

SEQUENCE LISTING

<110> Regeneron Pharmaceuticals, Inc.

<120> Anti-NPR1 Antibodies and Uses thereof

<130> 10471W001

<150> 62/749,557

<151> 2018-10-23

<150> 62/755,720

<151> 2018-11-05

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cctggacaag  ggcttgagtg  gatgggatgg  atcaaacctc  acagtgggtg  cacaaactct  180
gcacagaggt  ttcagggcag  aatcaccatg  acctgggaca  cgtccatcag  cacagcctac  240
atggaactga  gcaggctgag  atctgacgac  acggccgtgt  attactgttc  gagagggggc  300
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Ser Val Thr Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
          20          25          30
Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
          35          40          45
Gly Trp Ile Lys Pro Asn Ser Gly Gly Thr Asn Ser Ala Gln Arg Phe
          50          55          60
Gln Gly Arg Ile Thr Met Thr Trp Asp Thr Ser Ile Ser Thr Ala Tyr
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65					70					75				80
Met	Glu	Leu	Ser	Arg	Leu	Arg	Ser	Asp	Asp	Thr	Ala	Val	Tyr	Tyr
				85					90				95	Cys
Ser	Arg	Gly	Gly	Pro	Val	Met	Asn	Tyr	Tyr	Tyr	Tyr	Tyr	Gly	Met
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		115					120							

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<210> 9
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ggtaaagccc ctaaactcct gatctatgtt gcatccagtt tgcaaagtgg ggtcccatca 180
aggttcagtg gcagtggatc tgggaaagat ttcactctca ccatcagcag tctgcaacct 240
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			20					25					30		
Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile
		35					40					45			
Tyr	Val	Ala	Ser	Ser	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
	50					55				60					
Ser	Gly	Ser	Gly	Lys	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	Ile	Pro	Thr
				85				90						95	
Phe	Gly	Gln	Gly	Thr	Arg	Leu	Glu	Ile	Lys						
			100					105							

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<400> 13
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Gln Gln Ser Tyr Ser Ile Pro Thr

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ccagggaagg gcctggagtg ggtctcaggt attagttgga atagtgggtac cataggctat 180
gcggactctg tgaagggccg attcaccatg tccagagaca acgccaagaa ctccctgtat 240
ctgcaaatga acagtctgag acctgaagac acggccttgt attattgtgc aaaagatatg 300
ggcgtatcac tggcactatg gggggccttt gatatctggg gccaaggac aatggtcacc 360
gtctcttca 369

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<212> PRT

<213> Artificial Sequence

<220>

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

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<400> 19
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<220>
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<400> 20
 Gly Phe Thr Phe Asp Asp Tyr Ala
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<210> 21
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<400> 21
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<210> 22
<211> 8
<212> PRT
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<400> 22
Ile Ser Trp Asn Ser Gly Thr Ile
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gcaaaagata tgggcgtatc actggcacta tggggggcctt ttgatatc 48

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Ala Lys Asp Met Gly Val Ser Leu Ala Leu Trp Gly Ala Phe Asp Ile
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gggaaagccc ctaagggtcct gatctctact gcatccagtt tgcaaagtgg ggtcccatca 180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg cagttttcta ctgtcaacag agtttcggta tccctcggac gttcggccaa 300
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Asp Lys Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Arg Thr Tyr
20 25 30
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile
35 40 45
Ser Thr 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 Val Phe Tyr Cys Gln Gln Ser Phe Gly Ile Pro Arg
85 90 95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

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<400> 28
Gln Asn Ile Arg Thr Tyr
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<400> 29
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9

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Thr Ala Ser
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<400> 32
Gln Gln Ser Phe Gly Ile Pro Arg Thr
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ccaggcaagg ggctggagtg ggtggcactt atatggaatg atggaagtaa taaatactat 180
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctggat 240
ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gaggctgaat 300
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tcctca

366

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

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<220>
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Gly Phe Thr Phe Ser Thr Tyr Gly
1 5

<210> 37
<211> 24

<212> DNA
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<400> 37
atatggaatg atggaagtaa taaa

24

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<400> 38
Ile Trp Asn Asp Gly Ser Asn Lys
1 5

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gggaaagccc ctaacctcct gatctatggg gcatacactt tgcaaagtgg ggtcccatca 180
aggttccgtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg cgacttacta ctgtcaacag acttacagta cccctccgat caccttcggc 300
caagggacac gactggagat taaa 324

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<212> PRT

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<400> 42

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

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<400> 43

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<212> PRT

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<400> 44

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<400> 45
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<210> 46
<211> 3
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Gly Ala Tyr
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<400> 47
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Gln Gln Thr Tyr Ser Thr Pro Pro Ile Thr
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cagaccccag ggaggggact ggagtggatt gggaatatct tttttgatgg gaacacttac 180
tataccccgt ccctcaagag tcgagtcatc atatccgttg acatgtccca gaaccaattc 240
tccctgaggc tgacctctgt gaccgccgca gacacggctc tgtattactg tgcgagacat 300
aagagggtcca tgacagcttg ggggttcttt gactattggg gccagggaac cctggtcacc 360
gtctcctca                                     369
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Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Asn Asp Asn
      20             25             30
Ser Phe Phe Trp Asp Trp Ile Arg Gln Thr Pro Gly Arg Gly Leu Glu
      35             40             45
Trp Ile Gly Asn Ile Phe Phe Asp Gly Asn Thr Tyr Tyr Thr Pro Ser
      50             55             60
Leu Lys Ser Arg Val Ile Ile Ser Val Asp Met Ser Gln Asn Gln Phe
65             70             75             80
Ser Leu Arg Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Leu Tyr Tyr
      85             90             95
Cys Ala Arg His Lys Arg Ser Met Thr Ala Trp Gly Phe Phe Asp Tyr
      100            105            110
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
      115            120
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Gly Gly Ser Ile Asn Asp Asn Ser Phe Phe
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21

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<212> PRT

<213> Artificial Sequence

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Ile Phe Phe Asp Gly Asn Thr
1 5

<210> 55

<211> 45

<212> DNA

<213> Artificial Sequence

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<223> synthetic

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<212> PRT

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<400> 56

Ala Arg His Lys Arg Ser Met Thr Ala Trp Gly Phe Phe Asp Tyr
1 5 10 15

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<220>
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<400> 57
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 ggtaaagccc ctaaagttct gatctattct gcatccaatt tgcaaagtgg ggtcccctca 180
 cggttcagtg gcagtggatc tgggacagat ttcactctca ccatcaacag tctgcaacct 240
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 caaggacac gactggagat taaa 324

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

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<400> 59
 aagagaatta acacctat 18

<210> 60
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<220>

<223> synthetic

<400> 60

Lys Arg Ile Asn Thr Tyr

1

5

<210> 61

<211> 9

<212> DNA

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<223> synthetic

<400> 61

tctgcatcc

9

<210> 62

<211> 3

<212> PRT

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<220>

<223> synthetic

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<223> synthetic

<400> 63

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<212> PRT

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<400> 64

Gln Gln Ser Phe Ser Ala Pro Pro Ile Thr

1

5

10

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<212> DNA

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ccagggaagg gactggagtg ggtcgcattc attagtagta gtagtagttt cattaattat 180
gcagactcat tgaagggccg attcaccatc tccagagaca acgcccagaa ctcactgtat 240
ctacaaatga acagcctgag agccgaggac acggctatct attactgtgc gagagcggcg 300
ggtaacgatg ttttgcctgg tcgtatggac gtctggggcc aaggggacctc ggtcaccgtc 360
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<223> synthetic

<400> 66

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

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<210> 67

<211> 24

<212> DNA

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<400> 67
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<400> 68
Gly Phe Thr Phe Arg Ile Tyr Thr
1 5

<210> 69
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<400> 69
attagtagta gtagtagttt catt 24

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

<220>
<223> synthetic

<400> 70
Ile Ser Ser Ser Ser Ser Phe Ile
1 5

<210> 71
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 71
gcgagagcgg cgggtaacga tgttttgcct ggtcgtatgg acgtc 45

<210> 72
<211> 15
<212> PRT
<213> Artificial Sequence

<220>

<223> synthetic

<400> 72

Ala	Arg	Ala	Ala	Gly	Asn	Asp	Val	Leu	Pro	Gly	Arg	Met	Asp	Val
1				5				10					15	

<210> 73

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 73

gaaattgtgt	tgacgcagtc	tccaggcacc	ctgtctttgt	ctccagggga	aagagccacc	60
ctctcctgca	gggccagtc	gagtgttagc	agcaactact	tagcgtggta	ccagcagaaa	120
cctggccagg	ttcccagtc	cctcatctat	ggtgcatcca	gcagggccac	tggcatccca	180
gacaggttca	gtggcagcgg	gtctgggaca	gacttcactc	tcaccatcac	cagactggag	240
cctgaagatt	ttgcagtgt	ttactgtcag	cagtatggta	tctcaccttg	gacgttcggc	300
caagggacca	aggtggaaat	caaa				324

<210> 74

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 74

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

<210> 75

<211> 21

<212> DNA

<213> Artificial Sequence

<220>
 <223> synthetic

<400> 75
 cagagtgtta gcagcaacta c 21

<210> 76
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 76
 Gln Ser Val Ser Ser Asn Tyr
 1 5

<210> 77
 <211> 9
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 77
 ggtgcatcc 9

<210> 78
 <211> 3
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 78
 Gly Ala Ser
 1

<210> 79
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 79
 cagcagtatg gtatctcacc ttggacg 27

<210> 80

<211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 80
 Gln Gln Tyr Gly Ile Ser Pro Trp Thr
 1 5

<210> 81
 <211> 372
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 81
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 tcctgcaagg cttctggata caccttcacc ggctactata tacactgggt gcgacaggcc 120
 cctggacaag gacttgagtg gatgggatgg atcaacccta acagtattgg cacaaactat 180
 gcacagaagt ttcagggcag ggtcaccttg accagggaca cgtccatcag tacagcctac 240
 atggagctga gcagtctgag atctgacgac acggccgtgt attactgtgc gagaggggggt 300
 agcagctcat attactacta ctactacggg atggacgtct ggggccaagg gaccacggctc 360
 accgtctcct ca 372

<210> 82
 <211> 124
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 82
 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 Gly Tyr
 20 25 30
 Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Trp Ile Asn Pro Asn Ser Ile Gly Thr Asn Tyr Ala Gln Lys Phe
 50 55 60
 Gln Gly Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Gly Gly Ser Ser Ser Tyr Tyr Tyr Tyr Tyr Tyr Gly Met Asp
 100 105 110
 Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 83
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 83
ggatacacct tcaccggcta ctat

24

<210> 84
<211> 8
<212> PRT
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<220>
<223> synthetic

<400> 84
Gly Tyr Thr Phe Thr Gly Tyr Tyr
1 5

<210> 85
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 85
atcaacccta acagtattgg caca

24

<210> 86
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 86
Ile Asn Pro Asn Ser Ile Gly Thr
1 5

<210> 87
<211> 51
<212> DNA
<213> Artificial Sequence

<220>

<223> synthetic

<400> 87

gcgagagggg gtagcagctc atattactac tactactacg gtagggacgt c 51

<210> 88

<211> 17

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<223> synthetic

<400> 88

Ala	Arg	Gly	Gly	Ser	Ser	Ser	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Gly	Met	Asp
1				5				10					15		
Val															

<210> 89

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 89

gacatccaga	tgaccagtc	tccatcctcc	ctgtctgcat	ctgtaggaga	cagagtcacc	60
atcacttgcc	gggcaagtca	gagcattgac	aactatttaa	attggtatca	gcagaaacca	120
gggaaagccc	ctaagctcct	gatctatgtt	gcatccagtt	tgcaaagtgg	ggtcccatca	180
aggttcagtg	gcagtggatc	tgggacagat	ttcactctca	ccatcagcag	tctgcaacct	240
gaagattttg	caacttacta	ctgtcaacag	agttacagta	ccccgctcac	tttcggcgga	300
gggaccaagg	tggagatcaa	a				321

<210> 90

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 90

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	Ala	Ser	Gln	Ser	Ile	Asp	Asn	Tyr
			20					25				30			
Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile
			35				40				45				
Tyr	Val	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	Leu
				85					90					95	
Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys					
			100					105							

<210> 91
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 91
 cagagcattg acaactat 18

<210> 92
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 92
 Gln Ser Ile Asp Asn Tyr
 1 5

<210> 93
 <211> 9
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 93
 gttgcatcc 9

<210> 94
 <211> 3
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 94
 Val Ala Ser
 1

<210> 95

<211> 27
<212> DNA
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<220>
<223> synthetic

<400> 95
caacagagtt acagtacccc gctcact

27

<210> 96
<211> 9
<212> PRT
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<220>
<223> synthetic

<400> 96
Gln Gln Ser Tyr Ser Thr Pro Leu Thr
1 5

<210> 97
<211> 372
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 97
caggtgcagc tgggtgcagtc tggggctgag gtgatgaagc ctggggcctc agtgaaggtc 60
tcctgcaagg cttctggata caccttcacc ggctactata ttcattgggt acgacaggcc 120
cctggacaag ggcttgagt gatgggatgg atcacccta acagtggcgc cacaaactat 180
gcacagaagt ttcagggcag ggtcaccctg accagggaca cgtccatcag cacagcctac 240
atggaactga ccaggctgaa atctgacgac acggccgttt attattgtgc gagaggggggt 300
cagttggagt tcttctatta ctactacggg atggacgtct ggggccaagg gaccacggtc 360
accgtctcct ca 372

<210> 98
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 98
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Met Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
20 25 30
Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

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

<210> 99
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 99
 ggatacacct tcaccggcta ctat

24

<210> 100
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 100
 Gly Tyr Thr Phe Thr Gly Tyr Tyr
 1 5

<210> 101
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 101
 atcaccccta acagtggcgc caca

24

<210> 102
 <211> 8
 <212> PRT
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<220>
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<400> 102
Ile Thr Pro Asn Ser Gly Ala Thr
1 5

<210> 103
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 103
gcgagagggg gtcagttgga gttcttctat tactactacg gtatggacgt c 51

<210> 104
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 104
Ala Arg Gly Gly Gln Leu Glu Phe Phe Tyr Tyr Tyr Tyr Gly Met Asp
1 5 10 15
Val

<210> 105
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 105
gacatccaga tgaccagtc tccatcctcc ctctctgcat ctgcaggaga cagagtcacc 60
atcacttgcc gggcaagtca gagcattgac agctatttaa attggtatca gcagaaacca 120
gggaaagccc ctaaactcct gatctctgct acatccggtt tccaaagtgg ggtcccatca 180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg gaacttacta ctgtcaacag agttacacta cccctatcac cttcggccaa 300
gggacacgac tggagattaa a 321

<210> 106
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 106
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ala Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Asp Ser Tyr
 20 25 30
 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Ser Ala Thr Ser Gly Phe 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 Gly Thr Tyr Tyr Cys Gln Gln Ser Tyr Thr Thr Pro Ile
 85 90 95
 Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
 100 105

<210> 107
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 107
 cagagcattg acagctat 18

<210> 108
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 108
 Gln Ser Ile Asp Ser Tyr
 1 5

<210> 109
 <211> 9
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 109
 gctacatcc 9

<210> 110
 <211> 3
 <212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 110

Ala Thr Ser

1

<210> 111

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 111

caacagagtt acactacccc tatcacc

27

<210> 112

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 112

Gln Gln Ser Tyr Thr Thr Pro Ile Thr

1

5

<210> 113

<211> 372

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 113

caggtgcagc tgggtgcagtc tggggctgag gtgaaggagc ctggggcctc agtgaaggtc 60
tcctgtaagg cttctggata caccttcacc gactactata tacactgggt gcgacaggcc 120
cctggacaag ggcttgagtg gatgggatgg atcaatctta acagtgggtg caaaaaccat 180
gcacagaagt ttcagggcag ggtcaccgtg accagtgaca cgtccatcaa cacagcctat 240
atcgaactgg gcaggctgag aggtgacgac acggccgtgt attactgttc gagaggggggt 300
ggaagtcact actattatta ttatcacggg atggacgtct ggggcccaagg aaccacggtc 360
accgtctcct ca 372

<210> 114

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 114

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

<210> 115

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 115

ggatacacct tcaccgacta ctat

24

<210> 116

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 116

Gly	Tyr	Thr	Phe	Thr	Asp	Tyr	Tyr
1				5			

<210> 117

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 117
atcaatctta acagtgggtgg caaa 24

<210> 118
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 118
Ile Asn Leu Asn Ser Gly Gly Lys
1 5

<210> 119
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 119
tcgagagggg gtggaagtca ctactattat tattatcacg gtatggacgt c 51

<210> 120
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 120
Ser Arg Gly Gly Gly Ser His Tyr Tyr Tyr Tyr Tyr His Gly Met Asp
1 5 10 15
Val

<210> 121
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
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<400> 121
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atcacttgcc gggcaagtca cagcattgac agctatttaa attggtatca gcagaaacca 120
gggaaagccc ctaaactcct gatctatcct gcatccactt tgcaaagtgg ggtcccatca 180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattctg caatttacta ctgtcaacag agttacagta ccccgctcac tttcggcgga 300
 gggaccaagg tggagatcaa a 321

<210> 122
 <211> 107
 <212> PRT
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<220>
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<400> 122
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Ile Thr Ile Thr Cys Arg Ala Ser His Ser Ile Asp 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 Pro Ala Ser Thr 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 Ser Ala Ile Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu
 85 90 95
 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 123
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 123
 cacagcattg acagctat 18

<210> 124
 <211> 6
 <212> PRT
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<220>
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<400> 124
 His Ser Ile Asp Ser Tyr
 1 5

<210> 125
 <211> 9
 <212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 125

cctgcatcc

9

<210> 126

<211> 3

<212> PRT

<213> Artificial Sequence

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Pro Ala Ser

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<210> 127

<211> 27

<212> DNA

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<400> 127

caacagagtt acagtacccc gctcact

27

<210> 128

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 128

Gln Gln Ser Tyr Ser Thr Pro Leu Thr

1

5

<210> 129

<211> 372

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 129

caggtgcagc tgggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgtag cgtctggatt caccttcagt agctatggca tggctctgggt ccgccagact 120
ccaggcaagg ggctggagt ggtggcagtt atatggcatg atggaactaa taattactat 180
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cagctgtat 240
ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagagaacca 300
tggctggtac ggggctacta ctactacgct atggacgtct ggggccaagg gaccacggtc 360
accgtctcct ca 372

<210> 130

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 130

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

<210> 131

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 131

ggattcacct tcagtagcta tggc

24

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<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 132

Gly Phe Thr Phe Ser Ser Tyr Gly

1 5

<210> 133
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 133
atatggcatg atggaactaa taat 24

<210> 134
<211> 8
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<220>
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<400> 134
Ile Trp His Asp Gly Thr Asn Asn
1 5

<210> 135
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 135
gcgagagaac catggctggt acggggctac tactactacg ctatggacgt c 51

<210> 136
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
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<400> 136
Ala Arg Glu Pro Trp Leu Val Arg Gly Tyr Tyr Tyr Tyr Ala Met Asp
1 5 10 15
Val

<210> 137
<211> 321

<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 137
gacatccaga tgaccagtc tccttcacc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggccagtc gagtattagt agttgggttg cctggtatca gcagaaacca 120
gggaaagccc ctaagctcct gatctataag gcgtctagtt tagaaagtgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcagcct 240
gatgattttg caacttatta ctgccaacag tataatagtt attctcggac gttcggccaa 300
gggaccaagg tggaatcaa a 321

<210> 138
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 138
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Trp
20 25 30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45
Tyr Lys Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Ser Arg
85 90 95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 139
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 139
cagagtatta gtagttgg 18

<210> 140
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 140
Gln Ser Ile Ser Ser Trp
1 5

<210> 141
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 141
aaggcgtct

9

<210> 142
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 142
Lys Ala Ser
1

<210> 143
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 143
caacagtata atagttattc tcggacg

27

<210> 144
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 144
Gln Gln Tyr Asn Ser Tyr Ser Arg Thr
1 5

<210> 145
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 145
cagctgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60
acctgcactg tctctggtgg ctccatcagc agtagtagtt actactgggg ctggatccgc 120
cagccccag ggaagggact ggagtggatt gggagtatct attatagtgg gagccccctac 180
tacatcccg tccctcaagag tcgagtcacc atatccgtag acacgtccaa gaaccagttc 240
tccctgaagc tgagctctgt gaccgccgca gacacggcta tgtattactg tgcgagacag 300
gggcggggca tagccagggc tgggtccctt gactactggg gccaggggaa cctggtcacc 360
gtctcctca 369

<210> 146
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 146
Gln Leu Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Ser
20 25 30
Ser Tyr Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
35 40 45
Trp Ile Gly Ser Ile Tyr Tyr Ser Gly Ser Pro Tyr Tyr Ile Pro Ser
50 55 60
Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80
Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Met Tyr Tyr
85 90 95
Cys Ala Arg Gln Gly Arg Gly Ile Ala Arg Ala Gly Pro Phe Asp Tyr
100 105 110
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 147
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 147
ggtggctcca tcagcagtag tagttactac

<210> 148
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 148
Gly Gly Ser Ile Ser Ser Ser Ser Tyr Tyr
1 5 10

<210> 149
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 149
atctattata gtgggagccc c 21

<210> 150
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 150
Ile Tyr Tyr Ser Gly Ser Pro
1 5

<210> 151
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 151
gcgagacagg ggcggggcat agccagggct ggtccctttg actac 45

<210> 152
<211> 15
<212> PRT
<213> Artificial Sequence

<220>

<223> synthetic

<400> 152

Ala	Arg	Gln	Gly	Arg	Gly	Ile	Ala	Arg	Ala	Gly	Pro	Phe	Asp	Tyr
1				5					10					15

<210> 153

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 153

gacatccaga	tgaccagtc	tccatcctcc	ctgtctgcat	ctgtaggaga	cagagtcacc	60
atcacttgcc	gggcgagtca	gggcattagc	aattatttag	cctggtatca	ggagaaacca	120
gggaaagtgc	ctaaactcct	gatctatgct	gcatccactt	tgcaatcagg	gggtcccatct	180
cggttcagtg	gcagtggatc	tgggacagat	ttcactctca	ccatcaccag	cctgcagtct	240
gaagatgttg	caacttatta	ctgtcaaaag	tataacagtg	cccctccgtg	gacgttcggc	300
caagggacca	aggtggaaat	caaa				324

<210> 154

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 154

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

<210> 155

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 155
cagggcatta gcaattat 18

<210> 156
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 156
Gln Gly Ile Ser Asn Tyr
1 5

<210> 157
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 157
gctgcatcc 9

<210> 158
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 158
Ala Ala Ser
1

<210> 159
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 159
caaaagtata acagtgcccc tccgtggacg 30

<210> 160
<211> 10
<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 160

Gln Lys Tyr Asn Ser Ala Pro Pro Trp Thr
1 5 10

<210> 161

<211> 357

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 161

gaggtgcagc tgggtggagtc tggggggaggt gtggtacggc ctgggggggtc cctcagactc 60
tcctgtgcag cctctggatt caacgttgat gattatggca tgagctgggt ccgccaaatt 120
ccagggaagg ggctggagtg gatctctggt attaattgga atggtggttag gatataattat 180
gctgactcta tgaagggccg aatcaccatc tccagagaca acgccaagaa ctccctatat 240
ctacaaatga acagtctgag agccgaggac acggccttat atcactgtgt gagagatcag 300
tggctggtac gaggacttga ctactggggc cagggaaccc tggtcaccgt ctctca 357

<210> 162

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 162

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

<210> 163

<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 163
ggattcaacg ttgatgatta tggc

24

<210> 164
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 164
Gly Phe Asn Val Asp Asp Tyr Gly
1 5

<210> 165
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 165
attaattgga atggtggttag gata

24

<210> 166
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 166
Ile Asn Trp Asn Gly Gly Arg Ile
1 5

<210> 167
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 167

gtgagagatc agtggctggg acgaggactt gactac

36

<210> 168

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 168

Val Arg Asp Gln Trp Leu Val Arg Gly Leu Asp Tyr
1 5 10

<210> 169

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 169

gacatccaga tgaccagtc tccatcctca ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgtc gggcgagtca gggcatttac aattatcttag cctgggtttca gcagaaacca 120
gggaaagccc ctaagtccct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
aagttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240
gaagattttg caacttatta ctgccaacaa tataatactt acccgtagac ttttgccag 300
gggaccaagc tggagatcaa a 321

<210> 170

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 170

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 Ala Ser Gln Gly Ile Tyr Asn Tyr
20 25 30
Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Ser Leu Ile
35 40 45
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Lys 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 Tyr Asn Thr Tyr Pro Tyr
85 90 95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 171
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 171
cagggcattt acaattat

18

<210> 172
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 172
Gln Gly Ile Tyr Asn Tyr
1 5

<210> 173
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 173
gctgcatcc

9

<210> 174
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 174
Ala Ala Ser
1

<210> 175
<211> 27
<212> DNA
<213> Artificial Sequence

<220>

<223> synthetic

<400> 175

caacaatata atacttaccc gtacact

27

<210> 176

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 176

Gln Gln Tyr Asn Thr Tyr Pro Tyr Thr

1

5

<210> 177

<211> 384

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 177

cagggtgcagc tgggtggagtc tggggggaggc ttggtcaagc ctggagggtc cctgagactc 60
tcctgtgcag cctctggatt caccttcagt gactaccacc tgagctggat ccgccaggct 120
ccagggaagg ggctggagtg ggtttcttac attagaagta gtggtaggac catagactac 180
gcagcctctg tgaagggccg attcaccatc tccagggaca acgccaagaa ttactgtat 240
ctgcaaatga acagcctgag agtcgaggat acggccgtgt attactgtgc gagagagaac 300
tggtattgtgc taaaggtata tgctgggtata gtgggagccc ctcttgacca atgggggtcag 360
ggaaccctgg tcaccgtctc ctca 384

<210> 178

<211> 128

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 178

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

				85					90					95			
Ala	Arg	Glu	Asn	Trp	Ile	Val	Leu	Lys	Val	Tyr	Ala	Gly	Ile	Val	Gly		
			100					105					110				
Ala	Pro	Leu	Asp	Gln	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser		
		115					120					125					

<210> 179
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 179
 ggattcacct tcagtgacta ccac

24

<210> 180
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 180
 Gly Phe Thr Phe Ser Asp Tyr His
 1 5

<210> 181
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 181
 attagaagta gtggtaggac cata

24

<210> 182
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 182
 Ile Arg Ser Ser Gly Arg Thr Ile
 1 5

<210> 183
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 183
gcgagagaga actggattgt gctaaaggta tatgctggta tagtgggagc ccctcttgac 60
caa 63

<210> 184
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 184
Ala Arg Glu Asn Trp Ile Val Leu Lys Val Tyr Ala Gly Ile Val Gly
1 5 10 15
Ala Pro Leu Asp Gln
20

<210> 185
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 185
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatcca 180
gacagggtca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gctcaccttg gacgttcggc 300
caagggacca aggtggaaat caaa 324

<210> 186
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 186
Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser

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

<210> 187
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 187
 cagagtgtta gcagcagcta c 21

<210> 188
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 188
 Gln Ser Val Ser Ser Ser Tyr
 1 5

<210> 189
 <211> 9
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 189
 ggtgcatcc 9

<210> 190
 <211> 3
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 190
Gly Ala Ser
1

<210> 191
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 191
cagcagtatg gtagctcacc ttggacg

27

<210> 192
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 192
Gln Gln Tyr Gly Ser Ser Pro Trp Thr
1 5

<210> 193
<211> 1061
<212> PRT
<213> Artificial Sequence

<220>
<223> hNPR1

<400> 193
Met Pro Gly Pro Arg Arg Pro Ala Gly Ser Arg Leu Arg Leu Leu Leu
1 5 10 15
Leu Leu Leu Leu Pro Pro Leu Leu Leu Leu Arg Gly Ser His Ala
20 25 30
Gly Asn Leu Thr Val Ala Val Val Leu Pro Leu Ala Asn Thr Ser Tyr
35 40 45
Pro Trp Ser Trp Ala Arg Val Gly Pro Ala Val Glu Leu Ala Leu Ala
50 55 60
Gln Val Lys Ala Arg Pro Asp Leu Leu Pro Gly Trp Thr Val Arg Thr
65 70 75 80
Val Leu Gly Ser Ser Glu Asn Ala Leu Gly Val Cys Ser Asp Thr Ala
85 90 95
Ala Pro Leu Ala Ala Val Asp Leu Lys Trp Glu His Asn Pro Ala Val
100 105 110
Phe Leu Gly Pro Gly Cys Val Tyr Ala Ala Ala Pro Val Gly Arg Phe
115 120 125

Thr	Ala	His	Trp	Arg	Val	Pro	Leu	Leu	Thr	Ala	Gly	Ala	Pro	Ala	Leu
130						135					140				
Gly	Phe	Gly	Val	Lys	Asp	Glu	Tyr	Ala	Leu	Thr	Thr	Arg	Ala	Gly	Pro
145				150						155					160
Ser	Tyr	Ala	Lys	Leu	Gly	Asp	Phe	Val	Ala	Ala	Leu	His	Arg	Arg	Leu
			165						170					175	
Gly	Trp	Glu	Arg	Gln	Ala	Leu	Met	Leu	Tyr	Ala	Tyr	Arg	Pro	Gly	Asp
			180					185					190		
Glu	Glu	His	Cys	Phe	Phe	Leu	Val	Glu	Gly	Leu	Phe	Met	Arg	Val	Arg
		195					200					205			
Asp	Arg	Leu	Asn	Ile	Thr	Val	Asp	His	Leu	Glu	Phe	Ala	Glu	Asp	Asp
	210					215					220				
Leu	Ser	His	Tyr	Thr	Arg	Leu	Leu	Arg	Thr	Met	Pro	Arg	Lys	Gly	Arg
225					230					235					240
Val	Ile	Tyr	Ile	Cys	Ser	Ser	Pro	Asp	Ala	Phe	Arg	Thr	Leu	Met	Leu
				245					250					255	
Leu	Ala	Leu	Glu	Ala	Gly	Leu	Cys	Gly	Glu	Asp	Tyr	Val	Phe	Phe	His
			260					265					270		
Leu	Asp	Ile	Phe	Gly	Gln	Ser	Leu	Gln	Gly	Gly	Gln	Gly	Pro	Ala	Pro
		275					280					285			
Arg	Arg	Pro	Trp	Glu	Arg	Gly	Asp	Gly	Gln	Asp	Val	Ser	Ala	Arg	Gln
	290					295					300				
Ala	Phe	Gln	Ala	Ala	Lys	Ile	Ile	Thr	Tyr	Lys	Asp	Pro	Asp	Asn	Pro
305					310					315					320
Glu	Tyr	Leu	Glu	Phe	Leu	Lys	Gln	Leu	Lys	His	Leu	Ala	Tyr	Glu	Gln
				325					330					335	
Phe	Asn	Phe	Thr	Met	Glu	Asp	Gly	Leu	Val	Asn	Thr	Ile	Pro	Ala	Ser
			340					345					350		
Phe	His	Asp	Gly	Leu	Leu	Leu	Tyr	Ile	Gln	Ala	Val	Thr	Glu	Thr	Leu
		355					360						365		
Ala	His	Gly	Gly	Thr	Val	Thr	Asp	Gly	Glu	Asn	Ile	Thr	Gln	Arg	Met
	370					375					380				
Trp	Asn	Arg	Ser	Phe	Gln	Gly	Val	Thr	Gly	Tyr	Leu	Lys	Ile	Asp	Ser
385					390					395					400
Ser	Gly	Asp	Arg	Glu	Thr	Asp	Phe	Ser	Leu	Trp	Asp	Met	Asp	Pro	Glu
				405					410					415	
Asn	Gly	Ala	Phe	Arg	Val	Val	Leu	Asn	Tyr	Asn	Gly	Thr	Ser	Gln	Glu
			420					425					430		
Leu	Val	Ala	Val	Ser	Gly	Arg	Lys	Leu	Asn	Trp	Pro	Leu	Gly	Tyr	Pro
		435					440					445			
Pro	Pro	Asp	Ile	Pro	Lys	Cys	Gly	Phe	Asp	Asn	Glu	Asp	Pro	Ala	Cys
	450					455					460				
Asn	Gln	Asp	His	Leu	Ser	Thr	Leu	Glu	Val	Leu	Ala	Leu	Val	Gly	Ser
465					470					475					480
Leu	Ser	Leu	Leu	Gly	Ile	Leu	Ile	Val	Ser	Phe	Phe	Ile	Tyr	Arg	Lys
				485					490					495	
Met	Gln	Leu	Glu	Lys	Glu	Leu	Ala	Ser	Glu	Leu	Trp	Arg	Val	Arg	Trp
			500					505					510		
Glu	Asp	Val	Glu	Pro	Ser	Ser	Leu	Glu	Arg	His	Leu	Arg	Ser	Ala	Gly
		515					520					525			
Ser	Arg	Leu	Thr	Leu	Ser	Gly	Arg	Gly	Ser	Asn	Tyr	Gly	Ser	Leu	Leu
	530					535					540				
Thr	Thr	Glu	Gly	Gln	Phe	Gln	Val	Phe	Ala	Lys	Thr	Ala	Tyr	Tyr	Lys
545					550					555					560
Gly	Asn	Leu	Val	Ala	Val	Lys	Arg	Val	Asn	Arg	Lys	Arg	Ile	Glu	Leu

				565				570					575				
Thr	Arg	Lys	Val	Leu	Phe	Glu	Leu	Lys	His	Met	Arg	Asp	Val	Gln	Asn		
			580					585					590				
Glu	His	Leu	Thr	Arg	Phe	Val	Gly	Ala	Cys	Thr	Asp	Pro	Pro	Asn	Ile		
		595					600					605					
Cys	Ile	Leu	Thr	Glu	Tyr	Cys	Pro	Arg	Gly	Ser	Leu	Gln	Asp	Ile	Leu		
	610					615					620						
Glu	Asn	Glu	Ser	Ile	Thr	Leu	Asp	Trp	Met	Phe	Arg	Tyr	Ser	Leu	Thr		
625				630						635					640		
Asn	Asp	Ile	Val	Lys	Gly	Met	Leu	Phe	Leu	His	Asn	Gly	Ala	Ile	Cys		
			645					650						655			
Ser	His	Gly	Asn	Leu	Lys	Ser	Ser	Asn	Cys	Val	Val	Asp	Gly	Arg	Phe		
		660					665					670					
Val	Leu	Lys	Ile	Thr	Asp	Tyr	Gly	Leu	Glu	Ser	Phe	Arg	Asp	Leu	Asp		
	675					680					685						
Pro	Glu	Gln	Gly	His	Thr	Val	Tyr	Ala	Lys	Lys	Leu	Trp	Thr	Ala	Pro		
	690				695					700							
Glu	Leu	Leu	Arg	Met	Ala	Ser	Pro	Pro	Val	Arg	Gly	Ser	Gln	Ala	Gly		
705				710					715						720		
Asp	Val	Tyr	Ser	Phe	Gly	Ile	Ile	Leu	Gln	Glu	Ile	Ala	Leu	Arg	Ser		
			725			730								735			
Gly	Val	Phe	His	Val	Glu	Gly	Leu	Asp	Leu	Ser	Pro	Lys	Glu	Ile	Ile		
		740				745						750					
Glu	Arg	Val	Thr	Arg	Gly	Glu	Gln	Pro	Pro	Phe	Arg	Pro	Ser	Leu	Ala		
	755					760						765					
Leu	Gln	Ser	His	Leu	Glu	Glu	Leu	Gly	Leu	Leu	Met	Gln	Arg	Cys	Trp		
	770				775					780							
Ala	Glu	Asp	Pro	Gln	Glu	Arg	Pro	Pro	Phe	Gln	Gln	Ile	Arg	Leu	Thr		
785				790					795						800		
Leu	Arg	Lys	Phe	Asn	Arg	Glu	Asn	Ser	Ser	Asn	Ile	Leu	Asp	Asn	Leu		
			805					810						815			
Leu	Ser	Arg	Met	Glu	Gln	Tyr	Ala	Asn	Asn	Leu	Glu	Glu	Leu	Val	Glu		
		820						825					830				
Glu	Arg	Thr	Gln	Ala	Tyr	Leu	Glu	Glu	Lys	Arg	Lys	Ala	Glu	Ala	Leu		
	835					840						845					
Leu	Tyr	Gln	Ile	Leu	Pro	His	Ser	Val	Ala	Glu	Gln	Leu	Lys	Arg	Gly		
	850				855						860						
Glu	Thr	Val	Gln	Ala	Glu	Ala	Phe	Asp	Ser	Val	Thr	Ile	Tyr	Phe	Ser		
865				870					875						880		
Asp	Ile	Val	Gly	Phe	Thr	Ala	Leu	Ser	Ala	Glu	Ser	Thr	Pro	Met	Gln		
			885					890						895			
Val	Val	Thr	Leu	Leu	Asn	Asp	Leu	Tyr	Thr	Cys	Phe	Asp	Ala	Val	Ile		
	900							905					910				
Asp	Asn	Phe	Asp	Val	Tyr	Lys	Val	Glu	Thr	Ile	Gly	Asp	Ala	Tyr	Met		
	915					920						925					
Val	Val	Ser	Gly	Leu	Pro	Val	Arg	Asn	Gly	Arg	Leu	His	Ala	Cys	Glu		
	930				935						940						
Val	Ala	Arg	Met	Ala	Leu	Ala	Leu	Leu	Asp	Ala	Val	Arg	Ser	Phe	Arg		
945				950					955						960		
Ile	Arg	His	Arg	Pro	Gln	Glu	Gln	Leu	Arg	Leu	Arg	Ile	Gly	Ile	His		
			965					970						975			
Thr	Gly	Pro	Val	Cys	Ala	Gly	Val	Val	Gly	Leu	Lys	Met	Pro	Arg	Tyr		
		980					985						990				
Cys	Leu	Phe	Gly	Asp	Thr	Val	Asn	Thr	Ala	Ser	Arg	Met	Glu	Ser	Asn		
	995					1000						1005					

Gly Glu Ala Leu Lys Ile His Leu Ser Ser Glu Thr Lys Ala Val Leu
 1010 1015 1020
 Glu Glu Phe Gly Gly Phe Glu Leu Glu Leu Arg Gly Asp Val Glu Met
 1025 1030 1035 1040
 Lys Gly Lys Gly Lys Val Arg Thr Tyr Trp Leu Leu Gly Glu Arg Gly
 1045 1050 1055
 Ser Ser Thr Arg Gly
 1060

<210> 194
 <211> 469
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hNPR1-mmH
 aa 1-441: hNPR1 aa G32-E473 from NM_000906.3; aa
 442-469: Myc-Myc-hexahistidine tag

<400> 194
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 1 5 10 15
 Pro Trp Ser Trp Ala Arg Val Gly Pro Ala Val Glu Leu Ala Leu Ala
 20 25 30
 Gln Val Lys Ala Arg Pro Asp Leu Leu Pro Gly Trp Thr Val Arg Thr
 35 40 45
 Val Leu Gly Ser Ser Glu Asn Ala Leu Gly Val Cys Ser Asp Thr Ala
 50 55 60
 Ala Pro Leu Ala Ala Val Asp Leu Lys Trp Glu His Asn Pro Ala Val
 65 70 75 80
 Phe Leu Gly Pro Gly Cys Val Tyr Ala Ala Ala Pro Val Gly Arg Phe
 85 90 95
 Thr Ala His Trp Arg Val Pro Leu Leu Thr Ala Gly Ala Pro Ala Leu
 100 105 110
 Gly Phe Gly Val Lys Asp Glu Tyr Ala Leu Thr Thr Arg Ala Gly Pro
 115 120 125
 Ser Tyr Ala Lys Leu Gly Asp Phe Val Ala Ala Leu His Arg Arg Leu
 130 135 140
 Gly Trp Glu Arg Gln Ala Leu Met Leu Tyr Ala Tyr Arg Pro Gly Asp
 145 150 155 160
 Glu Glu His Cys Phe Phe Leu Val Glu Gly Leu Phe Met Arg Val Arg
 165 170 175
 Asp Arg Leu Asn Ile Thr Val Asp His Leu Glu Phe Ala Glu Asp Asp
 180 185 190
 Leu Ser His Tyr Thr Arg Leu Leu Arg Thr Met Pro Arg Lys Gly Arg
 195 200 205
 Val Ile Tyr Ile Cys Ser Ser Pro Asp Ala Phe Arg Thr Leu Met Leu
 210 215 220
 Leu Ala Leu Glu Ala Gly Leu Cys Gly Glu Asp Tyr Val Phe Phe His
 225 230 235 240
 Leu Asp Ile Phe Gly Gln Ser Leu Gln Gly Gly Gln Gly Pro Ala Pro
 245 250 255
 Arg Arg Pro Trp Glu Arg Gly Asp Gly Gln Asp Val Ser Ala Arg Gln

			100					105					110				
Gly	Phe	Gly	Val	Lys	Asp	Glu	Tyr	Ala	Leu	Thr	Thr	Arg	Ala	Gly	Pro		
		115					120					125					
Ser	Tyr	Ala	Lys	Leu	Gly	Asp	Phe	Val	Ala	Ala	Leu	His	Arg	Arg	Leu		
	130					135					140						
Gly	Trp	Glu	Arg	Gln	Ala	Leu	Met	Leu	Tyr	Ala	Tyr	Arg	Pro	Gly	Asp		
145				150						155					160		
Glu	Glu	His	Cys	Phe	Phe	Leu	Val	Glu	Gly	Leu	Phe	Met	Arg	Val	Arg		
			165						170					175			
Asp	Arg	Leu	Asn	Ile	Thr	Val	Asp	His	Leu	Glu	Phe	Ala	Glu	Asp	Asp		
			180					185					190				
Leu	Ser	His	Tyr	Thr	Arg	Leu	Leu	Arg	Thr	Met	Pro	Arg	Lys	Gly	Arg		
	195						200					205					
Val	Ile	Tyr	Ile	Cys	Ser	Ser	Pro	Asp	Ala	Phe	Arg	Thr	Leu	Met	Leu		
	210					215					220						
Leu	Ala	Leu	Glu	Ala	Gly	Leu	Cys	Gly	Glu	Asp	Tyr	Val	Phe	Phe	His		
225				230						235					240		
Leu	Asp	Ile	Phe	Gly	Gln	Ser	Leu	Gln	Gly	Gly	Gln	Gly	Pro	Ala	Pro		
			245					250						255			
Arg	Arg	Pro	Trp	Glu	Arg	Gly	Asp	Gly	Gln	Asp	Val	Ser	Ala	Arg	Gln		
			260					265					270				
Ala	Phe	Gln	Ala	Ala	Lys	Ile	Ile	Thr	Tyr	Lys	Glu	Pro	Asp	Asn	Pro		
	275						280					285					
Glu	Tyr	Leu	Glu	Phe	Leu	Lys	Gln	Leu	Lys	His	Leu	Ala	Arg	Glu	Gln		
	290					295					300						
Phe	Asn	Phe	Thr	Met	Glu	Asp	Gly	Leu	Val	Asn	Thr	Ile	Pro	Ala	Ser		
305				310						315					320		
Phe	His	Asp	Gly	Leu	Leu	Leu	Tyr	Ile	Gln	Ala	Val	Thr	Glu	Thr	Leu		
			325					330						335			
Ala	His	Gly	Gly	Thr	Val	Thr	Asp	Gly	Glu	Asn	Ile	Thr	Gln	Arg	Met		
		340					345						350				
Trp	Asn	Arg	Ser	Phe	Gln	Gly	Val	Thr	Gly	Tyr	Leu	Lys	Ile	Asp	Ser		
	355					360						365					
Ser	Gly	Asp	Arg	Glu	Thr	Asp	Phe	Ser	Leu	Trp	Asp	Met	Asp	Pro	Glu		
	370					375					380						
Thr	Gly	Ala	Phe	Arg	Val	Val	Leu	Asn	Tyr	Asn	Gly	Thr	Ser	Gln	Glu		
385				390						395					400		
Leu	Val	Ala	Val	Ser	Gly	Arg	Lys	Leu	Asn	Trp	Pro	Leu	Gly	Tyr	Pro		
			405					410						415			
Pro	Pro	Asp	Ile	Pro	Lys	Cys	Gly	Phe	Asp	Asn	Glu	Asp	Pro	Ala	Cys		
		420					425					430					
Asn	Gln	Asp	His	Leu	Ser	Thr	Leu	Glu	Glu	Gln	Lys	Leu	Ile	Ser	Glu		
	435					440					445						
Glu	Asp	Leu	Gly	Gly	Glu	Gln	Lys	Leu	Ile	Ser	Glu	Glu	Asp	Leu	His		
	450					455					460						
His	His	His	His	His													
465																	

<210> 196

<211> 469

<212> PRT

<213> Artificial Sequence

<220>

<223> mNPR1-mmH

aa 1-441: mouse NPR1 aa S29-E469 from NM_008727.5;

aa 442-469: Myc-Myc-hexahistidine tag

<400> 196

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

385					390					395				400	
Leu	Met	Ala	Val	Ser	Glu	His	Arg	Leu	Tyr	Trp	Pro	Leu	Gly	Tyr	Pro
				405					410					415	
Pro	Pro	Asp	Ile	Pro	Lys	Cys	Gly	Phe	Asp	Asn	Glu	Asp	Pro	Ala	Cys
			420					425					430		
Asn	Gln	Asp	His	Phe	Ser	Thr	Leu	Glu	Gln	Lys	Leu	Ile	Ser	Glu	
		435					440				445				
Glu	Asp	Leu	Gly	Gly	Glu	Gln	Lys	Leu	Ile	Ser	Glu	Glu	Asp	Leu	His
	450					455					460				
His	His	His	His	His											
465															

<210> 197

<211> 674

<212> PRT

<213> Artificial Sequence

<220>

<223> hNPR1-mFc

aa 1-441: human NPR1 amino acid G32-E473 from

NM_000906.3; aa 442-674: Mouse IgG2a Fc tag

<400> 197

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

Arg	Arg	Pro	Trp	245	Glu	Arg	Gly	Asp	Gly	250	Gln	Asp	Val	Ser	Ala	255	Arg	Gln
			260						265						270			
Ala	Phe	Gln	Ala	Ala	Lys	Ile	Ile	Thr	Tyr	Lys	Asp	Pro	Asp	Asn	Pro			
		275					280							285				
Glu	Tyr	Leu	Glu	Phe	Leu	Lys	Gln	Leu	Lys	His	Leu	Ala	Tyr	Glu	Gln			
	290					295					300							
Phe	Asn	Phe	Thr	Met	Glu	Asp	Gly	Leu	Val	Asn	Thr	Ile	Pro	Ala	Ser			
305					310					315					320			
Phe	His	Asp	Gly	Leu	Leu	Leu	Tyr	Ile	Gln	Ala	Val	Thr	Glu	Thr	Leu			
				325					330						335			
Ala	His	Gly	Gly	Thr	Val	Thr	Asp	Gly	Glu	Asn	Ile	Thr	Gln	Arg	Met			
			340					345						350				
Trp	Asn	Arg	Ser	Phe	Gln	Gly	Val	Thr	Gly	Tyr	Leu	Lys	Ile	Asp	Ser			
	355					360						365						
Ser	Gly	Asp	Arg	Glu	Thr	Asp	Phe	Ser	Leu	Trp	Asp	Met	Asp	Pro	Glu			
	370					375					380							
Asn	Gly	Ala	Phe	Arg	Val	Val	Leu	Asn	Tyr	Asn	Gly	Thr	Ser	Gln	Glu			
385					390					395					400			
Leu	Val	Ala	Val	Ser	Gly	Arg	Lys	Leu	Asn	Trp	Pro	Leu	Gly	Tyr	Pro			
			405						410						415			
Pro	Pro	Asp	Ile	Pro	Lys	Cys	Gly	Phe	Asp	Asn	Glu	Asp	Pro	Ala	Cys			
			420					425						430				
Asn	Gln	Asp	His	Leu	Ser	Thr	Leu	Glu	Glu	Pro	Arg	Gly	Pro	Thr	Ile			
		435					440					445						
Lys	Pro	Cys	Pro	Pro	Cys	Lys	Cys	Pro	Ala	Pro	Asn	Leu	Leu	Gly	Gly			
	450					455					460							
Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Lys	Ile	Lys	Asp	Val	Leu	Met	Ile			
465					470					475					480			
Ser	Leu	Ser	Pro	Ile	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Glu	Asp			
			485						490						495			
Asp	Pro	Asp	Val	Gln	Ile	Ser	Trp	Phe	Val	Asn	Asn	Val	Glu	Val	His			
			500					505						510				
Thr	Ala	Gln	Thr	Gln	Thr	His	Arg	Glu	Asp	Tyr	Asn	Ser	Thr	Leu	Arg			
		515					520						525					
Val	Val	Ser	Ala	Leu	Pro	Ile	Gln	His	Gln	Asp	Trp	Met	Ser	Gly	Lys			
	530					535					540							
Glu	Phe	Lys	Cys	Lys	Val	Asn	Asn	Lys	Asp	Leu	Pro	Ala	Pro	Ile	Glu			
545					550					555					560			
Arg	Thr	Ile	Ser	Lys	Pro	Lys	Gly	Ser	Val	Arg	Ala	Pro	Gln	Val	Tyr			
			565						570						575			
Val	Leu	Pro	Pro	Pro	Glu	Glu	Glu	Met	Thr	Lys	Lys	Gln	Val	Thr	Leu			
			580					585						590				
Thr	Cys	Met	Val	Thr	Asp	Phe	Met	Pro	Glu	Asp	Ile	Tyr	Val	Glu	Trp			
		595				600						605						
Thr	Asn	Asn	Gly	Lys	Thr	Glu	Leu	Asn	Tyr	Lys	Asn	Thr	Glu	Pro	Val			
	610					615					620							
Leu	Asp	Ser	Asp	Gly	Ser	Tyr	Phe	Met	Tyr	Ser	Lys	Leu	Arg	Val	Glu			
625					630					635					640			
Lys	Lys	Asn	Trp	Val	Glu	Arg	Asn	Ser	Tyr	Ser	Cys	Ser	Val	Val	His			
			645						650						655			
Glu	Gly	Leu	His	Asn	His	His	Thr	Thr	Lys	Ser	Phe	Ser	Arg	Thr	Pro			
			660					665							670			
Gly	Lys																	

<210> 198
 <211> 674
 <212> PRT
 <213> Artificial Sequence

<220>

<223> mfNPR1-mFc

aa 1-441: mf NPR1 amino acid G33-E473 of isoform
 X2 of XP_005541810.1; aa 442-674: Mouse IgG2a Fc
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<400> 198

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

Ala	His	Gly	Gly	Thr	Val	Thr	Asp	Gly	Glu	Asn	Ile	Thr	Gln	Arg	Met
			340					345					350		
Trp	Asn	Arg	Ser	Phe	Gln	Gly	Val	Thr	Gly	Tyr	Leu	Lys	Ile	Asp	Ser
		355					360					365			
Ser	Gly	Asp	Arg	Glu	Thr	Asp	Phe	Ser	Leu	Trp	Asp	Met	Asp	Pro	Glu
	370					375					380				
Thr	Gly	Ala	Phe	Arg	Val	Val	Leu	Asn	Tyr	Asn	Gly	Thr	Ser	Gln	Glu
385					390					395					400
Leu	Val	Ala	Val	Ser	Gly	Arg	Lys	Leu	Asn	Trp	Pro	Leu	Gly	Tyr	Pro
				405					410					415	
Pro	Pro	Asp	Ile	Pro	Lys	Cys	Gly	Phe	Asp	Asn	Glu	Asp	Pro	Ala	Cys
			420					425					430		
Asn	Gln	Asp	His	Leu	Ser	Thr	Leu	Glu	Glu	Pro	Arg	Gly	Pro	Thr	Ile
	435						440					445			
Lys	Pro	Cys	Pro	Pro	Cys	Lys	Cys	Pro	Ala	Pro	Asn	Leu	Leu	Gly	Gly
	450					455					460				
Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Lys	Ile	Lys	Asp	Val	Leu	Met	Ile
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Ser	Leu	Ser	Pro	Ile	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Glu	Asp
				485					490					495	
Asp	Pro	Asp	Val	Gln	Ile	Ser	Trp	Phe	Val	Asn	Asn	Val	Glu	Val	His
			500					505					510		
Thr	Ala	Gln	Thr	Gln	Thr	His	Arg	Glu	Asp	Tyr	Asn	Ser	Thr	Leu	Arg
		515					520					525			
Val	Val	Ser	Ala	Leu	Pro	Ile	Gln	His	Gln	Asp	Trp	Met	Ser	Gly	Lys
	530					535					540				
Glu	Phe	Lys	Cys	Lys	Val	Asn	Asn	Lys	Asp	Leu	Pro	Ala	Pro	Ile	Glu
545					550					555					560
Arg	Thr	Ile	Ser	Lys	Pro	Lys	Gly	Ser	Val	Arg	Ala	Pro	Gln	Val	Tyr
				565					570					575	
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			580					585					590		
Thr	Cys	Met	Val	Thr	Asp	Phe	Met	Pro	Glu	Asp	Ile	Tyr	Val	Glu	Trp
		595					600					605			
Thr	Asn	Asn	Gly	Lys	Thr	Glu	Leu	Asn	Tyr	Lys	Asn	Thr	Glu	Pro	Val
	610					615					620				
Leu	Asp	Ser	Asp	Gly	Ser	Tyr	Phe	Met	Tyr	Ser	Lys	Leu	Arg	Val	Glu
625					630					635					640
Lys	Lys	Asn	Trp	Val	Glu	Arg	Asn	Ser	Tyr	Ser	Cys	Ser	Val	Val	His
				645					650					655	
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Gly Lys

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 <211> 674
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> mNPR1-mFc
 aa 1-441: mouse NPR1 aa S29-E469 from NM_008727.5;

aa 442-674: Mouse IgG2a Fc tag

<400> 199

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

Pro	Pro	Asp	Ile	Pro	Lys	Cys	Gly	Phe	Asp	Asn	Glu	Asp	Pro	Ala	Cys
			420					425					430		
Asn	Gln	Asp	His	Phe	Ser	Thr	Leu	Glu	Glu	Pro	Arg	Gly	Pro	Thr	Ile
		435					440					445			
Lys	Pro	Cys	Pro	Pro	Cys	Lys	Cys	Pro	Ala	Pro	Asn	Leu	Leu	Gly	Gly
	450					455					460				
Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Lys	Ile	Lys	Asp	Val	Leu	Met	Ile
465					470					475					480
Ser	Leu	Ser	Pro	Ile	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Glu	Asp
				485					490					495	
Asp	Pro	Asp	Val	Gln	Ile	Ser	Trp	Phe	Val	Asn	Asn	Val	Glu	Val	His
			500					505					510		
Thr	Ala	Gln	Thr	Gln	Thr	His	Arg	Glu	Asp	Tyr	Asn	Ser	Thr	Leu	Arg
		515					520					525			
Val	Val	Ser	Ala	Leu	Pro	Ile	Gln	His	Gln	Asp	Trp	Met	Ser	Gly	Lys
	530					535					540				
Glu	Phe	Lys	Cys	Lys	Val	Asn	Asn	Lys	Asp	Leu	Pro	Ala	Pro	Ile	Glu
545					550					555					560
Arg	Thr	Ile	Ser	Lys	Pro	Lys	Gly	Ser	Val	Arg	Ala	Pro	Gln	Val	Tyr
				565					570					575	
Val	Leu	Pro	Pro	Pro	Glu	Glu	Glu	Met	Thr	Lys	Lys	Gln	Val	Thr	Leu
			580					585					590		
Thr	Cys	Met	Val	Thr	Asp	Phe	Met	Pro	Glu	Asp	Ile	Tyr	Val	Glu	Trp
		595					600					605			
Thr	Asn	Asn	Gly	Lys	Thr	Glu	Leu	Asn	Tyr	Lys	Asn	Thr	Glu	Pro	Val
	610					615					620				
Leu	Asp	Ser	Asp	Gly	Ser	Tyr	Phe	Met	Tyr	Ser	Lys	Leu	Arg	Val	Glu
625					630					635					640
Lys	Lys	Asn	Trp	Val	Glu	Arg	Asn	Ser	Tyr	Ser	Cys	Ser	Val	Val	His
				645					650					655	
Glu	Gly	Leu	His	Asn	His	His	Thr	Thr	Lys	Ser	Phe	Ser	Arg	Thr	Pro
			660					665					670		
Gly	Lys														