

SEQUENCE LISTING

<110> TEIJIN PHARMA LIMITED

<120> ANTI-IGF-1 RECEPTOR HUMANIZED ANTIBODY

<130>

<150> JP 2020-096344

<151> 2020-06-02

<160> 84

<170> PatentIn version 3.5

<210> 1

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR-H1

<400> 1

Ser Tyr Trp Met His

1 5

<210> 2

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<223> CDR-H1

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<400> 3

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1				5					10					15	

Ser

<210> 4
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51

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Glu Thr Asn Pro Ser Ser Ser Val Thr Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

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gaaacaaacc caagcagctc cgtcactaac tacgccaga agtttcaagg a 51

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Gly Arg Gly Arg Gly Phe Ala Tyr
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<210> 8
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<223> CDR-H3

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ggaaggggaa ggggattgc ttac

24

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<211> 11

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<223> CDR-L1

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Arg Ala Ser Gln Asn Ile Asn Phe Trp Leu Ser

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<210> 10

<211> 33

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<213> Artificial Sequence

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<223> CDR-L1

<400> 10

agggcctccc agaacatcaa cttctggctc agc

33

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<400> 11

Lys Ala Ser Asn Leu His Thr
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<212> DNA

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<223> CDR-L2

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21

<210> 13

<211> 9

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<223> CDR-L3

<400> 13

Leu Gln Gly Gln Ser Tyr Pro Tyr Thr
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<210> 14

<211> 27

<212> DNA

<213> Artificial Sequence

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<223> CDR-L3

<400> 14

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<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> FW1_VH1

<400> 15

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 Ser Tyr
20 25 30

Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Glu Thr Asn Pro Ser Asn Ser Val Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Leu Thr Val Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Thr Ile Gly Arg Gly Arg Gly Phe Ala Tyr Trp Gly Gln Gly Thr Leu

100

105

110

Val Thr Val Ser Ser

115

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<223> FW1_VH1

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tcttgtaagg cctccggcta caccttcacc tcctactgga tgcactgggt gaggcaagct 120

cccggccaag gtttagagtg gatgggcgag accaaccctt ccaactccgt gaccaactac 180

gcccagaagt tccaaggctg tgtgacttta accgtggaca cctccacctc caccgcctac 240

atggagctgt cctctttaag gtccgaggac accgccgtgt actactgtac catcggtcgt 300

ggccggggct ttgcttattg gggacaaggt actttagtga ccgtgagcag c 351

<210> 17

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<213> Artificial Sequence

<220>

<223> FW1_VH2

<400> 17

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

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cccgggtcaag	gtttagagt	gatgggcgag	accaaccct	ccaactccgt	gaccaactac	180
gcccagaagt	tccaaggctg	tgtgacttta	accgtggaca	cctccacctc	caccgcctac	240
atggagctgt	cctctttaag	gtccgaggac	accgccacct	actactgtac	catcggtcgt	300
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<210> 19

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> FW2_VH1

<400> 19

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

Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gln Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser Thr Ala Tyr

80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Thr Ile Gly Arg Gly Arg Gly Phe Ala Tyr Trp Gly Gln Gly Thr Leu

100

105

110

Val Thr Val Ser Ser

115

<210> 20

<211> 351

<212> DNA

〈213〉 Artificial Sequence

 $\langle 220 \rangle$

<223> FW2_VH1

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cccggtcaag gtttagagt gatgggcgag accaaccct ccaactcgt gaccaactac 180

gccagaagt tccaaggtcg tgtgacttta accgtggaca agtccacctc caccgcctac 240

atggagctgt cctctttaag gtccgaggac accgccgtgt actactgtac catcggtcgt 300

ggccggggct ttgcttattg gggacaaggt actttagtga ccgtgagcag c 351

<210> 21

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> FW1_VL1

<400> 21

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Val	Ser	Ala	Ser	Val	Gly
1				5				10					15		

Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Asn	Ile	Asn	Phe	Trp
			20					25					30		

Leu	Ser	Trp	Cys	Gln	Gln	Lys	Pro	Gly	Lys	Ile	Pro	Lys	Leu	Leu	Ile
		35					40					45			

Tyr	Lys	Ala	Ser	Asn	Leu	His	Thr	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	Leu	Gln	Gly	Gln	Ser	Tyr	Pro	Tyr
				85					90					95	

Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys
			100				105			

<210> 22

<211> 321

<212> DNA

<213> Artificial Sequence

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<223> FW1_VL1

<400> 22

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attacttgtc gggcctccca gaacatcaac ttctggctga gctggtgtca gcagaagccc 120
ggcaagatcc ccaagttatt aatctacaag gccagcaatt tacacaccgg agtgccttct 180
cgtttctcgc gcagcggcag cggaaccgac ttacttttaa ccattctctc ttacagccc 240
gaggacttcg ccacctacta ttgtttacaa ggtcagtcct atccctacac cttcggcggc 300
ggaaccaagt tagaaatcaa g 321

<210> 23

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> FW1_VL3

<400> 23

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Asn Phe Trp
20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Lys Ala Ser Asn Leu His Thr 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 Leu Gln Gly Gln Ser Tyr Pro Tyr		
	85	90 95
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys		
	100	105

<210> 24
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 <213> Artificial Sequence

<220>
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atcacttgta gggcctccca gaacatcaac ttctggctga gctggtatca gcagaagccc	120
ggcaaagccc ctaagctgct gatctacaag gctagcaatc tgcacactgg cgtcccttcc	180
agattcagcg gtcccggcag cggcactgac ttactctca caatcagctc tctgcagcca	240
gaggacttcg ctacatacta ctgcctccaa ggccagtcct atccttacac attcggaggc	300
ggcacaaagc tggagatcaa g	321

<210> 25
 <211> 107
 <212> PRT

<213> Artificial Sequence

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<223> FW1_VL4

<400> 25

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Asn Phe Trp
20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Lys Ala Ser Asn Leu His Thr 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 Leu Gln Gly Gln Ser Tyr Pro Tyr
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 26

<211> 321

<212> DNA

<213> Artificial Sequence

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<223> FW1_VL4

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ggcaaagccc ctaggtgct gatctacaag gctagcaatc tgcacactgg cgtcccttcc 180
agattcagcg gtcccggcag cggcactgac ttactctca caatcagctc totgcagcca 240
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ggcacaaagc tggagatcaa g 321

<210> 27

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> FW2_VL2

<400> 27

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 Asn Ile Asn Phe Trp
20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ile Pro Lys Leu Leu Ile
35 40 45

Tyr Lys Ala Ser Asn Leu His Thr 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 Val Ala Thr Tyr Tyr Cys Leu Gln Gly Gln Ser Tyr Pro Tyr		
	85	90 95
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys		
	100	105

<210> 28
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 <212> DNA
 <213> Artificial Sequence

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 <223> FW2_VL2

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ggcaagatcc ctaagctgct gatctacaag gccagcaacc tccacactgg agtcccatct	180
aggttttagcg gatccggcag cggaactgac ttactctca caatcagctc tctgcagcca	240
gaggacgtgg ctacatacta ctgcctccaa ggccagtcct acccttacac attcggcggc	300
ggcacaaaac tggagatcaa g	321

<210> 29
 <211> 117
 <212> PRT

<213> Artificial Sequence

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<223> FW1_VH1_mH1

<400> 29

Gln Ile Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Pro Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Glu Thr Asn Pro Ser Asn Ser Val Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Leu Thr Val Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Thr Ile Gly Arg Gly Arg Gly Phe Ala Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 30

<211> 351
<212> DNA
<213> Artificial Sequence

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<223> FW1_VH1_mH1

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agctgtaagg cccccggcta cactttcaca tcctactgga tgcactgggt gagacaagcc 120
cccgccaag gactggagtg gatgggcgag acaaacccta gcaactccgt cactaactac 180
gcccagaagt tccaaggaag ggtgactctc acagtggaca ctagcacatc cacagcctac 240
atggaactgt ccagcctcag atccgaggac actgctgtgt actactgcac aatcggcaga 300
ggaaggggat tcgcttactg gggccaaggc acactcgtga ctgtcagctc c 351

<210> 31
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> FW1_VH1_mH2

<400> 31

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 Ser Tyr
20 25 30

Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile

35

40

45

Gly Glu Thr Asn Pro Ser Asn Ser Val Thr Asn Tyr Ala Gln Lys Phe

50

55

60

Gln Gly Arg Val Thr Leu Thr Val Asp Thr Ser Thr Ser Thr Ala Tyr

65

70

75

80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Thr Ile Gly Arg Gly Arg Gly Phe Ala Tyr Trp Gly Gln Gly Thr Leu

100

105

110

Val Thr Val Ser Ser

115

<210> 32

<211> 351

<212> DNA

〈213〉 Artificial Sequence

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<223> FW1_VH1_mH2

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agctgcaaag cctccggcta cacattcaca tctactgga tgcactgggt caagcagagg 120

cccggccaag gactggagtg gatcggcgaa acaaaccctt ccaacagcgt cactaactac 180

gccagaagt ttcaaggaag ggtgacactg actgtcgaca ctagcactag cactgcctat 240

atggagctga gctctctgag gagcgaggac actgccgtct attactgcac tatcggaagg 300

ggcagaggat tcgcctactg gggccaaggc actctcgtga cagtcagcag c 351

<210> 33

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> FW1_VH1_mH3

<400> 33

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 Ser Tyr
20 25 30

Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Glu Thr Asn Pro Ser Asn Ser Val Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Thr Ile Gly Arg Gly Arg Gly Phe Ala Tyr Trp Gly Gln Gly Thr Leu

100

105

110

Val Thr Val Ser Ala

115

<210> 34

<211> 351

<212> DNA

<213> Artificial Sequence

<220>

<223> FW1_VH1_mH3

<400> 34

caagtgcaac tggcgcagtc cggcgccgag gtgaagaagc cggcgccag cgtgaaggtg 60

agctgtaaag ccagcggcta cacattcaca tcctactgga tgcactgggt gagacaagcc 120

cccggccaag gactggagtg gatgggcgaa actaaccctt ccaacagcgt cacaattat 180

gctcagaaat tccaggggaag ggtgacactg acagtcgaca aaagcagcag cacagcctat 240

atgcagctga gctctctgac tagcgaggac tccgccgtgt actactgcac aattggaagg 300

ggcagaggat tcgcctactg gggacaaggc actctggtga cagtcagcgc c 351

<210> 35

<211> 107

<212> PRT

<213> Artificial Sequence

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<223> FW1_VL3_mL1

<400> 35

Asp Ile Gln Met Asn Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly

1 5 10 15

Asp Thr Ile Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Asn Phe Trp
20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Lys Ala Ser Asn Leu His Thr 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 Leu Gln Gly Gln Ser Tyr Pro Tyr
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 36

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> FW1_VL3_mL1

<400> 36

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atcacttgta gggccagcca gaacatcaac ttctggctga gctggtacca gcaaaagccc 120

ggcaaagccc ctaagctgct gatttacaag gcctccaacc tccacactgg agtgcctagc 180
agattctccg gcagcggcag cggaacagac ttactctca caatcagctc tctgcagcca 240
gaggacttcg ctacatacta ctgcctccaa ggccagtcct atccttacac attcggcggc 300
ggcactaagc tggagatcaa g 321

<210> 37
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> FW1_VL3_mL2+L3

<400> 37

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Asn Phe Trp
20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Asn Ile Pro Lys Leu Leu Ile
35 40 45

Tyr Lys Ala Ser Asn Leu His Thr 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 Ile Ala Thr Tyr Tyr Cys Leu Gln Gly Gln Ser Tyr Pro Tyr

85

90

95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

100

105

<210> 38

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> FW1_VL3_mL2+L3

<400> 38

gacattcaga tgacacagtc cccaagctcc gtgtccgcta gcgtcggaga cagagtgaca 60

atcacatgta gggctagcca gaacatcaac ttctggctga gctggtacca gcagaagccc 120

ggcaacatcc ctaagctgct gatctacaag gcctccaatc tgcacactgg cgtgcctagc 180

agattcagcg gatccggctc cggaactgac ttactctca caatcagctc tctgcagcca 240

gaggacatcg ctacatacta ctgcctccaa ggccagagct atccttacac attoggaggc 300

ggcacaagc tggagatcaa g 321

<210> 39

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> IGF11-16_VH

<400> 39

Gln Ile Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala

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

<210> 40
 <211> 351
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> IGF11-16_VH

<400> 40

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tcttgtaagg cccccggta cactttcaca agctactgga tgcactgggt caagcagaga	120
cccggtcaag gtttagaatg gatcggcgaa acaaatcctt ccaacagcgt gacaaactat	180
aacgagaagt tcaagagcaa ggctactctg actgtggaca agagcagcag cactgcctat	240
atgcagctgt cctctttaac aagcgaggac agcgccgtgt actactgtac aatcggtcgt	300
ggtcgtggat ttgcctactg gggacaaggt aactggtga cagtgtccgc c	351

<210> 41
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> IGF11-16_VL

<400> 41

Asp	Ile	Gln	Met	Asn	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Leu	Gly
1				5				10						15	

Asp	Thr	Ile	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Asn	Ile	Asn	Phe	Trp
		20					25						30		

Leu	Ser	Trp	Cys	Gln	Gln	Lys	Pro	Gly	Asn	Ile	Pro	Lys	Leu	Leu	Ile
		35					40					45			

Tyr	Lys	Ala	Ser	Asn	Leu	His	Thr	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	Ile	Ala	Thr	Tyr	Tyr	Cys	Leu	Gln	Gly	Gln	Ser	Tyr	Pro	Tyr
				85					90					95	
Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys					
			100					105							

<210> 42
 <211> 321
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> IGF11-16_VL

<400> 42	
gacatccaga tgaatcagag ccctagctct ttaagcgctt ctttaggaga cactatcact	60
atcacttgta gggccagcca gaacatcaac ttctggctga gctggtgcca gcagaagccc	120
ggtaacatcc caaagctgct gatctacaaa gccagcaatt tacacactgg tgtoccttct	180
cgttttagcg gctccggcag cggcacagac ttactctga caatctctc ttacagcca	240
gaggacatcg ccacttacta ctgtttacaa ggtcagagct acccttacac ttttgcggcg	300
ggcactaaac tggagatcaa g	321

<210> 43
 <211> 117
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> VH13_PN

<400> 43

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 Pro Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Glu Thr Asn Pro Ser Asn Ser Val Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Leu Thr Val Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

Thr Ile Gly Arg Gly Arg Gly Phe Ala Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 44

<211> 351

<212> DNA

<213> Artificial Sequence

<220>

<223> VH13_PN

<400> 44

```
caagtgcagc tggccagag cggagccgaa gtgaaaaagc ccggcgcctc cgtcaaagtc      60
agctgcaagg cccctggcta caccttcacc tcctactgga tgcactgggt gaggcaagct      120
cccggtcaag gtttagagt gatgggcgag accaaccctt ccaactccgt gaccaactac      180
gccagaagt tccaaggctg tgtgacttta accgtggaca cctccacctc caccgcctac      240
atggagctgt cctctttaag gtccgaggac accgccacct actactgtac catcggtcgt      300
ggccggggct ttgcttattg gggacaaggt actttagtga ccgtgagcag c              351
```

<210> 45

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> VH13_PQ

<400> 45

```
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 Pro Gly Tyr Thr Phe Thr Ser Tyr
20              25              30
```

```
Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35              40              45
```

```
Gly Glu Thr Asn Pro Ser Gln Ser Val Thr Asn Tyr Ala Gln Lys Phe
```

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

<210> 46
 <211> 351
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> VH13_PQ

<400> 46	
caagtgcagc tggccagag cggagccgaa gtgaaaaagc ccggcgcctc cgtcaaagtc	60
agctgcaagg cccctggcta caccttcacc tcctactgga tgcactgggt gaggcaagct	120
cccggtaag gtttagagt gatgggcgag accaaccct ccagtcctg gaccaactac	180
gccagaagt tccaaggctg tgtgacttta accgtggaca cctccacctc caccgcctac	240
atggagctgt cctctttaag gtccgaggac accgccacct actactgtac catcggtcgt	300
ggccggggct ttgcttattg gggacaaggt actttagtga ccgtgagcag c	351

<210> 47
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> VH13_PS

<400> 47

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 Pro Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Glu Thr Asn Pro Ser Ser Ser Val Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Leu Thr Val Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

Thr Ile Gly Arg Gly Arg Gly Phe Ala Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser

115

<210> 48
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> VH13_PS

<400> 48
caagtccaac tgggccagtc cggagccgaa gtgaagaaac ccggcgctag cgtcaaggtc 60
agctgtaagg cccccggcta cacattcact agctactgga tgcactgggt gaggcaagcc 120
cccgccaag gactggagt gatgggcgaa acaaaccxaa gcagctccgt cactaactac 180
gccagaagt ttcaaggaag ggtgactctc acagtggaca catccacaag cactgcctat 240
atggagctca gtcctctcag aagcgaggat acagccactt actactgcac tatoggaagg 300
ggaaggggat tcgcttactg gggccaaggc aactggtca cagtcagctc c 351

<210> 49
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> VH23_PN

<400> 49

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 Pro Gly Tyr Thr Phe Thr Ser Tyr

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

<210> 50
 <211> 351
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> VH23_PN

<400> 50
 caagtgcagc tggccagag cggagccgaa gtgaaaaagc ccggcgcctc cgtcaaagtc 60
 agctgcaagg cccctggcta caccttcacc tcctactgga tgcactgggt gaggcaagct 120

85

90

95

Thr Ile Gly Arg Gly Arg Gly Phe Ala Tyr Trp Gly Gln Gly Thr Leu

100

105

110

Val Thr Val Ser Ser

115

<210> 52

<211> 351

<212> DNA

<213> Artificial Sequence

<220>

<223> VH23_PQ

<400> 52

caagtgcagc tgggccagag cggagccgaa gtgaaaaagc cgggcgcctc cgtcaaagtc 60

agctgcaagg cccctggcta caccttcacc tcctactgga tgcactgggt gaggcaagct 120

cccggccaag gtttagagt gatgggcgag accaaccct cccagtcctg gaccaactac 180

gccagaagt tccaaggctg tgtgacttta accgtggaca agtcacctc caccgcctac 240

atggagctgt cctctttaag gtccgaggac accgccgtgt actactgtac catcggtcgt 300

ggccggggct ttgcttattg gggacaaggt actttagtga ccgtgagcag c 351

<210> 53

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> VH23_PS

<400> 53

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 Pro Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Glu Thr Asn Pro Ser Ser Ser Val Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Thr Ile Gly Arg Gly Arg Gly Phe Ala Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 54

<211> 351

<212> DNA

<213> Artificial Sequence

<220>

<223> VH23_PS

<400> 54

```
caagtccaac tgggccagtc cggagccgaa gtgaagaaac ccggcgctag cgtcaaggtc      60
agctgtaagg cccccggcta cacattcact agctactgga tgcactgggt gaggcaagcc      120
cccgccaag gactggagtg gatgggcgaa acaaaccxaa gcagctccgt cactaactac      180
gccagaagt ttcaaggaag ggtgactctc acagtggaca agtcacaag cactgcctat      240
atggagctca gctccctcag aagcgaggat acagccgtgt actactgcac tatcggaagg      300
ggaaggggat tcgcttactg gggccaaggc aactgggtca cagtcagctc c              351
```

<210> 55

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> VH25_PN

<400> 55

```
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 Pro Gly Tyr Thr Phe Thr Ser Tyr
20              25              30
```

```
Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35              40              45
```

```
Gly Glu Thr Asn Pro Ser Asn Ser Val Thr Asn Tyr Ala Gln Lys Phe
```

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

<210> 56
 <211> 351
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> VH25_PN

<400> 56	
caagtgcagc tggccagag cggagccgaa gtgaaaaagc cggcgccctc cgtcaaagtc	60
agctgcaagg cccctggcta caccttcacc tcctactgga tgcactgggt gaggcaagct	120
cccggccaag gtttagagtg gatgggcgag accaaccctt ccaactccgt gaccaactac	180
gccagaagt tccaaggctg tgtgacttta accgtggaca cctccacctc caccgcctac	240
atggagctgt cctctttaag gtccgaggac accgccgtgt actactgtac catcggtcgt	300
ggccggggct ttgcttattg gggacaaggt actttagtga ccgtgagcag c	351

<210> 57
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> VH25_PQ

<400> 57

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 Pro Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Glu Thr Asn Pro Ser Gln Ser Val Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Leu Thr Val Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Thr Ile Gly Arg Gly Arg Gly Phe Ala Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser

<210> 58
 <211> 351
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> VH25_PQ

<400> 58
 caagtgcagc tgggccagag cggagccgaa gtgaaaaagc ccggcgcctc cgtcaaagtc 60
 agctgcaagg ccctggcta caccttcacc tcctactgga tgcactgggt gaggcaagct 120
 cccgggtcaag gtttagagt gatgggcgag accaaccctt ccagtcctg gaccaactac 180
 gccagaagt tccaaggctg tgtgacttta accgtggaca cctccacctc caccgcctac 240
 atggagctgt cctctttaag gtccgaggac accgccgtgt actactgtac catoggtcgt 300
 ggccggggct ttgcttattg gggacaaggt actttagtga ccgtgagcag c 351

<210> 59
 <211> 117
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> VH25_PS

<400> 59

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 Pro Gly Tyr Thr Phe Thr Ser Tyr

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

<210> 60
 <211> 351
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> VH25_PS

<400> 60
 caagtccaac tggccagtc cggagccgaa gtgaagaaac ccggcgctag cgtcaagtc 60
 agctgtaagg cccccggcta cacattcact agctactgga tgcactgggt gaggcaagcc 120

cccggccaag gactggagtg gatgggcgaa acaaacccaa gcagctccgt cactaactac 180
 gcccaagaag ttcaaggaag ggtgactctc acagtggaca catccacaag cactgcctat 240
 atggagctca gctccctcag aagcgaggat acagccgtgt actactgcac tatcggaagg 300
 ggaaggggat tcgcttactg gggccaaggc acactggtca cagtcagctc c 351

<210> 61
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> VL13

<400> 61

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Asn Phe Trp
 20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Lys Ala Ser Asn Leu His Thr 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 Leu Gln Gly Gln Ser Tyr Pro Tyr

85

90

95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

100

105

<210> 62

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> VL13

<400> 62

gacatccaga tgactcagag cccttcctcc gtcagcgctt ccgtgggaga tagggtgact 60

atcacttgta gggcctccca gaacatcaac ttctggctga gctggtatca gcagaagccc 120

ggcaaagccc ctaagctgct gatctacaag gctagcaatc tgcacactgg cgtoccttcc 180

agattcagcg gtcccggcag cggcactgac ttactctca caatcagctc tctgcagcca 240

gaggacttcg ctacatacta ctgcctccaa ggccagtcct atccttacac attoggaggc 300

ggcacaagc tggagatcaa g 321

<210> 63

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> VL14

<400> 63

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Asn Phe Trp
20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Lys Ala Ser Asn Leu His Thr 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 Leu Gln Gly Gln Ser Tyr Pro Tyr
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 64

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> VL14

<400> 64

gacatccaga tgactcagag cccttcctcc gtcagcgctt ccgtgggaga tagggtgact 60

atcacttgta gggcctccca gaacatcaac ttctggctga gctggtatca gcagaagccc 120

ggcaaagccc ctaggtgtgt gatctacaag gctagcaatc tgcacactgg cgtcccttcc	180
agattcagcg gctccggcag cggcactgac ttactctca caatcagctc tctgcagcca	240
gaggacttgc ctacatacta ctgcctccaa ggccagtcct atccttacac attcggaggc	300
ggcacaagc tggagatcaa g	321

<210> 65
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> VL22

<400> 65

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	Asn	Ile	Asn	Phe	Trp
			20					25					30		

Leu	Ser	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ile	Pro	Lys	Leu	Leu	Ile
		35					40					45			

Tyr	Lys	Ala	Ser	Asn	Leu	His	Thr	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	Val	Ala	Thr	Tyr	Tyr	Cys	Leu	Gln	Gly	Gln	Ser	Tyr	Pro	Tyr
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

85

90

95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

100

105

<210> 66

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> VL22

<400> 66

gatatccaga tgactcagag cccaagctct ctgagcgcta gcgtcggaga tagggtcaca 60

atcacttgta gggcctccca gaacatcaac ttctggctca gctggtacca gcagaaaccc 120

ggcaagatcc ctaagctgct gatctacaag gccagcaacc tocacactgg agtoccattt 180

aggtttagcg gatccggcag cggaactgac ttactctca caatcagctc tctgcagcca 240

gaggacgtgg ctacatacta ctgcctccaa ggccagtcct acccttacac attoggcggc 300

ggcacaaaac tggagatcaa g 321

<210> 67

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> VL23

<400> 67

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 Asn Ile Asn Phe Trp
20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile
35 40 45

Tyr Lys Ala Ser Asn Leu His Thr 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 Val Ala Thr Tyr Tyr Cys Leu Gln Gly Gln Ser Tyr Pro Tyr
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 68

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> VL23

<400> 68

gatatccaga tgactcagag cccaagctct ctgagcgcta gcgtcggaga tagggtcaca 60

atcacttgta gggcctccca gaacatcaac ttctggctca gctggtacca gcagaaaccc 120

ggcaaggtcc ctaagctgct gatctacaag gccagcaacc tccacactgg agtcccatct	180
aggtttagcg gatccggcag cggaactgac ttcactctca caatcagctc tctgcagcca	240
gaggacgtgg ctacatacta ctgcctccaa ggccagtcct acccttacac attcggcggc	300
ggcacaaaaac tggagatcaa g	321

<210> 69
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> VL24

<400> 69

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	Asn	Ile	Asn	Phe	Trp
		20						25					30		

Leu	Ser	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Val	Pro	Lys	Leu	Leu	Ile
		35					40					45			

Tyr	Lys	Ala	Ser	Asn	Arg	His	Thr	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	Val	Ala	Thr	Tyr	Tyr	Cys	Leu	Gln	Gly	Gln	Ser	Tyr	Pro	Tyr
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

85

90

95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

100

105

<210> 70

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> VL24

<400> 70

gatatccaga tgactcagag cccaagctct ctgagcgcta gcgtcggaga tagggtcaca 60

atcacttgta gggcctccca gaacatcaac ttctggctca gctggtacca gcagaaaccc 120

ggcaaggtcc ctaagctgct gatctacaag gccagcaaca ggcacactgg agtcccatct 180

aggttttagcg gatccggcag cggaactgac ttactctca caatcagctc tctgcagcca 240

gaggacgtgg ctacatacta ctgcctccaa ggccagtcct acccttacac attoggcggc 300

ggcacaaaac tggagatcaa g 321

<210> 71

<211> 1367

<212> PRT

<213> Homo sapiens

<220>

<223> Homo sapiens IGF-I receptor

<400> 71

Met Lys Ser Gly Ser Gly Gly Gly Ser Pro Thr Ser Leu Trp Gly Leu

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

	165		170		175
Glu Cys Gly Asp Leu Cys Pro Gly Thr Met Glu Glu Lys Pro Met Cys					
	180		185		190
Glu Lys Thr Thr Ile Asn Asn Glu Tyr Asn Tyr Arg Cys Trp Thr Thr					
	195		200		205
Asn Arg Cys Gln Lys Met Cys Pro Ser Thr Cys Gly Lys Arg Ala Cys					
	210		215		220
Thr Glu Asn Asn Glu Cys Cys His Pro Glu Cys Leu Gly Ser Cys Ser					
	225		230		235
					240
Ala Pro Asp Asn Asp Thr Ala Cys Val Ala Cys Arg His Tyr Tyr Tyr					
	245		250		255
Ala Gly Val Cys Val Pro Ala Cys Pro Pro Asn Thr Tyr Arg Phe Glu					
	260		265		270
Gly Trp Arg Cys Val Asp Arg Asp Phe Cys Ala Asn Ile Leu Ser Ala					
	275		280		285
Glu Ser Ser Asp Ser Glu Gly Phe Val Ile His Asp Gly Glu Cys Met					
	290		295		300
Gln Glu Cys Pro Ser Gly Phe Ile Arg Asn Gly Ser Gln Ser Met Tyr					
	305		310		315
					320
Cys Ile Pro Cys Glu Gly Pro Cys Pro Lys Val Cys Glu Glu Glu Lys					

	325		330		335
Lys Thr Lys Thr Ile Asp Ser Val Thr Ser Ala Gln Met Leu Gln Gly					
	340		345		350
Cys Thr Ile Phe Lys Gly Asn Leu Leu Ile Asn Ile Arg Arg Gly Asn					
	355		360		365
Asn Ile Ala Ser Glu Leu Glu Asn Phe Met Gly Leu Ile Glu Val Val					
	370		375		380
Thr Gly Tyr Val Lys Ile Arg His Ser His Ala Leu Val Ser Leu Ser					
	385		390		400
Phe Leu Lys Asn Leu Arg Leu Ile Leu Gly Glu Glu Gln Leu Glu Gly					
	405		410		415
Asn Tyr Ser Phe Tyr Val Leu Asp Asn Gln Asn Leu Gln Gln Leu Trp					
	420		425		430
Asp Trp Asp His Arg Asn Leu Thr Ile Lys Ala Gly Lys Met Tyr Phe					
	435		440		445
Ala Phe Asn Pro Lys Leu Cys Val Ser Glu Ile Tyr Arg Met Glu Glu					
	450		455		460
Val Thr Gly Thr Lys Gly Arg Gln Ser Lys Gly Asp Ile Asn Thr Arg					
	465		470		480
Asn Asn Gly Glu Arg Ala Ser Cys Glu Ser Asp Val Leu His Phe Thr					

485

490

495

Ser Thr Thr Thr Ser Lys Asn Arg Ile Ile Ile Thr Trp His Arg Tyr
500 505 510

Arg Pro Pro Asp Tyr Arg Asp Leu Ile Ser Phe Thr Val Tyr Tyr Lys
515 520 525

Glu Ala Pro Phe Lys Asn Val Thr Glu Tyr Asp Gly Gln Asp Ala Cys
530 535 540

Gly Ser Asn Ser Trp Asn Met Val Asp Val Asp Leu Pro Pro Asn Lys
545 550 555 560

Asp Val Glu Pro Gly Ile Leu Leu His Gly Leu Lys Pro Trp Thr Gln
565 570 575

Tyr Ala Val Tyr Val Lys Ala Val Thr Leu Thr Met Val Glu Asn Asp
580 585 590

His Ile Arg Gly Ala Lys Ser Glu Ile Leu Tyr Ile Arg Thr Asn Ala
595 600 605

Ser Val Pro Ser Ile Pro Leu Asp Val Leu Ser Ala Ser Asn Ser Ser
610 615 620

Ser Gln Leu Ile Val Lys Trp Asn Pro Pro Ser Leu Pro Asn Gly Asn
625 630 635 640

Leu Ser Tyr Tyr Ile Val Arg Trp Gln Arg Gln Pro Gln Asp Gly Tyr

				645					650					655			
Leu	Tyr	Arg	His	Asn	Tyr	Cys	Ser	Lys	Asp	Lys	Ile	Pro	Ile	Arg	Lys		
			660					665						670			
Tyr	Ala	Asp	Gly	Thr	Ile	Asp	Ile	Glu	Glu	Val	Thr	Glu	Asn	Pro	Lys		
		675					680					685					
Thr	Glu	Val	Cys	Gly	Gly	Glu	Lys	Gly	Pro	Cys	Cys	Ala	Cys	Pro	Lys		
	690					695					700						
Thr	Glu	Ala	Glu	Lys	Gln	Ala	Glu	Lys	Glu	Glu	Ala	Glu	Tyr	Arg	Lys		
705					710					715					720		
Val	Phe	Glu	Asn	Phe	Leu	His	Asn	Ser	Ile	Phe	Val	Pro	Arg	Pro	Glu		
			725					730					735				
Arg	Lys	Arg	Arg	Asp	Val	Met	Gln	Val	Ala	Asn	Thr	Thr	Met	Ser	Ser		
			740					745					750				
Arg	Ser	Arg	Asn	Thr	Thr	Ala	Ala	Asp	Thr	Tyr	Asn	Ile	Thr	Asp	Pro		
	755						760					765					
Glu	Glu	Leu	Glu	Thr	Glu	Tyr	Pro	Phe	Phe	Glu	Ser	Arg	Val	Asp	Asn		
770						775					780						
Lys	Glu	Arg	Thr	Val	Ile	Ser	Asn	Leu	Arg	Pro	Phe	Thr	Leu	Tyr	Arg		
785				790					795						800		
Ile	Asp	Ile	His	Ser	Cys	Asn	His	Glu	Ala	Glu	Lys	Leu	Gly	Cys	Ser		

	805		810		815
Ala Ser Asn Phe Val Phe Ala Arg Thr Met Pro Ala Glu Gly Ala Asp					
	820		825		830
Asp Ile Pro Gly Pro Val Thr Trp Glu Pro Arg Pro Glu Asn Ser Ile					
	835		840		845
Phe Leu Lys Trp Pro Glu Pro Glu Asn Pro Asn Gly Leu Ile Leu Met					
	850		855		860
Tyr Glu Ile Lys Tyr Gly Ser Gln Val Glu Asp Gln Arg Glu Cys Val					
865		870		875	880
Ser Arg Gln Glu Tyr Arg Lys Tyr Gly Gly Ala Lys Leu Asn Arg Leu					
	885		890		895
Asn Pro Gly Asn Tyr Thr Ala Arg Ile Gln Ala Thr Ser Leu Ser Gly					
	900		905		910
Asn Gly Ser Trp Thr Asp Pro Val Phe Phe Tyr Val Gln Ala Lys Thr					
	915		920		925
Gly Tyr Glu Asn Phe Ile His Leu Ile Ile Ala Leu Pro Val Ala Val					
	930		935		940
Leu Leu Ile Val Gly Gly Leu Val Ile Met Leu Tyr Val Phe His Arg					
945		950		955	960
Lys Arg Asn Asn Ser Arg Leu Gly Asn Gly Val Leu Tyr Ala Ser Val					

965

970

975

Asn Pro Glu Tyr Phe Ser Ala Ala Asp Val Tyr Val Pro Asp Glu Trp

980

985

990

Glu Val Ala Arg Glu Lys Ile Thr Met Ser Arg Glu Leu Gly Gln Gly

995

1000

1005

Ser Phe Gly Met Val Tyr Glu Gly Val Ala Lys Gly Val Val Lys

1010

1015

1020

Asp Glu Pro Glu Thr Arg Val Ala Ile Lys Thr Val Asn Glu Ala

1025

1030

1035

Ala Ser Met Arg Glu Arg Ile Glu Phe Leu Asn Glu Ala Ser Val

1040

1045

1050

Met Lys Glu Phe Asn Cys His His Val Val Arg Leu Leu Gly Val

1055

1060

1065

Val Ser Gln Gly Gln Pro Thr Leu Val Ile Met Glu Leu Met Thr

1070

1075

1080

Arg Gly Asp Leu Lys Ser Tyr Leu Arg Ser Leu Arg Pro Glu Met

1085

1090

1095

Glu Asn Asn Pro Val Leu Ala Pro Pro Ser Leu Ser Lys Met Ile

1100

1105

1110

Gln Met Ala Gly Glu Ile Ala Asp Gly Met Ala Tyr Leu Asn Ala

1115	1120	1125
Asn Lys Phe Val His Arg Asp Leu Ala Ala Arg Asn Cys Met Val		
1130	1135	1140
Ala Glu Asp Phe Thr Val Lys Ile Gly Asp Phe Gly Met Thr Arg		
1145	1150	1155
Asp Ile Tyr Glu Thr Asp Tyr Tyr Arg Lys Gly Gly Lys Gly Leu		
1160	1165	1170
Leu Pro Val Arg Trp Met Ser Pro Glu Ser Leu Lys Asp Gly Val		
1175	1180	1185
Phe Thr Thr Tyr Ser Asp Val Trp Ser Phe Gly Val Val Leu Trp		
1190	1195	1200
Glu Ile Ala Thr Leu Ala Glu Gln Pro Tyr Gln Gly Leu Ser Asn		
1205	1210	1215
Glu Gln Val Leu Arg Phe Val Met Glu Gly Gly Leu Leu Asp Lys		
1220	1225	1230
Pro Asp Asn Cys Pro Asp Met Leu Phe Glu Leu Met Arg Met Cys		
1235	1240	1245
Trp Gln Tyr Asn Pro Lys Met Arg Pro Ser Phe Leu Glu Ile Ile		
1250	1255	1260
Ser Ser Ile Lys Glu Glu Met Glu Pro Gly Phe Arg Glu Val Ser		

1265		1270		1275
Phe Tyr Tyr Ser Glu Glu Asn Lys Leu Pro Glu Pro Glu Glu Leu				
1280		1285		1290
Asp Leu Glu Pro Glu Asn Met Glu Ser Val Pro Leu Asp Pro Ser				
1295		1300		1305
Ala Ser Ser Ser Ser Leu Pro Leu Pro Asp Arg His Ser Gly His				
1310		1315		1320
Lys Ala Glu Asn Gly Pro Gly Pro Gly Val Leu Val Leu Arg Ala				
1325		1330		1335
Ser Phe Asp Glu Arg Gln Pro Tyr Ala His Met Asn Gly Gly Arg				
1340		1345		1350
Lys Asn Glu Arg Ala Leu Pro Leu Pro Gln Ser Ser Thr Cys				
1355		1360		1365

<210> 72
 <211> 4101
 <212> DNA
 <213> Homo sapiens

<220>
 <223> Homo sapiens IGF-I receptor

<400> 72
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aacgactatc agcagctgaa ggcctggag aactgcacgg tgatcgaggg ctacctccac	180
atcctgtctca tctccaaggc cgaggactac cgcagctacc gcttcccca gctcacggtc	240
attaccgagt acttgtgtgt gttccgagtg gctggcctcg agagcctcgg agacctcttc	300
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gagatgacca atctcaagga tattgggctt tacaacctga ggaacattac tcggggggcc	420
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ctggatgcgg tgtccaataa ctacattgtg gggaataagc ccccaaagga atgtggggac	540
ctgtgtocag ggacatgga ggagaagccg atgtgtgaga agaccacat caacaatgag	600
tacaactacc gctgctggac cacaaccgc tgccagaaaa tgtgccaag cacgtgtggg	660
aagcgggcgt gcaccagaa caatgagtgc tgccaccccg agtgccctggg cagctgcagc	720
ggcctgaca acgacacggc ctgtgtagct tgccgccact actactatgc cgggtgtctgt	780
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ctcattaaca tccgacgggg gaataacatt gcttcagagc tggagaactt catggggctc	1140
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aacaacgggg agagagcctc ctgtgaaagt gacgtcctgc atttcacctc caccaccacg	1500
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caggatgcct gcggctccaa cagctggaac atggtggacg tggacctccc gcccaacaag	1680
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gtggtgaaag atgaacctga aaccagagtg gccattaaaa cagtgaacga ggccgcaagc	3120
atgcgtgaga ggattgagtt tctcaacgaa gcttctgtga tgaaggagtt caattgtcac	3180
catgtggtgc gattgctggg tgtggtgtcc caaggccagc caacactggt catcatggaa	3240
ctgatgacac ggggcgatct caaaagtat ctccggtctc tgaggccaga aatggagaat	3300
aatccagtcc tagcacctcc aagcctgagc aagatgattc agatggccgg agagattgca	3360
gacggcatgg catacctcaa cgccaataag ttctgccaca gagaccttgc tgcccgaat	3420
tgcatggtag ccgaagattt cacagtcaaa atcggagatt ttggtatgac gcgagatata	3480
tatgagacag actattaccg gaaaggaggg aaagggtgc tgcccgtgcg ctggatgtct	3540
cctgagtccc tcaaggatgg agtcctcacc acttactcgg acgtctggtc cttcggggtc	3600
gtcctctggg agatgccac actggccgag cagccctacc agggcttgtc caacgagcaa	3660
gtccttcgct tcgtcatgga gggcggcctt ctggacaagc cagacaactg tcttgacatg	3720

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 ctgccccagt cttcgacctg c 4101

<210> 73

<211> 1367

<212> PRT

<213> *Macaca fascicularis*

<220>

<223> *Macaca fascicularis* IGF-I receptor

<400> 73

Met	Lys	Ser	Gly	Ser	Gly	Glu	Gly	Ser	Pro	Thr	Ser	Leu	Trp	Gly	Leu
1			5					10						15	

Leu	Phe	Leu	Ser	Ala	Ala	Leu	Ser	Leu	Trp	Pro	Thr	Ser	Gly	Glu	Ile
		20					25						30		

Cys	Gly	Pro	Gly	Ile	Asp	Ile	Arg	Asn	Asp	Tyr	Gln	Gln	Leu	Lys	Arg
		35					40					45			

Leu	Glu	Asn	Cys	Thr	Val	Ile	Glu	Gly	Tyr	Leu	His	Ile	Leu	Leu	Ile
	50						55					60			

Ser Lys Ala Glu Asp Tyr Arg Ser Tyr Arg Phe Pro Lys Leu Thr Val
65 70 75 80

Ile Thr Glu Tyr Leu Leu Phe Arg Val Ala Gly Leu Glu Ser Leu
85 90 95

Gly Asp Leu Phe Pro Asn Leu Thr Val Ile Arg Gly Trp Lys Leu Phe
100 105 110

Tyr Asn Tyr Ala Leu Val Ile Phe Glu Met Thr Asn Leu Lys Asp Ile
115 120 125

Gly Leu Tyr Asn Leu Arg Asn Ile Thr Arg Gly Ala Ile Arg Ile Glu
130 135 140

Lys Asn Ala Asp Leu Cys Tyr Leu Ser Thr Val Asp Trp Ser Leu Ile
145 150 155 160

Leu Asp Ala Val Ser Asn Asn Tyr Ile Val Gly Asn Lys Pro Pro Lys
165 170 175

Glu Cys Gly Asp Leu Cys Pro Gly Thr Met Glu Glu Lys Pro Met Cys
180 185 190

Glu Lys Thr Thr Ile Asn Asn Glu Tyr Asn Tyr Arg Cys Trp Thr Thr
195 200 205

Asn Arg Cys Gln Lys Met Cys Pro Ser Ala Cys Gly Lys Arg Ala Cys
210 215 220

Thr Glu Asn Asn Glu Cys Cys His Pro Glu Cys Leu Gly Ser Cys Ser
225 230 235 240

Ala Pro Asp Asn Asp Thr Ala Cys Val Ala Cys Arg His Tyr Tyr Tyr
245 250 255

Ala Gly Val Cys Val Pro Ala Cys Pro Pro Asn Thr Tyr Arg Phe Glu
260 265 270

Gly Trp Arg Cys Val Asp Arg Asp Phe Cys Ala Asn Ile Leu Ser Ala
275 280 285

Glu Ser Ser Asp Ser Glu Gly Phe Val Ile His Asp Gly Glu Cys Met
290 295 300

Gln Glu Cys Pro Ser Gly Phe Ile Arg Asn Gly Ser Gln Ser Met Tyr
305 310 315 320

Cys Ile Pro Cys Glu Gly Pro Cys Pro Lys Val Cys Glu Glu Glu Lys
325 330 335

Lys Thr Lys Thr Ile Asp Ser Val Thr Ser Ala Gln Met Leu Gln Gly
340 345 350

Cys Thr Ile Phe Lys Gly Asn Leu Leu Ile Asn Ile Arg Arg Gly Asn
355 360 365

Asn Ile Ala Ser Glu Leu Glu Asn Phe Met Gly Leu Ile Glu Val Val
370 375 380

Thr Gly Tyr Val Lys Ile Arg His Ser His Ala Leu Val Ser Leu Ser
385 390 395 400

Phe Leu Lys Asn Leu Arg Leu Ile Leu Gly Glu Glu Gln Leu Glu Gly
405 410 415

Asn Tyr Ser Phe Tyr Val Leu Asp Asn Gln Asn Leu Gln Gln Leu Trp
420 425 430

Asp Trp Asp His Arg Asn Leu Thr Ile Lys Ala Gly Lys Met Tyr Phe
435 440 445

Ala Phe Asn Pro Lys Leu Cys Val Ser Glu Ile Tyr Arg Met Glu Glu
450 455 460

Val Thr Gly Thr Lys Gly Arg Gln Ser Lys Gly Asp Ile Asn Thr Arg
465 470 475 480

Asn Asn Gly Glu Arg Ala Ser Cys Glu Ser Asp Val Leu His Phe Thr
485 490 495

Ser Thr Thr Thr Trp Lys Asn Arg Ile Ile Ile Thr Trp His Arg Tyr
500 505 510

Arg Pro Pro Asp Tyr Arg Asp Leu Ile Ser Phe Thr Val Tyr Tyr Lys
515 520 525

Glu Ala Pro Phe Lys Asn Val Thr Glu Tyr Asp Gly Gln Asp Ala Cys
530 535 540

Gly Ser Asn Ser Trp Asn Met Val Asp Val Asp Leu Pro Pro Asn Lys
545 550 555 560

Asp Val Glu Pro Gly Ile Leu Leu His Gly Leu Lys Pro Trp Thr Gln
565 570 575

Tyr Ala Val Tyr Val Lys Ala Val Thr Leu Thr Met Val Glu Asn Asp
580 585 590

His Ile Arg Gly Ala Lys Ser Glu Ile Leu Tyr Ile Arg Thr Asn Ala
595 600 605

Ser Val Pro Ser Ile Pro Leu Asp Val Leu Ser Ala Ser Asn Ser Ser
610 615 620

Ser Gln Leu Ile Val Lys Trp Asn Pro Pro Ser Leu Pro Asn Gly Asn
625 630 635 640

Leu Ser Tyr Tyr Ile Val Arg Trp Gln Arg Gln Pro Gln Asp Gly Tyr
645 650 655

Leu Tyr Arg His Asn Tyr Cys Ser Lys Asp Lys Ile Pro Ile Arg Lys
660 665 670

Tyr Ala Asp Gly Thr Ile Asp Ile Glu Glu Val Thr Glu Asn Pro Lys
675 680 685

Thr Glu Val Cys Gly Gly Glu Lys Gly Pro Cys Cys Ala Cys Pro Lys
690 695 700

Thr Glu Ala Glu Lys Gln Ala Glu Lys Glu Glu Ala Glu Tyr Arg Lys
705 710 715 720

Val Phe Glu Asn Phe Leu His Asn Ser Ile Phe Val Pro Arg Pro Glu
725 730 735

Arg Lys Arg Arg Asp Val Met Gln Val Ala Asn Thr Thr Met Ser Ser
740 745 750

Arg Ser Arg Asn Thr Thr Val Ala Asp Thr Tyr Asn Ile Thr Asp Leu
755 760 765

Glu Glu Leu Glu Thr Glu Tyr Pro Phe Phe Glu Ser Arg Val Asp Asn
770 775 780

Lys Glu Arg Thr Val Ile Ser Asn Leu Arg Pro Phe Thr Leu Tyr Arg
785 790 795 800

Ile Asp Ile His Ser Cys Asn His Glu Ala Glu Lys Leu Gly Cys Ser
805 810 815

Ala Ser Asn Phe Val Phe Ala Arg Thr Met Pro Ala Glu Gly Ala Asp
820 825 830

Asp Ile Pro Gly Pro Val Thr Trp Glu Pro Arg Pro Glu Asn Ser Ile
835 840 845

Phe Leu Lys Trp Pro Glu Pro Glu Asn Pro Asn Gly Leu Ile Leu Met
850 855 860

Tyr Glu Ile Lys Tyr Gly Ser Gln Val Glu Asp Gln Arg Glu Cys Val
865 870 875 880

Ser Arg Gln Glu Tyr Arg Lys Tyr Gly Gly Ala Lys Leu Asn Arg Leu
885 890 895

Asn Pro Gly Asn Tyr Thr Ala Arg Ile Gln Ala Thr Ser Leu Ser Gly
900 905 910

Asn Gly Ser Trp Thr Asp Pro Val Phe Phe Tyr Val Gln Ala Lys Thr
915 920 925

Gly Tyr Glu Asn Phe Ile His Leu Ile Ile Ala Leu Pro Val Ala Val
930 935 940

Leu Leu Ile Val Gly Gly Leu Val Ile Met Leu Tyr Val Phe His Arg
945 950 955 960

Lys Arg Asn Asn Ser Arg Leu Gly Asn Gly Val Leu Tyr Ala Ser Val
965 970 975

Asn Pro Glu Tyr Phe Ser Ala Ala Asp Val Tyr Val Pro Asp Glu Trp
980 985 990

Glu Val Ala Arg Glu Lys Ile Thr Met Ser Arg Glu Leu Gly Gln Gly
995 1000 1005

Ser Phe Gly Met Val Tyr Glu Gly Val Ala Lys Gly Val Val Lys
1010 1015 1020

Asp Glu Pro Glu Thr Arg Val Ala Ile Lys Thr Val Asn Glu Ala
1025 1030 1035

Ala Ser Met Arg Glu Arg Ile Glu Phe Leu Asn Glu Ala Ser Val
1040 1045 1050

Met Lys Glu Phe Asn Cys His His Val Val Arg Leu Leu Gly Val
1055 1060 1065

Val Ser Gln Gly Gln Pro Thr Leu Val Ile Met Glu Leu Met Thr
1070 1075 1080

Arg Gly Asp Leu Lys Ser Tyr Leu Arg Ser Leu Arg Pro Glu Met
1085 1090 1095

Glu Asn Asn Pro Val Leu Ala Pro Pro Ser Leu Ser Lys Met Ile
1100 1105 1110

Gln Met Ala Gly Glu Ile Ala Asp Gly Met Ala Tyr Leu Asn Ala
1115 1120 1125

Asn Lys Phe Val His Arg Asp Leu Ala Ala Arg Asn Cys Met Val
1130 1135 1140

Ala Glu Asp Phe Thr Val Lys Ile Gly Asp Phe Gly Met Thr Arg
1145 1150 1155

Asp Ile Tyr Glu Thr Asp Tyr Tyr Arg Lys Gly Gly Lys Gly Leu
1160 1165 1170

Leu Pro Val Arg Trp Met Ser Pro Glu Ser Leu Lys Asp Gly Val
1175 1180 1185

Phe Thr Thr Tyr Ser Asp Val Trp Ser Phe Gly Val Val Leu Trp
1190 1195 1200

Glu Ile Ala Thr Leu Ala Glu Gln Pro Tyr Gln Gly Leu Ser Asn
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Glu Gln Val Leu Arg Phe Val Met Glu Gly Gly Leu Leu Asp Lys
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Pro Asp Asn Cys Pro Asp Met Leu Phe Glu Leu Met Arg Met Cys
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Trp Gln Tyr Asn Pro Lys Met Arg Pro Ser Phe Leu Glu Ile Ile
1250 1255 1260

Ser Ser Ile Lys Asp Glu Met Glu Pro Gly Phe Arg Glu Val Ser
1265 1270 1275

Phe Tyr Tyr Ser Glu Glu Asn Lys Leu Pro Glu Pro Glu Glu Leu
1280 1285 1290

Asp Leu Glu Pro Glu Asn Met Glu Ser Val Pro Leu Asp Pro Ser
1295 1300 1305

Ala Ser Ser Ser Ser Leu Pro Leu Pro Asp Arg His Ser Gly His
1310 1315 1320

Lys Ala Glu Asn Gly Pro Gly Pro Gly Val Leu Val Leu Arg Ala
1325 1330 1335

Ser Phe Asp Glu Arg Gln Pro Tyr Ala His Met Asn Gly Gly Arg
1340 1345 1350

Lys Asn Glu Arg Ala Leu Pro Leu Pro Gln Ser Ser Thr Cys
1355 1360 1365

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<212> DNA
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gcgcctgaca acgacacggc ctgtgtagct tgccgccact actactacgc cgggtgtctgc	780
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<211> 1425

<212> PRT

<213> Oryctolagus cuniculus

<220>

<223> Oryctolagus cuniculus IGF-I receptor

<400> 75

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Leu Phe Leu Ser Ala Ala Leu Ser Val Trp Pro Thr Ser Gly Glu Ile
20 25 30

Cys Gly Pro Gly Ile Asp Ile Arg Asn Asp Phe Gln Gln Leu Lys Arg
35 40 45

Leu Glu Asn Cys Thr Val Ile Glu Gly Phe Leu His Ile Leu Leu Ile
50 55 60

Ser Lys Ala Glu Asp Tyr Arg Asn Tyr Arg Phe Pro Lys Leu Thr Val
65 70 75 80

Ile Thr Glu Tyr Leu Leu Leu Phe Arg Val Ala Gly Leu Glu Ser Leu
85 90 95

Gly Asp Leu Phe Pro Asn Leu Thr Val Ile Arg Gly Trp Lys Leu Phe
100 105 110

Tyr Asn Tyr Ala Leu Val Ile Phe Glu Met Thr Asn Leu Lys Asp Ile

115	120	125
Gly Leu Tyr Asn Leu Arg Asn Ile Thr Arg Gly Ala Ile Arg Ile Glu		
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Lys Asn Ala Asp Leu Cys Tyr Leu Ser Thr Val Asp Trp Ser Leu Ile		
145	150	155 160
Leu Asp Ala Val Ser Asn Asn Tyr Ile Val Gly Asn Lys Ser Pro Lys		
165	170	175
Glu Cys Gly Asp Met Cys Pro Gly Thr Leu Glu Glu Lys Pro Leu Cys		
180	185	190
Glu Lys Thr Ala Ile Asn Asn Glu Tyr Asn Tyr Arg Cys Trp Thr Thr		
195	200	205
Asn Arg Cys Gln Lys Met Cys Pro Ser Ala Cys Gly Lys Arg Ala Cys		
210	215	220
Thr Glu Asn Asn Glu Cys Cys His Pro Glu Cys Leu Gly Ser Cys His		
225	230	235 240
Ala Pro Asp Asp Asp Thr Ala Cys Val Ala Cys Arg His Tyr Tyr Phe		
245	250	255
Ser Gly Val Cys Val Pro Ala Cys Pro Pro Asn Thr Tyr Arg Phe Glu		
260	265	270
Gly Trp Arg Cys Val Asp Arg Asp Phe Cys Ala Asn Ile Pro Asn Ala		

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

435

440

445

Ala Phe Asn Pro Lys Leu Cys Val Ser Glu Ile Tyr Arg Met Glu Asp
450 455 460

Val Thr Gly Thr Lys Gly Arg Gln Ser Lys Gly Asp Ile Asn Thr Arg
465 470 475 480

Asn Asn Gly Glu Arg Ala Ser Cys Glu Ser Asp Ile Leu His Phe Thr
485 490 495

Ser Thr Asn Thr Trp Lys Asn Arg Ile Ile Leu Thr Trp His Arg Tyr
500 505 510

Arg Pro Pro Asp Tyr Arg Asp Leu Ile Ser Phe Thr Val Tyr Tyr Lys
515 520 525

Glu Ala Pro Phe Lys Asn Val Thr Glu Tyr Asp Gly Gln Asp Ala Cys
530 535 540

Gly Ser Asn Ser Trp Asn Met Val Asp Val Asp Leu Pro Pro Asn Lys
545 550 555 560

Asp Leu Glu Pro Gly Ile Leu Leu Gln Gly Leu Lys Pro Trp Thr Gln
565 570 575

Tyr Ala Val Tyr Val Lys Ala Val Thr Leu Thr Met Val Glu Asn Asp
580 585 590

His Ile Arg Gly Ala Lys Ser Glu Ile Leu Tyr Ile Arg Thr Asn Ala

595	600	605
Ser Val Pro Ser Ile Pro Leu Asp Ile Leu Ser Ala Ser Asn Ser Ser		
610	615	620
Ser Gln Leu Ile Val Lys Trp Ser Pro Pro Ser Leu Pro Asn Gly Asn		
625	630	635 640
Leu Ser Tyr Tyr Ile Val Arg Trp Gln Arg Gln Pro Gln Asp Gly Tyr		
	645	650 655
Leu Tyr Arg His Asn Tyr Cys Ser Lys Asp Lys Ile Pro Ile Arg Lys		
	660	665 670
Tyr Ala Asp Gly Thr Ile Asp Val Glu Glu Val Thr Glu Asn Pro Lys		
	675	680 685
Thr Glu Val Cys Gly Gly Glu Lys Gly Pro Cys Cys Ala Cys Pro Lys		
690	695	700
Thr Glu Ala Glu Lys Gln Ala Glu Lys Glu Glu Ala Glu Tyr Arg Lys		
705	710	715 720
Val Phe Glu Asn Phe Leu His Asn Ser Ile Phe Val Pro Arg Pro Glu		
	725	730 735
Arg Lys Arg Arg Asp Val Ala Gln Val Ala Asn Thr Thr Leu Ser Gly		
	740	745 750
Arg Gly Arg Asn Gly Thr Ala Val Asp Met Tyr Asn Ser Thr Asp Leu		

755	760	765
Glu Glu Leu Glu Thr Glu Tyr Pro Phe Phe Glu Thr Arg Val Asp Lys		
770	775	780
Glu Ile Thr Val Ile Ser Asn Leu Arg Pro Phe Thr Ser Tyr Arg Ile		
785	790	795 800
Asp Ile His Ser Cys Asn His Glu Ala Glu Lys Leu Gly Cys Ser Ala		
805	810	815
Ser Asn Phe Val Phe Ala Arg Thr Lys Pro Ala Glu Gly Ala Asp Asp		
820	825	830
Ile Pro Gly Pro Val Thr Trp Glu Ala Arg Pro Glu Asn Ser Ile Phe		
835	840	845
Leu Lys Trp Pro Glu Pro Glu Asn Pro Asn Gly Leu Ile Leu Met Tyr		
850	855	860
Glu Ile Lys Tyr Gly Ser Gln Ile Glu Asp Gln Arg Glu Cys Val Ser		
865	870	875 880
Arg Gln Gln Tyr Arg Lys Tyr Gly Gly Ala Lys Leu Asn Arg Leu Asn		
885	890	895
Pro Gly Asn Tyr Thr Ala Arg Ile Gln Ala Thr Ser Leu Ser Gly Asn		
900	905	910
Gly Ser Trp Thr Glu Pro Val Phe Phe Tyr Val Pro Ala Lys Ala Thr		

915

920

925

Tyr Glu Ser Phe Met His Leu Ile Ile Ala Leu Pro Val Ala Ile Leu
930 935 940

Leu Ile Val Gly Gly Leu Leu Ile Val Leu Tyr Val Phe His Arg Lys
945 950 955 960

Arg Ser Asn Ser Arg Leu Gly Asn Gly Val Leu Tyr Ala Ser Val Asn
965 970 975

Pro Glu Tyr Phe Ser Ala Ala Asp Val Tyr Val Pro Asp Glu Trp Glu
980 985 990

Val Ala Arg Glu Lys Ile Thr Met Ser Arg Glu Leu Gly Gln Gly Ser
995 1000 1005

Phe Gly Met Val Tyr Glu Gly Val Ala Lys Gly Val Val Lys Asp
1010 1015 1020

Glu Pro Glu Thr Arg Val Ala Ile Lys Thr Val Asn Glu Ala Ala
1025 1030 1035

Ser Met Arg Glu Arg Ile Glu Phe Leu Asn Glu Ala Ser Val Met
1040 1045 1050

Lys Glu Phe Asn Cys His His Val Val Arg Leu Leu Gly Val Val
1055 1060 1065

Ser Gln Gly Gln Pro Thr Leu Val Ile Met Glu Leu Met Thr Arg

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1115		1120		1125
Gly Arg Ser Gln Gln Pro Gly Ala Ser Ser Gly Ser Pro Thr Arg				
1130		1135		1140
Val Gln Gly Pro Lys Asp Leu Gly His Leu Pro Leu Pro Ser Gln				
1145		1150		1155
Asn Arg Ala Pro Ala Pro Pro Ser Leu Ser Lys Met Ile Gln Met				
1160		1165		1170
Ala Gly Glu Ile Ala Asp Gly Met Ala Tyr Leu Asn Ala Asn Lys				
1175		1180		1185
Phe Val His Arg Asp Leu Ala Ala Arg Asn Cys Met Val Ala Glu				
1190		1195		1200
Asp Phe Thr Val Lys Ile Gly Asp Phe Gly Met Thr Arg Asp Ile				
1205		1210		1215
Tyr Glu Thr Asp Tyr Tyr Arg Lys Gly Gly Lys Gly Leu Leu Pro				

1220		1225		1230
Val Arg Trp Met Ser Pro Glu Ser Leu Lys Asp Gly Val Phe Thr				
1235		1240		1245
Thr His Ser Asp Val Trp Ser Phe Gly Val Val Leu Trp Glu Ile				
1250		1255		1260
Ala Thr Leu Ala Glu Gln Pro Tyr Gln Gly Phe Ser Asn Glu Gln				
1265		1270		1275
Val Leu Arg Phe Val Met Glu Gly Gly Leu Leu Asp Lys Pro Asp				
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Asn Cys Pro Asp Met Leu Phe Glu Leu Met Arg Met Cys Trp Gln				
1295		1300		1305
Tyr Asn Pro Lys Met Arg Pro Ser Phe Leu Glu Ile Ile Gly Ser				
1310		1315		1320
Val Arg Asp Glu Met Glu Pro Gly Phe Arg Glu Val Ser Phe Tyr				
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Tyr Ser Glu Glu Asn Lys Pro Pro Glu Ala Glu Glu Leu Asp Leu				
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Glu Pro Glu Asn Met Glu Ser Val Pro Leu Asp Pro Ser Ala Asn				
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Ala Ala Ala Ala Val Ala Ala Leu Gln Pro Asp Arg His Lys Ala				

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Glu Asn Gly Pro Ser Ala Gly Ala Met Val Leu Arg Ala Ser Phe		
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<400> 76

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

Leu Glu Asn Cys Thr Val Ile Glu Gly Tyr Leu His Ile Leu Leu Ile
 50 55 60

Ser Lys Ala Glu Asp Tyr Arg Ser Tyr Arg Phe Pro Lys Leu Thr Val
 65 70 75 80

Ile Thr Glu Tyr Leu Leu Leu Phe Arg Val Ala Gly Leu Glu Ser Leu

85

90

95

Gly Asp Leu Phe Pro Asn Leu Thr Val Ile Arg Gly Trp Lys Leu Phe

100

105

110

Tyr Asn Tyr Ala Leu Val Ile Phe Glu Met Thr Asn Leu Lys Asp Ile

115

120

125

Gly Leu Tyr Asn Leu Arg Asn Ile Thr Arg Gly Ala Ile Arg Ile Glu

130

135

140

Lys Asn Ala Asp Leu Cys Tyr Leu Ser Thr Val Asp Trp Ser Leu Ile

145

150

155

160

Leu Asp Ala Val Ser Asn Asn Tyr Ile Val Gly Asn Lys Ser Pro Lys

165

170

175

Glu Cys Gly Asp Leu Cys Pro Gly Thr Met Glu Glu Lys Pro Leu Cys

180

185

190

Glu Lys Thr Thr Ile Asn Asn Glu Tyr Asn Tyr Arg Cys Trp Thr Thr

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200

205

Asn Arg Cys Gln Lys Met Cys Pro Ser Ala Cys Gly Lys Arg Ala Cys

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215

220

Thr Glu Tyr Gln Glu Cys Cys His Pro Glu Cys Leu Gly Ser Cys His

225

230

235

240

Ala Pro Asp Asp Asp Thr Ala Cys Val Ala Cys Arg His Phe Tyr Tyr

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

	405		410		415
Asn Tyr Ser Phe Tyr Val Leu Asp Asn Gln Asn Leu Gln Gln Leu Trp					
	420		425		430
Asp Trp Asp His Arg Asn Leu Thr Ile Lys Ser Gly Lys Met Tyr Phe					
	435		440		445
Ala Phe Asn Pro Lys Leu Cys Val Ser Glu Ile Tyr Arg Met Glu Glu					
	450		455		460
Val Thr Gly Thr Lys Gly Arg Gln Ser Lys Gly Asp Ile Asn Thr Arg					
465		470		475	480
Asn Asn Gly Glu Arg Ala Ser Cys Glu Ser Asp Val Leu Arg Phe Thr					
	485		490		495
Ser Thr Thr Thr Ser Lys Asn Arg Ile Ile Ile Thr Trp His Arg Tyr					
	500		505		510
Arg Pro Pro Asp Tyr Arg Asp Leu Ile Ser Phe Thr Val Tyr Tyr Lys					
	515		520		525
Glu Ala Pro Phe Lys Asn Val Thr Glu Tyr Asp Gly Gln Asp Ala Cys					
	530		535		540
Gly Ser Asn Ser Trp Asn Met Val Asp Val Asp Leu Pro Pro Asn Lys					
545		550		555	560
Asp Ala Glu Pro Gly Ile Leu Leu His Gly Leu Lys Pro Trp Thr Gln					

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Tyr	Ala	Val	Tyr	Val	Lys	Ala	Val	Thr	Leu	Thr	Met	Val	Glu	Asn	Asp
			580					585					590		
His	Ile	Arg	Gly	Ala	Lys	Ser	Glu	Ile	Leu	Tyr	Ile	Arg	Thr	Asn	Ala
			595				600					605			
Ser	Val	Pro	Ser	Ile	Pro	Leu	Asp	Val	Leu	Ser	Ala	Ser	Asn	Ser	Ser
			610				615				620				
Ser	Gln	Leu	Ile	Val	Lys	Trp	Asn	Pro	Pro	Ser	Leu	Pro	Asn	Gly	Asn
625					630					635				640	
Leu	Ser	Tyr	Tyr	Ile	Val	Arg	Trp	Gln	Arg	Gln	Pro	Gln	Asp	Ser	Tyr
				645				650					655		
Leu	Tyr	Arg	His	Asn	Tyr	Cys	Ser	Lys	Asp	Lys	Ile	Pro	Ile	Arg	Lys
			660					665				670			
Tyr	Ala	Asp	Gly	Thr	Ile	Asp	Val	Glu	Glu	Val	Thr	Glu	Asn	Pro	Lys
		675					680					685			
Thr	Glu	Val	Cys	Gly	Gly	Glu	Lys	Gly	Pro	Cys	Cys	Ala	Cys	Pro	Lys
		690				695					700				
Thr	Glu	Ala	Glu	Lys	Gln	Ala	Glu	Lys	Glu	Glu	Ala	Glu	Tyr	Arg	Lys
705					710				715				720		
Val	Phe	Glu	Asn	Phe	Leu	His	Asn	Ser	Ile	Phe	Val	Pro	Arg	Pro	Glu

735

750

765

780

800

815

830

845

860

880

Ser Arg Gln Glu Tyr Arg Lys Tyr Gly Gly Ala Lys Leu Ser Arg Leu

	885		890		895										
Asn	Pro	Gly	Asn	Tyr	Thr	Ala	Arg	Ile	Gln	Ala	Thr	Ser	Leu	Ser	Gly
	900		905		910										
Asn	Gly	Ser	Trp	Thr	Asp	Pro	Val	Phe	Phe	Tyr	Val	Pro	Ala	Lys	Thr
	915		920		925										
Thr	Tyr	Glu	Asn	Phe	Ile	His	Leu	Ile	Ile	Ala	Leu	Pro	Val	Ala	Ile
	930		935		940										
Leu	Leu	Ile	Val	Ala	Gly	Leu	Ala	Ile	Met	Leu	Tyr	Val	Phe	His	Arg
	945		950		955										
Lys	Arg	Asn	Ser	Ser	Arg	Leu	Gly	Asn	Gly	Val	Leu	Tyr	Ala	Ser	Val
			965		970									975	
Asn	Pro	Glu	Tyr	Phe	Ser	Ala	Ala	Asp	Val	Tyr	Val	Pro	Asp	Glu	Trp
	980		985		990										
Glu	Val	Ala	Arg	Glu	Lys	Ile	Thr	Met	Ser	Arg	Glu	Leu	Gly	Gln	Gly
	995		1000		1005										
Ser	Phe	Gly	Met	Val	Tyr	Glu	Gly	Val	Ala	Lys	Gly	Val	Val	Lys	
	1010		1015		1020										
Asp	Glu	Pro	Glu	Thr	Arg	Val	Ala	Ile	Lys	Thr	Val	Asn	Glu	Ala	
	1025		1030		1035										
Ala	Ser	Met	Arg	Glu	Arg	Ile	Glu	Phe	Leu	Asn	Glu	Ala	Ser	Val	

1040		1045		1050
Met Lys Glu Phe Asn Cys His	His Val Val Arg Leu	Leu Gly Val		
1055	1060	1065		
Val Ser Gln Gly Gln Pro Thr	Leu Val Ile Met Glu	Leu Met Thr		
1070	1075	1080		
Arg Gly Asp Leu Lys Ser Tyr	Leu Arg Ser Leu Arg	Pro Glu Val		
1085	1090	1095		
Glu Asn Ser Pro Ile Leu Ala	Pro Pro Ser Leu Ser	Lys Met Ile		
1100	1105	1110		
Gln Met Ala Gly Glu Ile Ala	Asp Gly Met Ala Tyr	Leu Asn Ala		
1115	1120	1125		
Asn Lys Phe Val His Arg Asp	Leu Ala Ala Arg Asn	Cys Met Val		
1130	1135	1140		
Ala Glu Asp Phe Thr Val Lys	Ile Gly Asp Phe Gly	Met Thr Arg		
1145	1150	1155		
Asp Ile Tyr Glu Thr Asp Tyr	Tyr Arg Lys Gly Gly	Lys Gly Leu		
1160	1165	1170		
Leu Pro Val Arg Trp Met Ser	Pro Glu Ser Leu Lys	Asp Gly Val		
1175	1180	1185		
Phe Thr Thr His Ser Asp Val	Trp Ser Phe Gly Val	Val Leu Trp		

1190		1195		1200
Glu Ile Ala Thr Leu Ala Glu Gln Pro Tyr Gln Gly Leu Ser Asn				
1205		1210		1215
Glu Gln Val Leu Arg Phe Val Met Glu Gly Gly Leu Leu Asp Lys				
1220		1225		1230
Pro Asp Asn Cys Pro Asp Met Leu Phe Glu Leu Met Arg Met Cys				
1235		1240		1245
Trp Gln Tyr Asn Pro Lys Met Arg Pro Ser Phe Leu Glu Ile Ile				
1250		1255		1260
Ser Ser Val Lys Asp Glu Leu Glu Ala Gly Phe Arg Glu Val Ser				
1265		1270		1275
Phe Tyr Tyr Ser Glu Glu Asn Lys Pro Pro Glu Pro Glu Glu Leu				
1280		1285		1290
Asp Leu Glu Pro Glu Asn Met Glu Ser Val Pro Leu Asp Pro Ser				
1295		1300		1305
Ala Ser Ser Ser Ser Leu Pro Pro Pro Asp Arg His Ser Gly His				
1310		1315		1320
Lys Gly Glu Asn Gly Pro Gly Pro Gly Val Leu Val Leu Arg Ala				
1325		1330		1335
Ser Phe Asp Glu Arg Gln Pro Tyr Ala His Met Asn Gly Gly Arg				

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<210> 78
 <211> 4104
 <212> DNA
 <213> *Cavia porcellus*

<220>
 <223> *Cavia porcellus* IGF-I receptor

<400> 78

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<210> 79

<211> 1371

<212> PRT

<213> Rattus norvegicus

<220>

<223> Rattus norvegicus IGF-I receptor

<400> 79

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Val Phe Leu Ser Ala Ala Leu Ser Leu Trp Pro Thr Ser Gly Glu Ile
20 25 30

Cys Gly Pro Gly Ile Asp Ile Arg Asn Asp Tyr Gln Gln Leu Lys Arg
35 40 45

Leu Glu Asn Cys Thr Val Ile Glu Gly Phe Leu His Ile Leu Leu Ile
50 55 60

Ser Lys Ala Glu Asp Tyr Arg Ser Tyr Arg Phe Pro Lys Leu Thr Val
65 70 75 80

Ile Thr Glu Tyr Leu Leu Leu Phe Arg Val Ala Gly Leu Glu Ser Leu
85 90 95

Gly Asp Leu Phe Pro Asn Leu Thr Val Ile Arg Gly Trp Lys Leu Phe
100 105 110

Tyr Asn Tyr Ala Leu Val Ile Phe Glu Met Thr Asn Leu Lys Asp Ile
115 120 125

Gly Leu Tyr Asn Leu Arg Asn Ile Thr Arg Gly Ala Ile Arg Ile Glu
130 135 140

Lys Asn Ala Asp Leu Cys Tyr Leu Ser Thr Ile Asp Trp Ser Leu Ile
145 150 155 160

Leu Asp Ala Val Ser Asn Asn Tyr Ile Val Gly Asn Lys Pro Pro Lys
165 170 175

Glu Cys Gly Asp Leu Cys Pro Gly Thr Leu Glu Glu Lys Pro Met Cys
180 185 190

Glu Lys Thr Thr Ile Asn Asn Glu Tyr Asn Tyr Arg Cys Trp Thr Thr
195 200 205

Asn Arg Cys Gln Lys Met Cys Pro Ser Val Cys Gly Lys Arg Ala Cys
210 215 220

Thr Glu Asn Asn Glu Cys Cys His Pro Glu Cys Leu Gly Ser Cys His
225 230 235 240

Thr Pro Asp Asp Asn Thr Thr Cys Val Ala Cys Arg His Tyr Tyr Tyr
245 250 255

Lys Gly Val Cys Val Pro Ala Cys Pro Pro Gly Thr Tyr Arg Phe Glu
260 265 270

Gly Trp Arg Cys Val Asp Arg Asp Phe Cys Ala Asn Ile Pro Asn Ala
275 280 285

Glu Ser Ser Asp Ser Asp Gly Phe Val Ile His Asp Gly Glu Cys Met
290 295 300

Gln Glu Cys Pro Ser Gly Phe Ile Arg Asn Ser Thr Gln Ser Met Tyr
305 310 315 320

Cys Ile Pro Cys Glu Gly Pro Cys Pro Lys Val Cys Gly Asp Glu Glu
325 330 335

Lys Lys Thr Lys Thr Ile Asp Ser Val Thr Ser Ala Gln Met Leu Gln
340 345 350

Gly Cys Thr Ile Leu Lys Gly Asn Leu Leu Ile Asn Ile Arg Arg Gly
355 360 365

Asn Asn Ile Ala Ser Glu Leu Glu Asn Phe Met Gly Leu Ile Glu Val
370 375 380

Val Thr Gly Tyr Val Lys Ile Arg His Ser His Ala Leu Val Ser Leu
385 390 395 400

Ser Phe Leu Lys Asn Leu Arg Leu Ile Leu Gly Glu Glu Gln Leu Glu
405 410 415

Gly Asn Tyr Ser Phe Tyr Val Leu Asp Asn Gln Asn Leu Gln Gln Leu
420 425 430

Trp Asp Trp Asn His Arg Asn Leu Thr Val Arg Ser Gly Lys Met Tyr
435 440 445

Phe Ala Phe Asn Pro Lys Leu Cys Val Ser Glu Ile Tyr Arg Met Glu
450 455 460

Glu Val Thr Gly Thr Lys Gly Arg Gln Ser Lys Gly Asp Ile Asn Thr
465 470 475 480

Arg Asn Asn Gly Glu Arg Ala Ser Cys Glu Ser Asp Val Leu Arg Phe
485 490 495

Thr Ser Thr Thr Thr Trp Lys Asn Arg Ile Ile Ile Thr Trp His Arg
500 505 510

Tyr Arg Pro Pro Asp Tyr Arg Asp Leu Ile Ser Phe Thr Val Tyr Tyr
515 520 525

Lys Glu Ala Pro Phe Lys Asn Val Thr Glu Tyr Asp Gly Gln Asp Ala
530 535 540

Cys Gly Ser Asn Ser Trp Asn Met Val Asp Val Asp Leu Pro Pro Asn
545 550 555 560

Lys Glu Gly Glu Pro Gly Ile Leu Leu His Gly Leu Lys Pro Trp Thr
565 570 575

Gln Tyr Ala Val Tyr Val Lys Ala Val Thr Leu Thr Met Val Glu Asn
580 585 590

Asp His Ile Arg Gly Ala Lys Ser Glu Ile Leu Tyr Ile Arg Thr Asn
595 600 605

Ala Ser Val Pro Ser Ile Pro Leu Asp Val Leu Ser Ala Ser Asn Ser
610 615 620

Ser Ser Gln Leu Ile Val Lys Trp Asn Pro Pro Thr Leu Pro Asn Gly
625 630 635 640

Asn Leu Ser Tyr Tyr Ile Val Arg Trp Gln Arg Gln Pro Gln Asp Gly
645 650 655

Tyr Leu Phe Arg His Asn Tyr Cys Ser Lys Asp Lys Ile Pro Ile Arg
660 665 670

Lys Tyr Ala Asp Gly Thr Ile Asp Val Glu Glu Val Thr Glu Asn Pro
675 680 685

Lys Thr Glu Val Cys Gly Gly Asp Lys Gly Pro Cys Cys Ala Cys Pro
690 695 700

Lys Thr Glu Ala Glu Lys Gln Ala Glu Lys Glu Glu Ala Glu Tyr Arg
705 710 715 720

Lys Val Phe Glu Asn Phe Leu His Asn Ser Ile Phe Val Pro Arg Pro
725 730 735

Glu Arg Arg Arg Arg Asp Val Leu Gln Val Ala Asn Thr Thr Met Ser
740 745 750

Ser Arg Ser Arg Asn Thr Thr Val Ala Asp Thr Tyr Asn Ile Thr Asp
755 760 765

Pro Glu Glu Phe Glu Thr Glu Tyr Pro Phe Phe Glu Ser Arg Val Asp
770 775 780

Asn Lys Glu Arg Thr Val Ile Ser Asn Leu Arg Pro Phe Thr Leu Tyr
785 790 795 800

Arg Ile Asp Ile His Ser Cys Asn His Glu Ala Glu Lys Leu Gly Cys
805 810 815

Ser Ala Ser Asn Phe Val Phe Ala Arg Thr Met Pro Ala Glu Gly Ala
820 825 830

Asp Asp Ile Pro Gly Pro Val Thr Trp Glu Pro Arg Pro Glu Asn Ser
835 840 845

Ile Phe Leu Lys Trp Pro Glu Pro Glu Asn Pro Asn Gly Leu Ile Leu
850 855 860

Met Tyr Glu Ile Lys Tyr Gly Ser Gln Val Glu Asp Gln Arg Glu Cys
865 870 875 880

Val Ser Arg Gln Glu Tyr Arg Lys Tyr Gly Gly Ala Lys Leu Asn Arg
885 890 895

Leu Asn Pro Gly Asn Tyr Thr Ala Arg Ile Gln Ala Thr Ser Leu Ser
900 905 910

Gly Asn Gly Ser Trp Thr Asp Pro Val Phe Phe Tyr Val Pro Ala Lys
915 920 925

Thr Thr Tyr Glu Asn Phe Met His Leu Ile Ile Ala Leu Pro Val Ala
930 935 940

Ile Leu Leu Ile Val Gly Gly Leu Val Ile Met Leu Tyr Val Phe His
945 950 955 960

Arg Lys Arg Asn Asn Ser Arg Leu Gly Asn Gly Val Leu Tyr Ala Ser
965 970 975

Val Asn Pro Glu Tyr Phe Ser Ala Ala Asp Val Tyr Val Pro Asp Glu
980 985 990

Trp Glu Val Ala Arg Glu Lys Ile Thr Met Asn Arg Glu Leu Gly Gln
995 1000 1005

Gly Ser Phe Gly Met Val Tyr Glu Gly Val Ala Lys Gly Val Val
1010 1015 1020

Lys Asp Glu Pro Glu Thr Arg Val Ala Ile Lys Thr Val Asn Glu
1025 1030 1035

Ala Ala Ser Met Arg Glu Arg Ile Glu Phe Leu Asn Glu Ala Ser
1040 1045 1050

Val Met Lys Glu Phe Asn Cys His His Val Val Arg Leu Leu Gly
1055 1060 1065

Val Val Ser Gln Gly Gln Pro Thr Leu Val Ile Met Glu Leu Met
1070 1075 1080

Thr Arg Gly Asp Leu Lys Ser Tyr Leu Arg Ser Leu Arg Pro Glu
1085 1090 1095

Val Glu Gln Asn Asn Leu Val Leu Ile Pro Pro Ser Leu Ser Lys
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Met Ile Gln Met Ala Gly Glu Ile Ala Asp Gly Met Ala Tyr Leu
1115 1120 1125

Asn Ala Asn Lys Phe Val His Arg Asp Leu Ala Ala Arg Asn Cys
1130 1135 1140

Met Val Ala Glu Asp Phe Thr Val Lys Ile Gly Asp Phe Gly Met
1145 1150 1155

Thr Arg Asp Ile Tyr Glu Thr Asp Tyr Tyr Arg Lys Gly Gly Lys
1160 1165 1170

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Gly Val Phe Thr Thr His Ser Asp Val Trp Ser Phe Gly Val Val
1190 1195 1200

Leu Trp Glu Ile Ala Thr Leu Ala Glu Gln Pro Tyr Gln Gly Leu
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Ser Asn Glu Gln Val Leu Arg Phe Val Met Glu Gly Gly Leu Leu
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Asp Lys Pro Asp Asn Cys Pro Asp Met Leu Phe Glu Leu Met Arg
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Met Cys Trp Gln Tyr Asn Pro Lys Met Arg Pro Ser Phe Leu Glu
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Ile Ile Gly Ser Ile Lys Asp Glu Met Glu Pro Ser Phe Gln Glu
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Val Ser Phe Tyr Tyr Ser Glu Glu Asn Lys Pro Pro Glu Pro Glu
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Val Pro Leu Asp Pro Ser Ala Ser Ser Ala Ser Leu Pro Leu Pro
1310 1315 1320

Glu Arg His Ser Gly His Lys Ala Glu Asn Gly Pro Gly Val Leu
1325 1330 1335

Val Leu Arg Ala Ser Phe Asp Glu Arg Gln Pro Tyr Ala His Met
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Asn Gly Gly Arg Ala Asn Glu Arg Ala Leu Pro Leu Pro Gln Ser
1355 1360 1365

Ser Thr Cys
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<210> 80

<211> 4116

<212> DNA

<213> Rattus norvegicus

<220>

<223> Rattus norvegicus IGF-I receptor

<400> 80

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<211> 1373

<212> PRT

<213> Mus musculus

<220>

<223> Mus musculus IGF-I receptor

<400> 81

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Cys Gly Pro Gly Ile Asp Ile Arg Asn Asp Tyr Gln Gln Leu Lys Arg
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Leu Glu Asn Cys Thr Val Ile Glu Gly Phe Leu His Ile Leu Leu Ile
 50 55 60

Ser Lys Ala Glu Asp Tyr Arg Ser Tyr Arg Phe Pro Lys Leu Thr Val
65 70 75 80

Ile Thr Glu Tyr Leu Leu Leu Phe Arg Val Ala Gly Leu Glu Ser Leu
 85 90 95

Gly Asp Leu Phe Pro Asn Leu Thr Val Ile Arg Gly Trp Lys Leu Phe
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Tyr Asn Tyr Ala Leu Val Ile Phe Glu Met Thr Asn Leu Lys Asp Ile
 115 120 125

Gly Leu Tyr Asn Leu Arg Asn Ile Thr Arg Gly Ala Ile Arg Ile Glu
 130 135 140

Lys Asn Ala Asp Leu Cys Tyr Leu Ser Thr Ile Asp Trp Ser Leu Ile
145 150 155 160

Leu Asp Ala Val Ser Asn Asn Tyr Ile Val Gly Asn Lys Pro Pro Lys
 165 170 175

Glu Cys Gly Asp Leu Cys Pro Gly Thr Leu Glu Glu Lys Pro Met Cys

Lys Lys Thr Lys Thr Ile Asp Ser Val Thr Ser Ala Gln Met Leu Gln

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Val	Thr	Gly	Tyr	Val	Lys
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Leu	Val	Ser	Leu		
	395				
	400				
Ser	Phe	Leu	Lys	Asn	Leu
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Arg	Leu	Ile	Leu	Gly	Glu
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Gln	Leu	Glu			
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Gly	Asn	Tyr	Ser	Phe	Tyr
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Val	Leu	Asp	Asn	Gln	Asn
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Leu	Gln	Gln	Leu		
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Trp	Asp	Trp	Asn	His	Arg
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Gly	Lys	Met	Tyr		
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Tyr	Arg	Met	Glu		
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Glu	Val	Thr	Gly	Thr	Lys
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Asp	Ile	Asn	Thr		
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Ala	Ser	Cys	Glu	Ser	Asp
	490				
Val	Leu	Arg	Phe		
	495				
Thr	Ser	Thr	Thr	Thr	Trp
Lys	Asn	Arg	Ile	Ile	Ile
Thr	Trp	His	Arg		

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Tyr	Arg	Pro	Pro	Asp	Tyr	Arg	Asp	Leu	Ile	Ser	Phe	Thr	Val	Tyr	Tyr
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Lys	Glu	Ala	Pro	Phe	Lys	Asn	Val	Thr	Glu	Tyr	Asp	Gly	Gln	Asp	Ala
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Cys	Gly	Ser	Asn	Ser	Trp	Asn	Met	Val	Asp	Val	Asp	Leu	Pro	Pro	Asn
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Lys	Glu	Gly	Glu	Pro	Gly	Ile	Leu	Leu	His	Gly	Leu	Lys	Pro	Trp	Thr
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Gln	Tyr	Ala	Val	Tyr	Val	Lys	Ala	Val	Thr	Leu	Thr	Met	Val	Glu	Asn
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Asp	His	Ile	Arg	Gly	Ala	Lys	Ser	Glu	Ile	Leu	Tyr	Ile	Arg	Thr	Asn
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Ala	Ser	Val	Pro	Ser	Ile	Pro	Leu	Asp	Val	Leu	Ser	Ala	Ser	Asn	Ser
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Ser	Ser	Gln	Leu	Ile	Val	Lys	Trp	Asn	Pro	Pro	Thr	Leu	Pro	Asn	Gly
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Asn	Leu	Ser	Tyr	Tyr	Ile	Val	Arg	Trp	Gln	Arg	Gln	Pro	Gln	Asp	Gly
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Tyr	Leu	Tyr	Arg	His	Asn	Tyr	Cys	Ser	Lys	Asp	Lys	Ile	Pro	Ile	Arg

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Lys Thr Glu Val Cys Gly Gly Asp Lys Gly Pro Cys Cys Ala Cys Pro		
690	695	700
Lys Thr Glu Ala Glu Lys Gln Ala Glu Lys Glu Glu Ala Glu Tyr Arg		
705	710	715
Lys Val Phe Glu Asn Phe Leu His Asn Ser Ile Phe Val Pro Arg Pro		
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Glu Arg Arg Arg Arg Asp Val Met Gln Val Ala Asn Thr Thr Met Ser		
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Ser Arg Ser Arg Asn Thr Thr Val Ala Asp Thr Tyr Asn Ile Thr Asp		
755	760	765
Pro Glu Glu Phe Glu Thr Glu Tyr Pro Phe Phe Glu Ser Arg Val Asp		
770	775	780
Asn Lys Glu Arg Thr Val Ile Ser Asn Leu Arg Pro Phe Thr Leu Tyr		
785	790	795
Arg Ile Asp Ile His Ser Cys Asn His Glu Ala Glu Lys Leu Gly Cys		
805	810	815
Ser Ala Ser Asn Phe Val Phe Ala Arg Thr Met Pro Ala Glu Gly Ala		

	820		825		830										
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Ile	Leu	Leu	Ile	Val	Gly	Gly	Leu	Val	Ile	Met	Leu	Tyr	Val	Phe	His
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Val Met Lys Glu Phe Asn Cys His His Val Val Arg Leu Leu Gly		
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Val Val Ser Gln Gly Gln Pro Thr Leu Val Ile Met Glu Leu Met		
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Thr Arg Gly Asp Leu Lys Ser Tyr Leu Arg Ser Leu Arg Pro Glu		
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Val Glu Gln Asn Asn Leu Val Leu Ile Pro Pro Ser Leu Ser Lys		
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Thr Arg Asp Ile Tyr Glu Thr	Asp Tyr Tyr Arg Lys	Gly Gly Lys		
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Gly Leu Leu Pro Val Arg Trp	Met Ser Pro Glu Ser	Leu Lys Asp		
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Ser Asn Glu Gln Val Leu Arg	Phe Val Met Glu Gly	Gly Leu Leu		
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Met Cys Trp Gln Tyr Asn Pro	Lys Met Arg Pro Ser	Phe Leu Glu		
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Val Ser Phe Tyr Tyr Ser Glu	Glu Asn Lys Pro Pro	Glu Pro Glu		

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Glu Arg His Ser Gly His Lys Ala Glu Asn Gly Pro Gly Pro Gly				
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Val Leu Val Leu Arg Ala Ser Phe Asp Glu Arg Gln Pro Tyr Ala				
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 <213> Mus musculus

<220>
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<211> 70

<212> PRT

<213> Homo sapiens

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<223> IGF-I

<400> 83

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Phe Arg Ser Cys Asp Leu Arg Arg Leu Glu Met Tyr Cys Ala Pro Leu
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Lys Pro Ala Lys Ser Ala
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<400> 85

Ser Tyr Trp Met His
1 5

<210> 86
<211> 17
<212> PRT
<213> Mus musculus

<220>

<223> IGF11-16 CDR-H2

<400> 86

Glu	Thr	Asn	Pro	Ser	Asn	Ser	Val	Thr	Asn	Tyr	Asn	Glu	Lys	Phe	Lys
1				5					10					15	

Ser

<210> 87

<211> 8

<212> PRT

<213> Mus musculus

<220>

<223> IGF11-16 CDR-H3

<400> 87

Gly	Arg	Gly	Arg	Gly	Phe	Ala	Tyr
1				5			

<210> 88

<211> 11

<212> PRT

<213> Mus musculus

<220>

<223> IGF11-16 CDR-L1

<400> 88

Arg	Ala	Ser	Gln	Asn	Ile	Asn	Phe	Trp	Leu	Ser
1				5				10		

<210> 89
<211> 7
<212> PRT
<213> Mus musculus

<220>
<223> IGF11-16 CDR-L2

<400> 89

Lys Ala Ser Asn Leu His Thr
1 5

<210> 90
<211> 9
<212> PRT
<213> Mus musculus

<220>
<223> IGF11-16 CDR-L3

<400> 90

Leu Gln Gly Gln Ser Tyr Pro Tyr Thr
1 5

<210> 91
<211> 234
<212> PRT
<213> Mus musculus

<220>
<223> IGF11-16 Light chain

<400> 91

Met Lys Leu Leu Ala Glu Leu Leu Gly Leu Leu Leu Phe Cys Phe Leu
1 5 10 15

Gly Val Arg Cys Asp Ile Gln Met Asn Gln Ser Pro Ser Ser Leu Ser
20 25 30

Ala Ser Leu Gly Asp Thr Ile Thr Ile Thr Cys Arg Ala Ser Gln Asn
35 40 45

Ile Asn Phe Trp Leu Ser Trp Cys Gln Gln Lys Pro Gly Asn Ile Pro
50 55 60

Lys Leu Leu Ile Tyr Lys Ala Ser Asn Leu His Thr Gly Val Pro Ser
65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
85 90 95

Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Leu Gln Gly Gln
100 105 110

Ser Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
115 120 125

Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln
130 135 140

Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr
145 150 155 160

Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln
165 170 175

Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr
180 185 190

Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg
195 200 205

His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro
210 215 220

Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
225 230

<210> 92

<211> 705

<212> DNA

<213> Mus musculus

<220>

<223> IGF11-16 Light chain

<400> 92

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atcacttgcc gtgccagtca gaacattaat ttttggttaa gctggtgcca gcagaaacca 180

ggaaatattc ctaaaactatt gatctataag gcttccaact tgcacacagg cgtcccatca 240

aggtttagtg gcagtggatc tggaacagat ttacattaa ccatcagcag totgcagcct 300

gaagacattg ccacttacta ctgtctacag ggtcaaagtt atccgtacac gttoggaggg 360

gggaccaagc tggaaataaa acgggctgat gctgcaccaa ctgtatccat cttoaccacca	420
tccagtgagc agttaacatc tggaggtgcc tcagtcgtgt gcttcttgaa caacttctac	480
cccaaagaca tcaatgtcaa gtggaagatt gatggcagtg aacgacaaaa tggcgtcctg	540
aacagttgga ctgatcagga cagcaaagac agcacctaca gcatgagcag caccctcacg	600
ttgaccaagg acgagtatga acgacataac agctatacct gtgaggccac tcacaagaca	660
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<210> 93

<211> 460

<212> PRT

<213> Mus musculus

<220>

<223> IGF11-16 Heavy chain

<400> 93

Met	Gly	Trp	Ser	Tyr	Ile	Ile	Leu	Phe	Leu	Val	Ala	Thr	Val	Thr	Asp
1				5					10					15	

Val	His	Ser	Gln	Ile	Gln	Leu	Gln	Gln	Pro	Gly	Ala	Glu	Leu	Val	Lys
			20				25						30		

Pro	Gly	Ala	Ser	Val	Lys	Leu	Ser	Cys	Lys	Ala	Pro	Gly	Tyr	Thr	Phe
		35					40					45			

Thr	Ser	Tyr	Trp	Met	His	Trp	Val	Lys	Gln	Arg	Pro	Gly	Gln	Gly	Leu
	50					55					60				

Glu Trp Ile Gly Glu Thr Asn Pro Ser Asn Ser Val Thr Asn Tyr Asn
65 70 75 80

Glu Lys Phe Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser
85 90 95

Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
100 105 110

Tyr Tyr Cys Thr Ile Gly Arg Gly Arg Gly Phe Ala Tyr Trp Gly Gln
115 120 125

Gly Thr Leu Val Thr Val Ser Ala Ala Lys Thr Thr Pro Pro Ser Val
130 135 140

Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr
145 150 155 160

Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr
165 170 175

Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val
180 185 190

Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser
195 200 205

Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His Pro Ala
210 215 220

Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly Cys
225 230 235 240

Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe Ile Phe
245 250 255

Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val
260 265 270

Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu Val Gln Phe
275 280 285

Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr Gln Pro
290 295 300

Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu Pro
305 310 315 320

Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys Arg Val
325 330 335

Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr
340 345 350

Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro Pro Lys
355 360 365

Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met Ile Thr Asp
370 375 380

Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Ala Gln Pro
 385 390 395 400

Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr Asp Gly Ser
 405 410 415

Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn Trp Glu Ala
 420 425 430

Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn His
 435 440 445

His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys
 450 455 460

<210> 94

<211> 1383

<212> DNA

<213> Mus musculus

<220>

<223> IGF11-16 Heavy chain

<400> 94

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tgcaaggctc ccggctacac cttcaccago tatttgatgc actgggtgaa gcagaggcct 180

ggacaaggcc ttgagtggat tggagagact aatcctagca atagtgttac taactacaat 240

gagaagttca agagcaaggc cacactgact gtagacaaat cctccagcac agcctacatg 300

caactcagca gcctgacatc tgaggactct gcggtctatt actgtacaat agggagggga 360

cggggatttg cttactgggg ccaagggact ctggtcactg tctctgcagc caaaacgaca	420
cccccatctg tctatccact ggcccctgga tctgctgccc aaactaactc catggtgacc	480
ctgggatgcc tggtaaggg ctatttccct gagccagtga cagtgcctg gaactctgga	540
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cagacgcaac cccgggagga gcagttcaac agcactttcc gctcagtcag tgaacttccc	960
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gcgggagaact acaagaacac tcagcccatc atggacacag atggctctta ctctgtctac	1260
agcaagctca atgtgcagaa gagcaactgg gaggcaggaa atactttcac ctgctctgtg	1320
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tga	1383

<210> 95

<211> 98

<212> PRT

<213> Homo sapiens

<220>

<223> VH-1-46

<400> 95

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 Ser Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg

<210> 96

<211> 98

<212> PRT

<213> Homo sapiens

<220>

<223> VH-1-e

<400> 96

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

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

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg

<210> 97

<211> 15

<212> PRT

<213> Homo sapiens

<220>

<223> JH4

<400> 97

Tyr	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser
1				5					10					15

<210> 98

<211> 95

<212> PRT

<213> Homo sapiens

<220>

<223> VK1-L5

<400> 98

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Val	Ser	Ala	Ser	Val	Gly
1				5					10						15

Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Gly	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	Ala	Ala	Ser	Ser	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
	50					55					60				

Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro
65					70					75					80

Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Ala	Asn	Ser	Phe	Pro
				85					90					95

<210> 99
<211> 95
<212> PRT
<213> Homo sapiens

<220>
<223> VK1-A20

<400> 99

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 Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe 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 Val Ala Thr Tyr Tyr Cys Gln Lys Tyr Asn Ser Ala Pro
85 90 95

<210> 100
<211> 12
<212> PRT
<213> Homo sapiens

<220>

<223> JK2

<400> 100

Tyr	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Leu	Glu	Ile	Lys
1				5					10		