

SEQUENCE LISTING

<110> Jones, Phil C; BOKU - University of Natural Resources and Life Sciences
 <120> Heterodimers and Purification Thereof
 <130> GB application
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33

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gaggctcttc tgtgtgaagc ggttgtgcag agcctc

36

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cttctcatgc tccgtgagcc atgaggctct gcacagccac tacacacag

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ggtgagcgtg ctgaccgtcc tgcaccagga ctggctgaat ggcaaggagt acaagtgc 58

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gcacttgtag tccttgccat tcagccagtc ctgggtgcagg acggtcagca cgctcacc 58

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cacggtgagc ttgctggtga ggaagaagga gccg

34

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36

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ccgggatggg ggcaggggtgc acacctgtgg ttctcg

36

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accctgcccc catgccggga tgagctgacc aagaac

36

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gttcttggtc agctcatccc ggcatggggg cagggt

36

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cccgagaca gggagaggct cttctgtgtg tagcggttgt gcagagcctc

50

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<220>

<223> Oligonucleotide

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cccgagaca gggagaggct cttctgtgtg tggaggctgt gcagagcctc atggctcacg 60
gagcatgaga a 71

<210> 21
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<400> 21

accgtcctgc accaggactg gctgaatggc aaggagtaca agtgc 45

<210> 22
<211> 224
<212> PRT
<213> Feline
<220>

<223> IgG Fc
<400> 22

Cys Pro Lys Cys Pro Pro Pro Glu Met Leu Gly Gly Pro Ser Ile Phe
1 5 10 15
Ile Phe Pro Pro Lys Pro Lys Asp Thr Leu Ser Ile Ser Arg Thr Pro
20 25 30
Glu Val Thr Cys Leu Val Val Asp Leu Gly Pro Asp Asp Ser Asp Val
35 40 45
Gln Ile Thr Trp Phe Val Asp Asn Thr Gln Val Tyr Thr Ala Lys Thr
50 55 60
Ser Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val
65 70 75 80
Leu Pro Ile Leu His Gln Asp Trp Leu Lys Gly Lys Glu Phe Lys Cys
85 90 95

Lys Val Asn Ser Lys Ser Leu Pro Ser Pro Ile Glu Arg Thr Ile Ser
 100 105 110
 Lys Asp Lys Gly Gln Pro His Glu Pro Gln Val Tyr Val Leu Pro Pro
 115 120 125
 Ala Gln Glu Glu Leu Ser Arg Asn Lys Val Ser Val Thr Cys Leu Ile
 130 135 140
 Glu Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ile Thr Gly
 145 150 155 160
 Gln Pro Glu Pro Glu Asn Asn Tyr Arg Thr Thr Pro Pro Gln Leu Asp
 165 170 175
 Ser Asp Gly Thr Tyr Phe Leu Tyr Ser Arg Leu Ser Val Asp Arg Ser
 180 185 190
 Arg Trp Gln Arg Gly Asn Thr Tyr Thr Cys Ser Val Ser His Glu Ala
 195 200 205
 Leu His Ser His His Thr Gln Lys Ser Leu Thr Gln Ser Pro Gly Lys
 210 215 220

<210> 23

<211> 222

<212> PRT

<213> Homo Sapiens

<220>

<223> IgG1 Fc

<400> 23

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
 1 5 10 15
 Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
 20 25 30
 Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
 35 40 45
 Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
 50 55 60
 Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val

65		70		75		80
Leu Thr Val	Leu His Gln Asp Trp	Leu Asn Gly Lys Glu Tyr	Lys Cys			
	85	90	95			
Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser						
	100	105	110			
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro						
	115	120	125			
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val						
	130	135	140			
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly						
145	150	155	160			
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp						
	165	170	175			
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp						
	180	185	190			
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His						
	195	200	205			
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys						
	210	215	220			

<210> 24
<211> 222
<212> PRT
<213> Homo Sapiens
<220>
<223> IgG3 Fc
<400> 24

Cys Pro Arg Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe			
1	5	10	15
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro			
	20	25	30
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val			
	35	40	45

Gln Phe Lys Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
 50 55 60
 Lys Leu Arg Glu Glu Gln Tyr Asn Ser Thr Phe Arg Val Val Ser Val
 65 70 75 80
 Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
 85 90 95
 Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
 100 105 110
 Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
 115 120 125
 Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
 130 135 140
 Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
 145 150 155 160
 Gln Pro Glu Asn Asn Tyr Asn Thr Thr Pro Pro Met Leu Asp Ser Asp
 165 170 175
 Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
 180 185 190
 Gln Gln Gly Asn Ile Phe Ser Cys Ser Val Met His Glu Ala Leu His
 195 200 205
 Asn Arg Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 210 215 220

<210> 25**<211> 330****<212> PRT****<213> Homo Sapiens****<220>****<223> IGHG1 (IgG1 constant heavy chain CH1-CH3)****<400> 25**

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
 1 5 10 15
 Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
 20 25 30
 Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
 35 40 45

Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser
50						55					60				
Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr
65					70				75					80	
Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys
			85						90					95	
Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys
			100					105					110		
Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro
			115				120					125			
Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys
			130			135					140				
Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp
145					150					155					160
Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu
			165						170					175	
Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu
			180					185					190		
His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn
		195				200						205			
Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly
		210				215					220				
Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu
225					230					235					240
Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr
			245						250					255	
Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn
			260					265					270		
Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe
		275					280					285			
Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn
		290				295					300				
Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr
305					310					315					320
Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys						
				325					330						

<210> 26

<211> 326

<212> PRT

<213> Homo Sapiens

<220>

<223> IGHG2 (IgG2 constant heavy chain CH1-CH3)

<400> 26

Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg
1				5					10					15	
Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr
			20					25					30		
Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser
		35				40						45			
Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser
		50				55					60				

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Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr
65          70          75          80
Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
      85          90          95
Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro
      100          105          110
Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
      115          120          125
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
      130          135          140
Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
145          150          155          160
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
      165          170          175
Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp
      180          185          190
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
      195          200          205
Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu
      210          215          220
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
225          230          235          240
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
      245          250          255
Ser Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
      260          265          270
Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
      275          280          285
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
      290          295          300
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
305          310          315          320
Ser Leu Ser Pro Gly Lys
      325

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<210> 27**<211> 377****<212> PRT****<213> Homo Sapiens****<220>****<223> IGHG3 (IgG3 constant heavy chain CH1-CH3)****<400> 27**

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Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
1          5          10          15
Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
      20          25          30
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
      35          40          45
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
      50          55          60
Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65          70          75          80

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Tyr Thr Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
      85                      90                      95
Arg Val Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr Cys Pro
      100                      105                      110
Arg Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg
      115                      120                      125
Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys
      130                      135                      140
Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro
      145                      150                      155                      160
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
      165                      170                      175
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
      180                      185                      190
Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Lys Trp Tyr
      195                      200                      205
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Leu Arg Glu Glu
      210                      215                      220
Gln Tyr Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Leu His
      225                      230                      235                      240
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
      245                      250                      255
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
      260                      265                      270
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
      275                      280                      285
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
      290                      295                      300
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
      305                      310                      315                      320
Tyr Asn Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu
      325                      330                      335
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Ile
      340                      345                      350
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Tyr Thr Gln
      355                      360                      365
Lys Ser Leu Ser Leu Ser Pro Gly Lys
      370                      375

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<210> 28**<211> 327****<212> PRT****<213> Homo Sapiens****<220>****<223> IGHG4 (IgG4 constant heavy chain CH1-CH3)****<400> 28**

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Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
1      5                      10                      15
Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
      20                      25                      30
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
      35                      40                      45
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser

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50		55		60											
Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr
65					70					75					80
Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys
			85						90					95	
Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Ser	Cys	Pro	Ala	Pro
			100					105					110		
Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys
		115					120					125			
Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val
	130					135					140				
Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp
145					150				155						160
Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe
			165					170						175	
Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp
		180					185					190			
Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu
	195					200					205				
Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg
	210					215					220				
Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys
225					230					235					240
Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp
			245					250						255	
Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys
		260					265						270		
Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser
	275						280					285			
Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser
	290					295					300				
Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser
305					310				315						320
Leu	Ser	Leu	Ser	Leu	Gly	Lys									
				325											

<210> 29

<211> 319

<212> PRT

<213> Homo Sapiens

<220>

<223> IgG1-Fc sequence with the N-terminal a-mating factor leader
sequence of the pPICZaA vector

<400> 29

Met	Arg	Phe	Pro	Ser	Ile	Phe	Thr	Ala	Val	Leu	Phe	Ala	Ala	Ser	Ser
1				5					10					15	
Ala	Leu	Ala	Ala	Pro	Val	Asn	Thr	Thr	Thr	Glu	Asp	Glu	Thr	Ala	Gln
			20					25					30		
Ile	Pro	Ala	Glu	Ala	Val	Ile	Gly	Tyr	Ser	Asp	Leu	Glu	Gly	Asp	Phe
		35					40					45			
Asp	Val	Ala	Val	Leu	Pro	Phe	Ser	Asn	Ser	Thr	Asn	Asn	Gly	Leu	Leu
	50					55				60					
Phe	Ile	Asn	Thr	Thr	Ile	Ala	Ser	Ile	Ala	Ala	Lys	Glu	Glu	Gly	Val

65					70					75				80
Ser	Leu	Glu	Lys	Arg	Glu	Ala	Glu	Ala	Glu	Phe	Thr	Cys	Pro	Pro Cys
				85					90				95	
Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro Pro
			100					105					110	
Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr Cys
		115					120					125		
Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn Trp
	130					135					140			
Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg Glu
145					150					155				160
Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val Leu
			165					170					175	
His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser Asn
		180						185					190	
Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys Gly
	195						200					205		
Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp Glu
	210				215						220			
Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe Tyr
225					230					235				240
Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu Asn
			245					250					255	
Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe Phe
		260					265					270		
Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly Asn
	275					280					285			
Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr Thr
	290					300				305				
Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys					
310					315									

<210> 30**<211> 942****<212> DNA****<213> Homo Sapiens and Pichia pastoris****<220>****<223> IgG1-Fc sequence with the N-terminal a-mating factor leader sequence used in the Pichia pastoris pPICZaA vector****<400> 30**

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tactcagatt tagaagggga tttcgatggt gctgttttgc cattttccaa cagcacaaat 180
aacgggttat tgtttataaa tactactatt gccagcattg ctgctaaaga agaaggggta 240
tctctcgaga aaagagaggc tgaagctgaa ttcacatgcc caccgtgccc agcacctgaa 300
ctcctggggg gaccgtcagt cttcctcttc cccccaaaac ccaaggacac cctcatgata 360
tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga gccacgaaga ccctgagggtc 420
aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgcgggag 480
gagcagtaca acagcacgta ccgtgtggtc agcgtcctca ccgtcctgca ccaggactgg 540
ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag ccctcccagc ccccatcgag 600
aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca 660

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tccccgggatg agctgaccaa gaaccagggtc agcctgacct gcctgggtcaa aggcttctat 720
cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc 780
acgcctcccg tgctggactc cgacggctcc ttcttcctct acagcaagct caccgtggac 840
aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac 900
aaccactaca cacagaagag cctctccctg tctccgggta aa 942

```

<210> 31

<211> 242

<212> PRT

<213> Homo Sapiens

<220>

<223> IgG1-Fc sequence with the N-terminal leader sequence used in the pTT5 mammalian expression vector

<400> 31

```

Met Glu Leu Gly Leu Ser Trp Ile Phe Leu Leu Ala Ile Leu Lys Gly
1      5      10      15
Val Gln Cys Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
20      25      30
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
35      40      45
Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
50      55      60
Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
65      70      75      80
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
85      90      95
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
100     105     110
Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
115     120     125
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
130     135     140
Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
145     150     155     160
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
165     170     175
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
180     185     190
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
195     200     205
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
210     215     220
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
225     230     235     240
Gly Lys

```

<210> 32

<211> 726

<212> DNA

<213> Homo Sapiens

<220>

<223> IgG1-Fc sequence with the N-terminal leader sequence used in the pTT5 mammalian expression vector

<400> 32

```
atggagctgg gcctgagctg gatcttctctg ctggccatcc tgaagggcgt gcagtgcacg 60
tgtcccccat gtcccgcccc tgagctgctg ggcggccctt cctgtttcct gttccctccc 120
aagccaaagg acaccctgat gatctcccgg acccctgagg tgacctgtgt ggtggtggac 180
gtgagccacg aggaccacaga ggtgaagtgc aactggtacg tggacggcgt ggaggtgcac 240
aacgccaaaga ccaagcctag agaggagcag tacaacagca cctaccgcgt ggtgagcgtg 300
ctgaccgtgc tgcaccagga ttggctgaat ggcaaggagt acaagtgcaa ggtgagcaac 360
aaggccctgc ctgcccccat cgagaagacc atctccaagg ccaagggccca gcctcgagaa 420
ccacaggtgt acaccctgcc cccatcccgg gatgagctga ccaagaacca ggtcagcctg 480
acctgcctgg tcaaaggctt ctatcccagc gacatcgccg tggagtggga gagcaatggg 540
cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctcttctctc 600
ctctacagca agctcaccgt ggacaagagc aggtggcagc aggggaacgt cttctcatgc 660
tccgtgatgc atgaggctct gcacaaccac tacacacaga agagcctctc cctgtctccg 720

ggtaaa 726
```

<210> 33

<211> 725

<212> DNA

<213> Homo Sapiens

<220>

<223> IgG1-Fc sequence with the N-terminal leader sequence with an EcoN1 restriction site, used in the pTT5 mammalian expression vector

<400> 33

```
atggagctgg gcctgagctg gatcttctctg ctggccatcc tgaagggcgt gcagtgcacg 60
tgtcccccat gtcccgcccc tgagctgctg ggcggccctt cctgtttcct gttccctccc 120
aagccaaagg acaccctgat gatctcccgg acccctgagg tgacctgtgt ggtggtggac 180
gtgagccacg aggaccacaga ggtgaagtgc aactggtacg tggacggcgt ggaggtgcac 240
aacgccaaaga ccaagcctag agaggagcag tacaacagca cctaccgcgt ggtgagcgtg 300
ctgaccgtgc tgcaccagga ctggctgaat ggcaaggagt acaagtgcaa ggtgagcaac 360
aaggccctgc ctgcccccat cgagaagacc atctccaagg ccaagggccca gcctcgagaa 420
ccacaggtgt acaccctgcc cccatcccgg gatgagctga ccaagaacca ggtcagcctg 480
acctgcctgg tcaaaggctt ctatcccagc gacatcgccg tggagtggga gagcaatggg 540
cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctcttctctc 600
ctctacagca agctcaccgt ggacaagagc aggtggcagc aggggaacgt cttctcatgc 660
tccgtgatgc atgaggctct gcacaaccac tacacacaga agagcctctc cctgtctccg 720

ggtaa 725
```

<210> 34

<211> 330
 <212> PRT
 <213> Homo Sapiens
 <220>
 <223> IgG1 constant heavy chain (CH1-CH3)
 <400> 34

Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	1	5	10	15
Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	20	25	30	
Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	35	40	45	
Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	50	55	60	
Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	65	70	75	80
Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	85	90	95	
Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	100	105	110	
Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	115	120	125	
Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	130	135	140	
Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	145	150	155	160
Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	165	170	175	
Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	180	185	190	
His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	195	200	205	
Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	210	215	220	
Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	225	230	235	240
Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	245	250	255	
Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	260	265	270	
Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	275	280	285	
Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	290	295	300	
Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	305	310	315	320
Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys							325	330		

<210> 35
 <211> 219

<212> **PRT**
 <213> **Homo Sapiens**
 <220>
 <223> **IgG1-Fc incorporating CH2 and CH3 domains**
 <400> **35**

```

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
1      5      10      15
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
20      25      30
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
35      40      45
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
50      55      60
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
65      70      75      80
Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
85      90      95
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
100     105     110
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
115     120     125
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
130     135     140
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
145     150     155     160
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
165     170     175
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
180     185     190
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
195     200     205
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
210     215

```

<210> **36**
 <211> **219**
 <212> **PRT**
 <213> **Homo Sapiens**
 <220>
 <223> **IgG1-Fc with M428S/N434S**
 <400> **36**

```

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
1      5      10      15
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
20      25      30
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
35      40      45

```

Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg
50						55					60				
Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val
65					70					75					80
Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser
			85						90					95	
Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys
		100						105					110		
Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp
		115					120					125			
Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe
130						135				140					
Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu
145					150					155					160
Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe
				165					170					175	
Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly
				180				185					190		
Asn	Val	Phe	Ser	Cys	Ser	Val	Ser	His	Glu	Ala	Leu	His	Ser	His	Tyr
		195					200					205			
Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys					
210						215									

<210> 37

<211> 224

<212> PRT

<213> Homo Sapiens

<220>

<223> IgG1-Fc with M428S/N434S/Y436H

<400> 37

Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro
1				5					10					15	
Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr
			20					25					30		
Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn
		35					40					45			
Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg
50						55					60				
Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val
65					70					75					80
Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser
			85						90					95	
Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys
		100						105					110		
Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp
		115					120					125			
Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe
130						135				140					
Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu
145					150					155					160
Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe
				165					170					175	
Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly

<210>	38
<211>	219
<212>	PRT
<213>	Homo Sapiens
<220>	
<223>	IgG1-Fc with M428S/N434S/H435R/Y436H
<400>	38

Cys 1	Pro	Ala	Pro	Glu 5	Leu	Leu	Gly	Gly	Pro 10	Ser	Val	Phe	Leu	Phe 15	Pro
Pro	Lys	Pro	Lys 20	Asp	Thr	Leu	Met	Ile 25	Ser	Arg	Thr	Pro	Glu 30	Val	Thr
Cys	Val	Val	Val 35	Asp	Val	Ser	His 40	Glu	Asp	Pro	Glu	Val 45	Lys	Phe	Asn
Trp	Tyr 50	Val	Asp	Gly	Val	Glu 55	Val	His	Asn	Ala	Lys 60	Thr	Lys	Pro	Arg
Glu 65	Glu	Gln	Tyr	Asn 70	Ser	Thr	Tyr	Arg	Val 75	Val	Ser	Val	Leu	Thr 80	Val
Leu	His	Gln	Asp	Trp 85	Leu	Asn	Gly	Lys	Glu 90	Tyr	Lys	Cys	Lys 95	Val	Ser
Asn	Lys	Ala	Leu 100	Pro	Ala	Pro	Ile	Glu 105	Lys	Thr	Ile	Ser	Lys 110	Ala	Lys
Gly	Gln	Pro	Arg 115	Glu	Pro	Gln	Val 120	Tyr	Thr	Leu	Pro	Pro 125	Ser	Arg	Asp
Glu	Leu 130	Thr	Lys	Asn	Gln	Val 135	Ser	Leu	Thr	Cys	Leu 140	Val	Lys	Gly	Phe
Tyr 145	Pro	Ser	Asp	Ile 150	Ala	Val	Glu	Trp	Glu 155	Ser	Asn	Gly	Gln 160	Pro	Glu
Asn	Asn	Tyr	Lys	Thr 165	Thr	Pro	Pro	Val	Leu 170	Asp	Ser	Asp	Gly 175	Ser	Phe
Phe	Leu	Tyr	Ser 180	Lys	Leu	Thr	Val	Asp 185	Lys	Ser	Arg	Trp	Gln 190	Gln	Gly
Asn	Val	Phe 195	Ser	Cys	Ser	Val	Ser 200	His	Glu	Ala	Leu	His 205	Ser	Arg	His
Thr	Gln 210	Lys	Ser	Leu	Ser	Leu 215	Ser	Pro	Gly	Lys					

<210>	39
<211>	326
<212>	PRT
<213>	Homo Sapiens
<220>	

<223> IgG2 constant heavy chain (CH1-CH3)

<400> 39

```

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
1      5      10
Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
      20      25      30
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
      35      40      45
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
      50      55      60
Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr
65      70      75      80
Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
      85      90      95
Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro
      100      105      110
Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
      115      120      125
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
      130      135      140
Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
145      150      155      160
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
      165      170      175
Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp
      180      185      190
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
      195      200      205
Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu
      210      215      220
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
225      230      235      240
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
      245      250      255
Ser Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
      260      265      270
Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
      275      280      285
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
      290      295      300
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
305      310      315      320
Ser Leu Ser Pro Gly Lys
      325

```

<210> 40

<211> 216

<212> PRT

<213> Homo Sapiens

<220>

<223> IgG2-Fc incorporating CH2 and CH3 domains

<400> 40

```

Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
1      5      10      15
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
20      25      30
Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val
35      40      45
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
50      55      60
Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln
65      70      75      80
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly
85      90      95
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro
100     105     110
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
115     120     125
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
130     135     140
Asp Ile Ser Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
145     150     155     160
Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
165     170     175
Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
180     185     190
Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
195     200     205
Ser Leu Ser Leu Ser Pro Gly Lys
210     215

```

<210> 41

<211> 216

<212> PRT

<213> Homo Sapiens

<220>

<223> IgG2-Fc with M428S/N434S

<400> 41

```

Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
1      5      10      15
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
20      25      30
Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val
35      40      45
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
50      55      60
Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln
65      70      75      80
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly
85      90      95
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro

```

```

      100      105      110
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
      115      120      125
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
      130      135      140
Asp Ile Ser Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
145      150      155      160
Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
      165      170      175
Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
      180      185      190
Ser Cys Ser Val Ser His Glu Ala Leu His Ser His Tyr Thr Gln Lys
      195      200      205
Ser Leu Ser Leu Ser Pro Gly Lys
210      215

```

```

<210>      42
<211>      216
<212>      PRT
<213>      Homo Sapiens
<220>
<223>      IgG2-Fc with M428S/N434S/Y436H
<400>      42

```

```

Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
1      5      10      15
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
      20      25      30
Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val
      35      40      45
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
50      55      60
Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln
65      70      75      80
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly
      85      90      95
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro
      100      105      110
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
      115      120      125
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
      130      135      140
Asp Ile Ser Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
145      150      155      160
Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
      165      170      175
Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
      180      185      190
Ser Cys Ser Val Ser His Glu Ala Leu His Ser His His Thr Gln Lys
      195      200      205
Ser Leu Ser Leu Ser Pro Gly Lys
210      215

```


<210> 43
 <211> 216
 <212> PRT
 <213> Homo Sapiens
 <220>
 <223> IgG2-Fc with M428S/N434S/H435R/Y436H
 <400> 43

```

Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
1      5      10      15
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
20      25      30
Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val
35      40      45
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
50      55      60
Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln
65      70      75      80
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly
85      90      95
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro
100     105     110
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
115     120     125
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
130     135     140
Asp Ile Ser Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
145     150     155     160
Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
165     170     175
Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
180     185     190
Ser Cys Ser Val Ser His Glu Ala Leu His Ser Arg His Thr Gln Lys
195     200     205
Ser Leu Ser Leu Ser Pro Gly Lys
210      215
  
```

<210> 44
 <211> 377
 <212> PRT
 <213> Homo Sapiens
 <220>
 <223> IgG3 constant heavy chain (CH1-CH3)
 <400> 44

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg

```

1           5           10           15
Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
                20                25                30
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
                35                40                45
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
                50                55                60
Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65                70                75                80
Tyr Thr Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                90                95
Arg Val Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr Cys Pro
                100                105                110
Arg Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg
                115                120                125
Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys
                130                135                140
Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro
145                150                155                160
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                165                170                175
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
                180                185                190
Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Lys Trp Tyr
                195                200                205
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Leu Arg Glu Glu
                210                215                220
Gln Tyr Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Leu His
225                230                235                240
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                245                250                255
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
                260                265                270
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
                275                280                285
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
                290                295                300
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
305                310                315                320
Tyr Asn Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu
                325                330                335
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Ile
                340                345                350
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Tyr Thr Gln
                355                360                365
Lys Ser Leu Ser Leu Ser Pro Gly Lys
                370                375

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<210> 45**<211> 217****<212> PRT****<213> Homo Sapiens****<220>****<223> IgG3-Fc incorporating CH2 and CH3 domains****<400> 45**

Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys
1			5						10					15	
Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val
			20					25					30		
Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Gln	Phe	Lys	Trp	Tyr
		35					40					45			
Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Leu	Arg	Glu	Glu
	50					55					60				
Gln	Tyr	Asn	Ser	Thr	Phe	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His
65					70					75					80
Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys
				85					90					95	
Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln
			100					105					110		
Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met
		115					120					125			
Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro
	130					135					140				
Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn
145					150					155					160
Tyr	Asn	Thr	Thr	Pro	Met	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	
				165				170					175		
Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Ile
			180				185						190		
Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	Arg	Tyr	Thr	Gln
		195					200					205			
Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys							
		210					215								

<210> 46
<211> 217
<212> PRT
<213> Homo Sapiens
<220>
<223> IgG3-Fc with M428S/N434S
<400> 46

Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys
1			5						10					15	
Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val
			20					25					30		
Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Gln	Phe	Lys	Trp	Tyr
		35					40					45			
Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Leu	Arg	Glu	Glu
	50					55					60				
Gln	Tyr	Asn	Ser	Thr	Phe	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His
65					70					75					80
Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys
				85					90					95	
Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln
			100					105					110		

```

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
    115                      120                      125
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    130                      135                      140
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
145                      150                      155                      160
Tyr Asn Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu
    165                      170                      175
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Ile
    180                      185                      190
Phe Ser Cys Ser Val Ser His Glu Ala Leu His Ser Arg Tyr Thr Gln
    195                      200                      205
Lys Ser Leu Ser Leu Ser Pro Gly Lys
    210                      215

```

<210> 47

<211> 217

<212> PRT

<213> Homo Sapiens

<220>

<223> IgG3-Fc with M428S/N434S/Y436H or F436H

<400> 47

```

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
1      5      10      15
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
    20      25      30
Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Lys Trp Tyr
    35      40      45
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Leu Arg Glu Glu
    50      55      60
Gln Tyr Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Leu His
65      70      75      80
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
    85      90      95
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
    100     105     110
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
    115     120     125
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    130     135     140
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
145     150     155     160

Tyr Asn Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu
    165     170     175
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Ile
    180     185     190
Phe Ser Cys Ser Val Ser His Glu Ala Leu His Ser Arg His Thr Gln
    195     200     205
Lys Ser Leu Ser Leu Ser Pro Gly Lys
    210     215

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<210> 48
 <211> 327
 <212> PRT
 <213> Homo Sapiens
 <220>
 <223> IgG4 constant heavy chain (CH1-CH3)
 <400> 48

Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	1	5	10	15
Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	20	25	30	
Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	35	40	45	
Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	50	55	60	
Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	65	70	75	80
Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	85	90	95	
Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Ser	Cys	Pro	Ala	Pro	100	105	110	
Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	115	120	125	
Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	130	135	140	
Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	145	150	155	160
Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	165	170	175	
Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	180	185	190	
Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	195	200	205	
Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	210	215	220	
Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	225	230	235	240
Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	245	250	255	
Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	260	265	270	
Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	275	280	285	
Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	290	295	300	
Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	305	310	315	320
Leu	Ser	Leu	Ser	Leu	Gly	Lys										325			

<210> 49
 <211> 217

<212> **PRT**
 <213> **Homo Sapiens**
 <220>
 <223> **IgG4 -Fc incorporating CH2 and CH3 domains**
 <400> **49**

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Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
1          5          10          15
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
          20          25          30
Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
          35          40          45
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
          50          55          60
Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65          70          75          80
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
          85          90          95
Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
          100          105          110
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met
          115          120          125
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
          130          135          140
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
145          150          155          160
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
          165          170          175
Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val
          180          185          190
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
          195          200          205
Lys Ser Leu Ser Leu Ser Leu Gly Lys
          210          215

```

<210> **50**
 <211> **217**
 <212> **PRT**
 <213> **Homo Sapiens**
 <220>
 <223> **IgG4-Fc with M428S/N434S**
 <400> **50**

```

Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
1          5          10          15
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
          20          25          30
Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
          35          40          45
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu

```

50		55		60
Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His				
65		70		75
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys				
	85		90	95
Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln				
	100		105	110
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met				
	115		120	125
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro				
	130		135	140
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn				
145		150		155
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu				
	165		170	175
Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val				
	180		185	190
Phe Ser Cys Ser Val Ser His Glu Ala Leu His Ser His Tyr Thr Gln				
	195		200	205
Lys Ser Leu Ser Leu Ser Leu Gly Lys				
210		215		

<210> 51

<211> 217

<212> PRT

<213> Homo Sapiens

<220>

<223> IgG4 with M428S/N434S/Y436H

<400> 51

Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys				
1	5		10	15
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val				
	20		25	30
Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr				
	35		40	45
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu				
	50		55	60
Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His				
65		70		75
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys				
	85		90	95
Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln				
	100		105	110
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met				
	115		120	125
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro				
	130		135	140
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn				
145		150		155
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu				
	165		170	175
Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val				
	180		185	190
Phe Ser Cys Ser Val Ser His Glu Ala Leu His Ser His His Thr Gln				

195 200 205
 Lys Ser Leu Ser Leu Ser Leu Gly Lys
 210 215

<210> 52
 <211> 217
 <212> PRT
 <213> Homo Sapiens
 <220>
 <223> IgG4 with M428S/N434S/H435R/Y436H
 <400> 52

Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 1 5 10 15
 Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 20 25 30
 Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
 35 40 45
 Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 50 55 60
 Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 65 70 75 80
 Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 85 90 95
 Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 100 105 110
 Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met
 115 120 125
 Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 130 135 140
 Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 145 150 155 160
 Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 165 170 175
 Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val
 180 185 190
 Phe Ser Cys Ser Val Ser His Glu Ala Leu His Ser Arg His Thr Gln
 195 200 205
 Lys Ser Leu Ser Leu Ser Leu Gly Lys
 210 215

<210> 53
 <211> 27
 <212> PRT
 <213> Homo Sapiens
 <220>
 <223> Peptide from IgG1 positions 419-445

<400> 53

```

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
1           5           10           15
His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
20           25

```

210> 54

<211> 27

<212> PRT

<213> Homo Sapiens and Influenza A virus

<220>

<223> Peptide from IgG1 positions 419-445 conatining 9 residues from the hemagglutinun (HA) peptide of the influenza A virus (position 10-18 in the sequence below)

<400> 54

```

Gln Gly Asn Val Phe Ser Cys Ser Val Tyr Val Lys Gln Asn Thr Leu
1           5           10           15
Lys Leu Thr Gln Lys Ser Leu Ser Leu Ser Pro
20           25

```

210> 55

<211> 10

<212> PRT

<213> Homo Sapiens

<220>

<223> Peptide from IgG1 positions 434-443 with N434S mutation

<400> 55

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Ser His Tyr Thr Gln Lys Ser Leu Ser Leu
1           5           10

```

210> 56

<211> 10

<212> PRT

<213> Homo Sapiens

<220>

<223> Peptide from IgG1 positions 435-444 with Y436H mutation

<400> 56

His	His	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser
1				5					10

210> 57

<211> 10

<212> PRT

<213> Homo Sapiens

<220>

<223> Peptide from IgG1 positions 434-443 with N434A mutation

<400> 57

Ala	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu
1				5					10

210> 58

<211> 10

<212> PRT

<213> Homo Sapiens

<220>

<223> Peptide from IgG1 positions 434-443

<400> 58

Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu
1				5					10

210> 59

<211> 10

<212> PRT

<213> Influenza A virus H3N2

<220>

<223> Sequence from part of the hemagglutinin (HA) peptide of the influenza A peptide

<400> 59

Val Tyr Val Lys Arg Asn Thr Leu Lys Leu
1 5 10

210> 60

<211> 10

<212> PRT

<213> Influenza A virus H3N2

<220>

<223> Sequence from part of the HA peptide of the influenza A virus

<400> 60

Tyr Val Lys Arg Asn Thr Leu Lys Leu Thr
1 5 10

210> 61

<211> 10

<212> PRT

<213> Homo Sapiens

<220>

<223> Peptide from IgG1 positions 437-443, preceded by three amino acids Leu-Lys-Leu derived from the the last three resdiues of the HA peptide

<400> 61

Leu Lys Leu Thr Gln Lys Ser Leu Ser Leu
1 5 10

<210> 62

<211> 807

<212> DNA

<213> Homo Sapiens

<220>

<223> IgG2-Fc sequence with the N-terminal leader sequence with EcoR1 and BamH1 restriction sites, used in the pTT5 mammalian expression vector

<400> 62

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CTCCCAGGTC CAAGTTTAAA CGGATCTCTA GCGAATTCCA CCATGGAGCT GGGCCTGAGC      60
TGGATCTTCC TGCTGGCCAT CCTGAAGGGC GTGCAGTGCG AGTGCCCTCC TTGTCTTGCT      120
CCTCCAGTGG CCGGACCTAG CGTGTTCTTG TTCCCCCAA AGCCCAAGGA CACCCTGATG      180
ATCAGCCGGA CCCCCGAAGT GACCTGCGTG GTGGTGGATG TGTCCACGA GGACCCGAG      240
GTGCAGTTCA ATTGGTACGT GGACGGCGTG GAAGTGCACA ACGCCAAGAC CAAGCCCAGA      300
GAGGAACAGT TCAACAGCAC CTTCCGGGTG GTGTCCGTGC TGACCGTGGT GCATCAGGAC      360
TGGCTGAACG GCAAAGAGTA CAAGTGCAAG GTGTCCAACA AGGGCCTGCC TGCCCCATC      420
GAGAAAACCA TCAGCAAGAC AAAGGGCCAG CCCC GCGAGC CCCAGGTGTA CACTGCCT      480
CCAAGCCGGG AAGAGATGAC CAAGAACCAG GTGTCCCTGA CCTGTCTCGT GAAGGGCTTC      540
TACCCAGCG ACATCAGCGT GGAATGGGAG AGCAACGGCC AGCCCGAGAA CACTACAAG      600
ACCACCCCCC CCATGCTGGA CTCCGACGGC TCCTTCTTCC TCTACAGCA GCTCACCCTG      660
GACAAGAGCA GGTGGCAGCA GGGGAACGTC TTCTCATGCT CCGTGATGCA TGAGGCTCTG      720
CACAACCACT ACACACAGAA GAGCCTCTCC CTGTCTCCGG GTAAATGAGG ATCCCCGAC      780
CTCGACCTCT GGCTAATAAA GGAAATT      807

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<210> 63

<211> 810

<212> DNA

<213> Homo Sapiens

<220>

<223> IgG4-Fc sequence with the N-terminal leader sequence with EcoR1 and BamH1 restriction sites, used in the pTT5 mammalian expression vector

<400> 63

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CTCCCAGGTC CAAGTTTAAA CGGATCTCTA GCGAATTCCA CCATGGAGCT GGGCCTGAGC      60
TGGATCTTCC TGCTGGCCAT CCTGAAGGGC GTGCAGTGCC CTTGCCCTTC TTGTCCCGCC      120
CCTGAGTTTC TGGGCGGACC CAGCGTGTTT CTGTTCCCCC CAAAGCCCAA GGACACCCTG      180
ATGATCAGCC GGACCCCCGA AGTGACCTGC GTGGTGGTGG ATGTGTCCCA GGAAGATCCC      240
GAGGTGCAGT TCAATTGGTA CGTGGACGGC GTGGAAGTGC ACAACGCCAA GACCAAGCCC      300
AGAGAGGAAC AGTTCAACAG CACCTACCGG GTGGTGTCCG TGCTGACCGT GCTGCACCAG      360
GACTGGCTGA ACGGCAAAGA GTACAAGTGC AAGGTGTCCA ACAAGGGCCT GCCCAGCAGC      420
ATCGAGAAAA CCATCAGCAA GGCCAAGGGC CAGCCCCGCG AACCACAGGT GTACACACTG      480
CCTCCAAGCC AGGAAGAGAT GACCAAGAAC CAGGTGTCCC TGACCTGTCT CGTGAAGGGC      540
TTCTACCCCT CCGATATCGC CGTGGAATGG GAGAGCAACG GCCAGCCCGA GAACAACCTAC      600
AAGACCACCC CCCCTGTGCT GGACAGCGAC GGCTCATTCT TCCTGTACAG CAGACTGACC      660
GTGGACAAGA GCCGGTGGCA GGAAGGGAAC GTCTTCTCAT GCTCCGTGAT GCATGAGGCT      720
CTGCACAACC ACTACACACA GAAGAGCCTC TCCCTGTCTC TGGGTAAATG AGGATCCCCC      780
GACCTCGACC TCTGGCTAAT AAAGGAAATT      810

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<210> 64
 <211> 46
 <212> DNA
 <213> Artificial
 <220>
 <223> Oligonucleotide
 <400> 64

GAGGCTCTGC ACAACCGCTA CACACAGAAG AGCCTCTCCC TGTCTC

46

<210> 65
 <211> 46
 <212> DNA
 <213> Artificial
 <220>
 <223> Oligonucleotide
 <400> 65

GAGACAGGGA GAGGCTCTTC TGTGTGTAGC GGTGTGCAG AGCCTC

46

<210> 66
 <211> 67
 <212> DNA
 <213> Artificial
 <220>
 <223> Oligonucleotide
 <400> 66

TTCTCATGCT CCGTGAGCCA TGAGGCTCTG CACAGCCACC ACACACAGAA GAGCCTCTCC
 CTGTCTC

67

<210> 67
<211> 67
<212> DNA
<213> Artificial
<220>
<223> Oligonucleotide
<400> 67

GAGACAGGGA GAGGCTCTTC TGTGTGTGGT GGCTGTGCAG AGCCTCATGG CTCACGGAGC
ATGAGAA

67

<210> 68
<211> 55
<212> DNA
<213> Artificial
<220>
<223> Oligonucleotide
<400> 68

TGCTCCGTGA GCCATGAGGC TCTGCACAGC CGCCACACAC AGAAGAGCCT CTCCC

55

<210> 69
<211> 55
<212> DNA
<213> Artificial
<220>
<223> Oligonucleotide
<400> 69

GGGAGAGGCT CTTCTGTGTG TGGCGGCTGT GCAGAGCCTC ATGGCTCACG GAGCA

55