

FIGURE 1

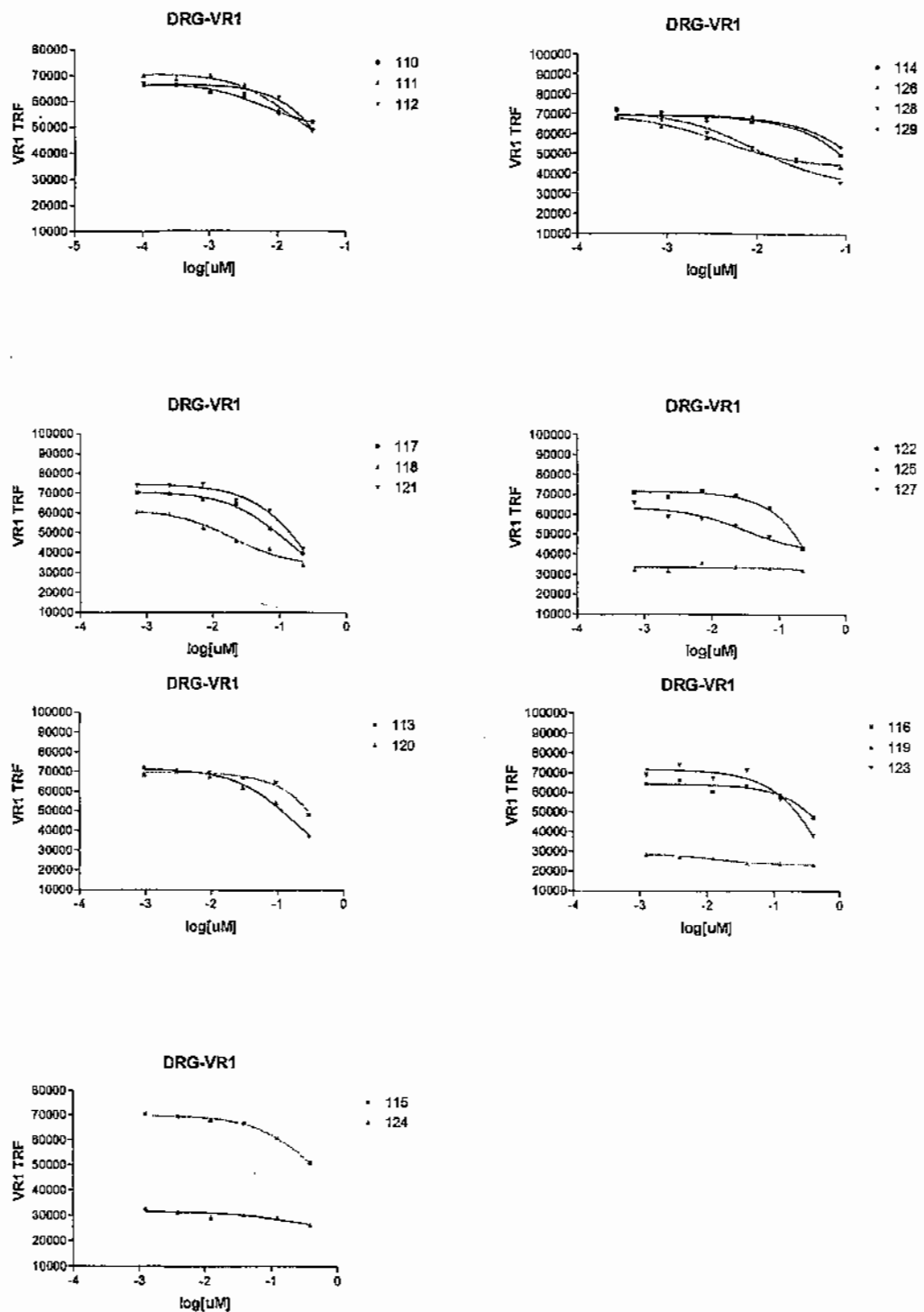


FIGURE 2

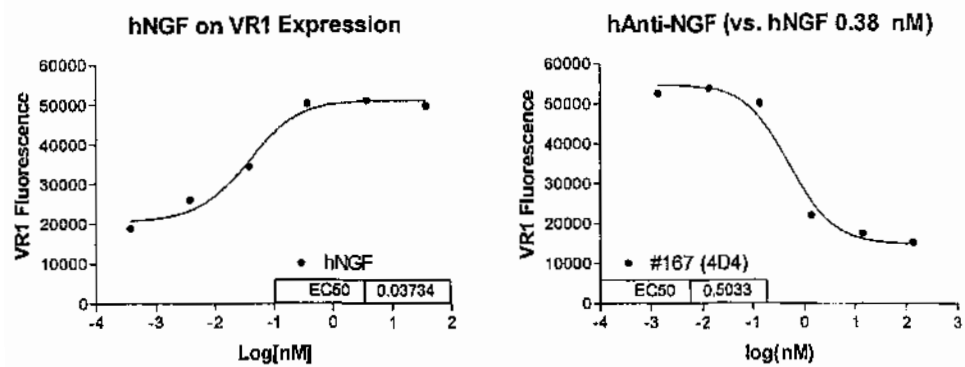


FIGURE 3

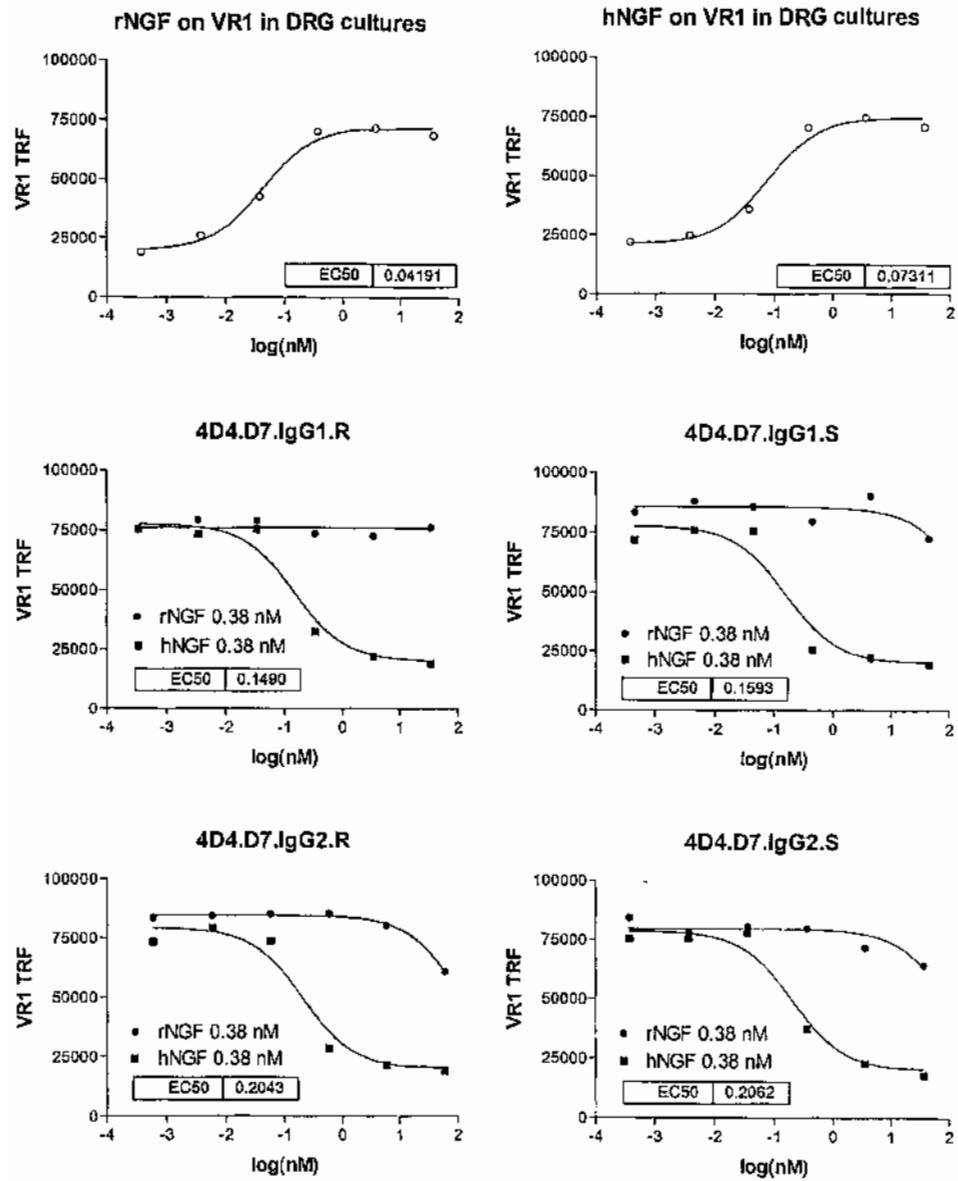


FIGURE 4

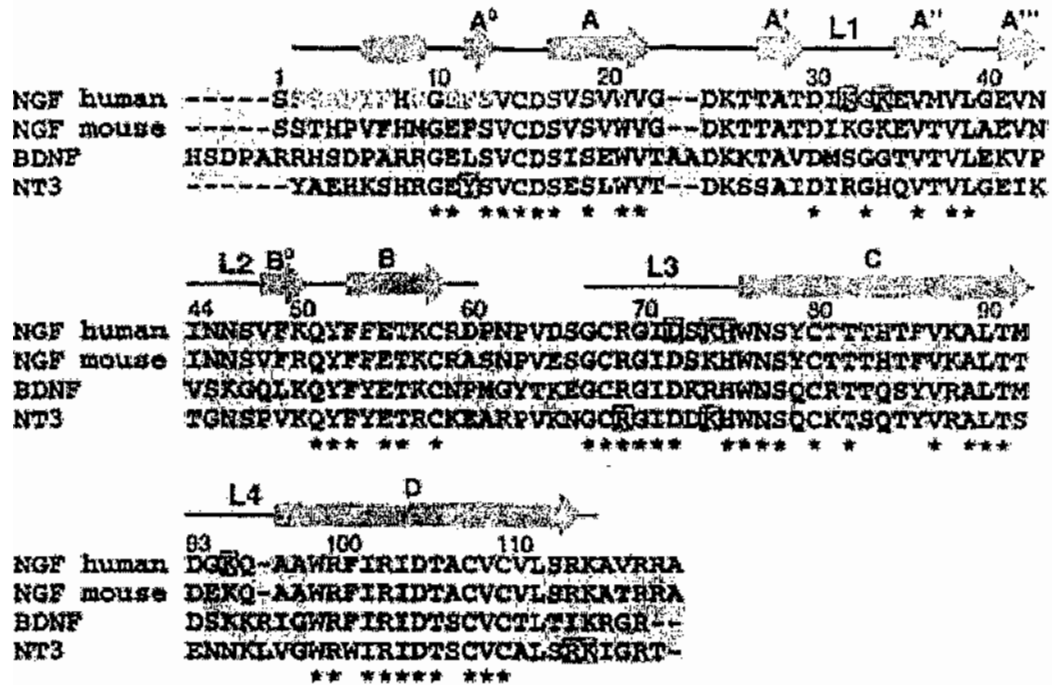


FIGURE 5

NGF CDR1 heavy chain alignments/ % identity

(1) 1 5
 14D10 HC CDR1 (1) DYAMH
 6H9 HC CDR1 (1) DYAMH
 7H2 HC CDR1 (1) DYAMH
 4G6 HC CDR1 (1) DYGMN
 14D11 HC CDR1 (1) TYWEG
 4D4 HC CDR1 (1) SYGMN

	14D10 HC CDR1	6H9 HC CDR1	7H2 HC CDR1	4G6 HC CDR1	14D11 HC CDR1	4D4 HC CDR1
14D10 HC CDR1	100	100	100	60	20	40
6H9 HC CDR1		100	100	60	20	40
7H2 HC CDR1			100	60	20	40
4G6 HC CDR1				100	20	60
14D11 HC CDR1					100	20
4D4 HC CDR1						100

FIGURE 6

NGF CDR2 heavy chain alignments/% identity

```

(1) 1 17
14D10 HC CDR2 (1) GISWNRGIIGYADSVRG
6H9 HC CDR2 (1) GISWNRGIIGYAGSVRG
7H2 HC CDR2 (1) GITWNSGIIGYADSVRG
4G6 HC CDR2 (1) DINWNGGSTGYADSVRG
4D4 HC CDR2 (1) YISRSBHTIFYADSVRG
14D11 HC CDR2 (1) ILYPGDSDTKYSPSFQG

```

	14D10 HC CDR2	6H9 HC CDR2	14D11 HC CDR2	4D4 HC CDR2	4G6 HC CDR2	7H2 HC CDR2
14D10 HC CDR2	100	94	24	59	70	82
6H9 HC CDR2		100	24	53	65	76
14D11 HC CDR2			100	24	29	24
4D4 HC CDR2				100	47	53
4G6 HC CDR2					100	70
7H2 HC CDR2						100

FIGURE 7

NGF CDR3 heavy chain alignments/% identity

```

(1) 1 17
14D10 HC CDR3 (1) GYYGSGRPGYFYVMDV
6H9 HC CDR3 (1) GYYGSGRPGYFYVMDV
14D11 HC CDR3 (1) -NYYGSGTYVYVYGMNV
4G6 HC CDR3 (1) --EQWLDPYVYVYGMNV
4D4 HC CDR3 (1) -VYS-SGWHVSDY-FDY
7H2 HC CDR3 (1) ---EGSGR---YYNFDY

```

	14D10 HC CDR3	6H9 HC CDR3	14D11 HC CDR3	4G6 HC CDR3	4D4 HC CDR3	7H2 HC CDR3
14D10 HC CDR3	100	100	35	41	18	18
6H9 HC CDR3		100	35	41	18	18
14D11 HC CDR3			100	53	29	35
4G6 HC CDR3				100	18	29
4D4 HC CDR3					100	41
7H2 HC CDR3						100

FIGURE 8

NGF CDR1 light chain alignments/% identity

	(1)	1	12
14D11 LC CDR1	(1)	RASQGVSSSYIA-	
4G6 LC CDR1 20031028340	(1)	RASQGVSSSYIA-	
4D4 LC CDR1	(1)	RASQGVSSSYIA-	
4G6 LC CDR1 20031028351	(1)	RASQGVSSSYIA-	
14D10 LC CDR1	(1)	RASQGVSSSYIA-	
4G6 LC CDR1 20031000528	(1)	RASQGVSSSYIA-	
4G6 LC CDR1 20031071526	(1)	RASQGVSSSYIA-	
6H9 LC CDR1	(1)	RASQGVSSSYIA-	
7H2 LC CDR1	(1)	RASQGVSSSYIA-	
NGF 4G6 LC CDR1 20031028344	(1)	RASQGVSSSYIA-	

	14D11 LC CDR1	4G6 LC CDR1 20031028340	4D4 LC CDR1	4G6 LC CDR1 20031028351	14D10 LC CDR1	4G6 LC CDR1 20031000528	4G6 LC CDR1 20031071526	6H9 LC CDR1
14D11 LC CDR1	100	92	83	75	42	67	42	42
4G6 LC CDR1 20031028340		100	92	83	50	75	50	50
4D4 LC CDR1			100	83	50	75	50	50
4G6 LC CDR1 20031028351				100	58	92	58	58
14D10 LC CDR1					100	67	83	83
4G6 LC CDR1 20031000528						100	67	67
4G6 LC CDR1 20031071526							100	100
6H9 LC CDR1								100
7H2 LC CDR1								
NGF 4G6 LC CDR1 20031028344								

FIGURE 9

NGF CDR2 light chain alignments/% identity

(1) 1 7
 14D11 LC CDR2 (1) PASSRAT
 4G6 LC CDR2 20031028340 (1) PASSRAT
 4D4 LC CDR2 (1) PASSRAT
 4G6 LC CDR2 20031000528 (1) PASSRAT
 4G6 LC CDR2 20031028351 (1) PASSRAT
 6H9 LC CDR2 (1) PASSRAT
 14D10 LC CDR2 (1) PASSRAT
 4G6 LC CDR2 20031071526 (1) PASSRAT
 7H2 LC CDR2 (1) PASSRAT
 NGF 4G6 LC CDR2 20031028344 (1) PASSRAT

	14D11 LC CDR2	4G6 LC CDR2 20031028340	4D4 LC CDR2	4G6 LC CDR2 20031000528	4G6 LC CDR2 20031028351	6H9 LC CDR2	14D10 LC CDR2	4G6 LC CDR2 20031071526	7H2 LC CDR2	NGF 4G6 LC CDR2 20031028344
14D11 LC CDR2	100	100	71	28	28	43	43	43	43	43
4G6 LC CDR2 20031028340		100	71	28	28	43	43	43	43	43
4D4 LC CDR2			100	43	43	43	43	43	43	43
4G6 LC CDR2 20031000528				100	100	71	71	71	71	71
4G6 LC CDR2 20031028351					100	71	71	71	71	71
6H9 LC CDR2						100	86	86	86	86
14D10 LC CDR2							100	100	100	100
4G6 LC CDR2 20031071526								100	100	100
7H2 LC CDR2									100	100
NGF 4G6 LC CDR2 20031028344										100

FIGURE 10

NGF CDR3 light chain alignments/% identity

(1) 1 9
 14D10 LC CDR3 (1) QQYGGSPYT
 7H2 LC CDR3 (1) QQYGGSPYT
 6H9 LC CDR3 (1) QQYGGSPYT
 4G6 LC CDR3 20031000528 (1) QQRSNWPHY
 4G6 LC CDR3 20031028351 (1) QQRSNWPHY
 14D11 LC CDR3 (1) QQANSPPHY
 4D4 LC CDR3 (1) QQYNAPPHY
 4G6 LC CDR3 20031028340 (1) QQYNAPPHY
 4G6 LC CDR3 20031071526 (1) QQYNAPPHY
 NGF 4G6 LC CDR3 20031028344 (1) QQYGGSPYT

	14D10 LC CDR3	7H2 LC CDR3	6H9 LC CDR3	4G6 LC CDR3 20031000528	4G6 LC CDR3 20031028351	14D11 LC CDR3	4D4 LC CDR3	4G6 LC CDR3 20031028340	4G6 LC CDR3 20031071526	NGF 4G6 LC CDR3 20031028344
14D10 LC CDR3	100	89	100	44	33	56	56	67	67	100
7H2 LC CDR3		100	89	33	33	44	44	56	66	89
6H9 LC CDR3			100	44	33	56	56	67	67	100
4G6 LC CDR3 20031000528				100	78	56	44	56	56	44
4G6 LC CDR3 20031028351					100	33	33	33	33	33
14D11 LC CDR3						100	67	78	78	56
4D4 LC CDR3							100	78	78	56
4G6 LC CDR3 20031028340								100	100	67
4G6 LC CDR3 20031071526									100	67
NGF 4G6 LC CDR3 20031028344										100

FIGURE 11

Alignment of light chain variable regions of mAbs 4G6, 7H2, 14D10, 14D11, 4G6, 4D4

		CDR 1	CDR 2	Section 1			
	(1)	10	20	30	40	50	67
4D4 VK	(1)	AIQLTQSPSSLSASVGDQVETL	CRASQGVSS-ALAWYQQRPGKAPKLLIY	DASSLESSMPSPSPSSSG			
NGF 4G6 kappa 20031071526 rc V region	(1)	EIVLTQSEPTLSLSPGERATLSC	CRASQGVSSSYLAHYQQRPGQAPRLIY	SASSRATFIPDRFSSSG			
NGF 4G6 LC 20031028344rv region	(1)	EIVLTQSEPTLSLSPGERATLSC	CRASQGVSSSYLAHYQQRPGQAPRLIY	SASSRATFIPDRFSSSG			
NGF 4G6 LC 20031028340rv region	(1)	EIVLTQSPSSLSASVGDQVETL	CRASQGVSS-ALAWYQQRPGKAPKLLIY	DASSLESSMPSPSPSSSG			
NGF 4G6 LC 20031028361rv region	(1)	EIVLTQSEPTLSLSPGERATLSC	CRASQGVSS-ALAWYQQRPGQAPRLIY	DASSRATFIPDRFSSSG			
NGF LC 4G6 GR5' pCR4 20031000528V region#2	(1)	EIVLTQSEPTLSLSPGERATLSC	CRASQGVSS-ALAWYQQRPGQAPRLIY	DASSRATFIPDRFSSSG			
NGF 14D10 LC 20031028386 rc v region	(1)	EIVLTQSEPTLSLSPGERATLSC	CRASQGVSSSYLAHYQQRPGQAPRLIY	SASSRATFIPDRFSSSG			
NGF 14D11 lc 20031028405 rc v region	(1)	EIVLTQSPSSLSASVGDQVETL	CRASQGVSS-ALAWYQQRPGKAPKLLIY	DASSLESSMPSPSPSSSG			
NGF 6H9 Hu kappa V region no sp 2002120980	(1)	EIVLTQSEPTLSLSPGERATLSC	CRASQGVSSSYLAHYQQRPGQAPRLIY	SASSRATFIPDRFSSSG			
NGF 7H2 Hu kappa 2002120984 V region no sp	(1)	EIVLTQSEPTLSLSPGERATLSC	CRASQGVSSSYLAHYQQRPGQAPRLIY	SASSRATFIPDRFSSSG			
							Section 2
	(68)	BB	BD	CDR 3	108		
4D4 VK	(67)	SGTDFTLTISLQPEDFATYYC	QQYNWYPTFGQSTKVEIK				
NGF 4G6 kappa 20031071526 rc V region	(68)	SGTGFDTLTISLQPEDFAVYYC	QQYNWYPTFGQSTKVEIK				
NGF 4G6 LC 20031028344rv region	(68)	SGTDFTLTISLQPEDFATYYC	QQYGSSTPTFGQSTKLEIK				
NGF 4G6 LC 20031028340rv region	(67)	SGTDFTLTISLQPEDFATYYC	QQYNWYPTFGQSTKVEIK				
NGF 4G6 LC 20031028361rv region	(67)	SGTDFTLTISLQPEDFAVYYC	QQRSNMWPTFGQSTKVEIK				
NGF LC 4G6 GR5' pCR4 20031000528V region#2	(67)	SGTDFTLTISLQPEDFATYYC	QQRSNMWPTFGQSTKVEIK				
NGF 14D10 LC 20031028386 rc v region	(68)	SGTDFTLTISLQPEDFAVYYC	QQYGSSTPTFGQSTKLEIK				
NGF 14D11 lc 20031028405 rc v region	(67)	SGTDFTLTISLQPEDFATYYC	QQANWYPTFGQSTKVEIK				
NGF 6H9 Hu kappa V region no sp 2002120980	(68)	SGTDFTLTISLQPEDFAVYYC	QQYGSSTPTFGQSTKLEIK				
NGF 7H2 Hu kappa 2002120984 V region no sp	(68)	SGTDFTLTISLQPEDFAVYYC	QQYGSSTPTFGQSTKLEIK				

FIGURE 12

Alignment of heavy chain variable regions of mAbs 4D4, 4G6, 14D10, 14D11, 7H2, 6H9

[illegible]

02-1240.ST25
SEQUENCE LISTING

<110> Kenneth, Wild
Treanor, James
Huang, Haichun
Inoue, Heather
Zhang, Tie J.
Martin, Frank

<120> Human anti-NGF Neutralizing Antibodies as Selective NGF Pathway Inhibitors

<130> 02-1240

<150> US 60/487,431

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35     40     45
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50     55     60
Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65     70     75     80
Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85     90     95
Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100    105    110
Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
115    120    125
Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
130    135    140
Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
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Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
165    170    175
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 Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
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 Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
 275 280 285
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 35 40 45
 Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
 50 55 60
 Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr
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 Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
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 Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro
 100 105 110
 Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
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 Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
 130 135 140
 Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
 145 150 155 160
 Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
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 Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp
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 Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
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 225 230 235 240
 Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
 245 250 255
 Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
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 tggaagggtgg ataacgccct ccaatcgggt aactcccagg agagtgtcac agagcaggac 180
 agcaaggaca gcacctacag cctcagcagc accctgacgc tgagcaaagc agactacgag 240
 aaacacaaaag tctacgcctg cgaagtcacc catcagggcc tgagctcgcc cgtcacaag 300
 agcttcaaca ggggagagtg t 321

<210> 8

<211> 107

<212> PRT

<213> Homo sapiens

<400> 8

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

<210> 9

<211> 369

<212> DNA

<213> Homo sapiens

<400> 9
 gaggtgcagc tgggtggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
 tcctgtgcag cctctggctt caccttaaga agttatagca tgaactgggt tcgccaggct 120
 ccagggaagg ggctggagtg ggtttcatatc attagtcgta gtagtcatac catattctac 180

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gcagactctg tgaagggccg attcaccatc tccagagaca atgccaagaa ttcactgtat 240
 ctgcaaatgg acagcctgag agacgaggac acggctatgt attactgtgc gagagtatat 300
 agcagtggct ggcacgtctc tgattatttt gactactggg gccaggggaat cctgggcacc 360
 gtttcctca 369

<210> 10

<211> 123

<212> PRT

<213> Homo sapiens

<400> 10

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

<210> 11

<211> 321

<212> DNA

<213> Homo sapiens

<400> 11

gccatccagt tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
 atcacttgcc gggcaagtca gggcattagc agtgcttag cctggtatca gcagaaacca 120
 gggaaagctc ctaagctcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca 180
 aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240
 gaagattttg caacttatta ctgtcaacag tttaatagtt acccgctcac ttccggcgga 300
 gggaccaagg tggagatcaa a 321

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<210> 12

<211> 107

<212> PRT

<213> Homo sapiens

<400> 12

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

<210> 13

<211> 42

<212> DNA

<213> Homo sapiens

<400> 13

gtatatagca gtggctggca cgtctctgat tattttgact ac

42

<210> 14

<211> 14

<212> PRT

<213> Homo sapiens

<400> 14

Val Tyr Ser Ser Gly Trp His Val Ser Asp Tyr Phe Asp Tyr
1 5 10

<210> 15

<211> 27

<212> DNA

<213> Homo sapiens

<400> 15

caacagttta atagttaccc gctcact

27

<210> 16

<211> 9

<212> PRT

<213> Homo sapiens

<400> 16

Gln Gln Phe Asn Ser Tyr Pro Leu Thr
1 5

<210> 17

<211> 51

<212> DNA

<213> Homo sapiens

<400> 17

tacattagtc gtagtagtca taccatattc tacgcagact ctgtgaaggg c

51

<210> 18

<211> 17

<212> PRT

<213> Homo sapiens

<400> 18

Tyr Ile Ser Arg Ser Ser His Thr Ile Phe Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 19

<211> 21

<212> DNA

<213> Homo sapiens

<400> 19

gatgcctcca gtttggaag t

21

<210> 20

<211> 7

<212> PRT

<213> Homo sapiens

<400> 20

Asp Ala Ser Ser Leu Glu Ser
1 5

<210> 21

<211> 15

<212> DNA

<213> Homo sapiens

<400> 21
agttatagca tgaac

15

<210> 22

<211> 5

<212> PRT

<213> Homo sapiens

<400> 22

Ser Tyr Ser Met Asn
1 5

<210> 23

<211> 33

<212> DNA

<213> Homo sapiens

<400> 23
cgggcaagtc agggcattag cagtgttta gcc

33

<210> 24

<211> 11

<212> PRT

<213> Homo sapiens

<400> 24

Arg Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala
1 5 10

<210> 25

<211> 1131

<212> DNA

<213> Homo sapiens

<400> 25

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gcctccacca agggcccatc ggtcttcccc ctggcgccct gctccaggag cacctctggg      60
ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacgggtgtcg    120
tggaactcag gcgccctgac cagcggcggtg cacaccttcc cggctgtcct acagtccctca    180
ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg caccagacc      240
tacacctgca acgtgaatca caagcccagc aacaccaagg tggacaagag agttgagctc     300
aaaacccac ttggtgacac aactcacaca tgcccacggt gcccagagcc caaatcttgt      360
gacacacctc ccccggtgcc acggtgccc gagcccaa atctgtgacac acctcccccg      420
tgcccacggt gcccagagcc caaatcttgt gacacacctc ccccatgccc acggtgccc      480
gcacctgaac tcctgggagg accgtcagtc ttctcttcc ccccaaaacc caaggatacc     540
cttatgattt cccggacccc tgaggtcacg tgcgtggtgg tggacgtgag ccacgaagac     600
cccagggtcc agttcaagtg gtacgtggac ggcgtggagg tgcataatgc caagacaaag     660
ccgcgggagg agcagttcaa cagcacgttc cgtgtggtca gcgtcctcac cgtcctgcac     720
caggactggc tgaacggcaa ggagtacaag tgcaagggtc ccaacaaagc cctcccagcc     780
cccatcgaga aaaccatctc caaaaccaa ggacagcccc gagaaccaca ggtgtacacc     840
ctgcccccat cccgggagga gatgaccaag aaccagggtc gcctgacctg cctgggtcaaa     900
ggcttctacc ccagcgacat cgccgtggag tgggagagca gcgggcagcc ggagaacaac     960
tacaacacca cgctcccat gctggactcc gacggctcct tcttctctca cagcaagctc    1020
accgtggaca agagcagggt gcagcagggg aacatcttct catgctccgt gatgcatgag    1080
gctctgcaca accgcttcac gcagaagagc ctctccctgt ctccgggtaa a              1131

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<210> 26

<211> 376

<212> PRT

<213> Homo sapiens

<400> 26

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

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Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe Thr Gln
 355 360 365

Lys Ser Leu Ser Leu Ser Pro Gly
 370 375

<210> 27

<211> 29

<212> DNA

<213> Artificial

<220>

<223> PCR primer for human NGF

<400> 27

acaccacata tgcatcatc ccatcccat

29

<210> 28

<211> 40

<212> DNA

<213> Artificial

<220>

<223> PCR Primer for human NGF

<400> 28

accacaggat cctccttatg cagcagcac agctttacgg

40

<210> 29

<211> 375

<212> DNA

<213> Artificial

<220>

<223> Nucleotide sequence encoding recombinant human met-NGF

<400> 29

catatgtcat catcccatcc catcttcac aggggcgaat tctcgggtgtg tgacagtgtc	60
agcgtgtggg ttggggataa gaccaccgcc acagacatca agggcaagga ggtgatgggtg	120
ttgggagagg tgaacattaa caacagtgtg ttcaaacagt acttttttga gaccaagtgc	180
cgggacccaa atcccgttga cagcgggtgc cggggcattg actcaaagca ctggaactca	240
tattgtacca cgactcacac ctttgtcaag ggcgtgacca tggatggcaa gcaggctgcc	300
tggcggttta tccggataga tacggcctgt gtgtgtgtgc tcagccgtaa agctgtgcgt	360

cgtgcataag gatcc

375

<210> 30

<211> 121

<212> PRT

<213> Artificial

<220>

<223> amino acid sequence of recombinant human met-NGF (1-120)

<400> 30

Met Ser Ser Ser His Pro Ile Phe His Arg Gly Glu Phe Ser Val Cys
 1 5 10 15

Asp Ser Val Ser Val Trp Val Gly Asp Lys Thr Thr Ala Thr Asp Ile
 20 25 30

Lys Gly Lys Glu Val Met Val Leu Gly Glu Val Asn Ile Asn Asn Ser
 35 40 45

Val Phe Lys Gln Tyr Phe Phe Glu Thr Lys Cys Arg Asp Pro Asn Pro
 50 55 60

Val Asp Ser Gly Cys Arg Gly Ile Asp Ser Lys His Trp Asn Ser Tyr
 65 70 75 80

Cys Thr Thr Thr His Thr Phe Val Lys Ala Leu Thr Met Asp Gly Lys
 85 90 95

Gln Ala Ala Trp Arg Phe Ile Arg Ile Asp Thr Ala Cys Val Cys Val
 100 105 110

Leu Ser Arg Lys Ala Val Arg Arg Ala
 115 120

<210> 31

<211> 55

<212> DNA

<213> Artificial

<220>

<223> 5' primer sequence to generate expression vector pCFM1656 (ATCC # 69576)

<400> 31

cgatttgatt ctagaaggag gaataacata tgggtaacgc gttggaattc ggtac 55

<210> 32

<211> 49

<212> DNA

<213> Artificial

<220>

<223> 3' primer sequence to generate expression vector pCFM1656 (ATCC # 69576

<400> 32
taaactaaga tcttcctcct tattgtatac caattgcgca accttaagc 49

<210> 33

<211> 24

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<220>

<221> Unsure

<222> (18)..(23)

<223> n is a, c, t, or g

<400> 33
ggccggatag gcctccannn nnnt 24

<210> 34

<211> 21

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 34
ggggtcaggc tggaactgag g 21

<210> 35

<211> 19

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 35
tgaggacgct gaccacacg

19

<210> 36

<211> 54

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 36
cagcagaagc ttctagacca ccatggacat gaggggtgccc gctcagctcc tggg

54

<210> 37

<211> 34

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 37
cttgtcgact caacactctc ccctgttgaa gctc

34

<210> 38

<211> 55

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 38
cagcagaagc ttctagacca ccatggagtt ggggctgtgc tgggttttcc ttgtt

55

<210> 39

<211> 34

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 39

gcatgtcgac tcatttaccc ggagacaggg agag

34

<210> 40

<211> 449

<212> PRT

<213> Homo sapiens

<400> 40

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

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Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro
 225 230 235 240
 Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
 245 250 255
 Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
 260 265 270
 Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
 275 280 285
 Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val
 290 295 300
 Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu
 305 310 315 320
 Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys
 325 330 335
 Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
 340 345 350
 Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
 355 360 365
 Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
 370 375 380
 Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu
 385 390 395 400
 Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
 405 410 415
 Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
 420 425 430
 Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 435 440 445

Lys

<210> 41

<211> 453

<212> PRT

<213> Homo sapiens

<400> 41

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

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

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420 425 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
 435 440 445

Leu Ser Pro Gly Lys
 450

<210> 42

<211> 450

<212> PRT

<213> Homo sapiens

<400> 42

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Arg Ser Tyr
 20 25 30

Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Tyr Ile Ser Arg Ser Ser His Thr Ile Phe Tyr Ala Asp 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 Asp Ser Leu Arg Asp Glu Asp Thr Ala Met Tyr Tyr Cys
 85 90 95

Ala Arg Val Tyr Ser Ser Gly Trp His Val Ser Asp Tyr Phe Asp Tyr
 100 105 110

Trp Gly Gln Gly Ile Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
 115 120 125

Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser
 130 135 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
 145 150 155 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
 165 170 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
 180 185 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val
 195 200 205

Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys
 210 215 220

Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu Phe Leu Gly Gly
 225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
 245 250 255

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Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu
 260 265 270
 Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 275 280 285
 Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg
 290 295 300
 Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 305 310 315 320
 Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu
 325 330 335
 Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 340 345 350
 Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu
 355 360 365
 Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 370 375 380
 Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 385 390 395 400
 Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp
 405 410 415
 Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His
 420 425 430
 Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu
 435 440 445
 Gly Lys
 450

<210> 43

<211> 499

<212> PRT

<213> Homo sapiens

<400> 43

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

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

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450		455		460	
Val 465	Asp	Lys	Ser	Arg	Trp 470
					Gln Gln Gly Asn Ile Phe Ser Cys Ser Val 480
Met	His	Glu	Ala	Leu 485	His Asn Arg Phe Thr 490
					Gln Lys Ser Leu Ser Leu 495
Ser Pro Gly					

<210> 44

<211> 214

<212> PRT

<213> Homo sapiens

<400> 44

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

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Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ala Lys Asn Ser Leu Tyr
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Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
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Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
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<210> 134

<211> 9

<212> PRT

<213> homo sapien

<400> 134

Gln Gln Tyr Gly Ser Ser Pro Tyr Thr
 1 5

<210> 135

<211> 120

<212> PRT

<213> homo sapien

<400> 135

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

<210> 136

<211> 120

<212> PRT

<213> mus musculus

<400> 136

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

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

<210> 137

<211> 126

<212> PRT

<213> homo sapien

<400> 137

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

<210> 138

<211> 119

<212> PRT

<213> homo sapien

<400> 138

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

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35

40

45

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