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(54) **ANTI-CSP ANTIBODIES**

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None
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(57) **ABSTRACT**

The present disclosure provides anti-circumsporozoite (CSP) antibodies, compositions comprising such antibodies. Also disclosed are methods of producing the disclosed antibodies and methods of treating or preventing malaria using the same.

31 Claims, 86 Drawing Sheets

Specification includes a Sequence Listing.

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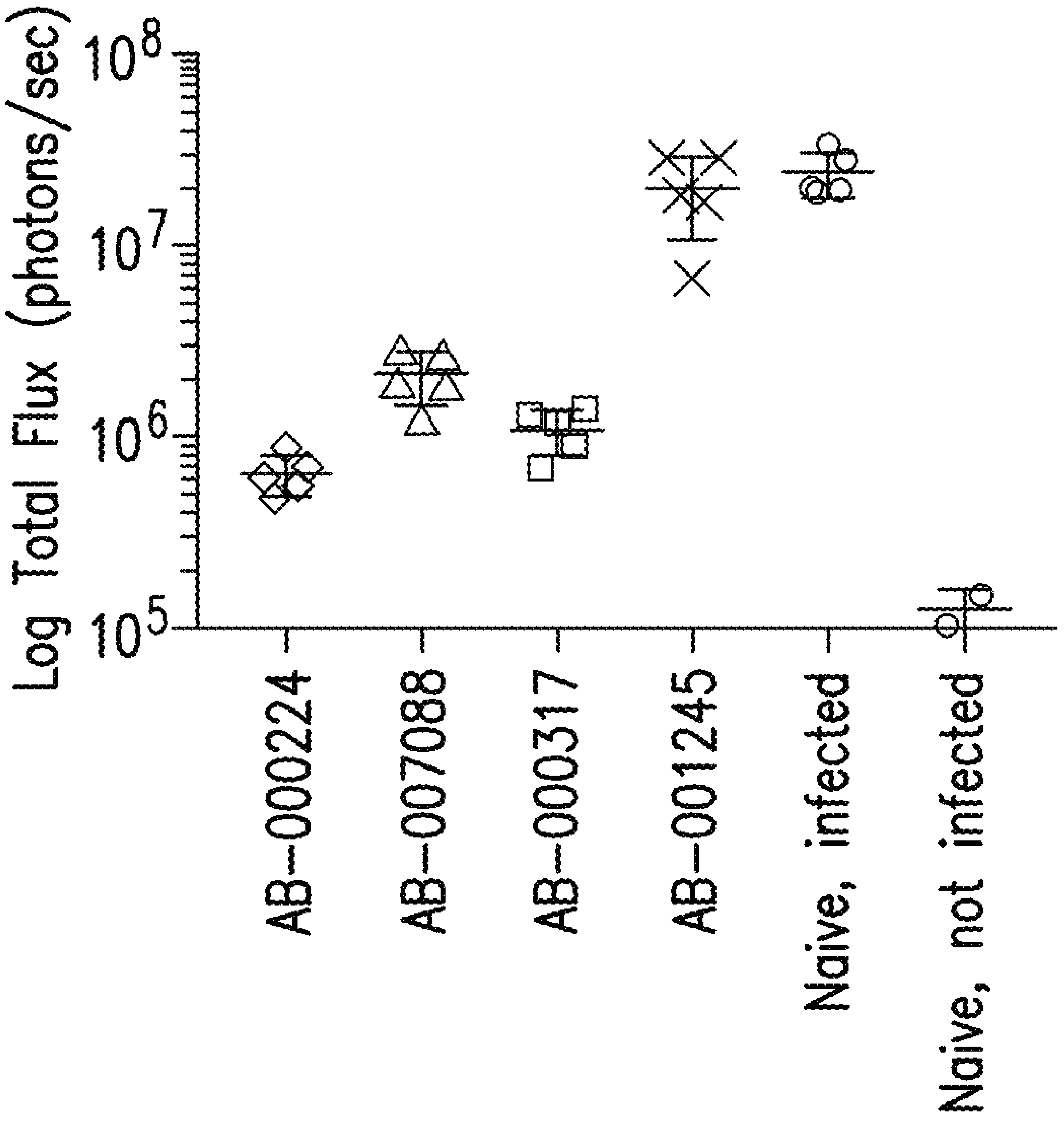

Log Total Flux (photons/sec)
10^8
10^7
10^6
10^5
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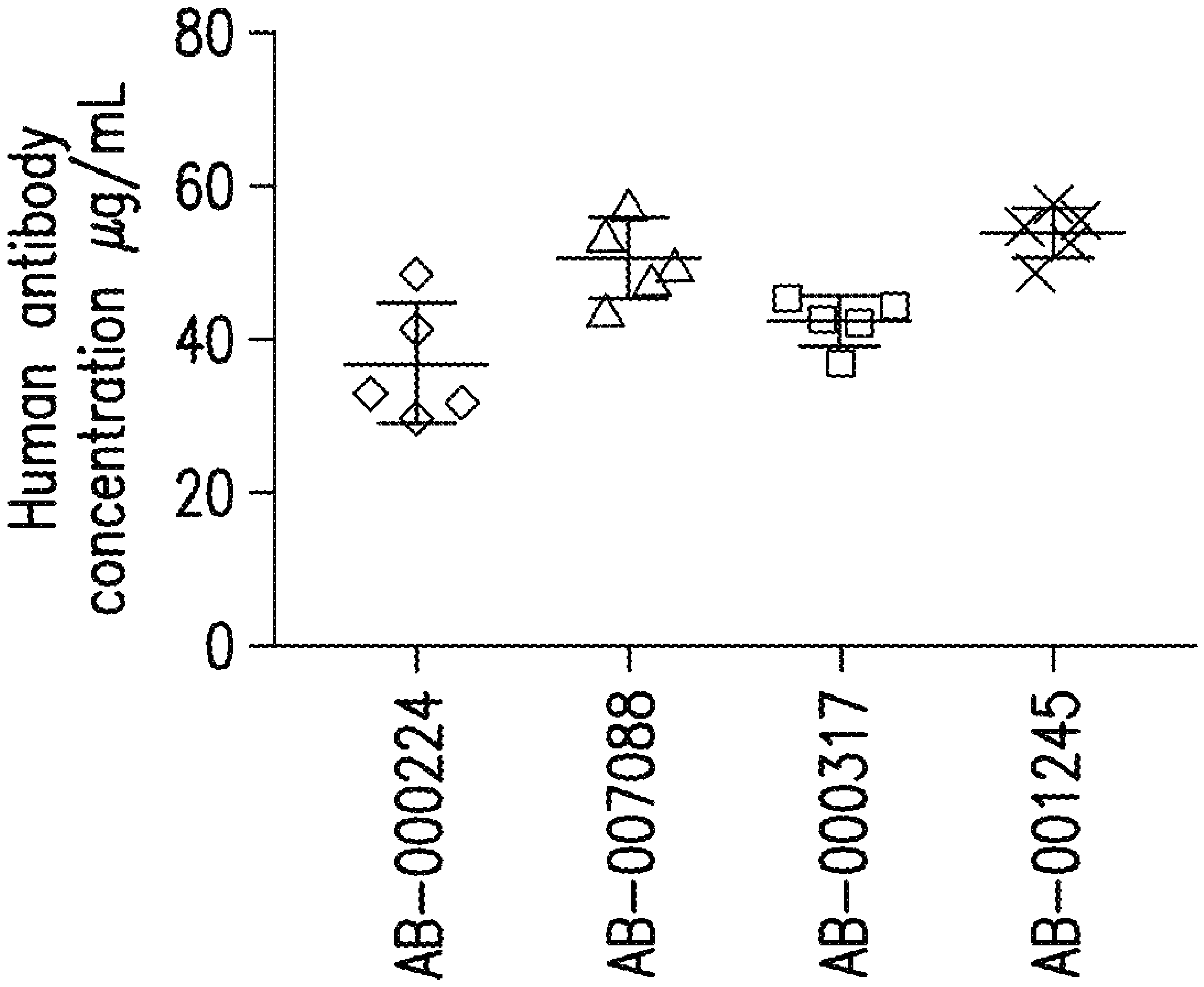
AB-007088
AB-000317
AB-001245
Naive, infected
Naive, not infected

FIG. 1A



Human antibody concentration μg/mL
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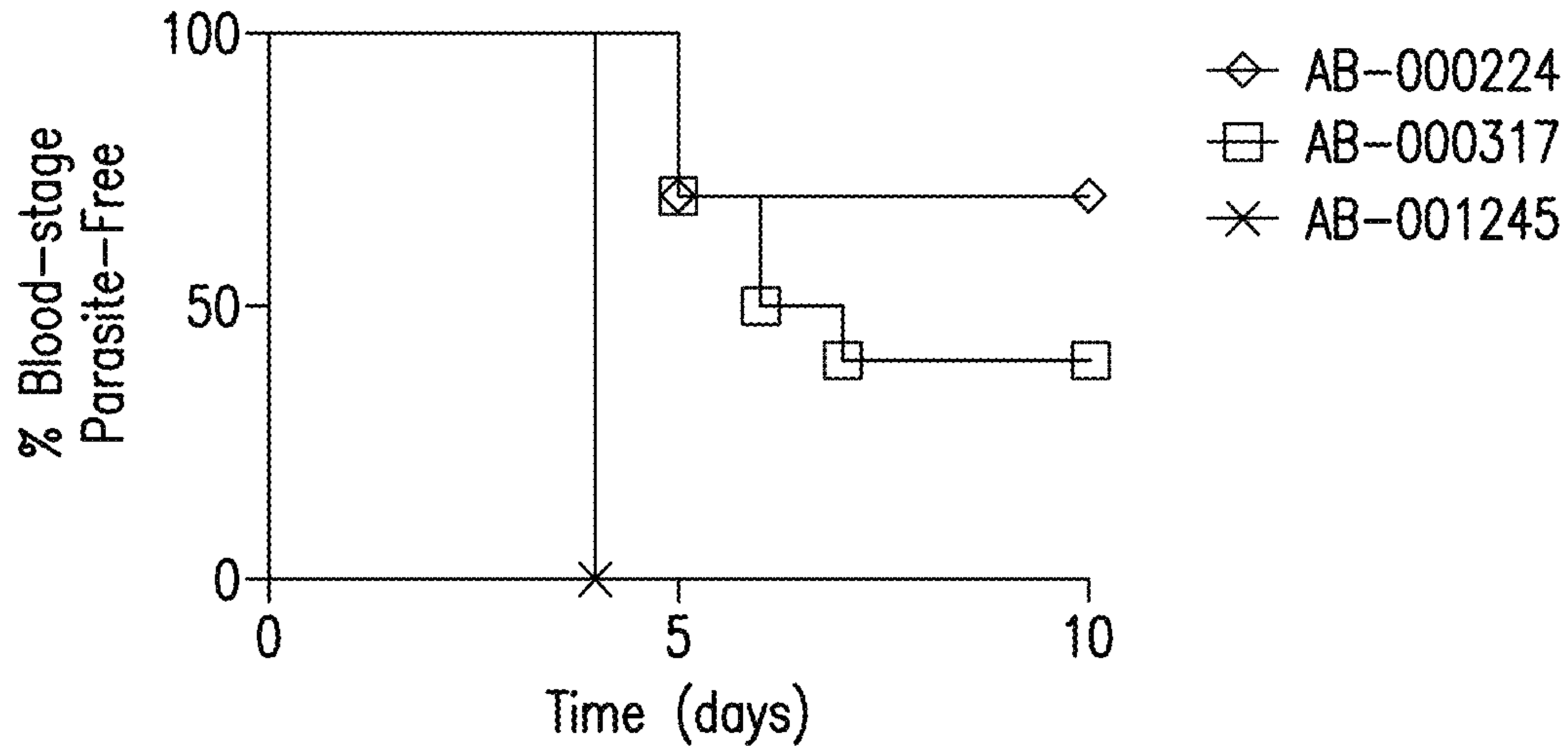
60
40
20
0
AB-000224
AB-007088
AB-000317
AB-001245

FIG. 1B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50
0
% Blood-stage Parasite-Free
0
5
10
Time (days)
AB-000224
AB-000317
AB-001245

FIG. 2A

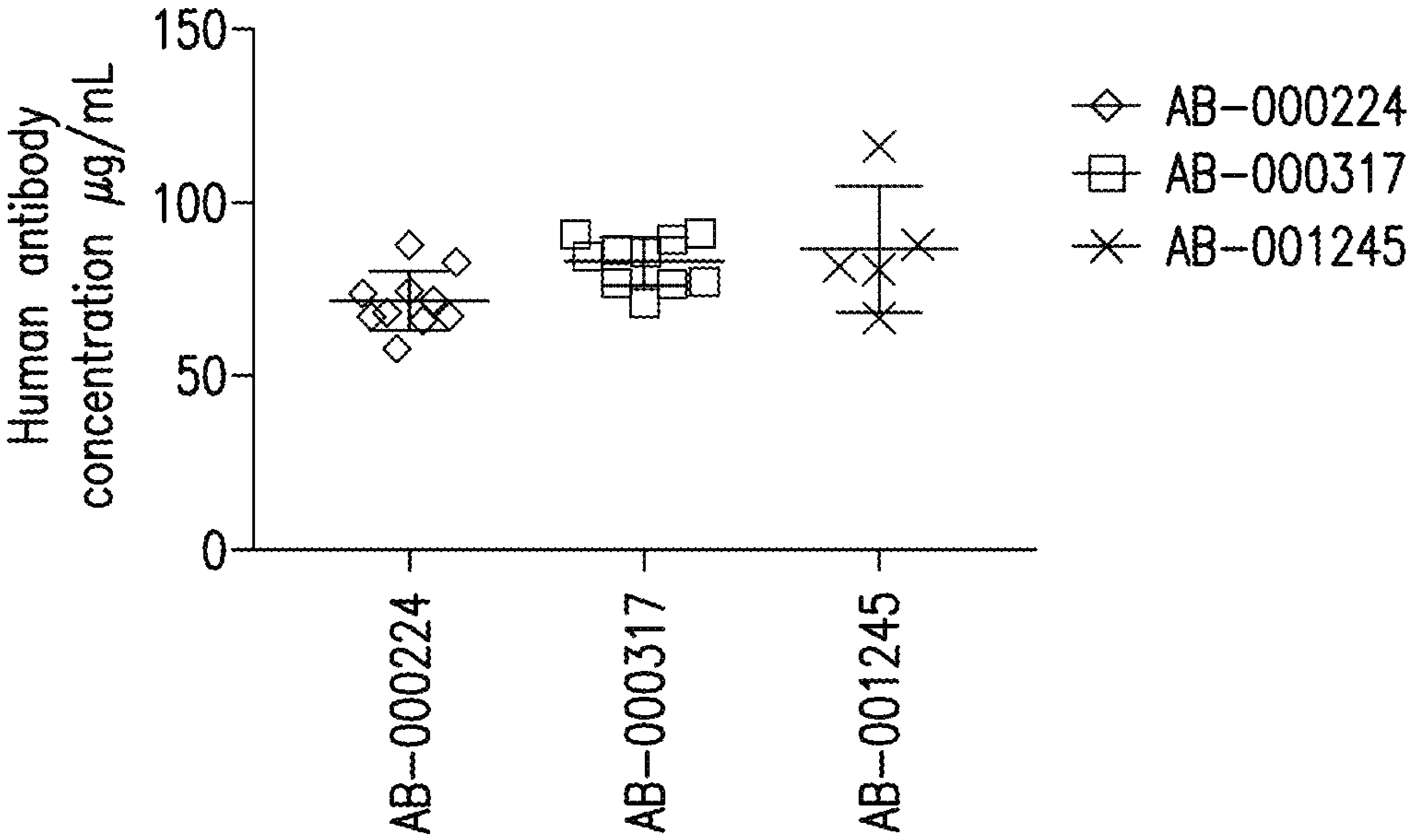

150
100
50
0
Human antibody concentration μg/mL
AB-000224
AB-000317
AB-001245
AB-000224
AB-000317
AB-001245

FIG. 2B

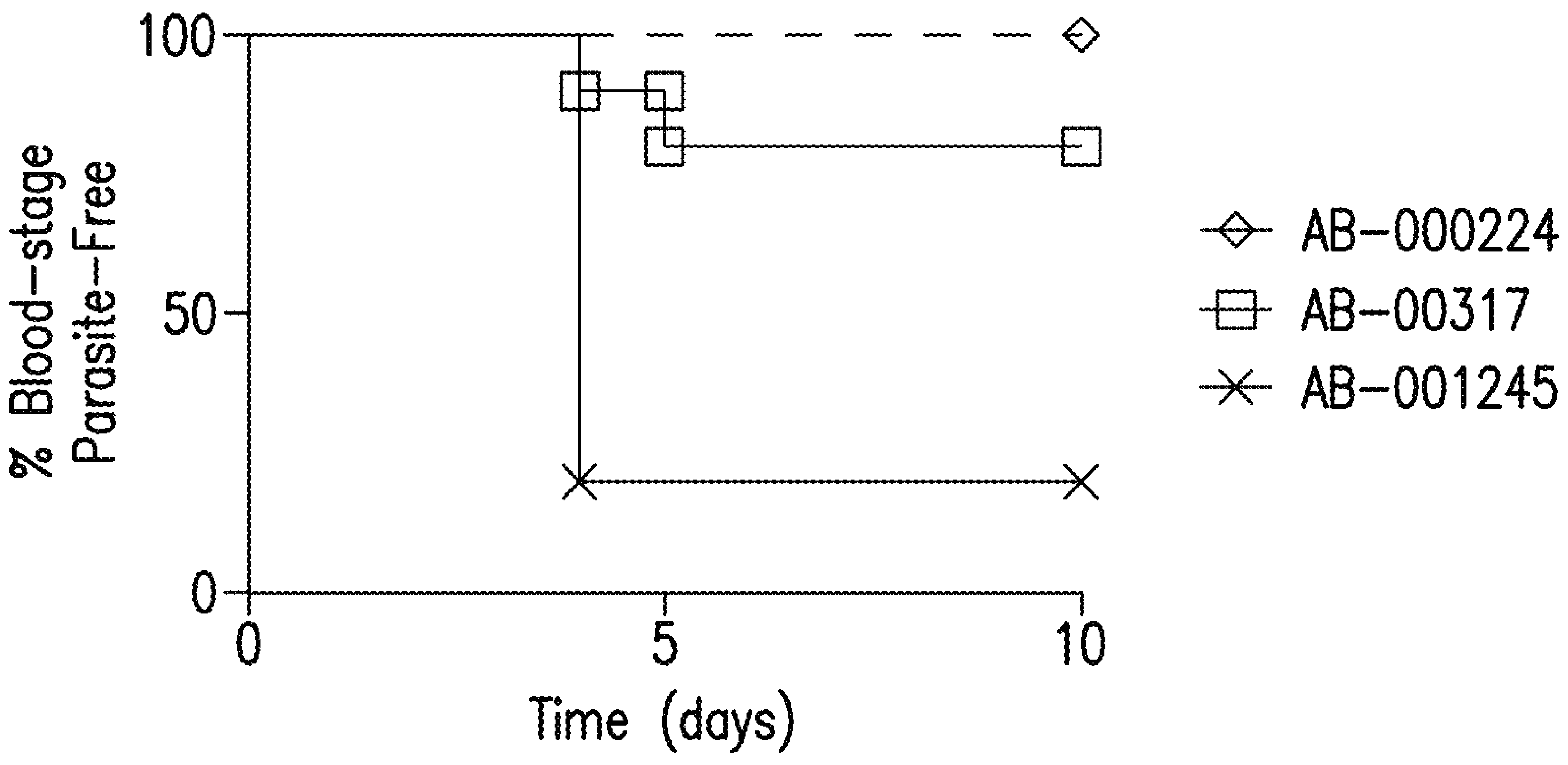
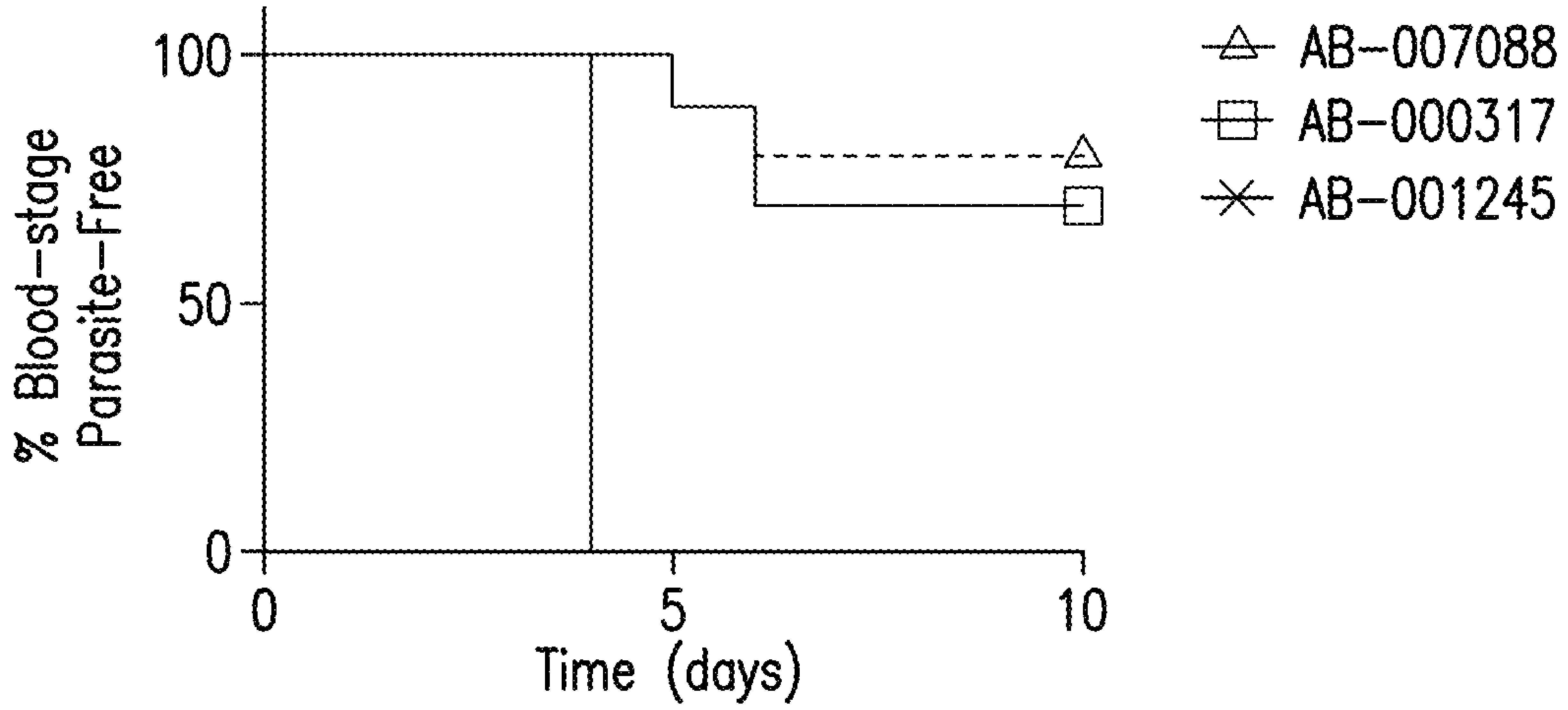

100
50
0
% Blood-stage Parasite-Free
0
5
10
Time (days)
AB-000224
AB-00317
AB-001245

FIG. 2C


% Blood-stage Parasite-Free
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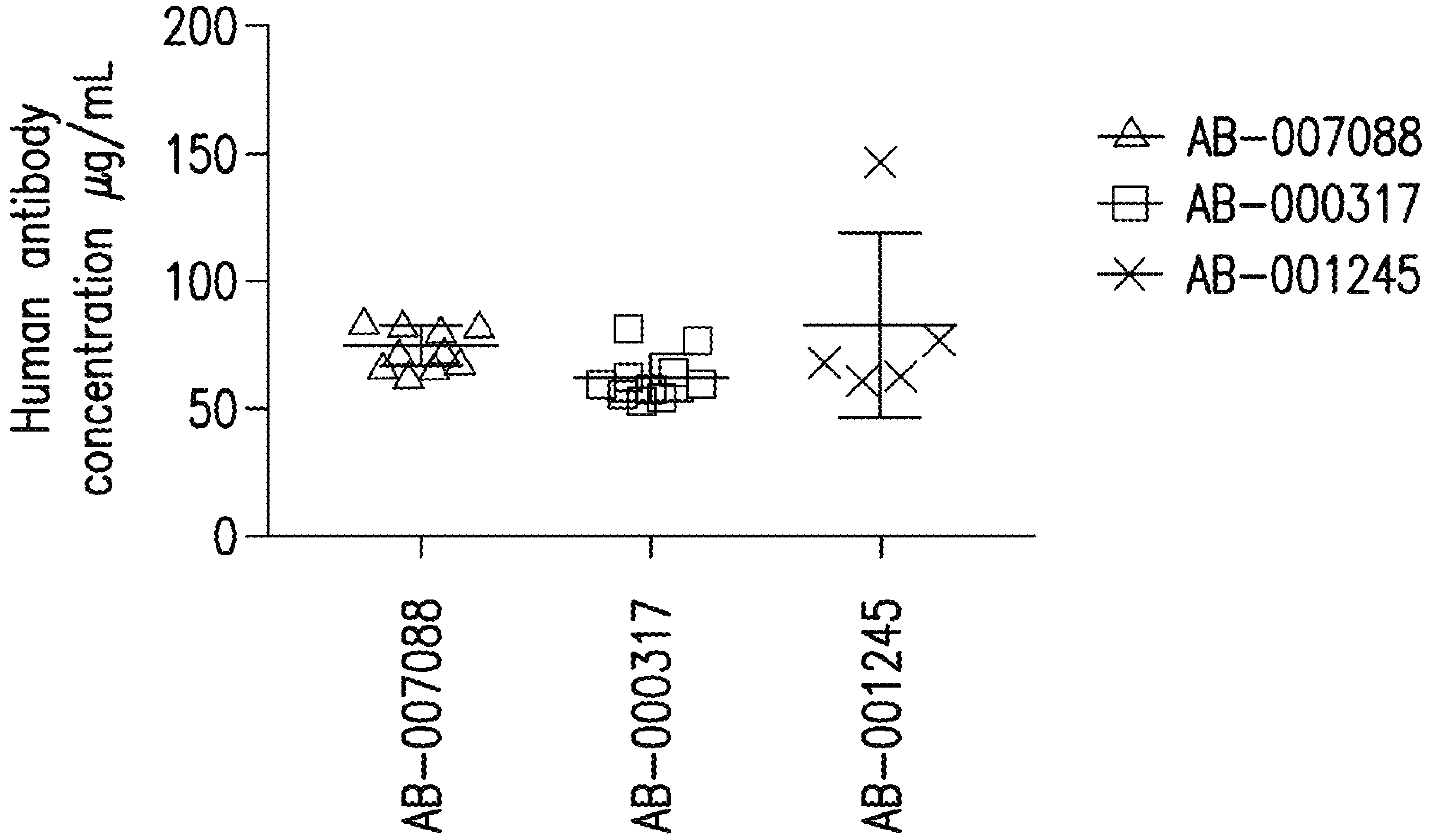
50
0
0
5
10
Time (days)
AB-007088
AB-000317
AB-001245

FIG. 3A


Human antibody concentration μg/mL
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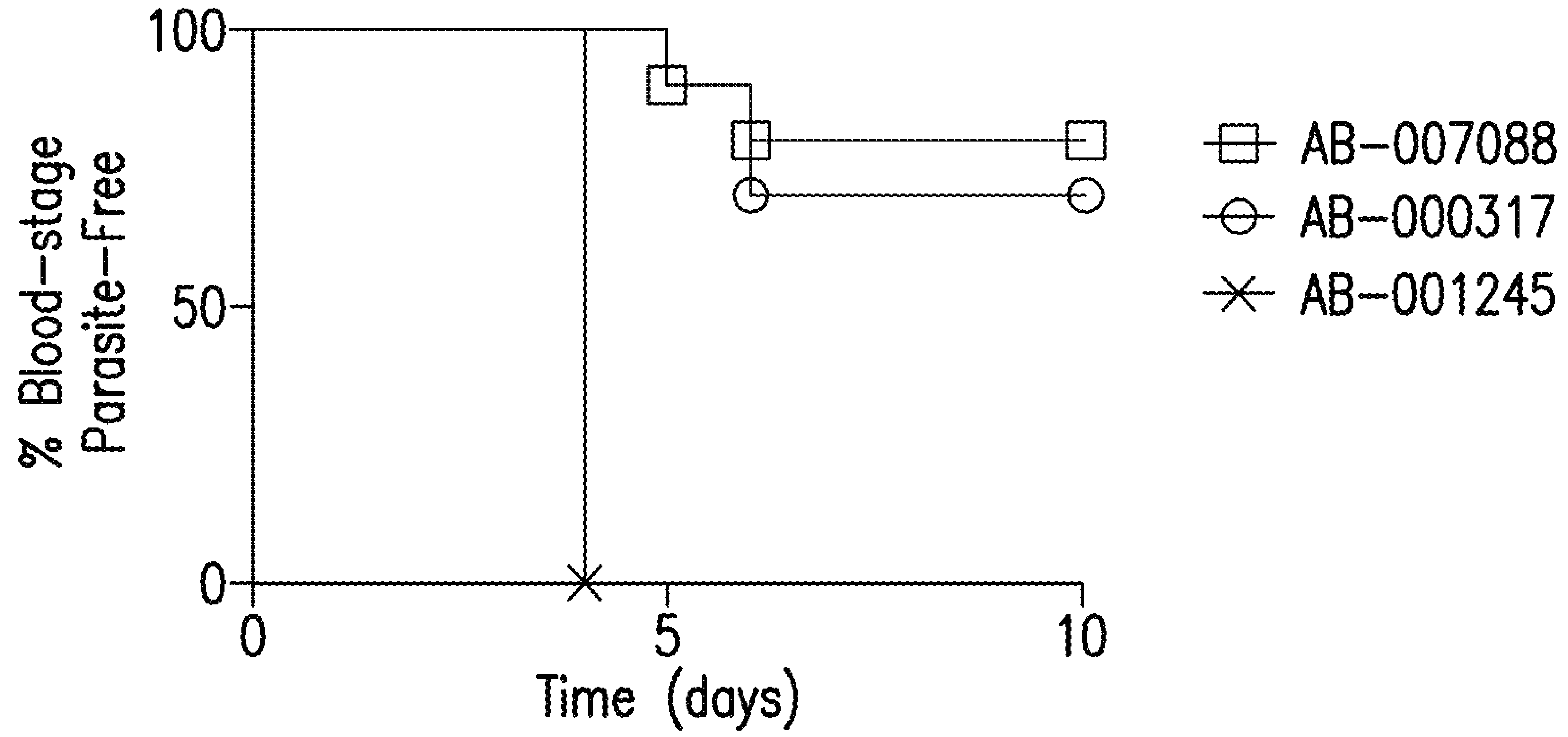
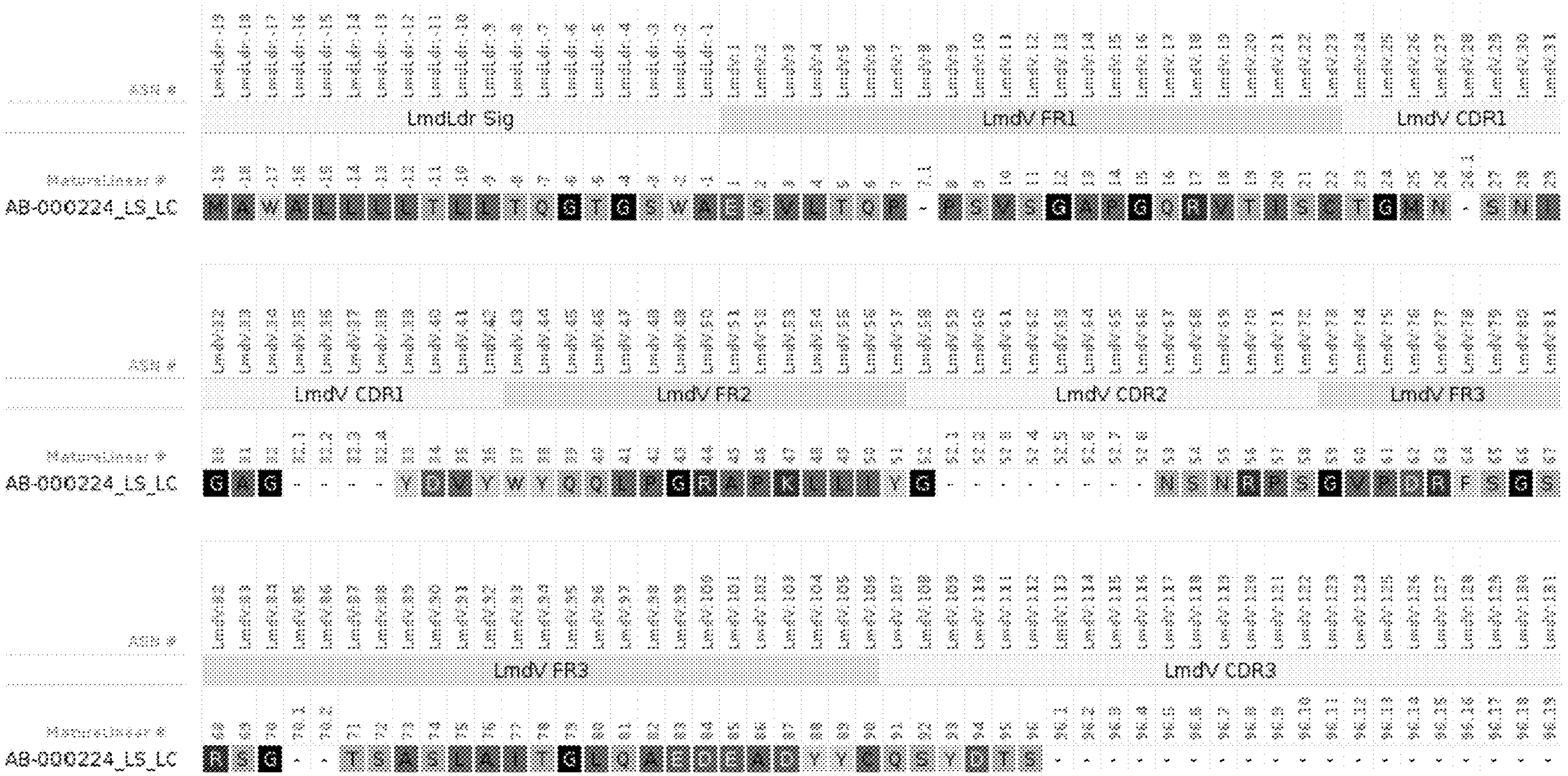
150
100
50
0
AB-007088
AB-000317
AB-001245
AB-007088
AB-000317
AB-001245

FIG. 3B



100
50
0
% Blood-stage Parasite-Free
0
5
10
Time (days)
AB-007088
AB-000317
AB-001245

FIG. 3C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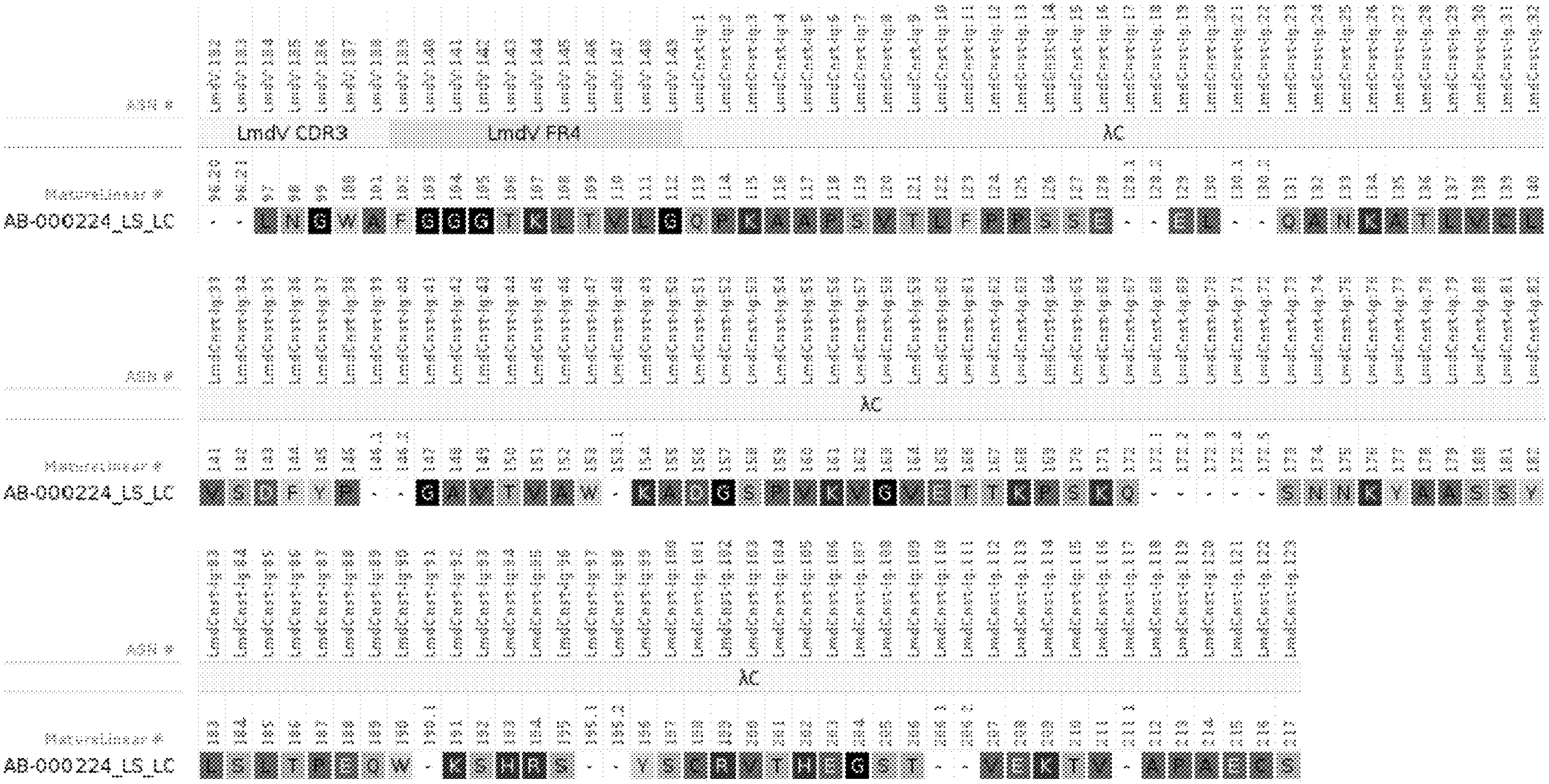
LmdV CDR1
LmdV FR2
LmdV CDR2
LmdV FR3
LmdV CDR3

FIG. 4A



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	LmdV CDR3							LmdV FR4											λC																															
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AB-000224_LS_LC	-	-	[illegible]	N	G	W	V	F	G	G	G	T	K	L	T	V	L	G	Q	P	K	A	A	P	S	V	T	L	F	P	P	S	S	E	-	-	E	L	-	-	Q	A	N	K	A	T	L	V	C	L

AHo #	LmdCnstlg.33	LmdCnstlg.34	LmdCnstlg.35	LmdCnstlg.36	LmdCnstlg.37	LmdCnstlg.38	LmdCnstlg.39	LmdCnstlg.40	LmdCnstlg.41	LmdCnstlg.42	LmdCnstlg.43	LmdCnstlg.44	LmdCnstlg.45	LmdCnstlg.46	LmdCnstlg.47	LmdCnstlg.48	LmdCnstlg.49	LmdCnstlg.50	LmdCnstlg.51	LmdCnstlg.52	LmdCnstlg.53	LmdCnstlg.54	LmdCnstlg.55	LmdCnstlg.56	LmdCnstlg.57	LmdCnstlg.58	LmdCnstlg.59	LmdCnstlg.60	LmdCnstlg.61	LmdCnstlg.62	LmdCnstlg.63	LmdCnstlg.64	LmdCnstlg.65	LmdCnstlg.66	LmdCnstlg.67	LmdCnstlg.68	LmdCnstlg.69	LmdCnstlg.70	LmdCnstlg.71	LmdCnstlg.72	LmdCnstlg.73	LmdCnstlg.74	LmdCnstlg.75	LmdCnstlg.76	LmdCnstlg.77	LmdCnstlg.78	LmdCnstlg.79	LmdCnstlg.80	LmdCnstlg.81	LmdCnstlg.82
	λC																																																	
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AHo #	LmdCnstlg.83	LmdCnstlg.84	LmdCnstlg.85	LmdCnstlg.86	LmdCnstlg.87	LmdCnstlg.88	LmdCnstlg.89	LmdCnstlg.90	LmdCnstlg.91	LmdCnstlg.92	LmdCnstlg.93	LmdCnstlg.94	LmdCnstlg.95	LmdCnstlg.96	LmdCnstlg.97	LmdCnstlg.98	LmdCnstlg.99	LmdCnstlg.100	LmdCnstlg.101	LmdCnstlg.102	LmdCnstlg.103	LmdCnstlg.104	LmdCnstlg.105	LmdCnstlg.106	LmdCnstlg.107	LmdCnstlg.108	LmdCnstlg.109	LmdCnstlg.110	LmdCnstlg.111	LmdCnstlg.112	LmdCnstlg.113	LmdCnstlg.114	LmdCnstlg.115	LmdCnstlg.116	LmdCnstlg.117	LmdCnstlg.118	LmdCnstlg.119	LmdCnstlg.120	LmdCnstlg.121	LmdCnstlg.122	LmdCnstlg.123
	λC																																								
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FIG. 4A Continued

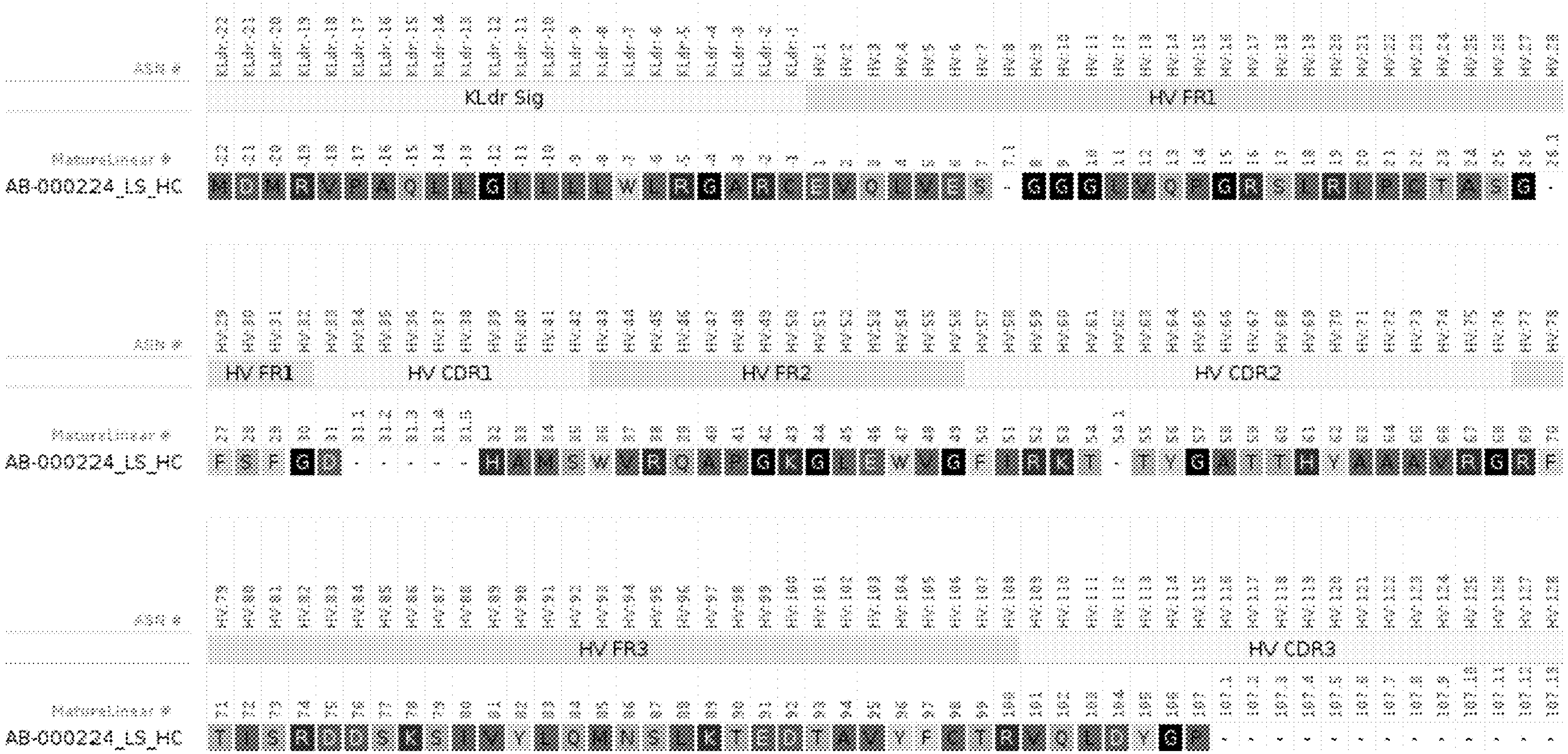
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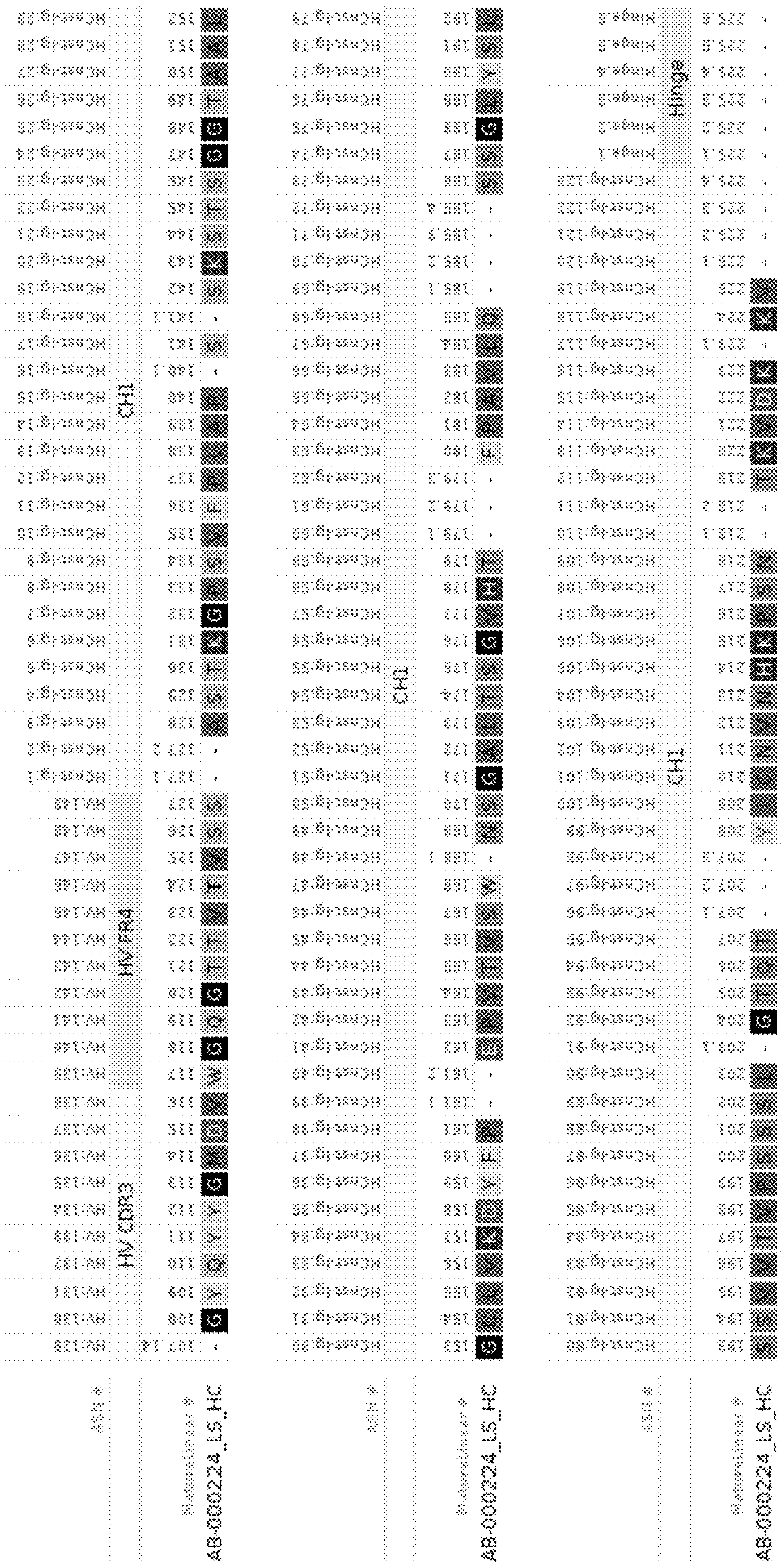
FIG. 4B



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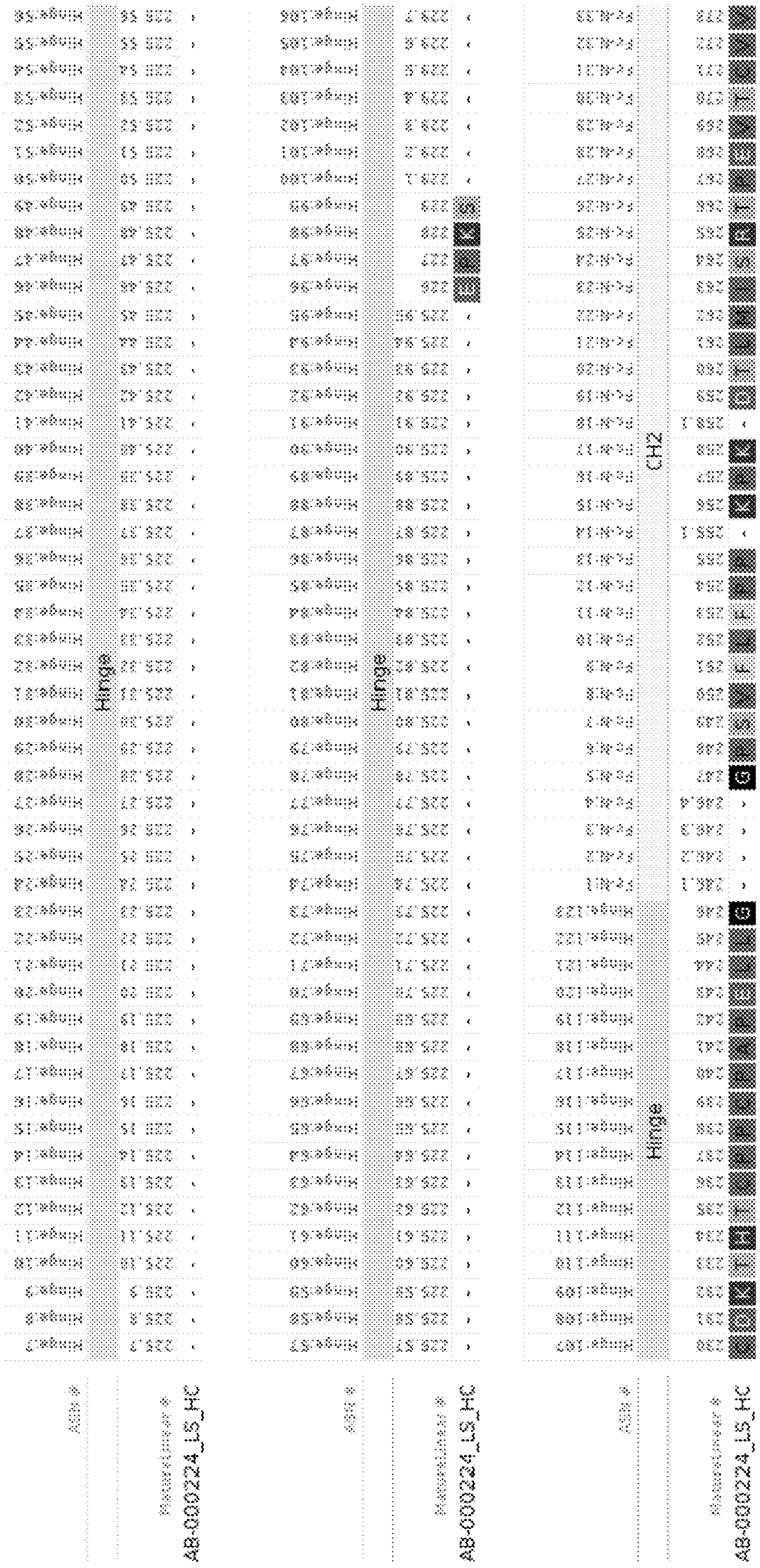
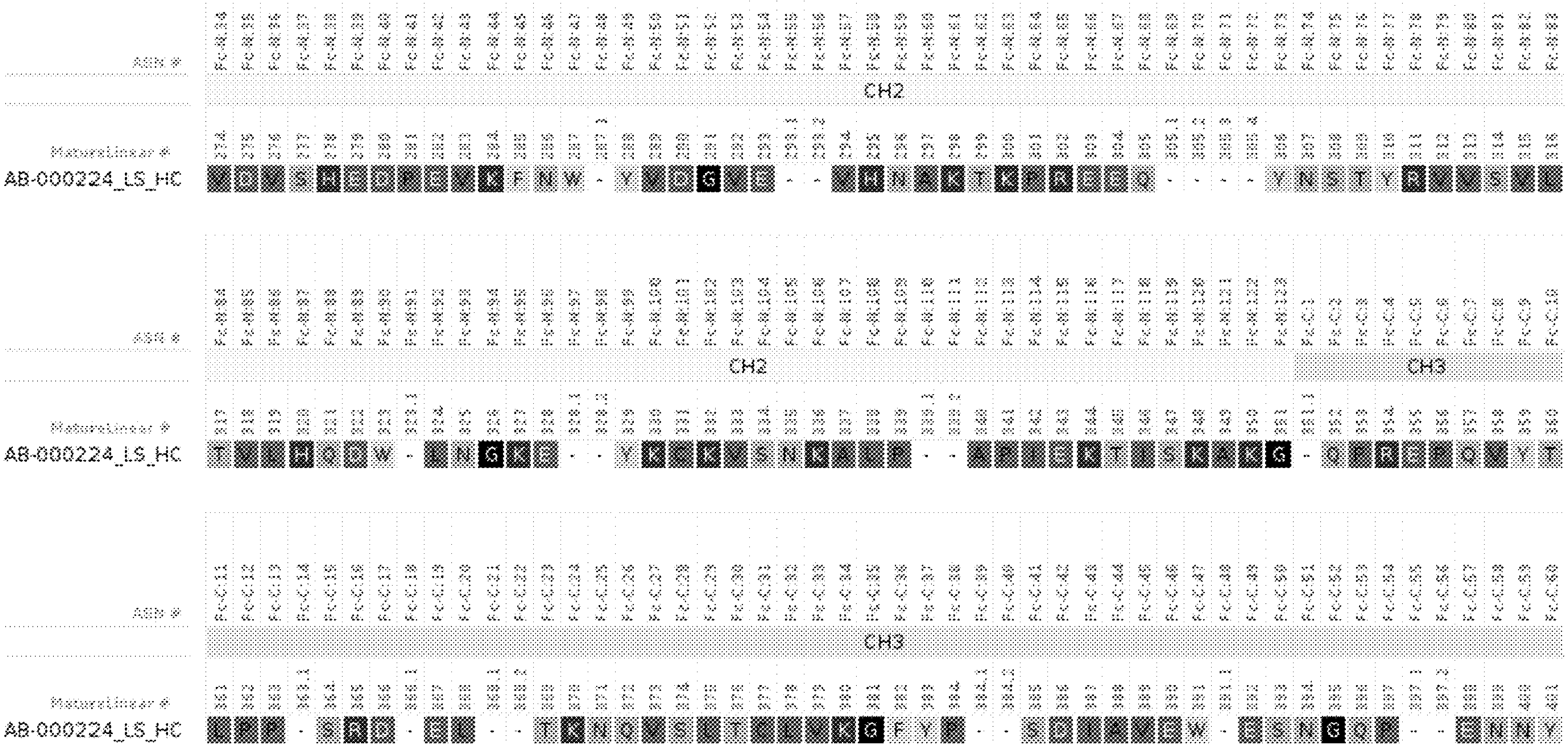


FIG. 4B Continued



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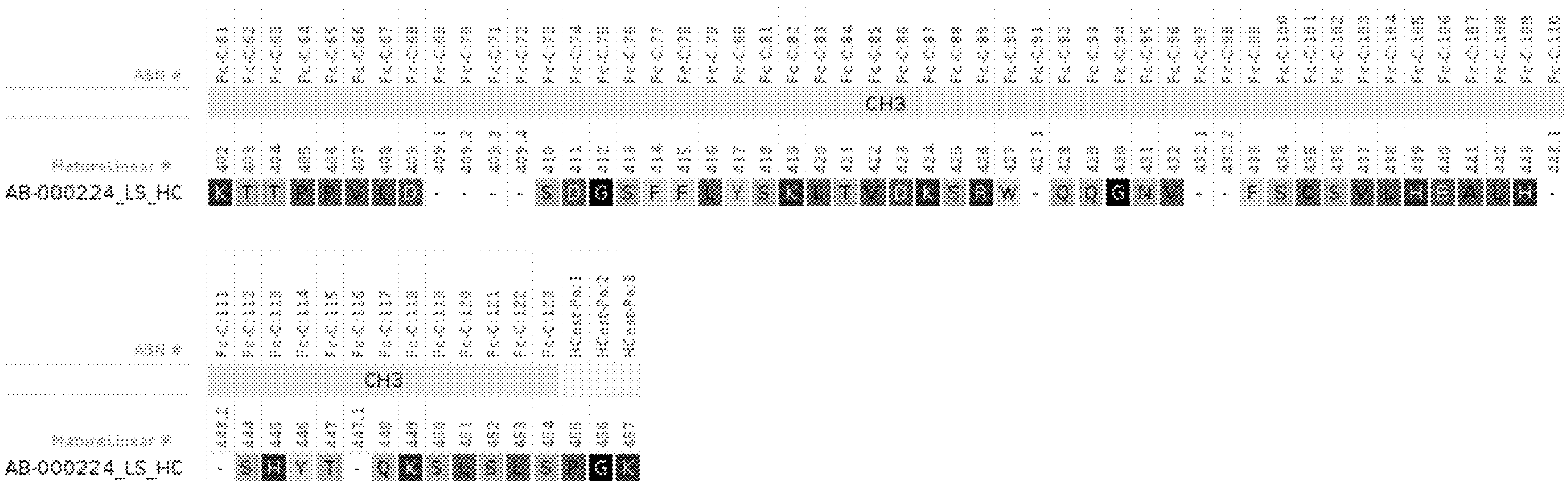

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ASR #	Fc-C111	Fc-C112	Fc-C113	Fc-C114	Fc-C115	Fc-C116	Fc-C117	Fc-C118	Fc-C119	Fc-C120	Fc-C121	Fc-C122	Fc-C123	HCcatPos1	HCcatPos2	HCcatPos3
	CH3															
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FIG. 4B Continued

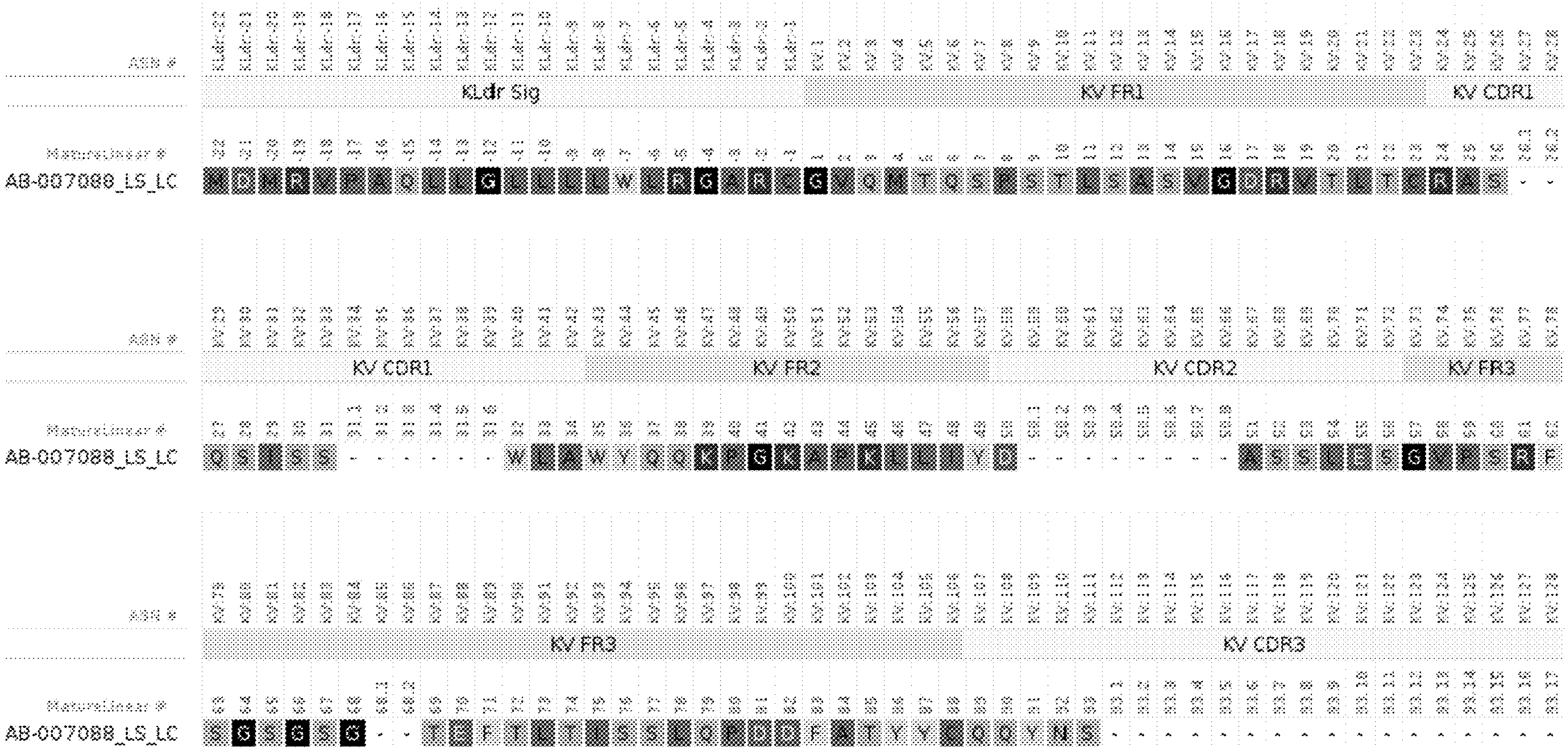
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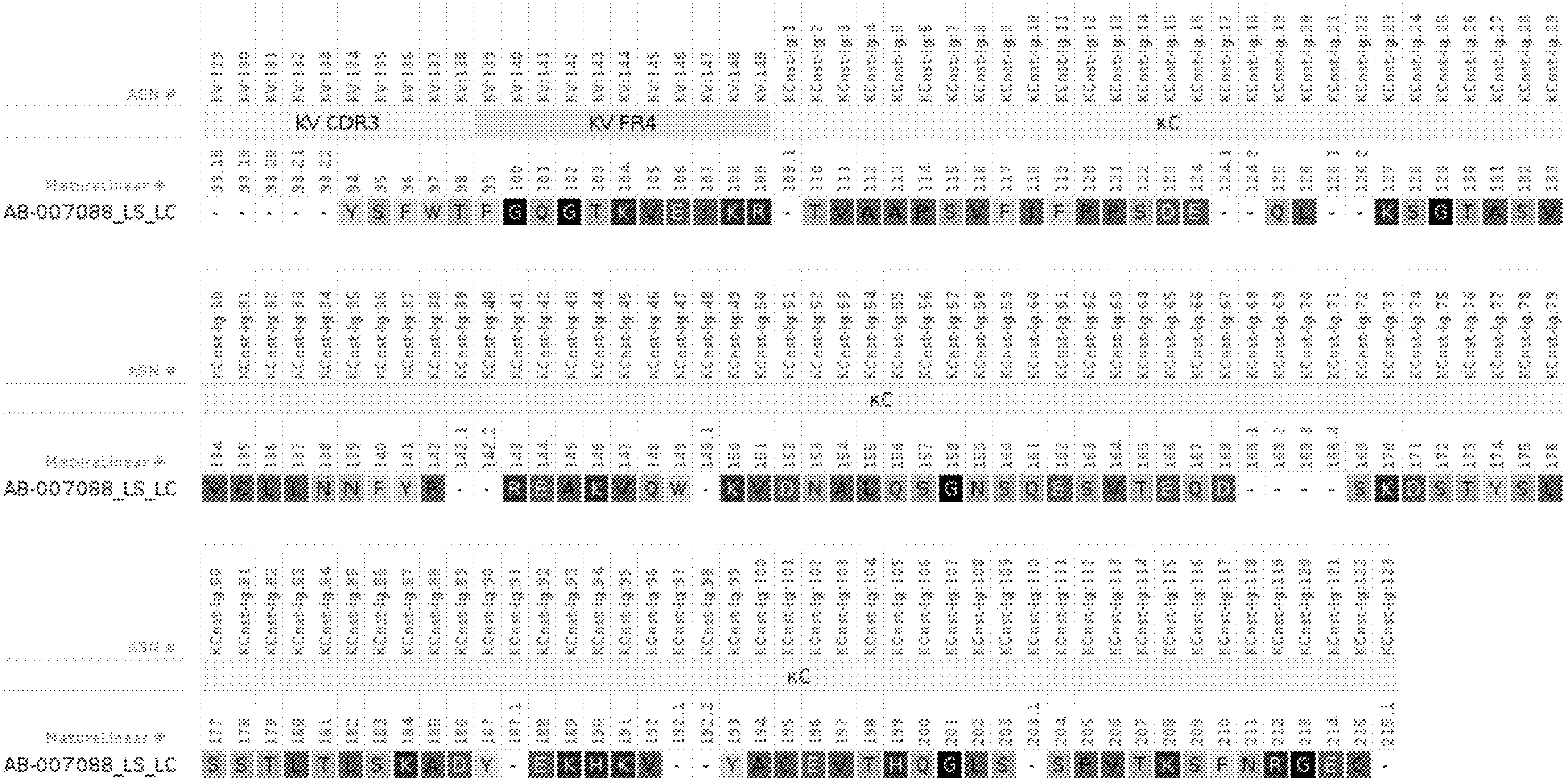
FIG. 5A



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	KV CDR3										KV FR4											κC																												
MatureLinear #	93.18	93.19	93.20	93.21	93.22	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	109.1	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	124.1	124.2	125	126	126.1	126.2	127	128	129	130	131	132	133
AB-007088_LS_LC	-	-	-	-	-	Y	S	F	W	T	F	G	Q	G	T	K	V	E	I	K	R	-	T	V	A	A	P	S	V	F	I	F	P	P	S	D	E	-	-	Q	L	-	-	K	S	G	T	A	S	V

AHo #	KConst-Ig.30	KConst-Ig.31	KConst-Ig.32	KConst-Ig.33	KConst-Ig.34	KConst-Ig.35	KConst-Ig.36	KConst-Ig.37	KConst-Ig.38	KConst-Ig.39	KConst-Ig.40	KConst-Ig.41	KConst-Ig.42	KConst-Ig.43	KConst-Ig.44	KConst-Ig.45	KConst-Ig.46	KConst-Ig.47	KConst-Ig.48	KConst-Ig.49	KConst-Ig.50	KConst-Ig.51	KConst-Ig.52	KConst-Ig.53	KConst-Ig.54	KConst-Ig.55	KConst-Ig.56	KConst-Ig.57	KConst-Ig.58	KConst-Ig.59	KConst-Ig.60	KConst-Ig.61	KConst-Ig.62	KConst-Ig.63	KConst-Ig.64	KConst-Ig.65	KConst-Ig.66	KConst-Ig.67	KConst-Ig.68	KConst-Ig.69	KConst-Ig.70	KConst-Ig.71	KConst-Ig.72	KConst-Ig.73	KConst-Ig.74	KConst-Ig.75	KConst-Ig.76	KConst-Ig.77	KConst-Ig.78	KConst-Ig.79
	κC																																																	
MatureLinear #	134	135	136	137	138	139	140	141	142	142.1	142.2	143	144	145	146	147	148	149	149.1	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	168.1	168.2	168.3	168.4	169	170	171	172	173	174	175	176
AB-007088_LS_LC	V	C	L	L	N	N	F	Y	P	-	-	R	E	A	K	V	Q	W	-	K	V	D	N	A	L	Q	S	G	N	S	Q	E	S	V	T	E	Q	D	-	-	-	-	S	K	D	S	T	Y	S	L

AHo #	KConst-Ig.80	KConst-Ig.81	KConst-Ig.82	KConst-Ig.83	KConst-Ig.84	KConst-Ig.85	KConst-Ig.86	KConst-Ig.87	KConst-Ig.88	KConst-Ig.89	KConst-Ig.90	KConst-Ig.91	KConst-Ig.92	KConst-Ig.93	KConst-Ig.94	KConst-Ig.95	KConst-Ig.96	KConst-Ig.97	KConst-Ig.98	KConst-Ig.99	KConst-Ig.100	KConst-Ig.101	KConst-Ig.102	KConst-Ig.103	KConst-Ig.104	KConst-Ig.105	KConst-Ig.106	KConst-Ig.107	KConst-Ig.108	KConst-Ig.109	KConst-Ig.110	KConst-Ig.111	KConst-Ig.112	KConst-Ig.113	KConst-Ig.114	KConst-Ig.115	KConst-Ig.116	KConst-Ig.117	KConst-Ig.118	KConst-Ig.119	KConst-Ig.120	KConst-Ig.121	KConst-Ig.122	KConst-Ig.123
	κC																																											
MatureLinear #	177	178	179	180	181	182	183	184	185	186	187	187.1	188	189	190	191	192	192.1	192.2	193	194	195	196	197	198	199	200	201	202	203	203.1	204	205	206	207	208	209	210	211	212	213	214	215	215.1
AB-007088_LS_LC	S	S	T	L	T	L	S	K	A	D	Y	-	E	K	H	K	V	-	-	Y	A	C	E	V	T	H	Q	G	L	S	-	S	P	V	T	K	S	F	N	R	G	E	C	-

FIG. 5A Continued

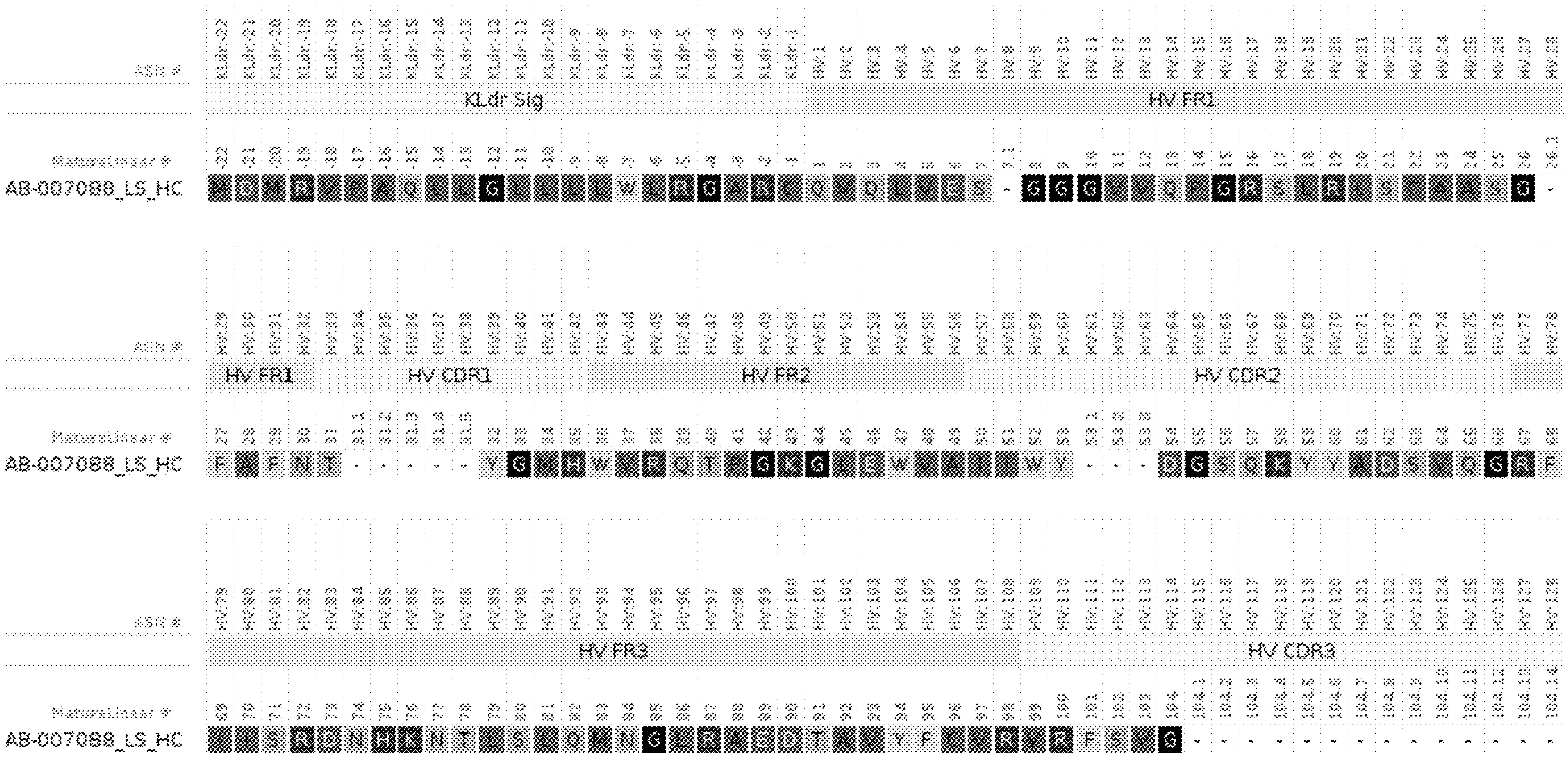

ASN #
KLdr Sig
HV FR1
MatureLinear #
AB-007088_LS_HC
HV FR1
HV CDR1
HV FR2
HV CDR2
HV FR3
HV CDR3

FIG. 5B

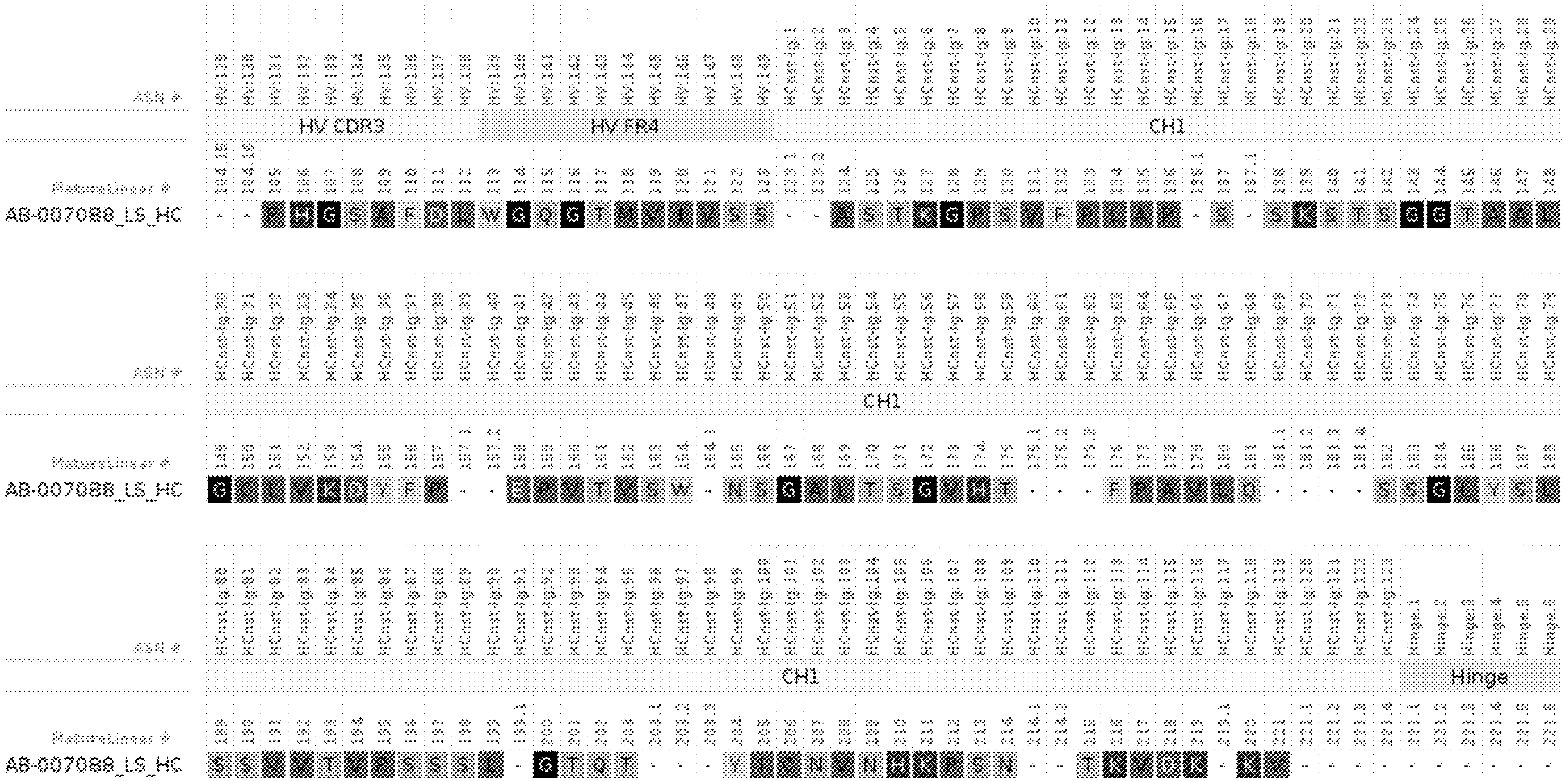


FIG. 5B Continued

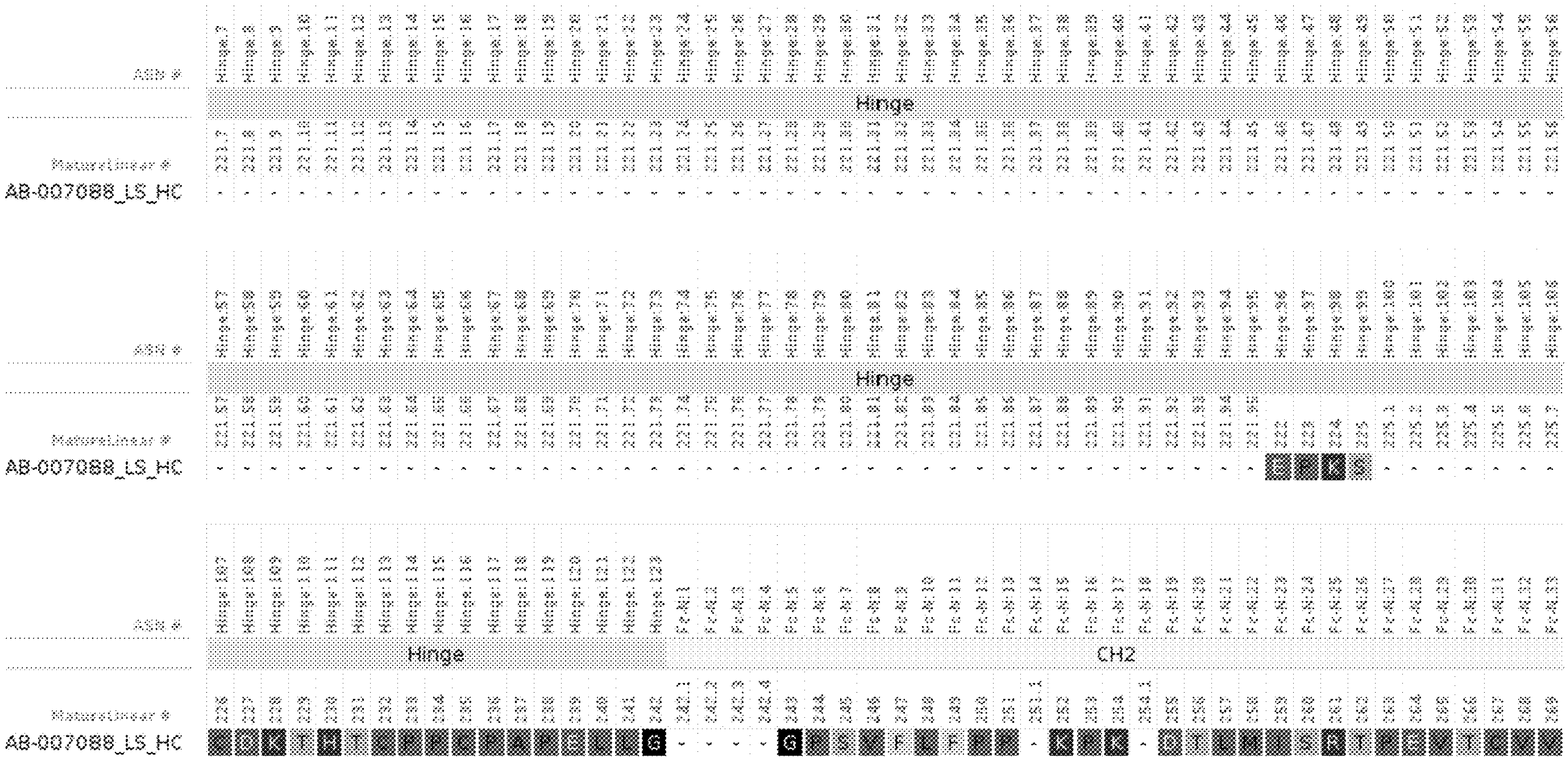


FIG. 5B Continued

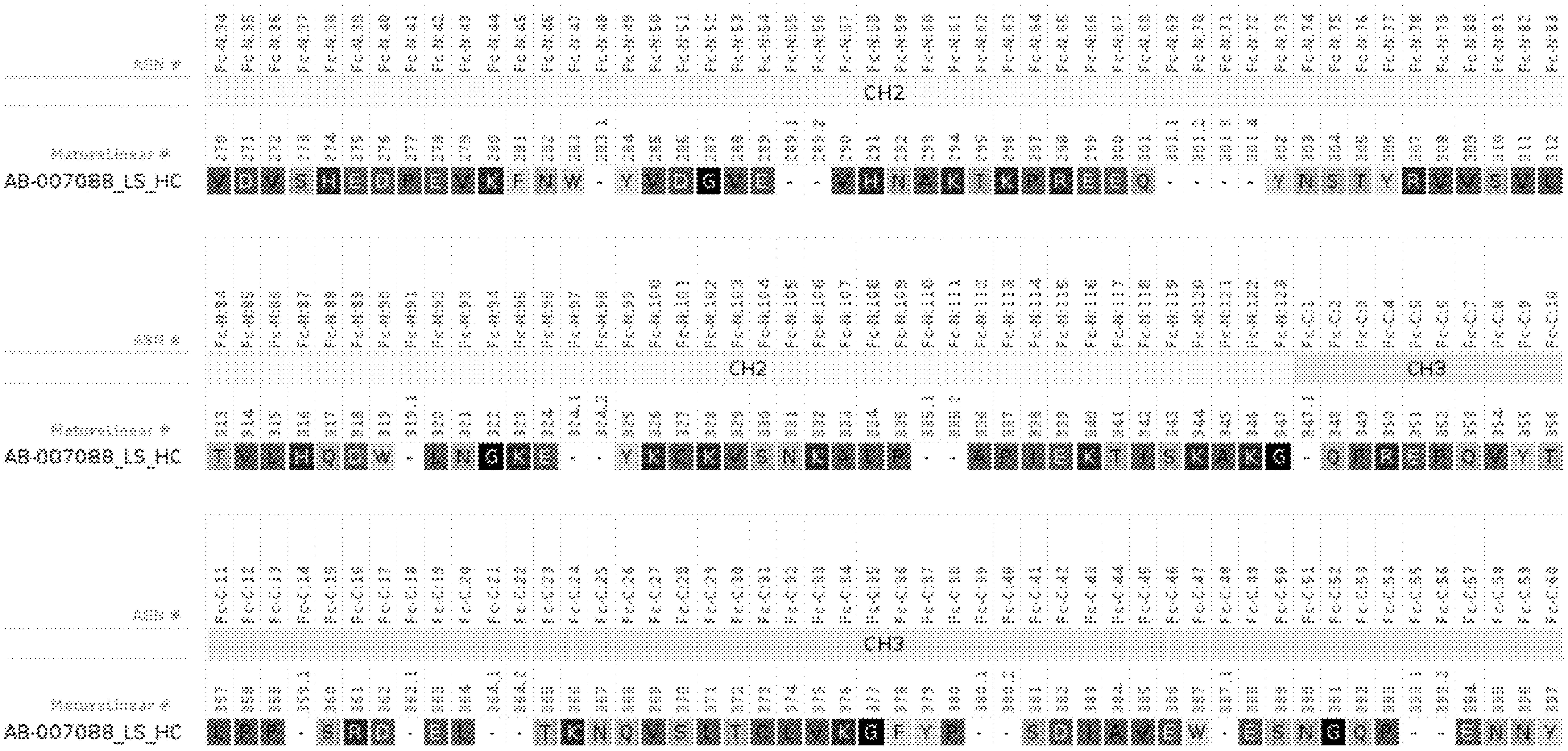


FIG. 5B Continued

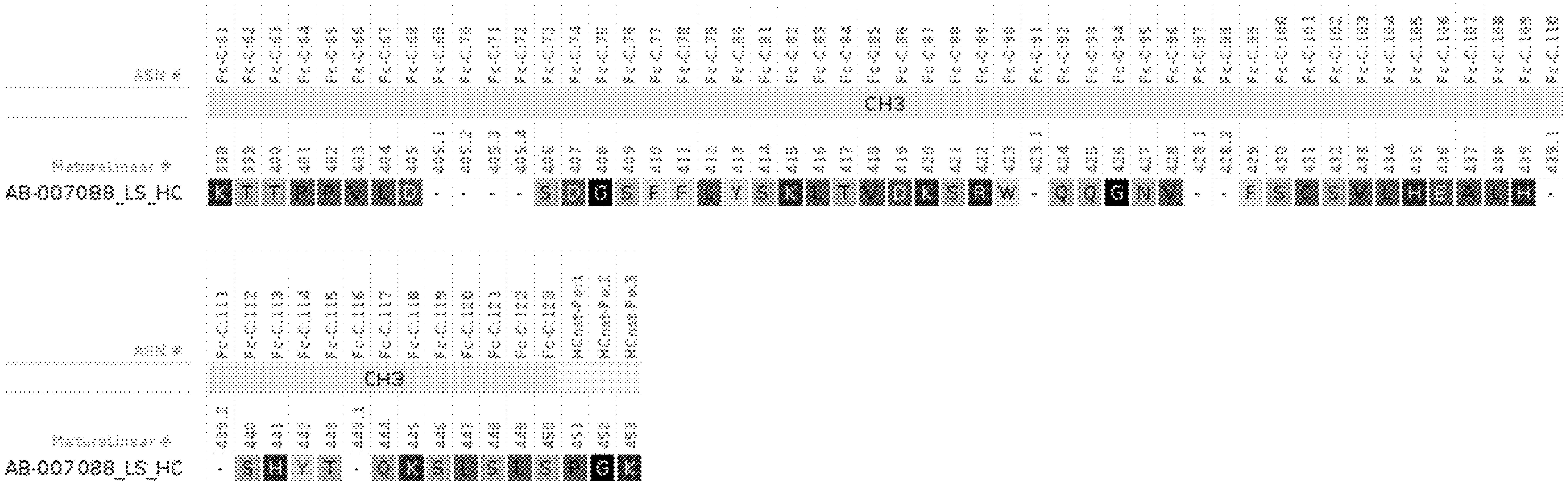


FIG. 5B Continued

AB-000224_LS Light Chain			
Residue	**Linear #**	**Mat. Linear #**	**ASN #**
M	1	-19	LmdLdr:-19
A	2	-18	LmdLdr:-18
W	3	-17	LmdLdr:-17
A	4	-16	LmdLdr:-16
L	5	-15	LmdLdr:-15
L	6	-14	LmdLdr:-14
L	7	-13	LmdLdr:-13
L	8	-12	LmdLdr:-12
T	9	-11	LmdLdr:-11
L	10	-10	LmdLdr:-10
L	11	-9	LmdLdr:-9
T	12	-8	LmdLdr:-8
Q	13	-7	LmdLdr:-7
G	14	-6	LmdLdr:-6
T	15	-5	LmdLdr:-5
G	16	-4	LmdLdr:-4
S	17	-3	LmdLdr:-3
W	18	-2	LmdLdr:-2
A	19	-1	LmdLdr:-1
E	20	1	LmdV:1
S	21	2	LmdV:2
V	22	3	LmdV:3
L	23	4	LmdV:4
T	24	5	LmdV:5
Q	25	6	LmdV:6
P	26	7	LmdV:7
-	26.1	7.1	LmdV:8
P	27	8	LmdV:9
S	28	9	LmdV:10
V	29	10	LmdV:11
S	30	11	LmdV:12
G	31	12	LmdV:13
A	32	13	LmdV:14
P	33	14	LmdV:15
G	34	15	LmdV:16
Q	35	16	LmdV:17
R	36	17	LmdV:18
V	37	18	LmdV:19
T	38	19	LmdV:20
I	39	20	LmdV:21
S	40	21	LmdV:22
C	41	22	LmdV:23

FIG. 6

AB-000224_LS Light Chain			
Residue	**Linear #**	**Mat. Linear #**	**ASN #**
T	42	23	LmdV:24
G	43	24	LmdV:25
M	44	25	LmdV:26
N	45	26	LmdV:27
-	45.1	26.1	LmdV:28
S	46	27	LmdV:29
N	47	28	LmdV:30
I	48	29	LmdV:31
G	49	30	LmdV:32
A	50	31	LmdV:33
G	51	32	LmdV:34
-	51.1	32.1	LmdV:35
-	51.2	32.2	LmdV:36
-	51.3	32.3	LmdV:37
-	51.4	32.4	LmdV:38
Y	52	33	LmdV:39
D	53	34	LmdV:40
V	54	35	LmdV:41
Y	55	36	LmdV:42
W	56	37	LmdV:43
Y	57	38	LmdV:44
Q	58	39	LmdV:45
Q	59	40	LmdV:46
L	60	41	LmdV:47
P	61	42	LmdV:48
G	62	43	LmdV:49
R	63	44	LmdV:50
A	64	45	LmdV:51
P	65	46	LmdV:52
K	66	47	LmdV:53
L	67	48	LmdV:54
L	68	49	LmdV:55
I	69	50	LmdV:56
Y	70	51	LmdV:57
G	71	52	LmdV:58
-	71.1	52.1	LmdV:59
-	71.2	52.2	LmdV:60
-	71.3	52.3	LmdV:61
-	71.4	52.4	LmdV:62
-	71.5	52.5	LmdV:63
-	71.6	52.6	LmdV:64
-	71.7	52.7	LmdV:65

FIG. 6 Continued

AB-000224_LS Light Chain			
Residue	**Linear #**	**Mat. Linear #**	**ASN #**
-	71.8	52.8	LmdV:66
N	72	53	LmdV:67
S	73	54	LmdV:68
N	74	55	LmdV:69
R	75	56	LmdV:70
P	76	57	LmdV:71
S	77	58	LmdV:72
G	78	59	LmdV:73
V	79	60	LmdV:74
P	80	61	LmdV:75
D	81	62	LmdV:76
R	82	63	LmdV:77
F	83	64	LmdV:78
S	84	65	LmdV:79
G	85	66	LmdV:80
S	86	67	LmdV:81
R	87	68	LmdV:82
S	88	69	LmdV:83
G	89	70	LmdV:84
-	89.1	70.1	LmdV:85
-	89.2	70.2	LmdV:86
T	90	71	LmdV:87
S	91	72	LmdV:88
A	92	73	LmdV:89
S	93	74	LmdV:90
L	94	75	LmdV:91
A	95	76	LmdV:92
I	96	77	LmdV:93
T	97	78	LmdV:94
G	98	79	LmdV:95
L	99	80	LmdV:96
Q	100	81	LmdV:97
A	101	82	LmdV:98
E	102	83	LmdV:99
D	103	84	LmdV:100
E	104	85	LmdV:101
A	105	86	LmdV:102
D	106	87	LmdV:103
Y	107	88	LmdV:104
Y	108	89	LmdV:105
C	109	90	LmdV:106
Q	110	91	LmdV:107

FIG. 6 Continued

AB-000224_LS Light Chain			
Residue	**Linear #**	**Mat. Linear #**	**ASN #**
S	111	92	LmdV:108
Y	112	93	LmdV:109
D	113	94	LmdV:110
T	114	95	LmdV:111
S	115	96	LmdV:112
-	115.1	96.1	LmdV:113
-	115.2	96.2	LmdV:114
-	115.3	96.3	LmdV:115
-	115.4	96.4	LmdV:116
-	115.5	96.5	LmdV:117
-	115.6	96.6	LmdV:118
-	115.7	96.7	LmdV:119
-	115.8	96.8	LmdV:120
-	115.9	96.9	LmdV:121
-	115.10	96.10	LmdV:122
-	115.11	96.11	LmdV:123
-	115.12	96.12	LmdV:124
-	115.13	96.13	LmdV:125
-	115.14	96.14	LmdV:126
-	115.15	96.15	LmdV:127
-	115.16	96.16	LmdV:128
-	115.17	96.17	LmdV:129
-	115.18	96.18	LmdV:130
-	115.19	96.19	LmdV:131
-	115.20	96.20	LmdV:132
-	115.21	96.21	LmdV:133
L	116	97	LmdV:134
N	117	98	LmdV:135
G	118	99	LmdV:136
W	119	100	LmdV:137
A	120	101	LmdV:138
F	121	102	LmdV:139
G	122	103	LmdV:140
G	123	104	LmdV:141
G	124	105	LmdV:142
T	125	106	LmdV:143
K	126	107	LmdV:144
L	127	108	LmdV:145
T	128	109	LmdV:146
V	129	110	LmdV:147
L	130	111	LmdV:148
G	131	112	LmdV:149

FIG. 6 Continued

AB-000224_LS Light Chain			
Residue	**Linear #**	**Mat. Linear #**	**ASN #**
Q	132	113	LmdCnst-Ig:1
P	133	114	LmdCnst-Ig:2
K	134	115	LmdCnst-Ig:3
A	135	116	LmdCnst-Ig:4
A	136	117	LmdCnst-Ig:5
P	137	118	LmdCnst-Ig:6
S	138	119	LmdCnst-Ig:7
V	139	120	LmdCnst-Ig:8
T	140	121	LmdCnst-Ig:9
L	141	122	LmdCnst-Ig:10
F	142	123	LmdCnst-Ig:11
P	143	124	LmdCnst-Ig:12
P	144	125	LmdCnst-Ig:13
S	145	126	LmdCnst-Ig:14
S	146	127	LmdCnst-Ig:15
E	147	128	LmdCnst-Ig:16
-	147.1	128.1	LmdCnst-Ig:17
-	147.2	128.2	LmdCnst-Ig:18
E	148	129	LmdCnst-Ig:19
L	149	130	LmdCnst-Ig:20
-	149.1	130.1	LmdCnst-Ig:21
-	149.2	130.2	LmdCnst-Ig:22
Q	150	131	LmdCnst-Ig:23
A	151	132	LmdCnst-Ig:24
N	152	133	LmdCnst-Ig:25
K	153	134	LmdCnst-Ig:26
A	154	135	LmdCnst-Ig:27
T	155	136	LmdCnst-Ig:28
L	156	137	LmdCnst-Ig:29
V	157	138	LmdCnst-Ig:30
C	158	139	LmdCnst-Ig:31
L	159	140	LmdCnst-Ig:32
V	160	141	LmdCnst-Ig:33
S	161	142	LmdCnst-Ig:34
D	162	143	LmdCnst-Ig:35
F	163	144	LmdCnst-Ig:36
Y	164	145	LmdCnst-Ig:37
P	165	146	LmdCnst-Ig:38
-	165.1	146.1	LmdCnst-Ig:39
-	165.2	146.2	LmdCnst-Ig:40
G	166	147	LmdCnst-Ig:41
A	167	148	LmdCnst-Ig:42

FIG. 6 Continued

AB-000224_LS Light Chain			
Residue	**Linear #**	**Mat. Linear #**	**ASN #**
V	168	149	LmdCnst-Ig:43
T	169	150	LmdCnst-Ig:44
V	170	151	LmdCnst-Ig:45
A	171	152	LmdCnst-Ig:46
W	172	153	LmdCnst-Ig:47
-	172.1	153.1	LmdCnst-Ig:48
K	173	154	LmdCnst-Ig:49
A	174	155	LmdCnst-Ig:50
D	175	156	LmdCnst-Ig:51
G	176	157	LmdCnst-Ig:52
S	177	158	LmdCnst-Ig:53
P	178	159	LmdCnst-Ig:54
V	179	160	LmdCnst-Ig:55
K	180	161	LmdCnst-Ig:56
V	181	162	LmdCnst-Ig:57
G	182	163	LmdCnst-Ig:58
V	183	164	LmdCnst-Ig:59
E	184	165	LmdCnst-Ig:60
T	185	166	LmdCnst-Ig:61
T	186	167	LmdCnst-Ig:62
K	187	168	LmdCnst-Ig:63
P	188	169	LmdCnst-Ig:64
S	189	170	LmdCnst-Ig:65
K	190	171	LmdCnst-Ig:66
Q	191	172	LmdCnst-Ig:67
-	191.1	172.1	LmdCnst-Ig:68
-	191.2	172.2	LmdCnst-Ig:69
-	191.3	172.3	LmdCnst-Ig:70
-	191.4	172.4	LmdCnst-Ig:71
-	191.5	172.5	LmdCnst-Ig:72
S	192	173	LmdCnst-Ig:73
N	193	174	LmdCnst-Ig:74
N	194	175	LmdCnst-Ig:75
K	195	176	LmdCnst-Ig:76
Y	196	177	LmdCnst-Ig:77
A	197	178	LmdCnst-Ig:78
A	198	179	LmdCnst-Ig:79
S	199	180	LmdCnst-Ig:80
S	200	181	LmdCnst-Ig:81
Y	201	182	LmdCnst-Ig:82
L	202	183	LmdCnst-Ig:83
S	203	184	LmdCnst-Ig:84

FIG. 6 Continued

AB-000224_LS Light Chain			
Residue	**Linear #**	**Mat. Linear #**	**ASN #**
L	204	185	LmdCnst-Ig:85
T	205	186	LmdCnst-Ig:86
P	206	187	LmdCnst-Ig:87
E	207	188	LmdCnst-Ig:88
Q	208	189	LmdCnst-Ig:89
W	209	190	LmdCnst-Ig:90
-	209.1	190.1	LmdCnst-Ig:91
K	210	191	LmdCnst-Ig:92
S	211	192	LmdCnst-Ig:93
H	212	193	LmdCnst-Ig:94
R	213	194	LmdCnst-Ig:95
S	214	195	LmdCnst-Ig:96
-	214.1	195.1	LmdCnst-Ig:97
-	214.2	195.2	LmdCnst-Ig:98
Y	215	196	LmdCnst-Ig:99
S	216	197	LmdCnst-Ig:100
C	217	198	LmdCnst-Ig:101
R	218	199	LmdCnst-Ig:102
V	219	200	LmdCnst-Ig:103
T	220	201	LmdCnst-Ig:104
H	221	202	LmdCnst-Ig:105
E	222	203	LmdCnst-Ig:106
G	223	204	LmdCnst-Ig:107
S	224	205	LmdCnst-Ig:108
T	225	206	LmdCnst-Ig:109
-	225.1	206.1	LmdCnst-Ig:110
-	225.2	206.2	LmdCnst-Ig:111
V	226	207	LmdCnst-Ig:112
E	227	208	LmdCnst-Ig:113
K	228	209	LmdCnst-Ig:114
T	229	210	LmdCnst-Ig:115
V	230	211	LmdCnst-Ig:116
-	230.1	211.1	LmdCnst-Ig:117
A	231	212	LmdCnst-Ig:118
P	232	213	LmdCnst-Ig:119
A	233	214	LmdCnst-Ig:120
E	234	215	LmdCnst-Ig:121
C	235	216	LmdCnst-Ig:122
S	236	217	LmdCnst-Ig:123

FIG. 6 Continued

AB-000224_LS_Heavy Chain			
Residue	**Linear #**	**Mat. Linear #**	**ASN #**
M	1	-22	KLdr:-22
D	2	-21	KLdr:-21
M	3	-20	KLdr:-20
R	4	-19	KLdr:-19
V	5	-18	KLdr:-18
P	6	-17	KLdr:-17
A	7	-16	KLdr:-16
Q	8	-15	KLdr:-15
L	9	-14	KLdr:-14
L	10	-13	KLdr:-13
G	11	-12	KLdr:-12
L	12	-11	KLdr:-11
L	13	-10	KLdr:-10
L	14	-9	KLdr:-9
L	15	-8	KLdr:-8
W	16	-7	KLdr:-7
L	17	-6	KLdr:-6
R	18	-5	KLdr:-5
G	19	-4	KLdr:-4
A	20	-3	KLdr:-3
R	21	-2	KLdr:-2
C	22	-1	KLdr:-1
E	23	1	HV:1
V	24	2	HV:2
Q	25	3	HV:3
L	26	4	HV:4
V	27	5	HV:5
E	28	6	HV:6
S	29	7	HV:7
~	29.1	7.1	HV:8
G	30	8	HV:9
G	31	9	HV:10
G	32	10	HV:11
L	33	11	HV:12
V	34	12	HV:13
Q	35	13	HV:14
P	36	14	HV:15
G	37	15	HV:16
R	38	16	HV:17
S	39	17	HV:18
L	40	18	HV:19

FIG. 7

AB-000224_LS_Heavy Chain			
Residue	Linear #	Mat. Linear #	ASN #
R	41	19	HV:20
L	42	20	HV:21
P	43	21	HV:22
C	44	22	HV:23
T	45	23	HV:24
A	46	24	HV:25
S	47	25	HV:26
G	48	26	HV:27
-	48.1	26.1	HV:28
F	49	27	HV:29
S	50	28	HV:30
F	51	29	HV:31
G	52	30	HV:32
D	53	31	HV:33
-	53.1	31.1	HV:34
-	53.2	31.2	HV:35
-	53.3	31.3	HV:36
-	53.4	31.4	HV:37
-	53.5	31.5	HV:38
H	54	32	HV:39
A	55	33	HV:40
M	56	34	HV:41
S	57	35	HV:42
W	58	36	HV:43
V	59	37	HV:44
R	60	38	HV:45
Q	61	39	HV:46
A	62	40	HV:47
P	63	41	HV:48
G	64	42	HV:49
K	65	43	HV:50
G	66	44	HV:51
L	67	45	HV:52
E	68	46	HV:53
W	69	47	HV:54
V	70	48	HV:55
G	71	49	HV:56
F	72	50	HV:57
I	73	51	HV:58
R	74	52	HV:59
K	75	53	HV:60
T	76	54	HV:61
-	76.1	54.1	HV:62

FIG. 7 Continued

AB-000224_LS_Heavy Chain			
Residue	**Linear #**	**Mat. Linear #**	**ASN #**
T	77	55	HV:63
Y	78	56	HV:64
G	79	57	HV:65
A	80	58	HV:66
T	81	59	HV:67
T	82	60	HV:68
H	83	61	HV:69
Y	84	62	HV:70
A	85	63	HV:71
A	86	64	HV:72
A	87	65	HV:73
V	88	66	HV:74
R	89	67	HV:75
G	90	68	HV:76
R	91	69	HV:77
F	92	70	HV:78
T	93	71	HV:79
I	94	72	HV:80
S	95	73	HV:81
R	96	74	HV:82
D	97	75	HV:83
D	98	76	HV:84
S	99	77	HV:85
K	100	78	HV:86
S	101	79	HV:87
I	102	80	HV:88
V	103	81	HV:89
Y	104	82	HV:90
L	105	83	HV:91
Q	106	84	HV:92
M	107	85	HV:93
N	108	86	HV:94
S	109	87	HV:95
L	110	88	HV:96
K	111	89	HV:97
T	112	90	HV:98
E	113	91	HV:99
D	114	92	HV:100
T	115	93	HV:101
A	116	94	HV:102
V	117	95	HV:103
Y	118	96	HV:104
F	119	97	HV:105

FIG. 7 Continued

AB-000224_LS_Heavy Chain			
Residue	Linear #	Mat. Linear #	ASN #
C	120	98	HV:106
T	121	99	HV:107
R	122	100	HV:108
V	123	101	HV:109
Q	124	102	HV:110
L	125	103	HV:111
D	126	104	HV:112
Y	127	105	HV:113
G	128	106	HV:114
P	129	107	HV:115
-	129.1	107.1	HV:116
-	129.2	107.2	HV:117
-	129.3	107.3	HV:118
-	129.4	107.4	HV:119
-	129.5	107.5	HV:120
-	129.6	107.6	HV:121
-	129.7	107.7	HV:122
-	129.8	107.8	HV:123
-	129.9	107.9	HV:124
-	129.10	107.10	HV:125
-	129.11	107.11	HV:126
-	129.12	107.12	HV:127
-	129.13	107.13	HV:128
-	129.14	107.14	HV:129
G	130	108	HV:130
Y	131	109	HV:131
Q	132	110	HV:132
Y	133	111	HV:133
Y	134	112	HV:134
G	135	113	HV:135
M	136	114	HV:136
D	137	115	HV:137
V	138	116	HV:138
W	139	117	HV:139
G	140	118	HV:140
Q	141	119	HV:141
G	142	120	HV:142
T	143	121	HV:143
T	144	122	HV:144
V	145	123	HV:145
T	146	124	HV:146
V	147	125	HV:147
S	148	126	HV:148

FIG. 7 Continued

AB-000224_LS_Heavy Chain			
Residue	**Linear #**	**Mat. Linear #**	**ASN #**
S	149	127	HV:149
-	149.1	127.1	HCnst-Ig:1
-	149.2	127.2	HCnst-Ig:2
A	150	128	HCnst-Ig:3
S	151	129	HCnst-Ig:4
T	152	130	HCnst-Ig:5
K	153	131	HCnst-Ig:6
G	154	132	HCnst-Ig:7
P	155	133	HCnst-Ig:8
S	156	134	HCnst-Ig:9
V	157	135	HCnst-Ig:10
F	158	136	HCnst-Ig:11
P	159	137	HCnst-Ig:12
L	160	138	HCnst-Ig:13
A	161	139	HCnst-Ig:14
P	162	140	HCnst-Ig:15
-	162.1	140.1	HCnst-Ig:16
S	163	141	HCnst-Ig:17
-	163.1	141.1	HCnst-Ig:18
S	164	142	HCnst-Ig:19
K	165	143	HCnst-Ig:20
S	166	144	HCnst-Ig:21
T	167	145	HCnst-Ig:22
S	168	146	HCnst-Ig:23
G	169	147	HCnst-Ig:24
G	170	148	HCnst-Ig:25
T	171	149	HCnst-Ig:26
A	172	150	HCnst-Ig:27
A	173	151	HCnst-Ig:28
L	174	152	HCnst-Ig:29
G	175	153	HCnst-Ig:30
C	176	154	HCnst-Ig:31
L	177	155	HCnst-Ig:32
V	178	156	HCnst-Ig:33
K	179	157	HCnst-Ig:34
D	180	158	HCnst-Ig:35
Y	181	159	HCnst-Ig:36
F	182	160	HCnst-Ig:37
P	183	161	HCnst-Ig:38
-	183.1	161.1	HCnst-Ig:39
-	183.2	161.2	HCnst-Ig:40
E	184	162	HCnst-Ig:41
P	185	163	HCnst-Ig:42

FIG. 7 Continued

AB-000224_LS_Heavy Chain			
Residue	Linear #	Mat. Linear #	ASN #
V	186	164	HCnst-Ig:43
T	187	165	HCnst-Ig:44
V	188	166	HCnst-Ig:45
S	189	167	HCnst-Ig:46
W	190	168	HCnst-Ig:47
-	190.1	168.1	HCnst-Ig:48
N	191	169	HCnst-Ig:49
S	192	170	HCnst-Ig:50
G	193	171	HCnst-Ig:51
A	194	172	HCnst-Ig:52
L	195	173	HCnst-Ig:53
T	196	174	HCnst-Ig:54
S	197	175	HCnst-Ig:55
G	198	176	HCnst-Ig:56
V	199	177	HCnst-Ig:57
H	200	178	HCnst-Ig:58
T	201	179	HCnst-Ig:59
-	201.1	179.1	HCnst-Ig:60
-	201.2	179.2	HCnst-Ig:61
-	201.3	179.3	HCnst-Ig:62
F	202	180	HCnst-Ig:63
P	203	181	HCnst-Ig:64
A	204	182	HCnst-Ig:65
V	205	183	HCnst-Ig:66
L	206	184	HCnst-Ig:67
Q	207	185	HCnst-Ig:68
-	207.1	185.1	HCnst-Ig:69
-	207.2	185.2	HCnst-Ig:70
-	207.3	185.3	HCnst-Ig:71
-	207.4	185.4	HCnst-Ig:72
S	208	186	HCnst-Ig:73
S	209	187	HCnst-Ig:74
G	210	188	HCnst-Ig:75
L	211	189	HCnst-Ig:76
Y	212	190	HCnst-Ig:77
S	213	191	HCnst-Ig:78
L	214	192	HCnst-Ig:79
S	215	193	HCnst-Ig:80
S	216	194	HCnst-Ig:81
V	217	195	HCnst-Ig:82
V	218	196	HCnst-Ig:83
T	219	197	HCnst-Ig:84
V	220	198	HCnst-Ig:85

FIG. 7 Continued

AB-000224_LS_Heavy Chain			
Residue	**Linear #**	**Mat. Linear #**	**ASN #**
P	221	199	HCnst-Ig:86
S	222	200	HCnst-Ig:87
S	223	201	HCnst-Ig:88
S	224	202	HCnst-Ig:89
L	225	203	HCnst-Ig:90
-	225.1	203.1	HCnst-Ig:91
G	226	204	HCnst-Ig:92
T	227	205	HCnst-Ig:93
Q	228	206	HCnst-Ig:94
T	229	207	HCnst-Ig:95
-	229.1	207.1	HCnst-Ig:96
-	229.2	207.2	HCnst-Ig:97
-	229.3	207.3	HCnst-Ig:98
Y	230	208	HCnst-Ig:99
I	231	209	HCnst-Ig:100
C	232	210	HCnst-Ig:101
N	233	211	HCnst-Ig:102
V	234	212	HCnst-Ig:103
N	235	213	HCnst-Ig:104
H	236	214	HCnst-Ig:105
K	237	215	HCnst-Ig:106
P	238	216	HCnst-Ig:107
S	239	217	HCnst-Ig:108
N	240	218	HCnst-Ig:109
-	240.1	218.1	HCnst-Ig:110
-	240.2	218.2	HCnst-Ig:111
T	241	219	HCnst-Ig:112
K	242	220	HCnst-Ig:113
V	243	221	HCnst-Ig:114
D	244	222	HCnst-Ig:115
K	245	223	HCnst-Ig:116
-	245.1	223.1	HCnst-Ig:117
K	246	224	HCnst-Ig:118
V	247	225	HCnst-Ig:119
-	247.1	225.1	HCnst-Ig:120
-	247.2	225.2	HCnst-Ig:121
-	247.3	225.3	HCnst-Ig:122
-	247.4	225.4	HCnst-Ig:123
-	247.5	225.1	Hinge:1
-	247.6	225.2	Hinge:2
-	247.7	225.3	Hinge:3
-	247.8	225.4	Hinge:4
-	247.9	225.5	Hinge:5

FIG. 7 Continued

AB-000224_LS_Heavy Chain			
Residue	**Linear #**	**Mat. Linear #**	**ASN #**
-	247.10	225.6	Hinge:6
-	247.11	225.7	Hinge:7
-	247.12	225.8	Hinge:8
-	247.13	225.9	Hinge:9
-	247.14	225.10	Hinge:10
-	247.15	225.11	Hinge:11
-	247.16	225.12	Hinge:12
-	247.17	225.13	Hinge:13
-	247.18	225.14	Hinge:14
-	247.19	225.15	Hinge:15
-	247.20	225.16	Hinge:16
-	247.21	225.17	Hinge:17
-	247.22	225.18	Hinge:18
-	247.23	225.19	Hinge:19
-	247.24	225.20	Hinge:20
-	247.25	225.21	Hinge:21
-	247.26	225.22	Hinge:22
-	247.27	225.23	Hinge:23
-	247.28	225.24	Hinge:24
-	247.29	225.25	Hinge:25
-	247.30	225.26	Hinge:26
-	247.31	225.27	Hinge:27
-	247.32	225.28	Hinge:28
-	247.33	225.29	Hinge:29
-	247.34	225.30	Hinge:30
-	247.35	225.31	Hinge:31
-	247.36	225.32	Hinge:32
-	247.37	225.33	Hinge:33
-	247.38	225.34	Hinge:34
-	247.39	225.35	Hinge:35
-	247.40	225.36	Hinge:36
-	247.41	225.37	Hinge:37
-	247.42	225.38	Hinge:38
-	247.43	225.39	Hinge:39
-	247.44	225.40	Hinge:40
-	247.45	225.41	Hinge:41
-	247.46	225.42	Hinge:42
-	247.47	225.43	Hinge:43
-	247.48	225.44	Hinge:44
-	247.49	225.45	Hinge:45
-	247.50	225.46	Hinge:46
-	247.51	225.47	Hinge:47
-	247.52	225.48	Hinge:48

FIG. 7 Continued

AB-000224_LS_Heavy Chain			
Residue	**Linear #**	**Mat. Linear #**	**ASN #**
-	247.53	225.49	Hinge:49
-	247.54	225.50	Hinge:50
-	247.55	225.51	Hinge:51
-	247.56	225.52	Hinge:52
-	247.57	225.53	Hinge:53
-	247.58	225.54	Hinge:54
-	247.59	225.55	Hinge:55
-	247.60	225.56	Hinge:56
-	247.61	225.57	Hinge:57
-	247.62	225.58	Hinge:58
-	247.63	225.59	Hinge:59
-	247.64	225.60	Hinge:60
-	247.65	225.61	Hinge:61
-	247.66	225.62	Hinge:62
-	247.67	225.63	Hinge:63
-	247.68	225.64	Hinge:64
-	247.69	225.65	Hinge:65
-	247.70	225.66	Hinge:66
-	247.71	225.67	Hinge:67
-	247.72	225.68	Hinge:68
-	247.73	225.69	Hinge:69
-	247.74	225.70	Hinge:70
-	247.75	225.71	Hinge:71
-	247.76	225.72	Hinge:72
-	247.77	225.73	Hinge:73
-	247.78	225.74	Hinge:74
-	247.79	225.75	Hinge:75
-	247.80	225.76	Hinge:76
-	247.81	225.77	Hinge:77
-	247.82	225.78	Hinge:78
-	247.83	225.79	Hinge:79
-	247.84	225.80	Hinge:80
-	247.85	225.81	Hinge:81
-	247.86	225.82	Hinge:82
-	247.87	225.83	Hinge:83
-	247.88	225.84	Hinge:84
-	247.89	225.85	Hinge:85
-	247.90	225.86	Hinge:86
-	247.91	225.87	Hinge:87
-	247.92	225.88	Hinge:88
-	247.93	225.89	Hinge:89
-	247.94	225.90	Hinge:90
-	247.95	225.91	Hinge:91

FIG. 7 Continued

AB-000224_LS_Heavy Chain			
Residue	**Linear #**	**Mat. Linear #**	**ASN #**
-	247.96	225.92	Hinge:92
-	247.97	225.93	Hinge:93
-	247.98	225.94	Hinge:94
-	247.99	225.95	Hinge:95
E	248	226	Hinge:96
P	249	227	Hinge:97
K	250	228	Hinge:98
S	251	229	Hinge:99
-	251.1	229.1	Hinge:100
-	251.2	229.2	Hinge:101
-	251.3	229.3	Hinge:102
-	251.4	229.4	Hinge:103
-	251.5	229.5	Hinge:104
-	251.6	229.6	Hinge:105
-	251.7	229.7	Hinge:106
C	252	230	Hinge:107
D	253	231	Hinge:108
K	254	232	Hinge:109
T	255	233	Hinge:110
H	256	234	Hinge:111
T	257	235	Hinge:112
C	258	236	Hinge:113
P	259	237	Hinge:114
P	260	238	Hinge:115
C	261	239	Hinge:116
P	262	240	Hinge:117
A	263	241	Hinge:118
P	264	242	Hinge:119
E	265	243	Hinge:120
L	266	244	Hinge:121
L	267	245	Hinge:122
G	268	246	Hinge:123
-	268.1	246.1	Fc-N:1
-	268.2	246.2	Fc-N:2
-	268.3	246.3	Fc-N:3
-	268.4	246.4	Fc-N:4
G	269	247	Fc-N:5
P	270	248	Fc-N:6
S	271	249	Fc-N:7
V	272	250	Fc-N:8
F	273	251	Fc-N:9
L	274	252	Fc-N:10
F	275	253	Fc-N:11

FIG. 7 Continued

AB-000224_LS_Heavy Chain			
Residue	Linear #	Mat. Linear #	ASN #
P	276	254	Fc-N:12
P	277	255	Fc-N:13
-	277.1	255.1	Fc-N:14
K	278	256	Fc-N:15
P	279	257	Fc-N:16
K	280	258	Fc-N:17
-	280.1	258.1	Fc-N:18
D	281	259	Fc-N:19
T	282	260	Fc-N:20
L	283	261	Fc-N:21
M	284	262	Fc-N:22
I	285	263	Fc-N:23
S	286	264	Fc-N:24
R	287	265	Fc-N:25
T	288	266	Fc-N:26
P	289	267	Fc-N:27
E	290	268	Fc-N:28
V	291	269	Fc-N:29
T	292	270	Fc-N:30
C	293	271	Fc-N:31
V	294	272	Fc-N:32
V	295	273	Fc-N:33
V	296	274	Fc-N:34
D	297	275	Fc-N:35
V	298	276	Fc-N:36
S	299	277	Fc-N:37
H	300	278	Fc-N:38
E	301	279	Fc-N:39
D	302	280	Fc-N:40
P	303	281	Fc-N:41
E	304	282	Fc-N:42
V	305	283	Fc-N:43
K	306	284	Fc-N:44
F	307	285	Fc-N:45
N	308	286	Fc-N:46
W	309	287	Fc-N:47
-	309.1	287.1	Fc-N:48
Y	310	288	Fc-N:49
V	311	289	Fc-N:50
D	312	290	Fc-N:51
G	313	291	Fc-N:52
V	314	292	Fc-N:53
E	315	293	Fc-N:54

FIG. 7 Continued

AB-000224_LS_Heavy Chain			
Residue	Linear #	Mat. Linear #	ASN #
-	315.1	293.1	Fc-N:55
-	315.2	293.2	Fc-N:56
V	316	294	Fc-N:57
H	317	295	Fc-N:58
N	318	296	Fc-N:59
A	319	297	Fc-N:60
K	320	298	Fc-N:61
T	321	299	Fc-N:62
K	322	300	Fc-N:63
P	323	301	Fc-N:64
R	324	302	Fc-N:65
E	325	303	Fc-N:66
E	326	304	Fc-N:67
Q	327	305	Fc-N:68
-	327.1	305.1	Fc-N:69
-	327.2	305.2	Fc-N:70
-	327.3	305.3	Fc-N:71
-	327.4	305.4	Fc-N:72
Y	328	306	Fc-N:73
N	329	307	Fc-N:74
S	330	308	Fc-N:75
T	331	309	Fc-N:76
Y	332	310	Fc-N:77
R	333	311	Fc-N:78
V	334	312	Fc-N:79
V	335	313	Fc-N:80
S	336	314	Fc-N:81
V	337	315	Fc-N:82
L	338	316	Fc-N:83
T	339	317	Fc-N:84
V	340	318	Fc-N:85
L	341	319	Fc-N:86
H	342	320	Fc-N:87
Q	343	321	Fc-N:88
D	344	322	Fc-N:89
W	345	323	Fc-N:90
-	345.1	323.1	Fc-N:91
L	346	324	Fc-N:92
N	347	325	Fc-N:93
G	348	326	Fc-N:94
K	349	327	Fc-N:95
E	350	328	Fc-N:96
-	350.1	328.1	Fc-N:97

FIG. 7 Continued

AB-000224_LS_Heavy Chain			
Residue	Linear #	Mat. Linear #	ASN #
-	350.2	328.2	Fc-N:98
Y	351	329	Fc-N:99
K	352	330	Fc-N:100
C	353	331	Fc-N:101
K	354	332	Fc-N:102
V	355	333	Fc-N:103
S	356	334	Fc-N:104
N	357	335	Fc-N:105
K	358	336	Fc-N:106
A	359	337	Fc-N:107
L	360	338	Fc-N:108
P	361	339	Fc-N:109
-	361.1	339.1	Fc-N:110
-	361.2	339.2	Fc-N:111
A	362	340	Fc-N:112
P	363	341	Fc-N:113
I	364	342	Fc-N:114
E	365	343	Fc-N:115
K	366	344	Fc-N:116
T	367	345	Fc-N:117
I	368	346	Fc-N:118
S	369	347	Fc-N:119
K	370	348	Fc-N:120
A	371	349	Fc-N:121
K	372	350	Fc-N:122
G	373	351	Fc-N:123
-	373.1	351.1	Fc-C:1
Q	374	352	Fc-C:2
P	375	353	Fc-C:3
R	376	354	Fc-C:4
E	377	355	Fc-C:5
P	378	356	Fc-C:6
Q	379	357	Fc-C:7
V	380	358	Fc-C:8
Y	381	359	Fc-C:9
T	382	360	Fc-C:10
L	383	361	Fc-C:11
P	384	362	Fc-C:12
P	385	363	Fc-C:13
-	385.1	363.1	Fc-C:14
S	386	364	Fc-C:15
R	387	365	Fc-C:16
D	388	366	Fc-C:17

FIG. 7 Continued

AB-000224_LS_Heavy Chain			
Residue	**Linear #**	**Mat. Linear #**	**ASN #**
-	388.1	366.1	Fc-C:18
E	389	367	Fc-C:19
L	390	368	Fc-C:20
-	390.1	368.1	Fc-C:21
-	390.2	368.2	Fc-C:22
T	391	369	Fc-C:23
K	392	370	Fc-C:24
N	393	371	Fc-C:25
Q	394	372	Fc-C:26
V	395	373	Fc-C:27
S	396	374	Fc-C:28
L	397	375	Fc-C:29
T	398	376	Fc-C:30
C	399	377	Fc-C:31
L	400	378	Fc-C:32
V	401	379	Fc-C:33
K	402	380	Fc-C:34
G	403	381	Fc-C:35
F	404	382	Fc-C:36
Y	405	383	Fc-C:37
P	406	384	Fc-C:38
-	406.1	384.1	Fc-C:39
-	406.2	384.2	Fc-C:40
S	407	385	Fc-C:41
D	408	386	Fc-C:42
I	409	387	Fc-C:43
A	410	388	Fc-C:44
V	411	389	Fc-C:45
E	412	390	Fc-C:46
W	413	391	Fc-C:47
-	413.1	391.1	Fc-C:48
E	414	392	Fc-C:49
S	415	393	Fc-C:50
N	416	394	Fc-C:51
G	417	395	Fc-C:52
Q	418	396	Fc-C:53
P	419	397	Fc-C:54
-	419.1	397.1	Fc-C:55
-	419.2	397.2	Fc-C:56
E	420	398	Fc-C:57
N	421	399	Fc-C:58
N	422	400	Fc-C:59
Y	423	401	Fc-C:60

FIG. 7 Continued

AB-000224_LS_Heavy Chain			
Residue	**Linear #**	**Mat. Linear #**	**ASN #**
K	424	402	Fc-C:61
T	425	403	Fc-C:62
T	426	404	Fc-C:63
P	427	405	Fc-C:64
P	428	406	Fc-C:65
V	429	407	Fc-C:66
L	430	408	Fc-C:67
D	431	409	Fc-C:68
-	431.1	409.1	Fc-C:69
-	431.2	409.2	Fc-C:70
-	431.3	409.3	Fc-C:71
-	431.4	409.4	Fc-C:72
S	432	410	Fc-C:73
D	433	411	Fc-C:74
G	434	412	Fc-C:75
S	435	413	Fc-C:76
F	436	414	Fc-C:77
F	437	415	Fc-C:78
L	438	416	Fc-C:79
Y	439	417	Fc-C:80
S	440	418	Fc-C:81
K	441	419	Fc-C:82
L	442	420	Fc-C:83
T	443	421	Fc-C:84
V	444	422	Fc-C:85
D	445	423	Fc-C:86
K	446	424	Fc-C:87
S	447	425	Fc-C:88
R	448	426	Fc-C:89
W	449	427	Fc-C:90
-	449.1	427.1	Fc-C:91
Q	450	428	Fc-C:92
Q	451	429	Fc-C:93
G	452	430	Fc-C:94
N	453	431	Fc-C:95
V	454	432	Fc-C:96
-	454.1	432.1	Fc-C:97
-	454.2	432.2	Fc-C:98
F	455	433	Fc-C:99
S	456	434	Fc-C:100
C	457	435	Fc-C:101
S	458	436	Fc-C:102
V	459	437	Fc-C:103

FIG. 7 Continued

AB-000224_LS_Heavy Chain			
Residue	Linear #	Mat. Linear #	ASN #
L	460	438	Fc-C:104
H	461	439	Fc-C:105
E	462	440	Fc-C:106
A	463	441	Fc-C:107
L	464	442	Fc-C:108
H	465	443	Fc-C:109
-	465.1	443.1	Fc-C:110
-	465.2	443.2	Fc-C:111
S	466	444	Fc-C:112
H	467	445	Fc-C:113
Y	468	446	Fc-C:114
T	469	447	Fc-C:115
-	469.1	447.1	Fc-C:116
Q	470	448	Fc-C:117
K	471	449	Fc-C:118
S	472	450	Fc-C:119
L	473	451	Fc-C:120
S	474	452	Fc-C:121
L	475	453	Fc-C:122
S	476	454	Fc-C:123
P	477	455	HCnst-Po:1
G	478	456	HCnst-Po:2
K	479	457	HCnst-Po:3
-	479.1	457.1	HCnst-Po:4
-	479.2	457.2	HCnst-Po:5
-	479.3	457.3	HCnst-Po:6
-	479.4	457.4	HCnst-Po:7
-	479.5	457.5	HCnst-Po:8
-	479.6	457.6	HCnst-Po:9
-	479.7	457.7	HCnst-Po:10
-	479.8	457.8	HCnst-Po:11
-	479.9	457.9	HCnst-Po:12
-	479.10	457.10	HCnst-Po:13
-	479.11	457.11	HCnst-Po:14
-	479.12	457.12	HCnst-Po:15
-	479.13	457.13	HCnst-Po:16
-	479.14	457.14	HCnst-Po:17
-	479.15	457.15	HCnst-Po:18
-	479.16	457.16	HCnst-Po:19
-	479.17	457.17	HCnst-Po:20
-	479.18	457.18	HCnst-Po:21
-	479.19	457.19	HCnst-Po:22
-	479.20	457.20	HCnst-Po:23

FIG. 7 Continued

AB-000224_LS_Heavy Chain			
Residue	Linear #	Mat. Linear #	ASN #
-	479.21	457.21	HCnst-Po:24
-	479.22	457.22	HCnst-Po:25
-	479.23	457.23	HCnst-Po:26
-	479.24	457.24	HCnst-Po:27
-	479.25	457.25	HCnst-Po:28
-	479.26	457.26	HCnst-Po:29
-	479.27	457.27	HCnst-Po:30
-	479.28	457.28	HCnst-Po:31
-	479.29	457.29	HCnst-Po:32
-	479.30	457.30	HCnst-Po:33
-	479.31	457.31	HCnst-Po:34
-	479.32	457.32	HCnst-Po:35
-	479.33	457.33	HCnst-Po:36
-	479.34	457.34	HCnst-Po:37
-	479.35	457.35	HCnst-Po:38
-	479.36	457.36	HCnst-Po:39
-	479.37	457.37	HCnst-Po:40
-	479.38	457.38	HCnst-Po:41
-	479.39	457.39	HCnst-Po:42
-	479.40	457.40	HCnst-Po:43
-	479.41	457.41	HCnst-Po:44
-	479.42	457.42	HCnst-Po:45
-	479.43	457.43	HCnst-Po:46
-	479.44	457.44	HCnst-Po:47
-	479.45	457.45	HCnst-Po:48
-	479.46	457.46	HCnst-Po:49
-	479.47	457.47	HCnst-Po:50
-	479.48	457.48	HCnst-Po:51
-	479.49	457.49	HCnst-Po:52
-	479.50	457.50	HCnst-Po:53
-	479.51	457.51	HCnst-Po:54
-	479.52	457.52	HCnst-Po:55
-	479.53	457.53	HCnst-Po:56
-	479.54	457.54	HCnst-Po:57
-	479.55	457.55	HCnst-Po:58
-	479.56	457.56	HCnst-Po:59
-	479.57	457.57	HCnst-Po:60
-	479.58	457.58	HCnst-Po:61
-	479.59	457.59	HCnst-Po:62
-	479.60	457.60	HCnst-Po:63
-	479.61	457.61	HCnst-Po:64
-	479.62	457.62	HCnst-Po:65
-	479.63	457.63	HCnst-Po:66

FIG. 7 Continued

AB-000224_LS_Heavy Chain			
Residue	**Linear #**	**Mat. Linear #**	**ASN #**
-	479.64	457.64	HCnst-Po:67
-	479.65	457.65	HCnst-Po:68
-	479.66	457.66	HCnst-Po:69
-	479.67	457.67	HCnst-Po:70
-	479.68	457.68	HCnst-Po:71
-	479.69	457.69	HCnst-Po:72
-	479.70	457.70	HCnst-Po:73
-	479.71	457.71	HCnst-Po:74
-	479.72	457.72	HCnst-Po:75
-	479.73	457.73	HCnst-Po:76
-	479.74	457.74	HCnst-Po:77
-	479.75	457.75	HCnst-Po:78
-	479.76	457.76	HCnst-Po:79
-	479.77	457.77	HCnst-Po:80
-	479.78	457.78	HCnst-Po:81
-	479.79	457.79	HCnst-Po:82
-	479.80	457.80	HCnst-Po:83
-	479.81	457.81	HCnst-Po:84
-	479.82	457.82	HCnst-Po:85
-	479.83	457.83	HCnst-Po:86
-	479.84	457.84	HCnst-Po:87
-	479.85	457.85	HCnst-Po:88
-	479.86	457.86	HCnst-Po:89
-	479.87	457.87	HCnst-Po:90
-	479.88	457.88	HCnst-Po:91
-	479.89	457.89	HCnst-Po:92
-	479.90	457.90	HCnst-Po:93
-	479.91	457.91	HCnst-Po:94
-	479.92	457.92	HCnst-Po:95
-	479.93	457.93	HCnst-Po:96
-	479.94	457.94	HCnst-Po:97
-	479.95	457.95	HCnst-Po:98
-	479.96	457.96	HCnst-Po:99
-	479.97	457.97	HCnst-Po:100
-	479.98	457.98	HCnst-Po:101
-	479.99	457.99	HCnst-Po:102
-	479.100	457.100	HCnst-Po:103
-	479.101	457.101	HCnst-Po:104
-	479.102	457.102	HCnst-Po:105
-	479.103	457.103	HCnst-Po:106
-	479.104	457.104	HCnst-Po:107
-	479.105	457.105	HCnst-Po:108
-	479.106	457.106	HCnst-Po:109

FIG. 7 Continued

AB-000224_LS_Heavy Chain			
Residue	**Linear #**	**Mat. Linear #**	**ASN #**
-	479.107	457.107	HCnst-Po:110
-	479.108	457.108	HCnst-Po:111
-	479.109	457.109	HCnst-Po:112
-	479.110	457.110	HCnst-Po:113
-	479.111	457.111	HCnst-Po:114
-	479.112	457.112	HCnst-Po:115
-	479.113	457.113	HCnst-Po:116
-	479.114	457.114	HCnst-Po:117
-	479.115	457.115	HCnst-Po:118
-	479.116	457.116	HCnst-Po:119
-	479.117	457.117	HCnst-Po:120
-	479.118	457.118	HCnst-Po:121
-	479.119	457.119	HCnst-Po:122
-	479.120	457.120	HCnst-Po:123

FIG. 7 Continued

AB-007088_LS_Light Chain			
Residue	Linear #	Mat. Linear #	ASN #
M	1	-22	KLdr:-22
D	2	-21	KLdr:-21
M	3	-20	KLdr:-20
R	4	-19	KLdr:-19
V	5	-18	KLdr:-18
P	6	-17	KLdr:-17
A	7	-16	KLdr:-16
Q	8	-15	KLdr:-15
L	9	-14	KLdr:-14
L	10	-13	KLdr:-13
G	11	-12	KLdr:-12
L	12	-11	KLdr:-11
L	13	-10	KLdr:-10
L	14	-9	KLdr:-9
L	15	-8	KLdr:-8
W	16	-7	KLdr:-7
L	17	-6	KLdr:-6
R	18	-5	KLdr:-5
G	19	-4	KLdr:-4
A	20	-3	KLdr:-3
R	21	-2	KLdr:-2
C	22	-1	KLdr:-1
G	23	1	KV:1
V	24	2	KV:2
Q	25	3	KV:3
M	26	4	KV:4
T	27	5	KV:5
Q	28	6	KV:6
S	29	7	KV:7
P	30	8	KV:8
S	31	9	KV:9
T	32	10	KV:10
L	33	11	KV:11
S	34	12	KV:12
A	35	13	KV:13
S	36	14	KV:14
V	37	15	KV:15
G	38	16	KV:16
D	39	17	KV:17
R	40	18	KV:18
V	41	19	KV:19
T	42	20	KV:20
L	43	21	KV:21

FIG. 8

T	44	22	KV:22
C	45	23	KV:23
R	46	24	KV:24
A	47	25	KV:25
S	48	26	KV:26
-	48.1	26.1	KV:27
-	48.2	26.2	KV:28
Q	49	27	KV:29
S	50	28	KV:30
I	51	29	KV:31
S	52	30	KV:32
S	53	31	KV:33
-	53.1	31.1	KV:34
-	53.2	31.2	KV:35
-	53.3	31.3	KV:36
-	53.4	31.4	KV:37
-	53.5	31.5	KV:38
-	53.6	31.6	KV:39
W	54	32	KV:40
L	55	33	KV:41
A	56	34	KV:42
W	57	35	KV:43
Y	58	36	KV:44
Q	59	37	KV:45
Q	60	38	KV:46
K	61	39	KV:47
P	62	40	KV:48
G	63	41	KV:49
K	64	42	KV:50
A	65	43	KV:51
P	66	44	KV:52
K	67	45	KV:53
L	68	46	KV:54
L	69	47	KV:55
I	70	48	KV:56
Y	71	49	KV:57
D	72	50	KV:58
-	72.1	50.1	KV:59
-	72.2	50.2	KV:60
-	72.3	50.3	KV:61
-	72.4	50.4	KV:62
-	72.5	50.5	KV:63
-	72.6	50.6	KV:64
-	72.7	50.7	KV:65
-	72.8	50.8	KV:66
A	73	51	KV:67

FIG. 8 Continued

S	74	52	KV:68
S	75	53	KV:69
L	76	54	KV:70
E	77	55	KV:71
S	78	56	KV:72
G	79	57	KV:73
V	80	58	KV:74
P	81	59	KV:75
S	82	60	KV:76
R	83	61	KV:77
F	84	62	KV:78
S	85	63	KV:79
G	86	64	KV:80
S	87	65	KV:81
G	88	66	KV:82
S	89	67	KV:83
G	90	68	KV:84
-	90.1	68.1	KV:85
-	90.2	68.2	KV:86
T	91	69	KV:87
E	92	70	KV:88
F	93	71	KV:89
T	94	72	KV:90
L	95	73	KV:91
T	96	74	KV:92
I	97	75	KV:93
S	98	76	KV:94
S	99	77	KV:95
L	100	78	KV:96
Q	101	79	KV:97
P	102	80	KV:98
D	103	81	KV:99
D	104	82	KV:100
F	105	83	KV:101
A	106	84	KV:102
T	107	85	KV:103
Y	108	86	KV:104
Y	109	87	KV:105
C	110	88	KV:106
Q	111	89	KV:107
Q	112	90	KV:108
Y	113	91	KV:109
N	114	92	KV:110
S	115	93	KV:111
-	115.1	93.1	KV:112
-	115.2	93.2	KV:113

FIG. 8 Continued

-	115.3	93.3	KV:114
-	115.4	93.4	KV:115
-	115.5	93.5	KV:116
-	115.6	93.6	KV:117
-	115.7	93.7	KV:118
-	115.8	93.8	KV:119
-	115.9	93.9	KV:120
-	115.10	93.10	KV:121
-	115.11	93.11	KV:122
-	115.12	93.12	KV:123
-	115.13	93.13	KV:124
-	115.14	93.14	KV:125
-	115.15	93.15	KV:126
-	115.16	93.16	KV:127
-	115.17	93.17	KV:128
-	115.18	93.18	KV:129
-	115.19	93.19	KV:130
-	115.20	93.20	KV:131
-	115.21	93.21	KV:132
-	115.22	93.22	KV:133
Y	116	94	KV:134
S	117	95	KV:135
F	118	96	KV:136
W	119	97	KV:137
T	120	98	KV:138
F	121	99	KV:139
G	122	100	KV:140
Q	123	101	KV:141
G	124	102	KV:142
T	125	103	KV:143
K	126	104	KV:144
V	127	105	KV:145
E	128	106	KV:146
I	129	107	KV:147
K	130	108	KV:148
R	131	109	KV:149
-	131.1	109.1	KCnst-Ig:1
T	132	110	KCnst-Ig:2
V	133	111	KCnst-Ig:3
A	134	112	KCnst-Ig:4
A	135	113	KCnst-Ig:5
P	136	114	KCnst-Ig:6
S	137	115	KCnst-Ig:7
V	138	116	KCnst-Ig:8
F	139	117	KCnst-Ig:9
I	140	118	KCnst-Ig:10

FIG. 8 Continued

F	141	119	KCnst-Ig:11
P	142	120	KCnst-Ig:12
P	143	121	KCnst-Ig:13
S	144	122	KCnst-Ig:14
D	145	123	KCnst-Ig:15
E	146	124	KCnst-Ig:16
-	146.1	124.1	KCnst-Ig:17
-	146.2	124.2	KCnst-Ig:18
Q	147	125	KCnst-Ig:19
L	148	126	KCnst-Ig:20
-	148.1	126.1	KCnst-Ig:21
-	148.2	126.2	KCnst-Ig:22
K	149	127	KCnst-Ig:23
S	150	128	KCnst-Ig:24
G	151	129	KCnst-Ig:25
T	152	130	KCnst-Ig:26
A	153	131	KCnst-Ig:27
S	154	132	KCnst-Ig:28
V	155	133	KCnst-Ig:29
V	156	134	KCnst-Ig:30
C	157	135	KCnst-Ig:31
L	158	136	KCnst-Ig:32
L	159	137	KCnst-Ig:33
N	160	138	KCnst-Ig:34
N	161	139	KCnst-Ig:35
F	162	140	KCnst-Ig:36
Y	163	141	KCnst-Ig:37
P	164	142	KCnst-Ig:38
-	164.1	142.1	KCnst-Ig:39
-	164.2	142.2	KCnst-Ig:40
R	165	143	KCnst-Ig:41
E	166	144	KCnst-Ig:42
A	167	145	KCnst-Ig:43
K	168	146	KCnst-Ig:44
V	169	147	KCnst-Ig:45
Q	170	148	KCnst-Ig:46
W	171	149	KCnst-Ig:47
-	171.1	149.1	KCnst-Ig:48
K	172	150	KCnst-Ig:49
V	173	151	KCnst-Ig:50
D	174	152	KCnst-Ig:51
N	175	153	KCnst-Ig:52
A	176	154	KCnst-Ig:53
L	177	155	KCnst-Ig:54
Q	178	156	KCnst-Ig:55
S	179	157	KCnst-Ig:56

FIG. 8 Continued

G	180	158	KCnst-Ig:57
N	181	159	KCnst-Ig:58
S	182	160	KCnst-Ig:59
Q	183	161	KCnst-Ig:60
E	184	162	KCnst-Ig:61
S	185	163	KCnst-Ig:62
V	186	164	KCnst-Ig:63
T	187	165	KCnst-Ig:64
E	188	166	KCnst-Ig:65
Q	189	167	KCnst-Ig:66
D	190	168	KCnst-Ig:67
-	190.1	168.1	KCnst-Ig:68
-	190.2	168.2	KCnst-Ig:69
-	190.3	168.3	KCnst-Ig:70
-	190.4	168.4	KCnst-Ig:71
S	191	169	KCnst-Ig:72
K	192	170	KCnst-Ig:73
D	193	171	KCnst-Ig:74
S	194	172	KCnst-Ig:75
T	195	173	KCnst-Ig:76
Y	196	174	KCnst-Ig:77
S	197	175	KCnst-Ig:78
L	198	176	KCnst-Ig:79
S	199	177	KCnst-Ig:80
S	200	178	KCnst-Ig:81
T	201	179	KCnst-Ig:82
L	202	180	KCnst-Ig:83
T	203	181	KCnst-Ig:84
L	204	182	KCnst-Ig:85
S	205	183	KCnst-Ig:86
K	206	184	KCnst-Ig:87
A	207	185	KCnst-Ig:88
D	208	186	KCnst-Ig:89
Y	209	187	KCnst-Ig:90
-	209.1	187.1	KCnst-Ig:91
E	210	188	KCnst-Ig:92
K	211	189	KCnst-Ig:93
H	212	190	KCnst-Ig:94
K	213	191	KCnst-Ig:95
V	214	192	KCnst-Ig:96
-	214.1	192.1	KCnst-Ig:97
-	214.2	192.2	KCnst-Ig:98
Y	215	193	KCnst-Ig:99
A	216	194	KCnst-Ig:100
C	217	195	KCnst-Ig:101
E	218	196	KCnst-Ig:102

FIG. 8 Continued

V	219	197	KCnst-Ig:103
T	220	198	KCnst-Ig:104
H	221	199	KCnst-Ig:105
Q	222	200	KCnst-Ig:106
G	223	201	KCnst-Ig:107
L	224	202	KCnst-Ig:108
S	225	203	KCnst-Ig:109
-	225.1	203.1	KCnst-Ig:110
S	226	204	KCnst-Ig:111
P	227	205	KCnst-Ig:112
V	228	206	KCnst-Ig:113
T	229	207	KCnst-Ig:114
K	230	208	KCnst-Ig:115
S	231	209	KCnst-Ig:116
F	232	210	KCnst-Ig:117
N	233	211	KCnst-Ig:118
R	234	212	KCnst-Ig:119
G	235	213	KCnst-Ig:120
E	236	214	KCnst-Ig:121
C	237	215	KCnst-Ig:122
-	237.1	215.1	KCnst-Ig:123

FIG. 8 Continued

AB-007088_LS_Heavy Chain			
Residue	**Linear #**	**Mat. Linear #**	**ASN #**
M	1	-22	KLdr:-22
D	2	-21	KLdr:-21
M	3	-20	KLdr:-20
R	4	-19	KLdr:-19
V	5	-18	KLdr:-18
P	6	-17	KLdr:-17
A	7	-16	KLdr:-16
Q	8	-15	KLdr:-15
L	9	-14	KLdr:-14
L	10	-13	KLdr:-13
G	11	-12	KLdr:-12
L	12	-11	KLdr:-11
L	13	-10	KLdr:-10
L	14	-9	KLdr:-9
L	15	-8	KLdr:-8
W	16	-7	KLdr:-7
L	17	-6	KLdr:-6
R	18	-5	KLdr:-5
G	19	-4	KLdr:-4
A	20	-3	KLdr:-3
R	21	-2	KLdr:-2
C	22	-1	KLdr:-1
Q	23	1	HV:1
V	24	2	HV:2
Q	25	3	HV:3
L	26	4	HV:4
V	27	5	HV:5
E	28	6	HV:6
S	29	7	HV:7
-	29.1	7.1	HV:8
G	30	8	HV:9
G	31	9	HV:10
G	32	10	HV:11
V	33	11	HV:12
V	34	12	HV:13
Q	35	13	HV:14
P	36	14	HV:15
G	37	15	HV:16
R	38	16	HV:17

FIG. 9

AB-007088_LS_Heavy Chain			
Residue	Linear #	Mat. Linear #	ASN #
S	39	17	HV:18
L	40	18	HV:19
R	41	19	HV:20
L	42	20	HV:21
S	43	21	HV:22
C	44	22	HV:23
A	45	23	HV:24
A	46	24	HV:25
S	47	25	HV:26
G	48	26	HV:27
-	48.1	26.1	HV:28
F	49	27	HV:29
A	50	28	HV:30
F	51	29	HV:31
N	52	30	HV:32
T	53	31	HV:33
-	53.1	31.1	HV:34
-	53.2	31.2	HV:35
-	53.3	31.3	HV:36
-	53.4	31.4	HV:37
-	53.5	31.5	HV:38
Y	54	32	HV:39
G	55	33	HV:40
M	56	34	HV:41
H	57	35	HV:42
W	58	36	HV:43
V	59	37	HV:44
R	60	38	HV:45
Q	61	39	HV:46
T	62	40	HV:47
P	63	41	HV:48
G	64	42	HV:49
K	65	43	HV:50
G	66	44	HV:51
L	67	45	HV:52
E	68	46	HV:53
W	69	47	HV:54
V	70	48	HV:55
A	71	49	HV:56
I	72	50	HV:57
I	73	51	HV:58
W	74	52	HV:59
Y	75	53	HV:60

FIG. 9 Continued

AB-007088_LS_Heavy Chain			
Residue	**Linear #**	**Mat. Linear #**	**ASN #**
-	75.1	53.1	HV:61
-	75.2	53.2	HV:62
-	75.3	53.3	HV:63
D	76	54	HV:64
G	77	55	HV:65
S	78	56	HV:66
Q	79	57	HV:67
K	80	58	HV:68
Y	81	59	HV:69
Y	82	60	HV:70
A	83	61	HV:71
D	84	62	HV:72
S	85	63	HV:73
V	86	64	HV:74
Q	87	65	HV:75
G	88	66	HV:76
R	89	67	HV:77
F	90	68	HV:78
I	91	69	HV:79
I	92	70	HV:80
S	93	71	HV:81
R	94	72	HV:82
D	95	73	HV:83
N	96	74	HV:84
H	97	75	HV:85
K	98	76	HV:86
N	99	77	HV:87
T	100	78	HV:88
L	101	79	HV:89
S	102	80	HV:90
L	103	81	HV:91
Q	104	82	HV:92
M	105	83	HV:93
N	106	84	HV:94
G	107	85	HV:95
L	108	86	HV:96
R	109	87	HV:97
A	110	88	HV:98
E	111	89	HV:99
D	112	90	HV:100
T	113	91	HV:101
A	114	92	HV:102
V	115	93	HV:103

FIG. 9 Continued

AB-007088_LS_Heavy Chain			
Residue	**Linear #**	**Mat. Linear #**	**ASN #**
Y	116	94	HV:104
F	117	95	HV:105
C	118	96	HV:106
V	119	97	HV:107
R	120	98	HV:108
V	121	99	HV:109
R	122	100	HV:110
F	123	101	HV:111
S	124	102	HV:112
V	125	103	HV:113
G	126	104	HV:114
-	126.1	104.1	HV:115
-	126.2	104.2	HV:116
-	126.3	104.3	HV:117
-	126.4	104.4	HV:118
-	126.5	104.5	HV:119
-	126.6	104.6	HV:120
-	126.7	104.7	HV:121
-	126.8	104.8	HV:122
-	126.9	104.9	HV:123
-	126.10	104.10	HV:124
-	126.11	104.11	HV:125
-	126.12	104.12	HV:126
-	126.13	104.13	HV:127
-	126.14	104.14	HV:128
-	126.15	104.15	HV:129
-	126.16	104.16	HV:130
P	127	105	HV:131
H	128	106	HV:132
G	129	107	HV:133
S	130	108	HV:134
A	131	109	HV:135
F	132	110	HV:136
D	133	111	HV:137
L	134	112	HV:138
W	135	113	HV:139
G	136	114	HV:140
Q	137	115	HV:141
G	138	116	HV:142
T	139	117	HV:143
M	140	118	HV:144
V	141	119	HV:145
I	142	120	HV:146

FIG. 9 Continued

AB-007088_LS_Heavy Chain			
Residue	**Linear #**	**Mat. Linear #**	**ASN #**
V	143	121	HV:147
S	144	122	HV:148
S	145	123	HV:149
-	145.1	123.1	HCnst-Ig:1
-	145.2	123.2	HCnst-Ig:2
A	146	124	HCnst-Ig:3
S	147	125	HCnst-Ig:4
T	148	126	HCnst-Ig:5
K	149	127	HCnst-Ig:6
G	150	128	HCnst-Ig:7
P	151	129	HCnst-Ig:8
S	152	130	HCnst-Ig:9
V	153	131	HCnst-Ig:10
F	154	132	HCnst-Ig:11
P	155	133	HCnst-Ig:12
L	156	134	HCnst-Ig:13
A	157	135	HCnst-Ig:14
P	158	136	HCnst-Ig:15
-	158.1	136.1	HCnst-Ig:16
S	159	137	HCnst-Ig:17
-	159.1	137.1	HCnst-Ig:18
S	160	138	HCnst-Ig:19
K	161	139	HCnst-Ig:20
S	162	140	HCnst-Ig:21
T	163	141	HCnst-Ig:22
S	164	142	HCnst-Ig:23
G	165	143	HCnst-Ig:24
G	166	144	HCnst-Ig:25
T	167	145	HCnst-Ig:26
A	168	146	HCnst-Ig:27
A	169	147	HCnst-Ig:28
L	170	148	HCnst-Ig:29
G	171	149	HCnst-Ig:30
C	172	150	HCnst-Ig:31
L	173	151	HCnst-Ig:32
V	174	152	HCnst-Ig:33
K	175	153	HCnst-Ig:34
D	176	154	HCnst-Ig:35
Y	177	155	HCnst-Ig:36
F	178	156	HCnst-Ig:37
P	179	157	HCnst-Ig:38
-	179.1	157.1	HCnst-Ig:39
-	179.2	157.2	HCnst-Ig:40

FIG. 9 Continued

AB-007088_LS_Heavy Chain			
Residue	Linear #	Mat. Linear #	ASN #
E	180	158	HCnst-Ig:41
P	181	159	HCnst-Ig:42
V	182	160	HCnst-Ig:43
T	183	161	HCnst-Ig:44
V	184	162	HCnst-Ig:45
S	185	163	HCnst-Ig:46
W	186	164	HCnst-Ig:47
-	186.1	164.1	HCnst-Ig:48
N	187	165	HCnst-Ig:49
S	188	166	HCnst-Ig:50
G	189	167	HCnst-Ig:51
A	190	168	HCnst-Ig:52
L	191	169	HCnst-Ig:53
T	192	170	HCnst-Ig:54
S	193	171	HCnst-Ig:55
G	194	172	HCnst-Ig:56
V	195	173	HCnst-Ig:57
H	196	174	HCnst-Ig:58
T	197	175	HCnst-Ig:59
-	197.1	175.1	HCnst-Ig:60
-	197.2	175.2	HCnst-Ig:61
-	197.3	175.3	HCnst-Ig:62
F	198	176	HCnst-Ig:63
P	199	177	HCnst-Ig:64
A	200	178	HCnst-Ig:65
V	201	179	HCnst-Ig:66
L	202	180	HCnst-Ig:67
Q	203	181	HCnst-Ig:68
-	203.1	181.1	HCnst-Ig:69
-	203.2	181.2	HCnst-Ig:70
-	203.3	181.3	HCnst-Ig:71
-	203.4	181.4	HCnst-Ig:72
S	204	182	HCnst-Ig:73
S	205	183	HCnst-Ig:74
G	206	184	HCnst-Ig:75
L	207	185	HCnst-Ig:76
Y	208	186	HCnst-Ig:77
S	209	187	HCnst-Ig:78
L	210	188	HCnst-Ig:79
S	211	189	HCnst-Ig:80
S	212	190	HCnst-Ig:81
V	213	191	HCnst-Ig:82
V	214	192	HCnst-Ig:83

FIG. 9 Continued

AB-007088_LS_Heavy Chain			
Residue	Linear #	Mat. Linear #	ASN #
T	215	193	HCnst-Ig:84
V	216	194	HCnst-Ig:85
P	217	195	HCnst-Ig:86
S	218	196	HCnst-Ig:87
S	219	197	HCnst-Ig:88
S	220	198	HCnst-Ig:89
L	221	199	HCnst-Ig:90
-	221.1	199.1	HCnst-Ig:91
G	222	200	HCnst-Ig:92
T	223	201	HCnst-Ig:93
Q	224	202	HCnst-Ig:94
T	225	203	HCnst-Ig:95
-	225.1	203.1	HCnst-Ig:96
-	225.2	203.2	HCnst-Ig:97
-	225.3	203.3	HCnst-Ig:98
Y	226	204	HCnst-Ig:99
I	227	205	HCnst-Ig:100
C	228	206	HCnst-Ig:101
N	229	207	HCnst-Ig:102
V	230	208	HCnst-Ig:103
N	231	209	HCnst-Ig:104
H	232	210	HCnst-Ig:105
K	233	211	HCnst-Ig:106
P	234	212	HCnst-Ig:107
S	235	213	HCnst-Ig:108
N	236	214	HCnst-Ig:109
-	236.1	214.1	HCnst-Ig:110
-	236.2	214.2	HCnst-Ig:111
T	237	215	HCnst-Ig:112
K	238	216	HCnst-Ig:113
V	239	217	HCnst-Ig:114
D	240	218	HCnst-Ig:115
K	241	219	HCnst-Ig:116
-	241.1	219.1	HCnst-Ig:117
K	242	220	HCnst-Ig:118
V	243	221	HCnst-Ig:119
-	243.1	221.1	HCnst-Ig:120
-	243.2	221.2	HCnst-Ig:121
-	243.3	221.3	HCnst-Ig:122
-	243.4	221.4	HCnst-Ig:123
-	243.5	221.1	Hinge:1
-	243.6	221.2	Hinge:2
-	243.7	221.3	Hinge:3

FIG. 9 Continued

AB-007088_LS_Heavy Chain			
Residue	Linear #	Mat. Linear #	ASN #
-	243.8	221.4	Hinge:4
-	243.9	221.5	Hinge:5
-	243.10	221.6	Hinge:6
-	243.11	221.7	Hinge:7
-	243.12	221.8	Hinge:8
-	243.13	221.9	Hinge:9
-	243.14	221.10	Hinge:10
-	243.15	221.11	Hinge:11
-	243.16	221.12	Hinge:12
-	243.17	221.13	Hinge:13
-	243.18	221.14	Hinge:14
-	243.19	221.15	Hinge:15
-	243.20	221.16	Hinge:16
-	243.21	221.17	Hinge:17
-	243.22	221.18	Hinge:18
-	243.23	221.19	Hinge:19
-	243.24	221.20	Hinge:20
-	243.25	221.21	Hinge:21
-	243.26	221.22	Hinge:22
-	243.27	221.23	Hinge:23
-	243.28	221.24	Hinge:24
-	243.29	221.25	Hinge:25
-	243.30	221.26	Hinge:26
-	243.31	221.27	Hinge:27
-	243.32	221.28	Hinge:28
-	243.33	221.29	Hinge:29
-	243.34	221.30	Hinge:30
-	243.35	221.31	Hinge:31
-	243.36	221.32	Hinge:32
-	243.37	221.33	Hinge:33
-	243.38	221.34	Hinge:34
-	243.39	221.35	Hinge:35
-	243.40	221.36	Hinge:36
-	243.41	221.37	Hinge:37
-	243.42	221.38	Hinge:38
-	243.43	221.39	Hinge:39
-	243.44	221.40	Hinge:40
-	243.45	221.41	Hinge:41
-	243.46	221.42	Hinge:42
-	243.47	221.43	Hinge:43
-	243.48	221.44	Hinge:44
-	243.49	221.45	Hinge:45
-	243.50	221.46	Hinge:46

FIG. 9 Continued

AB-007088_LS_Heavy Chain			
Residue	**Linear #**	**Mat. Linear #**	**ASN #**
-	243.51	221.47	Hinge:47
-	243.52	221.48	Hinge:48
-	243.53	221.49	Hinge:49
-	243.54	221.50	Hinge:50
-	243.55	221.51	Hinge:51
-	243.56	221.52	Hinge:52
-	243.57	221.53	Hinge:53
-	243.58	221.54	Hinge:54
-	243.59	221.55	Hinge:55
-	243.60	221.56	Hinge:56
-	243.61	221.57	Hinge:57
-	243.62	221.58	Hinge:58
-	243.63	221.59	Hinge:59
-	243.64	221.60	Hinge:60
-	243.65	221.61	Hinge:61
-	243.66	221.62	Hinge:62
-	243.67	221.63	Hinge:63
-	243.68	221.64	Hinge:64
-	243.69	221.65	Hinge:65
-	243.70	221.66	Hinge:66
-	243.71	221.67	Hinge:67
-	243.72	221.68	Hinge:68
-	243.73	221.69	Hinge:69
-	243.74	221.70	Hinge:70
-	243.75	221.71	Hinge:71
-	243.76	221.72	Hinge:72
-	243.77	221.73	Hinge:73
-	243.78	221.74	Hinge:74
-	243.79	221.75	Hinge:75
-	243.80	221.76	Hinge:76
-	243.81	221.77	Hinge:77
-	243.82	221.78	Hinge:78
-	243.83	221.79	Hinge:79
-	243.84	221.80	Hinge:80
-	243.85	221.81	Hinge:81
-	243.86	221.82	Hinge:82
-	243.87	221.83	Hinge:83
-	243.88	221.84	Hinge:84
-	243.89	221.85	Hinge:85
-	243.90	221.86	Hinge:86
-	243.91	221.87	Hinge:87
-	243.92	221.88	Hinge:88
-	243.93	221.89	Hinge:89

FIG. 9 Continued

AB-007088_LS_Heavy Chain			
Residue	**Linear #**	**Mat. Linear #**	**ASN #**
-	243.94	221.90	Hinge:90
-	243.95	221.91	Hinge:91
-	243.96	221.92	Hinge:92
-	243.97	221.93	Hinge:93
-	243.98	221.94	Hinge:94
-	243.99	221.95	Hinge:95
E	244	222	Hinge:96
P	245	223	Hinge:97
K	246	224	Hinge:98
S	247	225	Hinge:99
-	247.1	225.1	Hinge:100
-	247.2	225.2	Hinge:101
-	247.3	225.3	Hinge:102
-	247.4	225.4	Hinge:103
-	247.5	225.5	Hinge:104
-	247.6	225.6	Hinge:105
-	247.7	225.7	Hinge:106
C	248	226	Hinge:107
D	249	227	Hinge:108
K	250	228	Hinge:109
T	251	229	Hinge:110
H	252	230	Hinge:111
T	253	231	Hinge:112
C	254	232	Hinge:113
P	255	233	Hinge:114
P	256	234	Hinge:115
C	257	235	Hinge:116
P	258	236	Hinge:117
A	259	237	Hinge:118
P	260	238	Hinge:119
E	261	239	Hinge:120
L	262	240	Hinge:121
L	263	241	Hinge:122
G	264	242	Hinge:123
-	264.1	242.1	Fc-N:1
-	264.2	242.2	Fc-N:2
-	264.3	242.3	Fc-N:3
-	264.4	242.4	Fc-N:4
G	265	243	Fc-N:5
P	266	244	Fc-N:6
S	267	245	Fc-N:7
V	268	246	Fc-N:8
F	269	247	Fc-N:9

FIG. 9 Continued

AB-007088_LS_Heavy Chain			
Residue	Linear #	Mat. Linear #	ASN #
L	270	248	Fc-N:10
F	271	249	Fc-N:11
P	272	250	Fc-N:12
P	273	251	Fc-N:13
-	273.1	251.1	Fc-N:14
K	274	252	Fc-N:15
P	275	253	Fc-N:16
K	276	254	Fc-N:17
-	276.1	254.1	Fc-N:18
D	277	255	Fc-N:19
T	278	256	Fc-N:20
L	279	257	Fc-N:21
M	280	258	Fc-N:22
I	281	259	Fc-N:23
S	282	260	Fc-N:24
R	283	261	Fc-N:25
T	284	262	Fc-N:26
P	285	263	Fc-N:27
E	286	264	Fc-N:28
V	287	265	Fc-N:29
T	288	266	Fc-N:30
C	289	267	Fc-N:31
V	290	268	Fc-N:32
V	291	269	Fc-N:33
V	292	270	Fc-N:34
D	293	271	Fc-N:35
V	294	272	Fc-N:36
S	295	273	Fc-N:37
H	296	274	Fc-N:38
E	297	275	Fc-N:39
D	298	276	Fc-N:40
P	299	277	Fc-N:41
E	300	278	Fc-N:42
V	301	279	Fc-N:43
K	302	280	Fc-N:44
F	303	281	Fc-N:45
N	304	282	Fc-N:46
W	305	283	Fc-N:47
-	305.1	283.1	Fc-N:48
Y	306	284	Fc-N:49
V	307	285	Fc-N:50
D	308	286	Fc-N:51
G	309	287	Fc-N:52

FIG. 9 Continued

AB-007088_LS_Heavy Chain			
Residue	Linear #	Mat. Linear #	ASN #
V	310	288	Fc-N:53
E	311	289	Fc-N:54
-	311.1	289.1	Fc-N:55
-	311.2	289.2	Fc-N:56
V	312	290	Fc-N:57
H	313	291	Fc-N:58
N	314	292	Fc-N:59
A	315	293	Fc-N:60
K	316	294	Fc-N:61
T	317	295	Fc-N:62
K	318	296	Fc-N:63
P	319	297	Fc-N:64
R	320	298	Fc-N:65
E	321	299	Fc-N:66
E	322	300	Fc-N:67
Q	323	301	Fc-N:68
-	323.1	301.1	Fc-N:69
-	323.2	301.2	Fc-N:70
-	323.3	301.3	Fc-N:71
-	323.4	301.4	Fc-N:72
Y	324	302	Fc-N:73
N	325	303	Fc-N:74
S	326	304	Fc-N:75
T	327	305	Fc-N:76
Y	328	306	Fc-N:77
R	329	307	Fc-N:78
V	330	308	Fc-N:79
V	331	309	Fc-N:80
S	332	310	Fc-N:81
V	333	311	Fc-N:82
L	334	312	Fc-N:83
T	335	313	Fc-N:84
V	336	314	Fc-N:85
L	337	315	Fc-N:86
H	338	316	Fc-N:87
Q	339	317	Fc-N:88
D	340	318	Fc-N:89
W	341	319	Fc-N:90
-	341.1	319.1	Fc-N:91
L	342	320	Fc-N:92
N	343	321	Fc-N:93
G	344	322	Fc-N:94
K	345	323	Fc-N:95

FIG. 9 Continued

AB-007088_LS_Heavy Chain			
Residue	Linear #	Mat. Linear #	ASN #
E	346	324	Fc-N:96
-	346.1	324.1	Fc-N:97
-	346.2	324.2	Fc-N:98
Y	347	325	Fc-N:99
K	348	326	Fc-N:100
C	349	327	Fc-N:101
K	350	328	Fc-N:102
V	351	329	Fc-N:103
S	352	330	Fc-N:104
N	353	331	Fc-N:105
K	354	332	Fc-N:106
A	355	333	Fc-N:107
L	356	334	Fc-N:108
P	357	335	Fc-N:109
-	357.1	335.1	Fc-N:110
-	357.2	335.2	Fc-N:111
A	358	336	Fc-N:112
P	359	337	Fc-N:113
I	360	338	Fc-N:114
E	361	339	Fc-N:115
K	362	340	Fc-N:116
T	363	341	Fc-N:117
I	364	342	Fc-N:118
S	365	343	Fc-N:119
K	366	344	Fc-N:120
A	367	345	Fc-N:121
K	368	346	Fc-N:122
G	369	347	Fc-N:123
-	369.1	347.1	Fc-C:1
Q	370	348	Fc-C:2
P	371	349	Fc-C:3
R	372	350	Fc-C:4
E	373	351	Fc-C:5
P	374	352	Fc-C:6
Q	375	353	Fc-C:7
V	376	354	Fc-C:8
Y	377	355	Fc-C:9
T	378	356	Fc-C:10
L	379	357	Fc-C:11
P	380	358	Fc-C:12
P	381	359	Fc-C:13
-	381.1	359.1	Fc-C:14
S	382	360	Fc-C:15

FIG. 9 Continued

AB-007088_LS_Heavy Chain			
Residue	Linear #	Mat. Linear #	ASN #
R	383	361	Fc-C:16
D	384	362	Fc-C:17
-	384.1	362.1	Fc-C:18
E	385	363	Fc-C:19
L	386	364	Fc-C:20
-	386.1	364.1	Fc-C:21
-	386.2	364.2	Fc-C:22
T	387	365	Fc-C:23
K	388	366	Fc-C:24
N	389	367	Fc-C:25
Q	390	368	Fc-C:26
V	391	369	Fc-C:27
S	392	370	Fc-C:28
L	393	371	Fc-C:29
T	394	372	Fc-C:30
C	395	373	Fc-C:31
L	396	374	Fc-C:32
V	397	375	Fc-C:33
K	398	376	Fc-C:34
G	399	377	Fc-C:35
F	400	378	Fc-C:36
Y	401	379	Fc-C:37
P	402	380	Fc-C:38
-	402.1	380.1	Fc-C:39
-	402.2	380.2	Fc-C:40
S	403	381	Fc-C:41
D	404	382	Fc-C:42
I	405	383	Fc-C:43
A	406	384	Fc-C:44
V	407	385	Fc-C:45
E	408	386	Fc-C:46
W	409	387	Fc-C:47
-	409.1	387.1	Fc-C:48
E	410	388	Fc-C:49
S	411	389	Fc-C:50
N	412	390	Fc-C:51
G	413	391	Fc-C:52
Q	414	392	Fc-C:53
P	415	393	Fc-C:54
-	415.1	393.1	Fc-C:55
-	415.2	393.2	Fc-C:56
E	416	394	Fc-C:57
N	417	395	Fc-C:58

FIG. 9 Continued

AB-007088_LS_Heavy Chain			
Residue	Linear #	Mat. Linear #	ASN #
N	418	396	Fc-C:59
Y	419	397	Fc-C:60
K	420	398	Fc-C:61
T	421	399	Fc-C:62
T	422	400	Fc-C:63
P	423	401	Fc-C:64
P	424	402	Fc-C:65
V	425	403	Fc-C:66
L	426	404	Fc-C:67
D	427	405	Fc-C:68
-	427.1	405.1	Fc-C:69
-	427.2	405.2	Fc-C:70
-	427.3	405.3	Fc-C:71
-	427.4	405.4	Fc-C:72
S	428	406	Fc-C:73
D	429	407	Fc-C:74
G	430	408	Fc-C:75
S	431	409	Fc-C:76
F	432	410	Fc-C:77
F	433	411	Fc-C:78
L	434	412	Fc-C:79
Y	435	413	Fc-C:80
S	436	414	Fc-C:81
K	437	415	Fc-C:82
L	438	416	Fc-C:83
T	439	417	Fc-C:84
V	440	418	Fc-C:85
D	441	419	Fc-C:86
K	442	420	Fc-C:87
S	443	421	Fc-C:88
R	444	422	Fc-C:89
W	445	423	Fc-C:90
-	445.1	423.1	Fc-C:91
Q	446	424	Fc-C:92
Q	447	425	Fc-C:93
G	448	426	Fc-C:94
N	449	427	Fc-C:95
V	450	428	Fc-C:96
-	450.1	428.1	Fc-C:97
-	450.2	428.2	Fc-C:98
F	451	429	Fc-C:99
S	452	430	Fc-C:100
C	453	431	Fc-C:101

FIG. 9 Continued

AB-007088_LS_Heavy Chain			
Residue	Linear #	Mat. Linear #	ASN #
S	454	432	Fc-C:102
V	455	433	Fc-C:103
L	456	434	Fc-C:104
H	457	435	Fc-C:105
E	458	436	Fc-C:106
A	459	437	Fc-C:107
L	460	438	Fc-C:108
H	461	439	Fc-C:109
-	461.1	439.1	Fc-C:110
-	461.2	439.2	Fc-C:111
S	462	440	Fc-C:112
H	463	441	Fc-C:113
Y	464	442	Fc-C:114
T	465	443	Fc-C:115
-	465.1	443.1	Fc-C:116
Q	466	444	Fc-C:117
K	467	445	Fc-C:118
S	468	446	Fc-C:119
L	469	447	Fc-C:120
S	470	448	Fc-C:121
L	471	449	Fc-C:122
S	472	450	Fc-C:123
P	473	451	HCnst-Po:1
G	474	452	HCnst-Po:2
K	475	453	HCnst-Po:3
-	475.1	453.1	HCnst-Po:4
-	475.2	453.2	HCnst-Po:5
-	475.3	453.3	HCnst-Po:6
-	475.4	453.4	HCnst-Po:7
-	475.5	453.5	HCnst-Po:8
-	475.6	453.6	HCnst-Po:9
-	475.7	453.7	HCnst-Po:10
-	475.8	453.8	HCnst-Po:11
-	475.9	453.9	HCnst-Po:12
-	475.10	453.10	HCnst-Po:13
-	475.11	453.11	HCnst-Po:14
-	475.12	453.12	HCnst-Po:15
-	475.13	453.13	HCnst-Po:16
-	475.14	453.14	HCnst-Po:17
-	475.15	453.15	HCnst-Po:18
-	475.16	453.16	HCnst-Po:19
-	475.17	453.17	HCnst-Po:20
-	475.18	453.18	HCnst-Po:21

FIG. 9 Continued

AB-007088_LS_Heavy Chain			
Residue	Linear #	Mat. Linear #	ASN #
-	475.19	453.19	HCnst-Po:22
-	475.20	453.20	HCnst-Po:23
-	475.21	453.21	HCnst-Po:24
-	475.22	453.22	HCnst-Po:25
-	475.23	453.23	HCnst-Po:26
-	475.24	453.24	HCnst-Po:27
-	475.25	453.25	HCnst-Po:28
-	475.26	453.26	HCnst-Po:29
-	475.27	453.27	HCnst-Po:30
-	475.28	453.28	HCnst-Po:31
-	475.29	453.29	HCnst-Po:32
-	475.30	453.30	HCnst-Po:33
-	475.31	453.31	HCnst-Po:34
-	475.32	453.32	HCnst-Po:35
-	475.33	453.33	HCnst-Po:36
-	475.34	453.34	HCnst-Po:37
-	475.35	453.35	HCnst-Po:38
-	475.36	453.36	HCnst-Po:39
-	475.37	453.37	HCnst-Po:40
-	475.38	453.38	HCnst-Po:41
-	475.39	453.39	HCnst-Po:42
-	475.40	453.40	HCnst-Po:43
-	475.41	453.41	HCnst-Po:44
-	475.42	453.42	HCnst-Po:45
-	475.43	453.43	HCnst-Po:46
-	475.44	453.44	HCnst-Po:47
-	475.45	453.45	HCnst-Po:48
-	475.46	453.46	HCnst-Po:49
-	475.47	453.47	HCnst-Po:50
-	475.48	453.48	HCnst-Po:51
-	475.49	453.49	HCnst-Po:52
-	475.50	453.50	HCnst-Po:53
-	475.51	453.51	HCnst-Po:54
-	475.52	453.52	HCnst-Po:55
-	475.53	453.53	HCnst-Po:56
-	475.54	453.54	HCnst-Po:57
-	475.55	453.55	HCnst-Po:58
-	475.56	453.56	HCnst-Po:59
-	475.57	453.57	HCnst-Po:60
-	475.58	453.58	HCnst-Po:61
-	475.59	453.59	HCnst-Po:62
-	475.60	453.60	HCnst-Po:63
-	475.61	453.61	HCnst-Po:64

FIG. 9 Continued

AB-007088_LS_Heavy Chain			
Residue	**Linear #**	**Mat. Linear #**	**ASN #**
-	475.62	453.62	HCnst-Po:65
-	475.63	453.63	HCnst-Po:66
-	475.64	453.64	HCnst-Po:67
-	475.65	453.65	HCnst-Po:68
-	475.66	453.66	HCnst-Po:69
-	475.67	453.67	HCnst-Po:70
-	475.68	453.68	HCnst-Po:71
-	475.69	453.69	HCnst-Po:72
-	475.70	453.70	HCnst-Po:73
-	475.71	453.71	HCnst-Po:74
-	475.72	453.72	HCnst-Po:75
-	475.73	453.73	HCnst-Po:76
-	475.74	453.74	HCnst-Po:77
-	475.75	453.75	HCnst-Po:78
-	475.76	453.76	HCnst-Po:79
-	475.77	453.77	HCnst-Po:80
-	475.78	453.78	HCnst-Po:81
-	475.79	453.79	HCnst-Po:82
-	475.80	453.80	HCnst-Po:83
-	475.81	453.81	HCnst-Po:84
-	475.82	453.82	HCnst-Po:85
-	475.83	453.83	HCnst-Po:86
-	475.84	453.84	HCnst-Po:87
-	475.85	453.85	HCnst-Po:88
-	475.86	453.86	HCnst-Po:89
-	475.87	453.87	HCnst-Po:90
-	475.88	453.88	HCnst-Po:91
-	475.89	453.89	HCnst-Po:92
-	475.90	453.90	HCnst-Po:93
-	475.91	453.91	HCnst-Po:94
-	475.92	453.92	HCnst-Po:95
-	475.93	453.93	HCnst-Po:96
-	475.94	453.94	HCnst-Po:97
-	475.95	453.95	HCnst-Po:98
-	475.96	453.96	HCnst-Po:99
-	475.97	453.97	HCnst-Po:100
-	475.98	453.98	HCnst-Po:101
-	475.99	453.99	HCnst-Po:102
-	475.100	453.100	HCnst-Po:103
-	475.101	453.101	HCnst-Po:104
-	475.102	453.102	HCnst-Po:105
-	475.103	453.103	HCnst-Po:106
-	475.104	453.104	HCnst-Po:107

FIG. 9 Continued

AB-007088_LS_Heavy Chain			
Residue	**Linear #**	**Mat. Linear #**	**ASN #**
-	475.105	453.105	HCnst-Po:108
-	475.106	453.106	HCnst-Po:109
-	475.107	453.107	HCnst-Po:110
-	475.108	453.108	HCnst-Po:111
-	475.109	453.109	HCnst-Po:112
-	475.110	453.110	HCnst-Po:113
-	475.111	453.111	HCnst-Po:114
-	475.112	453.112	HCnst-Po:115
-	475.113	453.113	HCnst-Po:116
-	475.114	453.114	HCnst-Po:117
-	475.115	453.115	HCnst-Po:118
-	475.116	453.116	HCnst-Po:119
-	475.117	453.117	HCnst-Po:120
-	475.118	453.118	HCnst-Po:121
-	475.119	453.119	HCnst-Po:122
-	475.120	453.120	HCnst-Po:123

FIG. 9 Continued

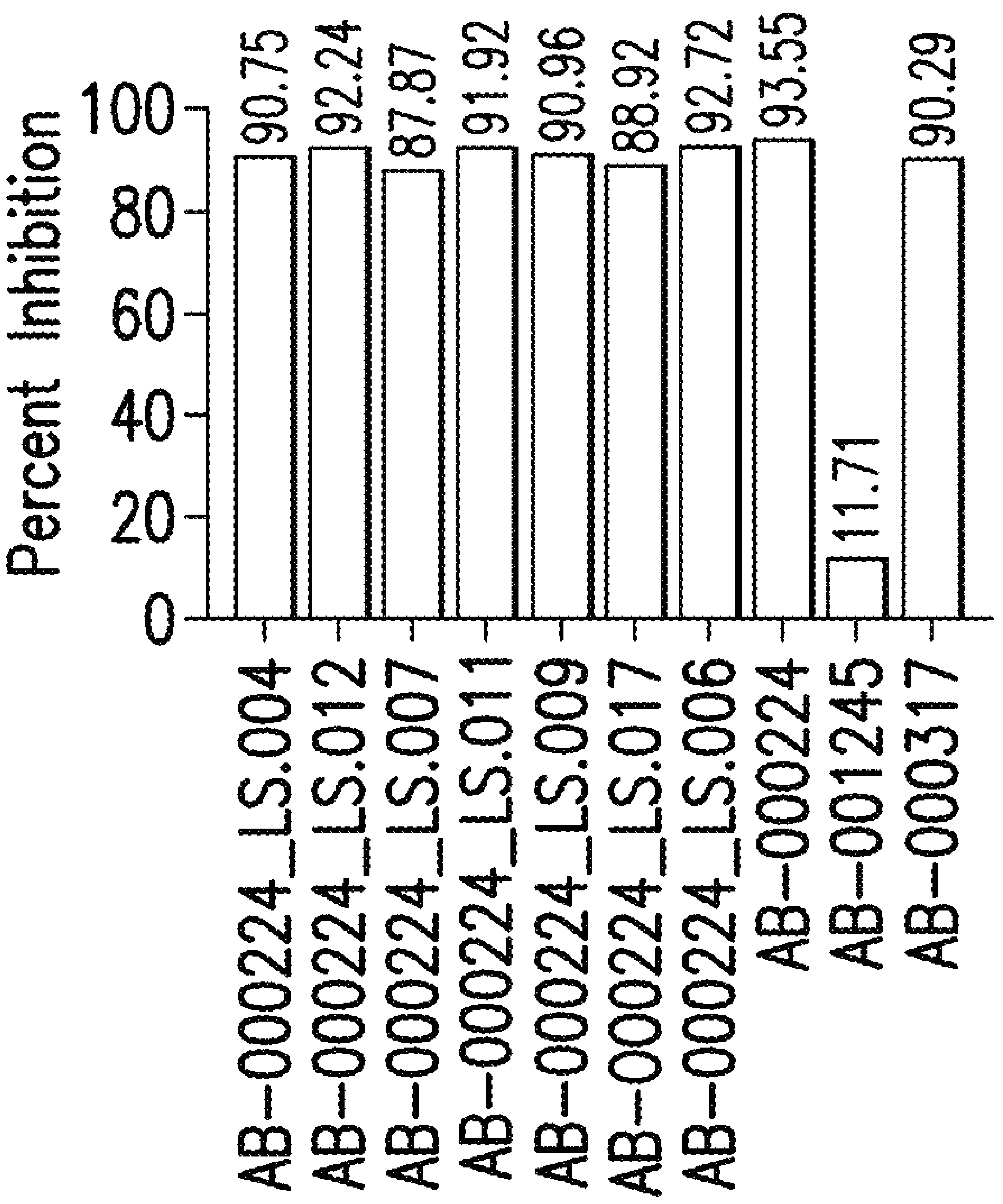


FIG. 10A

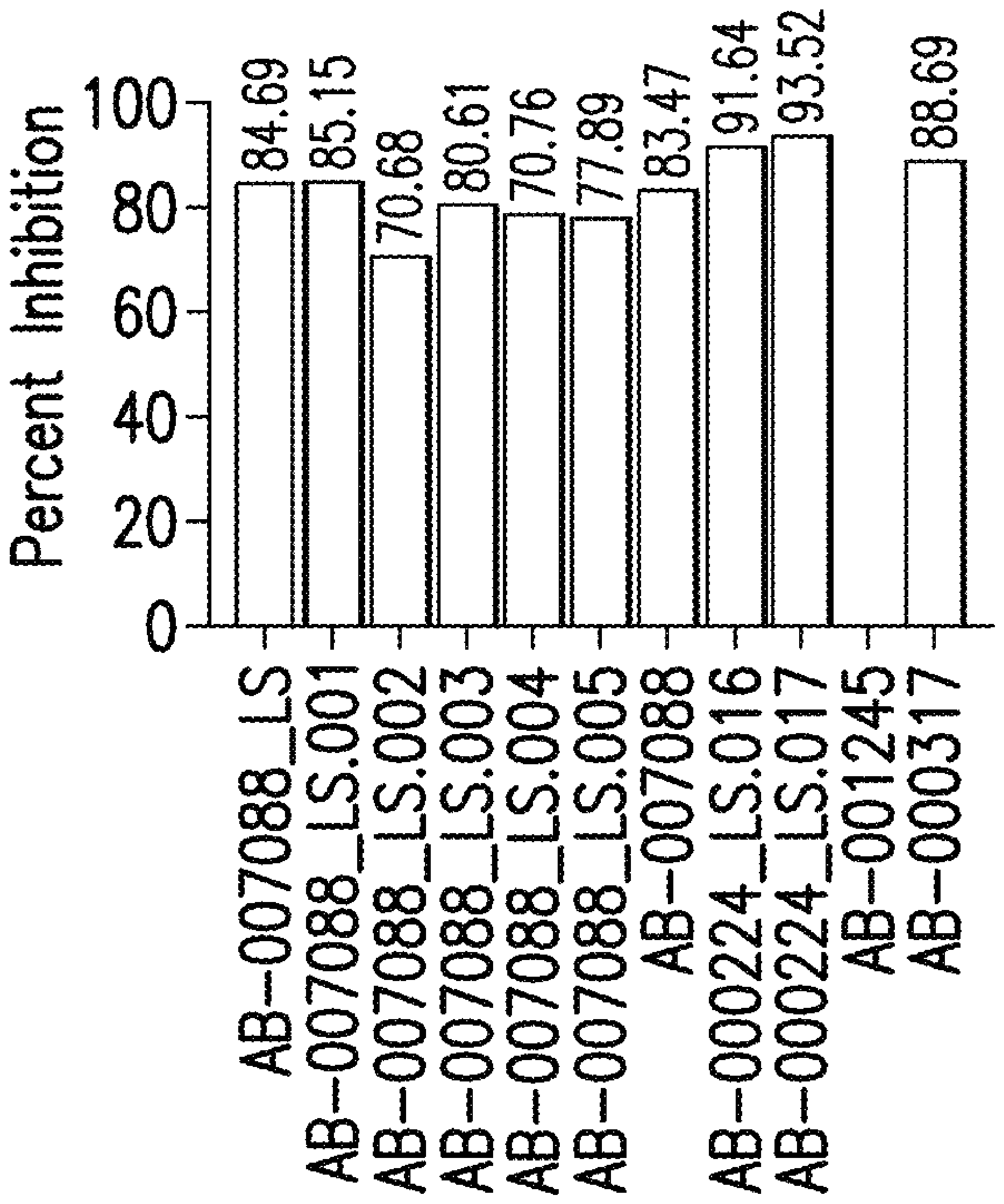


FIG. 10B

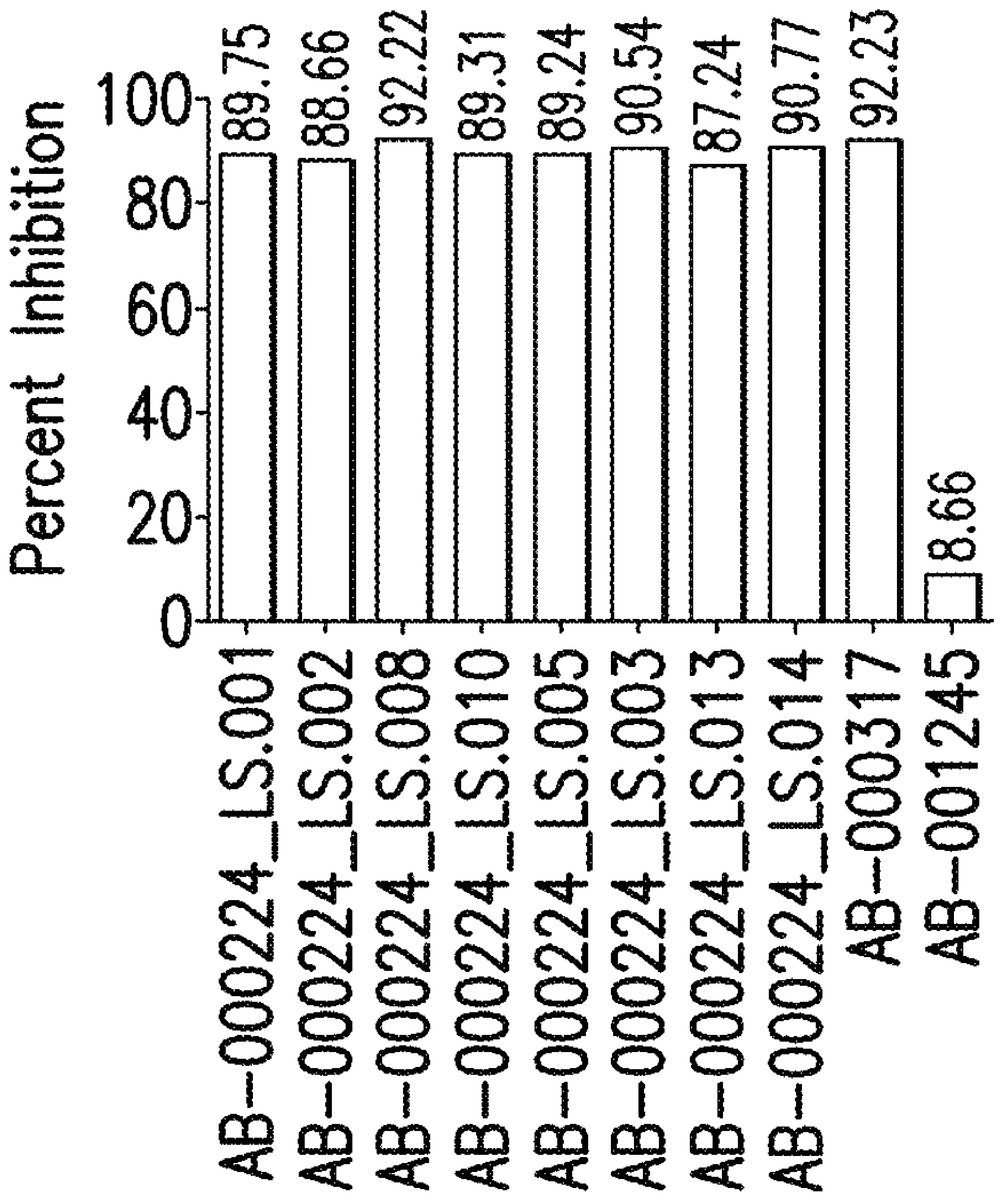


FIG. 10C

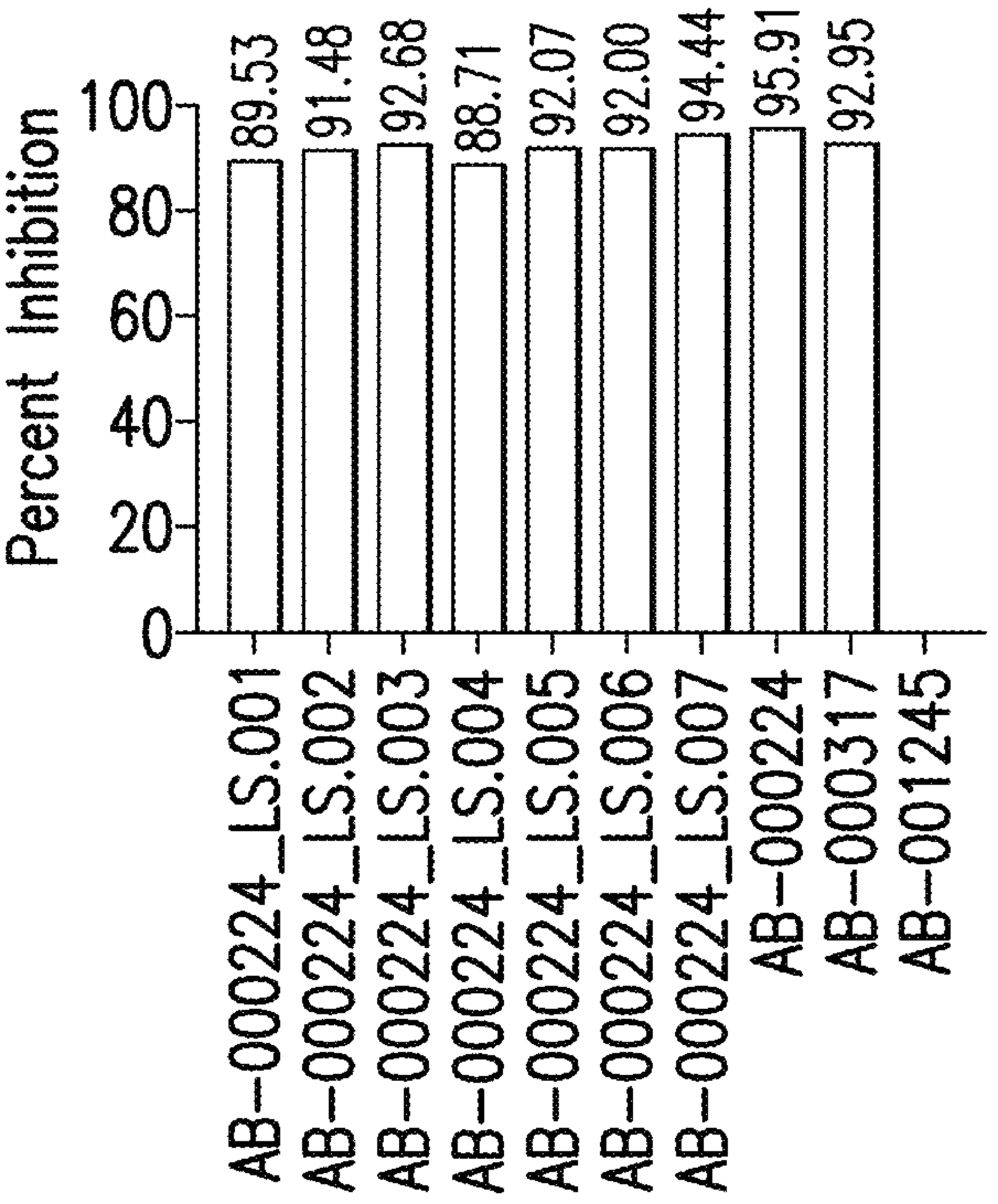


FIG. 10D

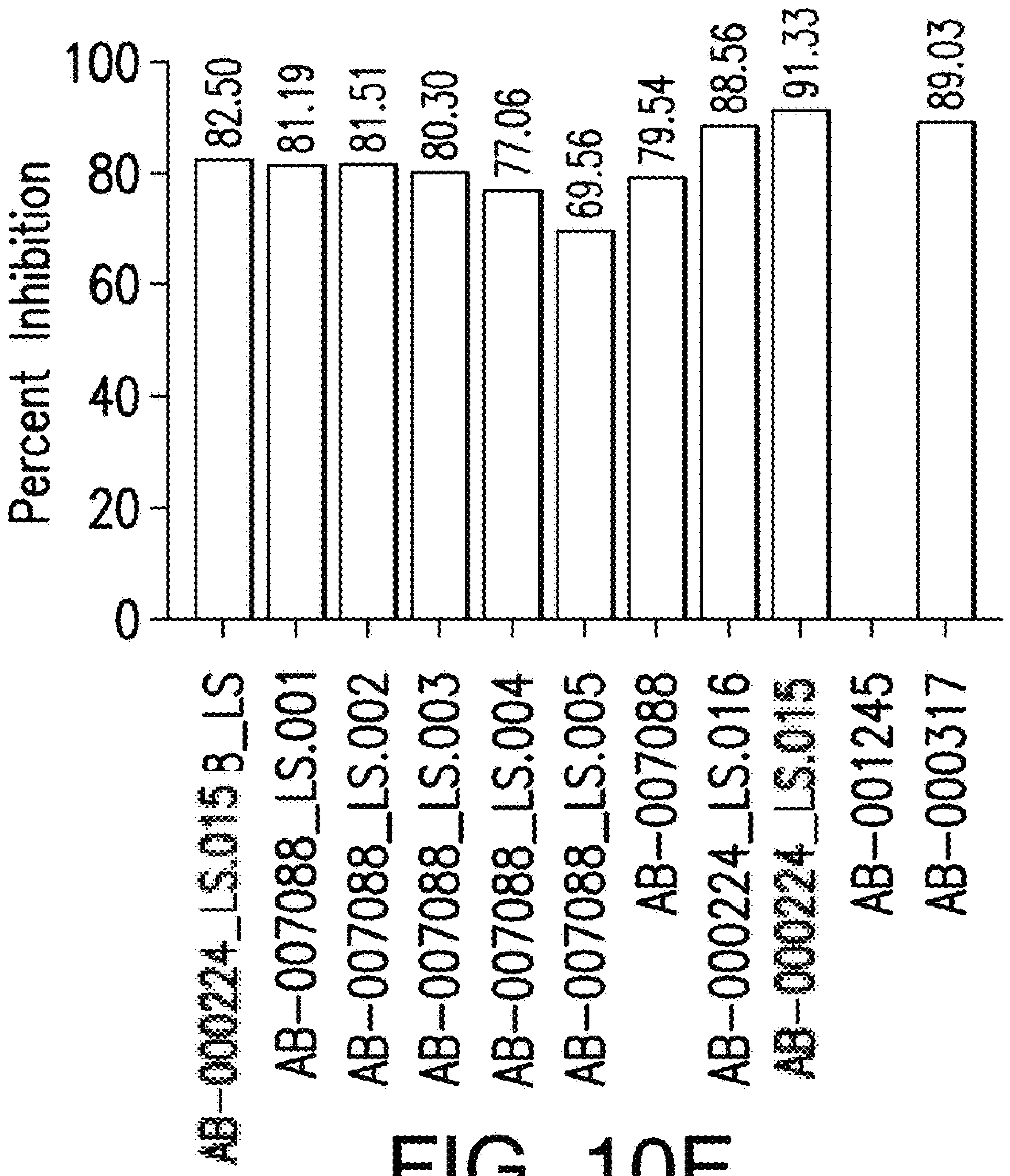


FIG. 10E

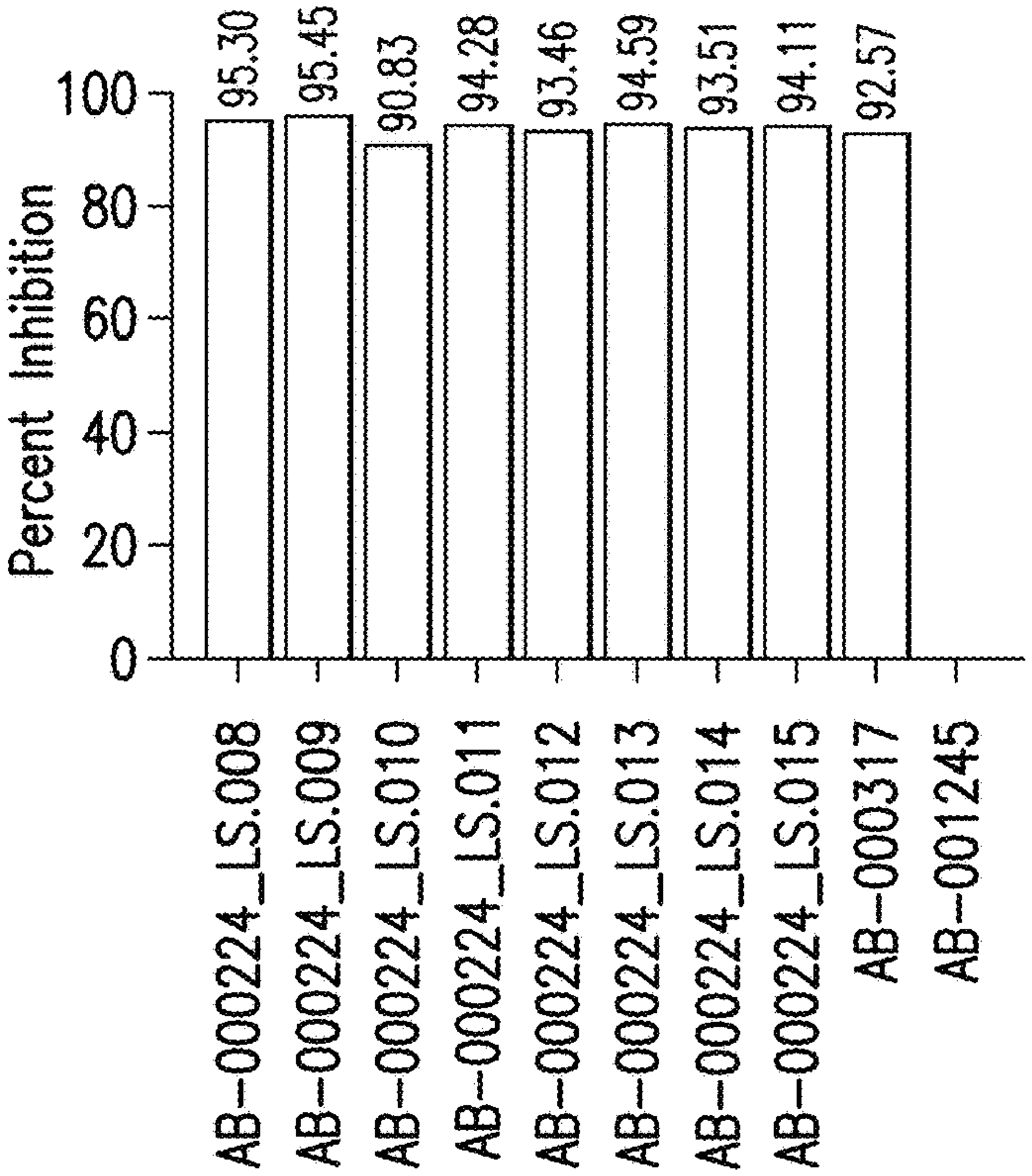


FIG. 10F

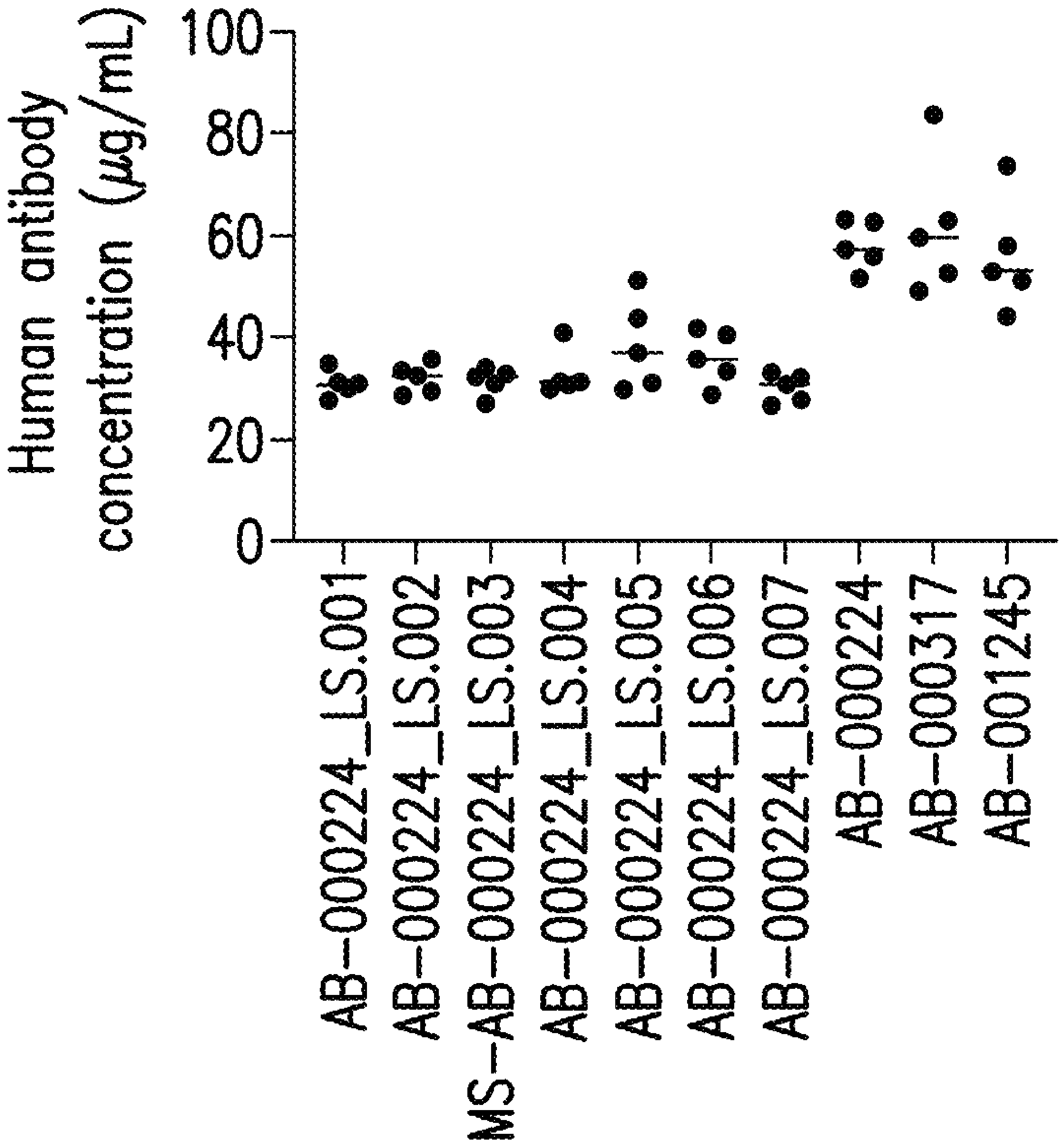


FIG. 10G

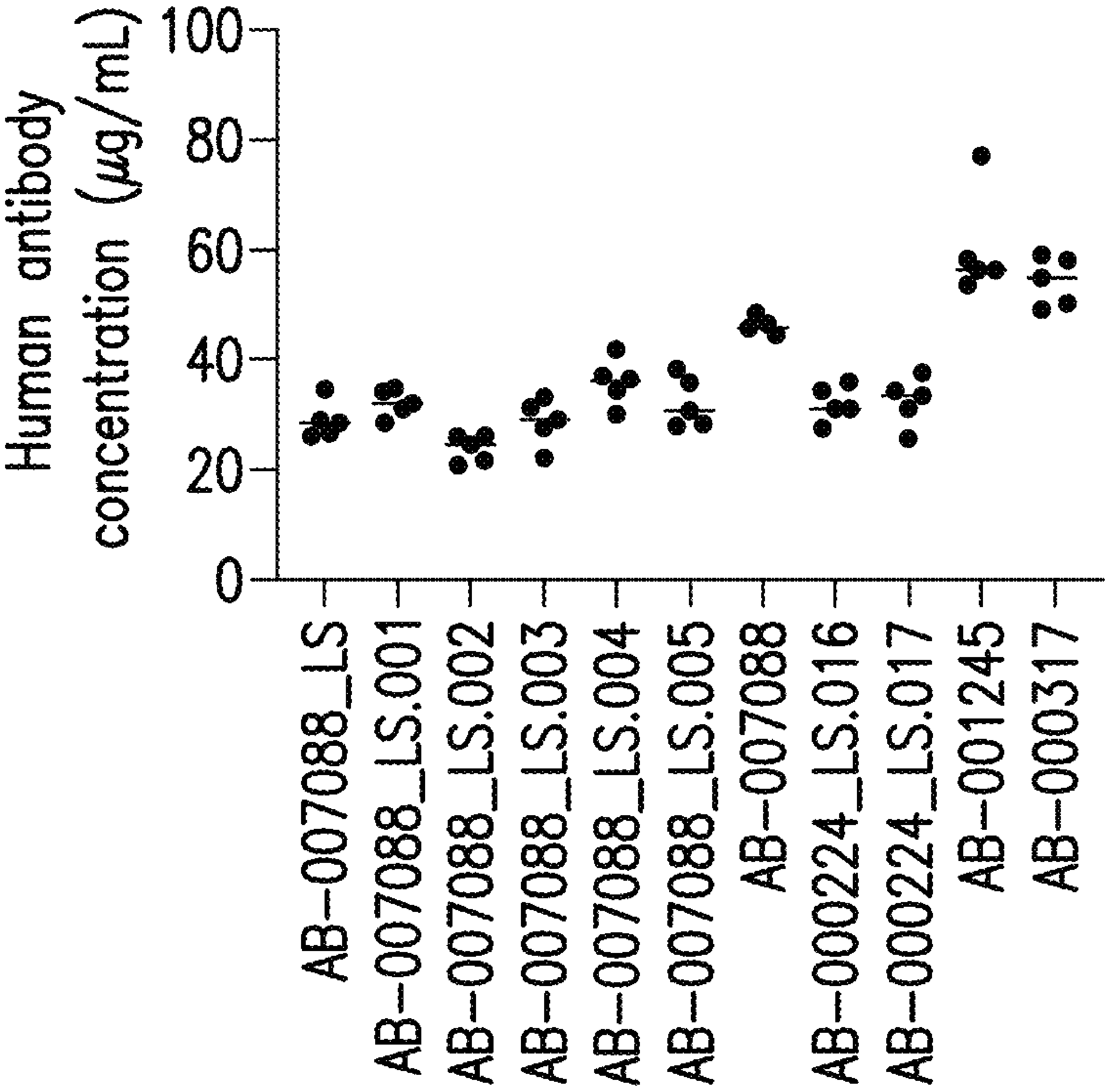


FIG. 10H

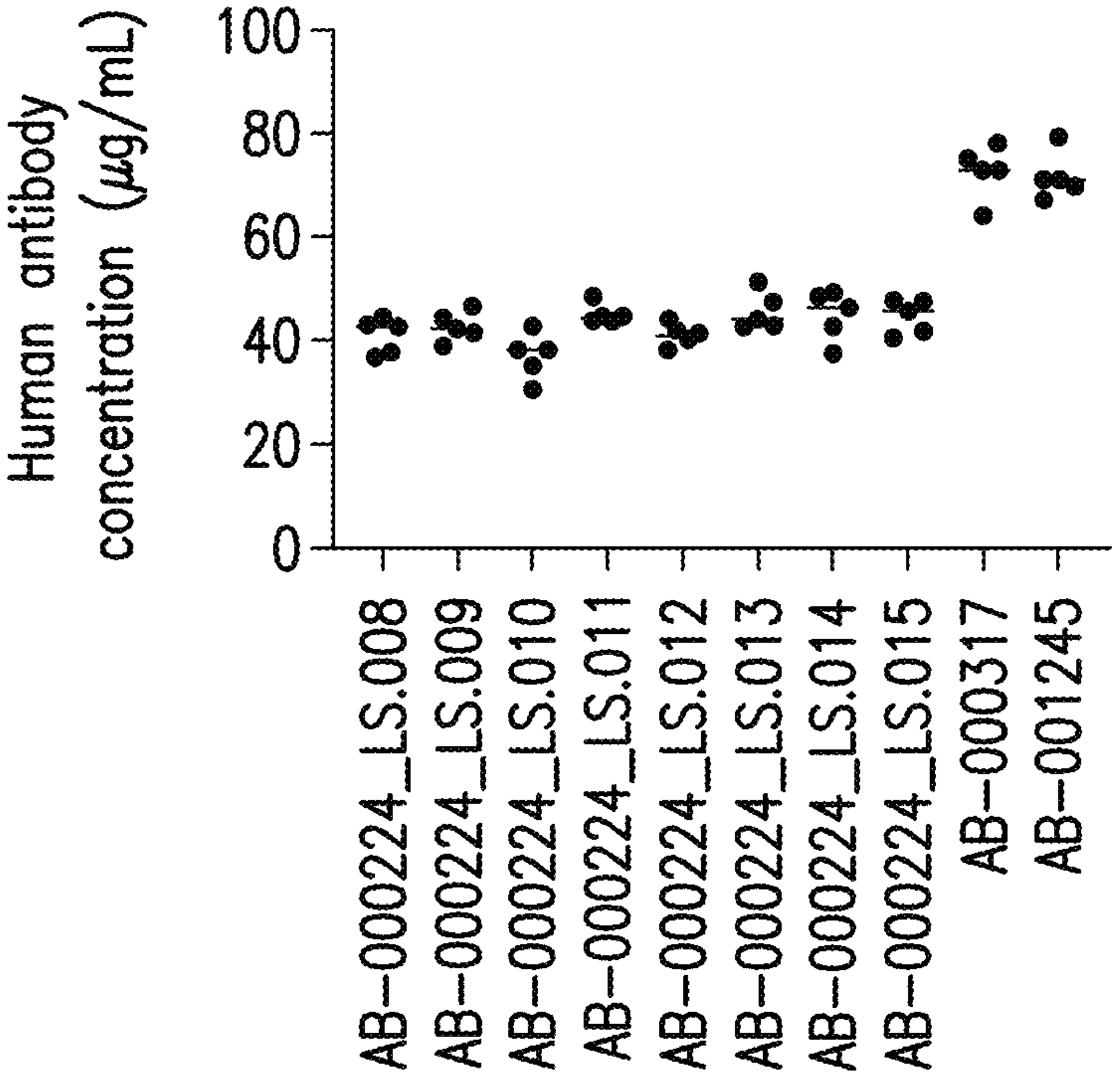

Human antibody concentration (μg/mL)
100
80
60
40
20
0
AB-000224_LS.008
AB-000224_LS.009
AB-000224_LS.010
AB-000224_LS.011
AB-000224_LS.012
AB-000224_LS.013
AB-000224_LS.014
AB-000224_LS.015
AB-000317
AB-001245

FIG. 10I

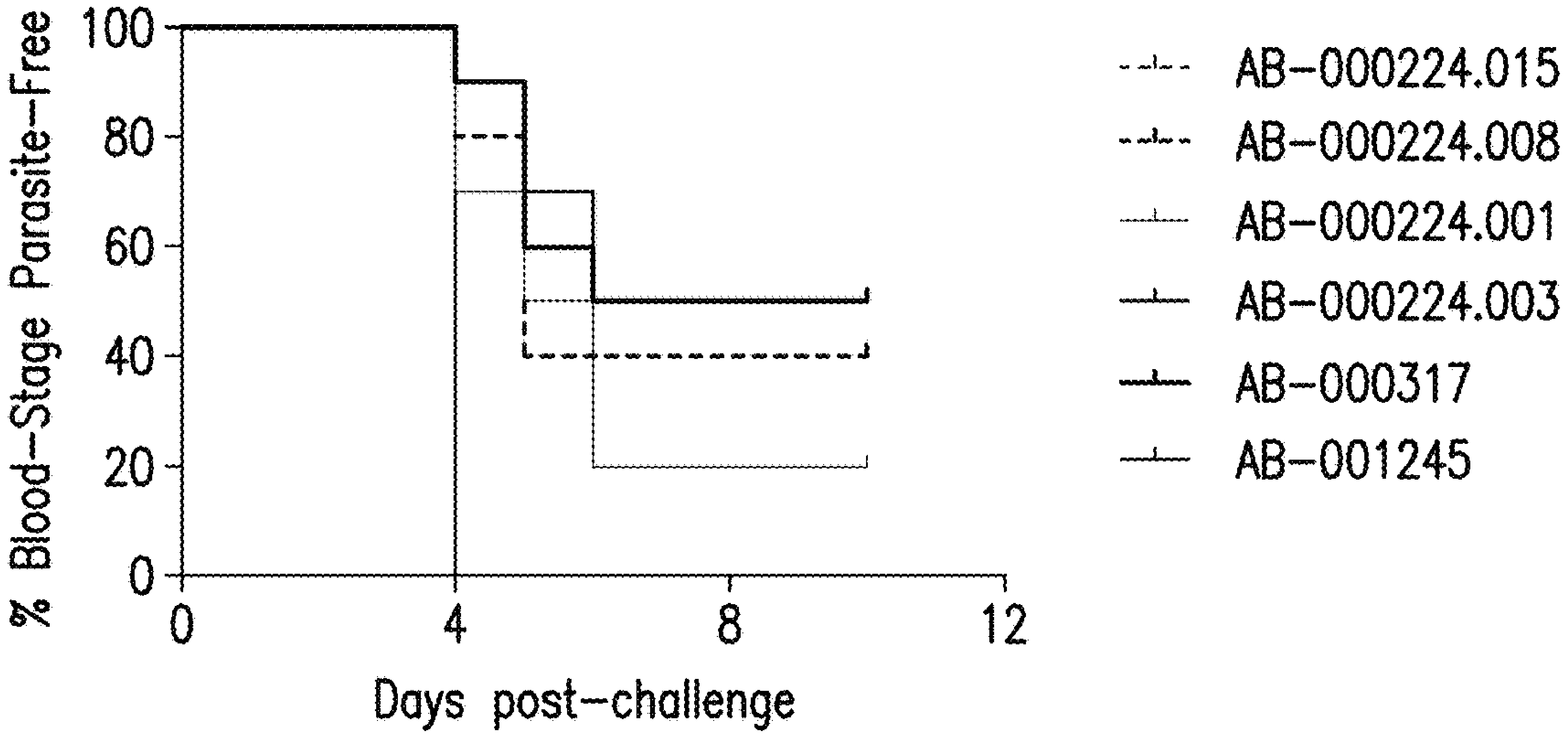


FIG. 11A

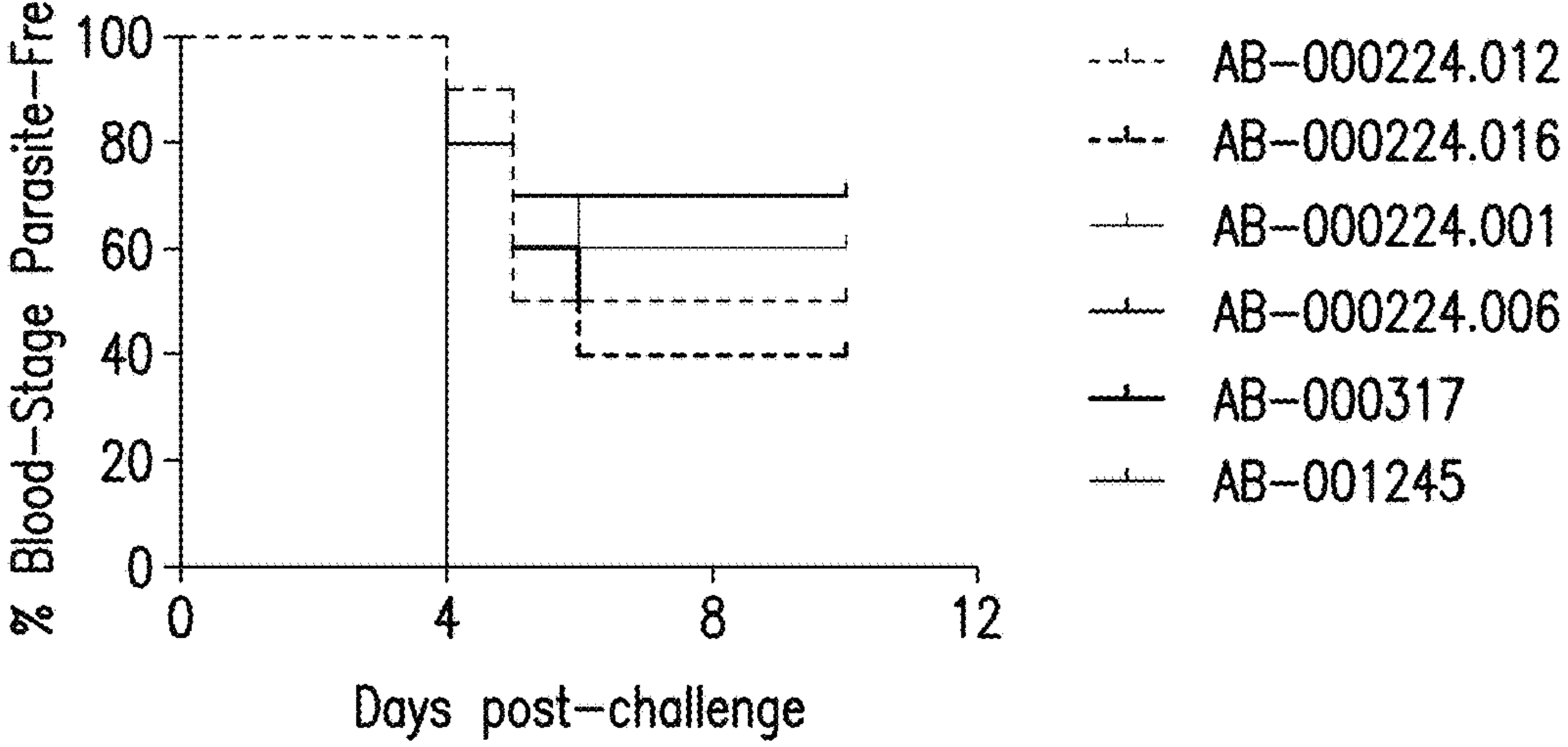


FIG. 11B

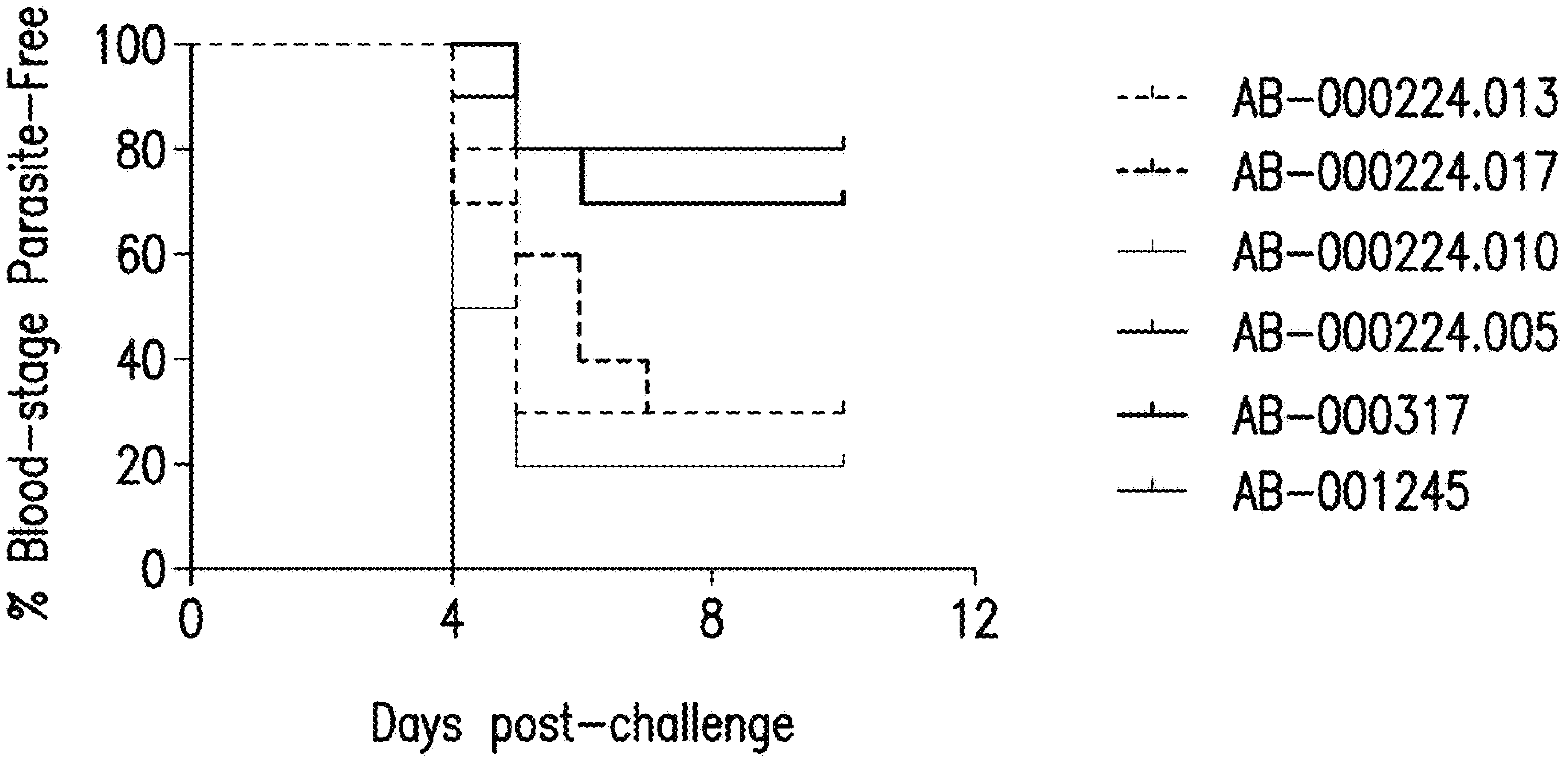


FIG. 11C

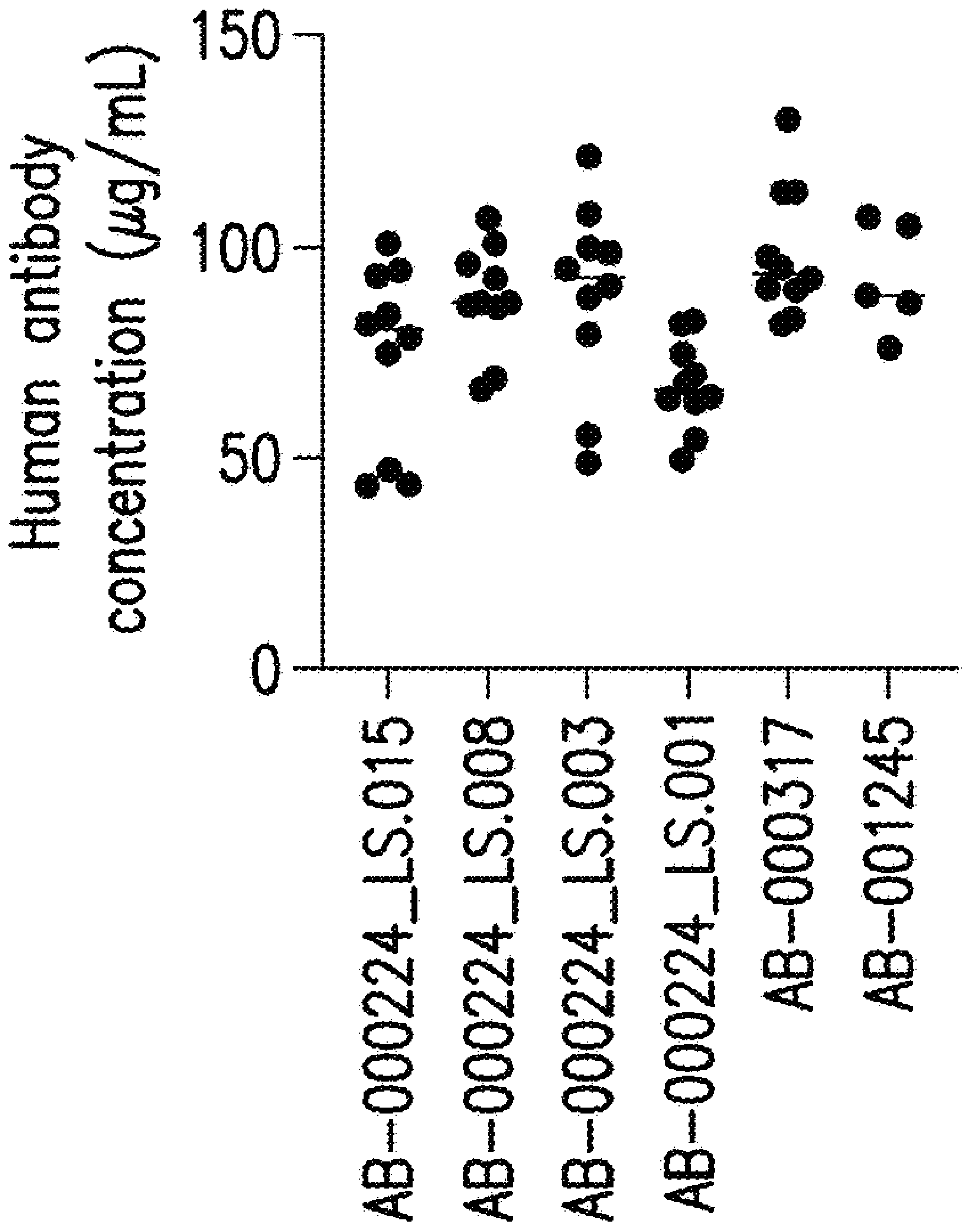


FIG. 11D

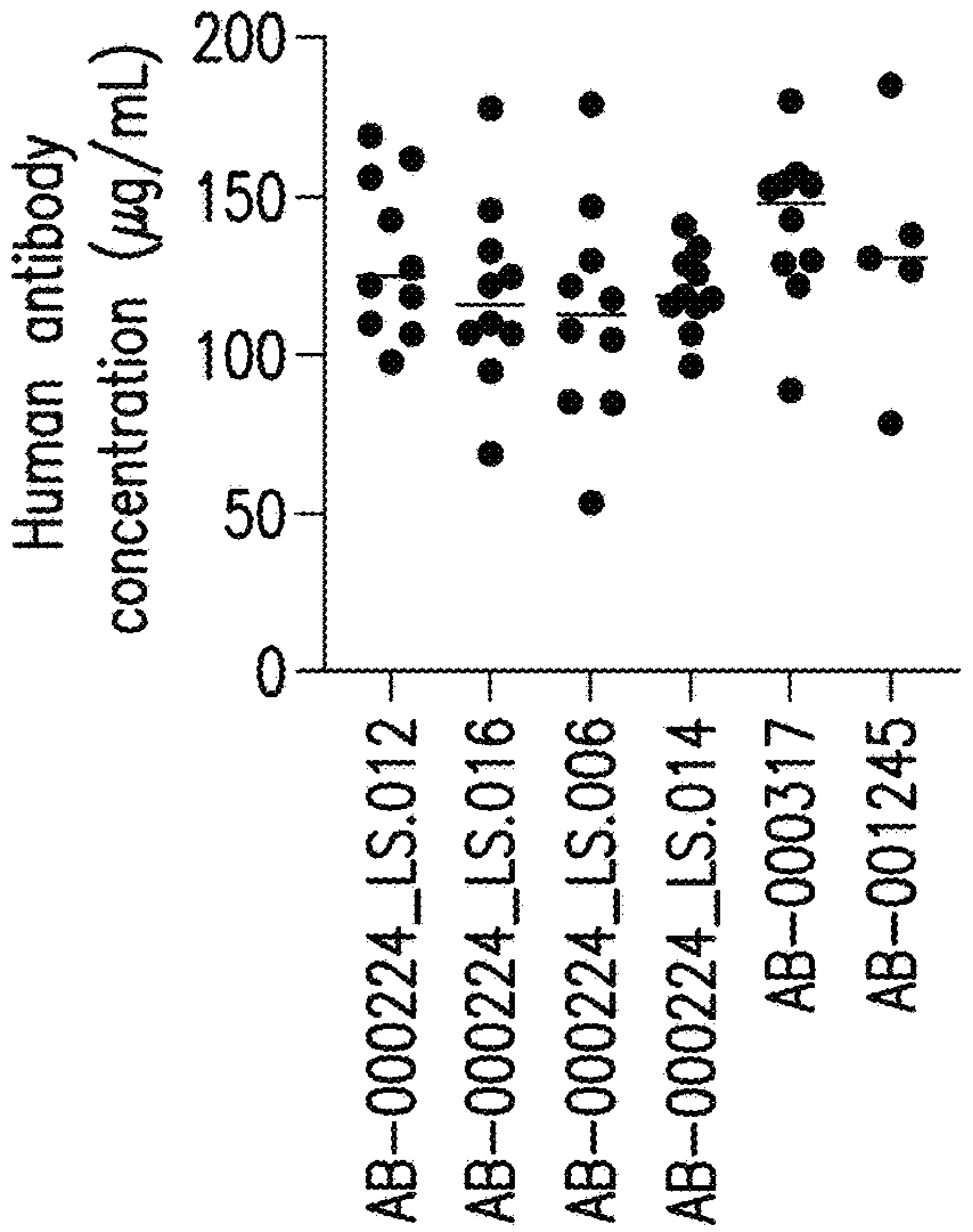


FIG. 11E

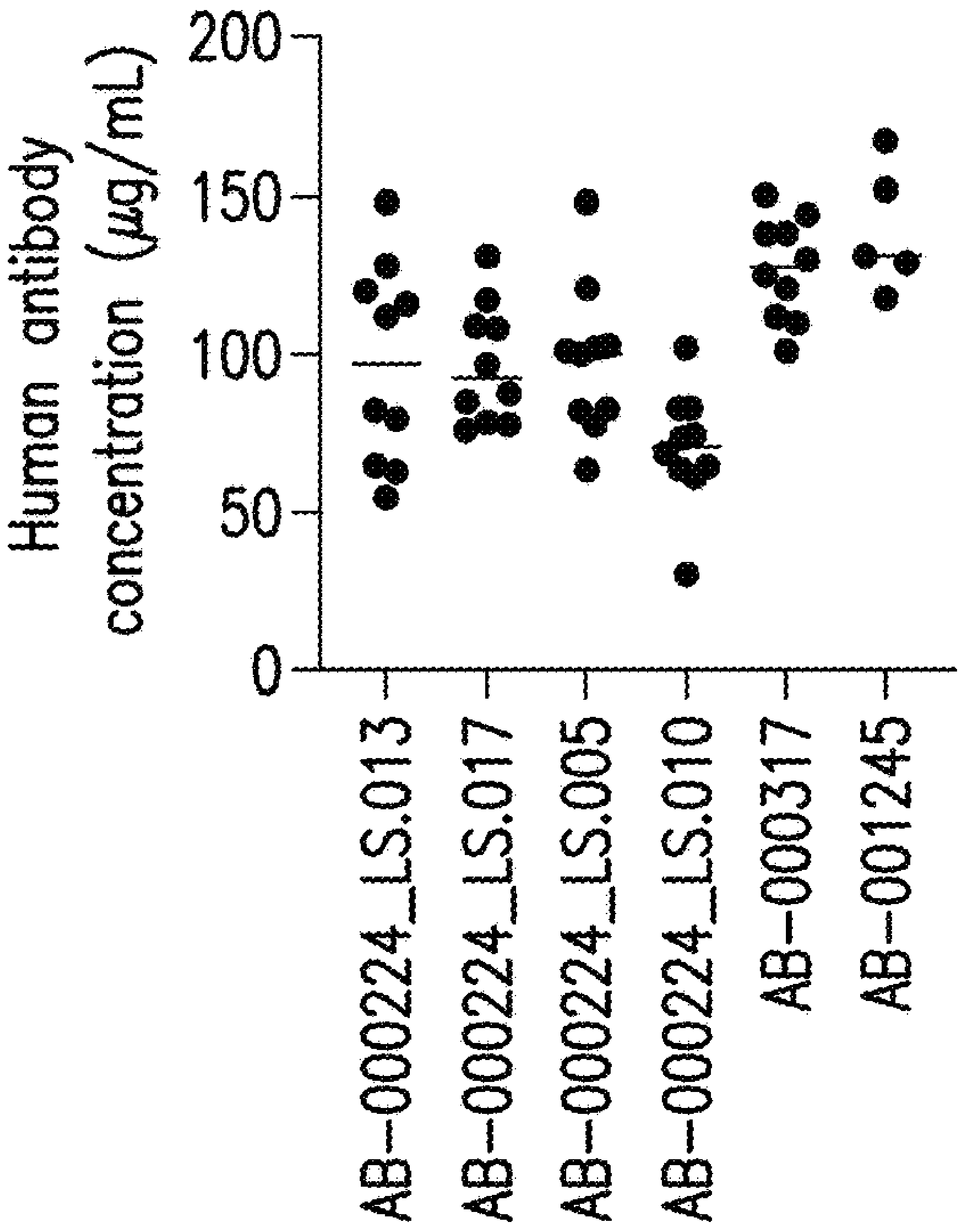


FIG. 11F

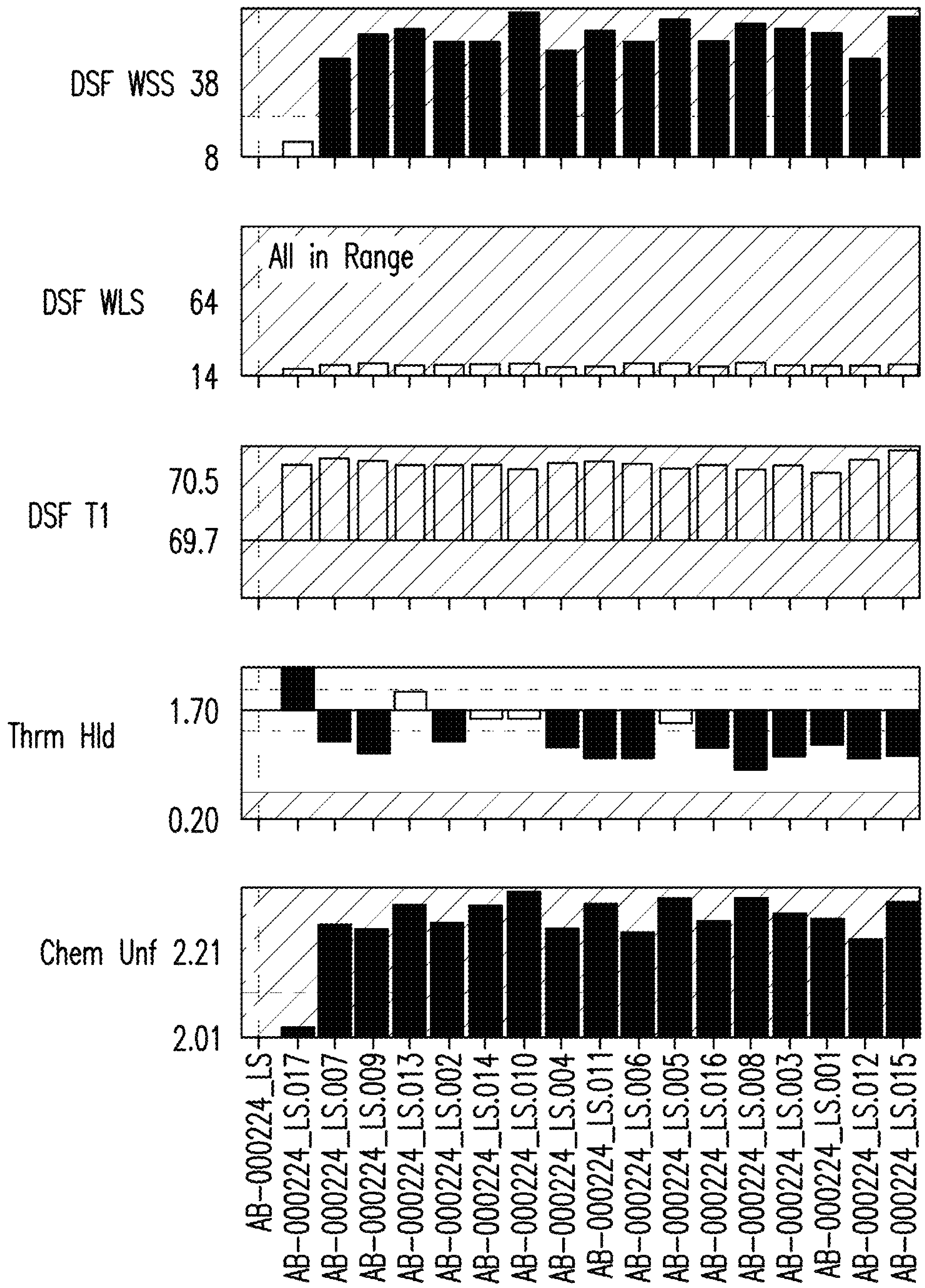

DSF WSS 38
8
DSF WLS 64
14
All in Range
DSF T1
70.5
69.7
Thrm Hld
1.70
0.20
Chem Unf 2.21
2.01
AB-000224_LS
AB-000224_LS.017
AB-000224_LS.007
AB-000224_LS.009
AB-000224_LS.013
AB-000224_LS.002
AB-000224_LS.014
AB-000224_LS.010
AB-000224_LS.004
AB-000224_LS.011
AB-000224_LS.006
AB-000224_LS.005
AB-000224_LS.016
AB-000224_LS.008
AB-000224_LS.003
AB-000224_LS.001
AB-000224_LS.012
AB-000224_LS.015

FIG. 12A

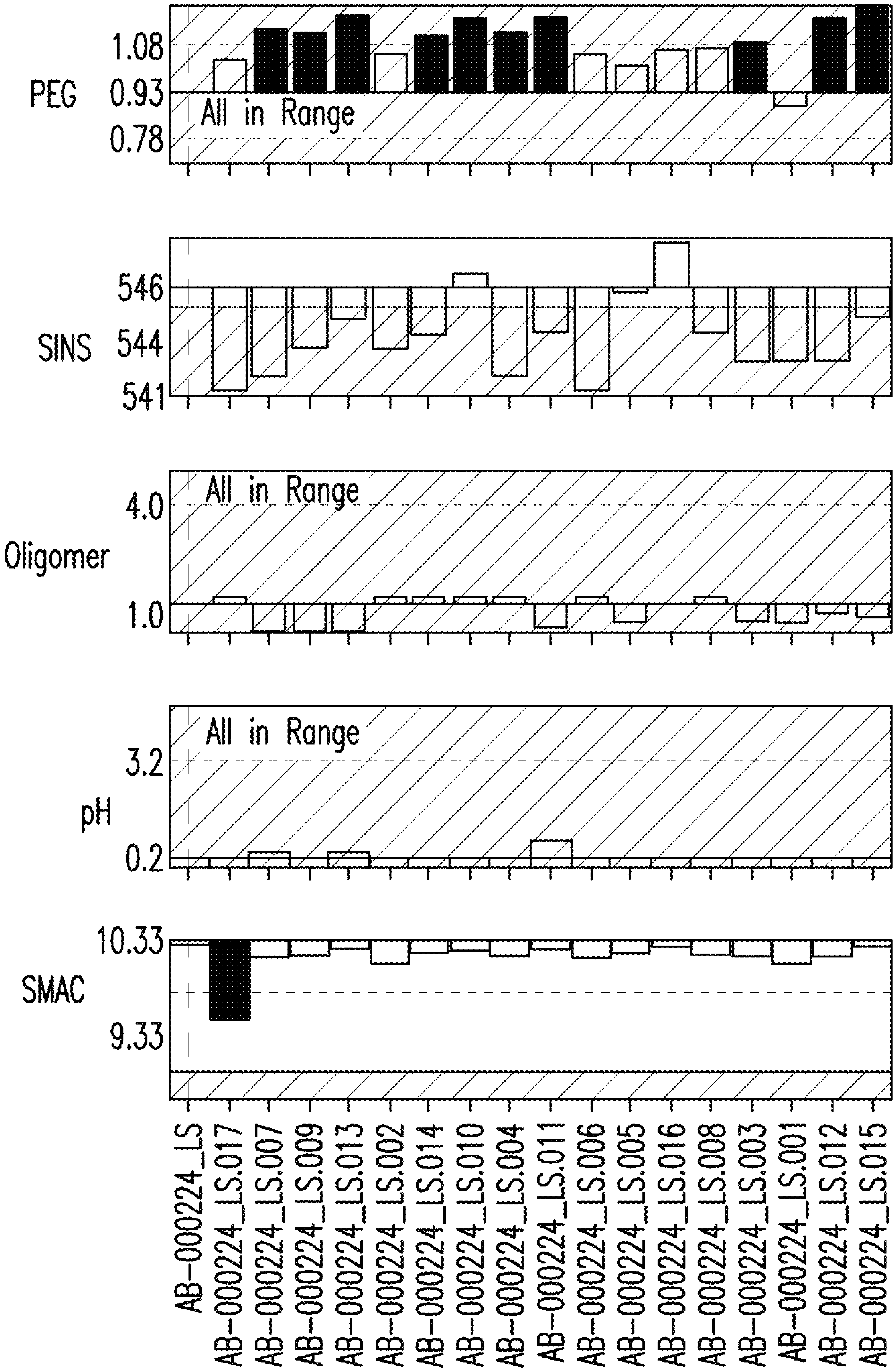


FIG. 12A Continued

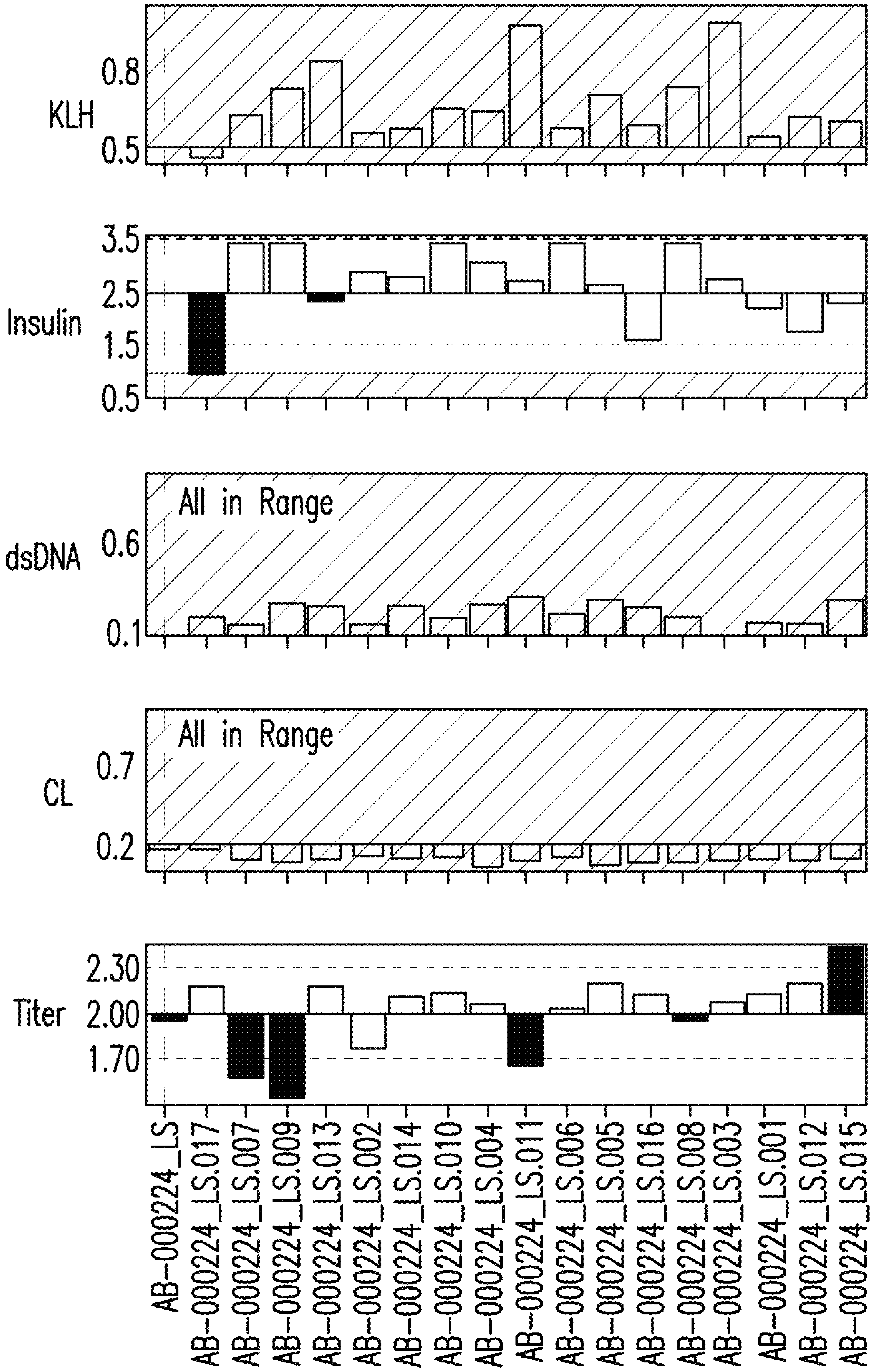
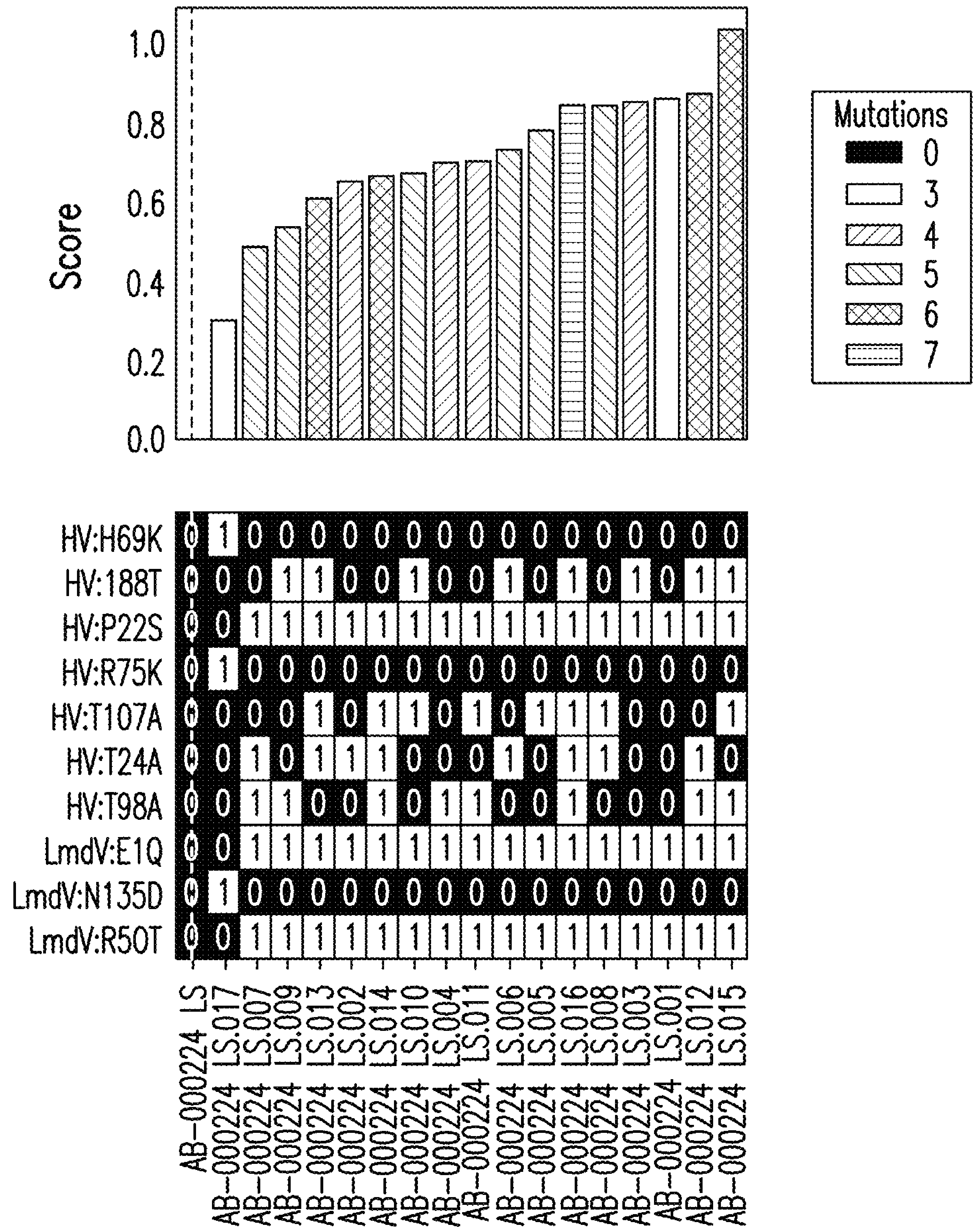
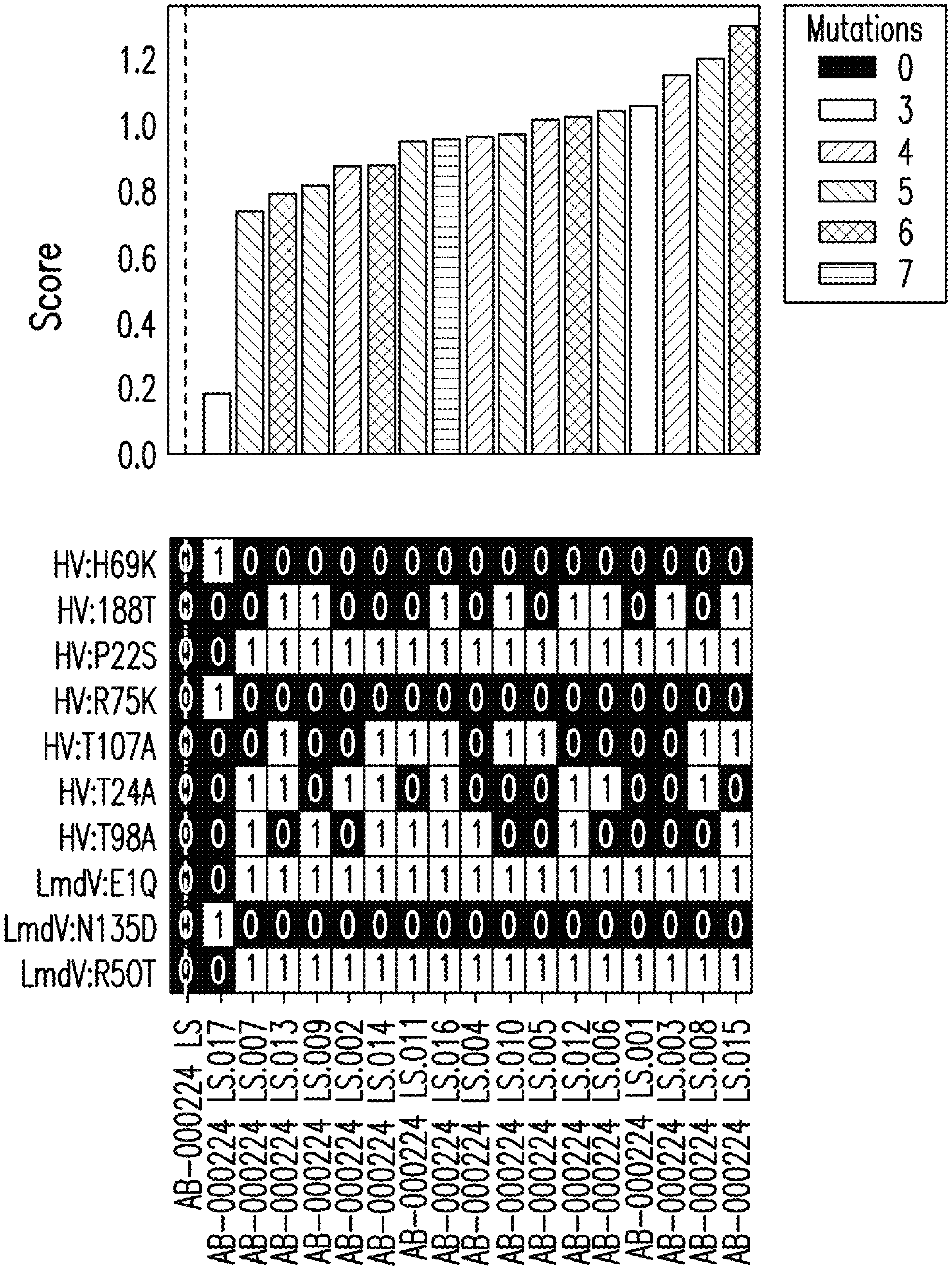


FIG. 12A Continued



	AB–000224_LS	AB–000224 LS.017	AB–000224 LS.007	AB–000224 LS.009	AB–000224 LS.013	AB–000224 LS.002	AB–000224 LS.014	AB–000224 LS.010	AB–000224 LS.004	AB–000224 LS.011	AB–000224 LS.006	AB–000224 LS.005	AB–000224 LS.016	AB–000224 LS.008	AB–000224 LS.003	AB–000224 LS.001	AB–000224 LS.012	AB–000224 LS.015
HV:H69K	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HV:188T	0	0	0	1	1	0	0	1	0	0	1	0	1	0	1	0	1	1
HV:P22S	0	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
HV:R75K	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HV:T107A	0	0	0	0	1	0	1	1	0	1	0	1	1	1	0	0	0	1
HV:T24A	0	0	1	0	1	1	1	0	0	0	1	0	1	1	0	0	1	0
HV:T98A	0	0	1	1	0	0	1	0	1	1	0	0	1	0	0	0	1	1
LmdV:E1Q	0	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
LmdV:N135D	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
LmdV:R50T	0	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1

FIG. 12B



	AB–000224 LS	AB–000224 LS.017	AB–000224 LS.007	AB–000224 LS.013	AB–000224 LS.009	AB–000224 LS.002	AB–000224 LS.014	AB–000224 LS.011	AB–000224 LS.016	AB–000224 LS.004	AB–000224 LS.010	AB–000224 LS.005	AB–000224 LS.012	AB–000224 LS.006	AB–000224 LS.001	AB–000224 LS.003	AB–000224 LS.008	AB–000224 LS.015
HV:H69K	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HV:188T	0	0	0	1	1	0	0	0	1	0	1	0	1	1	0	1	0	1
HV:P22S	0	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
HV:R75K	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HV:T107A	0	0	0	1	0	0	1	1	1	0	1	1	0	0	0	0	1	1
HV:T24A	0	0	1	1	0	1	1	0	1	0	0	0	1	1	0	0	1	0
HV:T98A	0	0	1	0	1	0	1	1	1	1	0	0	1	0	0	0	0	1
LmdV:E1Q	0	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
LmdV:N135D	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
LmdV:R50T	0	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1

FIG. 12C

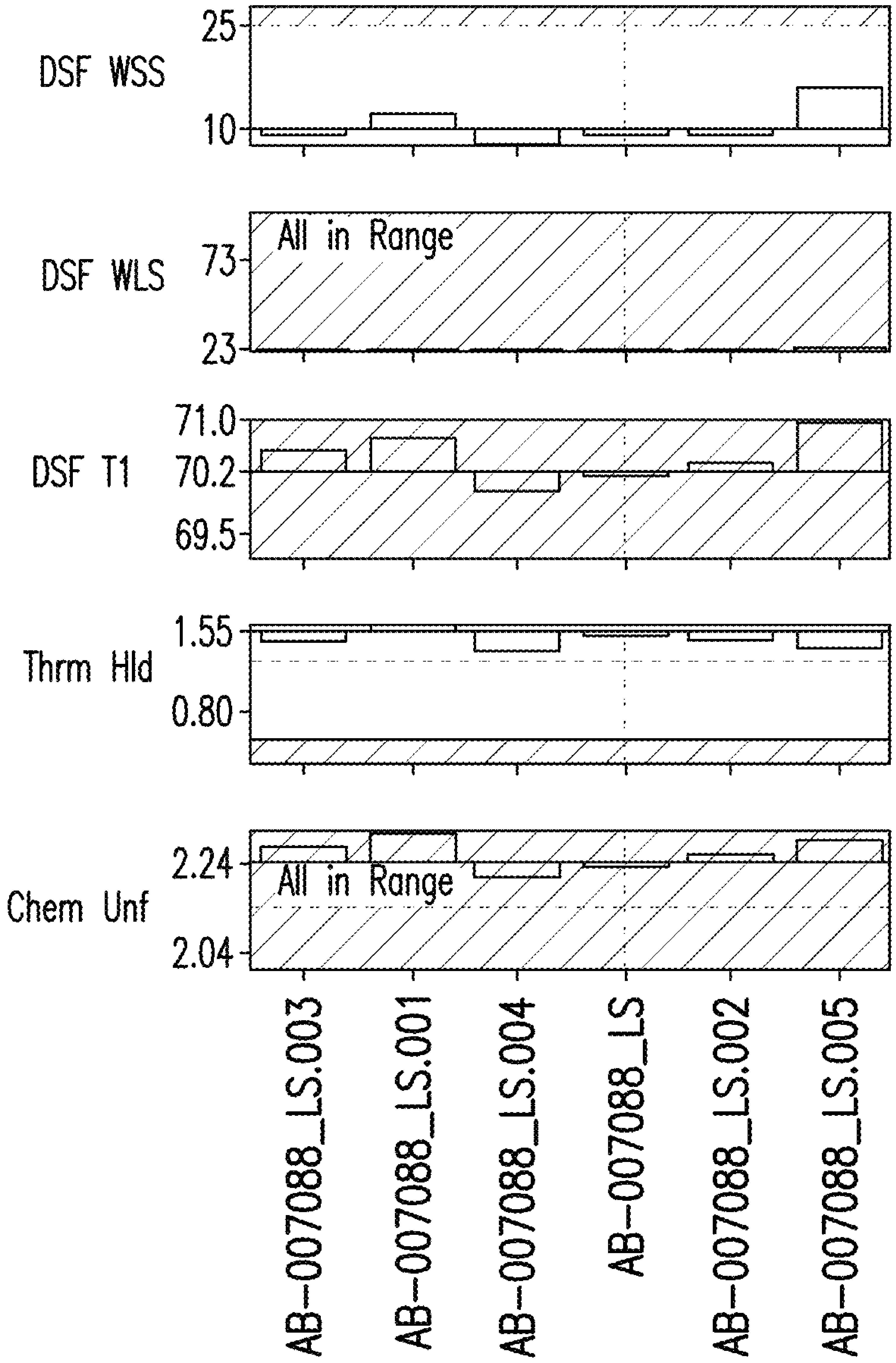

DSF WSS
25
10
DSF WLS
All in Range
73
23
DSF T1
71.0
70.2
69.5
Thrm Hld
1.55
0.80
Chem Unf
2.24
All in Range
2.04
AB-007088_LS.003
AB-007088_LS.001
AB-007088_LS.004
AB-007088_LS
AB-007088_LS.002
AB-007088_LS.005

FIG. 13A

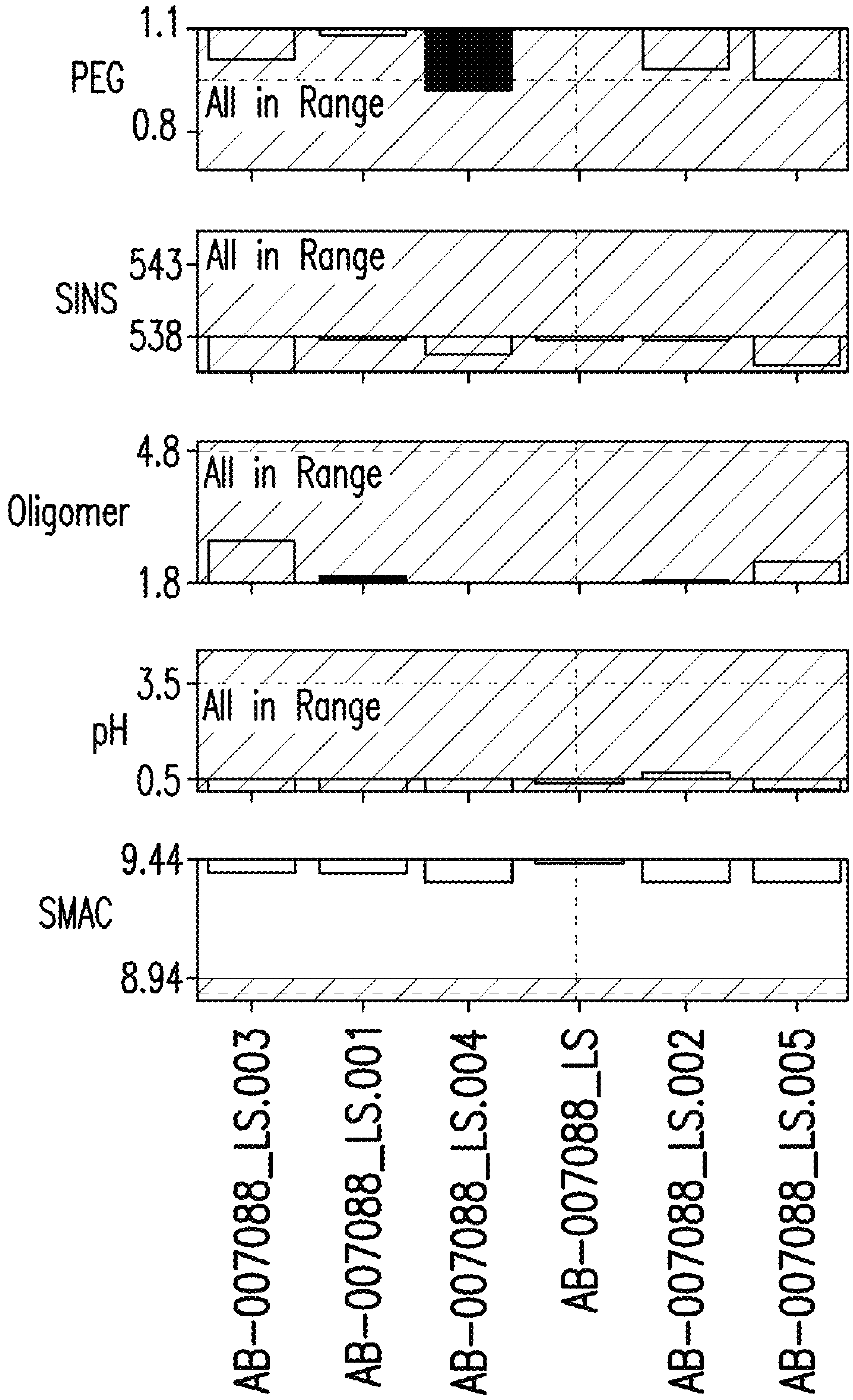


FIG. 13A Continued

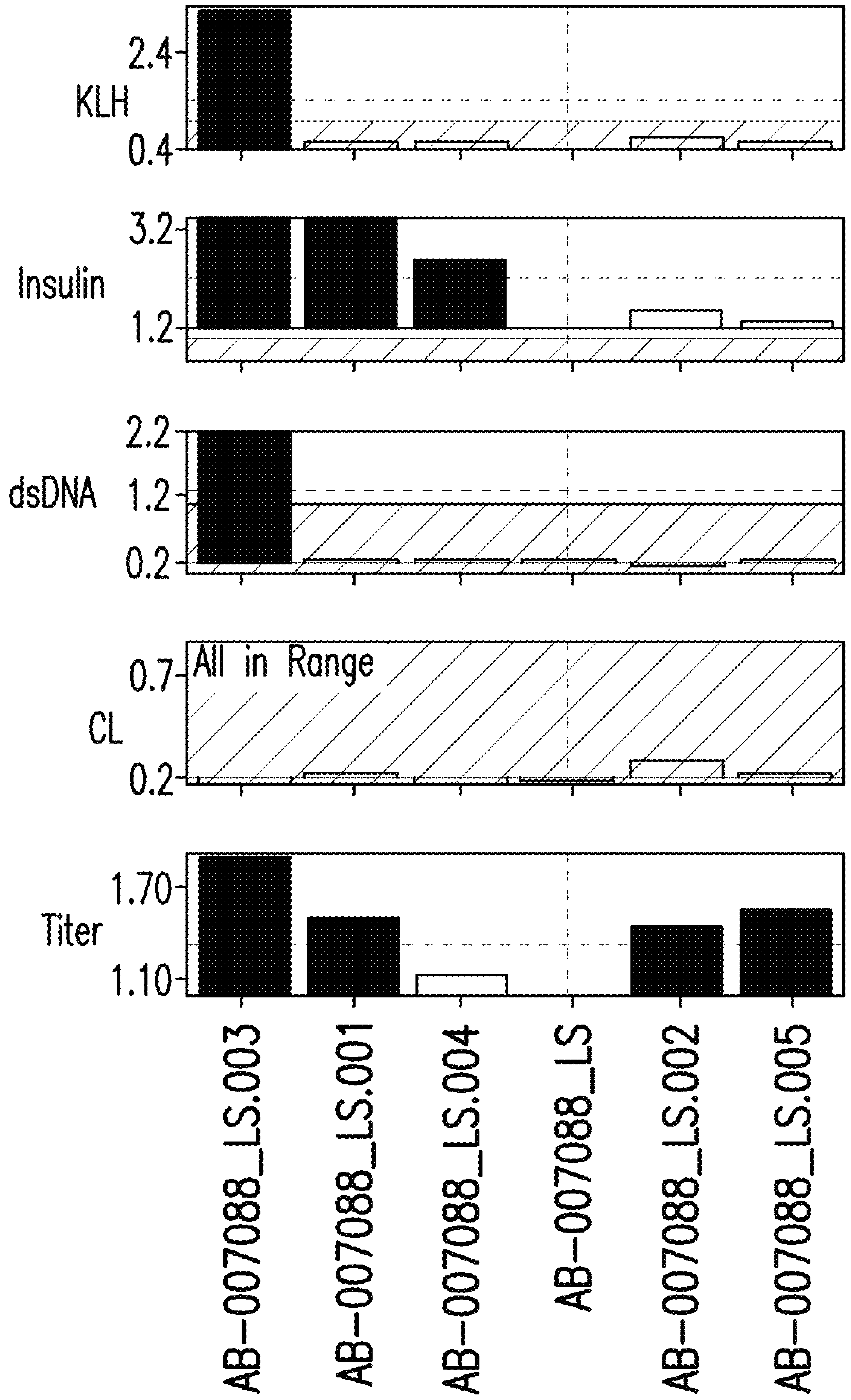
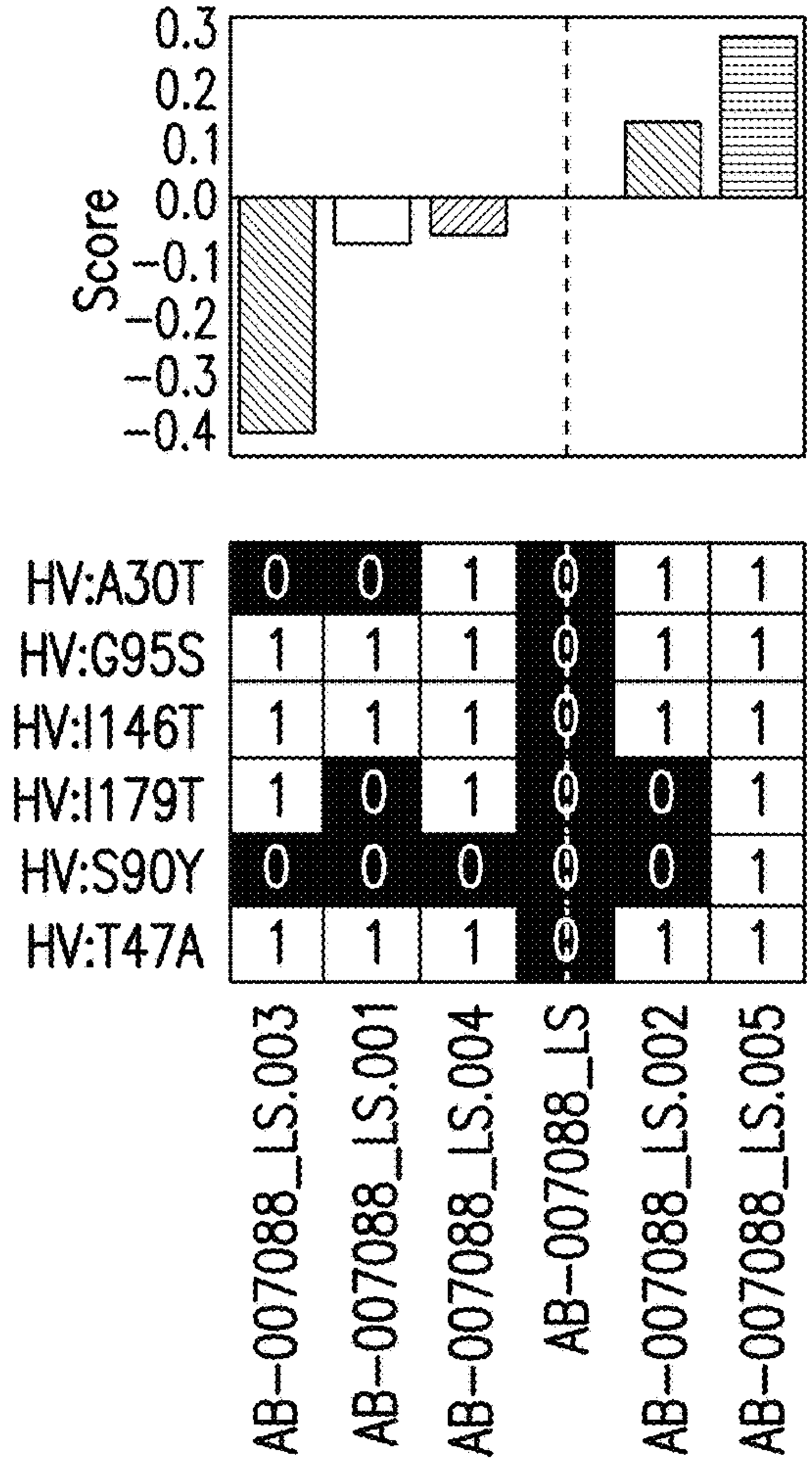
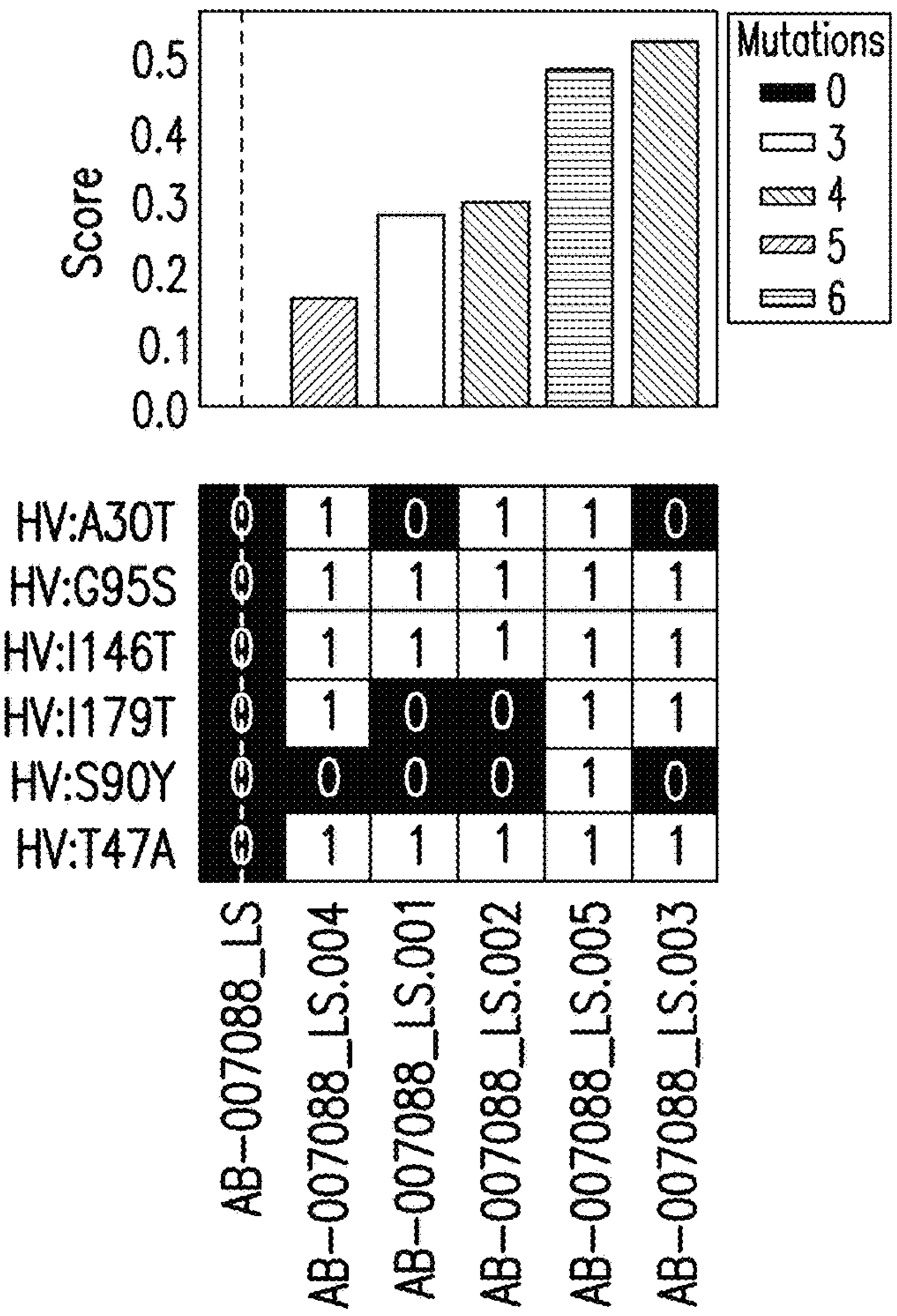


FIG. 13A Continued



	AB−007088_LS.003	AB−007088_LS.001	AB−007088_LS.004	AB−007088_LS	AB−007088_LS.002	AB−007088_LS.005
HV:A30T	0	0	1	0	1	1
HV:G95S	1	1	1	0	1	1
HV:I146T	1	1	1	0	1	1
HV:I179T	1	0	1	0	0	1
HV:S90Y	0	0	0	0	0	1
HV:T47A	1	1	1	0	1	1

FIG.13B



	AB−007088_LS	AB−007088_LS.004	AB−007088_LS.001	AB−007088_LS.002	AB−007088_LS.005	AB−007088_LS.003
HV:A30T	0	1	0	1	1	0
HV:G95S	0	1	1	1	1	1
HV:I146T	0	1	1	1	1	1
HV:I179T	0	1	0	0	1	1
HV:S90Y	0	0	0	0	1	0
HV:T47A	0	1	1	1	1	1

FIG.13C

ANTI-CSP ANTIBODIES

CROSS-REFERENCE TO RELATED APPLICATIONS

This application claims priority to U.S. Provisional Application No. 63/211,820, filed Jun. 17, 2021, the content of which is incorporated by reference in its entirety.

SEQUENCE LISTING

This application contains a Sequence Listing which has been submitted in ASCII format via EFS-Web and is hereby incorporated by reference in its entirety. Said ASCII copy, created on Jun. 16, 2022, is named 087996_0107_SL.txt and is 461,438 bytes in size.

FIELD

The present disclosure relates to compositions for treating or preventing malaria, and to antibodies conferring protection against infection by malarial parasites such as *Plasmodium falciparum* by insect vector transmission. The present disclosure also relates to methods for treating, preventing, or diagnosing *Plasmodium* infection in a mammal.

BACKGROUND

Malaria causes a large burden of morbidity and mortality, especially in the developing world. The causative agent of malaria is a protozoal parasite, which is transmitted by mosquitoes. Several infectious *Plasmodium* species cause malaria, the deadliest of which is *Plasmodium falciparum*. Others include *P. vivax*, *P. ovale*, and *P. malariae*. A first-generation vaccine (RTS,S) has been developed using portions of the malaria protein CSP, including part of the NANP repeats. CSP-based vaccines have consistently shown 30-50% efficacy in the prevention of erythrocytic-stage infection. This level of efficacy is not sufficient for eradication and new pre-erythrocytic treatments will need superior efficacy. Despite the existence of other anti-malarial products such as mefloquinine, doxycycline, and atovaquone/proguanil, there is a need for new antimalarials options for cases that are resistant to existing antimalarial drugs.

SUMMARY

The present disclosure provides to antibodies targeting *Plasmodium falciparum*. In certain non-limiting embodiments, the antibody is a recombinant anti-circumsporozoite (CSP) antibody. In certain embodiments, the recombinant antibody comprises a light chain variable region (VL) and a heavy chain variable region (VH), wherein the light chain variable region comprises a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 1, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO: 2, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO: 3; and the heavy chain variable region comprises a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 4, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO: 5, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO: 6.

In certain embodiments, the VL comprises the amino acid sequence set forth in SEQ ID NO: 163; the amino acid sequence set forth in SEQ ID NO: 23; the amino acid sequence set forth in SEQ ID NO: 33; the amino acid sequence set forth in SEQ ID NO: 43; the amino acid

sequence set forth in SEQ ID NO: 53; the amino acid sequence set forth in SEQ ID NO: 63; the amino acid sequence set forth in SEQ ID NO: 73; the amino acid sequence set forth in SEQ ID NO: 83; the amino acid sequence set forth in SEQ ID NO: 93; the amino acid sequence set forth in SEQ ID NO: 103; the amino acid sequence set forth in SEQ ID NO: 113; the amino acid sequence set forth in SEQ ID NO: 123; the amino acid sequence set forth in SEQ ID NO: 133; the amino acid sequence set forth in SEQ ID NO: 143; the amino acid sequence set forth in SEQ ID NO: 153; or the amino acid sequence set forth in SEQ ID NO: 173. In certain embodiments, the VH comprises the amino acid sequence set forth in SEQ ID NO: 164; the amino acid sequence set forth in SEQ ID NO: 24; the amino acid sequence set forth in SEQ ID NO: 34; the amino acid sequence set forth in SEQ ID NO: 44; the amino acid sequence set forth in SEQ ID NO: 54; the amino acid sequence set forth in SEQ ID NO: 64; the amino acid sequence set forth in SEQ ID NO: 74; the amino acid sequence set forth in SEQ ID NO: 84; the amino acid sequence set forth in SEQ ID NO: 94; the amino acid sequence set forth in SEQ ID NO: 104; the amino acid sequence set forth in SEQ ID NO: 114; the amino acid sequence set forth in SEQ ID NO: 124; the amino acid sequence set forth in SEQ ID NO: 134; the amino acid sequence set forth in SEQ ID NO: 144; the amino acid sequence set forth in SEQ ID NO: 154; or the amino acid sequence set forth in SEQ ID NO: 174.

In certain embodiments, the VL comprises the amino acid sequence set forth in SEQ ID NO: 163, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 164; the VL comprises the amino acid sequence set forth in SEQ ID NO: 33, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 34; the VL comprises the amino acid sequence set forth in SEQ ID NO: 43, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 44; the VL comprises the amino acid sequence set forth in SEQ ID NO: 53, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 54; the VL comprises the amino acid sequence set forth in SEQ ID NO: 63, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 64; the VL comprises the amino acid sequence set forth in SEQ ID NO: 73, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 74; the VL comprises the amino acid sequence set forth in SEQ ID NO: 83, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 84; the VL comprises the amino acid sequence set forth in SEQ ID NO: 93, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 94; the VL comprises the amino acid sequence set forth in SEQ ID NO: 103, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 104; the VL comprises the amino acid sequence set forth in SEQ ID NO: 113, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 114; the VL comprises the amino acid sequence set forth in SEQ ID NO: 123, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 124; the VL comprises the amino acid sequence set forth in SEQ ID NO: 133, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 134; the VL comprises the amino acid sequence set forth in SEQ ID NO: 143, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 144; the VL comprises the amino acid sequence set forth in SEQ ID NO: 153, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 154; or the VL comprises the amino acid sequence set forth in SEQ ID NO: 173, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 174.

In certain embodiments, the VL comprises the amino acid sequence set forth in SEQ ID NO: 63, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 64. In certain embodiments, the VL comprises the amino acid sequence set forth in SEQ ID NO: 133, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 134. In certain embodiments, the VL comprises the amino acid sequence set forth in SEQ ID NO: 163, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 164.

In certain embodiments, the recombinant antibody comprises a light chain (LC) and a heavy chain (HC). In certain embodiments, the LC comprises the amino acid sequence set forth in SEQ ID NO: 27; the amino acid sequence set forth in SEQ ID NO: 37; the amino acid sequence set forth in SEQ ID NO: 47; the amino acid sequence set forth in SEQ ID NO: 57; the amino acid sequence set forth in SEQ ID NO: 67; the amino acid sequence set forth in SEQ ID NO: 77; the amino acid sequence set forth in SEQ ID NO: 87; the amino acid sequence set forth in SEQ ID NO: 97; the amino acid sequence set forth in SEQ ID NO: 107; the amino acid sequence set forth in SEQ ID NO: 117; the amino acid sequence set forth in SEQ ID NO: 127; the amino acid sequence set forth in SEQ ID NO: 137; the amino acid sequence set forth in SEQ ID NO: 147; the amino acid sequence set forth in SEQ ID NO: 157; the amino acid sequence set forth in SEQ ID NO: 167; or the amino acid sequence set forth in SEQ ID NO: 177. In certain embodiments, the HC comprises the amino acid sequence set forth in SEQ ID NO: 28 or SEQ ID NO: 29; the amino acid sequence set forth in SEQ ID NO: 38 or SEQ ID NO: 39; the amino acid sequence set forth in SEQ ID NO: 48 or SEQ ID NO: 49; the amino acid sequence set forth in SEQ ID NO: 58 or SEQ ID NO: 59; the amino acid sequence set forth in SEQ ID NO: 68 or SEQ ID NO: 69; the amino acid sequence set forth in SEQ ID NO: 78 or SEQ ID NO: 79; the amino acid sequence set forth in SEQ ID NO: 88 or SEQ ID NO: 89; the amino acid sequence set forth in SEQ ID NO: 98 or SEQ ID NO: 99; the amino acid sequence set forth in SEQ ID NO: 108 or SEQ ID NO: 109; the amino acid sequence set forth in SEQ ID NO: 118 or SEQ ID NO: 119; the amino acid sequence set forth in SEQ ID NO: 128 or SEQ ID NO: 129; the amino acid sequence set forth in SEQ ID NO: 138 or SEQ ID NO: 139; the amino acid sequence set forth in SEQ ID NO: 148 or SEQ ID NO: 149; the amino acid sequence set forth in SEQ ID NO: 158 or SEQ ID NO: 159; the amino acid sequence set forth in SEQ ID NO: 168 or SEQ ID NO: 169; or the amino acid sequence set forth in SEQ ID NO: 178 or SEQ ID NO: 179.

In certain embodiments, the LC comprises the amino acid sequence set forth in SEQ ID NO: 27, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 28 or SEQ ID NO: 29; the LC comprises the amino acid sequence set forth in SEQ ID NO: 37, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 38 or SEQ ID NO: 39; the LC comprises the amino acid sequence set forth in SEQ ID NO: 47, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 48 or SEQ ID NO: 49; the LC comprises the amino acid sequence set forth in SEQ ID NO: 57, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 58 or SEQ ID NO: 59; the LC comprises the amino acid sequence set forth in SEQ ID NO: 67, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 68 or SEQ ID NO: 69; the LC comprises the amino acid sequence set forth in SEQ ID NO: 77, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 78 or SEQ ID NO: 79; the LC comprises the amino acid sequence set forth in SEQ ID NO: 87, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 88 or SEQ ID NO: 89; the LC comprises the amino acid sequence set forth in SEQ ID NO: 97, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 98 or SEQ ID NO: 99; the LC comprises the amino acid sequence set forth in SEQ ID NO: 107, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 108 or SEQ ID NO: 109; the LC comprises the amino acid sequence set forth in SEQ ID NO: 117, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 118 or SEQ ID NO: 119; the LC comprises the amino acid sequence set forth in SEQ ID NO: 127, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 128 or SEQ ID NO: 129; the LC comprises the amino acid sequence set forth in SEQ ID NO: 137, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 138 or SEQ ID NO: 139; the LC comprises the amino acid sequence set forth in SEQ ID NO: 147, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 148 or SEQ ID NO: 149; the LC comprises the amino acid sequence set forth in SEQ ID NO: 157, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 158 or SEQ ID NO: 159; the LC comprises the amino acid sequence set forth in SEQ ID NO: 167, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 168 or SEQ ID NO: 169; or the LC comprises the amino acid sequence set forth in SEQ ID NO: 177, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 178 or SEQ ID NO: 179.

In certain embodiments, the LC comprises the amino acid sequence set forth in SEQ ID NO: 67, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 69. In certain embodiments, the LC comprises the amino acid sequence set forth in SEQ ID NO: 137, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 139. In certain embodiments, the LC comprises the amino acid sequence set forth in SEQ ID NO: 167, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 169.

In certain embodiments, the recombinant antibody comprises a light chain variable region (VL) and a heavy chain variable region (VH), wherein the VL comprises the amino acid sequence set forth in SEQ ID NO: 13. In certain embodiments, the VL comprises at least one amino acid substitution. In certain embodiments, the at least one amino acid substitution is at position 1 and/or at position 44. In certain embodiments, the amino acid substitution at position 1 is E1Q. In certain embodiments, the amino acid substitution at position 44 is R44T. In certain embodiments, the VH comprises the amino acid sequence set forth in SEQ ID NO: 14. In certain embodiments, the VH comprises at least one amino acid substitution. In certain embodiments, the at least one amino acid substitution is at position 21, position 23, position 88, position 98, or a combination thereof. In certain embodiments, the amino acid substitution at position 1 is E1Q. In certain embodiments, the amino acid substitution at position 44 is R44T. In certain embodiments, the amino acid substitution at position 21 is P21S. In certain embodiments, the amino acid substitution at position 23 is T23A. In certain embodiments, the amino acid substitution at position 80 is I80T. In certain embodiments, the amino acid substitution at position 90 is T90A.

In certain embodiments, the recombinant antibody comprises a heavy chain (HC) comprising the amino acid sequence set forth in SEQ ID NO: 18. In certain embodiments, the HC comprises at least one amino acid substitution. In certain embodiments, the at least one amino acid substitution is at position 438 and/or or at position 444. In certain embodiments, the amino acid substitution at position

438 is M438L. In certain embodiments, the amino acid substitution at position 444 is N444S.

In certain non-limiting embodiments, the present disclosure also provides a recombinant anti-circumsporozoite (CSP) antibody comprising a light chain variable region (VL) and a heavy chain variable region (VH), wherein the VL comprises the amino acid sequence set forth in SEQ ID NO: 163 and the VH comprises the amino acid sequence set forth in SEQ ID NO: 164. In certain embodiments, the recombinant antibody comprises a light chain (LC) and a heavy chain (HC), wherein the LC comprises the amino acid sequence set forth in SEQ ID NO: 167 and the HC comprises the amino acid sequence set forth in SEQ ID NO: 169.

In certain non-limiting embodiments, the present disclosure provides a recombinant anti-circumsporozoite (CSP) antibody comprising a light chain variable region (VL) and a heavy chain variable region (VH), wherein the VL comprises the amino acid sequence set forth in SEQ ID NO: 63 and the VH comprises the amino acid sequence set forth in SEQ ID NO: 64. In certain embodiments, the recombinant antibody comprises a light chain (LC) and a heavy chain (HC), wherein the LC comprises the amino acid sequence set forth in SEQ ID NO: 67 and the HC comprises the amino acid sequence set forth in SEQ ID NO: 69.

In certain non-limiting embodiments, the present disclosure further provides a recombinant anti-circumsporozoite (CSP) antibody comprising a light chain variable region (VL) and a heavy chain variable region (VH), wherein the VL comprises the amino acid sequence set forth in SEQ ID NO: 133 and the VH comprises the amino acid sequence set forth in SEQ ID NO: 134. In certain embodiments, the recombinant antibody comprises a light chain (LC) and a heavy chain (HC), wherein the LC comprises the amino acid sequence set forth in SEQ ID NO: 137 and the HC comprises the amino acid sequence set forth in SEQ ID NO: 139.

In certain non-limiting embodiments, the present disclosure provides a recombinant anti-circumsporozoite (CSP) antibody comprising a light chain variable region (VL) and a heavy chain variable region (VH), wherein the light chain variable region comprises a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 183, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO: 184, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO: 185; and the heavy chain variable region comprises a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 186, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO: 187, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO: 188. In certain embodiments, the VL comprises the amino acid sequence set forth in SEQ ID NO: 195, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 196. In certain embodiments, the antibody comprises comprising a LC and a HC. In certain embodiments, the LC comprises the amino acid sequence set forth in SEQ ID NO: 199, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 200 or SEQ ID NO: 201.

In certain non-limiting embodiments, the present disclosure provides a recombinant anti-circumsporozoite (CSP) antibody comprising a light chain variable region (VL) and a heavy chain variable region (VH), wherein the light chain variable region comprises a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 205, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO: 206, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO: 207; and the heavy chain variable region comprises a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 208, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO: 209, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO: 210.

In certain embodiments, the amino acid sequence set forth in SEQ ID NO: 227; the amino acid sequence set forth in SEQ ID NO: 237; the amino acid sequence set forth in SEQ ID NO: 247; the amino acid sequence set forth in SEQ ID NO: 257; or the amino acid sequence set forth in SEQ ID NO: 267. In certain embodiments, the VH comprises the amino acid sequence set forth in SEQ ID NO: 228; the amino acid sequence set forth in SEQ ID NO: 238; the amino acid sequence set forth in SEQ ID NO: 248; the amino acid sequence set forth in SEQ ID NO: 258; or the amino acid sequence set forth in SEQ ID NO: 268.

In certain embodiments, the VL comprises the amino acid sequence set forth in SEQ ID NO: 227, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 228; the VL comprises the amino acid sequence set forth in SEQ ID NO: 237, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 238; the VL comprises the amino acid sequence set forth in SEQ ID NO: 247, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 248; the VL comprises the amino acid sequence set forth in SEQ ID NO: 257, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 258; or the VL comprises the amino acid sequence set forth in SEQ ID NO: 267, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 268.

In certain embodiments, the recombinant antibody comprises a LC and a HC. In certain embodiments, the LC comprises the amino acid sequence set forth in SEQ ID NO: 231; the amino acid sequence set forth in SEQ ID NO: 241; the amino acid sequence set forth in SEQ ID NO: 251; the amino acid sequence set forth in SEQ ID NO: 261; or the amino acid sequence set forth in SEQ ID NO: 271. In certain embodiments, the HC comprises the amino acid sequence set forth in SEQ ID NO: 232 or SEQ ID NO: 233; the amino acid sequence set forth in SEQ ID NO: 242 or SEQ ID NO: 243; the amino acid sequence set forth in SEQ ID NO: 252 or SEQ ID NO: 253; the amino acid sequence set forth in SEQ ID NO: 262 or SEQ ID NO: 263; or the amino acid sequence set forth in SEQ ID NO: 272 or SEQ ID NO: 273.

In certain embodiments, the LC comprises the amino acid sequence set forth in SEQ ID NO: 231, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 232 or SEQ ID NO: 233; the LC comprises the amino acid sequence set forth in SEQ ID NO: 241, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 242 or SEQ ID NO: 243; the LC comprises the amino acid sequence set forth in SEQ ID NO: 251, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 252 or SEQ ID NO: 253; the LC comprises the amino acid sequence set forth in SEQ ID NO: 261, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 262 or SEQ ID NO: 263; or the LC comprises the amino acid sequence set forth in SEQ ID NO: 271, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 272 or SEQ ID NO: 273.

In certain embodiments, the VH comprises the amino acid sequence set forth in SEQ ID NO: 218. In certain embodiments, the VH comprises at least one amino acid substitution. In certain embodiments, the at least one amino acid substitution is at position 40, position 69, position 80, position 85, position 120, or a combination thereof. In certain embodiments, the amino acid substitution at position 40 is T40A. In certain embodiments, the amino acid substitution at position 69 is I69T. In certain embodiments, the amino acid substitution at position 80 is 580Y. In certain embodiments, the amino acid substitution at position 85 is G85S. In certain embodiments, the amino acid substitution at position 120 is 1120T. In certain embodiments, the HC comprises the amino acid sequence set forth in SEQ ID NO: 222. In certain embodiments, the HC comprises at least one amino acid substitution. In certain embodiments, the at least one amino acid substitution is at position 434 and/or at position 440. In certain embodiments, the amino acid substitution at position 434 is M434L. In certain embodiments, the amino acid substitution at position 440 is N440S.

In certain embodiments, the recombinant antibody exhibits at least 20% reduction in parasite liver load as compared to a reference antibody. In certain embodiments, the recombinant antibody exhibits at least 20% increase in survival rate as compared to a reference antibody. In certain embodiments, the recombinant antibody exhibits increased conformational stability as compared to a reference antibody. In certain embodiments, the recombinant antibody exhibits increased colloidal stability as compared to a reference antibody. In certain embodiments, the reference antibody is AB-000317. In certain embodiments, the reference antibody is AB-000224. In certain embodiments, the reference antibody is AB-007088.

In certain embodiments, the recombinant antibody binds to a NANP repeat region. In certain embodiments, the recombinant antibody binds to a polypeptide comprising or consisting of the amino acid sequence set forth in SEQ ID NO: 280.

In certain embodiments, the recombinant antibody comprises at least one modification relative to the native AB-000224 variable heavy chain amino acid sequence set forth in SEQ ID NO: 14. In certain embodiments, the recombinant antibody comprises at least one modification relative to the native AB-000224 variable light chain amino acid sequence set forth in SEQ ID NO: 13. In certain embodiments, the recombinant antibody comprises at least one modification relative to the native AB-000224 variable heavy chain amino acid sequence set forth in SEQ ID NO: 14 and at least one modification relative to the native AB-000224 variable light chain amino acid sequence set forth in SEQ ID NO: 13.

In certain embodiments, the recombinant antibody comprises at least one modification relative to the native AB-007088 variable heavy chain amino acid sequence set forth in SEQ ID NO: 218. In certain embodiments, the recombinant antibody comprises at least one modification relative to the native AB-007088 variable light chain amino acid sequence set forth in SEQ ID NO: 217. In certain embodiments, the recombinant antibody comprises at least one modification relative to the native AB-007088 variable heavy chain amino acid sequence set forth in SEQ ID NO: 218 and at least one modification relative to the native AB-000224 variable light chain amino acid sequence set forth in SEQ ID NO: 217.

In certain non-limiting embodiments, the present disclosure provides a polynucleotide encoding an antibody disclosed herein. In certain non-limiting embodiments, the present disclosure provides an expression vector comprising the polynucleotide disclosed herein. In certain non-limiting embodiments, the present disclosure provides a host cell comprising the expression vector or the polynucleotide disclosed herein.

In certain non-limiting embodiments, the present disclosure provides a composition comprising the antibody disclosed herein. In certain embodiments, the composition further comprises a pharmaceutically acceptable carrier.

In certain non-limiting embodiments, the present disclosure provides a method of preventing and/or treating malaria in a subject in need thereof, comprising administering an effective amount of the antibody disclosed herein or of the composition disclosed herein. In certain embodiments, the subject is a pediatric patient.

In certain non-limiting embodiments, the present disclosure provides the antibodies or compositions disclosed herein for use in the prevention and/or treatment of malaria in a subject in need thereof. Additionally, in certain non-limiting embodiments, the present disclosure provides the antibodies or compositions disclosed herein for the manufacture of a medicament for the prevention and/or treatment of malaria in a subject in need thereof. Furthermore, the present disclosure provides use of the antibodies or compositions disclosed herein for the prevention and/or treatment and/or prevention of malaria in a subject in need thereof. In certain embodiments, the subject is a pediatric patient.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. **1**A illustrates parasite liver load following administration of experimental anti-CSP antibodies, AB-000224 and AB-007088. Parasite liver burden load was measured by bioluminescence (photons/sec) generated from the fluorescent sporozoites (y-axis). The individual points indicate the total amount of bioluminescence measured in a single mouse and by extension, the sporozoite liver burden. AB-001245 is a non-malaria-specific antibody that was used as a negative control. AB-000317 is a positive control. FIG. **1**B illustrates the associated human IgG serum concentrations determined by ELISA obtained 15 hours following antibody administration. The individual points indicate the total amount of human IgG in a single mouse. AB-001245 is a non-malaria-specific antibody that was used as a negative control. AB-000317 is a positive control.

FIGS. **2**A and **2**C illustrate the survival rate of mice following administration of anti-CSP antibody AB-000224 and exposure to mosquitoes infected with chimeric *P. berghei* expressing *P. falciparum* CSP protein in two experiments. FIG. **2**B shows the associated human IgG serum concentrations determined by ELISA obtained 15 hours following antibody administration in the experiment shown in FIG. **2**A. AB-001245 is a non-malaria-specific antibody that was used as a negative control. AB-000317 is a positive control.

FIGS. **3**A and **3**C illustrate the survival rate of mice following administration of anti-CSP antibody AB-007088 and exposure to mosquitoes infected with chimeric *P. berghei* expressing *P. falciparum* CSP protein in two experiments. FIG. **3**B shows the associated human IgG serum concentrations determined by ELISA obtained 15 hours following antibody administration in the experiment shown in FIG. **3**A. AB-001245 is a non-malaria-specific antibody that was used as a negative control. AB-000317 is a positive control.

FIGS. **4**A-**4**B illustrate sequences for the AB-000224 antibody. FIG. **4**A shows the AB-000224 Lambda Light Chain sequence (SEQ ID NO: 286). FIG. **4**B shows the AB-000224 IgG1 Heavy Chain sequence (SEQ ID NO: 287). Framework and CDR regions are designated using the ASN system.

FIGS. **5**A-**5**B illustrate sequences for the AB-007088 antibody. FIG. **5**A shows the AB-007088 Lambda Light Chain sequence (SEQ ID NO: 288). FIG. **5**B shows the

AB-007088 IgG1 Heavy Chain sequence (SEQ ID NO: 289). Framework and CDR regions are designated using the ASN system.

FIG. **6** shows the ASN numbering system for the light chain of AB-000224.

FIG. **7** shows the ASN numbering system for the heavy chain of AB-000224.

FIG. **8** shows the ASN numbering system for the light chain of AB-007088.

FIG. **9** shows the ASN numbering system for the heavy chain of AB-007088.

FIGS. **10**A-**10**F illustrate parasite liver load following administration of experimental anti-CSP antibodies variants disclosed herein. Results are expressed as percentage inhibition, where naïve infected were considered as 100%. FIGS. **10**G-**10**I show concentration of human antibodies that were circulating in the mice at the time of infection as determined by ELISA for the assays shown in FIGS. **10**D-F, respectively. AB-001245 is a non-malaria-specific antibody that was used as a negative control. AB-000317 is a positive control.

FIGS. **11**A-**11**C illustrate the survival rate of mice following administration of anti-CSP antibody variants disclosed herein and exposure to mosquitoes infected with chimeric *P. berghei* expressing *P. falciparum* CSP protein. FIGS. **11**D-F show concentration of human antibodies that were circulating in the mice at the time of infection as determined by ELISA for the assays shown in FIGS. **11**A-C, respectively. AB-001245 is a non-malaria-specific antibody that was used as a negative control. AB-000317 is a positive control.

FIG. **12**A illustrates the biophysical characterization of AB-000224 and variants thereof. FIG. **12**B shows the ranking of the AB-000224 and variants thereof based on all data obtained during biophysical characterization. FIG. **12**C shows the ranking of the AB-000224 and variants thereof excluding polyreactivity and including titer.

FIG. **13**A illustrates the biophysical characterization of AB-007088 and variants thereof. FIG. **13**B shows the ranking of the AB-007088 and variants thereof based on all data obtained during biophysical characterization. FIG. **13**C shows the ranking of the AB-007088 and variants thereof excluding polyreactivity and including titer.

DETAILED DESCRIPTION

The present disclosure is based, at least in part, on the finding of several anti-CSP antibody variants. The present disclosure surprisingly shows that the disclosed anti-CSP antibodies and variants thereof have superior properties as compared to previously disclosed antibodies.

Definitions

For purposes of interpreting this specification, the following definitions will apply and whenever appropriate, terms used in the singular will also include the plural and vice versa. In the event that any definition set forth below conflicts with any document incorporated herein by reference, the definition set forth below shall control.

Unless defined otherwise, technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Singleton et al., Dictionary of Microbiology and Molecular Biology 2nd ed., J. Wiley & Sons (New York, N.Y. 1994), and March, Advanced Organic Chemistry Reactions, Mechanisms and Structure 4th ed., John Wiley & Sons (New York, N.Y. 1992), provide one skilled in the art with a general guide to many of the terms used in the present application.

As used in this specification and the appended claims, the singular forms "a," "an" and "the" include plural referents unless the context dictates otherwise. Thus, for example, reference to "a protein" or an "antibody" includes a plurality of proteins or antibodies, respectively; reference to "a cell" includes mixtures of cells and the like.

As used herein, the term "about" or "approximately" refers to the usual error range for the respective value readily known to the skilled person in this technical field, for example, ±20%, ±10%, or ±5%, are within the intended meaning of the recited value.

As used herein, the term "antibody" means an isolated or recombinant binding agent that comprises the necessary variable region sequences to specifically bind an antigenic epitope. Therefore, an "antibody" as used herein is any form of antibody or fragment thereof that exhibits the desired biological activity, e.g., binding the specific target antigen. Thus, it is used in the broadest sense and specifically covers a monoclonal antibody (including full-length monoclonal antibodies), human antibodies, chimeric antibodies, nanobodies, diabodies, multispecific antibodies (e.g., bispecific antibodies), and antibody fragments including but not limited to scFv, Fab, and the like so long as they exhibit the desired biological activity.

"Antibody fragments" comprise a portion of an intact antibody, for example, the antigen-binding or variable region of the intact antibody. Examples of antibody fragments include Fab, Fab', F(ab')2, and Fv fragments; diabodies; linear antibodies (e.g., Zapata et al., Protein Eng. 8(10): 1057-1062 (1995)); single-chain antibody molecules (e.g., scFv); and multispecific antibodies formed from antibody fragments. Papain digestion of antibodies produces two identical antigen-binding fragments, called "Fab" fragments, each with a single antigen-binding site, and a residual "Fc" fragment, a designation reflecting the ability to crystallize readily. Pepsin treatment yields an F(ab')2 fragment that has two antigen combining sites and is still capable of cross-linking antigen.

As used herein, "recombinant antibody" refers to an antibody wherein the exact amino acid sequence of the antibody is not naturally found in a given organism (e.g., an antibody from a mammal). In certain embodiments, this term can refer to an antibody including one or more amino acid residues that are not found in a naturally occurring antibody. In certain embodiments, a recombinant antibody can have a CDR including an amino acid residue that is not found in a naturally occurring antibody (e.g., an antibody from a mammal). In another exemplary embodiment, a recombinant antibody can have a framework (FR) including an amino acid residue that is not found in a naturally occurring antibody (e.g., an antibody from a mammal). In certain embodiments, a recombinant antibody can have a constant region including an amino acid residue that is not found in a naturally occurring antibody (e.g., an antibody from a mammal). In certain embodiments, a recombinant antibody is variant of a naturally occurring antibody (e.g., AB-000224) including at least one modification, e.g., substitution, relative to the native variable heavy chain amino acid sequence or variable light chain amino acid sequence. For example, but without any limitation, a recombinant antibody can be an anti-CSP antibody AB-000224 disclosed herein comprising at least one modification, e.g., substitution, relative to the native AB-000224 variable heavy chain amino acid sequence (SEQ ID NO: 14) or variable light chain amino acid sequence (SEQ ID NO: 13) described herein. A recombinant antibody has improved developability, e.g., decreased heterogeneity, increased yield, increased stability, improved net charges to improve pharmacokinetics, and/or reduced immunogenicity.

As used herein, the terms, "anti-CSP antibody" and "CSP antibody" are used synonymously and refer to an antibody that binds to *Plasmodium falciparum* circumsporozoite (CSP) antigen.

An "antibody that binds to the same epitope" as a reference antibody refers to an antibody that blocks binding of the reference antibody to its antigen in a competition assay by 50% or more, and conversely, the reference antibody blocks binding of the antibody to its antigen in a competition assay by 50% or more.

As used herein, "V-region" refers to an antibody variable region domain comprising the segments of Framework 1, CDR1, Framework 2, CDR2, Framework 3, CDR3, and Framework 4. The heavy chain V-region, VH, is a consequence of rearrangement of a V-gene (HV), a D-gene (HD), and a J-gene (HJ), in what is known as V(D)J recombination during B-cell differentiation. The light chain V-region, VL, is a consequence of the rearrangement of a V-gene (LV) and a J-gene. In certain embodiments, the terms "VH" and "heavy chain variable" refer to the heavy chain V-region of an antibody. In certain embodiments, the terms "VL" and "light chain variable" refer to the light chain V-region of an antibody.

As used herein, "complementarity-determining region (CDR)" refers to the three hypervariable regions (HVRs) in each chain that interrupt the four "framework" regions established by the light and heavy chain variable regions. The CDRs are the primary contributors to binding to an epitope of an antigen. The CDRs of each chain are referred to as CDR1, CDR2, and CDR3 numbered sequentially starting from the N-terminus, and are also identified by the chain in which the particular CDR is located. Thus, a VH CDR3 (HCDR3) is located in the variable domain of the heavy chain of the antibody in which it is found, whereas a VL CDR3 (LCDR3) is the CDR3 from the variable domain of the light chain of the antibody in which it is found. The term "CDR" is used interchangeably with "HVR" when referring to CDR sequences.

The amino acid sequences of the CDRs and framework regions can be determined using various definitions in the art, e.g., Kabat, Chothia, international ImMunoGeneTics database (IMGT), and AbM (see, e.g., Chothia & Lesk, 1987, Canonical structures for the hypervariable regions of immunoglobulins. J. Mol. Biol. 196, 901-917; Chothia C. et al., 1989, Conformations of immunoglobulin hypervariable regions. Nature 342, 877-883; Chothia C. et al., 1992, Structural repertoire of the human VH segments J. Mol. Biol. 227, 799-817; Al-Lazikani et al., J. Mol. Biol 1997, 273(4)). Definitions of antigen combining sites are also described in the following: Ruiz et al., IMGT, the international ImMunoGeneTics database. Nucleic Acids Res., 28, 219-221 (2000); and Lefranc, M.-P. IMGT, the international ImMunoGeneTics database. Nucleic Acids Res. January 1; 29(1):207-9 (2001); MacCallum et al, Antibody-antigen interactions: Contact analysis and binding site topography, J. Mol. Biol., 262 (5), 732-745 (1996); and Martin et al, Proc. Natl Acad. Sci. USA, 86, 9268-9272 (1989); Martin, et al, Methods Enzymol., 203, 121-153, (1991); Pedersen et al, Immunomethods, 1, 126, (1992); and Rees et al, In Sternberg M. J. E. (ed.), Protein Structure Prediction. Oxford University Press, Oxford, 141-172 1996). Reference to CDRs as determined by Kabat numbering is based, for example, on Kabat et al., Sequences of Proteins of Immunological Interest, 5th Ed. Public Health Service, National Institute of Health, Bethesda, Md. (1991)). Chothia CDRs are determined as defined by Chothia (see, e.g., Chothia and Lesk J. Mol. Biol. 196:901-917 (1987)). In certain embodiments, the amino acid sequences of the CDRs and framework regions are numbered using the Antibody Structural Numbering (ASN) system. Antibody Structural Numbering (ASN) is a numbering system developed based on the AHo numbering system (Honegger & Pluckthun, J. Mol. Biol. 309:657-670 (2001)) defined by Annemarie Honegger for the variable region, but extended to include constant domains. FIGS. **6-7** illustrates ASN numbering for AB-000224-LS light and heavy chain, respectively. FIGS. **8-9** illustrates ASN numbering for AB-007088-LS light and heavy chain, respectively.

An "Fc region" refers to the constant region of an antibody excluding the first constant region immunoglobulin domain. Thus, Fc refers to the last two constant region immunoglobulin domains of IgA, IgD, and IgG, and the last three constant region immunoglobulin domains of IgE and IgM, and the flexible hinge N-terminal to these domains. For IgA and IgM Fc may include the J chain. For IgG, Fc comprises immunoglobulin domains Cγ2 and Cγ3 and the hinge between Cγ1 and Cγ. It is understood in the art that the boundaries of the Fc region may vary, however, the human IgG heavy chain Fc region is usually defined to comprise residues C226 or P230 to its carboxyl-terminus, using the numbering according to the EU index as in Kabat et al. (1991, NIH Publication 91-3242, National Technical Information Service, Springfield, Va.). The term "Fc region" may refer to this region in isolation or this region in the context of an antibody or antibody fragment. "Fc region" includes naturally occurring allelic variants of the Fc region as well as modifications that modulate effector function. Fc regions also include variants that don't result in alterations to biological function. For example, one or more amino acids can be deleted from the N-terminus or C-terminus of the Fc region of an immunoglobulin without substantial loss of biological function. Such variants can be selected according to general rules known in the art to have minimal effect on activity (see, e.g., Bowie, et al., Science 247:306-1310, 1990). For example, for IgG4 antibodies, a single amino acid substitution (S228P according to Kabat numbering; designated IgG4Pro) may be introduced to abolish the heterogeneity observed in recombinant IgG4 antibodies (see, e.g., Angal, et al., Mol Immunol 30:105-108, 1993). In certain embodiments, the Fc region includes substitutions that improve pharmacokinetics properties of an antibody, e.g., increased serum half-life. Non-limiting examples of substitutions of the Fc region can be found in U.S. Pat. No. 8,088,376, the content of which is incorporated by reference in its entirety.

The term "equilibrium dissociation constant" abbreviated (KD), refers to the dissociation rate constant (kd, time^{-1}) divided by the association rate constant (ka, $\text{time}^{-1}\ M^{-1}$). Equilibrium dissociation constants can be measured using any method. Thus, in certain embodiments, the antibodies of the present disclosure have a KD of less than about 50 nM, typically less than about 25 nM, or less than 10 nM, e.g., less than about 5 nM, or than about 1 nM and often less than about 10 nM as determined by surface plasmon resonance analysis using a biosensor system such as a Biacore® system performed at 37° C. In certain embodiments, an antibody of the present disclosure has a KD of less than 5×10^{-5} M, less than 10^{-5} M, less than 5×10^{-6} M, less than 10^{-6} M, less than 5×10^{-7} M, less than 10^{-7} M, less than 5×10^{-8} M, less than

10^{-8} M, less than 5×10^{-9} M, less than 10^{-9} M, less than 5×10^{-10} M, less than 10^{-10} M, less than 5×10^{-11M}, less than 10^{-11} M, less than 5×10^{-12} M, less than 10^{-12} M, less than 5×10^{-13} M, less than 10^{-13} M, less than 5×10^{-14} M, less than 10^{-14} M, less than 5×10^{-15} M, or less than 10^{-15} M or lower as measured as a bivalent antibody. As used herein, an "improved" KD refers to a lower KD. In certain embodiments, an antibody of the present disclosure has a KD of less than 5×10^{-5} M, less than 10^{-5} M, less than 5×10^{-6} M, less than 10^{-6} M, less than 5×10^{-7} M, less than 10^{-7} M, less than 5×10^{-8} M, less than 10^{-8} M, less than 5×10^{-9} M, less than 10^{-9} M, less than 5×10^{-10} M, less than 10^{-10} M, less than 5×10^{-11} M, less than 10^{-11} M, less than 5×10^{-12}M, less than 10^{-12} M, less than 5×10^{-13} M, less than 10^{-13} M, less than 5×10^{-14} M, less than 10^{-14} M, less than 5×10^{-15} M, or less than 10^{-15}M or lower as measured as a monovalent antibody, such as a monovalent Fab. In certain embodiments, an anti-CSP antibody of the present disclosure has KD less than 100 pM, e.g., or less than 75 pM, e.g., in the range of 1 to 100 pM, when measured by surface plasmon resonance analysis using a biosensor system such as a Biacore® system performed at 37° C. In certain embodiments, an anti-CSP antibody of the present disclosure has KD of greater than 100 pM, e.g., in the range of 100-1000 pM or 500-1000 pM when measured by surface plasmon resonance analysis using a biosensor system such as a Biacore® system performed at 37° C.

The term "monovalent molecule" as used herein refers to a molecule that has one antigen-binding site, e.g., a Fab or scFv.

The term "bivalent molecule" as used herein refers to a molecule that has two antigen-binding sites. In certain embodiments, a bivalent molecule of the present invention is a bivalent antibody or a bivalent fragment thereof. In certain embodiments, a bivalent molecule of the present invention is a bivalent antibody. In certain embodiments, a bivalent molecule of the present invention is an IgG. In certain embodiments, monoclonal antibodies have a bivalent basic structure. IgG and IgE have only one bivalent unit, while IgA and IgM consist of multiple bivalent units (2 and 5, respectively) and thus have higher valencies. This bivalency increases the avidity of antibodies for antigens.

The terms "monovalent binding" or "monovalently binds to" as used herein refer to the binding of one antigen-binding site to its antigen.

The terms "bivalent binding" or "bivalently binds to" as used herein refer to the binding of both antigen-binding sites of a bivalent molecule to its antigen. In certain embodiments, both antigen-binding sites of a bivalent molecule share the same antigen specificity.

The term "valency" as used herein refers to the number of different binding sites of an antibody for an antigen. A monovalent antibody includes one binding site for an antigen. A bivalent antibody (e.g., a bivalent IgG antibody) includes two binding sites for the same antigen.

The term "affinity" as used herein refers to either the single or combined strength of one or both arms of an antibody (e.g., an IgG antibody) binding to either a simple or complex antigen-expressing one or more epitopes. As defined here, the term "affinity" does not imply a specific number of valencies between the two binding partners.

The phrase "specifically (or selectively) binds" to an antigen or target or "specifically (or selectively) immunoreactive with," when referring to a protein or peptide, refers to a binding reaction whereby the antibody binds to the antigen or target of interest with an affinity that can be distinguished from non-specific interactions occurring between two proteins.

The terms "identical" or percent "identity," in the context of two or more polypeptide sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues that are the same (e.g., at least 70%, at least 75%, at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or higher) identity over a specified region, e.g., the length of the two sequences, when compared and aligned for maximum correspondence over a comparison window or designated region. Alignment for purposes of determining percent amino acid sequence identity can be performed in various methods, including, without any limitation, BLAST, BLAST-2, ALIGN, or Megalign (DNASTAR) software. Examples of algorithms that are suitable for determining percent sequence identity and sequence similarity the BLAST 2.0 algorithms, which are described in Altschul et al., Nuc. Acids Res. 25:3389-3402 (1977) and Altschul et al., J. Mol. Biol. 215:403-410 (1990). In certain embodiments, BLAST 2.0 can be used with the default parameters to determine percent sequence identity.

A "substitution," as used herein, denotes the replacement of one or more amino acids or nucleotides by different amino acids or nucleotides, respectively.

A "conservative" substitution as used herein refers to a substitution of an amino acid such that charge, polarity, hydropathy (hydrophobic, neutral, or hydrophilic), and/or size of the side group chain is maintained. Illustrative sets of amino acids that may be substituted for one another include (i) positively-charged amino acids Lys and Arg; and His at pH of about 6; (ii) negatively charged amino acids Glu and Asp; (iii) aromatic amino acids Phe, Tyr and Trp; (iv) nitrogen ring amino acids His and Trp; (v) aliphatic hydrophobic amino acids Ala, Val, Leu and Ile, (vi) hydrophobic sulfur-containing amino acids Met and Cys, which are not as hydrophobic as Val, Leu, and Ile, (vii) small polar uncharged amino acids Ser, Thr, Asp, and Asn (viii) small hydrophobic or neutral amino acids Gly, Ala, and Pro; (ix) amide-comprising amino acids Asn and Gln; and (xi) beta-branched amino acids Thr, Val, and Ile. Reference to the charge of an amino acid refers to the charge at pH 6-7.

As used herein, the terms "nucleic acid" and "polynucleotide" are used interchangeably and as used herein refer to both sense and anti-sense strands of RNA, cDNA, genomic DNA, and synthetic forms and mixed polymers of the above. In certain embodiments, a polynucleotide refers to a polyribonucleotide, polydeoxynucleotide or a modified form of either type of nucleotide, and combinations thereof. The terms also include, but are not limited to, single- and double-stranded forms of DNA. In addition, a polynucleotide, e.g., a cDNA or mRNA, may include either or both naturally occurring and modified nucleotides linked together by naturally occurring and/or non-naturally occurring nucleotide linkages. The nucleic acid molecules may be modified chemically or biochemically or may contain non-natural or derivatized nucleotide bases, as will be readily appreciated by those of skill in the art. Such modifications include, for example, labels, methylation, substitutions of one or more of the naturally occurring nucleotides with an analogue, internucleotide modifications such as uncharged linkages (e.g., methyl phosphonates, phosphotriesters, phosphoramidates, carbamates, etc.), charged linkages (e.g., phosphorothioates, phosphorodithioates, etc.), pendent moieties (e.g., polypeptides), intercalators (e.g., acridine, psoralen, etc.), chelators, alkylators, and modified linkages (e.g., alpha anomeric nucleic acids, etc.). The above term is also intended to include any topological conformation, including single-stranded, double-stranded, partially duplexed, triplex, hairpinned, circular, and padlocked conformations. A reference to a nucleic acid sequence encompasses its complement unless otherwise specified. Thus, a reference to a nucleic acid molecule having a particular sequence should be understood to encompass its complementary strand, with its complementary sequence. The term also includes codon-optimized nucleic acids that encode the same polypeptide sequence.

An "isolated" nucleic acid refers to a nucleic acid molecule that has been separated from a component of its natural environment. An isolated nucleic acid includes a nucleic acid molecule contained in cells that ordinarily contain the nucleic acid molecule, but the nucleic acid molecule is present extrachromosomally or at a chromosomal location that is different from its natural chromosomal location.

"Isolated nucleic acid encoding an antibody or fragment thereof" refers to one or more nucleic acid molecules encoding antibody heavy and light chains (or fragments thereof), including such nucleic acid molecule(s) in a single vector or separate vectors, and such nucleic acid molecule(s) present at one or more locations in a host cell.

The term "vector," as used herein, refers to a nucleic acid molecule capable of propagating another nucleic acid to which it is linked. The term includes the vector as a self-replicating nucleic acid structure as well as the vector incorporated into the genome of a host cell into which it has been introduced. A "vector," as used herein, refers to a recombinant construct in which a nucleic acid sequence of interest is inserted into the vector. Certain vectors can direct the expression of nucleic acids to which they are operatively linked. Such vectors are referred to herein as "expression vectors".

The terms "host cell," "host cell line," and "host cell culture" are used interchangeably and refer to cells into which exogenous nucleic acid has been introduced, including the progeny of such cells. A host cell can be a recombinant host cell and includes the primary transformed cell and progeny derived therefrom without regard to the number of passages.

A polypeptide "variant," as the term is used herein, is a polypeptide that typically differs from a polypeptide specifically disclosed herein in one or more substitutions, deletions, additions, and/or insertions. In the present invention, a "variant" with reference to the sequences described in the "Anti-CSP Antibody Variants" section refers to an engineered sequence, rather than a naturally occurring sequence.

The term "comparable," in the context of describing the strength of binding of two antibodies to the same target, refers to two dissociation constant (KD) values calculated from two binding reactions that are within three (3) fold from each other. In certain embodiments, the ratio between the first KD (the KD of the binding reaction between the first antibody and the target) and the second KD (the KD of the binding reaction between the second antibody and the target) is within the range of 1:3 or 3:1, endpoints exclusive. A lower KD value denotes stronger binding. For example, without any limitation, an antibody variant that has stronger binding as compared to AB-000224 binds to the target with a KD that is at least ⅓ of the KD measured against the same target for AB-000224.

Anti-CSP Antibodies

The present disclosure provides anti-CSP antibodies AB-000224 and AB-007088 and variants thereof. AB-000224 and AB-007088 were discovered in antibody repertoires generated by Immune Repertoire Capture® (IRC®) technology from plasmablast B cells isolated from two donors enrolled in a Phase 2a study evaluating the efficacy of the RTS,S vaccine in preventing malaria infection. The IRC® technology and its use in antibody discovery is well known and disclosed in, e.g., WO 2012148497A2, the entire content of which is herein incorporated by reference. The RTS,S vaccine is a pseudo-viral particle vaccine that combines the hepatitis B surface antigen and the central repeat and C-terminal regions of the *Plasmodium falciparum* (*P. falciparum*) circumsporozoite protein (CSP). RTS,S consists of two polypeptides; RTS is a single polypeptide chain corresponding to amino acids 207 to 395 of *P. falciparum* (3D7) that is fused to HBsAg and S is a polypeptide of 226 amino acids that corresponds to HBsAg. Stoute, et. al., N Engl J Med; 336:86-91(1997); RTS,S Clinical Trials Partnership, PLoS Med. 11(7):e1001685, (2014), WO1993/10152.

CSP is composed of an N-terminal domain containing a heparan sulfate binding site for hepatocyte adhesion, a central repeat region, and a structured C-terminal α-thrombospondin repeat (αTSR) that is followed by a GPI anchor, which attaches CSP to the sporozoite membrane. The central repeat region of CSP is highly immunogenic, and in all *P. falciparum* strains with a CSP sequence available, the repeat region is composed of 1 NPDP repeat, 3-5 NVDP repeats, and 35-41 NANP repeats (e.g., a total of 1/4/38 of NPDP/NVDP/NANP motifs are present in the *P. falciparum* 3D7 strain). The repeat region begins with the junctional NPDP sequence, typically followed by three alternations of NANP and NVDP sequences, and continues with the remaining NANP repeats, with most *P. falciparum* strains having one NVDP interspersed in the middle of the long NANP repeat region. Pholcharee, T. et al., J. Mol. Bio. 432: 1048-1063 (2020).

In certain embodiments, the anti-CSP antibodies disclosed herein bind to the central repeat region of *P. falciparum* CSP. In certain embodiments, the antibodies disclosed herein bind to *P. falciparum* CSP protein in the repeat and/or junctional regions that contain NPNA, NPDP, and/or NVDP motifs. In certain embodiments, the anti-CSP antibodies disclosed herein bind to the NANP repeat region of *P. falciparum* CSP. In certain embodiments, the anti-CSP antibodies disclosed herein bind to a polypeptide comprising the amino acid sequence of (NPNA)3 (SEQ ID NO: 280).

In certain embodiments, the present disclosure provides anti-CSP antibody variants of AB-000224. In certain embodiments, the present disclosure provides anti-CSP antibody variants of AB-007088. In certain embodiments, the variants exhibit protective effects in vivo, e.g., as shown by a reduction in parasite number in a mouse model of malaria infection.

In certain embodiments, the anti-CSP variants disclosed herein maintain the binding specificity, activity and stability and/or manufacturing properties of the parental antibody. In certain embodiments, the anti-CSP variants disclosed herein generated have improved developability, e.g., as identified through various in vitro assays, such as aggregation assessment by HPLC or UPLC, hydrophobic interaction chromatography (HIC), polyspecificity assays (e.g., baculovirus particle binding), self-interaction nanoparticle spectroscopy (SINS), or mass spec analysis after incubation in an accelerated degradation condition such as high temperature, low pH, high pH, or oxidative H_2O_2. Mutations are successful if the activity is maintained (or enhanced) while removing or reducing the severity of the liability.

Antibody liabilities are further described in Table 1 below:

TABLE 1

Description of potential development liabilities			
Free cysteine[1]	Yield, heterogeneity, stability, activity	sequence comprises an odd number of cysteines	High
N-linked glycosylation	Yield, heterogeneity, activity	N(-P)(S, T)[2]	High
Abnormal net charge	Platform fit, PK	Sharma 2014[3]	High
Patches of hydrophobicity	Stability, PK	Sharma 2014	High
Patches of same charge	Stability, PK	N/A (based on structure)	Medium
Proteolysis	Stability, PK	(K, R)(K, R)[4]	Medium
Proteolysis	Stability, PK	DP	Medium
Asparagine deamidation	Heterogeneity, stability, activity	NG; N(A, N, S, T)[5]	Medium; Low
Aspartate isomerization	Heterogeneity, stability, activity	DG; D(A, D, S, T)[6]	Medium; Low
Lysine glycation	Heterogeneity, stability, activity	K	Low
Methionine oxidation	Heterogeneity, stability, activity	M	Low
Tryptophan oxidation	Heterogeneity, stability, activity	W	Low

[1] "Free cysteine" refers to a cysteine that does not form a disulfide bond with another cysteine and thus is left "free" as thiols. The presence of free cysteines in the antibody can be a potential development liability.
Typically, an odd net number of cysteines in the protein shows a likelihood there is a free cysteine.

[2] The N-linked glycosylation site is N-X-S/T, where X is any residue other than proline.

[3] Sharma et al., Proc. Natl. Acad. Sci. USA 111:18601-18606, 2014.

[4] This motif consists of a K or R, followed by a K or R. Stated differently, the motif can be KK, KR, RK, or RR.

[5] The dipeptide NG poses a medium risk of development liability. The dipeptides NA, NN, NS, and NT pose a low risk of development liability. N may also exhibit low risk of liability for other successor residues, e.g., D, H, or P. Stated differently, dipeptide ND, NH, or NP poses a low risk of development liability.

[6] Similarly to the above, the dipeptide DG poses a medium risk of development liability. The dipeptides DA, DD, DS, and DT pose a low risk of development liability. D may also exhibit low risk of development liability for other successor residues, e.g., N, H, or P.

Another goal for engineering variants is to reduce the risk of clinical immunogenicity. For example, reducing the generation of anti-drug antibodies against the therapeutic antibody. In certain embodiments, the anti-CSP antibody variants have reduced immunogenicity as compared to the parental antibody.

The factors that drive clinical immunogenicity can be classified into two groups. First are factors that are intrinsic to the drug, such as sequence, post-translational modifications, aggregates, degradation products, and contaminants. Second are factors related to how the drug is used, such as dose level, dose frequency, route of administration, patient immune status, and patient HLA type.

One approach to engineering a variant to be as much like self as possible is to identify a close germline sequence and mutate as many mismatched positions (also known as "germline deviations") to the germline residue type as possible. This approach applies for germline genes IGHV, IGHJ, IGKV, IGKJ, IGLV, and IGLJ, and accounts for all of the variable heavy (V11) and variable light (VL) regions except for part of H-CDR3. Germline gene IGHD codes for part of the H-CDR3 region but typically exhibits too much variation in how it is recombined with IGHV and IGHJ (e.g., forward or reverse orientation, any of three translation frames, and 5' and 3' modifications and non-templated additions) to present a "self" sequence template from a population perspective.

Each germline gene can present as different alleles in the population. The least immunogenic drug candidate, in terms of minimizing the percent of patients with an immunogenic response, would likely be one that matches an allele commonly found in the patient population. Single nucleotide polymorphism (SNP) data from the human genome can be used to approximate the frequency of alleles in the population.

Another approach to engineering a lead for reduced immunogenicity risk is to use in silico predictions of immunogenicity, such as the prediction of T cell epitopes, or use in vitro assays of immunogenicity, such as ex vivo human T cell activation. For example, services such as those offered by Lonza, United Kingdom, are available that employ platforms for prediction of HLA binding and in vitro assessment to further identify potential epitopes.

In certain embodiments, antibody variants are additionally designed to enhance the efficacy of the antibody. Design parameters for this aspect focused on CDRs, e.g., CDR3. Positions to be mutated were identified based on structural analysis of antibody-antigen co-crystals (Oyen et al., Proc. Natl. Acad Sci. USA 114:E10438-E10445, 2017) and based on sequence information of other antibodies from the same lineage as AB-000224 or AB-007088.

1. Approaches to Mutation Design

Development liabilities can be removed or reduced by one or more mutations. Mutations are designed to preserve antibody structure and function while removing or reducing development liabilities and to improve function. In certain embodiments, mutations to chemically similar residues were identified to maintain size, shape, charge, and/or polarity. Non-limiting examples of mutations are described in Table 2 below:

TABLE 2

Free cysteine	Odd #C	High	C(A, S)
N-linked glycosylation	N(-P)(S, T)	High	N-*(Q, D, S, A); (S, T)-*(A, N)
Proteolytic cleavage	(K, R)(K, R)	Medium	K, R-*(Q, S, A)
Proteolytic cleavage	DP	Medium	D(E, S, A)
Asparagine deamidation	NG; N(A, N, S, T)*	Medium; Low	N-*(Q ,S, A); G-*(A, S)
Aspartate isomerization	DG; D(A, D, S, T)*	Medium; Low	D-*(E, S, A); G-*(A, S)
Lysine glycation	K	Low	K(R, Q, S, A)
Methionine oxidation	M	Low	M-*(Q, L, S, A)
Tryptophan oxidation	W	Low	W-*(Y, F)
Proteolytic cleavage	(K, R)(K, R)	Medium	K, R-*(Q, S, A)

2. Anti-CSP Antibody Variants of AB-000224

In certain embodiments, a variant of an anti-CSP antibody AB-000224 disclosed herein comprises modifications compared to AB-000224 that provide improved pharmacokinetic properties, increased serum stability, stronger binding, and/or improved in vivo protective effects compared to AB-000224. In certain embodiments, a variant of an anti-CSP antibody AB-000224 disclosed herein exhibits reduced immunogenicity and/or increased manufacturability as compared to AB-000224. In certain embodiments, a variant of an anti-CSP antibody AB-000224 disclosed herein has at least one modification, e.g., substitution, relative to the native AB-000224 variable heavy chain amino acid sequence (SEQ ID NO: 14) or variable light chain amino acid sequence (SEQ ID NO: 13) described herein, and has improved developability, e.g., decreased heterogeneity, increased yield, increased stability, improved net charges to improve pharmacokinetics, and/or reduced immunogenicity. In certain embodiments, a VH region or a VL region of such a variant of an anti-CSP antibody AB-000224 disclosed herein has at least two, three, four, five, or six, or more modifications, e.g., substitutions. In certain embodiments, a variant of the an anti-CSP antibody AB-000224 disclosed herein has a total of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50 modifications, e.g. substitutions, including both variable regions, compared to AB-000224.

In certain embodiments, a variant of an anti-CSP antibody AB-000224 disclosed herein exhibits increased serum half-life as compared to AB-000224. In certain embodiments, a variant of an anti-CSP antibody AB-000224 disclosed herein has at least one modification, e.g., substitution, relative to the native AB-000224 Fc region of the heavy chain sequence described herein, and has improved pharmacokinetics properties, e.g., half-life. In certain embodiments, an Fc region of the heavy chain of such a variant of an anti-CSP antibody AB-000224 disclosed herein has at least two, three, four, five, or six, or more modifications, e.g., substitutions. In certain embodiments, a variant of an anti-CSP antibody AB-000224 disclosed herein has a total of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50 modifications, e.g. substitutions, including both heavy and light chains, compared to AB-000224. In certain non-limiting embodiments, an Fc region of the heavy chain of a variant of an anti-CSP antibody AB-000224 disclosed herein can include an isoleucine at position 250, a tyrosine at position 252, an isoleucine at position 259, a glutamine at position 307, a phenylalanine at position 308, a leucine at position 319, a leucine at position 428, a histidine at position 434, a phenylalanine at position 434, an alanine at position 434, a serine at position 434, a methionine at position 434, or a combination thereof, wherein the numbering is defined by EU index as in Kabat. In certain embodiments, an Fc region of the heavy chain of a variant of an anti-CSP antibody AB-000224 disclosed herein includes a leucine at position 428 and a serine at position 434, wherein the numbering is defined by EU index as in Kabat.

The light and heavy chain CDRs of AB-000224 as defined by Kabat numbering system are shown in Table 3 below:

TABLE 3

AB-000224 CDR sequences (Kabat)			
	CDRI	CDR2	CDR3
VL region	TGMNSNIGAGYDVY (SEQ ID NO: 1)	GNSNRPS (SEQ ID NO: 2)	QSYDTSLNGWA (SEQ ID NO: 3)
VH region	DHAMS (SEQ ID NO: 4)	FIRKTTYGATTHYA AAVRG (SEQ ID NO: 5)	VQLDYGPGYQYYGM DV (SEQ ID NO: 6)

The light and heavy chain CDRs of AB-000224 as defined by ASN numbering system are shown in Table 4 below:

TABLE 4

AB-000224 CDR sequences (ASN)			
	CDRI	CDR2	CDR3
VL region	TGMNSNIGAGYDVY (SEQ ID NO: 7)	GNSNRPS (SEQ ID NO: 8)	QSYDTSLNGWA (SEQ ID NO: 9)
VH region	DHAMS (SEQ ID NO: 10)	FI RKTTYGATTHY AAAVRG (SEQ ID NO: 11)	VQLDYGPGYQYYGM DV (SEQ ID NO: 12)

The heavy chain variable region (VH) and light chain variable region (VL) sequences and heavy and light chain sequences of AB-000224 are shown in Table 5 below:

TABLE 5

AB-000224 variable region and full chain sequences	
VL region	ESVLTQPPSVSGAPGQRVTISCTGMNSNIGAGYDVYWYQQLPGRAPKLLIYGNSNRPSGVPDRFSGSRSGTSASLAITGLQAEDEADYYCQSYDTSLNGWAFGGGTKLTVLG (SEQ ID NO: 13)
VH region	EVQLVESGGGLVQPGRSLRLPCTASGFSFGDHAMSWVRQAPGKGLEWVGFIRKTTYGATTHYAAAVRGRFTISRDDSKSIVYLQMNSLKTEDTAVYFCTRVQLDYGPGYQYYGMDVWGQGTTVTVSS (SEQ ID NO: 14)
DNA for VL region	GAGTCTGTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAGGGTCACCATCTCCTGCACTGGGATGAACTCCAACATCGGGGCAGGTTATGATGTATACTGGTACCAACAACTTCCAGGAAGAGCCCCCAAACTCCTCATCTATGGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAGGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACACCAGCCTGAATGGTTGGGCTTTCGGCGGAGGGACCAAGTTGACCGTCCTAGGC [SEQ ID NO: 15]
DNA for VH region	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCAGGGCGGTCCCTGAGACTCCCCTGTACAGCCTCTGGGTTTAGTTTTGGTGATCATGCTATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTAGGTTTCATTAGAAAGACAACTTATGGTGCGACAACACACTACGCCGCGGCTGTGAGAGGCAGATTCACCATCTCGCGAGATGATTCTAAAAGCATTGTCTATCTGCAAATGAACAGCCTGAAAACCGAGGACACAGCCGTGTATTTCTGTACTAGAGTGCAGCTTGACTATGGCCCGGGATACCAGTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA [SEQ ID NO: 16]
Light Chain	ESVLTQPPSVSGAPGQRVTISCTGMNSNIGAGYDVYWYQQLPGRAPKLLIYGNSNRPSGVPDRFSGSRSGTSASLAITGLQAEDEADYYCQSYDTSLNGWAFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLVSDFYPGAVTVAWKADGSPVKVGVETTKPSKQSNNKYAASSYLSLTPEQWKSHRSYSCRVTHEGSTVEKTVAPAECS [SEQ ID NO:17]
Heavy Chain version 1	EVQLVESGGGLVQPGRSLRLPCTASGFSFGDHAMSWVRQAPGKGLEWVGFIRKTTYGATTHYAAAVRGRFTISRDDSKSIVYLQMNSLKTEDTAVYFCTRVQLDYGPGYQYYGMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSWTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPK

TABLE 5-continued

AB-000224 variable region and full chain sequences	
	SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF NWYVDGVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNHYTQKSLSLSPGK [SEQ ID NO: 18]
Heavy Chain version 2	EVQLVESGGGLVQPGRSLRLPCTASGFSFGDHAMSWVRQAPGKGLEWVGFIRKTTYG ATTHYAAAVRGRFTISRDDSKSIVYLQMNSLKTEDTAVYFCTRVQLDYGPGYQYYGM DVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSG ALTSGVHTFPAVLQSSGLYSLSSWTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPK SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF NWYVDGVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN nykttppvldsdgsfflyskltvdksrwqqgnvfscsvlhealhshytqkslslspg K [SEQ ID NO: 19]
DNA for Light Chain	GAGTCTGTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAGGGTCACC ATCTCCTGCACTGGGATGAACTCCAACATCGGGGCAGGTTATGATGTATACTGGTAC CAACAACTTCCAGGAAGAGCCCCCAAACTCCTCATCTATGGTAACAGCAATCGGCCC TCAGGGGTCCCTGACCGATTCTCTGGCTCCAGGTCTGGCACCTCAGCCTCCCTGGCC ATCACTGGGCTCCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACACC AGCCTGAATGGTTGGGCTTTCGGCGGAGGGACCAAGTTGACCGTCCTAGGCCAGCCC AAGGCTGCCCCCTCGGTCACTCTGTTCCCACCCTCCTCTGAGGAGCTTCAAGCCAAC AAGGCCACACTGGTGTGTCTCGTAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCC TGGAAGGCAGATGGCAGCCCCGTCAAGGTGGGAGTGGAGACCACCAAACCCTCCAAA CAAAGCAACAACAAGTATGCGGCCAGCAGCTACCTGAGCCTGACGCCCGAGCAGTGG AAGTCCCACAGAAGCTACAGCTGCCGGGTCACGCATGAAGGGAGCACCGTGGAGAAG ACAGTGGCCCCTGCAGAATGCTCT [SEQ ID NO: 20]
DNA for Heavy Chain version 1	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGG TACAGCCAGGGCGGTCCCTGAGACTCCCCTGTACAGCCTCTGGGTTTAGT TTTGGTGATCATGCTATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCT GGAGTGGGTAGGTTTCATTAGAAAGACAACTTATGGTGCGACAACACACT ACGCCGCGGCTGTGAGAGGCAGATTCACCATCTCGCGAGATGATTCTAAA AGCATTGTCTATCTGCAAATGAACAGCCTGAAAACCGAGGACACAGCCGT GTATTTCTGTACTAGAGTGCAGCTTGACTATGGCCCGGGATACCAGTACT ACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGCC TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCAC CTCTGGGGGCACAGCAGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCG AACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCAC ACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGT GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACG TGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAA TCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCT GGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCA TGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCAC GAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCA TAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTG TGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAAC CATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGC CCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTG GTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGG GCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACG GCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAA [SEQ ID NO: 21]
DNA for Heavy Chain version 2	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGG TACAGCCAGGGCGGTCCCTGAGACTCCCCTGTACAGCCTCTGGGTTTAGT TTTGGTGATCATGCTATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCT GGAGTGGGTAGGTTTCATTAGAAAGACAACTTATGGTGCGACAACACACT ACGCCGCGGCTGTGAGAGGCAGATTCACCATCTCGCGAGATGATTCTAAA AGCATTGTCTATCTGCAAATGAACAGCCTGAAAACCGAGGACACAGCCGT GTATTTCTGTACTAGAGTGCAGCTTGACTATGGCCCGGGATACCAGTACT ACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGCC TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCAC CTCTGGGGGCACAGCAGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCG AACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCAC ACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGT GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACG TGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAA TCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCT GGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCA TGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCAC GAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCA TAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTG

TABLE 5-continued

AB-000224 variable region and full chain sequences
TGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAAC CATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGC CCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTG GTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGG GCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACG GCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGCTGCATGAGGCTCTGCACTCCCA CTACACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAA [SEQ ID NO: 22]

In certain embodiments, a variant of an anti-CSP antibody includes one, two, or three CDRs of a VL sequence of Table 5. In certain embodiments, a variant of an anti-CSP antibody includes at least one mutation, e.g., substitution, and no more than 10, 20, 30, 40, or 50 mutations in the VL amino acid sequence set forth in SEQ ID NO: 13. In certain embodiments, the VL of the variant of an anti-CSP antibody includes at least one, at least two, or at least three mutations, e.g., substitutions, in the CDR1 amino acid sequence set forth in SEQ ID NO: 1. In certain embodiments, the VL of the variant of an anti-CSP antibody includes at least one, at least two, or at least three mutations, e.g., substitutions, in the CDR2 amino acid sequence set forth in SEQ ID NO: 2. In certain embodiments, the VL of the variant of an anti-CSP antibody includes at least one, at least two, or at least three mutations, e.g., substitutions, in the CDR3 amino acid sequence set forth in SEQ ID NO: 3. In certain embodiments, the VL of the variant of an anti-CSP antibody includes at least one, at least two, or at least three mutations, e.g., substitutions, in the CDR1 amino acid sequence set forth in SEQ ID NO: 7. In certain embodiments, the VL of the variant of an anti-CSP antibody includes at least one, at least two, or at least three mutations, e.g., substitutions, in the CDR2 amino acid sequence set forth in SEQ ID NO: 8. In certain embodiments, the VL of the variant of an anti-CSP antibody includes at least one, at least two, or at least three mutations, e.g., substitutions, in the CDR3 amino acid sequence set forth in SEQ ID NO: 9. In certain embodiments, the mutation is a conservative substitution. In certain embodiments, the VL of the variant of an anti-CSP antibody includes at least one, at least two, or at least three mutations, e.g., substitutions, in the framework of the amino acid sequence set forth in SEQ ID NO: 13. An exemplary nucleic acid sequence of SEQ ID NO: 13 is set forth in SEQ ID NO: 15. In certain embodiments, the VL of the variant of an anti-CSP antibody includes a substitution at position 1 of the SEQ ID NO: 13. In certain embodiments, the substitution is E1Q. In certain embodiments, the VL of the variant of an anti-CSP antibody includes a substitution at position 4 of the SEQ ID NO: 13. In certain embodiments, the substitution is R44T.

In certain embodiments, a variant of an anti-CSP antibody includes one, two, or three CDRs of a VH sequence of Table 5. In certain embodiments, a variant of an anti-CSP antibody includes at least one mutation, e.g., substitutions, and no more than 10, 20, 30, 40, or 50 mutations in the VH amino acid sequence set forth in SEQ ID NO: 14. In certain embodiments, the VH of the variant of an anti-CSP antibody includes at least one, at least two, or at least three mutations, e.g., substitutions, in the CDR1 amino acid sequence set forth in SEQ ID NO: 4. In certain embodiments, the VH of the variant of an anti-CSP antibody includes at least one, at least two, or at least three mutations, e.g., substitutions, in the CDR2 amino acid sequence set forth in SEQ ID NO: 5. In certain embodiments, the VH of the variant of an anti-CSP antibody includes at least one, at least two, or at least three mutations, e.g., substitutions, in the CDR3 amino acid sequence set forth in SEQ ID NO: 6. In certain embodiments, the VH of the variant of an anti-CSP antibody includes at least one, at least two, or at least three mutations, e.g., substitutions, in the CDR1 amino acid sequence set forth in SEQ ID NO: 10. In certain embodiments, the VH of the variant of an anti-CSP antibody includes at least one, at least two, or at least three mutations, e.g., substitutions, in the CDR2 amino acid sequence set forth in SEQ ID NO: 11. In certain embodiments, the VH of the variant of an anti-CSP antibody includes at least one, at least two, or at least three mutations, e.g., substitutions, in the CDR3 amino acid sequence set forth in SEQ ID NO: 12. In certain embodiments, the mutation is a conservative substitution. In certain embodiments, the VH of the variant of an anti-CSP antibody includes a CDR2 having a substitution at position 12 of the SEQ ID NO: 5. In certain embodiments, the substitution is H12K. In certain embodiments, the VH of the variant of an anti-CSP antibody includes a CDR2 having a substitution at position 18 of the SEQ ID NO: 5. In certain embodiments, the substitution is R18K. In certain embodiments, the mutation is a conservative substitution. In certain embodiments, the VH of the variant of an anti-CSP antibody includes a CDR2 having a substitution at position 12 of the SEQ ID NO: 11. In certain embodiments, the substitution is H12K. In certain embodiments, the VH of the variant of an anti-CSP antibody includes a CDR2 having a substitution at position 18 of the SEQ ID NO: 11. In certain embodiments, the substitution is R18K. In certain embodiments, the VH of the variant of an anti-CSP antibody includes at least one, at least two, at least three mutations, or at least four mutations, e.g., substitutions, in the framework of the amino acid sequence set forth in SEQ ID NO: 14. An exemplary nucleic acid sequence of SEQ ID NO: 14 is set forth in SEQ ID NO: 16. In certain embodiments, the VH of the variant of an anti-CSP antibody includes a substitution at position 21 of the SEQ ID NO: 14. In certain embodiments, the substitution is P21S. In certain embodiments, the VH of the variant of an anti-CSP antibody includes a substitution at position 23 of the SEQ ID NO: 14. In certain embodiments, the substitution is T23A. In certain embodiments, the VH of the variant of an anti-CSP antibody includes a substitution at position 80 of the SEQ ID NO: 14. In certain embodiments, the substitution is I80T. In certain embodiments, the VH of the variant of an anti-CSP antibody includes a substitution at position 90 of the SEQ ID NO: 14. In certain embodiments, the substitution is T90A. In certain embodiments, the VH of the variant of an anti-CSP antibody includes a substitution at position 99 of the SEQ ID NO: 14. In certain embodiments, the substitution is T99A.

In certain embodiments, a variant of an anti-CSP antibody includes at least one mutation, e.g., substitution, and no more than 10, 20, 30, 40, or 50 mutations in the Fc region of the heavy chain amino acid sequence set forth in SEQ ID NO: 18. In certain embodiments, the heavy chain of the variant of an anti-CSP antibody has an amino acid sequence set forth in SEQ ID NO: 18. An exemplary nucleic acid sequence of SEQ ID NO: 18 is set forth in SEQ ID NO: 21. In certain embodiments, the heavy chain of the variant of an anti-CSP antibody includes a substitution at position 438 of the SEQ ID NO: 18. In certain embodiments, the substitution is M438L. In certain embodiments, the heavy chain of the variant of an anti-CSP antibody includes a substitution at position 444 of the SEQ ID NO: 18. In certain embodiments, the substitution is N444S. In certain embodiments, the heavy chain of the variant of an anti-CSP antibody includes a substitution at position 438 of the SEQ ID NO: 18 and a substitution at position 444 of the SEQ ID NO: 18. In certain embodiments, the substitutions are M438L and N444S. In certain embodiments, the heavy chain of the variant of an anti-CSP antibody has an amino acid sequence set forth in SEQ ID NO: 19. An exemplary nucleic acid sequence of SEQ ID NO: 19 is set forth in SEQ ID NO: 22.

In certain embodiments, the light chain of the anti-CSP antibody AB-000224 and variants thereof comprises a signal peptide. In certain embodiments, the signal peptide is an IGLV2-8 signal peptide. In certain embodiments, the signal peptide has an amino acid sequence set forth in SEQ ID NO: 277. In certain embodiments, the heavy chain of the anti-CSP antibody AB-000224 and variants thereof comprises a signal peptide. In certain embodiments, the signal peptide is an IGKV1-39 signal peptide. In certain embodiments, the signal peptide has an amino acid sequence set forth in SEQ ID NO: 278. SEQ ID NO: 277 and SEQ ID NO: 278 are provided below:

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                                        [SEQ ID NO: 277]
MAWALLLLTLLTQGTGSWA

                                        [SEQ ID NO: 278]
MDMRVPAQLLGLLLLWLRGARC
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In certain embodiments, the anti-CSP antibody variant comprises a light chain variable region comprising a CDR1, a CDR2, and a CDR3 and having the amino acid sequence set forth in SEQ ID NO: 23, as shown in Table 6. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 and having the amino acid sequence set forth in SEQ ID NO: 24, as shown in Table 6. In certain embodiments, the anti-CSP antibody variant comprises a light chain having the amino acid sequence set forth in SEQ ID NO: 27, as shown in Table 6. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain having the amino acid sequence set forth in SEQ ID NO: 28, as shown in Table 6. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain having the amino acid sequence set forth in SEQ ID NO: 29, as shown in Table 6. Exemplary nucleic acid sequences of SEQ ID NOS: 23, 24, 27, 28, and 29 are provided in Table 6 below.

TABLE 6

	Antibody ID: AB-000224.001	
	KABAT	ASN
CDRI-VL	TGMNSNIGAGYDVY [SEQ ID NO: 1]	TGMNSNIGAGYDVY [SEQ ID NO: 7]
CDR2-VL	GNSNRPS [SEQ ID NO: 2]	GNSNRPS [SEQ ID NO: 8]
CDR3-VL	QSYDTSLNGWA [SEQ ID NO: 3]	QSYDTSLNGWA [SEQ ID NO: 9]
CDRI-VH	DHAMS [SEQ ID NO: 4]	DHAMS [SEQ ID NO: 10]
CDR2-VH	FIRKTTYGATTHYAAAVRG [SEQ ID NO: 5]	FIRKTTYGATTHYAAAVRG [SEQ ID NO: 11]
CDR3-VH	VQLDYGPGYQYYGMDV [SEQ ID NO: 6]	VQLDYGPGYQYYGMDV [SEQ ID NO: 12]
VL	QSVLTQPPSVSGAPGQRVTISCTGMNSNIGAGYDVYWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSRSGTSASLAITGLQAEDEADYYCQSYDTSLNGWAFGGGTKLTVLG [SEQ ID NO: 23]	
VH	EVQLVESGGGLVQPGRSLRLSCTASGFSFGDHAMSWVRQAPGKGLEWVGFIRKTTYGATTHYAAAVRGRFTISRDDSKSIVYLQMNSLKTEDTAVYFCTRVQLDYGPGYQYYGMDVWGQGTTVTVSS [SEQ ID NO: 24]	
DNA for VL	CAGTCTGTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAGGGTCACCATCTCCTGCACTGGGATGAACTCCAACATCGGGGCAGGTTATGATGTATACTGGTACCAACAACTTCCAGGAACTGCCCCCAAACTCCTCATCTATGGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAGGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACACCAGCCTGAATGGTTGGGCTTTCGGCGGAGGGACCAAGTTGACCGTCCTAGGC [SEQ ID NO: 25]	
DNA for VH	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCAGGGCGGTCCCTGAGACTCAGCTGTACAGCCTCTGGGTTTAGTTTTGGTGATCATGCTATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTAGGTTTCATTAGAAAGACAACTTATGGTGCGACAACACACTACGCCGCGGCTGTGAGAGGCAGATTCACCATCTCGCGAGATGATTCTAAAAGCATTGTCTATCTGCAAATGAACAGCCTGAAAACCGAGGACACAGCCGTGTATTTCTGTACTAGAGTGCAGCTTGACTATGGCCCGGGATACCAGTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA [SEQ ID NO: 26]	

TABLE 6-continued

Antibody ID: AB-000224.001

	KABAT ASN
Light Chain	QSVLTQPPSVSGAPGQRVTISCTGMNSNIGA GYDVYWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSRSGTSASLAITGLQ AEDEADYYCQSYDTSLNGWAFGGGTKLTVLGQPKAAPSVTLFPPSSEELQ ANKATLVCLVSDFYPGAVTVAWKADGSPVKVGVETTKPSKQSNNKYAASS YLSLTPEQWKSHRSYSCRVTHEGSTVEKTVAPAECS [SEQ ID NO: 27]
Heavy Chain version 1	EVQLVESGGGLVQPGRSLRLSCTASGFSFGDHAMSWVRQAPGKGLEWVGFIRKTTYGA TTHYAAAVRGRFTISRDDSKSIVYLQMNSLKTEDTAVYFCTRVQLDYGPGYQYYGMDV WGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDK THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK [SEQ ID NO: 28]
Heavy Chain version 2	EVQLVESGGGLVQPGRSLRLSCTASGFSFGDHAMSWVRQAPGKGLEWVGFIRKTTYGA TTHYAAAVRGRFTISRDDSKSIVYLQMNSLKTEDTAVYFCTRVQLDYGPGYQYYGMDV WGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDK THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK [SEQ ID NO: 29]
DNA for Light Chain	CAGTCTGTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAGGGTCACCA TCTCCTGCACTGGGATGAACTCCAACATCGGGGCAGGTTATGATGTATACTGGTACCA ACAACTTCCAGGAACTGCCCCCAAACTCCTCATCTATGGTAACAGCAATCGGCCCTCA GGGGTCCCTGACCGATTCTCTGGCTCCAGGTCTGGCACCTCAGCCTCCCTGGCCATCA CTGGGCTCCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACACCAGCCT GAATGGTTGGGCTTTCGGCGGAGGGACCAAGTTGACCGTCCTAGGCCAGCCCAAGGCT GCCCCCTCGGTCACTCTGTTCCCACCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCA CACTGGTGTGTCTCGTAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGC AGATGGCAGCCCCGTCAAGGTGGGAGTGGAGACCACCAAACCCTCCAAACAAAGCAAC AACAAGTATGCGGCCAGCAGCTACCTGAGCCTGACGCCCGAGCAGTGGAAGTCCCACA GAAGCTACAGCTGCCGGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCC TGCAGAATGCTCT [SEQ ID NO: 30]
DNA for Heavy Chain version 1	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCAGGGCGGTCCCTGAGAC TCAGCTGTACAGCCTCTGGGTTTAGTTTTGGTGATCATGCTATGAGCTGGGTCCGCCA GGCTCCAGGGAAGGGGCTGGAGTGGGTAGGTTTCATTAGAAAGACAACTTATGGTGCG ACAACACACTACGCCGCGGCTGTGAGAGGCAGATTCACCATCTCGCGAGATGATTCTA AAAGCATTGTCTATCTGCAAATGAACAGCCTGAAAACCGAGGACACAGCCGTGTATTT CTGTACTAGAGTGCAGCTTGACTATGGCCCGGGATACCAGTACTACGGTATGGACGTC TGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCT TCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCAGCCCTGGGCTGCCT GGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACC AGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCA GCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAA TCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAAA ACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCC TCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATG CGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGT ACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTA CAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGC TGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACAT CGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCC GTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCA GGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAA [SEQ ID NO: 31]
DNA for Heavy Chain version 2	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCAGGGCGGTCCCTGAGAC TCAGCTGTACAGCCTCTGGGTTTAGTTTTGGTGATCATGCTATGAGCTGGGTCCGCCA GGCTCCAGGGAAGGGGCTGGAGTGGGTAGGTTTCATTAGAAAGACAACTTATGGTGCG ACAACACACTACGCCGCGGCTGTGAGAGGCAGATTCACCATCTCGCGAGATGATTCTA AAAGCATTGTCTATCTGCAAATGAACAGCCTGAAAACCGAGGACACAGCCGTGTATTT CTGTACTAGAGTGCAGCTTGACTATGGCCCGGGATACCAGTACTACGGTATGGACGTC TGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCT TCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCAGCCCTGGGCTGCCT GGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACC AGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCA GCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAA TCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAAA

TABLE 6-continued

Antibody ID: AB-000224.001		
	KABAT	ASN
	ACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGCTGCATGAGGCTCTGCACTCCCACTACACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAA [SEQ ID NO: 32]	

In certain embodiments, the anti-CSP antibody variant comprises a light chain variable region comprising a CDR1, a CDR2, and a CDR3 and having the amino acid sequence set forth in SEQ ID NO: 33, as shown in Table 7. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 and having the amino acid sequence set forth in SEQ ID NO: 34, as shown in Table 75. In certain embodiments, the anti-CSP antibody variant comprises a light chain having the amino acid sequence set forth in SEQ ID NO: 37, as shown in Table 7. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain having the amino acid sequence set forth in SEQ ID NO: 38, as shown in Table 7. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain having the amino acid sequence set forth in SEQ ID NO: 39, as shown in Table 7. Exemplary nucleic acid sequences of SEQ ID NOS: 33, 34, 37, 38, and 39 are provided in Table 7 below.

TABLE 7

Antibody ID: AB-000224.002		
	KABAT	ASN
CDR1-VL	TGMNSNIGAGYDVY [SEQ ID NO: 1]	TGMNSNIGAGYDVY [SEQ ID NO: 7]
CDR2-VL	GNSNRPS [SEQ ID NO: 2]	GNSNRPS [SEQ ID NO: 8]
CDR3-VL	QSYDTSLNGWA [SEQ ID NO: 3]	QSYDTSLNGWA [SEQ ID NO: 9]
CDRI-VH	DHAMS [SEQ ID NO: 4]	DHAMS [SEQ ID NO: 10]
CDR2-VH	FIRKTTYGATTHYAAAVRG [SEQ ID NO: 5]	FIRKTTYGATTHYAAAVRG [SEQ ID NO: 11]
CDR3-VH	VQLDYGPGYQYYGMDV [SEQ ID NO: 6]	VQLDYGPGYQYYGMDV [SEQ ID NO: 12]
VL	QSVLTQPPSVSGAPGQRVTISCTGMNSNIGAGYDVYWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSRSGTSASLAITGLQAEDEADYYCQSYDTSLNGWAFGGGTKLTVLG [SEQ ID NO: 33]	
VH	EVQLVESGGGLVQPGRSLRLSCAASGFSFGDHAMSWVRQAPGKGLEWVGFIRKTTYGATTHYAAAVRGRFTISRDDSKSIVYLQMNSLKTEDTAVYFCTRVQLDYGPGYQYYGMDVWGQGTTVTVSS [SEQ ID NO: 34]	
DNA for VL	CAGTCTGTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAGGGTCACCATCTCCTGCACTGGGATGAACTCCAACATCGGGGCAGGTTATGATGTATACTGGTACCAACAACTTCCAGGAACTGCCCCCAAACTCCTCATCTATGGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAGGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACACCAGCCTGAATGGTTGGGCTTTCGGCGGAGGGACCAAGTTGACCGTCCTAGGC [SEQ ID NO: 35]	
DNA forVH	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCAGGGCGGTCCCTGAGACTCAGCTGTGCGGCCTCTGGGTTTAGTTTTGGTGATCATGCTATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTAGGTTTCATTAGAAAGACAACTTATGGTGCGACAACACACTACGCCGCGGCTGTGAGAGGCAGATTCACCATCTCGCGAGATGATTCTAAAAGCATTGTCTATCTGCAAATGAACAGCCTGAAAACCGAGGACACAGCCGTGTATTTCTGTACTAGAGTGCAGCTTGACTATGGCCCGGGATACCAGTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA [SEQ ID NO: 36]	

TABLE 7-continued

Antibody ID: AB-000224.002		
	KABAT	ASN
Light Chain	QSVLTQPPSVSGAPGQRVTISCTGMNSNIGA GYDVYWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSRSGTSASLAITGLQ AEDEADYYCQSYDTSLNGWAFGGGTKLTVLGQPKAAPSVTLFPPSSEELQ AN KAT LVC LVS D FY P GAVTVAWKADGS PVKVGVETT KPSKQSNNKYAAS S YLSLTPEQWKSHRSYSCRVTHEGSTVEKTVAPAECS[SEQ ID NO: 37]	
Heavy Chain version 1	EVQLVESGGGLVQPGRSLRLSCAASGFS FGDHAMSWVRQAPGKGLEWVGFIRKTTYGATTHYAAAVRGRFTISRDDSK SIVYLQMNSLKTEDTAVYFCTRVQLDYGPGYQYYGMDVWGQGTTVTVSSA STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPK SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNHYTQKSLSLSPGK [SEQ ID NO: 38]	
Heavy Chain version 2	EVQLVESGGGLVQPGRSLRLSCAASGFS FGDHAMSWVRQAPGKGLEWVGFIRKTTYGATTHYAAAVRGRFTISRDDSK SIVYLQMNSLKTEDTAVYFCTRVQLDYGPGYQYYGMDVWGQGTTVTVSSA STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPK SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVLHEALHSHYTQKSLSLSPGK [SEQ ID NO: 39]	
DNA for Light Chain	CAGTCTGTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAG GGCAGAGGGTCACCATCTCCTGCACTGGGATGAACTCCAACATCGGGGCA GGTTATGATGTATACTGGTACCAACAACTTCCAGGAACTGCCCCCAAACT CCTCATCTATGGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGATTCT CTGGCTCCAGGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAG GCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACACCAGCCTGAA TGGTTGGGCTTTCGGCGGAGGGACCAAGTTGACCGTCCTAGGCCAGCCCA AGGCTGCCCCCTCGGTCACTCTGTTCCCACCCTCCTCTGAGGAGCTTCAA GCCAACAAGGCCACACTGGTGTGTCTCGTAAGTGACTTCTACCCGGGAGC CGTGACAGTGGCCTGGAAGGCAGATGGCAGCCCCGTCAAGGTGGGAGTGG AGACCACCAAACCCTCCAAACAAAGCAACAACAAGTATGCGGCCAGCAGC TACCTGAGCCTGACGCCCGAGCAGTGGAAGTCCCACAGAAGCTACAGCTG CCGGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTGCAG AATGCTCT [SEQ ID NO: 40]	
DNA for Heavy Chain version 1	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCAGGGCGGTCCCTGAGACTCA GCTGTGCGGCCTCTGGGTTTAGTTTTGGTGATCATGCTATGAGCTGGGTCCGCCAGGCTCC AGGGAAGGGGCTGGAGTGGGTAGGTTTCATTAGAAAGACAACTTATGGTGCGACAACACAC TACGCCGCGGCTGTGAGAGGCAGATTCACCATCTCGCGAGATGATTCTAAAAGCATTGTCT ATCTGCAAATGAACAGCCTGAAAACCGAGGACACAGCCGTGTATTTCTGTACTAGAGTGCA GCTTGACTATGGCCCGGGATACCAGTACTACGGTATGGACGTCTGGGGCCAAGGGACCACG GTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCA AGAGCACCTCTGGGGGCACAGCAGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACC GGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTC CTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGG GCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAA AGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTC CTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTT CAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAG TACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATG GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCAT CTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAT GAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACA TCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGT GCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGG CAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACAC AGAAGAGCCTCTCCCTGTCTCCGGGTAAA [SEQ ID NO: 41]	
DNA for Heavy Chain version 1	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCAGGGCGGTCCCTGAGACTCA GCTGTGCGGCCTCTGGGTTTAGTTTTGGTGATCATGCTATGAGCTGGGTCCGCCAGGCTCC AGGGAAGGGGCTGGAGTGGGTAGGTTTCATTAGAAAGACAACTTATGGTGCGACAACACAC TACGCCGCGGCTGTGAGAGGCAGATTCACCATCTCGCGAGATGATTCTAAAAGCATTGTCT ATCTGCAAATGAACAGCCTGAAAACCGAGGACACAGCCGTGTATTTCTGTACTAGAGTGCA GCTTGACTATGGCCCGGGATACCAGTACTACGGTATGGACGTCTGGGGCCAAGGGACCACG GTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCA AGAGCACCTCTGGGGGCACAGCAGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACC	

TABLE 7-continued

Antibody ID: AB-000224.002		
	KABAT	ASN
	GGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGCTGCATGAGGCTCTGCACTCCCACTACACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAA [SEQ ID NO: 42]	

In certain embodiments, the anti-CSP antibody variant comprises a light chain variable region comprising a CDR1, a CDR2, and a CDR3 and having the amino acid sequence set forth in SEQ ID NO: 43, as shown in Table 8. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 and having the amino acid sequence set forth in SEQ ID NO: 44, as shown in Table 8. In certain embodiments, the anti-CSP antibody variant comprises a light chain having the amino acid sequence set forth in SEQ ID NO: 47, as shown in Table 8. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain having the amino acid sequence set forth in SEQ ID NO: 48, as shown in Table 8. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain having the amino acid sequence set forth in SEQ ID NO: 49, as shown in Table 8. Exemplary nucleic acid sequences of SEQ ID NOS: 43, 44, 47, 48, and 49 are provided in Table 8 below.

TABLE 8

Antibody ID: AB-000224.003		
	KABAT	ASN
CDR1-VL	TGMNSNIGAGYDVY [SEQ ID NO: 1]	TGMNSNIGAGYDVY [SEQ ID NO: 7]
CDR2-VL	GNSNRPS [SEQ ID NO: 2]	GNSNRPS [SEQ ID NO: 8]
CDR3-VL	QSYDTSLNGWA [SEQ ID NO: 3]	QSYDTSLNGWA [SEQ ID NO: 9]
CDR1-VH	DHAMS [SEQ ID NO: 4]	DHAMS [SEQ ID NO: 10]
CDR2-VH	FIRKTTYGATTHYAAAVRG [SEQ ID NO: 5]	FIRKTTYGATTHYAAAVRG [SEQ ID NO: 11]
CDR3-VH	VQLDYGPGYQYYGMDV [SEQ ID NO: 6]	VQLDYGPGYQYYGMDV [SEQ ID NO: 12]
VL	QSVLTQPPSVSGAPGQRVTISCTGMNSNIGAGYDVYWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSRSGTSASLAITGLQAEDEADYYCQSYDTSLNGWAFGGGTKLTVLG [SEQ ID NO: 43]	
VH	EVQLVESGGGLVQPGRSLRLSCTASGFSFGDHAMSWVRQAPGKGLEWVGFIRKTTYGATTHYAAAVRGRFTISRDDSKSTVYLQMNSLKTEDTAVYFCTRVQLDYGPGYQYYGMDVWGQGTTVTVSS [SEQ ID NO: 44]	
DNA for VL	CAGTCTGTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAGGGTCACCATCTCCTGCACTGGGATGAACTCCAACATCGGGGCAGGTTATGATGTATACTGGTACCAACAACTTCCAGGAACTGCCCCCAAACTCCTCATCTATGGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAGGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACACCAGCCTGAATGGTTGGGCTTTCGGCGGAGGGACCAAGTTGACCGTCCTAGGC [SEQ ID NO: 45]	
DNA for VH	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCAGGGCGGTCCCTGAGACTCAGCTGTACAGCCTCTGGGTTTAGTTTTGGTGATCATGCTATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTAGGTTTCATTAGAAAGACAACTTATGGTGCGACAACACACTACGCCGCGGCTGTGAGAGGCAGATTCACCATCTCGCGAGATGATTCTAAA	

TABLE 8-continued

Antibody ID: AB-000224.003		
	KABAT	ASN
	AGCACTGTCTATCTGCAAATGAACAGCCTGAAAACCGAGGACACAGCCGTGTATTTCTGTACTAGAGTGCAGCTTGACTATGGCCCGGGATACCAGTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA [SEQ ID NO: 46]	
Light Chain	QSVLTQPPSVSGAPGQRVTISCTGMNSNIGAGYDVYWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSRSGTSASLAITGLQAEDEADYYCQSYDTSLNGWAFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLVSDFYPGAVTVAWKADGSPVKVGVETTKPSKQSNNKYAASSYLSLTPEQWKSHRSYSCRVTHEGSTVEKTVAPAECS [SEQ ID NO: 47]	
Heavy Chain version 1	EVQLVESGGGLVQPGRSLRLSCTASGFSFGDHAMSWVRQAPGKGLEWVGFIRKTTYGATTHYAAAVRGRFTISRDDSKSTVYLQMNSLKTEDTAVYFCTRVQLDYGPGYQYYGMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK [SEQ ID NO: 48]	
Heavy Chain version 2	EVQLVESGGGLVQPGRSLRLSCTASGFSFGDHAMSWVRQAPGKGLEWVGFIRKTTYGATTHYAAAVRGRFTISRDDSKSTVYLQMNSLKTEDTAVYFCTRVQLDYGPGYQYYGMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK [SEQ ID NO: 49]	
DNA for Light Chain	CAGTCTGTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAGGGTCACCATCTCCTGCACTGGGATGAACTCCAACATCGGGGCAGGTTATGATGTATACTGGTACCAACAACTTCCAGGAACTGCCCCCAAACTCCTCATCTATGGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAGGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACACCAGCCTGAATGGTTGGGCTTTCGGCGGAGGGACCAAGTTGACCGTCCTAGGCCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCACCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCGTAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATGGCAGCCCCGTCAAGGTGGGAGTGGAGACCACCAAACCCTCCAAACAAAGCAACAACAAGTATGCGGCCAGCAGCTACCTGAGCCTGACGCCCGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCGGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTGCAGAATGCTCT [SEQ ID NO: 50]	
DNA for Heavy Chain version 1	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCAGGGCGGTCCCTGAGACTCAGCTGTACAGCCTCTGGGTTTAGTTTTGGTGATCATGCTATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTAGGTTTCATTAGAAAGACAACTTATGGTGCGACAACACACTACGCCGCGGCTGTGAGAGGCAGATTCACCATCTCGCGAGATGATTCTAAAAGCACTGTCTATCTGCAAATGAACAGCCTGAAAACCGAGGACACAGCCGTGTATTTCTGTACTAGAGTGCAGCTTGACTATGGCCCGGGATACCAGTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCAGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAA [SEQ ID NO: 51]	

TABLE 8-continued

Antibody ID: AB-000224.003		
	KABAT	ASN
DNA for Heavy Chain version 2	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCAGGGCGGTCCCTGAGACTCA GCTGTACAGCCTCTGGGTTTAGTTTTGGTGATCATGCTATGAGCTGGGTCCGCCAGGCTCC AGGGAAGGGGCTGGAGTGGGTAGGTTTCATTAGAAAGACAACTTATGGTGCGACAACACAC TACGCCGCGGCTGTGAGAGGCAGATTCACCATCTCGCGAGATGATTCTAAAAGCACTGTCT ATCTGCAAATGAACAGCCTGAAAACCGAGGACACAGCCGTGTATTTCTGTACTAGAGTGCA GCTTGACTATGGCCCGGGATACCAGTACTACGGTATGGACGTCTGGGGCCAAGGGACCACG GTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCA AGAGCACCTCTGGGGGCACAGCAGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACC GGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTC CTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGG GCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAA AGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTC CTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTT CAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAG TACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATG GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCAT CTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAT GAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACA TCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGT GCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGG CAGCAGGGGAACGTCTTCTCATGCTCCGTGCTGCATGAGGCTCTGCACTCCCACTACACAC AGAAGAGCCTCTCCCTGTCTCCGGGTAAA [SEQ ID NO: 52]	

In certain embodiments, the anti-CSP antibody variant comprises a light chain variable region comprising a CDR1, a CDR2, and a CDR3 and having the amino acid sequence set forth in SEQ ID NO: 53, as shown in Table 9. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 and having the amino acid sequence set forth in SEQ ID NO: 55, as shown in Table 9. In certain embodiments, the anti-CSP antibody variant comprises a light chain having the amino acid sequence set forth in SEQ ID NO: 57, as shown in Table 9. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain having the amino acid sequence set forth in SEQ ID NO: 58, as shown in Table 9. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain having the amino acid sequence set forth in SEQ ID NO: 59, as shown in Table 9. Exemplary nucleic acid sequences of SEQ ID NOS: 53, 54, 57, 58, and 59 are provided in Table 9 below.

TABLE 9

Antibody ID: AB-000224.004		
	KABAT	ASN
CDR1-VL	TGMNSNIGAGYDVY [SEQ ID NO: 1]	TGMNSNIGAGYDVY [SEQ ID NO: 7]
CDR2-VL	GNSNRPS [SEQ ID NO: 2]	GNSNRPS [SEQ ID NO: 8]
CDR3-VL	QSYDTSLNGWA [SEQ ID NO: 3]	QSYDTSLNGWA [SEQ ID NO: 9]
CDR1-VH	DHAMS [SEQ ID NO: 4]	DHAMS [SEQ ID NO: 10]
CDR2-VH	FIRKTTYGATTHYAAAVRG [SEQ ID NO: 5]	FIRKTTYGATTHYAAAVRG [SEQ ID NO: 11]
CDR3-VH	VQLDYGPGYQYYGMDV [SEQ ID NO: 6]	VQLDYGPGYQYYGMDV [SEQ ID NO: 12]
VL	QSVLTQPPSVSGAPGQRVTISCTGMNSNIGAGYDVYWYQQLPGTAPKLLIYGNSNRPSGVP DRFSGSRSGTSASLAITGLQAEDEADYYCQSYDTSLNGWAFGGGTKLTVLG [SEQ ID NO: 53]	
VH	EVQLVESGGGLVQPGRSLRLSCTASGFSFGDHAMSWVRQAPGKGLEWVGFIRKTTYGATTH YAAAVRGRFTISRDDSKSIVYLQMNSLKAEDTAVYFCTRVQLDYGPGYQYYGMDVWGQGTT VTVSS [SEQ ID NO: 54]	
DNA for VL	CAGTCTGTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAG GGCAGAGGGTCACCATCTCCTGCACTGGGATGAACTCCAACATCGGGGCA GGTTATGATGTATACTGGTACCAACAACTTCCAGGAACTGCCCCCAAACT CCTCATCTATGGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGATTCT	

TABLE 9-continued

	Antibody ID: AB-000224.004	
	KABAT	ASN
	CTGGCTCCAGGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAG GCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACACCAGCCTGAA TGGTTGGGCTTTCGGCGGAGGGACCAAGTTGACCGTCCTAGGC [SEQ ID NO: 55]	
DNA for VH	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGG TACAGCCAGGGCGGTCCCTGAGACTCAGCTGTACAGCCTCTGGGTTTAGT TTTGGTGATCATGCTATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCT GGAGTGGGTAGGTTTCATTAGAAAGACAACTTATGGTGCGACAACACACT ACGCCGCGGCTGTGAGAGGCAGATTCACCATCTCGCGAGATGATTCTAAA AGOATTGTOTATCTGCAAATGAACAGCCTGAAAGCAGAGGACACAGCCGT GTATTTCTGTACTAGAGTGCAGCTTGACTATGGCCCGGGATACCAGTACT ACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA [SEQ ID NO: 56]	
Light Chain	QSVLTQPPSVSGAPGQRVTISCTGMNSNIGA GYDVYWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSRSGTSASLAITGLQ AEDEADYYCQSYDTSLNGWAFGGGTKLTVLGQPKAAPSVTLFPPSSEELQ ANKATLVCLVSDFYPGAVTVAWKADGSPVKVGVETTKPSKQSNNKYAASS YLSLTPEQWKSHRSYSCRVTHEGSTVEKTVAPAECS[SEQ ID NO: 57]	
Heavy Chain version 1	EVQLVESGGGLVQPGRSLRLSCTASGFS FGDHAMSWVRQAPGKGLEWVGFIRKTTYGATTHYAAAVRGRFTISRDDSK SIVYLQMNSLKAEDTAVYFCTRVQLDYGPGYQYYGMDVWGQGTTVTVSSA STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPK SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNHYTQKSLSLSPGK[SEQ ID NO: 58]	
Heavy Chain version 2	EVQLVESGGGLVQPGRSLRLSCTASGFS FGDHAMSWVRQAPGKGLEWVGFIRKTTYGATTHYAAAVRGRFTISRDDSK SIVYLQMNSLKAEDTAVYFCTRVQLDYGPGYQYYGMDVWGQGTTVTVSSA STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPK SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVLHEALHSHYTQKSLSLSPGK [SEQ ID NO: 59]	
DNA for Light Chain	CAGTCTGTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAG GGCAGAGGGTCACCATCTCCTGCACTGGGATGAACTCCAACATCGGGGCA GGTTATGATGTATACTGGTACCAACAACTTCCAGGAACTGCCCCCAAACT CCTCATCTATGGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGATTCT CTGGCTCCAGGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAG GCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACACCAGCCTGAA TGGTTGGGCTTTCGGCGGAGGGACCAAGTTGACCGTCCTAGGCCAGCCCA AGGCTGCCCCCTCGGTCACTCTGTTCCCACCCTCCTCTGAGGAGCTTCAA GCCAACAAGGCCACACTGGTGTGTCTCGTAAGTGACTTCTACCCGGGAGC CGTGACAGTGGCCTGGAAGGCAGATGGCAGCCCCGTCAAGGTGGGAGTGG AGACCACCAAACCCTCCAAACAAAGCAACAACAAGTATGCGGCCAGCAGC TACCTGAGCCTGACGCCCGAGCAGTGGAAGTCCCACAGAAGCTACAGCTG CCGGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTGCAG AATGCTCT [SEQ ID NO: 60]	
DNA for Heavy Chain version 1	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGG TACAGCCAGGGCGGTCCCTGAGACTCAGCTGTACAGCCTCTGGGTTTAGT TTTGGTGATCATGCTATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCT GGAGTGGGTAGGTTTCATTAGAAAGACAACTTATGGTGCGACAACACACT ACGCCGCGGCTGTGAGAGGCAGATTCACCATCTCGCGAGATGATTCTAAA AGCATTGTOTATCTGCAAATGAACAGCCTGAAAGCAGAGGACACAGCCGT GTATTTCTGTACTAGAGTGCAGCTTGACTATGGCCCGGGATACCAGTACT ACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGCC TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCAC CTCTGGGGGCACAGCAGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCG AACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCAC ACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGT GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACG TGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAA TCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCT GGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCA TGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCAC GAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCA TAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTG	

TABLE 9-continued

Antibody ID: AB-000224.004		
	KABAT	ASN
	TGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAAC CATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGC CCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTG GTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGG GCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACG GCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAA [SEQ ID NO: 61]	
DNA for Heavy Chain version 2	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGG TACAGCCAGGGCGGTCCCTGAGACTCAGCTGTACAGCCTCTGGGTTTAGT TTTGGTGATCATGCTATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCT GGAGTGGGTAGGTTTCATTAGAAAGACAACTTATGGTGCGACAACACACT ACGCCGCGGCTGTGAGAGGCAGATTCACCATCTCGCGAGATGATTCTAAA AGGATTGTCTATGTGCAAATGAACAGCCTGAAAGCAGAGGACACAGCCGT GTATTTCTGTACTAGAGTGCAGCTTGACTATGGCCCGGGATACCAGTACT ACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGCC TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCAC CTCTGGGGGCACAGCAGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCG AACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCAC ACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGT GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACG TGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAA TCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCT GGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCA TGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCAC GAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCA TAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTG TGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAAC CATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGC CCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTG GTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGG GCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACG GCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGCTGCATGAGGCTCTGCACTCCCA CTACACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAA [SEQ ID NO: 62]	

In certain embodiments, the anti-CSP antibody variant comprises a light chain variable region comprising a CDR1, a CDR2, and a CDR3 and having the amino acid sequence set forth in SEQ ID NO: 63, as shown in Table 10. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 and having the amino acid sequence set forth in SEQ ID NO: 64, as shown in Table 10. In certain embodiments, the anti-CSP antibody variant comprises a light chain having the amino acid sequence set forth in SEQ ID NO: 67, as shown in Table 10. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain having the amino acid sequence set forth in SEQ ID NO: 68, as shown in Table 10. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain having the amino acid sequence set forth in SEQ ID NO: 69, as shown in Table 10. Exemplary nucleic acid sequences of SEQ ID NOS: 63, 64, 67, 68, and 69 are provided in Table 10 below.

TABLE 10

Antibody ID: AB-000224.005		
	KABAT	ASN
CDR1-VL	TGMNSNIGAGYDVY [SEQ ID NO: 1]	TGMNSNIGAGYDVY [SEQ ID NO: 7]
CDR2-VL	GNSNRPS [SEQ ID NO: 2]	GNSNRPS [SEQ ID NO: 8]
CDR3-VL	QSYDTSLNGWA [SEQ ID NO: 3]	QSYDTSLNGWA [SEQ ID NO: 9]
CDR1-VH	DHAMS [SEQ ID NO: 4]	DHAMS [SEQ ID NO: 10]
CDR2-VH	FIRKTTYGATTHYAAAVRG [SEQ ID NO: 5]	FIRKTTYGATTHYAAAVRG [SEQ ID NO: 11]
CDR3-VH	VQLDYGPGYQYYGMDV [SEQ ID NO: 6]	VQLDYGPGYQYYGMDV [SEQ ID NO: 12]

TABLE 10-continued

	Antibody ID: AB-000224.005	
	KABAT	ASN
VL	QSVLTQPPSVSGAPGQRVTISCTGMNSNIGA GYDVYWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSRSGTSASLAITGLQ AEDEADYYCQSYDTSLNGWAFGGGTKLTVLG [SEQ ID NO: 63]	
VH	EVQLVESGGGLVQPGRSLRLSCTASGFS FGDHAMSWVRQAPGKGLEWVGFIRKTTYGATTHYAAAVRGRFTISRDDSK SIVYLQMNSLKTEDTAVYFCARVQLDYGPGYQYYGMDVWGQGTTVTVSS [SEQ ID NO: 64]	
DNA for VL	CAGTCTGTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAG GGCAGAGGGTCACCATCTCCTGCACTGGGATGAACTCCAACATCGGGGCA GGTTATGATGTATACTGGTACCAACAACTTCCAGGAACTGCCCCCAAACT CCTCATCTATGGTAACAGCAATCG6CCCTCAGGGGTCCCTGACCGATTCT CTGGCTCCAGGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAG GCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACACCAGCCTGAA TGGTTGGGCTTTCGGCGGAGGGACCAAGTTGACCGTCCTAGGC [SEQ ID NO: 65]	
DNA for VH	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGG TACAGCCAGGGCGGTCCCTGAGACTCAGCTGTACAGCCTCTGGGTTTAGT TTTGGTGATCATGCTATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCT GGAGTGGGTAGGTTTCATTAGAAAGACAACTTATGGTGCGACAACACACT ACGCCGCGGCTGTGAGAGGCAGATTCACCATCTCGCGAGATGATTCTAAA AGCATTGTCTATCTGCAAATGAACAGCCTGAAAACCGAGGACACAGCCGT GTATTTCTGTGCTAGAGTGCAGCTTGACTATGGCCCGGGATACCAGTACT ACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA [SEQ ID NO: 66]	
Light Chain	QSVLTQPPSVSGAPGQRVTISCTGMNSNIGA GYDVYWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSRSGTSASLAITGLQ AEDEADYYCQSYDTSLNGWAFGGGTKLTVLGQPKAAPSVTLFPPSSEELQ ANKATLVCLVSDFYPGAVTVAWKADGSPVKVGVETTKPSKQSNNKYAASS YLSLTPEQWKSHRSYSCRVTHEGSTVEKTVAPAECS [SEQ ID NO: 67]	
Heavy Chain version 1	EVQLVESGGGLVQPGRSLRLSCTASGFS FGDHAMSWVRQAPGKGLEWVGFIRKTTYGATTHYAAAVRGRFTISRDDSK SIVYLQMNSLKTEDTAVYFCARVQLDYGPGYQYYGMDVWGQGTTVTVSSA STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPK SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNHYTQKSLSLSPGK [SEQ ID NO: 68]	
Heavy Chain version 2	EVQLVESGGGLVQPGRSLRLSCTASGFS FGDHAMSWVRQAPGKGLEWVGFIRKTTYGATTHYAAAVRGRFTISRDDSK SIVYLQMNSLKTEDTAVYFCARVQLDYGPGYQYYGMDVWGQGTTVTVSSA STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPK SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVLHEALHSHYTQKSLSLSPGK [SEQ ID NO: 69]	
DNA for Light Chain	CAGTCTGTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAG GGCAGAGGGTCACCATCTCCTGCACTGGGATGAACTCCAACATCGGGGCA GGTTATGATGTATACTGGTACCAACAACTTCCAGGAACTGCCCCCAAACT CCTCATCTATGGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGATTCT CTGGCTCCAGGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAG GCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACACCAGCCTGAA TGGTTGGGCTTTCGGCGGAGGGACCAAGTTGACCGTCCTAGGCCAGCCCA AGGCTGCCCCCTCGGTCACTCTGTTCCCACCCTCCTCTGAGGAGCTTCAA GCCAACAAGGCCACACTGGTGTGTCTCGTAAGTGACTTCTACCCGGGAGC CGTGACAGTGGCCTGGAAGGCAGATGGCAGCCCCGTCAAGGTGGGAGTGG AGACCACCAAACCCTCCAAACAAAGCAACAACAAGTATGCGGCCAGCAGC TACCTGAGCCTGACGCCCGAGCAGTGGAAGTCCCACAGAAGCTACAGCTG CCGGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTGCAG AATGCTCT [SEQ ID NO: 70]	

TABLE 10-continued

	Antibody ID: AB-000224.005	
	KABAT	ASN
DNA for Heavy Chain version 1	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGG TACAGCCAGGGCGGTCCCTGAGACTCAGCTGTACAGCCTCTGGGTTTAGT TTTGGTGATCATGCTATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCT GGAGTGGGTAGGTTTCATTAGAAAGACAACTTATGGTGCGACAACACACT ACGCCGCGGCTGTGAGAGGCAGATTCACCATCTCGCGAGATGATTCTAAA AGCATTGTCTATCTGCAAATGAACAGCCTGAAAACCGAGGACACAGCCGT GTATTTCTGTGCTAGAGTGCAGCTTGACTATGGCCCGGGATACCAGTACT ACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGCC TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCAC CTCTGGGGGCACAGCAGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCG AACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCAC ACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGT GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACG TGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAA TCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCT GGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCA TGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCAC GAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCA TAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTG TGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAAC CATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGC CCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTG GTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGG GCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACG GCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAA [SEQ ID NO: 71]	
DNA for Heavy Chain version 2	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGG TACAGCCAGGGCGGTCCCTGAGACTCAGCTGTACAGCCTCTGGGTTTAGT TTTGGTGATCATGCTATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCT GGAGTGGGTAGGTTTCATTAGAAAGACAACTTATGGTGCGACAACACACT ACGCCGCGGCTGTGAGAGGCAGATTCACCATCTCGCGAGATGATTCTAAA AGCATTGTCTATCTGCAAATGAACAGCCTGAAAACCGAGGACACAGCCGT GTATTTCTGTGCTAGAGTGCAGCTTGACTATGGCCCGGGATACCAGTACT ACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGCC TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCAC CTCTGGGGGCACAGCAGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCG AACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCAC ACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGT GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACG TGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAA TCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCT GGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCA TGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCAC GAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCA TAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTG TGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAAC CATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGC CCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTG GTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGG GCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACG GCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGCTGCATGAGGCTCTGCACTCCCA CTACACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAA [SEQ ID NO: 72]	

In certain embodiments, the anti-CSP antibody variant comprises a light chain variable region comprising a CDR1, a CDR2, and a CDR3 and having the amino acid sequence set forth in SEQ ID NO: 73, as shown in Table 11. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 and having the amino acid sequence set forth in SEQ ID NO: 74, as shown in Table 11. In certain embodiments, the anti-CSP antibody variant comprises a light chain having the amino acid sequence set forth in SEQ ID NO: 77, as shown in Table 11. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain having the amino acid sequence set forth in SEQ ID NO: 78, as shown in Table 11. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain having the amino acid sequence set forth in SEQ ID NO: 79, as shown in Table 11. Exemplary nucleic acid sequences of SEQ ID NOS: 73, 74, 77, 78, and 79 are provided in Table 11 below.

TABLE 11

	Antibody ID: AB-000224.006	
	KABAT	ASN
CDR1-VL	TGMNSNIGAGYDVY [SEQ ID NO: 1]	TGMNSNIGAGYDVY [SEQ ID NO: 7]
CDR2-VL	GNSNRPS [SEQ ID NO: 2]	GNSNRPS [SEQ ID NO: 8]
CDR3-VL	QSYDTSLNGWA [SEQ ID NO: 3]	QSYDTSLNGWA [SEQ ID NO: 9]
CDR1-VH	DHAMS [SEQ ID NO: 4]	DHAMS [SEQ ID NO: 10]
CDR2-VH	FIRKTTYGATTHYAAAVRG [SEQ ID NO: 5]	FIRKTTYGATTHYAAAVRG [SEQ ID NO: 11]
CDR3-VH	VQLDYGPGYQYYGMDV [SEQ ID NO: 6]	VQLDYGPGYQYYGMDV [SEQ ID NO: 12]
VL	QSVLTQPPSVSGAPGQRVTISCTGMNSNIGA GYDVYWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSRSGTSASLAITGLQ AEDEADYYCQSYDTSLNGWAFGGGTKLTVLG [SEQ ID NO: 73]	
VH	EVQLVESGGGLVQPGRSLRLSCAASGFS FGDHAMSWVRQAPGKGLEWVGFIRKTTYGATTHYAAAVRGRFTISRDDSK STVYLQMNSLKTEDTAVYFCTRVQLDYGPGYQYYGMDVWGQGTTVTVSS [SEQ ID NO: 74]	
DNA for VL	CAGTCTGTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAG GGCAGAGGGTCACCATCTCCTGCACTGGGATGAACTCCAACATCGGGGCA GGTTATGATGTATACTGGTACCAACAACTTCCAGGAACTGCCCCCAAACT CCTCATCTATGGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGATTCT CTGGCTCCAGGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAG GCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACACCAGCCTGAA TGGTTGGGCTTTCGGCGGAGGGACCAAGTTGACCGTCCTAGGC [SEQ ID NO: 75]	
DNA for VH	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGG TACAGCCAGGGCGGTCCCTGAGACTCAGCTGTGCGGCCTCTGGGTTTAGT TTTGGTGATCATGCTATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCT GGAGTGGGTAGGTTTCATTAGAAAGACAACTTATGGTGCGACAACACACT ACGCCGCGGCTGTGAGAGGCAGATTCACCATCTCGCGAGATGATTCTAAA AGCACTGTCTATCTGCAAATGAACAGCCTGAAAACCGAGGACACAGCCGT GTATTTCTGTACTAGAGTGCAGCTTGACTATGGCCCGGGATACCAGTACT ACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA [SEQ ID NO: 76]	
Light Chain	QSVLTQPPSVSGAPGQRVTISCTGMNSNIGA GYDVYWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSRSGTSASLAITGLQ AEDEADYYCQSYDTSLNGWAFGGGTKLTVLGQPKAAPSVTLFPPSSEELQ ANKATLVCLVSDFYPGAVTVAWKADGSPVKVGVETTKPSKQSNNKYAASS YLSLTPEQWKSHRSYSCRVTHEGSTVEKTVAPAECS [SEQ ID NO: 77]	
Heavy Chain version 1	EVQLVESGGGLVQPGRSLRLSCAASGFS FGDHAMSWVRQAPGKGLEWVGFIRKTTYGATTHYAAAVRGRFTISRDDSK STVYLQMNSLKTEDTAVYFCTRVQLDYGPGYQYYGMDVWGQGTTVTVSSA STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPK SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNHYTQKSLSLSPGK [SEQ ID NO: 78]	
Heavy Chain version 2	EVQLVESGGGLVQPGRSLRLSCAASGFS FGDHAMSWVRQAPGKGLEWVGFIRKTTYGATTHYAAAVRGRFTISRDDSK STVYLQMNSLKTEDTAVYFCTRVQLDYGPGYQYYGMDVWGQGTTVTVSSA STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPK SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH	

TABLE 11-continued

	Antibody ID: AB-000224.006	
	KABAT	ASN
	EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK [SEQ ID NO: 79]	
DNA for Light Chain	CAGTCTGTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAGGGTCACCATCTCCTGCACTGGGATGAACTCCAACATCGGGGCAGGTTATGATGTATACTGGTACCAACAACTTCCAGGAACTGCCCCCAAACTCCTCATCTATGGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAGGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACACCAGCCTGAATGGTTGGGCTTTCGGCGGAGGGACCAAGTTGACCGTCCTAGGCCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCACCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCGTAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATGGCAGCCCCGTCAAGGTGGGAGTGGAGACCACCAAACCCTCCAAACAAAGCAACAACAAGTATGCGGCCAGCAGCTACCTGAGCCTGACGCCCGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCGGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTGCAGAATGCTCT [SEQ ID NO: 80]	
DNA for Heavy Chain version 1	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCAGGGCGGTCCCTGAGACTCAGCTGTGCGGCCTCTGGGTTTAGTTTTGGTGATCATGCTATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTAGGTTTCATTAGAAAGACAACTTATGGTGCGACAACACACTACGCCGCGGCTGTGAGAGGCAGATTCACCATCTCGCGAGATGATTCTAAAAGCACTGTCTATCTGCAAATGAACAGCCTGAAAACCGAGGACACAGCCGTGTATTTCTGTACTAGAGTGCAGCTTGACTATGGCCCGGGATACCAGTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCAGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAA [SEQ ID NO: 81]	
DNA for Heavy Chain version 2	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCAGGGCGGTCCCTGAGACTCAGCTGTGCGGCCTCTGGGTTTAGTTTTGGTGATCATGCTATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTAGGTTTCATTAGAAAGACAACTTATGGTGCGACAACACACTACGCCGCGGCTGTGAGAGGCAGATTCACCATCTCGCGAGATGATTCTAAAAGCACTGTCTATCTGCAAATGAACAGCCTGAAAACCGAGGACACAGCCGTGTATTTCTGTACTAGAGTGCAGCTTGACTATGGCCCGGGATACCAGTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCAGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACG	

TABLE 11-continued

Antibody ID: AB-000224.006		
	KABAT	ASN
	GCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGCTGCATGAGGCTCTGCACTCCCA CTACACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAA [SEQ ID NO: 82]	

In certain embodiments, the anti-CSP antibody variant comprises a light chain variable region comprising a CDR1, a CDR2, and a CDR3 and having the amino acid sequence set forth in SEQ ID NO: 83, as shown in Table 12. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 and having the amino acid sequence set forth in SEQ ID NO: 84, as shown in Table 12. In certain embodiments, the anti-CSP antibody variant comprises a light chain having the amino acid sequence set forth in SEQ ID NO: 87, as shown in Table 12. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain having the amino acid sequence set forth in SEQ ID NO: 88, as shown in Table 12. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain having the amino acid sequence set forth in SEQ ID NO: 89, as shown in Table 12. Exemplary nucleic acid sequences of SEQ ID NOS: 83, 84, 87, 88, and 89 are provided in Table 12 below.

TABLE 12

Antibody ID: AB-000224.007		
	KABAT	ASN
CDR1-VL	TGMNSNIGAGYDVY [SEQ ID NO: 1]	TGMNSNIGAGYDVY [SEQ ID NO: 7]
CDR2-VL	GNSNRPS [SEQ ID NO: 2]	GNSNRPS [SEQ ID NO: 8]
CDR3-VL	QSYDTSLNGWA [SEQ ID NO: 3]	QSYDTSLNGWA [SEQ ID NO: 9]
CDR1-VH	DHAMS [SEQ ID NO: 4]	DHAMS [SEQ ID NO: 10]
CDR2-VH	FIRKTTYGATTHYAAAVRG [SEQ ID NO: 5]	FIRKTTYGATTHYAAAVRG [SEQ ID NO: 11]
CDR3-VH	VQLDYGPGYQYYGMDV [SEQ ID NO: 6]	VQLDYGPGYQYYGMDV [SEQ ID NO: 12]
VL	QSVLTQPPSVSGAPGQRVTISCTGMNSNIGA GYDVYWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSRSGTSASLAITGLQ AEDEADYYCQSYDTSLNGWAFGGGTKLTVLG [SEQ ID NO: 83]	
VH	EVQLVESGGGLVQPGRSLRLSCAASGFS FGDHAMSWVRQAPGKGLEWVGFIRKTTYGATTHYAAAVRGRFTISRDDSK SIVYLQMNSLKAEDTAVYFCTRVQLDYGPGYQYYGMDVWGQGTTVTVSS [SEQ ID NO: 84]	
DNA for VL	CAGTCTGTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAG GGCAGAGGGTCACCATCTCCTGCACTGGGATGAACTCCAACATCGGGGCA GGTTATGATGTATACTGGTACCAACAACTTCCAGGAACTGCCCCCAAACT CCTCATCTATGGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGATTCT CTGGCTCCAGGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAG GCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACACCAGCCTGAA TGGTTGGGCTTTCGGCGGAGGGACCAAGTTGACCGTCCTAGGC [SEQ ID NO: 85]	
DNA for VH	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGG TACAGCCAGGGCGGTCCCTGAGACTCAGCTGTGCGGCCTCTGGGTTTAGT TTTGGTGATCATGCTATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCT GGAGTGGGTAGGTTTCATTAGAAAGACAACTTATGGTGCGACAACACACT ACGCCGCGGCTGTGAGAGGCAGATTCACCATCTCGCGAGATGATTCTAAA AGOATTGTOTATCTGCAAATGAACAGCCTGAAAGCAGAGGACACAGCCGT GTATTTCTGTACTAGAGTGCAGCTTGACTATGGCCCGGGATACCAGTACT ACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA [SEQ ID NO: 86]	

TABLE 12-continued

	Antibody ID: AB-000224.007	
	KABAT	ASN
Light Chain	QSVLTQPPSVSGAPGQRVTISCTGMNSNIGA GYDVYWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSRSGTSASLAITGLQ AEDEADYYCQSYDTSLNGWAFGGGTKLTVLGQPKAAPSVTLFPPSSEELQ ANKATLVCLVSDFYPGAVTVAWKADGSPVKVGVETTKPSKQSNNKYAASS YLSLTPEQWKSHRSYSCRVTHEGSTVEKTVAPAECS [SEQ ID NO: 87]	
Heavy Chain version 1	EVQLVESGGGLVQPGRSLRLSCAASGFS FGDHAMSWVRQAPGKGLEWVGFIRKTTYGATTHYAAAVRGRFTISRDDSK SIVYLQMNSLKAEDTAVYFCTRVQLDYGPGYQYYGMDVWGQGTTVTVSSA STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPK SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNHYTQKSLSLSPGK [SEQ ID NO: 88]	
Heavy Chain version 2	EVQLVESGGGLVQPGRSLRLSCAASGFS FGDHAMSWVRQAPGKGLEWVGFIRKTTYGATTHYAAAVRGRFTISRDDSK SIVYLQMNSLKAEDTAVYFCTRVQLDYGPGYQYYGMDVWGQGTTVTVSSA STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPK SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVLHEALHSHYTQKSLSLSPGK [SEQ ID NO: 89]	
DNA for Light Chain	CAGTCTGTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAG GGCAGAGGGTCACCATCTCCTGCACTGGGATGAACTCCAACATCGGGGCA GGTTATGATGTATACTGGTACCAACAACTTCCAGGAACTGCCCCCAAACT CCTCATCTATGGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGATTCT CTGGCTCCAGGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAG GCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACACCAGCCTGAA TGGTTGGGCTTTCGGCGGAGGGACCAAGTTGACCGTCCTAGGCCAGCCCA AGGCTGCCCCCTCGGTCACTCTGTTCCCACCCTCCTCTGAGGAGCTTCAA GCCAACAAGGCCACACTGGTGTGTCTCGTAAGTGACTTCTACCCGGGAGC CGTGACAGTGGCCTGGAAGGCAGATGGCAGCCCCGTCAAGGTGGGAGTGG AGACCACCAAACCCTCCAAACAAAGCAACAACAAGTATGCGGCCAGCAGC TACCTGAGCCTGACGCCCGAGCAGTGGAAGTCCCACAGAAGCTACAGCTG CCGGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTGCAG AATGCTCT [SEQ ID NO: 90]	
DNA for Heavy Chain version 1	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGG TACAGCCAGGGCGGTCCCTGAGACTCAGCTGTGCGGCCTCTGGGTTTAGT TTTGGTGATCATGCTATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCT GGAGTGGGTAGGTTTCATTAGAAAGACAACTTATGGTGCGACAACACACT ACGCCGCGGCTGTGAGAGGCAGATTCACCATCTCGCGAGATGATTCTAAA AGGATTGTCTATGTGCAAATGAACAGCCTGAAAGCAGAGGACACAGCCGT GTATTTCTGTACTAGAGTGCAGCTTGACTATGGCCCGGGATACCAGTACT ACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGCC TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCAC CTCTGGGGGCACAGCAGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCG AACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCAC ACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGT GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACG TGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAA TCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCT GGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCA TGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCAC GAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCA TAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTG TGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAAC CATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGC CCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTG GTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGG GCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACG GCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAA [SEQ ID NO: 91]	

TABLE 12-continued

Antibody ID: AB-000224.007		
	KABAT	ASN
DNA for Heavy Chain version 2	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGG TACAGCCAGGGCGGTCCCTGAGACTCAGCTGTGCGGCCTCTGGGTTTAGT TTTGGTGATCATGCTATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCT GGAGTGGGTAGGTTTCATTAGAAAGACAACTTATGGTGCGACAACACACT ACGCCGCGGCTGTGAGAGGCAGATTCACCATCTCGCGAGATGATTCTAAA AGCATTGTCTATCTGCAAATGAACAGCCTGAAAGCAGAGGACACAGCCGT GTATTTCTGTACTAGAGTGCAGCTTGACTATGGCCCGGGATACCAGTACT ACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGCC TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCAC CTCTGGGGGCACAGCAGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCG AACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCAC ACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGT GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACG TGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAA TCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCT GGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCA TGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCAC GAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCA TAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTG TGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAAC CATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGC CCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTG GTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGG GCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACG GCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGCTGCATGAGGCTCTGCACTCCCA CTACACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAA [SEQ ID NO: 92]	

In certain embodiments, the anti-CSP antibody variant comprises a light chain variable region comprising a CDR1, a CDR2, and a CDR3 and having the amino acid sequence set forth in SEQ ID NO: 93, as shown in Table 13. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 and having the amino acid sequence set forth in SEQ ID NO: 94, as shown in Table 13. In certain embodiments, the anti-CSP antibody variant comprises a light chain having the amino acid sequence set forth in SEQ ID NO: 97, as shown in Table 13. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain having the amino acid sequence set forth in SEQ ID NO: 98, as shown in Table 13. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain having the amino acid sequence set forth in SEQ ID NO: 99, as shown in Table 13. Exemplary nucleic acid sequences of SEQ ID NOS: 93, 94, 97, 98, and 99 are provided in Table 13 below.

TABLE 13

Antibody ID: AB-000224.008		
	KABAT	ASN
CDR1-VL	TGMNSNIGAGYDVY [SEQ ID NO: 1]	TGMNSNIGAGYDVY [SEQ ID NO: 7]
CDR2-VL	GNSNRPS [SEQ ID NO: 2]	GNSNRPS [SEQ ID NO: 8]
CDR3-VL	QSYDTSLNGWA [SEQ ID NO: 3]	QSYDTSLNGWA [SEQ ID NO: 9]
CDR1-VH	DHAMS [SEQ ID NO: 4]	DHAMS [SEQ ID NO: 10]
CDR2-VH	FIRKTTYGATTHYAAAVRG [SEQ ID NO: 5]	FIRKTTYGATTHYAAAVRG [SEQ ID NO: 11]
CDR3-VH	VQLDYGPGYQYYGMDV [SEQ ID NO: 6]	VQLDYGPGYQYYGMDV [SEQ ID NO: 12]
VL	QSVLTQPPSVSGAPGQRVTISCTGMNSNIGA GYDVYWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSRSGTSASLAITGLQ AEDEADYYCQSYDTSLNGWAFGGGTKLTVLG [SEQ ID NO: 93]	
VH	EVQLVESGGGLVQPGRSLRLSCAASGFS FGDHAMSWVRQAPGKGLEWVGFIRKTTYGATTHYAAAVRGRFTISRDDSK SIVYLQMNSLKTEDTAVYFCARVQLDYGPGYQYYGMDVWGQGTTVTVSS [SEQ ID NO: 94]	

TABLE 13-continued

	Antibody ID: AB-000224.008
	KABAT ASN
DNA for VL	CAGTCTGTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAGGGTCACCATCTCCTGCACTGGGATGAACTCCAACATCGGGGCAGGTTATGATGTATACTGGTACCAACAACTTCCAGGAACTGCCCCCAAACTCCTCATCTATGGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAGGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACACCAGCCTGAATGGTTGGGCTTTCGGCGGAGGGACCAAGTTGACCGTCCTAGGC [SEQ ID NO: 95]
DNA for VH	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCAGGGCGGTCCCTGAGACTCAGCTGTGCGGCCTCTGGGTTTAGTTTTGGTGATCATGCTATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTAGGTTTCATTAGAAAGACAACTTATGGTGCGACAACACACTACGCCGCGGCTGTGAGAGGCAGATTCACCATCTCGCGAGATGATTCTAAAAGCATTGTCTATCTGCAAATGAACAGCCTGAAAACCGAGGACACAGCCGTGTATTTCTGTGCTAGAGTGCAGCTTGACTATGGCCCGGGATACCAGTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA [SEQ ID NO: 96]
Light Chain	QSVLTQPPSVSGAPGQRVTISCTGMNSNIGAGYDVYWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSRSGTSASLAITGLQAEDEADYYCQSYDTSLNGWAFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLVSDFYPGAVTVAWKADGSPVKVGVETTKPSKQSNNKYAASSYLSLTPEQWKSHRSYSCRVTHEGSTVEKTVAPAECS [SEQ ID NO: 97]
Heavy Chain version 1	EVQLVESGGGLVQPGRSLRLSCAASGFSFGDHAMSWVRQAPGKGLEWVGFIRKTTYGATTHYAAAVRGRFTISRDDSKSIVYLQMNSLKTEDTAVYFCARVQLDYGPGYQYYGMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK [SEQ ID NO: 98]
Heavy Chain version 2	EVQLVESGGGLVQPGRSLRLSCAASGFSFGDHAMSWVRQAPGKGLEWVGFIRKTTYGATTHYAAAVRGRFTISRDDSKSIVYLQMNSLKTEDTAVYFCARVQLDYGPGYQYYGMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK [SEQ ID NO: 99]
DNA for Light Chain	CAGTCTGTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAGGGTCACCATCTCCTGCACTGGGATGAACTCCAACATCGGGGCAGGTTATGATGTATACTGGTACCAACAACTTCCAGGAACTGCCCCCAAACTCCTCATCTATGGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAGGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACACCAGCCTGAATGGTTGGGCTTTCGGCGGAGGGACCAAGTTGACCGTCCTAGGCCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCACCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCGTAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATGGCAGCCCCGTCAAGGTGGGAGTGGAGACCACCAAACCCTCCAAACAAAGCAACAACAAGTATGCGGCCAGCAGCTACCTGAGCCTGACGCCCGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCGGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTGCAGAATGCTCT [SEQ ID NO: 100]
DNA for Heavy Chain version 1	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCAGGGCGGTCCCTGAGACTCAGCTGTGCGGCCTCTGGGTTTAGTTTTGGTGATCATGCTATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTAGGTTTCATTAGAAAGACAACTTATGGTGCGACAACACACTACGCCGCGGCTGTGAGAGGCAGATTCACCATCTCGCGAGATGATTCTAAAAGCATTGTCTATCTGCAAATGAACAGCCTGAAAACCGAGGACACAGCCGTGTATTTCTGTGCTAGAGTGCAGCTTGACTATGGCCCGGGATACCAGTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCAGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCG

TABLE 13-continued

Antibody ID: AB-000224.008		
	KABAT	ASN
	AACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCAC ACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGT GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACG TGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAA TCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCT GGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCA TGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCAC GAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCA TAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTG TGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAAC CATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGC CCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTG GTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGG GCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACG GCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAA [SEQ ID NO: 101]	
DNA for Heavy Chain version 2	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGG TACAGCCAGGGCGGTCCCTGAGACTCAGCTGTGCGGCCTCTGGGTTTAGT TTTGGTGATCATGCTATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCT GGAGTGGGTAGGTTTCATTAGAAAGACAACTTATGGTGCGACAACACACT ACGCCGCGGCTGTGAGAGGCAGATTCACCATCTCGCGAGATGATTCTAAA AGCATTGTCTATCTGCAAATGAACAGCCTGAAAACCGAGGACACAGCCGT GTATTTCTGTGCTAGAGTGCAGCTTGACTATGGCCCGGGATACCAGTACT ACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGCC TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCAC CTCTGGGGGCACAGCAGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCG AACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCAC ACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGT GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACG TGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAA TCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCT GGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCA TGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCAC GAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCA TAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTG TGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAAC CATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGC CCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTG GTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGG GCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACG GCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGCTGCATGAGGCTCTGCACTCCCA CTACACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAA [SEQ ID NO: 102]	

In certain embodiments, the anti-CSP antibody variant comprises a light chain variable region comprising a CDR1, a CDR2, and a CDR3 and having the amino acid sequence set forth in SEQ ID NO: 103, as shown in Table 14. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 and having the amino acid sequence set forth in SEQ ID NO: 104, as shown in Table 14. In certain embodiments, the anti-CSP antibody variant comprises a light chain having the amino acid sequence set forth in SEQ ID NO: 107, as shown in Table 14. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain having the amino acid sequence set forth in SEQ ID NO: 108, as shown in Table 14. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain having the amino acid sequence set forth in SEQ ID NO: 109, as shown in Table 14. Exemplary nucleic acid sequences of SEQ ID NOS: 103, 104, 107, 108, and 109 are provided in Table 14 below.

TABLE 14

Antibody ID: AB-000224.009		
	KABAT	ASN
CDR1-VL	TGMNSNIGAGYDVY [SEQ ID NO: 1]	TGMNSNIGAGYDVY [SEQ ID NO: 7]
CDR2-VL	GNSNRPS [SEQ ID NO: 2]	GNSNRPS [SEQ ID NO: 8]

TABLE 14-continued

	Antibody ID: AB-000224.009	
	KABAT	ASN
CDR3-VL	QSYDTSLNGWA [SEQ ID NO: 3]	QSYDTSLNGWA [SEQ ID NO: 9]
CDR1-VH	DHAMS [SEQ ID NO: 4]	DHAMS [SEQ ID NO: 10]
CDR2-VH	FIRKTTYGATTHYAAAVRG [SEQ ID NO: 5]	FIRKTTYGATTHYAAAVRG [SEQ ID NO: 11]
CDR3-VH	VQLDYGPGYQYYGMDV [SEQ ID NO: 6]	VQLDYGPGYQYYGMDV [SEQ ID NO: 12]
VL	QSVLTQPPSVSGAPGQRVTISCTGMNSNIGA GYDVYWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSRSGTSASLAITGLQ AEDEADYYCQSYDTSLNGWAFGGGTKLTVLG [SEQ ID NO: 103]	
VH	EVQLVESGGGLVQPGRSLRLSCTASGFS FGDHAMSWVRQAPGKGLEWVGFIRKTTYGATTHYAAAVRGRFTISRDDSK STVYLQMNSLKAEDTAVYFCTRVQLDYGPGYQYYGMDVWGQGTTVTVSS [SEQ ID NO: 104]	
DNA for VL	CAGTCTGTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAG GGCAGAGGGTCACCATCTCCTGCACTGGGATGAACTCCAACATCGGGGCA GGTTATGATGTATACTGGTACCAACAACTTCCAGGAACTGCCCCCAAACT CCTCATCTATGGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGATTCT CTGGCTCCAGGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAG GCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACACCAGCCTGAA TGGTTGGGCTTTCGGCGGAGGGACCAAGTTGACCGTCCTAGGC [SEQ ID NO: 105]	
DNA for VH	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGG TACAGCCAGGGCGGTCCCTGAGACTCAGCTGTACAGCCTCTGGGTTTAGT TTTGGTGATCATGCTATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCT GGAGTGGGTAGGTTTCATTAGAAAGACAACTTATGGTGCGACAACACACT ACGCCGCGGCTGTGAGAGGCAGATTCACCATCTCGCGAGATGATTCTAAA AGOACTGTOTATCTGCAAATGAACAGCCTGAAAGCAGAGGACACAGCCGT GTATTTCTGTACTAGAGTGCAGCTTGACTATGGCCCGGGATACCAGTACT ACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA [SEQ ID NO: 106]	
Light Chain	QSVLTQPPSVSGAPGQRVTISCTGMNSNIGA GYDVYWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSRSGTSASLAITGLQ AEDEADYYCQSYDTSLNGWAFGGGTKLTVLGQPKAAPSVTLFPPSSEELQ ANKATLVCLVSDFYPGAVTVAWKADGSPVKVGVETTKPSKQSNNKYAASS YLSLTPEQWKSHRSYSCRVTHEGSTVEKTVAPAECS [SEQ ID NO: 107]	
Heavy Chain version 1	EVQLVESGGGLVQPGRSLRLSCTASGFS FGDHAMSWVRQAPGKGLEWVGFIRKTTYGATTHYAAAVRGRFTISRDDSK STVYLQMNSLKAEDTAVYFCTRVQLDYGPGYQYYGMDVWGQGTTVTVSSA STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPK SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNHYTQKSLSLSPGK [SEQ ID NO: 108]	
Heavy Chain version 2	EVQLVESGGGLVQPGRSLRLSCTASGFS FGDHAMSWVRQAPGKGLEWVGFIRKTTYGATTHYAAAVRGRFTISRDDSK STVYLQMNSLKAEDTAVYFCTRVQLDYGPGYQYYGMDVWGQGTTVTVSSA STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPK SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVLHEALHSHYTQKSLSLSPGK [SEQ ID NO: 109]	

TABLE 14-continued

Antibody ID: AB-000224.009

	KABAT	ASN
DNA for Light Chain	CAGTCTGTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAGGGTCACCATCTCCTGCACTGGGATGAACTCCAACATCGGGGCAGGTTATGATGTATACTGGTACCAACAACTTCCAGGAACTGCCCCCAAACTCCTCATCTATGGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAGGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACACCAGCCTGAATGGTTGGGCTTTCGGCGGAGGGACCAAGTTGACCGTCCTAGGCCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCACCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCGTAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATGGCAGCCCCGTCAAGGTGGGAGTGGAGACCACCAAACCCTCCAAACAAAGCAACAACAAGTATGCGGCCAGCAGCTACCTGAGCCTGACGCCCGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCGGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTGCAGAATGCTCT [SEQ ID NO: 110]	
DNA for Heavy Chain version 1	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCAGGGCGGTCCCTGAGACTCAGCTGTACAGCCTCTGGGTTTAGTTTTGGTGATCATGCTATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTAGGTTTCATTAGAAAGACAACTTATGGTGCGACAACACACTACGCCGCGGCTGTGAGAGGCAGATTCACCATCTCGCGAGATGATTCTAAAAGOACTGTOTATCTGCAAATGAACAGCCTGAAAGCAGAGGACACAGCCGTGTATTTCTGTACTAGAGTGCAGCTTGACTATGGCCCGGGATACCAGTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCAGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAA [SEQ ID NO: 111]	
DNA for Heavy Chain version 2	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCAGGGCGGTCCCTGAGACTCAGCTGTACAGCCTCTGGGTTTAGTTTTGGTGATCATGCTATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTAGGTTTCATTAGAAAGACAACTTATGGTGCGACAACACACTACGCCGCGGCTGTGAGAGGCAGATTCACCATCTCGCGAGATGATTCTAAAAGCACTGTCTATCTGCAAATGAACAGCCTGAAAGCAGAGGACACAGCCGTGTATTTCTGTACTAGAGTGCAGCTTGACTATGGCCCGGGATACCAGTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCAGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGCTGCATGAGGCTCTGCACTCCCACTACACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAA [SEQ ID NO: 112]	

In certain embodiments, the anti-CSP antibody variant comprises a light chain variable region comprising a CDR1, a CDR2, and a CDR3 and having the amino acid sequence set forth in SEQ ID NO: 113, as shown in Table 15. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 and having the amino acid sequence set forth in SEQ ID NO: 114, as shown in Table 15. In certain embodiments, the anti-CSP antibody variant comprises a light chain having the amino acid sequence set forth in SEQ ID NO: 117, as shown in Table 15. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain having the amino acid sequence set forth in SEQ ID NO: 118, as shown in Table 15. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain having the amino acid sequence set forth in SEQ ID NO: 119, as shown in Table 15. Exemplary nucleic acid sequences of SEQ ID NOS: 113, 114, 117, 118, and 119 are provided in Table 15 below.

TABLE 15

	Antibody ID: AB-000224.010	
	KABAT	ASN
CDR1-VL	TGMNSNIGAGYDVY [SEQ ID NO: 1]	TGMNSNIGAGYDVY [SEQ ID NO: 7]
CDR2-VL	GNSNRPS [SEQ ID NO: 2]	GNSNRPS [SEQ ID NO: 8]
CDR3-VL	QSYDTSLNGWA [SEQ ID NO: 3]	QSYDTSLNGWA [SEQ ID NO: 9]
CDR1-VH	DHAMS [SEQ ID NO: 4]	DHAMS [SEQ ID NO: 10]
CDR2-VH	FIRKTTYGATTHYAAAVRG [SEQ ID NO: 5]	FIRKTTYGATTHYAAAVRG [SEQ ID NO: 11]
CDR3-VH	VQLDYGPGYQYYGMDV [SEQ ID NO: 6]	VQLDYGPGYQYYGMDV [SEQ ID NO: 12]
VL	QSVLTQPPSVSGAPGQRVTISCTGMNSNIGA GYDVYWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSRSGTSASLAITGLQ AEDEADYYCQSYDTSLNGWAFGGGTKLTVLG [SEQ ID NO: 113]	
VH	EVQLVESGGGLVQPGRSLRLSCTASGFS FGDHAMSWVRQAPGKGLEWVGFIRKTTYGATTHYAAAVRGRFTISRDDSK STVYLQMNSLKTEDTAVYFCARVQLDYGPGYQYYGMDVWGQGTTVTVSS [SEQ ID NO: 114]	
DNA for VL	CAGTCTGTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAG GGCAGAGGGTCACCATCTCCTGCACTGGGATGAACTCCAACATCGGGGCA GGTTATGATGTATACTGGTACCAACAACTTCCAGGAACTGCCCCCAAACT CCTCATCTATGGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGATTCT CTGGCTCCAGGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAG GCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACACCAGCCTGAA TGGTTGGGCTTTCGGCGGAGGGACCAAGTTGACCGTCCTAGGC [SEQ ID NO: 115]	
DNA for VH	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGG TACAGCCAGGGCGGTCCCTGAGACTCAGCTGTACAGCCTCTGGGTTTAGT TTTGGTGATCATGCTATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCT GGAGTGGGTAGGTTTCATTAGAAAGACAACTTATGGTGCGACAACACACT ACGCCGCGGCTGTGAGAGGCAGATTCACCATCTCGCGAGATGATTCTAAA AGCACTGTCTATCTGCAAATGAACAGCCTGAAAACCGAGGACACAGCCGT GTATTTCTGTGCTAGAGTGCAGCTTGACTATGGCCCGGGATACCAGTACT ACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA [SEQ ID NO: 116]	
Light Chain	QSVLTQPPSVSGAPGQRVTISCTGMNSNIGA GYDVYWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSRSGTSASLAITGLQ AEDEADYYCQSYDTSLNGWAFGGGTKLTVLGQPKAAPSVTLFPPSSEELQ ANKATLVCLVSDFYPGAVTVAWKADGSPVKVGVETTKPSKQSNNKYAASS YLSLTPEQWKSHRSYSCRVTHEGSTVEKTVAPAECS [SEQ ID NO: 117]	
Heavy Chain version 1	EVQLVESGGGLVQPGRSLRLSCTASGFS FGDHAMSWVRQAPGKGLEWVGFIRKTTYGATTHYAAAVRGRFTISRDDSK STVYLQMNSLKTEDTAVYFCARVQLDYGPGYQYYGMDVWGQGTTVTVSSA STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPK SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH	

TABLE 15-continued

Antibody ID: AB-000224.010		
	KABAT	ASN
	EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNHYTQKSLSLSPGK [SEQ ID NO: 118]	
Heavy Chain version 2	EVQLVESGGGLVQPGRSLRLSCTASGFS FGDHAMSWVRQAPGKGLEWVGFIRKTTYGATTHYAAAVRGRFTISRDDSK STVYLQMNSLKTEDTAVYFCARVQLDYGPGYQYYGMDVWGQGTTVTVSSA STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPK SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVLHEALHSHYTQKSLSLSPGK [SEQ ID NO: 119]	
DNA for Light Chain	CAGTCTGTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAG GGCAGAGGGTCACCATCTCCTGCACTGGGATGAACTCCAACATCGGGGCA GGTTATGATGTATACTGGTACCAACAACTTCCAGGAACTGCCCCCAAACT CCTCATCTATGGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGATTCT CTGGCTCCAGGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAG GCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACACCAGCCTGAA TGGTTGGGCTTTCGGCGGAGGGACCAAGTTGACCGTCCTAGGCCAGCCCA AGGCTGCCCCCTCGGTCACTCTGTTCCCACCCTCCTCTGAGGAGCTTCAA GCCAACAAGGCCACACTGGTGTGTCTCGTAAGTGACTTCTACCCGGGAGC CGTGACAGTGGCCTGGAAGGCAGATGGCAGCCCCGTCAAGGTGGGAGTGG AGACCACCAAACCCTCCAAACAAAGCAACAACAAGTATGCGGCCAGCAGC TACCTGAGCCTGACGCCCGAGCAGTGGAAGTCCCACAGAAGCTACAGCTG CCGGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTGCAG AATGCTCT [SEQ ID NO: 120]	
DNA for Heavy Chain version 1	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGG TACAGCCAGGGCGGTCCCTGAGACTCAGCTGTACAGCCTCTGGGTTTAGT TTTGGTGATCATGCTATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCT GGAGTGGGTAGGTTTCATTAGAAAGACAACTTATGGTGCGACAACACACT ACGCCGCGGCTGTGAGAGGCAGATTCACCATCTCGCGAGATGATTCTAAA AGCACTGTCTATCTGCAAATGAACAGCCTGAAAACCGAGGACACAGCCGT GTATTTCTGTGCTAGAGTGCAGCTTGACTATGGCCCGGGATACCAGTACT ACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGCC TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCAC CTCTGGGGGCACAGCAGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCG AACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCAC ACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGT GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACG TGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAA TCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCT GGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCA TGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCAC GAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCA TAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTG TGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAAC CATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGC CCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTG GTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGG GCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACG GCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAA [SEQ ID NO: 121]	
DNA for Heavy Chain version 2	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGG TACAGCCAGGGCGGTCCCTGAGACTCAGCTGTACAGCCTCTGGGTTTAGT TTTGGTGATCATGCTATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCT GGAGTGGGTAGGTTTCATTAGAAAGACAACTTATGGTGCGACAACACACT ACGCCGCGGCTGTGAGAGGCAGATTCACCATCTCGCGAGATGATTCTAAA AGCACTGTCTATCTGCAAATGAACAGCCTGAAAACCGAGGACACAGCCGT GTATTTCTGTGCTAGAGTGCAGCTTGACTATGGCCCGGGATACCAGTACT ACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGCC TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCAC CTCTGGGGGCACAGCAGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCG AACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCAC ACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGT GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACG TGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAA TCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCT	

TABLE 15-continued

Antibody ID: AB-000224.010	
KABAT	ASN
GGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCA TGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCAC GAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCA TAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTG TGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAAC CATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGC CCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTG GTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGG GCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACG GCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGCTGCATGAGGCTCTGCACTCCCA CTACACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAA [SEQ ID NO: 122]	

In certain embodiments, the anti-CSP antibody variant comprises a light chain variable region comprising a CDR1, a CDR2, and a CDR3 and having the amino acid sequence set forth in SEQ ID NO: 123, as shown in Table 16. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 and having the amino acid sequence set forth in SEQ ID NO: 124, as shown in Table 16. In certain embodiments, the anti-CSP antibody variant comprises a light chain having the amino acid sequence set forth in SEQ ID NO: 127, as shown in Table 16. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain having the amino acid sequence set forth in SEQ ID NO: 128, as shown in Table 16. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain having the amino acid sequence set forth in SEQ ID NO: 129, as shown in Table 16. Exemplary nucleic acid sequences of SEQ ID NOS: 123, 124, 127, 128, and 129 are provided in Table 16 below.

TABLE 16

Antibody ID: AB-000224.011		
	KABAT	ASN
CDR1-VL	TGMNSNIGAGYDVY [SEQ ID NO: 1]	TGMNSNIGAGYDVY [SEQ ID NO: 7]
CDR2-VL	GNSNRPS [SEQ ID NO: 2]	GNSNRPS [SEQ ID NO: 8]
CDR3-VL	QSYDTSLNGWA [SEQ ID NO: 3]	QSYDTSLNGWA [SEQ ID NO: 9]
CDR1-VH	DHAMS [SEQ ID NO: 4]	DHAMS [SEQ ID NO: 10]
CDR2-VH	FIRKTTYGATTHYAAAVRG [SEQ ID NO: 5]	FIRKTTYGATTHYAAAVRG [SEQ ID NO: 11]
CDR3-VH	VQLDYGPGYQYYGMDV [SEQ ID NO: 6]	VQLDYGPGYQYYGMDV [SEQ ID NO: 12]
VL	QSVLTQPPSVSGAPGQRVTISCTGMNSNIGA GYDVYWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSRSGTSASLAITGLQ AEDEADYYCQSYDTSLNGWAFGGGTKLTVLG [SEQ ID NO: 123]	
VH	EVQLVESGGGLVQPGRSLRLSCTASGFS FGDHAMSWVRQAPGKGLEWVGFIRKTTYGATTHYAAAVRGRFTISRDDSK SIVYLQMNSLKAEDTAVYFCARVQLDYGPGYQYYGMDVWGQGTTVTVSS [SEQ ID NO: 124]	
DNA for VL	CAGTCTGTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAG GGCAGAGGGTCACCATCTCCTGCACTGGGATGAACTCCAACATCGGGGCA GGTTATGATGTATACTGGTACCAACAACTTCCAGGAACTGCCCCCAAACT CCTCATCTATGGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGATTCT CTGGCTCCAGGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAG GCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACACCAGCCTGAA TGGTTGGGCTTTCGGCGGAGGGACCAAGTTGACCGTCCTAGGC [SEQ ID NO: 125]	
DNA forVH	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGG TACAGCCAGGGCGGTCCCTGAGACTCAGCTGTACAGCCTCTGGGTTTAGT TTTGGTGATCATGCTATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCT GGAGTGGGTAGGTTTCATTAGAAAGACAACTTATGGTGCGACAACACACT	

TABLE 16-continued

	Antibody ID: AB-000224.011	
	KABAT	ASN
	ACGCCGCGGCTGTGAGAGGCAGATTCACCATCTCGCGAGATGATTCTAAA AGOATTGTOTATCTGCAAATGAACAGCCTGAAAGCAGAGGACACAGCCGT GTATTTCTGTGCTAGAGTGCAGCTTGACTATGGCCCGGGATACCAGTACT ACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA [SEQ ID NO: 126]	
Light Chain	QSVLTQPPSVSGAPGQRVTISCTGMNSNIGA GYDVYWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSRSGTSASLAITGLQ AEDEADYYCQSYDTSLNGWAFGGGTKLTVLGQPKAAPSVTLFPPSSEELQ ANKATLVCLVSDFYPGAVTVAWKADGSPVKVGVETTKPSKQSNNKYAASS YLSLTPEQWKSHRSYSCRVTHEGSTVEKTVAPAECS [SEQ ID NO: 127]	
Heavy Chain version 1	EVQLVESGGGLVQPGRSLRLSCTASGFS FGDHAMSWVRQAPGKGLEWVGFIRKTTYGATTHYAAAVRGRFTISRDDSK SIVYLQMNSLKAEDTAVYFCARVQLDYGPGYQYYGMDVWGQGTTVTVSSA STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPK SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNHYTQKSLSLSPGK [SEQ ID NO: 128]	
Heavy Chain version 2	EVQLVESGGGLVQPGRSLRLSCTASGFS FGDHAMSWVRQAPGKGLEWVGFIRKTTYGATTHYAAAVRGRFTISRDDSK SIVYLQMNSLKAEDTAVYFCARVQLDYGPGYQYYGMDVWGQGTTVTVSSA STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPK SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVLHEALHSHYTQKSLSLSPGK [SEQ ID NO: 129]	
DNA for Light Chain	CAGTCTGTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAG GGCAGAGGGTCACCATCTCCTGCACTGGGATGAACTCCAACATCGGGGCA GGTTATGATGTATACTGGTACCAACAACTTCCAGGAACTGCCCCCAAACT CCTCATCTATGGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGATTCT CTGGCTCCAGGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAG GCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACACCAGCCTGAA TGGTTGGGCTTTCGGCGGAGGGACCAAGTTGACCGTCCTAGGCCAGCCCA AGGCTGCCCCCTCGGTCACTCTGTTCCCACCCTCCTCTGAGGAGCTTCAA GCCAACAAGGCCACACTGGTGTGTCTCGTAAGTGACTTCTACCCGGGAGC CGTGACAGTGGCCTGGAAGGCAGATGGCAGCCCCGTCAAGGTGGGAGTGG AGACCACCAAACCCTCCAAACAAAGCAACAACAAGTATGCGGCCAGCAGC TACCTGAGCCTGACGCCCGAGCAGTGGAAGTCCCACAGAAGCTACAGCTG CCGGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTGCAG AATGCTCT [SEQ ID NO: 130]	
DNA for Heavy Chain version 1	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGG TACAGCCAGGGCGGTCCCTGAGACTCAGCTGTACAGCCTCTGGGTTTAGT TTTGGTGATCATGCTATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCT GGAGTGGGTAGGTTTCATTAGAAAGACAACTTATGGTGCGACAACACACT ACGCCGCGGCTGTGAGAGGCAGATTCACCATCTCGCGAGATGATTCTAAA AGCATTGTCTATCTGCAAATGAACAGCCTGAAAGCAGAGGACACAGCCGT GTATTTCTGTGCTAGAGTGCAGCTTGACTATGGCCCGGGATACCAGTACT ACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGCC TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCAC CTCTGGGGGCACAGCAGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCG AACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCAC ACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGT GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACG TGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAA TCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCT GGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCA TGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCAC GAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCA TAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTG TGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAAC CATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGC CCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTG GTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGG	

TABLE 16-continued

Antibody ID: AB-000224.011		
	KABAT	ASN
	GCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACG GCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAA [SEQ ID NO: 131]	
DNA for Heavy Chain version 2	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGG TACAGCCAGGGCGGTCCCTGAGACTCAGCTGTACAGCCTCTGGGTTTAGT TTTGGTGATCATGCTATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCT GGAGTGGGTAGGTTTCATTAGAAAGACAACTTATGGTGCGACAACACACT ACGCCGCGGCTGTGAGAGGCAGATTCACCATCTCGCGAGATGATTCTAAA AGCATTGTCTATCTGCAAATGAACAGCCTGAAAGCAGAGGACACAGCCGT GTATTTCTGTGCTAGAGTGCAGCTTGACTATGGCCCGGGATACCAGTACT ACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGCC TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCAC CTCTGGGGGCACAGCAGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCG AACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCAC ACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGT GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACG TGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAA TCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCT GGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCA TGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCAC GAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCA TAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTG TGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAAC CATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGC CCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTG GTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGG GCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACG GCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGCTGCATGAGGCTCTGCACTCCCA CTACACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAA [SEQ ID NO: 132]	

In certain embodiments, the anti-CSP antibody variant comprises a light chain variable region comprising a CDR1, a CDR2, and a CDR3 and having the amino acid sequence set forth in SEQ ID NO: 133, as shown in Table 17. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 and having the amino acid sequence set forth in SEQ ID NO: 134, as shown in Table 17. In certain embodiments, the anti-CSP antibody variant comprises a light chain having the amino acid sequence set forth in SEQ ID NO: 137, as shown in Table 17. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain having the amino acid sequence set forth in SEQ ID NO: 138, as shown in Table 17. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain having the amino acid sequence set forth in SEQ ID NO: 139, as shown in Table 17. Exemplary nucleic acid sequences of SEQ ID NOS: 133, 134, 137, 138, and 139 are provided in Table 17 below.

TABLE 17

Antibody ID: AB-000224.012		
	KABAT	ASN
CDR1-VL	TGMNSNIGAGYDVY [SEQ ID NO: 1]	TGMNSNIGAGYDVY [SEQ ID NO: 7]
CDR2-VL	GNSNRPS [SEQ ID NO: 2]	GNSNRPS [SEQ ID NO: 8]
CDR3-VL	QSYDTSLNGWA [SEQ ID NO: 3]	QSYDTSLNGWA [SEQ ID NO: 9]
CDR1-VH	DHAMS [SEQ ID NO: 4]	DHAMS [SEQ ID NO: 10]
CDR2-VH	FIRKTTYGATTHYAAAVRG [SEQ ID NO: 5]	FIRKTTYGATTHYAAAVRG [SEQ ID NO: 11]
CDR3-VH	VQLDYGPGYQYYGMDV [SEQ ID NO: 6]	VQLDYGPGYQYYGMDV [SEQ ID NO: 12]

TABLE 17-continued

	Antibody ID: AB-000224.012	
	KABAT	ASN
VL	QSVLTQPPSVSGAPGQRVTISCTGMNSNIGA GYDVYWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSRSGTSASLAITGLQ AEDEADYYCQSYDTSLNGWAFGGGTKLTVLG [SEQ ID NO: 133]	
VH	EVQLVESGGGLVQPGRSLRLSCAASGFS FGDHAMSWVRQAPGKGLEWVGFIRKTTYGATTHYAAAVRGRFTISRDDSK STVYLQMNSLKAEDTAVYFCTRVQLDYGPGYQYYGMDVWGQGTTVTVSS [SEQ ID NO: 134]	
DNA for VL	CAGTCTGTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAG GGCAGAGGGTCACCATCTCCTGCACTGGGATGAACTCCAACATCGGGGCA GGTTATGATGTATACTGGTACCAACAACTTCCAGGAACTGCCCCCAAACT CCTCATCTATGGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGATTCT CTGGCTCCAGGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAG GCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACACCAGCCTGAA TGGTTGGGCTTTCGGCGGAGGGACCAAGTTGACCGTCCTAGGC [SEQ ID NO: 135]	
DNA forVH	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGG TACAGCCAGGGCGGTCCCTGAGACTCAGCTGTGCGGCCTCTGGGTTTAGT TTTGGTGATCATGCTATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCT GGAGTGGGTAGGTTTCATTAGAAAGACAACTTATGGTGCGACAACACACT ACGCCGCGGCTGTGAGAGGCAGATTCACCATCTCGCGAGATGATTCTAAA AGGACTGTCTATCTGCAAATGAACAGCCTGAAAGCAGAGGACACAGCCGT GTATTTCTGTACTAGAGTGCAGCTTGACTATGGCCCGGGATACCAGTACT ACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA [SEQ ID NO: 136]	
Light Chain	QSVLTQPPSVSGAPGQRVTISCTGMNSNIGA GYDVYWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSRSGTSASLAITGLQ AEDEADYYCQSYDTSLNGWAFGGGTKLTVLGQPKAAPSVTLFPPSSEELQ ANKATLVCLVSDFYPGAVTVAWKADGSPVKVGVETTKPSKQSNNKYAASS YLSLTPEQWKSHRSYSCRVTHEGSTVEKTVAPAECS [SEQ ID NO: 137]	
Heavy Chain version 1	EVQLVESGGGLVQPGRSLRLSCAASGFS FGDHAMSWVRQAPGKGLEWVGFIRKTTYGATTHYAAAVRGRFTISRDDSK STVYLQMNSLKAEDTAVYFCTRVQLDYGPGYQYYGMDVWGQGTTVTVSSA STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPK SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNHYTQKSLSLSPGK [SEQ ID NO: 138]	
Heavy Chain version 2	EVQLVESGGGLVQPGRSLRLSCAASGFS FGDHAMSWVRQAPGKGLEWVGFIRKTTYGATTHYAAAVRGRFTISRDDSK STVYLQMNSLKAEDTAVYFCTRVQLDYGPGYQYYGMDVWGQGTTVTVSSA STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPK SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVLHEALHSHYTQKSLSLSPGK [SEQ ID NO: 139]	
DNA for Light Chain	CAGTCTGTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAG GGCAGAGGGTCACCATCTCCTGCACTGGGATGAACTCCAACATCGGGGCA GGTTATGATGTATACTGGTACCAACAACTTCCAGGAACTGCCCCCAAACT CCTCATCTATGGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGATTCT CTGGCTCCAGGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAG GCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACACCAGCCTGAA TGGTTGGGCTTTCGGCGGAGGGACCAAGTTGACCGTCCTAGGCCAGCCCA AGGCTGCCCCCTCGGTCACTCTGTTCCCACCCTCCTCTGAGGAGCTTCAA GCCAACAAGGCCACACTGGTGTGTCTCGTAAGTGACTTCTACCCGGGAGC CGTGACAGTGGCCTGGAAGGCAGATGGCAGCCCCGTCAAGGTGGAGTGG AGACCACCAAACCCTCCAAACAAAGCAACAACAAGTATGCGGCCAGCAGC TACCTGAGCCTGACGCCCGAGCAGTGGAAGTCCCACAGAAGCTACAGCTG CCGGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTGCAG AATGCTCT[SEQ ID NO: 140]	

TABLE 17-continued

	Antibody ID: AB-000224.012	
	KABAT	ASN
DNA for Heavy Chain version 1	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGG TACAGCCAGGGCGGTCCCTGAGACTCAGCTGTGCGGCCTCTGGGTTTAGT TTTGGTGATCATGCTATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCT GGAGTGGGTAGGTTTCATTAGAAAGACAACTTATGGTGCGACAACACACT ACGCCGCGGCTGTGAGAGGCAGATTCACCATCTCGCGAGATGATTCTAAA AGCACTGTCTATCTGCAAATGAACAGCCTGAAAGCAGAGGACACAGCCGT GTATTTCTGTACTAGAGTGCAGCTTGACTATGGCCCGGGATACCAGTACT ACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGCC TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCAC CTCTGGGGGCACAGCAGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCG AACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCAC ACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGT GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACG TGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAA TCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCT GGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCA TGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCAC GAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCA TAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTG TGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAAC CATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGC CCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTG GTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGG GCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACG GCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAA [SEQ ID NO: 141]	
DNA for Heavy Chain version 2	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGG TACAGCCAGGGCGGTCCCTGAGACTCAGCTGTGCGGCCTCTGGGTTTAGT TTTGGTGATCATGCTATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCT GGAGTGGGTAGGTTTCATTAGAAAGACAACTTATGGTGCGACAACACACT ACGCCGCGGCTGTGAGAGGCAGATTCACCATCTCGCGAGATGATTCTAAA AGGACTGTCTATCTGCAAATGAACAGCCTGAAAGCAGAGGACACAGCCGT GTATTTCTGTACTAGAGTGCAGCTTGACTATGGCCCGGGATACCAGTACT ACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGCC TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCAC CTCTGGGGGCACAGCAGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCG AACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCAC ACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGT GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACG TGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAA TCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCT GGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCA TGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCAC GAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCA TAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTG TGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAAC CATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGC CCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTG GTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGG GCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACG GCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGCTGCATGAGGCTCTGCACTCCCA CTACACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAA [SEQ ID NO: 142]	

In certain embodiments, the anti-CSP antibody variant comprises a light chain variable region comprising a CDR1, a CDR2, and a CDR3 and having the amino acid sequence set forth in SEQ ID NO: 143, as shown in Table 18. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 and having the amino acid sequence set forth in SEQ ID NO: 144, as shown in Table 18. In certain embodiments, the anti-CSP antibody variant comprises a light chain having the amino acid sequence set forth in SEQ ID NO: 147, as shown in Table 18. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain having the amino acid sequence set forth in SEQ ID NO: 148, as shown in Table 18. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain having the amino acid sequence set forth in SEQ ID NO: 149, as shown in Table 18. Exemplary nucleic acid sequences of SEQ ID NOS: 143, 144, 147, 148, and 149 are provided in Table 18 below.

TABLE 18

Antibody ID: AB-000224.013		
	KABAT	ASN
CDR1-VL	TGMNSNIGAGYDVY [SEQ ID NO: 1]	TGMNSNIGAGYDVY [SEQ ID NO: 7]
CDR2-VL	GNSNRPS [SEQ ID NO: 2]	GNSNRPS [SEQ ID NO: 8]
CDR3-VL	QSYDTSLNGWA [SEQ ID NO: 3]	QSYDTSLNGWA [SEQ ID NO: 9]
CDR1-VH	DHAMS [SEQ ID NO: 4]	DHAMS [SEQ ID NO: 10]
CDR2-VH	FIRKTTYGATTHYAAAVRG [SEQ ID NO: 5]	FIRKTTYGATTHYAAAVRG [SEQ ID NO: 11]
CDR3-VH	VQLDYGPGYQYYGMDV [SEQ ID NO: 6]	VQLDYGPGYQYYGMDV [SEQ ID NO: 12]
VL	QSVLTQPPSVSGAPGQRVTISCTGMNSNIGAGYDVYWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSRSGTSASLAITGLQAEDEADYYCQSYDTSLNGWAFGGGTKLTVLG [SEQ ID NO: 143]	
VH	EVQLVESGGGLVQPGRSLRLSCAASGFSFGDHAMSWVRQAPGKGLEWVGFIRKTTYGATTHYAAAVRGRFTISRDDSKSTVYLQMNSLKTEDTAVYFCARVQLDYGPGYQYYGMDVWGQGTTVTVSS [SEQ ID NO: 144]	
DNA for VL	CAGTCTGTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAGGGTCACCATCTCCTGCACTGGGATGAACTCCAACATCGGGGCAGGTTATGATGTATACTGGTACCAACAACTTCCAGGAACTGCCCCCAAACTCCTCATCTATGGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAGGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACACCAGCCTGAATGGTTGGGCTTTCGGCGGAGGGACCAAGTTGACCGTCCTAGGC [SEQ ID NO: 145]	
DNA for VH	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCAGGGCGGTCCCTGAGACTCAGCTGTGCGGCCTCTGGGTTTAGTTTTGGTGATCATGCTATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTAGGTTTCATTAGAAAGACAACTTATGGTGCGACAACACACTACGCCGCGGCTGTGAGAGGCAGATTCACCATCTCGCGAGATGATTCTAAAAGCACTGTCTATCTGCAAATGAACAGCCTGAAAACCGAGGACACAGCCGTGTATTTCTGTGCTAGAGTGCAGCTTGACTATGGCCCGGGATACCAGTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA [SEQ ID NO: 146]	
Light Chain	QSVLTQPPSVSGAPGQRVTISCTGMNSNIGAGYDVYWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSRSGTSASLAITGLQAEDEADYYCQSYDTSLNGWAFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLVSDFYPGAVTVAWKADGSPVKVGVETTKPSKQSNNKYAASSYLSLTPEQWKSHRSYSCRVTHEGSTVEKTVAPAECS [SEQ ID NO: 147]	
Heavy Chain version 1	EVQLVESGGGLVQPGRSLRLSCAASGFSFGDHAMSWVRQAPGKGLEWVGFIRKTTYGATTHYAAAVRGRFTISRDDSKSTVYLQMNSLKTEDTAVYFCARVQLDYGPGYQYYGMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK [SEQ ID NO: 148]	
Heavy Chain version 2	EVQLVESGGGLVQPGRSLRLSCAASGFSFGDHAMSWVRQAPGKGLEWVGFIRKTTYGATTHYAAAVRGRFTISRDDSKSTVYLQMNSLKTEDTAVYFCARVQLDYGPGYQYYGMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK [SEQ ID NO: 149]	

TABLE 18-continued

	Antibody ID: AB-000224.013	
	KABAT	ASN
DNA for Light Chain	CAGTCTGTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAGGGTCACCATCTCCTGCACTGGGATGAACTCCAACATCGGGGCAGGTTATGATGTATACTGGTACCAACAACTTCCAGGAACTGCCCCCAAACTCCTCATCTATGGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAGGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACACCAGCCTGAATGGTTGGGCTTTCGGCGGAGGGACCAAGTTGACCGTCCTAGGCCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCACCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCGTAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATGGCAGCCCCGTCAAGGTGGGAGTGGAGACCACCAAACCCTCCAAACAAAGCAACAACAAGTATGCGGCCAGCAGCTACCTGAGCCTGACGCCCGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCGGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTGCAGAATGCTCT [SEQ ID NO: 150]	
DNA for Heavy Chain version 1	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCAGGGCGGTCCCTGAGACTCAGCTGTGCGGCCTCTGGGTTTAGTTTTGGTGATCATGCTATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTAGGTTTCATTAGAAAGACAACTTATGGTGCGACAACACACTACGCCGCGGCTGTGAGAGGCAGATTCACCATCTCGCGAGATGATTCTAAAAGCACTGTCTATCTGCAAATGAACAGCCTGAAAACCGAGGACACAGCCGTGTATTTCTGTGCTAGAGTGCAGCTTGACTATGGCCCGGGATACCAGTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCAGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAA [SEQ ID NO: 151]	
DNA for Heavy Chain version 2	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCAGGGCGGTCCCTGAGACTCAGCTGTGCGGCCTCTGGGTTTAGTTTTGGTGATCATGCTATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTAGGTTTCATTAGAAAGACAACTTATGGTGCGACAACACACTACGCCGCGGCTGTGAGAGGCAGATTCACCATCTCGCGAGATGATTCTAAAAGCACTGTCTATCTGCAAATGAACAGCCTGAAAACCGAGGACACAGCCGTGTATTTCTGTGCTAGAGTGCAGCTTGACTATGGCCCGGGATACCAGTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCAGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGCTGCATGAGGCTCTGCACTCCCACTACACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAA [SEQ ID NO: 152]	

In certain embodiments, the anti-CSP antibody variant comprises a light chain variable region comprising a CDR1, a CDR2, and a CDR3 and having the amino acid sequence set forth in SEQ ID NO: 153, as shown in Table 19. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 and having the amino acid sequence set forth in SEQ ID NO: 154, as shown in Table 19. In certain embodiments, the anti-CSP antibody variant comprises a light chain having the amino acid sequence set forth in SEQ ID NO: 157, as shown in Table 19. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain having the amino acid sequence set forth in SEQ ID NO: 158, as shown in Table 19. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain having the amino acid sequence set forth in SEQ ID NO: 159, as shown in Table 19. Exemplary nucleic acid sequences of SEQ ID NOS: 153, 154, 157, 158, and 159 are provided in Table 19 below.

TABLE 19

Antibody ID: AB-000224.014		
	KABAT	ASN
CDR1-VL	TGMNSNIGAGYDVY [SEQ ID NO: 1]	TGMNSNIGAGYDVY [SEQ ID NO: 7]
CDR2-VL	GNSNRPS [SEQ ID NO: 2]	GNSNRPS [SEQ ID NO: 8]
CDR3-VL	QSYDTSLNGWA [SEQ ID NO: 3]	QSYDTSLNGWA [SEQ ID NO: 9]
CDR1-VH	DHAMS [SEQ ID NO: 4]	DHAMS [SEQ ID NO: 10]
CDR2-VH	FIRKTTYGATTHYAAAVRG [SEQ ID NO: 5]	FIRKTTYGATTHYAAAVRG [SEQ ID NO: 11]
CDR3-VH	VQLDYGPGYQYYGMDV [SEQ ID NO: 6]	VQLDYGPGYQYYGMDV [SEQ ID NO: 12]
VL	QSVLTQPPSVSGAPGQRVTISCTGMNSNIGA GYDVYWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSRSGTSASLAITGLQ AEDEADYYCQSYDTSLNGWAFGGGTKLTVLG [SEQ ID NO: 153]	
VH	EVQLVESGGGLVQPGRSLRLSCAASGFS FGDHAMSWVRQAPGKGLEWVGFIRKTTYGATTHYAAAVRGRFTISRDDSK SIVYLQMNSLKAEDTAVYFCARVQLDYGPGYQYYGMDVWGQGTTVTVSS [SEQ ID NO: 154]	
DNA for VL	CAGTCTGTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAG GGCAGAGGGTCACCATCTCCTGCACTGGGATGAACTCCAACATCGGGGCA GGTTATGATGTATACTGGTACCAACAACTTCCAGGAACTGCCCCCAAACT CCTCATCTATGGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGATTCT CTGGCTCCAGGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAG GCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACACCAGCCTGAA TGGTTGGGCTTTCGGCGGAGGGACCAAGTTGACCGTCCTAGGC [SEQ ID NO: 155]	
DNA for VH	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGG TACAGCCAGGGCGGTCCCTGAGACTCAGCTGTGCGGCCTCTGGGTTTAGT TTTGGTGATCATGCTATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCT GGAGTGGGTAGGTTTCATTAGAAAGACAACTTATGGTGCGACAACACACT ACGCCGCGGCTGTGAGAGGCAGATTCACCATCTCGCGAGATGATTCTAAA AGOATTGTOTATCTGCAAATGAACAGCCTGAAAGCAGAGGACACAGCCGT GTATTTCTGTGCTAGAGTGCAGCTTGACTATGGCCCGGGATACCAGTACT ACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA [SEQ ID NO: 156]	
Light Chain	QSVLTQPPSVSGAPGQRVTISCTGMNSNIGA GYDVYWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSRSGTSASLAITGLQ AEDEADYYCQSYDTSLNGWAFGGGTKLTVLGQPKAAPSVTLFPPSSEELQ ANKATLVCLVSDFYPGAVTVAWKADGSPVKVGVETTKPSKQSNNKYAASS YLSLTPEQWKSHRSYSCRVTHEGSTVEKTVAPAECS [SEQ ID NO: 157]	
Heavy Chain version 1	EVQLVESGGGLVQPGRSLRLSCAASGFS FGDHAMSWVRQAPGKGLEWVGFIRKTTYGATTHYAAAVRGRFTISRDDSK SIVYLQMNSLKAEDTAVYFCARVQLDYGPGYQYYGMDVWGQGTTVTVSSA STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPK SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH	

TABLE 19-continued

Antibody ID: AB-000224.014		
	KABAT	ASN
	EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK [SEQ ID NO: 158]	
Heavy Chain version 2	EVQLVESGGGLVQPGRSLRLSCAASGFSFGDHAMSWVRQAPGKGLEWVGFIRKTTYGATTHYAAAVRGRFTISRDDSKSIVYLQMNSLKAEDTAVYFCARVQLDYGPGYQYYGMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK [SEQ ID NO: 159]	
DNA for Light Chain	CAGTCTGTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAGGGTCACCATCTCCTGCACTGGGATGAACTCCAACATCGGGGCAGGTTATGATGTATACTGGTACCAACAACTTCCAGGAACTGCCCCCAAACTCCTCATCTATGGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAGGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACACCAGCCTGAATGGTTGGGCTTTCGGCGGAGGGACCAAGTTGACCGTCCTAGGCCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCACCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCGTAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATGGCAGCCCCGTCAAGGTGGGAGTGGAGACCACCAAACCCTCCAAACAAAGCAACAACAAGTATGCGGCCAGCAGCTACCTGAGCCTGACGCCCGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCGGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTGCAGAATGCTCT [SEQ ID NO: 160]	
DNA for Heavy Chain version 1	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCAGGGCGGTCCCTGAGACTCAGCTGTGCGGCCTCTGGGTTTAGTTTTGGTGATCATGCTATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTAGGTTTCATTAGAAAGACAACTTATGGTGCGACAACACACTACGCCGCGGCTGTGAGAGGCAGATTCACCATCTCGCGAGATGATTCTAAAAGCATTGTCTATCTGCAAATGAACAGCCTGAAAGCAGAGGACACAGCCGTGTATTTCTGTGCTAGAGTGCAGCTTGACTATGGCCCGGGATACCAGTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCAGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAA [SEQ ID NO: 161]	
DNA for Heavy Chain version 2	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCAGGGCGGTCCCTGAGACTCAGCTGTGCGGCCTCTGGGTTTAGTTTTGGTGATCATGCTATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTAGGTTTCATTAGAAAGACAACTTATGGTGCGACAACACACTACGCCGCGGCTGTGAGAGGCAGATTCACCATCTCGCGAGATGATTCTAAAAGGATTGTCTATGTGCAAATGAACAGCCTGAAAGCAGAGGACACAGCCGTGTATTTCTGTGCTAGAGTGCAGCTTGACTATGGCCCGGGATACCAGTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCAGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCT	

TABLE 19-continued

Antibody ID: AB-000224.014	
KABAT	ASN
GGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCA TGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCAC GAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCA TAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTG TGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAAC CATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGC CCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTG GTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGG GCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACG GCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGCTGCATGAGGCTCTGCACTCCCA CTACACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAA [SEQ ID NO: 162]	

In certain embodiments, the anti-CSP antibody variant comprises a light chain variable region comprising a CDR1, a CDR2, and a CDR3 and having the amino acid sequence set forth in SEQ ID NO: 163, as shown in Table 20. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 and having the amino acid sequence set forth in SEQ ID NO: 164, as shown in Table 20. In certain embodiments, the anti-CSP antibody variant comprises a light chain having the amino acid sequence set forth in SEQ ID NO: 167, as shown in Table 20. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain having the amino acid sequence set forth in SEQ ID NO: 168, as shown in Table 20. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain having the amino acid sequence set forth in SEQ ID NO: 169, as shown in Table 20. Exemplary nucleic acid sequences of SEQ ID NOS: 163, 164, 167, 168, and 169 are provided in Table 20 below.

TABLE 20

Antibody ID: AB-000224.015		
	KABAT	ASN
CDR1-VL	TGMNSNIGAGYDVY [SEQ ID NO: 1]	TGMNSNIGAGYDVY [SEQ ID NO: 7]
CDR2-VL	GNSNRPS [SEQ ID NO: 2]	GNSNRPS [SEQ ID NO: 8]
CDR3-VL	QSYDTSLNGWA [SEQ ID NO: 3]	QSYDTSLNGWA [SEQ ID NO: 9]
CDR1-VH	DHAMS [SEQ ID NO: 4]	DHAMS [SEQ ID NO: 10]
CDR2-VH	FIRKTTYGATTHYAAAVRG [SEQ ID NO: 5]	FIRKTTYGATTHYAAAVRG [SEQ ID NO: 11]
CDR3-VH	VQLDYGPGYQYYGMDV [SEQ ID NO: 6]	VQLDYGPGYQYYGMDV [SEQ ID NO: 12]
VL	QSVLTQPPSVSGAPGQRVTISCTGMNSNIGA GYDVYWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSRSGTSASLAITGLQ AEDEADYYCQSYDTSLNGWAFGGGTKLTVLG [SEQ ID NO: 163]	
VH	EVQLVESGGGLVQPGRSLRLSCTASGFS FGDHAMSWVRQAPGKGLEWVGFIRKTTYGATTHYAAAVRGRFTISRDDSK STVYLQMNSLKAEDTAVYFCARVQLDYGPGYQYYGMDVWGQGTTVTVSS [SEQ ID NO: 164]	
DNA for VL	CAGTCTGTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAG GGCAGAGGGTCACCATCTCCTGCACTGGGATGAACTCCAACATCGGGGCA GGTTATGATGTATACTGGTACCAACAACTTCCAGGAACTGCCCCCAAACT CCTCATCTATGGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGATTCT CTGGCTCCAGGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAG GCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACACCAGCCTGAA TGGTTGGGCTTTCGGCGGAGGGACCAAGTTGACCGTCCTAGGC [SEQ ID NO: 165]	
DNA forVH	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGG TACAGCCAGGGCGGTCCCTGAGACTCAGCTGTACAGCCTCTGGGTTTAGT TTTGGTGATCATGCTATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCT GGAGTGGGTAGGTTTCATTAGAAAGACAACTTATGGTGCGACAACACACT	

TABLE 20-continued

Antibody ID: AB-000224.015		
	KABAT	ASN
	ACGCCGCGGCTGTGAGAGGCAGATTCACCATCTCGCGAGATGATTCTAAA AGOACTGTOTATCTGCAAATGAACAGCCTGAAAGCAGAGGACACAGCCGT GTATTTCTGTGCTAGAGTGCAGCTTGACTATGGCCCGGGATACCAGTACT ACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA [SEQ ID NO: 166]	
Light Chain	QSVLTQPPSVSGAPGQRVTISCTGMNSNIGA GYDVYWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSRSGTSASLAITGLQ AEDEADYYCQSYDTSLNGWAFGGGTKLTVLGQPKAAPSVTLFPPSSEELQ ANKATLVCLVSDFYPGAVTVAWKADGSPVKVGVETTKPSKQSNNKYAASS YLSLTPEQWKSHRSYSCRVTHEGSTVEKTVAPAECS [SEQ ID NO: 167]	
Heavy Chain version 1	EVQLVESGGGLVQPGRSLRLSCTASGFS FGDHAMSWVRQAPGKGLEWVGFIRKTTYGATTHYAAAVRGRFTISRDDSK STVYLQMNSLKAEDTAVYFCARVQLDYGPGYQYYGMDVWGQGTTVTVSSA STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPK SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNHYTQKSLSLSPGK [SEQ ID NO: 168]	
Heavy Chain version 2	EVQLVESGGGLVQPGRSLRLSCTASGFS FGDHAMSWVRQAPGKGLEWVGFIRKTTYGATTHYAAAVRGRFTISRDDSK STVYLQMNSLKAEDTAVYFCARVQLDYGPGYQYYGMDVWGQGTTVTVSSA STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPK SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVLHEALHSHYTQKSLSLSPGK [SEQ ID NO: 169]	
DNA for Light Chain	CAGTCTGTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAG GGCAGAGGGTCACCATCTCCTGCACTGGGATGAACTCCAACATCGGGGCA GGTTATGATGTATACTGGTACCAACAACTTCCAGGAACTGCCCCCAAACT CCTCATCTATGGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGATTCT CTGGCTCCAGGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAG GCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACACCAGCCTGAA TGGTTGGGCTTTCGGCGGAGGGACCAAGTTGACCGTCCTAGGCCAGCCCA AGGCTGCCCCCTCGGTCACTCTGTTCCCACCCTCCTCTGAGGAGCTTCAA GCCAACAAGGCCACACTGGTGTGTCTCGTAAGTGACTTCTACCCGGGAGC CGTGACAGTGGCCTGGAAGGCAGATGGCAGCCCCGTCAAGGTGGGAGTGG AGACCACCAAACCCTCCAAACAAAGCAACAACAAGTATGCGGCCAGCAGC TACCTGAGCCTGACGCCCGAGCAGTGGAAGTCCCACAGAAGCTACAGCTG CCGGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTGCAG AATGCTCT [SEQ ID NO: 170]	
DNA for Heavy Chain version 1	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGG TACAGCCAGGGCGGTCCCTGAGACTCAGCTGTACAGCCTCTGGGTTTAGT TTTGGTGATCATGCTATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCT GGAGTGGGTAGGTTTCATTAGAAAGACAACTTATGGTGCGACAACACACT ACGCCGCGGCTGTGAGAGGCAGATTCACCATCTCGCGAGATGATTCTAAA AGOACTGTOTATCTGCAAATGAACAGCCTGAAAGCAGAGGACACAGCCGT GTATTTCTGTGCTAGAGTGCAGCTTGACTATGGCCCGGGATACCAGTACT ACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGCC TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCAC CTCTGGGGGCACAGCAGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCG AACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCAC ACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGT GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACG TGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAA TCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCT GGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCA TGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCAC GAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCA TAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTG TGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAAC CATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGC CCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTG GTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGG GCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACG	

TABLE 20-continued

Antibody ID: AB-000224.015		
	KABAT	ASN
	GCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAA [SEQ ID NO: 171]	
DNA for Heavy Chain version 2	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGG TACAGCCAGGGCGGTCCCTGAGACTCAGCTGTACAGCCTCTGGGTTTAGT TTTGGTGATCATGCTATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCT GGAGTGGGTAGGTTTCATTAGAAAGACAACTTATGGTGCGACAACACACT ACGCCGCGGCTGTGAGAGGCAGATTCACCATCTCGCGAGATGATTCTAAA AGGACTGTCTATCTGCAAATGAACAGCCTGAAAGCAGAGGACACAGCCGT GTATTTCTGTGCTAGAGTGCAGCTTGACTATGGCCCGGGATACCAGTACT ACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGCC TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCAC CTCTGGGGGCACAGCAGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCG AACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCAC ACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGT GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACG TGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAA TCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCT GGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCA TGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCAC GAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCA TAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTG TGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAAC CATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGC CCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTG GTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGG GCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACG GCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGCTGCATGAGGCTCTGCACTCCCA CTACACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAA [SEQ ID NO: 172]	

In certain embodiments, the anti-CSP antibody variant comprises a light chain variable region comprising a CDR1, a CDR2, and a CDR3 and having the amino acid sequence set forth in SEQ ID NO: 173, as shown in Table 21. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 and having the amino acid sequence set forth in SEQ ID NO: 174, as shown in Table 21. In certain embodiments, the anti-CSP antibody variant comprises a light chain having the amino acid sequence set forth in SEQ ID NO: 177, as shown in Table 21. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain having the amino acid sequence set forth in SEQ ID NO: 178, as shown in Table 21. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain having the amino acid sequence set forth in SEQ ID NO: 179, as shown in Table 21. Exemplary nucleic acid sequences of SEQ ID NOS: 173, 174, 177, 178, and 179 are provided in Table 21 below.

TABLE 21

Antibody ID: AB-000224.016		
	KABAT	ASN
CDR1-VL	TGMNSNIGAGYDVY [SEQ ID NO: 1]	TGMNSNIGAGYDVY [SEQ ID NO: 7]
CDR2-VL	GNSNRPS [SEQ ID NO: 2]	GNSNRPS [SEQ ID NO: 8]
CDR3-VL	QSYDTSLNGWA [SEQ ID NO: 3]	QSYDTSLNGWA [SEQ ID NO: 9]
CDR1-VH	DHAMS [SEQ ID NO: 4]	DHAMS [SEQ ID NO: 10]
CDR2-VH	FIRKTTYGATTHYAAAVRG [SEQ ID NO: 5]	FIRKTTYGATTHYAAAVRG [SEQ ID NO: 11]
CDR3-VH	VQLDYGPGYQYYGMDV [SEQ ID NO: 6]	VQLDYGPGYQYYGMDV [SEQ ID NO: 12]
VL	QSVLTQPPSVSGAPGQRVTISCTGMNSNIGA GYDVYWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSRSGTSASLAITGLQ AEDEADYYCQSYDTSLNGWAFGGGTKLTVLG [SEQ ID NO: 173]	

TABLE 21-continued

	Antibody ID: AB-000224.016	
	KABAT	ASN
VH	EVQLVESGGGLVQPGRSLRLSCAASGFSFGDHAMSWVRQAPGKGLEWVGFIRKTTYGATTHYAAAVRGRFTISRDDSKSTVYLQMNSLKAEDTAVYFCARVQLDYGPGYQYYGMDVWGQGTTVTVSS [SEQ ID NO: 174]	
DNA for VL	CAGTCTGTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAGGGTCACCATCTCCTGCACTGGGATGAACTCCAACATCGGGGCAGGTTATGATGTATACTGGTACCAACAACTTCCAGGAACTGCCCCCAAACTCCTCATCTATGGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAGGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACACCAGCCTGAATGGTTGGGCTTTCGGCGGAGGGACCAAGTTGACCGTCCTAGGC [SEQ ID NO: 175]	
DNA forVH	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCAGGGCGGTCCCTGAGACTCAGCTGTGCGGCCTCTGGGTTTAGTTTTGGTGATCATGCTATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTAGGTTTCATTAGAAAGACAACTTATGGTGCGACAACACACTACGCCGCGGCTGTGAGAGGCAGATTCACCATCTCGCGAGATGATTCTAAAAGOACTGTOTATCTGCAAATGAACAGCCTGAAAGCAGAGGACACAGCCGTGTATTTCTGTGCTAGAGTGCAGCTTGACTATGGCCCGGGATACCAGTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA [SEQ ID NO: 176]	
Light Chain	QSVLTQPPSVSGAPGQRVTISCTGMNSNIGAGYDVYWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSRSGTSASLAITGLQAEDEADYYCQSYDTSLNGWAFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLVSDFYPGAVTVAWKADGSPVKVGVETTKPSKQSNNKYAASSYLSLTPEQWKSHRSYSCRVTHEGSTVEKTVAPAECS [SEQ ID NO: 177]	
Heavy Chain version 1	EVQLVESGGGLVQPGRSLRLSCAASGFSFGDHAMSWVRQAPGKGLEWVGFIRKTTYGATTHYAAAVRGRFTISRDDSKSTVYLQMNSLKAEDTAVYFCARVQLDYGPGYQYYGMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK [SEQ ID NO: 178]	
Heavy Chain version 2	EVQLVESGGGLVQPGRSLRLSCAASGFSFGDHAMSWVRQAPGKGLEWVGFIRKTTYGATTHYAAAVRGRFTISRDDSKSTVYLQMNSLKAEDTAVYFCARVQLDYGPGYQYYGMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK [SEQ ID NO: 179]	
DNA for Light Chain	CAGTCTGTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAGGGTCACCATCTCCTGCACTGGGATGAACTCCAACATCGGGGCAGGTTATGATGTATACTGGTACCAACAACTTCCAGGAACTGCCCCCAAACTCCTCATCTATGGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAGGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACACCAGCCTGAATGGTTGGGCTTTCGGCGGAGGGACCAAGTTGACCGTCCTAGGCCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCACCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCGTAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATGGCAGCCCCGTCAAGGTGGGAGTGGAGACCACCAAACCCTCCAAACAAAGCAACAACAAGTATGCGGCCAGCAGCTACCTGAGCCTGACGCCCGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCGGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTGCAGAATGCTCT [SEQ ID NO: 180]	

TABLE 21-continued

	Antibody ID: AB-000224.016
	KABAT ASN
DNA for Heavy Chain version 1	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCAGGGCGGTCCCTGAGACTCAGCTGTGCGGCCTCTGGGTTTAGTTTTGGTGATCATGCTATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTAGGTTTCATTAGAAAGACAACTTATGGTGCGACAACACACTACGCCGCGGCTGTGAGAGGCAGATTCACCATCTCGCGAGATGATTCTAAAAGOACTGTOTATCTGCAAATGAACAGCCTGAAAGCAGAGGACACAGCCGTGTATTTCTGTGCTAGAGTGCAGCTTGACTATGGCCCGGGATACCAGTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCAGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAA [SEQ ID NO: 181]
DNA for Heavy Chain version 2	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCAGGGCGGTCCCTGAGACTCAGCTGTGCGGCCTCTGGGTTTAGTTTTGGTGATCATGCTATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTAGGTTTCATTAGAAAGACAACTTATGGTGCGACAACACACTACGCCGCGGCTGTGAGAGGCAGATTCACCATCTCGCGAGATGATTCTAAAAGCACTGTCTATCTGCAAATGAACAGCCTGAAAGCAGAGGACACAGCCGTGTATTTCTGTGCTAGAGTGCAGCTTGACTATGGCCCGGGATACCAGTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCAGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGCTGCATGAGGCTCTGCACTCCCACTACACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAA [SEQ ID NO: 182]

In certain embodiments, the VL of the variant of an anti-CSP antibody includes at least one, at least two, or at least three mutations, e.g., substitutions, in the CDR1 amino acid sequence set forth in SEQ ID NO: 183. In certain embodiments, the VL of the variant of an anti-CSP antibody includes at least one, at least two, or at least three mutations, e.g., substitutions, in the CDR2 amino acid sequence set forth in SEQ ID NO: 184. In certain embodiments, the VL of the variant of an anti-CSP antibody includes at least one, at least two, or at least three mutations, e.g., substitutions, in the CDR3 amino acid sequence set forth in SEQ ID NO: 185. In certain embodiments, the VH of the variant of an anti-CSP antibody includes at least one, at least two, or at least three mutations, e.g., substitutions, in the CDR1 amino acid sequence set forth in SEQ ID NO: 186. In certain embodiments, the VL of the variant of an anti-CSP antibody includes at least one, at least two, or at least three mutations, e.g., substitutions, in the CDR2 amino acid sequence set forth in SEQ ID NO: 187. In certain embodiments, the VL of the variant of an anti-CSP antibody includes at least one, at least two, or at least three mutations, e.g., substitutions, in the CDR3 amino acid sequence set forth in SEQ ID NO: 188.

In certain embodiments, the VL of the variant of an anti-CSP antibody includes at least one, at least two, or at least three mutations, e.g., substitutions, in the CDR1 amino acid sequence set forth in SEQ ID NO: 189. In certain embodiments, the VL of the variant of an anti-CSP antibody includes at least one, at least two, or at least three mutations, e.g., substitutions, in the CDR2 amino acid sequence set forth in SEQ ID NO: 190. In certain embodiments, the VL of the variant of an anti-CSP antibody includes at least one, at least two, or at least three mutations, e.g., substitutions, in the CDR3 amino acid sequence set forth in SEQ ID NO: 191. In certain embodiments, the VH of the variant of an anti-CSP antibody includes at least one, at least two, or at least three mutations, e.g., substitutions, in the CDR1 amino acid sequence set forth in SEQ ID NO: 192. In certain embodiments, the VL of the variant of an anti-CSP antibody includes at least one, at least two, or at least three mutations, e.g., substitutions, in the CDR2 amino acid sequence set forth in SEQ ID NO: 193. In certain embodiments, the VL of the variant of an anti-CSP antibody includes at least one, at least two, or at least three mutations, e.g., substitutions, in the CDR3 amino acid sequence set forth in SEQ ID NO: 194.

In certain embodiments, the anti-CSP antibody variant comprises a light chain variable region comprising a CDR1, a CDR2, and a CDR3 and having the amino acid sequence set forth in SEQ ID NO: 195, as shown in Table 22. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 and having the amino acid sequence set forth in SEQ ID NO: 196, as shown in Table 22. In certain embodiments, the anti-CSP antibody variant comprises a light chain having the amino acid sequence set forth in SEQ ID NO: 199, as shown in Table 22. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain having the amino acid sequence set forth in SEQ ID NO: 200, as shown in Table 22. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain having the amino acid sequence set forth in SEQ ID NO: 201, as shown in Table 22. Exemplary nucleic acid sequences of SEQ ID NOS: 195, 196, 199, 200, and 201 are provided in Table 22 below.

TABLE 22

Antibody ID: AB-000224.017		
	KABAT	ASN
CDR1-VL	TGMNSNIGAGYDVY [SEQ ID NO: 183]	TGMNSNIGAGYDVY [SEQ ID NO: 189]
CDR2-VL	GNSNRPS [SEQ ID NO: 184]	GNSNRPS [SEQ ID NO: 190]
CDR3-VL	QSYDTSLDGWA [SEQ ID NO: 185]	QSYDTSLDGWA [SEQ ID NO: 191]
CDR1-VH	DHAMS [SEQ ID NO: 186]	DHAMS [SEQ ID NO: 192]
CDR2-VH	FIRKTTYGATTKYAAAVKG [SEQ ID NO: 187]	FIRKTTYGATTKYAAAVKG [SEQ ID NO: 193]
CDR3-VH	VQLDYGPGYQYYGMDV [SEQ ID NO: 188]	VQLDYGPGYQYYGMDV [SEQ ID NO: 194]
VL	ESVLTQPPSVSGAPGQRVTISCTGMNSNIGA GYDVYWYQQLPGRAPKLLIYGNSNRPSGVPDRFSGSRSGTSASLAITGLQ AEDEADYYCQSYDTSLDGWAFGGGTKLTVLG [SEQ ID NO: 195]	
VH	EVQLVESGGGLVQPGRSLRLPCTASGFS FGDHAMSWVRQAPGKGLEWVGFIRKTTYGATTKYAAAVKGRFTISRDDSK SIVYLQMNSLKTEDTAVYFCTRVQLDYGPGYQYYGMDVWGQGTTVTVSS [SEQ ID NO: 196]	
DNA for VL	GAGTCTGTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAG GGCAGAGGGTCACCATCTCCTGCACTGGGATGAACTCCAACATCGGGGCA GGTTATGATGTATACTGGTACCAACAACTTCCAGGAAGAGCCCCCAAACT CCTCATCTATGGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGATTCT CTGGCTCCAGGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAG GCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACACCAGCCTGGA CGGTTGGGCTTTCGGCGGAGGGACCAAGTTGACCGTCCTAGGC [SEQ ID NO: 197]	
DNA fo rVH	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGG TACAGCCAGGGCGGTCCCTGAGACTCCCCTGTACAGCCTCTGGGTTTAGT TTTGGTGATCATGCTATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCT GGAGTGGGTAGGTTTCATTAGAAAGACAACTTATGGTGCGACAACAAAGT ACGCCGCGGCTGTGAAGGGCAGATTCACCATCTCGCGAGATGATTCTAAA AGCATTGTCTATCTGCAAATGAACAGCCTGAAAACCGAGGACACAGCCGT GTATTTCTGTACTAGAGTGCAGCTTGACTATGGCCCGGGATACCAGTACT ACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA [SEQ ID NO: 198]	
Light Chain	ESVLTQPPSVSGAPGQRVTISCTGMNSNIGA GYDVYWYQQLPGRAPKLLIYGNSNRPSGVPDRFSGSRSGTSASLAITGLQ AEDEADYYCQSYDTSLDGWAFGGGTKLTVLGQPKAAPSVTLFPPSSEELQ	

TABLE 22-continued

	Antibody ID: AB-000224.017
	KABAT ASN
	ANKATLVCLVSDFYPGAVTVAWKADGSPVKVGVETTKPSKQSNNKYAASSYLSLTPEQWKSHRSYSCRVTHEGSTVEKTVAPAECS [SEQ ID NO: 199]
Heavy Chain version 1	EVQLVESGGGLVQPGRSLRLPCTASGFSFGDHAMSWVRQAPGKGLEWVGFIRKTTYGATTKYAAAVKGRFTISRDDSKSIVYLQMNSLKTEDTAVYFCTRVQLDYGPGYQYYGMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK [SEQ ID NO: 200]
Heavy Chain version 2	EVQLVESGGGLVQPGRSLRLPCTASGFSFGDHAMSWVRQAPGKGLEWVGFIRKTTYGATTKYAAAVKGRFTISRDDSKSIVYLQMNSLKTEDTAVYFCTRVQLDYGPGYQYYGMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK [SEQ ID NO: 201]
DNA for Light Chain	GAGTCTGTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAGGGTCACCATCTCCTGCACTGGGATGAACTCCAACATCGGGGCAGGTTATGATGTATACTGGTACCAACAACTTCCAGGAAGAGCCCCCAAACTCCTCATCTATGGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAGGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACACCAGCCTGGACGGTTGGGCTTTCGGCGGAGGGACCAAGTTGACCGTCCTAGGCCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCACCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCGTAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATGGCAGCCCCGTCAAGGTGGGAGTGGAGACCACCAAACCCTCCAAACAAAGCAACAACAAGTATGCGGCCAGCAGCTACCTGAGCCTGACGCCCGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCGGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTGCAGAATGCTCT [SEQ ID NO: 202]
DNA for Heavy Chain version 1	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCAGGGCGGTCCCTGAGACTCCCCTGTACAGCCTCTGGGTTTAGTTTTGGTGATCATGCTATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTAGGTTTCATTAGAAAGACAACTTATGGTGCGACAACAAAGTACGCCGCGGCTGTGAAGGGCAGATTCACCATCTCGCGAGATGATTCTAAAAGCATTGTCTATCTGCAAATGAACAGCCTGAAAACCGAGGACACAGCCGTGTATTTCTGTACTAGAGTGCAGCTTGACTATGGCCCGGGATACCAGTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCAGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAA [SEQ ID NO: 203]

TABLE 22-continued

	Antibody ID: AB-000224.017	
	KABAT	ASN
DNA for Heavy Chain version 2	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGG TACAGCCAGGGCGGTCCCTGAGACTCCCCTGTACAGCCTCTGGGTTTAGT TTTGGTGATCATGCTATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCT GGAGTGGGTAGGTTTCATTAGAAAGACAACTTATGGTGCGACAACAAAGT ACGCCGCGGCTGTGAAGGGCAGATTCACCATCTCGCGAGATGATTCTAAA AGCATTGTCTATCTGCAAATGAACAGCCTGAAAACCGAGGACACAGCCGT GTATTTCTGTACTAGAGTGCAGCTTGACTATGGCCCGGGATACCAGTACT ACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGCC TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCAC CTCTGGGGGCACAGCAGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCG AACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCAC ACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGT GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACG TGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAA TCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCT GGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCA TGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCAC GAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCA TAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTG TGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAAC CATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGC CCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTG GTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGG GCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACG GCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGCTGCATGAGGCTCTGCACTCCCA CTACACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAA [SEQ ID NO: 204]	

3. Anti-CSP Antibody Variants of AB-007088

In certain embodiments, a variant of an anti-CSP antibody AB-007088 disclosed herein comprises modifications compared to AB-007088 that provide improved pharmacokinetic properties, increased serum stability, stronger binding, and/or improved in vivo protective effects compared to AB-007088. In certain embodiments, a variant of an anti-CSP antibody AB-007088 disclosed herein exhibits reduced immunogenicity and/or increased manufacturability as compared to AB-007088. In certain embodiments, a variant of an anti-CSP antibody AB-007088 disclosed herein has at least one modification, e.g., substitution, relative to the native AB-007088 variable heavy chain amino acid sequence (SEQ ID NO: 196) or variable light chain amino acid sequence (SEQ ID NO: 195), and has improved developability, e.g., decreased heterogeneity, increased yield, increased stability, improved net charges to improve pharmacokinetics, and/or reduced immunogenicity. In certain embodiments, a VH region or a VL region of such a variant of an anti-CSP antibody AB-007088 disclosed herein has at least two, three, four, five, or six, or more modifications, e.g., substitutions. In certain embodiments, a variant of the an anti-CSP antibody AB-007088 disclosed herein has a total of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50 modifications, e.g. substitutions, including both variable regions, compared to AB-007088.

In certain embodiments, a variant of an anti-CSP antibody AB-007088 disclosed herein exhibits increased serum half-life as compared to AB-007088. In certain embodiments, a variant of an anti-CSP antibody AB-007088 disclosed herein has at least one modification, e.g., substitution, relative to the native AB-007088 Fc region of the heavy chain herein, and has improved pharmacokinetics properties, e.g., half-life. In certain embodiments, an Fc region of the heavy chain of such a variant of an anti-CSP antibody AB-007088 disclosed herein has at least two, three, four, five, or six, or more modifications, e.g., substitutions. In certain embodiments, a variant of the an anti-CSP antibody AB-007088 disclosed herein has a total of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50 modifications, e.g. substitutions, including both heavy and light chains, compared to AB-007088. In certain non-limiting embodiments, an Fc region of the heavy chain of a variant of an anti-CSP antibody AB-007088 disclosed herein can include an isoleucine at position 250, a tyrosine at position 252, an isoleucine at position 259, a glutamine at position 307, a phenylalanine at position 308, a leucine at position 319, a leucine at position 428, a histidine at position 434, a phenylalanine at position 434, an alanine at position 434, a serine at position 434, a methionine at position 434, or a combination thereof, wherein the numbering is defined by EU index as in Kabat. In certain embodiments, an Fc region of the heavy chain of a variant of an anti-CSP antibody AB-007088 disclosed herein includes a leucine at position 428 and a serine at position 434, wherein the numbering is defined by EU index as in Kabat.

The light and heavy chain CDRs of AB-007088 as defined by Kabat numbering system are shown in Table 23 below:

TABLE 23

AB-007088 CDR sequences (Kabat)

	CDR1	CDR2	CDR3
VL region	RASQSISSWLA (SEQ ID NO: 205)	DASSLES (SEQ ID NO: 206)	QQYNSYSFWT (SEQ ID NO: 207)
VH region	TYGMH (SEQ ID NO: 208)	IIWYDGSQKYYADSVQG (SEQ ID NO: 209)	VRFSVGPHGSAFDL (SEQ ID NO: 210)

The light and heavy chain CDRs of AB-007088 as defined by ASN are shown in Table 24 below:

TABLE 24

AB-007088 CDR sequences (ASN)

	CDRI	CDR2	CDR3
VL region	RASQSISSWLA (SEQ ID NO: 211)	DASSLES (SEQ ID NO: 212)	QQYNSYWT (SEQ ID NO: 213)
VH region	TYGMH (SEQ ID NO: 214)	IIWYDGSQKYYADSVQG (SEQ ID NO: 215)	SAFDL (SEQ ID NO: 216)

The heavy chain variable region (VH) and light chain variable region (VL) sequences and heavy and light chain sequences of AB-007088 are shown in Table 25 below:

TABLE 25

AB-007088 variable region and full-length sequences

VL region	GVQMTQSPSTLSASVGDRVTLTCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQYNSYSFWTFGQGTKVEIKR (SEQ ID NO: 217)
VH region	QVQLVESGGGWQPGRSLRLSCAASGFAFNTYGMHWVRQTPGKGLEWVAIIWYDGSQ KYYADSVQGRFIISRDNHKNTLSLQMNGLRAEDTAVYFCVRVRFSVGPHGSAFDLWG QGTMVIVSS (SEQ ID NO: 218)
DNA for VL region	GGCGTCCAGATGACCCAGTCTCCTTCCACCCTGT CTGCATCTGTGGGAGACAGAGTCACCCTCACTTGCCGGGCCAGTCAGAGT ATTAGTAGTTGGTTGGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAA ACTCCTGATCTATGATGCCTCCAGTTTGGAAAGTGGGGTCCCATCAAGGT TCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACCATCAGCAGCCTG CAACCTGATGATTTTGCAACTTATTACTGCCAACAGTATAATAGTTATTC TTTTTGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAACGC [SEQ ID NO: 219]
DNA for VH region	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTGG TCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGGTTCGCT TTCAATACCTATGGCATGCACTGGGTCCGCCAGACTCCAGGCAAGGGGCT GGAGTGGGTGGCAATTATCTGGTATGATGGGAGCCAGAAATACTATGCAG ACTCCGTGCAGGGCCGATTCATCATCTCCAGAGACAATCACAAGAACACG TTGTCTCTGCAAATGAACGGCCTGAGAGCCGAGGACACGGCTGTGTATTT CTGTGTGAGAGTCCGCTTTAGCGTTGGCCCCCACGGGAGTGCTTTTGATC TCTGGGGCCAGGGGACAATGGTCATCGTCTCTTCA [SEQ ID NO: 220]
Light Chain	GVQMTQSPSTLSASVGDRVTLTCRASQS ISSWLAWYQQKPGKAPKLLIYDASSLESGVPSRFSGSGSGTEFTLTISSL QPDDFATYYCQQYNSYSFWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKS GTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC [SEQ ID NO: 221]
Heavy Chain version 1	QVQLVESGGGVVQPGRSLRLSCAASGFA FNTYGMHWVRQTPGKGLEWVAIIWYDGSQKYYADSVQGRFIISRDNHKNT LSLQMNGLRAEDTAVYFCVRVRFSVGPHGSAFDLWGQGTMVIVSSASTKG PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDK

TABLE 25-continued

AB-007088 variable region and full-length sequences	
	THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK [SEQ ID NO: 222]
Heavy Chain version 2	QVQLVESGGGVVQPGRSLRLSCAASGFAFNTYGMHWVRQTPGKGLEWVAIIWYDGSQKYYADSVQGRFIISRDNHKNTLSLQMNGLRAEDTAVYFCVRVRFSVGPHGSAFDLWGQGTMVIVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK [SEQ ID NO: 223]
DNA for Light Chain	GGCGTCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTGGGAGACAGAGTCACCCTCACTTGCCGGGCCAGTCAGAGTATTAGTAGTTGGTTGGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAACTCCTGATCTATGATGCCTCCAGTTTGGAAAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACCATCAGCAGCCTGCAACCTGATGATTTTGCAACTTATTACTGCCAACAGTATAATAGTTATTCTTTTTGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAACGCACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT [SEQ ID NO: 224]
DNA for Heavy Chain version 1	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGGTTCGCTTTCAATACCTATGGCATGCACTGGGTCCGCCAGACTCCAGGCAAGGGGCTGGAGTGGGTGGCAATTATCTGGTATGATGGGAGCCAGAAATACTATGCAGACTCCGTGCAGGGCCGATTCATCATCTCCAGAGACAATCACAAGAACACGTTGTCTCTGCAAATGAACGGCCTGAGAGCCGAGGACACGGCTGTGTATTTCTGTGTGAGAGTCCGCTTTAGCGTTGGCCCCCACGGGAGTGCTTTTGATCTCTGGGGCCAGGGGACAATGGTCATCGTCTCTTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCAGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAA [SEQ ID NO: 225]
DNA for Heavy Chain version 2	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGGTTCGCTTTCAATACCTATGGCATGCACTGGGTCCGCCAGACTCCAGGCAAGGGGCTGGAGTGGGTGGCAATTATCTGGTATGATGGGAGCCAGAAATACTATGCAGACTCCGTGCAGGGCCGATTCATCATCTCCAGAGACAATCACAAGAACACGTTGTCTCTGCAAATGAACGGCCTGAGAGCCGAGGACACGGCTGTGTATTTCTGTGTGAGAGTCCGCTTTAGCGTTGGCCCCCACGGGAGTGCTTTTGATCTCTGGGGCCAGGGGACAATGGTCATCGTCTCTTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCAGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGA

TABLE 25-continued

AB-007088 variable region and full-length sequences
CCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAG GTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGAC AAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCC TCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAG GTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGC CAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGG ATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTC TATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAA CAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCC TCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTC TTCTCATGCTCCGTGCTGCATGAGGCTCTGCACTCCCACTACACACAGAA GAGCCTCTCCCTGTCTCCGGGTAAA [SEQ ID NO: 226]

In certain embodiments, a variant of an anti-CSP antibody includes one, two, or three CDRs of a VL sequence of Table 25. In certain embodiments, a variant of an anti-CSP antibody includes at least one mutation, e.g., a substitution, and no more than 10, 20, 30, 40, or 50 mutations in the VL amino acid sequence set forth in SEQ ID NO: 217. In certain embodiments, the VL of the variant of an anti-CSP antibody includes at least one, at least two, or at least three mutations, e.g., substitutions, in the CDR1 amino acid sequence set forth in SEQ ID NO: 205. In certain embodiments, the VL of the variant of an anti-CSP antibody includes at least one, at least two, or at least three mutations, e.g., substitutions, in the CDR2 amino acid sequence set forth in SEQ ID NO: 206. In certain embodiments, the VL of the variant of an anti-CSP antibody includes at least one, at least two, or at least three mutations, e.g., substitutions, in the CDR3 amino acid sequence set forth in SEQ ID NO: 207. In certain embodiments, the VL of the variant of an anti-CSP antibody includes at least one, at least two, or at least three mutations, e.g., substitutions, in the CDR1 amino acid sequence set forth in SEQ ID NO: 211. In certain embodiments, the VL of the variant of an anti-CSP antibody includes at least one, at least two, or at least three mutations, e.g., substitutions, in the CDR2 amino acid sequence set forth in SEQ ID NO: 212. In certain embodiments, the VL of the variant of an anti-CSP antibody includes at least one, at least two, or at least three mutations, e.g., substitutions, in the CDR3 amino acid sequence set forth in SEQ ID NO: 213. In certain embodiments, the mutation is a conservative substitution. In certain embodiments, the VL of the variant of an anti-CSP antibody includes at least one, at least two, or at least three mutations, e.g., substitutions, in the framework of the amino acid sequence set forth in SEQ ID NO: 217. An exemplary nucleic acid sequence of SEQ ID NO: 217 is set forth in SEQ ID NO: 219.

In certain embodiments, a variant of an anti-CSP antibody includes one, two, or three CDRs of a VH sequence of Table 25. In certain embodiments, a variant of an anti-CSP antibody includes at least one mutation, e.g., a substitution, and no more than 10, 20, 30, 40, or 50 mutations in the VH amino acid sequence set forth in SEQ ID NO: 218. In certain embodiments, the VH of the variant of an anti-CSP antibody includes at least one, at least two, or at least three mutations, e.g., substitutions, in the CDR1 amino acid sequence set forth in SEQ ID NO: 208. In certain embodiments, the VH of the variant of an anti-CSP antibody includes at least one, at least two, or at least three mutations, e.g., substitutions, in the CDR2 amino acid sequence set forth in SEQ ID NO: 209. In certain embodiments, the VH of the variant of an anti-CSP antibody includes at least one, at least two, or at least three mutations, e.g., substitutions, in the CDR3 amino acid sequence set forth in SEQ ID NO: 210. In certain embodiments, the VH of the variant of an anti-CSP antibody includes at least one, at least two, or at least three mutations, e.g., substitutions, in the CDR1 amino acid sequence set forth in SEQ ID NO: 214. In certain embodiments, the VH of the variant of an anti-CSP antibody includes at least one, at least two, or at least three mutations, e.g., substitutions, in the CDR2 amino acid sequence set forth in SEQ ID NO: 215. In certain embodiments, the VH of the variant of an anti-CSP antibody includes at least one, at least two, or at least three mutations, e.g., substitutions, in the CDR3 amino acid sequence set forth in SEQ ID NO: 216. In certain embodiments, the mutation is a conservative substitution. In certain embodiments, the VH of the variant of an anti-CSP antibody includes at least one, at least two, at least three mutations, at least four mutations, at least five mutations, or at least six mutations, e.g., substitutions, in the framework of the amino acid sequence set forth in SEQ ID NO: 218. An exemplary nucleic acid sequence of SEQ ID NO: 218 is set forth in SEQ ID NO: 220. In certain embodiments, the VH of the variant of an anti-CSP antibody includes a substitution at position 28 of the SEQ ID NO: 218. In certain embodiments, the substitution is A28T. In certain embodiments, the VH of the variant of an anti-CSP antibody includes a substitution at position 40 of the SEQ ID NO: 218. In certain embodiments, the substitution is T40A. In certain embodiments, the VH of the variant of an anti-CSP antibody includes a substitution at position 69 of the SEQ ID NO: 218. In certain embodiments, the substitution is I69T. In certain embodiments, the VH of the variant of an anti-CSP antibody includes a substitution at position 80 of the SEQ ID NO: 218. In certain embodiments, the substitution is 580Y. In certain embodiments, the VH of the variant of an anti-CSP antibody includes a substitution at position 85 of the SEQ ID NO: 218. In certain embodiments, the substitution is G85S. In certain embodiments, the VH of the variant of an anti-CSP antibody includes a substitution at position 120 of the SEQ ID NO: 218. In certain embodiments, the substitution is 1120T.

In certain embodiments, the light chain of the variant of an anti-CSP antibody has an amino acid sequence set forth in SEQ ID NO: 221. An exemplary nucleic acid sequence of SEQ ID NO: 221 is set forth in SEQ ID NO: 224. In certain embodiments, a variant of an anti-CSP antibody includes at least one mutation, e.g., substitution, and no more than 10, 20, 30, 40, or 50 mutations in the Fc region of the heavy chain amino acid sequence set forth in SEQ ID NO: 222. In certain embodiments, the heavy chain of the variant of an anti-CSP antibody has an amino acid sequence set forth in SEQ ID NO: 222. An exemplary nucleic acid sequence of SEQ ID NO: 222 is set forth in SEQ ID NO: 225. In certain embodiments, the heavy chain of the variant of an anti-CSP antibody includes a substitution at position 434 of the SEQ ID NO: 222. In certain embodiments, the substitution is M434L. In certain embodiments, the heavy chain of the variant of an anti-CSP antibody includes a substitution at position 440 of the SEQ ID NO: 222. In certain embodiments, the substitution is L440S. In certain embodiments, the heavy chain of the variant of an anti-CSP antibody includes a substitution at position 434 of the SEQ ID NO: 222 and a substitution at position 440 of the SEQ ID NO: 222. In certain embodiments, the substitutions are M434L and N440S. In certain embodiments, the heavy chain of the variant of an anti-CSP antibody has an amino acid sequence set forth in SEQ ID NO: 223. An exemplary nucleic acid sequence of SEQ ID NO: 223 is set forth in SEQ ID NO: 226.

In certain embodiments, the light chain of the anti-CSP antibody AB-007088 and variants thereof comprises a signal peptide. In certain embodiments, the signal peptide is an IGLV2-8 signal peptide. In certain embodiments, the signal peptide has an amino acid sequence set forth in SEQ ID NO: 277. In certain embodiments, the heavy chain of the anti-CSP antibody AB-007088 and variants thereof comprises a signal peptide. In certain embodiments, the signal peptide is an IGKV1-39 signal peptide. In certain embodiments, the signal peptide has an amino acid sequence set forth in SEQ ID NO: 278.

In certain embodiments, the anti-CSP antibody variant comprises a light chain variable region comprising a CDR1, a CDR2, and a CDR3 and having the amino acid sequence set forth in SEQ ID NO: 227, as shown in Table 26. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 and having the amino acid sequence set forth in SEQ ID NO: 228, as shown in Table 26. In certain embodiments, the anti-CSP antibody variant comprises a light chain having the amino acid sequence set forth in SEQ ID NO: 231, as shown in Table 26. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain having the amino acid sequence set forth in SEQ ID NO: 232, as shown in Table 26. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain having the amino acid sequence set forth in SEQ ID NO: 233, as shown in Table 26. Exemplary nucleic acid sequences of SEQ ID NOS: 227, 228, 231, 232, and 233 are provided in Table 26 below.

TABLE 26

Antibody ID: AB-007088.001		
	KABAT	ASN
CDRI-VL	RASQSISSWLA [SEQ ID NO: 205]	RASQSISSWLA [SEQ ID NO: 211]
CDR2-VL	DASSLES [SEQ ID NO: 206]	DASSLES [SEQ ID NO: 212]
CDR3-VL	QQYNSYSFWT [SEQ ID NO: 207]	QQYNSYSFWTF [SEQ ID NO: 213]
CDR1-VH	TYGMH [SEQ ID NO: 208]	TYGMH [SEQ ID NO: 214]
CDR2-VH	IIWYDGSQKYYADSVQG [SEQ ID NO: 209]	IIWYDGSQKYYADSVQG [SEQ ID NO: 215]
CDR3-VH	VRFSVGPHGSAFDL [SEQ ID NO: 210]	SAFDL [SEQ ID NO: 216]
VL	GVQMTQSPSTLSASVGDRVTLTCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQYNSYSFWTFGQGTKVEIKR [SEQ ID NO: 227]	
VH	QVQLVESGGGVVQPGRSLRLSCAASGFAFNTYGMHWVRQAPGKGLEWVAIIWYDGSQKYYADSVQGRFIISRDNHKNTLSLQMNSLRAEDTAVYFCVRVRFSVGPHGSAFDLWGQGTMVTVSS [SEQ ID NO: 228]	
DNA for VL	GGCGTCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTGGGAGACAGAGTCACCCTCACTTGCCGGGCCAGTCAGAGTATTAGTAGTTGGTTGGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAACTCCTGATCTATGATGCCTCCAGTTTGGAAAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACCATCAGCAGCCTGCAACCTGATGATTTTGCAACTTATTACTGCCAACAGTATAATAGTTATTCTTTTTGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAACGC [SEQ ID NO: 229]	
DNA for VH	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGGTTCGCTTTCAATACCTATGGCATGCACTGGGTCCGCCAGGCACCAGGCAAGGGGCTGGAGTGGGTGGCAATTATCTGGTATGATGGGAGCCAGAAATACTATGCAGACTCCGTGCAGGGCCGATTCATCATCTCCAGAGACAATCACAAGAACACGTTGTCTCTGCAAATGAACTCCCTGAGAGCCGAGGACACGGCTGTGTATTTCTGTGTGAGAGTCCGCTTTAGCGTTGGCCCCCACGGGAGTGCTTTTGATCTCTGGGGCCAGGGGACAATGGTCACAGTCTCTTCA [SEQ ID NO: 230]	

TABLE 26-continued

<table>
<tr><th colspan="3">Antibody ID: AB-007088.001</th></tr>
<tr><th></th><th>KABAT</th><th>ASN</th></tr>
<tr><td>Light Chain</td><td colspan="2">GVQMTQSPSTLSASVGDRVTLTCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQYNSYSFWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC [SEQ ID NO: 231]</td></tr>
<tr><td>Heavy Chain version 1</td><td colspan="2">QVQLVESGGGVVQPGRSLRLSCAASGFAFNTYGMHWVRQAPGKGLEWVAIIWYDGSQKYYADSVQGRFIISRDNHKNTLSLQMNSLRAEDTAVYFCVRVRFSVGPHGSAFDLWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK [SEQ ID NO: 232]</td></tr>
<tr><td>Heavy Chain version 2</td><td colspan="2">QVQLVESGGGVVQPGRSLRLSCAASGFAFNTYGMHWVRQAPGKGLEWVAIIWYDGSQKYYADSVQGRFIISRDNHKNTLSLQMNSLRAEDTAVYFCVRVRFSVGPHGSAFDLWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK [SEQ ID NO: 233]</td></tr>
<tr><td>DNA for Light Chain</td><td colspan="2">GGCGTCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTGGGAGACAGAGTCACCCTCACTTGCCGGGCCAGTCAGAGTATTAGTAGTTGGTTGGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAACTCCTGATCTATGATGCCTCCAGTTTGGAAAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACCATCAGCAGCCTGCAACCTGATGATTTTGCAACTTATTACTGCCAACAGTATAATAGTTATTCTTTTTGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAACGCACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT [SEQ ID NO: 234]</td></tr>
<tr><td>DNA for Heavy Chain version 1</td><td colspan="2">CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGGTTCGCTTTCAATACCTATGGCATGCACTGGGTCCGCCAGGCACCAGGCAAGGGGCTGGAGTGGGTGGCAATTATCTGGTATGATGGGAGCCAGAAATACTATGCAGACTCCGTGCAGGGCCGATTCATCATCTCCAGAGACAATCACAAGAACACGTTGTCTCTGCAAATGAACTCCCTGAGAGCCGAGGACACGGCTGTGTATTTCTGTGTGAGAGTCCGCTTTAGCGTTGGCCCCCACGGGAGTGCTTTTGATCTCTGGGGCCAGGGGACAATGGTCACAGTCTCTTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCAGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAA [SEQ ID NO: 235]</td></tr>
</table>

TABLE 26-continued

Antibody ID: AB-007088.001

	KABAT	ASN
DNA for Heavy Chain version 2	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGGTTCGCTTTCAATACCTATGGCATGCACTGGGTCCGCCAGGCACCAGGCAAGGGGCTGGAGTGGGTGGCAATTATCTGGTATGATGGGAGCCAGAAATACTATGCAGACTCCGTGCAGGGCCGATTCATCATCTCCAGAGACAATCACAAGAACACGTTGTCTCTGCAAATGAACTCCCTGAGAGCCGAGGACACGGCTGTGTATTTCTGTGTGAGAGTCCGCTTTAGCGTTGGCCCCCACGGGAGTGCTTTTGATCTCTGGGGCCAGGGGACAATGGTCACAGTCTCTTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCAGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGCTGCATGAGGCTCTGCACTCCCACTACACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAA [SEQ ID NO: 236]	

In certain embodiments, the anti-CSP antibody variant comprises a light chain variable region comprising a CDR1, a CDR2, and a CDR3 and having the amino acid sequence set forth in SEQ ID NO: 237, as shown in Table 27. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 and having the amino acid sequence set forth in SEQ ID NO: 238, as shown in Table 27. In certain embodiments, the anti-CSP antibody variant comprises a light chain having the amino acid sequence set forth in SEQ ID NO: 241, as shown in Table 27. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain having the amino acid sequence set forth in SEQ ID NO: 242, as shown in Table 27. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain having the amino acid sequence set forth in SEQ ID NO: 243, as shown in Table 27. Exemplary nucleic acid sequences of SEQ ID NOS: 237, 238, 241, 242, and 243 are provided in Table 27 below.

TABLE 27

Antibody ID: AB-007088.002

	KABAT	ASN
CDR1-VL	RASQSISSWLA [SEQ ID NO: 205]	RASQSISSWLA [SEQ ID NO: 211]
CDR2-VL	DASSLES [SEQ ID NO: 206]	DASSLES [SEQ ID NO: 212]
CDR3-VL	QQYNSYSFWT [SEQ ID NO: 207]	QQYNSYSFWTF [SEQ ID NO: 213]
CDR1-VH	TYGMH [SEQ ID NO: 208]	TYGMH [SEQ ID NO: 214]
CDR2-VH	IIWYDGSQKYYADSVQG [SEQ ID NO: 209]	IIWYDGSQKYYADSVQG [SEQ ID NO: 215]
CDR3-VH	VRFSVGPHGSAFDL [SEQ ID NO: 210]	SAFDL [SEQ ID NO: 216]
VL	GVQMTQSPSTLSASVGDRVTLTCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQYNSYSFWTFGQGTKVEIKR [SEQ ID NO: 237]	

TABLE 27-continued

	Antibody ID: AB-007088.002	
	KABAT	ASN
VH	QVQLVESGGGVVQPGRSLRLSCAASGFTFNTYGMHWVRQAPGKGLEWVAIIWYDGSQKYYADSVQGRFIISRDNHKNTLSLQMNSLRAEDTAVYFCVRVRFSVGPHGSAFDLWGQGTMVTVSS [SEQ ID NO: 238]	
DNA for VL	GGCGTCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTGGGAGACAGAGTCACCCTCACTTGCCGGGCCAGTCAGAGTATTAGTAGTTGGTTGGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAACTCCTGATCTATGATGCCTCCAGTTTGGAAAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACCATCAGCAGCCTGCAACCTGATGATTTTGCAACTTATTACTGCCAACAGTATAATAGTTATTCTTTTTGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAACGC [SEQ ID NO: 239]	
DNA forVH	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGGTTCACTTTCAATACCTATGGCATGCACTGGGTCCGCCAGGCACCAGGCAAGGGGCTGGAGTGGGTGGCAATTATCTGGTATGATGGGAGCCAGAAATACTATGCAGACTCCGTGCAGGGCCGATTCATCATCTCCAGAGACAATCACAAGAACACGTTGTCTCTGCAAATGAACTCCCTGAGAGCCGAGGACACGGCTGTGTATTTCTGTGTGAGAGTCCGCTTTAGCGTTGGCCCCCACGGGAGTGCTTTTGATCTCTGGGGCCAGGGGACAATGGTCACAGTCTCTTCA [SEQ ID NO: 240]	
Light Chain	GVQMTQSPSTLSASVGDRVTLTCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQYNSYSFWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC [SEQ ID NO: 241]	
Heavy Chain version 1	QVQLVESGGGVVQPGRSLRLSCAASGFTFNTYGMHWVRQAPGKGLEWVAIIWYDGSQKYYADSVQGRFIISRDNHKNTLSLQMNSLRAEDTAVYFCVRVRFSVGPHGSAFDLWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK [SEQ ID NO: 242]	
Heavy Chain version 2	QVQLVESGGGVVQPGRSLRLSCAASGFTFNTYGMHWVRQAPGKGLEWVAIIWYDGSQKYYADSVQGRFIISRDNHKNTLSLQMNSLRAEDTAVYFCVRVRFSVGPHGSAFDLWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK [SEQ ID NO: 243]	
DNA for Light Chain	GGCGTCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTGGGAGACAGAGTCACCCTCACTTGCCGGGCCAGTCAGAGTATTAGTAGTTGGTTGGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAACTCCTGATCTATGATGCCTCCAGTTTGGAAAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACCATCAGCAGCCTGCAACCTGATGATTTTGCAACTTATTACTGCCAACAGTATAATAGTTATTCTTTTTGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAACGCACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT [SEQ ID NO: 244]	

TABLE 27-continued

	Antibody ID: AB-007088.002
	KABAT ASN
DNA for Heavy Chain version 1	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGGTTCACTTTCAATACCTATGGCATGCACTGGGTCCGCCAGGCACCAGGCAAGGGGCTGGAGTGGGTGGCAATTATCTGGTATGATGGGAGCCAGAAATACTATGCAGACTCCGTGCAGGGCCGATTCATCATCTCCAGAGACAATCACAAGAACACGTTGTCTCTGCAAATGAACTCCCTGAGAGCCGAGGACACGGCTGTGTATTTCTGTGTGAGAGTCCGCTTTAGCGTTGGCCCCCACGGGAGTGCTTTTGATCTCTGGGGCCAGGGGACAATGGTCACAGTCTCTTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCAGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAA [SEQ ID NO: 245]
DNA for Heavy Chain version 2	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGGTTCACTTTCAATACCTATGGCATGCACTGGGTCCGCCAGGCACCAGGCAAGGGGCTGGAGTGGGTGGCAATTATCTGGTATGATGGGAGCCAGAAATACTATGCAGACTCCGTGCAGGGCCGATTCATCATCTCCAGAGACAATCACAAGAACACGTTGTCTCTGCAAATGAACTCCCTGAGAGCCGAGGACACGGCTGTGTATTTCTGTGTGAGAGTCCGCTTTAGCGTTGGCCCCCACGGGAGTGCTTTTGATCTCTGGGGCCAGGGGACAATGGTCACAGTCTCTTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCAGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGCTGCATGAGGCTCTGCACTCCCACTACACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAA [SEQ ID NO: 246]

In certain embodiments, the anti-CSP antibody variant comprises a light chain variable region comprising a CDR1, a CDR2, and a CDR3 and having the amino acid sequence set forth in SEQ ID NO: 247, as shown in Table 28. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 and having the amino acid sequence set forth in SEQ ID NO: 248, as shown in Table 28. In certain embodiments, the anti-CSP antibody variant comprises a light chain having the amino acid sequence set forth in SEQ ID NO: 251, as shown in Table 28. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain having the amino acid sequence set forth in SEQ ID NO: 252, as shown in Table 28. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain having the amino acid sequence set forth in SEQ ID NO: 253, as shown in Table 28. Exemplary nucleic acid sequences of SEQ ID NOS: 247, 248, 251, 252, and 253 are provided in Table 28 below.

TABLE 28

Antibody ID: AB-007088.003

	KABAT	ASN
CDR1-VL	RASQSISSWLA [SEQ ID NO: 205]	RASQSISSWLA [SEQ ID NO: 211]
CDR2-VL	DASSLES [SEQ ID NO: 206]	DASSLES [SEQ ID NO: 212]
CDR3-VL	QQYNSYSFWT [SEQ ID NO: 207]	QQYNSYSFWTF [SEQ ID NO: 213]
CDR1-VH	TYGMH [SEQ ID NO: 208]	TYGMH [SEQ ID NO: 214]
CDR2-VH	IIWYDGSQKYYADSVQG [SEQ ID NO: 209]	IIWYDGSQKYYADSVQG [SEQ ID NO: 215]
CDR3-VH	VRFSVGPHGSAFDL [SEQ ID NO: 210]	SAFDL [SEQ ID NO: 216]
VL	GVQMTQSPSTLSASVGDRVTLTCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQYNSYSFWTFGQGTKVEIKR [SEQ ID NO: 247]	
VH	QVQLVESGGGVVQPGRSLRLSCAASGFAFNTYGMHWVRQAPGKGLEWVAIIWYDGSQKYYADSVQGRFTISRDNHKNTLSLQMNSLRAEDTAVYFCVRVRFSVGPHGSAFDLWGQGTMVTVSS [SEQ ID NO: 248]	
DNA for VL	GGCGTCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTGGGAGACAGAGTCACCCTCACTTGCCGGGCCAGTCAGAGTATTAGTAGTTGGTTGGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAACTCCTGATCTATGATGCCTCCAGTTTGGAAAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACCATCAGCAGCCTGCAACCTGATGATTTTGCAACTTATTACTGCCAACAGTATAATAGTTATTCTTTTTGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAACGC [SEQ ID NO: 249]	
DNA forVH	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGGTTCGCTTTCAATACCTATGGCATGCACTGGGTCCGCCAGGCACCAGGCAAGGGGCTGGAGTGGGTGGCAATTATCTGGTATGATGGGAGCCAGAAATACTATGCAGACTCCGTGCAGGGCCGATTCACTATCTCCAGAGACAATCACAAGAACACGTTGTCTCTGCAAATGAACTCCCTGAGAGCCGAGGACACGGCTGTGTATTTCTGTGTGAGAGTCCGCTTTAGCGTTGGCCCCCACGGGAGTGCTTTTGATCTCTGGGGCCAGGGGACAATGGTCACAGTCTCTTCA [SEQ ID NO: 250]	
Light Chain	GVQMTQSPSTLSASVGDRVTLTCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQYNSYSFWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC [SEQ ID NO: 251]	
Heavy Chain version 1	QVQLVESGGGVVQPGRSLRLSCAASGFAFNTYGMHWVRQAPGKGLEWVAIIWYDGSQKYYADSVQGRFTISRDNHKNTLSLQMNSLRAEDTAVYFCVRVRFSVGPHGSAFDLWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK [SEQ ID NO: 252]	
Heavy Chain version 2	QVQLVESGGGVVQPGRSLRLSCAASGFAFNTYGMHWVRQAPGKGLEWVAIIWYDGSQKYYADSVQGRFTISRDNHKNTLSLQMNSLRAEDTAVYFCVRVRFSVGPHGSAFDLWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK [SEQ ID NO: 253]	

TABLE 28-continued

	Antibody ID: AB-007088.003
	KABAT ASN
DNA for Light Chain	GGCGTCCAGATGACCCAGTCTCCTTCCACCCTGT CTGCATCTGTGGGAGACAGAGTCACCCTCACTTGCCGGGCCAGTCAGAGT ATTAGTAGTTGGTTGGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAA ACTCCTGATCTATGATGCCTCCAGTTTGGAAAGTGGGGTCCCATCAAGGT TCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACCATCAGCAGCCTG CAACCTGATGATTTTGCAACTTATTACTGCCAACAGTATAATAGTTATTC TTTTTGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAACGCACTGTGG CTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCT GGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGC CAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGG AGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGC ACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTG CGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT [SEQ ID NO: 254]
DNA for Heavy Chain version 1	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTGG TCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGGTTCGCT TTCAATACCTATGGCATGCACTGGGTCCGCCAGGCACCAGGCAAGGGGCT GGAGTGGGTGGCAATTATCTGGTATGATGGGAGCCAGAAATACTATGCAG ACTCCGTGCAGGGCCGATTCACTATCTCCAGAGACAATCACAAGAACACG TTGTCTCTGCAAATGAACTCCCTGAGAGCCGAGGACACGGCTGTGTATTT CTGTGTGAGAGTCCGCTTTAGCGTTGGCCCCCACGGGAGTGCTTTTGATC TCTGGGGCCAGGGGACAATGGTCACAGTCTCTTCAGCCTCCACCAAGGGC CCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCAC AGCAGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGG TGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCT GTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCC CTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGC CCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAAA ACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTC AGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGA CCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAG GTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGAC AAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCC TCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAG GTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGC CAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGG ATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTC TATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAA CAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCC TCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTC TTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACACAGAA GAGCCTCTCCCTGTCTCCGGGTAAA [SEQ ID NO: 255]
DNA for Heavy Chain version 2	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTGG TCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGGTTCGCT TTCAATACCTATGGCATGCACTGGGTCCGCCAGGCACCAGGCAAGGGGCT GGAGTGGGTGGCAATTATCTGGTATGATGGGAGCCAGAAATACTATGCAG ACTCCGTGCAGGGCCGATTCACTATCTCCAGAGACAATCACAAGAACACG TTGTCTCTGCAAATGAACTCCCTGAGAGCCGAGGACACGGCTGTGTATTT CTGTGTGAGAGTCCGCTTTAGCGTTGGCCCCCACGGGAGTGCTTTTGATC TCTGGGGCCAGGGGACAATGGTCACAGTCTCTTCAGCCTCCACCAAGGGC CCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCAC AGCAGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGG TGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCT GTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCC CTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGC CCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAAA ACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTC AGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGA CCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAG GTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGAC AAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCC TCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAG GTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGC CAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGG ATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTC TATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAA CAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCC TCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTC TTCTCATGCTCCGTGCTGCATGAGGCTCTGCACTCCCACTACACACAGAA GAGCCTCTCCCTGTCTCCGGGTAAA [SEQ ID NO: 256]

In certain embodiments, the anti-CSP antibody variant comprises a light chain variable region comprising a CDR1, a CDR2, and a CDR3 and having the amino acid sequence set forth in SEQ ID NO: 257, as shown in Table 29. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 and having the amino acid sequence set forth in SEQ ID NO: 258, as shown in Table 29. In certain embodiments, the anti-CSP antibody variant comprises a light chain having the amino acid sequence set forth in SEQ ID NO: 261, as shown in Table 29. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain having the amino acid sequence set forth in SEQ ID NO: 262, as shown in Table 29. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain having the amino acid sequence set forth in SEQ ID NO: 263, as shown in Table 29. Exemplary nucleic acid sequences of SEQ ID NOS: 257, 258, 261, 262, and 263 are provided in Table 29 below.

TABLE 29

	Antibody ID: AB-007088.004	
	KABAT	ASN
CDR1-VL	RASQSISSWLA [SEQ ID NO: 205]	RASQSISSWLA [SEQ ID NO: 211]
CDR2-VL	DASSLES [SEQ ID NO: 206]	DASSLES [SEQ ID NO: 212]
CDR3-VL	QQYNSYSFWT [SEQ ID NO: 207]	QQYNSYSFWTF [SEQ ID NO: 213]
CDR1-VH	TYGMH [SEQ ID NO: 208]	TYGMH [SEQ ID NO: 214]
CDR2-VH	IIWYDGSQKYYADSVQG [SEQ ID NO: 209]	IIWYDGSQKYYADSVQG [SEQ ID NO: 215]
CDR3-VH	VRFSVGPHGSAFDL [SEQ ID NO: 210]	SAFDL [SEQ ID NO: 216]
VL	GVQMTQSPSTLSASVGDRVTLTCRASQS ISSWLAWYQQKPGKAPKLLIYDASSLESGVPSRFSGSGSGTEFTLTISSL QPDDFATYYCQQYNSYSFWTFGQGTKVEIKR [SEQ ID NO: 257]	
VH	QVQLVESGGGVVQPGRSLRLSCAASGFT FNTYGMHWVRQAPGKGLEWVAIIWYDGSQKYYADSVQGRFTISRDNHKNT LSLQMNSLRAEDTAVYFCVRVRFSVGPHGSAFDLWGQGTMVTVSS [SEQ ID NO: 258]	
DNA for VL	GGCGTCCAGATGACCCAGTCTCCTTCCACCCTGT CTGCATCTGTGGGAGACAGAGTCACCCTCACTTGCCGGGCCAGTCAGAGT ATTAGTAGTTGGTTGGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAA ACTCCTGATCTATGATGCCTCCAGTTTGGAAAGTGGGGTCCCATCAAGGT TCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACCATCAGCAGCCTG CAACCTGATGATTTTGCAACTTATTACTGCCAACAGTATAATAGTTATTC TTTTTGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAACGC [SEQ ID NO: 259]	
DNA forVH	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTGG TCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGGTTCACT TTCAATACCTATGGCATGCACTGGGTCCGCCAGGCACCAGGCAAGGGGCT GGAGTGGGTGGCAATTATCTGGTATGATGGGAGCCAGAAATACTATGCAG ACTCCGTGCAGGGCCGATTCACTATCTCCAGAGACAATCACAAGAACACG TTGTCTCTGCAAATGAACTCCCTGAGAGCCGAGGACACGGCTGTGTATTT CTGTGTGAGAGTCCGCTTTAGCGTTGGCCCCCACGGGAGTGCTTTTGATC TCTGGGGCCAGGGGACAATGGTCACAGTCTCTTCA [SEQ ID NO: 260]	
Light Chain	GVQMTQSPSTLSASVGDRVTLTCRASQS ISSWLAWYQQKPGKAPKLLIYDASSLESGVPSRFSGSGSGTEFTLTISSL QPDDFATYYCQQYNSYSFWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKS GTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC [SEQ ID NO: 261]	
Heavy Chain version 1	QVQLVESGGGVVQPGRSLRLSCAASGFT FNTYGMHWVRQAPGKGLEWVAIIWYDGSQKYYADSVQGRFTISRDNHKNT LSLQMNSLRAEDTAVYFCVRVRFSVGPHGSAFDLWGQGTMVTVSSASTKG PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDK THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE	

TABLE 29-continued

Antibody ID: AB-007088.004		
	KABAT	ASN
	VKFNWYVDGVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSLSPGK [SEQ ID NO: 262]	
Heavy Chain version 2	QVQLVESGGGVVQPGRSLRLSCAASGFT FNTYGMHWVRQAPGKGLEWVAIIWYDGSQKYYADSVQGRFTISRDNHKNT LSLQMNSLRAEDTAVYFCVRVRFSVGPHGSAFDLWGQGTMVTVSSASTKG PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDK THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVLHEALHSHYTQKSLSLSPGK [SEQ ID NO: 263]	
DNA for Light Chain	GGCGTCCAGATGACCCAGTCTCCTTCCACCCTGT CTGCATCTGTGGGAGACAGAGTCACCCTCACTTGCCGGGCCAGTCAGAGT ATTAGTAGTTGGTTGGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAA ACTCCTGATCTATGATGCCTCCAGTTTGGAAAGTGGGGTCCCATCAAGGT TCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACCATCAGCAGCCTG CAACCTGATGATTTTGCAACTTATTACTGCCAACAGTATAATAGTTATTC TTTTTGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAACGCACTGTGG CTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCT GGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGC CAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGG AGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGC ACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTG CGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT [SEQ ID NO: 264]	
DNA for Heavy Chain version 1	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTGG TCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGGTTCACT TTCAATACCTATGGCATGCACTGGGTCCGCCAGGCACCAGGCAAGGGGCT GGAGTGGGTGGCAATTATCTGGTATGATGGGAGCCAGAAATACTATGCAG ACTCCGTGCAGGGCCGATTCACTATCTCCAGAGACAATCACAAGAACACG TTGTCTCTGCAAATGAACTCCCTGAGAGCCGAGGACACGGCTGTGTATTT CTGTGTGAGAGTCCGCTTTAGCGTTGGCCCCCACGGGAGTGCTTTTGATC TCTGGGGCCAGGGGACAATGGTCACAGTCTCTTCAGCCTCCACCAAGGGC CCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCAC AGCAGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGG TGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCT GTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCC CTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGC CCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAAA ACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTC AGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGA CCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAG GTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGAC AAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCC TCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAG GTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGC CAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGG ATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTC TATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAA CAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCC TCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTC TTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACACAGAA GAGCCTCTCCCTGTCTCCGGGTAAA [SEQ ID NO: 265]	
DNA for Heavy Chain version 2	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTGG TCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGGTTCACT TTCAATACCTATGGCATGCACTGGGTCCGCCAGGCACCAGGCAAGGGGCT GGAGTGGGTGGCAATTATCTGGTATGATGGGAGCCAGAAATACTATGCAG ACTCCGTGCAGGGCCGATTCACTATCTCCAGAGACAATCACAAGAACACG TTGTCTCTGCAAATGAACTCCCTGAGAGCCGAGGACACGGCTGTGTATTT CTGTGTGAGAGTCCGCTTTAGCGTTGGCCCCCACGGGAGTGCTTTTGATC TCTGGGGCCAGGGGACAATGGTCACAGTCTCTTCAGCCTCCACCAAGGGC CCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCAC AGCAGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGG TGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCT GTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCC CTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGC CCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAAA ACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTC	

TABLE 29-continued

Antibody ID: AB-007088.004	
KABAT	ASN
AGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGA CCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAG GTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGAC AAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCC TCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAG GTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGC CAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGG ATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTC TATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAA CAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCC TCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTC TTCTCATGCTCCGTGCTGCATGAGGCTCTGCACTCCCACTACACACAGAA GAGCCTCTCCCTGTCTCCGGGTAAA [SEQ ID NO: 266]	

In certain embodiments, the anti-CSP antibody variant comprises a light chain variable region comprising a CDR1, a CDR2, and a CDR3 and having the amino acid sequence set forth in SEQ ID NO: 267, as shown in Table 30. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 and having the amino acid sequence set forth in SEQ ID NO: 268, as shown in Table 30. In certain embodiments, the anti-CSP antibody variant comprises a light chain having the amino acid sequence set forth in SEQ ID NO: 271, as shown in Table 30. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain having the amino acid sequence set forth in SEQ ID NO: 272, as shown in Table 30. In certain embodiments, the anti-CSP antibody variant comprises a heavy chain having the amino acid sequence set forth in SEQ ID NO: 273, as shown in Table 30. Exemplary nucleic acid sequences of SEQ ID NOS: 267, 268, 271, 272, and 273 are provided in Table 30 below.

TABLE 30

Antibody ID: AB-007088.005		
	KABAT	ASN
CDR1-VL	RASQSISSWLA [SEQ ID NO: 205]	RASQSISSWLA [SEQ ID NO: 211]
CDR2-VL	DASSLES [SEQ ID NO: 206]	DASSLES [SEQ ID NO: 212]
CDR3-VL	QQYNSYSFWT [SEQ ID NO: 207]	QQYNSYSFWTF [SEQ ID NO: 213]
CDR1-VH	TYGMH [SEQ ID NO: 208]	TYGMH [SEQ ID NO: 214]
CDR2-VH	IIWYDGSQKYYADSVQG [SEQ ID NO: 209]	IIWYDGSQKYYADSVQG [SEQ ID NO: 215]
CDR3-VH	VRFSVGPHGSAFDL [SEQ ID NO: 210]	SAFDL [SEQ ID NO: 216]
VL	GVQMTQSPSTLSASVGDRVTLTCRASQS ISSWLAWYQQKPGKAPKLLIYDASSLESGVPSRFSGSGSGTEFTLTISSL QPDDFATYYCQQYNSYSFWTFGQGTKVEIKR [SEQ ID NO: 267]	
VH	QVQLVESGGGVVQPGRSLRLSCAASGFT FNTYGMHWVRQAPGKGLEWVAIIWYDGSQKYYADSVQGRFTISRDNHKNT LYLQMNSLRAEDTAVYFCVRVRFSVGPHGSAFDLWGQGTMVTVSS [SEQ ID NO: 268]	
DNA for VL	GGCGTCCAGATGACCCAGTCTCCTTCCACCCTGT CTGCATCTGTGGGAGACAGAGTCACCCTCACTTGCCGGGCCAGTCAGAGT ATTAGTAGTTGGTTGGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAA ACTCCTGATCTATGATGCCTCCAGTTTGGAAAGTGGGGTCCCATCAAGGT TCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACCATCAGCAGCCTG CAACCTGATGATTTTGCAACTTATTACTGCCAACAGTATAATAGTTATTC TTTTTGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAACGC [SEQ ID NO: 269]	
DNA forVH	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTGG TCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGGTTCACT TTCAATACCTATGGCATGCACTGGGTCCGCCAGGCACCAGGCAAGGGGCT GGAGTGGGTGGCAATTATCTGGTATGATGGGAGCCAGAAATACTATGCAG	

TABLE 30-continued

Antibody ID: AB-007088.005		
	KABAT	ASN
	ACTCCGTGCAGGGCCGATTCACTATCTCCAGAGACAATCACAAGAACACG TTGTACCTGCAAATGAACTCCCTGAGAGCCGAGGACACGGCTGTGTATTT CTGTGTGAGAGTCCGCTTTAGCGTTGGCCCCCACGGGAGTGCTTTTGATC TCTGGGGCCAGGGGACAATGGTCACAGTCTCTTCA [SEQ ID NO: 270]	
Light Chain	GVQMTQSPSTLSASVGDRVTLTCRASQS ISSWLAWYQQKPGKAPKLLIYDASSLESGVPSRFSGSGSGTEFTLTISSL QPDDFATYYCQQYNSYSFWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKS GTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC [SEQ ID NO: 271]	
Heavy Chain version 1	QVQLVESGGGVVQPGRSLRLSCAASGFT FNTYGMHWVRQAPGKGLEWVAIIWYDGSQKYYADSVQGRFTISRDNHKNT LYLQMNSLRAEDTAVYFCVRVRFSVGPHGSAFDLWGQGTMVTVSSASTKG PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDK THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSLSPGK [SEQ ID NO: 272]	
Heavy Chain version 2	QVQLVESGGGVVQPGRSLRLSCAASGFT FNTYGMHWVRQAPGKGLEWVAIIWYDGSQKYYADSVQGRFTISRDNHKNT LYLQMNSLRAEDTAVYFCVRVRFSVGPHGSAFDLWGQGTMVTVSSASTKG PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDK THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVLHEALHSHYTQKSLSLSPGK [SEQ ID NO: 273]	
DNA for Light Chain	GGCGTCCAGATGACCCAGTCTCCTTCCACCCTGT CTGCATCTGTGGGAGACAGAGTCACCCTCACTTGCCGGGCCAGTCAGAGT ATTAGTAGTTGGTTGGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAA ACTCCTGATCTATGATGCCTCCAGTTTGGAAAGTGGGGTCCCATCAAGGT TCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACCATCAGCAGCCTG CAACCTGATGATTTTGCAACTTATTACTGCCAACAGTATAATAGTTATTC TTTTTGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAACGCACTGTGG CTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCT GGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGC CAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGG AGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGC ACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTG CGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT [SEQ ID NO: 274]	
DNA for Heavy Chain version 1	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTGG TCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGGTTCACT TTCAATACCTATGGCATGCACTGGGTCCGCCAGGCACCAGGCAAGGGGCT GGAGTGGGTGGCAATTATCTGGTATGATGGGAGCCAGAAATACTATGCAG ACTCCGTGCAGGGCCGATTCACTATCTCCAGAGACAATCACAAGAACACG TTGTACCTGCAAATGAACTCCCTGAGAGCCGAGGACACGGCTGTGTATTT CTGTGTGAGAGTCCGCTTTAGCGTTGGCCCCCACGGGAGTGCTTTTGATC TCTGGGGCCAGGGGACAATGGTCACAGTCTCTTCAGCCTCCACCAAGGGC CCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCAC AGCAGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGG TGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCT GTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCC CTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGC CCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAAA ACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTC AGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGA CCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAG GTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGAC AAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCC TCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAG GTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGC CAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGG ATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTC TATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAA	

TABLE 30-continued

Antibody ID: AB-007088.005

	KABAT	ASN
	CAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCC TCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTC TTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACACAGAA GAGCCTCTCCCTGTCTCCGGGTAAA [SEQ ID NO: 275]	
DNA for Heavy Chain version 2	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTGG TCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGGTTCACT TTCAATACCTATGGCATGCACTGGGTCCGCCAGGCACCAGGCAAGGGGCT GGAGTGGGTGGCAATTATCTGGTATGATGGGAGCCAGAAATACTATGCAG ACTCCGTGCAGGGCCGATTCACTATCTCCAGAGACAATCACAAGAACACG TTGTACCTGCAAATGAACTCCCTGAGAGCCGAGGACACGGCTGTGTATTT CTGTGTGAGAGTCCGCTTTAGCGTTGGCCCCCACGGGAGTGCTTTTGATC TCTGGGGCCAGGGGACAATGGTCACAGTCTCTTCAGCCTCCACCAAGGGC CCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCAC AGCAGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGG TGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCT GTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCC CTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGC CCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAAA ACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTC AGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGA CCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAG GTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGAC AAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCC TCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAG GTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGC CAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGG ATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTC TATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAA CAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCC TCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTC TTCTCATGCTCCGTGCTGCATGAGGCTCTGCACTCCCACTACACACAGAA GAGCCTCTCCCTGTCTCCGGGTAAA [SEQ ID NO: 276]	

4. Glycosylation of Anti-CSP Antibodies and Variants Thereof

Glycosylation of antibodies and engineered antibodies has been previously disclosed (see, e.g., U.S. Pat. No. 6,602,684, the content of which is incorporated in its entirety). Antibody Fc regions are generally post-translationally modified via the addition of N-glycans at specific asparagine residues on the antibody heavy chain. IgG molecules bear a N-linked glycosylation asparagine of each heavy chain. It has been shown that a modified glycosylation profile can regulate the antibody functions. For example, without any limitation, altered glycosylation can improve the binding affinity or the half-life of the antibody as compared to the non-modified form.

In certain embodiments, the present disclosure provides anti-CSP antibodies and variants thereof with modified glycosylation. In certain embodiments, the antibodies disclosed herein include an Fc region with increased glycosylation. In certain non-limiting embodiments, the Fc region with increased glycosylation includes increased amounts of bisected oligosaccharides. In certain embodiments, the Fc region with increased glycosylation includes increased amounts of nonfucosylated oligosaccharides. In certain embodiments, the Fc region with increased glycosylation includes increased amounts of fucose-containing oligosaccharides.

In certain embodiments, the antibodies disclosed herein include an Fc region with decreased glycosylation. In certain non-limiting embodiments, the Fc region with decreased glycosylation includes reduced amounts of bisected oligosaccharides. In certain embodiments, the Fc region with decreased glycosylation includes reduced amounts of non-fucosylated oligosaccharides. In certain embodiments, the Fc region with increased glycosylation includes reduced amounts of fucose-containing oligosaccharides.

In certain embodiments, the antibodies disclosed herein include a V region with increased glycosylation. In certain non-limiting embodiments, the V region with increased glycosylation includes increased amounts of bisected oligosaccharides. In certain embodiments, the V region with increased glycosylation includes increased amounts of non-fucosylated oligosaccharides. In certain embodiments, the V region with increased glycosylation includes increased amounts of fucose-containing oligosaccharides.

In certain embodiments, the antibodies disclosed herein include a V region with decreased glycosylation. In certain non-limiting embodiments, the V region with decreased glycosylation includes reduced amounts of bisected oligosaccharides. In certain embodiments, the V region with decreased glycosylation includes reduced amounts of non-fucosylated oligosaccharides. In certain embodiments, the V region with increased glycosylation includes reduced amounts of fucose-containing oligosaccharides.

In certain embodiments, the modified glycosylation can be obtained by expressing any of the antibodies disclosed herein in a host cell with altered glycosylation machinery. For example, without any limitation, a host cell can include a functional disruption of the fucosyltransferase gene and antibodies expressed in this host cell with show reduced glycosylation, e.g., reduced fucosylation (see PCT Patent Publication No. WO 99/54342).

In certain embodiments, the present disclosure provides anti-CSP antibody variants disclosed herein including one or more amino acid substitution resulting in the alteration of a glycosylation acceptor site. In certain embodiments, the alteration includes the elimination of the glycosylation acceptor site. In certain embodiments, the alteration includes modification of a glycosylation acceptor site. In certain embodiments, the alteration includes insertion of a glycosylation acceptor site.

As used herein, "glycosylation acceptor site" refers to an amino acid residue of the light chain or heavy chain of the antibody which can be N- or O-glycosylated. In certain embodiments, the N-linked glycosylation acceptor site can be an asparagine residue. In certain embodiments, the O-linked glycosylation acceptor site can be a serine residue, a threonine residue, a tyrosine residue, a hydroxylysine residue, or a hydroxyproline residue.

In certain embodiments, the Fc region of the antibodies disclosed herein includes one or more glycosylation acceptor site. In certain embodiments, the V region of any of the antibodies disclosed herein includes one or more glycosylation acceptor site. In certain embodiments, the light chain of any of the antibodies disclosed herein includes one or more glycosylation acceptor site. In certain embodiments, the heavy chain of any one of the antibodies disclosed herein includes one or more glycosylation acceptor site. In certain embodiments, the light chain variable region of any of the antibodies disclosed herein includes one or more glycosylation acceptor site. In certain embodiments, the heavy chain variable region of any of the antibodies disclosed herein includes one or more glycosylation acceptor site.

5. PEGylation and Other Chemical Modifications of Anti-CSP Antibodies and Variants Thereof

The present disclosure provides anti-CSP antibodies and variants thereof including additional modifications. In certain embodiments, the modifications can improve pharmacological properties of the antibodies, e.g., half-life. In certain non-limiting embodiments, the modification includes PEGylation, deamination, derivatization with polymers, lipidation, removal and/or introduction of disulfide bonds, oxidation, and removal of C-terminal lysine

In certain embodiments, the modification is a PEGylation. PEGylation of antibodies and engineered antibodies includes attachment of one or more polyethylene glycol (PEG) to the antibody. In certain non-limitation embodiments, for example, the PEGylation can be carried out by an acylation reaction or an alkylation reaction with a reactive PEG molecule (or an analogous reactive water-soluble polymer). As used herein, the term "polyethylene glycol" refers to any of the forms of PEG that have been used to derivatize other proteins, such as mono (C1-C10) alkoxy- or aryloxy-polyethylene glycol or polyethylene glycol-maleimide.

In certain embodiments, the modification is the derivatization with a hydrophilic polymer. In certain non-limiting embodiments, for example, the hydrophilic polymer can be carboxymethylcellulose, dextran, polyvinyl alcohol, polyvinyl pyrrolidone, poly-1, 3-dioxolane, poly-1,3,6-trioxane, ethylene/maleic anhydride copolymer, polyaminoacids (either homopolymers or random copolymers), and dextran or poly(n-vinyl pyrrolidone)polyethylene glycol, propropylene glycol homopolymers, prolypropylene oxide/ethylene oxide co-polymers, polyoxyethylated polyols (e.g., glycerol), polyvinyl alcohol, and mixtures thereof.

In certain embodiments, the modification is a lipidation. Lipidation is the conjugation of a protein with a lipid. Lipidation of peptides improves metabolic stability, membrane permeability, bioavailability, and changes the pharmacokinetic and pharmacodynamic properties of the peptides. For example, a lipidated peptide has a high affinity with serum albumin resulting in increased half-life and stability. In certain non-limiting embodiments, for example, the lipid can be myristic acid, palmitic acid, stearic acid, lauric acid, cholesterol, and mixtures thereof.

In certain embodiments, the modification is a substitution of an amino acid residue to form a disulfide bond. In certain embodiments, the amino acid substitution introduces a cysteine. Under certain redox conditions, two cysteines can form a non-natural disulfide bond. In certain non-limiting embodiments, the disulfide bond improves the stability of the antibody, e.g., corrected pairing of the antibody chains. In certain embodiments, the cysteine is introduced in the V region. In certain embodiments, the cysteine is introduced in the Fc region. In certain embodiments, the modification is a substitution of an amino acid residue to remove a disulfide bond. In certain embodiments, the amino acid substitution removes a cysteine. In certain embodiments, the cysteine is substituted with a serine. In certain non-limiting embodiments, removing a cysteine improves the stability of the antibody, e.g., improved long-term stability. In certain embodiments, the cysteine is removed in the V region. In certain embodiments, the cysteine is removed in the Fc region.

6. Anti-CSP Antibody and Anti-CSP Antibody Variants Conjugates

In certain embodiments, the present disclosure provides an anti-CSP antibody or variant thereof conjugated or linked to therapeutic and/or imaging/detectable moieties. For example, without any limitation, the anti-CSP antibody or variant thereof can be conjugated to a detectable marker, a toxin, or a therapeutic agent. The moiety may be linked to the antibody covalently or by non-covalent linkages.

In certain embodiments, the antibody or variant thereof is conjugated to cytotoxic moiety or other moiety that inhibits cell proliferation. In certain embodiments, the antibody or variant thereof is conjugated to a cytotoxic agent including, but not limited to, a ricin A chain, doxorubicin, daunorubicin, a maytansinoid, taxol, ethidium bromide, mitomycin, etoposide, tenoposide, vincristine, vinblastine, colchicine, dihydroxy anthracin dione, actinomycin, a diphtheria toxin, extotoxin A from *Pseudomonas*, *Pseudomonas* exotoxin (PE) A, PE40, abrin, abrin A chain, modeccin A chain, alpha sarcin, gelonin, mitogellin, restrictocin, cobran venom factor, a ribonuclease, phenomycin, enomycin, curicin, crotin, calicheamicin, *Saponaria officinalis* inhibitor, glucocorticoid, auristatin, auromycin, yttrium, bismuth, combrestatin, duocarmycins, dolastatin, cc1065, or a cisplatin. In certain embodiments, the antibody or variant thereof can be linked to an agent such as an enzyme inhibitor, a proliferation inhibitor, a lytic agent, a DNA or RNA synthesis inhibitors, a membrane permeability modifier, a DNA metabolites, a dichloroethyl sulfide derivative, a protein production inhibitor, a ribosome inhibitor, or an inducer of apoptosis.

In certain embodiments, the antibody or variant thereof can be linked to a radionuclide, an iron-related compound, a dye, a fluorescent agent, or an imaging agent. In certain embodiments, an antibody may be linked to agents, such as, but not limited to, metals; metal chelators; lanthanides; lanthanide chelators; radiometals; radiometal chelators; positron-emitting nuclei; microbubbles (for ultrasound); liposomes; molecules microencapsulated in liposomes or nanosphere; monocrystalline iron oxide nano-compounds; magnetic resonance imaging contrast agents; light absorbing, reflecting and/or scattering agents; colloidal particles; fluorophores, such as near-infrared fluorophores.

In certain embodiments, the present disclosure provides bispecific molecules comprising an anti-CSP antibody, a variant thereof, or a fragment thereof, disclosed herein. The anti-CSP antibody, anti-CSP antibody variant or antigen-binding portions thereof can be derivatized or linked to another functional molecule, e.g., another peptide or protein (e.g., another antibody or ligand for a receptor) to generate a bispecific molecule that binds to at least two different binding sites or target molecules. The anti-CSP antibody or variant thereof disclosed herein can be derivatized or linked to more than one other functional molecule to generate multispecific molecules that bind to more than two different binding sites (e.g., two different epitopes on the CSP protein) and/or target molecules; such multispecific molecules are also intended to be encompassed by the term "bispecific molecule" as used herein. To create a bispecific molecule of the invention, an antibody of the invention can be functionally linked (e.g., by chemical coupling, genetic fusion, noncovalent association, or otherwise) to one or more other binding molecules, such as another antibody, antibody fragment, peptide or binding mimetic, such that a bispecific molecule results. In certain non-limiting embodiments, for example and without any limitation, the bispecific antibody can be created using the knobs-into-holes strategy. This strategy typically involves creation of a first half of a first antibody that recognizes a first antigen, e.g., CSP, and a second half of the antibody that recognizes a second antigen or binding site, and then joining the two halves to create the bispecific antibody. In certain embodiments, the first antigen and the second antigen are different epitopes of the CSP protein.

7. Activity

The activity of any of the anti-CSP antibodies disclosed herein can be assessed by using different endpoints. In certain embodiments, the activity is assessed for binding to CSP, either binding to a series of linear peptides with varying lengths representing the immunodominant regions of the CSP protein or to the entire CSP protein. In certain embodiments, the activity is assessed for the ability to protect against challenge with *Plasmodium* that comprises *P. falciparum* CSP, e.g., in in vivo animal models of malaria. In certain embodiments, effector function, e.g., ADCC, is also evaluated.

In certain embodiments, the binding activity of an anti-CSP antibody disclosed herein to *P. falciparum* CSP protein can be assessed by surface plasmon resonance (SPR) using a biosensor system. Systems suitable for use in SPR are, for example, and without any limitation, LSA™ (Carterra, Dublin, Calif.), Biacore™ (General Electric, Boston, Mass.), and OpenSPR (Nicoya, East Kitchener, ON, Canada). In an exemplary SPR assay, each antibody can be either directly immobilized to a Carterra CMD200M Chip or captured to the CMD200M Carterra Chip with a goat anti-human IgG Fc antibody. The uncoupled antibodies can be washed off and various concentration gradients of the targets can be flowed over the antibodies. In certain experimental conditions, the highest concentration of each target can be in the range of 0.5-8 μg/mL. For better accuracy, each antibody can be immobilized in different locations (e.g., at least 2) on the chip, and the affinity for each antibody-target combination can be determined using multiple (e.g., 4-5) target concentrations according to standard methods. If the variation between the two duplicates is >3-fold, the antibody-target measurement is repeated.

In certain embodiments, the binding activity of an anti-CSP antibody disclosed herein to *P. falciparum* CSP protein can be assessed by bio-layer interferometry (BLI). For BLI, each of the antigens (e.g., those disclosed in Table 35) can be immobilized on sensors according to the manufacturer's instructions. Systems suitable for use in BLI include, but are not limited to, Octet™ (ForteBio, Fremont, Calif.) and Gator™ (Probelife, Palo Alto, Calif.). In certain embodiments, for example and without any limitation, the antigen can be biotinylated and immobilized to streptavidin sensors. For better accuracy, each antibody can be evaluated in replicates at a suitable concentration (e.g., 5 μg/mL). If the variation between the two duplicates is >3-fold, the antibody-target measurement is repeated. The assays are typically performed under conditions according to the manufacturer's instructions. The assays can be performed under a temperature in the range of 20° C. to 37° C., for example, 20° C.-25° C. In certain embodiments, the assay is performed at 25° C. In certain embodiments, the assay is performed at 37° C.

In certain embodiments, binding to CSP protein is assessed in a competitive assay format with a reference antibody AB-000224 or a reference antibody having the variable regions of AB-000224. In certain embodiments, binding to CSP protein is assessed in a competitive assay format with a reference antibody AB-007088 or a reference antibody having the variable regions of AB-007088. In certain embodiments, a variant anti-CSP antibody disclosed herein can block binding of the reference antibody in a competition assay by about 50% or more.

Anti-CSP antibodies and anti-CSP antibody variants of the present disclosure may also be evaluated in various assays for their ability to mediate FcR-dependent activity. In certain embodiments, an antibody of the present disclosure has enhanced ADCC and/or serum stability compared to antibody AB-000224 when the antibodies are assayed in a human IgG1 isotype format. In certain embodiments, an antibody of the present disclosure has enhanced ADCC and/or serum stability compared to antibody AB-007088 when the antibodies are assayed in a human IgG1 isotype format.

In certain embodiments, the activity of an anti-CSP antibody can be evaluated in vivo in an animal model, e.g., as described in the Examples section. In certain non-limiting embodiments, for example, the mouse malaria liver burden assay can be used, as disclosed in, for example, Flores-Garcia Y, et al. Malar J. 2019; 18(1):426, doi:10.1186/s12936-019-3055-9, the content of which is herein incorporated by reference. Mice are administered antibody and infected with chimeric *P. berghei* expressing GFP-luciferase and *P. falciparum* CSP protein. Parasite liver load can be evaluated, e.g., by RT-qPCR or by measuring bioluminescence with an IVIS Spectrum imager. A reduction in parasite liver load reflects the prophylactic activity of an antibody.

In certain embodiments, the activity of an anti-CSP antibody can be determined by evaluating the in vivo protection and survival of animal models, e.g., mice. For example, but without any limitation, mice are administered antibody and challenged with chimeric *P. berghei* expressing *P. falciparum* CSP protein as disclosed in, for example, Espinosa, D., et al. npj Vaccines 2017; 2, 10 (2017); Espinosa, D., et al. Infect Immun. 2013 August; 81(8): 2882-2887. The in vivo protection can be determined by detecting blood-stage parasitaemia in microscopy. The survival rate can be determined using the absence of parasitaemia during an observation period, e.g., two weeks, immediately following the challenge. An increased survival rate reflects the prophylactic and/or therapeutic activity of an antibody.

In certain embodiments, an anti-CSP antibody, e.g., AB-000224 or AB-007088, disclosed herein has at least 20%, or at least 30%, or at least 40%, or at least 50%, or at least 60%, or 70%, or greater, of the activity of antibody AB-000317 when evaluated under the same assay conditions. In certain embodiments, an anti-CSP antibody exhibits improved activity, i.e., greater than 100%, activity compared to antibody AB-000317. In certain non-limiting embodiments, an anti-CSP antibody disclosed herein exhibits at least 20%, or at least 30%, or at least 40%, or at least 50%, or at least 60%, or 70%, or greater reduction in parasite liver load as compared to antibody AB-000317. In certain non-limiting embodiments, an anti-CSP antibody disclosed herein exhibits at least 20%, or at least 30%, or at least 40%, or at least 50%, or at least 60%, or 70%, or greater increase in survival rate as compared to antibody AB-000317.

In certain embodiments, an anti-CSP antibody variant disclosed herein has at least 50%, or at least 60%, or 70%, or greater, of the activity of AB-000224 when evaluated under the same assay conditions. In certain embodiments, an anti-CSP antibody exhibits improved activity, i.e., greater than 100%, activity compared to AB-000224. In certain embodiments, the anti-CSP antibody variants disclosed herein have similar activity against malaria infection as compared to AB-000224. In certain embodiment, an anti-CSP antibody variant disclosed herein has at least 50%, or at least 60%, or 70%, or greater, of the activity of AB-007088 when evaluated under the same assay conditions. In certain embodiments, an anti-CSP antibody exhibits improved activity, i.e., greater than 100%, activity compared to AB-007088. In certain embodiments, the anti-CSP antibody variants disclosed herein have similar activity against malaria infection as compared to AB-007088. The term "similar activity," when used to compare in vivo activity of antibodies, refers to that two measurements of the activity is no more than 30%, no more than 25%, no more than 20%, no more than 15% different, no more than 10%, no more than 8%, or no more than 5% different from each other.

In certain embodiments, the native anti-CSP antibody, AB-000224, is modified to have improved developability (i.e., reduced development liabilities), including but not limited to, decreased heterogeneity, increased yield, increased stability, improved net charges to improve pharmacokinetics, and or/reduced immunogenicity. In certain embodiments, antibodies having improved developability can be obtained by introducing mutations to reduce or eliminate potential development liabilities, as described in Table 1. In certain embodiments, antibodies having improved developability possess modifications as compared to AB-000224 in their amino acid sequence, as disclosed in Table 2.

In certain embodiments, the native anti-CSP antibody, AB-007088, is modified to have improved developability (i.e., reduced development liabilities), including but not limited to, decreased heterogeneity, increased yield, increased stability, improved net charges to improve pharmacokinetics, and or/reduced immunogenicity. In certain embodiments, antibodies having improved developability can be obtained by introducing mutations to reduce or eliminate potential development liabilities, as described in Table 1. In certain embodiments, antibodies having improved developability possess modifications as compared to AB-007088 in their amino acid sequence, as disclosed in Table 2.

In certain embodiments, the anti-CSP antibody variants disclosed herein have improved developability while maintaining comparable or improved binding affinity to the target as compared to AB-000224. Non-limiting examples of such anti-CSP antibody variants are disclosed herein. In certain embodiments, the anti-CSP antibody variants disclosed herein have improved developability while maintaining activities that are similar to AB-000224.

In certain embodiments, the anti-CSP antibody variants disclosed herein have improved developability while maintaining comparable or improved binding affinity to the target as compared to AB-007088. Non-limiting examples of such anti-CSP antibody variants are disclosed herein. In certain embodiments, the anti-CSP antibody variants disclosed herein have improved developability while maintaining activities that are similar to AB-007088.

8. Generation of Antibodies

CSP antibodies and variants thereof disclosed herein can be produced using vectors and recombinant methodology (see, e.g., Sambrook & Russell, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press; Ausubel, Current Protocols in Molecular Biology). Reagents, cloning vectors, and kits for genetic manipulation are available from commercial vendors.

The present disclosure provides isolated nucleic acids encoding a VH and/or VL region, or fragment thereof, of any of the anti-CSP antibodies and anti-CSP antibody variants disclosed herein. In certain embodiments, the present disclosure provides vectors comprising said nucleic acids and host cells into which the nucleic acids are introduced that are used to replicate the antibody-encoding nucleic acids and/or to express the antibodies. These nucleic acids can encode an amino acid sequence containing the VL, and/or an amino acid sequence containing the VH of the anti-CSP antibody or variant thereof (e.g., the light and/or heavy chains of the antibody). In certain embodiments, the host cell contains (1) a vector containing a polynucleotide that encodes the VL amino acid sequence and a polynucleotide that encodes the VH amino acid sequence, or (2) a first vector containing a polynucleotide that encodes the VL amino acid sequence and a second vector containing a polynucleotide that encodes the VH amino acid sequence.

In certain embodiments, the present disclosure provides a method of making an anti-CSP antibody disclosed herein. In certain embodiments, the method includes culturing a host cell previously described under conditions suitable for expression of the antibody. In certain embodiments, the antibody is subsequently recovered from the host cell (or host cell culture medium).

Suitable vectors containing polynucleotides encoding antibodies of the present disclosure, or fragments thereof, include cloning vectors and expression vectors. While the cloning vector selected can vary according to the host cell intended to be used, useful cloning vectors generally can self-replicate, can possess a single target for a particular restriction endonuclease, and/or may carry genes for a marker that can be used in selecting clones containing the vector. Non-limiting examples include plasmids and bacterial viruses, e.g., pUC18, pUC19, Bluescript (e.g., pBS SK+) and its derivatives, mp18, mp19, pBR322, pMB9, ColE1 plasmids, pCR1, RP4, phage DNAs, and shuttle vectors.

Expression vectors generally are replicable polynucleotide constructs that contain a nucleic acid of the present disclosure. The expression vector can replicate in the host cells either as episomes or as an integral part of the chromosomal DNA. Suitable expression vectors include, but are not limited to, plasmids and viral vectors, including adenoviruses, adeno-associated viruses, retroviruses, and any other vector.

Suitable host cells for expressing an anti-CSP antibody or anti-CSP antibody variant disclosed herein include both prokaryotic or eukaryotic cells. For example, but without any limitation, anti-CSP antibodies can be produced in bacteria, in particular when glycosylation and Fc effector function are not needed. After expression, the antibody can be isolated from the bacterial cell lysate in a soluble fraction and can be further purified. Alternatively, the host cell can be a eukaryotic host cell, including, without limitation, eukaryotic microorganisms, such as filamentous fungi or yeast, fungi and yeast strains whose glycosylation pathways have been "humanized," resulting in the production of an antibody with a partially or fully human glycosylation pattern, vertebrate, invertebrate, and plant cells. Non-limiting examples of invertebrate cells include insect cells. Numerous baculoviral strains have been identified which may be used in conjunction with insect cells. Plant cell cultures can also be utilized as host cells.

In certain embodiments, vertebrate host cells are used for producing anti-CSP antibodies of the present disclosure. For example, without any limitation, mammalian cell lines that can be used to express anti-CSP antibodies include monkey kidney CV1 line transformed by SV40 (COS-7); human embryonic kidney line (293 or 293 cells); baby hamster kidney cells (BHK); mouse Sertoli cells (TM4 cells); monkey kidney cells (CV1); African green monkey kidney cells (VERO-76); human cervical carcinoma cells (HELA); canine kidney cells (MDCK; buffalo rat liver cells (BRL 3A); human lung cells (W138); human liver cells (Hep G2); mouse mammary tumor (MMT 060562); TRI cells; MRC 5 cells; and FS4 cells. In certain embodiments, the mammalian cell line used to express anti-CSP antibodies can be Chinese hamster ovary (CHO) cell line; DHFR-CHO cell line (Urlaub et al., Proc. Natl. Acad. Sci. USA 77:4216, 1980); and myeloma cell lines such as YO, NSO, and Sp2/0. Host cells of the present disclosure also include, without limitation, isolated cells, in vitro cultured cells, and ex vivo cultured cells.

A host cell transfected with an expression vector encoding an anti-CSP antibody of the present disclosure, or fragment thereof, can be cultured under appropriate conditions to allow expression of the polypeptide to occur. The polypeptides can be secreted and isolated from a mixture of cells and medium containing the polypeptides. Alternatively, the polypeptide can be retained in the cytoplasm or a membrane fraction and the cells harvested, lysed, and the polypeptide isolated using a desired method.

In certain embodiments, the present disclosure provides a method of generating variants of an anti-CSP antibody disclosed herein. In certain non-limiting embodiments, for example and without any limitation, a construct encoding a variant of VH CDR2 as described in the "anti-CSP Antibody Variant" section can be additionally modified and the VH region encoded by the additionally modified construct can be tested for binding activity to CSP and/or in vivo protective efficacy in the context of a VH region comprising the native AB-000224 CDR1 and CDR3, or a variant CDR1 or CDR3 as described herein, that is paired with a native AB-000224 VL region or variant region as described herein. Similarly, a construct encoding a variant VL CDR3 as described in the "anti-CSP Antibody Variant" section can be additionally modified and the VL region encoded by the additionally modified construct can be tested for binding activity to CSP and/or protective efficacy. Such an analysis can also be performed with other CDRs or framework regions and an antibody having the desired activity can then be selected.

Pharmaceutical Compositions and Methods of Treatment

In certain embodiments, the present disclosure provides pharmaceutical compositions for the administration of an anti-CSP antibody and variants thereof. In certain embodiments, the pharmaceutical compositions can be administered to a mammalian subject, e.g., a human, who has malaria or is at risk for malaria, in a therapeutically effective amount and according to a schedule sufficient to prevent *Plasmodium* infection, e.g., infection with *Plasmodium falciparum* or a *Plasmodium* sp. having a cross-reactive CSP protein, or to reduce a symptom of malaria in the subject. In certain embodiments, the pharmaceutical compositions can include any of the anti-CSP antibodies and variants thereof disclosed herein, or a polynucleotide encoding the same, and a pharmaceutically acceptable diluent or carrier. In certain embodiments, a polynucleotide encoding the antibody can be contained in a plasmid vector for delivery, or a viral vector. In certain embodiments, the pharmaceutical composition comprises a therapeutically effective amount of the antibody. As used herein, a "therapeutically effective dose" or a "therapeutically effective amount" refers to an amount sufficient to prevent, cure, or at least partially arrest malaria or symptoms of malaria. A therapeutically effective dose can be determined by monitoring a patient's response to therapy. Typical benchmarks indicative of a therapeutically effective dose include amelioration or prevention of symptoms of malaria in the patient, including, for example, and without limitation, reduction in the number of parasites. Amounts effective for this use will depend upon the severity of the disease and the general state of the patient's health, including other factors such as age, weight, gender, administration route, etc. Single or multiple administrations of the antibody will be dependent on the dosage and frequency as required and tolerated by the patient.

In certain embodiments, the antibody is administered at a pre-erythrocyte stage of infection, i.e., the antibody is administered in a time frame to prevent or reduce hepatocyte infection.

Various pharmaceutically acceptable diluents, carriers, and excipients, and techniques for the preparation and use of pharmaceutical compositions are also disclosed herein. Illustrative pharmaceutical compositions and pharmaceutically acceptable diluents, carriers, and excipients are also described in Remington: The Science and Practice of Pharmacy 20th Ed. (Lippincott, Williams & Wilkins 2012). In certain embodiments, each carrier, diluent, or excipient is "acceptable" in the sense of being compatible with the other ingredients of the pharmaceutical composition and not injurious to the subject. Often, the pharmaceutically acceptable carrier is an aqueous pH-buffered solution. In certain non-limiting embodiments, for example, pharmaceutically-acceptable carriers, diluents or excipients include water; buffers, e.g., phosphate-buffered saline; sugars, such as lactose, glucose and sucrose; starches, such as corn starch and potato starch; cellulose, and its derivatives, such as sodium carboxymethyl cellulose, ethyl cellulose and cellulose acetate; powdered tragacanth; malt; gelatin; talc; excipients, such as cocoa butter and suppository waxes; oils, such as peanut oil, cottonseed oil, safflower oil, sesame oil, olive oil, corn oil and soybean oil; glycols, such as propylene glycol; polyols, such as glycerin, sorbitol, mannitol and polyethylene glycol; esters, such as ethyl oleate and ethyl laurate; agar; buffering agents, such as magnesium hydroxide and aluminum hydroxide; alginic acid; pyrogen-free water; isotonic saline; Ringer's solution; ethyl alcohol; phosphate buffer solutions; and other non-toxic compatible substances employed in pharmaceutical formulations. Wetting agents, emulsifiers and lubricants, such as sodium lauryl sulfate and magnesium stearate, as well as coloring agents, release agents, coating agents, sweetening, flavoring and perfuming agents, preservatives and antioxidants can also be present in the compositions.

In certain embodiments, the pharmaceutical composition can be formulated for any suitable route of administration, including for example, parenteral, intrapulmonary, intranasal, or local administration. Parenteral administration can include intramuscular, intravenous, intraarterial, intraperitoneal, oral, or subcutaneous administration. In certain embodiments, the pharmaceutical composition is formulated for intravenous administration and has a concentration of antibody of 10-100 mg/ml, 10-50 mg/ml, 20 to 40 mg/ml, or about 30 mg/ml. In certain embodiments, the pharmaceutical composition is formulated for subcutaneous injection and has a concentration of antibody of 50-500 mg/ml, 50-250 mg/ml, or 100 to 150 mg/ml, and a viscosity less than 50 cP, less than 30 cP, less than 20 cP, or about 10 cP. In certain embodiments, the pharmaceutical compositions are liquids or solids. In certain embodiments, the pharmaceutical compositions are formulated for parenteral, e.g., intravenous, subcutaneous, intraperitoneal, or intramuscular administration.

In certain embodiments, the formulation of and delivery methods of pharmaceutical compositions are adapted according to the site and the disease to be treated. For example, without any limitation, formulations include those in which the antibody is encapsulated in micelles, liposomes, or drug-release capsules (active agents incorporated within a biocompatible coating designed for slow-release); ingestible formulations; formulations for topical use, such as creams, ointments, and gels; and other formulations such as inhalants, aerosols, and sprays.

In certain non-limiting embodiments, for example for parenteral administration, the antibodies or antigen-binding fragments thereof are formulated in a unit dosage injectable form (solution, suspension, emulsion) in association with a pharmaceutically acceptable, parenteral vehicle. Non-limiting examples of vehicles include water, saline, Ringer's solution, dextrose solution, and 5% human serum albumin. Nonaqueous vehicles such as fixed oils and ethyl oleate may also be used.

The dose and dosage regimen depend upon a variety of factors readily determined by a physician, such as the nature of the infection, the characteristics of the subject, and the subject's history. In certain embodiments, the amount of antibody or antigen-binding fragment thereof administered or provided to the subject is in the range of about 0.1 mg/kg to about 50 mg/kg of the subject's body weight. Depending on the type and severity of the infection, in certain embodiments, about 0.1 mg/kg to about 50 mg/kg body weight (e.g., about 0.1-15 mg/kg/dose) of antibody or antigen-binding fragment thereof may be provided as an initial candidate dosage to the patient, whether, for example, by one or more separate administrations, or by continuous infusion. The progress of the therapy is readily monitored by conventional methods and assays and based on criteria known to the physician or other persons of skill in the art.

An antibody or variant thereof of the present disclosure can be administered to a subject using any route of administration, e.g., systemic, parenterally, locally, in accordance with known methods. Such routes include, but are not limited to, intravenous administration, e.g., as a bolus or by continuous infusion over a period of time, by intramuscular, intraperitoneal, intracerobrospinal, subcutaneous, intraarticular, intrasynovial, intrathecal, oral, topical, or inhalation routes. A subject can be administered an antibody of the present invention one or more times; and can be administered before, after, or concurrently with another therapeutic agent as further described below.

In certain embodiments, the antibodies or variants thereof of the present disclosure can be administered to prevent malaria. In certain embodiments, the antibodies disclosed herein can inhibit or reduce the risk of *Plasmodium* infection. In certain embodiments, the antibodies disclosed herein can inhibit or reduce the pre-erythrocytic or sporozoite stage of infection. In certain embodiments, the antibodies disclosed herein can prevent malaria by targeting the *Plasmodium* at an early stage of entry to the vertebrate of a subject, to thereby arrest the infection from taking place.

In certain embodiments, antibody or variant thereof of the present disclosure can be administered to treat malaria. In certain embodiments, the antibodies disclosed herein can inhibit or reduce the progression of *Plasmodium* infection in the blood stream. In certain embodiments, the antibodies disclosed herein can inhibit or reduce the risk of transmission of *Plasmodium* from a subject to another via insect feeding, e.g., mosquito bite or via contact with infected blood.

In certain embodiments, the pharmaceutical compositions disclosed herein can be administered to a pediatric patient. As used herein, the term "pediatric patient" refers to a patient up to the age of 18 years old. In certain embodiments, the pediatric patient is a patient from age 3 months to less than 12 years old. In certain non-limiting embodiments, the pediatric patient can be a patient between from about 1 year old to about 2 years old, from about 2 years old to about 3 years old, from about 3 years old to about 4 years old, from about 4 years old to about 5 years old, from about 5 years old to about 6 years old, from about 6 years old to about 7 years old, from about 7 years old to about 8 years old, from about 8 years old to about 9 years old, from about 9 years old to about 10 years old, or from about 11 years old to about 12 years old. In certain embodiments, the pediatric patient is not responsive or poorly responsive to another treatment to malaria. In certain embodiments, the pediatric patient is human.

In certain embodiments, the dose of the pharmaceutical compositions disclosed herein is administered based on the weight of the pediatric patient. In certain non-limiting embodiments, the dose of the pharmaceutical compositions is about 5 mg/kg, about 10 mg/kg, about 15 mg/kg, about 20 mg/kg about 25 mg/kg, about 50 mg/kg, about 75 mg/kg, about 100 mg/kg, about 150 mg/kg, about 200 mg/kg, about 250 mg/kg, about 300 mg/kg, or about 350 mg/kg. In certain embodiments, the pediatric patient has a weight of from about 2.5 kg to about 5 kg, from about 5 kg to about 10 kg, from about 10 kg to about 15 kg, from about 15 kg to about 20 kg, from about 20 kg to about 30 kg, or from about 30 kg to about 40 kg.

In certain embodiments, the antibody is provided to the subject in combination with one or more additional therapeutic agents used to treat or prevent malaria or a related disease or disorder. In certain embodiments, a method for treating or preventing malaria is provided, comprising administering to the human a therapeutically effective amount of an antibody as disclosed herein, or a pharmaceutically acceptable salt thereof, in combination with a therapeutically effective amount of one or more additional therapeutic agents. In certain embodiments, a method for treating malaria in a human having or at risk of having the infection is provided, comprising administering to the human a therapeutically effective amount of an antibody as disclosed herein, or a pharmaceutically acceptable salt thereof, in combination with a therapeutically effective amount of one or more additional therapeutic agents.

In certain embodiments, when an antibody of the present disclosure as described herein is combined with one or more additional therapeutic agents as described above, the components of the composition are administered as a simultaneous or sequential regimen. When administered sequentially, the combination may be administered in two or more administrations.

In certain embodiments, an antibody as disclosed herein is combined with one or more additional therapeutic agents in a unitary dosage form for simultaneous administration to a patient.

A "patient" refers to any subject receiving the antibody regardless of whether they have malaria. In certain embodiments, a "patient" is a non-human subject, e.g., an animal that is used as a model for evaluating the effects of antibody administration.

"Co-administration" of an antibody disclosed herein with one or more additional therapeutic agents generally refers to simultaneous or sequential administration of an antibody or fragment thereof disclosed herein and one or more additional therapeutic agents, such that therapeutically effective amounts of the antibody or fragment thereof disclosed herein and one or more additional therapeutic agents are both present in the body of the patient. Co-administration includes administration of unit dosages of the antibody disclosed herein before or after administration of unit dosages of one or more additional therapeutic agents, for example, and without limitation, administration of the antibody within seconds, minutes, or hours of the administration of one or more additional therapeutic agents. In certain non-limiting embodiments, for example, a unit dose of an antibody disclosed herein is administered first, followed within seconds or minutes by administration of a unit dose of one or more additional therapeutic agents. In certain non-limiting embodiments, a unit dose of one or more additional therapeutic agents is administered first, followed by administration of a unit dose of an antibody within seconds or minutes. In certain embodiments, a unit dose of an antibody disclosed herein is administered first, followed, after a period of hours (e.g., 1-12 hours), by administration of a unit dose of one or more additional therapeutic agents. In certain embodiments, a unit dose of one or more additional therapeutic agents is administered first, followed, after a period of hours (e.g., 1-12 hours), by administration of a unit dose of the antibody.

The combined administration may be co-administration, using separate pharmaceutical compositions or a single pharmaceutical composition, or consecutive administration in either order, wherein there is optionally a time period while both (or all) therapeutic agents simultaneously exert their biological activities. Such combined therapy may result in a synergistic therapeutic effect. In certain embodiments, it is desirable to combine administration of an antibody of the invention with another antibody directed against another *Plasmodium falciparum* antigen, or against a different CSP target epitope.

CSP has multiple domains and regions that include the N-terminal domain, the immunogenic central NANP repeat region, and the C-terminal (ctCSP) domain or α-thrombospondin repeat (αTSR) domain. Between the N-terminal domain and the central repeat region is the junctional region that contains an NPDP sequence and a minor repeat region that contains three NVDP motifs that are both related to the dominant NANP motif (Pholcharee, T. et al., J. Mol. Bio. 432: 1048-1063 (2020). In certain embodiments, an antibody disclosed herein is co-administered with an antibody that binds to ctCSP. In certain embodiments, an antibody disclosed herein is co-administered with an antibody that binds to the alpha epitope (α-ctCSP) domain of ctCSP. The α-ctCSP consists of an α-helix that includes the T-cell epitope Th2R (region III), and the CS flap, which contains another T-cell epitope Th3R (Beutler N, PLoS Pathog 18(3): e1010409 (2022), FIG. 2, incorporated by reference herein). In certain embodiments, an antibody disclosed herein is co-administered with an antibody that binds to the beta epitope (β-ctCSP) domain of ctCSP (Beutler N, PLoS Pathog 18(3):e1010409 (2022), FIG. 2).

In certain embodiments, the antibody can be administered by gene therapy via a nucleic acid comprising one or more polynucleotides encoding the antibody. In certain embodiments, the polynucleotide encodes an scFv. In certain embodiments, the polynucleotide comprises DNA, cDNA or RNA. In certain embodiments, the polynucleotide is present in a vector, e.g., a viral vector.

Exemplary Embodiments of the Presently Disclosed Subject Matter

The present disclosure provides to antibodies targeting *Plasmodium falciparum*. In certain non-limiting embodiments, the antibody is a recombinant anti-circumsporozoite (CSP) antibody. In certain embodiments, the recombinant antibody comprises a light chain variable region (VL) and a heavy chain variable region (VH), wherein the light chain variable region comprises a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 1, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO: 2, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO: 3; and the heavy chain variable region comprises a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 4, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO: 5, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO: 6.

In certain embodiments, the VL of the recombinant antibodies disclosed herein comprises the amino acid sequence set forth in SEQ ID NO: 163; the amino acid sequence set forth in SEQ ID NO: 23; the amino acid sequence set forth in SEQ ID NO: 33; the amino acid sequence set forth in SEQ ID NO: 43; the amino acid sequence set forth in SEQ ID NO: 53; the amino acid sequence set forth in SEQ ID NO: 63; the amino acid sequence set forth in SEQ ID NO: 73; the amino acid sequence set forth in SEQ ID NO: 83; the amino acid sequence set forth in SEQ ID NO: 93; the amino acid sequence set forth in SEQ ID NO: 103; the amino acid sequence set forth in SEQ ID NO: 113; the amino acid sequence set forth in SEQ ID NO: 123; the amino acid sequence set forth in SEQ ID NO: 133; the amino acid sequence set forth in SEQ ID NO: 143; the amino acid sequence set forth in SEQ ID NO: 153; or the amino acid sequence set forth in SEQ ID NO: 173. In certain embodiments, the VH of the recombinant antibodies disclosed herein comprises the amino acid sequence set forth in SEQ ID NO: 164; the amino acid sequence set forth in SEQ ID NO: 24; the amino acid sequence set forth in SEQ ID NO: 34; the amino acid sequence set forth in SEQ ID NO: 44; the amino acid sequence set forth in SEQ ID NO: 54; the amino acid sequence set forth in SEQ ID NO: 64; the amino acid sequence set forth in SEQ ID NO: 74; the amino acid sequence set forth in SEQ ID NO: 84; the amino acid sequence set forth in SEQ ID NO: 94; the amino acid sequence set forth in SEQ ID NO: 104; the amino acid sequence set forth in SEQ ID NO: 114; the amino acid sequence set forth in SEQ ID NO: 124; the amino acid sequence set forth in SEQ ID NO: 134; the amino acid sequence set forth in SEQ ID NO: 144; the amino acid sequence set forth in SEQ ID NO: 154; or the amino acid sequence set forth in SEQ ID NO: 174.

In certain embodiments of the recombinant antibodies disclosed herein, the VL comprises the amino acid sequence set forth in SEQ ID NO: 163, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 164; the VL comprises the amino acid sequence set forth in SEQ ID NO: 33, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 34; the VL comprises the amino acid sequence set forth in SEQ ID NO: 43, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 44; the VL comprises the amino acid sequence set forth in SEQ ID NO: 53, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 54; the VL comprises the amino acid sequence set forth in SEQ ID NO: 63, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 64; the VL comprises the amino acid sequence set forth in SEQ ID NO: 73, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 74; the VL comprises the amino acid sequence set forth in SEQ ID NO: 83, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 84; the VL comprises the amino acid sequence set forth in SEQ ID NO: 93, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 94; the VL comprises the amino acid sequence set forth in SEQ ID NO: 103, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 104; the VL comprises the amino acid sequence set forth in SEQ ID NO: 113, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 114; the VL comprises the amino acid sequence set forth in SEQ ID NO: 123, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 124; the VL comprises the amino acid sequence set forth in SEQ ID NO: 133, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 134; the VL comprises the amino acid sequence set forth in SEQ ID NO: 143, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 144; the VL comprises the amino acid sequence set forth in SEQ ID NO: 153, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 154; or the VL comprises the amino acid sequence set forth in SEQ ID NO: 173, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 174. In certain embodiments of the recombinant antibodies disclosed herein, the VL comprises the amino acid sequence set forth in SEQ ID NO: 63, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 64. In certain embodiments of the recombinant antibodies disclosed herein, the VL comprises the amino acid sequence set forth in SEQ ID NO: 133, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 134. In certain embodiments of the recombinant antibodies disclosed herein, the VL comprises the amino acid sequence set forth in SEQ ID NO: 163, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 164.

In certain embodiments, the recombinant antibodies disclosed herein comprise a light chain (LC) and a heavy chain (HC). In certain embodiments, the LC of the recombinant antibodies disclosed herein comprises the amino acid sequence set forth in SEQ ID NO: 27; the amino acid sequence set forth in SEQ ID NO: 37; the amino acid sequence set forth in SEQ ID NO: 47; the amino acid sequence set forth in SEQ ID NO: 57; the amino acid sequence set forth in SEQ ID NO: 67; the amino acid sequence set forth in SEQ ID NO: 77; the amino acid sequence set forth in SEQ ID NO: 87; the amino acid sequence set forth in SEQ ID NO: 97; the amino acid sequence set forth in SEQ ID NO: 107; the amino acid sequence set forth in SEQ ID NO: 117; the amino acid sequence set forth in SEQ ID NO: 127; the amino acid sequence set forth in SEQ ID NO: 137; the amino acid sequence set forth in SEQ ID NO: 147; the amino acid sequence set forth in SEQ ID NO: 157; the amino acid sequence set forth in SEQ ID NO: 167; or the amino acid sequence set forth in SEQ ID NO: 177. In certain embodiments, the HC of the recombinant antibodies disclosed herein comprises the amino acid sequence set forth in SEQ ID NO: 28 or SEQ ID NO: 29; the amino acid sequence set forth in SEQ ID NO: 38 or SEQ ID NO: 39; the amino acid sequence set forth in SEQ ID NO: 48 or SEQ ID NO: 49; the amino acid sequence set forth in SEQ ID NO: 58 or SEQ ID NO: 59; the amino acid sequence set forth in SEQ ID NO: 68 or SEQ ID NO: 69; the amino acid sequence set forth in SEQ ID NO: 78 or SEQ ID NO: 79; the amino acid sequence set forth in SEQ ID NO: 88 or SEQ ID NO: 89; the amino acid sequence set forth in SEQ ID NO: 98 or SEQ ID NO: 99; the amino acid sequence set forth in SEQ ID NO: 108 or SEQ ID NO: 109; the amino acid sequence set forth in SEQ ID NO: 118 or SEQ ID NO: 119; the amino acid sequence set forth in SEQ ID NO: 128 or SEQ ID NO: 129; the amino acid sequence set forth in SEQ ID NO: 138 or SEQ ID NO: 139; the amino acid sequence set forth in SEQ ID NO: 148 or SEQ ID NO: 149; the amino acid sequence set forth in SEQ ID NO: 158 or SEQ ID NO: 159; the amino acid sequence set forth in SEQ ID NO: 168 or SEQ ID NO: 169; or the amino acid sequence set forth in SEQ ID NO: 178 or SEQ ID NO: 179.

In certain embodiments of the recombinant antibodies disclosed herein, the LC comprises the amino acid sequence set forth in SEQ ID NO: 27, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 28 or SEQ ID NO: 29; the LC comprises the amino acid sequence set forth in SEQ ID NO: 37, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 38 or SEQ ID NO: 39; the LC comprises the amino acid sequence set forth in SEQ ID NO: 47, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 48 or SEQ ID NO: 49; the LC comprises the amino acid sequence set forth in SEQ ID NO: 57, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 58 or SEQ ID NO: 59; the LC comprises the amino acid sequence set forth in SEQ ID NO: 67, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 68 or SEQ ID NO: 69; the LC comprises the amino acid sequence set forth in SEQ ID NO: 77, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 78 or SEQ ID NO: 79; the LC comprises the amino acid sequence set forth in SEQ ID NO: 87, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 88 or SEQ ID NO: 89; the LC comprises the amino acid sequence set forth in SEQ ID NO: 97, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 98 or SEQ ID NO: 99; the LC comprises the amino acid sequence set forth in SEQ ID NO: 107, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 108 or SEQ ID NO: 109; the LC comprises the amino acid sequence set forth in SEQ ID NO: 117, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 118 or SEQ ID NO: 119; the LC comprises the amino acid sequence set forth in SEQ ID NO: 127, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 128 or SEQ ID NO: 129; the LC comprises the amino acid sequence set forth in SEQ ID NO: 137, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 138 or SEQ ID NO: 139; the LC comprises the amino acid sequence set forth in SEQ ID NO: 147, and the HC comprises the amino acid sequence set forth in SEQ ID NO:

148 or SEQ ID NO: 149; the LC comprises the amino acid sequence set forth in SEQ ID NO: 157, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 158 or SEQ ID NO: 159; the LC comprises the amino acid sequence set forth in SEQ ID NO: 167, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 168 or SEQ ID NO: 169; or the LC comprises the amino acid sequence set forth in SEQ ID NO: 177, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 178 or SEQ ID NO: 179. In certain embodiments of the recombinant antibodies disclosed herein, the LC comprises the amino acid sequence set forth in SEQ ID NO: 67, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 69. In certain embodiments, the LC comprises the amino acid sequence set forth in SEQ ID NO: 137, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 139. In certain embodiments, the LC comprises the amino acid sequence set forth in SEQ ID NO: 167, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 169.

In certain embodiments, the VL of the recombinant antibodies disclosed herein comprises the amino acid sequence set forth in SEQ ID NO: 13. In certain embodiments of the recombinant antibodies disclosed herein, the VL comprises at least one amino acid substitution. In certain embodiments of the recombinant antibodies disclosed herein, the at least one amino acid substitution is at position 1 and/or at position 44. In certain embodiments of the recombinant antibodies disclosed herein, the amino acid substitution at position 1 is E1Q. In certain embodiments of the recombinant antibodies disclosed herein, the amino acid substitution at position 44 is R44T.

In certain embodiments, the VH of the recombinant antibodies disclosed herein comprises the amino acid sequence set forth in SEQ ID NO: 14. In certain embodiments of the recombinant antibodies disclosed herein, the VH comprises at least one amino acid substitution. In certain embodiments of the recombinant antibodies disclosed herein, the at least one amino acid substitution is at position 21, position 23, position 88, position 98, or a combination thereof. In certain embodiments of the recombinant antibodies disclosed herein, the amino acid substitution at position 1 is E1Q. In certain embodiments of the recombinant antibodies disclosed herein, the amino acid substitution at position 44 is R44T. In certain embodiments of the recombinant antibodies disclosed herein, the amino acid substitution at position 21 is P21S. In certain embodiments of the recombinant antibodies disclosed herein, the amino acid substitution at position 23 is T23A. In certain embodiments of the recombinant antibodies disclosed herein, the amino acid substitution at position 80 is I80T. In certain embodiments, the amino acid substitution at position 90 is T90A.

In certain embodiments, the HC of the recombinant antibodies disclosed herein comprises the amino acid sequence set forth in SEQ ID NO: 18. In certain embodiments of the recombinant antibodies disclosed herein, the HC comprises at least one amino acid substitution. In certain embodiments of the recombinant antibodies disclosed herein, the at least one amino acid substitution is at position 438 and/or or at position 444. In certain embodiments, the amino acid substitution at position 438 is M438L. In certain embodiments of the recombinant antibodies disclosed herein, the amino acid substitution at position 444 is N444S.

In certain non-limiting embodiments, the present disclosure provides a recombinant anti-circumsporozoite (CSP) antibody comprising a light chain variable region (VL) and a heavy chain variable region (VH), wherein the VL comprises the amino acid sequence set forth in SEQ ID NO: 63 and the VH comprises the amino acid sequence set forth in SEQ ID NO: 64. In certain embodiments, the recombinant antibody comprises a light chain (LC) and a heavy chain (HC), wherein the LC comprises the amino acid sequence set forth in SEQ ID NO: 67 and the HC comprises the amino acid sequence set forth in SEQ ID NO: 69.

In certain non-limiting embodiments, the present disclosure further provides a recombinant anti-circumsporozoite (CSP) antibody comprising a light chain variable region (VL) and a heavy chain variable region (VH), wherein the VL comprises the amino acid sequence set forth in SEQ ID NO: 133 and the VH comprises the amino acid sequence set forth in SEQ ID NO: 134. In certain embodiments, the recombinant antibody comprises a light chain (LC) and a heavy chain (HC), wherein the LC comprises the amino acid sequence set forth in SEQ ID NO: 137 and the HC comprises the amino acid sequence set forth in SEQ ID NO: 139.

In certain non-limiting embodiments, the present disclosure also provides a recombinant anti-circumsporozoite (CSP) antibody comprising a light chain variable region (VL) and a heavy chain variable region (VH), wherein the VL comprises the amino acid sequence set forth in SEQ ID NO: 163 and the VH comprises the amino acid sequence set forth in SEQ ID NO: 164. In certain embodiments, the recombinant antibody comprises a light chain (LC) and a heavy chain (HC), wherein the LC comprises the amino acid sequence set forth in SEQ ID NO: 167 and the HC comprises the amino acid sequence set forth in SEQ ID NO: 169.

In certain non-limiting embodiments, the present disclosure provides a recombinant anti-circumsporozoite (CSP) antibody comprising a light chain variable region (VL) and a heavy chain variable region (VH), wherein the light chain variable region comprises a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 183, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO: 184, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO: 185; and the heavy chain variable region comprises a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 186, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO: 187, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO: 188. In certain embodiments, the VL comprises the amino acid sequence set forth in SEQ ID NO: 195, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 196. In certain embodiments, the recombinant antibody comprises comprising a LC and a HC. In certain embodiments of the recombinant antibodies disclosed herein, the LC comprises the amino acid sequence set forth in SEQ ID NO: 199, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 200 or SEQ ID NO: 201.

In certain non-limiting embodiments, the present disclosure provides a recombinant anti-circumsporozoite (CSP) antibody comprising a light chain variable region (VL) and a heavy chain variable region (VH), wherein the light chain variable region comprises a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 205, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO: 206, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO: 207; and the heavy chain variable region comprises a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 208, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO: 209, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO: 210.

In certain embodiments, the VL of the recombinant antibodies disclosed herein comprises the amino acid sequence set forth in SEQ ID NO: 227; the amino acid sequence set forth in SEQ ID NO: 237; the amino acid sequence set forth in SEQ ID NO: 247; the amino acid sequence set forth in SEQ ID NO: 257; or the amino acid sequence set forth in SEQ ID NO: 267. In certain embodiments, the VH of the recombinant antibodies disclosed herein comprises the amino acid sequence set forth in SEQ ID NO: 228; the amino acid sequence set forth in SEQ ID NO: 238; the amino acid sequence set forth in SEQ ID NO: 248; the amino acid sequence set forth in SEQ ID NO: 258; or the amino acid sequence set forth in SEQ ID NO: 268. In certain embodiments of the recombinant antibodies disclosed herein, the VL comprises the amino acid sequence set forth in SEQ ID NO: 227, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 228; the VL comprises the amino acid sequence set forth in SEQ ID NO: 237, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 238; the VL comprises the amino acid sequence set forth in SEQ ID NO: 247, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 248; the VL comprises the amino acid sequence set forth in SEQ ID NO: 257, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 258; or the VL comprises the amino acid sequence set forth in SEQ ID NO: 267, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 268.

In certain embodiments, the recombinant antibodies disclosed herein comprise a LC and a HC. In certain embodiments, the LC of the recombinant antibodies disclosed herein comprises the amino acid sequence set forth in SEQ ID NO: 231; the amino acid sequence set forth in SEQ ID NO: 241; the amino acid sequence set forth in SEQ ID NO: 251; the amino acid sequence set forth in SEQ ID NO: 261; or the amino acid sequence set forth in SEQ ID NO: 271. In certain embodiments, the HC of the recombinant antibodies disclosed herein comprises the amino acid sequence set forth in SEQ ID NO: 232 or SEQ ID NO: 233; the amino acid sequence set forth in SEQ ID NO: 242 or SEQ ID NO: 243; the amino acid sequence set forth in SEQ ID NO: 252 or SEQ ID NO: 253; the amino acid sequence set forth in SEQ ID NO: 262 or SEQ ID NO: 263; or the amino acid sequence set forth in SEQ ID NO: 272 or SEQ ID NO: 273. In certain embodiments of the recombinant antibodies disclosed herein, the LC comprises the amino acid sequence set forth in SEQ ID NO: 231, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 232 or SEQ ID NO: 233; the LC comprises the amino acid sequence set forth in SEQ ID NO: 241, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 242 or SEQ ID NO: 243; the LC comprises the amino acid sequence set forth in SEQ ID NO: 251, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 252 or SEQ ID NO: 253; the LC comprises the amino acid sequence set forth in SEQ ID NO: 261, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 262 or SEQ ID NO: 263; or the LC comprises the amino acid sequence set forth in SEQ ID NO: 271, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 272 or SEQ ID NO: 273.

In certain embodiments, the VH of the recombinant antibodies disclosed herein comprises the amino acid sequence set forth in SEQ ID NO: 218. In certain embodiments of the recombinant antibodies disclosed herein, the VH comprises at least one amino acid substitution. In certain embodiments of the recombinant antibodies disclosed herein, the at least one amino acid substitution is at position 40, position 69, position 80, position 85, position 120, or a combination thereof. In certain embodiments of the recombinant antibodies disclosed herein, the amino acid substitution at position 40 is T40A. In certain embodiments of the recombinant antibodies disclosed herein, the amino acid substitution at position 69 is I69T. In certain embodiments of the recombinant antibodies disclosed herein, the amino acid substitution at position 80 is S80Y. In certain embodiments of the recombinant antibodies disclosed herein, the amino acid substitution at position 85 is G85S. In certain embodiments of the recombinant antibodies disclosed herein, the amino acid substitution at position 120 is 1120T. In certain embodiment of the recombinant antibodies disclosed herein s, the HC comprises the amino acid sequence set forth in SEQ ID NO: 222. In certain embodiments of the recombinant antibodies disclosed herein, the HC comprises at least one amino acid substitution. In certain embodiments of the recombinant antibodies disclosed herein, the at least one amino acid substitution is at position 434 and/or at position 440. In certain embodiments of the recombinant antibodies disclosed herein, the amino acid substitution at position 434 is M434L. In certain embodiments of the recombinant antibodies disclosed herein, the amino acid substitution at position 440 is N440S.

In certain embodiments, the recombinant antibodies disclosed herein exhibit at least 20% reduction in parasite liver load as compared to a reference antibody. In certain embodiments, the recombinant antibodies disclosed herein exhibit at least 20% increase in survival rate as compared to a reference antibody. In certain embodiments, the recombinant antibodies disclosed herein exhibit increased conformational stability as compared to a reference antibody. In certain embodiments, the recombinant antibodies disclosed herein exhibit increased colloidal stability as compared to a reference antibody. In certain embodiments, the reference antibody is AB-000317. In certain embodiments, the reference antibody is AB-000224. In certain embodiments, the reference antibody is AB-007088.

In certain embodiments, the recombinant antibodies disclosed herein binds to a NANP repeat region. In certain embodiments, the recombinant antibodies disclosed herein binds to a polypeptide comprising or consisting of the amino acid sequence set forth in SEQ ID NO: 280.

In certain embodiments, the recombinant antibodies disclosed herein comprise at least one modification relative to the native AB-000224 variable heavy chain amino acid sequence set forth in SEQ ID NO: 14. In certain embodiments, the recombinant antibodies disclosed herein comprise at least one modification relative to the native AB-000224 variable light chain amino acid sequence set forth in SEQ ID NO: 13. In certain embodiments, the recombinant antibodies disclosed herein comprise at least one modification relative to the native AB-000224 variable heavy chain amino acid sequence set forth in SEQ ID NO: 14 and at least one modification relative to the native AB-000224 variable light chain amino acid sequence set forth in SEQ ID NO: 13.

In certain embodiments, the recombinant antibodies disclosed herein comprise at least one modification relative to the native AB-007088 variable heavy chain amino acid sequence set forth in SEQ ID NO: 218. In certain embodiments, the recombinant antibodies disclosed herein comprise at least one modification relative to the native AB-007088 variable light chain amino acid sequence set forth in SEQ ID NO: 217. In certain embodiments, the recombinant antibodies disclosed herein comprise at least one modification relative to the native AB-007088 variable heavy chain amino acid sequence set forth in SEQ ID NO:

218 and at least one modification relative to the native AB-000224 variable light chain amino acid sequence set forth in SEQ ID NO: 217. In certain non-limiting embodiments, the present disclosure provides a polynucleotide encoding a recombinant antibody disclosed herein. In certain non-limiting embodiments, the present disclosure provides an expression vector comprising the polynucleotide disclosed herein. In certain non-limiting embodiments, the present disclosure provides a host cell comprising the expression vector or the polynucleotide disclosed herein.

In certain non-limiting embodiments, the present disclosure provides a composition comprising the recombinant antibody disclosed herein. In certain embodiments, the composition further comprises a pharmaceutically acceptable carrier.

In certain non-limiting embodiments, the present disclosure provides a method of preventing and/or treating malaria in a subject in need thereof, comprising administering an effective amount of the recombinant antibody disclosed herein or of the composition disclosed herein. In certain embodiments, the subject is a pediatric patient.

In certain non-limiting embodiments, the present disclosure provides the recombinant antibodies or compositions disclosed herein for use in the prevention and/or treatment and/or prevention of malaria in a subject in need thereof. Additionally, in certain non-limiting embodiments, the present disclosure provides the recombinant antibodies or compositions disclosed herein for the manufacture of a medicament for the prevention and/or treatment and/or prevention of malaria in a subject in need thereof. Furthermore, the present disclosure provides use of the recombinant antibodies or compositions disclosed herein for the prevention and/or treatment and/or prevention of malaria in a subject in need thereof. In certain embodiments, the subject is a pediatric patient.

From the foregoing description, it will be apparent that variations and modifications may be made to the presently disclosed subject matter to adopt it to various usages and conditions. Such embodiments are also within the scope of the following claims.

The recitation of a listing of elements in any definition of a variable herein includes definitions of that variable as any single element or combination (or sub-combination) of listed elements. The recitation of an embodiment herein includes that embodiment as any single embodiment or in combination with any other embodiments or portions thereof.

All patents and publications mentioned in this specification are herein incorporated by reference to the same extent as if each independent patent and publication was specifically and individually indicated to be incorporated by reference.

All of the features disclosed in this specification may be combined in any combination. Each feature disclosed in this specification may be replaced by an alternative feature serving the same, equivalent, or similar purpose. Thus, unless expressly stated otherwise, each feature disclosed is only an example of a generic series of equivalent or similar features.

The foregoing written description is considered to be sufficient to enable one skilled in the art to practice the methods and/or obtain the compositions described herein. The following examples and detailed description are offered by way of illustration and not by way of limitation.

EXAMPLES

The Examples are offered for illustrative purposes only, and are not intended to limit the scope of the present invention in any way. Indeed, various modifications in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and fall within the scope of the appended claims.

It is understood that various other embodiments may be practiced, given the general description provided above.

Example 1. Identification of Functionally Active Anti-CSP Antibodies

AB-000224 and AB-007088 were discovered in antibody repertoires generated by Immune Repertoire Capture® (IRC®) technology from plasmablast B cells isolated from two donors enrolled in a Phase 2a study evaluating the efficacy of the RTS,S vaccine in preventing malaria infection. The IRC® technology and its use in antibody discovery is well known and disclosed in, e.g., WO 2012148497A2, the entire content of which is herein incorporated by reference. The RTS,S vaccine is a pseudo-viral particle vaccine that combines the hepatitis B surface antigen and the central repeat and C-terminal regions of the CSP protein. RTS,S consists of two polypeptides; RTS is a single polypeptide chain corresponding to amino acids 207 to 395 of *P. falciparum* (3D7) that is fused to HBsAg and S is a polypeptide of 226 amino acids that corresponds to HBsAg. Stoute, et. al., N Engl J Med; 336:86-91(1997); RTS,S Clinical Trials Partnership, PLoS Med. 11(7):e1001685, (2014), WO1993/10152. The RTS,S vaccine was administered with the adjuvant AS01B to increase efficacy. AS01B is a liposome-based formulation that contains the immunostimulants monophosphoryl lipid A (MPL) and QS21 and was shown to be more immunogenic than another adjuvant, AS02A, used in initial studies. Kester, et al., J Infect Dis 200: 337-346 (2009). All study participants were vaccinated with one of two vaccine schedules (standard full-dose: 0, 1, 2 M or fractional-third dose: 0, 1, 7 M), or placebo and subsequently challenged with a controlled human malaria parasite infection. The donors from whom AB-000224 and AB-007088 were identified and protected following challenge. Heavy and light chain AB-000224 sequences were expressed as a human IgG1 monoclonal antibody. Heavy and light chain AB-007088 sequences were expressed as a human IgG1 monoclonal antibody. Compared to other antibodies obtained from the same or different donors, AB-000224 and AB-007088 demonstrated strong binding and affinity to CSP protein in vitro, no binding to Hepatitis B protein, and exceptional functional activity when tested in vivo.

The present example provides the design of improved variants of AB-000224 or AB-007088. In certain embodiments, the variants generated have improved developability, e.g., as identified through various in vitro assays, such as aggregation assessment by HPLC or UPLC, hydrophobic interaction chromatography (HIC), polyspecificity assays (e.g., baculovirus particle binding), self-interaction nanoparticle spectroscopy (SINS), or mass spec analysis after incubation in an accelerated degradation condition such as high temperature, low pH, high pH, or oxidative H_2O_2. Mutations are successful if the activity is maintained (or enhanced) while removing or reducing the severity of the liability.

Example 2. Generation of Anti-CSP Antibody Variants

Assessment of AB-000224

In vivo generated antibodies undergo genomic recombination followed by somatic hypermutation. Germline information was obtained from the AB-000224 antibody and used for the optimization of variant design. FIGS. **4**A and **4**B show the alignment of the AB-0002224 to the putative V and J germlines genes. CDRs, germline deviations, and potential liabilities were identified. N-linked glycosylation sites, non-typical cysteine residues, and other potential liability motifs were identified across the VH and VL.

The close siblings to AB-000224 are AB-007110, AB-007111, and AB-007112. These were evaluated at the sequence and structure level to find any possible beneficial modifications to AB-000224. AB-007110 in particular has been shown in biophysical characterization to have improved thermal stability over AB-000224. The positions evaluated below differ from AB-000224 and are either consistent amongst the siblings or of structural interest.

Design of Variants of AB-000224

Framework and complementary-determining region (CDR) germline deviations in AB-000224 were analyzed for their potential to be mutated, individually or in combination, to germline sequence, without negatively impacting binding to the (NANP)3 region of the CSP protein or potency. For each of the candidate mutations from AB-000224 sequence to germline sequence, the risk of making the mutation was assessed based on: (1) the change in charge, if any, since change in charge is intrinsically risky, and a change to more positive charge is particularly risky given the already net positive charge of AB-000224 Fv; (2) conservation of the native AB-000224 residue in the lineage versus the presence of the germline residue or other mutations at that position in the lineage and (3) the structural location of the position with respect to the NANP motif. Some mutations were noted to be coupled to at least one other mutation, meaning that the risk prediction is based on making the mutation in conjunction with the other mutation(s). Proposed AB-000224 Residue Modifications according to the ASN numbering system are shown in Table 31 below:

TABLE 31

Site	Mutation	Design Group
LmdV:E1	Q	Standard
LmdV:R50	T	Standard
LmdV:N135	NS	Siblings
HV:P22	S	Standard
HV:T24	TA	Standard
HV:H69	HK	Siblings
HV:R75	RK	Siblings
HV:D84	DN	Do not repair
HV:I88	IT	Standard
HV:T98	TA	Standard
HV:F105	FY	Do not repair
HV:T107	TA	Standard

Mutations were built by grouping the "Standard" Design Group in all combinations. This results in 16 variants. Add a single variant using the "Sibling" Design Group with all three sites together. This totals 17 variants. Adding the parent results in 18 antibodies required for production. Mutation site positions in the AB-000224 variants according to the ASN numbering system are specified in the table below:

TABLE 32

Variant	LC-LmdV: E1	LC-LmdV: R50	LC-LmdV: N135	HV: P22	HV: T24	HV: H69	HV: R75	HV: I88	HV: T98	HV: T107
AB-000224_LS										
AB-000224.001	Q	T		S						
AB-000224.002	Q	T		S	A					
AB-000224.003	Q	T		S				T		
AB-000224.004	Q	T		S					A	
AB-000224.005	Q	T		S						A
AB-000224.006	Q	T		S	A			T		
AB-000224.007	Q	T		S	A				A	
AB-000224.008	Q	T		S	A					A
AB-000224.009	Q	T		S				T	A	
AB-000224.010	Q	T		S				T		A
AB-000224.011	Q	T		S					A	A
AB-000224.012	Q	T		S	A			T	A	
AB-000224.013	Q	T		S	A			T		A
AB-000224.014	Q	T		S	A				A	A
AB-000224.015	Q	T		S				T	A	A
AB-000224.016	Q	T		S	A			T	A	A
AB-000224.017			D			K	K			

Assessment of AB-007088

Germline information was obtained from the AB-007088 antibody and used for the optimization of variant design. FIGS. **5**A and **5**B show the alignment of the AB-0070884 to the putative V and J germlines genes. CDRs, germline deviations, and potential liabilities were identified. N-linked glycosylation sites, non-typical cysteine residues, and other potential liability motifs were identified across the VH and VL.

Design of Variants of AB-007088

Framework and complementary-determining region (CDR) germline deviations in AB-007088 were analyzed for their potential to be mutated, individually or in combination, to germline sequence, without negatively impacting binding to the (NANP)3 region of the CSP protein or potency. For each of the candidate mutations from AB-007088 sequence to germline sequence, the risk of making the mutation was assessed based on: (1) the change in charge, if any, since change in charge is intrinsically risky, and a change to more positive charge is particularly risky given the already net positive charge of AB-007088 Fv; (2) conservation of the native AB-007088 residue in the lineage versus the presence of the germline residue or other mutations at that position in the lineage and (3) the structural location of the position with respect to the NANP motif. Some mutations were noted to be coupled to at least one other mutation, meaning that the risk prediction is based on making the mutation in conjunction with the other mutation(s). Proposed AB-007088 Residue Modifications according to the ASN numbering system are shown in Table 33 below:

TABLE 33

Site	Mutation	Design Group
HV:A30	AT	Group 1
HV:T47	A	Group 1
HV:I79	IT	Group 1
HV:S90	SY	Group 2
HV:G95	S	Group 1
HV:I146	T	Group 1

Mutations were built by grouping the "Group 1" Design Group in all combinations. This resulted in 4 variants. By adding a single variant using HV:S90Y to the design with all mutations, a total of five designs were obtained. Mutation site positions in the AB-007088 variants according to the ASN numbering system are specified in the table below:

TABLE 34

Variant	HV: A30	HV: T47	HV: I79	HV: S90	HV: G95	HV: I146
AB-007088_LS						
AB-007088.001		A			S	T
AB-007088.002	T	A			S	T
AB-007088.003		A	T		S	T
AB-007088.004	T	A	T		S	T
AB-007088.005	T	A	T	Y	S	T

Example 3. Binding Assays

AB-000224 and AB-007088 were evaluated for binding to the complete CSP protein and a series of linear peptides representing the immunodominant NANP repeat region. Two assay platforms, bio-layer interferometry (BLI) and surface plasmon resonance (SPR), were used to quantify antibody-target binding strength. Five binding targets were evaluated in the SPR assay and six targets were evaluated in the BLI platform and described in Table 35 below:

TABLE 35

Target Name	Peptide Sequence	Used in BLI, SPR, or both assays
(NANP)6	NANPNANPNANPNANPNANPNANP (SEQ ID NO: 279)	Both
(NPNA)3	NPNANPNANPNA (SEQ ID NO: 280)	Both
(NVDP)3 (NANP)2	NVDPNANPNVDPNANPNVDP (SEQ ID NO: 281)	Both
NANPNV DPNANP	NPDPNANPNVDPNANP (SEQ ID NO: 282)	Both
NANPNV DP	DPNANPNVDPNA (SEQ ID NO: 283)	BLI only
N-Interface	KQPADGNPDPNANPN (SEQ ID NO: 284)	BLI only
CSP Protein	MMRKLAILSVSSFLFVEALFQEYQCYGSSSNTRVLNELNYDNAGINLYNELEMNYYGKQENWYSLKKNSRSLGENDDGNNNNGDNGREGKDEDKRDGNNEDNEKLRKPKHKKLKQPGDGNPDPNANPNVDPNANPNVDPNANPNVDPNANPNANPNANPNANPNANPNANPNANPNANPNANPNANPNANPNANPNANPNANPNANPNANPNANPNANPNANPNANPNANPNANPNANPNANPNANPNANPNANPNANPNANPNANPNANPNANPNANPNANPNANPNANPNKNNQGNGQGHNMPNDPNRNVDENANANNAVKNNNNEEPSDKHIEQYLKKIQNSLSTEWSPCSVTCGNGIQVRIKPGSANKPKDELDYENDIEKKICKMEKCSSVFNVVNSSIGLIMVLSFLFLN (SEQ ID NO: 285)	SPR only

For BLI, each of the targets specified in Table 35 was biotinylated and immobilized to streptavidin sensors. Each antibody was evaluated in duplicate at 5 μg/mL. If the variation between the two duplicates was >3-fold, the antibody-target measurement was repeated.

For SPR, each antibody was either directly coupled to a Carterra Chip or coupled using a goat anti-human Fc antibody. The uncoupled antibodies were washed off and various concentration gradients of the targets were flowed over the antibodies, where the highest concentration of each target was in the range 0.5-8 μg/mL. Each antibody was immobilized in two different locations on the chip to allow for duplicate measurements. The affinity for each antibody-target combination was determined using 4-5 target concentrations in Mathematica software. If the variation between the two duplicates was >3-fold, the antibody-target measurement was repeated.

While the data generated by the BLI and SPR assays are similar, the assays were designed with opposite orientations of the target and antibody. Specifically, the target was immobilized while the antibody flowed over it in the BLI assay, while the SPR assay was designed so that the antibody was immobilized and the target flowed over it. Given these orientations, an antibody, when evaluated in the BLI assay, would be more likely to engage in binding interactions that involve multiple target molecules. As such, the binding of antibodies to targets in the BLI assay may exhibit more similarities to binding the complete CSP protein, which coats the surface of the malaria sporozoite. In contrast, the activity measured in the SPR assay would more accurately represent an interaction between an antibody F(ab) and a single target molecule. The data generated for the antibodies AB-000224 and AB-007088 are summarized in Table 36 below:

TABLE 36

Antibody ID	AB-000224	AB-007088
NANP6 K_{ON} BLI	5.44	5.22
NANP6 K_{OFF} BLI	−4.75	−4.32
NANP6 K_D BLI	−10.19	−9.55
NANP6 K_{ON} SPR	5.01	5.52
NANP6 K_{OFF} SPR	−5.00	−4.14
NANP6 K_D SPR	−10.00	−9.63
NPNA3 K_{ON} BLI	5.35	5.23
NPNA3 K_{OFF} BLI	−4.32	−6.00
NPNA3 K_D BLI	−9.67	−11.23
NPNA3 K_{ON} SPR	4.87	5.08
NPNA3 K_{OFF} SPR	−3.47	−3.25
NPNA3 K_D SPR	−8.34	−8.33
NVDP3NANP2 K_{ON} BLI	5.53	4.94
NVDP3NANP2 K_{OFF} BLI	−5.12	−6.00
NVDP3NANP2 K_D BLI	−10.65	−10.94
NVDP3NANP2 K_{ON} SPR	4.81	4.29
NVDP3NANP2 K_{OFF} SPR	−4.02	−4.40
NVDP3NANP2 K_D SPR	−8.77	−8.71
NANPNVDPNANP K_{ON} BLI	5.59	5.03
NANPNVDPNANP K_{OFF} BLI	−2.68	−6.00
NANPNVDPNANP K_D BLI	−8.27	−11.03
NANPNVDPNANP K_{ON} SPR	4.08	<LLOQ
NANPNVDPNANP K_{OFF} SPR	−1.77	<LLOQ
NANPNVDPNANP K_D SPR	−5.85	<LLOQ
NANPNVDP K_{ON} BLI	<LLOQ	4.89
NANPNVDP K_{OFF} BLI	<LLOQ	−6.00
NANPNVDP K_D BLI	<LLOQ	−10.89
NVDPNANP K_{ON} BLI	5.35	5.02
NVDPNANP K_{OFF} BLI	−4.50	−6.00
NVDPNANP K_D BLI	−9.85	−11.02
N-Interface K_{ON} BLI	6.42	5.13
N-Interface K_{OFF} BLI	−1.92	−6.00
N-Interface K_D BLI	−8.34	−11.13
N-Interface K_{ON} SPR	<LLOQ	4.17
N-Interface K_{OFF} SPR	<LLOQ	−2.42
N-Interface K_D SPR	<LLOQ	−6.60
CSP K_{ON} SPR	5.47	5.08
CSP K_{OFF} SPR	−5.00	−4.59
CSP K_D SPR	−10.44	−9.67

Summary of AB-000224 Antibody Variants

Seventeen (17) variants (AB-000224.001, AB-000224.002, AB-000224.003, AB-000224.004, AB-000224.005, AB-000224.006, AB-000224.007, AB-000224.008, AB-000224.009, AB-000224.010, AB-000224.011, AB-000224.012, AB-000224.013, AB-000224.014, AB-000224.015, AB-000224.016, AB-000224.017)) were designed to germline antibodies by mutating residues in either the framework regions or CDRs to reduce the risk of antibody-directed immunogenicity.

Summary of AB-007088 Antibody Variants

Five (5) variants (AB-007088.001, AB-007088.002, AB-007088.003, AB-007088.004, AB-007088.005) were designed to germline antibodies by mutating residues in either the framework regions or CDRs to reduce the risk of antibody-directed immunogenicity.

Example 4. In Vivo Performance of the Antibodies

Liver Burden Assay

AB-000224 and AB-007088 and variants thereof (with those in format comprising Heavy Chain version 2 indicated with the "LS") were evaluated for in vivo activity in a mouse malaria liver burden assay, as described in Flores-Garcia Y, et al. Malar J. 2019; 18(1):426, doi:10.1186/s12936-019-3055-9. Experimental antibodies were compared to both positive (AB-000317) and negative (AB-001245) antibody controls. AB-000317 is an anti-CSP antibody described in WO2020/172220. AB-001245 is non-CSP isotype control.

For each antibody, five C57B1/6 mice per experimental or control arm were administered 100 of antibody 16 hours prior to intravenous infection with fluorescent chimeric *P. berghei* sporozoites expressing *P. falciparum* CSP protein. Forty-two (42) hours following parasite challenge, the sporozoite liver load was quantified by bioluminescence. For each experimental mouse, the percent liver burden was calculated by subtracting the average background luminescence measured from two untreated, naive mice and calculating the percent reduction as compared to the average luminescence measured in five untreated, infected mice. The average percent reduction was reported for each of the experimental antibody groups.

Mice administered AB-000224, AB-007088 or positive control antibody AB-000317 all exhibited a similar reduction in liver burden load as compared to naïve infected mice and mice treated with the negative control, AB-001245 (FIG. **1**A). The level of experimental and control human antibodies circulating in the mice at the time of infection was quantified via an ELISA assay (FIG. **1**B) and was similar between the experimental and control antibodies.

Variants of AB-000224 and AB-007088 drove reduction in liver burden load in treated mice that was comparable to the respective parent antibody AB-000224 or AB-007088 and the positive control antibody AB-000317. Liver burden levels measured in animals administered either the variants, the parent molecules or positive control antibody AB-000317 was significantly lower than liver burden levels in either the naïve infected mice or mice treated with the negative control, AB-001245 (FIGS. **10**A-**10**F). Biological replicates of each antibody variant are shown in FIGS. **10**A-**10**F. The concentration of human antibodies that were circulating in the mice at the time of infection was determined by ELISA and is shown in FIGS. **10**G-**10**I.

Bite Parasitemia Assay

AB-000224 and AB-007088 and variants thereof were also evaluated for their ability to protect against infection (with those in format comprising Heavy Chain version 2 indicated with the "LS"). In this experiment, animals were exposed to mosquitoes infected with chimeric *P. berghei* expressing *P. falciparum* CSP protein, as described in Espinosa, D., et al. npj Vaccines 2017; 2, 10 (2017); Espinosa, D., et al. Infect Immun. 2013 August; 81(8): 2882-2887.

C57B1/6 Mice were administered 150 μg of antibody and 16 hours later were exposed to six or seven chimeric *P. berghei*-infected mosquitoes. At least 70%-80% of the mosquito population are infected with chimeric *P. berghei* expressing *P. falciparum* CSP protein, resulting in exposure to at least one infectious event. Each mouse was subsequently evaluated for blood stage parasitemia from days

4-10 following infection by microscopy. Parasitemia data were recorded as positive or negative and the data used to generate a survival curve. Experimental antibodies were compared to both the positive (AB-000317) and negative (AB-001245) controls.

Mice treated with AB-000224, AB-007088 or the positive control AB-000317 were less likely to develop parasitemia as compared to mice treated with the negative control AB-001245. (FIGS. **2**A and **2**C show AB-000224 experimental data and FIGS. **3**A and **3**C show AB-007088 experimental data). The level of human antibodies circulating in the mice at the time of infection was quantified via an ELISA assay (FIGS. **2**B and **3**B) and was similar between the experimental and control antibodies.

Finally, mice administered variants of AB-000224 or AB-007088 were comparably likely to remain parasite-free as mice treated with either of the parent antibodies, or the positive control antibody AB-000317 (FIGS. **11**A-**11**C). The concentration of human antibodies that were circulating in the mice at the time of infection was determined by ELISA and is shown in FIGS. **11**D-**11**F.

Example 5. Biophysical Characterization

The present example describes the biophysical hallmarks of the anti-CSP antibody variants. AB-000224 and AB-007088 and variants thereof (all in the format comprising Heavy Chain version 2) were evaluated for their conformational stability and colloidal stability. Several methods were used to analyze these endpoints and are summarized in the Tables 37 and 38 below:

TABLE 37

Conformational Stability Methods				
Method Name	Attribute Measured	Characterization	Desired Outcome	Values that indicate instability
Differential scanning fluorimetry (DSF)	Melting temperature	Lower Tm(app) is indicative of decreased conformational stability	Increase in Tm or formation of additional Tm's indicating increased domain stability	Weighted Shoulder Score (WSS) Below 20
Thermal hold	Temperature induced aggregation	Define conditions for precipitation relating to potential destabilization during room temperature incubation	Increase in thermal stability indicated by the absence of precipitation	Absorbance at 350 nm is above 0.5
Low pH Aggregation	Low pH stability by high molecular weight	Molecules with an increase in high molecule weight following neutralization after low pH exposure may show increased aggregation during low pH viral inactivation	No significant increase in high molecular weight species following low pH exposure and neutralization	More than 10% aggregation after low pH exposure
Chemical Unfolding	Conformational stability	Molecules with an increased inflection point may show lower rates of aggregation during storage and are more conformationally stable	Increased inflection point compared to the parent molecule	Less than 2.1M inflection point

TABLE 38

Colloidal Stability Methods				
Method Name	Attribute Measured	Characterization	Desired Outcome	Values that indicate instability
Self-interaction nanoparticle spectroscopy (SINS)	Protein-protein interaction	Define relative protein self-association to help identify potential for higher viscosity during concentration and problems with filterability	Decrease in parameters indicating self-association of the molecule	Wavelength Maximum Above 550 nm

TABLE 38-continued

Colloidal Stability Methods				
Method Name	Attribute Measured	Characterization	Desired Outcome	Values that indicate instability
Standup Monolayer Affinity Chromatography (Zenix Column)	Colloidal stability	Molecules with reduced retention times may show increase solubility and lower rates of aggregation during storage	Decreased main peak retention time compared to parent molecule	Longer retention times, there is no established values correlating to instability at this time
Relative Solubility Analysis (RSA)	Polyethylene glycol based solubility analysis	Molecules with higher relative solubility may show lower rates of aggregation during storage	Increased solubility compared to parent molecule	50% Loss of protein occurring less than 7% PEG
Polyreactivity	Non-specific binding	Molecules that have the potential to non-specifically bind to an array of different antigens can potentially have a higher clearance rate.	Decreased non-specific binding compared to the parent molecule	Absorbance at 405 nm is above 1.5-2.0

AB-000224 Variants Showed Improved Stability

AB-000224 and variants thereof showed comparable harvest yield and titer results. Thus, additional end-points were assessed. AB-000224 and variants thereof were evaluated for their thermal stability by differential scanning fluorimetry (DSF). Thermal unfolding was monitored by measuring the intensity of an extrinsic dye (sypro orange) as the sample was heated from 20° C. to 90° C. The data was reported as Tm1 and Tm2 with the first transition correlating with the CH2 domain and the 2nd transition correlating with the unfolding of the Fab and CH3 domain regions. Higher unfolding temperatures are desirable and have been linked with an increase in a product's conformational stability. Lack of a Tm2 is indicative of the Fab unfolding at the same or similar temperature to the CH2 domain, reported as Tm1. Additional information is also obtained from a proprietary parameter termed the weighted shoulder score which accounts for multiple pieces of information from the unfolding curve. Again, higher values are indicative of greater conformational stability. The DSF analysis was conducted in PBS buffer, with all samples being diluted down to a final antibody concentration of 0.15 mg/mL.

The propensity to aggregate at elevated temperatures was assessed using the thermal aggregation method. Samples were place in a 96 well Biorad PCR plate and heated to various temperatures for 5 minutes using a Biorad Thermal Cycler. After heating, protein precipitation was determined by reading the absorbance at 350 nm (A350) using a Spectrostar nano plate reader. Almost all AB-000224 variants showed higher WSS as compared to the parent antibody AB-000224, a T2 that approached 80° C., and no precipitation during thermal hold assays. However, AB-000224.017 did not have a T2 and showed precipitation during thermal hold assay.

Further, AB-000224 and variants thereof were also evaluated for their chemical stability. Sensitivity to low pH was assessed by titrating the samples to pH 3.3 using acetic acid, holding the samples for 30 minutes, neutralizing the samples to pH 5 with tris base, and measuring aggregation by size exclusion HPLC. Samples that were diluted with PBS using the same volume of acetic acid and tris base as used in the test samples were used as a control. AB-000224 and all variants thereof did not show low pH instability.

AB-000224 and variants thereof were tested for stability against chemical unfolding as assayed by denaturation with guanidine. Chemical unfolding curves were produced by exposing the antibodies to increasing concentrations of guanidine hydrochloride. After 24 hours, the intrinsic fluorescence of the samples is measured using a SUPR-UV plate reader. The collected raw data was then processed and the chemical unfolding curve and its inflection point calculated from the processed data as a function of denaturant condition. Antibodies with denaturation inflection points higher than 2.1 M guanidine are considered to be conformationally stable by this method. AB-000224 and all variants showed inflection points above 2 M guanidine (Gdn). Notably, AB-000224.005, AB-000224.008, AB-000224.010, AB-000224.011, AB-000224.013, and AB-000224.015 showed improved stability against chemical unfolding as compared to AB-000224, each having an inflection point above 2.3 M guanidine.

AB-000224 and variants thereof were also evaluated for their colloidal stability by self-interaction nanoparticle spectroscopy (SINS) which monitors protein-protein interactions by capture on the surface of a gold colloid and measuring shifts of the wavelength of maximum absorption. Maximum absorption values of wavelengths higher than 550 nm are consider interacting and could manifest in increase viscosity and filterability issues. All variants had maximum absorption values less than 550 nm and showed a slight improvement in the SINS values as compared to AB-000224.

AB-000224 and variants thereof were tested for potential hydrophobic interactions that might results in manufacturability challenges by monitoring retention time on a Zenix HPLC column. Undiluted samples were loaded onto the Zenix column and eluted isocratically with a 100 mM sodium phosphate, pH 7.0 running buffer and monitored at 220 nm. Longer retention times indicates hydrophobic interactions. Most antibodies have a retention time of 8.5-9.0 minutes under conditions tested. AB-00224 and all variants thereof showed comparable retention times of approximately 10 minutes.

Solubility of AB-000224 and variants thereof was assayed by precipitating the antibody samples with increasing amounts of PEG 10,000, filtering the samples, and measuring the soluble protein concentration. For each parent molecule, an initial experiment was performed to determine the ideal PEG concentration to precipitate the parent by approximately 50%, subsequent experiments used this PEG concentration on all variants to assess if a variant is more or less soluble than the parent molecule. Antibodies that precipitate above 8-10% PEG are considered highly soluble while poorly soluble antibodies precipitate at 4-5% PEG. AB-000224 and all variants thereof showed high solubility.

Polyreactivity of AB-000224 and variants thereof was determined by testing the antibodies for binding to KLH, insulin and dsDNA by Elisa. Samples were diluted to 1 μg/mL and a secondary anti-human antibody was used to detect the amount of protein that has bound to the different antigens. After substrate addition, absorbance was measured at 405 nm. A polyreactive antibody was used as a positive control. Non-specific binding to such common physiological components can cause an increase clearance rate, negatively impacting pK. Absorbance values above 1.5 for KLH and Insulin and 2.0 for dsDNA could indicate non-specific binding issues for a molecule. While most of the AB-000224 variants did not show any polyreactivity, some variants showed polyreactive signal against insulin (AB-000224.006, AB-000224.007, AB-000224.008, AB-000224.009, AB-000224.010).

The AB-000224 and variants thereof were ranked based on the different assays and titer results and ranked as described in FIGS. **12**B and **12**C.

AB-007088 Variants Showed Improved Stability

The harvest yield and titer of the AB-007088 and variants thereof were initially evaluated. The AB-007088 variants showed comparable harvest yield and titer results. AB-007088 and variants thereof were evaluated to determine conformational and colloidal stability as described above for AB-000224 and variants thereof.

The AB-007088.005 variant showed improved thermal stability by the DFS method and a T2 that approached 75° C., while the other variants were similar to the parent AB-007088 with T1 values of approximately 70° C. and no measurable T2. In addition, AB-007088.005 showed a slightly reduced precipitation as compared to the parent AB-007088 and the other variants. When chemical stability was evaluated, AB-007088 and all variants thereof did not show low pH instability (at pH 3.3). Further, AB-007088 and all variants thereof showed stability against chemical unfolding with an inflection point above 2 M guanidine (Gdn). Notably, AB-007088.001 showed improved stability as compared to AB-007088 with an inflection point above 2.3 M guanidine.

AB-007088 and variants thereof were also evaluated for their colloidal stability. When protein-protein interactions were monitored (SINS), all variants showed very low SINS values, indicating absence of protein-protein interactions. In addition, AB-007088 and variants thereof showed comparable retention times on Zenix column. Notably, when PEG solubility was determined, AB-007088 and all variants thereof showed high solubility. Further, while most of the AB-007088 variants did not show any polyreactivity, some variants showed polyreactive signal against insulin (AB-007088.001, AB-007088.003, AB-007088.004).

The AB-007088 and variants thereof were ranked based on the different assays and titer results, and ranked as described in FIGS. **13**B and **13**C.

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        35                  40                  45

Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60

Ser Gly Ser Arg Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65                  70                  75                  80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Thr Ser
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        35                  40                  45

Gly Phe Ile Arg Lys Thr Thr Tyr Gly Ala Thr Thr His Tyr Ala Ala
    50                  55                  60

Ala Val Arg Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile
65                  70                  75                  80

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                85                  90                  95

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<211> LENGTH: 381
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 16

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc cagggcggtc cctgagactc     60

ccctgtacag cctctgggtt tagttttggt gatcatgcta tgagctgggt ccgccaggct    120

ccagggaagg ggctggagtg ggtaggtttc attagaaaga caacttatgg tgcgacaaca    180

cactacgccg cggctgtgag aggcagattc accatctcgc gagatgattc taaaagcatt    240

gtctatctgc aaatgaacag cctgaaaacc gaggacacag ccgtgtattt ctgtactaga    300

gtgcagcttg actatggccc gggataccag tactacggta tggacgtctg gggccaaggg    360

accacggtca ccgtctcctc a                                              381
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<210> SEQ ID NO 17
<211> LENGTH: 217
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 17

Glu Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15

Arg Val Thr Ile Ser Cys Thr Gly Met Asn Ser Asn Ile Gly Ala Gly
            20                  25                  30

Tyr Asp Val Tyr Trp Tyr Gln Gln Leu Pro Gly Arg Ala Pro Lys Leu
        35                  40                  45

Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60

Ser Gly Ser Arg Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65                  70                  75                  80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Thr Ser
                85                  90                  95

Leu Asn Gly Trp Ala Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu
        115                 120                 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Val Ser Asp Phe
    130                 135                 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro Val
145                 150                 155                 160

Lys Val Gly Val Glu Thr Thr Lys Pro Ser Lys Gln Ser Asn Asn Lys
                165                 170                 175

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
            180                 185                 190

His Arg Ser Tyr Ser Cys Arg Val Thr His Glu Gly Ser Thr Val Glu
        195                 200                 205

Lys Thr Val Ala Pro Ala Glu Cys Ser
    210                 215


<210> SEQ ID NO 18
<211> LENGTH: 457
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 18

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Pro Cys Thr Ala Ser Gly Phe Ser Phe Gly Asp His
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Gly Phe Ile Arg Lys Thr Thr Tyr Gly Ala Thr Thr His Tyr Ala Ala
    50                  55                  60

Ala Val Arg Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile
65                  70                  75                  80

Val Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
                85                  90                  95
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Phe Cys Thr Arg Val Gln Leu Asp Tyr Gly Pro Gly Tyr Gln Tyr Tyr
            100                 105                 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala
        115                 120                 125

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
    130                 135                 140

Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
145                 150                 155                 160

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
                165                 170                 175

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
            180                 185                 190

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
        195                 200                 205

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
    210                 215                 220

Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
225                 230                 235                 240

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                245                 250                 255

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            260                 265                 270

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        275                 280                 285

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    290                 295                 300

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
305                 310                 315                 320

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                325                 330                 335

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            340                 345                 350

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
        355                 360                 365

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    370                 375                 380

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
385                 390                 395                 400

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                405                 410                 415

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            420                 425                 430

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
        435                 440                 445

Lys Ser Leu Ser Leu Ser Pro Gly Lys
    450                 455


<210> SEQ ID NO 19
<211> LENGTH: 457
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 19
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Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Pro Cys Thr Ala Ser Gly Phe Ser Phe Gly Asp His
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Gly Phe Ile Arg Lys Thr Thr Tyr Gly Ala Thr Thr His Tyr Ala Ala
    50                  55                  60

Ala Val Arg Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile
65                  70                  75                  80

Val Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
                85                  90                  95

Phe Cys Thr Arg Val Gln Leu Asp Tyr Gly Pro Gly Tyr Gln Tyr Tyr
            100                 105                 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala
        115                 120                 125

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
    130                 135                 140

Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
145                 150                 155                 160

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
                165                 170                 175

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
            180                 185                 190

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
        195                 200                 205

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
    210                 215                 220

Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
225                 230                 235                 240

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                245                 250                 255

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            260                 265                 270

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        275                 280                 285

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    290                 295                 300

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
305                 310                 315                 320

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                325                 330                 335

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            340                 345                 350

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
        355                 360                 365

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    370                 375                 380

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
385                 390                 395                 400

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                405                 410                 415
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Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            420                 425                 430

Phe Ser Cys Ser Val Leu His Glu Ala Leu His Ser His Tyr Thr Gln
        435                 440                 445

Lys Ser Leu Ser Leu Ser Pro Gly Lys
    450                 455


<210> SEQ ID NO 20
<211> LENGTH: 651
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 20

gagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc      60

tcctgcactg ggatgaactc caacatcggg gcaggttatg atgtatactg gtaccaacaa     120

cttccaggaa gagcccccaa actcctcatc tatggtaaca gcaatcggcc ctcaggggtc     180

cctgaccgat tctctggctc caggtctggc acctcagcct ccctggccat cactgggctc     240

caggctgagg atgaggctga ttattactgc cagtcctatg acaccagcct gaatggttgg     300

gctttcggcg gagggaccaa gttgaccgtc ctaggccagc ccaaggctgc cccctcggtc     360

actctgttcc caccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc     420

gtaagtgact tctacccggg agccgtgaca gtggcctgga aggcagatgg cagccccgtc     480

aaggtgggag tggagaccac caaaccctcc aaacaaagca acaacaagta tgcggccagc     540

agctacctga gcctgacgcc cgagcagtgg aagtcccaca gaagctacag ctgccgggtc     600

acgcatgaag ggagcaccgt ggagaagaca gtggcccctg cagaatgctc t              651


<210> SEQ ID NO 21
<211> LENGTH: 1371
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 21

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc cagggcggtc cctgagactc      60

ccctgtacag cctctgggtt tagttttggt gatcatgcta tgagctgggt ccgccaggct     120

ccagggaagg ggctggagtg ggtaggtttc attagaaaga caacttatgg tgcgacaaca     180

cactacgccg cggctgtgag aggcagattc accatctcgc gagatgattc taaaagcatt     240

gtctatctgc aaatgaacag cctgaaaacc gaggacacag ccgtgtattt ctgtactaga     300

gtgcagcttg actatggccc gggataccag tactacggta tggacgtctg gggccaaggg     360

accacggtca ccgtctcctc agcctccacc aagggcccat cggtcttccc cctggcaccc     420

tcctccaaga gcacctctgg gggcacagca gccctgggct gcctggtcaa ggactacttc     480

cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc     540

ccggctgtcc tacagtcctc aggactctac tccctcagca gcgtggtgac cgtgccctcc     600

agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag     660

gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgccca     720

gcacctgaac tcctgggggg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc     780

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac     840
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cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag    900

ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac    960

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc   1020

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc   1080

ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa   1140

ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac   1200

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc   1260

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag   1320

gctctgcaca accactacac acagaagagc ctctccctgt ctccgggtaa a            1371


<210> SEQ ID NO 22
<211> LENGTH: 1371
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 22

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc cagggcggtc cctgagactc     60

ccctgtacag cctctgggtt tagttttggt gatcatgcta tgagctgggt ccgccaggct    120

ccagggaagg ggctggagtg ggtaggtttc attagaaaga caacttatgg tgcgacaaca    180

cactacgccg cggctgtgag aggcagattc accatctcgc gagatgattc taaaagcatt    240

gtctatctgc aaatgaacag cctgaaaacc gaggacacag ccgtgtattt ctgtactaga    300

gtgcagcttg actatggccc gggataccag tactacggta tggacgtctg ggccaaggg     360

accacggtca ccgtctcctc agcctccacc aagggcccat cggtcttccc cctggcaccc    420

tcctccaaga gcacctctgg gggcacagca gccctgggct gcctggtcaa ggactacttc    480

cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc    540

ccggctgtcc tacagtcctc aggactctac tccctcagca gcgtggtgac cgtgccctcc    600

agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag    660

gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgccca    720

gcacctgaac tcctgggggg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc    780

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac    840

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag    900

ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac    960

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc   1020

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc   1080

ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa   1140

ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac   1200

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc   1260

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gctgcatgag   1320

gctctgcact cccactacac acagaagagc ctctccctgt ctccgggtaa a            1371


<210> SEQ ID NO 23
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 23

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15

Arg Val Thr Ile Ser Cys Thr Gly Met Asn Ser Asn Ile Gly Ala Gly
            20                  25                  30

Tyr Asp Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35                  40                  45

Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60

Ser Gly Ser Arg Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65                  70                  75                  80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Thr Ser
                85                  90                  95

Leu Asn Gly Trp Ala Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110


<210> SEQ ID NO 24
<211> LENGTH: 127
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 24

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Ser Phe Gly Asp His
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Gly Phe Ile Arg Lys Thr Thr Tyr Gly Ala Thr Thr His Tyr Ala Ala
    50                  55                  60

Ala Val Arg Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile
65                  70                  75                  80

Val Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
                85                  90                  95

Phe Cys Thr Arg Val Gln Leu Asp Tyr Gly Pro Gly Tyr Gln Tyr Tyr
            100                 105                 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120                 125


<210> SEQ ID NO 25
<211> LENGTH: 336
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 25

cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc      60

tcctgcactg ggatgaactc caacatcggg gcaggttatg atgtatactg gtaccaacaa     120

cttccaggaa ctgcccccaa actcctcatc tatggtaaca gcaatcggcc ctcaggggtc     180

cctgaccgat tctctggctc caggtctggc acctcagcct ccctggccat cactgggctc     240

caggctgagg atgaggctga ttattactgc cagtcctatg acaccagcct gaatggttgg     300
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gctttcggcg gagggaccaa gttgaccgtc ctaggc                           336


<210> SEQ ID NO 26
<211> LENGTH: 381
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 26

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc cagggcggtc cctgagactc     60

agctgtacag cctctgggtt tagttttggt gatcatgcta tgagctgggt ccgccaggct    120

ccagggaagg ggctggagtg ggtaggtttc attagaaaga caacttatgg tgcgacaaca    180

cactacgccg cggctgtgag aggcagattc accatctcgc gagatgattc taaaagcatt    240

gtctatctgc aaatgaacag cctgaaaacc gaggacacag ccgtgtattt ctgtactaga    300

gtgcagcttg actatggccc gggataccag tactacggta tggacgtctg gggccaaggg    360

accacggtca ccgtctcctc a                                              381


<210> SEQ ID NO 27
<211> LENGTH: 217
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 27

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15

Arg Val Thr Ile Ser Cys Thr Gly Met Asn Ser Asn Ile Gly Ala Gly
            20                  25                  30

Tyr Asp Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35                  40                  45

Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60

Ser Gly Ser Arg Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65                  70                  75                  80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Thr Ser
                85                  90                  95

Leu Asn Gly Trp Ala Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu
        115                 120                 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Val Ser Asp Phe
    130                 135                 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro Val
145                 150                 155                 160

Lys Val Gly Val Glu Thr Thr Lys Pro Ser Lys Gln Ser Asn Asn Lys
                165                 170                 175

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
            180                 185                 190

His Arg Ser Tyr Ser Cys Arg Val Thr His Glu Gly Ser Thr Val Glu
        195                 200                 205

Lys Thr Val Ala Pro Ala Glu Cys Ser
    210                 215
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<210> SEQ ID NO 28
<211> LENGTH: 457
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 28

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Ser Phe Gly Asp His
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Gly Phe Ile Arg Lys Thr Thr Tyr Gly Ala Thr Thr His Tyr Ala Ala
    50                  55                  60

Ala Val Arg Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile
65                  70                  75                  80

Val Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
                85                  90                  95

Phe Cys Thr Arg Val Gln Leu Asp Tyr Gly Pro Gly Tyr Gln Tyr Tyr
            100                 105                 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala
        115                 120                 125

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
    130                 135                 140

Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
145                 150                 155                 160

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
                165                 170                 175

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
            180                 185                 190

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
        195                 200                 205

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
    210                 215                 220

Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
225                 230                 235                 240

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                245                 250                 255

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            260                 265                 270

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        275                 280                 285

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    290                 295                 300

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
305                 310                 315                 320

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                325                 330                 335

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            340                 345                 350

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
        355                 360                 365
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Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    370                 375                 380

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
385                 390                 395                 400

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                405                 410                 415

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            420                 425                 430

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
        435                 440                 445

Lys Ser Leu Ser Leu Ser Pro Gly Lys
    450                 455


<210> SEQ ID NO 29
<211> LENGTH: 457
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 29

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Ser Phe Gly Asp His
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Gly Phe Ile Arg Lys Thr Thr Tyr Gly Ala Thr Thr His Tyr Ala Ala
    50                  55                  60

Ala Val Arg Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile
65                  70                  75                  80

Val Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
                85                  90                  95

Phe Cys Thr Arg Val Gln Leu Asp Tyr Gly Pro Gly Tyr Gln Tyr Tyr
            100                 105                 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala
        115                 120                 125

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
    130                 135                 140

Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
145                 150                 155                 160

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
                165                 170                 175

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
            180                 185                 190

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
        195                 200                 205

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
    210                 215                 220

Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
225                 230                 235                 240

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                245                 250                 255

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            260                 265                 270
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Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        275                 280                 285

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    290                 295                 300

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
305                 310                 315                 320

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                325                 330                 335

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            340                 345                 350

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
        355                 360                 365

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    370                 375                 380

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
385                 390                 395                 400

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                405                 410                 415

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            420                 425                 430

Phe Ser Cys Ser Val Leu His Glu Ala Leu His Ser His Tyr Thr Gln
        435                 440                 445

Lys Ser Leu Ser Leu Ser Pro Gly Lys
    450                 455
```

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<210> SEQ ID NO 30
<211> LENGTH: 651
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 30

cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc     60

tcctgcactg ggatgaactc caacatcggg gcaggttatg atgtatactg gtaccaacaa    120

cttccaggaa ctgcccccaa actcctcatc tatggtaaca gcaatcggcc ctcaggggtc    180

cctgaccgat tctctggctc caggtctggc acctcagcct ccctggccat cactgggctc    240

caggctgagg atgaggctga ttattactgc cagtcctatg acaccagcct gaatggttgg    300

gctttcggcg gagggaccaa gttgaccgtc ctaggccagc ccaaggctgc cccctcggtc    360

actctgttcc caccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc    420

gtaagtgact tctacccggg agccgtgaca gtggcctgga aggcagatgg cagccccgtc    480

aaggtgggag tggagaccac caaaccctcc aaacaaagca acaacaagta tgcggccagc    540

agctacctga gcctgacgcc cgagcagtgg aagtcccaca gaagctacag ctgccgggtc    600

acgcatgaag ggagcaccgt ggagaagaca gtggcccctg cagaatgctc t             651


<210> SEQ ID NO 31
<211> LENGTH: 1371
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 31

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc cagggcggtc cctgagactc     60
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agctgtacag cctctgggtt tagttttggt gatcatgcta tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtaggtttc attagaaaga caacttatgg tgcgacaaca 180

cactacgccg cggctgtgag aggcagattc accatctcgc gagatgattc taaaagcatt 240

gtctatctgc aaatgaacag cctgaaaacc gaggacacag ccgtgtattt ctgtactaga 300

gtgcagcttg actatggccc gggataccag tactacggta tggacgtctg gggccaaggg 360

accacggtca ccgtctcctc agcctccacc aagggcccat cggtcttccc cctggcaccc 420

tcctccaaga gcacctctgg gggcacagca gccctgggct gcctggtcaa ggactacttc 480

cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc 540

ccggctgtcc tacagtcctc aggactctac tccctcagca gcgtggtgac cgtgccctcc 600

agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag 660

gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgccca 720

gcacctgaac tcctgggggg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 780

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 840

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 900

ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 960

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc 1020

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1080

ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 1140

ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1200

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1260

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1320

gctctgcaca accactacac acagaagagc ctctccctgt ctccgggtaa a 1371

<210> SEQ ID NO 32
<211> LENGTH: 1371
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 32

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc cagggcggtc cctgagactc 60

agctgtacag cctctgggtt tagttttggt gatcatgcta tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtaggtttc attagaaaga caacttatgg tgcgacaaca 180

cactacgccg cggctgtgag aggcagattc accatctcgc gagatgattc taaaagcatt 240

gtctatctgc aaatgaacag cctgaaaacc gaggacacag ccgtgtattt ctgtactaga 300

gtgcagcttg actatggccc gggataccag tactacggta tggacgtctg gggccaaggg 360

accacggtca ccgtctcctc agcctccacc aagggcccat cggtcttccc cctggcaccc 420

tcctccaaga gcacctctgg gggcacagca gccctgggct gcctggtcaa ggactacttc 480

cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc 540

ccggctgtcc tacagtcctc aggactctac tccctcagca gcgtggtgac cgtgccctcc 600

agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag 660

gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgccca 720

```
gcacctgaac tcctgggggg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc    780

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac    840

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag    900

ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac    960

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc   1020

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc   1080

ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa   1140

ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac   1200

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc   1260

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gctgcatgag   1320

gctctgcact cccactacac acagaagagc ctctccctgt ctccgggtaa a            1371
```

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<210> SEQ ID NO 33
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 33

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15

Arg Val Thr Ile Ser Cys Thr Gly Met Asn Ser Asn Ile Gly Ala Gly
            20                  25                  30

Tyr Asp Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35                  40                  45

Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60

Ser Gly Ser Arg Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65                  70                  75                  80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Thr Ser
                85                  90                  95

Leu Asn Gly Trp Ala Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110


<210> SEQ ID NO 34
<211> LENGTH: 127
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 34

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Gly Asp His
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Gly Phe Ile Arg Lys Thr Thr Tyr Gly Ala Thr Thr His Tyr Ala Ala
    50                  55                  60

Ala Val Arg Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile
65                  70                  75                  80

Val Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
```

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                85                  90                  95

Phe Cys Thr Arg Val Gln Leu Asp Tyr Gly Pro Gly Tyr Gln Tyr Tyr
            100                 105                 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120                 125


<210> SEQ ID NO 35
<211> LENGTH: 336
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 35

cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc      60

tcctgcactg ggatgaactc caacatcggg gcaggttatg atgtatactg gtaccaacaa     120

cttccaggaa ctgcccccaa actcctcatc tatggtaaca gcaatcggcc ctcaggggtc     180

cctgaccgat tctctggctc caggtctggc acctcagcct ccctggccat cactgggctc     240

caggctgagg atgaggctga ttattactgc cagtcctatg acaccagcct gaatggttgg     300

gctttcggcg gagggaccaa gttgaccgtc ctaggc                               336


<210> SEQ ID NO 36
<211> LENGTH: 381
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 36

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc cagggcggtc cctgagactc      60

agctgtgcgg cctctgggtt tagttttggt gatcatgcta tgagctgggt ccgccaggct     120

ccagggaagg ggctggagtg ggtaggtttc attagaaaga caacttatgg tgcgacaaca     180

cactacgccg cggctgtgag aggcagattc accatctcgc gagatgattc taaaagcatt     240

gtctatctgc aaatgaacag cctgaaaacc gaggacacag ccgtgtattt ctgtactaga     300

gtgcagcttg actatggccc gggataccag tactacggta tggacgtctg gggccaaggg     360

accacggtca ccgtctcctc a                                               381


<210> SEQ ID NO 37
<211> LENGTH: 217
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 37

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15

Arg Val Thr Ile Ser Cys Thr Gly Met Asn Ser Asn Ile Gly Ala Gly
            20                  25                  30

Tyr Asp Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35                  40                  45

Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60

Ser Gly Ser Arg Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65                  70                  75                  80
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Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Thr Ser
                85                  90                  95

Leu Asn Gly Trp Ala Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu
        115                 120                 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Val Ser Asp Phe
    130                 135                 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro Val
145                 150                 155                 160

Lys Val Gly Val Glu Thr Thr Lys Pro Ser Lys Gln Ser Asn Asn Lys
                165                 170                 175

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
            180                 185                 190

His Arg Ser Tyr Ser Cys Arg Val Thr His Glu Gly Ser Thr Val Glu
        195                 200                 205

Lys Thr Val Ala Pro Ala Glu Cys Ser
    210                 215


<210> SEQ ID NO 38
<211> LENGTH: 457
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 38

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Gly Asp His
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Gly Phe Ile Arg Lys Thr Thr Tyr Gly Ala Thr Thr His Tyr Ala Ala
    50                  55                  60

Ala Val Arg Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile
65                  70                  75                  80

Val Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
                85                  90                  95

Phe Cys Thr Arg Val Gln Leu Asp Tyr Gly Pro Gly Tyr Gln Tyr Tyr
            100                 105                 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala
        115                 120                 125

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
    130                 135                 140

Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
145                 150                 155                 160

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
                165                 170                 175

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
            180                 185                 190

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
        195                 200                 205

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
    210                 215                 220
```

```
Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
225                 230                 235                 240

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                245                 250                 255

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            260                 265                 270

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        275                 280                 285

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    290                 295                 300

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
305                 310                 315                 320

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                325                 330                 335

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            340                 345                 350

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
        355                 360                 365

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    370                 375                 380

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
385                 390                 395                 400

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                405                 410                 415

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            420                 425                 430

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
        435                 440                 445

Lys Ser Leu Ser Leu Ser Pro Gly Lys
    450                 455


<210> SEQ ID NO 39
<211> LENGTH: 457
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 39

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Gly Asp His
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Gly Phe Ile Arg Lys Thr Thr Tyr Gly Ala Thr Thr His Tyr Ala Ala
    50                  55                  60

Ala Val Arg Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile
65                  70                  75                  80

Val Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
                85                  90                  95

Phe Cys Thr Arg Val Gln Leu Asp Tyr Gly Pro Gly Tyr Gln Tyr Tyr
            100                 105                 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala
        115                 120                 125
```

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Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
    130                 135                 140

Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
145                 150                 155                 160

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
                165                 170                 175

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
            180                 185                 190

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
        195                 200                 205

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
    210                 215                 220

Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
225                 230                 235                 240

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                245                 250                 255

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            260                 265                 270

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        275                 280                 285

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    290                 295                 300

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
305                 310                 315                 320

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                325                 330                 335

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            340                 345                 350

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
        355                 360                 365

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    370                 375                 380

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
385                 390                 395                 400

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                405                 410                 415

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            420                 425                 430

Phe Ser Cys Ser Val Leu His Glu Ala Leu His Ser His Tyr Thr Gln
        435                 440                 445

Lys Ser Leu Ser Leu Ser Pro Gly Lys
    450                 455
```

<210> SEQ ID NO 40
<211> LENGTH: 651
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 40

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cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc     60

tcctgcactg ggatgaactc caacatcggg gcaggttatg atgtatactg gtaccaacaa    120

cttccaggaa ctgcccccaa actcctcatc tatggtaaca gcaatcggcc ctcaggggtc    180
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cctgaccgat tctctggctc caggtctggc acctcagcct ccctggccat cactgggctc 240

caggctgagg atgaggctga ttattactgc cagtcctatg acaccagcct gaatggttgg 300

gctttcggcg gagggaccaa gttgaccgtc ctaggccagc ccaaggctgc cccctcggtc 360

actctgttcc caccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420

gtaagtgact tctacccggg agccgtgaca gtggcctgga aggcagatgg cagccccgtc 480

aaggtgggag tggagaccac caaaccctcc aaacaaagca acaacaagta tgcggccagc 540

agctacctga gcctgacgcc cgagcagtgg aagtcccaca gaagctacag ctgccgggtc 600

acgcatgaag ggagcaccgt ggagaagaca gtggcccctg cagaatgctc t 651

<210> SEQ ID NO 41
<211> LENGTH: 1371
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 41

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc cagggcggtc cctgagactc 60

agctgtgcgg cctctgggtt tagttttggt gatcatgcta tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtaggtttc attagaaaga caacttatgg tgcgacaaca 180

cactacgccg cggctgtgag aggcagattc accatctcgc gagatgattc taaaagcatt 240

gtctatctgc aaatgaacag cctgaaaacc gaggacacag ccgtgtattt ctgtactaga 300

gtgcagcttg actatggccc gggataccag tactacggta tggacgtctg gggccaaggg 360

accacggtca ccgtctcctc agcctccacc aagggcccat cggtcttccc cctggcaccc 420

tcctccaaga gcacctctgg gggcacagca gccctgggct gcctggtcaa ggactacttc 480

cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc 540

ccggctgtcc tacagtcctc aggactctac tccctcagca gcgtggtgac cgtgccctcc 600

agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag 660

gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgccca 720

gcacctgaac tcctgggggg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 780

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 840

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 900

ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 960

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc 1020

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1080

ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 1140

ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1200

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1260

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1320

gctctgcaca accactacac acagaagagc ctctccctgt ctccgggtaa a 1371

<210> SEQ ID NO 42
<211> LENGTH: 1371
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 42

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc cagggcggtc cctgagactc 60

agctgtgcgg cctctgggtt tagttttggt gatcatgcta tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtaggtttc attagaaaga caacttatgg tgcgacaaca 180

cactacgccg cggctgtgag aggcagattc accatctcgc gagatgattc taaaagcatt 240

gtctatctgc aaatgaacag cctgaaaacc gaggacacag ccgtgtattt ctgtactaga 300

gtgcagcttg actatggccc gggataccag tactacggta tggacgtctg gggccaaggg 360

accacggtca ccgtctcctc agcctccacc aagggcccat cggtcttccc cctggcaccc 420

tcctccaaga gcacctctgg gggcacagca gccctgggct gcctggtcaa ggactacttc 480

cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc 540

ccggctgtcc tacagtcctc aggactctac tccctcagca gcgtggtgac cgtgccctcc 600

agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag 660

gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgccca 720

gcacctgaac tcctgggggg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 780

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 840

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 900

ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 960

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc 1020

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1080

ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 1140

ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1200

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1260

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gctgcatgag 1320

gctctgcact cccactacac acagaagagc ctctccctgt ctccgggtaa a 1371

<210> SEQ ID NO 43
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 43

```
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15

Arg Val Thr Ile Ser Cys Thr Gly Met Asn Ser Asn Ile Gly Ala Gly
            20                  25                  30

Tyr Asp Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35                  40                  45

Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60

Ser Gly Ser Arg Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65                  70                  75                  80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Thr Ser
                85                  90                  95

Leu Asn Gly Trp Ala Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110
```

<210> SEQ ID NO 44
<211> LENGTH: 127
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 44

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Ser Phe Gly Asp His
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Gly Phe Ile Arg Lys Thr Thr Tyr Gly Ala Thr Thr His Tyr Ala Ala
50 55 60

Ala Val Arg Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Val Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
85 90 95

Phe Cys Thr Arg Val Gln Leu Asp Tyr Gly Pro Gly Tyr Gln Tyr Tyr
100 105 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> SEQ ID NO 45
<211> LENGTH: 336
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 45

cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60

tcctgcactg ggatgaactc caacatcggg gcaggttatg atgtatactg gtaccaacaa 120

cttccaggaa ctgcccccaa actcctcatc tatggtaaca gcaatcggcc ctcaggggtc 180

cctgaccgat tctctggctc caggtctggc acctcagcct ccctggccat cactgggctc 240

caggctgagg atgaggctga ttattactgc cagtcctatg acaccagcct gaatggttgg 300

gctttcggcg gagggaccaa gttgaccgtc ctaggc 336

<210> SEQ ID NO 46
<211> LENGTH: 381
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 46

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc cagggcggtc cctgagactc 60

agctgtacag cctctgggtt tagttttggt gatcatgcta tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtaggtttc attagaaaga caacttatgg tgcgacaaca 180

cactacgccg cggctgtgag aggcagattc accatctcgc gagatgattc taaaagcact 240

gtctatctgc aaatgaacag cctgaaaacc gaggacacag ccgtgtattt ctgtactaga 300

gtgcagcttg actatggccc gggataccag tactacggta tggacgtctg gggccaaggg 360

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accacggtca ccgtctcctc a                                              381


<210> SEQ ID NO 47
<211> LENGTH: 217
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 47

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15

Arg Val Thr Ile Ser Cys Thr Gly Met Asn Ser Asn Ile Gly Ala Gly
            20                  25                  30

Tyr Asp Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35                  40                  45

Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60

Ser Gly Ser Arg Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65                  70                  75                  80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Thr Ser
                85                  90                  95

Leu Asn Gly Trp Ala Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu
        115                 120                 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Val Ser Asp Phe
    130                 135                 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro Val
145                 150                 155                 160

Lys Val Gly Val Glu Thr Thr Lys Pro Ser Lys Gln Ser Asn Asn Lys
                165                 170                 175

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
            180                 185                 190

His Arg Ser Tyr Ser Cys Arg Val Thr His Glu Gly Ser Thr Val Glu
        195                 200                 205

Lys Thr Val Ala Pro Ala Glu Cys Ser
    210                 215


<210> SEQ ID NO 48
<211> LENGTH: 457
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 48

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Ser Phe Gly Asp His
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Gly Phe Ile Arg Lys Thr Thr Tyr Gly Ala Thr Thr His Tyr Ala Ala
    50                  55                  60

Ala Val Arg Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65                  70                  75                  80
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Val Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
                85                  90                  95

Phe Cys Thr Arg Val Gln Leu Asp Tyr Gly Pro Gly Tyr Gln Tyr Tyr
            100                 105                 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala
        115                 120                 125

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
    130                 135                 140

Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
145                 150                 155                 160

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
                165                 170                 175

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
            180                 185                 190

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
        195                 200                 205

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
    210                 215                 220

Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
225                 230                 235                 240

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                245                 250                 255

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            260                 265                 270

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        275                 280                 285

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    290                 295                 300

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
305                 310                 315                 320

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                325                 330                 335

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            340                 345                 350

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
        355                 360                 365

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    370                 375                 380

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
385                 390                 395                 400

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                405                 410                 415

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            420                 425                 430

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
        435                 440                 445

Lys Ser Leu Ser Leu Ser Pro Gly Lys
    450                 455


<210> SEQ ID NO 49
<211> LENGTH: 457
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
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<400> SEQUENCE: 49

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Ser Phe Gly Asp His
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Gly Phe Ile Arg Lys Thr Thr Tyr Gly Ala Thr Thr His Tyr Ala Ala
    50                  55                  60

Ala Val Arg Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65                  70                  75                  80

Val Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
                85                  90                  95

Phe Cys Thr Arg Val Gln Leu Asp Tyr Gly Pro Gly Tyr Gln Tyr Tyr
            100                 105                 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala
        115                 120                 125

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
    130                 135                 140

Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
145                 150                 155                 160

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
                165                 170                 175

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
            180                 185                 190

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
        195                 200                 205

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
    210                 215                 220

Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
225                 230                 235                 240

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                245                 250                 255

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            260                 265                 270

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        275                 280                 285

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    290                 295                 300

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
305                 310                 315                 320

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                325                 330                 335

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            340                 345                 350

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
        355                 360                 365

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    370                 375                 380

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
385                 390                 395                 400

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
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            405                 410                 415

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
        420                 425                 430

Phe Ser Cys Ser Val Leu His Glu Ala Leu His Ser His Tyr Thr Gln
    435                 440                 445

Lys Ser Leu Ser Leu Ser Pro Gly Lys
    450                 455


<210> SEQ ID NO 50
<211> LENGTH: 651
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 50

cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc     60

tcctgcactg ggatgaactc caacatcggg gcaggttatg atgtatactg gtaccaacaa    120

cttccaggaa ctgcccccaa actcctcatc tatggtaaca gcaatcggcc ctcaggggtc    180

cctgaccgat tctctggctc caggtctggc acctcagcct ccctggccat cactgggctc    240

caggctgagg atgaggctga ttattactgc cagtcctatg acaccagcct gaatggttgg    300

gctttcggcg gagggaccaa gttgaccgtc ctaggccagc ccaaggctgc cccctcggtc    360

actctgttcc caccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc    420

gtaagtgact tctacccggg agccgtgaca gtggcctgga aggcagatgg cagccccgtc    480

aaggtgggag tggagaccac caaaccctcc aaacaaagca acaacaagta tgcggccagc    540

agctacctga gcctgacgcc cgagcagtgg aagtcccaca gaagctacag ctgccgggtc    600

acgcatgaag ggagcaccgt ggagaagaca gtggcccctg cagaatgctc t             651


<210> SEQ ID NO 51
<211> LENGTH: 1371
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 51

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc cagggcggtc cctgagactc     60

agctgtacag cctctgggtt tagttttggt gatcatgcta tgagctgggt ccgccaggct    120

ccagggaagg ggctggagtg ggtaggtttc attagaaaga caacttatgg tgcgacaaca    180

cactacgccg cggctgtgag aggcagattc accatctcgc gagatgattc taaaagcact    240

gtctatctgc aaatgaacag cctgaaaacc gaggacacag ccgtgtattt ctgtactaga    300

gtgcagcttg actatggccc gggataccag tactacggta tggacgtctg gggccaaggg    360

accacggtca ccgtctcctc agcctccacc aagggcccat cggtcttccc cctggcaccc    420

tcctccaaga gcacctctgg gggcacagca gccctgggct gcctggtcaa ggactacttc    480

cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc    540

ccggctgtcc tacagtcctc aggactctac tccctcagca gcgtggtgac cgtgccctcc    600

agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag    660

gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgccca    720

gcacctgaac tcctgggggg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc    780
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ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 840

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 900

ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 960

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc 1020

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1080

ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 1140

ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1200

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1260

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1320

gctctgcaca accactacac acagaagagc ctctccctgt ctccgggtaa a 1371

<210> SEQ ID NO 52
<211> LENGTH: 1371
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 52

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc cagggcggtc cctgagactc 60

agctgtacag cctctgggtt tagttttggt gatcatgcta tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtaggtttc attagaaaga caacttatgg tgcgacaaca 180

cactacgccg cggctgtgag aggcagattc accatctcgc gagatgattc taaaagcact 240

gtctatctgc aaatgaacag cctgaaaacc gaggacacag ccgtgtattt ctgtactaga 300

gtgcagcttg actatggccc gggataccag tactacggta tggacgtctg gggccaaggg 360

accacggtca ccgtctcctc agcctccacc aagggcccat cggtcttccc cctggcaccc 420

tcctccaaga gcacctctgg gggcacagca gccctgggct gcctggtcaa ggactacttc 480

cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc 540

ccggctgtcc tacagtcctc aggactctac tccctcagca gcgtggtgac cgtgccctcc 600

agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag 660

gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgccca 720

gcacctgaac tcctgggggg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 780

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 840

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 900

ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 960

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc 1020

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1080

ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 1140

ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1200

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1260

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gctgcatgag 1320

gctctgcact cccactacac acagaagagc ctctccctgt ctccgggtaa a 1371

<210> SEQ ID NO 53
<211> LENGTH: 112

```
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 53

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15

Arg Val Thr Ile Ser Cys Thr Gly Met Asn Ser Asn Ile Gly Ala Gly
            20                  25                  30

Tyr Asp Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35                  40                  45

Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60

Ser Gly Ser Arg Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65                  70                  75                  80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Thr Ser
                85                  90                  95

Leu Asn Gly Trp Ala Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110


<210> SEQ ID NO 54
<211> LENGTH: 127
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 54

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Ser Phe Gly Asp His
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Gly Phe Ile Arg Lys Thr Thr Tyr Gly Ala Thr Thr His Tyr Ala Ala
    50                  55                  60

Ala Val Arg Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile
65                  70                  75                  80

Val Tyr Leu Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr
                85                  90                  95

Phe Cys Thr Arg Val Gln Leu Asp Tyr Gly Pro Gly Tyr Gln Tyr Tyr
            100                 105                 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120                 125


<210> SEQ ID NO 55
<211> LENGTH: 336
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 55

cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc      60

tcctgcactg ggatgaactc caacatcggg gcaggttatg atgtatactg gtaccaacaa     120

cttccaggaa ctgcccccaa actcctcatc tatggtaaca gcaatcggcc ctcaggggtc     180

cctgaccgat tctctggctc caggtctggc acctcagcct ccctggccat cactgggctc     240
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caggctgagg atgaggctga ttattactgc cagtcctatg acaccagcct gaatggttgg    300

gctttcggcg gagggaccaa gttgaccgtc ctaggc                              336


<210> SEQ ID NO 56
<211> LENGTH: 381
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 56

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc cagggcggtc cctgagactc     60

agctgtacag cctctgggtt tagttttggt gatcatgcta tgagctgggt ccgccaggct    120

ccagggaagg ggctggagtg ggtaggtttc attagaaaga caacttatgg tgcgacaaca    180

cactacgccg cggctgtgag aggcagattc accatctcgc gagatgattc taaaagcatt    240

gtctatctgc aaatgaacag cctgaaagca gaggacacag ccgtgtattt ctgtactaga    300

gtgcagcttg actatggccc gggataccag tactacggta tggacgtctg gggccaaggg    360

accacggtca ccgtctcctc a                                              381


<210> SEQ ID NO 57
<211> LENGTH: 217
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 57

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15

Arg Val Thr Ile Ser Cys Thr Gly Met Asn Ser Asn Ile Gly Ala Gly
            20                  25                  30

Tyr Asp Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35                  40                  45

Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60

Ser Gly Ser Arg Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65                  70                  75                  80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Thr Ser
                85                  90                  95

Leu Asn Gly Trp Ala Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu
        115                 120                 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Val Ser Asp Phe
    130                 135                 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro Val
145                 150                 155                 160

Lys Val Gly Val Glu Thr Thr Lys Pro Ser Lys Gln Ser Asn Asn Lys
                165                 170                 175

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
            180                 185                 190

His Arg Ser Tyr Ser Cys Arg Val Thr His Glu Gly Ser Thr Val Glu
        195                 200                 205

Lys Thr Val Ala Pro Ala Glu Cys Ser
```

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    210                 215


<210> SEQ ID NO 58
<211> LENGTH: 457
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 58

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Ser Phe Gly Asp His
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Gly Phe Ile Arg Lys Thr Thr Tyr Gly Ala Thr Thr His Tyr Ala Ala
    50                  55                  60

Ala Val Arg Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile
65                  70                  75                  80

Val Tyr Leu Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr
                85                  90                  95

Phe Cys Thr Arg Val Gln Leu Asp Tyr Gly Pro Gly Tyr Gln Tyr Tyr
            100                 105                 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala
        115                 120                 125

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
    130                 135                 140

Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
145                 150                 155                 160

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
                165                 170                 175

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
            180                 185                 190

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
        195                 200                 205

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
    210                 215                 220

Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
225                 230                 235                 240

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                245                 250                 255

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            260                 265                 270

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        275                 280                 285

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    290                 295                 300

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
305                 310                 315                 320

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                325                 330                 335

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            340                 345                 350

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
```

```
        355                 360                 365

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    370                 375                 380

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
385                 390                 395                 400

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                405                 410                 415

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            420                 425                 430

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
        435                 440                 445

Lys Ser Leu Ser Leu Ser Pro Gly Lys
    450                 455


<210> SEQ ID NO 59
<211> LENGTH: 457
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 59

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Ser Phe Gly Asp His
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Gly Phe Ile Arg Lys Thr Thr Tyr Gly Ala Thr Thr His Tyr Ala Ala
    50                  55                  60

Ala Val Arg Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile
65                  70                  75                  80

Val Tyr Leu Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr
                85                  90                  95

Phe Cys Thr Arg Val Gln Leu Asp Tyr Gly Pro Gly Tyr Gln Tyr Tyr
            100                 105                 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala
        115                 120                 125

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
    130                 135                 140

Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
145                 150                 155                 160

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
                165                 170                 175

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
            180                 185                 190

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
        195                 200                 205

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
    210                 215                 220

Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
225                 230                 235                 240

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                245                 250                 255

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
```

```
            260                 265                 270

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        275                 280                 285

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    290                 295                 300

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
305                 310                 315                 320

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                325                 330                 335

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            340                 345                 350

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
        355                 360                 365

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    370                 375                 380

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
385                 390                 395                 400

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                405                 410                 415

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            420                 425                 430

Phe Ser Cys Ser Val Leu His Glu Ala Leu His Ser His Tyr Thr Gln
        435                 440                 445

Lys Ser Leu Ser Leu Ser Pro Gly Lys
    450                 455
```

<210> SEQ ID NO 60
<211> LENGTH: 651
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 60

```
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc      60

tcctgcactg ggatgaactc caacatcggg gcaggttatg atgtatactg gtaccaacaa     120

cttccaggaa ctgcccccaa actcctcatc tatggtaaca gcaatcggcc ctcaggggtc     180

cctgaccgat tctctggctc caggtctggc acctcagcct ccctggccat cactgggctc     240

caggctgagg atgaggctga ttattactgc cagtcctatg acaccagcct gaatggttgg     300

gctttcggcg gagggaccaa gttgaccgtc ctaggccagc ccaaggctgc cccctcggtc     360

actctgttcc caccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc     420

gtaagtgact tctacccggg agccgtgaca gtggcctgga aggcagatgg cagccccgtc     480

aaggtgggag tggagaccac caaaccctcc aaacaaagca acaacaagta tgcggccagc     540

agctacctga gcctgacgcc cgagcagtgg aagtcccaca gaagctacag ctgccgggtc     600

acgcatgaag ggagcaccgt ggagaagaca gtggcccctg cagaatgctc t              651
```

<210> SEQ ID NO 61
<211> LENGTH: 1371
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 61

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc cagggcggtc cctgagactc 60

agctgtacag cctctgggtt tagttttggt gatcatgcta tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtaggtttc attagaaaga caacttatgg tgcgacaaca 180

cactacgccg cggctgtgag aggcagattc accatctcgc gagatgattc taaaagcatt 240

gtctatctgc aaatgaacag cctgaaagca gaggacacag ccgtgtattt ctgtactaga 300

gtgcagcttg actatggccc gggataccag tactacggta tggacgtctg gggccaaggg 360

accacggtca ccgtctcctc agcctccacc aagggcccat cggtcttccc cctggcaccc 420

tcctccaaga gcacctctgg gggcacagca gccctgggct gcctggtcaa ggactacttc 480

cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc 540

ccggctgtcc tacagtcctc aggactctac tccctcagca gcgtggtgac cgtgccctcc 600

agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag 660

gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgccca 720

gcacctgaac tcctgggggg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 780

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 840

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 900

ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 960

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc 1020

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1080

ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 1140

ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1200

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1260

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1320

gctctgcaca accactacac acagaagagc ctctccctgt ctccgggtaa a 1371

<210> SEQ ID NO 62
<211> LENGTH: 1371
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 62

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc cagggcggtc cctgagactc 60

agctgtacag cctctgggtt tagttttggt gatcatgcta tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtaggtttc attagaaaga caacttatgg tgcgacaaca 180

cactacgccg cggctgtgag aggcagattc accatctcgc gagatgattc taaaagcatt 240

gtctatctgc aaatgaacag cctgaaagca gaggacacag ccgtgtattt ctgtactaga 300

gtgcagcttg actatggccc gggataccag tactacggta tggacgtctg gggccaaggg 360

accacggtca ccgtctcctc agcctccacc aagggcccat cggtcttccc cctggcaccc 420

tcctccaaga gcacctctgg gggcacagca gccctgggct gcctggtcaa ggactacttc 480

cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc 540

ccggctgtcc tacagtcctc aggactctac tccctcagca gcgtggtgac cgtgccctcc 600

agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag 660

```
gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgccca    720

gcacctgaac tcctgggggg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc    780

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac    840

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag    900

ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac    960

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc   1020

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc   1080

ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa   1140

ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac   1200

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc   1260

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gctgcatgag   1320

gctctgcact cccactacac acagaagagc ctctccctgt ctccgggtaa a            1371
```

<210> SEQ ID NO 63
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 63

```
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15

Arg Val Thr Ile Ser Cys Thr Gly Met Asn Ser Asn Ile Gly Ala Gly
            20                  25                  30

Tyr Asp Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35                  40                  45

Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60

Ser Gly Ser Arg Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65                  70                  75                  80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Thr Ser
                85                  90                  95

Leu Asn Gly Trp Ala Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110
```

<210> SEQ ID NO 64
<211> LENGTH: 127
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 64

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Ser Phe Gly Asp His
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Gly Phe Ile Arg Lys Thr Thr Tyr Gly Ala Thr Thr His Tyr Ala Ala
    50                  55                  60

Ala Val Arg Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile
65                  70                  75                  80
```

```
Val Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
                85                  90                  95

Phe Cys Ala Arg Val Gln Leu Asp Tyr Gly Pro Gly Tyr Gln Tyr Tyr
            100                 105                 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120                 125


<210> SEQ ID NO 65
<211> LENGTH: 336
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 65

cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc      60

tcctgcactg ggatgaactc caacatcggg gcaggttatg atgtatactg gtaccaacaa     120

cttccaggaa ctgcccccaa actcctcatc tatggtaaca gcaatcggcc ctcaggggtc     180

cctgaccgat tctctggctc caggtctggc acctcagcct ccctggccat cactgggctc     240

caggctgagg atgaggctga ttattactgc cagtcctatg acaccagcct gaatggttgg     300

gctttcggcg gagggaccaa gttgaccgtc ctaggc                               336


<210> SEQ ID NO 66
<211> LENGTH: 381
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 66

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc cagggcggtc cctgagactc      60

agctgtacag cctctgggtt tagttttggt gatcatgcta tgagctgggt ccgccaggct     120

ccagggaagg ggctggagtg ggtaggtttc attagaaaga caacttatgg tgcgacaaca     180

cactacgccg cggctgtgag aggcagattc accatctcgc gagatgattc taaaagcatt     240

gtctatctgc aaatgaacag cctgaaaacc gaggacacag ccgtgtattt ctgtgctaga     300

gtgcagcttg actatggccc gggataccag tactacggta tggacgtctg gggccaaggg     360

accacggtca ccgtctcctc a                                               381


<210> SEQ ID NO 67
<211> LENGTH: 217
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 67

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15

Arg Val Thr Ile Ser Cys Thr Gly Met Asn Ser Asn Ile Gly Ala Gly
            20                  25                  30

Tyr Asp Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35                  40                  45

Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60

Ser Gly Ser Arg Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
```

```
65                  70                  75                  80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Thr Ser
                85                  90                  95

Leu Asn Gly Trp Ala Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu
        115                 120                 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Val Ser Asp Phe
    130                 135                 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro Val
145                 150                 155                 160

Lys Val Gly Val Glu Thr Thr Lys Pro Ser Lys Gln Ser Asn Asn Lys
                165                 170                 175

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
            180                 185                 190

His Arg Ser Tyr Ser Cys Arg Val Thr His Glu Gly Ser Thr Val Glu
        195                 200                 205

Lys Thr Val Ala Pro Ala Glu Cys Ser
    210                 215


<210> SEQ ID NO 68
<211> LENGTH: 457
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 68

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Ser Phe Gly Asp His
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Gly Phe Ile Arg Lys Thr Thr Tyr Gly Ala Thr Thr His Tyr Ala Ala
    50                  55                  60

Ala Val Arg Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile
65                  70                  75                  80

Val Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
                85                  90                  95

Phe Cys Ala Arg Val Gln Leu Asp Tyr Gly Pro Gly Tyr Gln Tyr Tyr
            100                 105                 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala
        115                 120                 125

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
    130                 135                 140

Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
145                 150                 155                 160

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
                165                 170                 175

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
            180                 185                 190

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
        195                 200                 205

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
```

```
    210                 215                 220

Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
225                 230                 235                 240

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                245                 250                 255

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            260                 265                 270

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        275                 280                 285

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    290                 295                 300

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
305                 310                 315                 320

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                325                 330                 335

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            340                 345                 350

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
        355                 360                 365

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    370                 375                 380

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
385                 390                 395                 400

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                405                 410                 415

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            420                 425                 430

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
        435                 440                 445

Lys Ser Leu Ser Leu Ser Pro Gly Lys
    450                 455


<210> SEQ ID NO 69
<211> LENGTH: 457
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 69

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Ser Phe Gly Asp His
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Gly Phe Ile Arg Lys Thr Thr Tyr Gly Ala Thr Thr His Tyr Ala Ala
    50                  55                  60

Ala Val Arg Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile
65                  70                  75                  80

Val Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
                85                  90                  95

Phe Cys Ala Arg Val Gln Leu Asp Tyr Gly Pro Gly Tyr Gln Tyr Tyr
            100                 105                 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala
```

```
        115                 120                 125

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
    130                 135                 140

Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
145                 150                 155                 160

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
                165                 170                 175

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
            180                 185                 190

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
        195                 200                 205

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
    210                 215                 220

Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
225                 230                 235                 240

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                245                 250                 255

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            260                 265                 270

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        275                 280                 285

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    290                 295                 300

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
305                 310                 315                 320

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                325                 330                 335

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            340                 345                 350

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
        355                 360                 365

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    370                 375                 380

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
385                 390                 395                 400

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                405                 410                 415

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            420                 425                 430

Phe Ser Cys Ser Val Leu His Glu Ala Leu His Ser His Tyr Thr Gln
        435                 440                 445

Lys Ser Leu Ser Leu Ser Pro Gly Lys
    450                 455


<210> SEQ ID NO 70
<211> LENGTH: 651
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 70

cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc      60

tcctgcactg ggatgaactc caacatcggg gcaggttatg atgtatactg gtaccaacaa     120
```

cttccaggaa ctgcccccaa actcctcatc tatggtaaca gcaatcggcc ctcaggggtc 180

cctgaccgat tctctggctc caggtctggc acctcagcct ccctggccat cactgggctc 240

caggctgagg atgaggctga ttattactgc cagtcctatg acaccagcct gaatggttgg 300

gctttcggcg gagggaccaa gttgaccgtc ctaggccagc ccaaggctgc cccctcggtc 360

actctgttcc caccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420

gtaagtgact tctacccggg agccgtgaca gtggcctgga aggcagatgg cagccccgtc 480

aaggtgggag tggagaccac caaaccctcc aaacaaagca acaacaagta tgcggccagc 540

agctacctga gcctgacgcc cgagcagtgg aagtcccaca gaagctacag ctgccgggtc 600

acgcatgaag ggagcaccgt ggagaagaca gtggcccctg cagaatgctc t 651

<210> SEQ ID NO 71
<211> LENGTH: 1371
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 71

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc cagggcggtc cctgagactc 60

agctgtacag cctctgggtt tagttttggt gatcatgcta tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtaggtttc attagaaaga caacttatgg tgcgacaaca 180

cactacgccg cggctgtgag aggcagattc accatctcgc gagatgattc taaaagcatt 240

gtctatctgc aaatgaacag cctgaaaacc gaggacacag ccgtgtattt ctgtgctaga 300

gtgcagcttg actatggccc gggataccag tactacggta tggacgtctg gggccaaggg 360

accacggtca ccgtctcctc agcctccacc aagggcccat cggtcttccc cctggcaccc 420

tcctccaaga gcacctctgg gggcacagca gccctgggct gcctggtcaa ggactacttc 480

cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc 540

ccggctgtcc tacagtcctc aggactctac tccctcagca gcgtggtgac cgtgccctcc 600

agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag 660

gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgccca 720

gcacctgaac tcctgggggg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 780

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 840

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 900

ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 960

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc 1020

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1080

ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 1140

ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1200

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1260

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1320

gctctgcaca accactacac acagaagagc ctctccctgt ctccgggtaa a 1371

<210> SEQ ID NO 72
<211> LENGTH: 1371
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 72

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc cagggcggtc cctgagactc     60

agctgtacag cctctgggtt tagttttggt gatcatgcta tgagctgggt ccgccaggct    120

ccagggaagg ggctggagtg ggtaggtttc attagaaaga caacttatgg tgcgacaaca    180

cactacgccg cggctgtgag aggcagattc accatctcgc gagatgattc taaaagcatt    240

gtctatctgc aaatgaacag cctgaaaacc gaggacacag ccgtgtattt ctgtgctaga    300

gtgcagcttg actatggccc gggataccag tactacggta tggacgtctg gggccaaggg    360

accacggtca ccgtctcctc agcctccacc aagggcccat cggtcttccc cctggcaccc    420

tcctccaaga gcacctctgg gggcacagca gccctgggct gcctggtcaa ggactacttc    480

cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc    540

ccggctgtcc tacagtcctc aggactctac tccctcagca gcgtggtgac cgtgccctcc    600

agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag    660

gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgccca    720

gcacctgaac tcctgggggg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc    780

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac    840

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag    900

ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac    960

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc   1020

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc   1080

ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa   1140

ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac   1200

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc   1260

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gctgcatgag   1320

gctctgcact cccactacac acagaagagc ctctccctgt ctccgggtaa a            1371


<210> SEQ ID NO 73
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 73

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15

Arg Val Thr Ile Ser Cys Thr Gly Met Asn Ser Asn Ile Gly Ala Gly
            20                  25                  30

Tyr Asp Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35                  40                  45

Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60

Ser Gly Ser Arg Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65                  70                  75                  80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Thr Ser
                85                  90                  95
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Leu Asn Gly Trp Ala Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110


<210> SEQ ID NO 74
<211> LENGTH: 127
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 74

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Gly Asp His
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Gly Phe Ile Arg Lys Thr Thr Tyr Gly Ala Thr Thr His Tyr Ala Ala
    50                  55                  60

Ala Val Arg Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65                  70                  75                  80

Val Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
                85                  90                  95

Phe Cys Thr Arg Val Gln Leu Asp Tyr Gly Pro Gly Tyr Gln Tyr Tyr
            100                 105                 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120                 125


<210> SEQ ID NO 75
<211> LENGTH: 336
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 75

cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc     60

tcctgcactg ggatgaactc caacatcggg gcaggttatg atgtatactg gtaccaacaa    120

cttccaggaa ctgcccccaa actcctcatc tatggtaaca gcaatcggcc ctcaggggtc    180

cctgaccgat tctctggctc caggtctggc acctcagcct ccctggccat cactgggctc    240

caggctgagg atgaggctga ttattactgc cagtcctatg acaccagcct gaatggttgg    300

gctttcggcg gagggaccaa gttgaccgtc ctaggc                              336


<210> SEQ ID NO 76
<211> LENGTH: 381
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 76

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc cagggcggtc cctgagactc     60

agctgtgcgg cctctgggtt tagttttggt gatcatgcta tgagctgggt ccgccaggct    120

ccagggaagg ggctggagtg ggtaggtttc attagaaaga caacttatgg tgcgacaaca    180

cactacgccg cggctgtgag aggcagattc accatctcgc gagatgattc taaaagcact    240

gtctatctgc aaatgaacag cctgaaaacc gaggacacag ccgtgtattt ctgtactaga    300
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gtgcagcttg actatggccc gggataccag tactacggta tggacgtctg gggccaaggg    360

accacggtca ccgtctcctc a                                              381


<210> SEQ ID NO 77
<211> LENGTH: 217
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 77

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15

Arg Val Thr Ile Ser Cys Thr Gly Met Asn Ser Asn Ile Gly Ala Gly
            20                  25                  30

Tyr Asp Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35                  40                  45

Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60

Ser Gly Ser Arg Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65                  70                  75                  80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Thr Ser
                85                  90                  95

Leu Asn Gly Trp Ala Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu
        115                 120                 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Val Ser Asp Phe
    130                 135                 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro Val
145                 150                 155                 160

Lys Val Gly Val Glu Thr Thr Lys Pro Ser Lys Gln Ser Asn Asn Lys
                165                 170                 175

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
            180                 185                 190

His Arg Ser Tyr Ser Cys Arg Val Thr His Glu Gly Ser Thr Val Glu
        195                 200                 205

Lys Thr Val Ala Pro Ala Glu Cys Ser
    210                 215


<210> SEQ ID NO 78
<211> LENGTH: 457
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 78

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Gly Asp His
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Gly Phe Ile Arg Lys Thr Thr Tyr Gly Ala Thr Thr His Tyr Ala Ala
    50                  55                  60

Ala Val Arg Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
```

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65                  70                  75                  80

Val Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
                85                  90                  95

Phe Cys Thr Arg Val Gln Leu Asp Tyr Gly Pro Gly Tyr Gln Tyr Tyr
            100                 105                 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala
        115                 120                 125

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
    130                 135                 140

Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
145                 150                 155                 160

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
                165                 170                 175

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
            180                 185                 190

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
        195                 200                 205

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
    210                 215                 220

Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
225                 230                 235                 240

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                245                 250                 255

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            260                 265                 270

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        275                 280                 285

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    290                 295                 300

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
305                 310                 315                 320

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                325                 330                 335

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            340                 345                 350

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
        355                 360                 365

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    370                 375                 380

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
385                 390                 395                 400

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                405                 410                 415

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            420                 425                 430

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
        435                 440                 445

Lys Ser Leu Ser Leu Ser Pro Gly Lys
    450                 455


<210> SEQ ID NO 79
<211> LENGTH: 457
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 79

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Gly Asp His
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Gly Phe Ile Arg Lys Thr Thr Tyr Gly Ala Thr Thr His Tyr Ala Ala
    50                  55                  60

Ala Val Arg Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65                  70                  75                  80

Val Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
                85                  90                  95

Phe Cys Thr Arg Val Gln Leu Asp Tyr Gly Pro Gly Tyr Gln Tyr Tyr
            100                 105                 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala
        115                 120                 125

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
    130                 135                 140

Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
145                 150                 155                 160

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
                165                 170                 175

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
            180                 185                 190

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
        195                 200                 205

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
    210                 215                 220

Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
225                 230                 235                 240

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                245                 250                 255

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            260                 265                 270

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        275                 280                 285

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    290                 295                 300

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
305                 310                 315                 320

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                325                 330                 335

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            340                 345                 350

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
        355                 360                 365

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    370                 375                 380

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
385                 390                 395                 400
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Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
405 410 415

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
420 425 430

Phe Ser Cys Ser Val Leu His Glu Ala Leu His Ser His Tyr Thr Gln
435 440 445

Lys Ser Leu Ser Leu Ser Pro Gly Lys
450 455

<210> SEQ ID NO 80
<211> LENGTH: 651
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 80

cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60

tcctgcactg ggatgaactc caacatcggg gcaggttatg atgtatactg gtaccaacaa 120

cttccaggaa ctgcccccaa actcctcatc tatggtaaca gcaatcggcc ctcaggggtc 180

cctgaccgat tctctggctc caggtctggc acctcagcct ccctggccat cactgggctc 240

caggctgagg atgaggctga ttattactgc cagtcctatg acaccagcct gaatggttgg 300

gctttcggcg gagggaccaa gttgaccgtc ctaggccagc ccaaggctgc cccctcggtc 360

actctgttcc caccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420

gtaagtgact tctacccggg agccgtgaca gtggcctgga aggcagatgg cagccccgtc 480

aaggtgggag tggagaccac caaaccctcc aaacaaagca acaacaagta tgcggccagc 540

agctacctga gcctgacgcc cgagcagtgg aagtcccaca gaagctacag ctgccgggtc 600

acgcatgaag ggagcaccgt ggagaagaca gtggcccctg cagaatgctc t 651

<210> SEQ ID NO 81
<211> LENGTH: 1371
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 81

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc cagggcggtc cctgagactc 60

agctgtgcgg cctctgggtt tagttttggt gatcatgcta tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtaggtttc attagaaaga caacttatgg tgcgacaaca 180

cactacgccg cggctgtgag aggcagattc accatctcgc gagatgattc taaaagcact 240

gtctatctgc aaatgaacag cctgaaaacc gaggacacag ccgtgtattt ctgtactaga 300

gtgcagcttg actatggccc gggataccag tactacggta tggacgtctg gggccaaggg 360

accacggtca ccgtctcctc agcctccacc aagggcccat cggtcttccc cctggcaccc 420

tcctccaaga gcacctctgg gggcacagca gccctgggct gcctggtcaa ggactacttc 480

cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc 540

ccggctgtcc tacagtcctc aggactctac tccctcagca gcgtggtgac cgtgccctcc 600

agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag 660

gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgccca 720

-continued

gcacctgaac tcctgggggg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 780

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 840

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 900

ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 960

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc 1020

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1080

ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 1140

ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1200

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1260

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1320

gctctgcaca accactacac acagaagagc ctctccctgt ctccgggtaa a 1371

<210> SEQ ID NO 82
<211> LENGTH: 1371
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 82

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc cagggcggtc cctgagactc 60

agctgtgcgg cctctgggtt tagttttggt gatcatgcta tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtaggtttc attagaaaga caacttatgg tgcgacaaca 180

cactacgccg cggctgtgag aggcagattc accatctcgc gagatgattc taaaagcact 240

gtctatctgc aaatgaacag cctgaaaacc gaggacacag ccgtgtattt ctgtactaga 300

gtgcagcttg actatggccc gggataccag tactacggta tggacgtctg gggccaaggg 360

accacggtca ccgtctcctc agcctccacc aagggcccat cggtcttccc cctggcaccc 420

tcctccaaga gcacctctgg gggcacagca gccctgggct gcctggtcaa ggactacttc 480

cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc 540

ccggctgtcc tacagtcctc aggactctac tccctcagca gcgtggtgac cgtgccctcc 600

agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag 660

gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgccca 720

gcacctgaac tcctgggggg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 780

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 840

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 900

ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 960

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc 1020

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1080

ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 1140

ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1200

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1260

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gctgcatgag 1320

gctctgcact cccactacac acagaagagc ctctccctgt ctccgggtaa a 1371

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<210> SEQ ID NO 83
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 83

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15

Arg Val Thr Ile Ser Cys Thr Gly Met Asn Ser Asn Ile Gly Ala Gly
            20                  25                  30

Tyr Asp Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35                  40                  45

Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60

Ser Gly Ser Arg Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65                  70                  75                  80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Thr Ser
                85                  90                  95

Leu Asn Gly Trp Ala Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110


<210> SEQ ID NO 84
<211> LENGTH: 127
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 84

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Gly Asp His
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Gly Phe Ile Arg Lys Thr Thr Tyr Gly Ala Thr Thr His Tyr Ala Ala
    50                  55                  60

Ala Val Arg Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile
65                  70                  75                  80

Val Tyr Leu Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr
                85                  90                  95

Phe Cys Thr Arg Val Gln Leu Asp Tyr Gly Pro Gly Tyr Gln Tyr Tyr
            100                 105                 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120                 125


<210> SEQ ID NO 85
<211> LENGTH: 336
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 85

cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc      60

tcctgcactg ggatgaactc caacatcggg gcaggttatg atgtatactg gtaccaacaa     120

cttccaggaa ctgcccccaa actcctcatc tatggtaaca gcaatcggcc ctcaggggtc     180
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cctgaccgat tctctggctc caggtctggc acctcagcct ccctggccat cactgggctc    240

caggctgagg atgaggctga ttattactgc cagtcctatg acaccagcct gaatggttgg    300

gctttcggcg gagggaccaa gttgaccgtc ctaggc                              336


<210> SEQ ID NO 86
<211> LENGTH: 381
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 86

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc cagggcggtc cctgagactc     60

agctgtgcgg cctctgggtt tagttttggt gatcatgcta tgagctgggt ccgccaggct    120

ccagggaagg ggctggagtg ggtaggtttc attagaaaga caacttatgg tgcgacaaca    180

cactacgccg cggctgtgag aggcagattc accatctcgc gagatgattc taaaagcatt    240

gtctatctgc aaatgaacag cctgaaagca gaggacacag ccgtgtattt ctgtactaga    300

gtgcagcttg actatggccc gggataccag tactacggta tggacgtctg gggccaaggg    360

accacggtca ccgtctcctc a                                              381


<210> SEQ ID NO 87
<211> LENGTH: 217
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 87

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15

Arg Val Thr Ile Ser Cys Thr Gly Met Asn Ser Asn Ile Gly Ala Gly
            20                  25                  30

Tyr Asp Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35                  40                  45

Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60

Ser Gly Ser Arg Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65                  70                  75                  80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Thr Ser
                85                  90                  95

Leu Asn Gly Trp Ala Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu
        115                 120                 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Val Ser Asp Phe
    130                 135                 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro Val
145                 150                 155                 160

Lys Val Gly Val Glu Thr Thr Lys Pro Ser Lys Gln Ser Asn Asn Lys
                165                 170                 175

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
            180                 185                 190

His Arg Ser Tyr Ser Cys Arg Val Thr His Glu Gly Ser Thr Val Glu
        195                 200                 205
```

```
Lys Thr Val Ala Pro Ala Glu Cys Ser
    210                 215


<210> SEQ ID NO 88
<211> LENGTH: 457
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 88

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Gly Asp His
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Gly Phe Ile Arg Lys Thr Thr Tyr Gly Ala Thr Thr His Tyr Ala Ala
    50                  55                  60

Ala Val Arg Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile
65                  70                  75                  80

Val Tyr Leu Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr
                85                  90                  95

Phe Cys Thr Arg Val Gln Leu Asp Tyr Gly Pro Gly Tyr Gln Tyr Tyr
            100                 105                 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala
        115                 120                 125

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
    130                 135                 140

Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
145                 150                 155                 160

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
                165                 170                 175

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
            180                 185                 190

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
        195                 200                 205

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
    210                 215                 220

Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
225                 230                 235                 240

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                245                 250                 255

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            260                 265                 270

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        275                 280                 285

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    290                 295                 300

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
305                 310                 315                 320

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                325                 330                 335

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            340                 345                 350
```

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
355 360 365

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
370 375 380

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
385 390 395 400

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
405 410 415

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
420 425 430

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
435 440 445

Lys Ser Leu Ser Leu Ser Pro Gly Lys
450 455

<210> SEQ ID NO 89
<211> LENGTH: 457
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 89

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Gly Asp His
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Gly Phe Ile Arg Lys Thr Thr Tyr Gly Ala Thr Thr His Tyr Ala Ala
50 55 60

Ala Val Arg Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile
65 70 75 80

Val Tyr Leu Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr
85 90 95

Phe Cys Thr Arg Val Gln Leu Asp Tyr Gly Pro Gly Tyr Gln Tyr Tyr
100 105 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala
115 120 125

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
130 135 140

Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
145 150 155 160

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
165 170 175

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
180 185 190

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
195 200 205

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
210 215 220

Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
225 230 235 240

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
245 250 255

```
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            260                 265                 270

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        275                 280                 285

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    290                 295                 300

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
305                 310                 315                 320

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                325                 330                 335

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            340                 345                 350

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
        355                 360                 365

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    370                 375                 380

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
385                 390                 395                 400

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                405                 410                 415

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            420                 425                 430

Phe Ser Cys Ser Val Leu His Glu Ala Leu His Ser His Tyr Thr Gln
        435                 440                 445

Lys Ser Leu Ser Leu Ser Pro Gly Lys
    450                 455
```

<210> SEQ ID NO 90
<211> LENGTH: 651
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 90

```
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc     60

tcctgcactg ggatgaactc caacatcggg gcaggttatg atgtatactg gtaccaacaa    120

cttccaggaa ctgcccccaa actcctcatc tatggtaaca gcaatcggcc ctcaggggtc    180

cctgaccgat tctctggctc caggtctggc acctcagcct ccctggccat cactgggctc    240

caggctgagg atgaggctga ttattactgc cagtcctatg acaccagcct gaatggttgg    300

gctttcggcg gagggaccaa gttgaccgtc ctaggccagc ccaaggctgc cccctcggtc    360

actctgttcc caccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc    420

gtaagtgact tctacccggg agccgtgaca gtggcctgga aggcagatgg cagccccgtc    480

aaggtgggag tggagaccac caaaccctcc aaacaaagca acaacaagta tgcggccagc    540

agctacctga gcctgacgcc cgagcagtgg aagtcccaca gaagctacag ctgccgggtc    600

acgcatgaag ggagcaccgt ggagaagaca gtggcccctg cagaatgctc t             651
```

<210> SEQ ID NO 91
<211> LENGTH: 1371
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 91

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc cagggcggtc cctgagactc 60

agctgtgcgg cctctgggtt tagttttggt gatcatgcta tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtaggtttc attagaaaga caacttatgg tgcgacaaca 180

cactacgccg cggctgtgag aggcagattc accatctcgc gagatgattc taaaagcatt 240

gtctatctgc aaatgaacag cctgaaagca gaggacacag ccgtgtattt ctgtactaga 300

gtgcagcttg actatggccc gggataccag tactacggta tggacgtctg gggccaaggg 360

accacggtca ccgtctcctc agcctccacc aagggcccat cggtcttccc cctggcaccc 420

tcctccaaga gcacctctgg gggcacagca gccctgggct gcctggtcaa ggactacttc 480

cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc 540

ccggctgtcc tacagtcctc aggactctac tccctcagca gcgtggtgac cgtgccctcc 600

agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag 660

gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgccca 720

gcacctgaac tcctgggggg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 780

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 840

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 900

ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 960

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc 1020

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1080

ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 1140

ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1200

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1260

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1320

gctctgcaca accactacac acagaagagc ctctccctgt ctccgggtaa a 1371

<210> SEQ ID NO 92
<211> LENGTH: 1371
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 92

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc cagggcggtc cctgagactc 60

agctgtgcgg cctctgggtt tagttttggt gatcatgcta tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtaggtttc attagaaaga caacttatgg tgcgacaaca 180

cactacgccg cggctgtgag aggcagattc accatctcgc gagatgattc taaaagcatt 240

gtctatctgc aaatgaacag cctgaaagca gaggacacag ccgtgtattt ctgtactaga 300

gtgcagcttg actatggccc gggataccag tactacggta tggacgtctg gggccaaggg 360

accacggtca ccgtctcctc agcctccacc aagggcccat cggtcttccc cctggcaccc 420

tcctccaaga gcacctctgg gggcacagca gccctgggct gcctggtcaa ggactacttc 480

cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc 540

ccggctgtcc tacagtcctc aggactctac tccctcagca gcgtggtgac cgtgccctcc 600

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agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag    660

gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgccca    720

gcacctgaac tcctgggggg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc    780

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac    840

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag    900

ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac    960

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc   1020

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc   1080

ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa   1140

ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac   1200

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc   1260

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gctgcatgag   1320

gctctgcact cccactacac acagaagagc ctctccctgt ctccgggtaa a            1371
```

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<210> SEQ ID NO 93
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 93

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15

Arg Val Thr Ile Ser Cys Thr Gly Met Asn Ser Asn Ile Gly Ala Gly
            20                  25                  30

Tyr Asp Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35                  40                  45

Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60

Ser Gly Ser Arg Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65                  70                  75                  80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Thr Ser
                85                  90                  95

Leu Asn Gly Trp Ala Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110


<210> SEQ ID NO 94
<211> LENGTH: 127
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 94

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Gly Asp His
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Gly Phe Ile Arg Lys Thr Thr Tyr Gly Ala Thr Thr His Tyr Ala Ala
    50                  55                  60
```

```
Ala Val Arg Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile
65                  70                  75                  80

Val Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
                85                  90                  95

Phe Cys Ala Arg Val Gln Leu Asp Tyr Gly Pro Gly Tyr Gln Tyr Tyr
            100                 105                 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120                 125


<210> SEQ ID NO 95
<211> LENGTH: 336
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 95

cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc      60

tcctgcactg ggatgaactc caacatcggg gcaggttatg atgtatactg gtaccaacaa     120

cttccaggaa ctgcccccaa actcctcatc tatggtaaca gcaatcggcc ctcaggggtc     180

cctgaccgat tctctggctc caggtctggc acctcagcct ccctggccat cactgggctc     240

caggctgagg atgaggctga ttattactgc cagtcctatg acaccagcct gaatggttgg     300

gctttcggcg gagggaccaa gttgaccgtc ctaggc                               336


<210> SEQ ID NO 96
<211> LENGTH: 381
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 96

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc cagggcggtc cctgagactc      60

agctgtgcgg cctctgggtt tagttttggt gatcatgcta tgagctgggt ccgccaggct     120

ccagggaagg ggctggagtg ggtaggtttc attagaaaga caacttatgg tgcgacaaca     180

cactacgccg cggctgtgag aggcagattc accatctcgc gagatgattc taaaagcatt     240

gtctatctgc aaatgaacag cctgaaaacc gaggacacag ccgtgtattt ctgtgctaga     300

gtgcagcttg actatggccc gggataccag tactacggta tggacgtctg gggccaaggg     360

accacggtca ccgtctcctc a                                               381


<210> SEQ ID NO 97
<211> LENGTH: 217
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 97

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15

Arg Val Thr Ile Ser Cys Thr Gly Met Asn Ser Asn Ile Gly Ala Gly
            20                  25                  30

Tyr Asp Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35                  40                  45

Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60
```

```
Ser Gly Ser Arg Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65                  70                  75                  80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Thr Ser
                85                  90                  95

Leu Asn Gly Trp Ala Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu
        115                 120                 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Val Ser Asp Phe
    130                 135                 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro Val
145                 150                 155                 160

Lys Val Gly Val Glu Thr Thr Lys Pro Ser Lys Gln Ser Asn Asn Lys
                165                 170                 175

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
            180                 185                 190

His Arg Ser Tyr Ser Cys Arg Val Thr His Glu Gly Ser Thr Val Glu
        195                 200                 205

Lys Thr Val Ala Pro Ala Glu Cys Ser
    210                 215


<210> SEQ ID NO 98
<211> LENGTH: 457
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 98

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Gly Asp His
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Gly Phe Ile Arg Lys Thr Thr Tyr Gly Ala Thr Thr His Tyr Ala Ala
    50                  55                  60

Ala Val Arg Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile
65                  70                  75                  80

Val Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
                85                  90                  95

Phe Cys Ala Arg Val Gln Leu Asp Tyr Gly Pro Gly Tyr Gln Tyr Tyr
            100                 105                 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala
        115                 120                 125

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
    130                 135                 140

Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
145                 150                 155                 160

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
                165                 170                 175

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
            180                 185                 190

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
        195                 200                 205
```

```
Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
    210                 215                 220

Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
225                 230                 235                 240

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                245                 250                 255

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            260                 265                 270

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        275                 280                 285

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    290                 295                 300

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
305                 310                 315                 320

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                325                 330                 335

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            340                 345                 350

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
        355                 360                 365

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    370                 375                 380

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
385                 390                 395                 400

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                405                 410                 415

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            420                 425                 430

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
        435                 440                 445

Lys Ser Leu Ser Leu Ser Pro Gly Lys
    450                 455


<210> SEQ ID NO 99
<211> LENGTH: 457
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 99

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Gly Asp His
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Gly Phe Ile Arg Lys Thr Thr Tyr Gly Ala Thr Thr His Tyr Ala Ala
    50                  55                  60

Ala Val Arg Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile
65                  70                  75                  80

Val Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
                85                  90                  95

Phe Cys Ala Arg Val Gln Leu Asp Tyr Gly Pro Gly Tyr Gln Tyr Tyr
            100                 105                 110
```

```
Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala
        115                 120                 125

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
    130                 135                 140

Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
145                 150                 155                 160

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
                165                 170                 175

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
            180                 185                 190

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
        195                 200                 205

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
    210                 215                 220

Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
225                 230                 235                 240

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                245                 250                 255

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            260                 265                 270

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        275                 280                 285

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    290                 295                 300

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
305                 310                 315                 320

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                325                 330                 335

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            340                 345                 350

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
        355                 360                 365

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    370                 375                 380

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
385                 390                 395                 400

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                405                 410                 415

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            420                 425                 430

Phe Ser Cys Ser Val Leu His Glu Ala Leu His Ser His Tyr Thr Gln
        435                 440                 445

Lys Ser Leu Ser Leu Ser Pro Gly Lys
    450                 455
```

<210> SEQ ID NO 100
<211> LENGTH: 651
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 100

```
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc      60
```

-continued

tcctgcactg ggatgaactc caacatcggg gcaggttatg atgtatactg gtaccaacaa 120

cttccaggaa ctgcccccaa actcctcatc tatggtaaca gcaatcggcc ctcaggggtc 180

cctgaccgat tctctggctc caggtctggc acctcagcct ccctggccat cactgggctc 240

caggctgagg atgaggctga ttattactgc cagtcctatg acaccagcct gaatggttgg 300

gctttcggcg gagggaccaa gttgaccgtc ctaggccagc ccaaggctgc cccctcggtc 360

actctgttcc caccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420

gtaagtgact tctacccggg agccgtgaca gtggcctgga aggcagatgg cagccccgtc 480

aaggtgggag tggagaccac caaaccctcc aaacaaagca acaacaagta tgcggccagc 540

agctacctga gcctgacgcc cgagcagtgg aagtcccaca gaagctacag ctgccgggtc 600

acgcatgaag ggagcaccgt ggagaagaca gtggcccctg cagaatgctc t 651

<210> SEQ ID NO 101
<211> LENGTH: 1371
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 101

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc cagggcggtc cctgagactc 60

agctgtgcgg cctctgggtt tagttttggt gatcatgcta tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtaggtttc attagaaaga caacttatgg tgcgacaaca 180

cactacgccg cggctgtgag aggcagattc accatctcgc gagatgattc taaaagcatt 240

gtctatctgc aaatgaacag cctgaaaacc gaggacacag ccgtgtattt ctgtgctaga 300

gtgcagcttg actatggccc gggataccag tactacggta tggacgtctg gggccaaggg 360

accacggtca ccgtctcctc agcctccacc aagggcccat cggtcttccc cctggcaccc 420

tcctccaaga gcacctctgg gggcacagca gccctgggct gcctggtcaa ggactacttc 480

cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc 540

ccggctgtcc tacagtcctc aggactctac tccctcagca gcgtggtgac cgtgccctcc 600

agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag 660

gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgccca 720

gcacctgaac tcctgggggg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 780

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 840

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 900

ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 960

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc 1020

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1080

ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 1140

ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1200

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1260

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1320

gctctgcaca accactacac acagaagagc ctctccctgt ctccgggtaa a 1371

<210> SEQ ID NO 102
<211> LENGTH: 1371

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 102

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc cagggcggtc cctgagactc      60

agctgtgcgg cctctgggtt tagttttggt gatcatgcta tgagctgggt ccgccaggct     120

ccagggaagg ggctggagtg ggtaggtttc attagaaaga caacttatgg tgcgacaaca     180

cactacgccg cggctgtgag aggcagattc accatctcgc gagatgattc taaaagcatt     240

gtctatctgc aaatgaacag cctgaaaacc gaggacacag ccgtgtattt ctgtgctaga     300

gtgcagcttg actatggccc gggataccag tactacggta tggacgtctg gggccaaggg     360

accacggtca ccgtctcctc agcctccacc aagggcccat cggtcttccc cctggcaccc     420

tcctccaaga gcacctctgg gggcacagca gccctgggct gcctggtcaa ggactacttc     480

cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc     540

ccggctgtcc tacagtcctc aggactctac tccctcagca gcgtggtgac cgtgccctcc     600

agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag     660

gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgccca     720

gcacctgaac tcctgggggg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc     780

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac     840

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag     900

ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac     960

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc    1020

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc    1080

ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa    1140

ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac    1200

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc    1260

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gctgcatgag    1320

gctctgcact cccactacac acagaagagc ctctccctgt ctccgggtaa a             1371


<210> SEQ ID NO 103
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 103

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15

Arg Val Thr Ile Ser Cys Thr Gly Met Asn Ser Asn Ile Gly Ala Gly
            20                  25                  30

Tyr Asp Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35                  40                  45

Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60

Ser Gly Ser Arg Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65                  70                  75                  80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Thr Ser
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                85                  90                  95

Leu Asn Gly Trp Ala Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110


<210> SEQ ID NO 104
<211> LENGTH: 127
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 104

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Ser Phe Gly Asp His
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Gly Phe Ile Arg Lys Thr Thr Tyr Gly Ala Thr Thr His Tyr Ala Ala
    50                  55                  60

Ala Val Arg Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65                  70                  75                  80

Val Tyr Leu Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr
                85                  90                  95

Phe Cys Thr Arg Val Gln Leu Asp Tyr Gly Pro Gly Tyr Gln Tyr Tyr
            100                 105                 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120                 125


<210> SEQ ID NO 105
<211> LENGTH: 336
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 105

cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc      60

tcctgcactg ggatgaactc caacatcggg gcaggttatg atgtatactg gtaccaacaa     120

cttccaggaa ctgcccccaa actcctcatc tatggtaaca gcaatcggcc ctcaggggtc     180

cctgaccgat tctctggctc caggtctggc acctcagcct ccctggccat cactgggctc     240

caggctgagg atgaggctga ttattactgc cagtcctatg acaccagcct gaatggttgg     300

gctttcggcg gagggaccaa gttgaccgtc ctaggc                               336


<210> SEQ ID NO 106
<211> LENGTH: 381
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 106

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc cagggcggtc cctgagactc      60

agctgtacag cctctgggtt tagttttggt gatcatgcta tgagctgggt ccgccaggct     120

ccagggaagg ggctggagtg ggtaggtttc attagaaaga caacttatgg tgcgacaaca     180

cactacgccg cggctgtgag aggcagattc accatctcgc gagatgattc taaaagcact     240
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gtctatctgc aaatgaacag cctgaaagca gaggacacag ccgtgtattt ctgtactaga    300

gtgcagcttg actatggccc gggataccag tactacggta tggacgtctg ggccaaggg    360

accacggtca ccgtctcctc a                                               381


<210> SEQ ID NO 107
<211> LENGTH: 217
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 107

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15

Arg Val Thr Ile Ser Cys Thr Gly Met Asn Ser Asn Ile Gly Ala Gly
            20                  25                  30

Tyr Asp Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35                  40                  45

Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60

Ser Gly Ser Arg Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65                  70                  75                  80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Thr Ser
                85                  90                  95

Leu Asn Gly Trp Ala Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu
        115                 120                 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Val Ser Asp Phe
    130                 135                 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro Val
145                 150                 155                 160

Lys Val Gly Val Glu Thr Thr Lys Pro Ser Lys Gln Ser Asn Asn Lys
                165                 170                 175

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
            180                 185                 190

His Arg Ser Tyr Ser Cys Arg Val Thr His Glu Gly Ser Thr Val Glu
        195                 200                 205

Lys Thr Val Ala Pro Ala Glu Cys Ser
    210                 215


<210> SEQ ID NO 108
<211> LENGTH: 457
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 108

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Ser Phe Gly Asp His
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Gly Phe Ile Arg Lys Thr Thr Tyr Gly Ala Thr Thr His Tyr Ala Ala
    50                  55                  60
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Ala Val Arg Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65                  70                  75                  80

Val Tyr Leu Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr
                85                  90                  95

Phe Cys Thr Arg Val Gln Leu Asp Tyr Gly Pro Gly Tyr Gln Tyr Tyr
            100                 105                 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala
        115                 120                 125

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
    130                 135                 140

Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
145                 150                 155                 160

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
                165                 170                 175

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
            180                 185                 190

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
        195                 200                 205

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
    210                 215                 220

Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
225                 230                 235                 240

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                245                 250                 255

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            260                 265                 270

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        275                 280                 285

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    290                 295                 300

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
305                 310                 315                 320

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                325                 330                 335

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            340                 345                 350

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
        355                 360                 365

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    370                 375                 380

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
385                 390                 395                 400

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                405                 410                 415

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            420                 425                 430

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
        435                 440                 445

Lys Ser Leu Ser Leu Ser Pro Gly Lys
    450                 455


<210> SEQ ID NO 109
<211> LENGTH: 457
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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 109

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1   5   10   15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Ser Phe Gly Asp His
            20   25   30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Gly Phe Ile Arg Lys Thr Thr Tyr Gly Ala Thr Thr His Tyr Ala Ala
    50   55   60

Ala Val Arg Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65   70   75   80

Val Tyr Leu Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr
                85   90   95

Phe Cys Thr Arg Val Gln Leu Asp Tyr Gly Pro Gly Tyr Gln Tyr Tyr
            100   105   110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala
        115   120   125

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
    130   135   140

Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
145   150   155   160

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
                165   170   175

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
            180   185   190

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
        195   200   205

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
    210   215   220

Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
225   230   235   240

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                245   250   255

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            260   265   270

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        275   280   285

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    290   295   300

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
305   310   315   320

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                325   330   335

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            340   345   350

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
        355   360   365

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    370   375   380

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Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
385                 390                 395                 400

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                405                 410                 415

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            420                 425                 430

Phe Ser Cys Ser Val Leu His Glu Ala Leu His Ser His Tyr Thr Gln
    435                 440                 445

Lys Ser Leu Ser Leu Ser Pro Gly Lys
    450                 455


<210> SEQ ID NO 110
<211> LENGTH: 651
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 110

cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc      60

tcctgcactg ggatgaactc caacatcggg gcaggttatg atgtatactg gtaccaacaa     120

cttccaggaa ctgcccccaa actcctcatc tatggtaaca gcaatcggcc ctcaggggtc     180

cctgaccgat tctctggctc caggtctggc acctcagcct ccctggccat cactgggctc     240

caggctgagg atgaggctga ttattactgc cagtcctatg acaccagcct gaatggttgg     300

gctttcggcg gagggaccaa gttgaccgtc ctaggccagc ccaaggctgc cccctcggtc     360

actctgttcc caccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc     420

gtaagtgact tctacccggg agccgtgaca gtggcctgga aggcagatgg cagccccgtc     480

aaggtgggag tggagaccac caaaccctcc aaacaaagca acaacaagta tgcggccagc     540

agctacctga gcctgacgcc cgagcagtgg aagtcccaca gaagctacag ctgccgggtc     600

acgcatgaag ggagcaccgt ggagaagaca gtggcccctg cagaatgctc t              651


<210> SEQ ID NO 111
<211> LENGTH: 1371
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 111

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc cagggcggtc cctgagactc      60

agctgtacag cctctgggtt tagttttggt gatcatgcta tgagctgggt ccgccaggct     120

ccagggaagg ggctggagtg ggtaggtttc attagaaaga caacttatgg tgcgacaaca     180

cactacgccg cggctgtgag aggcagattc accatctcgc gagatgattc taaaagcact     240

gtctatctgc aaatgaacag cctgaaagca gaggacacag ccgtgtattt ctgtactaga     300

gtgcagcttg actatggccc gggataccag tactacggta tggacgtctg gggccaaggg     360

accacggtca ccgtctcctc agcctccacc aagggcccat cggtcttccc cctggcaccc     420

tcctccaaga gcacctctgg gggcacagca gccctgggct gcctggtcaa ggactacttc     480

cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc     540

ccggctgtcc tacagtcctc aggactctac tccctcagca gcgtggtgac cgtgccctcc     600

agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag     660
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gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgccca 720

gcacctgaac tcctgggggg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 780

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 840

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 900

ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 960

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc 1020

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1080

ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 1140

ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1200

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1260

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1320

gctctgcaca accactacac acagaagagc ctctccctgt ctccgggtaa a 1371

<210> SEQ ID NO 112
<211> LENGTH: 1371
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 112

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc cagggcggtc cctgagactc 60

agctgtacag cctctgggtt tagttttggt gatcatgcta tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtaggtttc attagaaaga caacttatgg tgcgacaaca 180

cactacgccg cggctgtgag aggcagattc accatctcgc gagatgattc taaaagcact 240

gtctatctgc aaatgaacag cctgaaagca gaggacacag ccgtgtattt ctgtactaga 300

gtgcagcttg actatggccc gggataccag tactacggta tggacgtctg gggccaaggg 360

accacggtca ccgtctcctc agcctccacc aagggcccat cggtcttccc cctggcaccc 420

tcctccaaga gcacctctgg gggcacagca gccctgggct gcctggtcaa ggactacttc 480

cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc 540

ccggctgtcc tacagtcctc aggactctac tccctcagca gcgtggtgac cgtgccctcc 600

agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag 660

gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgccca 720

gcacctgaac tcctgggggg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 780

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 840

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 900

ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 960

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc 1020

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1080

ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 1140

ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1200

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1260

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gctgcatgag 1320

gctctgcact cccactacac acagaagagc ctctccctgt ctccgggtaa a 1371

<210> SEQ ID NO 113
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 113

```
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15

Arg Val Thr Ile Ser Cys Thr Gly Met Asn Ser Asn Ile Gly Ala Gly
            20                  25                  30

Tyr Asp Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35                  40                  45

Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60

Ser Gly Ser Arg Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65              70                  75                      80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Thr Ser
                85                  90                  95

Leu Asn Gly Trp Ala Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110
```

<210> SEQ ID NO 114
<211> LENGTH: 127
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 114

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Ser Phe Gly Asp His
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Gly Phe Ile Arg Lys Thr Thr Tyr Gly Ala Thr Thr His Tyr Ala Ala
    50                  55                  60

Ala Val Arg Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65              70                  75                      80

Val Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
                85                  90                  95

Phe Cys Ala Arg Val Gln Leu Asp Tyr Gly Pro Gly Tyr Gln Tyr Tyr
            100                 105                 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120                 125
```

<210> SEQ ID NO 115
<211> LENGTH: 336
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 115

```
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc      60

tcctgcactg ggatgaactc caacatcggg gcaggttatg atgtatactg gtaccaacaa     120
```

```
cttccaggaa ctgcccccaa actcctcatc tatggtaaca gcaatcggcc ctcaggggtc    180

cctgaccgat tctctggctc caggtctggc acctcagcct ccctggccat cactgggctc    240

caggctgagg atgaggctga ttattactgc cagtcctatg acaccagcct gaatggttgg    300

gctttcggcg gagggaccaa gttgaccgtc ctaggc                              336


<210> SEQ ID NO 116
<211> LENGTH: 381
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 116

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc cagggcggtc cctgagactc     60

agctgtacag cctctgggtt tagttttggt gatcatgcta tgagctgggt ccgccaggct    120

ccagggaagg ggctggagtg ggtaggtttc attagaaaga caacttatgg tgcgacaaca    180

cactacgccg cggctgtgag aggcagattc accatctcgc gagatgattc taaaagcact    240

gtctatctgc aaatgaacag cctgaaaacc gaggacacag ccgtgtattt ctgtgctaga    300

gtgcagcttg actatggccc gggataccag tactacggta tggacgtctg gggccaaggg    360

accacggtca ccgtctcctc a                                              381


<210> SEQ ID NO 117
<211> LENGTH: 217
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 117

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15

Arg Val Thr Ile Ser Cys Thr Gly Met Asn Ser Asn Ile Gly Ala Gly
            20                  25                  30

Tyr Asp Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35                  40                  45

Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60

Ser Gly Ser Arg Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65                  70                  75                  80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Thr Ser
                85                  90                  95

Leu Asn Gly Trp Ala Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu
        115                 120                 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Val Ser Asp Phe
    130                 135                 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro Val
145                 150                 155                 160

Lys Val Gly Val Glu Thr Thr Lys Pro Ser Lys Gln Ser Asn Asn Lys
                165                 170                 175

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
            180                 185                 190
```

```
His Arg Ser Tyr Ser Cys Arg Val Thr His Glu Gly Ser Thr Val Glu
        195                 200                 205

Lys Thr Val Ala Pro Ala Glu Cys Ser
    210                 215


<210> SEQ ID NO 118
<211> LENGTH: 457
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 118

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Ser Phe Gly Asp His
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Gly Phe Ile Arg Lys Thr Thr Tyr Gly Ala Thr Thr His Tyr Ala Ala
    50                  55                  60

Ala Val Arg Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65                  70                  75                  80

Val Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
                85                  90                  95

Phe Cys Ala Arg Val Gln Leu Asp Tyr Gly Pro Gly Tyr Gln Tyr Tyr
            100                 105                 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala
        115                 120                 125

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
    130                 135                 140

Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
145                 150                 155                 160

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
                165                 170                 175

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
            180                 185                 190

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
        195                 200                 205

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
    210                 215                 220

Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
225                 230                 235                 240

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                245                 250                 255

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            260                 265                 270

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        275                 280                 285

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    290                 295                 300

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
305                 310                 315                 320

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                325                 330                 335
```

-continued

```
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            340                 345                 350

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
        355                 360                 365

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    370                 375                 380

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
385                 390                 395                 400

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                405                 410                 415

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            420                 425                 430

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
        435                 440                 445

Lys Ser Leu Ser Leu Ser Pro Gly Lys
    450                 455


<210> SEQ ID NO 119
<211> LENGTH: 457
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 119

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Ser Phe Gly Asp His
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Gly Phe Ile Arg Lys Thr Thr Tyr Gly Ala Thr Thr His Tyr Ala Ala
    50                  55                  60

Ala Val Arg Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65                  70                  75                  80

Val Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
                85                  90                  95

Phe Cys Ala Arg Val Gln Leu Asp Tyr Gly Pro Gly Tyr Gln Tyr Tyr
            100                 105                 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala
        115                 120                 125

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
    130                 135                 140

Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
145                 150                 155                 160

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
                165                 170                 175

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
            180                 185                 190

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
        195                 200                 205

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
    210                 215                 220

Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
225                 230                 235                 240
```

```
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                245                 250                 255

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            260                 265                 270

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        275                 280                 285

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    290                 295                 300

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
305                 310                 315                 320

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                325                 330                 335

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            340                 345                 350

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
        355                 360                 365

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    370                 375                 380

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
385                 390                 395                 400

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                405                 410                 415

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            420                 425                 430

Phe Ser Cys Ser Val Leu His Glu Ala Leu His Ser His Tyr Thr Gln
        435                 440                 445

Lys Ser Leu Ser Leu Ser Pro Gly Lys
    450                 455


<210> SEQ ID NO 120
<211> LENGTH: 651
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 120

cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc      60

tcctgcactg ggatgaactc caacatcggg gcaggttatg atgtatactg gtaccaacaa     120

cttccaggaa ctgcccccaa actcctcatc tatggtaaca gcaatcggcc ctcaggggtc     180

cctgaccgat tctctggctc caggtctggc acctcagcct ccctggccat cactgggctc     240

caggctgagg atgaggctga ttattactgc cagtcctatg acaccagcct gaatggttgg     300

gctttcggcg gagggaccaa gttgaccgtc ctaggccagc ccaaggctgc cccctcggtc     360

actctgttcc caccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc     420

gtaagtgact tctacccggg agccgtgaca gtggcctgga aggcagatgg cagccccgtc     480

aaggtgggag tggagaccac caaaccctcc aaacaaagca acaacaagta tgcggccagc     540

agctacctga gcctgacgcc cgagcagtgg aagtcccaca gaagctacag ctgccgggtc     600

acgcatgaag ggagcaccgt ggagaagaca gtggcccctg cagaatgctc t              651


<210> SEQ ID NO 121
<211> LENGTH: 1371
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
```

<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 121

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc cagggcggtc cctgagactc 60

agctgtacag cctctgggtt tagttttggt gatcatgcta tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtaggtttc attagaaaga caacttatgg tgcgacaaca 180

cactacgccg cggctgtgag aggcagattc accatctcgc gagatgattc taaaagcact 240

gtctatctgc aaatgaacag cctgaaaacc gaggacacag ccgtgtattt ctgtgctaga 300

gtgcagcttg actatggccc gggataccag tactacggta tggacgtctg gggccaaggg 360

accacggtca ccgtctcctc agcctccacc aagggcccat cggtcttccc cctggcaccc 420

tcctccaaga gcacctctgg gggcacagca gccctgggct gcctggtcaa ggactacttc 480

cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc 540

ccggctgtcc tacagtcctc aggactctac tccctcagca gcgtggtgac cgtgccctcc 600

agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag 660

gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgccca 720

gcacctgaac tcctgggggg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 780

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 840

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 900

ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 960

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc 1020

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1080

ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 1140

ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1200

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1260

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1320

gctctgcaca accactacac acagaagagc ctctccctgt ctccgggtaa a 1371

<210> SEQ ID NO 122
<211> LENGTH: 1371
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 122

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc cagggcggtc cctgagactc 60

agctgtacag cctctgggtt tagttttggt gatcatgcta tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtaggtttc attagaaaga caacttatgg tgcgacaaca 180

cactacgccg cggctgtgag aggcagattc accatctcgc gagatgattc taaaagcact 240

gtctatctgc aaatgaacag cctgaaaacc gaggacacag ccgtgtattt ctgtgctaga 300

gtgcagcttg actatggccc gggataccag tactacggta tggacgtctg gggccaaggg 360

accacggtca ccgtctcctc agcctccacc aagggcccat cggtcttccc cctggcaccc 420

tcctccaaga gcacctctgg gggcacagca gccctgggct gcctggtcaa ggactacttc 480

cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc 540

```
ccggctgtcc tacagtcctc aggactctac tccctcagca gcgtggtgac cgtgccctcc    600

agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag    660

gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgccca    720

gcacctgaac tcctgggggg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc    780

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac    840

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag    900

ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac    960

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc   1020

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc   1080

ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa   1140

ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac   1200

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc   1260

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gctgcatgag   1320

gctctgcact cccactacac acagaagagc ctctccctgt ctccgggtaa a            1371


<210> SEQ ID NO 123
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 123

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15

Arg Val Thr Ile Ser Cys Thr Gly Met Asn Ser Asn Ile Gly Ala Gly
            20                  25                  30

Tyr Asp Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35                  40                  45

Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60

Ser Gly Ser Arg Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65                  70                  75                  80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Thr Ser
                85                  90                  95

Leu Asn Gly Trp Ala Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110


<210> SEQ ID NO 124
<211> LENGTH: 127
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 124

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Ser Phe Gly Asp His
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Gly Phe Ile Arg Lys Thr Thr Tyr Gly Ala Thr Thr His Tyr Ala Ala
```

```
    50                  55                  60

Ala Val Arg Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile
65                  70                  75                  80

Val Tyr Leu Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr
                85                  90                  95

Phe Cys Ala Arg Val Gln Leu Asp Tyr Gly Pro Gly Tyr Gln Tyr Tyr
            100                 105                 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120                 125
```

```
<210> SEQ ID NO 125
<211> LENGTH: 336
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 125

cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc      60

tcctgcactg ggatgaactc caacatcggg gcaggttatg atgtatactg gtaccaacaa     120

cttccaggaa ctgcccccaa actcctcatc tatggtaaca gcaatcggcc ctcaggggtc     180

cctgaccgat tctctggctc caggtctggc acctcagcct ccctggccat cactgggctc     240

caggctgagg atgaggctga ttattactgc cagtcctatg acaccagcct gaatggttgg     300

gctttcggcg gagggaccaa gttgaccgtc ctaggc                               336
```

```
<210> SEQ ID NO 126
<211> LENGTH: 381
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 126

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc cagggcggtc cctgagactc      60

agctgtacag cctctgggtt tagttttggt gatcatgcta tgagctgggt ccgccaggct     120

ccagggaagg ggctggagtg ggtaggtttc attagaaaga caacttatgg tgcgacaaca     180

cactacgccg cggctgtgag aggcagattc accatctcgc gagatgattc taaaagcatt     240

gtctatctgc aaatgaacag cctgaaagca gaggacacag ccgtgtattt ctgtgctaga     300

gtgcagcttg actatggccc gggataccag tactacggta tggacgtctg gggccaaggg     360

accacggtca ccgtctcctc a                                               381
```

```
<210> SEQ ID NO 127
<211> LENGTH: 217
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 127

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15

Arg Val Thr Ile Ser Cys Thr Gly Met Asn Ser Asn Ile Gly Ala Gly
            20                  25                  30

Tyr Asp Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35                  40                  45
```

```
Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60

Ser Gly Ser Arg Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65                  70                  75                  80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Thr Ser
                85                  90                  95

Leu Asn Gly Trp Ala Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu
        115                 120                 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Val Ser Asp Phe
    130                 135                 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro Val
145                 150                 155                 160

Lys Val Gly Val Glu Thr Thr Lys Pro Ser Lys Gln Ser Asn Asn Lys
                165                 170                 175

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
            180                 185                 190

His Arg Ser Tyr Ser Cys Arg Val Thr His Glu Gly Ser Thr Val Glu
        195                 200                 205

Lys Thr Val Ala Pro Ala Glu Cys Ser
    210                 215


<210> SEQ ID NO 128
<211> LENGTH: 457
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 128

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Ser Phe Gly Asp His
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Gly Phe Ile Arg Lys Thr Thr Tyr Gly Ala Thr Thr His Tyr Ala Ala
    50                  55                  60

Ala Val Arg Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile
65                  70                  75                  80

Val Tyr Leu Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr
                85                  90                  95

Phe Cys Ala Arg Val Gln Leu Asp Tyr Gly Pro Gly Tyr Gln Tyr Tyr
            100                 105                 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala
        115                 120                 125

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
    130                 135                 140

Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
145                 150                 155                 160

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
                165                 170                 175

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
            180                 185                 190
```

```
Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
        195                 200                 205

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
    210                 215                 220

Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
225                 230                 235                 240

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                245                 250                 255

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            260                 265                 270

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        275                 280                 285

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    290                 295                 300

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
305                 310                 315                 320

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                325                 330                 335

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            340                 345                 350

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
        355                 360                 365

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    370                 375                 380

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
385                 390                 395                 400

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                405                 410                 415

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            420                 425                 430

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
        435                 440                 445

Lys Ser Leu Ser Leu Ser Pro Gly Lys
    450                 455


<210> SEQ ID NO 129
<211> LENGTH: 457
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 129

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Ser Phe Gly Asp His
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Gly Phe Ile Arg Lys Thr Thr Tyr Gly Ala Thr Thr His Tyr Ala Ala
    50                  55                  60

Ala Val Arg Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile
65                  70                  75                  80

Val Tyr Leu Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr
                85                  90                  95
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Phe Cys Ala Arg Val Gln Leu Asp Tyr Gly Pro Gly Tyr Gln Tyr Tyr
            100                 105                 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala
        115                 120                 125

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
    130                 135                 140

Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
145                 150                 155                 160

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
                165                 170                 175

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
            180                 185                 190

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
        195                 200                 205

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
    210                 215                 220

Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
225                 230                 235                 240

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                245                 250                 255

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            260                 265                 270

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        275                 280                 285

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    290                 295                 300

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
305                 310                 315                 320

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                325                 330                 335

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            340                 345                 350

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
        355                 360                 365

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    370                 375                 380

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
385                 390                 395                 400

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                405                 410                 415

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            420                 425                 430

Phe Ser Cys Ser Val Leu His Glu Ala Leu His Ser His Tyr Thr Gln
        435                 440                 445

Lys Ser Leu Ser Leu Ser Pro Gly Lys
    450                 455
```

<210> SEQ ID NO 130
<211> LENGTH: 651
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 130

cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60

tcctgcactg ggatgaactc caacatcggg gcaggttatg atgtatactg gtaccaacaa 120

cttccaggaa ctgcccccaa actcctcatc tatggtaaca gcaatcggcc ctcaggggtc 180

cctgaccgat tctctggctc caggtctggc acctcagcct ccctggccat cactgggctc 240

caggctgagg atgaggctga ttattactgc cagtcctatg acaccagcct gaatggttgg 300

gctttcggcg gagggaccaa gttgaccgtc ctaggccagc ccaaggctgc cccctcggtc 360

actctgttcc caccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420

gtaagtgact tctacccggg agccgtgaca gtggcctgga aggcagatgg cagccccgtc 480

aaggtgggag tggagaccac caaaccctcc aaacaaagca acaacaagta tgcggccagc 540

agctacctga gcctgacgcc cgagcagtgg aagtcccaca gaagctacag ctgccgggtc 600

acgcatgaag ggagcaccgt ggagaagaca gtggcccctg cagaatgctc t 651

<210> SEQ ID NO 131
<211> LENGTH: 1371
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 131

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc cagggcggtc cctgagactc 60

agctgtacag cctctgggtt tagttttggt gatcatgcta tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtaggtttc attagaaaga caacttatgg tgcgacaaca 180

cactacgccg cggctgtgag aggcagattc accatctcgc gagatgattc taaaagcatt 240

gtctatctgc aaatgaacag cctgaaagca gaggacacag ccgtgtattt ctgtgctaga 300

gtgcagcttg actatggccc gggataccag tactacggta tggacgtctg gggccaaggg 360

accacggtca ccgtctcctc agcctccacc aagggcccat cggtcttccc cctggcaccc 420

tcctccaaga gcacctctgg gggcacagca gccctgggct gcctggtcaa ggactacttc 480

cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc 540

ccggctgtcc tacagtcctc aggactctac tccctcagca gcgtggtgac cgtgccctcc 600

agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag 660

gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgccca 720

gcacctgaac tcctgggggg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 780

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 840

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 900

ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 960

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc 1020

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1080

ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 1140

ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1200

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1260

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1320

gctctgcaca accactacac acagaagagc ctctccctgt ctccgggtaa a 1371

<210> SEQ ID NO 132
<211> LENGTH: 1371
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 132

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc cagggcggtc cctgagactc 60

agctgtacag cctctgggtt tagttttggt gatcatgcta tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtaggtttc attagaaaga caacttatgg tgcgacaaca 180

cactacgccg cggctgtgag aggcagattc accatctcgc gagatgattc taaaagcatt 240

gtctatctgc aaatgaacag cctgaaagca gaggacacag ccgtgtattt ctgtgctaga 300

gtgcagcttg actatggccc gggataccag tactacggta tggacgtctg gggccaaggg 360

accacggtca ccgtctcctc agcctccacc aagggcccat cggtcttccc cctggcaccc 420

tcctccaaga gcacctctgg gggcacagca gccctgggct gcctggtcaa ggactacttc 480

cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc 540

ccggctgtcc tacagtcctc aggactctac tccctcagca gcgtggtgac cgtgccctcc 600

agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag 660

gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgccca 720

gcacctgaac tcctgggggg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 780

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 840

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 900

ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 960

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc 1020

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1080

ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 1140

ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1200

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1260

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gctgcatgag 1320

gctctgcact cccactacac acagaagagc ctctccctgt ctccgggtaa a 1371

<210> SEQ ID NO 133
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 133

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Met Asn Ser Asn Ile Gly Ala Gly
20 25 30

Tyr Asp Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
35 40 45

Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Arg Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65 70 75 80

```
Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Thr Ser
                85                  90                  95

Leu Asn Gly Trp Ala Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110


<210> SEQ ID NO 134
<211> LENGTH: 127
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 134

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Gly Asp His
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Gly Phe Ile Arg Lys Thr Thr Tyr Gly Ala Thr Thr His Tyr Ala Ala
    50                  55                  60

Ala Val Arg Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65                  70                  75                  80

Val Tyr Leu Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr
                85                  90                  95

Phe Cys Thr Arg Val Gln Leu Asp Tyr Gly Pro Gly Tyr Gln Tyr Tyr
            100                 105                 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120                 125


<210> SEQ ID NO 135
<211> LENGTH: 336
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 135

cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc      60

tcctgcactg ggatgaactc caacatcggg gcaggttatg atgtatactg gtaccaacaa     120

cttccaggaa ctgcccccaa actcctcatc tatggtaaca gcaatcggcc ctcaggggtc     180

cctgaccgat tctctggctc caggtctggc acctcagcct ccctggccat cactgggctc     240

caggctgagg atgaggctga ttattactgc cagtcctatg acaccagcct gaatggttgg     300

gctttcggcg gagggaccaa gttgaccgtc ctaggc                               336


<210> SEQ ID NO 136
<211> LENGTH: 381
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 136

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc cagggcggtc cctgagactc      60

agctgtgcgg cctctgggtt tagttttggt gatcatgcta tgagctgggt ccgccaggct     120

ccagggaagg ggctggagtg ggtaggtttc attagaaaga caacttatgg tgcgacaaca     180
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cactacgccg cggctgtgag aggcagattc accatctcgc gagatgattc taaaagcact    240

gtctatctgc aaatgaacag cctgaaagca gaggacacag ccgtgtattt ctgtactaga    300

gtgcagcttg actatggccc gggataccag tactacggta tggacgtctg ggccaaggg     360

accacggtca ccgtctcctc a                                              381


<210> SEQ ID NO 137
<211> LENGTH: 217
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 137

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15

Arg Val Thr Ile Ser Cys Thr Gly Met Asn Ser Asn Ile Gly Ala Gly
            20                  25                  30

Tyr Asp Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35                  40                  45

Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60

Ser Gly Ser Arg Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65                  70                  75                  80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Thr Ser
                85                  90                  95

Leu Asn Gly Trp Ala Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu
        115                 120                 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Val Ser Asp Phe
    130                 135                 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro Val
145                 150                 155                 160

Lys Val Gly Val Glu Thr Thr Lys Pro Ser Lys Gln Ser Asn Asn Lys
                165                 170                 175

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
            180                 185                 190

His Arg Ser Tyr Ser Cys Arg Val Thr His Glu Gly Ser Thr Val Glu
        195                 200                 205

Lys Thr Val Ala Pro Ala Glu Cys Ser
    210                 215


<210> SEQ ID NO 138
<211> LENGTH: 457
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 138

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Gly Asp His
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
```

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Gly Phe Ile Arg Lys Thr Thr Tyr Gly Ala Thr Thr His Tyr Ala Ala
    50                  55                  60

Ala Val Arg Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65                  70                  75                  80

Val Tyr Leu Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr
                85                  90                  95

Phe Cys Thr Arg Val Gln Leu Asp Tyr Gly Pro Gly Tyr Gln Tyr Tyr
            100                 105                 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala
        115                 120                 125

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
    130                 135                 140

Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
145                 150                 155                 160

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
                165                 170                 175

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
            180                 185                 190

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
        195                 200                 205

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
    210                 215                 220

Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
225                 230                 235                 240

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                245                 250                 255

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            260                 265                 270

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        275                 280                 285

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    290                 295                 300

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
305                 310                 315                 320

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                325                 330                 335

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            340                 345                 350

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
        355                 360                 365

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    370                 375                 380

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
385                 390                 395                 400

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                405                 410                 415

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            420                 425                 430

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
        435                 440                 445

Lys Ser Leu Ser Leu Ser Pro Gly Lys
    450                 455
```

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<210> SEQ ID NO 139
<211> LENGTH: 457
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 139

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Gly Asp His
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Gly Phe Ile Arg Lys Thr Thr Tyr Gly Ala Thr Thr His Tyr Ala Ala
    50                  55                  60

Ala Val Arg Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65                  70                  75                  80

Val Tyr Leu Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr
                85                  90                  95

Phe Cys Thr Arg Val Gln Leu Asp Tyr Gly Pro Gly Tyr Gln Tyr Tyr
            100                 105                 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala
        115                 120                 125

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
    130                 135                 140

Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
145                 150                 155                 160

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
                165                 170                 175

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
            180                 185                 190

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
        195                 200                 205

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
    210                 215                 220

Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
225                 230                 235                 240

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                245                 250                 255

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            260                 265                 270

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        275                 280                 285

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    290                 295                 300

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
305                 310                 315                 320

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                325                 330                 335

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            340                 345                 350

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
        355                 360                 365

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
```

```
    370                 375                 380

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
385                 390                 395                 400

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                405                 410                 415

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            420                 425                 430

Phe Ser Cys Ser Val Leu His Glu Ala Leu His Ser His Tyr Thr Gln
        435                 440                 445

Lys Ser Leu Ser Leu Ser Pro Gly Lys
    450                 455
```

<210> SEQ ID NO 140
<211> LENGTH: 651
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 140

```
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc      60

tcctgcactg ggatgaactc caacatcggg gcaggttatg atgtatactg gtaccaacaa     120

cttccaggaa ctgcccccaa actcctcatc tatggtaaca gcaatcggcc ctcaggggtc     180

cctgaccgat tctctggctc caggtctggc acctcagcct ccctggccat cactgggctc     240

caggctgagg atgaggctga ttattactgc cagtcctatg acaccagcct gaatggttgg     300

gctttcggcg gagggaccaa gttgaccgtc ctaggccagc ccaaggctgc cccctcggtc     360

actctgttcc caccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc     420

gtaagtgact tctacccggg agccgtgaca gtggcctgga aggcagatgg cagccccgtc     480

aaggtgggag tggagaccac caaaccctcc aaacaaagca acaacaagta tgcggccagc     540

agctacctga gcctgacgcc cgagcagtgg aagtcccaca gaagctacag ctgccgggtc     600

acgcatgaag ggagcaccgt ggagaagaca gtggcccctg cagaatgctc t              651
```

<210> SEQ ID NO 141
<211> LENGTH: 1371
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 141

```
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc cagggcggtc cctgagactc      60

agctgtgcgg cctctgggtt tagttttggt gatcatgcta tgagctgggt ccgccaggct     120

ccagggaagg ggctggagtg ggtaggtttc attagaaaga caacttatgg tgcgacaaca     180

cactacgccg cggctgtgag aggcagattc accatctcgc gagatgattc taaaagcact     240

gtctatctgc aaatgaacag cctgaaagca gaggacacag ccgtgtattt ctgtactaga     300

gtgcagcttg actatggccc gggataccag tactacggta tggacgtctg gggccaaggg     360

accacggtca ccgtctcctc agcctccacc aagggcccat cggtcttccc cctggcaccc     420

tcctccaaga gcacctctgg gggcacagca gccctgggct gcctggtcaa ggactacttc     480

cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc     540

ccggctgtcc tacagtcctc aggactctac tccctcagca gcgtggtgac cgtgccctcc     600
```

agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag 660

gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgccca 720

gcacctgaac tcctgggggg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 780

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 840

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 900

ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 960

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc 1020

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1080

ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 1140

ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1200

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1260

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1320

gctctgcaca accactacac acagaagagc ctctccctgt ctccgggtaa a 1371

<210> SEQ ID NO 142
<211> LENGTH: 1371
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 142

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc cagggcggtc cctgagactc 60

agctgtgcgg cctctgggtt tagttttggt gatcatgcta tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtaggtttc attagaaaga caacttatgg tgcgacaaca 180

cactacgccg cggctgtgag aggcagattc accatctcgc gagatgattc taaaagcact 240

gtctatctgc aaatgaacag cctgaaagca gaggacacag ccgtgtattt ctgtactaga 300

gtgcagcttg actatggccc gggataccag tactacggta tggacgtctg gggccaaggg 360

accacggtca ccgtctcctc agcctccacc aagggcccat cggtcttccc cctggcaccc 420

tcctccaaga gcacctctgg gggcacagca gccctgggct gcctggtcaa ggactacttc 480

cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc 540

ccggctgtcc tacagtcctc aggactctac tccctcagca gcgtggtgac cgtgccctcc 600

agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag 660

gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgccca 720

gcacctgaac tcctgggggg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 780

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 840

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 900

ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 960

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc 1020

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1080

ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 1140

ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1200

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1260

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gctgcatgag 1320

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gctctgcact cccactacac acagaagagc ctctccctgt ctccgggtaa a           1371


<210> SEQ ID NO 143
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 143

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15

Arg Val Thr Ile Ser Cys Thr Gly Met Asn Ser Asn Ile Gly Ala Gly
                20                  25                  30

Tyr Asp Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35                  40                  45

Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60

Ser Gly Ser Arg Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65                  70                  75                  80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Thr Ser
                85                  90                  95

Leu Asn Gly Trp Ala Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110


<210> SEQ ID NO 144
<211> LENGTH: 127
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 144

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Gly Asp His
                20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Gly Phe Ile Arg Lys Thr Thr Tyr Gly Ala Thr Thr His Tyr Ala Ala
    50                  55                  60

Ala Val Arg Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65                  70                  75                  80

Val Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
                85                  90                  95

Phe Cys Ala Arg Val Gln Leu Asp Tyr Gly Pro Gly Tyr Gln Tyr Tyr
            100                 105                 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120                 125


<210> SEQ ID NO 145
<211> LENGTH: 336
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 145

cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc     60
```

tcctgcactg ggatgaactc caacatcggg gcaggttatg atgtatactg gtaccaacaa 120

cttccaggaa ctgcccccaa actcctcatc tatggtaaca gcaatcggcc ctcaggggtc 180

cctgaccgat tctctggctc caggtctggc acctcagcct ccctggccat cactgggctc 240

caggctgagg atgaggctga ttattactgc cagtcctatg acaccagcct gaatggttgg 300

gctttcggcg gagggaccaa gttgaccgtc ctaggc 336

<210> SEQ ID NO 146
<211> LENGTH: 381
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 146

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc cagggcggtc cctgagactc 60

agctgtgcgg cctctgggtt tagttttggt gatcatgcta tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtaggtttc attagaaaga caacttatgg tgcgacaaca 180

cactacgccg cggctgtgag aggcagattc accatctcgc gagatgattc taaaagcact 240

gtctatctgc aaatgaacag cctgaaaacc gaggacacag ccgtgtattt ctgtgctaga 300

gtgcagcttg actatggccc gggataccag tactacggta tggacgtctg gggccaaggg 360

accacggtca ccgtctcctc a 381

<210> SEQ ID NO 147
<211> LENGTH: 217
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 147

```
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15

Arg Val Thr Ile Ser Cys Thr Gly Met Asn Ser Asn Ile Gly Ala Gly
            20                  25                  30

Tyr Asp Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35                  40                  45

Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60

Ser Gly Ser Arg Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65                  70                  75                  80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Thr Ser
                85                  90                  95

Leu Asn Gly Trp Ala Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu
        115                 120                 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Val Ser Asp Phe
    130                 135                 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro Val
145                 150                 155                 160

Lys Val Gly Val Glu Thr Thr Lys Pro Ser Lys Gln Ser Asn Asn Lys
                165                 170                 175

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
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            180                 185                 190

His Arg Ser Tyr Ser Cys Arg Val Thr His Glu Gly Ser Thr Val Glu
        195                 200                 205

Lys Thr Val Ala Pro Ala Glu Cys Ser
    210                 215


<210> SEQ ID NO 148
<211> LENGTH: 457
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 148

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Gly Asp His
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Gly Phe Ile Arg Lys Thr Thr Tyr Gly Ala Thr Thr His Tyr Ala Ala
    50                  55                  60

Ala Val Arg Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65                  70                  75                  80

Val Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
                85                  90                  95

Phe Cys Ala Arg Val Gln Leu Asp Tyr Gly Pro Gly Tyr Gln Tyr Tyr
            100                 105                 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala
        115                 120                 125

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
    130                 135                 140

Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
145                 150                 155                 160

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
                165                 170                 175

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
            180                 185                 190

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
        195                 200                 205

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
    210                 215                 220

Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
225                 230                 235                 240

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                245                 250                 255

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            260                 265                 270

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        275                 280                 285

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    290                 295                 300

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
305                 310                 315                 320

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
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                325                 330                 335

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            340                 345                 350

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
        355                 360                 365

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    370                 375                 380

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
385                 390                 395                 400

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                405                 410                 415

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            420                 425                 430

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
        435                 440                 445

Lys Ser Leu Ser Leu Ser Pro Gly Lys
    450                 455


<210> SEQ ID NO 149
<211> LENGTH: 457
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 149

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Gly Asp His
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Gly Phe Ile Arg Lys Thr Thr Tyr Gly Ala Thr Thr His Tyr Ala Ala
    50                  55                  60

Ala Val Arg Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65                  70                  75                  80

Val Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
                85                  90                  95

Phe Cys Ala Arg Val Gln Leu Asp Tyr Gly Pro Gly Tyr Gln Tyr Tyr
            100                 105                 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala
        115                 120                 125

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
    130                 135                 140

Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
145                 150                 155                 160

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
                165                 170                 175

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
            180                 185                 190

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
        195                 200                 205

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
    210                 215                 220

Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
```

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225                 230                 235                 240

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                245                 250                 255

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            260                 265                 270

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        275                 280                 285

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    290                 295                 300

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
305                 310                 315                 320

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                325                 330                 335

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            340                 345                 350

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
        355                 360                 365

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    370                 375                 380

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
385                 390                 395                 400

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                405                 410                 415

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            420                 425                 430

Phe Ser Cys Ser Val Leu His Glu Ala Leu His Ser His Tyr Thr Gln
        435                 440                 445

Lys Ser Leu Ser Leu Ser Pro Gly Lys
    450                 455
```

<210> SEQ ID NO 150
<211> LENGTH: 651
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 150

```
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc     60

tcctgcactg ggatgaactc caacatcggg gcaggttatg atgtatactg gtaccaacaa    120

cttccaggaa ctgcccccaa actcctcatc tatggtaaca gcaatcggcc ctcaggggtc    180

cctgaccgat tctctggctc caggtctggc acctcagcct ccctggccat cactgggctc    240

caggctgagg atgaggctga ttattactgc cagtcctatg acaccagcct gaatggttgg    300

gctttcggcg gagggaccaa gttgaccgtc ctaggccagc ccaaggctgc cccctcggtc    360

actctgttcc caccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc    420

gtaagtgact tctacccggg agccgtgaca gtggcctgga aggcagatgg cagccccgtc    480

aaggtgggag tggagaccac caaaccctcc aaacaaagca acaacaagta tgcggccagc    540

agctacctga gcctgacgcc cgagcagtgg aagtcccaca gaagctacag ctgccgggtc    600

acgcatgaag ggagcaccgt ggagaagaca gtggcccctg cagaatgctc t             651
```

<210> SEQ ID NO 151
<211> LENGTH: 1371

<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 151

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc cagggcggtc cctgagactc 60

agctgtgcgg cctctgggtt tagttttggt gatcatgcta tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtaggtttc attagaaaga caacttatgg tgcgacaaca 180

cactacgccg cggctgtgag aggcagattc accatctcgc gagatgattc taaaagcact 240

gtctatctgc aaatgaacag cctgaaaacc gaggacacag ccgtgtattt ctgtgctaga 300

gtgcagcttg actatggccc gggataccag tactacggta tggacgtctg gggccaaggg 360

accacggtca ccgtctcctc agcctccacc aagggcccat cggtcttccc cctggcaccc 420

tcctccaaga gcacctctgg gggcacagca gccctgggct gcctggtcaa ggactacttc 480

cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc 540

ccggctgtcc tacagtcctc aggactctac tccctcagca gcgtggtgac cgtgccctcc 600

agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag 660

gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgccca 720

gcacctgaac tcctgggggg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 780

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 840

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 900

ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 960

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc 1020

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1080

ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 1140

ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1200

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1260

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1320

gctctgcaca accactacac acagaagagc ctctccctgt ctccgggtaa a 1371

<210> SEQ ID NO 152
<211> LENGTH: 1371
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 152

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc cagggcggtc cctgagactc 60

agctgtgcgg cctctgggtt tagttttggt gatcatgcta tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtaggtttc attagaaaga caacttatgg tgcgacaaca 180

cactacgccg cggctgtgag aggcagattc accatctcgc gagatgattc taaaagcact 240

gtctatctgc aaatgaacag cctgaaaacc gaggacacag ccgtgtattt ctgtgctaga 300

gtgcagcttg actatggccc gggataccag tactacggta tggacgtctg gggccaaggg 360

accacggtca ccgtctcctc agcctccacc aagggcccat cggtcttccc cctggcaccc 420

tcctccaaga gcacctctgg gggcacagca gccctgggct gcctggtcaa ggactacttc 480

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cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc     540

ccggctgtcc tacagtcctc aggactctac tccctcagca gcgtggtgac cgtgccctcc     600

agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag     660

gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgccca     720

gcacctgaac tcctgggggg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc     780

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac     840

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag     900

ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac     960

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc    1020

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc    1080

ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa    1140

ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac    1200

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc    1260

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gctgcatgag    1320

gctctgcact cccactacac acagaagagc ctctccctgt ctccgggtaa a             1371


<210> SEQ ID NO 153
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 153

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15

Arg Val Thr Ile Ser Cys Thr Gly Met Asn Ser Asn Ile Gly Ala Gly
            20                  25                  30

Tyr Asp Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35                  40                  45

Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60

Ser Gly Ser Arg Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65                  70                  75                  80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Thr Ser
                85                  90                  95

Leu Asn Gly Trp Ala Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110


<210> SEQ ID NO 154
<211> LENGTH: 127
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 154

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Gly Asp His
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
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Gly Phe Ile Arg Lys Thr Thr Tyr Gly Ala Thr Thr His Tyr Ala Ala
    50                  55                  60

Ala Val Arg Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile
65                  70                  75                  80

Val Tyr Leu Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr
                85                  90                  95

Phe Cys Ala Arg Val Gln Leu Asp Tyr Gly Pro Gly Tyr Gln Tyr Tyr
            100                 105                 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120                 125


<210> SEQ ID NO 155
<211> LENGTH: 336
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 155

cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc     60

tcctgcactg ggatgaactc caacatcggg gcaggttatg atgtatactg gtaccaacaa    120

cttccaggaa ctgcccccaa actcctcatc tatggtaaca gcaatcggcc ctcaggggtc    180

cctgaccgat tctctggctc caggtctggc acctcagcct ccctggccat cactgggctc    240

caggctgagg atgaggctga ttattactgc cagtcctatg acaccagcct gaatggttgg    300

gctttcggcg gagggaccaa gttgaccgtc ctaggc                              336


<210> SEQ ID NO 156
<211> LENGTH: 381
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 156

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc cagggcggtc cctgagactc     60

agctgtgcgg cctctgggtt tagttttggt gatcatgcta tgagctgggt ccgccaggct    120

ccagggaagg ggctggagtg ggtaggtttc attagaaaga caacttatgg tgcgacaaca    180

cactacgccg cggctgtgag aggcagattc accatctcgc gagatgattc taaaagcatt    240

gtctatctgc aaatgaacag cctgaaagca gaggacacag ccgtgtattt ctgtgctaga    300

gtgcagcttg actatggccc gggataccag tactacggta tggacgtctg gggccaaggg    360

accacggtca ccgtctcctc a                                              381


<210> SEQ ID NO 157
<211> LENGTH: 217
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 157

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15

Arg Val Thr Ile Ser Cys Thr Gly Met Asn Ser Asn Ile Gly Ala Gly
            20                  25                  30

Tyr Asp Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
```

```
        35                  40                  45

Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60

Ser Gly Ser Arg Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65                  70                  75                  80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Thr Ser
                85                  90                  95

Leu Asn Gly Trp Ala Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu
        115                 120                 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Val Ser Asp Phe
    130                 135                 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro Val
145                 150                 155                 160

Lys Val Gly Val Glu Thr Thr Lys Pro Ser Lys Gln Ser Asn Asn Lys
                165                 170                 175

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
            180                 185                 190

His Arg Ser Tyr Ser Cys Arg Val Thr His Glu Gly Ser Thr Val Glu
        195                 200                 205

Lys Thr Val Ala Pro Ala Glu Cys Ser
    210                 215


<210> SEQ ID NO 158
<211> LENGTH: 457
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 158

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Gly Asp His
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Gly Phe Ile Arg Lys Thr Thr Tyr Gly Ala Thr Thr His Tyr Ala Ala
    50                  55                  60

Ala Val Arg Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile
65                  70                  75                  80

Val Tyr Leu Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr
                85                  90                  95

Phe Cys Ala Arg Val Gln Leu Asp Tyr Gly Pro Gly Tyr Gln Tyr Tyr
            100                 105                 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala
        115                 120                 125

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
    130                 135                 140

Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
145                 150                 155                 160

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
                165                 170                 175

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
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            180                 185                 190

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
        195                 200                 205

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
    210                 215                 220

Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
225                 230                 235                 240

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                245                 250                 255

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            260                 265                 270

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        275                 280                 285

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    290                 295                 300

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
305                 310                 315                 320

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                325                 330                 335

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            340                 345                 350

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
        355                 360                 365

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    370                 375                 380

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
385                 390                 395                 400

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                405                 410                 415

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            420                 425                 430

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
        435                 440                 445

Lys Ser Leu Ser Leu Ser Pro Gly Lys
    450                 455


<210> SEQ ID NO 159
<211> LENGTH: 457
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 159

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Gly Asp His
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Gly Phe Ile Arg Lys Thr Thr Tyr Gly Ala Thr Thr His Tyr Ala Ala
    50                  55                  60

Ala Val Arg Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile
65                  70                  75                  80

Val Tyr Leu Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr
```

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                85                  90                  95

Phe Cys Ala Arg Val Gln Leu Asp Tyr Gly Pro Gly Tyr Gln Tyr Tyr
            100                 105                 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala
        115                 120                 125

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
    130                 135                 140

Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
145                 150                 155                 160

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
                165                 170                 175

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
            180                 185                 190

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
        195                 200                 205

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
    210                 215                 220

Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
225                 230                 235                 240

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                245                 250                 255

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            260                 265                 270

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        275                 280                 285

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    290                 295                 300

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
305                 310                 315                 320

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                325                 330                 335

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            340                 345                 350

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
        355                 360                 365

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    370                 375                 380

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
385                 390                 395                 400

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                405                 410                 415

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            420                 425                 430

Phe Ser Cys Ser Val Leu His Glu Ala Leu His Ser His Tyr Thr Gln
        435                 440                 445

Lys Ser Leu Ser Leu Ser Pro Gly Lys
    450                 455


<210> SEQ ID NO 160
<211> LENGTH: 651
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
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<400> SEQUENCE: 160

cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60

tcctgcactg ggatgaactc caacatcggg gcaggttatg atgtatactg gtaccaacaa 120

cttccaggaa ctgcccccaa actcctcatc tatggtaaca gcaatcggcc ctcaggggtc 180

cctgaccgat tctctggctc caggtctggc acctcagcct ccctggccat cactgggctc 240

caggctgagg atgaggctga ttattactgc cagtcctatg acaccagcct gaatggttgg 300

gctttcggcg gagggaccaa gttgaccgtc ctaggccagc ccaaggctgc cccctcggtc 360

actctgttcc caccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420

gtaagtgact tctacccggg agccgtgaca gtggcctgga aggcagatgg cagccccgtc 480

aaggtgggag tggagaccac caaaccctcc aaacaaagca acaacaagta tgcggccagc 540

agctacctga gcctgacgcc cgagcagtgg aagtcccaca gaagctacag ctgccgggtc 600

acgcatgaag ggagcaccgt ggagaagaca gtggcccctg cagaatgctc t 651

<210> SEQ ID NO 161
<211> LENGTH: 1371
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 161

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc cagggcggtc cctgagactc 60

agctgtgcgg cctctgggtt tagttttggt gatcatgcta tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtaggtttc attagaaaga caacttatgg tgcgacaaca 180

cactacgccg cggctgtgag aggcagattc accatctcgc gagatgattc taaaagcatt 240

gtctatctgc aaatgaacag cctgaaagca gaggacacag ccgtgtattt ctgtgctaga 300

gtgcagcttg actatggccc gggataccag tactacggta tggacgtctg gggccaaggg 360

accacggtca ccgtctcctc agcctccacc aagggcccat cggtcttccc cctggcaccc 420

tcctccaaga gcacctctgg gggcacagca gccctgggct gcctggtcaa ggactacttc 480

cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc 540

ccggctgtcc tacagtcctc aggactctac tccctcagca gcgtggtgac cgtgccctcc 600

agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag 660

gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgccca 720

gcacctgaac tcctgggggg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 780

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 840

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 900

ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 960

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc 1020

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1080

ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 1140

ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1200

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1260

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1320

gctctgcaca accactacac acagaagagc ctctccctgt ctccgggtaa a 1371

<210> SEQ ID NO 162
<211> LENGTH: 1371
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 162

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc cagggcggtc cctgagactc 60

agctgtgcgg cctctgggtt tagttttggt gatcatgcta tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtaggtttc attagaaaga caacttatgg tgcgacaaca 180

cactacgccg cggctgtgag aggcagattc accatctcgc gagatgattc taaaagcatt 240

gtctatctgc aaatgaacag cctgaaagca gaggacacag ccgtgtattt ctgtgctaga 300

gtgcagcttg actatggccc gggataccag tactacggta tggacgtctg ggccaaggg 360

accacggtca ccgtctcctc agcctccacc aagggcccat cggtcttccc cctggcaccc 420

tcctccaaga gcacctctgg gggcacagca gccctgggct gcctggtcaa ggactacttc 480

cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc 540

ccggctgtcc tacagtcctc aggactctac tccctcagca gcgtggtgac cgtgccctcc 600

agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag 660

gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgccca 720

gcacctgaac tcctgggggg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 780

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 840

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 900

ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 960

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc 1020

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1080

ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 1140

ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1200

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1260

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gctgcatgag 1320

gctctgcact cccactacac acagaagagc ctctccctgt ctccgggtaa a 1371

<210> SEQ ID NO 163
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 163

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Met Asn Ser Asn Ile Gly Ala Gly
20 25 30

Tyr Asp Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
35 40 45

Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
50 55 60

```
Ser Gly Ser Arg Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65                  70                  75                  80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Thr Ser
                85                  90                  95

Leu Asn Gly Trp Ala Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110
```

<210> SEQ ID NO 164
<211> LENGTH: 127
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 164

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Ser Phe Gly Asp His
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Gly Phe Ile Arg Lys Thr Thr Tyr Gly Ala Thr Thr His Tyr Ala Ala
    50                  55                  60

Ala Val Arg Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65                  70                  75                  80

Val Tyr Leu Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr
                85                  90                  95

Phe Cys Ala Arg Val Gln Leu Asp Tyr Gly Pro Gly Tyr Gln Tyr Tyr
            100                 105                 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120                 125
```

<210> SEQ ID NO 165
<211> LENGTH: 336
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 165

```
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc     60

tcctgcactg ggatgaactc caacatcggg gcaggttatg atgtatactg gtaccaacaa    120

cttccaggaa ctgcccccaa actcctcatc tatggtaaca gcaatcggcc ctcaggggtc    180

cctgaccgat tctctggctc caggtctggc acctcagcct ccctggccat cactgggctc    240

caggctgagg atgaggctga ttattactgc cagtcctatg acaccagcct gaatggttgg    300

gctttcggcg gagggaccaa gttgaccgtc ctaggc                              336
```

<210> SEQ ID NO 166
<211> LENGTH: 381
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 166

```
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc cagggcggtc cctgagactc     60

agctgtacag cctctgggtt tagttttggt gatcatgcta tgagctgggt ccgccaggct    120
```

```
ccagggaagg ggctggagtg ggtaggtttc attagaaaga caacttatgg tgcgacaaca    180

cactacgccg cggctgtgag aggcagattc accatctcgc gagatgattc taaaagcact    240

gtctatctgc aaatgaacag cctgaaagca gaggacacag ccgtgtattt ctgtgctaga    300

gtgcagcttg actatggccc gggataccag tactacggta tggacgtctg gggccaaggg    360

accacggtca ccgtctcctc a                                              381


<210> SEQ ID NO 167
<211> LENGTH: 217
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 167

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15

Arg Val Thr Ile Ser Cys Thr Gly Met Asn Ser Asn Ile Gly Ala Gly
            20                  25                  30

Tyr Asp Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35                  40                  45

Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60

Ser Gly Ser Arg Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65                  70                  75                  80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Thr Ser
                85                  90                  95

Leu Asn Gly Trp Ala Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu
        115                 120                 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Val Ser Asp Phe
    130                 135                 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro Val
145                 150                 155                 160

Lys Val Gly Val Glu Thr Thr Lys Pro Ser Lys Gln Ser Asn Asn Lys
                165                 170                 175

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
            180                 185                 190

His Arg Ser Tyr Ser Cys Arg Val Thr His Glu Gly Ser Thr Val Glu
        195                 200                 205

Lys Thr Val Ala Pro Ala Glu Cys Ser
    210                 215


<210> SEQ ID NO 168
<211> LENGTH: 457
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 168

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Ser Phe Gly Asp His
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
```

-continued

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        35                  40                  45

Gly Phe Ile Arg Lys Thr Thr Tyr Gly Ala Thr Thr His Tyr Ala Ala
    50                  55                  60

Ala Val Arg Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65                  70                  75                  80

Val Tyr Leu Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr
                85                  90                  95

Phe Cys Ala Arg Val Gln Leu Asp Tyr Gly Pro Gly Tyr Gln Tyr Tyr
            100                 105                 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala
        115                 120                 125

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
    130                 135                 140

Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
145                 150                 155                 160

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
                165                 170                 175

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
            180                 185                 190

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
        195                 200                 205

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
    210                 215                 220

Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
225                 230                 235                 240

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                245                 250                 255

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            260                 265                 270

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        275                 280                 285

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    290                 295                 300

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
305                 310                 315                 320

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                325                 330                 335

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            340                 345                 350

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
        355                 360                 365

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    370                 375                 380

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
385                 390                 395                 400

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                405                 410                 415

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            420                 425                 430

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
        435                 440                 445

Lys Ser Leu Ser Leu Ser Pro Gly Lys
    450                 455
```

```
<210> SEQ ID NO 169
<211> LENGTH: 457
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 169

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Ser Phe Gly Asp His
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Gly Phe Ile Arg Lys Thr Thr Tyr Gly Ala Thr Thr His Tyr Ala Ala
    50                  55                  60

Ala Val Arg Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65                  70                  75                  80

Val Tyr Leu Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr
                85                  90                  95

Phe Cys Ala Arg Val Gln Leu Asp Tyr Gly Pro Gly Tyr Gln Tyr Tyr
            100                 105                 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala
        115                 120                 125

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
    130                 135                 140

Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
145                 150                 155                 160

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
                165                 170                 175

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
            180                 185                 190

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
        195                 200                 205

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
    210                 215                 220

Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
225                 230                 235                 240

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                245                 250                 255

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            260                 265                 270

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        275                 280                 285

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    290                 295                 300

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
305                 310                 315                 320

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                325                 330                 335

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            340                 345                 350

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
        355                 360                 365
```

```
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    370                 375                 380

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
385                 390                 395                 400

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                405                 410                 415

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            420                 425                 430

Phe Ser Cys Ser Val Leu His Glu Ala Leu His Ser His Tyr Thr Gln
        435                 440                 445

Lys Ser Leu Ser Leu Ser Pro Gly Lys
    450                 455
```

<210> SEQ ID NO 170
<211> LENGTH: 651
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 170

```
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc     60

tcctgcactg ggatgaactc caacatcggg gcaggttatg atgtatactg gtaccaacaa    120

cttccaggaa ctgcccccaa actcctcatc tatggtaaca gcaatcggcc ctcaggggtc    180

cctgaccgat tctctggctc caggtctggc acctcagcct ccctggccat cactgggctc    240

caggctgagg atgaggctga ttattactgc cagtcctatg acaccagcct gaatggttgg    300

gctttcggcg gagggaccaa gttgaccgtc ctaggccagc ccaaggctgc cccctcggtc    360

actctgttcc caccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc    420

gtaagtgact tctacccggg agccgtgaca gtggcctgga aggcagatgg cagccccgtc    480

aaggtgggag tggagaccac caaaccctcc aaacaaagca acaacaagta tgcggccagc    540

agctacctga gcctgacgcc cgagcagtgg aagtcccaca gaagctacag ctgccgggtc    600

acgcatgaag ggagcaccgt ggagaagaca gtggcccctg cagaatgctc t             651
```

<210> SEQ ID NO 171
<211> LENGTH: 1371
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 171

```
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc cagggcggtc cctgagactc     60

agctgtacag cctctgggtt tagttttggt gatcatgcta tgagctgggt ccgccaggct    120

ccagggaagg ggctggagtg ggtaggtttc attagaaaga caacttatgg tgcgacaaca    180

cactacgccg cggctgtgag aggcagattc accatctcgc gagatgattc taaaagcact    240

gtctatctgc aaatgaacag cctgaaagca gaggacacag ccgtgtattt ctgtgctaga    300

gtgcagcttg actatggccc gggataccag tactacggta tggacgtctg gggccaaggg    360

accacggtca ccgtctcctc agcctccacc aagggcccat cggtcttccc cctggcaccc    420

tcctccaaga gcacctctgg gggcacagca gccctgggct gcctggtcaa ggactacttc    480

cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc    540
```

ccggctgtcc tacagtcctc aggactctac tccctcagca gcgtggtgac cgtgccctcc 600

agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag 660

gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgccca 720

gcacctgaac tcctgggggg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 780

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 840

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 900

ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 960

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc 1020

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1080

ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 1140

ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1200

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1260

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1320

gctctgcaca accactacac acagaagagc ctctccctgt ctccgggtaa a 1371

<210> SEQ ID NO 172
<211> LENGTH: 1371
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 172

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc cagggcggtc cctgagactc 60

agctgtacag cctctgggtt tagttttggt gatcatgcta tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtaggtttc attagaaaga caacttatgg tgcgacaaca 180

cactacgccg cggctgtgag aggcagattc accatctcgc gagatgattc taaaagcact 240

gtctatctgc aaatgaacag cctgaaagca gaggacacag ccgtgtattt ctgtgctaga 300

gtgcagcttg actatggccc gggataccag tactacggta tggacgtctg ggcccaaggg 360

accacggtca ccgtctcctc agcctccacc aagggcccat cggtcttccc cctggcaccc 420

tcctccaaga gcacctctgg gggcacagca gccctgggct gcctggtcaa ggactacttc 480

cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc 540

ccggctgtcc tacagtcctc aggactctac tccctcagca gcgtggtgac cgtgccctcc 600

agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag 660

gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgccca 720

gcacctgaac tcctgggggg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 780

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 840

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 900

ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 960

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc 1020

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1080

ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 1140

ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1200

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1260

```
accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gctgcatgag   1320

gctctgcact cccactacac acagaagagc ctctccctgt ctccgggtaa a            1371
```

<210> SEQ ID NO 173
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 173

```
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15

Arg Val Thr Ile Ser Cys Thr Gly Met Asn Ser Asn Ile Gly Ala Gly
            20                  25                  30

Tyr Asp Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35                  40                  45

Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60

Ser Gly Ser Arg Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65                  70                  75                  80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Thr Ser
                85                  90                  95

Leu Asn Gly Trp Ala Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110
```

<210> SEQ ID NO 174
<211> LENGTH: 127
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 174

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Gly Asp His
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Gly Phe Ile Arg Lys Thr Thr Tyr Gly Ala Thr Thr His Tyr Ala Ala
    50                  55                  60

Ala Val Arg Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65                  70                  75                  80

Val Tyr Leu Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr
                85                  90                  95

Phe Cys Ala Arg Val Gln Leu Asp Tyr Gly Pro Gly Tyr Gln Tyr Tyr
            100                 105                 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120                 125
```

<210> SEQ ID NO 175
<211> LENGTH: 336
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 175

```
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc     60

tcctgcactg ggatgaactc caacatcggg gcaggttatg atgtatactg gtaccaacaa    120

cttccaggaa ctgcccccaa actcctcatc tatggtaaca gcaatcggcc ctcaggggtc    180

cctgaccgat tctctggctc caggtctggc acctcagcct ccctggccat cactgggctc    240

caggctgagg atgaggctga ttattactgc cagtcctatg acaccagcct gaatggttgg    300

gctttcggcg gagggaccaa gttgaccgtc ctaggc                               336


<210> SEQ ID NO 176
<211> LENGTH: 381
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 176

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc cagggcggtc cctgagactc     60

agctgtgcgg cctctgggtt tagttttggt gatcatgcta tgagctgggt ccgccaggct    120

ccagggaagg ggctggagtg ggtaggtttc attagaaaga caacttatgg tgcgacaaca    180

cactacgccg cggctgtgag aggcagattc accatctcgc gagatgattc taaaagcact    240

gtctatctgc aaatgaacag cctgaaagca gaggacacag ccgtgtattt ctgtgctaga    300

gtgcagcttg actatggccc gggataccag tactacggta tggacgtctg gggccaaggg    360

accacggtca ccgtctcctc a                                              381


<210> SEQ ID NO 177
<211> LENGTH: 217
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 177

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15

Arg Val Thr Ile Ser Cys Thr Gly Met Asn Ser Asn Ile Gly Ala Gly
            20                  25                  30

Tyr Asp Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35                  40                  45

Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60

Ser Gly Ser Arg Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65                  70                  75                  80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Thr Ser
                85                  90                  95

Leu Asn Gly Trp Ala Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu
        115                 120                 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Val Ser Asp Phe
    130                 135                 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro Val
145                 150                 155                 160

Lys Val Gly Val Glu Thr Thr Lys Pro Ser Lys Gln Ser Asn Asn Lys
                165                 170                 175
```

```
Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
            180                 185                 190

His Arg Ser Tyr Ser Cys Arg Val Thr His Glu Gly Ser Thr Val Glu
        195                 200                 205

Lys Thr Val Ala Pro Ala Glu Cys Ser
    210                 215


<210> SEQ ID NO 178
<211> LENGTH: 457
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 178

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Gly Asp His
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Gly Phe Ile Arg Lys Thr Thr Tyr Gly Ala Thr Thr His Tyr Ala Ala
    50                  55                  60

Ala Val Arg Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65                  70                  75                  80

Val Tyr Leu Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr
                85                  90                  95

Phe Cys Ala Arg Val Gln Leu Asp Tyr Gly Pro Gly Tyr Gln Tyr Tyr
            100                 105                 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala
        115                 120                 125

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
    130                 135                 140

Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
145                 150                 155                 160

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
                165                 170                 175

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
            180                 185                 190

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
        195                 200                 205

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
    210                 215                 220

Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
225                 230                 235                 240

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                245                 250                 255

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            260                 265                 270

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        275                 280                 285

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    290                 295                 300

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
305                 310                 315                 320
```

```
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                325                 330                 335

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            340                 345                 350

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
        355                 360                 365

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    370                 375                 380

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
385                 390                 395                 400

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                405                 410                 415

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            420                 425                 430

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
        435                 440                 445

Lys Ser Leu Ser Leu Ser Pro Gly Lys
    450                 455


<210> SEQ ID NO 179
<211> LENGTH: 457
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 179

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Gly Asp His
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Gly Phe Ile Arg Lys Thr Thr Tyr Gly Ala Thr Thr His Tyr Ala Ala
    50                  55                  60

Ala Val Arg Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65                  70                  75                  80

Val Tyr Leu Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr
                85                  90                  95

Phe Cys Ala Arg Val Gln Leu Asp Tyr Gly Pro Gly Tyr Gln Tyr Tyr
            100                 105                 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala
        115                 120                 125

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
    130                 135                 140

Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
145                 150                 155                 160

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
                165                 170                 175

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
            180                 185                 190

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
        195                 200                 205

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
    210                 215                 220
```

```
Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
225                 230                 235                 240

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                245                 250                 255

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            260                 265                 270

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        275                 280                 285

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    290                 295                 300

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
305                 310                 315                 320

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                325                 330                 335

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            340                 345                 350

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
        355                 360                 365

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    370                 375                 380

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
385                 390                 395                 400

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                405                 410                 415

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            420                 425                 430

Phe Ser Cys Ser Val Leu His Glu Ala Leu His Ser His Tyr Thr Gln
        435                 440                 445

Lys Ser Leu Ser Leu Ser Pro Gly Lys
    450                 455


<210> SEQ ID NO 180
<211> LENGTH: 651
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 180

cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc      60

tcctgcactg ggatgaactc caacatcggg gcaggttatg atgtatactg gtaccaacaa     120

cttccaggaa ctgcccccaa actcctcatc tatggtaaca gcaatcggcc ctcaggggtc     180

cctgaccgat tctctggctc caggtctggc acctcagcct ccctggccat cactgggctc     240

caggctgagg atgaggctga ttattactgc cagtcctatg acaccagcct gaatggttgg     300

gctttcggcg gagggaccaa gttgaccgtc ctaggccagc ccaaggctgc cccctcggtc     360

actctgttcc caccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc     420

gtaagtgact tctacccggg agccgtgaca gtggcctgga aggcagatgg cagccccgtc     480

aaggtgggag tggagaccac caaaccctcc aaacaaagca acaacaagta tgcggccagc     540

agctacctga gcctgacgcc cgagcagtgg aagtcccaca gaagctacag ctgccgggtc     600

acgcatgaag ggagcaccgt ggagaagaca gtggcccctg cagaatgctc t              651
```

<210> SEQ ID NO 181
<211> LENGTH: 1371
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 181

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc cagggcggtc cctgagactc 60

agctgtgcgg cctctgggtt tagttttggt gatcatgcta tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtaggtttc attagaaaga caacttatgg tgcgacaaca 180

cactacgccg cggctgtgag aggcagattc accatctcgc gagatgattc taaaagcact 240

gtctatctgc aaatgaacag cctgaaagca gaggacacag ccgtgtattt ctgtgctaga 300

gtgcagcttg actatggccc gggataccag tactacggta tggacgtctg gggccaaggg 360

accacggtca ccgtctcctc agcctccacc aagggcccat cggtcttccc cctggcaccc 420

tcctccaaga gcacctctgg gggcacagca gccctgggct gcctggtcaa ggactacttc 480

cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc 540

ccggctgtcc tacagtcctc aggactctac tccctcagca gcgtggtgac cgtgccctcc 600

agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag 660

gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgccca 720

gcacctgaac tcctgggggg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 780

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 840

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 900

ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 960

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc 1020

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1080

ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 1140

ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1200

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1260

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1320

gctctgcaca accactacac acagaagagc ctctccctgt ctccgggtaa a 1371

<210> SEQ ID NO 182
<211> LENGTH: 1371
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 182

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc cagggcggtc cctgagactc 60

agctgtgcgg cctctgggtt tagttttggt gatcatgcta tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtaggtttc attagaaaga caacttatgg tgcgacaaca 180

cactacgccg cggctgtgag aggcagattc accatctcgc gagatgattc taaaagcact 240

gtctatctgc aaatgaacag cctgaaagca gaggacacag ccgtgtattt ctgtgctaga 300

gtgcagcttg actatggccc gggataccag tactacggta tggacgtctg gggccaaggg 360

accacggtca ccgtctcctc agcctccacc aagggcccat cggtcttccc cctggcaccc 420 tcctccaaga gcacctctgg gggcacagca gccctgggct gcctggtcaa ggactacttc 480

cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc 540

ccggctgtcc tacagtcctc aggactctac tccctcagca gcgtggtgac cgtgccctcc 600

agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag 660

gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgccca 720

gcacctgaac tcctgggggg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 780

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 840

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 900

ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 960

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc 1020

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1080

ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 1140

ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1200

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1260

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gctgcatgag 1320

gctctgcact cccactacac acagaagagc ctctccctgt ctccgggtaa a 1371

<210> SEQ ID NO 183
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 183

Thr Gly Met Asn Ser Asn Ile Gly Ala Gly Tyr Asp Val Tyr
1 5 10

<210> SEQ ID NO 184
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 184

Gly Asn Ser Asn Arg Pro Ser
1 5

<210> SEQ ID NO 185
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 185

Gln Ser Tyr Asp Thr Ser Leu Asp Gly Trp Ala
1 5 10

<210> SEQ ID NO 186
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

```
<400> SEQUENCE: 186

Asp His Ala Met Ser
1               5


<210> SEQ ID NO 187
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 187

Phe Ile Arg Lys Thr Thr Tyr Gly Ala Thr Thr Lys Tyr Ala Ala Ala
1               5                   10                  15

Val Lys Gly


<210> SEQ ID NO 188
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 188

Val Gln Leu Asp Tyr Gly Pro Gly Tyr Gln Tyr Tyr Gly Met Asp Val
1               5                   10                  15


<210> SEQ ID NO 189
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 189

Thr Gly Met Asn Ser Asn Ile Gly Ala Gly Tyr Asp Val Tyr
1               5                   10


<210> SEQ ID NO 190
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 190

Gly Asn Ser Asn Arg Pro Ser
1               5


<210> SEQ ID NO 191
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 191

Gln Ser Tyr Asp Thr Ser Leu Asp Gly Trp Ala
1               5                   10


<210> SEQ ID NO 192
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
```

```
<400> SEQUENCE: 192

Asp His Ala Met Ser
1               5


<210> SEQ ID NO 193
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 193

Phe Ile Arg Lys Thr Thr Tyr Gly Ala Thr Thr Lys Tyr Ala Ala Ala
1               5                   10                  15

Val Lys Gly


<210> SEQ ID NO 194
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 194

Val Gln Leu Asp Tyr Gly Pro Gly Tyr Gln Tyr Tyr Gly Met Asp Val
1               5                   10                  15


<210> SEQ ID NO 195
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 195

Glu Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15

Arg Val Thr Ile Ser Cys Thr Gly Met Asn Ser Asn Ile Gly Ala Gly
            20                  25                  30

Tyr Asp Val Tyr Trp Tyr Gln Gln Leu Pro Gly Arg Ala Pro Lys Leu
        35                  40                  45

Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60

Ser Gly Ser Arg Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65                  70                  75                  80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Thr Ser
                85                  90                  95

Leu Asp Gly Trp Ala Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110


<210> SEQ ID NO 196
<211> LENGTH: 127
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 196

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Pro Cys Thr Ala Ser Gly Phe Ser Phe Gly Asp His
```

```
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Gly Phe Ile Arg Lys Thr Thr Tyr Gly Ala Thr Thr Lys Tyr Ala Ala
    50                  55                  60

Ala Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile
65                  70                  75                  80

Val Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
                85                  90                  95

Phe Cys Thr Arg Val Gln Leu Asp Tyr Gly Pro Gly Tyr Gln Tyr Tyr
            100                 105                 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120                 125


<210> SEQ ID NO 197
<211> LENGTH: 336
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 197

gagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc      60

tcctgcactg ggatgaactc caacatcggg gcaggttatg atgtatactg gtaccaacaa     120

cttccaggaa gagcccccaa actcctcatc tatggtaaca gcaatcggcc ctcaggggtc     180

cctgaccgat tctctggctc caggtctggc acctcagcct ccctggccat cactgggctc     240

caggctgagg atgaggctga ttattactgc cagtcctatg acaccagcct ggacggttgg     300

gctttcggcg gagggaccaa gttgaccgtc ctaggc                               336


<210> SEQ ID NO 198
<211> LENGTH: 381
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 198

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc cagggcggtc cctgagactc      60

ccctgtacag cctctgggtt tagttttggt gatcatgcta tgagctgggt ccgccaggct     120

ccagggaagg ggctggagtg ggtaggtttc attagaaaga caacttatgg tgcgacaaca     180

aagtacgccg cggctgtgaa gggcagattc accatctcgc gagatgattc taaaagcatt     240

gtctatctgc aaatgaacag cctgaaaacc gaggacacag ccgtgtattt ctgtactaga     300

gtgcagcttg actatggccc gggataccag tactacggta tggacgtctg gggccaaggg     360

accacggtca ccgtctcctc a                                               381


<210> SEQ ID NO 199
<211> LENGTH: 217
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 199

Glu Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15
```

```
Arg Val Thr Ile Ser Cys Thr Gly Met Asn Ser Asn Ile Gly Ala Gly
            20                  25                  30

Tyr Asp Val Tyr Trp Tyr Gln Gln Leu Pro Gly Arg Ala Pro Lys Leu
        35                  40                  45

Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60

Ser Gly Ser Arg Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65                  70                  75                  80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Thr Ser
                85                  90                  95

Leu Asp Gly Trp Ala Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu
        115                 120                 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Val Ser Asp Phe
    130                 135                 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro Val
145                 150                 155                 160

Lys Val Gly Val Glu Thr Thr Lys Pro Ser Lys Gln Ser Asn Asn Lys
                165                 170                 175

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
            180                 185                 190

His Arg Ser Tyr Ser Cys Arg Val Thr His Glu Gly Ser Thr Val Glu
        195                 200                 205

Lys Thr Val Ala Pro Ala Glu Cys Ser
    210                 215


<210> SEQ ID NO 200
<211> LENGTH: 457
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 200

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Pro Cys Thr Ala Ser Gly Phe Ser Phe Gly Asp His
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Gly Phe Ile Arg Lys Thr Thr Tyr Gly Ala Thr Thr Lys Tyr Ala Ala
    50                  55                  60

Ala Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile
65                  70                  75                  80

Val Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
                85                  90                  95

Phe Cys Thr Arg Val Gln Leu Asp Tyr Gly Pro Gly Tyr Gln Tyr Tyr
            100                 105                 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala
        115                 120                 125

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
    130                 135                 140

Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
145                 150                 155                 160
```

-continued

```
Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
                165                 170                 175

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
            180                 185                 190

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
        195                 200                 205

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
    210                 215                 220

Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
225                 230                 235                 240

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                245                 250                 255

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            260                 265                 270

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        275                 280                 285

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    290                 295                 300

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
305                 310                 315                 320

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                325                 330                 335

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            340                 345                 350

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
        355                 360                 365

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    370                 375                 380

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
385                 390                 395                 400

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                405                 410                 415

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            420                 425                 430

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
        435                 440                 445

Lys Ser Leu Ser Leu Ser Pro Gly Lys
    450                 455


<210> SEQ ID NO 201
<211> LENGTH: 457
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 201

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Pro Cys Thr Ala Ser Gly Phe Ser Phe Gly Asp His
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Gly Phe Ile Arg Lys Thr Thr Tyr Gly Ala Thr Thr Lys Tyr Ala Ala
    50                  55                  60
```

```
Ala Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile
65                  70                  75                  80

Val Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
                85                  90                  95

Phe Cys Thr Arg Val Gln Leu Asp Tyr Gly Pro Gly Tyr Gln Tyr Tyr
            100                 105                 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala
        115                 120                 125

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
    130                 135                 140

Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
145                 150                 155                 160

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
                165                 170                 175

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
            180                 185                 190

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
        195                 200                 205

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
    210                 215                 220

Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
225                 230                 235                 240

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                245                 250                 255

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            260                 265                 270

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        275                 280                 285

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    290                 295                 300

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
305                 310                 315                 320

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                325                 330                 335

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            340                 345                 350

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
        355                 360                 365

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    370                 375                 380

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
385                 390                 395                 400

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                405                 410                 415

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            420                 425                 430

Phe Ser Cys Ser Val Leu His Glu Ala Leu His Ser His Tyr Thr Gln
        435                 440                 445

Lys Ser Leu Ser Leu Ser Pro Gly Lys
    450                 455


<210> SEQ ID NO 202
<211> LENGTH: 651
<212> TYPE: DNA
```

<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 202

gagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60

tcctgcactg ggatgaactc caacatcggg gcaggttatg atgtatactg gtaccaacaa 120

cttccaggaa gagcccccaa actcctcatc tatggtaaca gcaatcggcc ctcaggggtc 180

cctgaccgat tctctggctc caggtctggc acctcagcct ccctggccat cactgggctc 240

caggctgagg atgaggctga ttattactgc cagtcctatg acaccagcct ggacggttgg 300

gctttcggcg gagggaccaa gttgaccgtc ctaggccagc ccaaggctgc cccctcggtc 360

actctgttcc caccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420

gtaagtgact tctacccggg agccgtgaca gtggcctgga aggcagatgg cagccccgtc 480

aaggtgggag tggagaccac caaaccctcc aaacaaagca acaacaagta tgcggccagc 540

agctacctga gcctgacgcc cgagcagtgg aagtcccaca gaagctacag ctgccgggtc 600

acgcatgaag ggagcaccgt ggagaagaca gtggcccctg cagaatgctc t 651

<210> SEQ ID NO 203
<211> LENGTH: 1371
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 203

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc cagggcggtc cctgagactc 60

ccctgtacag cctctgggtt tagttttggt gatcatgcta tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtaggtttc attagaaaga caacttatgg tgcgacaaca 180

aagtacgccg cggctgtgaa gggcagattc accatctcgc gagatgattc taaaagcatt 240

gtctatctgc aaatgaacag cctgaaaacc gaggacacag ccgtgtattt ctgtactaga 300

gtgcagcttg actatggccc gggataccag tactacggta tggacgtctg gggccaaggg 360

accacggtca ccgtctcctc agcctccacc aagggcccat cggtcttccc cctggcaccc 420

tcctccaaga gcacctctgg gggcacagca gccctgggct gcctggtcaa ggactacttc 480

cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc 540

ccggctgtcc tacagtcctc aggactctac tccctcagca gcgtggtgac cgtgccctcc 600

agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag 660

gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgccca 720

gcacctgaac tcctgggggg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 780

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 840

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 900

ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 960

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc 1020

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1080

ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 1140

ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1200

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1260 accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1320

gctctgcaca accactacac acagaagagc ctctccctgt ctccgggtaa a 1371

<210> SEQ ID NO 204
<211> LENGTH: 1371
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 204

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc cagggcggtc cctgagactc 60

ccctgtacag cctctgggtt tagttttggt gatcatgcta tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtaggtttc attagaaaga caacttatgg tgcgacaaca 180

aagtacgccg cggctgtgaa gggcagattc accatctcgc gagatgattc taaaagcatt 240

gtctatctgc aaatgaacag cctgaaaacc gaggacacag ccgtgtattt ctgtactaga 300

gtgcagcttg actatggccc gggataccag tactacggta tggacgtctg gggccaaggg 360

accacggtca ccgtctcctc agcctccacc aagggcccat cggtcttccc cctggcaccc 420

tcctccaaga gcacctctgg gggcacagca gccctgggct gcctggtcaa ggactacttc 480

cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc 540

ccggctgtcc tacagtcctc aggactctac tccctcagca gcgtggtgac cgtgccctcc 600

agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag 660

gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgccca 720

gcacctgaac tcctgggggg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 780

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 840

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 900

ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 960

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc 1020

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1080

ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 1140

ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1200

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1260

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gctgcatgag 1320

gctctgcact cccactacac acagaagagc ctctccctgt ctccgggtaa a 1371

<210> SEQ ID NO 205
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 205

Arg Ala Ser Gln Ser Ile Ser Ser Trp Leu Ala
1 5 10

<210> SEQ ID NO 206
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence

```
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 206

Asp Ala Ser Ser Leu Glu Ser
1               5


<210> SEQ ID NO 207
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 207

Gln Gln Tyr Asn Ser Tyr Ser Phe Trp Thr
1               5                   10


<210> SEQ ID NO 208
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 208

Thr Tyr Gly Met His
1               5


<210> SEQ ID NO 209
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 209

Ile Ile Trp Tyr Asp Gly Ser Gln Lys Tyr Tyr Ala Asp Ser Val Gln
1               5                   10                  15

Gly


<210> SEQ ID NO 210
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 210

Val Arg Phe Ser Val Gly Pro His Gly Ser Ala Phe Asp Leu
1               5                   10


<210> SEQ ID NO 211
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 211

Arg Ala Ser Gln Ser Ile Ser Ser Trp Leu Ala
1               5                   10


<210> SEQ ID NO 212
<211> LENGTH: 7
<212> TYPE: PRT
```

```
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 212

Asp Ala Ser Ser Leu Glu Ser
1               5


<210> SEQ ID NO 213
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 213

Gln Gln Tyr Asn Ser Tyr Ser Phe Trp Thr Phe
1               5                   10


<210> SEQ ID NO 214
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 214

Thr Tyr Gly Met His
1               5


<210> SEQ ID NO 215
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 215

Ile Ile Trp Tyr Asp Gly Ser Gln Lys Tyr Tyr Ala Asp Ser Val Gln
1               5                   10                  15

Gly


<210> SEQ ID NO 216
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 216

Ser Ala Phe Asp Leu
1               5


<210> SEQ ID NO 217
<211> LENGTH: 109
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 217

Gly Val Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1               5                   10                  15

Asp Arg Val Thr Leu Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Trp
            20                  25                  30
```

```
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Ser Phe
                85                  90                  95

Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105
```

<210> SEQ ID NO 218
<211> LENGTH: 123
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 218

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Asn Thr Tyr
            20                  25                  30

Gly Met His Trp Val Arg Gln Thr Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ala Ile Ile Trp Tyr Asp Gly Ser Gln Lys Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Gln Gly Arg Phe Ile Ile Ser Arg Asp Asn His Lys Asn Thr Leu Ser
65                  70                  75                  80

Leu Gln Met Asn Gly Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys
                85                  90                  95

Val Arg Val Arg Phe Ser Val Gly Pro His Gly Ser Ala Phe Asp Leu
            100                 105                 110

Trp Gly Gln Gly Thr Met Val Ile Val Ser Ser
        115                 120
```

<210> SEQ ID NO 219
<211> LENGTH: 327
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 219

```
ggcgtccaga tgacccagtc tccttccacc ctgtctgcat ctgtgggaga cagagtcacc     60

ctcacttgcc gggccagtca gagtattagt agttggttgg cctggtatca gcagaaacca    120

gggaaagccc ctaaactcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca    180

aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcaacct    240

gatgattttg caacttatta ctgccaacag tataatagtt attctttttg gacgttcggc    300

caagggacca aggtggaaat caaacgc                                        327
```

<210> SEQ ID NO 220
<211> LENGTH: 369
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

```
<400> SEQUENCE: 220

caggtgcaac tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc      60

tcctgtgcag cgtctgggtt cgctttcaat acctatggca tgcactgggt ccgccagact     120

ccaggcaagg ggctggagtg ggtggcaatt atctggtatg atgggagcca gaaatactat     180

gcagactccg tgcagggccg attcatcatc tccagagaca atcacaagaa cacgttgtct     240

ctgcaaatga acggcctgag agccgaggac acggctgtgt atttctgtgt gagagtccgc     300

tttagcgttg gcccccacgg gagtgctttt gatctctggg gccaggggac aatggtcatc     360

gtctcttca                                                             369


<210> SEQ ID NO 221
<211> LENGTH: 215
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 221

Gly Val Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1               5                   10                  15

Asp Arg Val Thr Leu Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Trp
            20                  25                  30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Ser Phe
                85                  90                  95

Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala
            100                 105                 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
        115                 120                 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
    130                 135                 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145                 150                 155                 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
                165                 170                 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
            180                 185                 190

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
        195                 200                 205

Ser Phe Asn Arg Gly Glu Cys
    210                 215


<210> SEQ ID NO 222
<211> LENGTH: 453
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 222

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
```

-continued

```
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Asn Thr Tyr
            20                  25                  30

Gly Met His Trp Val Arg Gln Thr Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ala Ile Ile Trp Tyr Asp Gly Ser Gln Lys Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Gln Gly Arg Phe Ile Ile Ser Arg Asp Asn His Lys Asn Thr Leu Ser
65                  70                  75                  80

Leu Gln Met Asn Gly Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys
                85                  90                  95

Val Arg Val Arg Phe Ser Val Gly Pro His Gly Ser Ala Phe Asp Leu
            100                 105                 110

Trp Gly Gln Gly Thr Met Val Ile Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys
    210                 215                 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
225                 230                 235                 240

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
        355                 360                 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430
```

```
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445

Leu Ser Pro Gly Lys
    450


<210> SEQ ID NO 223
<211> LENGTH: 453
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 223

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Asn Thr Tyr
            20                  25                  30

Gly Met His Trp Val Arg Gln Thr Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ala Ile Ile Trp Tyr Asp Gly Ser Gln Lys Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Gln Gly Arg Phe Ile Ile Ser Arg Asp Asn His Lys Asn Thr Leu Ser
65                  70                  75                  80

Leu Gln Met Asn Gly Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys
                85                  90                  95

Val Arg Val Arg Phe Ser Val Gly Pro His Gly Ser Ala Phe Asp Leu
            100                 105                 110

Trp Gly Gln Gly Thr Met Val Ile Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys
    210                 215                 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
225                 230                 235                 240

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335
```

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
340 345 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
355 360 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
370 375 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385 390 395 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
405 410 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
420 425 430

Val Leu His Glu Ala Leu His Ser His Tyr Thr Gln Lys Ser Leu Ser
435 440 445

Leu Ser Pro Gly Lys
450

<210> SEQ ID NO 224
<211> LENGTH: 645
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 224

ggcgtccaga tgacccagtc tccttccacc ctgtctgcat ctgtgggaga cagagtcacc 60

ctcacttgcc gggccagtca gagtattagt agttggttgg cctggtatca gcagaaacca 120

gggaaagccc ctaaactcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcaacct 240

gatgattttg caacttatta ctgccaacag tataatagtt attctttttg gacgttcggc 300

caagggacca aggtggaaat caaacgcact gtggctgcac catctgtctt catcttcccg 360

ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 420

tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc 480

caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 540

acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag 600

ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgt 645

<210> SEQ ID NO 225
<211> LENGTH: 1359
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 225

caggtgcaac tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cgtctgggtt cgctttcaat acctatggca tgcactgggt ccgccagact 120

ccaggcaagg ggctggagtg ggtggcaatt atctggtatg atgggagcca gaaatactat 180

gcagactccg tgcagggccg attcatcatc tccagagaca atcacaagaa cacgttgtct 240

ctgcaaatga acggcctgag agccgaggac acggctgtgt atttctgtgt gagagtccgc 300

tttagcgttg gcccccacgg gagtgctttt gatctctggg gccaggggac aatggtcatc 360 gtctcttcag cctccaccaa gggcccatcg gtcttccccc tggcaccctc ctccaagagc 420

acctctgggg gcacagcagc cctgggctgc ctggtcaagg actacttccc cgaaccggtg 480

acggtgtcgt ggaactcagg cgccctgacc agcggcgtgc acaccttccc ggctgtccta 540

cagtcctcag gactctactc cctcagcagc gtggtgaccg tgccctccag cagcttgggc 600

acccagacct acatctgcaa cgtgaatcac aagcccagca acaccaaggt ggacaagaaa 660

gttgagccca aatcttgtga caaaactcac acatgcccac cgtgcccagc acctgaactc 720

ctggggggac cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc 780

cggacccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagaccc tgaggtcaag 840

ttcaactggt acgtggacgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag 900

cagtacaaca gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg 960

aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa 1020

accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gcccccatcc 1080

cgggatgagc tgaccaagaa ccaggtcagc ctgacctgcc tggtcaaagg cttctatccc 1140

agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 1200

cctcccgtgc tggactccga cggctccttc ttcctctaca gcaagctcac cgtggacaag 1260

agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac 1320

cactacacac agaagagcct ctccctgtct ccgggtaaa 1359

<210> SEQ ID NO 226
<211> LENGTH: 1359
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 226

caggtgcaac tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cgtctgggtt cgctttcaat acctatggca tgcactgggt ccgccagact 120

ccaggcaagg ggctggagtg ggtggcaatt atctggtatg atgggagcca gaaatactat 180

gcagactccg tgcagggccg attcatcatc tccagagaca atcacaagaa cacgttgtct 240

ctgcaaatga acggcctgag agccgaggac acggctgtgt atttctgtgt gagagtccgc 300

tttagcgttg gcccccacgg gagtgctttt gatctctggg gccaggggac aatggtcatc 360

gtctcttcag cctccaccaa gggcccatcg gtcttccccc tggcaccctc ctccaagagc 420

acctctgggg gcacagcagc cctgggctgc ctggtcaagg actacttccc cgaaccggtg 480

acggtgtcgt ggaactcagg cgccctgacc agcggcgtgc acaccttccc ggctgtccta 540

cagtcctcag gactctactc cctcagcagc gtggtgaccg tgccctccag cagcttgggc 600

acccagacct acatctgcaa cgtgaatcac aagcccagca acaccaaggt ggacaagaaa 660

gttgagccca aatcttgtga caaaactcac acatgcccac cgtgcccagc acctgaactc 720

ctggggggac cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc 780

cggacccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagaccc tgaggtcaag 840

ttcaactggt acgtggacgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag 900

cagtacaaca gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg 960

aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa 1020

accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gcccccatcc 1080

```
cgggatgagc tgaccaagaa ccaggtcagc ctgacctgcc tggtcaaagg cttctatccc   1140

agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg   1200

cctcccgtgc tggactccga cggctccttc ttcctctaca gcaagctcac cgtggacaag   1260

agcaggtggc agcaggggaa cgtcttctca tgctccgtgc tgcatgaggc tctgcactcc   1320

cactacacac agaagagcct ctccctgtct ccgggtaaa                         1359


<210> SEQ ID NO 227
<211> LENGTH: 109
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 227

Gly Val Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1               5                   10                  15

Asp Arg Val Thr Leu Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Trp
            20                  25                  30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Ser Phe
                85                  90                  95

Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> SEQ ID NO 228
<211> LENGTH: 123
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 228

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Asn Thr Tyr
            20                  25                  30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ala Ile Ile Trp Tyr Asp Gly Ser Gln Lys Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Gln Gly Arg Phe Ile Ile Ser Arg Asp Asn His Lys Asn Thr Leu Ser
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys
                85                  90                  95

Val Arg Val Arg Phe Ser Val Gly Pro His Gly Ser Ala Phe Asp Leu
            100                 105                 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115                 120


<210> SEQ ID NO 229
<211> LENGTH: 327
```

```
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 229

ggcgtccaga tgacccagtc tccttccacc ctgtctgcat ctgtgggaga cagagtcacc     60

ctcacttgcc gggccagtca gagtattagt agttggttgg cctggtatca gcagaaacca    120

gggaaagccc ctaaactcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca    180

aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcaacct    240

gatgattttg caacttatta ctgccaacag tataatagtt attctttttg gacgttcggc    300

caagggacca aggtggaaat caaacgc                                        327


<210> SEQ ID NO 230
<211> LENGTH: 369
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 230

caggtgcaac tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc     60

tcctgtgcag cgtctgggtt cgctttcaat acctatggca tgcactgggt ccgccaggca    120

ccaggcaagg ggctggagtg ggtggcaatt atctggtatg atgggagcca gaaatactat    180

gcagactccg tgcagggccg attcatcatc tccagagaca atcacaagaa cacgttgtct    240

ctgcaaatga actccctgag agccgaggac acggctgtgt atttctgtgt gagagtccgc    300

tttagcgttg gcccccacgg gagtgctttt gatctctggg gccaggggac aatggtcaca    360

gtctcttca                                                            369


<210> SEQ ID NO 231
<211> LENGTH: 215
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 231

Gly Val Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1               5                   10                  15

Asp Arg Val Thr Leu Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Trp
            20                  25                  30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Ser Phe
                85                  90                  95

Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala
            100                 105                 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
        115                 120                 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
    130                 135                 140
```

```
Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145                 150                 155                 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
                165                 170                 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
            180                 185                 190

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
        195                 200                 205

Ser Phe Asn Arg Gly Glu Cys
    210                 215


<210> SEQ ID NO 232
<211> LENGTH: 453
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 232

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Asn Thr Tyr
            20                  25                  30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ala Ile Ile Trp Tyr Asp Gly Ser Gln Lys Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Gln Gly Arg Phe Ile Ile Ser Arg Asp Asn His Lys Asn Thr Leu Ser
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys
                85                  90                  95

Val Arg Val Arg Phe Ser Val Gly Pro His Gly Ser Ala Phe Asp Leu
            100                 105                 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys
    210                 215                 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
225                 230                 235                 240

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285
```

```
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
        355                 360                 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445

Leu Ser Pro Gly Lys
    450
```

```
<210> SEQ ID NO 233
<211> LENGTH: 453
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 233

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Asn Thr Tyr
            20                  25                  30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ala Ile Ile Trp Tyr Asp Gly Ser Gln Lys Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Gln Gly Arg Phe Ile Ile Ser Arg Asp Asn His Lys Asn Thr Leu Ser
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys
                85                  90                  95

Val Arg Val Arg Phe Ser Val Gly Pro His Gly Ser Ala Phe Asp Leu
            100                 105                 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190
```

```
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys
    210                 215                 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
225                 230                 235                 240

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
        355                 360                 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430

Val Leu His Glu Ala Leu His Ser His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445

Leu Ser Pro Gly Lys
    450


<210> SEQ ID NO 234
<211> LENGTH: 645
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 234

ggcgtccaga tgacccagtc tccttccacc ctgtctgcat ctgtgggaga cagagtcacc      60

ctcacttgcc gggccagtca gagtattagt agttggttgg cctggtatca gcagaaacca     120

gggaaagccc ctaaactcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca     180

aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcaacct     240

gatgattttg caacttatta ctgccaacag tataatagtt attctttttg gacgttcggc     300

caagggacca aggtggaaat caaacgcact gtggctgcac catctgtctt catcttcccg     360

ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc     420

tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc     480

caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg     540
```

acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag 600

ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgt 645

<210> SEQ ID NO 235
<211> LENGTH: 1359
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 235

caggtgcaac tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cgtctgggtt cgctttcaat acctatggca tgcactgggt ccgccaggca 120

ccaggcaagg ggctggagtg ggtggcaatt atctggtatg atgggagcca gaaatactat 180

gcagactccg tgcagggccg attcatcatc tccagagaca atcacaagaa cacgttgtct 240

ctgcaaatga actccctgag agccgaggac acggctgtgt atttctgtgt gagagtccgc 300

tttagcgttg gcccccacgg gagtgctttt gatctctggg gccaggggac aatggtcaca 360

gtctcttcag cctccaccaa gggcccatcg gtcttccccc tggcaccctc ctccaagagc 420

acctctgggg gcacagcagc cctgggctgc ctggtcaagg actacttccc cgaaccggtg 480

acggtgtcgt ggaactcagg cgccctgacc agcggcgtgc acaccttccc ggctgtccta 540

cagtcctcag gactctactc cctcagcagc gtggtgaccg tgccctccag cagcttgggc 600

acccagacct acatctgcaa cgtgaatcac aagcccagca acaccaaggt ggacaagaaa 660

gttgagccca aatcttgtga caaaactcac acatgcccac cgtgcccagc acctgaactc 720

ctggggggac cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc 780

cggacccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagaccc tgaggtcaag 840

ttcaactggt acgtggacgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag 900

cagtacaaca gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg 960

aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa 1020

accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gcccccatcc 1080

cgggatgagc tgaccaagaa ccaggtcagc ctgacctgcc tggtcaaagg cttctatccc 1140

agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 1200

cctcccgtgc tggactccga cggctccttc ttcctctaca gcaagctcac cgtggacaag 1260

agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac 1320

cactacacac agaagagcct ctccctgtct ccgggtaaa 1359

<210> SEQ ID NO 236
<211> LENGTH: 1359
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 236

caggtgcaac tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cgtctgggtt cgctttcaat acctatggca tgcactgggt ccgccaggca 120

ccaggcaagg ggctggagtg ggtggcaatt atctggtatg atgggagcca gaaatactat 180

gcagactccg tgcagggccg attcatcatc tccagagaca atcacaagaa cacgttgtct 240

```
ctgcaaatga actccctgag agccgaggac acggctgtgt atttctgtgt gagagtccgc    300

tttagcgttg gcccccacgg gagtgctttt gatctctggg gccaggggac aatggtcaca    360

gtctcttcag cctccaccaa gggcccatcg gtcttccccc tggcaccctc ctccaagagc    420

acctctgggg gcacagcagc cctgggctgc ctggtcaagg actacttccc cgaaccggtg    480

acggtgtcgt ggaactcagg cgccctgacc agcggcgtgc acaccttccc ggctgtccta    540

cagtcctcag gactctactc cctcagcagc gtggtgaccg tgccctccag cagcttgggc    600

acccagacct acatctgcaa cgtgaatcac aagcccagca acaccaaggt ggacaagaaa    660

gttgagccca aatcttgtga caaaactcac acatgcccac cgtgcccagc acctgaactc    720

ctggggggac cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc    780

cggacccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagaccc tgaggtcaag    840

ttcaactggt acgtggacgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag    900

cagtacaaca gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg    960

aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa   1020

accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gcccccatcc   1080

cgggatgagc tgaccaagaa ccaggtcagc ctgacctgcc tggtcaaagg cttctatccc   1140

agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg   1200

cctcccgtgc tggactccga cggctccttc ttcctctaca gcaagctcac cgtggacaag   1260

agcaggtggc agcaggggaa cgtcttctca tgctccgtgc tgcatgaggc tctgcactcc   1320

cactacacac agaagagcct ctccctgtct ccgggtaaa                          1359
```

<210> SEQ ID NO 237
<211> LENGTH: 109
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 237

```
Gly Val Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1               5                   10                  15

Asp Arg Val Thr Leu Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Trp
            20                  25                  30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Ser Phe
                85                  90                  95

Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105
```

<210> SEQ ID NO 238
<211> LENGTH: 123
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 238

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Thr Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Ile Ile Trp Tyr Asp Gly Ser Gln Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Gln Gly Arg Phe Ile Ile Ser Arg Asp Asn His Lys Asn Thr Leu Ser
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys
85 90 95

Val Arg Val Arg Phe Ser Val Gly Pro His Gly Ser Ala Phe Asp Leu
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> SEQ ID NO 239
<211> LENGTH: 327
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 239

ggcgtccaga tgacccagtc tccttccacc ctgtctgcat ctgtgggaga cagagtcacc 60

ctcacttgcc gggccagtca gagtattagt agttggttgg cctggtatca gcagaaacca 120

gggaaagccc ctaaactcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcaacct 240

gatgattttg caacttatta ctgccaacag tataatagtt attctttttg gacgttcggc 300

caagggacca aggtggaaat caaacgc 327

<210> SEQ ID NO 240
<211> LENGTH: 369
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 240

caggtgcaac tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cgtctgggtt cactttcaat acctatggca tgcactgggt ccgccaggca 120

ccaggcaagg ggctggagtg ggtggcaatt atctggtatg atgggagcca gaaatactat 180

gcagactccg tgcagggccg attcatcatc tccagagaca atcacaagaa cacgttgtct 240

ctgcaaatga actccctgag agccgaggac acggctgtgt atttctgtgt gagagtccgc 300

tttagcgttg gcccccacgg gagtgctttt gatctctggg gccaggggac aatggtcaca 360

gtctcttca 369

<210> SEQ ID NO 241
<211> LENGTH: 215
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 241

```
Gly Val Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1               5                   10                  15

Asp Arg Val Thr Leu Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Trp
            20                  25                  30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Ser Phe
                85                  90                  95

Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala
            100                 105                 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
        115                 120                 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
    130                 135                 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145                 150                 155                 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
                165                 170                 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
            180                 185                 190

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
        195                 200                 205

Ser Phe Asn Arg Gly Glu Cys
    210                 215


<210> SEQ ID NO 242
<211> LENGTH: 453
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 242

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Thr Tyr
            20                  25                  30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ala Ile Ile Trp Tyr Asp Gly Ser Gln Lys Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Gln Gly Arg Phe Ile Ile Ser Arg Asp Asn His Lys Asn Thr Leu Ser
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys
                85                  90                  95

Val Arg Val Arg Phe Ser Val Gly Pro His Gly Ser Ala Phe Asp Leu
            100                 105                 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140
```

```
Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys
    210                 215                 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
225                 230                 235                 240

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
        355                 360                 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445

Leu Ser Pro Gly Lys
    450


<210> SEQ ID NO 243
<211> LENGTH: 453
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 243

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Thr Tyr
            20                  25                  30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
```

```
Ala Ile Ile Trp Tyr Asp Gly Ser Gln Lys Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Gln Gly Arg Phe Ile Ile Ser Arg Asp Asn His Lys Asn Thr Leu Ser
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys
                85                  90                  95

Val Arg Val Arg Phe Ser Val Gly Pro His Gly Ser Ala Phe Asp Leu
            100                 105                 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys
    210                 215                 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
225                 230                 235                 240

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
        355                 360                 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430

Val Leu His Glu Ala Leu His Ser His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445

Leu Ser Pro Gly Lys
    450
```

<210> SEQ ID NO 244
<211> LENGTH: 645
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 244

ggcgtccaga tgacccagtc tccttccacc ctgtctgcat ctgtgggaga cagagtcacc 60

ctcacttgcc gggccagtca gagtattagt agttggttgg cctggtatca gcagaaacca 120

gggaaagccc ctaaactcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcaacct 240

gatgattttg caacttatta ctgccaacag tataatagtt attctttttg gacgttcggc 300

caagggacca aggtggaaat caaacgcact gtggctgcac catctgtctt catcttcccg 360

ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 420

tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc 480

caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 540

acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag 600

ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgt 645

<210> SEQ ID NO 245
<211> LENGTH: 1359
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 245

caggtgcaac tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cgtctgggtt cactttcaat acctatggca tgcactgggt ccgccaggca 120

ccaggcaagg ggctggagtg ggtggcaatt atctggtatg atgggagcca gaaatactat 180

gcagactccg tgcagggccg attcatcatc tccagagaca atcacaagaa cacgttgtct 240

ctgcaaatga actccctgag agccgaggac acggctgtgt atttctgtgt gagagtccgc 300

tttagcgttg gcccccacgg gagtgctttt gatctctggg gccaggggac aatggtcaca 360

gtctcttcag cctccaccaa gggcccatcg gtcttccccc tggcaccctc ctccaagagc 420

acctctgggg gcacagcagc cctgggctgc ctggtcaagg actacttccc cgaaccggtg 480

acggtgtcgt ggaactcagg cgccctgacc agcggcgtgc acaccttccc ggctgtccta 540

cagtcctcag gactctactc cctcagcagc gtggtgaccg tgccctccag cagcttgggc 600

acccagacct acatctgcaa cgtgaatcac aagcccagca acaccaaggt ggacaagaaa 660

gttgagccca aatcttgtga caaaactcac acatgcccac cgtgcccagc acctgaactc 720

ctggggggac cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc 780

cggacccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagaccc tgaggtcaag 840

ttcaactggt acgtggacgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag 900

cagtacaaca gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg 960

aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa 1020

accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gcccccatcc 1080

cgggatgagc tgaccaagaa ccaggtcagc ctgacctgcc tggtcaaagg cttctatccc 1140 agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 1200

cctcccgtgc tggactccga cggctccttc ttcctctaca gcaagctcac cgtggacaag 1260

agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac 1320

cactacacac agaagagcct ctccctgtct ccgggtaaa 1359

<210> SEQ ID NO 246
<211> LENGTH: 1359
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 246

caggtgcaac tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cgtctgggtt cactttcaat acctatggca tgcactgggt ccgccaggca 120

ccaggcaagg ggctggagtg ggtggcaatt atctggtatg atgggagcca gaaatactat 180

gcagactccg tgcagggccg attcatcatc tccagagaca atcacaagaa cacgttgtct 240

ctgcaaatga actccctgag agccgaggac acggctgtgt atttctgtgt gagagtccgc 300

tttagcgttg gcccccacgg gagtgctttt gatctctggg gccaggggac aatggtcaca 360

gtctcttcag cctccaccaa gggcccatcg gtcttccccc tggcaccctc ctccaagagc 420

acctctgggg gcacagcagc cctgggctgc ctggtcaagg actacttccc cgaaccggtg 480

acggtgtcgt ggaactcagg cgccctgacc agcggcgtgc acaccttccc ggctgtccta 540

cagtcctcag gactctactc cctcagcagc gtggtgaccg tgccctccag cagcttgggc 600

acccagacct acatctgcaa cgtgaatcac aagcccagca acaccaaggt ggacaagaaa 660

gttgagccca aatcttgtga caaaactcac acatgcccac cgtgcccagc acctgaactc 720

ctggggggac cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc 780

cggacccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagaccc tgaggtcaag 840

ttcaactggt acgtggacgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag 900

cagtacaaca gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg 960

aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa 1020

accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gcccccatcc 1080

cgggatgagc tgaccaagaa ccaggtcagc ctgacctgcc tggtcaaagg cttctatccc 1140

agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 1200

cctcccgtgc tggactccga cggctccttc ttcctctaca gcaagctcac cgtggacaag 1260

agcaggtggc agcaggggaa cgtcttctca tgctccgtgc tgcatgaggc tctgcactcc 1320

cactacacac agaagagcct ctccctgtct ccgggtaaa 1359

<210> SEQ ID NO 247
<211> LENGTH: 109
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 247

Gly Val Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Leu Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Trp

            20   25   30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45

Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Ser Phe
                85   90   95

Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100   105

<210> SEQ ID NO 248
<211> LENGTH: 123
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 248

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Asn Thr Tyr
            20   25   30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ala Ile Ile Trp Tyr Asp Gly Ser Gln Lys Tyr Tyr Ala Asp Ser Val
    50   55   60

Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn His Lys Asn Thr Leu Ser
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys
                85   90   95

Val Arg Val Arg Phe Ser Val Gly Pro His Gly Ser Ala Phe Asp Leu
            100   105   110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115   120

<210> SEQ ID NO 249
<211> LENGTH: 327
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 249

ggcgtccaga tgacccagtc tccttccacc ctgtctgcat ctgtgggaga cagagtcacc 60

ctcacttgcc gggccagtca gagtattagt agttggttgg cctggtatca gcagaaacca 120

gggaaagccc ctaaactcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcaacct 240

gatgattttg caacttatta ctgccaacag tataatagtt attctttttg gacgttcggc 300

caagggacca aggtggaaat caaacgc 327

<210> SEQ ID NO 250
<211> LENGTH: 369
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 250

caggtgcaac tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cgtctgggtt cgctttcaat acctatggca tgcactgggt ccgccaggca 120

ccaggcaagg ggctggagtg ggtggcaatt atctggtatg atgggagcca gaaatactat 180

gcagactccg tgcagggccg attcactatc tccagagaca atcacaagaa cacgttgtct 240

ctgcaaatga actccctgag agccgaggac acggctgtgt atttctgtgt gagagtccgc 300

tttagcgttg gcccccacgg gagtgctttt gatctctggg gccaggggac aatggtcaca 360

gtctcttca 369

<210> SEQ ID NO 251
<211> LENGTH: 215
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 251

Gly Val Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1   5   10   15

Asp Arg Val Thr Leu Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Trp
            20   25   30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45

Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Ser Phe
                85   90   95

Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala
            100   105   110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
        115   120   125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
    130   135   140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145   150   155   160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
                165   170   175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
            180   185   190

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
        195   200   205

Ser Phe Asn Arg Gly Glu Cys
    210   215

<210> SEQ ID NO 252
<211> LENGTH: 453
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 252

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Asn Thr Tyr
            20                  25                  30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ala Ile Ile Trp Tyr Asp Gly Ser Gln Lys Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn His Lys Asn Thr Leu Ser
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys
                85                  90                  95

Val Arg Val Arg Phe Ser Val Gly Pro His Gly Ser Ala Phe Asp Leu
            100                 105                 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys
    210                 215                 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
225                 230                 235                 240

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
        355                 360                 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415
```

```
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445

Leu Ser Pro Gly Lys
    450


<210> SEQ ID NO 253
<211> LENGTH: 453
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 253

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Asn Thr Tyr
            20                  25                  30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ala Ile Ile Trp Tyr Asp Gly Ser Gln Lys Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn His Lys Asn Thr Leu Ser
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys
                85                  90                  95

Val Arg Val Arg Phe Ser Val Gly Pro His Gly Ser Ala Phe Asp Leu
            100                 105                 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys
    210                 215                 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
225                 230                 235                 240

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320
```

```
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
        355                 360                 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430

Val Leu His Glu Ala Leu His Ser His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445

Leu Ser Pro Gly Lys
    450
```

<210> SEQ ID NO 254
<211> LENGTH: 645
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 254

```
ggcgtccaga tgacccagtc tccttccacc ctgtctgcat ctgtgggaga cagagtcacc     60

ctcacttgcc gggccagtca gagtattagt agttggttgg cctggtatca gcagaaacca    120

gggaaagccc ctaaactcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca    180

aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcaacct    240

gatgattttg caacttatta ctgccaacag tataatagtt attctttttg gacgttcggc    300

caagggacca aggtggaaat caaacgcact gtggctgcac catctgtctt catcttcccg    360

ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc    420

tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc    480

caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg    540

acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag    600

ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgt                     645
```

<210> SEQ ID NO 255
<211> LENGTH: 1359
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 255

```
caggtgcaac tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc     60

tcctgtgcag cgtctgggtt cgctttcaat acctatggca tgcactgggt ccgccaggca    120

ccaggcaagg ggctggagtg ggtggcaatt atctggtatg atgggagcca gaaatactat    180

gcagactccg tgcagggccg attcactatc tccagagaca atcacaagaa cacgttgtct    240

ctgcaaatga actccctgag agccgaggac acggctgtgt atttctgtgt gagagtccgc    300
```

-continued

tttagcgttg gcccccacgg gagtgctttt gatctctggg gccaggggac aatggtcaca 360

gtctcttcag cctccaccaa gggcccatcg gtcttccccc tggcaccctc ctccaagagc 420

acctctgggg gcacagcagc cctgggctgc ctggtcaagg actacttccc cgaaccggtg 480

acggtgtcgt ggaactcagg cgccctgacc agcggcgtgc acaccttccc ggctgtccta 540

cagtcctcag gactctactc cctcagcagc gtggtgaccg tgccctccag cagcttgggc 600

acccagacct acatctgcaa cgtgaatcac aagcccagca acaccaaggt ggacaagaaa 660

gttgagccca aatcttgtga caaaactcac acatgcccac cgtgcccagc acctgaactc 720

ctggggggac cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc 780

cggacccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagaccc tgaggtcaag 840

ttcaactggt acgtggacgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag 900

cagtacaaca gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg 960

aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa 1020

accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gcccccatcc 1080

cgggatgagc tgaccaagaa ccaggtcagc ctgacctgcc tggtcaaagg cttctatccc 1140

agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 1200

cctcccgtgc tggactccga cggctccttc ttcctctaca gcaagctcac cgtggacaag 1260

agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac 1320

cactacacac agaagagcct ctccctgtct ccgggtaaa 1359

<210> SEQ ID NO 256
<211> LENGTH: 1359
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 256

caggtgcaac tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cgtctgggtt cgctttcaat acctatggca tgcactgggt ccgccaggca 120

ccaggcaagg ggctggagtg ggtggcaatt atctggtatg atgggagcca gaaatactat 180

gcagactccg tgcagggccg attcactatc tccagagaca atcacaagaa cacgttgtct 240

ctgcaaatga actccctgag agccgaggac acggctgtgt atttctgtgt gagagtccgc 300

tttagcgttg gcccccacgg gagtgctttt gatctctggg gccaggggac aatggtcaca 360

gtctcttcag cctccaccaa gggcccatcg gtcttccccc tggcaccctc ctccaagagc 420

acctctgggg gcacagcagc cctgggctgc ctggtcaagg actacttccc cgaaccggtg 480

acggtgtcgt ggaactcagg cgccctgacc agcggcgtgc acaccttccc ggctgtccta 540

cagtcctcag gactctactc cctcagcagc gtggtgaccg tgccctccag cagcttgggc 600

acccagacct acatctgcaa cgtgaatcac aagcccagca acaccaaggt ggacaagaaa 660

gttgagccca aatcttgtga caaaactcac acatgcccac cgtgcccagc acctgaactc 720

ctggggggac cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc 780

cggacccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagaccc tgaggtcaag 840

ttcaactggt acgtggacgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag 900

cagtacaaca gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg 960

aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa 1020

```
accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gcccccatcc   1080

cgggatgagc tgaccaagaa ccaggtcagc ctgacctgcc tggtcaaagg cttctatccc   1140

agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg   1200

cctcccgtgc tggactccga cggctccttc ttcctctaca gcaagctcac cgtggacaag   1260

agcaggtggc agcaggggaa cgtcttctca tgctccgtgc tgcatgaggc tctgcactcc   1320

cactacacac agaagagcct ctccctgtct ccgggtaaa                          1359
```

<210> SEQ ID NO 257
<211> LENGTH: 109
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 257

```
Gly Val Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1               5                   10                  15

Asp Arg Val Thr Leu Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Trp
            20                  25                  30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Ser Phe
                85                  90                  95

Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105
```

<210> SEQ ID NO 258
<211> LENGTH: 123
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 258

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Thr Tyr
            20                  25                  30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ala Ile Ile Trp Tyr Asp Gly Ser Gln Lys Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn His Lys Asn Thr Leu Ser
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys
                85                  90                  95

Val Arg Val Arg Phe Ser Val Gly Pro His Gly Ser Ala Phe Asp Leu
            100                 105                 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115                 120
```

```
<210> SEQ ID NO 259
<211> LENGTH: 327
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 259

ggcgtccaga tgacccagtc tccttccacc ctgtctgcat ctgtgggaga cagagtcacc      60

ctcacttgcc gggccagtca gagtattagt agttggttgg cctggtatca gcagaaacca     120

gggaaagccc ctaaactcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca     180

aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcaacct     240

gatgattttg caacttatta ctgccaacag tataatagtt attctttttg gacgttcggc     300

caagggacca aggtggaaat caaacgc                                         327


<210> SEQ ID NO 260
<211> LENGTH: 369
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 260

caggtgcaac tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc      60

tcctgtgcag cgtctgggtt cactttcaat acctatggca tgcactgggt ccgccaggca     120

ccaggcaagg ggctggagtg ggtggcaatt atctggtatg atgggagcca gaaatactat     180

gcagactccg tgcagggccg attcactatc tccagagaca atcacaagaa cacgttgtct     240

ctgcaaatga actccctgag agccgaggac acggctgtgt atttctgtgt gagagtccgc     300

tttagcgttg gcccccacgg gagtgctttt gatctctggg gccaggggac aatggtcaca     360

gtctcttca                                                             369


<210> SEQ ID NO 261
<211> LENGTH: 215
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 261

Gly Val Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1               5                   10                  15

Asp Arg Val Thr Leu Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Trp
            20                  25                  30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Ser Phe
                85                  90                  95

Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala
            100                 105                 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
        115                 120                 125
```

```
Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
    130                 135                 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145                 150                 155                 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
                165                 170                 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
            180                 185                 190

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
        195                 200                 205

Ser Phe Asn Arg Gly Glu Cys
    210                 215
```

<210> SEQ ID NO 262
<211> LENGTH: 453
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 262

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Thr Tyr
            20                  25                  30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ala Ile Ile Trp Tyr Asp Gly Ser Gln Lys Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn His Lys Asn Thr Leu Ser
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys
                85                  90                  95

Val Arg Val Arg Phe Ser Val Gly Pro His Gly Ser Ala Phe Asp Leu
            100                 105                 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys
    210                 215                 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
225                 230                 235                 240

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270
```

```
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
        355                 360                 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445

Leu Ser Pro Gly Lys
    450


<210> SEQ ID NO 263
<211> LENGTH: 453
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 263

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Thr Tyr
            20                  25                  30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ala Ile Ile Trp Tyr Asp Gly Ser Gln Lys Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn His Lys Asn Thr Leu Ser
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys
                85                  90                  95

Val Arg Val Arg Phe Ser Val Gly Pro His Gly Ser Ala Phe Asp Leu
            100                 105                 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175
```

```
Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys
    210                 215                 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
225                 230                 235                 240

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
        355                 360                 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430

Val Leu His Glu Ala Leu His Ser His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445

Leu Ser Pro Gly Lys
    450
```

<210> SEQ ID NO 264
<211> LENGTH: 645
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 264

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ggcgtccaga tgacccagtc tccttccacc ctgtctgcat ctgtgggaga cagagtcacc     60

ctcacttgcc gggccagtca gagtattagt agttggttgg cctggtatca gcagaaacca    120

gggaaagccc ctaaactcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca    180

aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcaacct    240

gatgattttg caacttatta ctgccaacag tataatagtt attctttttg gacgttcggc    300

caagggacca aggtggaaat caaacgcact gtggctgcac catctgtctt catcttcccg    360

ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc    420

tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc    480
```

caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 540

acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag 600

ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgt 645

<210> SEQ ID NO 265
<211> LENGTH: 1359
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 265

caggtgcaac tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cgtctgggtt cactttcaat acctatggca tgcactgggt ccgccaggca 120

ccaggcaagg ggctggagtg ggtggcaatt atctggtatg atgggagcca gaaatactat 180

gcagactccg tgcagggccg attcactatc tccagagaca atcacaagaa cacgttgtct 240

ctgcaaatga actccctgag agccgaggac acggctgtgt atttctgtgt gagagtccgc 300

tttagcgttg gcccccacgg gagtgctttt gatctctggg gccaggggac aatggtcaca 360

gtctcttcag cctccaccaa gggcccatcg gtcttccccc tggcaccctc ctccaagagc 420

acctctgggg gcacagcagc cctgggctgc ctggtcaagg actacttccc cgaaccggtg 480

acggtgtcgt ggaactcagg cgccctgacc agcggcgtgc acaccttccc ggctgtccta 540

cagtcctcag gactctactc cctcagcagc gtggtgaccg tgccctccag cagcttgggc 600

acccagacct acatctgcaa cgtgaatcac aagcccagca acaccaaggt ggacaagaaa 660

gttgagccca aatcttgtga caaaactcac acatgcccac cgtgcccagc acctgaactc 720

ctggggggac cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc 780

cggacccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagaccc tgaggtcaag 840

ttcaactggt acgtggacgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag 900

cagtacaaca gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg 960

aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa 1020

accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gcccccatcc 1080

cgggatgagc tgaccaagaa ccaggtcagc ctgacctgcc tggtcaaagg cttctatccc 1140

agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 1200

cctcccgtgc tggactccga cggctccttc ttcctctaca gcaagctcac cgtggacaag 1260

agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac 1320

cactacacac agaagagcct ctccctgtct ccgggtaaa 1359

<210> SEQ ID NO 266
<211> LENGTH: 1359
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 266

caggtgcaac tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cgtctgggtt cactttcaat acctatggca tgcactgggt ccgccaggca 120

ccaggcaagg ggctggagtg ggtggcaatt atctggtatg atgggagcca gaaatactat 180

```
gcagactccg tgcagggccg attcactatc tccagagaca atcacaagaa cacgttgtct    240

ctgcaaatga actccctgag agccgaggac acggctgtgt atttctgtgt gagagtccgc    300

tttagcgttg gcccccacgg gagtgctttt gatctctggg gccaggggac aatggtcaca    360

gtctcttcag cctccaccaa gggcccatcg gtcttccccc tggcaccctc ctccaagagc    420

acctctgggg gcacagcagc cctgggctgc ctggtcaagg actacttccc cgaaccggtg    480

acggtgtcgt ggaactcagg cgccctgacc agcggcgtgc acaccttccc ggctgtccta    540

cagtcctcag gactctactc cctcagcagc gtggtgaccg tgccctccag cagcttgggc    600

acccagacct acatctgcaa cgtgaatcac aagcccagca acaccaaggt ggacaagaaa    660

gttgagccca aatcttgtga caaaactcac acatgcccac cgtgcccagc acctgaactc    720

ctggggggac cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc    780

cggacccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagaccc tgaggtcaag    840

ttcaactggt acgtggacgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag    900

cagtacaaca gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg    960

aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa   1020

accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gcccccatcc   1080

cgggatgagc tgaccaagaa ccaggtcagc ctgacctgcc tggtcaaagg cttctatccc   1140

agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg   1200

cctcccgtgc tggactccga cggctccttc ttcctctaca gcaagctcac cgtggacaag   1260

agcaggtggc agcaggggaa cgtcttctca tgctccgtgc tgcatgaggc tctgcactcc   1320

cactacacac agaagagcct ctccctgtct ccgggtaaa                          1359
```

```
<210> SEQ ID NO 267
<211> LENGTH: 109
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 267

Gly Val Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1               5                   10                  15

Asp Arg Val Thr Leu Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Trp
            20                  25                  30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Ser Phe
                85                  90                  95

Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> SEQ ID NO 268
<211> LENGTH: 123
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
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```
<400> SEQUENCE: 268

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Thr Tyr
            20                  25                  30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ala Ile Ile Trp Tyr Asp Gly Ser Gln Lys Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn His Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys
                85                  90                  95

Val Arg Val Arg Phe Ser Val Gly Pro His Gly Ser Ala Phe Asp Leu
            100                 105                 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115                 120


<210> SEQ ID NO 269
<211> LENGTH: 327
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 269

ggcgtccaga tgacccagtc tccttccacc ctgtctgcat ctgtgggaga cagagtcacc      60

ctcacttgcc gggccagtca gagtattagt agttggttgg cctggtatca gcagaaacca     120

gggaaagccc ctaaactcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca     180

aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcaacct     240

gatgattttg caacttatta ctgccaacag tataatagtt attctttttg gacgttcggc     300

caagggacca aggtggaaat caaacgc                                         327


<210> SEQ ID NO 270
<211> LENGTH: 369
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 270

caggtgcaac tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc      60

tcctgtgcag cgtctgggtt cactttcaat acctatggca tgcactgggt ccgccaggca     120

ccaggcaagg ggctggagtg ggtggcaatt atctggtatg atgggagcca gaaatactat     180

gcagactccg tgcagggccg attcactatc tccagagaca atcacaagaa cacgttgtac     240

ctgcaaatga actccctgag agccgaggac acggctgtgt atttctgtgt gagagtccgc     300

tttagcgttg gcccccacgg gagtgctttt gatctctggg gccaggggac aatggtcaca     360

gtctcttca                                                             369


<210> SEQ ID NO 271
<211> LENGTH: 215
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
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<400> SEQUENCE: 271

Gly Val Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1               5                   10                  15

Asp Arg Val Thr Leu Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Trp
            20                  25                  30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Ser Phe
                85                  90                  95

Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala
            100                 105                 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
        115                 120                 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
    130                 135                 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145                 150                 155                 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
                165                 170                 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
            180                 185                 190

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
        195                 200                 205

Ser Phe Asn Arg Gly Glu Cys
    210                 215


<210> SEQ ID NO 272
<211> LENGTH: 453
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 272

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Thr Tyr
            20                  25                  30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ala Ile Ile Trp Tyr Asp Gly Ser Gln Lys Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn His Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys
                85                  90                  95

Val Arg Val Arg Phe Ser Val Gly Pro His Gly Ser Ala Phe Asp Leu
            100                 105                 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125
```

```
Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys
    210                 215                 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
225                 230                 235                 240

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
        355                 360                 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445

Leu Ser Pro Gly Lys
    450


<210> SEQ ID NO 273
<211> LENGTH: 453
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 273

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Thr Tyr
            20                  25                  30
```

-continued

```
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ala Ile Ile Trp Tyr Asp Gly Ser Gln Lys Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn His Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys
                85                  90                  95

Val Arg Val Arg Phe Ser Val Gly Pro His Gly Ser Ala Phe Asp Leu
            100                 105                 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys
    210                 215                 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
225                 230                 235                 240

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
        355                 360                 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430

Val Leu His Glu Ala Leu His Ser His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445

Leu Ser Pro Gly Lys
```

450

<210> SEQ ID NO 274
<211> LENGTH: 645
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 274

ggcgtccaga tgacccagtc tccttccacc ctgtctgcat ctgtgggaga cagagtcacc 60

ctcacttgcc gggccagtca gagtattagt agttggttgg cctggtatca gcagaaacca 120

gggaaagccc ctaaactcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcaacct 240

gatgattttg caacttatta ctgccaacag tataatagtt attctttttg gacgttcggc 300

caagggacca aggtggaaat caaacgcact gtggctgcac catctgtctt catcttcccg 360

ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 420

tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc 480

caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 540

acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag 600

ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgt 645

<210> SEQ ID NO 275
<211> LENGTH: 1359
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 275

caggtgcaac tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cgtctgggtt cactttcaat acctatggca tgcactgggt ccgccaggca 120

ccaggcaagg ggctggagtg ggtggcaatt atctggtatg atgggagcca gaaatactat 180

gcagactccg tgcagggccg attcactatc tccagagaca atcacaagaa cacgttgtac 240

ctgcaaatga actccctgag agccgaggac acggctgtgt atttctgtgt gagagtccgc 300

tttagcgttg gcccccacgg gagtgctttt gatctctggg gccaggggac aatggtcaca 360

gtctcttcag cctccaccaa gggcccatcg gtcttccccc tggcaccctc ctccaagagc 420

acctctgggg gcacagcagc cctgggctgc ctggtcaagg actacttccc cgaaccggtg 480

acggtgtcgt ggaactcagg cgccctgacc agcggcgtgc acaccttccc ggctgtccta 540

cagtcctcag gactctactc cctcagcagc gtggtgaccg tgccctccag cagcttgggc 600

acccagacct acatctgcaa cgtgaatcac aagcccagca acaccaaggt ggacaagaaa 660

gttgagccca aatcttgtga caaaactcac acatgcccac cgtgcccagc acctgaactc 720

ctggggggac cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc 780

cggacccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagaccc tgaggtcaag 840

ttcaactggt acgtggacgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag 900

cagtacaaca gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg 960

aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa 1020

accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gcccccatcc 1080 cgggatgagc tgaccaagaa ccaggtcagc ctgacctgcc tggtcaaagg cttctatccc 1140

agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 1200

cctcccgtgc tggactccga cggctccttc ttcctctaca gcaagctcac cgtggacaag 1260

agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac 1320

cactacacac agaagagcct ctccctgtct ccgggtaaa 1359

<210> SEQ ID NO 276
<211> LENGTH: 1359
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 276

caggtgcaac tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cgtctgggtt cactttcaat acctatggca tgcactgggt ccgccaggca 120

ccaggcaagg ggctggagtg ggtggcaatt atctggtatg atgggagcca gaaatactat 180

gcagactccg tgcagggccg attcactatc tccagagaca atcacaagaa cacgttgtac 240

ctgcaaatga actccctgag agccgaggac acggctgtgt atttctgtgt gagagtccgc 300

tttagcgttg gcccccacgg gagtgctttt gatctctggg gccaggggac aatggtcaca 360

gtctcttcag cctccaccaa gggcccatcg gtcttccccc tggcaccctc ctccaagagc 420

acctctgggg gcacagcagc cctgggctgc ctggtcaagg actacttccc cgaaccggtg 480

acggtgtcgt ggaactcagg cgccctgacc agcggcgtgc acaccttccc ggctgtccta 540

cagtcctcag gactctactc cctcagcagc gtggtgaccg tgccctccag cagcttgggc 600

acccagacct acatctgcaa cgtgaatcac aagcccagca acaccaaggt ggacaagaaa 660

gttgagccca aatcttgtga caaaactcac acatgcccac cgtgcccagc acctgaactc 720

ctggggggac cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc 780

cggacccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagaccc tgaggtcaag 840

ttcaactggt acgtggacgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag 900

cagtacaaca gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg 960

aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa 1020

accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gcccccatcc 1080

cgggatgagc tgaccaagaa ccaggtcagc ctgacctgcc tggtcaaagg cttctatccc 1140

agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 1200

cctcccgtgc tggactccga cggctccttc ttcctctaca gcaagctcac cgtggacaag 1260

agcaggtggc agcaggggaa cgtcttctca tgctccgtgc tgcatgaggc tctgcactcc 1320

cactacacac agaagagcct ctccctgtct ccgggtaaa 1359

<210> SEQ ID NO 277
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 277

Met Ala Trp Ala Leu Leu Leu Leu Thr Leu Leu Thr Gln Gly Thr Gly
1 5 10 15

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Ser Trp Ala


<210> SEQ ID NO 278
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 278

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1               5                   10                  15

Leu Arg Gly Ala Arg Cys
            20


<210> SEQ ID NO 279
<211> LENGTH: 24
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 279

Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro
1               5                   10                  15

Asn Ala Asn Pro Asn Ala Asn Pro
            20


<210> SEQ ID NO 280
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 280

Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala
1               5                   10


<210> SEQ ID NO 281
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 281

Asn Val Asp Pro Asn Ala Asn Pro Asn Val Asp Pro Asn Ala Asn Pro
1               5                   10                  15

Asn Val Asp Pro
            20


<210> SEQ ID NO 282
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 282

Asn Pro Asp Pro Asn Ala Asn Pro Asn Val Asp Pro Asn Ala Asn Pro
1               5                   10                  15


<210> SEQ ID NO 283
```

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<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 283

Asp Pro Asn Ala Asn Pro Asn Val Asp Pro Asn Ala
1               5                   10


<210> SEQ ID NO 284
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 284

Lys Gln Pro Ala Asp Gly Asn Pro Asp Pro Asn Ala Asn Pro Asn
1               5                   10                  15


<210> SEQ ID NO 285
<211> LENGTH: 424
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 285

Met Met Arg Lys Leu Ala Ile Leu Ser Val Ser Ser Phe Leu Phe Val
1               5                   10                  15

Glu Ala Leu Phe Gln Glu Tyr Gln Cys Tyr Gly Ser Ser Ser Asn Thr
            20                  25                  30

Arg Val Leu Asn Glu Leu Asn Tyr Asp Asn Ala Gly Ile Asn Leu Tyr
        35                  40                  45

Asn Glu Leu Glu Met Asn Tyr Tyr Gly Lys Gln Glu Asn Trp Tyr Ser
    50                  55                  60

Leu Lys Lys Asn Ser Arg Ser Leu Gly Glu Asn Asp Asp Gly Asn Asn
65                  70                  75                  80

Asn Asn Gly Asp Asn Gly Arg Glu Gly Lys Asp Glu Asp Lys Arg Asp
                85                  90                  95

Gly Asn Asn Glu Asp Asn Glu Lys Leu Arg Lys Pro Lys His Lys Lys
            100                 105                 110

Leu Lys Gln Pro Gly Asp Gly Asn Pro Asp Pro Asn Ala Asn Pro Asn
        115                 120                 125

Val Asp Pro Asn Ala Asn Pro Asn Val Asp Pro Asn Ala Asn Pro Asn
    130                 135                 140

Val Asp Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn
145                 150                 155                 160

Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn
                165                 170                 175

Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn
            180                 185                 190

Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn
        195                 200                 205

Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn
    210                 215                 220

Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn
225                 230                 235                 240
```

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Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn
                245                 250                 255

Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn
            260                 265                 270

Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn
        275                 280                 285

Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn Lys Asn Asn Gln
    290                 295                 300

Gly Asn Gly Gln Gly His Asn Met Pro Asn Asp Pro Asn Arg Asn Val
305                 310                 315                 320

Asp Glu Asn Ala Asn Ala Asn Asn Ala Val Lys Asn Asn Asn Asn Glu
                325                 330                 335

Glu Pro Ser Asp Lys His Ile Glu Gln Tyr Leu Lys Lys Ile Gln Asn
            340                 345                 350

Ser Leu Ser Thr Glu Trp Ser Pro Cys Ser Val Thr Cys Gly Asn Gly
        355                 360                 365

Ile Gln Val Arg Ile Lys Pro Gly Ser Ala Asn Lys Pro Lys Asp Glu
    370                 375                 380

Leu Asp Tyr Glu Asn Asp Ile Glu Lys Lys Ile Cys Lys Met Glu Lys
385                 390                 395                 400

Cys Ser Ser Val Phe Asn Val Val Asn Ser Ser Ile Gly Leu Ile Met
                405                 410                 415

Val Leu Ser Phe Leu Phe Leu Asn
            420


<210> SEQ ID NO 286
<211> LENGTH: 236
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 286

Met Ala Trp Ala Leu Leu Leu Leu Thr Leu Leu Thr Gln Gly Thr Gly
1               5                   10                  15

Ser Trp Ala Glu Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala
            20                  25                  30

Pro Gly Gln Arg Val Thr Ile Ser Cys Thr Gly Met Asn Ser Asn Ile
        35                  40                  45

Gly Ala Gly Tyr Asp Val Tyr Trp Tyr Gln Gln Leu Pro Gly Arg Ala
    50                  55                  60

Pro Lys Leu Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro
65                  70                  75                  80

Asp Arg Phe Ser Gly Ser Arg Ser Gly Thr Ser Ala Ser Leu Ala Ile
                85                  90                  95

Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr
            100                 105                 110

Asp Thr Ser Leu Asn Gly Trp Ala Phe Gly Gly Gly Thr Lys Leu Thr
        115                 120                 125

Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro
    130                 135                 140

Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Val
145                 150                 155                 160

Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Gly
                165                 170                 175
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Ser Pro Val Lys Val Gly Val Glu Thr Thr Lys Pro Ser Lys Gln Ser
            180   185   190

Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln
        195   200   205

Trp Lys Ser His Arg Ser Tyr Ser Cys Arg Val Thr His Glu Gly Ser
    210   215   220

Thr Val Glu Lys Thr Val Ala Pro Ala Glu Cys Ser
225   230   235

<210> SEQ ID NO 287
<211> LENGTH: 479
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 287

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1   5   10   15

Leu Arg Gly Ala Arg Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly
            20   25   30

Leu Val Gln Pro Gly Arg Ser Leu Arg Leu Pro Cys Thr Ala Ser Gly
        35   40   45

Phe Ser Phe Gly Asp His Ala Met Ser Trp Val Arg Gln Ala Pro Gly
    50   55   60

Lys Gly Leu Glu Trp Val Gly Phe Ile Arg Lys Thr Thr Tyr Gly Ala
65   70   75   80

Thr Thr His Tyr Ala Ala Ala Val Arg Gly Arg Phe Thr Ile Ser Arg
                85   90   95

Asp Asp Ser Lys Ser Ile Val Tyr Leu Gln Met Asn Ser Leu Lys Thr
            100   105   110

Glu Asp Thr Ala Val Tyr Phe Cys Thr Arg Val Gln Leu Asp Tyr Gly
        115   120   125

Pro Gly Tyr Gln Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr
    130   135   140

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
145   150   155   160

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
                165   170   175

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
            180   185   190

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
        195   200   205

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
    210   215   220

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
225   230   235   240

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
                245   250   255

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
            260   265   270

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
        275   280   285

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
    290   295   300

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Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
305 310 315 320

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
325 330 335

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
340 345 350

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
355 360 365

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
370 375 380

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
385 390 395 400

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
405 410 415

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
420 425 430

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
435 440 445

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Leu His Glu Ala Leu
450 455 460

His Ser His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475

<210> SEQ ID NO 288
<211> LENGTH: 237
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 288

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

Leu Arg Gly Ala Arg Cys Gly Val Gln Met Thr Gln Ser Pro Ser Thr
20 25 30

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Leu Thr Cys Arg Ala Ser
35 40 45

Gln Ser Ile Ser Ser Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
50 55 60

Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val
65 70 75 80

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr
85 90 95

Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
100 105 110

Tyr Asn Ser Tyr Ser Phe Trp Thr Phe Gly Gln Gly Thr Lys Val Glu
115 120 125

Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser
130 135 140

Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn
145 150 155 160

Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala
165 170 175

Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys
180 185 190

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Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp
        195                 200                 205

Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu
    210                 215                 220

Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230                 235


<210> SEQ ID NO 289
<211> LENGTH: 475
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 289

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1               5                   10                  15

Leu Arg Gly Ala Arg Cys Gln Val Gln Leu Val Glu Ser Gly Gly Gly
            20                  25                  30

Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
        35                  40                  45

Phe Ala Phe Asn Thr Tyr Gly Met His Trp Val Arg Gln Thr Pro Gly
    50                  55                  60

Lys Gly Leu Glu Trp Val Ala Ile Ile Trp Tyr Asp Gly Ser Gln Lys
65                  70                  75                  80

Tyr Tyr Ala Asp Ser Val Gln Gly Arg Phe Ile Ile Ser Arg Asp Asn
                85                  90                  95

His Lys Asn Thr Leu Ser Leu Gln Met Asn Gly Leu Arg Ala Glu Asp
            100                 105                 110

Thr Ala Val Tyr Phe Cys Val Arg Val Arg Phe Ser Val Gly Pro His
        115                 120                 125

Gly Ser Ala Phe Asp Leu Trp Gly Gln Gly Thr Met Val Ile Val Ser
    130                 135                 140

Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser
145                 150                 155                 160

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
                165                 170                 175

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
            180                 185                 190

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
        195                 200                 205

Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
    210                 215                 220

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
225                 230                 235                 240

Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
                245                 250                 255

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
            260                 265                 270

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
        275                 280                 285

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
    290                 295                 300

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
305                 310                 315                 320
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Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
                325                 330                 335

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
            340                 345                 350

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
        355                 360                 365

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
    370                 375                 380

Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
385                 390                 395                 400

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
                405                 410                 415

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
            420                 425                 430

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
        435                 440                 445

Asn Val Phe Ser Cys Ser Val Leu His Glu Ala Leu His Ser His Tyr
    450                 455                 460

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465                 470                 475
```

What is claimed is:

1. A recombinant anti-circumsporozoite (CSP) antibody comprising a light chain variable region (VL) and a heavy chain variable region (VH), wherein:

a) the light chain variable region comprises a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 1, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO: 2, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO: 3; and the heavy chain variable region comprises a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 4, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO: 5, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO: 6;

b) the light chain variable region comprises a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 183, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO: 184, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO: 185; and the heavy chain variable region comprises a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 186, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO: 187, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO: 188;

c) the light chain variable region comprises a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 205, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO: 206, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO: 207; and the heavy chain variable region comprises a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 208, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO: 209, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO: 210.

2. The recombinant antibody of claim 1, wherein the light chain variable region (VL) comprises:

a) the amino acid sequence set forth in SEQ ID NO: 23;
b) the amino acid sequence set forth in SEQ ID NO: 33;
c) the amino acid sequence set forth in SEQ ID NO: 43;
d) the amino acid sequence set forth in SEQ ID NO: 53;
e) the amino acid sequence set forth in SEQ ID NO: 63;
f) the amino acid sequence set forth in SEQ ID NO: 73;
g) the amino acid sequence set forth in SEQ ID NO: 83;
h) the amino acid sequence set forth in SEQ ID NO: 93;
i) the amino acid sequence set forth in SEQ ID NO: 103;
j) the amino acid sequence set forth in SEQ ID NO: 113;
k) the amino acid sequence set forth in SEQ ID NO: 123;
l) The amino acid sequence set forth in SEQ ID NO: 133;
m) the amino acid sequence set forth in SEQ ID NO: 143;
n) the amino acid sequence set forth in SEQ ID NO: 153;
o) the amino acid sequence set forth in SEQ ID NO: 163;
p) the amino acid sequence set forth in SEQ ID NO: 173;
q) the amino acid sequence set forth in SEQ ID NO: 195;
r) the amino acid sequence set forth in SEQ ID NO: 227;
s) the amino acid sequence set forth in SEQ ID NO: 237;
t) the amino acid sequence set forth in SEQ ID NO: 247;
u) the amino acid sequence set forth in SEQ ID NO: 257; or
v) the amino acid sequence set forth in SEQ ID NO: 267.

3. The recombinant antibody of claim 1, wherein the heavy chain variable region (VH) comprises:

a) the amino acid sequence set forth in SEQ ID NO: 24;
b) the amino acid sequence set forth in SEQ ID NO: 34;
c) the amino acid sequence set forth in SEQ ID NO: 44;
d) the amino acid sequence set forth in SEQ ID NO: 54;
e) the amino acid sequence set forth in SEQ ID NO: 64;
f) the amino acid sequence set forth in SEQ ID NO: 74;
g) the amino acid sequence set forth in SEQ ID NO: 84;
h) the amino acid sequence set forth in SEQ ID NO: 94;

i) the amino acid sequence set forth in SEQ ID NO: 104;
j) the amino acid sequence set forth in SEQ ID NO: 114;
k) the amino acid sequence set forth in SEQ ID NO: 124;
l) The amino acid sequence set forth in SEQ ID NO: 134;
m) the amino acid sequence set forth in SEQ ID NO: 144;
n) the amino acid sequence set forth in SEQ ID NO: 154;
o) the amino acid sequence set forth in SEQ ID NO: 164;
p) the amino acid sequence set forth in SEQ ID NO: 174;
q) the amino acid sequence set forth in SEQ ID NO: 196;
r) the amino acid sequence set forth in SEQ ID NO: 228;
s) the amino acid sequence set forth in SEQ ID NO: 238;
t) the amino acid sequence set forth in SEQ ID NO: 248;
u) the amino acid sequence set forth in SEQ ID NO: 258; or
v) the amino acid sequence set forth in SEQ ID NO: 268.

4. The recombinant antibody of claim **1**, wherein:
a) the VL comprises the amino acid sequence set forth in SEQ ID NO: 23, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 24;
b) the VL comprises the amino acid sequence set forth in SEQ ID NO: 33, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 34;
c) the VL comprises the amino acid sequence set forth in SEQ ID NO: 43, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 44;
d) the VL comprises the amino acid sequence set forth in SEQ ID NO: 53, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 54;
e) the VL comprises the amino acid sequence set forth in SEQ ID NO: 63, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 64;
f) the VL comprises the amino acid sequence set forth in SEQ ID NO: 73, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 74;
g) the VL comprises the amino acid sequence set forth in SEQ ID NO: 83, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 84;
h) the VL comprises the amino acid sequence set forth in SEQ ID NO: 93, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 94;
i) the VL comprises the amino acid sequence set forth in SEQ ID NO: 103, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 104;
j) the VL comprises the amino acid sequence set forth in SEQ ID NO: 113, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 114;
k) the VL comprises the amino acid sequence set forth in SEQ ID NO: 123, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 124;
l) the VL comprises the amino acid sequence set forth in SEQ ID NO: 133, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 134;
m) the VL comprises the amino acid sequence set forth in SEQ ID NO: 143, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 144;
n) the VL comprises the amino acid sequence set forth in SEQ ID NO: 153, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 154;
o) the VL comprises the amino acid sequence set forth in SEQ ID NO: 163, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 164;
p) the VL comprises the amino acid sequence set forth in SEQ ID NO: 173, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 174;
q) the VL comprises the amino acid sequence set forth in SEQ ID NO: 195, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 196;

r) the VL comprises the amino acid sequence set forth in SEQ ID NO: 227, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 228;
s) the VL comprises the amino acid sequence set forth in SEQ ID NO: 237, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 238;
t) the VL comprises the amino acid sequence set forth in SEQ ID NO: 247, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 248;
u) the VL comprises the amino acid sequence set forth in SEQ ID NO: 257, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 258; or
v) the VL comprises the amino acid sequence set forth in SEQ ID NO: 267, and the VH comprises the amino acid sequence set forth in SEQ ID NO: 268.

5. The recombinant antibody of claim **1** comprising a light chain (LC) and a heavy chain (HC), wherein the LC comprises:
a) the amino acid sequence set forth in SEQ ID NO: 27;
b) the amino acid sequence set forth in SEQ ID NO: 37;
c) the amino acid sequence set forth in SEQ ID NO: 47;
d) the amino acid sequence set forth in SEQ ID NO: 57;
e) the amino acid sequence set forth in SEQ ID NO: 67;
f) the amino acid sequence set forth in SEQ ID NO: 77;
g) the amino acid sequence set forth in SEQ ID NO: 87;
h) the amino acid sequence set forth in SEQ ID NO: 97;
i) the amino acid sequence set forth in SEQ ID NO: 107;
j) the amino acid sequence set forth in SEQ ID NO: 117;
k) the amino acid sequence set forth in SEQ ID NO: 127;
l) The amino acid sequence set forth in SEQ ID NO: 137;
m) the amino acid sequence set forth in SEQ ID NO: 147;
n) the amino acid sequence set forth in SEQ ID NO: 157;
o) the amino acid sequence set forth in SEQ ID NO: 167;
p) the amino acid sequence set forth in SEQ ID NO: 177;
q) the amino acid sequence set forth in SEQ ID NO: 199;
r) the amino acid sequence set forth in SEQ ID NO: 231;
s) the amino acid sequence set forth in SEQ ID NO: 241;
t) the amino acid sequence set forth in SEQ ID NO: 251;
u) the amino acid sequence set forth in SEQ ID NO: 261; or
v) the amino acid sequence set forth in SEQ ID NO: 271.

6. The recombinant antibody of claim **1** comprising a light chain (LC) and a heavy chain (HC), wherein the HC comprises:
a) the amino acid sequence set forth in SEQ ID NO: 28 or SEQ ID NO: 29;
b) the amino acid sequence set forth in SEQ ID NO: 38 or SEQ ID NO: 39;
c) the amino acid sequence set forth in SEQ ID NO: 48 or SEQ ID NO: 49;
d) the amino acid sequence set forth in SEQ ID NO: 58 or SEQ ID NO: 59;
e) the amino acid sequence set forth in SEQ ID NO: 68 or SEQ ID NO: 69;
f) the amino acid sequence set forth in SEQ ID NO: 78 or SEQ ID NO: 79;
g) the amino acid sequence set forth in SEQ ID NO: 88 or SEQ ID NO: 89;
h) the amino acid sequence set forth in SEQ ID NO: 98 or SEQ ID NO: 99;
i) the amino acid sequence set forth in SEQ ID NO: 108 or SEQ ID NO: 109;
j) the amino acid sequence set forth in SEQ ID NO: 118 or SEQ ID NO: 119;
k) the amino acid sequence set forth in SEQ ID NO: 128 or SEQ ID NO: 129;

l) The amino acid sequence set forth in SEQ ID NO: 138 or SEQ ID NO: 139;

m) the amino acid sequence set forth in SEQ ID NO: 148 or SEQ ID NO: 149;

n) the amino acid sequence set forth in SEQ ID NO: 158 or SEQ ID NO: 159;

o) the amino acid sequence set forth in SEQ ID NO: 168 or SEQ ID NO: 169;

p) the amino acid sequence set forth in SEQ ID NO: 178 or SEQ ID NO: 179;

q) the amino acid sequence set forth in SEQ ID NO: 200 or SEQ ID NO: 201;

r) the amino acid sequence set forth in SEQ ID NO: 232 or SEQ ID NO: 233;

s) the amino acid sequence set forth in SEQ ID NO: 242 or SEQ ID NO: 243;

t) the amino acid sequence set forth in SEQ ID NO: 252 or SEQ ID NO: 253;

u) the amino acid sequence set forth in SEQ ID NO: 262 or SEQ ID NO: 263; or

v) the amino acid sequence set forth in SEQ ID NO: 272 or SEQ ID NO: 273.

7. The recombinant antibody of claim **1** comprising a light chain (LC) and a heavy chain (HC), wherein:

a) the LC comprises the amino acid sequence set forth in SEQ ID NO: 27, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 28 or SEQ ID NO: 29;

b) the LC comprises the amino acid sequence set forth in SEQ ID NO: 37, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 38 or SEQ ID NO: 39;

c) the LC comprises the amino acid sequence set forth in SEQ ID NO: 47, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 48 or SEQ ID NO: 49;

d) the LC comprises the amino acid sequence set forth in SEQ ID NO: 57, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 58 or SEQ ID NO: 59;

e) the LC comprises the amino acid sequence set forth in SEQ ID NO: 67, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 68 or SEQ ID NO: 69;

f) the LC comprises the amino acid sequence set forth in SEQ ID NO: 77, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 78 or SEQ ID NO: 79;

g) the LC comprises the amino acid sequence set forth in SEQ ID NO: 87, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 88 or SEQ ID NO: 89;

h) the LC comprises the amino acid sequence set forth in SEQ ID NO: 97, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 98 or SEQ ID NO: 99;

i) the LC comprises the amino acid sequence set forth in SEQ ID NO: 107, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 108 or SEQ ID NO: 109;

j) the LC comprises the amino acid sequence set forth in SEQ ID NO: 117, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 118 or SEQ ID NO: 119;

k) the LC comprises the amino acid sequence set forth in SEQ ID NO: 127, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 128 or SEQ ID NO: 129;

l) The LC comprises the amino acid sequence set forth in SEQ ID NO: 137, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 138 or SEQ ID NO: 139;

m) the LC comprises the amino acid sequence set forth in SEQ ID NO: 147, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 148 or SEQ ID NO: 149;

n) the LC comprises the amino acid sequence set forth in SEQ ID NO: 157, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 158 or SEQ ID NO: 159;

o) the LC comprises the amino acid sequence set forth in SEQ ID NO: 167, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 168 or SEQ ID NO: 169;

p) the LC comprises the amino acid sequence set forth in SEQ ID NO: 177, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 178 or SEQ ID NO: 179;

q) the LC comprises the amino acid sequence set forth in SEQ ID NO: 199, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 200 or SEQ ID NO: 201;

r) the LC comprises the amino acid sequence set forth in SEQ ID NO: 231, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 232 or SEQ ID NO: 233;

s) the LC comprises the amino acid sequence set forth in SEQ ID NO: 241, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 242 or SEQ ID NO: 243;

t) the LC comprises the amino acid sequence set forth in SEQ ID NO: 251, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 252 or SEQ ID NO: 253;

u) the LC comprises the amino acid sequence set forth in SEQ ID NO: 261, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 262 or SEQ ID NO: 263; or

v) the LC comprises the amino acid sequence set forth in SEQ ID NO: 271, and the HC comprises the amino acid sequence set forth in SEQ ID NO: 272 or SEQ ID NO: 273.

8. The recombinant antibody of claim **1**, wherein the VL comprises the amino acid sequence set forth in SEQ ID NO: 13 and at least one amino acid substitution at position 1 and/or at position 44.

9. The recombinant antibody of claim **8**, wherein the amino acid substitution at position 1 is E1Q and the amino acid substitution at position 44 is R44T.

10. The recombinant antibody of claim **1**, wherein the VH comprises the amino acid sequence set forth in SEQ ID NO: 14 and at least one amino acid substitution at position 21, position 23, position 88, position 98, or a combination thereof.

11. The recombinant antibody of claim **10**, wherein

a) the amino acid substitution at position 21 is P21S;

b) the amino acid substitution at position 23 is T23A;

c) the amino acid substitution at position 80 is 180T; and

d) the amino acid substitution at position 90 is T90A.

12. The recombinant antibody of claim **1**, wherein the antibody comprises a heavy chain (HC) comprising the amino acid sequence set forth in SEQ ID NO: 18 and at least one amino acid substitution at position 438 and/or or at position 444.

13. The recombinant antibody of claim **12**, wherein the amino acid substitution at position 438 is M438L and the amino acid substitution at position 444 is N444S.

14. The recombinant antibody of claim **1**, wherein the VH comprises the amino acid sequence set forth in SEQ ID NO: 218 and at least one amino acid substitution at position 40, position 69, position 80, position 85, position 120, or a combination thereof.

15. The recombinant antibody of claim **14**, wherein

a) the amino acid substitution at position 40 is T40A;

b) the amino acid substitution at position 69 is I69T;

c) the amino acid substitution at position 80 is 580Y;

d) the amino acid substitution at position 85 is G85S; and

e) the amino acid substitution at position 120 is 1120T.

16. The recombinant antibody of claim **1**, wherein the HC comprises the amino acid sequence set forth in SEQ ID NO: 222 and at least one amino acid substitution at position 434 and/or at position 440.

17. The recombinant antibody of claim **16**, wherein the amino acid substitution at position 434 is M434L and the amino acid substitution at position 440 is N440S.

18. The recombinant antibody of claim **1**, wherein the antibody exhibits at

a) least 20% reduction in parasite liver load as compared to a reference antibody;

b) at least 20% increase in survival rate as compared to a reference antibody;

c) increased conformational stability as compared to a reference antibody;

d) increased colloidal stability as compared to a reference antibody;

wherein the reference antibody is selected from the group consisting of AB-000317, AB-000224, and AB-007088.

19. An anti-circumsporozoite (CSP) recombinant antibody comprising a light chain variable region (VL) and a heavy chain variable region (VH), wherein

a) the VL comprises the amino acid sequence set forth in SEQ ID NO: 63 and the VH comprises the amino acid sequence set forth in SEQ ID NO: 64;

b) the VL comprises the amino acid sequence set forth in SEQ ID NO: 133 and the VH comprises the amino acid sequence set forth in SEQ ID NO: 134;

c) the VL comprises the amino acid sequence set forth in SEQ ID NO: 163 and the VH comprises the amino acid sequence set forth in SEQ ID NO: 164.

20. The recombinant antibody of claim **19** comprising a light chain (LC) and a heavy chain (HC), wherein

a) the LC comprises the amino acid sequence set forth in SEQ ID NO: 67 and the HC comprises the amino acid sequence set forth in SEQ ID NO: 69;

b) the LC comprises the amino acid sequence set forth in SEQ ID NO: 137 and the HC comprises the amino acid sequence set forth in SEQ ID NO: 139; or

c) the LC comprises the amino acid sequence set forth in SEQ ID NO: 167 and the HC comprises the amino acid sequence set forth in SEQ ID NO: 169.

21. A recombinant anti-circumsporozoite (CSP) antibody comprising a light chain variable region (VL) and a heavy chain variable region (VH), wherein the VL comprises a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 1, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO: 2, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO: 3; and the VH comprises a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 4, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO: 5, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO: 6.

22. A recombinant anti-circumsporozoite (CSP) antibody comprising a light chain variable region (VL) comprising the amino acid sequence set forth in SEQ ID NO: 163 and a heavy chain variable region (VH) comprising the amino acid sequence set forth in SEQ ID NO: 164.

23. A recombinant anti-circumsporozoite (CSP) antibody comprising a light chain (LC) comprising the amino acid sequence set forth in SEQ ID NO: 167 and a heavy chain (HC) comprising the amino acid sequence set forth in SEQ ID NO: 168 or SEQ ID NO: 169.

24. A polynucleotide encoding the antibody of any one of claims **1**, **4**, **7**, **19**, **20**, **21**, **22**, and **23**.

25. A host cell comprising the polynucleotide of claim **24**.

26. A composition comprising the antibody of any one of claims **1**, **4**, **7**, **19**, **20**, **21**, **22**, and **23**.

27. The composition of claim **26**, further comprising a pharmaceutically acceptable carrier.

28. A method of preventing and/or treating malaria in a subject in need thereof, comprising administering an effective amount of the antibody of any one of claims **1**, **4**, **7**, **19**, **20**, **21**, **22**, and **23**.

29. The method of claim **28**, wherein the subject is a pediatric patient.

30. A method of preventing and/or treating malaria in a subject in need thereof, comprising administering an effective amount of the composition of any one of claim **26** or **27**.

31. The method of claim **30**, wherein the subject is a pediatric patient.

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