

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

<160> 104

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ccaggcaagg gactggagtg ggtgtcagtt atatcatatg atggaattaa tacatactat 180
acagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcaaatga acggcctgag agctgaggac acggctcttt attactgtgt gcaaggggtca 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
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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
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 Gly Phe Ser Phe Ser Ser Phe Gly
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 Ile Ser Tyr Asp Gly Ile Asn Thr

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gggaaagtgc ctaaactcct gatctatgct gcatccactt tacaatcagg ggtcccatct 180
cggttcggtg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240
gaagatgttg caacttatta ctgtcaaaag tataccagtg ccccatcac tttcggccct 300
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Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

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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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Thr	Phe	Gly	Pro	Gly	Thr	Lys	Val	Asp	Ile	Lys					
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 Gln Gly Ile Ser Asn Tyr
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Ala Ala Ser
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caaaagtata ccagtgtccc attcact 27

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Gln Lys Tyr Thr Ser Ala Pro Phe Thr
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tccgggaaag ggctggagtg gattggccgt attagaaaca aggctaacag ttacgcgaca 180
gcatatggtg cgtcggtgac aggcaggttc accatctcca gagatgattc aaagaacacg 240
gcgtatctgc aaatgaacag cctgaaaacc gaggacacgg ccgtttatta ctgtactttc 300
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tcctca 366

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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								
		115					120										

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<400> 19

gggttcacct tcagtggctc tggt

24

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attagaaaca aggctaacag ttacgcgaca 30

<210> 22
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<400> 22
Ile Arg Asn Lys Ala Asn Ser Tyr Ala Thr
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Thr Phe Pro Gly Val Val Gly Arg Gly Gly Phe Asp Tyr
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tggtaccaac agaaaccagg acagcctcct aagttgctct tttactgggc atctaccg 180
gaatccgggg tccctgaccg attcgggtggc agcgggtctg ggacagattt ctctctcacc 240
atcaacagcc tgcagactga agatgtggca gtttattact gtctccaata ttatagtatt 300

ccgtggacgt tcggccaagg gaccaaggtg gaaatcaaa

339

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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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<211> 36

<212> DNA

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<223> synthetic

<400> 27

cagagtgttt tattcagctc caacaataag aactac

36

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<211> 12

<212> PRT

<213> Artificial Sequence

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<223> synthetic

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Gln	Ser	Val	Leu	Phe	Ser	Ser	Asn	Asn	Lys	Asn	Tyr
1			5						10		

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<220>
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<400> 29
tgggcatct

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<210> 30
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<400> 30
Trp Ala Ser
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<210> 31
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<212> DNA
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<400> 31
ctccaatatt atagtattcc gtggacg

27

<210> 32
<211> 9
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<400> 32
Leu Gln Tyr Tyr Ser Ile Pro Trp Thr
1 5

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ccagggaagg ggctggagtg gatttcatac attagtaata gtgggttatac catatactac 180
gcagactctg tgaagggccg attcaccatc tccagagaca acgccaggaa ctcaatatat 240
ctgcaagtga acagcctgag agccgaggac acggctgttt attactgttc gagacgtact 300
actatgattc ggggcattag ggcgtactac tattacggtc tggacgtctg gggccaaggg 360
accacgggtca 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
100 105 110
Gly Leu Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

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<400> 35
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<210> 36
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<400> 36

Gly Phe Asn Phe Arg Asp Tyr Glu
1 5

<210> 37

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<400> 37

attagtaata gtggttatac cata

24

<210> 38

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<400> 38

Ile Ser Asn Ser Gly Tyr Thr Ile
1 5

<210> 39

<211> 60

<212> DNA

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<400> 39

tcgagacgta ctactatgat tcggggcatt agggcgtact actattacgg tctggacgtc 60

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<400> 40

Ser Arg Arg Thr Thr Met Ile Arg Gly Ile Arg Ala Tyr Tyr Tyr Tyr
1 5 10 15

Gly Leu Asp Val
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atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 120
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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<400> 42
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
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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

cagagcatta gcagctat

18

<210> 44

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

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<400> 44

Gln Ser Ile Ser Ser Tyr

1

5

<210> 45

<211> 9

<212> DNA

<213> Artificial Sequence

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<223> synthetic

<400> 45

gctgcatcc

9

<210> 46

<211> 3

<212> PRT

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<220>

<223> synthetic

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Ala Ala Ser

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<212> DNA

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<210> 48

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<400> 48

Gln Gln Ser Tyr Ser Thr Pro Pro Ile Thr
1 5 10

<210> 49

<211> 123

<212> PRT

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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

<210> 50

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<213> Artificial Sequence

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<223> M2aM14173N HCDR1

<400> 50

Gly Phe Thr Phe Ser Ser Ser Ala
1 5

<210> 51

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<212> PRT

<213> Artificial Sequence

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<223> M2aM14173N HCDR2

<400> 51

Ile Ser Asp Arg Gly Ser Tyr Thr
1 5

<210> 52

<211> 16

<212> PRT

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<223> M2aM14173N HCDR3

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Ala Arg Gly Lys Gly Glu Lys Ala Tyr Tyr Thr Ala Phe Phe Ala Tyr
1 5 10 15

<210> 53

<211> 107

<212> PRT

<213> Artificial Sequence

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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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<400> 55
Asn Ala Glu
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<223> M2aM14173N LCDR3

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

<210> 57
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
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<400> 57
Ala Lys Thr Thr Ala Pro Ser Val Tyr Pro Leu Ala Pro Val Cys Gly
1 5 10 15
Asp Thr Thr Gly Ser Ser Val Thr Leu Gly Cys Leu Val Lys Gly Tyr
20 25 30
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	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						

<210> 58

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<212> PRT

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<220>

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<400> 58

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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							

<210> 59
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> M2aM14178N HCVR

<400> 59
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15
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

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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

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<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

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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

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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
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
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
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
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
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
 145 150 155 160
 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 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> 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
			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											

Phe Ser Arg Thr Pro Gly Lys
625 630

<210> 81
<211> 625
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse TrkB (C32-H429).hFc
aa 1-398: aa 32 through 429 of NP_001020245; aa
399-625 human Fc domain

<400> 81
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 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
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

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

<210> 86

<211> 605

<212> PRT

<213> Artificial Sequence

<220>

<223> Human TrkA(A34-T414).hFc

aa 1-375: aa 34 through 414 of NP_001012331.1 with

V263L, C300S; aa 376-378 GPG Linker; aa 379-605
human Fc domain

<400> 86

Ala	Pro	Cys	Pro	Asp	Ala	Cys	Cys	Pro	His	Gly	Ser	Ser	Gly	Leu	Arg	1	5	10	15
Cys	Thr	Arg	Asp	Gly	Ala	Leu	Asp	Ser	Leu	His	His	Leu	Pro	Gly	Ala	20	25	30	
Glu	Asn	Leu	Thr	Glu	Leu	Tyr	Ile	Glu	Asn	Gln	Gln	His	Leu	Gln	His	35	40	45	
Leu	Glu	Leu	Arg	Asp	Leu	Arg	Gly	Leu	Gly	Glu	Leu	Arg	Asn	Leu	Thr	50	55	60	
Ile	Val	Lys	Ser	Gly	Leu	Arg	Phe	Val	Ala	Pro	Asp	Ala	Phe	His	Phe	65	70	75	80
Thr	Pro	Arg	Leu	Ser	Arg	Leu	Asn	Leu	Ser	Phe	Asn	Ala	Leu	Glu	Ser	85	90	95	
Leu	Ser	Trp	Lys	Thr	Val	Gln	Gly	Leu	Ser	Leu	Gln	Glu	Leu	Val	Leu	100	105	110	
Ser	Gly	Asn	Pro	Leu	His	Cys	Ser	Cys	Ala	Leu	Arg	Trp	Leu	Gln	Arg	115	120	125	
Trp	Glu	Glu	Glu	Gly	Leu	Gly	Gly	Val	Pro	Glu	Gln	Lys	Leu	Gln	Cys	130	135	140	
His	Gly	Gln	Gly	Pro	Leu	Ala	His	Met	Pro	Asn	Ala	Ser	Cys	Gly	Val	145	150	155	160
Pro	Thr	Leu	Lys	Val	Gln	Val	Pro	Asn	Ala	Ser	Val	Asp	Val	Gly	Asp	165	170	175	
Asp	Val	Leu	Leu	Arg	Cys	Gln	Val	Glu	Gly	Arg	Gly	Leu	Glu	Gln	Ala	180	185	190	
Gly	Trp	Ile	Leu	Thr	Glu	Leu	Glu	Gln	Ser	Ala	Thr	Val	Met	Lys	Ser	195	200	205	
Gly	Gly	Leu	Pro	Ser	Leu	Gly	Leu	Thr	Leu	Ala	Asn	Val	Thr	Ser	Asp	210	215	220	
Leu	Asn	Arg	Lys	Asn	Leu	Thr	Cys	Trp	Ala	Glu	Asn	Asp	Val	Gly	Arg	225	230	235	240
Ala	Glu	Val	Ser	Val	Gln	Val	Asn	Val	Ser	Phe	Pro	Ala	Ser	Val	Gln	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													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													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
	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	Gly	Pro	Ala	Ser	Val	Ile	Ser	Asn	Asp	Asp	Asp	Ser	Ala	Ser	435	440	445	
Pro	Leu	His	His	Ile	Ser	Asn	Gly	Ser	Asn	Thr	Pro	Ser	Ser	Ser	Glu	450	455	460	
Gly	Gly	Pro	Asp	Ala	Val	Ile	Ile	Gly	Met	Thr	Lys	Ile	Pro	Val	Ile	465	470	475	480
Glu	Asn	Pro	Gln	Tyr	Phe	Gly	Ile	Thr	Asn	Ser	Gln	Leu	Lys	Pro	Asp	485	490	495	
Thr	Phe	Val	Gln	His	Ile	Lys	Arg	His	Asn	Ile	Val	Leu	Lys	Arg	Glu	500	505	510	
Leu	Gly	Glu	Gly	Ala	Phe	Gly	Lys	Val	Phe	Leu	Ala	Glu	Cys	Tyr	Asn	515	520	525	
Leu	Cys	Pro	Glu	Gln	Asp	Lys	Ile	Leu	Val	Ala	Val	Lys	Thr	Leu	Lys	530	535	540	
Asp	Ala	Ser	Asp	Asn	Ala	Arg	Lys	Asp	Phe	His	Arg	Glu	Ala	Glu	Leu	545	550	555	560
Leu	Thr	Asn	Leu	Gln	His	Glu	His	Ile	Val	Lys	Phe	Tyr	Gly	Val	Cys	565	570	575	
Val	Glu	Gly	Asp	Pro	Leu	Ile	Met	Val	Phe	Glu	Tyr	Met	Lys	His	Gly	580	585	590	
Asp	Leu	Asn	Lys	Phe	Leu	Arg	Ala	His	Gly	Pro	Asp	Ala	Val	Leu	Met	595	600	605	
Ala	Glu	Gly	Asn	Pro	Pro	Thr	Glu	Leu	Thr	Gln	Ser	Gln	Met	Leu	His	610	615	620	
Ile	Ala	Gln	Gln	Ile	Ala	Ala	Gly	Met	Val	Tyr	Leu	Ala	Ser	Gln	His	625	630	635	640
Phe	Val	His	Arg	Asp	Leu	Ala	Thr	Arg	Asn	Cys	Leu	Val	Gly	Glu	Asn	645	650	655	

Leu	Leu	Val	Lys	Ile	Gly	Asp	Phe	Gly	Met	Ser	Arg	Asp	Val	Tyr	Ser
			660					665					670		
Thr	Asp	Tyr	Tyr	Arg	Val	Gly	Gly	His	Thr	Met	Leu	Pro	Ile	Arg	Trp
		675					680					685			
Met	Pro	Pro	Glu	Ser	Ile	Met	Tyr	Arg	Lys	Phe	Thr	Thr	Glu	Ser	Asp
		690				695					700				
Val	Trp	Ser	Leu	Gly	Val	Val	Leu	Trp	Glu	Ile	Phe	Thr	Tyr	Gly	Lys
705					710					715					720
Gln	Pro	Trp	Tyr	Gln	Leu	Ser	Asn	Asn	Glu	Val	Ile	Glu	Cys	Ile	Thr
				725					730					735	
Gln	Gly	Arg	Val	Leu	Gln	Arg	Pro	Arg	Thr	Cys	Pro	Gln	Glu	Val	Tyr
			740					745					750		
Glu	Leu	Met	Leu	Gly	Cys	Trp	Gln	Arg	Glu	Pro	His	Met	Arg	Lys	Asn
		755					760					765			
Ile	Lys	Gly	Ile	His	Thr	Leu	Leu	Gln	Asn	Leu	Ala	Lys	Ala	Ser	Pro
	770					775					780				
Val	Tyr	Leu	Asp	Ile	Leu	Gly									
785					790										

<210> 92

<211> 445

<212> PRT

<213> Artificial Sequence

<220>

<223> Mouse TrkB

aa 1-446: aa 32 through 476 of NP_032771.1

<400> 92

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	Leu	Leu	Leu	Lys	Leu	Ala	Arg	His	Ser	Lys	Phe	Gly	Met		
		420					425						430				
Lys	Gly	Phe	Val	Leu	Phe	His	Lys	Ile	Pro	Leu	Asp	Gly					
	435						440					445					

<210> 93

<211> 790

<212> PRT

<213> Artificial Sequence

<220>

<223> Chimera TrkB (pRG984.mTrkB ecto-hTrkB TM/Cyto)
aa 1-398: aa 32 through 429 of NP_001020245.1 or
Uniprot number P15209-1; Human TrkB TM/Cyto
399-790 (aaa 431 through 822 of NP_001018074.1)

<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 20	Ile	Val	Ala	Phe	Pro 25	Arg	Leu	Glu	Pro	Asn 30	Ser	Val
Asp	Pro	Glu 35	Asn	Ile	Thr	Glu	Ile 40	Leu	Ile	Ala	Asn	Gln 45	Lys	Arg	Leu
Glu	Ile 50	Ile	Asn	Glu	Asp	Asp 55	Val	Glu	Ala	Tyr	Val 60	Gly	Leu	Arg	Asn
Leu 65	Thr	Ile	Val	Asp	Ser 70	Gly	Leu	Lys	Phe	Val 75	Ala	Tyr	Lys	Ala	Phe 80
Leu	Lys	Asn	Ser	Asn 85	Leu	Arg	His	Ile	Asn 90	Phe	Thr	Arg	Asn	Lys 95	Leu
Thr	Ser	Leu	Ser 100	Arg	Arg	His	Phe	Arg 105	His	Leu	Asp	Leu	Ser	Asp	Leu
Ile	Leu	Thr 115	Gly	Asn	Pro	Phe	Thr 120	Cys	Ser	Cys	Asp	Ile 125	Met	Trp	Leu
Lys	Thr 130	Leu	Gln	Glu	Thr	Lys 135	Ser	Ser	Pro	Asp	Thr 140	Gln	Asp	Leu	Tyr
Cys 145	Leu	Asn	Glu	Ser	Ser 150	Lys	Asn	Met	Pro	Leu	Ala 155	Asn	Leu	Gln	Ile 160
Pro	Asn	Cys	Gly 165	Leu	Pro	Ser	Ala	Arg 170	Leu	Ala	Ala	Pro	Asn	Leu	Thr 175
Val	Glu	Glu	Gly 180	Lys	Ser	Val	Thr	Leu 185	Ser	Cys	Ser	Val	Gly	Gly	Asp
Pro	Leu	Pro 195	Thr	Leu	Tyr	Trp	Asp 200	Val	Gly	Asn	Leu	Val 205	Ser	Lys	His
Met	Asn 210	Glu	Thr	Ser	His	Thr 215	Gln	Gly	Ser	Leu	Arg 220	Ile	Thr	Asn	Ile
Ser 225	Ser	Asp	Asp	Ser	Gly 230	Lys	Gln	Ile	Ser	Cys 235	Val	Ala	Glu	Asn	Leu 240
Val	Gly	Glu	Asp 245	Gln	Asp	Ser	Val	Asn 250	Leu	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
Pro	Phe 275	Thr	Val	Arg	Gly	Asn 280	Pro	Lys	Pro	Ala	Leu	Gln 285	Trp	Phe	Tyr
Asn	Gly 290	Ala	Ile	Leu	Asn 295	Glu	Ser	Lys	Tyr	Ile	Cys 300	Thr	Lys	Ile	His
Val 305	Thr	Asn	His	Thr	Glu 310	Tyr	His	Gly	Cys	Leu	Gln 315	Leu	Asp	Asn	Pro 320
Thr	His	Met	Asn 325	Asn	Gly	Asp	Tyr	Thr 330	Leu	Met	Ala	Lys	Asn	Glu	Tyr 335
Gly	Lys	Asp	Glu 340	Arg	Gln	Ile	Ser	Ala 345	His	Phe	Met	Gly	Arg	Pro	Gly
Val	Asp	Tyr 355	Glu	Thr	Asn	Pro	Asn 360	Tyr	Pro	Glu	Val	Leu 365	Tyr	Glu	Asp
Trp	Thr 370	Thr	Pro	Thr	Asp 375	Ile	Gly	Asp	Thr	Thr	Asn 380	Lys	Ser	Asn	Glu
Ile 385	Pro	Ser	Thr	Asp	Val 390	Ala	Asp	Gln	Ser	Asn 395	Arg	Glu	His	Leu	Ser 400
Val	Tyr	Ala	Val 405	Val	Val	Ile	Ala	Ser	Val	Val	Gly	Phe	Cys	Leu	Leu 415
Val	Met	Leu	Phe 420	Leu	Leu	Lys	Leu	Ala 425	Arg	His	Ser	Lys	Phe	Gly	Met
Lys	Gly	Pro 435	Ala	Ser	Val	Ile	Ser	Asn 440	Asp	Asp	Asp	Ser	Ala	Ser	Pro

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

<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
						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
						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		
			260					265				270					
Val	Gln	Phe	Ser	Trp	Phe	Val	Asp	Asp	Val	Glu	Val	His	Thr	Ala	Gln		
		275					280					285					
Thr	Gln	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Phe	Arg	Ser	Val	Ser		
		290				295					300						
Glu	Leu	Pro	Ile	Met	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Phe	Lys		
305				310					315						320		
Cys	Arg	Val	Asn	Ser	Ala	Ala	Phe	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile		
			325					330						335			
Ser	Lys	Thr	Lys	Gly	Arg	Pro	Lys	Ala	Pro	Gln	Val	Tyr	Thr	Ile	Pro		
		340						345					350				
Pro	Pro	Lys	Glu	Gln	Met	Ala	Lys	Asp	Lys	Val	Ser	Leu	Thr	Cys	Met		
		355					360					365					
Ile	Thr	Asp	Phe	Phe	Pro	Glu	Asp	Ile	Thr	Val	Glu	Trp	Gln	Trp	Asn		
	370					375					380						
Gly	Gln	Pro	Ala	Glu	Asn	Tyr	Lys	Asn	Thr	Gln	Pro	Ile	Met	Asp	Thr		
385				390						395				400			
Asp	Gly	Ser	Tyr	Phe	Val	Tyr	Ser	Lys	Leu	Asn	Val	Gln	Lys	Ser	Asn		
			405					410					415				
Trp	Glu	Ala	Gly	Asn	Thr	Phe	Thr	Cys	Ser	Val	Leu	His	Glu	Gly	Leu		
		420					425					430					
His	Asn	His	His	Thr	Glu	Lys	Ser	Leu	Ser	His	Ser	Pro	Gly	Lys			
	435						440					445					

<210> 98

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> H1M8037C light chain

<400> 98

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

Asn	Val	Lys	Trp	Lys	Ile	Asp	Gly	Ser	Glu	Arg	Gln	Asn	Gly	Val	Leu
145					150					155					160
Asn	Ser	Trp	Thr	Asp	Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Met	Ser
				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

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

<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

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

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							