

1/78
FIG. 1A

Anti-TIM-3 13A3 VH1

V segment: 4-39

D segment: 4-17

J segment: JH5b

1	Q	L	Q	L	Q	E	S	G	P	G	L	V	K	P	S	E	T
	CAG	CTG	CAG	CTG	CAG	GAG	TCG	GGC	CCA	GGA	CTG	GTG	AAG	CCT	TCG	GAG	ACC
52	L	S	L	T	C	T	V	S	G	G	S	I	S	<u>CDR1</u>			
	CTG	TCC	CTC	ACC	TGC	ACT	GTC	TCT	GGT	GGC	TCC	ATC	AGC	AGT	AGA	AGT	TAC
103	Y	W	G	W	I	R	Q	P	P	G	K	G	L	E	W	I	G
	TAC	TGG	GGC	TGG	ATC	CGC	CAG	CCC	CCA	GGG	AAG	GGG	CTG	GAG	TGG	ATT	GGG
154	<u>CDR2</u>																
	S	I	Y	Y	S	G	F	T	Y	Y	N	P	S	L	K	S	R
	AGT	ATC	TAT	TAT	AGT	GGG	TTC	ACC	TAC	TAC	AAC	CCG	TCC	CTC	AAG	AGT	CGA
205	V	T	I	S	V	D	T	S	K	N	Q	F	S	L	K	L	S
	GTC	ACC	ATA	TCC	GTT	GAC	ACG	TCC	AAG	AAC	CAG	TTC	TCC	CTG	AAG	CTG	AGC
256	S	V	T	A	A	D	T	A	V	Y	Y	C	A	T	<u>CDR3</u>		
	TCT	GTG	ACC	GCC	GCA	GAC	ACG	GCT	GTG	TAT	TAT	TGT	GCG	ACA	GGG	GGG	CCC
307	Y	G	D	Y	A	H	W	F	D	P	W	G	Q	G	T	L	V
	TAC	GGT	GAC	TAC	GCC	CAC	TGG	TTC	GAC	CCC	TGG	GGC	CAG	GGA	ACC	CTG	GTC
358	T	V	S	S													
	ACC	GTC	TCC	TCA													

J segment: JK5

[illegible]

3/78
FIG. 1C

13A3 _NT_VH1

ATGAAGCACCTGTGGTTCTTCCTCCTGCTGGTGGCGGCTCCCAGATGGGTCCCTGTCCCAGCTGCAGCTGCAGGAG
TCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCACTGTCTCTGGTGGCTCCATCAGCAGT
AGAAGTTACTACTGGGGCTGGATCCGCCAGCCCCAGGGAAGGGGCTGGAGTGGATTGGGAGTATCTATTATAGT
GGGTTCACCTACTACAACCCGTCCCTCAAGAGTCGAGTCACCATATCCGTTGACACGTCCAAGAACCAGTTCTCC
CTGAAGCTGAGCTCTGTGACCGCCGCAGACACGGCTGTGTATTATTGTGCGACAGGGGGGCCCTACGGTGACTAC
GCCCCTGGTTCGACCCCTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA

13A3 _AA_VH1

MKHLWFFLLLVAAPRWVLSQLQLQESGPGLVKPSSETLSLTCTVSGGSISSRSYYWGWIROPKPGLEWIGSIYYS
GFTYYNPSLKSRTVISVDTSKNQFSLKLSSVTAADTAVYYCATGGPYGDYAHWFDPWGQGLVTVSS

13A3 _NT_VK1

ATGGAAACCCAGCGCAGCTTCTCTTCCTCCTGCTACTCTGGCTCCCAGATACCACCGGAGAAATTGTGTTGACG
CAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGC
AGCAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCAGCAGG
GCCACTGGCATCCCAGACAGGTTCACTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAG
CCTGAAGATTTTGAGTGTATTACTGTCAGCAGTATGGTAGCTCACCGATCACCTTCGGCCAAGGGACACGACTG
GAGATTAAA

13A3 _AA_VK1

METPAQLLFLLLLWLDPDTTGEIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYGASSR
ATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQYQGSSPITFGQGRLEIK

4/78
FIG. 2A

Anti-TIM-3 8B9 VH1

V segment: 4-59

D segment: 4-17

J segment: JH6b

1	Q	V	Q	L	Q	E	S	G	P	G	L	V	K	P	S	E	T
	CAG	GTG	CAG	CTG	CAG	GAG	TCG	GGC	CCA	GGA	CTG	GTG	AAG	CCT	TCG	GAG	ACC
52	L	S	L	T	C	T	V	S	G	G	S	I	S	CDR1			
	CTG	TCC	CTC	ACC	TGC	ACT	GTC	TCT	GGT	GGC	TCC	ATC	AGT	CGT	CAC	TAC	TGG
103	N	W	I	R	Q	P	P	G	K	G	L	E	W	I	G	CDR2	
	AAC	TGG	ATC	CGG	CAG	CCC	CCA	GGG	AAG	GGA	CTG	GAG	TGG	ATT	GGG	TAT	ATC
154	H	Y	S	G	S	T	N	Y	N	S	S	L	K	S	R	V	T
	CAT	TAC	AGT	GGA	AGC	ACC	AAC	TAC	AAT	TCC	TCC	CTC	AAG	AGT	CGA	GTC	ACC
205	I	S	V	D	T	S	K	N	Q	F	S	L	K	L	S	S	V
	ATA	TCA	GTA	GAC	ACG	TCC	AAG	AAC	CAG	TTC	TCC	CTG	AAG	CTG	AGC	TCT	GTG
256	T	A	A	D	T	A	V	Y	Y	C	A	R	CDR3				
	ACC	GCT	GCG	GAC	ACG	GCC	GTG	TAT	TAC	TGT	GCG	AGA	GAT	ACT	GGG	TAC	TAC
307	G	M	D	I	W	G	Q	G	T	T	V	T	V	S	S		
	GGT	ATG	GAC	ATC	TGG	GGC	CAA	GGG	ACC	ACG	GTC	ACC	GTC	TCC	TCA		

J segment: JK4

	E	I	V	L	T	Q	S	P	G	T	L	S	L	S	P	G	E		
1	GAA	ATT	GTG	TTG	ACG	CAG	TCT	CCA	GGC	ACC	CTG	TCT	TTG	TCT	CCA	GGG	GAA		
							<u>CDR1</u>												
	R	A	T	L	S	C	R	A	S	Q	S	V	S	S	S	Y	L		
52	AGA	GCC	ACC	CTC	TCC	TGC	AGG	GCC	AGT	CAG	AGT	GTT	AGC	AGC	AGC	TAC	TTA		
	A	W	Y	Q	Q	K	P	G	Q	A	P	R	L	L	I	Y	G		
103	GCC	TGG	TAC	CAG	CAG	AAA	CCT	GGC	CAG	GCT	CCC	AGG	CTC	CTC	ATC	TAT	GGT		
	<u>CDR2</u>																		
	A	S	S	R	A	T	G	I	P	D	R	F	S	G	S	G	S		
154	GCA	TCC	AGC	AGG	GCC	ACT	GGC	ATC	CCA	GAC	AGG	TTC	AGT	GGC	AGT	GGG	TCT		
	G	T	D	F	T	L	T	I	S	R	L	E	P	E	D	F	A		
205	GGG	ACA	GAC	TTC	ACT	CTC	ACC	ATC	AGC	AGA	CTG	GAG	CCT	GAA	GAT	TTT	GCA		
							<u>CDR3</u>												
	V	Y	Y	C	Q	Q	Y	G	S	S	P	L	T	F	G	G	G		
256	GTG	TAT	TAC	TGT	CAG	CAG	TAT	GGT	AGC	TCA	CCT	CTC	ACT	TTC	GGC	GGA	GGG		
	T	K	V	E	I	K													
307	ACC	AAG	GTG	GAG	ATC	AAA													

6/78
FIG. 2C

8B9 NT_VH1

ATGAAACATCTGTGGTTCTTCCTTCTCCTGGTGGCAGCTCCCAGATGGGTCTGTCCCAGGTGCAGCTGCAGGAG
TCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCACTGTCTCTGGTGGCTCCATCAGTCGT
CACTACTGGAAGTGGATCCGGCAGCCCCAGGGAAGGGACTGGAGTGGATTGGGTATATCCATTACAGTGGGAAGC
ACCAACTACAATTCTCCCTCAAGAGTCGAGTCACCATATCAGTAGACACGTCCAAGAACCAGTTCTCCCTGAAG
CTGAGCTCTGTGACCGCTGCGGACACGGCCGTGTATTACTGTGCGAGAGATACTGGGTACTACGGTATGGACATC
TGGGGCCAAGGACCACGGTCACCGTCTCCTCA

8B9 _AA_VH1

MKHLWFFLLLVAAAPRWVLSQVQLQESGPGLVKPSSETLSLTCTVSGGSISRHYWNWIRQPPGKLEWIGYIHYSGS
TNYNSSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDTGYYGMDIWGQGTTVTVSS

8B9 _NT_VK1

ATGGAAACCCAGCGCAGCTTCTCTTCCTCCTGCTACTCTGGCTCCCAGATACCACCGGAGAAATTGTGTTGACG
CAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGC
AGCAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCAGCAGG
GCCACTGGCATCCCAGACAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAG
CCTGAAGATTTTGAGTGTATTACTGTCAGCAGTATGGTAGCTCACCTCTCACTTTCGG
CGGAGGGACCAAGGTGGAGATCAA

8B9 _AA_VK1

METPAQLLFLLLLWLDPDTTGEIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSR
ATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQYQYGSPLTFGGGTKVEIK

7/78
FIG. 3A

Anti-TIM-3 8C4 VH1

V segment: 4-59

D segment: 4-17

J segment: JH6b

1	Q	V	Q	L	Q	E	S	G	P	G	L	V	K	P	S	E	T
	CAG	GTG	CAG	CTG	CAG	GAG	TCG	GGC	CCA	GGA	CTG	GTG	AAG	CCT	TCG	GAG	ACC
52	L	S	L	T	C	T	V	S	G	G	S	I	S	CDR1			
	CTG	TCC	CTC	ACC	TGC	ACT	GTC	TCT	GGT	GGC	TCC	ATC	AGT	CGT	TAC	TAC	TGG
103	S	W	I	R	Q	P	P	G	K	G	L	E	W	I	G	CDR2	
	AGC	TGG	ATC	CGG	CAG	CCC	CCA	GGG	AAG	GGA	CTG	GAG	TGG	ATT	GGG	TAT	ATC
154	H	Y	T	G	S	T	N	Y	N	P	S	L	K	S	R	V	T
	CAT	TAC	ACT	GGG	AGC	ACC	AAC	TAC	AAC	CCC	TCC	CTC	AAG	AGT	CGA	GTC	ACC
205	I	S	V	D	T	S	K	N	Q	F	S	L	K	L	S	S	V
	ATA	TCA	GTA	GAC	ACG	TCC	AAG	AAC	CAG	TTC	TCC	CTG	AAG	CTG	AGC	TCT	GTG
256	T	A	A	D	T	A	V	Y	Y	C	A	T	CDR3				
	ACC	GCA	GCG	GAC	ACG	GCC	GTG	TAT	TAC	TGT	GCG	ACA	GAT	ACG	GGC	TAC	
307	Y	G	M	D	V	W	G	Q	G	T	T	V	T	V	S	S	
	TAC	GGT	ATG	GAC	GTC	TGG	GGC	CAA	GGG	ACC	ACG	GTC	ACC	GTC	TCC	TCA	

J segment: JK4

[illegible]

9/78
FIG. 3C

8C4_NT_VH1

ATGAAACATCTGTGGTTCTTCCTTCTCCTGGTGGCAGCTCCCAGATGGGTCTGTCCCAGGTGCAGCTGCAGGAG
TCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCACTGTCTCTGGTGGCTCCATCAGTCGT
TACTACTGGAGCTGGATCCGGCAGCCCCAGGGAAGGACTGGAGTGGATTGGGTATATCCATTACACTGGGAGC
ACCAACTACAACCCCTCCCTCAAGAGTCGAGTCACCATATCAGTAGACACGTCCAAGAACCAGTTCTCCCTGAAG
CTGAGCTCTGTGACCGCAGCGGACACGGCCGTGTATTACTGTGCGACAGATACGGGCTACTACGGTATGGACGTC
TGGGGCCAAGGGACACGGTCACCGTCTCCTCA

8C4_AA_VH1

MKHLWFFLLLVAAPRWVLSQVQLQESGPLVKPSETLSLTCTVSGGSISRYYWSWIRQPPGKLEWIGYIHYTGS
TNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCATDTGYYGMDVWGQGT'TVTVSS

8C4_NT_VK1

ATGGAAACCCAGCGCAGCTTCTCTTCTCCTGCTACTCTGGCTCCCAGATACCACCGGAGAAATTGTGTTGACG
CAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGC
AGCAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCAGCAGG
GCCACTGGCATCCCAGACAGGTTCACTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAG
CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGCTCACCGCTCACTTTCGGCGGAGGGACCAAGGTG
GAGATCAA

8C4_AA_VK1

METPAQLLFLLLLWLDPDTTGEIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSR
ATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQYGGSSPLTFGGGTKVEIK

Anti-TIM-3 17C3 VH1

V segment: 1-46

D segment: 3-10

J segment: JH6b

1	Q	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	A	S		
	CAG	GTG	CAG	TTG	GTG	CAG	TCT	GGG	GCT	GAG	GTG	AAG	AAG	CCT	GGG	GCC	TCA		
52	V	K	V	S	C	K	A	S	G	Y	T	F	T	CDR1					
	GTG	AAG	GTC	TCC	TGC	AAG	GCA	TCT	GGA	TAC	ACT	TTC	ACC	S	Y	Y	M		
103	H				W	V	R	Q	A	P	G	Q	G	L	E	W	M	CDR2	
	CAC	TGG	GTG	CGA	CAG	GCC	CCT	GGA	CAA	GGG	CTT	GAG	TGG	ATG	GGA	ATA	ATC	I	I
154	N	P	R	G	D	S	I	I	Y	A	Q	K	F	Q	G	R	V		
	AAC	CCT	AGG	GGT	GAT	AGC	ATA	ATC	TAC	GCA	CAG	AAG	TTC	CAG	GGC	AGA	GTC		
205	T	M	T	R	D	T	S	T	S	T	V	Y	M	E	L	S	S		
	ACC	ATG	ACC	AGG	GAC	ACG	TCC	ACG	AGC	ACA	GTC	TAC	ATG	GAG	CTG	AGC	AGC		
256	L	R	S	E	D	T	A	V	Y	Y	C	A	R	CDR3					
	CTG	AGA	TCT	GAG	GAC	ACG	GCC	GTG	TAT	TAC	TGT	GCG	AGA	D	F	Y	G		
307	S	G	N	Y	Y	Y	G	M	D	V	W	G	Q	G	T	T	V		
	TCG	GGA	AAC	TAC	TAC	TAC	GGT	ATG	GAC	GTC	TGG	GGC	CAA	GGG	ACC	ACG	GTC		
358	T	V	S	S															
	ACC	GTC	TCC	TCA															

J segment: JK5

	E	I	V	L	T	Q	S	P	G	T	L	S	L	S	P	G	E		
1	GAA	ATT	GTG	TTG	ACG	CAG	TCT	CCA	GGC	ACC	CTG	TCT	TTG	TCT	CCA	GGG	GAA		
							<u>CDR1</u>												
52	R	A	T	L	S	C	R	A	S	Q	S	V	S	S	S	Y	L		
	AGA	GCC	ACC	CTC	TCC	TGC	AGG	GCC	AGT	CAG	AGT	GTT	AGC	AGC	AGC	TAC	TTA		
	A	W	Y	Q	Q	K	P	G	Q	A	P	R	L	L	I	Y	G		
103	GCC	TGG	TAC	CAG	CAG	AAA	CCT	GGC	CAG	GCT	CCC	AGG	CTC	CTC	ATC	TAT	GGT		
	<u>CDR2</u>																		
154	A	S	S	R	A	T	G	I	P	D	R	F	S	G	S	G	S		
	GCA	TCC	AGC	AGG	GCC	ACT	GGC	ATC	CCA	GAC	AGG	TTC	AGT	GGC	AGT	GGG	TCT		
	G	T	D	F	T	L	T	I	S	R	L	E	P	E	D	F	A		
205	GGG	ACA	GAC	TTC	ACT	CTC	ACC	ATC	AGC	AGA	CTG	GAG	CCT	GAA	GAT	TTT	GCA		
	<u>CDR3</u>																		
256	V	Y	Y	C	Q	Q	Y	G	S	S	P	I	T	F	G	Q	G		
	GTG	TAT	TAC	TGT	CAG	CAG	TAT	GGT	AGC	TCA	CCG	ATC	ACC	TTC	GGC	CAA	GGG		
	T	R	L	E	I	K													
307	ACA	CGA	CTG	GAG	ATT	AAA													

12/78
FIG. 4C

17C3_NT_VH1

ATGGACTGGACCTGGAGGGTCTTCTGCTTGCTGGCTGTAGCTCCAGGTGCTCACTCCCAGGTGCAGTTGGTGCAG
TCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCATCTGGATACACTTTCACCAGC
TACTATATGCACTGGGTGCGACAGGCCCTGGACAAGGGCTTGAGTGGATGGGAATAATCAACCCTAGGGGTGAT
AGCATAATCTACGCACAGAAGTTCCAGGGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTACATG
GAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATTCTATGGTTCGGGAAACTAC
TACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA

17C3_AA_VH1

MDWTWRVFCLLAVAPGAHSQVQLVQSGAEVKKPGASVKVSCKASGYTFFTSYMHWVRQAPGQGLEWMGIINPRGD
SIIYAQKFQGRVTMTTRDTSTSTVYMESSLRSEDVAVYYCARDIFYGSGNYYYGMDVWGQGTITVTVSS

17C3_NT_VK1

ATGGAAACCCAGCGCAGCTTCTCTTCTCCTGCTACTCTGGCTCCCAGATACCACCGGAGAAATTGTGTTGACG
CAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGC
AGCAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCAGCAGG
GCCACTGGCATCCCAGACAGGTTCACTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAG
CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGCTCACCGATCACCTTCGGCCAAGGGACACGACTG
GAGATTAAA

17C3_AA_VK1

METPAQLLFLLLLLWLPDTTGEIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSR
ATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQYGSSPITFGQGRLEIK

Anti-TIM-3 9F6 VH1

V segment: 3-11

D segment: 6-19

J segment: JH6b

1	Q	V	Q	L	V	E	S	G	G	G	L	V	K	P	G	G	S
	CAG	GTG	CAG	CTG	GTG	GAG	TCT	GGG	GGA	GGC	TTG	GTC	AAG	CCT	GGA	GGG	TCC
52	L	R	L	S	C	A	A	S	G	F	T	F	S	CDR1			
	CTG	AGA	CTC	TCC	TGT	GCA	GCC	TCT	GGA	TTC	ACC	TTC	AGT	GAC	TAC	TAC	ATG
103	S	W	I	R	Q	A	P	G	K	G	L	E	W	V	S	CDR2	
	AGC	TGG	ATC	CGC	CAG	GCT	CCA	GGG	AAG	GGG	CTG	GAG	TGG	GTT	TCA	TTC	ATT
154	S	G	G	G	S	T	I	Y	Y	A	D	S	V	K	G	R	F
	AGT	GGT	GGT	GGT	AGT	ACC	ATA	TAC	TAC	GCA	GAC	TCT	GTG	AAG	GGC	CGA	TTC
205	T	I	S	R	D	N	A	K	N	S	L	F	L	Q	M	N	S
	ACC	ATC	TCC	AGG	GAC	AAC	GCC	AAG	AAC	TCG	CTG	TTT	CTG	CAA	ATG	AAC	AGC
256	L	R	V	E	D	T	A	V	Y	Y	C	A	R	CDR3			
	CTG	AGA	GTC	GAG	GAC	ACG	GCT	GTG	TAT	TAC	TGT	GCG	AGA	GAT	GGC	TAT	AGC
307	S	G	W	Y	Y	Y	G	M	D	V	W	G	Q	G	T	A	V
	AGT	GGC	TGG	TAC	TAC	TAC	GGT	ATG	GAC	GTC	TGG	GGC	CAA	GGG	ACC	GCG	GTC
358	T	V	S	S													
	ACC	GTC	TCC	TCA													

J segment: JK1

[illegible]

J segment: JK4

	E	I	V	L	T	Q	S	P	G	T	L	S	L	S	P	G	E		
1	GAA	ATT	GTG	TTG	ACG	CAG	TCT	CCA	GGC	ACC	CTG	TCT	TTG	TCT	CCA	GGG	GAA		
							<u>CDR1</u>												
52	R	A	T	L	S	C	R	A	S	Q	S	V	S	S	S	Y	L		
	AGA	GCC	ACC	CTC	TCC	TGC	AGG	GCC	AGT	CAG	AGT	GTT	AGC	AGC	AGC	TAC	TTA		
	<u>A</u>	<u>W</u>	<u>Y</u>	<u>Q</u>	<u>Q</u>	<u>K</u>	<u>P</u>	<u>G</u>	<u>Q</u>	<u>A</u>	<u>P</u>	<u>R</u>	<u>L</u>	<u>L</u>	<u>I</u>	<u>Y</u>	<u>G</u>		
103	GCC	TGG	TAC	CAG	CAG	AAA	CCT	GGC	CAG	GCT	CCC	AGG	CTC	CTC	ATC	TAT	GGT		
	<u>CDR2</u>																		
154	A	S	S	R	A	T	G	I	P	D	R	F	S	G	S	G	S		
	GCA	TCC	AGC	AGG	GCC	ACT	GGC	ATC	CCA	GAC	AGG	TTC	AGT	GGC	AGT	GGG	TCT		
205	G	T	D	F	T	L	T	I	S	R	L	E	P	E	D	F	A		
	GGG	ACA	GAC	TTC	ACT	CTC	ACC	ATC	AGC	AGA	CTG	GAG	CCT	GAA	GAT	TTT	GCA		
							<u>CDR3</u>												
256	V	Y	Y	C	Q	Q	Y	G	S	S	L	T	F	G	G	G	T		
	GTG	TAT	TAC	TGT	CAG	CAG	TAT	GGT	AGC	TCA	CTC	ACT	TTC	GGC	GGA	GGG	ACC		
307	K	V	E	I	K														
	AAG	GTG	GAG	ATC	AAA														

J segment: JK4

	E	I	V	L	T	Q	S	P	G	T	L	S	L	S	P	G	E		
1	GAA	ATT	GTG	TTG	ACG	CAG	TCT	CCA	GGC	ACC	CTG	TCT	TTG	TCT	CCA	GGG	GAA		
							<u>CDR1</u>												
	R	A	T	L	S	C	R	A	S	Q	S	V	S	S	S	Y	L		
52	AGA	GCC	ACC	CTC	TCC	TGC	AGG	GCC	AGT	CAG	AGT	GTT	AGC	AGC	AGC	TAC	TTA		
	A	W	Y	Q	Q	K	P	G	Q	A	P	R	L	L	I	Y	G		
103	GCC	TGG	TAC	CAG	CAG	AAA	CCT	GGC	CAG	GCT	CCC	AGG	CTC	CTC	ATC	TAT	GGT		
	<u>CDR2</u>																		
	A	S	S	R	A	T	G	I	P	D	R	F	S	G	S	G	S		
154	GCA	TCC	AGC	AGG	GCC	ACT	GGC	ATC	CCA	GAC	AGG	TTC	AGT	GGC	AGT	GGG	TCT		
	G	T	D	F	T	L	T	I	S	R	L	E	P	E	D	F	A		
205	GGG	ACA	GAC	TTC	ACT	CTC	ACC	ATC	AGC	AGA	CTG	GAG	CCT	GAA	GAT	TTT	GCA		
	<u>CDR3</u>																		
	V	Y	Y	C	Q	Q	Y	G	S	S	P	L	T	F	G	G	G		
256	GTG	TAT	TAC	TGT	CAG	CAG	TAT	GGT	AGC	TCA	CCG	CTC	ACT	TTC	GGC	GGA	GGG		
	T	K	V	E	I	K													
307	ACC	AAG	GTG	GAG	ATC	AAA													

17/78
FIG. 5E

9F6_NT_VH1

TGGAGTTTGGGCTGAGCTGGGTTTTTCCTTGTTGCTATTATAAAAGGTGTCCAGTGTCAGGTGCAGCTGGTGGAGT
CTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTCAGTGACT
ACTACATGAGCTGGATCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTTTCATTATTAGTGGTGGTGGTAGTA
CCATATACTACGCAGACTCTGTGAAGGGCCGATTACCATCTCCAGGGACAACGCCAAGAAGCTCGCTGTTTCTGC
AAATGAACAGCCTGAGAGTCGAGGACACGGCTGTGTATTACTGTGCGAGAGATGGCTATAGCAGTGGCTGGTACT
ACTACGGTATGGACGTCTGGGGCCAAGGGACCGCGTACCGTCTCCTCA

9F6_AA_VH1

MEFGLSWVFLVAIIKGVQCQVQLVESGGGLVKPGGSLRLSCAASGFTFSDIYMSWIRQAPKGLEWVSFISGGGS
TIYYADSVKGRFTISRDNAKNSLFLQMNSLRVEDTAVIYCARDGYSSGWYYYGMDVWGQGTAVTVSS

9F6_NT_VK1

ATGGACATGAGGGTCCCCGCTCAGCTCCTGGGGCTTCTGCTGCTCTGGCTCCCAGGTGCCAGATGTGCCATCCAG
TTGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCGGGCAAGTCAGGGC
ATTAGCAGTGCTTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCTCCTAAGCTCCTGATCTATGATGCCTCCAGT
TTGGAAAGTGGGGTCCCATCAAGGTTACGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTG
CAGCCTGAAGATTTTGCAACTTATTACTGTCAACAGTTTAATAGTTACCCTCGGACGTTTCGGCCAAGGGACCAAG
GTGGAAATCAAA

9F6_AA_VK1

MDMRVPAQLLGLLLWLPGARCAIQLTQSPSSLSASVGDRVITICRASQGISSALAWYQQKPKAPKLLIYDASS
LESGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQFNISYPRTFGQGTKVEIK

9F6_NT_VK2

ATGGAAACCCAGCGCAGCTTCTCTTCTCCTGCTACTCTGGCTCCCAGATAACCACCGGAGAAATTGTGTTGACG
CAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGC
AGCAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCAGCAGG
GCCACTGGCATCCCAGACAGGTTCACTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAG
CCTGAAGATTTTGCAGTGTATTACTGTGAGCAGTATGGTAGCTCACTCACTTTCGGCGGAGGGACCAAGGTGGAG
ATCAAA

9F6_AA_VK2

METPAQLLFLLLLWLPTTGEIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSR
ATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSSLTFGGGTKVEIK

9F6_NT_VK3

ATGGAAACCCAGCGCAGCTTCTCTTCTCCTGCTACTCTGGCTCCCAGATAACCACCGGAGAAATTGTGTTGACG
CAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGC
AGCAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCAGCAGG
GCCACTGGCATCCCAGACAGGTTCACTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAG
CCTGAAGATTTTGCAGTGTATTACTGTGAGCAGTATGGTAGCTCACCGCTCACTTTCGG
CGGAGGGACCAAGGTGGAGATCAAA

9F6_AA_VK3

METPAQLLFLLLLWLPTTGEIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSR
ATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSSLTFGGGTKVEIK

Anti-TIM-3 3G4 VH1

D segment: 6-13

J segment: JH6b

[illegible]

Anti-TIM-3 3G4 VK1

V segment: A27

J segment: JK5

1	E	I	V	L	T	Q	S	P	G	T	L	S	L	S	P	G	E		
	GAA	ATT	GTG	TTG	ACG	CAG	TCT	CCA	GGC	ACC	CTG	TCT	TTG	TCT	CCA	GGG	GAA		
							CDR1												
52	R	A	T	L	S	C	R	A	S	Q	S	V	S	S	S	Y	L		
	AGA	GCC	ACC	CTC	TCC	TGC	AGG	GCC	AGT	CAG	AGT	GTT	AGC	AGC	AGC	TAC	TTA		
103	A	W	Y	Q	Q	K	P	G	Q	A	P	R	L	L	I	Y	G		
	GCC	TGG	TAC	CAG	CAG	AAA	CCT	GGC	CAG	GCT	CCC	AGG	CTC	CTC	ATC	TAT	GGT		
	CDR2																		
154	A	S	S	R	A	T	G	I	P	D	R	F	S	G	S	G	S		
	GCA	TCC	AGC	AGG	GCC	ACT	GGC	ATC	CCA	GAC	AGG	TTC	AGT	GGC	AGT	GGG	TCT		
205	G	T	D	F	T	L	T	I	S	R	L	E	P	E	D	F	A		
	GGG	ACA	GAC	TTC	ACT	CTC	ACC	ATC	AGC	AGA	CTG	GAG	CCT	GAA	GAT	TTT	GCA		
					CDR3														
256	V	Y	Y	C	Q	Q	Y	G	S	S	P	I	T	F	G	Q	G		
	GTG	TAT	TAC	TGT	CAG	CAG	TAT	GGT	AGC	TCA	CCG	ATC	ACC	TTC	GGC	CAA	GGG		
307	T	R	L	E	I	K													
	ACA	CGA	CTG	GAG	ATT	AAA													

20/78
FIG. 6C

3G4_NT_VH1

ATGGAGTTTGGGCTGAGCTGGGTTTTCTTGTTGCTATTATAAAAGGTGTCCAGTGTCAGGTGCAGCTGGTGGAG
TCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTCAGTGAC
TACTACATGAGCTGGATCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTTTCATTCATTAGTACTAGTGGTAGT
ATCATATACTACGCAGACTCTGTGAAGGGCCGATTACCATCTCCAGGGACAACGCCAAGAACTCACTGTATCTG
CAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGAAGGGTATAGCAGCAGCTGGTCC
TACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA

3G4_AA_VH1

MEFGLSWVFLVAIIKGVQCQVQLVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPKGLEWVSFISTSGS
IIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAREGYSSWSYYYGMDVWGQGTTVTVSS

3G4_NT_VK1

ATGGAAACCCAGCGCAGCTTCTCTTCCTCCTGCTACTCTGGCTCCCAGATACCACCGGAGAAATTGTGTTGACG
CAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGC
AGCAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCAGCAGG
GCCACTGGCATCCCAGACAGGTTCACTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAG
CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGCTCACCGATCACCTTCGGCCAAGGGACACGACTG
GAGATTAA

3G4_AA_VK1

METPAQLLFLLLLWLDPDTTGEIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSR
ATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPITFGQGTREIK

Anti-TIM-3 17C8 VH1

D segment: 6-19

J segment: JH6b

1	Q	V	Q	L	V	E	S	G	G	G	L	V	K	P	G	G	S		
	CAG	GTG	CAG	CTG	GTG	GAG	TCT	GGG	GGA	GGC	TTG	GTC	AAG	CCT	GGA	GGG	TCC		
52	L	R	L	S	C	A	A	S	G	F	T	F	S	CDR1					
	CTG	AGA	CTC	TCC	TGT	GCA	GCC	TCT	GGA	TTC	ACC	TTC	AGT	GAC	TAC	TAC	ATG		
103	S	W	I	R	Q	A	P	G	K	G	L	E	W	V	S	F	I		
	AGC	TGG	ATC	CGC	CAG	GCT	CCA	GGG	AAG	GGG	CTG	GAG	TGG	GTT	TCA	TTC	ATT		
154	CDR2																	R	F
	S	S	S	G	S	I	I	Y	Y	A	D	S	V	K	G	CGA	TTC		
	AGT	AGT	AGT	GGT	AGT	ATC	ATA	TAC	TAC	GCA	GAC	TCT	GTG	AAG	GGC				
205	T	I	S	R	D	N	A	K	N	S	L	Y	L	Q	M	N	S		
	ACC	ATC	TCC	AGG	GAC	AAC	GCC	AAG	AAC	TCA	CTG	TAT	CTG	CAA	ATG	AAC	AGC		
256														CDR3					
	L	R	A	E	D	T	A	V	Y	Y	C	A	R	D	G	Y	S		
	CTG	AGA	GCC	GAG	GAC	ACG	GCT	GTG	TAT	TAC	TGT	GCG	AGA	GAT	GGG	TAT	AGC		
307	S	G	W	E	Y	Y	G	M	D	V	W	G	Q	G	T	T	V		
	AGT	GGC	TGG	GAG	TAC	TAC	GGT	ATG	GAC	GTC	TGG	GGC	CAA	GGG	ACC	ACG	GTC		
358	T	V	S	S															
	ACC	GTC	TCC	TCA															

J segment: JK4

23/78
FIG. 7C

17C8_NT_VH1

ATGGAGTTTGGGCTGAGCTGGGTTTTCTTGTTGCTATTATAAAAGGTGTCCAGTGTCAGGTGCAGCTGGTGGAG
TCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTCAGTGAC
TACTACATGAGCTGGATCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTTTCATTCATTAGTAGTAGTGGTAGT
ATCATATACTACGCAGACTCTGTGAAGGGCCGATTACCATCTCCAGGGACAACGCCAAGAACTCACTGTATCTG
CAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATGGGTATAGCAGTGGCTGGGAG
TACTACGGTATGGACGTCTGGGGCCAAGGGACCAGGTACCGTCTCCTCA

17C8_AA_VH1

MEFGLSWVFLVAIIKGVQCQVQLVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPKGLEWVSFISSSGS
IIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDGYSSGWEYYGMDVWGQGT'TVTVSS

17C8_NT_VK1

ATGGAAACCCAGCGCAGCTTCTCTTCTCCTGCTACTCTGGCTCCCAGATACCACCGGAGAAATTGTGTTGACG
CAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGC
AGCAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCAGCAGG
GCCACTGGCATCCCAGACAGGTTCACTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAG
CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGCTCACCGCTCACTTTCGGCGGAGGGACCAAGGTG
GAGATCAAA

17C8_AA_VK1

METPAQLLFLLLLWLPD'TTGEIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSR
ATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQYQYSSPLTFGGGT'KVEIK

FIG. 8A

Sequence Alignment for Heavy Chain Variable Regions

	FR1	CDR1	FR2	CDR2	
13A3	QLQLQESGPGLVKPSETLSLTCTVSGGSIS	SRSYYWGWIRQPPGKGLEWIGSI	YIYSGFT-		59
8B9	QVQLQESGPGLVKPSETLSLTCTVSGGSIS	--RHYWNWIRQPPGKGLEWIGYI	HYSGST-		57
8C4	QVQLQESGPGLVKPSETLSLTCTVSGGSIS	--RYYWSWIRQPPGKGLEWIGYI	HYTGST-		57
17C3	QVQLVQSGAEVKKPGASVKVSKASGYTFT	--SYMHVWRQAPGGGLEWMGI	INPRGDSI		58
9F6	QVQLVESGGGLVKPGGSLRLSCAASGFTFS	--DYYMSWIRQAPGKGLEWVSFI	SGGSTI		58
3G4	QVQLVESGGGLVKPGGSLRLSCAASGFTFS	--DYYMSWIRQAPGKGLEWVSFI	STSGSII		58
17C8	QVQLVESGGGLVKPGGSLRLSCAASGFTFS	--DYYMSWIRQAPGKGLEWVSFI	SSSGSII		58
	*:** : ** : ** . :: : * . ** :::	: *	* : ** . ** : ** * : * : .	* *	

	CDR2	FR3	CDR3				
13A3	YYNP SLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAT	----	GG----	PYGDYAHWFDP	112		
8B9	NYNP SLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARD	----	TG----	YYG----	MDI	106	
8C4	NYNP SLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCATD	----	TG----	YYG----	MDV	106	
17C3	IYAQKFQGRVTIMTRDTSTSTVYME LSSLRSEDTAVYYCARD	DFYGS	GN Y-YYG----	MDV	112		
9F6	YYADSVKGRFTISRDNAKNSLFLQMNSLRVEDTAVYYCARD	DGYSS	GWY-YYG----	MDV	112		
3G4	YYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARD	EGYSS	SWSYYYG----	MDV	113		
17C8	YYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARD	DGYSS	SGWE-YYG----	MDV	112		
	* *	* . * : : *	: : : . * :	*****	.	**	: *

	FR4	
13A3	WGQGT LVT VSS	123
8B9	WGQGT T V T VSS	117
8C4	WGQGT T V T VSS	117
17C3	WGQGT T V T VSS	123
9F6	WGQGT A V T VSS	123
3G4	WGQGT T V T VSS	124
17C8	WGQGT T V T VSS	123
	*****	*****

FIG. 8B

VH Region Sequence Designation

SEQ ID NO:									
	VH	CDR1	CDR2	CDR3	VH Variants				
13A3.	34	41	46	53	112 (N60Q)	113 (N60S)	114 (N60A)	115 (D101E)	116 (P102V)
					117 (P102Y)	118 (P102L)	119 (N60Q, P102Y)	364 (N60Q, D101E)	
8B9.	35	42	47	54	120 (S61P)				
8C4.	36	43	48	55					
17C3.	37	44	49	56					
9F6.	38	45	50	57	121 (A108T)				
3G4.	39	45	51	58					
17C8.	40	45	52	59					

Sequence Alignment for Light Chain Variable Regions

	FR1	CDR1	FR2	CDR2	
13A3	EIVLTQSPGTL	SLSPGERATL	SCRASQSVSSSYLA	WYQKPGQAPRLLI	YGASSRATGIP 60
17C3	EIVLTQSPGTL	SLSPGERATL	SCRASQSVSSSYLA	WYQKPGQAPRLLI	YGASSRATGIP 60
3G4	EIVLTQSPGTL	SLSPGERATL	SCRASQSVSSSYLA	WYQKPGQAPRLLI	YGASSRATGIP 60
8B9	EIVLTQSPGTL	SLSPGERATL	SCRASQSVSSSYLA	WYQKPGQAPRLLI	YGASSRATGIP 60
8C4	EIVLTQSPGTL	SLSPGERATL	SCRASQSVSSSYLA	WYQKPGQAPRLLI	YGASSRATGIP 60
9F6_VK3	EIVLTQSPGTL	SLSPGERATL	SCRASQSVSSSYLA	WYQKPGQAPRLLI	YGASSRATGIP 60
17C8	EIVLTQSPGTL	SLSPGERATL	SCRASQSVSSSYLA	WYQKPGQAPRLLI	YGASSRATGIP 60
9F6_VK2	EIVLTQSPGTL	SLSPGERATL	SCRASQSVSSSYLA	WYQKPGQAPRLLI	YGASSRATGIP 60
9F6_VK1	AIQLTQSPSSL	SASVGD	RVTTITCRASQGISSA-L	AWYQKPGKAPKLLI	YDASSLES
	* *****.:** * *:*.:*****.:*: *****:*.**:****.*** :*:*				
	FR3	CDR3	FR4		
13A3	DRFSGSGSGTDFTLTISRLEPEDFAVYYC	QQYGSSPIT	FGQGTRLEIK	108	
17C3	DRFSGSGSGTDFTLTISRLEPEDFAVYYC	QQYGSSPIT	FGQGTRLEIK	108	
3G4	DRFSGSGSGTDFTLTISRLEPEDFAVYYC	QQYGSSPIT	FGQGTRLEIK	108	
8B9	DRFSGSGSGTDFTLTISRLEPEDFAVYYC	QQYGSSPLT	FGGGTKVEIK	108	
8C4	DRFSGSGSGTDFTLTISRLEPEDFAVYYC	QQYGSSPLT	FGGGTKVEIK	108	
9F6_VK3	DRFSGSGSGTDFTLTISRLEPEDFAVYYC	QQYGSSPLT	FGGGTKVEIK	108	
17C8	DRFSGSGSGTDFTLTISRLEPEDFAVYYC	QQYGSSPLT	FGGGTKVEIK	108	
9F6_VK2	DRFSGSGSGTDFTLTISRLEPEDFAVYYC	QQYGSS-LT	FGGGTKVEIK	107	
9F6_VK1	SRFSGSGSGTDFTLTISLQPEDFATYYC	QQFNSYPR	TFGQGT	KVEIK 107	
	.*****:***** *:*****.*****.* *** **:***				

FIG. 9B

Light Chain Sequence Designation

	SEQ ID NO:			
	VL	CDR1	CDR2	CDR3
13A3	60	64	66	68
8B9	61	64	66	69
8C4	61	64	66	69
17C3	60	64	66	68
9F6 (VK1)	62	65	67	70
9F6 (VK2)	63	64	66	71
9F6 (VK3)	61	64	66	69
3G4	60	64	66	68
17C8.	61	64	66	69

26/78
FIG. 10

Sequence alignment of the heavy chain of 13A3.IgG1.3f and variants

TIM3.5	<u>QLQLQESGPGLVKVPSETLSLTCTVSGGSISSRSYYWGWIRQPPGKGLEWIGSIYYSGFTY</u>
TIM3.11	<u>QLQLQESGPGLVKVPSETLSLTCTVSGGSISSRSYYWGWIRQPPGKGLEWIGSIYYSGFTY</u>
TIM3.12	<u>QLQLQESGPGLVKVPSETLSLTCTVSGGSISSRSYYWGWIRQPPGKGLEWIGSIYYSGFTY</u>
TIM3.13	<u>QLQLQESGPGLVKVPSETLSLTCTVSGGSISSRSYYWGWIRQPPGKGLEWIGSIYYSGFTY</u>
TIM3.10	<u>QLQLQESGPGLVKVPSETLSLTCTVSGGSISSRSYYWGWIRQPPGKGLEWIGSIYYSGFTY</u>
TIM3.18	<u>QLQLQESGPGLVKVPSETLSLTCTVSGGSISSRSYYWGWIRQPPGKGLEWIGSIYYSGFTY</u>
TIM3.14	<u>QLQLQESGPGLVKVPSETLSLTCTVSGGSISSRSYYWGWIRQPPGKGLEWIGSIYYSGFTY</u>
TIM3.16	<u>QLQLQESGPGLVKVPSETLSLTCTVSGGSISSRSYYWGWIRQPPGKGLEWIGSIYYSGFTY</u>
TIM3.15	<u>QLQLQESGPGLVKVPSETLSLTCTVSGGSISSRSYYWGWIRQPPGKGLEWIGSIYYSGFTY</u>
TIM3.17	<u>QLQLQESGPGLVKVPSETLSLTCTVSGGSISSRSYYWGWIRQPPGKGLEWIGSIYYSGFTY</u>

TIM3.5	<u>YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCATGGPYGDYAHWFDPWGQGLT</u>
TIM3.11	<u>YPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCATGGPYGDYAHWFDPWGQGLT</u>
TIM3.12	<u>YAPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCATGGPYGDYAHWFDPWGQGLT</u>
TIM3.13	<u>YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCATGGPYGDYAHWFDPWGQGLT</u>
TIM3.10	<u>YQPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCATGGPYGDYAHWFDPWGQGLT</u>
TIM3.18	<u>YQPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCATGGPYGDYAHWFDPWGQGLT</u>
TIM3.14	<u>YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCATGGPYGDYAHWFDPWGQGLT</u>
TIM3.16	<u>YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCATGGPYGDYAHWFDPWGQGLT</u>
TIM3.15	<u>YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCATGGPYGDYAHWFDPWGQGLT</u>
TIM3.17	<u>YQPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCATGGPYGDYAHWFDPWGQGLT</u>
	* ***** :
TIM3.5	<u>VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL</u>
TIM3.11	<u>VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL</u>
TIM3.12	<u>VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL</u>
TIM3.13	<u>VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL</u>
TIM3.10	<u>VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL</u>
TIM3.18	<u>VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL</u>
TIM3.14	<u>VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL</u>
TIM3.16	<u>VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL</u>
TIM3.15	<u>VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL</u>
TIM3.17	<u>VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL</u>

TIM3.5	<u>QSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEA</u>
TIM3.11	<u>QSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEA</u>
TIM3.12	<u>QSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEA</u>
TIM3.13	<u>QSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEA</u>
TIM3.10	<u>QSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEA</u>
TIM3.18	<u>QSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEA</u>
TIM3.14	<u>QSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEA</u>
TIM3.16	<u>QSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEA</u>
TIM3.15	<u>QSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEA</u>
TIM3.17	<u>QSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEA</u>

TIM3.5	<u>EGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE</u>
TIM3.11	<u>EGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE</u>
TIM3.12	<u>EGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE</u>
TIM3.13	<u>EGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE</u>
TIM3.10	<u>EGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE</u>
TIM3.18	<u>EGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE</u>
TIM3.14	<u>EGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE</u>
TIM3.16	<u>EGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE</u>
TIM3.15	<u>EGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE</u>
TIM3.17	<u>EGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE</u>

27/78
FIG. 10 (Cont.)

TIM3.5 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS
TIM3.11 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS
TIM3.12 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS
TIM3.13 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS
TIM3.10 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS
TIM3.18 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS
TIM3.14 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS
TIM3.16 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS
TIM3.15 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS
TIM3.17 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS

TIM3.5 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK
TIM3.11 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK
TIM3.12 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK
TIM3.13 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK
TIM3.10 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK
TIM3.18 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK
TIM3.14 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK
TIM3.16 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK
TIM3.15 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK
TIM3.17 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK

TIM3.5 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
TIM3.11 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
TIM3.12 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
TIM3.13 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
TIM3.10 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
TIM3.18 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
TIM3.14 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
TIM3.16 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
TIM3.15 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
TIM3.17 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

28/78
FIG. 11**Sequence alignment of the heavy chain of 9F6.IgG1.3f and variant (A108T)**

9F6	<u>QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSFISGGGSTIYY</u>
TIM3.7	<u>QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSFISGGGSTIYY</u> *****
9F6	<u>ADSVKGRFTISRDNAKNSLFLQMNSLRVEDTAVYYCARDGYSSGWYYYGMDVWGQGTAVT</u>
TIM3.7	<u>ADSVKGRFTISRDNAKNSLFLQMNSLRVEDTAVYYCARDGYSSGWYYYGMDVWGQGTAVT</u> *****;
9F6	<u>VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL</u>
TIM3.7	<u>VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL</u> *****
9F6	<u>QSSGLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEA</u>
TIM3.7	<u>QSSGLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEA</u> *****
9F6	<u>EGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE</u>
TIM3.7	<u>EGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE</u> *****
9F6	<u>QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS</u>
TIM3.7	<u>QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS</u> *****
9F6	<u>REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK</u>
TIM3.7	<u>REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK</u> *****
9F6	<u>SRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK</u>
TIM3.7	<u>SRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK</u> *****

29/78
FIG. 12**Sequence alignment of the heavy chain of 8B9.IgG1.3f and variant (S61P)**

8B9	<u>QVQLQESGPGLVKPSSETLSLTCTVSGGSISRHYWNWIRQPPGKGLEWIGYIHYSGSTNYN</u>
TIM3.8	<u>QVQLQESGPGLVKPSSETLSLTCTVSGGSISRHYWNWIRQPPGKGLEWIGYIHYSGSTNYN</u> *****
8B9	<u>SSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDTGYYGMDIWGQGTTVTVSSAST</u>
TIM3.8	<u>PSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDTGYYGMDIWGQGTTVTVSSAST</u> .******
8B9	KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY
TIM3.8	KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY *****
8B9	SLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAEGAPSV
TIM3.8	SLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAEGAPSV *****
8B9	FLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
TIM3.8	FLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY *****
8B9	RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTK
TIM3.8	RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTK *****
8B9	NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG
TIM3.8	NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG *****
8B9	NVFSCSVMHEALHNHYTQKSLSLSPGK
TIM3.8	NVFSCSVMHEALHNHYTQKSLSLSPGK *****

FIG. 13

H.n.*	Rec. Ab name	Heavy chain						Light chain					
		HC	VH	CDR1	CDR2	CDR3	HC isotype	LC	VL	CDR1	CDR2	CDR3	LC isotype
13A3	-	301, 302	34	41	46	53	IgG4	29	VK1	60	66	68	hKappa
-	TIM3.5-IgG1.1f	1, 8*					IgG1.1f						
	13A3-IgG1.1f						IgG1.1f						
	13A3-IgG1.3f	15,22					IgG1.3f						
	13A3-IgG4P	303, 304					IgG4						
	TIM3.10-IgG1.1f	72, 82	112		122		IgG1.1f						
	(13A3 VH-N60Q)												
	TIM3.10-IgG1.3f	92, 102					IgG1.3f						
	TIM3.10-IgG4P	305, 306					IgG4P						
	TIM3.11-IgG1.1f	73, 83	113		123		IgG1.1f						
	(13A3 VH-N60S)												
	TIM3.11-IgG1.3f	93, 103					IgG1.3f						
	TIM3.11-IgG4P	307, 308					IgG4P						
	TIM3.12-IgG1.1f	74, 84	114		124		IgG1.1f						
	(13A3 VH-N60A)												
	TIM3.12-IgG1.3f	94, 104					IgG1.3f						
	TIM3.12-IgG4P	309, 310					IgG4P						
	TIM3.13-IgG1.1f	75, 85	115		46	126	IgG1.1f						
	(13A3 VH-D101E)												
	TIM3.13-IgG1.3f	95, 105					IgG1.3f						
	TIM3.13-IgG4P	311, 312					IgG4P						
	TIM3.14-IgG1.1	76, 86	116			127	IgG1.1f						
	(13A3 VH-P102V)												
	TIM3.14-IgG1.3f	96, 106					IgG1.3f						
	TIM3.14-IgG4P	313, 314					IgG4P						
	TIM3.15-IgG1.1f	77, 87	117			128	IgG1.1f						
	(13A3 VH-P102Y)												
	TIM3.15-IgG1.3f	97, 107					IgG1.3f						
	TIM3.15-IgG4P	315, 316					IgG4P						
	TIM3.16-IgG1.1f	78, 88	118			129	IgG1.1f						
	(13A3 VH-P102L)												
	TIM3.16-IgG1.3f	98, 108					IgG1.3f						

FIG. 13 (Cont.)

H.n.*	Rec. Ab name	Heavy chain						Light chain					
		HC	VH	CDR1	CDR2	CDR3	HC isotype	LC	VL	CDR1	CDR2	CDR3	LC isotype
	TIM3.16-IgG4P	317, 318					IgG4P						
	TIM3.17-IgG1.1f (13A3-VH-N60Q, P102Y)	79, 89	119		122	128	IgG1.1f						
	TIM3.17-IgG1.3f	99, 109					IgG1.3f						
	TIM3.17-IgG4P	319, 320					IgG4P						
	TIM3.18-IgG1.1f (13A3-VH-N60Q, D101E)	349, 350	364			126	IgG1.1f						
	TIM3.18-IgG1.3f (13A3-VH-N60Q, D101E)	351, 352					IgG1.3f						
	TIM3.18-IgG4P (13A3-VH-N60Q, D101E)	353, 354					IgG4P						
889	-	321, 322	35	42	47	54	IgG1za	30	VK1			69	
	889-IgG1.1f	2,9					IgG1.1f						
	889-IgG1.3f	16,23					IgG1.3f						
	889-IgG4P	323, 324					IgG4P						
	TIM3.8-IgG1.1f (8B9 VH S61P)	80,90	120		125		IgG1.1f						
	TIM3.8-IgG1.3f	100,110					IgG1.3f						
	TIM3.8-IgG4P	325, 326					IgG4P						
8C4	-	327, 328	36	43	48	55	IgG1za						
	TIM3.6-IgG1.1f (8C4)	3,10					IgG1.1f						
	TIM3.6-IgG1.3f	17,24					IgG1.3f						
	TIM3.6-IgG4P	329, 330					IgG4P						
17C3	-	331, 332	37	44	49	56	IgG1za	29	VK1			68	

FIG. 13 (Cont.)

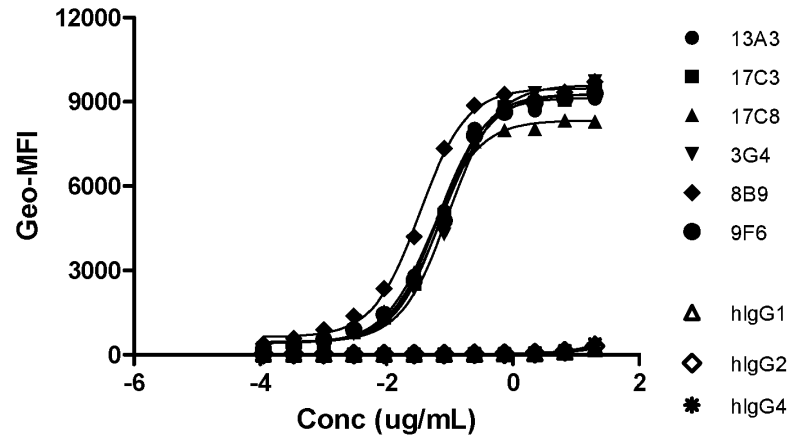
H.n.*	Rec. Ab name	Heavy chain						Light chain					
		HC	VH	CDR1	CDR2	CDR3	HC isotype	LC	VL	CDR1	CDR2	CDR3	LC isotype
	TIM3.2-IgG1.1f (17C3- IgG1.1f)	4,11					IgG1.1f						
	TIM3.2-IgG1.3f	18,25					IgG1.3f						
	TIM3.2-IgG4P	333, 334					IgG4P						
9F6	-	335, 336	38	45	50	57	IgG1za	32	VK1	62	67	70	
								33	VK2	63	66	71	
								31	VK3	61		69	
-	9F6-IgG1.1f	5,12					IgG1.1f	33	VK2	63		71	
	9F6-IgG1.3f	19,26					IgG1.3f						
	9F6-IgG4P	337, 338					IgG4P						
	TIM3.7-IgG1.1f (9F6 VK2 VH-A108T)	81,91	121				IgG1.1f						
	TIM3.7-IgG1.3f	101,111					IgG1.3f						
	TIM3.7-IgG4P	339, 340					IgG4P						
3G4	-	341, 342	39		51	58	IgG1za	29	VK1	60		68	
-	TIM3.4-IgG1.1f	6,13					IgG1.1f						
	3G4-IgG1.1f												
	TIM3.4-IgG1.3f	20,27					IgG1.3f						
	TIM3.4-IgG4P	343, 344					IgG4P						

FIG. 13 (Cont.)

H.n.*	Rec. Ab name	Heavy chain					Light chain						
		HC	VH	CDR1	CDR2	CDR3	HC isotype	LC	VL	CDR1	CDR2	CDR3	LC isotype
17C8	-	345, 346	40		52	59	IgG4	30	VK1	61		69	
-	TIM3.9-IgG1.1f (17C8)	7,14					IgG1.1f						
	TIM3.9-IgG1.3f	21,28					IgG1.3f						
	TIM3.9-IgG4P	347, 348					IgG4P						

34/78
FIG. 14A

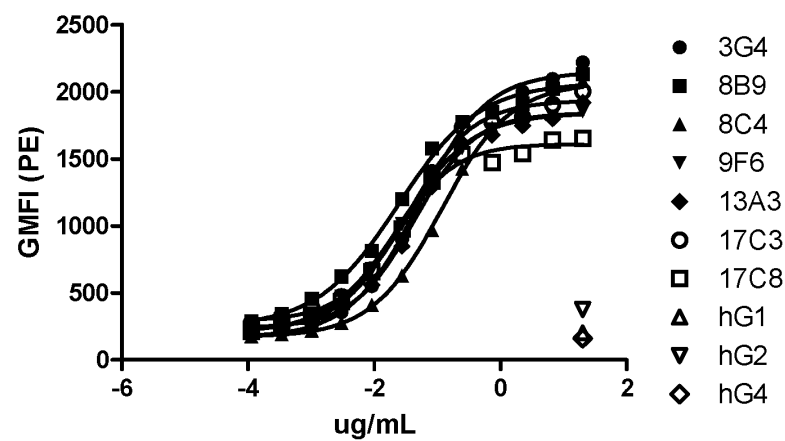
Binding of TIM-3 antibodies to CHO-huTIM3 transfectant



	EC50
13A3	0.06358
17C3	0.07208
17C8	0.05160
3G4	0.09602
8B9	0.03371
9F6	0.07401
hIgG1	39740
hIgG2	42256
hIgG4	29319

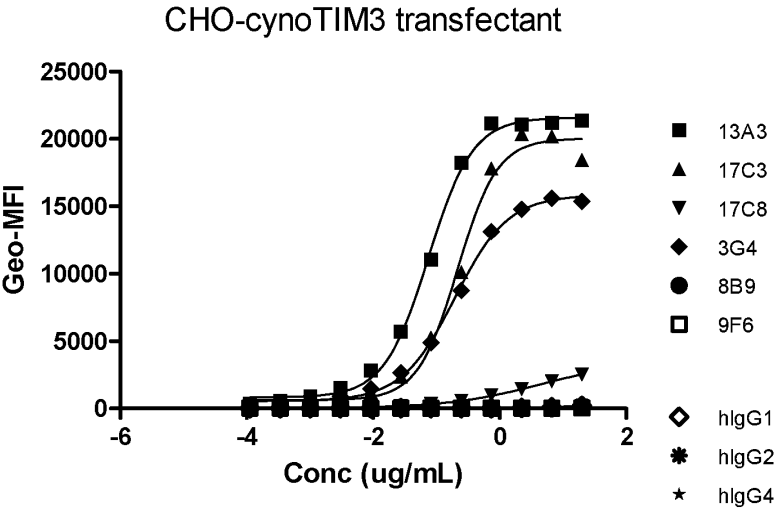
35/78
FIG. 14B

Binding of anti-TIM-3 to activated human T cells



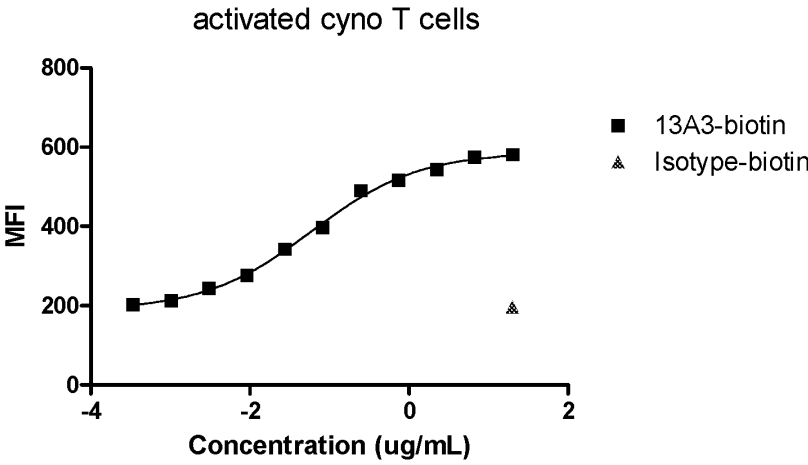
	EC50
3G4	0.05043
8B9	0.02392
8C4	0.1149
9F6	0.02660
13A3	0.04274
17C3	0.03621
17C8	0.02083

36/78
FIG. 15A



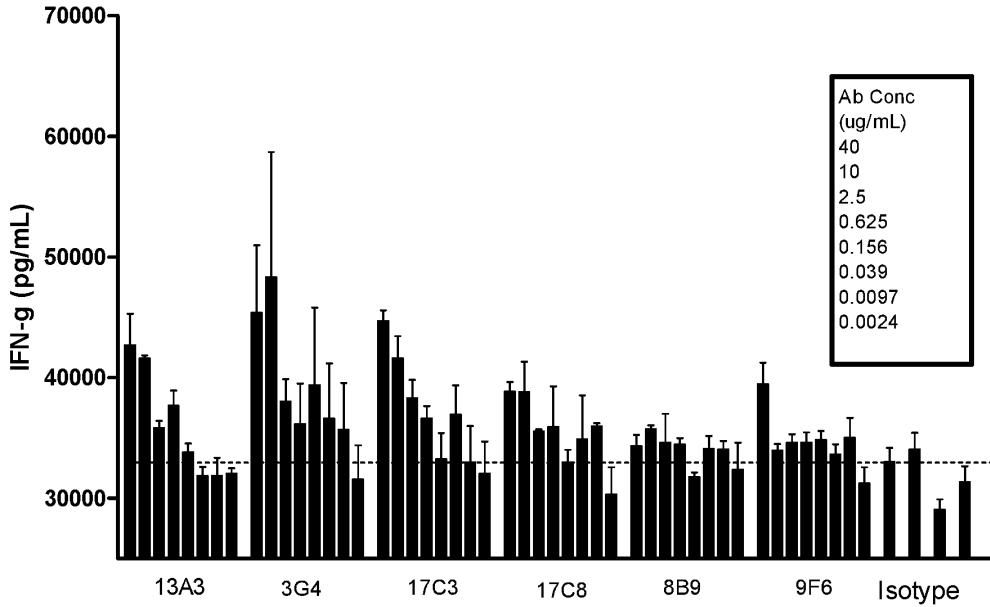
	EC50
13A3	0.07486
17C3	0.2159
17C8	4.709
3G4	0.1952
8B9	~ 2.532
9F6	~ 7.465
hlgG1	75731
hlgG2	44504
hlgG4	54134

37/78
FIG. 15B

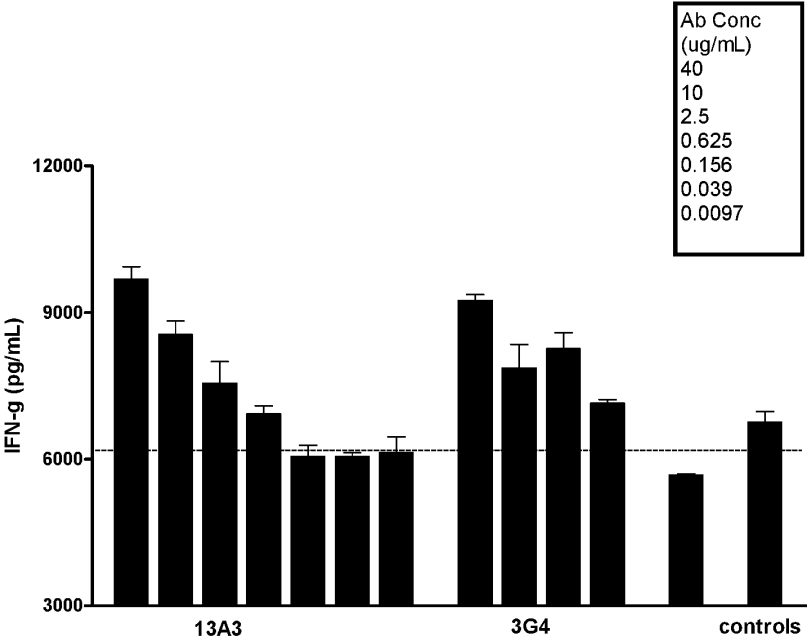


	13A3-biotin
EC50	0.06018

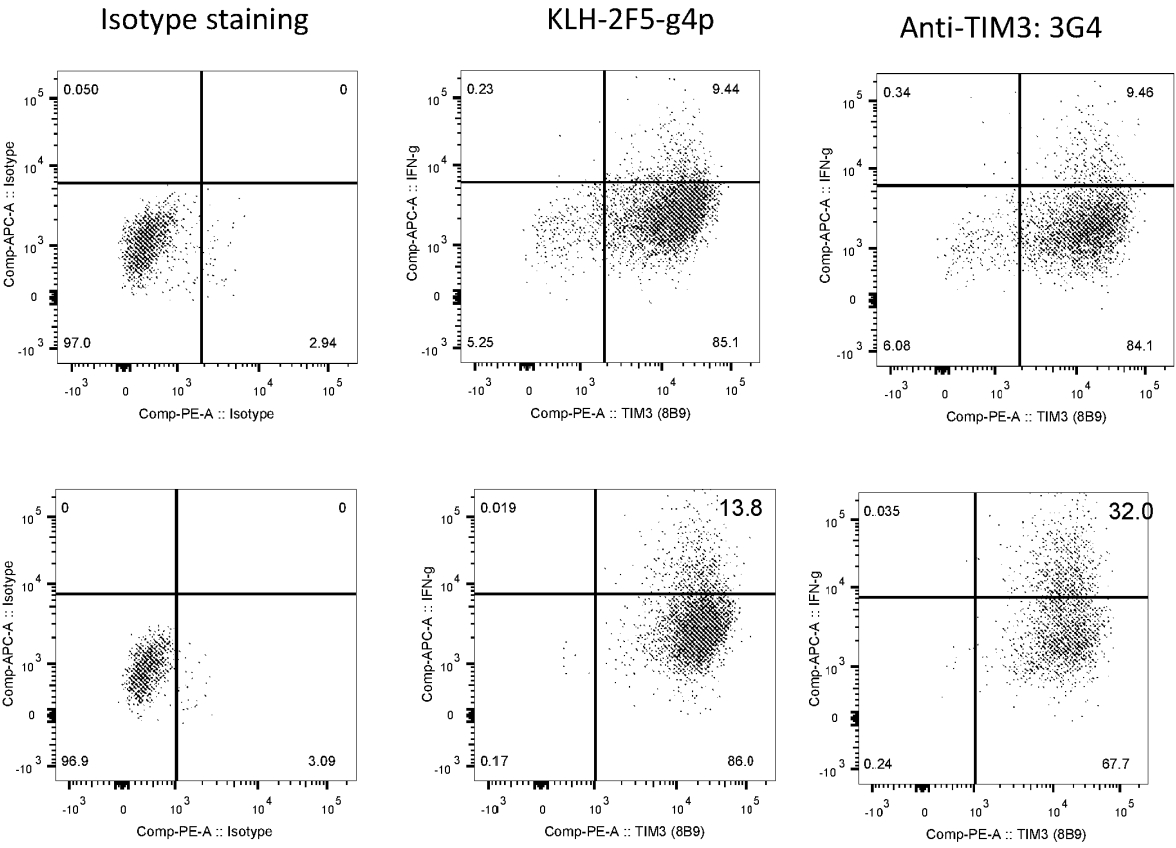
38/78
FIG. 16



39/78
FIG. 17A



Ab treatment



41/78
FIG. 18

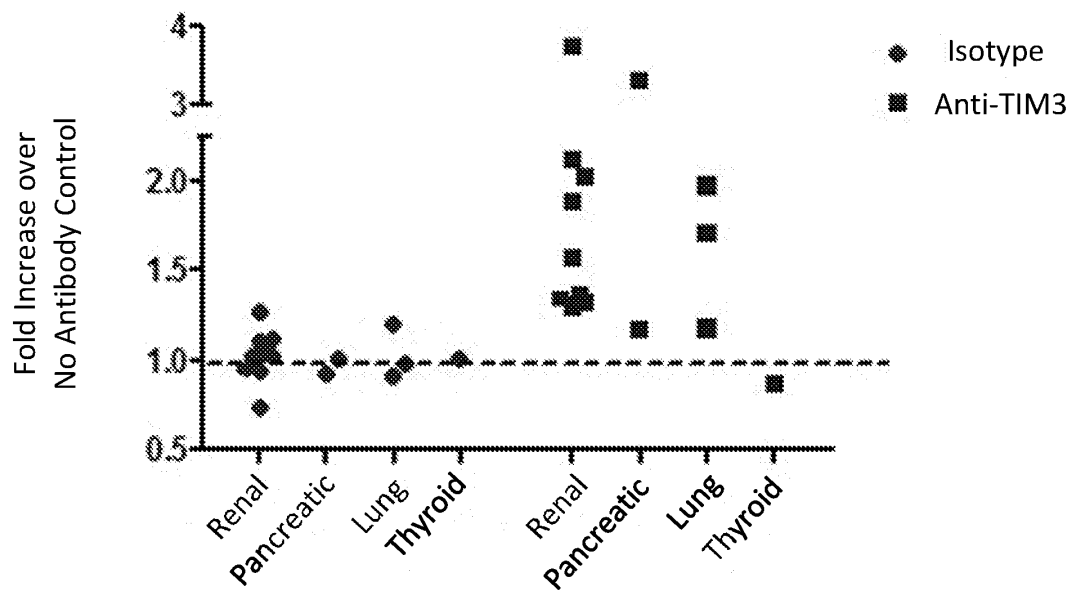


FIG. 19

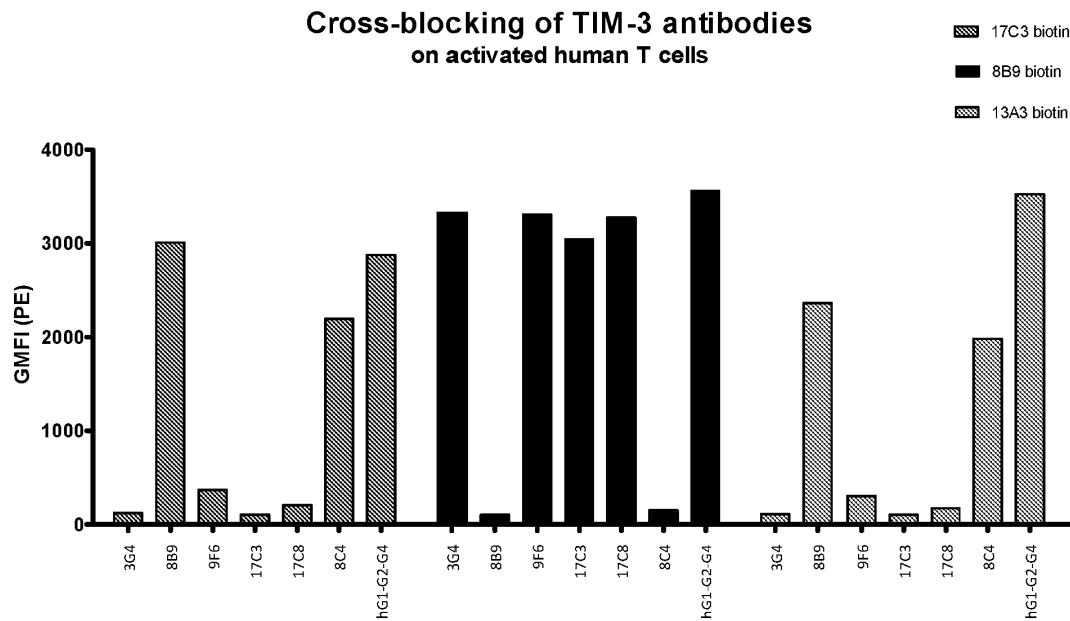


FIG. 20

Epitope residues on TIM3 protein

TIM3	10	20	30	40	50	60
13A3	<u>MFSLHPFDCV LLLLLLLLTR</u>					
3G4						CP
17C3						CPV
8B9					L	CPV
	70	80	90	100	110	120
TIM3	FECGNVVLRT	DERDVNYWTS	RYWLN G DFRK	GDVSLTIENV	TLADSGIYCC	RIQIPGIMND
13A3	FEC				<u>D</u>	R Q D
3G4	FEC				D	G M
17C3	FECG				D	G
8B9		W S R WL GD R			D	
	130	140	150	160	170	180
TIM3	EKFN L KLVIK	PAKVTPAPTR	QRDFTAAPR	MLTTRGHGPA	ETQTLGSLPD	INLTQISTLA
13A3						
3G4						
17C3						
8B9						
TIM3	190	200	210	220	230	240
	NELRDSRLAN	DLRDSGATIR	<u>IGIYIGAGIC</u>	AGLALALIFG	ALIFKWYSHS	KEKIQNLSLI
TIM3	250	260	270	280	290	300
	SLANLPPSGL	ANAVAEGIRS	EENIYTTIEN	VYEVEEPNEY	YCYVSSRQQP	SQPLGCRFAMP

43/78
FIG. 21A

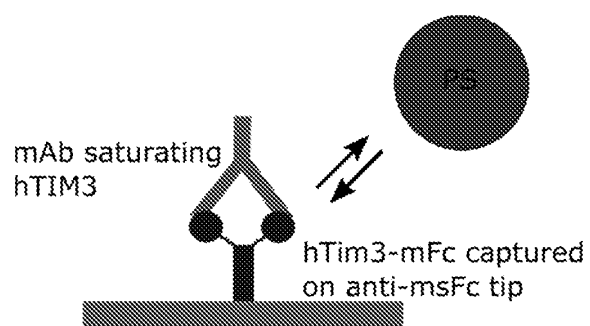
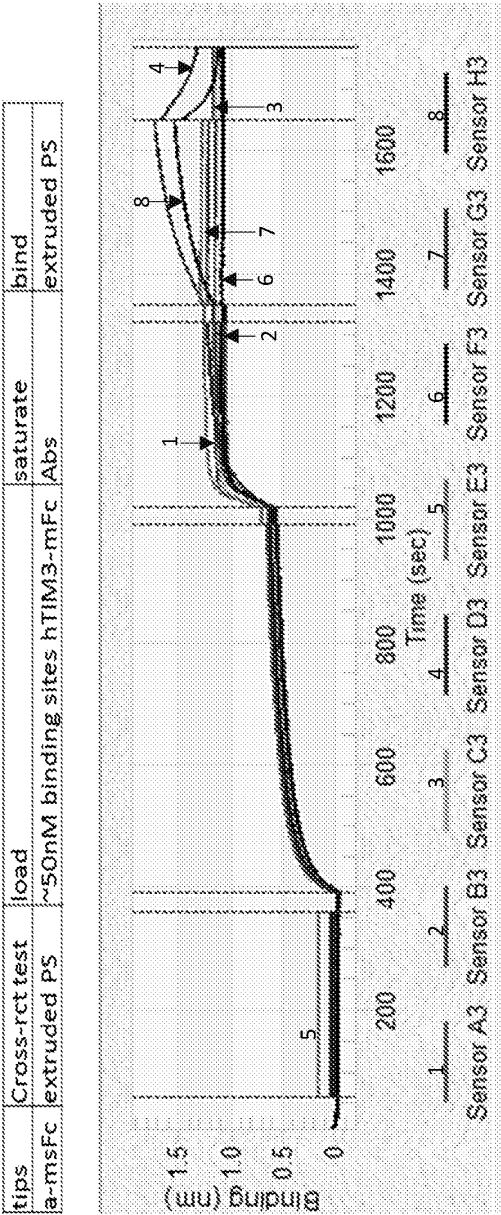


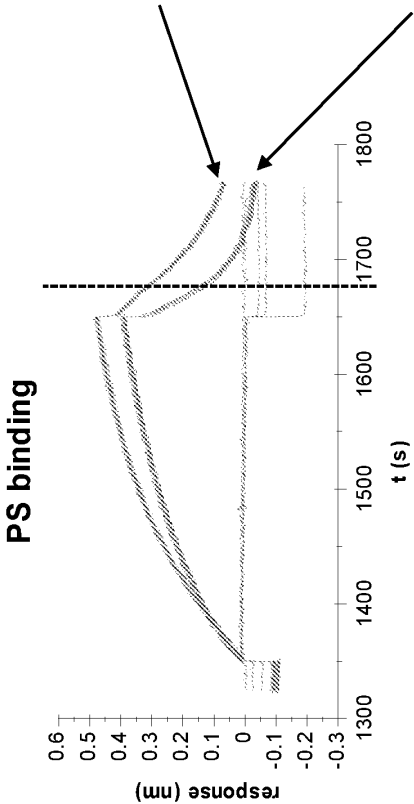
FIG. 21B



Octet HTX, 25C, PBS pH 7.4 with 1mg/mL BSA, hTIM3-ECD-mFc captured, anti-TIM3 Ab panel bound, binding of extruded PS tested at 1/2 dilution.

FIG. 21B (Cont.)

mAb	PS reponse (nm) t=1630s	PS binding
3G4	0.0061	No
Ab A	0.4725	Yes
13A3	0.0003	No
17C3	0.0077	No
17C8	-0.0039	No
Ab B	0.3803	Yes



mAb	PS reponse (nm) t=1310s	PS binding
Ab A	0.084	Yes
8B9	-0.0103	No
8C4	-0.0158	No
9F6	-0.0302	No
blank 1	0.1841	Yes
blank 2	0.1193	Yes

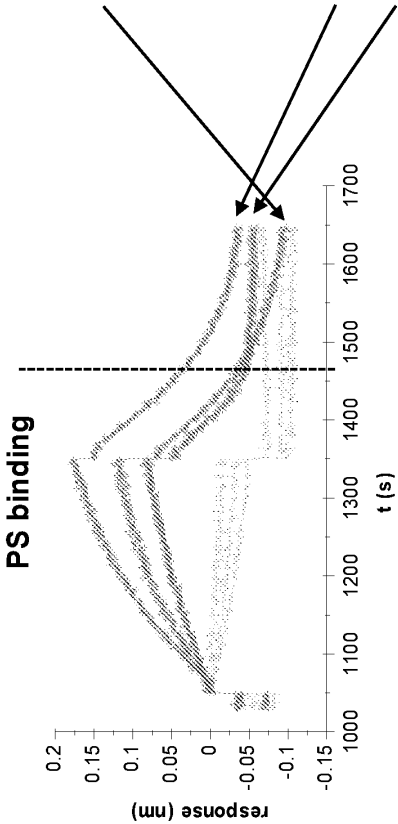


FIG. 22**Summary of Functional Activity of Anti-TIM3 Antibodies**

Clone	Binding Assay (EC50 nM)				T Cell Assay	TIL Assay	PS-TIM3 Blocking
	Human T cells (nM)	Cyno T cells (nM)	CHO-huTIM (nM)	CHO-cynoTIM3 (nM)			
13A3 (IgG4)	0.27	0.4	0.4	0.47	N/A	Dose dep	Yes
3G4 (IgG2)	0.3	Non-C	0.67	1.3	Dose dep	Dose dep	Yes
17C3 (IgG1)	0.24	Non-C	0.47	1.4	Dose dep	Dose dep	Yes
17C8 (IgG1)	0.13	Non-C	0.33	Non-C	Dose dep	Dose Dep	Yes
9F6 (IgG1)	0.13	Non-C	0.47	Non-C	Weak	No activity	Yes
8B9 (IgG4)	0.13	Non-C	0.2	Non-C	Weak	No activity	Yes
8C4 (IgG1)	0.73	Non-C	N/A	Non-C	Weak	No activity	Yes

FIG. 23**Description of Sequences Represented by the SEQ ID NOs**

SEQ ID NO.	Antibody	Description	AA/NT
1	13A3	IgG1.1f HC	Amino Acid
2	8B9	IgG1.1f HC	Amino Acid
3	8C4	IgG1.1f HC	Amino Acid
4	17C3	IgG1.1f HC	Amino Acid
5	9F6	IgG1.1f HC	Amino Acid
6	3G4	IgG1.1f HC	Amino Acid
7	17C8	IgG1.1f HC	Amino Acid
8	13A3	IgG1.1f HC (no C-terminal K)	Amino Acid
9	8B9	IgG1.1f HC (no C-terminal K)	Amino Acid
10	8C4	IgG1.1f HC (no C-terminal K)	Amino Acid
11	17C3	IgG1.1f HC (no C-terminal K)	Amino Acid
12	9F6	IgG1.1f HC (no C-terminal K)	Amino Acid
13	3G4	IgG1.1f HC (no C-terminal K)	Amino Acid
14	17C8	IgG1.1f HC (no C-terminal K)	Amino Acid
15	13A3	IgG1.3f HC	Amino Acid
16	8B9	IgG1.3f HC	Amino Acid
17	8C4	IgG1.3f HC	Amino Acid
18	17C3	IgG1.3f HC	Amino Acid
19	9F6	IgG1.3f HC	Amino Acid
20	3G4	IgG1.3f HC	Amino Acid
21	17C8	IgG1.3f HC	Amino Acid
22	13A3	IgG1.3f HC (no C-terminal K)	Amino Acid
23	8B9	IgG1.3f HC (no C-terminal K)	Amino Acid
24	8C4	IgG1.3f HC (no C-terminal K)	Amino Acid
25	17C3	IgG1.3f HC (no C-terminal K)	Amino Acid
26	9F6	IgG1.3f HC (no C-terminal K)	Amino Acid
27	3G4	IgG1.3f HC (no C-terminal K)	Amino Acid
28	17C8	IgG1.3f HC (no C-terminal K)	Amino Acid
29	13A3, 17C3, 3G4	LC	Amino Acid
30	8B9, 8C4, 17C8	LC	Amino Acid
31	9F6 (VK3)	LC	Amino Acid
32	9F6 (VK1)	LC	Amino Acid
33	9F6 (VK2)	LC	Amino Acid
34	13A3	VH	Amino Acid
35	8B9	VH	Amino Acid

FIG. 23 (Cont).

SEQ ID NO.	Antibody	Description	AA/NT
36	8C4	VH	Amino Acid
37	17C3	VH	Amino Acid
38	9F6	VH	Amino Acid
39	3G4	VH	Amino Acid
40	17C8	VH	Amino Acid
41	13A3, including the following 13A3 variants: N60Q; N60S; N60A; D101E; P102V; P102Y; P102L; N60Q and P102Y; N60Q and D101E	CDR1 (VH)	Amino Acid
42	8B9, including the 8B9 (S61P) variant	CDR1 (VH)	Amino Acid
43	8C4	CDR1 (VH)	Amino Acid
44	17C3	CDR1 (VH)	Amino Acid
45	9F6, including the 9F6 (A108T) variant; 3G4; 17C8	CDR1 (VH)	Amino Acid
46	13A3, including the following 13A3 variants: D101E, P102V, P102Y, and P102L	CDR2 (VH)	Amino Acid
47	8B9	CDR2 (VH)	Amino Acid
48	8C4	CDR2 (VH)	Amino Acid
49	17C3	CDR2 (VH)	Amino Acid
50	9F6, including the 9F6 (A108T) variant	CDR2 (VH)	Amino Acid
51	3G4	CDR2 (VH)	Amino Acid
52	17C8	CDR2 (VH)	Amino Acid
53	13A3, including the following 13A3 variants: N60Q, N60S, N60A	CDR3 (VH)	Amino Acid
54	8B9, including the 8B9 (S61P) variant	CDR3 (VH)	Amino Acid
55	8C4	CDR3 (VH)	Amino Acid
56	17C3	CDR3 (VH)	Amino Acid
57	9F6, including the 9F6 (A108T) variant	CDR3 (VH)	Amino Acid
58	3G4	CDR3 (VH)	Amino Acid

FIG. 23 (Cont).

SEQ ID NO.	Antibody	Description	AA/NT
59	17C8	CDR3 (VH)	Amino Acid
60	13A3, 17C3, 3G4	VL	Amino Acid
61	8B9, 8C4, 17C8, 9F6 (VK3)	VL	Amino Acid
62	9F6 (VK1)	VL	Amino Acid
63	9F6 (VK2)	VL	Amino Acid
64	13A3, 8B9, 8C4, 17C3, 9F6 (VK2, VK3), 3G4, 17C8	CDR1 (VL)	Amino Acid
65	9F6 (VK1)	CDR1 (VL)	Amino Acid
66	13A3, 8B9, 8C4, 17C3, 9F6 (VK2, VK3), 3G4, 17C8	CDR2 (VL)	Amino Acid
67	9F6 (VK1)	CDR2 (VL)	Amino Acid
68	13A3, 17C3, 3G4	CDR3 (VL)	Amino Acid
69	8B9, 8C4, 9F6 (VK3), 17C8	CDR3 (VL)	Amino Acid
70	9F6 (VK1)	CDR3 (VL)	Amino Acid
71	9F6 (VK2)	CDR3 (VL)	Amino Acid
72	13A3 (N60Q)	IgG1.1f HC	Amino Acid
73	13A3 (N60S)	IgG1.1f HC	Amino Acid
74	13A3 (N60A)	IgG1.1f HC	Amino Acid
75	13A3 (D101E)	IgG1.1f HC	Amino Acid
76	13A3 (P102V)	IgG1.1f HC	Amino Acid
77	13A3 (P102Y)	IgG1.1f HC	Amino Acid
78	13A3 (P102L)	IgG1.1f HC	Amino Acid
79	13A3 (N60Q, P102Y)	IgG1.1f HC	Amino Acid
349	13A3 (N60Q, D101E)	IgG1.1f HC	Amino Acid
80	8B9 (S61P)	IgG1.1f HC	Amino Acid
81	9F6 (A108T)	IgG1.1f HC	Amino Acid
82	13A3 (N60Q)	IgG1.1f HC (no C-terminal K)	Amino Acid
83	13A3 (N60S)	IgG1.1f HC (no C-terminal K)	Amino Acid
84	13A3 (N60A)	IgG1.1f HC (no C-terminal K)	Amino Acid
85	13A3 (D101E)	IgG1.1f HC (no C-terminal K)	Amino Acid
86	13A3 (P102V)	IgG1.1f HC (no C-terminal K)	Amino Acid
87	13A3 (P102Y)	IgG1.1f HC (no C-terminal K)	Amino Acid
88	13A3 (P102L)	IgG1.1f HC (no C-terminal K)	Amino Acid
89	13A3 (N60Q, P102Y)	IgG1.1f HC (no C-terminal K)	Amino Acid
350	13A3 (N60Q, D101E)	IgG1.1f HC (no C-terminal K)	Amino Acid

FIG. 23 (Cont).

SEQ ID NO.	Antibody	Description	AA/NT
90	8B9 (S61P)	IgG1.1f HC (no C-terminal K)	Amino Acid
91	9F6 (A108T)	IgG1.1f HC (no C-terminal K)	Amino Acid
92	13A3 (N60Q)	IgG1.3f HC	Amino Acid
93	13A3 (N60S)	IgG1.3f HC	Amino Acid
94	13A3 (N60A)	IgG1.3f HC	Amino Acid
95	13A3 (D101E)	IgG1.3f HC	Amino Acid
96	13A3 (P102V)	IgG1.3f HC	Amino Acid
97	13A3 (P102Y)	IgG1.3f HC	Amino Acid
98	13A3 (P102L)	IgG1.3f HC	Amino Acid
99	13A3 (N60Q, P102Y)	IgG1.3f HC	Amino Acid
351	13A3 (N60Q, D101E)	IgG1.3f HC	Amino Acid
100	8B9 (S61P)	IgG1.3f HC	Amino Acid
101	9F6 (A108T)	IgG1.3f HC	Amino Acid
102	13A3 (N60Q)	IgG1.3f HC (no C-terminal K)	Amino Acid
103	13A3 (N60S)	IgG1.3f HC (no C-terminal K)	Amino Acid
104	13A3 (N60A)	IgG1.3f HC (no C-terminal K)	Amino Acid
105	13A3 (D101E)	IgG1.3f HC (no C-terminal K)	Amino Acid
106	13A3 (P102V)	IgG1.3f HC (no C-terminal K)	Amino Acid
107	13A3 (P102Y)	IgG1.3f HC (no C-terminal K)	Amino Acid
108	13A3 (P102L)	IgG1.3f HC (no C-terminal K)	Amino Acid
109	13A3 (N60Q, P102Y)	IgG1.3f HC (no C-terminal K)	Amino Acid
352	13A3 (N60Q, D101E)	IgG1.3f HC (no C-terminal K)	Amino Acid
110	8B9 (S61P)	IgG1.3f HC (no C-terminal K)	Amino Acid
111	9F6 (A108T)	IgG1.3f HC (no C-terminal K)	Amino Acid
112	13A3 (N60Q)	VH	Amino Acid
113	13A3 (N60S)	VH	Amino Acid
114	13A3 (N60A)	VH	Amino Acid
115	13A3 (D101E)	VH	Amino Acid
116	13A3 (P102V)	VH	Amino Acid
117	13A3 (P102Y)	VH	Amino Acid
118	13A3 (P102L)	VH	Amino Acid
119	13A3 (N60Q, P102Y)	VH	Amino Acid
364	13A3 (N60Q, D101E)	VH	Amino Acid
120	8B9 (S61P)	VH	Amino Acid
121	9F6 (A108T)	VH	Amino Acid

FIG. 23 (Cont).

SEQ ID NO.	Antibody	Description	AA/NT
122	13A3 (N60Q); 13A3 (N60Q, P102Y); 13A3 (N60Q, D101E)	CDR2 (VH)	Amino Acid
123	13A3 (N60S)	CDR2 (VH)	Amino Acid
124	13A3 (N60A)	CDR2 (VH)	Amino Acid
125	8B9 (S61P)	CDR2 (VH)	Amino Acid
126	13A3 (D101E); 13A3 (N60Q, D101E)	CDR3 (VH)	Amino Acid
127	13A3 (P102V)	CDR3 (VH)	Amino Acid
128	13A3 (P102Y); 13A3 (N60Q, P102Y)	CDR3 (VH)	Amino Acid
129	13A3 (P102L)	CDR3 (VH)	Amino Acid
130	All antibodies	HC Constant Domain (IgG1.1f)	Amino Acid
131	All antibodies	HC Constant Domain (IgG1.1f) (no C-terminal K)	Amino Acid
132	All antibodies	HC Constant Domain (IgG1.3f)	Amino Acid
133	All antibodies	HC Constant Domain (IgG1.3f) (no C-terminal K)	Amino Acid
134	13A3	IgG1.1f HC	Nucleotide
135	8B9	IgG1.1f HC	Nucleotide
136	8C4	IgG1.1f HC	Nucleotide
137	17C3	IgG1.1f HC	Nucleotide
138	9F6	IgG1.1f HC	Nucleotide
139	3G4	IgG1.1f HC	Nucleotide
140	17C8	IgG1.1f HC	Nucleotide
141	13A3	IgG1.1f HC (no C-terminal K)	Nucleotide
142	8B9	IgG1.1f HC (no C-terminal K)	Nucleotide
143	8C4	IgG1.1f HC (no C-terminal K)	Nucleotide
144	17C3	IgG1.1f HC (no C-terminal K)	Nucleotide
145	9F6	IgG1.1f HC (no C-terminal K)	Nucleotide
146	3G4	IgG1.1f HC (no C-terminal K)	Nucleotide
147	17C8	IgG1.1f HC (no C-terminal K)	Nucleotide
148	13A3	IgG1.3f HC	Nucleotide
149	8B9	IgG1.3f HC	Nucleotide
150	8C4	IgG1.3f HC	Nucleotide
151	17C3	IgG1.3f HC	Nucleotide
152	9F6	IgG1.3f HC	Nucleotide
153	3G4	IgG1.3f HC	Nucleotide
154	17C8	IgG1.3f HC	Nucleotide
155	13A3	IgG1.3f HC (no C-terminal K)	Nucleotide
156	8B9	IgG1.3f HC (no C-terminal K)	Nucleotide

FIG. 23 (Cont).

SEQ ID NO.	Antibody	Description	AA/NT
157	8C4	IgG1.3f HC (no C-terminal K)	Nucleotide
158	17C3	IgG1.3f HC (no C-terminal K)	Nucleotide
159	9F6	IgG1.3f HC (no C-terminal K)	Nucleotide
160	3G4	IgG1.3f HC (no C-terminal K)	Nucleotide
161	17C8	IgG1.3f HC (no C-terminal K)	Nucleotide
162	13A3, 17C3, 3G4	LC	Nucleotide
163	8B9, 8C4, 17C8	LC	Nucleotide
164	9F6 (VK3)	LC	Nucleotide
165	9F6 (VK1)	LC	Nucleotide
166	9F6 (VK2)	LC	Nucleotide
167	13A3	VH	Nucleotide
168	8B9	VH	Nucleotide
169	8C4	VH	Nucleotide
170	17C3	VH	Nucleotide
171	9F6	VH	Nucleotide
172	3G4	VH	Nucleotide
173	17C8	VH	Nucleotide
174	13A3, including the following 13A3 variants: N60Q; N60S; N60A; D101E; P102V; P102Y; P102L; N60Q and P102Y; 13A3 (N60Q, D101E)	CDR1 (VH)	Nucleotide
175	8B9, including the 8B9 (S61P) variant	CDR1 (VH)	Nucleotide
176	8C4	CDR1 (VH)	Nucleotide
177	17C3	CDR1 (VH)	Nucleotide
178	9F6, including the 9F6 (A108T) variant; 3G4; 17C8	CDR1 (VH)	Nucleotide
179	13A3, including the following 13A3 variants: D101E, P102V, P102Y, and P102L	CDR2 (VH)	Nucleotide
180	8B9	CDR2 (VH)	Nucleotide
181	8C4	CDR2 (VH)	Nucleotide
182	17C3	CDR2 (VH)	Nucleotide
183	9F6, including the 9F6 (A108T) variant	CDR2 (VH)	Nucleotide

FIG. 23 (Cont).

SEQ ID NO.	Antibody	Description	AA/NT
184	3G4	CDR2 (VH)	Nucleotide
185	17C8	CDR2 (VH)	Nucleotide
186	13A3, including the following 13A3 variants: N60Q, N60S, N60A	CDR3 (VH)	Nucleotide
187	8B9, including the 8B9 (S61P) variant	CDR3 (VH)	Nucleotide
188	8C4	CDR3 (VH)	Nucleotide
189	17C3	CDR3 (VH)	Nucleotide
190	9F6, including the 9F6 (A108T) variant	CDR3 (VH)	Nucleotide
191	3G4	CDR3 (VH)	Nucleotide
192	17C8	CDR3 (VH)	Nucleotide
193	13A3, 17C3, 3G4	VL	Nucleotide
194	8B9, 8C4, 17C8, 9F6 (VK3)	VL	Nucleotide
195	9F6 (VK1)	VL	Nucleotide
196	9F6 (VK2)	VL	Nucleotide
197	13A3, 8B9, 8C4, 17C3, 9F6 (VK2, VK3), 3G4, 17C8	CDR1 (VL)	Nucleotide
198	9F6 (VK1)	CDR1 (VL)	Nucleotide
199	13A3, 8B9, 8C4, 17C3, 9F6 (VK2, VK3), 3G4, 17C8	CDR2 (VL)	Nucleotide
200	9F6 (VK1)	CDR2 (VL)	Nucleotide
201	13A3, 17C3, 3G4	CDR3 (VL)	Nucleotide
202	8B9, 8C4, 9F6 (VK3), 17C8	CDR3 (VL)	Nucleotide
203	9F6 (VK1)	CDR3 (VL)	Nucleotide
204	9F6 (VK2)	CDR3 (VL)	Nucleotide
205	13A3 (N60Q)	IgG1.1f HC	Nucleotide
206	13A3 (N60S)	IgG1.1f HC	Nucleotide
207	13A3 (N60A)	IgG1.1f HC	Nucleotide
208	13A3 (D101E)	IgG1.1f HC	Nucleotide
209	13A3 (P102V)	IgG1.1f HC	Nucleotide
210	13A3 (P102Y)	IgG1.1f HC	Nucleotide
211	13A3 (P102L)	IgG1.1f HC	Nucleotide
212	13A3 (N60Q, P102Y)	IgG1.1f HC	Nucleotide
355	13A3 (N60Q, D101E)	IgG1.1f HC	Nucleotide

FIG. 23 (Cont).

SEQ ID NO.	Antibody	Description	AA/NT
213	8B9 (S61P)	IgG1.1f HC	Nucleotide
214	9F6 (A108T)	IgG1.1f HC	Nucleotide
215	13A3 (N60Q)	IgG1.1f HC (no C-terminal K)	Nucleotide
216	13A3 (N60S)	IgG1.1f HC (no C-terminal K)	Nucleotide
217	13A3 (N60A)	IgG1.1f HC (no C-terminal K)	Nucleotide
218	13A3 (D101E)	IgG1.1f HC (no C-terminal K)	Nucleotide
219	13A3 (P102V)	IgG1.1f HC (no C-terminal K)	Nucleotide
220	13A3 (P102Y)	IgG1.1f HC (no C-terminal K)	Nucleotide
221	13A3 (P102L)	IgG1.1f HC (no C-terminal K)	Nucleotide
222	13A3 (N60Q, P102Y)	IgG1.1f HC (no C-terminal K)	Nucleotide
356	13A3 (N60Q, D101E)	IgG1.1f HC (no C-terminal K)	Nucleotide
223	8B9 (S61P)	IgG1.1f HC (no C-terminal K)	Nucleotide
224	9F6 (A108T)	IgG1.1f HC (no C-terminal K)	Nucleotide
225	13A3 (N60Q)	IgG1.3f HC	Nucleotide
226	13A3 (N60S)	IgG1.3f HC	Nucleotide
227	13A3 (N60A)	IgG1.3f HC	Nucleotide
228	13A3 (D101E)	IgG1.3f HC	Nucleotide
229	13A3 (P102V)	IgG1.3f HC	Nucleotide
230	13A3 (P102Y)	IgG1.3f HC	Nucleotide
231	13A3 (P102L)	IgG1.3f HC	Nucleotide
232	13A3 (N60Q, P102Y)	IgG1.3f HC	Nucleotide
357	13A3 (N60Q, D101E)	IgG1.3f HC	Nucleotide
233	8B9 (S61P)	IgG1.3f HC	Nucleotide
234	9F6 (A108T)	IgG1.3f HC	Nucleotide
235	13A3 (N60Q)	IgG1.3f HC (no C-terminal K)	Nucleotide
236	13A3 (N60S)	IgG1.3f HC (no C-terminal K)	Nucleotide
237	13A3 (N60A)	IgG1.3f HC (no C-terminal K)	Nucleotide
238	13A3 (D101E)	IgG1.3f HC (no C-terminal K)	Nucleotide
239	13A3 (P102V)	IgG1.3f HC (no C-terminal K)	Nucleotide
240	13A3 (P102Y)	IgG1.3f HC (no C-terminal K)	Nucleotide
241	13A3 (P102L)	IgG1.3f HC (no C-terminal K)	Nucleotide
242	13A3 (N60Q, P102Y)	IgG1.3f HC (no C-terminal K)	Nucleotide
358	13A3 (N60Q, D101E)	IgG1.3f HC (no C-terminal K)	Nucleotide
374	13A3 (N60Q, D101E) (TIM3.18) (T168C)	IgG1.3f HC (no C-terminal K)	Nucleotide
243	8B9 (S61P)	IgG1.3f HC (no C-terminal K)	Nucleotide
244	9F6 (A108T)	IgG1.3f HC (no C-terminal K)	Nucleotide

FIG. 23 (Cont).

SEQ ID NO.	Antibody	Description	AA/NT
245	13A3 (N60Q)	VH	Nucleotide
246	13A3 (N60S)	VH	Nucleotide
247	13A3 (N60A)	VH	Nucleotide
248	13A3 (D101E)	VH	Nucleotide
249	13A3 (P102V)	VH	Nucleotide
250	13A3 (P102Y)	VH	Nucleotide
251	13A3 (P102L)	VH	Nucleotide
252	13A3 (N60Q, P102Y)	VH	Nucleotide
359	13A3 (N60Q, D101E)	VH	Nucleotide
253	8B9 (S61P)	VH	Nucleotide
254	9F6 (A108T)	VH	Nucleotide
255	13A3 (N60Q); 13A3 (N60Q, P102Y); 13A3 (N60Q, D101E)	CDR2 (VH)	Nucleotide
256	13A3 (N60S)	CDR2 (VH)	Nucleotide
257	13A3 (N60A)	CDR2 (VH)	Nucleotide
258	8B9 (S61P)	CDR2 (VH)	Nucleotide
259	13A3 (D101E)	CDR3 (VH)	Nucleotide
260	13A3 (P102V)	CDR3 (VH)	Nucleotide
261	13A3 (P102Y); 13A3 (N60Q, P102Y); 13A3 (N60Q, D101E)	CDR3 (VH)	Nucleotide
262	13A3 (P102L)	CDR3 (VH)	Nucleotide
263	All antibodies	HC Constant Domain (IgG1.1f)	Nucleotide
264	All antibodies	HC Constant Domain (IgG1.1f) (no C-terminal K)	Nucleotide
265	All antibodies	HC Constant Domain (IgG1.3f)	Nucleotide
266	All antibodies	HC Constant Domain (IgG1.3f) (no C-terminal K)	Nucleotide
267		Signal Peptide	amino acid
268		Signal Peptide	amino acid
269		Signal Peptide	amino acid
270		Signal Peptide	amino acid
271		Signal Peptide	amino acid
361		Signal Peptide (TIM3.2-TIM3.18)	amino acid
272		Signal Peptide	Nucleotide
273		Signal Peptide	Nucleotide
274		Signal Peptide	Nucleotide
275		Signal Peptide	Nucleotide
276		Signal Peptide	Nucleotide

FIG. 23 (Cont).

SEQ ID NO.	Antibody	Description	AA/NT
362		Signal Peptide (TIM3.2-TIM3.18 HC)	Nucleotide
363		Signal Peptide (TIM3.2-TIM3.18 LC)	Nucleotide
277		human IgG1 (allotypic variant)	Amino Acid
278		human IgG1 kappa light chain	Amino Acid
279		LSPGK (C-terminal end of heavy chain)	Amino Acid
280		LSPG (C-terminal end of heavy chain)	Amino Acid
281		LSP (C-terminal end of heavy chain)	Amino Acid
282		X1X2X3X4YX5X6 (VH CDR1 degenerate)	Amino Acid
283		X1IX2X3X4GX5X6X7X8YX9X10X11X12X13X14 (VH CDR2 degenerate)	Amino Acid
284		X1X2X3X4X5X6YGX7X8X9X10YGX11X12DX13X14X15X16 X17X18 (VH CDR3 degenerate)	Amino Acid
285		QQX1X2SX3X4X5T (VL CDR1 degenerate)	Amino Acid
286		TIM3 Isoform 1 (aa)	Amino Acid
287		TIM3 Isoform 2 (aa)	Amino Acid
288		TIM3 Isoform 1 (nt)	Nucleotide
289		TIM3 Isoform 2 (nt)	Nucleotide
290		Extracellular domain of TIM3	Amino Acid
291		WT human IgG1 constant domain (same as IgG1za)	Amino Acid
292		human IgG4 constant domain	Amino Acid
293		9F6 VK2 IgG1 light chain	Amino Acid
294		IgG1.1 constant domain (used in anti-TIM3 antibodies)	Amino Acid
295		IgG1.3 constant domain (used in anti-TIM3 antibodies)	Amino Acid
296		residues 37-43 of mature TIM3 ECD	Amino Acid
297		residues 57-83 of mature TIM3 ECD	Amino Acid
298		residues 90-99 of mature TIM3 ECD	Amino Acid
299		residues 1-99 of mature TIM3 ECD	Amino Acid
300		Linker	Amino Acid
360		Cynomolgus TIM3 Protein	Amino Acid
301	13A3	hIgG4 HC	Amino Acid
302	13A3	hIgG4 HC (without C-terminal K)	Amino Acid
303	TIM3.5 – 13A3	IgG4P HC	Amino Acid
304	TIM3.5 – 13A3	IgG4P HC (without C-terminal K)	Amino Acid
305	TIM3.10 – 13A3 (N60Q)	IgG4P HC	Amino Acid
306	TIM3.10 – 13A3 (N60Q)	IgG4P HC (without C-terminal K)	Amino Acid
307	TIM3.11 – 13A3 (N60S)	IgG4P HC	Amino Acid

FIG. 23 (Cont).

SEQ ID NO.	Antibody	Description	AA/NT
308	TIM3.11 – 13A3 (N60S)	IgG4P HC (without C-terminal K)	Amino Acid
309	TIM3.12 – 13A3 (N60A)	IgG4P HC	Amino Acid
310	TIM3.12 – 13A3 (N60A)	IgG4P HC (without C-terminal K)	Amino Acid
311	TIM3.13 – 13A3 (D101E)	IgG4P HC	Amino Acid
312	TIM3.13 – 13A3 (D101E)	IgG4P HC (without C-terminal K)	Amino Acid
313	TIM 3.14 – 13A3 (P102V)	IgG4P HC	Amino Acid
314	TIM 3.14 – 13A3 (P102V)	IgG4P HC (without C-terminal K)	Amino Acid
315	TIM3.15 – 13A3 (P102Y)	IgG4P HC	Amino Acid
316	TIM3.15 – 13A3 (P102Y)	IgG4P HC (without C-terminal K)	Amino Acid
317	TIM3.16 – 13A3 (P102L)	IgG4P HC	Amino Acid
318	TIM3.16 – 13A3 (P102L)	IgG4P HC (without C-terminal K)	Amino Acid
319	TIM3.17 – 13A3 (N60Q, P102Y)	IgG4P HC	Amino Acid
320	TIM3.17 – 13A3 (N60Q, P102Y)	IgG4P HC (without C-terminal K)	Amino Acid
353	TIM3.18 – 13A3 (N60Q, D101E)	IgG4P HC	Amino Acid
354	TIM3.18 – 13A3 (N60Q, D101E)	IgG4P HC (without C-terminal K)	Amino Acid
321	8B9	IgG1za HC	Amino Acid
322	8B9	IgG1za HC (without C-terminal K)	Amino Acid
323	8B9	IgG4P HC	Amino Acid
324	8B9	IgG4P HC (without C-terminal K)	Amino Acid
325	TIM3.8 – 8B9 (S61P)	IgG4P HC	Amino Acid
326	TIM3.8 – 8B9 (S61P)	IgG4P HC (without C-terminal K)	Amino Acid
327	8C4	IgG1za HC	Amino Acid
328	8C4	IgG1za HC (without C-terminal K)	Amino Acid
329	TIM3.6 – 8C4	IgG4P HC	Amino Acid
330	TIM3.6 – 8C4	IgG4P HC (without C-terminal K)	Amino Acid
331	17C3	IgG1za HC	Amino Acid
332	17C3	IgG1za HC (without C-terminal K)	Amino Acid
333	TIM3.2 – 17C3	IgG4P HC	Amino Acid
334	TIM3.2 – 17C3	IgG4P HC (without C-terminal K)	Amino Acid
335	9F6	IgG1za HC	Amino Acid

FIG. 23 (Cont).

SEQ ID NO.	Antibody	Description	AA/NT
336	9F6	IgG1za HC (without C-terminal K)	Amino Acid
337	9F6	IgG4P HC	Amino Acid
338	9F6	IgG4P HC (without C-terminal K)	Amino Acid
339	TIM3.7 – 9F6 (A108T)	IgG4P HC	Amino Acid
340	TIM3.7 – 9F6 (A108T)	IgG4P HC (without C-terminal K)	Amino Acid
341	3G4	IgG1za HC	Amino Acid
342	3G4	IgG1za HC (without C-terminal K)	Amino Acid
343	TIM3.4 – 3G4	IgG4P HC	Amino Acid
344	TIM3.4 – 3G4	IgG4P HC (without C-terminal K)	Amino Acid
345	17C8	IgG4 HC	Amino Acid
346	17C8	IgG4 HC	Amino Acid
347	TIM3.9 – 17C8	IgG4P HC	Amino Acid
348	TIM3.9 – 17C8	IgG4P HC (without C-terminal K)	Amino Acid
365	13A3	Heavy Chain Fab 6X His	Amino Acid
366	TIM3.18 – 13A3 (N60Q, D101E)	Heavy Chain ab 6X His	Amino Acid
367		Residues 49-62 of Mature Human TIM3 Extracellular Domain	Amino Acid
368		Residues 111-127 of Mature Human TIM3 Extracellular Domain	Amino Acid
369		Residues 40-62 of Mature Human TIM3 Extracellular Domain	Amino Acid
370		Residues 66-77 of Mature Human TIM3 Extracellular Domain	Amino Acid
371		Residues 78-95 of Mature Human TIM3 Extracellular Domain	Amino Acid
372		Residues 110-127 of Mature Human TIM3 Extracellular Domain	Amino Acid
373		Residues 119-127 of Mature Human TIM3 Extracellular Domain	Amino Acid
375		hTIM3-mFc	Amino Acid
376		Cyno TIM3-MycHisAvi	Amino Acid
377		hTIM3_IgV	Amino Acid
378	TIM3.18 – 13A3 (N60Q, D101E)	IgG1.3f HC with signal peptide	Amino Acid
379	TIM3.18 – 13A3 (N60Q, D101E)	IgG1.3f HC (no C-terminal K) with signal peptide	Amino Acid
380	TIM3.18 – 13A3 (N60Q, D101E)	IgG1.3f HC with signal sequence	Nucleotide
381	TIM3.18 – 13A3 (N60Q, D101E)	IgG1.3f HC (no C-terminal K) with signal sequence	Nucleotide
382	TIM3.18 – 13A3 (N60Q, D101E)	IgG1.3f HC (T168C) with signal sequence	Nucleotide

FIG. 23 (Cont).

SEQ ID NO.	Antibody	Description	AA/NT
383	TIM3.18 – 13A3 (N60Q, D101E)	IgG1.3f HC (T168C) (no C-terminal K) with signal sequence	Nucleotide
384	TIM3.18 – 13A3 (N60Q, D101E)	LC with signal peptide	Amino Acid
385	TIM3.18 – 13A3 (N60Q, D101E)	LC with signal sequence	Nucleotide

FIG. 24A

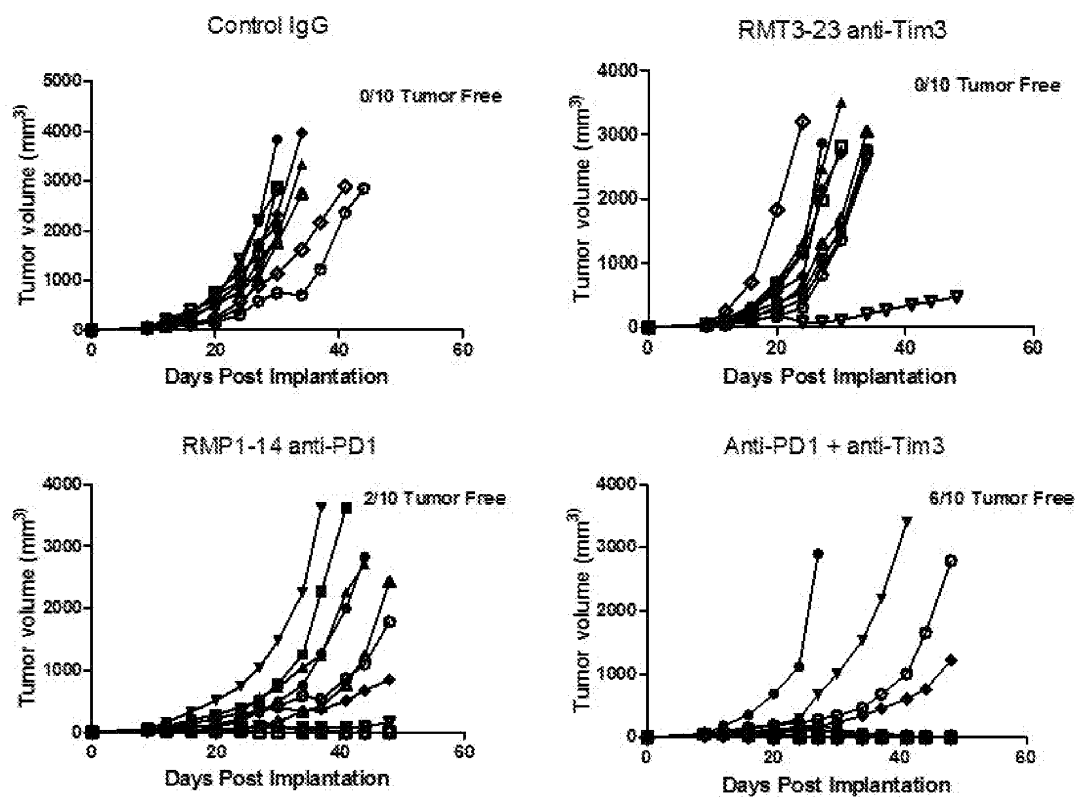


FIG. 24B

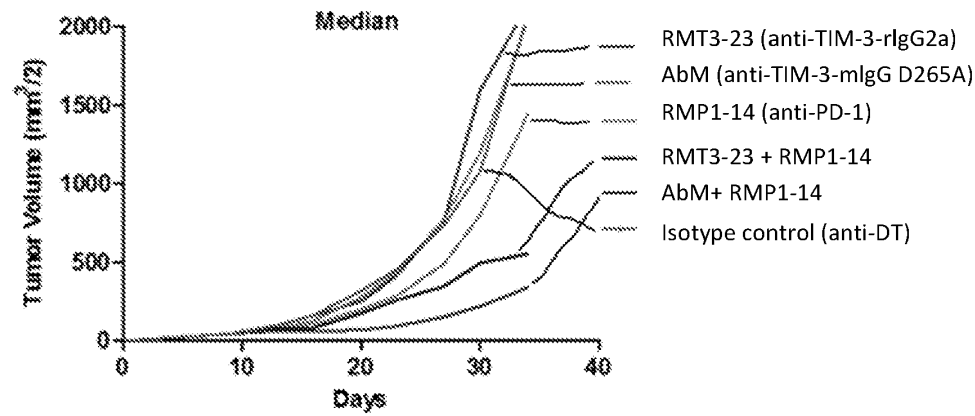


FIG. 25

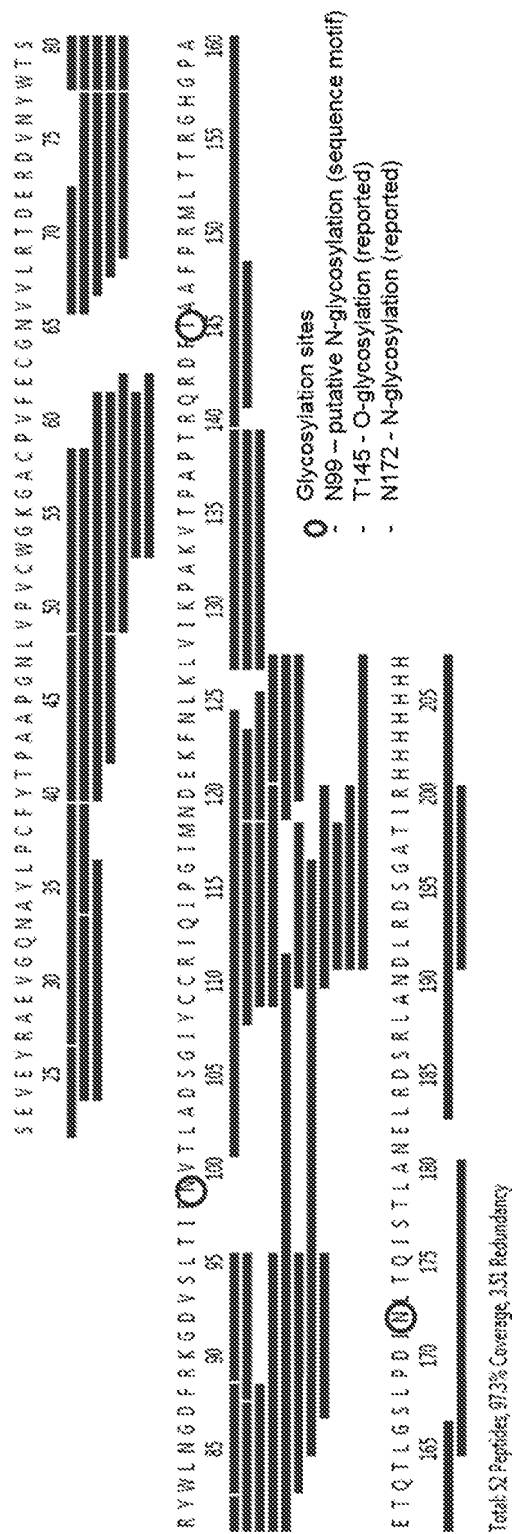
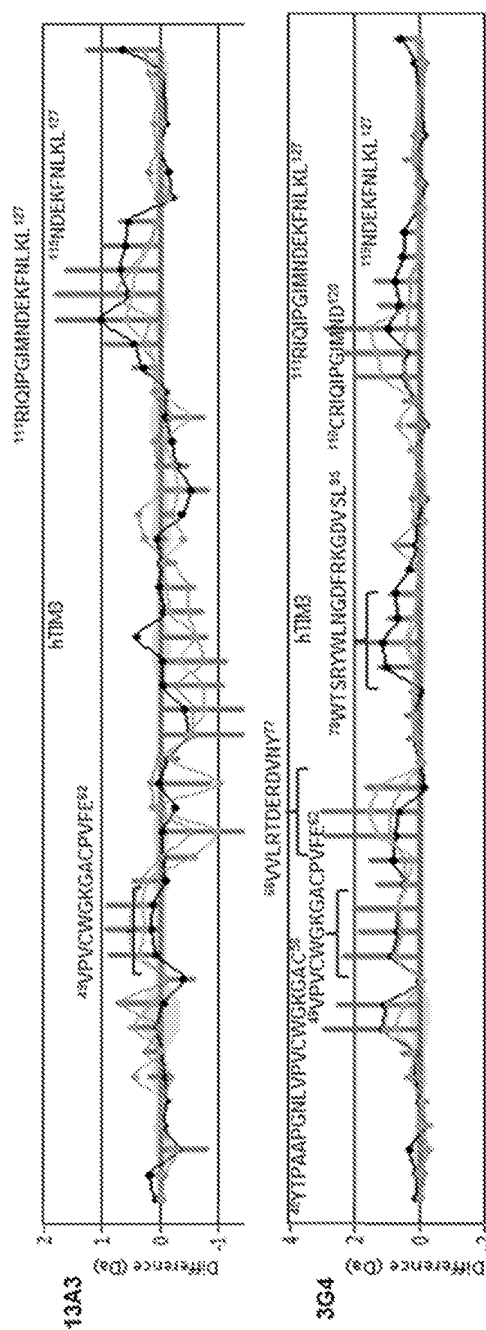
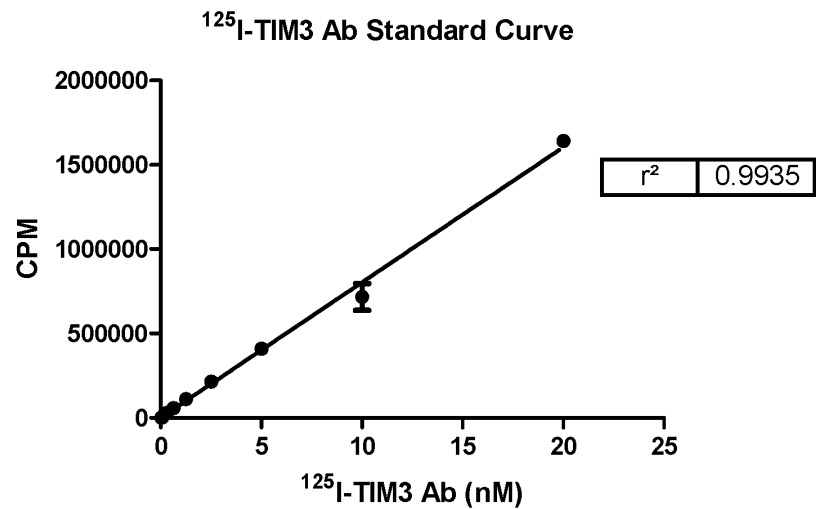


FIG. 26



64/78
FIG. 27A

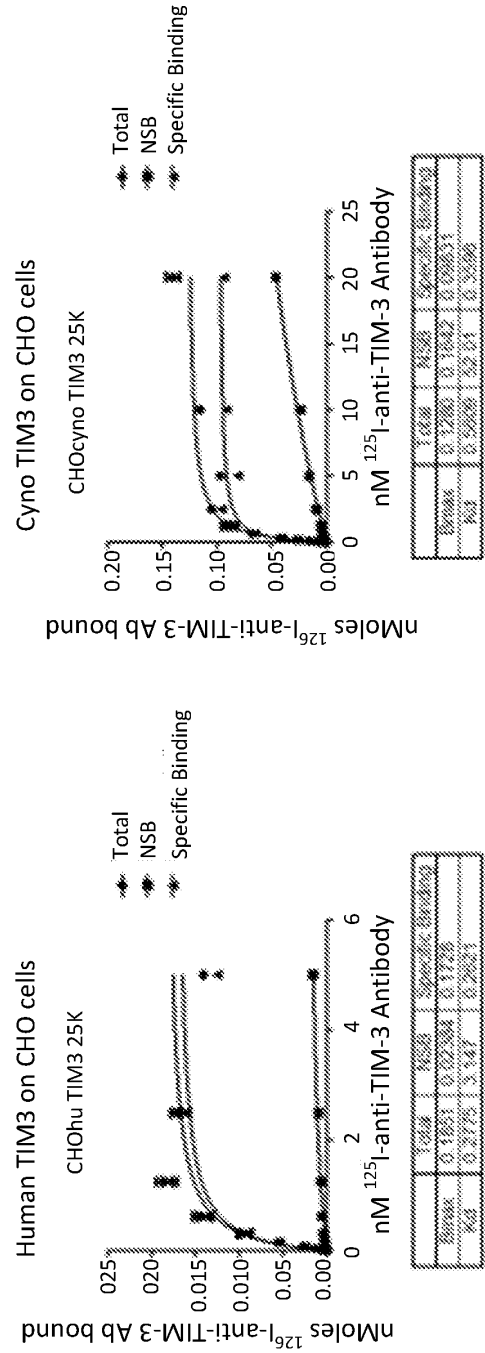


$Y = mX + b$
 $Y = 80220(1\text{nM}) + 899.3$
 $Y = 81119.3$

1nM 125I-Ab = 81119.3 cpm

Slope	80220 ± 1526
Y-intercept when X=0.0	899.3 ± 11140

FIG. 27B



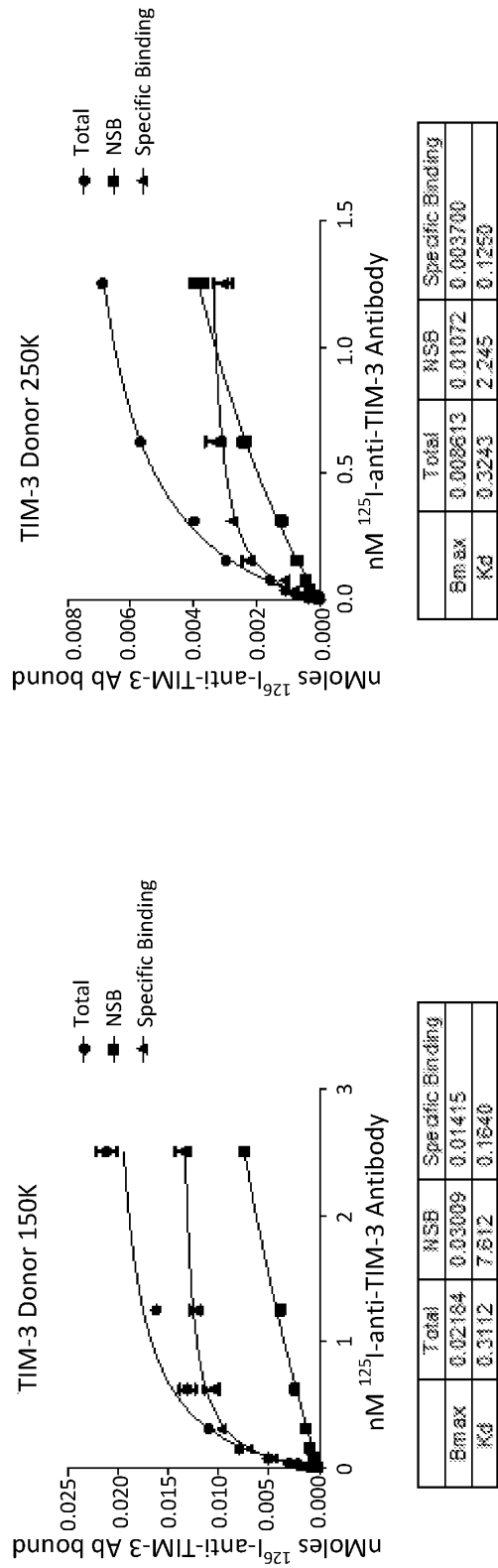
Affinity of 0.26-0.48 nM for overexpressed human TIM3

414,720 receptors per cell

Affinity of 0.36-0.48 nM for overexpressed cyno TIM3

235,944 receptors per cell

FIG. 28



Receptors per cell = 16,980

Receptors per cell = 4,440

FIG. 29A

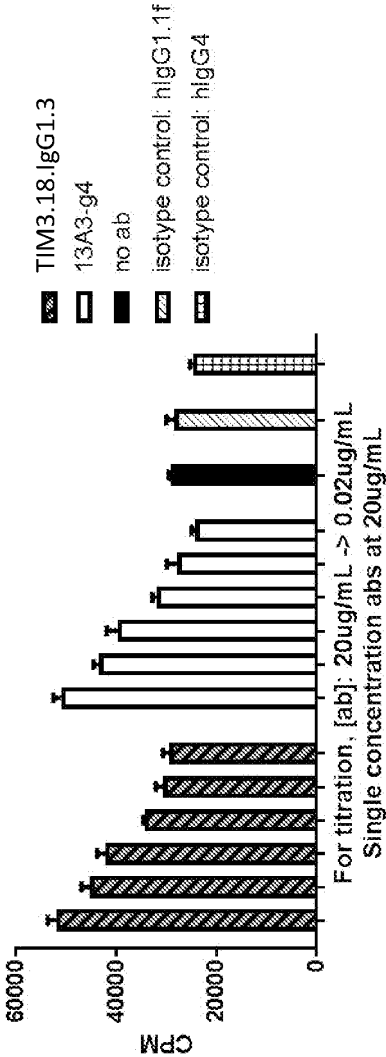


FIG. 29B

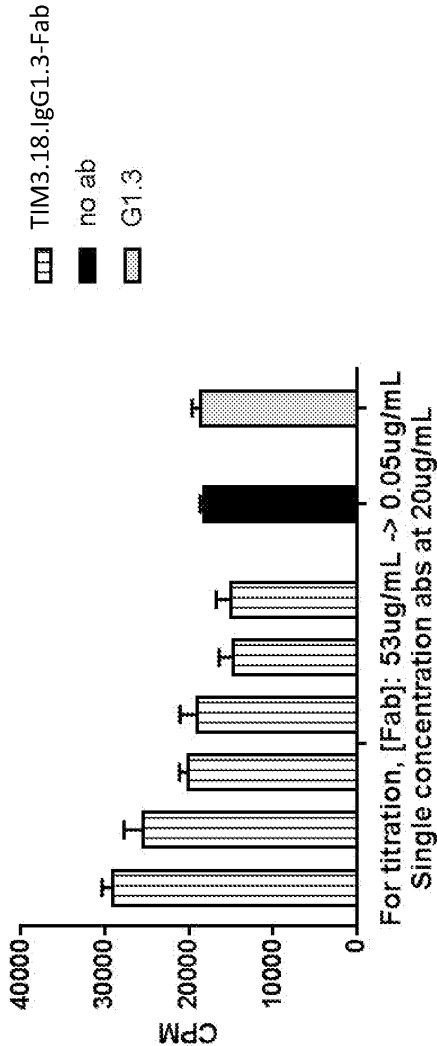


FIG. 30

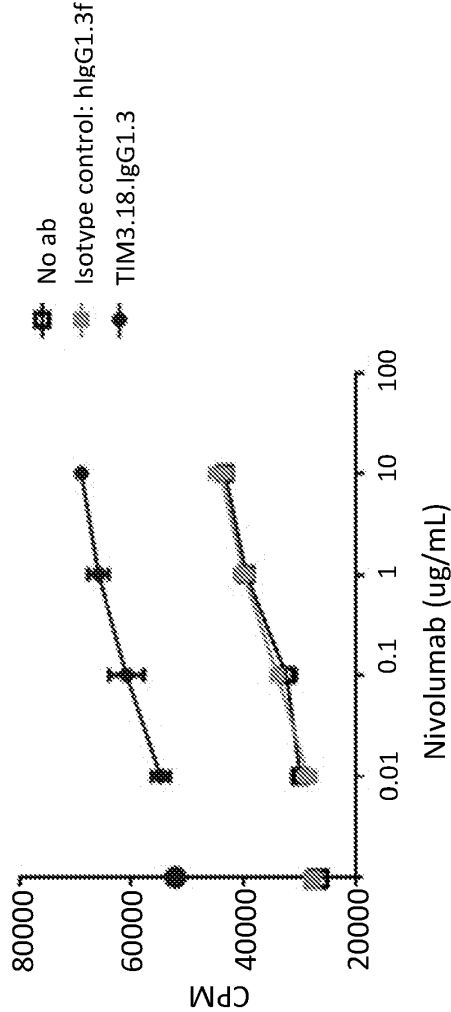


FIG. 31

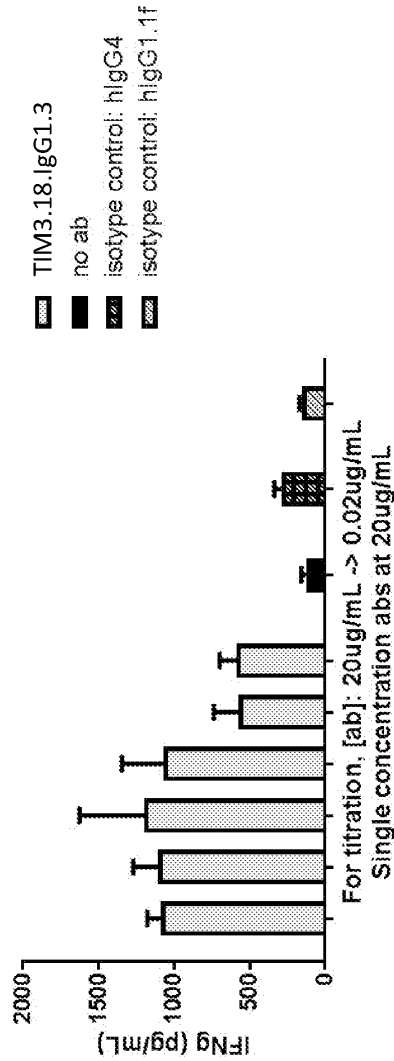


FIG. 32

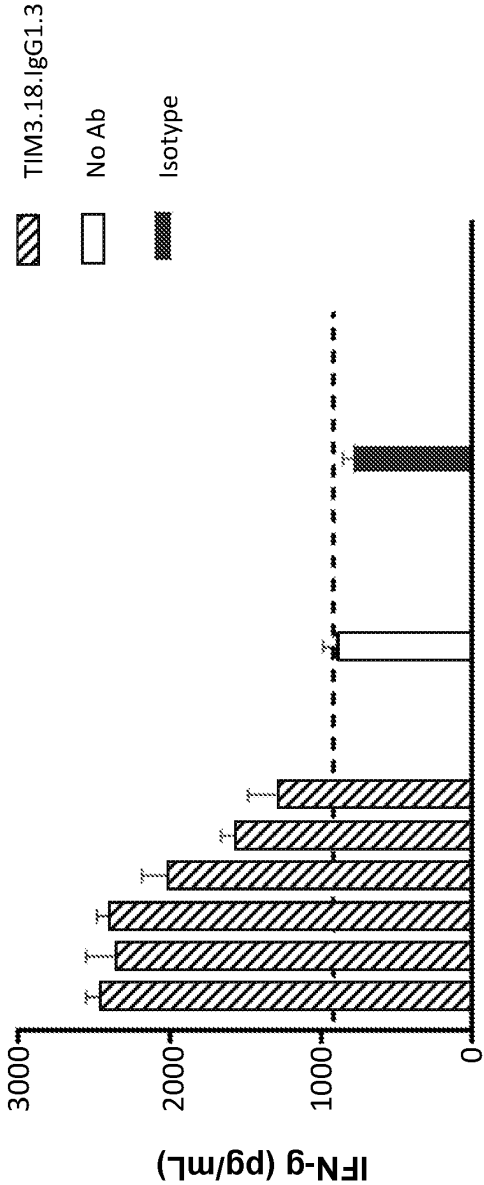


FIG. 33

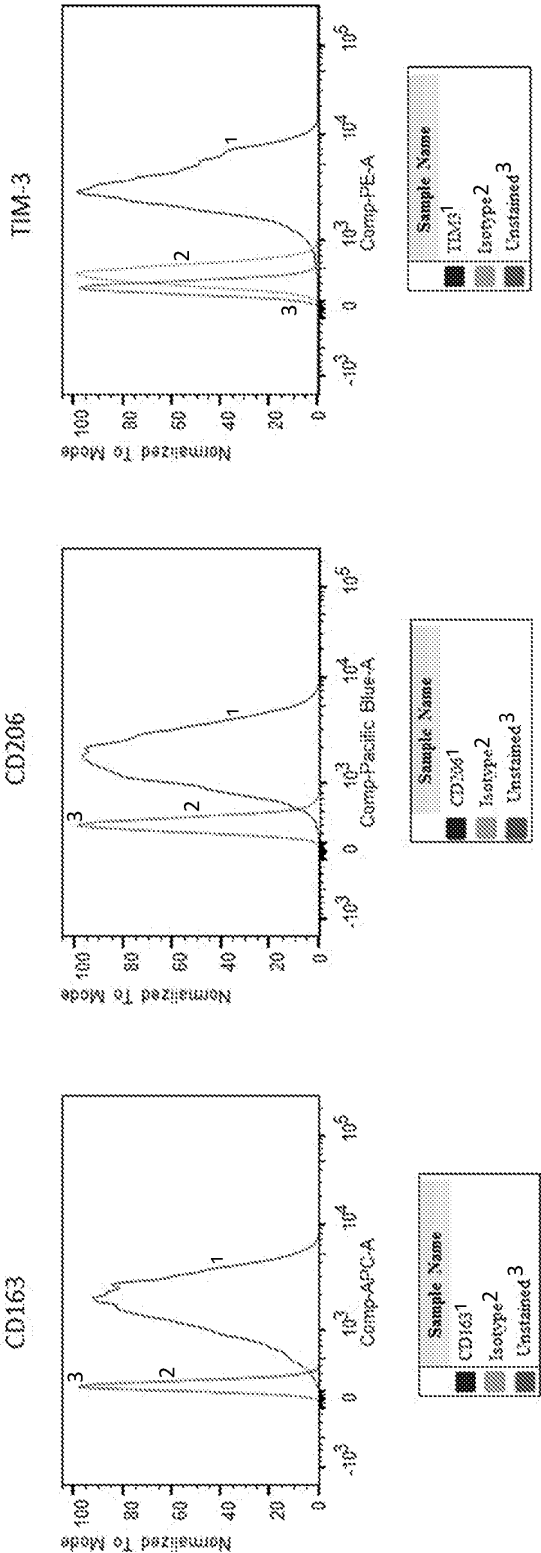


FIG. 34

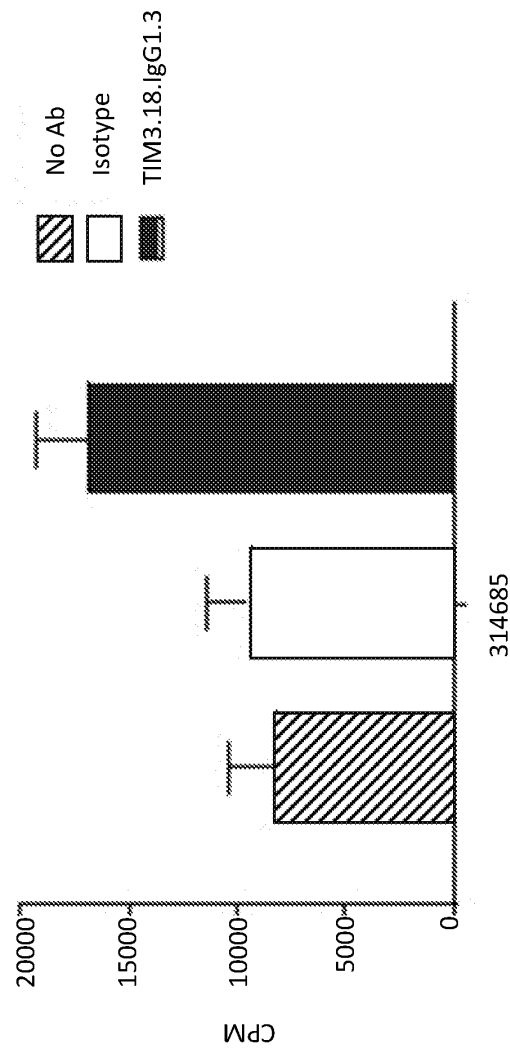


FIG. 35

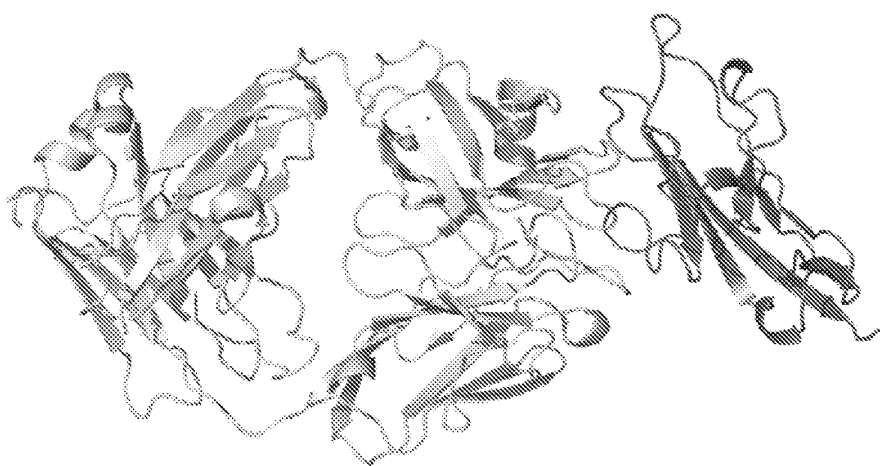


FIG. 36

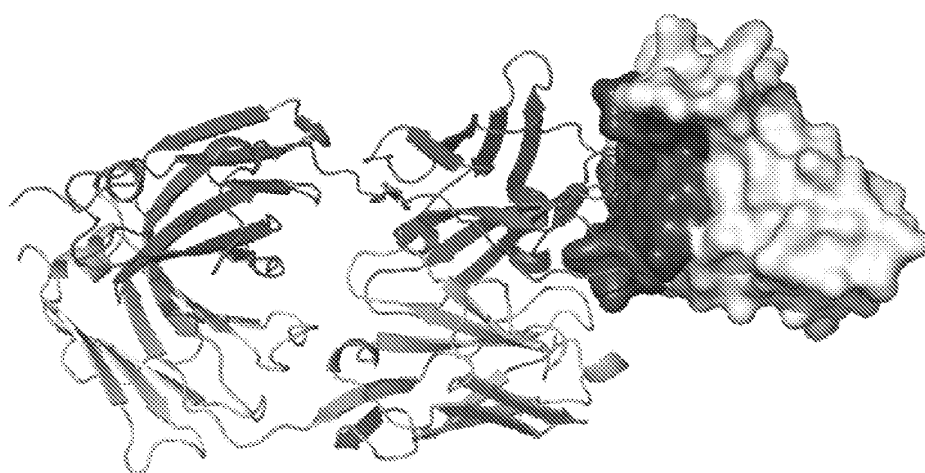


FIG. 37

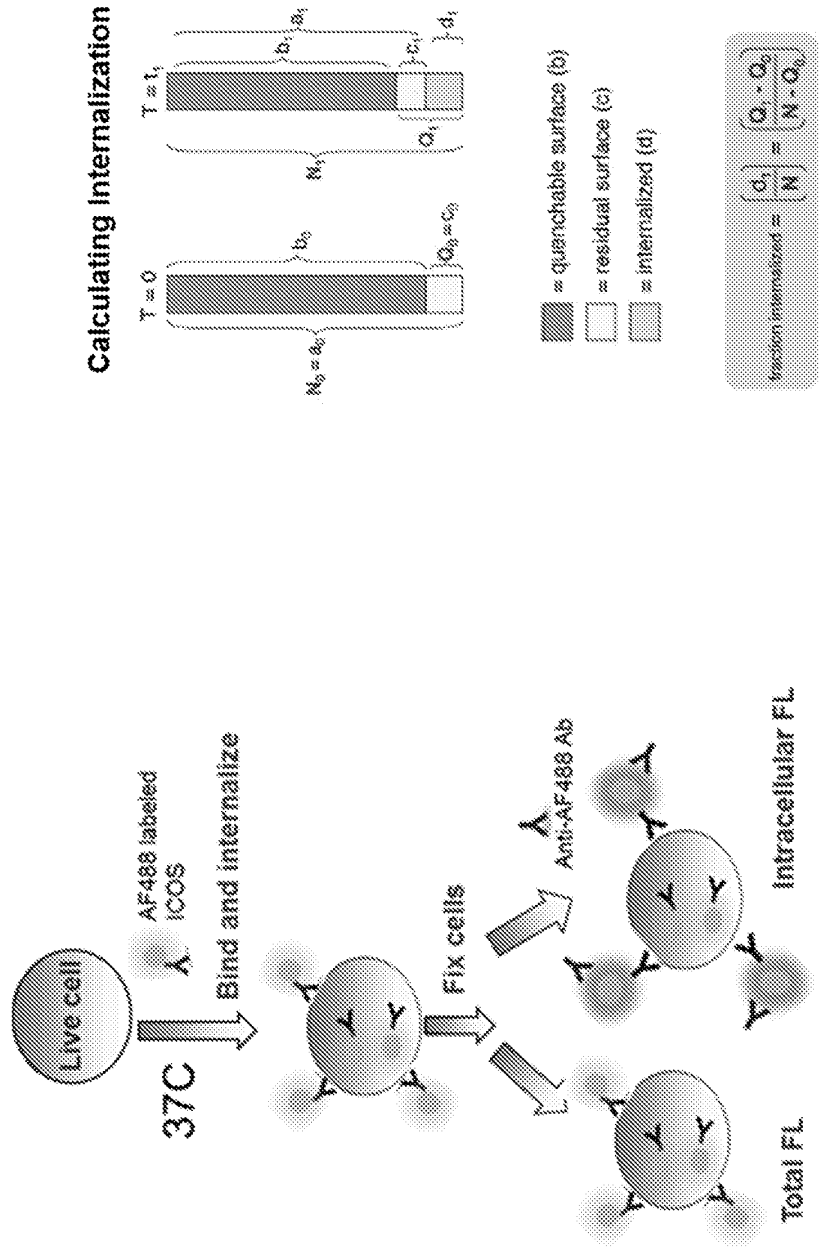


FIG. 38

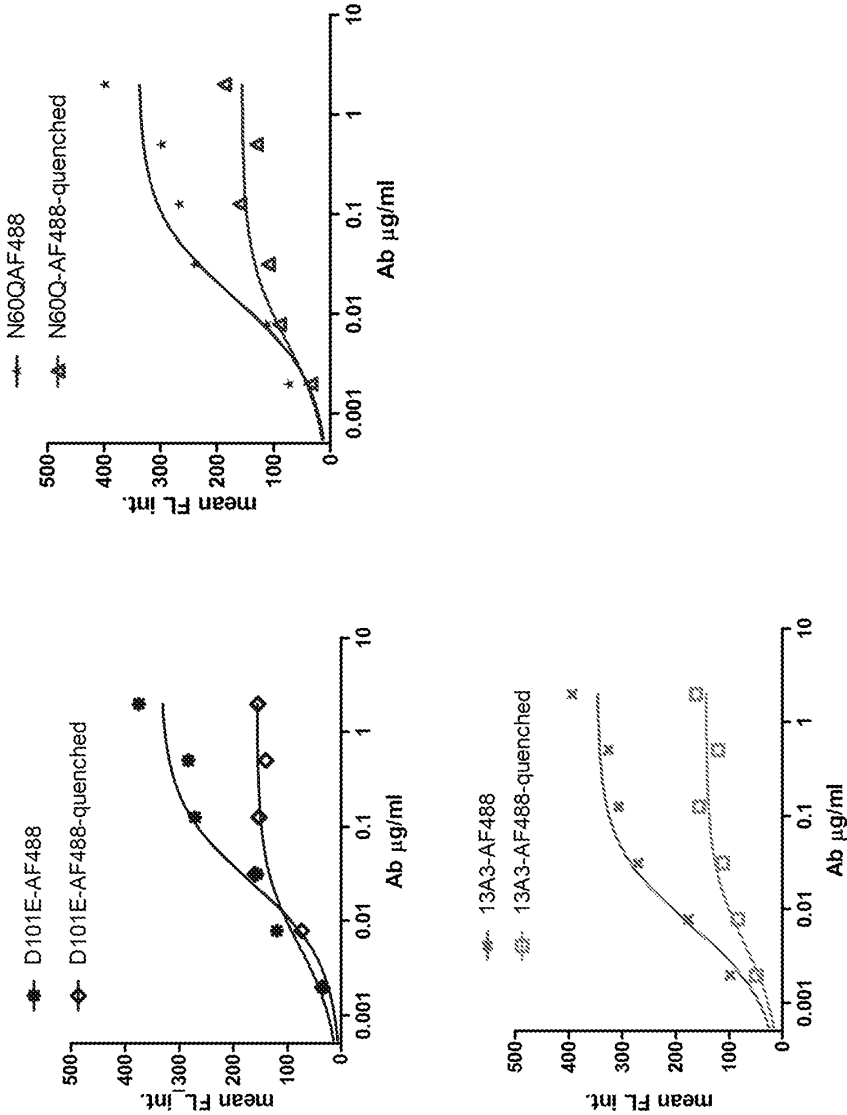
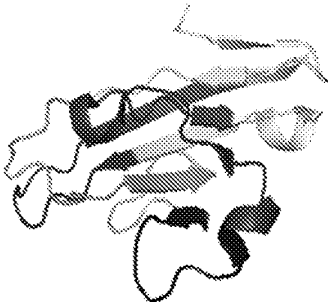


FIG. 39B

3G4



40YTPAAPGCHLVPCWCKGAC⁵³
49VPVCWCKGACPVEE⁶²

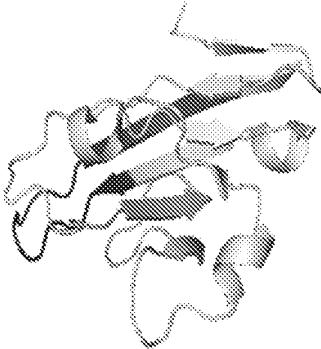
63WLRDTERDNY⁷⁷

75WTSRYWLNKGDFRKGDVSL⁸⁶

111RIQIPGIMNDEKFNLKL¹²⁷

FIG. 39A

13A3



49VPVCWCKGACPVEE⁶²

111RIQIPGIMNDEKFNLKL¹²⁷