Figure 1a

IgG1 wild type CH1 & hinge

(A)STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV

DKKV(E)PKSCDKTHTCPPCPAPELGGP (SEQ ID NO:227)

IgG4 wild type CH1 & hinge

(A)STKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKV

DKRV(E)SKYGPPCPSCPAPEFLGGP (SEQ ID NO:228)

Ig wild type kappa constant light chain

TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSP

VTKSFNRGEC (SEQ ID NO:229)

Figure 1b

Light chain	C_L			
Human κ	FNRGEC (SEQ ID NO:228)			
Heavy chain	**C_H1 (N-term)**	**UPPER**	**CORE**	**LOWER**
Human IgGγ1	LAPSSKSTS (SEQ ID NO:230)	EPKSCDKTHT (SEQ ID NO:231)	CPPCP	APELLGGP
Human IgGγ2	LAPCSRSTS (SEQ ID NO:232)	ERK (SEQ ID NO:233)	CCVECPPCP	APPVA GP
Human IgGγ3	LAPCSRSTS (SEQ ID NO:234)	ELKTPLGDTTHT (SEQ ID NO:235)	CPRCP(EPKSCDTPPPCPRCP)$_3$	APELLGGP
Human IgGγ4	LAPCSRSTS ↑ C127 (SEQ ID NO:236)	ESKYGPP ↑ G230 (SEQ ID NO:237)	CPSCP ↑ C239 ↑ C242	APEFLGGP
Heavy chain	**C_H1 (N-term)**	**Hinge**		
Human IgD	IISGCRHPK (SEQ ID NO:238)	(E)SPKAQASSVPTAQPQAEGSLAKATTAPATTRNT (SEQ ID NO:239)		
Heavy chain	**C_H1 (N-term)**	**C_H1 (C-term)**	**C_H2 (N-term)**	
Human IgM	LVSCENSPS (SEQ ID NO:240)	EKNVPLP (SEQ ID NO:241)	(V)IAELPPKVSV (SEQ ID NO:242)	

Figure 2a

	CH1	HINGE													
EU Numbering for IgG1	**131**	**216**	**217**	**218**	**221**			**222**	**223**	**224**	**225**	**226**	**227**	**228**	**229**	**230**
Kabat Numbering for IgG1	**127**	**226**	**227**	**228**	**232**	**233**	**234**	**235**	**236**	**237**	**238**	**239**	**240**	**241**	**242**	**243**
IMGT Numbering for IgG1	**10**	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**	**14**	**15**
IgG1 wt residues	S	E	P	K	S	C	D	K	T	H	T	C	P	P	C	P
EU Numbering for IgG4	**131**	**216**	**217**	**218**	**219**	**220**	**224**	**225**	**-**	**-**	**-**	**226**	**227**	**228**	**229**	**230**
Kabat Numbering for IgG4	**127**	**226**	**227**	**228**	**229**	**230**	**237**	**238**	**-**	**-**	**-**	**239**	**240**	**241**	**242**	**243**
IMGT Numbering for IgG4	**10**	**1**	**2**	**3**	**4**	**5**	**6**	**7**				**8**	**9**	**10**	**11**	**12**
IgG4 wt residues	C	E	S	K	Y	G	P	P	-	-	-	C	P	S	C	P
Mutations to IgG4	S		C or P	C	C or S	C	D	K	A or T	A or H	A or T	S		P	S	

Figure 2b

	CH1	HINGE						
Kabat Numbering	**127**	**226**	**227**	**228**	**229**	**230**	**232**	**233**
IMGT Numbering for IgG3	**10**	**1**	**2**	**3**	**4**	**5**	**6**	**7**
IgG3 wt residues	C	E	L	K	T	P	L	G
Mutations to IgG3	S	C	C	C	C	C	C	C

Figure 2c

	CH1					CH2		
Kabat numbering for IgM	**127**	**223**	**223A**	**223B**	**223C**	**243G**	**243H**	**243I**
IMGT Numbering for IgM	**10**	**121**	**122**	**123**	**124**	**1.5**	**1.4**	**1.3**
IgM wt residues	C	V	P	L	P	V	I	A
Mutations to IgM	S	C	C	C	C	C	C	C

Figure 2d

	CH1	Hinge						
Kabat numbering for IgD	**128**	**227**	**228**	**229**	**230**	**231**	**232**	**233**
IMGT Numbering for IgD	**11**	**1**	**2**	**3**	**4**	**5**	**6**	**7**
IgD wt residues	C	E	S	P	K	A	Q	A
Mutations to IgD	S	C	C	C	C	C	C	C

Figure 3a

	ANTIBODIES																		
Mutations	**G4**	**G1**	**1**	**2**	**3**	**4**	**5**	**5P**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**	**14**	**15**	**16**
C127S			•	•	•	•			•	•	•							•	•
G230C							•	•	•	•	•	•	•	•				•	•
C239S				•		•			•		•	•		•	•		•		
S241P								•											•
C242S					•	•				•	•		•	•		•	•		

Figure 3b

	ANTIBODIES																	
HC Cys position	**G4**	**G1**	**1**	**2**	**3**	**4**	**5**	**5P**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**	**14**	**15**	**16**
127	LC						LC	LC				LC	LC	LC	LC	LC	LC		
230							HC	HC	LC	LC	LC	HC	HC	HC				HC or LC	HC or LC
230 (G4) 233 (G1)		LC																	
239	HC	HC	LC or HC		LC		HC	HC		HC			HC			HC		HC or LC	HC or LC
242	HC	HC	LC or HC	LC			HC	HC	HC			HC			HC			HC or LC	HC or LC

Figure 4a

	ANTIBODIES																	
Mutations to G4	**G4**	**G1**	**28**	**29**	**30**	**31**	**32**	**33**	**34**	**35**	**36**	**37**	**38**	**39**	**44**	**45**	**46**	**47**
C127S			•	•	•	•	•	•	•	•	•	•	•	•	•	•	•	•
S227C											•	•	•	•				
K228C							•	•	•	•								
Y229C			•	•	•	•												
G230C															•	•	•	•
P238PAAA															•	•	•	•
C239S				•		•		•		•		•		•		•		•
S241P																		
C242S					•	•			•	•			•	•			•	•

Figure 4b

	ANTIBODIES																	
HC Cys position	**G4**	**G1**	**28**	**29**	**30**	**31**	**32**	**33**	**34**	**35**	**36**	**37**	**38**	**39**	**44**	**45**	**46**	**47**
127	LC																	
227											LC or HC	LC	LC	LC				
228							LC or HC	LC	LC	LC								
229 (G4)			LC or HC	LC	LC	LC												
230 (G4) 233(G1)		LC													LC or HC	LC	LC	LC
239	HC	HC	HC or LC		H C		HC or LC		HC		HC or LC		H C		HC or LC		H C	
242	HC	HC	HC or LC	HC			HC or LC	H C			HC or LC	H C			HC or LC	H C		

Figure 5

(Ab 6) (SEQ ID NO:243)
(A) STKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV(E) SKYCPPSPSCPAPEFLGGP

(Ab 7) (SEQ ID NO:244)
(A) STKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV(E) SKYCPPCPSSPAPEFLGGP

(Ab 8) (SEQ ID NO:245)
(A) STKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV(E) SKYCPPSPSSPAPEFLGGP

(Ab 15) (SEQ ID NO:246)
(A) STKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV(E) SKYCPPCPSCPAPEFLGGP

(Ab 16) (SEQ ID NO:247)
(A) STKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV(E) SKYCPPCPPCPAPEFLGGP

(Ab 28) (SEQ ID NO:248)
(A) STKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV(E) SKCGPPCPSCPAPEFLGGP

(Ab 29) (SEQ ID NO:249)
(A) STKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV(E) SKCGPPSPSCPAPEFLGGP

(Ab 30) (SEQ ID NO:250)
(A) STKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV (E) SKCGPPCPSSPAPEFLGGP

(Ab 31) (SEQ ID NO:251)
(A) STKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV (E) SKCGPPSPSSPAPEFLGGP

(Ab 32) (SEQ ID NO:252)
(A) STKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV (E) SCYGPPCPSCPAPEFLGGP

(Ab 33) (SEQ ID NO:253)
(A) STKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV (E) SCYGPPSPSCPAPEFLGGP

(Ab 34) (SEQ ID NO:254)
(A) STKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV (E) SCYGPPCPSSPAPEFLGGP

(Ab 35) (SEQ ID NO:255)
(A) STKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV (E) SCYGPPSPSSPAPEFLGGP

(Ab 36) (SEQ ID NO:256)
(A) STKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV (E) CKYGPPCPSCPAPEFLGGP

(Ab 37) (SEQ ID NO:257)
(A) STKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV (E) CKYGPPSPSCPAPEFLGGP

(Ab 38) (SEQ ID NO:258)
(A) STKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV (E) CKYGPPCPSSPAPEFLGGP

(Ab 39) (SEQ ID NO:259)
(A) STKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV (E) CKYGPPSPSSPAPEFLGGP

(Ab 44) (SEQ ID NO:260)
(A) STKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV (E) SKYCPPAAACPSCPAPEFLGGP

(Ab 45) (SEQ ID NO:261)
(A) STKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV (E) SKYCPPAAASPSCPAPEFLGGP

(Ab 46) (SEQ ID NO:262)
(A) STKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV (E) SKYCPPAAACPSSPAPEFLGGP

(Ab 47) (SEQ ID NO:263)
(A) STKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV (E) SKYCPPAAASPSSPAPEFLGGP

(Ab 2) (SEQ ID NO:264)
(A) STKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV (E) SKYGPPSPSCPAPEFLGGP

(Ab 3) (SEQ ID NO:265)
(A)STKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV(E)SKYGPPCPSSPAPEFLGGP

(Ab 48) (SEQ ID NO:266)
(A)STKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV(E)PKSCDKTHTCPPCPAPEFLGGP

(Ab 28P) (SEQ ID NO:267)
(A)STKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV(E)SKCGPPCPPCPAPEFLGGP

(Ab 44P) (SEQ ID NO:268)
(A)STKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV(E)SKYCPPAAACPPCPAPEFLGGP

(Ab 1) (SEQ ID NO:269)
(A)STKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV(E)SKYGPPCPSCPAPEFLGGP

(Ab 4) (SEQ ID NO:270)
(A)STKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV(E)SKYGPPSPSSPAPEFLGGP

Ab5 (SEQ ID NO:271)
(A)STKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV(E)SKYCPPCPSCPAPEFLGGP

Ab5P (SEQ ID NO:272)
(A)STKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV(E)SKYCPPCPPCPAPEFLGGP

Ab9 (SEQ ID NO:273)
(A) STKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV (E) SKYCPPSPSCPAPEFLGGP

Ab10 (SEQ ID NO:274)
(A) STKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV (E) SKYCPPCPSSPAPEFLGGP

Ab11 (SEQ ID NO:275)
(A) STKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV (E) SKYCPPSPSSPAPEFLGGP

Ab12 (SEQ ID NO:276)
(A) STKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV (E) SKYGPPSPSCPAPEFLGGP

Ab13 (SEQ ID NO:277)
(A) STKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV (E) SKYGPPCPSSPAPEFLGGP

Ab14 (SEQ ID NO:278)
(A) STKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV (E) SKYGPPSPSSPAPEFLGGP

Figure 6

IgG4 CH2 and CH3: (SEQ ID NO:279)
SVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKG
LPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSR
WQEGNVFSCSVMHEALHNHYTQKSLSLSLGK

IgG4 CH2 IgG1 CH3: (SEQ ID NO:280)
SVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKG
LPSSIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR
WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

(Ab 6) (SEQ ID NO:281)
(A) STKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV(E) SKYCPPSPSCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREE
QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWES
NGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK

(Ab 7) (SEQ ID NO:282)
(A) STKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV(E) SKYCPPCPSSPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREE
QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWES
NGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK

(Ab 8) (SEQ ID NO:283)
(A) STKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV(E) SKYCPPSPSSPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREE
QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWES
NGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK

(Ab 15) (SEQ ID NO:284)
(A) STKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV(E) SKYCPPCPSCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREE
QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWES
NGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK

(Ab 16) (SEQ ID NO:285)
(A) STKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV(E) SKYCPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREE
QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWES
NGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK

(Ab 28) (SEQ ID NO:286)
(A) STKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV(E) SKCGPPCPSCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREE
QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWES
NGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK

(Ab 29) (SEQ ID NO:287)
(A) STKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV(E) SKCGPPSPSCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREE
QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWES
NGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK

(Ab 30) (SEQ ID NO:288)
(A) STKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV(E) SKCGPPCPSSPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREE
QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWES
NGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK

(Ab 31) (SEQ ID NO:289)
(A) STKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV(E) SKCGPPSPSSPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREE
QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWES
NGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK

(Ab 32) (SEQ ID NO:290)
(A) STKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV(E) SCYGPPCPSCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREE
QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWES
NGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK

(Ab 33) (SEQ ID NO:291)
(A) STKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV(E) SCYGPPSPSCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREE
QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWES
NGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK

(Ab 34) (SEQ ID NO:292)
(A) STKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV(E) SCYGPPCPSSPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREE
QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWES
NGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK

(Ab 35) (SEQ ID NO:293)
(A) STKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV(E) SCYGPPSPSSPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREE
QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWES
NGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK

(Ab 36) (SEQ ID NO:294)
(A) STKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV(E)CKYGPPCPSCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREE
QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWES
NGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK

(Ab 37) (SEQ ID NO:295)
(A) STKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV(E)CKYGPPSPSCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREE
QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWES
NGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK

(Ab 38) (SEQ ID NO:296)
(A) STKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV(E)CKYGPPCPSSPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREE
QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWES
NGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK

(Ab 39) (SEQ ID NO:297)
(A) STKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV(E)CKYGPPSPSSPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREE
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NGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK

(Ab 44) (SEQ ID NO:298)
(A) STKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV(E)SKYCPPAAACPSCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP
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WESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK

(Ab 45) (SEQ ID NO:299)
(A) STKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV(E) SKYCPPAAASPSCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP
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WESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK

(Ab 46) (SEQ ID NO:300)
(A) STKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV(E) SKYCPPAAACPSSPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP
REEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVE
WESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK

(Ab 47) (SEQ ID NO:301)
(A) STKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV(E) SKYCPPAAASPSSPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP
REEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVE
WESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK

(Ab 2) (SEQ ID NO:302)
(A) STKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV(E) SKYGPPSPSCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREE
QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWES
NGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK

(Ab 3) (SEQ ID NO:303)
(A) STKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV(E) SKYGPPCPSSPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREE
QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWES
NGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK

(Ab 48) (SEQ ID NO:304)
(A) STKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV(E)PKSCDKTHTCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP
REEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVE
WESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK

(Ab 28P) (SEQ ID NO:305)
(A) STKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV(E)SKCGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREE
QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWES
NGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK

(Ab 44P) (SEQ ID NO:306)
(A) STKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV(E)SKYCPPAAACPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP
REEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVE
WESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK

(Ab 1) (SEQ ID NO:307)
(A) STKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV(E)SKYGPPCPSCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREE
QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWES
NGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK

(Ab 4) (SEQ ID NO:308)
(A) STKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV(E)SKYGPPSPSSPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREE
QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWES
NGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK

Ab5 (SEQ ID NO:309)

(A)STKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV(E)SKYCPPCPSCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREE
QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWES
NGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK

Ab5P (SEQ ID NO:310)

(A)STKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV(E)SKYCPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREE
QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWES
NGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK

Ab9 (SEQ ID NO:311)

(A)STKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV(E)SKYCPPSPSCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREE
QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWES
NGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK

Ab10 (SEQ ID NO:312)

(A)STKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV(E)SKYCPPCPSSPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREE
QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWES
NGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK

Ab11 (SEQ ID NO:313)

(A)STKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV(E)SKYCPPSPSSPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREE
QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWES
NGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK

Ab12 (SEQ ID NO:314)

(A)STKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV(E)SKYGPPSPSCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREE
QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWES
NGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK

Ab13 (SEQ ID NO:315)

(A)STKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV(E)SKYGPPCPSSPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREE
QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWES
NGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK

Ab14 (SEQ ID NO:316)

(A)STKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH
KPSNTKVDKRV(E)SKYGPPSPSSPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREE
QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWES
NGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK

Figure 7

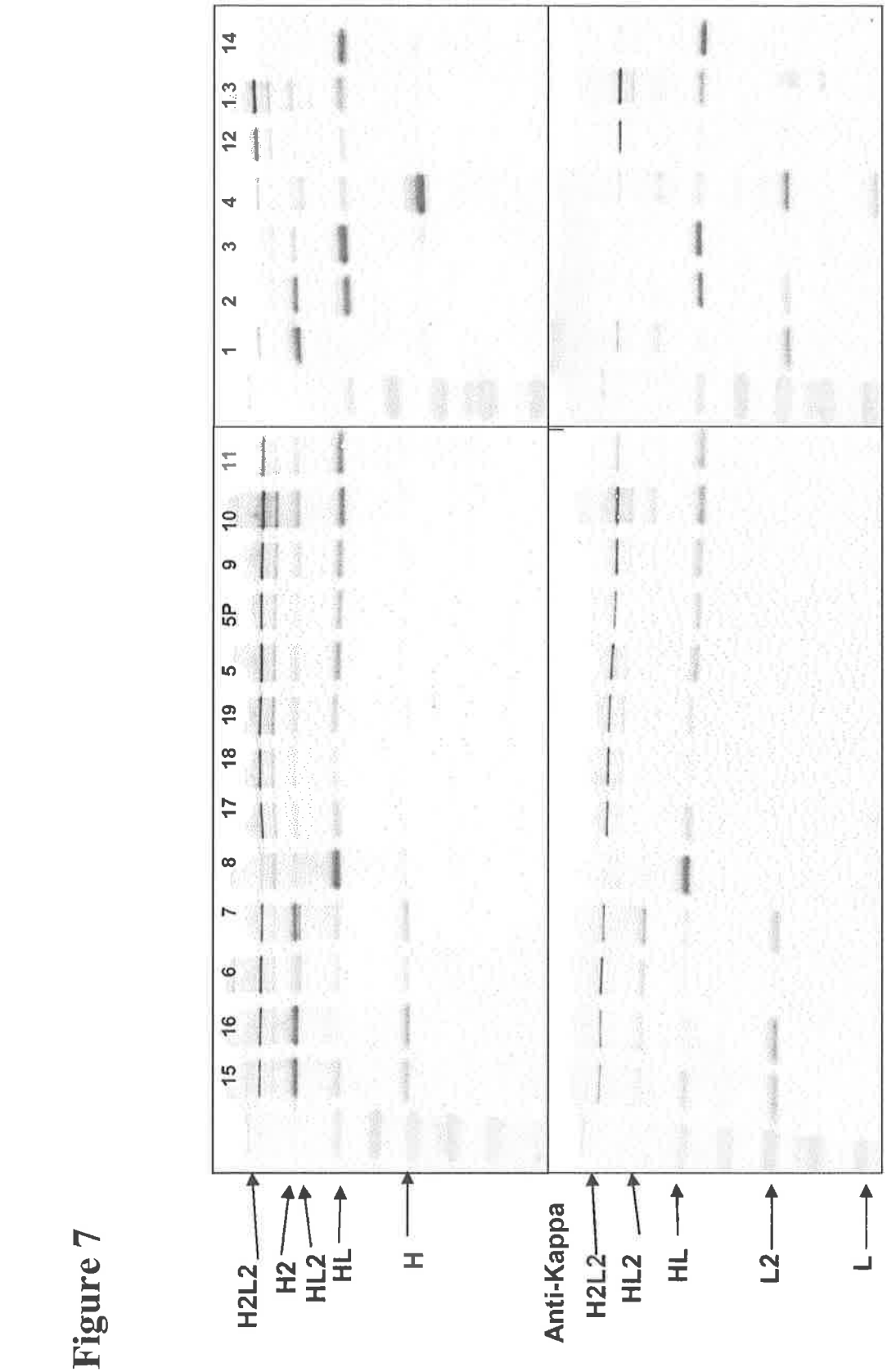

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11
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H2
HL2
HL
H
Anti-Kappa
H2L2
HL2
HL
L2
L

Figure 8

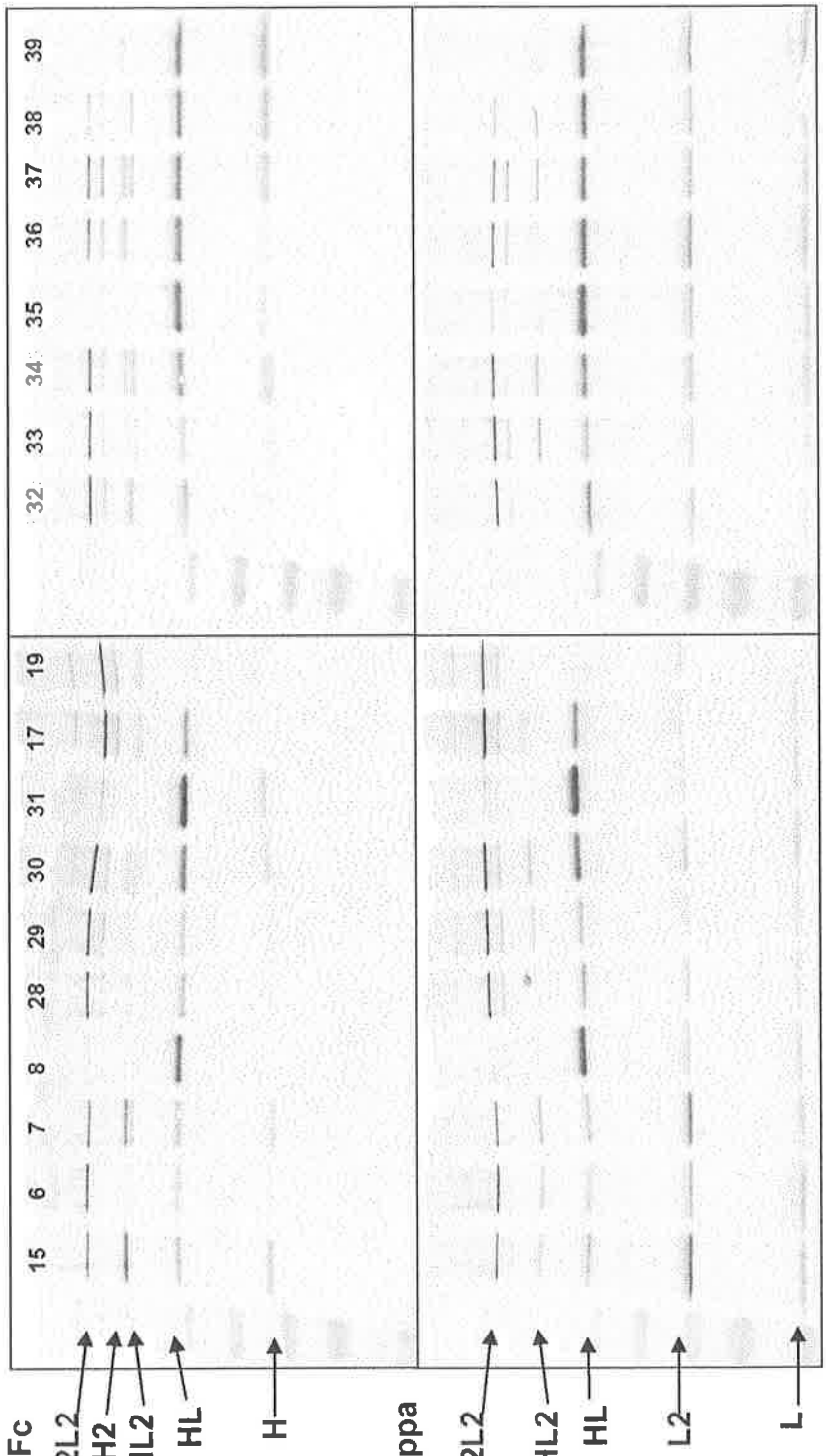

Anti-hFc
H2L2
H2
HL2
HL
H
Anti-Kappa
H2L2
HL2
HL
L2
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Figure 9

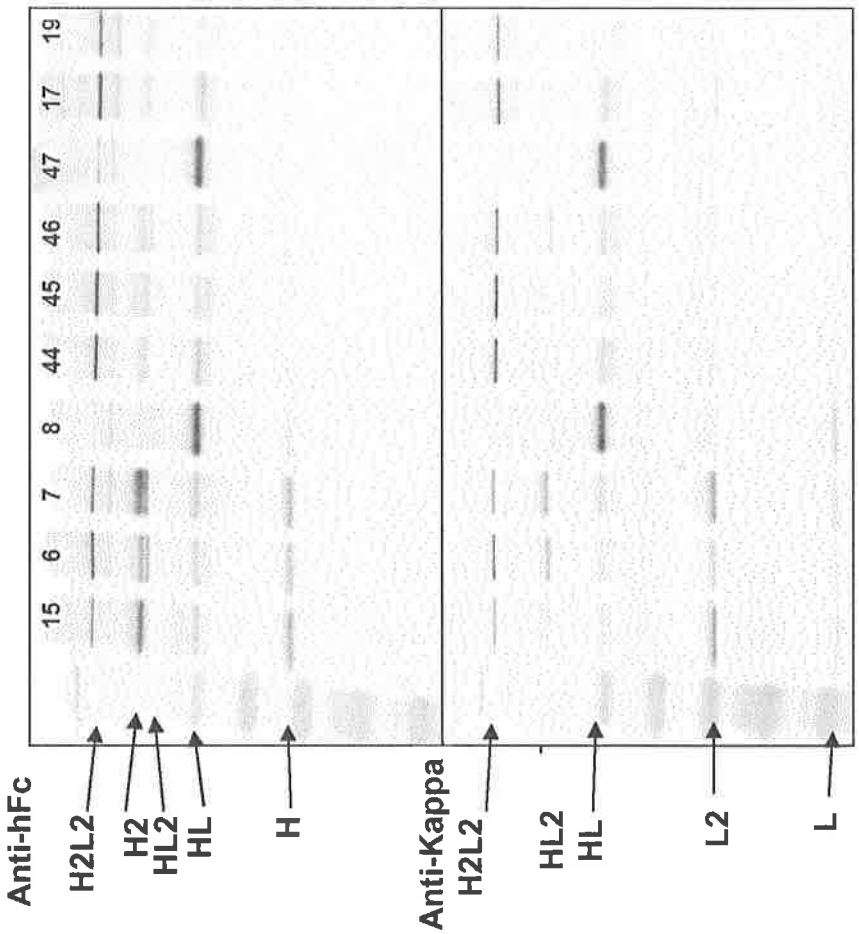

Anti-hFc
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HL2
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Anti-Kappa
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Figure 10

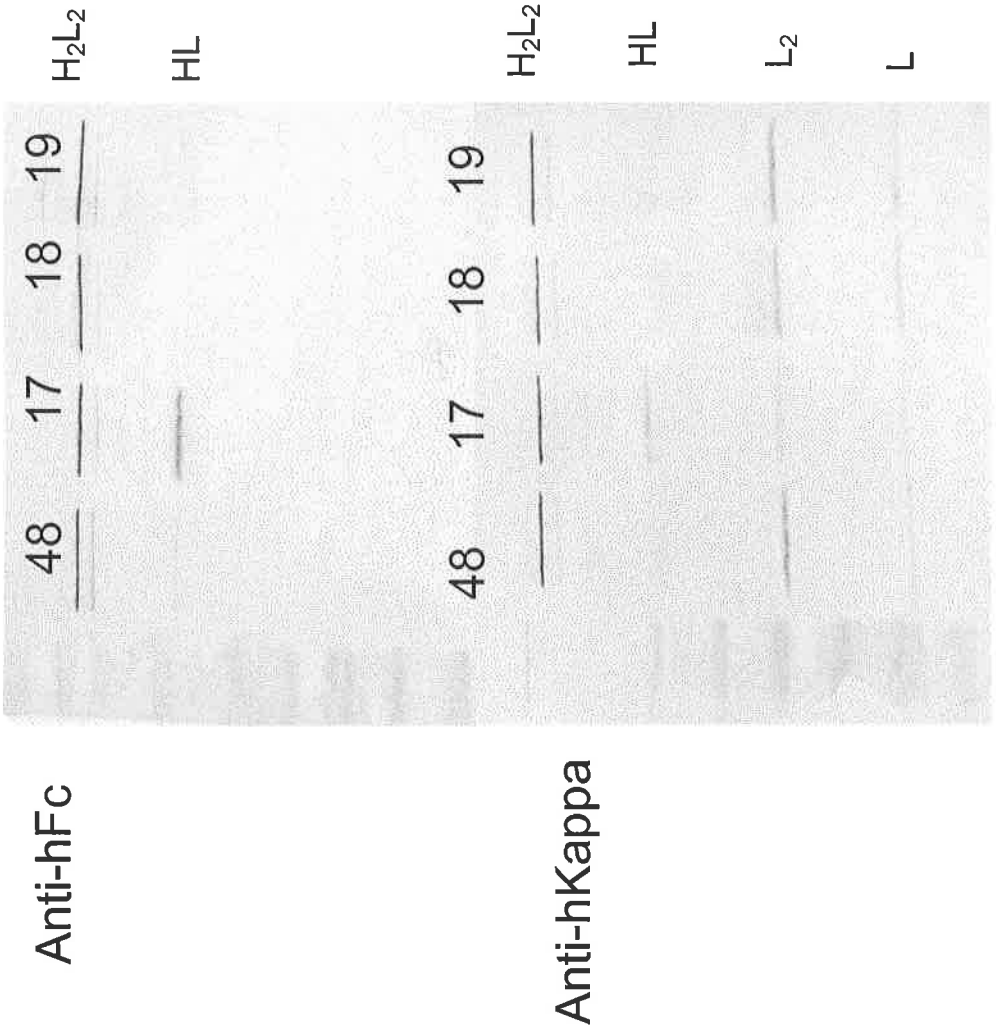


Figure 11

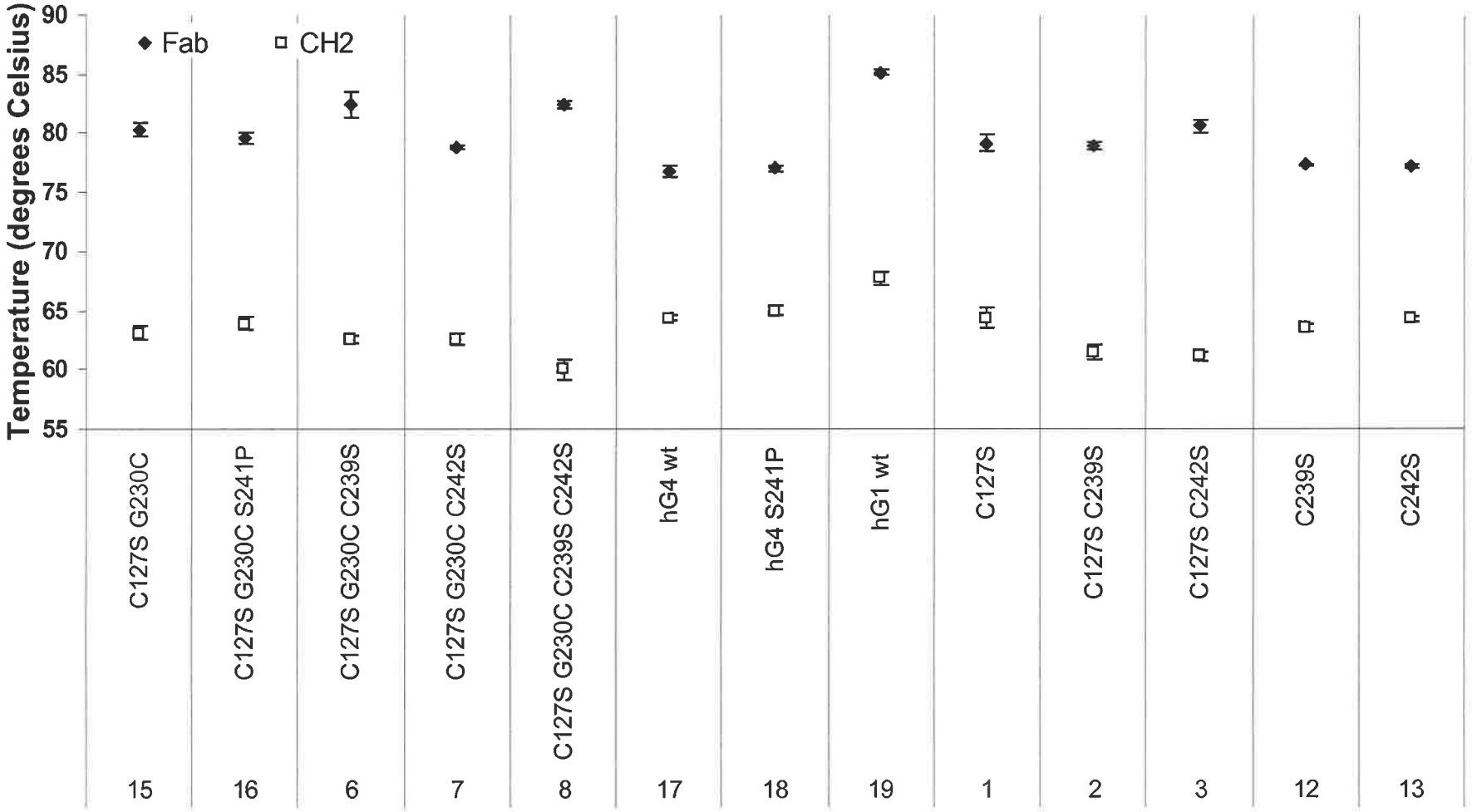

Temperature (degrees Celsius)
90
85
80
75
70
65
60
55
Fab
CH2
C127S G230C
C127S G230C S241P
C127S G230C C239S
C127S G230C C242S
C127S G230C C239S C242S
hG4 wt
hG4 S241P
hG1 wt
C127S
C127S C239S
C127S C242S
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3
12
13

Figure 12

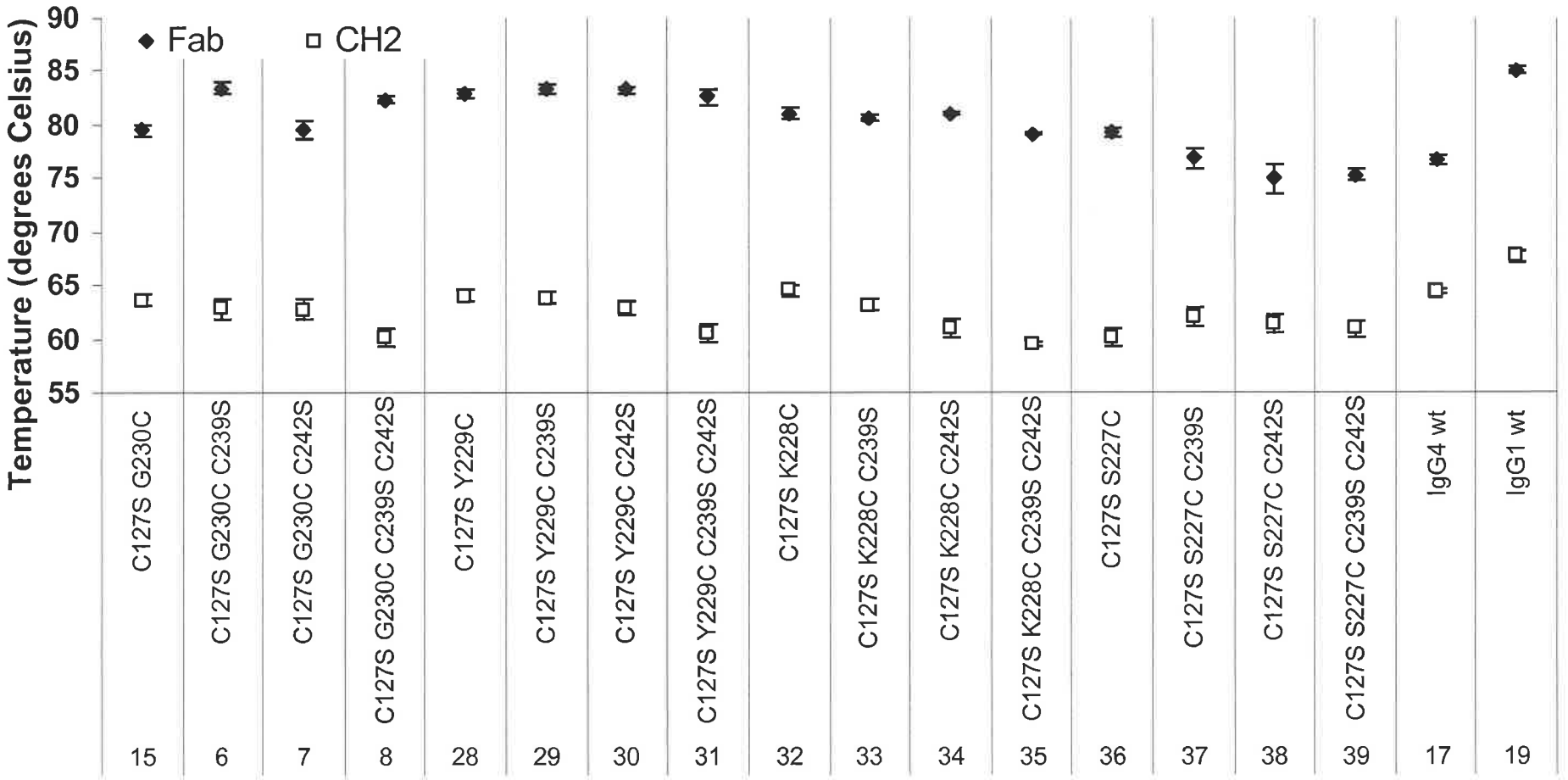

Temperature (degrees Celsius)
90
85
80
75
70
65
60
55
◆ Fab
□ CH2
C127S G230C
C127S G230C C239S
C127S G230C C242S
C127S G230C C239S C242S
C127S Y229C
C127S Y229C C239S
C127S Y229C C242S
C127S Y229C C239S C242S
C127S K228C
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C127S K228C C242S
C127S K228C C239S C242S
C127S S227C
C127S S227C C239S
C127S S227C C242S
C127S S227C C239S C242S
IgG4 wt
IgG1 wt
15
6
7
8
28
29
30
31
32
33
34
35
36
37
38
39
17
19

Figure 13

Temperature (degrees Celsius)
90
85
80
75
70
65
60
55
◆ Fab
□ CH2
15 C127S G230C
6 C127S G230C S241P
7 C127S G230C C239S
8 C127S G230C C242S
44 C127S G230C P238PAA
45 C127S G230C C239S P238PAA
46 C127S G230C C242S P238PAA
47 C127S G230C C239S C242S P238PAA
17 IgG4 wt
19 IgG1 wt

Figure 14

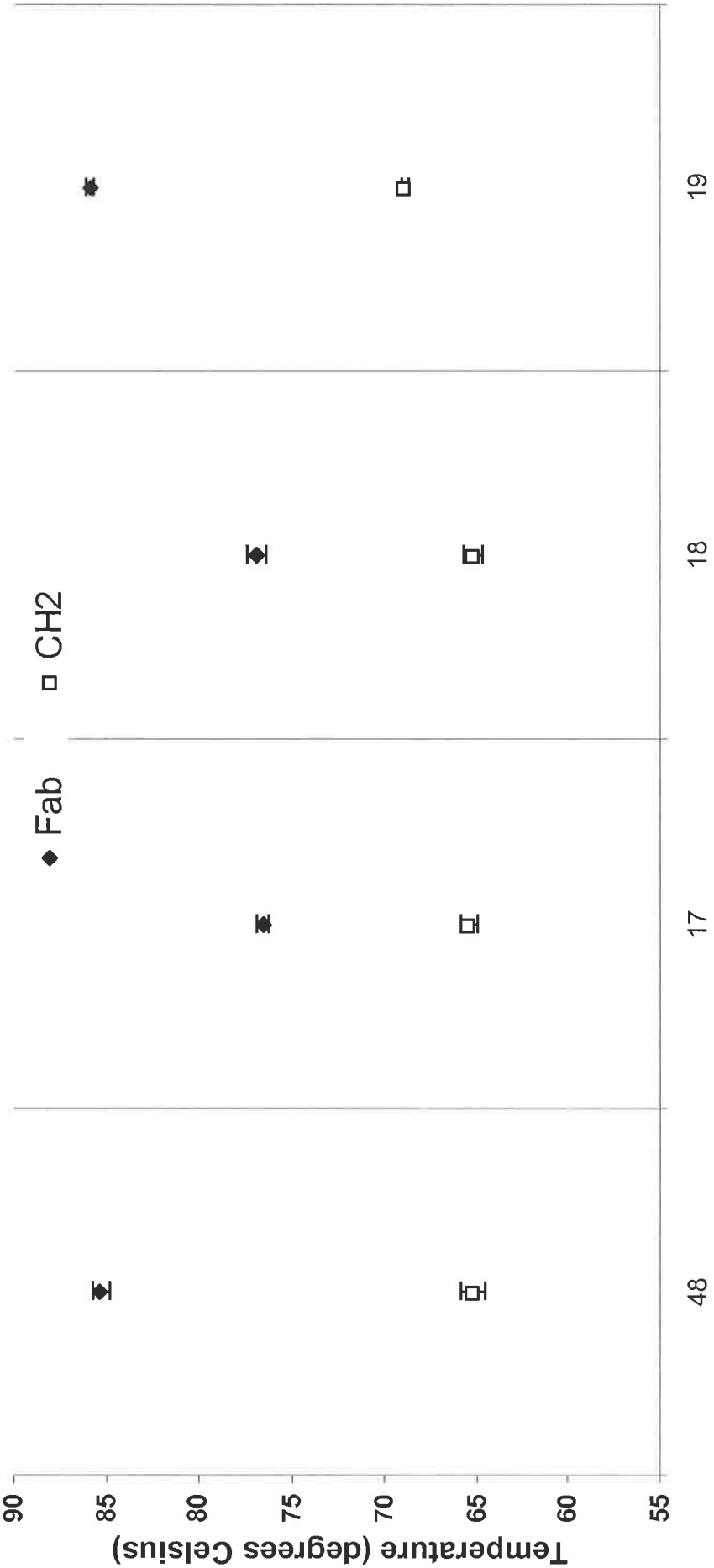

Temperature (degrees Celsius)
90
85
80
75
70
65
60
55
48
17
18
19
◆ Fab
□ CH2

Figure 15

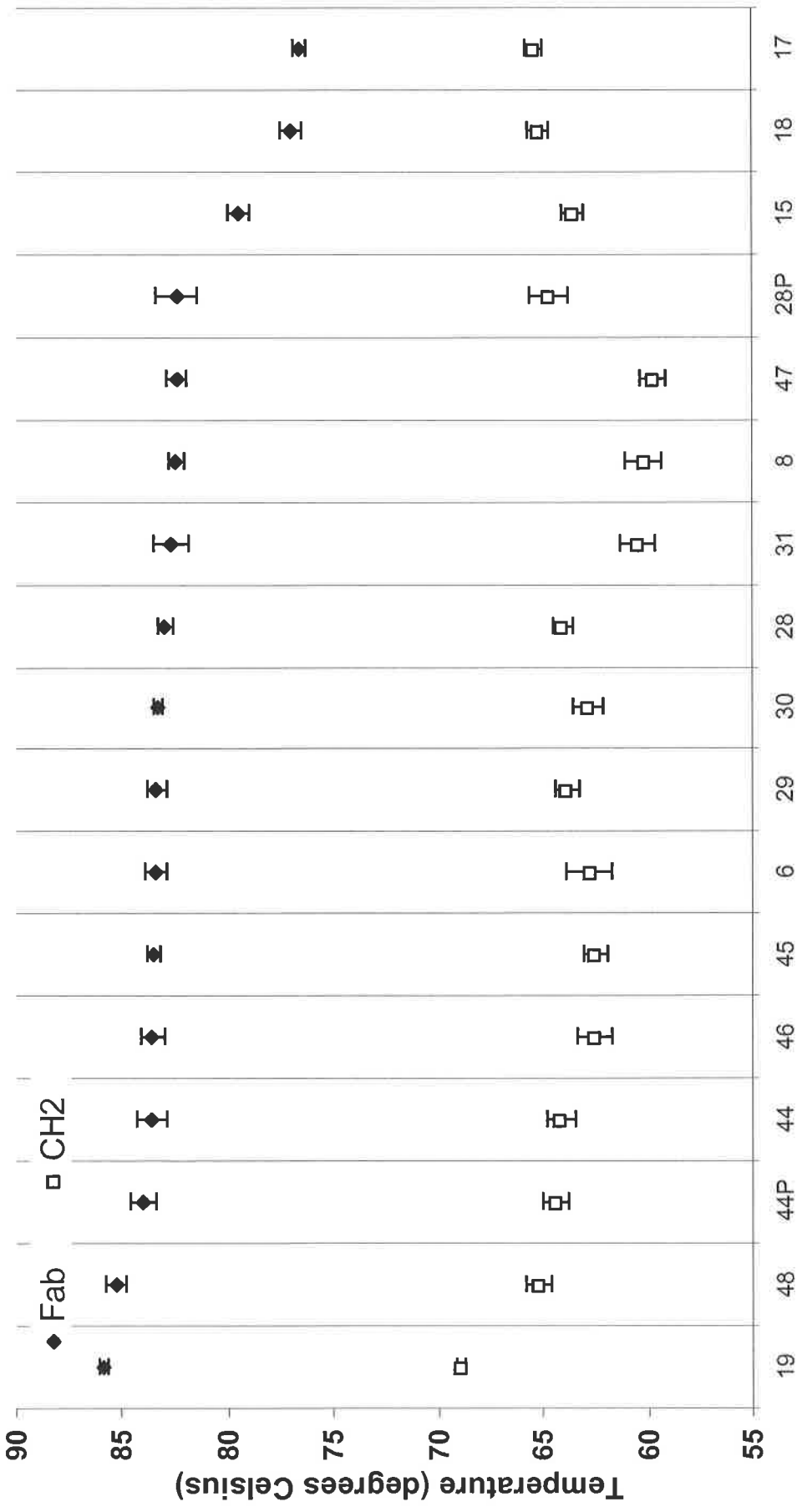

Temperature (degrees Celsius)
90
85
80
75
70
65
60
55
Fab
CH2
19
48
44P
44
46
45
6
29
30
28
31
8
47
28P
15
18
17

Figure 16

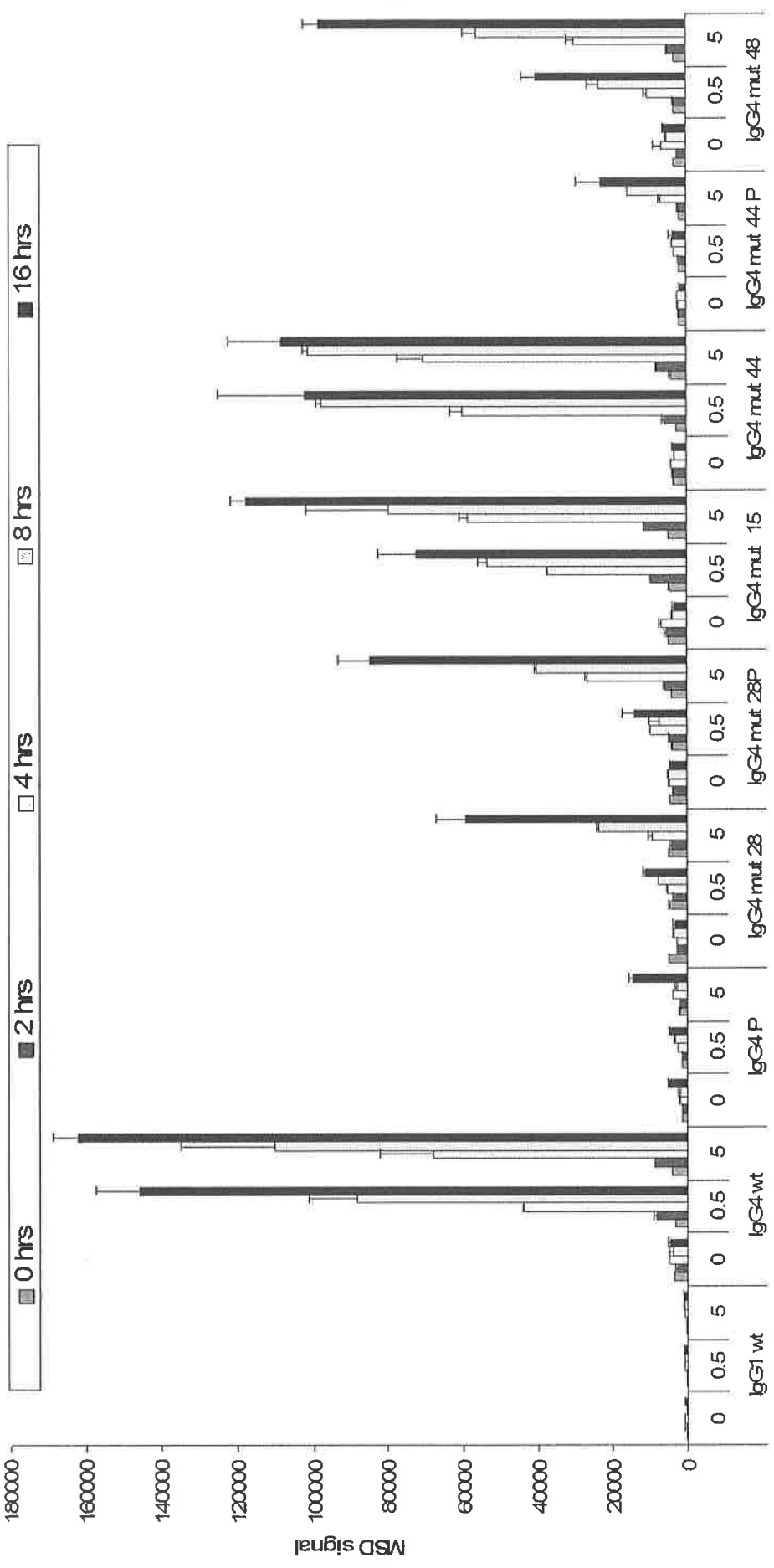

0 hrs
2 hrs
4 hrs
8 hrs
16 hrs
MSD signal
180000
160000
140000
120000
100000
80000
60000
40000
20000
0
0
0.5
5
0
0.5
5
0
0.5
5
0
0.5
5
0
0.5
5
0
0.5
5
0
0.5
5
0
0.5
5
IgG1 wt
IgG4 wt
IgG4 P
IgG4 mut 28
IgG4 mut 28P
IgG4 mut 15
IgG4 mut 44
IgG4 mut 44 P
IgG4 mut 48
GSH Conc

Figure 17

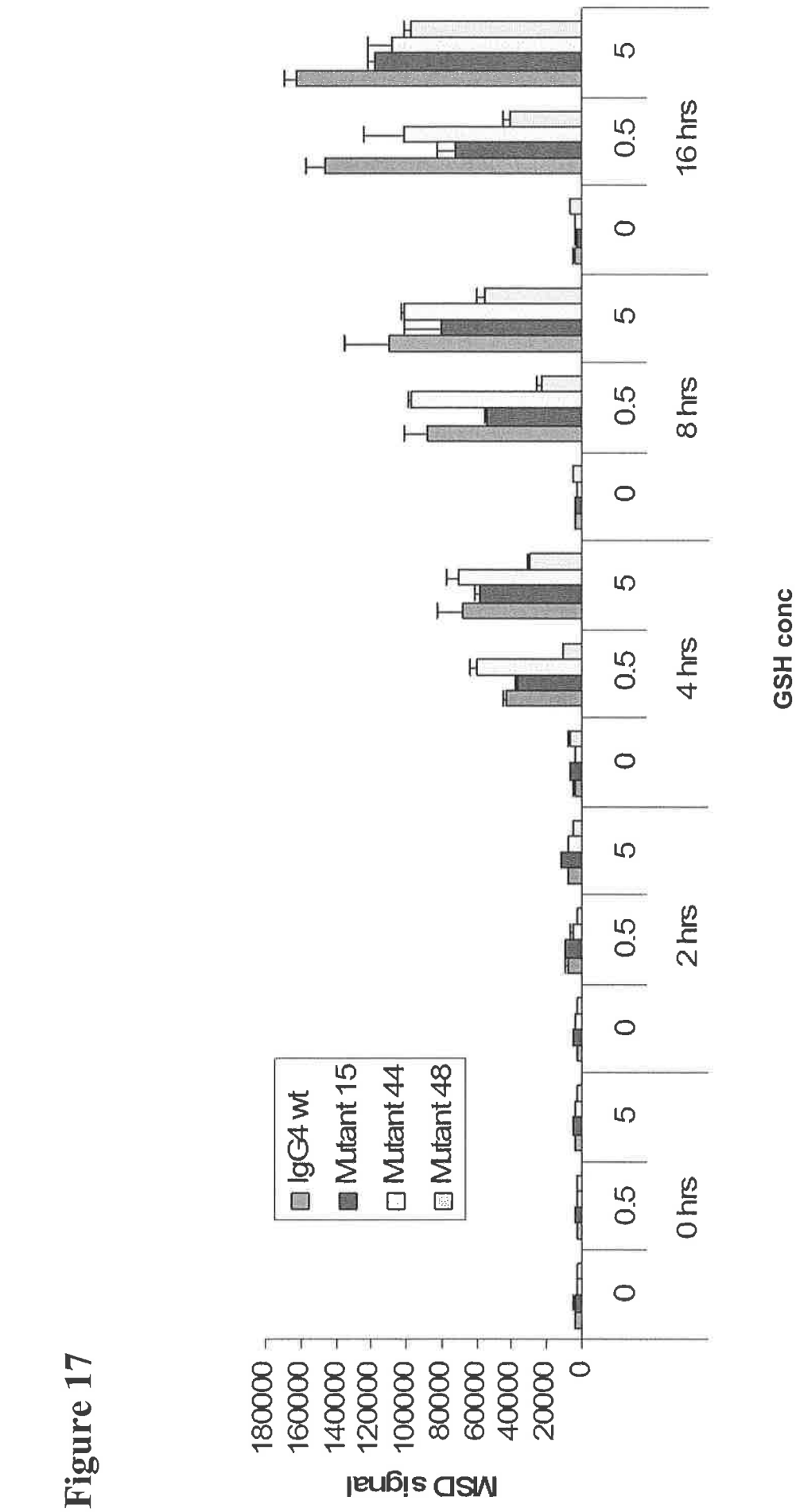

MSD signal
180000
160000
140000
120000
100000
80000
60000
40000
20000
0
IgG4 wt
Mutant 15
Mutant 44
Mutant 48
0
0.5
5
0 hrs
0
0.5
2 hrs
0
0.5
5
4 hrs
0
0.5
5
8 hrs
0
0.5
5
16 hrs
GSH conc

Figure 18

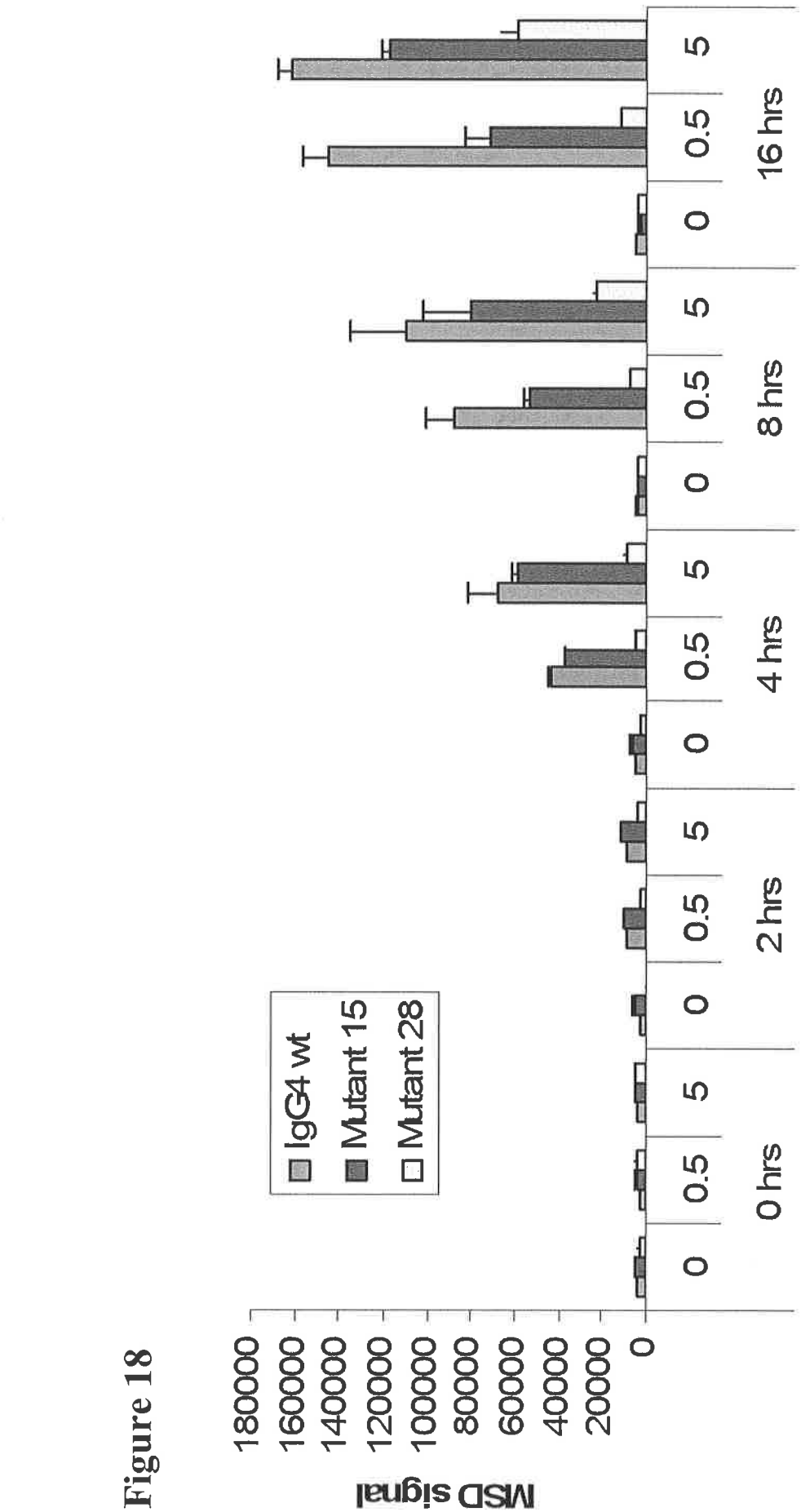

MSD signal
180000
160000
140000
120000
100000
80000
60000
40000
20000
0
IgG4 wt
Mutant 15
Mutant 28
0
0.5
5
0
0.5
5
0
0.5
5
0
0.5
5
0
0.5
5
0 hrs
2 hrs
4 hrs
8 hrs
16 hrs
GSH Conc

Figure 19

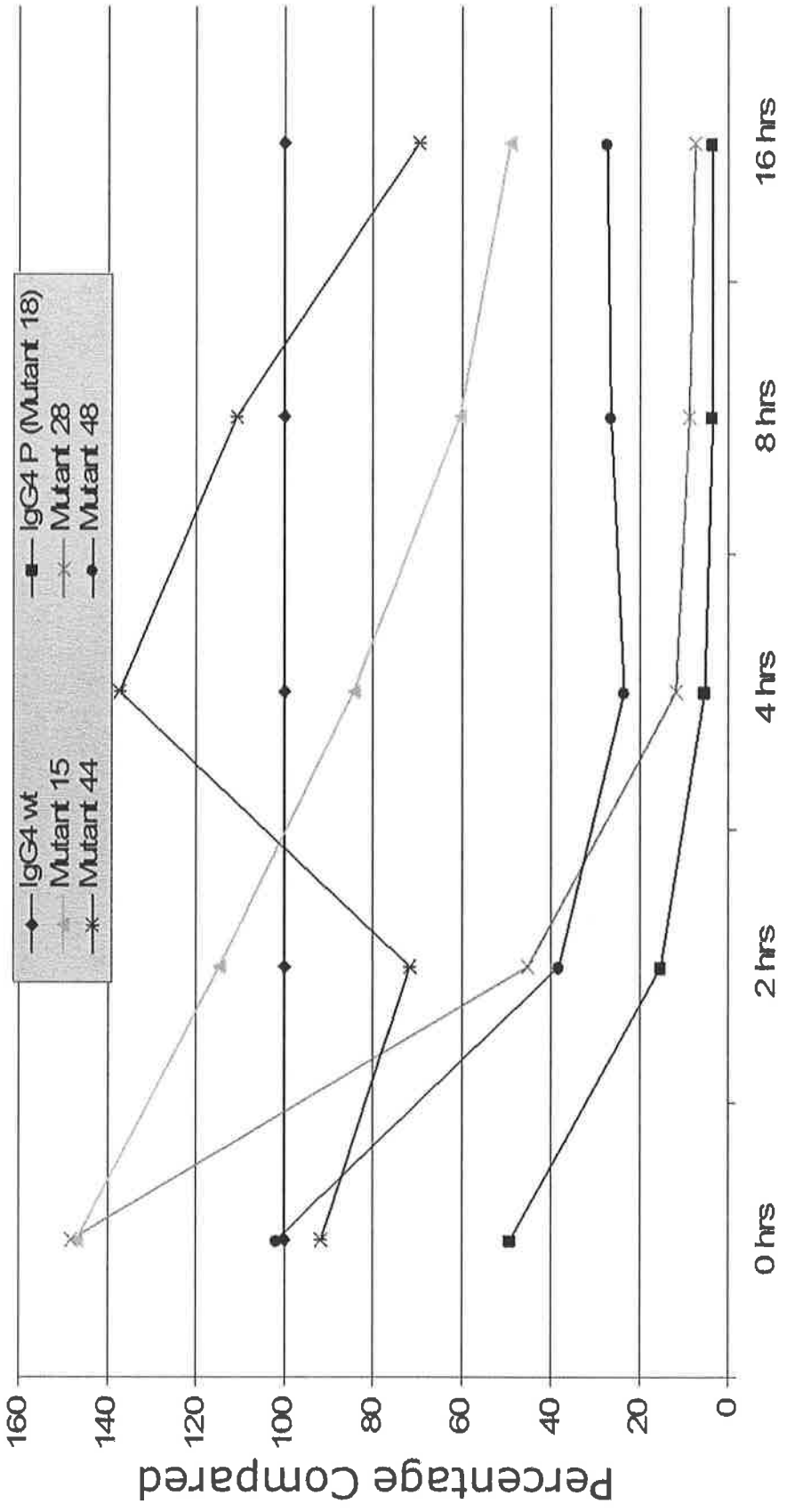

IgG4 wt
IgG4 P (Mutant 18)
Mutant 15
Mutant 28
Mutant 44
Mutant 48
Percentage Compared
160
140
120
100
80
60
40
20
0
0 hrs
2 hrs
4 hrs
8 hrs
16 hrs

Figure 20

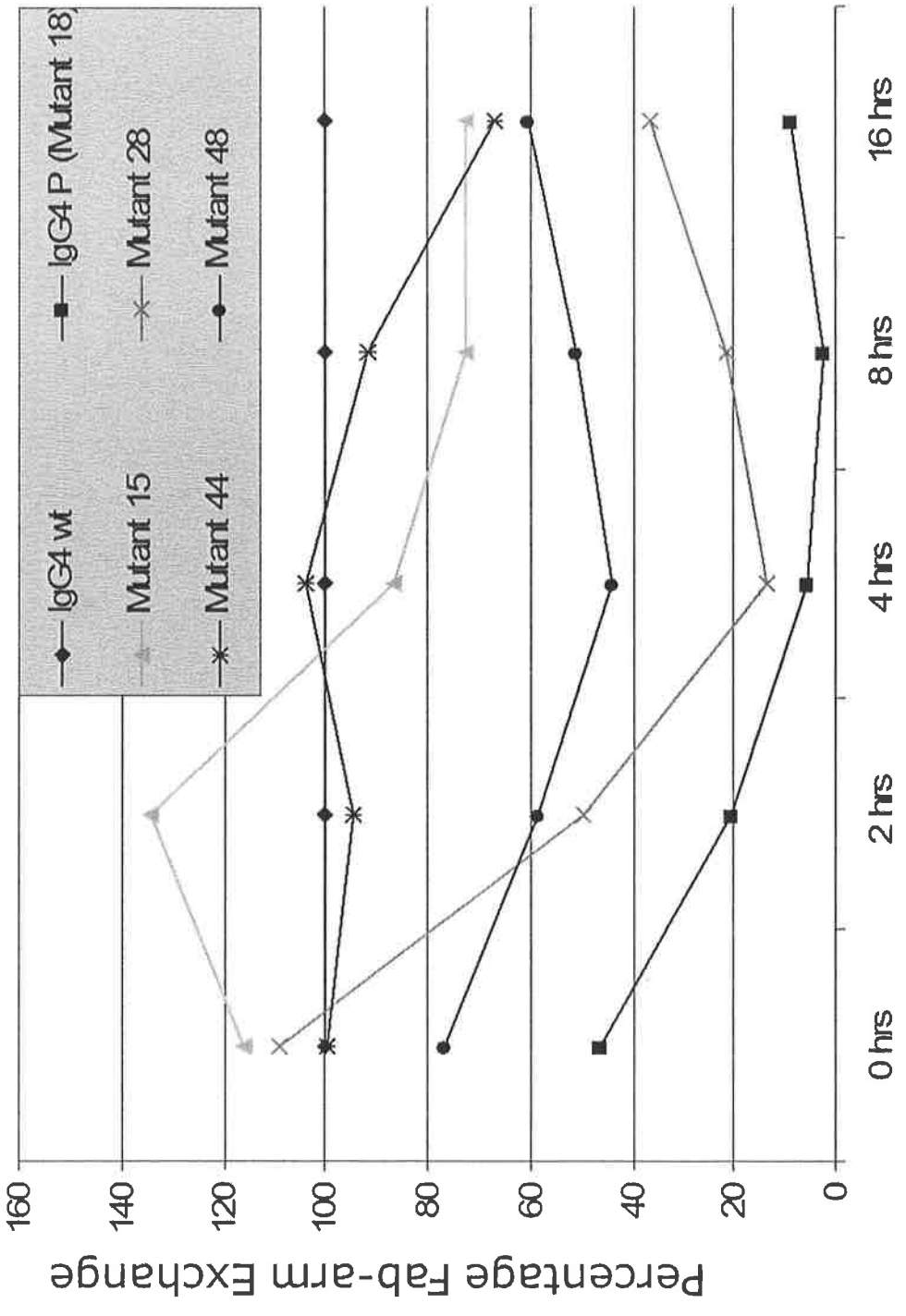

Percentage Fab-arm Exchange
160
140
120
100
80
60
40
20
0
0 hrs
2 hrs
4 hrs
8 hrs
16 hrs
IgG4 wt
IgG4 P (Mutant 18)
Mutant 15
Mutant 28
Mutant 44
Mutant 48

Figure 21 Symmetrical arm exchange analysis of IgG4 mutants with alternative residues at position 241.

