

SEQUENCE LISTING

<110> Regeneron Pharmaceuticals, Inc.

<120> Anti-TrkB Monoclonal Antibodies and
Methods of Use

<130> 10395W001 (REGN-029W0)

<140> To be assigned

<141> 2018-11-28

<150> 62/592,657

<151> 2017-11-30

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tcctgtgcag cctctggatt cagcttcagt agctttggca tgcactgggt ccgccaggct 120
ccaggcaagg gactggagtg ggtgtcagtt atatcatatg atggaattaa tacatactat 180
acagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcaaatga acggcctgag agctgaggac acggctcttt attactgtgt gcaagggtca 300
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Ser Phe
 20          25          30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35          40          45
Ser Val Ile Ser Tyr Asp Gly Ile Asn Thr Tyr Tyr Thr Asp Ser Val
 50          55          60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65          70          75          80
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Leu	Gln	Met	Asn	Gly	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Leu	Tyr	Tyr	Cys
				85					90					95	
Val	Gln	Gly	Ser	Ile	Gly	Thr	Val	Phe	Glu	Tyr	Trp	Gly	Gln	Gly	Thr
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Val Gln Gly Ser Ile Gly Thr Val Phe Glu Tyr
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gggaaagttc ctaaactcct gatctatgct gcatccactt tacaatcagg ggtcccatct 180
cggttcggtg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240
gaagatgttg caacttatta ctgtcaaaag tataccagtg cccattcac tttcggccct 300
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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Tyr
20 25 30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile

		35					40				45						
Tyr	Ala	Ala	Ser	Thr	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Gly	Gly		
	50					55					60						
Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro		
65					70					75					80		
Glu	Asp	Val	Ala	Thr	Tyr	Tyr	Cys	Gln	Lys	Tyr	Thr	Ser	Ala	Pro	Phe		
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tccgggaaaag ggctggagtg gattggccgt attagaaaca aggctaacag ttacgcgaca 180
gcatatggtg cgtcgggtgac aggcagggtc accatctcca gagatgattc aaagaacacg 240
gcgtatctgc aaatgaacag cctgaaaacc gaggacacgg ccgtttatta ctgtactttc 300
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			20					25					30			
Val	Ile	His	Trp	Val	Arg	Gln	Ala	Ser	Gly	Lys	Gly	Leu	Glu	Trp	Ile	
		35					40					45				
Gly	Arg	Ile	Arg	Asn	Lys	Ala	Asn	Ser	Tyr	Ala	Thr	Ala	Tyr	Gly	Ala	
	50					55					60					
Ser	Val	Thr	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asp	Ser	Lys	Asn	Thr	
65					70					75					80	
Ala	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Lys	Thr	Glu	Asp	Thr	Ala	Val	Tyr	
				85					90					95		
Tyr	Cys	Thr	Phe	Pro	Gly	Val	Val	Gly	Arg	Gly	Gly	Phe	Asp	Tyr	Trp	
			100					105					110			
Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser							
		115					120									

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<210> 21
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<400> 21
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tggtaccaac	agaaaccagg	acagcctcct	aagtgtctct	tttactgggc	atctaccgg	180
gaatccgggg	tccctgaccg	attcgggtggc	agcgggtctg	ggacagattt	ctctctcacc	240
atcaacagcc	tgcagactga	agatgtggca	gtttattact	gtctccaata	ttatagtatt	300
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Glu Gly Ala Thr Ile Asn Cys Met Ser Ser Gln Ser Val Leu Phe Ser
20 25 30
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45
Pro Pro Lys Leu Leu Phe Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60
Pro Asp Arg Phe Gly Gly Ser Gly Ser Gly Thr Asp Phe Ser Leu Thr
65 70 75 80
Ile Asn Ser Leu Gln Thr Glu Asp Val Ala Val Tyr Tyr Cys Leu Gln
85 90 95
Tyr Tyr Ser Ile Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110
Lys

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<400> 28

Gln Ser Val Leu Phe Ser Ser Asn Asn Lys Asn Tyr
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<211> 9

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<213> Artificial Sequence

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<400> 29

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<400> 30

Trp Ala Ser

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<211> 27

<212> DNA

<213> Artificial Sequence

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<223> synthetic

<400> 31

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<210> 32

<211> 9

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<223> synthetic

<400> 32

Leu Gln Tyr Tyr Ser Ile Pro Trp Thr

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5

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<211> 381

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ccagggaagg ggctggagtg gatttcatac attagtaata gtggttatac catatactac 180
gcagactctg tgaagggccg attcaccatc tccagagaca acgccaggaa ctcaatatat 240
ctgcaagtga acagcctgag agccgaggac acggctgttt attactgttc gagacgtact 300
actatgattc ggggcattag ggcgtactac tattacggtc tggacgtctg gggccaaggg 360
accacggtca ccgtctcctc a 381

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

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Gly Leu Asp Val

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gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccgtca 180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg caacttacta ctgtcaacag agttacagta cccctccgat caccttcggc 300
caagggacac gactggagat taaa 324

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

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<400> 43
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<210> 44
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<400> 44
Gln Ser Ile Ser Ser Tyr

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<400> 48
Gln Gln Ser Tyr Ser Thr Pro Pro Ile Thr
1 5 10

<210> 49
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<223> M2aM14173N HCVR

<400> 49

Asn	Val	Ser	Leu	Val	Glu	Ser	Gly	Gly	Gly	Ser	Val	Lys	Pro	Gly	Gly		
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Ser	Leu	Gln	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Ser	Ser		
			20					25					30				
Ala	Met	Ser	Trp	Ile	Arg	Gln	Thr	Pro	Glu	Met	Arg	Leu	Glu	Trp	Val		
		35					40					45					
Ala	Thr	Ile	Ser	Asp	Arg	Gly	Ser	Tyr	Thr	Tyr	Tyr	Pro	Asp	Ser	Val		
	50					55					60						
Glu	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Ile	Leu	Tyr		
65					70				75					80			
Leu	Gln	Met	Ser	His	Leu	Met	Ser	Glu	Asp	Thr	Ala	Met	Tyr	Tyr	Cys		
				85					90				95				
Ala	Arg	Gly	Lys	Gly	Glu	Lys	Ala	Tyr	Tyr	Thr	Ala	Phe	Phe	Ala	Tyr		
			100					105					110				
Trp	Gly	Gln	Gly	Ser	Leu	Val	Thr	Val	Ser	Ala							
		115					120										

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<223> M2aM14173N HCDR1

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Gly	Phe	Thr	Phe	Ser	Ser	Ser	Ala										
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Ile	Ser	Asp	Arg	Gly	Ser	Tyr	Thr										
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Ala Arg Gly Lys Gly Glu Lys Ala Tyr Tyr Thr Ala Phe Phe Ala Tyr
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<210> 53

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<223> M2aM14173N LCVR

<400> 53

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

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<223> M2aM14173N LCDR1

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Glu Asn Ile Tyr Ser Tyr
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<223> M2aM14173N LCDR2

<400> 55

Asn Ala Glu

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<400> 56
Gln His His Tyr Ser Ser Pro Trp Thr
1 5

<210> 57
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Asp Thr Thr Gly Ser Ser Val Thr Leu Gly Cys Leu Val Lys Gly Tyr
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Phe Pro Glu Pro Val Thr Leu Thr Trp Asn Ser Gly Ser Leu Ser Ser
35 40 45
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu
50 55 60
Ser Ser Ser Val Thr Val Thr Ser Ser Thr Trp Pro Ser Gln Ser Ile
65 70 75 80
Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys
85 90 95
Ile Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys
100 105 110
Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro
115 120 125
Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys
130 135 140
Val Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp
145 150 155 160
Phe Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg
165 170 175
Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln
180 185 190
His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn
195 200 205
Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly
210 215 220
Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu Glu
225 230 235 240

Met	Thr	Lys	Lys	Gln	Val	Thr	Leu	Thr	Cys	Met	Val	Thr	Asp	Phe	Met
				245					250					255	
Pro	Glu	Asp	Ile	Tyr	Val	Glu	Trp	Thr	Asn	Asn	Gly	Lys	Thr	Glu	Leu
			260					265					270		
Asn	Tyr	Lys	Asn	Thr	Glu	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Tyr	Phe
		275					280					285			
Met	Tyr	Ser	Lys	Leu	Arg	Val	Glu	Lys	Lys	Asn	Trp	Val	Glu	Arg	Asn
	290					295					300				
Ser	Tyr	Ser	Cys	Ser	Val	Val	His	Glu	Gly	Leu	His	Asn	His	His	Thr
305					310					315					320
Thr	Lys	Ser	Phe	Ser	Arg	Thr	Pro	Gly	Lys						
				325					330						

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

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

50						55						60					
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Asn	Leu	Tyr		
65					70					75					80		
Leu	Gln	Met	Ser	His	Leu	Glu	Ser	Glu	Asp	Thr	Ala	Met	Tyr	Tyr	Cys		
				85					90					95			
Ile	Arg	Gly	Asp	Val	Tyr	Tyr	Val	Arg	Phe	Ala	Tyr	Trp	Gly	Gln	Gly		
			100					105					110				
Thr	Leu	Val	Thr	Val	Ser	Ala											
			115														

<210> 60
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> M2aM14178N HCDR1

<400> 60
 Gly Phe Thr Phe Ser Ser Tyr Ala
 1 5

<210> 61
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> M2aM14178N HCDR2

<400> 61
 Ile Ser Asp Gly Gly Thr Tyr Thr
 1 5

<210> 62
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> M2aM14178N HCDR3

<400> 62
 Ile Arg Gly Asp Val Tyr Tyr Val Arg Phe Ala Tyr
 1 5 10

<210> 63
 <211> 109
 <212> PRT
 <213> Artificial Sequence

<220>

<223> M2aM14178N LCVR

<400> 63

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

<210> 64

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> M2aM14178N LCDR1

<400> 64

Thr	Gly	Ala	Val	Thr	Ser	Ser	Asn	His
1				5				

<210> 65

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> M2aM14178N LCDR2

<400> 65

Gly	Thr	Asn
1		

<210> 66

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> M2aM14178N LCDR3

<400> 66

Ala Leu Trp His Ser Asn His Trp Val
 1 5

<210> 67
 <211> 106
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> M2aM14178N Constant LC

<400> 67
 Gly Gln Pro Lys Ser Ser Pro Ser Val Thr Leu Phe Pro Pro Ser Ser
 1 5 10 15
 Glu Glu Leu Glu Thr Asn Lys Ala Thr Leu Val Cys Thr Ile Thr Asp
 20 25 30
 Phe Tyr Pro Gly Val Val Thr Val Asp Trp Lys Val Asp Gly Thr Pro
 35 40 45
 Val Thr Gln Gly Met Glu Thr Thr Gln Pro Ser Lys Gln Ser Asn Asn
 50 55 60
 Lys Tyr Met Ala Ser Ser Tyr Leu Thr Leu Thr Ala Arg Ala Trp Glu
 65 70 75 80
 Arg His Ser Ser Tyr Ser Cys Gln Val Thr His Glu Gly His Thr Val
 85 90 95
 Glu Lys Ser Leu Ser Arg Ala Asp Cys Ser
 100 105

<210> 68
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> M2aM14179N HCVR

<400> 68
 Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Leu Thr Asp Tyr
 20 25 30
 Tyr Met Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
 35 40 45
 Gly Asp Ile Asn Pro Asn Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
 50 55 60
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Gly Ala Tyr Tyr Ser Asn Tyr Phe Asp Tyr Trp Gly Gln Gly
 100 105 110
 Thr Thr Leu Thr Val Ser Ser
 115

<210> 69
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> M2aM14179N HCDR1

<400> 69
Gly Tyr Thr Leu Thr Asp Tyr Tyr
1 5

<210> 70
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> M2aM14179N HCDR2

<400> 70
Ile Asn Pro Asn Asn Gly Gly Thr
1 5

<210> 71
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> M2aM14179N HCDR3

<400> 71
Ala Arg Gly Ala Tyr Tyr Ser Asn Tyr Phe Asp Tyr
1 5 10

<210> 72
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> M2aM14179N LCVR

<400> 72
Asp Ile Val Met Ser Gln Ser Pro Ser Ser Leu Ala Val Ser Ala Gly
1 5 10 15
Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30
Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Trp	Ala	Ser	Thr	Arg	Glu	Ser	Gly	Val
50						55					60				
Pro	Asp	Arg	Phe	Thr	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr
65					70					75					80
Ile	Ser	Ser	Val	Gln	Ala	Glu	Asp	Leu	Ala	Val	Tyr	Tyr	Cys	Lys	Gln
				85					90					95	
Ser	Tyr	Ile	Leu	Phe	Thr	Phe	Gly	Ser	Gly	Thr	Gln	Leu	Glu	Ile	Lys
			100					105					110		

<210> 73
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> M2aM14179N LCDR1

<400> 73
 Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr
 1 5 10

<210> 74
 <211> 3
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> M2aM14179N LCDR2

<400> 74
 Trp Ala Ser
 1

<210> 75
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> M2aM14179N LCDR3

<400> 75
 Lys Gln Ser Tyr Ile Leu Phe Thr
 1 5

<210> 76
 <211> 427
 <212> PRT
 <213> Artificial Sequence

<220>

<223> TrkB(C32-H430).mmH

aa 1-399: aa 32 through 430 of NP_001018074.1; aa
400-427 myc-myc-hexahistidine tag

<400> 76

Cys	Pro	Thr	Ser	Cys	Lys	Cys	Ser	Ala	Ser	Arg	Ile	Trp	Cys	Ser	Asp
1				5					10					15	
Pro	Ser	Pro	Gly	Ile	Val	Ala	Phe	Pro	Arg	Leu	Glu	Pro	Asn	Ser	Val
			20					25					30		
Asp	Pro	Glu	Asn	Ile	Thr	Glu	Ile	Phe	Ile	Ala	Asn	Gln	Lys	Arg	Leu
		35				40					45				
Glu	Ile	Ile	Asn	Glu	Asp	Asp	Val	Glu	Ala	Tyr	Val	Gly	Leu	Arg	Asn
50					55					60					
Leu	Thr	Ile	Val	Asp	Ser	Gly	Leu	Lys	Phe	Val	Ala	His	Lys	Ala	Phe
65				70					75					80	
Leu	Lys	Asn	Ser	Asn	Leu	Gln	His	Ile	Asn	Phe	Thr	Arg	Asn	Lys	Leu
			85					90					95		
Thr	Ser	Leu	Ser	Arg	Lys	His	Phe	Arg	His	Leu	Asp	Leu	Ser	Glu	Leu
			100					105					110		
Ile	Leu	Val	Gly	Asn	Pro	Phe	Thr	Cys	Ser	Cys	Asp	Ile	Met	Trp	Ile
		115					120					125			
Lys	Thr	Leu	Gln	Glu	Ala	Lys	Ser	Ser	Pro	Asp	Thr	Gln	Asp	Leu	Tyr
		130				135				140					
Cys	Leu	Asn	Glu	Ser	Ser	Lys	Asn	Ile	Pro	Leu	Ala	Asn	Leu	Gln	Ile
145					150					155					160
Pro	Asn	Cys	Gly	Leu	Pro	Ser	Ala	Asn	Leu	Ala	Ala	Pro	Asn	Leu	Thr
			165					170						175	
Val	Glu	Glu	Gly	Lys	Ser	Ile	Thr	Leu	Ser	Cys	Ser	Val	Ala	Gly	Asp
			180					185					190		
Pro	Val	Pro	Asn	Met	Tyr	Trp	Asp	Val	Gly	Asn	Leu	Val	Ser	Lys	His
		195					200					205			
Met	Asn	Glu	Thr	Ser	His	Thr	Gln	Gly	Ser	Leu	Arg	Ile	Thr	Asn	Ile
	210					215					220				
Ser	Ser	Asp	Asp	Ser	Gly	Lys	Gln	Ile	Ser	Cys	Val	Ala	Glu	Asn	Leu
225					230					235					240
Val	Gly	Glu	Asp	Gln	Asp	Ser	Val	Asn	Leu	Thr	Val	His	Phe	Ala	Pro
			245					250						255	
Thr	Ile	Thr	Phe	Leu	Glu	Ser	Pro	Thr	Ser	Asp	His	His	Trp	Cys	Ile
			260					265					270		
Pro	Phe	Thr	Val	Lys	Gly	Asn	Pro	Lys	Pro	Ala	Leu	Gln	Trp	Phe	Tyr
		275				280						285			
Asn	Gly	Ala	Ile	Leu	Asn	Glu	Ser	Lys	Tyr	Ile	Cys	Thr	Lys	Ile	His
	290					295					300				
Val	Thr	Asn	His	Thr	Glu	Tyr	His	Gly	Cys	Leu	Gln	Leu	Asp	Asn	Pro
305					310					315					320
Thr	His	Met	Asn	Asn	Gly	Asp	Tyr	Thr	Leu	Ile	Ala	Lys	Asn	Glu	Tyr
			325					330						335	
Gly	Lys	Asp	Glu	Lys	Gln	Ile	Ser	Ala	His	Phe	Met	Gly	Trp	Pro	Gly
		340						345					350		
Ile	Asp	Asp	Gly	Ala	Asn	Pro	Asn	Tyr	Pro	Asp	Val	Ile	Tyr	Glu	Asp
		355				360						365			
Tyr	Gly	Thr	Ala	Ala	Asn	Asp	Ile	Gly	Asp	Thr	Thr	Asn	Arg	Ser	Asn
	370					375					380				
Glu	Ile	Pro	Ser	Thr	Asp	Val	Thr	Asp	Lys	Thr	Gly	Arg	Glu	His	Glu

385					390					395				400	
Gln	Lys	Leu	Ile	Ser	Glu	Glu	Asp	Leu	Gly	Gly	Glu	Gln	Lys	Leu	Ile
				405					410					415	
Ser	Glu	Glu	Asp	Leu	His	His	His	His	His	His					
			420					425							

<210> 77

<211> 632

<212> PRT

<213> Artificial Sequence

<220>

<223> Human TrkB (C32-H430).mFc

aa 1-399: aa 32 through 430 of NP_001018074.1; aa
400-632 mouse Fc domain

<400> 77

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

Asn	Gly	Ala	Ile	Leu	Asn	Glu	Ser	Lys	Tyr	Ile	Cys	Thr	Lys	Ile	His
290					295					300					
Val	Thr	Asn	His	Thr	Glu	Tyr	His	Gly	Cys	Leu	Gln	Leu	Asp	Asn	Pro
305					310					315					320
Thr	His	Met	Asn	Asn	Gly	Asp	Tyr	Thr	Leu	Ile	Ala	Lys	Asn	Glu	Tyr
			325						330					335	
Gly	Lys	Asp	Glu	Lys	Gln	Ile	Ser	Ala	His	Phe	Met	Gly	Trp	Pro	Gly
			340					345					350		
Ile	Asp	Asp	Gly	Ala	Asn	Pro	Asn	Tyr	Pro	Asp	Val	Ile	Tyr	Glu	Asp
		355					360					365			
Tyr	Gly	Thr	Ala	Ala	Asn	Asp	Ile	Gly	Asp	Thr	Thr	Asn	Arg	Ser	Asn
	370					375						380			
Glu	Ile	Pro	Ser	Thr	Asp	Val	Thr	Asp	Lys	Thr	Gly	Arg	Glu	His	Glu
385					390					395					400
Pro	Arg	Gly	Pro	Thr	Ile	Lys	Pro	Cys	Pro	Pro	Cys	Lys	Cys	Pro	Ala
			405						410					415	
Pro	Asn	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Lys	Ile
		420						425					430		
Lys	Asp	Val	Leu	Met	Ile	Ser	Leu	Ser	Pro	Ile	Val	Thr	Cys	Val	Val
	435					440						445			
Val	Asp	Val	Ser	Glu	Asp	Asp	Pro	Asp	Val	Gln	Ile	Ser	Trp	Phe	Val
	450					455					460				
Asn	Asn	Val	Glu	Val	His	Thr	Ala	Gln	Thr	Gln	Thr	His	Arg	Glu	Asp
465					470					475					480
Tyr	Asn	Ser	Thr	Leu	Arg	Val	Val	Ser	Ala	Leu	Pro	Ile	Gln	His	Gln
			485						490					495	
Asp	Trp	Met	Ser	Gly	Lys	Glu	Phe	Lys	Cys	Lys	Val	Asn	Asn	Lys	Asp
		500						505					510		
Leu	Pro	Ala	Pro	Ile	Glu	Arg	Thr	Ile	Ser	Lys	Pro	Lys	Gly	Ser	Val
		515					520						525		
Arg	Ala	Pro	Gln	Val	Tyr	Val	Leu	Pro	Pro	Pro	Glu	Glu	Glu	Met	Thr
	530					535					540				
Lys	Lys	Gln	Val	Thr	Leu	Thr	Cys	Met	Val	Thr	Asp	Phe	Met	Pro	Glu
545					550					555					560
Asp	Ile	Tyr	Val	Glu	Trp	Thr	Asn	Asn	Gly	Lys	Thr	Glu	Leu	Asn	Tyr
			565						570					575	
Lys	Asn	Thr	Glu	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Tyr	Phe	Met	Tyr
		580						585					590		
Ser	Lys	Leu	Arg	Val	Glu	Lys	Lys	Asn	Trp	Val	Glu	Arg	Asn	Ser	Tyr
	595					600						605			
Ser	Cys	Ser	Val	Val	His	Glu	Gly	Leu	His	Asn	His	His	Thr	Thr	Lys
	610					615					620				
Ser	Phe	Ser	Arg	Thr	Pro	Gly	Lys								
625					630										

<210> 78

<211> 626

<212> PRT

<213> Artificial Sequence

<220>

<223> Human TrkB (C32-H430).hFc

aa 1-399: aa 32 through 430 of NP_001018074.1; aa

400-626: human Fc domain

<400> 78

Cys	Pro	Thr	Ser	Cys	Lys	Cys	Ser	Ala	Ser	Arg	Ile	Trp	Cys	Ser	Asp
1				5					10					15	
Pro	Ser	Pro	Gly	Ile	Val	Ala	Phe	Pro	Arg	Leu	Glu	Pro	Asn	Ser	Val
			20					25					30		
Asp	Pro	Glu	Asn	Ile	Thr	Glu	Ile	Phe	Ile	Ala	Asn	Gln	Lys	Arg	Leu
		35					40					45			
Glu	Ile	Ile	Asn	Glu	Asp	Asp	Val	Glu	Ala	Tyr	Val	Gly	Leu	Arg	Asn
	50					55					60				
Leu	Thr	Ile	Val	Asp	Ser	Gly	Leu	Lys	Phe	Val	Ala	His	Lys	Ala	Phe
65				70					75						80
Leu	Lys	Asn	Ser	Asn	Leu	Gln	His	Ile	Asn	Phe	Thr	Arg	Asn	Lys	Leu
				85					90					95	
Thr	Ser	Leu	Ser	Arg	Lys	His	Phe	Arg	His	Leu	Asp	Leu	Ser	Glu	Leu
			100					105					110		
Ile	Leu	Val	Gly	Asn	Pro	Phe	Thr	Cys	Ser	Cys	Asp	Ile	Met	Trp	Ile
		115					120					125			
Lys	Thr	Leu	Gln	Glu	Ala	Lys	Ser	Ser	Pro	Asp	Thr	Gln	Asp	Leu	Tyr
	130					135					140				
Cys	Leu	Asn	Glu	Ser	Ser	Lys	Asn	Ile	Pro	Leu	Ala	Asn	Leu	Gln	Ile
145					150					155					160
Pro	Asn	Cys	Gly	Leu	Pro	Ser	Ala	Asn	Leu	Ala	Ala	Pro	Asn	Leu	Thr
				165					170					175	
Val	Glu	Glu	Gly	Lys	Ser	Ile	Thr	Leu	Ser	Cys	Ser	Val	Ala	Gly	Asp
			180					185					190		
Pro	Val	Pro	Asn	Met	Tyr	Trp	Asp	Val	Gly	Asn	Leu	Val	Ser	Lys	His
		195					200					205			
Met	Asn	Glu	Thr	Ser	His	Thr	Gln	Gly	Ser	Leu	Arg	Ile	Thr	Asn	Ile
	210					215					220				
Ser	Ser	Asp	Asp	Ser	Gly	Lys	Gln	Ile	Ser	Cys	Val	Ala	Glu	Asn	Leu
225					230					235					240
Val	Gly	Glu	Asp	Gln	Asp	Ser	Val	Asn	Leu	Thr	Val	His	Phe	Ala	Pro
				245					250					255	
Thr	Ile	Thr	Phe	Leu	Glu	Ser	Pro	Thr	Ser	Asp	His	His	Trp	Cys	Ile
			260					265					270		
Pro	Phe	Thr	Val	Lys	Gly	Asn	Pro	Lys	Pro	Ala	Leu	Gln	Trp	Phe	Tyr
		275					280					285			
Asn	Gly	Ala	Ile	Leu	Asn	Glu	Ser	Lys	Tyr	Ile	Cys	Thr	Lys	Ile	His
	290					295					300				
Val	Thr	Asn	His	Thr	Glu	Tyr	His	Gly	Cys	Leu	Gln	Leu	Asp	Asn	Pro
305					310					315					320
Thr	His	Met	Asn	Asn	Gly	Asp	Tyr	Thr	Leu	Ile	Ala	Lys	Asn	Glu	Tyr
				325					330					335	
Gly	Lys	Asp	Glu	Lys	Gln	Ile	Ser	Ala	His	Phe	Met	Gly	Trp	Pro	Gly
			340					345					350		
Ile	Asp	Asp	Gly	Ala	Asn	Pro	Asn	Tyr	Pro	Asp	Val	Ile	Tyr	Glu	Asp
		355					360					365			
Tyr	Gly	Thr	Ala	Ala	Asn	Asp	Ile	Gly	Asp	Thr	Thr	Asn	Arg	Ser	Asn
	370					375					380				
Glu	Ile	Pro	Ser	Thr	Asp	Val	Thr	Asp	Lys	Thr	Gly	Arg	Glu	His	Asp
385					390					395					400
Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly
				405					410					415	

Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile
			420					425					430		
Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu
		435					440					445			
Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His
	450					455					460				
Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg
465					470					475					480
Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys
				485					490					495	
Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu
			500					505					510		
Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr
		515					520					525			
Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu
	530					535					540				
Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp
545					550					555					560
Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val
				565					570					575	
Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp
			580					585					590		
Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His
		595					600				605				
Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro
	610					615					620				
Gly	Lys														
625															

<210> 79

<211> 426

<212> PRT

<213> Artificial Sequence

<220>

<223> Mouse TrkB (C32-H429)mmH

aa 1-398: aa 32 through 429 of NP_001020245; aa

399-426: myc-myc-hexahistidine tag

<400> 79

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

Thr	Ser	Leu	Ser	Arg	Arg	His	Phe	Arg	His	Leu	Asp	Leu	Ser	Asp	Leu	100	105	110
Ile	Leu	Thr	Gly	Asn	Pro	Phe	Thr	Cys	Ser	Cys	Asp	Ile	Met	Trp	Leu	115	120	125
Lys	Thr	Leu	Gln	Glu	Thr	Lys	Ser	Ser	Pro	Asp	Thr	Gln	Asp	Leu	Tyr	130	135	140
Cys	Leu	Asn	Glu	Ser	Ser	Lys	Asn	Met	Pro	Leu	Ala	Asn	Leu	Gln	Ile	145	150	155
Pro	Asn	Cys	Gly	Leu	Pro	Ser	Ala	Arg	Leu	Ala	Ala	Pro	Asn	Leu	Thr	165	170	175
Val	Glu	Glu	Gly	Lys	Ser	Val	Thr	Leu	Ser	Cys	Ser	Val	Gly	Gly	Asp	180	185	190
Pro	Leu	Pro	Thr	Leu	Tyr	Trp	Asp	Val	Gly	Asn	Leu	Val	Ser	Lys	His	195	200	205
Met	Asn	Glu	Thr	Ser	His	Thr	Gln	Gly	Ser	Leu	Arg	Ile	Thr	Asn	Ile	210	215	220
Ser	Ser	Asp	Asp	Ser	Gly	Lys	Gln	Ile	Ser	Cys	Val	Ala	Glu	Asn	Leu	225	230	235
Val	Gly	Glu	Asp	Gln	Asp	Ser	Val	Asn	Leu	Thr	Val	His	Phe	Ala	Pro	245	250	255
Thr	Ile	Thr	Phe	Leu	Glu	Ser	Pro	Thr	Ser	Asp	His	His	Trp	Cys	Ile	260	265	270
Pro	Phe	Thr	Val	Arg	Gly	Asn	Pro	Lys	Pro	Ala	Leu	Gln	Trp	Phe	Tyr	275	280	285
Asn	Gly	Ala	Ile	Leu	Asn	Glu	Ser	Lys	Tyr	Ile	Cys	Thr	Lys	Ile	His	290	295	300
Val	Thr	Asn	His	Thr	Glu	Tyr	His	Gly	Cys	Leu	Gln	Leu	Asp	Asn	Pro	305	310	315
Thr	His	Met	Asn	Asn	Gly	Asp	Tyr	Thr	Leu	Met	Ala	Lys	Asn	Glu	Tyr	325	330	335
Gly	Lys	Asp	Glu	Arg	Gln	Ile	Ser	Ala	His	Phe	Met	Gly	Arg	Pro	Gly	340	345	350
Val	Asp	Tyr	Glu	Thr	Asn	Pro	Asn	Tyr	Pro	Glu	Val	Leu	Tyr	Glu	Asp	355	360	365
Trp	Thr	Thr	Pro	Thr	Asp	Ile	Gly	Asp	Thr	Thr	Asn	Lys	Ser	Asn	Glu	370	375	380
Ile	Pro	Ser	Thr	Asp	Val	Ala	Asp	Gln	Ser	Asn	Arg	Glu	His	Glu	Gln	385	390	395
Lys	Leu	Ile	Ser	Glu	Glu	Asp	Leu	Gly	Gly	Glu	Gln	Lys	Leu	Ile	Ser	405	410	415
Glu	Glu	Asp	Leu	His	His	His	His	His	His	His						420	425	

<210> 80

<211> 631

<212> PRT

<213> Artificial Sequence

<220>

<223> Mouse TrkB (C32-H429).mFc

aa 1-398: aa 32 through 429 of NP_001020245; aa
399-631 Mouse Fc domain

<400> 80

Cys	Pro	Thr	Ser	Cys	Lys	Cys	Ser	Ser	Ala	Arg	Ile	Trp	Cys	Thr	Glu
1				5					10					15	
Pro	Ser	Pro	Gly	Ile	Val	Ala	Phe	Pro	Arg	Leu	Glu	Pro	Asn	Ser	Val
			20					25					30		
Asp	Pro	Glu	Asn	Ile	Thr	Glu	Ile	Leu	Ile	Ala	Asn	Gln	Lys	Arg	Leu
		35					40					45			
Glu	Ile	Ile	Asn	Glu	Asp	Asp	Val	Glu	Ala	Tyr	Val	Gly	Leu	Arg	Asn
	50					55					60				
Leu	Thr	Ile	Val	Asp	Ser	Gly	Leu	Lys	Phe	Val	Ala	Tyr	Lys	Ala	Phe
65				70					75						80
Leu	Lys	Asn	Ser	Asn	Leu	Arg	His	Ile	Asn	Phe	Thr	Arg	Asn	Lys	Leu
				85					90					95	
Thr	Ser	Leu	Ser	Arg	Arg	His	Phe	Arg	His	Leu	Asp	Leu	Ser	Asp	Leu
			100					105						110	
Ile	Leu	Thr	Gly	Asn	Pro	Phe	Thr	Cys	Ser	Cys	Asp	Ile	Met	Trp	Leu
		115					120					125			
Lys	Thr	Leu	Gln	Glu	Thr	Lys	Ser	Ser	Pro	Asp	Thr	Gln	Asp	Leu	Tyr
	130					135					140				
Cys	Leu	Asn	Glu	Ser	Ser	Lys	Asn	Met	Pro	Leu	Ala	Asn	Leu	Gln	Ile
145					150					155					160
Pro	Asn	Cys	Gly	Leu	Pro	Ser	Ala	Arg	Leu	Ala	Ala	Pro	Asn	Leu	Thr
				165					170					175	
Val	Glu	Glu	Gly	Lys	Ser	Val	Thr	Leu	Ser	Cys	Ser	Val	Gly	Gly	Asp
			180					185					190		
Pro	Leu	Pro	Thr	Leu	Tyr	Trp	Asp	Val	Gly	Asn	Leu	Val	Ser	Lys	His
		195					200					205			
Met	Asn	Glu	Thr	Ser	His	Thr	Gln	Gly	Ser	Leu	Arg	Ile	Thr	Asn	Ile
	210					215					220				
Ser	Ser	Asp	Asp	Ser	Gly	Lys	Gln	Ile	Ser	Cys	Val	Ala	Glu	Asn	Leu
225					230					235					240
Val	Gly	Glu	Asp	Gln	Asp	Ser	Val	Asn	Leu	Thr	Val	His	Phe	Ala	Pro
				245					250					255	
Thr	Ile	Thr	Phe	Leu	Glu	Ser	Pro	Thr	Ser	Asp	His	His	Trp	Cys	Ile
			260					265					270		
Pro	Phe	Thr	Val	Arg	Gly	Asn	Pro	Lys	Pro	Ala	Leu	Gln	Trp	Phe	Tyr
		275					280					285			
Asn	Gly	Ala	Ile	Leu	Asn	Glu	Ser	Lys	Tyr	Ile	Cys	Thr	Lys	Ile	His
	290					295					300				
Val	Thr	Asn	His	Thr	Glu	Tyr	His	Gly	Cys	Leu	Gln	Leu	Asp	Asn	Pro
305					310					315					320
Thr	His	Met	Asn	Asn	Gly	Asp	Tyr	Thr	Leu	Met	Ala	Lys	Asn	Glu	Tyr
				325					330					335	
Gly	Lys	Asp	Glu	Arg	Gln	Ile	Ser	Ala	His	Phe	Met	Gly	Arg	Pro	Gly
			340					345					350		
Val	Asp	Tyr	Glu	Thr	Asn	Pro	Asn	Tyr	Pro	Glu	Val	Leu	Tyr	Glu	Asp
		355					360					365			
Trp	Thr	Thr	Pro	Thr	Asp	Ile	Gly	Asp	Thr	Thr	Asn	Lys	Ser	Asn	Glu
	370					375					380				
Ile	Pro	Ser	Thr	Asp	Val	Ala	Asp	Gln	Ser	Asn	Arg	Glu	His	Glu	Pro
385					390					395					400
Arg	Gly	Pro	Thr	Ile	Lys	Pro	Cys	Pro	Pro	Cys	Lys	Cys	Pro	Ala	Pro
				405					410					415	
Asn	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Lys	Ile	Lys

Ile	Leu	Thr	Gly	Asn	Pro	Phe	Thr	Cys	Ser	Cys	Asp	Ile	Met	Trp	Leu
	115						120					125			
Lys	Thr	Leu	Gln	Glu	Thr	Lys	Ser	Ser	Pro	Asp	Thr	Gln	Asp	Leu	Tyr
	130					135				140					
Cys	Leu	Asn	Glu	Ser	Ser	Lys	Asn	Met	Pro	Leu	Ala	Asn	Leu	Gln	Ile
145					150					155					160
Pro	Asn	Cys	Gly	Leu	Pro	Ser	Ala	Arg	Leu	Ala	Ala	Pro	Asn	Leu	Thr
			165						170					175	
Val	Glu	Glu	Gly	Lys	Ser	Val	Thr	Leu	Ser	Cys	Ser	Val	Gly	Gly	Asp
			180					185					190		
Pro	Leu	Pro	Thr	Leu	Tyr	Trp	Asp	Val	Gly	Asn	Leu	Val	Ser	Lys	His
	195						200					205			
Met	Asn	Glu	Thr	Ser	His	Thr	Gln	Gly	Ser	Leu	Arg	Ile	Thr	Asn	Ile
	210					215					220				
Ser	Ser	Asp	Asp	Ser	Gly	Lys	Gln	Ile	Ser	Cys	Val	Ala	Glu	Asn	Leu
225					230					235					240
Val	Gly	Glu	Asp	Gln	Asp	Ser	Val	Asn	Leu	Thr	Val	His	Phe	Ala	Pro
			245						250					255	
Thr	Ile	Thr	Phe	Leu	Glu	Ser	Pro	Thr	Ser	Asp	His	His	Trp	Cys	Ile
			260					265					270		
Pro	Phe	Thr	Val	Arg	Gly	Asn	Pro	Lys	Pro	Ala	Leu	Gln	Trp	Phe	Tyr
	275						280					285			
Asn	Gly	Ala	Ile	Leu	Asn	Glu	Ser	Lys	Tyr	Ile	Cys	Thr	Lys	Ile	His
	290					295					300				
Val	Thr	Asn	His	Thr	Glu	Tyr	His	Gly	Cys	Leu	Gln	Leu	Asp	Asn	Pro
305					310					315					320
Thr	His	Met	Asn	Asn	Gly	Asp	Tyr	Thr	Leu	Met	Ala	Lys	Asn	Glu	Tyr
			325						330					335	
Gly	Lys	Asp	Glu	Arg	Gln	Ile	Ser	Ala	His	Phe	Met	Gly	Arg	Pro	Gly
			340					345					350		
Val	Asp	Tyr	Glu	Thr	Asn	Pro	Asn	Tyr	Pro	Glu	Val	Leu	Tyr	Glu	Asp
	355						360					365			
Trp	Thr	Thr	Pro	Thr	Asp	Ile	Gly	Asp	Thr	Thr	Asn	Lys	Ser	Asn	Glu
	370					375					380				
Ile	Pro	Ser	Thr	Asp	Val	Ala	Asp	Gln	Ser	Asn	Arg	Glu	His	Asp	Lys
385					390					395					400
Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro
			405						410					415	
Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser
			420					425					430		
Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp
	435						440					445			
Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn
	450					455					460				
Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val
465					470					475					480
Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu
			485						490					495	
Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys
			500					505					510		
Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr
	515						520					525			
Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr
	530					535					540				
Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu

545					550					555					560
Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu
				565					570					575	
Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys
			580					585					590		
Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu
		595					600					605			
Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly
	610					615					620				
Lys															
625															

<210> 82
 <211> 427
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Rabbit TrkB (C32-H430)mmH
 aa 1-399: aa32 through 430 of XP_002721319.1; aa
 400-427: myc-myc-hexahistidine tag

<400> 82

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

Val	Gly	Glu	Asp	Gln	Asp	Ser	Val	Asn	Leu	Thr	Val	His	Phe	Ala	Pro
				245					250					255	
Thr	Ile	Thr	Phe	Leu	Glu	Ser	Pro	Thr	Ser	Asp	His	His	Trp	Cys	Ile
			260					265					270		
Pro	Phe	Thr	Val	Lys	Gly	Asn	Pro	Lys	Pro	Thr	Leu	Gln	Trp	Phe	Tyr
		275					280					285			
Asn	Gly	Ala	Ile	Leu	Asn	Glu	Ser	Lys	Tyr	Ile	Cys	Thr	Lys	Ile	His
	290					295					300				
Val	Thr	Asn	His	Thr	Glu	Tyr	His	Gly	Cys	Leu	Gln	Leu	Asp	Asn	Pro
305					310					315					320
Thr	His	Met	Asn	Asn	Gly	Asp	Tyr	Thr	Leu	Ile	Ala	Lys	Asn	Glu	Tyr
				325					330					335	
Gly	Lys	Asp	Glu	Arg	Gln	Ile	Ser	Ala	His	Phe	Met	Gly	Trp	Pro	Gly
			340					345					350		
Ile	Asp	Asp	Asp	Pro	Asn	Leu	Asn	Tyr	Pro	Asp	Val	Ile	Tyr	Ala	Asp
		355					360					365			
Tyr	Gly	Thr	Ala	Ala	Asn	Asp	Ile	Gly	Asp	Thr	Thr	Asn	Arg	Ser	Asn
	370					375					380				
Glu	Ile	Pro	Pro	Thr	Gly	Ala	Ala	Asp	Asn	Ala	Gly	Arg	Glu	His	Glu
385					390					395					400
Gln	Lys	Leu	Ile	Ser	Glu	Glu	Asp	Leu	Gly	Gly	Glu	Gln	Lys	Leu	Ile
				405					410					415	
Ser	Glu	Glu	Asp	Leu	His	His	His	His	His	His					
			420					425							

<210> 83

<211> 632

<212> PRT

<213> Artificial Sequence

<220>

<223> Rabbit TrkB (C32-H430)mFc

aa 1-399: aa32 through 430 of XP_002721319.1; aa

400-632 Mouse Fc domain

<400> 83

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

Lys	Asn	Thr	Glu	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Tyr	Phe	Met	Tyr
			580					585					590		
Ser	Lys	Leu	Arg	Val	Glu	Lys	Lys	Asn	Trp	Val	Glu	Arg	Asn	Ser	Tyr
		595					600					605			
Ser	Cys	Ser	Val	Val	His	Glu	Gly	Leu	His	Asn	His	His	Thr	Thr	Lys
	610					615					620				
Ser	Phe	Ser	Arg	Thr	Pro	Gly	Lys								
625					630										

<210> 84

<211> 426

<212> PRT

<213> Artificial Sequence

<220>

<223> Rat TrkB (C32-H429)mmH

aa 1-398: aa 32 through 429 of NP_036863.1; aa

399-426 myc-myc-hexahistidine tag

<400> 84

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

Thr	Ile	Thr	Phe	Leu	Glu	Ser	Pro	Thr	Ser	Asp	His	His	Trp	Cys	Ile
			260					265					270		
Pro	Phe	Thr	Val	Arg	Gly	Asn	Pro	Lys	Pro	Ala	Leu	Gln	Trp	Phe	Tyr
		275					280					285			
Asn	Gly	Ala	Ile	Leu	Asn	Glu	Ser	Lys	Tyr	Ile	Cys	Thr	Lys	Ile	His
	290					295					300				
Val	Thr	Asn	His	Thr	Glu	Tyr	His	Gly	Cys	Leu	Gln	Leu	Asp	Asn	Pro
305					310					315					320
Thr	His	Met	Asn	Asn	Gly	Asp	Tyr	Thr	Leu	Met	Ala	Lys	Asn	Glu	Tyr
			325						330					335	
Gly	Lys	Asp	Glu	Arg	Gln	Ile	Ser	Ala	His	Phe	Met	Gly	Arg	Pro	Gly
		340						345					350		
Val	Asp	Tyr	Glu	Thr	Asn	Pro	Asn	Tyr	Pro	Glu	Val	Leu	Tyr	Glu	Asp
	355						360					365			
Trp	Thr	Thr	Pro	Thr	Asp	Ile	Gly	Asp	Thr	Thr	Asn	Lys	Ser	Asn	Glu
	370					375					380				
Ile	Pro	Ser	Thr	Asp	Val	Ala	Asp	Gln	Thr	Asn	Arg	Glu	His	Glu	Gln
385					390					395					400
Lys	Leu	Ile	Ser	Glu	Glu	Asp	Leu	Gly	Gly	Glu	Gln	Lys	Leu	Ile	Ser
			405					410						415	
Glu	Glu	Asp	Leu	His	His	His	His	His	His						
			420					425							

<210> 85

<211> 631

<212> PRT

<213> Artificial Sequence

<220>

<223> Rat TrkB (C32-H429)mFc

aa 1-398: aa 32 through 429 of NP_036863.1; aa

399-631 Mouse Fc domain

<400> 85

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

Cys	Leu	Asn	Glu	Ser	Ser	Lys	Asn	Thr	Pro	Leu	Ala	Asn	Leu	Gln	Ile
145					150					155					160
Pro	Asn	Cys	Gly	Leu	Pro	Ser	Ala	Arg	Leu	Ala	Ala	Pro	Asn	Leu	Thr
				165					170						175
Val	Glu	Glu	Gly	Lys	Ser	Val	Thr	Ile	Ser	Cys	Ser	Val	Gly	Gly	Asp
			180					185					190		
Pro	Leu	Pro	Thr	Leu	Tyr	Trp	Asp	Val	Gly	Asn	Leu	Val	Ser	Lys	His
		195					200					205			
Met	Asn	Glu	Thr	Ser	His	Thr	Gln	Gly	Ser	Leu	Arg	Ile	Thr	Asn	Ile
	210					215					220				
Ser	Ser	Asp	Asp	Ser	Gly	Lys	Gln	Ile	Ser	Cys	Val	Ala	Glu	Asn	Leu
225					230					235					240
Val	Gly	Glu	Asp	Gln	Asp	Ser	Val	Asn	Leu	Thr	Val	His	Phe	Ala	Pro
				245					250						255
Thr	Ile	Thr	Phe	Leu	Glu	Ser	Pro	Thr	Ser	Asp	His	His	Trp	Cys	Ile
			260					265					270		
Pro	Phe	Thr	Val	Arg	Gly	Asn	Pro	Lys	Pro	Ala	Leu	Gln	Trp	Phe	Tyr
		275					280					285			
Asn	Gly	Ala	Ile	Leu	Asn	Glu	Ser	Lys	Tyr	Ile	Cys	Thr	Lys	Ile	His
	290					295					300				
Val	Thr	Asn	His	Thr	Glu	Tyr	His	Gly	Cys	Leu	Gln	Leu	Asp	Asn	Pro
305					310					315					320
Thr	His	Met	Asn	Asn	Gly	Asp	Tyr	Thr	Leu	Met	Ala	Lys	Asn	Glu	Tyr
				325					330					335	
Gly	Lys	Asp	Glu	Arg	Gln	Ile	Ser	Ala	His	Phe	Met	Gly	Arg	Pro	Gly
			340					345					350		
Val	Asp	Tyr	Glu	Thr	Asn	Pro	Asn	Tyr	Pro	Glu	Val	Leu	Tyr	Glu	Asp
		355					360					365			
Trp	Thr	Thr	Pro	Thr	Asp	Ile	Gly	Asp	Thr	Thr	Asn	Lys	Ser	Asn	Glu
	370					375						380			
Ile	Pro	Ser	Thr	Asp	Val	Ala	Asp	Gln	Thr	Asn	Arg	Glu	His	Glu	Pro
385					390					395					400
Arg	Gly	Pro	Thr	Ile	Lys	Pro	Cys	Pro	Pro	Cys	Lys	Cys	Pro	Ala	Pro
				405					410					415	
Asn	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Lys	Ile	Lys
			420					425					430		
Asp	Val	Leu	Met	Ile	Ser	Leu	Ser	Pro	Ile	Val	Thr	Cys	Val	Val	Val
		435					440					445			
Asp	Val	Ser	Glu	Asp	Asp	Pro	Asp	Val	Gln	Ile	Ser	Trp	Phe	Val	Asn
		450				455					460				
Asn	Val	Glu	Val	His	Thr	Ala	Gln	Thr	Gln	Thr	His	Arg	Glu	Asp	Tyr
465					470					475					480
Asn	Ser	Thr	Leu	Arg	Val	Val	Ser	Ala	Leu	Pro	Ile	Gln	His	Gln	Asp
				485					490					495	
Trp	Met	Ser	Gly	Lys	Glu	Phe	Lys	Cys	Lys	Val	Asn	Asn	Lys	Asp	Leu
			500					505					510		
Pro	Ala	Pro	Ile	Glu	Arg	Thr	Ile	Ser	Lys	Pro	Lys	Gly	Ser	Val	Arg
		515					520					525			
Ala	Pro	Gln	Val	Tyr	Val	Leu	Pro	Pro	Pro	Glu	Glu	Glu	Met	Thr	Lys
		530				535						540			
Lys	Gln	Val	Thr	Leu	Thr	Cys	Met	Val	Thr	Asp	Phe	Met	Pro	Glu	Asp
545					550					555					560
Ile	Tyr	Val	Glu	Trp	Thr	Asn	Asn	Gly	Lys	Thr	Glu	Leu	Asn	Tyr	Lys
				565					570					575	
Asn	Thr	Glu	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Tyr	Phe	Met	Tyr	Ser

				245				250					255				
Leu	His	Thr	Ala	Val	Glu	Met	His	His	Trp	Ser	Ile	Pro	Phe	Ser	Val		
			260					265					270				
Asp	Gly	Gln	Pro	Ala	Pro	Ser	Leu	Arg	Trp	Leu	Phe	Asn	Gly	Ser	Val		
		275					280					285					
Leu	Asn	Glu	Thr	Ser	Phe	Ile	Phe	Thr	Glu	Phe	Leu	Glu	Pro	Ala	Ala		
	290					295					300						
Asn	Glu	Thr	Val	Arg	His	Gly	Cys	Leu	Arg	Leu	Asn	Gln	Pro	Thr	His		
305					310					315					320		
Val	Asn	Asn	Gly	Asn	Tyr	Thr	Leu	Leu	Ala	Ala	Asn	Pro	Phe	Gly	Gln		
				325					330					335			
Ala	Ser	Ala	Ser	Ile	Met	Ala	Ala	Phe	Met	Asp	Asn	Pro	Phe	Glu	Phe		
			340					345					350				
Asn	Pro	Glu	Asp	Pro	Ile	Pro	Asp	Thr	Asn	Ser	Thr	Ser	Gly	Asp	Pro		
	355						360					365					
Val	Glu	Lys	Lys	Asp	Glu	Thr	Gly	Pro	Gly	Asp	Lys	Thr	His	Thr	Cys		
	370					375					380						
Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu		
385					390					395					400		
Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu		
			405						410					415			
Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys		
			420					425					430				
Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys		
	435					440						445					
Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu		
	450					455					460						
Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys		
465					470					475					480		
Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys		
				485					490					495			
Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser		
			500					505					510				
Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys		
	515						520					525					
Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln		
	530					535					540						
Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly		
545					550					555					560		
Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln		
				565					570					575			
Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn		
			580					585					590				
His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys					
		595					600					605					

<210> 87

<211> 426

<212> PRT

<213> Artificial Sequence

<220>

<223> Human TrkC(C32-T429).mmH

aa 1-398: aa 32 through 429 of NP_001012338.1; aa

399-426 myc-myc-hexahistidine tag

<400> 87

Cys	Pro	Ala	Asn	Cys	Val	Cys	Ser	Lys	Thr	Glu	Ile	Asn	Cys	Arg	Arg
1				5					10					15	
Pro	Asp	Asp	Gly	Asn	Leu	Phe	Pro	Leu	Leu	Glu	Gly	Gln	Asp	Ser	Gly
			20					25					30		
Asn	Ser	Asn	Gly	Asn	Ala	Ser	Ile	Asn	Ile	Thr	Asp	Ile	Ser	Arg	Asn
		35					40					45			
Ile	Thr	Ser	Ile	His	Ile	Glu	Asn	Trp	Arg	Ser	Leu	His	Thr	Leu	Asn
	50					55					60				
Ala	Val	Asp	Met	Glu	Leu	Tyr	Thr	Gly	Leu	Gln	Lys	Leu	Thr	Ile	Lys
65					70					75					80
Asn	Ser	Gly	Leu	Arg	Ser	Ile	Gln	Pro	Arg	Ala	Phe	Ala	Lys	Asn	Pro
				85					90					95	
His	Leu	Arg	Tyr	Ile	Asn	Leu	Ser	Ser	Asn	Arg	Leu	Thr	Thr	Leu	Ser
			100					105					110		
Trp	Gln	Leu	Phe	Gln	Thr	Leu	Ser	Leu	Arg	Glu	Leu	Gln	Leu	Glu	Gln
		115					120					125			
Asn	Phe	Phe	Asn	Cys	Ser	Cys	Asp	Ile	Arg	Trp	Met	Gln	Leu	Trp	Gln
	130					135					140				
Glu	Gln	Gly	Glu	Ala	Lys	Leu	Asn	Ser	Gln	Asn	Leu	Tyr	Cys	Ile	Asn
145					150					155					160
Ala	Asp	Gly	Ser	Gln	Leu	Pro	Leu	Phe	Arg	Met	Asn	Ile	Ser	Gln	Cys
				165					170					175	
Asp	Leu	Pro	Glu	Ile	Ser	Val	Ser	His	Val	Asn	Leu	Thr	Val	Arg	Glu
			180					185					190		
Gly	Asp	Asn	Ala	Val	Ile	Thr	Cys	Asn	Gly	Ser	Gly	Ser	Pro	Leu	Pro
		195					200					205			
Asp	Val	Asp	Trp	Ile	Val	Thr	Gly	Leu	Gln	Ser	Ile	Asn	Thr	His	Gln
	210					215					220				
Thr	Asn	Leu	Asn	Trp	Thr	Asn	Val	His	Ala	Ile	Asn	Leu	Thr	Leu	Val
225				230					235						240
Asn	Val	Thr	Ser	Glu	Asp	Asn	Gly	Phe	Thr	Leu	Thr	Cys	Ile	Ala	Glu
				245					250					255	
Asn	Val	Val	Gly	Met	Ser	Asn	Ala	Ser	Val	Ala	Leu	Thr	Val	Tyr	Tyr
			260				265						270		
Pro	Pro	Arg	Val	Val	Ser	Leu	Glu	Glu	Pro	Glu	Leu	Arg	Leu	Glu	His
		275					280					285			
Cys	Ile	Glu	Phe	Val	Val	Arg	Gly	Asn	Pro	Pro	Pro	Thr	Leu	His	Trp
	290					295					300				
Leu	His	Asn	Gly	Gln	Pro	Leu	Arg	Glu	Ser	Lys	Ile	Ile	His	Val	Glu
305					310					315					320
Tyr	Tyr	Gln	Glu	Gly	Glu	Ile	Ser	Glu	Gly	Cys	Leu	Leu	Phe	Asn	Lys
				325					330					335	
Pro	Thr	His	Tyr	Asn	Asn	Gly	Asn	Tyr	Thr	Leu	Ile	Ala	Lys	Asn	Pro
			340				345						350		
Leu	Gly	Thr	Ala	Asn	Gln	Thr	Ile	Asn	Gly	His	Phe	Leu	Lys	Glu	Pro
		355				360						365			
Phe	Pro	Glu	Ser	Thr	Asp	Asn	Phe	Ile	Leu	Phe	Asp	Glu	Val	Ser	Pro
		370				375					380				

Thr	Pro	Pro	Ile	Thr	Val	Thr	His	Lys	Pro	Glu	Glu	Asp	Thr	Glu	Gln
385					390					395					400
Lys	Leu	Ile	Ser	Glu	Glu	Asp	Leu	Gly	Gly	Glu	Gln	Lys	Leu	Ile	Ser
			405					410						415	
Glu	Glu	Asp	Leu	His	His	His	His	His	His						
			420					425							

<210> 88

<211> 426

<212> PRT

<213> Artificial Sequence

<220>

<223> Mouse TrkC(C32-T429).mmH

aa 1-398: aa 32 through 429 of NP_032772.3; aa

399-426 myc-myc-hexahistidine tag

<400> 88

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

				245					250					255			
Asn	Val	Val	Gly	Met	Ser	Asn	Ala	Ser	Val	Ala	Leu	Thr	Val	Tyr	Tyr		
			260					265					270				
Pro	Pro	Arg	Val	Val	Ser	Leu	Val	Glu	Pro	Glu	Val	Arg	Leu	Glu	His		
		275					280					285					
Cys	Ile	Glu	Phe	Val	Val	Arg	Gly	Asn	Pro	Thr	Pro	Thr	Leu	His	Trp		
	290					295					300						
Leu	Tyr	Asn	Gly	Gln	Pro	Leu	Arg	Glu	Ser	Lys	Ile	Ile	His	Met	Asp		
305					310					315					320		
Tyr	Tyr	Gln	Glu	Gly	Glu	Val	Ser	Glu	Gly	Cys	Leu	Leu	Phe	Asn	Lys		
				325					330						335		
Pro	Thr	His	Tyr	Asn	Asn	Gly	Asn	Tyr	Thr	Leu	Ile	Ala	Lys	Asn	Ala		
			340					345					350				
Leu	Gly	Thr	Ala	Asn	Gln	Thr	Ile	Asn	Gly	His	Phe	Leu	Lys	Glu	Pro		
	355						360					365					
Phe	Pro	Glu	Ser	Thr	Asp	Phe	Phe	Asp	Phe	Glu	Ser	Asp	Ala	Ser	Pro		
	370					375					380						
Thr	Pro	Pro	Ile	Thr	Val	Thr	His	Lys	Pro	Glu	Glu	Asp	Thr	Glu	Gln		
385					390					395					400		
Lys	Leu	Ile	Ser	Glu	Glu	Asp	Leu	Gly	Gly	Glu	Gln	Lys	Leu	Ile	Ser		
			405					410						415			
Glu	Glu	Asp	Leu	His	His	His	His	His	His								
			420					425									

<210> 89

<211> 426

<212> PRT

<213> Artificial Sequence

<220>

<223> MF TrkC(C32-T429).mmH

aa 1-398: aa 32 through 429 of XP_015308837.1; aa

399-426 myc-myc-hexahistidine tag

<400> 89

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

Trp	Gln	Leu	Phe	Gln	Thr	Leu	Ser	Leu	Arg	Glu	Leu	Arg	Leu	Glu	Gln
	115						120					125			
Asn	Phe	Phe	Asn	Cys	Ser	Cys	Asp	Ile	Arg	Trp	Met	Gln	Leu	Trp	Gln
	130					135					140				
Glu	Gln	Gly	Glu	Ala	Lys	Leu	Asn	Asn	Gln	Asn	Leu	Tyr	Cys	Ile	Asn
145					150					155					160
Ala	Asp	Gly	Ser	Gln	Leu	Pro	Leu	Phe	Arg	Met	Asn	Ile	Ser	Gln	Cys
				165					170					175	
Asp	Leu	Pro	Glu	Ile	Ser	Val	Ser	His	Val	Asn	Leu	Thr	Val	Arg	Glu
			180					185					190		
Gly	Asp	Asn	Ala	Val	Ile	Thr	Cys	Asn	Gly	Ser	Gly	Ser	Pro	Leu	Pro
	195						200					205			
Asp	Val	Asp	Trp	Ile	Val	Thr	Gly	Leu	Gln	Ser	Ile	Asn	Thr	His	Gln
	210					215					220				
Thr	Asn	Leu	Asn	Trp	Thr	Asn	Val	His	Ala	Ile	Asn	Leu	Thr	Leu	Val
225					230					235					240
Asn	Val	Thr	Ser	Glu	Asp	Asn	Gly	Phe	Thr	Leu	Thr	Cys	Ile	Ala	Glu
			245					250						255	
Asn	Val	Val	Gly	Met	Ser	Asn	Ala	Ser	Val	Ala	Leu	Thr	Val	Tyr	Tyr
			260					265					270		
Pro	Pro	Arg	Val	Val	Ser	Leu	Glu	Glu	Pro	Glu	Leu	Arg	Leu	Glu	His
		275					280					285			
Cys	Ile	Glu	Phe	Val	Val	Arg	Gly	Asn	Pro	Pro	Pro	Thr	Leu	His	Trp
	290					295					300				
Leu	His	Asn	Gly	Gln	Pro	Leu	Arg	Glu	Ser	Lys	Ile	Ile	His	Val	Glu
305					310					315					320
Tyr	Tyr	Gln	Glu	Gly	Glu	Ile	Ser	Glu	Gly	Cys	Leu	Leu	Phe	Asn	Lys
			325						330					335	
Pro	Thr	His	Tyr	Asn	Asn	Gly	Asn	Tyr	Thr	Leu	Ile	Ala	Lys	Asn	Pro
			340					345					350		
Leu	Gly	Thr	Ala	Asn	Gln	Thr	Ile	Asn	Gly	His	Phe	Leu	Lys	Glu	Pro
	355						360					365			
Phe	Pro	Glu	Ser	Thr	Asp	Asn	Phe	Ile	Leu	Phe	Asp	Glu	Val	Ser	Pro
	370					375					380				
Thr	Pro	Pro	Ile	Thr	Val	Thr	His	Lys	Pro	Glu	Glu	Asp	Thr	Glu	Gln
385					390					395					400
Lys	Leu	Ile	Ser	Glu	Glu	Asp	Leu	Gly	Gly	Glu	Gln	Lys	Leu	Ile	Ser
			405						410					415	
Glu	Glu	Asp	Leu	His	His	His	His	His	His						
			420					425							

<210> 90

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> BDNF_isoform A

aa 1-120: aa 129 through 247 of NP_733928.1 with a
Met added on the N-term

<400> 90

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

<210> 91

<211> 791

<212> PRT

<213> Artificial Sequence

<220>

<223> TrkB (pRG984.hTrkB ecto-hTrkB TM/Cyto)

aa 1-792: aa 32 through 822 of NP_001018074.1 or

Uniprot number Q16620-1 TM/Cyto 399-790

<400> 91

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

Cys 145	Leu	Asn	Glu	Ser	Ser 150	Lys	Asn	Ile	Pro	Leu	Ala	Asn	Leu	Gln	Ile 160
Pro	Asn	Cys	Gly	Leu 165	Pro	Ser	Ala	Asn	Leu 170	Ala	Ala	Pro	Asn	Leu	Thr 175
Val	Glu	Glu	Gly 180	Lys	Ser	Ile	Thr	Leu 185	Ser	Cys	Ser	Val	Ala	Gly	Asp 190
Pro	Val	Pro 195	Asn	Met	Tyr	Trp	Asp 200	Val	Gly	Asn	Leu	Val	Ser	Lys	His 205
Met	Asn 210	Glu	Thr	Ser	His	Thr 215	Gln	Gly	Ser	Leu	Arg	Ile	Thr	Asn	Ile 220
Ser 225	Ser	Asp	Asp	Ser	Gly 230	Lys	Gln	Ile	Ser	Cys	Val	Ala	Glu	Asn	Leu 240
Val	Gly	Glu	Asp	Gln 245	Asp	Ser	Val	Asn	Leu 250	Thr	Val	His	Phe	Ala	Pro 255
Thr	Ile	Thr	Phe 260	Leu	Glu	Ser	Pro	Thr 265	Ser	Asp	His	His	Trp	Cys	Ile 270
Pro	Phe	Thr 275	Val	Lys	Gly	Asn	Pro 280	Lys	Pro	Ala	Leu	Gln	Trp	Phe	Tyr 285
Asn	Gly 290	Ala	Ile	Leu	Asn	Glu 295	Ser	Lys	Tyr	Ile	Cys	Thr	Lys	Ile	His 300
Val 305	Thr	Asn	His	Thr	Glu 310	Tyr	His	Gly	Cys	Leu	Gln	Leu	Asp	Asn	Pro 320
Thr	His	Met	Asn	Asn	Gly 325	Asp	Tyr	Thr	Leu 330	Ile	Ala	Lys	Asn	Glu	Tyr 335
Gly	Lys	Asp	Glu	Lys	Gln	Ile	Ser	Ala 345	His	Phe	Met	Gly	Trp	Pro	Gly 350
Ile	Asp	Asp 355	Gly	Ala	Asn	Pro	Asn	Tyr 360	Pro	Asp	Val	Ile	Tyr	Glu	Asp 365
Tyr	Gly 370	Thr	Ala	Ala	Asn	Asp 375	Ile	Gly	Asp	Thr	Thr	Asn	Arg	Ser	Asn 380
Glu 385	Ile	Pro	Ser	Thr	Asp 390	Val	Thr	Asp	Lys	Thr	Gly	Arg	Glu	His	Leu 400
Ser	Val	Tyr	Ala	Val	Val	Val	Ile	Ala	Ser	Val	Val	Gly	Phe	Cys	Leu 415
Leu	Val	Met	Leu 420	Phe	Leu	Leu	Lys	Leu 425	Ala	Arg	His	Ser	Lys	Phe	Gly 430
Met	Lys	Gly 435	Pro	Ala	Ser	Val	Ile	Ser 440	Asn	Asp	Asp	Asp	Ser	Ala	Ser 445
Pro	Leu 450	His	His	Ile	Ser	Asn	Gly 455	Ser	Asn	Thr	Pro	Ser	Ser	Ser	Glu 460
Gly 465	Gly	Pro	Asp	Ala	Val	Ile	Ile	Gly 475	Met	Thr	Lys	Ile	Pro	Val	Ile 480
Glu	Asn	Pro	Gln	Tyr 485	Phe	Gly	Ile	Thr	Asn 490	Ser	Gln	Leu	Lys	Pro	Asp 495
Thr	Phe	Val	Gln 500	His	Ile	Lys	Arg	His 505	Asn	Ile	Val	Leu	Lys	Arg	Glu 510
Leu	Gly	Glu	Gly 515	Ala	Phe	Gly	Lys	Val 520	Phe	Leu	Ala	Glu	Cys	Tyr	Asn 525
Leu	Cys 530	Pro	Glu	Gln	Asp	Lys 535	Ile	Leu	Val	Ala	Val	Lys	Thr	Leu	Lys 540
Asp 545	Ala	Ser	Asp	Asn	Ala	Arg	Lys	Asp	Phe	His	Arg	Glu	Ala	Glu	Leu 555
Leu	Thr	Asn	Leu	Gln 565	His	Glu	His	Ile	Val 570	Lys	Phe	Tyr	Gly	Val	Cys 575
Val	Glu	Gly	Asp	Pro	Leu	Ile	Met	Val	Phe	Glu	Tyr	Met	Lys	His	Gly

<400> 93

Cys	Pro	Thr	Ser	Cys	Lys	Cys	Ser	Ser	Ala	Arg	Ile	Trp	Cys	Thr	Glu
1				5					10					15	
Pro	Ser	Pro	Gly	Ile	Val	Ala	Phe	Pro	Arg	Leu	Glu	Pro	Asn	Ser	Val
			20					25					30		
Asp	Pro	Glu	Asn	Ile	Thr	Glu	Ile	Leu	Ile	Ala	Asn	Gln	Lys	Arg	Leu
		35					40					45			
Glu	Ile	Ile	Asn	Glu	Asp	Asp	Val	Glu	Ala	Tyr	Val	Gly	Leu	Arg	Asn
	50					55					60				
Leu	Thr	Ile	Val	Asp	Ser	Gly	Leu	Lys	Phe	Val	Ala	Tyr	Lys	Ala	Phe
65				70					75						80
Leu	Lys	Asn	Ser	Asn	Leu	Arg	His	Ile	Asn	Phe	Thr	Arg	Asn	Lys	Leu
				85					90					95	
Thr	Ser	Leu	Ser	Arg	Arg	His	Phe	Arg	His	Leu	Asp	Leu	Ser	Asp	Leu
			100					105						110	
Ile	Leu	Thr	Gly	Asn	Pro	Phe	Thr	Cys	Ser	Cys	Asp	Ile	Met	Trp	Leu
		115					120					125			
Lys	Thr	Leu	Gln	Glu	Thr	Lys	Ser	Ser	Pro	Asp	Thr	Gln	Asp	Leu	Tyr
	130					135					140				
Cys	Leu	Asn	Glu	Ser	Ser	Lys	Asn	Met	Pro	Leu	Ala	Asn	Leu	Gln	Ile
145					150					155					160
Pro	Asn	Cys	Gly	Leu	Pro	Ser	Ala	Arg	Leu	Ala	Ala	Pro	Asn	Leu	Thr
				165					170					175	
Val	Glu	Glu	Gly	Lys	Ser	Val	Thr	Leu	Ser	Cys	Ser	Val	Gly	Gly	Asp
			180					185					190		
Pro	Leu	Pro	Thr	Leu	Tyr	Trp	Asp	Val	Gly	Asn	Leu	Val	Ser	Lys	His
		195					200					205			
Met	Asn	Glu	Thr	Ser	His	Thr	Gln	Gly	Ser	Leu	Arg	Ile	Thr	Asn	Ile
	210					215					220				
Ser	Ser	Asp	Asp	Ser	Gly	Lys	Gln	Ile	Ser	Cys	Val	Ala	Glu	Asn	Leu
225					230					235					240
Val	Gly	Glu	Asp	Gln	Asp	Ser	Val	Asn	Leu	Thr	Val	His	Phe	Ala	Pro
				245					250					255	
Thr	Ile	Thr	Phe	Leu	Glu	Ser	Pro	Thr	Ser	Asp	His	His	Trp	Cys	Ile
			260					265					270		
Pro	Phe	Thr	Val	Arg	Gly	Asn	Pro	Lys	Pro	Ala	Leu	Gln	Trp	Phe	Tyr
		275					280					285			
Asn	Gly	Ala	Ile	Leu	Asn	Glu	Ser	Lys	Tyr	Ile	Cys	Thr	Lys	Ile	His
	290					295					300				
Val	Thr	Asn	His	Thr	Glu	Tyr	His	Gly	Cys	Leu	Gln	Leu	Asp	Asn	Pro
305					310					315					320
Thr	His	Met	Asn	Asn	Gly	Asp	Tyr	Thr	Leu	Met	Ala	Lys	Asn	Glu	Tyr
				325					330					335	
Gly	Lys	Asp	Glu	Arg	Gln	Ile	Ser	Ala	His	Phe	Met	Gly	Arg	Pro	Gly
			340					345					350		
Val	Asp	Tyr	Glu	Thr	Asn	Pro	Asn	Tyr	Pro	Glu	Val	Leu	Tyr	Glu	Asp
		355					360					365			
Trp	Thr	Thr	Pro	Thr	Asp	Ile	Gly	Asp	Thr	Thr	Asn	Lys	Ser	Asn	Glu
	370					375					380				
Ile	Pro	Ser	Thr	Asp	Val	Ala	Asp	Gln	Ser	Asn	Arg	Glu	His	Leu	Ser
385					390					395					400

Val	Tyr	Ala	Val	Val	Val	Ile	Ala	Ser	Val	Val	Gly	Phe	Cys	Leu	Leu			
				405					410					415				
Val	Met	Leu	Phe	Leu	Leu	Lys	Leu	Ala	Arg	His	Ser	Lys	Phe	Gly	Met			
			420					425					430					
Lys	Gly	Pro	Ala	Ser	Val	Ile	Ser	Asn	Asp	Asp	Asp	Ser	Ala	Ser	Pro			
		435					440					445						
Leu	His	His	Ile	Ser	Asn	Gly	Ser	Asn	Thr	Pro	Ser	Ser	Ser	Glu	Gly			
	450					455					460							
Gly	Pro	Asp	Ala	Val	Ile	Ile	Gly	Met	Thr	Lys	Ile	Pro	Val	Ile	Glu			
465					470					475					480			
Asn	Pro	Gln	Tyr	Phe	Gly	Ile	Thr	Asn	Ser	Gln	Leu	Lys	Pro	Asp	Thr			
				485				490						495				
Phe	Val	Gln	His	Ile	Lys	Arg	His	Asn	Ile	Val	Leu	Lys	Arg	Glu	Leu			
			500				505						510					
Gly	Glu	Gly	Ala	Phe	Gly	Lys	Val	Phe	Leu	Ala	Glu	Cys	Tyr	Asn	Leu			
		515				520						525						
Cys	Pro	Glu	Gln	Asp	Lys	Ile	Leu	Val	Ala	Val	Lys	Thr	Leu	Lys	Asp			
	530				535						540							
Ala	Ser	Asp	Asn	Ala	Arg	Lys	Asp	Phe	His	Arg	Glu	Ala	Glu	Leu	Leu			
545				550					555						560			
Thr	Asn	Leu	Gln	His	Glu	His	Ile	Val	Lys	Phe	Tyr	Gly	Val	Cys	Val			
				565				570						575				
Glu	Gly	Asp	Pro	Leu	Ile	Met	Val	Phe	Glu	Tyr	Met	Lys	His	Gly	Asp			
			580					585					590					
Leu	Asn	Lys	Phe	Leu	Arg	Ala	His	Gly	Pro	Asp	Ala	Val	Leu	Met	Ala			
		595				600						605						
Glu	Gly	Asn	Pro	Pro	Thr	Glu	Leu	Thr	Gln	Ser	Gln	Met	Leu	His	Ile			
	610					615					620							
Ala	Gln	Gln	Ile	Ala	Ala	Gly	Met	Val	Tyr	Leu	Ala	Ser	Gln	His	Phe			
625				630					635						640			
Val	His	Arg	Asp	Leu	Ala	Thr	Arg	Asn	Cys	Leu	Val	Gly	Glu	Asn	Leu			
				645				650						655				
Leu	Val	Lys	Ile	Gly	Asp	Phe	Gly	Met	Ser	Arg	Asp	Val	Tyr	Ser	Thr			
			660				665						670					
Asp	Tyr	Tyr	Arg	Val	Gly	Gly	His	Thr	Met	Leu	Pro	Ile	Arg	Trp	Met			
		675				680						685						
Pro	Pro	Glu	Ser	Ile	Met	Tyr	Arg	Lys	Phe	Thr	Thr	Glu	Ser	Asp	Val			
	690				695						700							
Trp	Ser	Leu	Gly	Val	Val	Leu	Trp	Glu	Ile	Phe	Thr	Tyr	Gly	Lys	Gln			
705				710					715						720			
Pro	Trp	Tyr	Gln	Leu	Ser	Asn	Asn	Glu	Val	Ile	Glu	Cys	Ile	Thr	Gln			
				725				730					735					
Gly	Arg	Val	Leu	Gln	Arg	Pro	Arg	Thr	Cys	Pro	Gln	Glu	Val	Tyr	Glu			
		740				745						750						
Leu	Met	Leu	Gly	Cys	Trp	Gln	Arg	Glu	Pro	His	Met	Arg	Lys	Asn	Ile			
		755				760					765							
Lys	Gly	Ile	His	Thr	Leu	Leu	Gln	Asn	Leu	Ala	Lys	Ala	Ser	Pro	Val			
	770				775						780							
Tyr	Leu	Asp	Ile	Leu	Gly													
785					790													

<210> 94
 <211> 791
 <212> PRT

<213> Artificial Sequence

<220>

<223> AGM TrkB (pRGN984.agmTrkB)

1-791: aa 32 through 822 of XP_007967815.1

<400> 94

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

<210> 95
 <211> 807
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MM TrkB (mmTrkB)
 1-807: aa 32 through 838 of NP_001248226.1

<400> 95
 Cys Pro Thr Ser Cys Lys Cys Ser Ala Ser Arg Ile Trp Cys Ser Asp
 1 5 10 15
 Pro Ser Pro Gly Ile Val Ala Phe Pro Arg Leu Glu Pro Asn Ser Val
 20 25 30
 Asp Pro Glu Asn Ile Thr Glu Ile Phe Ile Ala Asn Gln Lys Arg Leu
 35 40 45
 Glu Ile Ile Asn Glu Asp Asp Val Glu Ala Tyr Val Gly Leu Arg Asn
 50 55 60
 Leu Thr Ile Val Asp Ser Gly Leu Lys Phe Val Ala His Lys Ala Phe
 65 70 75 80
 Leu Lys Asn Ser Asn Leu Gln His Ile Asn Phe Thr Arg Asn Lys Leu
 85 90 95
 Thr Ser Leu Ser Arg Lys His Phe Arg His Leu Asp Leu Ser Glu Leu
 100 105 110
 Ile Leu Val Gly Asn Pro Phe Thr Cys Ser Cys Asp Ile Met Trp Ile
 115 120 125
 Lys Thr Leu Gln Glu Ala Lys Ser Ser Pro Asp Thr Gln Asp Leu Tyr
 130 135 140
 Cys Leu Asn Glu Ser Ser Lys Asn Ile Pro Leu Ala Asn Leu Gln Ile
 145 150 155 160
 Pro Asn Cys Gly Leu Pro Ser Ala Asn Leu Ala Ala Pro Asn Leu Thr
 165 170 175
 Val Glu Glu Gly Lys Ser Ile Thr Leu Ser Cys Ser Val Ala Gly Asp
 180 185 190
 Pro Val Pro Asn Met Tyr Trp Asp Val Gly Asn Leu Val Ser Lys His
 195 200 205
 Met Asn Glu Thr Ser His Thr Gln Gly Ser Leu Arg Ile Thr Asn Ile
 210 215 220
 Ser Ser Asp Asp Ser Gly Lys Gln Ile Ser Cys Val Ala Glu Asn Leu
 225 230 235 240
 Val Gly Glu Asp Gln Asp Ser Val Asn Leu Thr Val His Phe Ala Pro
 245 250 255
 Thr Ile Thr Phe Leu Glu Ser Pro Thr Ser Asp His His Trp Cys Ile
 260 265 270
 Pro Phe Thr Val Lys Gly Asn Pro Lys Pro Ala Leu Gln Trp Phe Tyr
 275 280 285
 Asn Gly Ala Ile Leu Asn Glu Ser Lys Tyr Ile Cys Thr Lys Ile His
 290 295 300
 Val Thr Asn His Thr Glu Tyr His Gly Cys Leu Gln Leu Asp Asn Pro
 305 310 315 320

Thr	His	Met	Asn	Asn	Gly	Asp	Tyr	Thr	Leu	Ile	Ala	Lys	Asn	Glu	Tyr	
				325					330					335		
Gly	Lys	Asp	Glu	Lys	Gln	Ile	Ser	Ala	His	Phe	Met	Gly	Trp	Pro	Gly	
			340					345					350			
Ile	Asp	Asp	Gly	Ala	Asn	Pro	Asn	Tyr	Pro	Asp	Val	Ile	Tyr	Glu	Asp	
		355					360					365				
Tyr	Gly	Thr	Ala	Ala	Asn	Asp	Ile	Gly	Asp	Thr	Thr	Asn	Arg	Ser	Asn	
	370					375					380					
Glu	Ile	Pro	Ser	Thr	Asp	Val	Thr	Asp	Lys	Thr	Gly	Arg	Glu	His	Leu	
385					390					395					400	
Ser	Val	Tyr	Ala	Val	Val	Val	Ile	Ala	Ser	Val	Val	Gly	Phe	Cys	Leu	
			405					410						415		
Leu	Val	Met	Leu	Phe	Leu	Leu	Lys	Leu	Ala	Arg	His	Ser	Lys	Phe	Gly	
		420					425						430			
Met	Lys	Asp	Phe	Ser	Trp	Phe	Gly	Phe	Gly	Lys	Val	Lys	Ser	Arg	Gln	
	435					440						445				
Gly	Val	Gly	Pro	Ala	Ser	Val	Ile	Ser	Asn	Asp	Asp	Asp	Ser	Ala	Ser	
	450				455					460						
Pro	Leu	His	His	Ile	Ser	Asn	Gly	Ser	Asn	Thr	Pro	Ser	Ser	Ser	Glu	
465				470						475					480	
Gly	Gly	Pro	Asp	Ala	Val	Ile	Ile	Gly	Met	Thr	Lys	Ile	Pro	Val	Ile	
			485					490						495		
Glu	Asn	Pro	Gln	Tyr	Phe	Gly	Ile	Thr	Asn	Ser	Gln	Leu	Lys	Pro	Asp	
		500					505						510			
Thr	Phe	Val	Gln	His	Ile	Lys	Arg	His	Asn	Ile	Val	Leu	Lys	Arg	Glu	
	515					520						525				
Leu	Gly	Glu	Gly	Ala	Phe	Gly	Lys	Val	Phe	Leu	Ala	Glu	Cys	Tyr	Asn	
	530					535			540							
Leu	Cys	Pro	Glu	Gln	Asp	Lys	Ile	Leu	Val	Ala	Val	Lys	Thr	Leu	Lys	
545				550					555						560	
Asp	Ala	Ser	Asp	Asn	Ala	Arg	Lys	Asp	Phe	His	Arg	Glu	Ala	Glu	Leu	
			565					570						575		
Leu	Thr	Asn	Leu	Gln	His	Glu	His	Ile	Val	Lys	Phe	Tyr	Gly	Val	Cys	
		580					585						590			
Val	Glu	Gly	Asp	Pro	Leu	Ile	Met	Val	Phe	Glu	Tyr	Met	Lys	His	Gly	
	595					600						605				
Asp	Leu	Asn	Lys	Phe	Leu	Arg	Ala	His	Gly	Pro	Asp	Ala	Val	Leu	Met	
	610				615					620						
Ala	Glu	Gly	Asn	Pro	Pro	Thr	Glu	Leu	Thr	Gln	Ser	Gln	Met	Leu	His	
625				630					635						640	
Ile	Ala	Gln	Gln	Ile	Ala	Ala	Gly	Met	Val	Tyr	Leu	Ala	Ser	Gln	His	
			645					650						655		
Phe	Val	His	Arg	Asp	Leu	Ala	Thr	Arg	Asn	Cys	Leu	Val	Gly	Glu	Asn	
	660						665						670			
Leu	Leu	Val	Lys	Ile	Gly	Asp	Phe	Gly	Met	Ser	Arg	Asp	Val	Tyr	Ser	
	675				680							685				
Thr	Asp	Tyr	Tyr	Arg	Val	Gly	Gly	His	Thr	Met	Leu	Pro	Ile	Arg	Trp	
	690				695					700						
Met	Pro	Pro	Glu	Ser	Ile	Met	Tyr	Arg	Lys	Phe	Thr	Thr	Glu	Ser	Asp	
705				710					715						720	
Val	Trp	Ser	Leu	Gly	Val	Val	Leu	Trp	Glu	Ile	Phe	Thr	Tyr	Gly	Lys	
			725					730						735		
Gln	Pro	Trp	Tyr	Gln	Leu	Ser	Asn	Asn	Glu	Val	Ile	Glu	Cys	Ile	Thr	
	740						745						750			
Gln	Gly	Arg	Val	Leu	Gln	Arg	Pro	Arg	Thr	Cys	Pro	Gln	Glu	Val	Tyr	

		755				760				765					
Glu	Leu	Met	Leu	Gly	Cys	Trp	Gln	Arg	Glu	Pro	His	Met	Arg	Lys	Asn
	770					775					780				
Ile	Lys	Gly	Ile	His	Thr	Leu	Leu	Gln	Asn	Leu	Ala	Lys	Ala	Ser	Pro
785					790					795					800
Val	Tyr	Leu	Asp	Ile	Leu	Gly									
				805											

<210> 96

<211> 807

<212> PRT

<213> Artificial Sequence

<220>

<223> MF TrkB (mfTrkB)

1-807 : aa 32 through 838 of XP_005582102.1

<400> 96

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

Asn	Gly	Ala	Ile	Leu	Asn	Glu	Ser	Lys	Tyr	Ile	Cys	Thr	Lys	Ile	His
290					295					300					
Val	Thr	Asn	His	Thr	Glu	Tyr	His	Gly	Cys	Leu	Gln	Leu	Asp	Asn	Pro
305					310					315					320
Thr	His	Met	Asn	Asn	Gly	Asp	Tyr	Thr	Leu	Ile	Ala	Lys	Asn	Glu	Tyr
			325						330					335	
Gly	Lys	Asp	Glu	Lys	Gln	Ile	Ser	Ala	His	Phe	Met	Gly	Trp	Pro	Gly
			340					345					350		
Ile	Asp	Asp	Gly	Ala	Asn	Pro	Asn	Tyr	Pro	Asp	Val	Ile	Tyr	Glu	Asp
		355					360					365			
Tyr	Gly	Thr	Ala	Ala	Asn	Asp	Ile	Gly	Asp	Thr	Thr	Asn	Arg	Ser	Asn
	370					375					380				
Glu	Ile	Pro	Ser	Thr	Asp	Val	Thr	Asp	Lys	Thr	Gly	Arg	Glu	His	Leu
385					390					395					400
Ser	Val	Tyr	Ala	Val	Val	Val	Ile	Ala	Ser	Val	Val	Gly	Phe	Cys	Leu
			405					410						415	
Leu	Val	Met	Leu	Phe	Leu	Leu	Lys	Leu	Ala	Arg	His	Ser	Lys	Phe	Gly
		420					425						430		
Met	Lys	Asp	Phe	Ser	Trp	Phe	Gly	Phe	Gly	Lys	Val	Lys	Ser	Arg	Gln
		435				440						445			
Gly	Val	Gly	Pro	Ala	Ser	Val	Ile	Ser	Asn	Asp	Asp	Asp	Ser	Ala	Ser
	450					455				460					
Pro	Leu	His	His	Ile	Ser	Asn	Gly	Ser	Asn	Thr	Pro	Ser	Ser	Ser	Glu
465					470					475					480
Gly	Gly	Pro	Asp	Ala	Val	Ile	Ile	Gly	Met	Thr	Lys	Ile	Pro	Val	Ile
				485				490						495	
Glu	Asn	Pro	Gln	Tyr	Phe	Gly	Ile	Thr	Asn	Ser	Gln	Leu	Lys	Pro	Asp
			500					505					510		
Thr	Phe	Val	Gln	His	Ile	Lys	Arg	His	Asn	Ile	Val	Leu	Lys	Arg	Glu
		515					520					525			
Leu	Gly	Glu	Gly	Ala	Phe	Gly	Lys	Val	Phe	Leu	Ala	Glu	Cys	Tyr	Asn
	530					535					540				
Leu	Cys	Pro	Glu	Gln	Asp	Lys	Ile	Leu	Val	Ala	Val	Lys	Thr	Leu	Lys
545					550					555					560
Asp	Ala	Ser	Asp	Asn	Ala	Arg	Lys	Asp	Phe	His	Arg	Glu	Ala	Glu	Leu
				565					570					575	
Leu	Thr	Asn	Leu	Gln	His	Glu	His	Ile	Val	Lys	Phe	Tyr	Gly	Val	Cys
		580						585					590		
Val	Glu	Gly	Asp	Pro	Leu	Ile	Met	Val	Phe	Glu	Tyr	Met	Lys	His	Gly
		595					600					605			
Asp	Leu	Asn	Lys	Phe	Leu	Arg	Ala	His	Gly	Pro	Asp	Ala	Val	Leu	Met
	610					615				620					
Ala	Glu	Gly	Asn	Pro	Pro	Thr	Glu	Leu	Thr	Gln	Ser	Gln	Met	Leu	His
625					630					635					640
Ile	Ala	Gln	Gln	Ile	Ala	Ala	Gly	Met	Val	Tyr	Leu	Ala	Ser	Gln	His
				645					650					655	
Phe	Val	His	Arg	Asp	Leu	Ala	Thr	Arg	Asn	Cys	Leu	Val	Gly	Glu	Asn
			660					665					670		
Leu	Leu	Val	Lys	Ile	Gly	Asp	Phe	Gly	Met	Ser	Arg	Asp	Val	Tyr	Ser
		675					680					685			
Thr	Asp	Tyr	Tyr	Arg	Val	Gly	Gly	His	Thr	Met	Leu	Pro	Ile	Arg	Trp
	690					695					700				
Met	Pro	Pro	Glu	Ser	Ile	Met	Tyr	Arg	Lys	Phe	Thr	Thr	Glu	Ser	Asp
705					710					715					720
Val	Trp	Ser	Leu	Gly	Val	Val	Leu	Trp	Glu	Ile	Phe	Thr	Tyr	Gly	Lys

				725					730					735			
Gln	Pro	Trp	Tyr	Gln	Leu	Ser	Asn	Asn	Glu	Val	Ile	Glu	Cys	Ile	Thr		
			740					745					750				
Gln	Gly	Arg	Val	Leu	Gln	Arg	Pro	Arg	Thr	Cys	Pro	Gln	Glu	Val	Tyr		
		755					760					765					
Glu	Leu	Met	Leu	Gly	Cys	Trp	Gln	Arg	Glu	Pro	His	Met	Arg	Lys	Asn		
	770				775						780						
Ile	Lys	Gly	Ile	His	Thr	Leu	Leu	Gln	Asn	Leu	Ala	Lys	Ala	Ser	Pro		
785					790					795					800		
Val	Tyr	Leu	Asp	Ile	Leu	Gly											
				805													

<210> 97

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> H1M8037C heavy chain

<400> 97

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

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

<210> 99

<211> 445

<212> PRT

<213> Artificial Sequence

<220>

<223> H4H9780P Full length heavy chain

<400> 99

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

290	295	300
Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys		
305	310	315
Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys		
	325	330
Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser		
	340	345
Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys		
	355	360
Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln		
	370	375
Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly		
385	390	395
Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln		
	405	410
Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn		
	420	425
His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys		
	435	440
		445

<210> 100

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> H4H9780P Full length light chain

<400> 100

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly	
1	5
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Tyr	
	20
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile	
	35
Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Gly Gly	
	50
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro	
65	70
Glu Asp Val Ala Thr Tyr Tyr Cys Gln Lys Tyr Thr Ser Ala Pro Phe	
	85
Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala Ala	
	100
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly	
	115
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala	
	130
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln	
145	150
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser	
	165
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr	
	180
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser	
	185
	190

195
Phe Asn Arg Gly Glu Cys
210

200

205

<210> 101
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> H4H9814P Full length heavy chain

<400> 101
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Lys Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe Ser Gly Ser
20 25 30
Val Ile His Trp Val Arg Gln Ala Ser Gly Lys Gly Leu Glu Trp Ile
35 40 45
Gly Arg Ile Arg Asn Lys Ala Asn Ser Tyr Ala Thr Ala Tyr Gly Ala
50 55 60
Ser Val Thr Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
65 70 75 80
Ala Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
85 90 95
Tyr Cys Thr Phe Pro Gly Val Val Gly Arg Gly Gly Phe Asp Tyr Trp
100 105 110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
115 120 125
Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr
130 135 140
Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
145 150 155 160
Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
165 170 175
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
180 185 190
Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp
195 200 205
His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr
210 215 220
Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro
225 230 235 240
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
245 250 255
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp
260 265 270
Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
275 280 285
Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val
290 295 300
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305 310 315 320
Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys

				325					330				335			
Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	
			340					345					350			
Leu	Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	
		355					360					365				
Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	
	370					375					380					
Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	
385					390					395					400	
Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	
			405						410					415		
Ser	Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	
			420					425					430			
Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	
		435					440					445				

Lys

<210> 102

<211> 220

<212> PRT

<213> Artificial Sequence

<220>

<223> H4H9814P Full length light chain

<400> 102

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

210

215

220

<210> 103

<211> 454

<212> PRT

<213> Artificial Sequence

<220>

<223> H4H9816P2 Full length heavy chain

<400> 103

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

			340					345				350					
Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn		
			355				360					365					
Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile		
			370				375				380						
Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr		
385					390					395					400		
Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg		
				405				410						415			
Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys		
			420					425					430				
Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	Arg	Phe	Thr	Gln	Lys	Ser	Leu		
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Ser	Leu	Ser	Pro	Gly	Lys												
		450															

<210> 104

<211> 215

<212> PRT

<213> Artificial Sequence

<220>

<223> H4H9816P2 Full length light chain

<400> 104

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