Variable Light Chain

Kabat#	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	a	b	c	d	e	f	28	29	30	31	32	33	34	35
																								CDR-L1																				
huKI	D	I	Q	M	T	Q	S	P	S	S	L	S	A	S	V	G	D	R	V	T	I	T	C	R	A	S	Q							S	I	S	N	Y	L	A	W
mu5D5	D	I	M	M	S	Q	S	P	S	S	L	T	V	S	V	G	E	K	V	T	V	S	C	K	S	S	Q	S	L	L	Y	T	S	S	Q	K	N	Y	L	A	W
5D5 Graft	D	I	Q	M	T	Q	S	P	S	S	L	S	A	S	V	G	D	R	V	T	I	T	C	K	S	S	Q	S	L	L	Y	T	S	S	Q	K	N	Y	L	A	W

Kabat#	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75
															CDR-L2																											
huKI	Y	Q	Q	K	P	G	K	A	P	K	L	L	I	Y	A	A	S	S	L	E	S	G	V	P	S	R	F	S	G	S	G	S	G	T	D	F	T	L	T	I
mu5D5	Y	Q	Q	K	P	G	Q	S	P	K	L	L	I	Y	W	A	S	T	R	E	S	G	V	P	D	R	F	T	G	S	G	S	G	T	D	F	T	L	T	I
5D5 Graft	Y	Q	Q	K	P	G	K	A	P	K	L	L	I	Y	W	A	S	T	R	E	S	G	V	P	S	R	F	S	G	S	G	S	G	T	D	F	T	L	T	I

Kabat#	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	
														CDR-L3																				
huKI	S	S	L	Q	P	E	D	F	A	T	Y	Y	C	Q	Q	Y	N	S	L	P	W	T	F	G	Q	G	T	K	V	E	I	K	R	SEQ ID NO: 11
mu5D5	T	S	V	K	A	D	D	L	A	V	Y	Y	C	Q	Q	Y	Y	A	Y	P	W	T	F	G	G	G	T	K	L	E	I	K	R	SEQ ID NO: 9
5D5 Graft	S	S	L	Q	P	E	D	F	A	T	Y	Y	C	Q	Q	Y	Y	A	Y	P	W	T	F	G	Q	G	T	K	V	E	I	K	R	SEQ ID NO: 12

FIG. 1A

Variable Heavy Chain

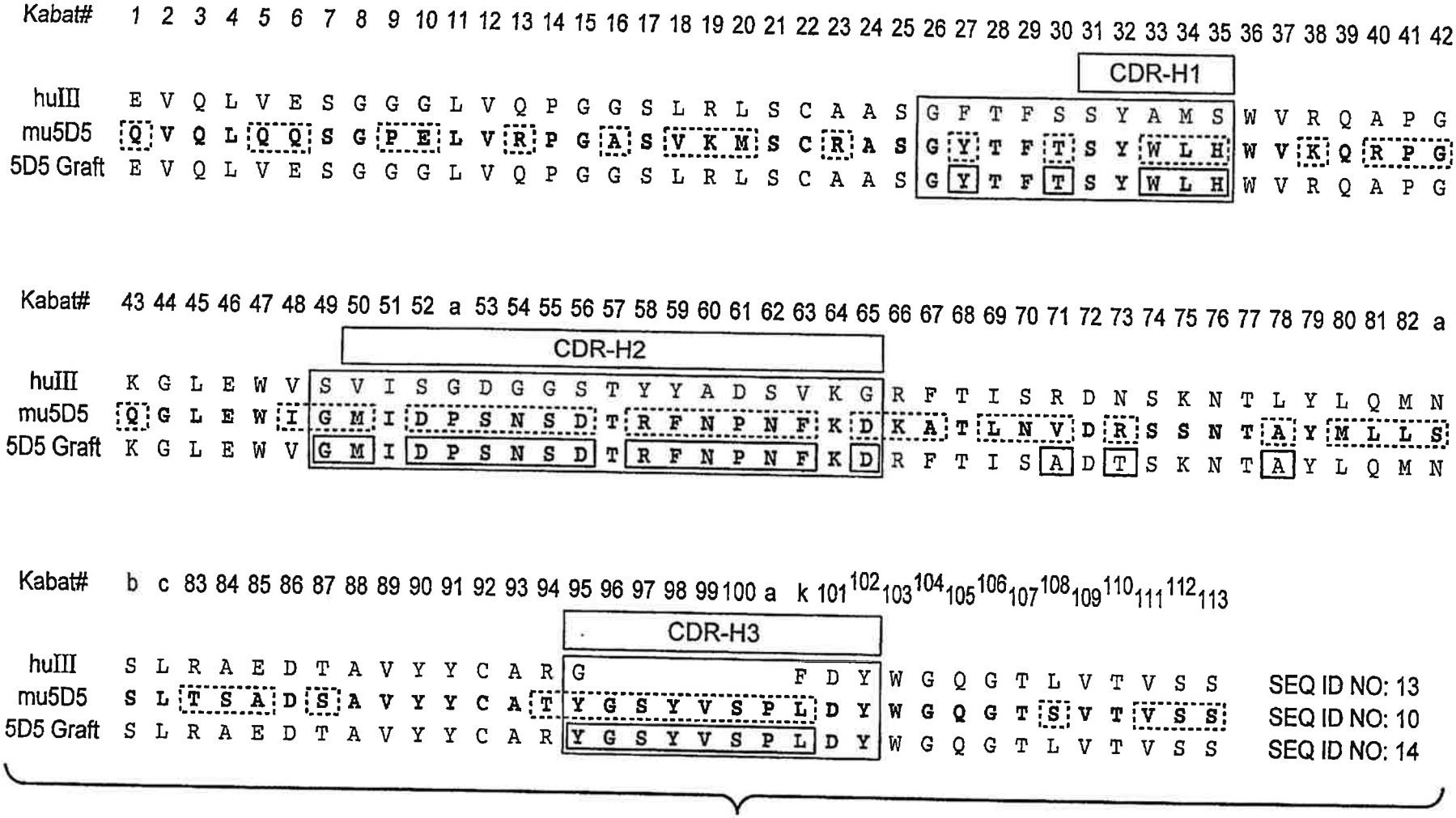


FIG. 1B

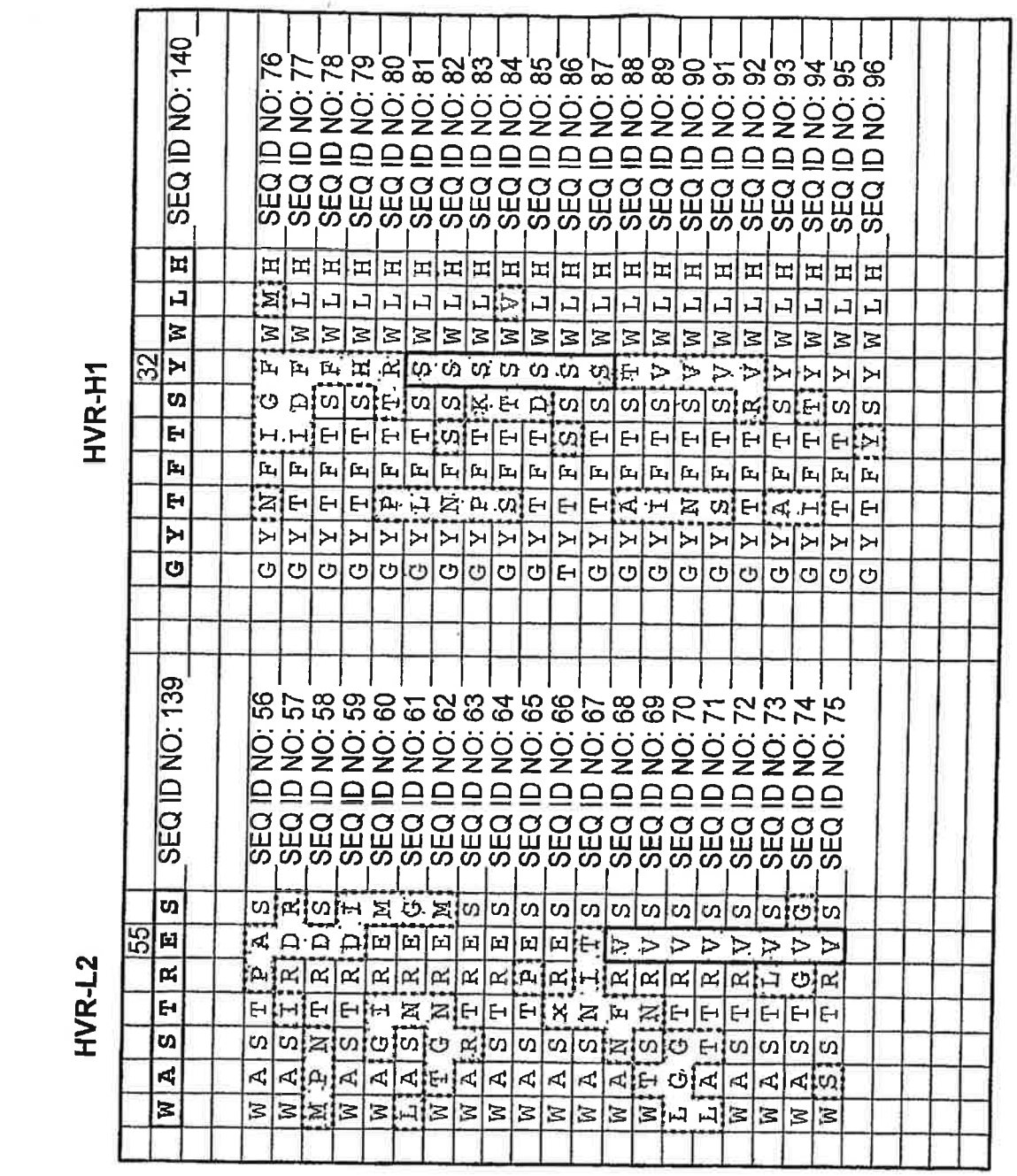


FIG. 2A

FIG. 2

FIG. 2A FIG. 2B

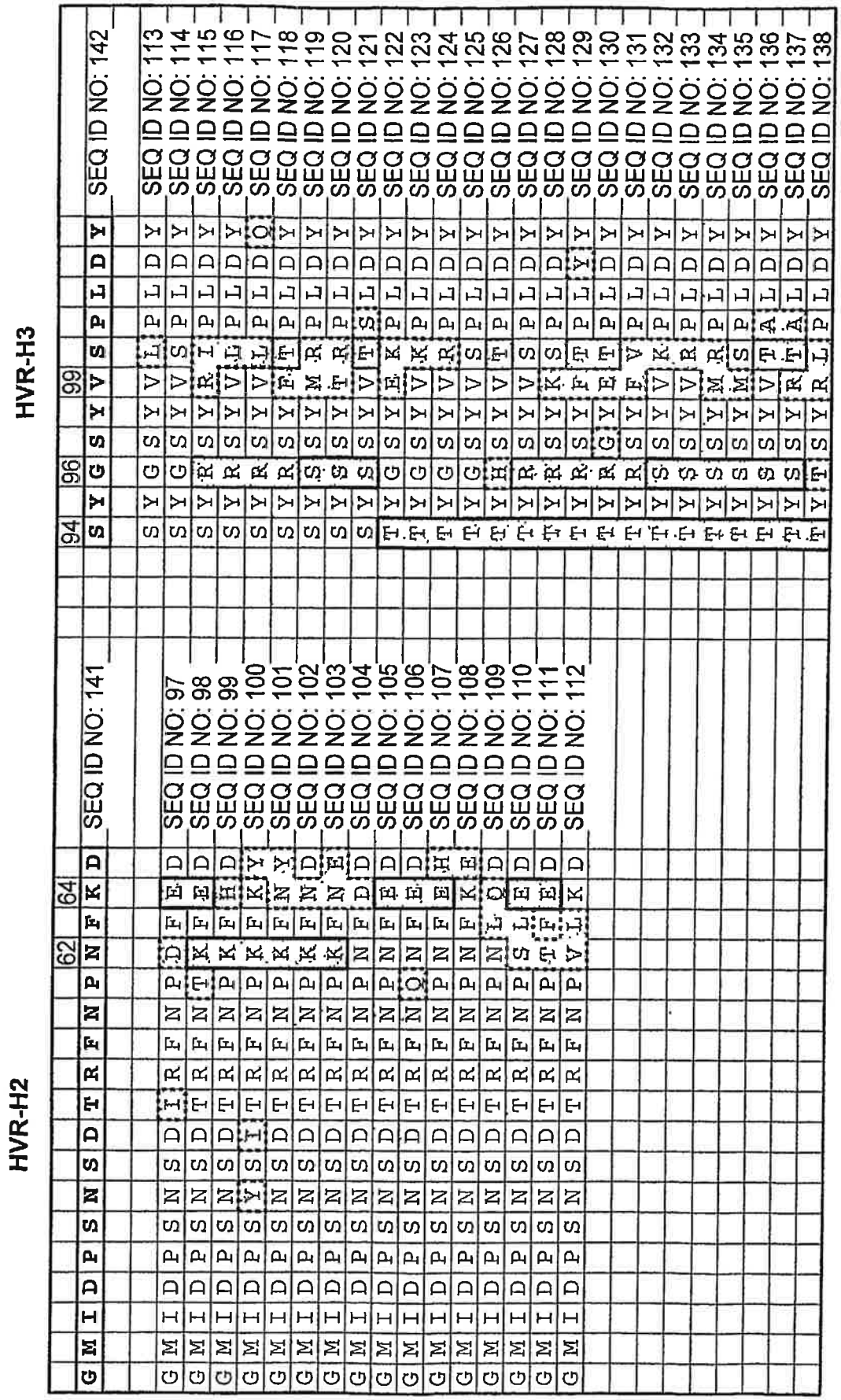

HVR-H2
HVR-H3
SEQ ID NO: 141
SEQ ID NO: 142
SEQ ID NO: 97
SEQ ID NO: 98
SEQ ID NO: 99
SEQ ID NO: 100
SEQ ID NO: 101
SEQ ID NO: 102
SEQ ID NO: 103
SEQ ID NO: 104
SEQ ID NO: 105
SEQ ID NO: 106
SEQ ID NO: 107
SEQ ID NO: 108
SEQ ID NO: 109
SEQ ID NO: 110
SEQ ID NO: 111
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SEQ ID NO: 130
SEQ ID NO: 131
SEQ ID NO: 132
SEQ ID NO: 133
SEQ ID NO: 134
SEQ ID NO: 135
SEQ ID NO: 136
SEQ ID NO: 137
SEQ ID NO: 138

FIG. 2B

HVR-H3

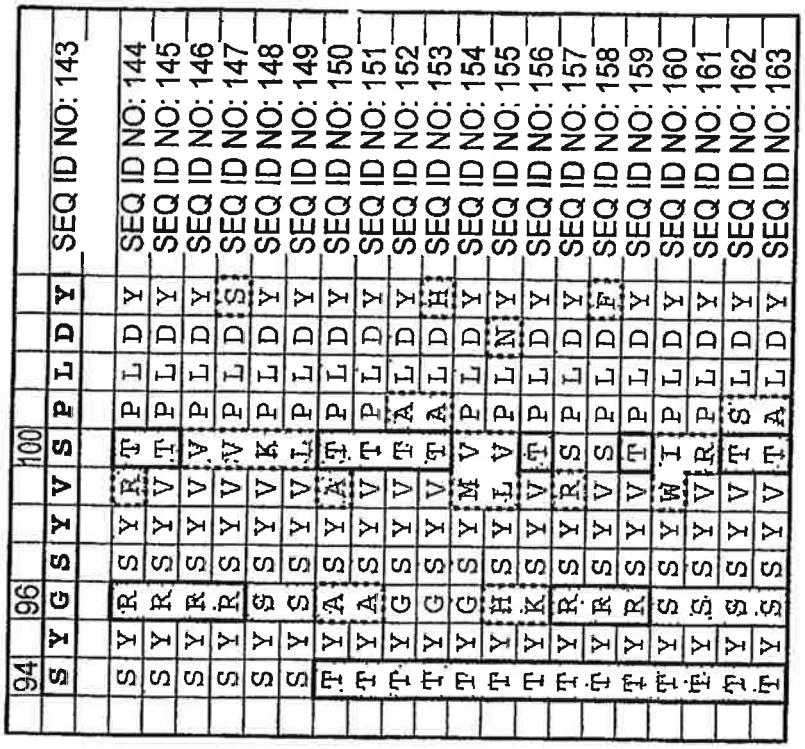
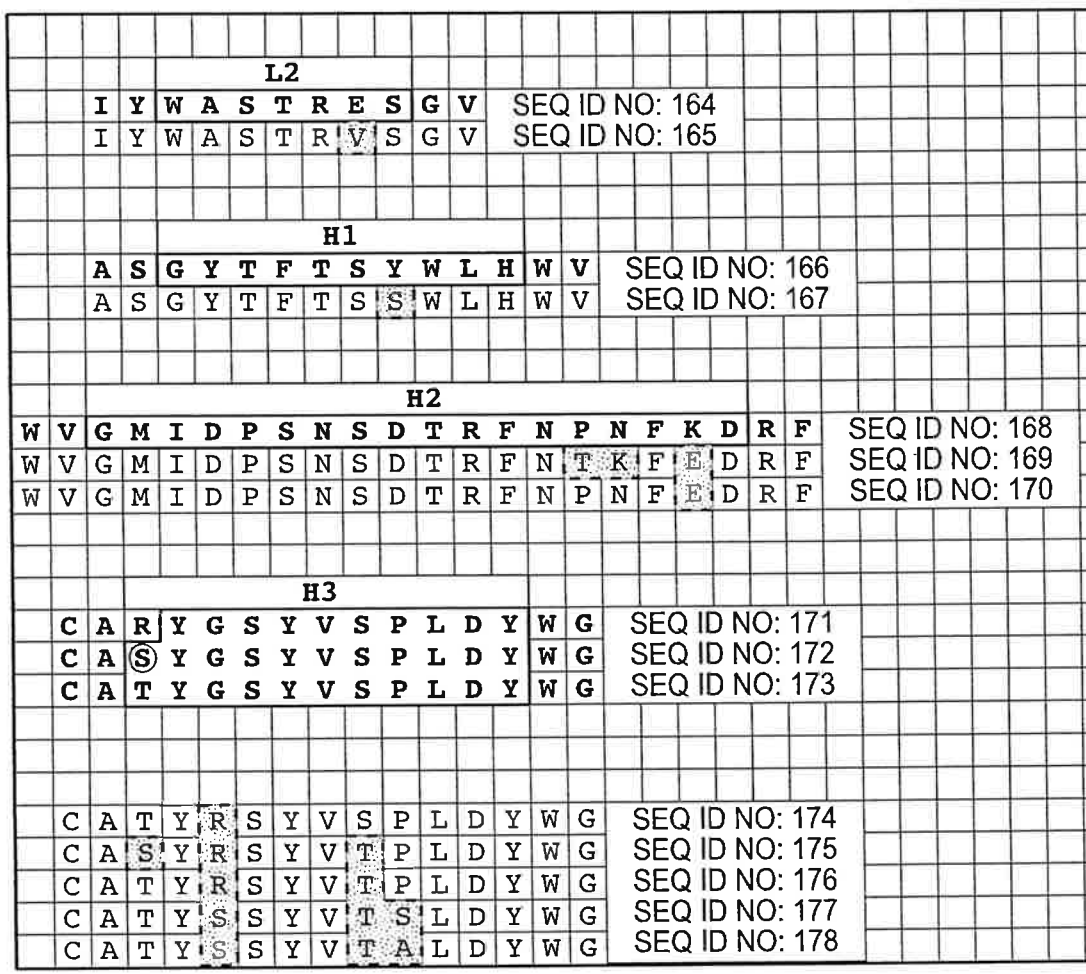

94 96 100
S Y G S Y V S P L D Y SEQ ID NO: 143
SEQ ID NO: 144
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SEQ ID NO: 149
SEQ ID NO: 150
SEQ ID NO: 151
SEQ ID NO: 152
SEQ ID NO: 153
SEQ ID NO: 154
SEQ ID NO: 155
SEQ ID NO: 156
SEQ ID NO: 157
SEQ ID NO: 158
SEQ ID NO: 159
SEQ ID NO: 160
SEQ ID NO: 161
SEQ ID NO: 162
SEQ ID NO: 163

FIG. 3



5D5 Variants	ka (1/Ms)	kd (1/s)	KD (nM)
#34	4.87E+04	3.52E-04	7.22
#94	*1.18E+04*	*4.50E-04*	*38.1*
#4	6.30E+04	4.92E-04	7.81
#12	5.98E+04	5.06E-04	8.46
graft	no detectable binding at 500 nM		
R94S	5.16E+04	5.07E-04	9.83
OA-5D5	8.98E+04	7.43E-04	8.27
#49	*2.86E+03*	*2.24E-04*	*78.3*
#92	1.99E+05	2.09E-04	1.05
#78	2.36E+05	1.47E-04	0.625
#75	8.31E+04	1.58E-04	1.9
#95	9.05E+04	2.29E-04	2.53

FIG. 4

FIG. 5

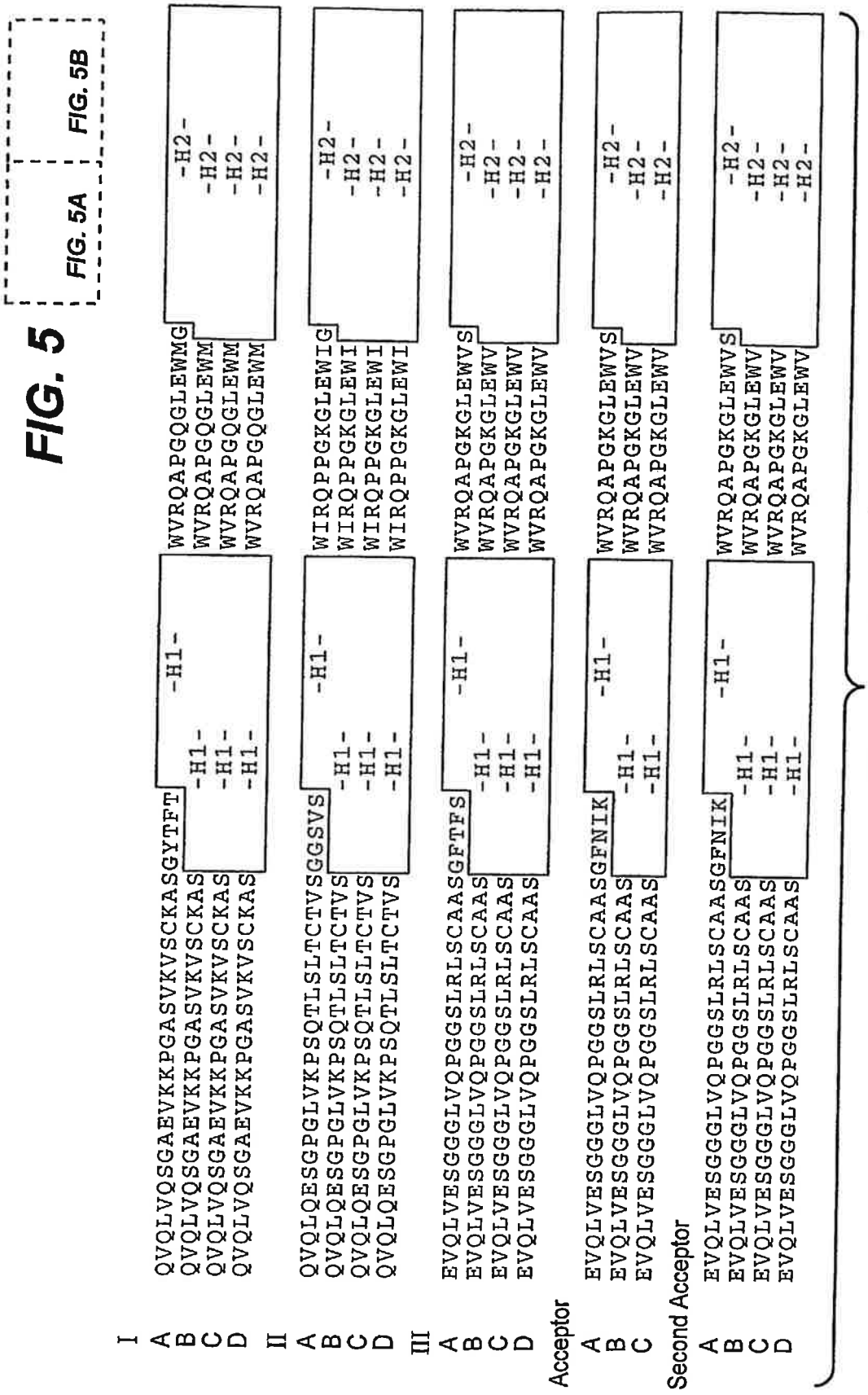

FIG. 5A
FIG. 5B
I
A QVQLVQSGAEVKKPGASVKVSCKASGYTFT -H1- WVRQAPGQGLEWMG -H2-
B QVQLVQSGAEVKKPGASVKVSCKAS -H1- WVRQAPGQGLEWM -H2-
C QVQLVQSGAEVKKPGASVKVSCKAS -H1- WVRQAPGQGLEWM -H2-
D QVQLVQSGAEVKKPGASVKVSCKAS -H1- WVRQAPGQGLEWM -H2-
II
A QVQLQESGPGLVKPSQTLSLTCTVSGGSVS -H1- WIRQPPGKGLEWIG -H2-
B QVQLQESGPGLVKPSQTLSLTCTVS -H1- WIRQPPGKGLEWI -H2-
C QVQLQESGPGLVKPSQTLSLTCTVS -H1- WIRQPPGKGLEWI -H2-
D QVQLQESGPGLVKPSQTLSLTCTVS -H1- WIRQPPGKGLEWI -H2-
III
A EVQLVESGGGLVQPGGSLRLSCAASGFTFS -H1- WVRQAPGKGLEWVS -H2-
B EVQLVESGGGLVQPGGSLRLSCAAS -H1- WVRQAPGKGLEWV -H2-
C EVQLVESGGGLVQPGGSLRLSCAAS -H1- WVRQAPGKGLEWV -H2-
D EVQLVESGGGLVQPGGSLRLSCAAS -H1- WVRQAPGKGLEWV -H2-
Acceptor
A EVQLVESGGGLVQPGGSLRLSCAASGFNIK -H1- WVRQAPGKGLEWVS -H2-
B EVQLVESGGGLVQPGGSLRLSCAAS -H1- WVRQAPGKGLEWV -H2-
C EVQLVESGGGLVQPGGSLRLSCAAS -H1- WVRQAPGKGLEWV -H2-
Second Acceptor
A EVQLVESGGGLVQPGGSLRLSCAASGFNIK -H1- WVRQAPGKGLEWVS -H2-
B EVQLVESGGGLVQPGGSLRLSCAAS -H1- WVRQAPGKGLEWV -H2-
C EVQLVESGGGLVQPGGSLRLSCAAS -H1- WVRQAPGKGLEWV -H2-
D EVQLVESGGGLVQPGGSLRLSCAAS -H1- WVRQAPGKGLEWV -H2-

FIG. 5A

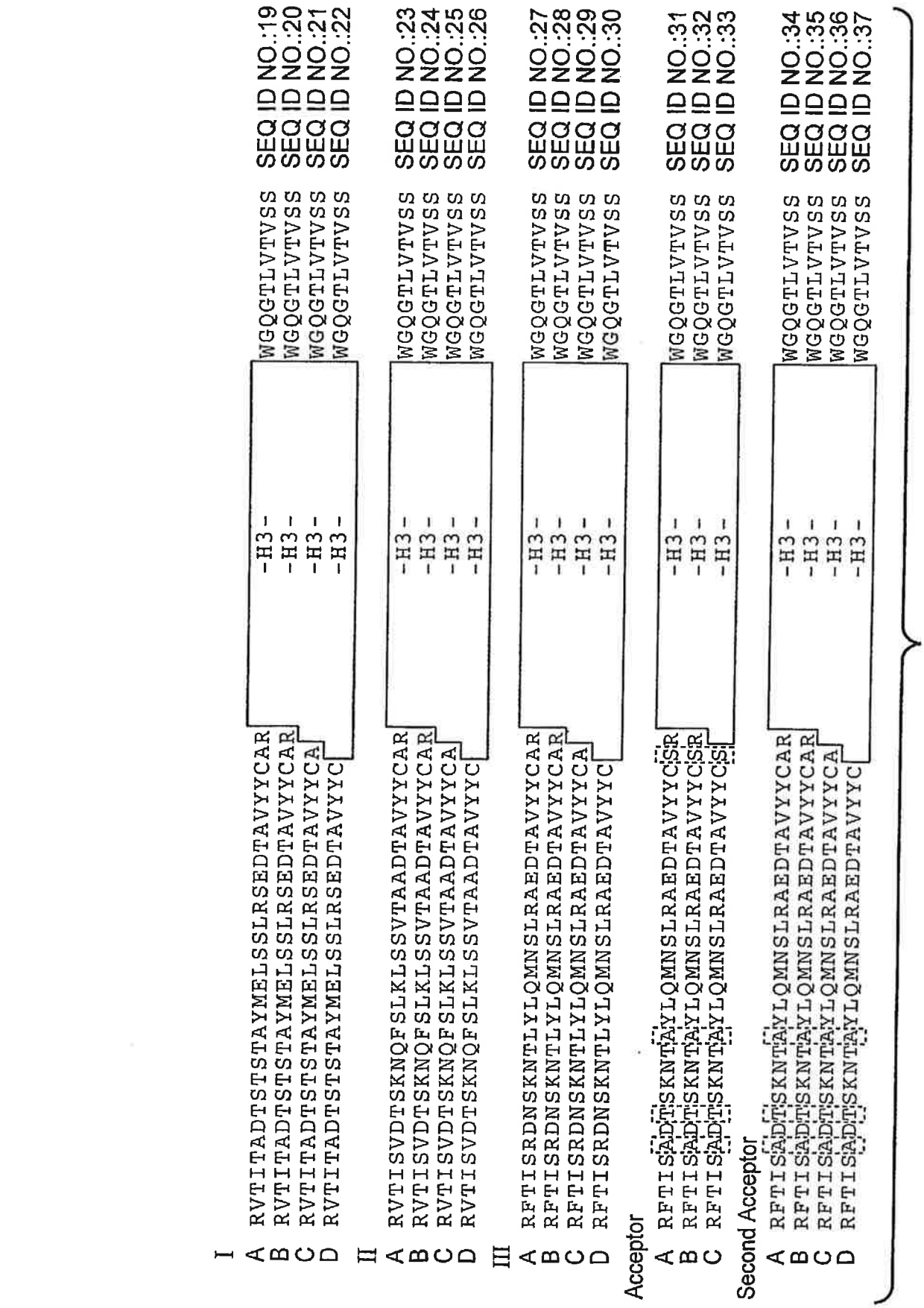

I
A RVTITADTSTSTAYMELSSLRSEDTAVYYCAR -H3- WGQGTLVTVSS SEQ ID NO.:19
B RVTITADTSTSTAYMELSSLRSEDTAVYYCAR -H3- WGQGTLVTVSS SEQ ID NO.:20
C RVTITADTSTSTAYMELSSLRSEDTAVYYCA -H3- WGQGTLVTVSS SEQ ID NO.:21
D RVTITADTSTSTAYMELSSLRSEDTAVYYC -H3- WGQGTLVTVSS SEQ ID NO.:22
II
A RVTISVDTSKNQFSLKLSSVTAADTAVYYCAR -H3- WGQGTLVTVSS SEQ ID NO.:23
B RVTISVDTSKNQFSLKLSSVTAADTAVYYCAR -H3- WGQGTLVTVSS SEQ ID NO.:24
C RVTISVDTSKNQFSLKLSSVTAADTAVYYCA -H3- WGQGTLVTVSS SEQ ID NO.:25
D RVTISVDTSKNQFSLKLSSVTAADTAVYYC -H3- WGQGTLVTVSS SEQ ID NO.:26
III
A RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR -H3- WGQGTLVTVSS SEQ ID NO.:27
B RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR -H3- WGQGTLVTVSS SEQ ID NO.:28
C RFTISRDNSKNTLYLQMNSLRAEDTAVYYCA -H3- WGQGTLVTVSS SEQ ID NO.:29
D RFTISRDNSKNTLYLQMNSLRAEDTAVYYC -H3- WGQGTLVTVSS SEQ ID NO.:30
Acceptor
A RFTISADTSKNTAYLQMNSLRAEDTAVYYCSR -H3- WGQGTLVTVSS SEQ ID NO.:31
B RFTISADTSKNTAYLQMNSLRAEDTAVYYCSR -H3- WGQGTLVTVSS SEQ ID NO.:32
C RFTISADTSKNTAYLQMNSLRAEDTAVYYCS -H3- WGQGTLVTVSS SEQ ID NO.:33
Second Acceptor
A RFTISADTSKNTAYLQMNSLRAEDTAVYYCAR -H3- WGQGTLVTVSS SEQ ID NO.:34
B RFTISADTSKNTAYLQMNSLRAEDTAVYYCAR -H3- WGQGTLVTVSS SEQ ID NO.:35
C RFTISADTSKNTAYLQMNSLRAEDTAVYYCA -H3- WGQGTLVTVSS SEQ ID NO.:36
D RFTISADTSKNTAYLQMNSLRAEDTAVYYC -H3- WGQGTLVTVSS SEQ ID NO.:37

FIG. 5B

kv1 DIQMTQSPSSLSASVGDRVTITC -L1- WYQQKPGKAPKLLIY -L2- GVPSRFSGSGSGTDFTLTISSLQP

kv2 DIVMTQSPLSLPVTPGEPASISC -L1- WYLQKPGQSPQLLIY -L2- GVPDRFSGSGSGTDFTLKISRVEA

kv3 EIVLTQSPGTLSLSPGERATLSC -L1- WYQQKPGQAPRLLIY -L2- GIPDRFSGSGSGTDFTLTISRLEP

kv4 DIVMTQSPDSLAVSLGERATINC -L1- WYQQKPGQPPKLLIY -L2- GVPDRFSGSGSGTDFTLTISSLQA

FIG. 6A

kv1 EDFATYYC -L3- FGQGTKVEIK SEQ ID NO.:38

kv2 EDVGVYYC -L3- FGQGTKVEIK SEQ ID NO.:39

kv3 EDFAVYYC -L3- FGQGTKVEIK SEQ ID NO.:40

kv4 EDVAVYYC -L3- FGQGTKVEIK SEQ ID NO.:41

FIG. 6B

LC

Kabat#	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	a	b	c	d	e	f
mu5D5	D	I	M	M	S	Q	S	P	S	S	L	T	V	S	V	G	E	K	V	T	V	S	C	K	S	S	Q	S	L	L	Y	T	S

	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61
	S	Q	K	N	Y	L	A	W	Y	Q	Q	K	P	G	Q	S	P	K	L	L	I	Y	W	A	S	T	R	E	S	G	V	P	D	R

	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93
	F	T	G	S	G	S	G	T	D	F	T	L	T	I	T	S	V	K	A	D	D	L	A	V	Y	Y	C	Q	Q	Y	Y	A	

	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	
	Y	P	W	T	F	G	G	G	T	K	L	E	I	K	R	(SEQ ID NO: 9)

HC

Kabat#	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
mu5D5	Q	V	Q	L	Q	Q	S	G	P	E	L	V	R	P	G	A	S	V	K	M	S	C	R	A	S	G	Y	T	F	T	S	Y	W

	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	a	53	54	55	56	57	58	59	60	61	62	63	64	65
	L	H	W	V	K	Q	R	P	G	Q	G	L	E	W	I	G	M	I	D	P	S	N	S	D	T	R	F	N	P	N	F	K	D

	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	a	b	c	83	84	85	86	87	88	89	90	91	92	93	94	95
	K	A	T	L	N	V	D	R	S	S	N	T	A	Y	M	L	L	S	S	L	T	S	A	D	S	A	V	Y	Y	C	A	T	Y

	96	97	98	99	100	a	k	101	102	103	104	105	106	107	108	109	110	111	112	113	
	G	S	Y	V	S	P	L	D	Y	W	G	Q	G	T	S	V	T	V	S	S	(SEQ ID NO: 10)

FIG. 7

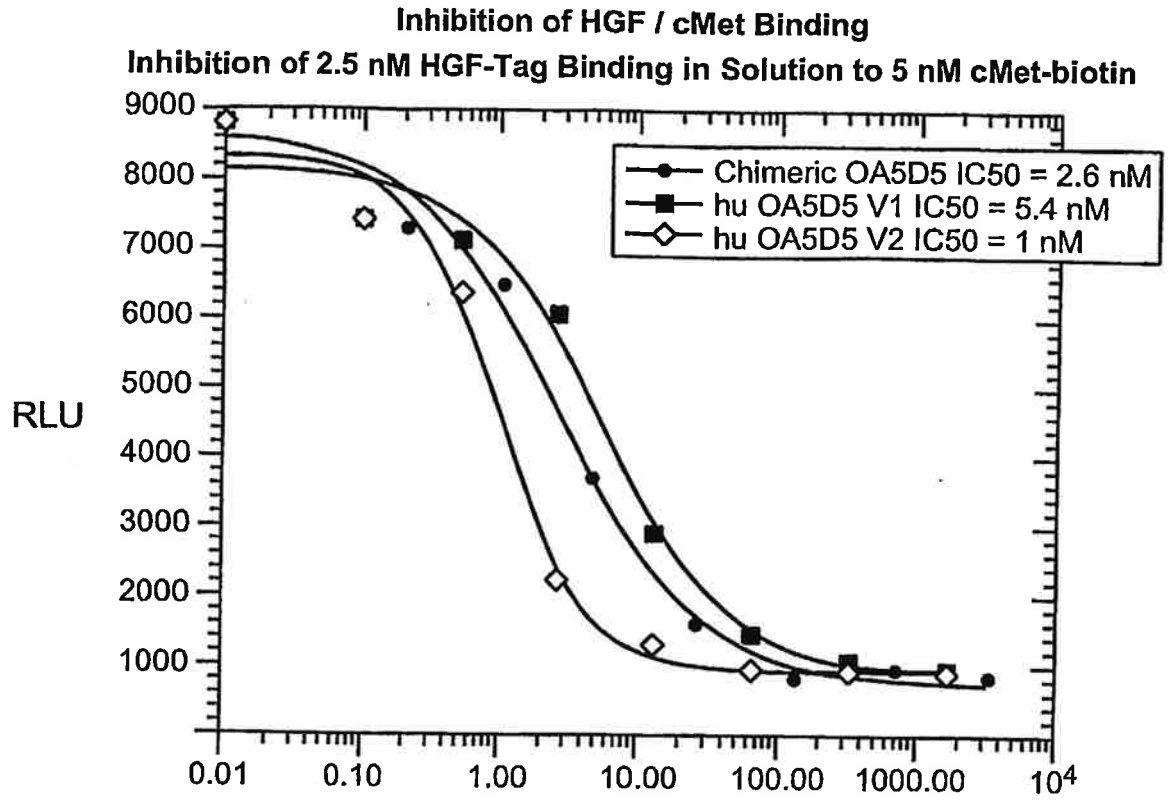

Inhibition of HGF / cMet Binding
Inhibition of 2.5 nM HGF-Tag Binding in Solution to 5 nM cMet-biotin
RLU
9000
8000
7000
6000
5000
4000
3000
2000
1000
0.01
0.10
1.00
10.00
100.00
1000.00
10^4
Chimeric OA5D5 IC50 = 2.6 nM
hu OA5D5 V1 IC50 = 5.4 nM
hu OA5D5 V2 IC50 = 1 nM
OA5D5 (Anti-cMet Antibody) (nM)

FIG. 8

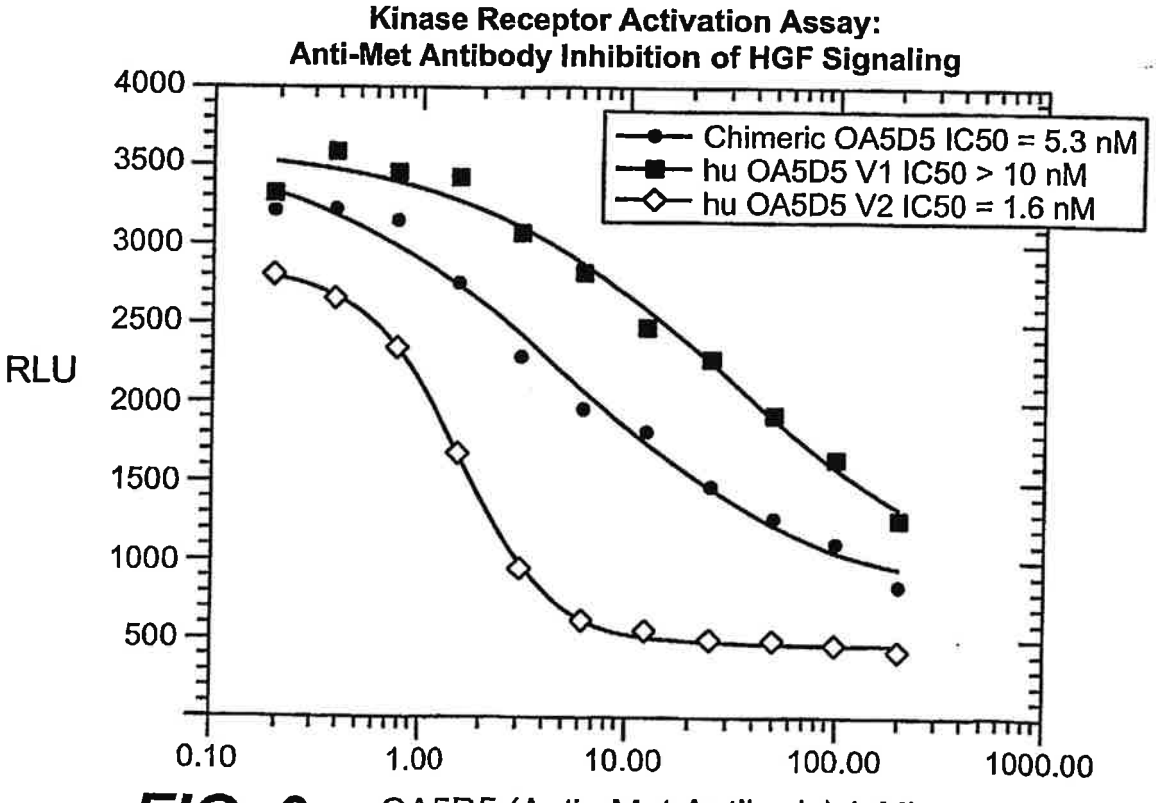

Kinase Receptor Activation Assay:
Anti-Met Antibody Inhibition of HGF Signaling
RLU
4000
3500
3000
2500
2000
1500
1000
500
0.10
1.00
10.00
100.00
1000.00
Chimeric OA5D5 IC50 = 5.3 nM
hu OA5D5 V1 IC50 > 10 nM
hu OA5D5 V2 IC50 = 1.6 nM
OA5D5 (Anti-cMet Antibody) (nM)

FIG. 9

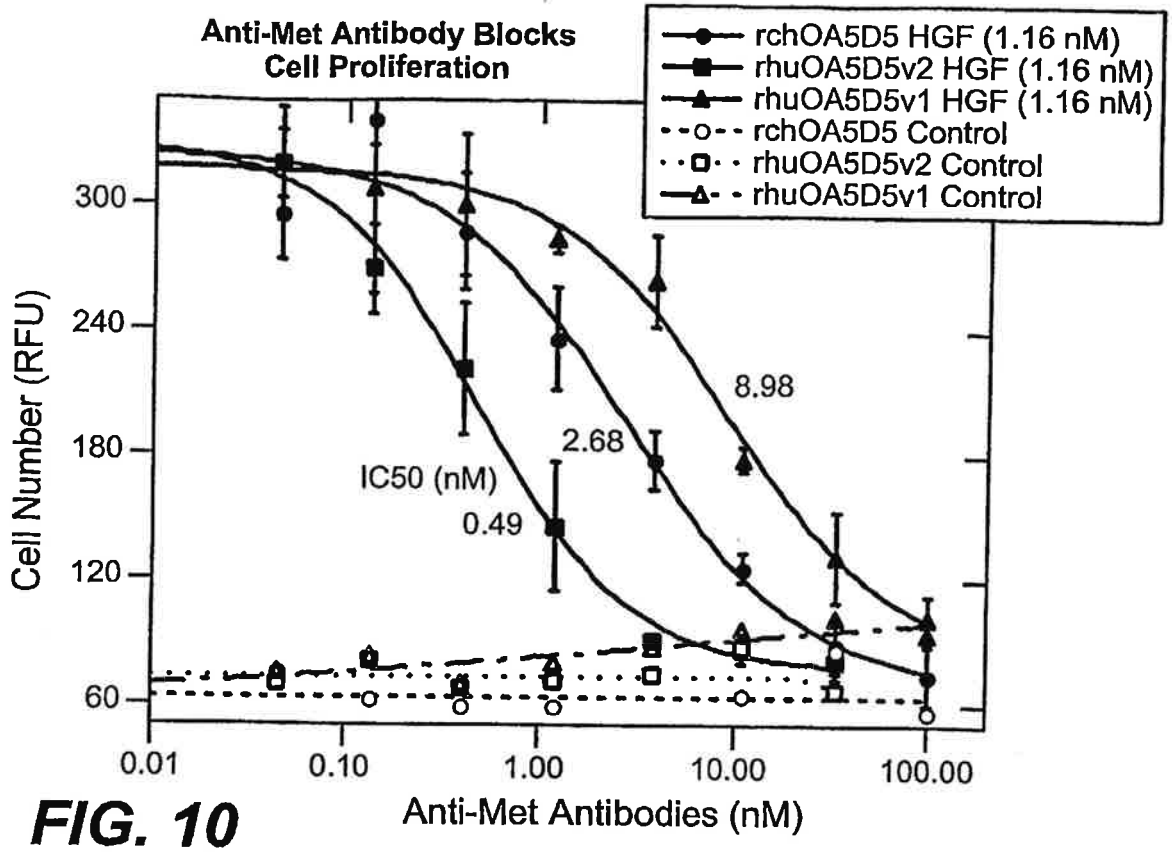

Anti-Met Antibody Blocks
Cell Proliferation
rchOA5D5 HGF (1.16 nM)
rhuOA5D5v2 HGF (1.16 nM)
rhuOA5D5v1 HGF (1.16 nM)
rchOA5D5 Control
rhuOA5D5v2 Control
rhuOA5D5v1 Control
Cell Number (RFU)
300
240
180
120
60
8.98
2.68
IC50 (nM)
0.49
0.01
0.10
1.00
10.00
100.00
Anti-Met Antibodies (nM)

FIG. 10

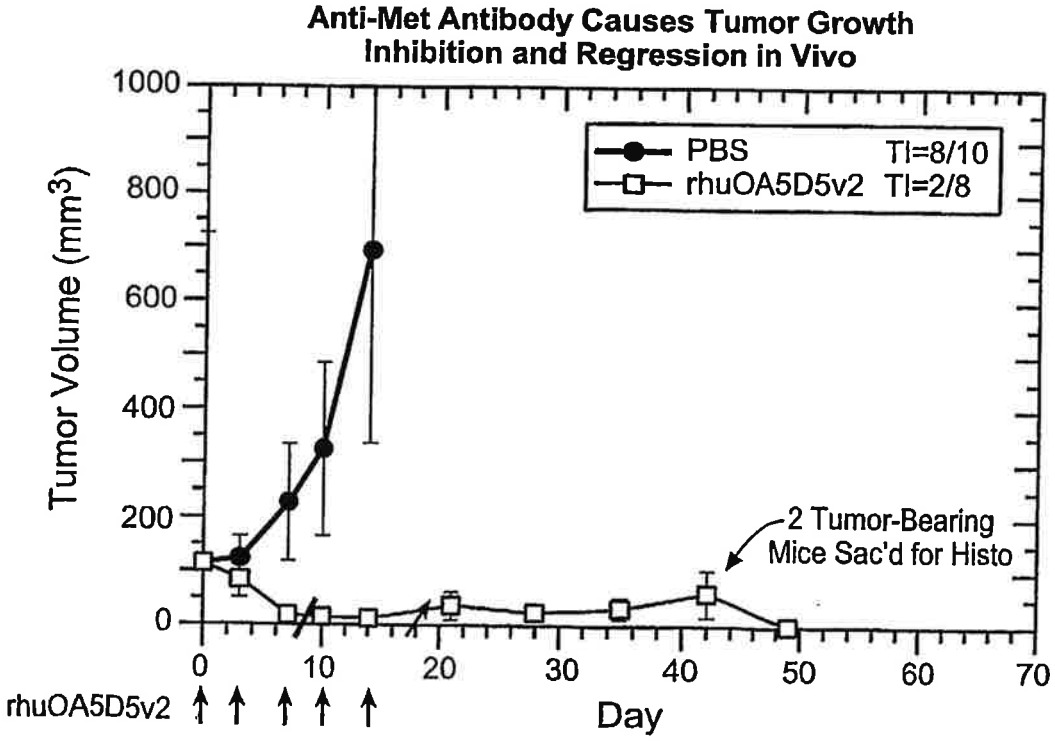

Anti-Met Antibody Causes Tumor Growth
Inhibition and Regression in Vivo
PBS TI=8/10
rhuOA5D5v2 TI=2/8
Tumor Volume (mm3)
1000
800
600
400
200
0
2 Tumor-Bearing
Mice Sac'd for Histo
0
10
20
30
40
50
60
70
rhuOA5D5v2
Day

FIG. 12

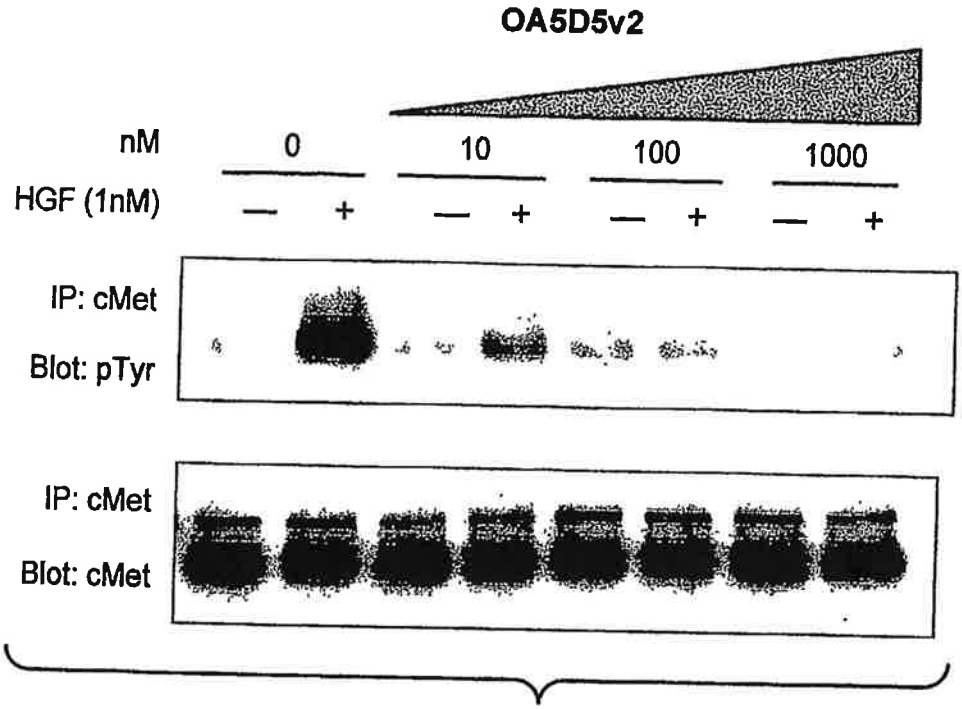


FIG. 11A

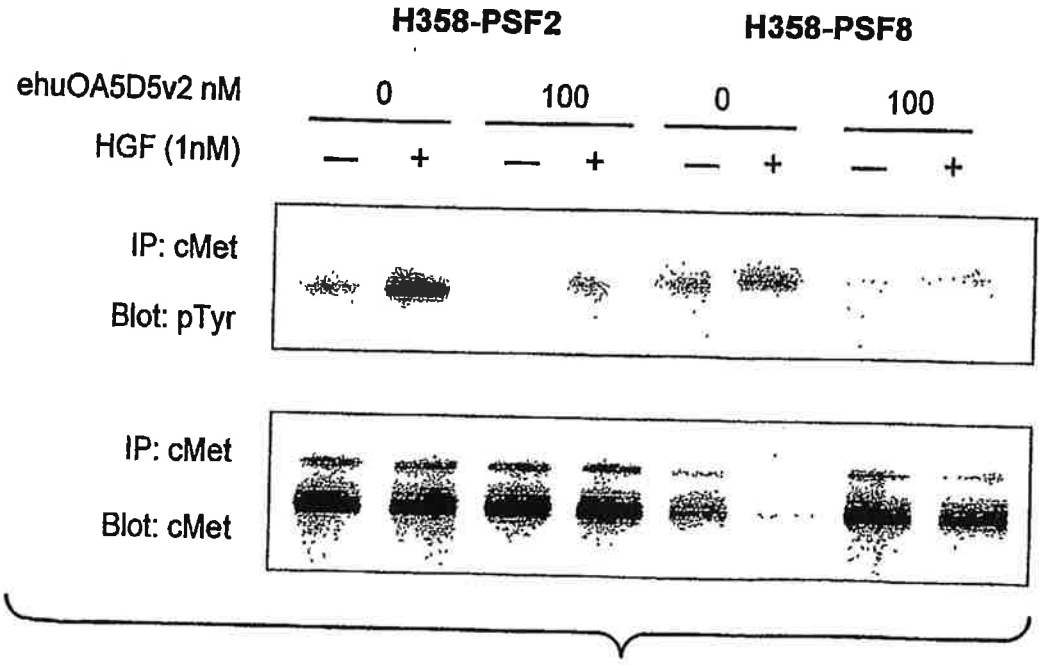


FIG. 11B

5D5.v2 Light Chain

FR1-LC: DIQMTQSPSSLSASVGDRVTITC (SEQ ID NO: 179)
FR2-LC: WYQQKPGKAPKLLIY (SEQ ID NO: 180)
FR3-LC: GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC (SEQ ID NO: 181)
FR4-LC: FGQGTKVEIKR (SEQ ID NO: 182)
HVR1-LC: KSSQSLLYTSSQKNYLA (SEQ ID NO: 183)
HVR2-LC: WASTRES (SEQ ID NO: 184)
HVR3-LC: QQYYAYPWT (SEQ ID NO: 185)
CL1: TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK
DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 186)

5D5.v2 Heavy Chain

FR1-HC: EVQLVESGGGLVQPGGSLRLSCAAS (SEQ ID NO: 187)
FR2-HC: WVRQAPGKGLEWV (SEQ ID NO: 188)
FR3-HC: RFTISADTSKNTAYLQMNSLRAEDTAVYYC (SEQ ID NO: 189)
FR4-HC: WGQGTLVTVSS (SEQ ID NO: 190)
HVR1-HC: GYTFTSYWLH (SEQ ID NO: 191)
HVR2-HC: GMIDPSNSDTRFNPNFKD (SEQ ID NO: 192)
HVR3-HC: ATYRSYVTPLDY (SEQ ID NO: 193)
CH1: ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA
VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT (SEQ ID NO: 194)
Fc: CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH
NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
QVYTLPPSREEMTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL
VSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 195)

FIG. 13

CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED
PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE
YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLWCL
VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW
QQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 196)

FIG. 14