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<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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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
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Gln	Gly	Arg	Ile	Thr	Met	Thr	Trp	Asp	Thr	Ser	Ile	Ser	Thr	Ala	Tyr
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Met	Glu	Leu	Ser	Arg	Leu	Arg	Ser	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				85				90						95	
Ser	Arg	Gly	Gly	Pro	Val	Met	Asn	Tyr	Tyr	Tyr	Tyr	Tyr	Gly	Met	Asp
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Val	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser				
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aggttcagtg gcagtggatc tgggaaagat ttcactctca ccatcagcag tctgcaacct 240
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 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
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ccaggaagg gcctggagtg ggtctcaggt attagtggga atagtggtag cataggctat 180
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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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gggaaagccc ctaaggtcct gatctctact gcatccagtt tgcaaagtgg ggtcccatca 180
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 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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Gln Gln Ser Phe Gly Ile Pro Arg Thr
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gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctggat 240
ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gaggctgaat 300
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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
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Gly Phe Thr Phe Ser Thr Tyr Gly
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 aggttccgtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
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 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
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tccctgaggc tgacctctgt gaccgccgca gacacggctc tgtattactg tgcgagacat 300
aagaggtcca tgacagcttg ggggttcttt gactattggg gccaggaac cctggtcacc 360
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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
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ggtaaagccc	ctaaagttct	gatctattct	gcatccaatt	tgcaaagtgg	gggtcccctca	180
cggttcagtg	gcagtggatc	tgggacagat	ttcactctca	ccatcaacag	tctgcaacct	240
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		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
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ccaggaagg gactggagtg ggtcgcaccc attagtagta gtagtagttt cattaattat 180
gcagactcat tgaagggccg attcaccatc tccagagaca acgcccagaa ctcactgtat 240
ctacaaatga acagcctgag agccgaggac acggctatctt attactgtgc gagagcggcg 300
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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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 Gly Phe Thr Phe Arg Ile Tyr Thr
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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>
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<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>
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<400> 73
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgca gggccagtca gagtgttagc agcaactact tagcgtggta ccagcagaaa 120
cctggccagg ttccagtcct cctcatctat ggtgcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagcgg gtctggggaca gacttcactc tcaccatcac cagactggag 240
cctgaagatt ttgcagtgtg 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
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<220>
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<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
cagggtgcagc tgggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggctc 60
tcctgcaagg cttctggata caccttcacc ggctactata tacactgggt gcgacaggcc 120
cctggacaag gacttgagt gatgggatgg atcaacccta acagtattgg cacaaactat 180
gcacagaagt ttcagggcag ggtcaccttg accagggaca cgtccatcag tacagcctac 240
atggagctga gcagtctgag atctgacgac acggccgtgt attactgtgc gagaggggggt 300
agcagctcat attactacta ctactacggg atggacgtct ggggcccaagg gaccacgggtc 360
accgtctcct ca 372

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

<220>

<223> synthetic

<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

<213> Artificial Sequence

<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>
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<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 gtatggacgt c 51

<210> 88
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<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 gatctatggt 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>
 <223> synthetic

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

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

<220>
<223> synthetic

<400> 93
gttgcattcc

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
<213> Artificial Sequence

<220>
<223> synthetic

<400> 95
caacagagtt acagtacccc gctcact

27

<210> 96
<211> 9
<212> PRT
<213> Artificial Sequence

<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

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tcctgcaagg cttctggata caccttcacc ggctactata ttcattgggt acgacaggcc 120
cctggacaag ggcttgagtg gatgggatgg atcaccccta 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
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<210> 98

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 98

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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
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<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

<213> Artificial Sequence

<220>

<223> synthetic

<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 ctaaaactcct 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

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<210> 111

<211> 27

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<400> 111

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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

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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  gagagggggg  300
ggaagtcact  actattatta  ttatcacggg  atggacgtct  ggggccaagg  aaccacggtc  360
accgtctcct  ca                                     372
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<210> 114

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 114

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

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

<220>
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<400> 119
tcgagagggg gtggaagtca ctactattat tattatcacg gtatggacgt c 51

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

<220>
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<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
<213> Artificial Sequence

<220>
<223> synthetic

<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
 <213> Artificial Sequence

<220>
 <223> synthetic

<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

<220>
 <223> synthetic

<400> 126
 Pro Ala Ser
 1

<210> 127
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 127
caacagagtt acagtacccc gtcact 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
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tcctgtgtag cgtctggatt caccttcagt agctatggca tggctctgggt ccgccagact 120
ccaggcaagg ggctggagtg ggtggcagtt atatggcatg atggaactaa taattactat 180
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 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

<210> 132
 <211> 8
 <212> PRT
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<220>
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<400> 132
 Gly Phe Thr Phe Ser Ser Tyr Gly
 1 5

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

<220>
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<400> 133
 atatggcatg atggaactaa taat

24

<210> 134
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 <212> PRT
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<220>

<223> synthetic

<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 catggctggc acggggctac tactactacg ctatggacgt c 51

<210> 136

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<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

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gggaaagccc ctaagctcct gatctataag gcgtctagtt tagaaagtgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcagcct 240
gatgattttg caacttatta ctgccaacag tataatagtt attctcggac gttcggccaa 300
gggaccaagg tggaaatcaa 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 gagcccctac 180
tacatcccggt ccctcaagag tcgagtcacc atatccgtag acacgtccaa gaaccagttc 240
tccctgaagc tgagctctgt gaccgccgca gacacggcta tgtattactg tgcgagacag 300
gggcggggca tagccagggc tgggtccctt gactactggg gccagggaac 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

30

<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 agccagggt 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 gggcgagtc gggcattagc aattatttag cctgggtatca ggagaaacca 120
gggaaagtgc ctaaacctct gatctatgct gcatccactt tgcaatcagg ggtcccatct 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 acagtgtccc 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 atggtggtag gatataattat 180
gctgactcta tgaagggccg aatcaccatc tccagagaca acgccaagaa ctccctatat 240
ctacaaatga acagtctgag agccgaggac acggccttat atcactgtgt gagagatcag 300
tggctggtac gaggacttga ctactggggc cagggaaccc tggtcaccgt ctcctca 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

<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 atggtggtag 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 agtggctggt 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 aattatttag cctggtttca gcagaaacca 120
gggaaagccc ctaagtccct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
aagttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240
gaagattttg caacttatta ctgccaacaa tataatactt acccgtagac ttttggccag 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 atacttacc 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

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cagggtgcagc tgggtggagtc tggggggaggc ttgggtcaagc ctggagggtc cctgagactc 60
tcctgtgcag cctctggatt caccttcagt gactaccacc tgagctggat ccgccaggct 120
ccagggaagg ggctggagtg ggtttcttac attagaagta gtggtaggac catagactac 180
gcagcctctg tgaagggccg attcaccatc tccagggaca acgccaagaa ttcactgtat 240
ctgcaaataa acagcctgag agtcgaggat acggccgtgt attactgtgc gagagagaac 300
tggattgtgc taaaggtata tgctgggtata gtggggagccc ctcttgacca atgggggtcag 360
ggaaccctgg tcaccgtctc ctca 384
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<210> 178

<211> 128

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 178

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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
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<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 gagggttagc agcagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtggt 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																						

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						
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						
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						
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						
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						
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

Gly	Asn	Leu	Thr	Val	Ala	Val	Val	Leu	Pro	Leu	Ala	Asn	Thr	Ser	Tyr
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

<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
1				5				10						15	
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	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 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
 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 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
Leu Asp Ile Phe Gly Gln Ser Leu Gln Gly Gly Gln Gly Pro Ala Pro		240
	245	250
Arg Arg Pro Trp Glu Arg Gly Asp Gly Gln Asp Val Ser Ala Arg Gln		255
	260	265
Ala Phe Gln Ala Ala Lys Ile Ile Thr Tyr Lys Asp Pro Asp Asn Pro		270
	275	280
Glu Tyr Leu Glu Phe Leu Lys Gln Leu Lys His Leu Ala Tyr Glu Gln		285
	290	295
Phe Asn Phe Thr Met Glu Asp Gly Leu Val Asn Thr Ile Pro Ala Ser		300
305	310	315
Phe His Asp Gly Leu Leu Leu Tyr Ile Gln Ala Val Thr Glu Thr Leu		320
	325	330
Ala His Gly Gly Thr Val Thr Asp Gly Glu Asn Ile Thr Gln Arg Met		335
	340	345
Trp Asn Arg Ser Phe Gln Gly Val Thr Gly Tyr Leu Lys Ile Asp Ser		350
	355	360
Ser Gly Asp Arg Glu Thr Asp Phe Ser Leu Trp Asp Met Asp Pro Glu		365
	370	375
Asn Gly Ala Phe Arg Val Val Leu Asn Tyr Asn Gly Thr Ser Gln Glu		380
385	390	395
Leu Val Ala Val Ser Gly Arg Lys Leu Asn Trp Pro Leu Gly Tyr Pro		400
	405	410
Pro Pro Asp Ile Pro Lys Cys Gly Phe Asp Asn Glu Asp Pro Ala Cys		415
	420	425
Asn Gln Asp His Leu Ser Thr Leu Glu Glu Pro Arg Gly Pro Thr Ile		430
	435	440
Lys Pro Cys Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly Gly		445
	450	455
Pro Ser Val Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile		460
465	470	475
Ser Leu Ser Pro Ile Val Thr Cys Val Val Val Asp Val Ser Glu Asp		480
	485	490
Asp Pro Asp Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His		495
	500	505
Thr Ala Gln Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg		510
	515	520
Val Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys		525
	530	535
Glu Phe Lys Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu		540
545	550	555
Arg Thr Ile Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr		560
	565	570
Val Leu Pro Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu		575
	580	585
Thr Cys Met Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp		590
	595	600
Thr Asn Asn Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val		605
	610	615
Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu		620
625	630	635
Lys Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His		640

				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
 tag

<400> 198

Gly	Asn	Leu	Thr	Val	Ala	Val	Val	Leu	Pro	Leu	Ala	Asn	Thr	Ser	Tyr	
1				5				10						15		
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	

<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

Ser	Asp	Leu	Thr	Val	Ala	Val	Val	Leu	Pro	Leu	Thr	Asn	Thr	Ser	Tyr
1				5				10						15	
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	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	

[illegible]