SEQUENCE LISTING

<110> Mark, Chiu
Sheri, Moores
Joost, Neijssen
Paul, Parren
Janine, Schuuman

<120> Bispecific EGFR/c-Met Antibodies

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<151> 2013-03-14

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<151> 2013-04-08

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<170> PatentIn version 3.5

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Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Asn Leu Thr
35 40 45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
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20 25 30

Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Asn Leu Thr
35 40 45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
50 55 60

Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys Asp
65 70 75 80

Thr Asn Met Arg Gly Leu Pro Leu Ser Ala Glu Phe Thr Thr
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Leu Arg Leu Ser Trp Thr Tyr Asp Arg Asp Gly Tyr Asp Ser Phe Leu
20 25 30

Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Asn Leu Thr
35 40 45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
50 55 60

Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys Asp
65 70 75 80

Thr Asn Met Arg Gly Leu Pro Leu Ser Ala Glu Phe Thr Thr
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Leu Arg Leu Ser Trp Gly Tyr Asn Gly Asp His Phe Asp Ser Phe Leu
20 25 30

Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Asn Leu Thr
35 40 45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
50 55 60

Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys Asp
65 70 75 80

Thr Asn Met Arg Gly Leu Pro Leu Ser Ala Glu Phe Thr Thr
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Leu Arg Leu Ser Trp Asp Asp Pro Arg Gly Phe Tyr Glu Ser Phe Leu
20 25 30

Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Asn Leu Thr
35 40 45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
50 55 60

Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys Asp
65 70 75 80

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Leu Arg Leu Ser Trp Thr Trp Pro Tyr Ala Asp Leu Asp Ser Phe Leu
20 25 30

Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Asn Leu Thr
35 40 45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
50 55 60

Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys Asp
65 70 75 80

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

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
50 55 60

Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys Asp
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Leu Arg Leu Ser Trp Asp Tyr Asp Leu Gly Val Tyr Phe Asp Ser Phe
20 25 30

Leu Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Asn Leu
35 40 45

Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro
50 55 60

Gly Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys
65 70 75 80

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

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
50 55 60

Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys Asp
65 70 75 80

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

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
50 55 60

Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val Leu Gly Ser Tyr Val Phe
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Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu Thr
35 40 45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
50 55 60

Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys Asp
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Thr Asn Met Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr
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20 25 30

Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu Thr
35 40 45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
50 55 60

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

Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Asn Leu Thr
35 40 45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
50 55 60

Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys Asp
65 70 75 80

Thr Asn Met Arg Gly Leu Pro Leu Ser Ala Glu Phe Thr Thr
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Ala Thr Gly Cys Thr Gly Cys Cys Gly Gly Cys Gly Cys Cys Gly Ala
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Ala Ala Ala Ala Cys
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Thr Thr Thr Ala Ala Thr Gly Gly Thr Gly Ala Thr Gly Gly Thr Gly
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Ala Thr Gly Gly Thr Gly Ala Cys Cys Ala Cys Cys Gly Gly Thr Gly
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Gly Thr Gly Ala Ala Gly Ala Thr Cys Gly Cys Ala Gly Ala Cys Ala
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20 25 30

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35 40 45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
50 55 60

Thr Glu Tyr Tyr Val Asn Ile Leu Gly Val Lys Gly Gly Ser Ile Ser
65 70 75 80

Val Pro Leu Ser Ala Ile Phe Thr Thr
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20 25 30

Ile Arg Tyr Asp Glu Phe Leu Arg Ser Gly Glu Ala Ile Val Leu Thr
35 40 45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
50 55 60

Thr Glu Tyr Trp Val Thr Ile Leu Gly Val Lys Gly Gly Leu Val Ser
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20 25 30

Ile Arg Tyr Phe Glu Phe Leu Gly Ser Gly Glu Ala Ile Val Leu Thr
35 40 45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
50 55 60

Thr Glu Tyr Ile Val Asn Ile Met Gly Val Lys Gly Gly Ser Ile Ser
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20 25 30

Ile Arg Tyr Phe Glu Phe Leu Gly Ser Gly Glu Ala Ile Val Leu Thr
35 40 45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
50 55 60

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35 40 45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
50 55 60

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Ile Pro Leu Ser Ala Ile Phe Thr Thr
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35 40 45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
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35 40 45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
50 55 60

Thr Glu Tyr Val Val Gly Ile Asn Gly Val Lys Gly Gly Tyr Ile Ser
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Tyr Pro Leu Ser Ala Ile Phe Thr Thr
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<223> c-Met binding FN3 domain

<400> 39

Leu Pro Ala Pro Lys Asn Leu Val Val Ser Arg Val Thr Glu Asp Ser
1 5 10 15

Ala Arg Leu Ser Trp Thr Ala Pro Asp Ala Ala Phe Asp Ser Phe Trp
20 25 30

Ile Arg Tyr Phe Glu Phe Leu Gly Ser Gly Glu Ala Ile Val Leu Thr
35 40 45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Asp Leu Lys Pro Gly
50 55 60

Thr Glu Tyr Gly Val Thr Ile Asn Gly Val Lys Gly Gly Arg Val Ser
65 70 75 80

Thr Pro Leu Ser Ala Ile Phe Thr Thr
85

<210> 40
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> c-Met binding FN3 domain

<400> 40

Leu Pro Ala Pro Lys Asn Leu Val Val Ser Arg Val Thr Glu Asp Ser
1 5 10 15

Ala Arg Leu Ser Trp Thr Ala Pro Asp Ala Ala Phe Asp Ser Phe Trp
20 25 30

Ile Arg Tyr Phe Glu Phe Leu Gly Ser Gly Glu Ala Ile Val Leu Thr
35 40 45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
50 55 60

Thr Glu Tyr Val Val Gln Ile Ile Gly Val Lys Gly Gly His Ile Ser
65 70 75 80

Leu Pro Leu Ser Ala Ile Phe Thr Thr
85

<210> 41
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> c-Met binding FN3 domain

<400> 41

Leu Pro Ala Pro Lys Asn Leu Val Val Ser Arg Val Thr Glu Asp Ser
1 5 10 15

Ala Arg Leu Ser Trp Thr Ala Pro Asp Ala Ala Phe Asp Ser Phe Trp
20 25 30

Ile Arg Tyr Phe Glu Phe Leu Gly Ser Gly Glu Ala Ile Val Leu Thr
35 40 45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
50 55 60

Thr Glu Tyr Val Val Asn Ile Met Gly Val Lys Gly Gly Lys Ile Ser
65 70 75 80

Pro Pro Leu Ser Ala Ile Phe Thr Thr
85

<210> 42
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> c-Met binding FN3 domain

<400> 42

Leu Pro Ala Pro Lys Asn Leu Val Val Ser Arg Val Thr Glu Asp Ser
1 5 10 15

Ala Arg Leu Ser Trp Thr Ala Pro Asp Ala Ala Phe Asp Ser Phe Trp
20 25 30

Ile Arg Tyr Phe Glu Phe Leu Gly Ser Gly Glu Ala Ile Val Leu Thr
35 40 45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
50 55 60

Thr Glu Tyr Ala Val Asn Ile Met Gly Val Lys Gly Gly Arg Val Ser
65 70 75 80

Val Pro Leu Ser Ala Ile Phe Thr Thr
85

<210> 43
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> c-Met binding FN3 domain

<400> 43

Leu Pro Ala Pro Lys Asn Leu Val Val Ser Arg Val Thr Glu Asp Ser
1 5 10 15

Ala Arg Leu Ser Trp Thr Ala Pro Asp Ala Ala Phe Asp Ser Phe Trp
20 25 30

Ile Arg Tyr Phe Glu Phe Leu Gly Ser Gly Glu Ala Ile Val Leu Thr
35 40 45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
50 55 60

Thr Glu Tyr Val Val Gln Ile Leu Gly Val Lys Gly Gly Ser Ile Ser
65 70 75 80

Val Pro Leu Ser Ala Ile Phe Thr Thr
85

<210> 44
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> c-Met binding FN3 domain

<400> 44

Leu Pro Ala Pro Lys Asn Leu Val Val Ser Arg Val Thr Glu Asp Ser
1 5 10 15

Ala Arg Leu Ser Trp Thr Ala Pro Asp Ala Ala Phe Asp Ser Phe Trp
20 25 30

Ile Arg Tyr Phe Glu Phe Leu Gly Ser Gly Glu Ala Ile Val Leu Thr
35 40 45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
50 55 60

Thr Glu Tyr Val Val Asn Ile Met Gly Val Lys Gly Gly Ser Ile Ser
65 70 75 80

Tyr Pro Leu Ser Ala Ile Phe Thr Thr
85

<210> 45
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> c-Met binding FN3 domain

<400> 45

Leu Pro Ala Pro Lys Asn Leu Val Val Ser Arg Val Thr Glu Asp Ser
1 5 10 15

Ala Arg Leu Ser Trp Thr Ala Pro Asp Ala Ala Phe Asp Ser Phe Trp
20 25 30

Ile Arg Tyr Phe Glu Phe Leu Gly Ser Gly Glu Ala Ile Val Leu Thr
35 40 45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
50 55 60

Thr Glu Tyr Val Val Gln Ile Leu Gly Val Lys Gly Gly Tyr Ile Ser
65 70 75 80

Ile Pro Leu Ser Ala Ile Phe Thr Thr
85

<210> 46
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> c-Met binding FN3 domain

<400> 46

Leu Pro Ala Pro Lys Asn Leu Val Val Ser Arg Val Thr Glu Asp Ser
1 5 10 15

Ala Arg Leu Ser Trp Thr Ala Pro Asp Ala Ala Phe Asp Ser Phe Trp
20 25 30

Ile Arg Tyr Phe Glu Phe Leu Gly Ser Gly Glu Ala Ile Val Leu Thr
35 40 45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
50 55 60

Thr Glu Tyr Val Val Gln Ile Met Gly Val Lys Gly Gly Thr Val Ser
65 70 75 80

Pro Pro Leu Ser Ala Ile Phe Thr Thr
85

<210> 47
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> c-Met binding FN3 domain

<400> 47

Leu Pro Ala Pro Lys Asn Leu Val Val Ser Arg Val Thr Glu Asp Ser
1 5 10 15

Ala Arg Leu Ser Trp Thr Ala Pro Asp Ala Ala Phe Asp Ser Phe Trp
20 25 30

Ile Arg Tyr Phe Glu Phe Thr Thr Ala Gly Glu Ala Ile Val Leu Thr
35 40 45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
50 55 60

Thr Glu Tyr Val Val Asn Ile Met Gly Val Lys Gly Gly Ser Ile Ser
65 70 75 80

Pro Pro Leu Ser Ala Ile Phe Thr Thr
85

<210> 48
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> c-Met binding FN3 domain

<400> 48

Leu Pro Ala Pro Lys Asn Leu Val Val Ser Arg Val Thr Glu Asp Ser
1 5 10 15

Ala Arg Leu Ser Trp Thr Ala Pro Asp Ala Ala Phe Asp Ser Phe Trp
20 25 30

Ile Arg Tyr Phe Glu Leu Leu Ser Thr Gly Glu Ala Ile Val Leu Thr
35 40 45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
50 55 60

Thr Glu Tyr Val Val Asn Ile Met Gly Val Lys Gly Gly Ser Ile Ser
65 70 75 80

Pro Pro Leu Ser Ala Ile Phe Thr Thr
85

<210> 49
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> c-Met binding FN3 domain

<400> 49

Leu Pro Ala Pro Lys Asn Leu Val Val Ser Arg Val Thr Glu Asp Ser
1 5 10 15

Ala Arg Leu Ser Trp Thr Ala Pro Asp Ala Ala Phe Asp Ser Phe Trp
20 25 30

Ile Arg Tyr Phe Glu Phe Val Ser Lys Gly Glu Ala Ile Val Leu Thr
35 40 45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
50 55 60

Thr Glu Tyr Val Val Asn Ile Met Gly Val Lys Gly Gly Ser Ile Ser
65 70 75 80

Pro Pro Leu Ser Ala Ile Phe Thr Thr
85

<210> 50
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> bispecific EGFR/cMet binding molecule

<400> 50

Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Glu Val Thr Glu Asp
1 5 10 15

Ser Ala Arg Leu Ser Trp Asp Asp Pro Trp Ala Phe Tyr Glu Ser Phe
20 25 30

Leu Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu
35 40 45

Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro
50 55 60

Gly Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys
65 70 75 80

Asp Thr Asn Met Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Gly
85 90 95

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
100 105 110

Gly Gly Ser Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Arg Val
115 120 125

Thr Glu Asp Ser Ala Arg Leu Ser Trp Thr Ala Pro Asp Ala Ala Phe
130 135 140

Asp Ser Phe Trp Ile Arg Tyr Asp Glu Val Val Val Gly Gly Glu Ala
145 150 155 160

Ile Val Leu Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly
165 170 175

Leu Lys Pro Gly Thr Glu Tyr Tyr Val Asn Ile Leu Gly Val Lys Gly
180 185 190

Gly Ser Ile Ser Val Pro Leu Ser Ala Ile Phe Thr Thr
195 200 205

<210> 51
<211> 204
<212> PRT
<213> Artificial Sequence

<220>
<223> bispecific EGFR/cMet binding molecule

<400> 51

Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Glu Val Thr Glu Asp
1 5 10 15

Ser Ala Arg Leu Ser Trp Asp Asp Pro Trp Ala Phe Tyr Glu Ser Phe
20 25 30

Leu Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu
35 40 45

Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro
50 55 60

Gly Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys
65 70 75 80

Asp Thr Asn Met Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Gly
85 90 95

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
100 105 110

Gly Gly Ser Leu Pro Ala Pro Lys Asn Leu Val Val Ser Arg Val Thr
115 120 125

Glu Asp Ser Ala Arg Leu Ser Trp Thr Ala Pro Asp Ala Ala Phe Asp
130 135 140

Ser Phe Trp Ile Arg Tyr Phe Glu Phe Leu Gly Ser Gly Glu Ala Ile
145 150 155 160

Val Leu Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu
165 170 175

Lys Pro Gly Thr Glu Tyr Val Val Asn Ile Met Gly Val Lys Gly Gly
180 185 190

Lys Ile Ser Pro Pro Leu Ser Ala Ile Phe Thr Thr
195 200

<210> 52
<211> 205

<212> PRT
<213> Artificial Sequence

<220>
<223> bispecific EGFR/cMet binding molecule

<400> 52

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Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Glu Val Thr Glu Asp
1               5                  10                  15

Ser Ala Arg Leu Ser Trp Asp Asp Pro Trp Ala Phe Tyr Glu Ser Phe
            20                  25                  30

Leu Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu
        35                  40                  45

Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro
    50                  55                  60

Gly Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys
65                  70                  75                  80

Asp Thr Asn Met Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Gly
                85                  90                  95

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
            100                 105                 110

Gly Gly Ser Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Arg Val
        115                 120                 125

Thr Glu Asp Ser Ala Arg Leu Ser Trp Thr Ala Pro Asp Ala Ala Phe
    130                 135                 140

Asp Ser Phe Trp Ile Arg Tyr Phe Glu Phe Leu Gly Ser Gly Glu Ala
145                 150                 155                 160

Ile Val Leu Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly
                165                 170                 175

Leu Lys Pro Gly Thr Glu Tyr Val Val Gln Ile Ile Gly Val Lys Gly
            180                 185                 190

Gly His Ile Ser Leu Pro Leu Ser Ala Ile Phe Thr Thr
        195                 200                 205
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<210> 53
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> bispecific EGFR/cMet binding molecule

<400> 53

Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Glu Val Thr Glu Asp
1 5 10 15

Ser Ala Arg Leu Ser Trp Asp Asp Pro Trp Ala Phe Tyr Glu Ser Phe
20 25 30

Leu Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu
35 40 45

Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro
50 55 60

Gly Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys
65 70 75 80

Asp Thr Asn Met Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Gly
85 90 95

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
100 105 110

Gly Gly Ser Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Arg Val
115 120 125

Thr Glu Asp Ser Ala Arg Leu Ser Trp Thr Ala Pro Asp Ala Ala Phe
130 135 140

Asp Ser Phe Phe Ile Arg Tyr Asp Glu Phe Leu Arg Ser Gly Glu Ala
145 150 155 160

Ile Val Leu Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly
165 170 175

Leu Lys Pro Gly Thr Glu Tyr Trp Val Thr Ile Leu Gly Val Lys Gly
180 185 190

Gly Leu Val Ser Thr Pro Leu Ser Ala Ile Phe Thr Thr
195 200 205

<210> 54
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> bispecific EGFR/cMet binding molecule

<400> 54

Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Glu Val Thr Glu Asp
1 5 10 15

Ser Ala Arg Leu Ser Trp Ala Asp Pro His Gly Phe Tyr Asp Ser Phe
20 25 30

Leu Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu
35 40 45

Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro
50 55 60

Gly Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys
65 70 75 80

Asp Thr Asn Met Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Gly
85 90 95

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
100 105 110

Gly Gly Ser Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Arg Val
115 120 125

Thr Glu Asp Ser Ala Arg Leu Ser Trp Thr Ala Pro Asp Ala Ala Phe
130 135 140

Asp Ser Phe Trp Ile Arg Tyr Phe Glu Phe Leu Gly Ser Gly Glu Ala
145 150 155 160

Ile Val Leu Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly
165 170 175

Leu Lys Pro Gly Thr Glu Tyr Val Val Asn Ile Met Gly Val Lys Gly
180 185 190

Gly Lys Ile Ser Pro Pro Leu Ser Ala Ile Phe Thr Thr
195 200 205

<210> 55
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> bispecific EGFR/cMet binding molecule

<400> 55

Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Glu Val Thr Glu Asp
1 5 10 15

Ser Ala Arg Leu Ser Trp Ala Asp Pro His Gly Phe Tyr Asp Ser Phe
20 25 30

Leu Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu
35 40 45

Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro
50 55 60

Gly Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys
65 70 75 80

Asp Thr Asn Met Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Gly
85 90 95

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
100 105 110

Gly Gly Ser Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Arg Val
115 120 125

Thr Glu Asp Ser Ala Arg Leu Ser Trp Thr Ala Pro Asp Ala Ala Phe
130 135 140

Asp Ser Phe Trp Ile Arg Tyr Phe Glu Phe Leu Gly Ser Gly Glu Ala
145 150 155 160

Ile Val Leu Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly
165 170 175

Leu Lys Pro Gly Thr Glu Tyr Val Val Gln Ile Ile Gly Val Lys Gly
180 185 190

Gly His Ile Ser Leu Pro Leu Ser Ala Ile Phe Thr Thr
195 200 205

<210> 56
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> bispecific EGFR/cMet binding molecule

<400> 56

Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Glu Val Thr Glu Asp
1 5 10 15

Ser Ala Arg Leu Ser Trp Ala Asp Pro His Gly Phe Tyr Asp Ser Phe
20 25 30

Leu Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu
35 40 45

Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro
50 55 60

Gly Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys
65 70 75 80

Asp Thr Asn Met Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Gly
85 90 95

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
100 105 110

Gly Gly Ser Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Arg Val
115 120 125

Thr Glu Asp Ser Ala Arg Leu Ser Trp Thr Ala Pro Asp Ala Ala Phe
130 135 140

Asp Ser Phe Trp Ile Arg Tyr Phe Glu Phe Leu Gly Ser Gly Glu Ala
145 150 155 160

Ile Val Leu Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly
165 170 175

Leu Lys Pro Gly Thr Glu Tyr Val Val Gln Ile Ile Gly Val Lys Gly
180 185 190

Gly His Ile Ser Leu Pro Leu Ser Ala Ile Phe Thr Thr
195 200 205

<210> 57
<211> 194
<212> PRT
<213> Artificial Sequence

<220>
<223> bispecific EGFR/cMet binding molecule

<400> 57

Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Glu Val Thr Glu Asp
1 5 10 15

Ser Ala Arg Leu Ser Trp Asp Asp Pro Trp Ala Phe Tyr Glu Ser Phe
20 25 30

Leu Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu
35 40 45

Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro
50 55 60

Gly Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys
65 70 75 80

Asp Thr Asn Met Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Ala
85 90 95

```
Pro Ala Pro Ala Pro Ala Pro Ala Pro Leu Pro Ala Pro Lys Asn Leu
            100                 105                 110

Val Val Ser Arg Val Thr Glu Asp Ser Ala Arg Leu Ser Trp Thr Ala
        115                 120                 125

Pro Asp Ala Ala Phe Asp Ser Phe Trp Ile Arg Tyr Phe Glu Phe Leu
    130                 135                 140

Gly Ser Gly Glu Ala Ile Val Leu Thr Val Pro Gly Ser Glu Arg Ser
145                 150                 155                 160

Tyr Asp Leu Thr Gly Leu Lys Pro Gly Thr Glu Tyr Val Val Asn Ile
                165                 170                 175

Met Gly Val Lys Gly Gly Lys Ile Ser Pro Pro Leu Ser Ala Ile Phe
            180                 185                 190

Thr Thr
```

<210> 58
<211> 194
<212> PRT
<213> Artificial Sequence

<220>
<223> bispecific EGFR/cMet binding molecule

<400> 58

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Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Glu Val Thr Glu Asp
1               5                   10                  15

Ser Ala Arg Leu Ser Trp Asp Asp Pro Trp Ala Phe Tyr Glu Ser Phe
            20                  25                  30

Leu Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu
        35                  40                  45

Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro
    50                  55                  60

Gly Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys
65                  70                  75                  80

Asp Thr Asn Met Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Ala
                85                  90                  95

Pro Ala Pro Ala Pro Ala Pro Ala Pro Leu Pro Ala Pro Lys Asn Leu
            100                 105                 110
```

Val Val Ser Arg Val Thr Glu Asp Ser Ala Arg Leu Ser Trp Thr Ala
115 120 125

Pro Asp Ala Ala Phe Asp Ser Phe Trp Ile Arg Tyr Asp Glu Val Val
130 135 140

Val Gly Gly Glu Ala Ile Val Leu Thr Val Pro Gly Ser Glu Arg Ser
145 150 155 160

Tyr Asp Leu Thr Gly Leu Lys Pro Gly Thr Glu Tyr Tyr Val Asn Ile
165 170 175

Leu Gly Val Lys Gly Gly Ser Ile Ser Val Pro Leu Ser Ala Ile Phe
180 185 190

Thr Thr

<210> 59
<211> 195
<212> PRT
<213> Artificial Sequence

<220>
<223> bispecific EGFR/cMet binding molecule

<400> 59

Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Glu Val Thr Glu Asp
1 5 10 15

Ser Ala Arg Leu Ser Trp Ala Asp Pro His Gly Phe Tyr Asp Ser Phe
20 25 30

Leu Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu
35 40 45

Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro
50 55 60

Gly Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys
65 70 75 80

Asp Thr Asn Met Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Ala
85 90 95

Pro Ala Pro Ala Pro Ala Pro Ala Pro Met Leu Pro Ala Pro Lys Asn
100 105 110

Leu Val Val Ser Arg Val Thr Glu Asp Ser Ala Arg Leu Ser Trp Thr
115 120 125

Ala Pro Asp Ala Ala Phe Asp Ser Phe Trp Ile Arg Tyr Phe Glu Phe
130 135 140

Leu Gly Ser Gly Glu Ala Ile Val Leu Thr Val Pro Gly Ser Glu Arg
145 150 155 160

Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly Thr Glu Tyr Val Val Asn
165 170 175

Ile Met Gly Val Lys Gly Gly Lys Ile Ser Pro Pro Leu Ser Ala Ile
180 185 190

Phe Thr Thr
195

<210> 60
<211> 194
<212> PRT
<213> Artificial Sequence

<220>
<223> bispecific EGFR/cMet binding molecule

<400> 60

Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Glu Val Thr Glu Asp
1 5 10 15

Ser Ala Arg Leu Ser Trp Ala Asp Pro His Gly Phe Tyr Asp Ser Phe
20 25 30

Leu Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu
35 40 45

Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro
50 55 60

Gly Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys
65 70 75 80

Asp Thr Asn Met Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Ala
85 90 95

Pro Ala Pro Ala Pro Ala Pro Ala Pro Leu Pro Ala Pro Lys Asn Leu
100 105 110

Val Val Ser Arg Val Thr Glu Asp Ser Ala Arg Leu Ser Trp Thr Ala
115 120 125

Pro Asp Ala Ala Phe Asp Ser Phe Trp Ile Arg Tyr Asp Glu Val Val
130 135 140

Val Gly Gly Glu Ala Ile Val Leu Thr Val Pro Gly Ser Glu Arg Ser
145 150 155 160

Tyr Asp Leu Thr Gly Leu Lys Pro Gly Thr Glu Tyr Tyr Val Asn Ile
165 170 175

Leu Gly Val Lys Gly Gly Ser Ile Ser Val Pro Leu Ser Ala Ile Phe
180 185 190

Thr Thr

<210> 61
<211> 194
<212> PRT
<213> Artificial Sequence

<220>
<223> bispecific EGFR/cMet binding molecule

<400> 61

Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Glu Val Thr Glu Asp
1 5 10 15

Ser Ala Arg Leu Ser Trp Asp Asp Pro Trp Ala Phe Tyr Glu Ser Phe
20 25 30

Leu Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu
35 40 45

Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro
50 55 60

Gly Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys
65 70 75 80

Asp Thr Asn Ile Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Ala
85 90 95

Pro Ala Pro Ala Pro Ala Pro Ala Pro Leu Pro Ala Pro Lys Asn Leu
100 105 110

Val Val Ser Arg Val Thr Glu Asp Ser Ala Arg Leu Ser Trp Thr Ala
115 120 125

Pro Asp Ala Ala Phe Asp Ser Phe Trp Ile Arg Tyr Phe Glu Phe Leu
130 135 140

Gly Ser Gly Glu Ala Ile Val Leu Thr Val Pro Gly Ser Glu Arg Ser
145 150 155 160

Tyr Asp Leu Thr Gly Leu Lys Pro Gly Thr Glu Tyr Val Val Asn Ile
165 170 175

Leu Gly Val Lys Gly Gly Lys Ile Ser Pro Pro Leu Ser Ala Ile Phe
180 185 190

Thr Thr

<210> 62
<211> 194
<212> PRT
<213> Artificial Sequence

<220>
<223> bispecific EGFR/cMet binding molecule

<400> 62

Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Glu Val Thr Glu Asp
1 5 10 15

Ser Ala Arg Leu Ser Trp Asp Asp Pro Trp Ala Phe Tyr Glu Ser Phe
20 25 30

Leu Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu
35 40 45

Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro
50 55 60

Gly Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys
65 70 75 80

Asp Thr Asn Ile Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Ala
85 90 95

Pro Ala Pro Ala Pro Ala Pro Ala Pro Leu Pro Ala Pro Lys Asn Leu
100 105 110

Val Val Ser Arg Val Thr Glu Asp Ser Ala Arg Leu Ser Trp Thr Ala
115 120 125

Pro Asp Ala Ala Phe Asp Ser Phe Trp Ile Arg Tyr Phe Glu Phe Val
130 135 140

Gly Ser Gly Glu Ala Ile Val Leu Thr Val Pro Gly Ser Glu Arg Ser
145 150 155 160

Tyr Asp Leu Thr Gly Leu Lys Pro Gly Thr Glu Tyr Val Val Asn Ile
165 170 175

Leu Gly Val Lys Gly Gly Ser Ile Ser Pro Pro Leu Ser Ala Ile Phe
180 185 190

Thr Thr

<210> 63
<211> 194
<212> PRT
<213> Artificial Sequence

<220>
<223> bispecific EGFR/cMet binding molecule

<400> 63

Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Glu Val Thr Glu Asp
1 5 10 15

Ser Ala Arg Leu Ser Trp Asp Asp Pro Trp Ala Phe Tyr Glu Ser Phe
20 25 30

Leu Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu
35 40 45

Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro
50 55 60

Gly Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys
65 70 75 80

Asp Thr Asn Ile Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Ala
85 90 95

Pro Ala Pro Ala Pro Ala Pro Ala Pro Leu Pro Ala Pro Lys Asn Leu
100 105 110

Val Val Ser Arg Val Thr Glu Asp Ser Ala Arg Leu Ser Trp Thr Ala
115 120 125

Pro Asp Ala Ala Phe Asp Ser Phe Trp Ile Arg Tyr Phe Glu Phe Val
130 135 140

Ser Lys Gly Asp Ala Ile Val Leu Thr Val Pro Gly Ser Glu Arg Ser
145 150 155 160

Tyr Asp Leu Thr Gly Leu Lys Pro Gly Thr Glu Tyr Val Val Asn Ile
165 170 175

Leu Gly Val Lys Gly Gly Ser Ile Ser Pro Pro Leu Ser Ala Ile Phe
180 185 190

Thr Thr

<210> 64
<211> 194
<212> PRT
<213> Artificial Sequence

<220>

<223> bispecific EGFR/cMet binding molecule

<400> 64

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Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Glu Val Thr Glu Asp
1               5                  10                  15

Ser Ala Arg Leu Ser Trp Asp Asp Pro Trp Ala Phe Tyr Glu Ser Phe
            20                  25                  30

Leu Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu
        35                  40                  45

Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro
    50                  55                  60

Gly Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys
65                  70                  75                  80

Asp Thr Asn Ile Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Ala
                85                  90                  95

Pro Ala Pro Ala Pro Ala Pro Ala Pro Leu Pro Ala Pro Lys Asn Leu
            100                 105                 110

Val Val Ser Arg Val Thr Glu Asp Ser Ala Arg Leu Ser Trp Thr Ala
        115                 120                 125

Pro Asp Ala Ala Phe Asp Ser Phe Trp Ile Arg Tyr Phe Glu Phe Leu
    130                 135                 140

Gly Ser Gly Glu Ala Ile Val Leu Thr Val Pro Gly Ser Glu Arg Ser
145                 150                 155                 160

Tyr Asp Leu Thr Gly Leu Lys Pro Gly Thr Glu Tyr Val Val Asn Ile
                165                 170                 175

Leu Ser Val Lys Gly Gly Ser Ile Ser Pro Pro Leu Ser Ala Ile Phe
            180                 185                 190

Thr Thr
```

<210> 65
<211> 194
<212> PRT
<213> Artificial Sequence

<220>
<223> bispecific EGFR/cMet binding molecule

<400> 65

```
Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Glu Val Thr Glu Asp
1               5                  10                  15
```

```
Ser Ala Arg Leu Ser Trp Asp Asp Pro His Ala Phe Tyr Glu Ser Phe
            20                  25                  30

Leu Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu
        35                  40                  45

Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro
    50                  55                  60

Gly Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys
65                  70                  75                  80

Asp Thr Asn Ile Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Ala
                85                  90                  95

Pro Ala Pro Ala Pro Ala Pro Ala Pro Leu Pro Ala Pro Lys Asn Leu
            100                 105                 110

Val Val Ser Arg Val Thr Glu Asp Ser Ala Arg Leu Ser Trp Thr Ala
        115                 120                 125

Pro Asp Ala Ala Phe Asp Ser Phe Trp Ile Arg Tyr Phe Glu Phe Leu
    130                 135                 140

Gly Ser Gly Glu Ala Ile Val Leu Thr Val Pro Gly Ser Glu Arg Ser
145                 150                 155                 160

Tyr Asp Leu Thr Gly Leu Lys Pro Gly Thr Glu Tyr Val Val Asn Ile
                165                 170                 175

Leu Gly Val Lys Gly Gly Lys Ile Ser Pro Pro Leu Ser Ala Ile Phe
            180                 185                 190

Thr Thr
```

<210> 66
<211> 194
<212> PRT
<213> Artificial Sequence

<220>
<223> bispecific EGFR/cMet binding molecule

<400> 66

```
Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Glu Val Thr Glu Asp
1               5                   10                  15

Ser Ala Arg Leu Ser Trp Asp Asp Pro His Ala Phe Tyr Glu Ser Phe
            20                  25                  30
```

Leu Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu
35 40 45

Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro
50 55 60

Gly Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys
65 70 75 80

Asp Thr Asn Ile Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Ala
85 90 95

Pro Ala Pro Ala Pro Ala Pro Ala Pro Leu Pro Ala Pro Lys Asn Leu
100 105 110

Val Val Ser Arg Val Thr Glu Asp Ser Ala Arg Leu Ser Trp Thr Ala
115 120 125

Pro Asp Ala Ala Phe Asp Ser Phe Trp Ile Arg Tyr Phe Glu Phe Val
130 135 140

Gly Ser Gly Glu Ala Ile Val Leu Thr Val Pro Gly Ser Glu Arg Ser
145 150 155 160

Tyr Asp Leu Thr Gly Leu Lys Pro Gly Thr Glu Tyr Val Val Asn Ile
165 170 175

Leu Gly Val Lys Gly Gly Ser Ile Ser Pro Pro Leu Ser Ala Ile Phe
180 185 190

Thr Thr

<210> 67
<211> 194
<212> PRT
<213> Artificial Sequence

<220>
<223> bispecific EGFR/cMet binding molecule

<400> 67

Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Glu Val Thr Glu Asp
1 5 10 15

Ser Ala Arg Leu Ser Trp Asp Asp Pro His Ala Phe Tyr Glu Ser Phe
20 25 30

Leu Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu
35 40 45

Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro
50 55 60

```
Gly Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys
65                  70                  75                  80

Asp Thr Asn Ile Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Ala
                85                  90                  95

Pro Ala Pro Ala Pro Ala Pro Ala Pro Leu Pro Ala Pro Lys Asn Leu
            100                 105                 110

Val Val Ser Arg Val Thr Glu Asp Ser Ala Arg Leu Ser Trp Thr Ala
        115                 120                 125

Pro Asp Ala Ala Phe Asp Ser Phe Trp Ile Arg Tyr Phe Glu Phe Val
    130                 135                 140

Ser Lys Gly Asp Ala Ile Val Leu Thr Val Pro Gly Ser Glu Arg Ser
145                 150                 155                 160

Tyr Asp Leu Thr Gly Leu Lys Pro Gly Thr Glu Tyr Val Val Asn Ile
                165                 170                 175

Leu Gly Val Lys Gly Gly Ser Ile Ser Pro Pro Leu Ser Ala Ile Phe
            180                 185                 190

Thr Thr
```

<210> 68
<211> 194
<212> PRT
<213> Artificial Sequence

<220>
<223> bispecific EGFR/cMet binding molecule

<400> 68

```
Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Glu Val Thr Glu Asp
1               5                   10                  15

Ser Ala Arg Leu Ser Trp Asp Asp Pro His Ala Phe Tyr Glu Ser Phe
            20                  25                  30

Leu Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu
        35                  40                  45

Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro
    50                  55                  60

Gly Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys
65                  70                  75                  80
```

```
Asp Thr Asn Ile Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Ala
                85                  90                  95

Pro Ala Pro Ala Pro Ala Pro Ala Pro Leu Pro Ala Pro Lys Asn Leu
            100                 105                 110

Val Val Ser Arg Val Thr Glu Asp Ser Ala Arg Leu Ser Trp Thr Ala
        115                 120                 125

Pro Asp Ala Ala Phe Asp Ser Phe Trp Ile Arg Tyr Phe Glu Phe Leu
    130                 135                 140

Gly Ser Gly Glu Ala Ile Val Leu Thr Val Pro Gly Ser Glu Arg Ser
145                 150                 155                 160

Tyr Asp Leu Thr Gly Leu Lys Pro Gly Thr Glu Tyr Val Val Asn Ile
                165                 170                 175

Leu Ser Val Lys Gly Gly Ser Ile Ser Pro Pro Leu Ser Ala Ile Phe
            180                 185                 190

Thr Thr
```

<210> 69
<211> 194
<212> PRT
<213> Artificial Sequence

<220>
<223> bispecific EGFR/cMet binding molecule

<400> 69

```
Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Glu Val Thr Glu Asp
1               5                   10                  15

Ser Ala Arg Leu Ser Trp Ala Asp Pro His Gly Phe Tyr Asp Ser Phe
            20                  25                  30

Leu Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu
        35                  40                  45

Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro
    50                  55                  60

Gly Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys
65                  70                  75                  80

Asp Thr Asn Ile Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Ala
                85                  90                  95

Pro Ala Pro Ala Pro Ala Pro Ala Pro Leu Pro Ala Pro Lys Asn Leu
            100                 105                 110
```

```
Val Val Ser Arg Val Thr Glu Asp Ser Ala Arg Leu Ser Trp Thr Ala
        115                 120                 125

Pro Asp Ala Ala Phe Asp Ser Phe Trp Ile Arg Tyr Phe Glu Phe Leu
    130                 135                 140

Gly Ser Gly Glu Ala Ile Val Leu Thr Val Pro Gly Ser Glu Arg Ser
145                 150                 155                 160

Tyr Asp Leu Thr Gly Leu Lys Pro Gly Thr Glu Tyr Val Val Asn Ile
                165                 170                 175

Leu Gly Val Lys Gly Gly Lys Ile Ser Pro Pro Leu Ser Ala Ile Phe
            180                 185                 190

Thr Thr
```

<210> 70
<211> 194
<212> PRT
<213> Artificial Sequence

<220>
<223> bispecific EGFR/cMet binding molecule

<400> 70

```
Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Glu Val Thr Glu Asp
1               5                   10                  15

Ser Ala Arg Leu Ser Trp Ala Asp Pro His Gly Phe Tyr Asp Ser Phe
            20                  25                  30

Leu Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu
        35                  40                  45

Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro
    50                  55                  60

Gly Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys
65                  70                  75                  80

Asp Thr Asn Ile Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Ala
                85                  90                  95

Pro Ala Pro Ala Pro Ala Pro Ala Pro Leu Pro Ala Pro Lys Asn Leu
            100                 105                 110

Val Val Ser Arg Val Thr Glu Asp Ser Ala Arg Leu Ser Trp Thr Ala
        115                 120                 125
```

Pro Asp Ala Ala Phe Asp Ser Phe Trp Ile Arg Tyr Phe Glu Phe Val
130 135 140

Gly Ser Gly Glu Ala Ile Val Leu Thr Val Pro Gly Ser Glu Arg Ser
145 150 155 160

Tyr Asp Leu Thr Gly Leu Lys Pro Gly Thr Glu Tyr Val Val Asn Ile
165 170 175

Leu Gly Val Lys Gly Gly Ser Ile Ser Pro Pro Leu Ser Ala Ile Phe
180 185 190

Thr Thr

<210> 71
<211> 194
<212> PRT
<213> Artificial Sequence

<220>
<223> bispecific EGFR/cMet binding molecule

<400> 71

Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Glu Val Thr Glu Asp
1 5 10 15

Ser Ala Arg Leu Ser Trp Ala Asp Pro His Gly Phe Tyr Asp Ser Phe
20 25 30

Leu Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu
35 40 45

Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro
50 55 60

Gly Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys
65 70 75 80

Asp Thr Asn Ile Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Ala
85 90 95

Pro Ala Pro Ala Pro Ala Pro Ala Pro Leu Pro Ala Pro Lys Asn Leu
100 105 110

Val Val Ser Arg Val Thr Glu Asp Ser Ala Arg Leu Ser Trp Thr Ala
115 120 125

Pro Asp Ala Ala Phe Asp Ser Phe Trp Ile Arg Tyr Phe Glu Phe Val
130 135 140

Ser Lys Gly Asp Ala Ile Val Leu Thr Val Pro Gly Ser Glu Arg Ser
145 150 155 160

Tyr Asp Leu Thr Gly Leu Lys Pro Gly Thr Glu Tyr Val Val Asn Ile
165 170 175

Leu Gly Val Lys Gly Gly Ser Ile Ser Pro Pro Leu Ser Ala Ile Phe
180 185 190

Thr Thr

<210> 72
<211> 194
<212> PRT
<213> Artificial Sequence

<220>
<223> bispecific EGFR/cMet binding molecule

<400> 72

Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Glu Val Thr Glu Asp
1 5 10 15

Ser Ala Arg Leu Ser Trp Ala Asp Pro His Gly Phe Tyr Asp Ser Phe
20 25 30

Leu Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu
35 40 45

Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro
50 55 60

Gly Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys
65 70 75 80

Asp Thr Asn Ile Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Ala
85 90 95

Pro Ala Pro Ala Pro Ala Pro Ala Pro Leu Pro Ala Pro Lys Asn Leu
100 105 110

Val Val Ser Arg Val Thr Glu Asp Ser Ala Arg Leu Ser Trp Thr Ala
115 120 125

Pro Asp Ala Ala Phe Asp Ser Phe Trp Ile Arg Tyr Phe Glu Phe Leu
130 135 140

Gly Ser Gly Glu Ala Ile Val Leu Thr Val Pro Gly Ser Glu Arg Ser
145 150 155 160

Tyr Asp Leu Thr Gly Leu Lys Pro Gly Thr Glu Tyr Val Val Asn Ile
165 170 175

Leu Ser Val Lys Gly Gly Ser Ile Ser Pro Pro Leu Ser Ala Ile Phe
180 185 190

Thr Thr

<210> 73
<211> 1210
<212> PRT
<213> HOMO SAPIENS

<400> 73

Met Arg Pro Ser Gly Thr Ala Gly Ala Ala Leu Leu Ala Leu Leu Ala
1 5 10 15

Ala Leu Cys Pro Ala Ser Arg Ala Leu Glu Glu Lys Lys Val Cys Gln
20 25 30

Gly Thr Ser Asn Lys Leu Thr Gln Leu Gly Thr Phe Glu Asp His Phe
35 40 45

Leu Ser Leu Gln Arg Met Phe Asn Asn Cys Glu Val Val Leu Gly Asn
50 55 60

Leu Glu Ile Thr Tyr Val Gln Arg Asn Tyr Asp Leu Ser Phe Leu Lys
65 70 75 80

Thr Ile Gln Glu Val Ala Gly Tyr Val Leu Ile Ala Leu Asn Thr Val
85 90 95

Glu Arg Ile Pro Leu Glu Asn Leu Gln Ile Ile Arg Gly Asn Met Tyr
100 105 110

Tyr Glu Asn Ser Tyr Ala Leu Ala Val Leu Ser Asn Tyr Asp Ala Asn
115 120 125

Lys Thr Gly Leu Lys Glu Leu Pro Met Arg Asn Leu Gln Glu Ile Leu
130 135 140

His Gly Ala Val Arg Phe Ser Asn Asn Pro Ala Leu Cys Asn Val Glu
145 150 155 160

Ser Ile Gln Trp Arg Asp Ile Val Ser Ser Asp Phe Leu Ser Asn Met
165 170 175

Ser Met Asp Phe Gln Asn His Leu Gly Ser Cys Gln Lys Cys Asp Pro
180 185 190

Ser Cys Pro Asn Gly Ser Cys Trp Gly Ala Gly Glu Glu Asn Cys Gln
195 200 205

Lys Leu Thr Lys Ile Ile Cys Ala Gln Gln Cys Ser Gly Arg Cys Arg

210 215 220

Gly Lys Ser Pro Ser Asp Cys Cys His Asn Gln Cys Ala Ala Gly Cys
225 230 235 240

Thr Gly Pro Arg Glu Ser Asp Cys Leu Val Cys Arg Lys Phe Arg Asp
245 250 255

Glu Ala Thr Cys Lys Asp Thr Cys Pro Pro Leu Met Leu Tyr Asn Pro
260 265 270

Thr Thr Tyr Gln Met Asp Val Asn Pro Glu Gly Lys Tyr Ser Phe Gly
275 280 285

Ala Thr Cys Val Lys Lys Cys Pro Arg Asn Tyr Val Val Thr Asp His
290 295 300

Gly Ser Cys Val Arg Ala Cys Gly Ala Asp Ser Tyr Glu Met Glu Glu
305 310 315 320

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

Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn
340 345 350

Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp
355 360 365

Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe Thr His Thr
370 375 380

Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val Lys Glu
385 390 395 400

Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp
405 410 415

Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln
420 425 430

His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile Thr Ser Leu
435 440 445

Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val Ile Ile Ser
450 455 460

Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu
465 470 475 480

Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn Arg Gly Glu

485 490 495

Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu Cys Ser Pro
500 505 510

Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser Cys Arg Asn
515 520 525

Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Leu Leu Glu Gly
530 535 540

Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln Cys His Pro
545 550 555 560

Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly Arg Gly Pro
565 570 575

Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro His Cys Val
580 585 590

Lys Thr Cys Pro Ala Gly Val Met Gly Glu Asn Asn Thr Leu Val Trp
595 600 605

Lys Tyr Ala Asp Ala Gly His Val Cys His Leu Cys His Pro Asn Cys
610 615 620

Thr Tyr Gly Cys Thr Gly Pro Gly Leu Glu Gly Cys Pro Thr Asn Gly
625 630 635 640

Pro Lys Ile Pro Ser Ile Ala Thr Gly Met Val Gly Ala Leu Leu Leu
645 650 655

Leu Leu Val Val Ala Leu Gly Ile Gly Leu Phe Met Arg Arg Arg His
660 665 670

Ile Val Arg Lys Arg Thr Leu Arg Arg Leu Leu Gln Glu Arg Glu Leu
675 680 685

Val Glu Pro Leu Thr Pro Ser Gly Glu Ala Pro Asn Gln Ala Leu Leu
690 695 700

Arg Ile Leu Lys Glu Thr Glu Phe Lys Lys Ile Lys Val Leu Gly Ser
705 710 715 720

Gly Ala Phe Gly Thr Val Tyr Lys Gly Leu Trp Ile Pro Glu Gly Glu
725 730 735

Lys Val Lys Ile Pro Val Ala Ile Lys Glu Leu Arg Glu Ala Thr Ser
740 745 750

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

```
        755                 760                 765

Val Asp Asn Pro His Val Cys Arg Leu Leu Gly Ile Cys Leu Thr Ser
    770                 775                 780

Thr Val Gln Leu Ile Thr Gln Leu Met Pro Phe Gly Cys Leu Leu Asp
785                 790                 795                 800

Tyr Val Arg Glu His Lys Asp Asn Ile Gly Ser Gln Tyr Leu Leu Asn
                805                 810                 815

Trp Cys Val Gln Ile Ala Lys Gly Met Asn Tyr Leu Glu Asp Arg Arg
            820                 825                 830

Leu Val His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Lys Thr Pro
        835                 840                 845

Gln His Val Lys Ile Thr Asp Phe Gly Leu Ala Lys Leu Leu Gly Ala
    850                 855                 860

Glu Glu Lys Glu Tyr His Ala Glu Gly Gly Lys Val Pro Ile Lys Trp
865                 870                 875                 880

Met Ala Leu Glu Ser Ile Leu His Arg Ile Tyr Thr His Gln Ser Asp
                885                 890                 895

Val Trp Ser Tyr Gly Val Thr Val Trp Glu Leu Met Thr Phe Gly Ser
            900                 905                 910

Lys Pro Tyr Asp Gly Ile Pro Ala Ser Glu Ile Ser Ser Ile Leu Glu
        915                 920                 925

Lys Gly Glu Arg Leu Pro Gln Pro Pro Ile Cys Thr Ile Asp Val Tyr
    930                 935                 940

Met Ile Met Val Lys Cys Trp Met Ile Asp Ala Asp Ser Arg Pro Lys
945                 950                 955                 960

Phe Arg Glu Leu Ile Ile Glu Phe Ser Lys Met Ala Arg Asp Pro Gln
                965                 970                 975

Arg Tyr Leu Val Ile Gln Gly Asp Glu Arg Met His Leu Pro Ser Pro
            980                 985                 990

Thr Asp Ser Asn Phe Tyr Arg Ala  Leu Met Asp Glu Glu  Asp Met Asp
        995                 1000                1005

Asp Val  Val Asp Ala Asp Glu  Tyr Leu Ile Pro Gln  Gln Gly Phe
    1010                1015                1020

Phe Ser  Ser Pro Ser Thr Ser  Arg Thr Pro Leu Leu  Ser Ser Leu
```

1025 1030 1035

Ser Ala Thr Ser Asn Asn Ser Thr Val Ala Cys Ile Asp Arg Asn
1040 1045 1050

Gly Leu Gln Ser Cys Pro Ile Lys Glu Asp Ser Phe Leu Gln Arg
1055 1060 1065

Tyr Ser Ser Asp Pro Thr Gly Ala Leu Thr Glu Asp Ser Ile Asp
1070 1075 1080

Asp Thr Phe Leu Pro Val Pro Glu Tyr Ile Asn Gln Ser Val Pro
1085 1090 1095

Lys Arg Pro Ala Gly Ser Val Gln Asn Pro Val Tyr His Asn Gln
1100 1105 1110

Pro Leu Asn Pro Ala Pro Ser Arg Asp Pro His Tyr Gln Asp Pro
1115 1120 1125

His Ser Thr Ala Val Gly Asn Pro Glu Tyr Leu Asn Thr Val Gln
1130 1135 1140

Pro Thr Cys Val Asn Ser Thr Phe Asp Ser Pro Ala His Trp Ala
1145 1150 1155

Gln Lys Gly Ser His Gln Ile Ser Leu Asp Asn Pro Asp Tyr Gln
1160 1165 1170

Gln Asp Phe Phe Pro Lys Glu Ala Lys Pro Asn Gly Ile Phe Lys
1175 1180 1185

Gly Ser Thr Ala Glu Asn Ala Glu Tyr Leu Arg Val Ala Pro Gln
1190 1195 1200

Ser Ser Glu Phe Ile Gly Ala
1205 1210

<210> 74
<211> 53
<212> PRT
<213> HOMO SAPIENS

<400> 74

Asn Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr Cys Leu His
1 5 10 15

Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys Asn
20 25 30

Cys Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr Arg Asp Leu Lys
35 40 45

Trp Trp Glu Leu Arg
50

<210> 75
<211> 2201
<212> PRT
<213> Homo sapiens

<400> 75

Met Gly Ala Met Thr Gln Leu Leu Ala Gly Val Phe Leu Ala Phe Leu
1 5 10 15

Ala Leu Ala Thr Glu Gly Gly Val Leu Lys Lys Val Ile Arg His Lys
20 25 30

Arg Gln Ser Gly Val Asn Ala Thr Leu Pro Glu Glu Asn Gln Pro Val
35 40 45

Val Phe Asn His Val Tyr Asn Ile Lys Leu Pro Val Gly Ser Gln Cys
50 55 60

Ser Val Asp Leu Glu Ser Ala Ser Gly Glu Lys Asp Leu Ala Pro Pro
65 70 75 80

Ser Glu Pro Ser Glu Ser Phe Gln Glu His Thr Val Asp Gly Glu Asn
85 90 95

Gln Ile Val Phe Thr His Arg Ile Asn Ile Pro Arg Arg Ala Cys Gly
100 105 110

Cys Ala Ala Ala Pro Asp Val Lys Glu Leu Leu Ser Arg Leu Glu Glu
115 120 125

Leu Glu Asn Leu Val Ser Ser Leu Arg Glu Gln Cys Thr Ala Gly Ala
130 135 140

Gly Cys Cys Leu Gln Pro Ala Thr Gly Arg Leu Asp Thr Arg Pro Phe
145 150 155 160

Cys Ser Gly Arg Gly Asn Phe Ser Thr Glu Gly Cys Gly Cys Val Cys
165 170 175

Glu Pro Gly Trp Lys Gly Pro Asn Cys Ser Glu Pro Glu Cys Pro Gly
180 185 190

Asn Cys His Leu Arg Gly Arg Cys Ile Asp Gly Gln Cys Ile Cys Asp
195 200 205

Asp Gly Phe Thr Gly Glu Asp Cys Ser Gln Leu Ala Cys Pro Ser Asp
210 215 220

```
Cys Asn Asp Gln Gly Lys Cys Val Asn Gly Val Cys Ile Cys Phe Glu
225                 230                 235                 240

Gly Tyr Ala Gly Ala Asp Cys Ser Arg Glu Ile Cys Pro Val Pro Cys
                245                 250                 255

Ser Glu Glu His Gly Thr Cys Val Asp Gly Leu Cys Val Cys His Asp
            260                 265                 270

Gly Phe Ala Gly Asp Asp Cys Asn Lys Pro Leu Cys Leu Asn Asn Cys
        275                 280                 285

Tyr Asn Arg Gly Arg Cys Val Glu Asn Glu Cys Val Cys Asp Glu Gly
    290                 295                 300

Phe Thr Gly Glu Asp Cys Ser Glu Leu Ile Cys Pro Asn Asp Cys Phe
305                 310                 315                 320

Asp Arg Gly Arg Cys Ile Asn Gly Thr Cys Tyr Cys Glu Glu Gly Phe
                325                 330                 335

Thr Gly Glu Asp Cys Gly Lys Pro Thr Cys Pro His Ala Cys His Thr
            340                 345                 350

Gln Gly Arg Cys Glu Glu Gly Gln Cys Val Cys Asp Glu Gly Phe Ala
        355                 360                 365

Gly Val Asp Cys Ser Glu Lys Arg Cys Pro Ala Asp Cys His Asn Arg
    370                 375                 380

Gly Arg Cys Val Asp Gly Arg Cys Glu Cys Asp Asp Gly Phe Thr Gly
385                 390                 395                 400

Ala Asp Cys Gly Glu Leu Lys Cys Pro Asn Gly Cys Ser Gly His Gly
                405                 410                 415

Arg Cys Val Asn Gly Gln Cys Val Cys Asp Glu Gly Tyr Thr Gly Glu
            420                 425                 430

Asp Cys Ser Gln Leu Arg Cys Pro Asn Asp Cys His Ser Arg Gly Arg
        435                 440                 445

Cys Val Glu Gly Lys Cys Val Cys Glu Gln Gly Phe Lys Gly Tyr Asp
    450                 455                 460

Cys Ser Asp Met Ser Cys Pro Asn Asp Cys His Gln His Gly Arg Cys
465                 470                 475                 480

Val Asn Gly Met Cys Val Cys Asp Asp Gly Tyr Thr Gly Glu Asp Cys
                485                 490                 495
```

```
Arg Asp Arg Gln Cys Pro Arg Asp Cys Ser Asn Arg Gly Leu Cys Val
            500                 505                 510

Asp Gly Gln Cys Val Cys Glu Asp Gly Phe Thr Gly Pro Asp Cys Ala
        515                 520                 525

Glu Leu Ser Cys Pro Asn Asp Cys His Gly Gln Gly Arg Cys Val Asn
    530                 535                 540

Gly Gln Cys Val Cys His Glu Gly Phe Met Gly Lys Asp Cys Lys Glu
545                 550                 555                 560

Gln Arg Cys Pro Ser Asp Cys His Gly Gln Gly Arg Cys Val Asp Gly
                565                 570                 575

Gln Cys Ile Cys His Glu Gly Phe Thr Gly Leu Asp Cys Gly Gln His
            580                 585                 590

Ser Cys Pro Ser Asp Cys Asn Asn Leu Gly Gln Cys Val Ser Gly Arg
        595                 600                 605

Cys Ile Cys Asn Glu Gly Tyr Ser Gly Glu Asp Cys Ser Glu Val Ser
    610                 615                 620

Pro Pro Lys Asp Leu Val Val Thr Glu Val Thr Glu Glu Thr Val Asn
625                 630                 635                 640

Leu Ala Trp Asp Asn Glu Met Arg Val Thr Glu Tyr Leu Val Val Tyr
                645                 650                 655

Thr Pro Thr His Glu Gly Gly Leu Glu Met Gln Phe Arg Val Pro Gly
            660                 665                 670

Asp Gln Thr Ser Thr Ile Ile Gln Glu Leu Glu Pro Gly Val Glu Tyr
        675                 680                 685

Phe Ile Arg Val Phe Ala Ile Leu Glu Asn Lys Lys Ser Ile Pro Val
    690                 695                 700

Ser Ala Arg Val Ala Thr Tyr Leu Pro Ala Pro Glu Gly Leu Lys Phe
705                 710                 715                 720

Lys Ser Ile Lys Glu Thr Ser Val Glu Val Glu Trp Asp Pro Leu Asp
                725                 730                 735

Ile Ala Phe Glu Thr Trp Glu Ile Ile Phe Arg Asn Met Asn Lys Glu
            740                 745                 750

Asp Glu Gly Glu Ile Thr Lys Ser Leu Arg Arg Pro Glu Thr Ser Tyr
        755                 760                 765
```

```
Arg Gln Thr Gly Leu Ala Pro Gly Gln Glu Tyr Glu Ile Ser Leu His
    770                 775                 780

Ile Val Lys Asn Asn Thr Arg Gly Pro Gly Leu Lys Arg Val Thr Thr
785                 790                 795                 800

Thr Arg Leu Asp Ala Pro Ser Gln Ile Glu Val Lys Asp Val Thr Asp
                805                 810                 815

Thr Thr Ala Leu Ile Thr Trp Phe Lys Pro Leu Ala Glu Ile Asp Gly
            820                 825                 830

Ile Glu Leu Thr Tyr Gly Ile Lys Asp Val Pro Gly Asp Arg Thr Thr
        835                 840                 845

Ile Asp Leu Thr Glu Asp Glu Asn Gln Tyr Ser Ile Gly Asn Leu Lys
    850                 855                 860

Pro Asp Thr Glu Tyr Glu Val Ser Leu Ile Ser Arg Arg Gly Asp Met
865                 870                 875                 880

Ser Ser Asn Pro Ala Lys Glu Thr Phe Thr Thr Gly Leu Asp Ala Pro
                885                 890                 895

Arg Asn Leu Arg Arg Val Ser Gln Thr Asp Asn Ser Ile Thr Leu Glu
            900                 905                 910

Trp Arg Asn Gly Lys Ala Ala Ile Asp Ser Tyr Arg Ile Lys Tyr Ala
        915                 920                 925

Pro Ile Ser Gly Gly Asp His Ala Glu Val Asp Val Pro Lys Ser Gln
    930                 935                 940

Gln Ala Thr Thr Lys Thr Thr Leu Thr Gly Leu Arg Pro Gly Thr Glu
945                 950                 955                 960

Tyr Gly Ile Gly Val Ser Ala Val Lys Glu Asp Lys Glu Ser Asn Pro
                965                 970                 975

Ala Thr Ile Asn Ala Ala Thr Glu Leu Asp Thr Pro Lys Asp Leu Gln
            980                 985                 990

Val Ser Glu Thr Ala Glu Thr Ser  Leu Thr Leu Leu Trp  Lys Thr Pro
        995                 1000                1005

Leu Ala  Lys Phe Asp Arg Tyr  Arg Leu Asn Tyr Ser  Leu Pro Thr
    1010                1015                1020

Gly Gln  Trp Val Gly Val Gln  Leu Pro Arg Asn Thr  Thr Ser Tyr
    1025                1030                1035
```

```
Val Leu  Arg Gly Leu Glu Pro  Gly Gln Glu Tyr Asn  Val Leu Leu
    1040                 1045                 1050

Thr Ala  Glu Lys Gly Arg His  Lys Ser Lys Pro Ala  Arg Val Lys
    1055                 1060                 1065

Ala Ser  Thr Glu Gln Ala Pro  Glu Leu Glu Asn Leu  Thr Val Thr
    1070                 1075                 1080

Glu Val  Gly Trp Asp Gly Leu  Arg Leu Asn Trp Thr  Ala Ala Asp
    1085                 1090                 1095

Gln Ala  Tyr Glu His Phe Ile  Ile Gln Val Gln Glu  Ala Asn Lys
    1100                 1105                 1110

Val Glu  Ala Ala Arg Asn Leu  Thr Val Pro Gly Ser  Leu Arg Ala
    1115                 1120                 1125

Val Asp  Ile Pro Gly Leu Lys  Ala Ala Thr Pro Tyr  Thr Val Ser
    1130                 1135                 1140

Ile Tyr  Gly Val Ile Gln Gly  Tyr Arg Thr Pro Val  Leu Ser Ala
    1145                 1150                 1155

Glu Ala  Ser Thr Gly Glu Thr  Pro Asn Leu Gly Glu  Val Val Val
    1160                 1165                 1170

Ala Glu  Val Gly Trp Asp Ala  Leu Lys Leu Asn Trp  Thr Ala Pro
    1175                 1180                 1185

Glu Gly  Ala Tyr Glu Tyr Phe  Phe Ile Gln Val Gln  Glu Ala Asp
    1190                 1195                 1200

Thr Val  Glu Ala Ala Gln Asn  Leu Thr Val Pro Gly  Gly Leu Arg
    1205                 1210                 1215

Ser Thr  Asp Leu Pro Gly Leu  Lys Ala Ala Thr His  Tyr Thr Ile
    1220                 1225                 1230

Thr Ile  Arg Gly Val Thr Gln  Asp Phe Ser Thr Thr  Pro Leu Ser
    1235                 1240                 1245

Val Glu  Val Leu Thr Glu Glu  Val Pro Asp Met Gly  Asn Leu Thr
    1250                 1255                 1260

Val Thr  Glu Val Ser Trp Asp  Ala Leu Arg Leu Asn  Trp Thr Thr
    1265                 1270                 1275

Pro Asp  Gly Thr Tyr Asp Gln  Phe Thr Ile Gln Val  Gln Glu Ala
    1280                 1285                 1290
```

```
Asp Gln  Val Glu Glu Ala His  Asn Leu Thr Val Pro  Gly Ser Leu
    1295                 1300                 1305

Arg Ser  Met Glu Ile Pro Gly  Leu Arg Ala Gly Thr  Pro Tyr Thr
    1310                 1315                 1320

Val Thr  Leu His Gly Glu Val  Arg Gly His Ser Thr  Arg Pro Leu
    1325                 1330                 1335

Ala Val  Glu Val Val Thr Glu  Asp Leu Pro Gln Leu  Gly Asp Leu
    1340                 1345                 1350

Ala Val  Ser Glu Val Gly Trp  Asp Gly Leu Arg Leu  Asn Trp Thr
    1355                 1360                 1365

Ala Ala  Asp Asn Ala Tyr Glu  His Phe Val Ile Gln  Val Gln Glu
    1370                 1375                 1380

Val Asn  Lys Val Glu Ala Ala  Gln Asn Leu Thr Leu  Pro Gly Ser
    1385                 1390                 1395

Leu Arg  Ala Val Asp Ile Pro  Gly Leu Glu Ala Ala  Thr Pro Tyr
    1400                 1405                 1410

Arg Val  Ser Ile Tyr Gly Val  Ile Arg Gly Tyr Arg  Thr Pro Val
    1415                 1420                 1425

Leu Ser  Ala Glu Ala Ser Thr  Ala Lys Glu Pro Glu  Ile Gly Asn
    1430                 1435                 1440

Leu Asn  Val Ser Asp Ile Thr  Pro Glu Ser Phe Asn  Leu Ser Trp
    1445                 1450                 1455

Met Ala  Thr Asp Gly Ile Phe  Glu Thr Phe Thr Ile  Glu Ile Ile
    1460                 1465                 1470

Asp Ser  Asn Arg Leu Leu Glu  Thr Val Glu Tyr Asn  Ile Ser Gly
    1475                 1480                 1485

Ala Glu  Arg Thr Ala His Ile  Ser Gly Leu Pro Pro  Ser Thr Asp
    1490                 1495                 1500

Phe Ile  Val Tyr Leu Ser Gly  Leu Ala Pro Ser Ile  Arg Thr Lys
    1505                 1510                 1515

Thr Ile  Ser Ala Thr Ala Thr  Thr Glu Ala Leu Pro  Leu Leu Glu
    1520                 1525                 1530

Asn Leu  Thr Ile Ser Asp Ile  Asn Pro Tyr Gly Phe  Thr Val Ser
    1535                 1540                 1545
```

```
Trp Met  Ala Ser Glu Asn Ala  Phe Asp Ser Phe Leu  Val Thr Val
    1550                 1555                 1560

Val Asp  Ser Gly Lys Leu Leu  Asp Pro Gln Glu Phe  Thr Leu Ser
    1565                 1570                 1575

Gly Thr  Gln Arg Lys Leu Glu  Leu Arg Gly Leu Ile  Thr Gly Ile
    1580                 1585                 1590

Gly Tyr  Glu Val Met Val Ser  Gly Phe Thr Gln Gly  His Gln Thr
    1595                 1600                 1605

Lys Pro  Leu Arg Ala Glu Ile  Val Thr Glu Ala Glu  Pro Glu Val
    1610                 1615                 1620

Asp Asn  Leu Leu Val Ser Asp  Ala Thr Pro Asp Gly  Phe Arg Leu
    1625                 1630                 1635

Ser Trp  Thr Ala Asp Glu Gly  Val Phe Asp Asn Phe  Val Leu Lys
    1640                 1645                 1650

Ile Arg  Asp Thr Lys Lys Gln  Ser Glu Pro Leu Glu  Ile Thr Leu
    1655                 1660                 1665

Leu Ala  Pro Glu Arg Thr Arg  Asp Ile Thr Gly Leu  Arg Glu Ala
    1670                 1675                 1680

Thr Glu  Tyr Glu Ile Glu Leu  Tyr Gly Ile Ser Lys  Gly Arg Arg
    1685                 1690                 1695

Ser Gln  Thr Val Ser Ala Ile  Ala Thr Thr Ala Met  Gly Ser Pro
    1700                 1705                 1710

Lys Glu  Val Ile Phe Ser Asp  Ile Thr Glu Asn Ser  Ala Thr Val
    1715                 1720                 1725

Ser Trp  Arg Ala Pro Thr Ala  Gln Val Glu Ser Phe  Arg Ile Thr
    1730                 1735                 1740

Tyr Val  Pro Ile Thr Gly Gly  Thr Pro Ser Met Val  Thr Val Asp
    1745                 1750                 1755

Gly Thr  Lys Thr Gln Thr Arg  Leu Val Lys Leu Ile  Pro Gly Val
    1760                 1765                 1770

Glu Tyr  Leu Val Ser Ile Ile  Ala Met Lys Gly Phe  Glu Glu Ser
    1775                 1780                 1785

Glu Pro  Val Ser Gly Ser Phe  Thr Thr Ala Leu Asp  Gly Pro Ser
    1790                 1795                 1800
```

```
Gly Leu  Val Thr Ala Asn Ile  Thr Asp Ser Glu Ala  Leu Ala Arg
    1805                 1810                 1815

Trp Gln  Pro Ala Ile Ala Thr  Val Asp Ser Tyr Val  Ile Ser Tyr
    1820                 1825                 1830

Thr Gly  Glu Lys Val Pro Glu  Ile Thr Arg Thr Val  Ser Gly Asn
    1835                 1840                 1845

Thr Val  Glu Tyr Ala Leu Thr  Asp Leu Glu Pro Ala  Thr Glu Tyr
    1850                 1855                 1860

Thr Leu  Arg Ile Phe Ala Glu  Lys Gly Pro Gln Lys  Ser Ser Thr
    1865                 1870                 1875

Ile Thr  Ala Lys Phe Thr Thr  Asp Leu Asp Ser Pro  Arg Asp Leu
    1880                 1885                 1890

Thr Ala  Thr Glu Val Gln Ser  Glu Thr Ala Leu Leu  Thr Trp Arg
    1895                 1900                 1905

Pro Pro  Arg Ala Ser Val Thr  Gly Tyr Leu Leu Val  Tyr Glu Ser
    1910                 1915                 1920

Val Asp  Gly Thr Val Lys Glu  Val Ile Val Gly Pro  Asp Thr Thr
    1925                 1930                 1935

Ser Tyr  Ser Leu Ala Asp Leu  Ser Pro Ser Thr His  Tyr Thr Ala
    1940                 1945                 1950

Lys Ile  Gln Ala Leu Asn Gly  Pro Leu Arg Ser Asn  Met Ile Gln
    1955                 1960                 1965

Thr Ile  Phe Thr Thr Ile Gly  Leu Leu Tyr Pro Phe  Pro Lys Asp
    1970                 1975                 1980

Cys Ser  Gln Ala Met Leu Asn  Gly Asp Thr Thr Ser  Gly Leu Tyr
    1985                 1990                 1995

Thr Ile  Tyr Leu Asn Gly Asp  Lys Ala Glu Ala Leu  Glu Val Phe
    2000                 2005                 2010

Cys Asp  Met Thr Ser Asp Gly  Gly Gly Trp Ile Val  Phe Leu Arg
    2015                 2020                 2025

Arg Lys  Asn Gly Arg Glu Asn  Phe Tyr Gln Asn Trp  Lys Ala Tyr
    2030                 2035                 2040

Ala Ala  Gly Phe Gly Asp Arg  Arg Glu Glu Phe Trp  Leu Gly Leu
    2045                 2050                 2055
```

Asp Asn Leu Asn Lys Ile Thr Ala Gln Gly Gln Tyr Glu Leu Arg
2060 2065 2070

Val Asp Leu Arg Asp His Gly Glu Thr Ala Phe Ala Val Tyr Asp
2075 2080 2085

Lys Phe Ser Val Gly Asp Ala Lys Thr Arg Tyr Lys Leu Lys Val
2090 2095 2100

Glu Gly Tyr Ser Gly Thr Ala Gly Asp Ser Met Ala Tyr His Asn
2105 2110 2115

Gly Arg Ser Phe Ser Thr Phe Asp Lys Asp Thr Asp Ser Ala Ile
2120 2125 2130

Thr Asn Cys Ala Leu Ser Tyr Lys Gly Ala Phe Trp Tyr Arg Asn
2135 2140 2145

Cys His Arg Val Asn Leu Met Gly Arg Tyr Gly Asp Asn Asn His
2150 2155 2160

Ser Gln Gly Val Asn Trp Phe His Trp Lys Gly His Glu His Ser
2165 2170 2175

Ile Gln Phe Ala Glu Met Lys Leu Arg Pro Ser Asn Phe Arg Asn
2180 2185 2190

Leu Glu Gly Arg Arg Lys Arg Ala
2195 2200

<210> 76
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Fibcon FN3 domain

<400> 76

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

Ile Thr Val Ser Trp Thr Pro Pro Ser Ala Thr Ile Thr Gly Tyr Arg
20 25 30

Ile Thr Tyr Thr Pro Ser Asn Gly Pro Gly Glu Pro Lys Glu Leu Thr
35 40 45

Val Pro Pro Ser Ser Thr Ser Val Thr Ile Thr Gly Leu Thr Pro Gly
50 55 60

Val Glu Tyr Val Val Ser Leu Tyr Ala Leu Lys Asp Asn Gln Glu Ser

65 70 75 80

Pro Pro Leu Val Gly Thr Gln Thr Thr
85

<210> 77
<211> 94
<212> PRT
<213> Homo sapiens

<400> 77

Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro Thr
1 5 10 15

Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Val Thr Val Arg Tyr Tyr
20 25 30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
35 40 45

Thr Val Pro Gly Ser Lys Ser Thr Ala Thr Ile Ser Gly Leu Lys Pro
50 55 60

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

Ser Pro Ala Ser Ser Lys Pro Ile Ser Ile Asn Tyr Arg Thr
85 90

<210> 78
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<400> 78

Gly Ser Gly Ser
1

<210> 79
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<400> 79

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Ser
20 25

<210> 80
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<400> 80

Ala Pro Ala Pro
1

<210> 81
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<400> 81

Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro
1 5 10

<210> 82
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<400> 82

Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro
1 5 10 15

Ala Pro Ala Pro
20

<210> 83
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<400> 83

Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro
1 5 10 15

Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro
20 25 30

Ala Pro Ala Pro Ala Pro Ala Pro
35 40

<210> 84
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<400> 84

Ala Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys
1 5 10 15

Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Ala Ala Ala
20 25

<210> 85
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> tencon BC loop

<400> 85

Thr Ala Pro Asp Ala Ala Phe Asp
1 5

<210> 86
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> tencon FG loop

<400> 86

Lys Gly Gly His Arg Ser Asn
1 5

<210> 87
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR binding FN3 domain BC loop

<400> 87

Ala Asp Pro His Gly Phe Tyr Asp
1 5

<210> 88
<211> 8
<212> PRT
<213> Artificial Sequence

<220>

<223> EGFR binding FN3 domain BC loop

<400> 88

Thr Tyr Asp Arg Asp Gly Tyr Asp
1 5

<210> 89
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR binding FN3 domain BC loop

<400> 89

Trp Asp Pro Phe Ser Phe Tyr Asp
1 5

<210> 90
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR binding FN3 domain BC loop

<400> 90

Asp Asp Pro Arg Gly Phe Tyr Glu
1 5

<210> 91
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR binding FN3 domain BC loop

<400> 91

Thr Trp Pro Tyr Ala Asp Leu Asp
1 5

<210> 92
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR binding FN3 domain BC loop

<400> 92

Gly Tyr Asn Gly Asp His Phe Asp
1 5

<210> 93
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR binding FN3 domain BC loop

<400> 93

Asp Tyr Asp Leu Gly Val Tyr Asp
1   5

<210> 94
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR binding FN3 domain BC loop

<400> 94

Asp Asp Pro Trp Asp Phe Tyr Glu
1   5

<210> 95
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR binding FN3 domain FG loop

<400> 95

His Asn Val Tyr Lys Asp Thr Asn Met Arg Gly Leu
1   5   10

<210> 96
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR binding FN3 domain FG loop

<400> 96

Leu Gly Ser Tyr Val Phe Glu His Asp Val Met
1   5   10

<210> 97
<211> 285
<212> DNA
<213> Artificial Sequence

<220>
<223> EGFR binding FN3 domain from ECB97; P54AR4-83V22

<400> 97
atgttgccag cgccgaagaa cctggtagtt agcgaggtta ctgaggacag cgcgcgtctg 60

agctgggacg atccgtgggc gttctacgag agctttctga tccagtatca agagagcgag 120

aaagtcggtg aagcgattgt gctgaccgtc ccgggctccg agcgttccta cgacctgacc 180

ggtttgaagc cgggtaccga gtatacggtg agcatctacg gtgttcacaa tgtctataag 240

gacactaata tccgcggtct gcctctgagc gccattttca ccacc 285

<210> 98
<211> 285
<212> DNA
<213> Artificial Sequence

<220>
<223> EGFR binding FN3 domain from ECB15; P54AR4-83V2

<400> 98
atgctgccag cccctaagaa tctggtcgtg agcgaagtaa ccgaggacag cgcccgcctg 60

agctgggacg acccgtgggc gttctatgag tctttcctga ttcagtatca agaaagcgaa 120

aaagttggcg aagcgatcgt cctgaccgtc ccgggtagcg agcgctccta cgatctgacc 180

ggcctgaaac cgggtacgga gtacacggtg tccatttacg gtgttcacaa tgtgtataaa 240

gacaccaaca tgcgtggcct gccgctgtcg gcgattttca ccacc 285

<210> 99
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> tencon27 FN3 domain

<400> 99

Leu Pro Ala Pro Lys Asn Leu Val Val Ser Arg Val Thr Glu Asp Ser
1 5 10 15

Ala Arg Leu Ser Trp Thr Ala Pro Asp Ala Ala Phe Asp Ser Phe Leu
20 25 30

Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu Thr
35 40 45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
50 55 60

Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val Lys Gly Gly His Arg Ser
65 70 75 80

Asn Pro Leu Ser Ala Ile Phe Thr Thr
85

<210> 100
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> TCL14 library

<220>

<221> MISC_FEATURE
<222> (32)..(32)
<223> Xaa is any amino acid

<220>
<221> MISC_FEATURE
<222> (34)..(34)
<223> Xaa is any amino acid

<220>
<221> MISC_FEATURE
<222> (36)..(36)
<223> Xaa is any amino acid

<220>
<221> MISC_FEATURE
<222> (38)..(38)
<223> Xaa is any amino acid

<220>
<221> MISC_FEATURE
<222> (39)..(39)
<223> Xaa is any amino acid

<220>
<221> MISC_FEATURE
<222> (40)..(40)
<223> Xaa is any amino acid

<220>
<221> MISC_FEATURE
<222> (41)..(41)
<223> Xaa is any amino acid

<220>
<221> MISC_FEATURE
<222> (68)..(68)
<223> Xaa is any amino acid

<220>
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<222> (70)..(70)
<223> Xaa is any amino acid

<220>
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<222> (72)..(72)
<223> Xaa is any amino acid

<220>
<221> MISC_FEATURE
<222> (78)..(78)
<223> Xaa is any amino acid

<220>
<221> MISC_FEATURE
<222> (79)..(79)
<223> Xaa is any amino acid

<220>
<221> MISC_FEATURE
<222> (81)..(81)
<223> Xaa is any amino acid

<400> 100

Leu Pro Ala Pro Lys Asn Leu Val Val Ser Arg Val Thr Glu Asp Ser
1 5 10 15

Ala Arg Leu Ser Trp Thr Ala Pro Asp Ala Ala Phe Asp Ser Phe Xaa
            20   25   30

Ile Xaa Tyr Xaa Glu Xaa Xaa Xaa Xaa Gly Glu Ala Ile Val Leu Thr
        35   40   45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
    50   55   60

Thr Glu Tyr Xaa Val Xaa Ile Xaa Gly Val Lys Gly Gly Xaa Xaa Ser
65   70   75   80

Xaa Pro Leu Ser Ala Ile Phe Thr Thr
                85

<210> 101
<211> 1408
<212> PRT
<213> HOMO SAPIENS

<400> 101

Met Lys Ala Pro Ala Val Leu Ala Pro Gly Ile Leu Val Leu Leu Phe
1   5   10   15

Thr Leu Val Gln Arg Ser Asn Gly Glu Cys Lys Glu Ala Leu Ala Lys
            20   25   30

Ser Glu Met Asn Val Asn Met Lys Tyr Gln Leu Pro Asn Phe Thr Ala
        35   40   45

Glu Thr Pro Ile Gln Asn Val Ile Leu His Glu His His Ile Phe Leu
    50   55   60

Gly Ala Thr Asn Tyr Ile Tyr Val Leu Asn Glu Glu Asp Leu Gln Lys
65   70   75   80

Val Ala Glu Tyr Lys Thr Gly Pro Val Leu Glu His Pro Asp Cys Phe
                85   90   95

Pro Cys Gln Asp Cys Ser Ser Lys Ala Asn Leu Ser Gly Gly Val Trp
            100   105   110

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

Gln Leu Ile Ser Cys Gly Ser Val Asn Arg Gly Thr Cys Gln Arg His
    130   135   140

Val Phe Pro His Asn His Thr Ala Asp Ile Gln Ser Glu Val His Cys
145   150   155   160

```
Ile Phe Ser Pro Gln Ile Glu Glu Pro Ser Gln Cys Pro Asp Cys Val
                165                 170                 175

Val Ser Ala Leu Gly Ala Lys Val Leu Ser Ser Val Lys Asp Arg Phe
            180                 185                 190

Ile Asn Phe Phe Val Gly Asn Thr Ile Asn Ser Ser Tyr Phe Pro Asp
        195                 200                 205

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

Gly Phe Met Phe Leu Thr Asp Gln Ser Tyr Ile Asp Val Leu Pro Glu
225                 230                 235                 240

Phe Arg Asp Ser Tyr Pro Ile Lys Tyr Val His Ala Phe Glu Ser Asn
                245                 250                 255

Asn Phe Ile Tyr Phe Leu Thr Val Gln Arg Glu Thr Leu Asp Ala Gln
            260                 265                 270

Thr Phe His Thr Arg Ile Ile Arg Phe Cys Ser Ile Asn Ser Gly Leu
        275                 280                 285

His Ser Tyr Met Glu Met Pro Leu Glu Cys Ile Leu Thr Glu Lys Arg
    290                 295                 300

Lys Lys Arg Ser Thr Lys Lys Glu Val Phe Asn Ile Leu Gln Ala Ala
305                 310                 315                 320

Tyr Val Ser Lys Pro Gly Ala Gln Leu Ala Arg Gln Ile Gly Ala Ser
                325                 330                 335

Leu Asn Asp Asp Ile Leu Phe Gly Val Phe Ala Gln Ser Lys Pro Asp
            340                 345                 350

Ser Ala Glu Pro Met Asp Arg Ser Ala Met Cys Ala Phe Pro Ile Lys
        355                 360                 365

Tyr Val Asn Asp Phe Phe Asn Lys Ile Val Asn Lys Asn Asn Val Arg
    370                 375                 380

Cys Leu Gln His Phe Tyr Gly Pro Asn His Glu His Cys Phe Asn Arg
385                 390                 395                 400

Thr Leu Leu Arg Asn Ser Ser Gly Cys Glu Ala Arg Arg Asp Glu Tyr
                405                 410                 415

Arg Thr Glu Phe Thr Thr Ala Leu Gln Arg Val Asp Leu Phe Met Gly
            420                 425                 430
```

```
Gln Phe Ser Glu Val Leu Leu Thr Ser Ile Ser Thr Phe Ile Lys Gly
        435                 440                 445

Asp Leu Thr Ile Ala Asn Leu Gly Thr Ser Glu Gly Arg Phe Met Gln
    450                 455                 460

Val Val Val Ser Arg Ser Gly Pro Ser Thr Pro His Val Asn Phe Leu
465                 470                 475                 480

Leu Asp Ser His Pro Val Ser Pro Glu Val Ile Val Glu His Thr Leu
                485                 490                 495

Asn Gln Asn Gly Tyr Thr Leu Val Ile Thr Gly Lys Lys Ile Thr Lys
            500                 505                 510

Ile Pro Leu Asn Gly Leu Gly Cys Arg His Phe Gln Ser Cys Ser Gln
        515                 520                 525

Cys Leu Ser Ala Pro Pro Phe Val Gln Cys Gly Trp Cys His Asp Lys
    530                 535                 540

Cys Val Arg Ser Glu Glu Cys Leu Ser Gly Thr Trp Thr Gln Gln Ile
545                 550                 555                 560

Cys Leu Pro Ala Ile Tyr Lys Val Phe Pro Asn Ser Ala Pro Leu Glu
                565                 570                 575

Gly Gly Thr Arg Leu Thr Ile Cys Gly Trp Asp Phe Gly Phe Arg Arg
            580                 585                 590

Asn Asn Lys Phe Asp Leu Lys Lys Thr Arg Val Leu Leu Gly Asn Glu
        595                 600                 605

Ser Cys Thr Leu Thr Leu Ser Glu Ser Thr Met Asn Thr Leu Lys Cys
    610                 615                 620

Thr Val Gly Pro Ala Met Asn Lys His Phe Asn Met Ser Ile Ile Ile
625                 630                 635                 640

Ser Asn Gly His Gly Thr Thr Gln Tyr Ser Thr Phe Ser Tyr Val Asp
                645                 650                 655

Pro Val Ile Thr Ser Ile Ser Pro Lys Tyr Gly Pro Met Ala Gly Gly
            660                 665                 670

Thr Leu Leu Thr Leu Thr Gly Asn Tyr Leu Asn Ser Gly Asn Ser Arg
        675                 680                 685

His Ile Ser Ile Gly Gly Lys Thr Cys Thr Leu Lys Ser Val Ser Asn
    690                 695                 700
```

```
Ser Ile Leu Glu Cys Tyr Thr Pro Ala Gln Thr Ile Ser Thr Glu Phe
705                 710                 715                 720

Ala Val Lys Leu Lys Ile Asp Leu Ala Asn Arg Glu Thr Ser Ile Phe
                725                 730                 735

Ser Tyr Arg Glu Asp Pro Ile Val Tyr Glu Ile His Pro Thr Lys Ser
            740                 745                 750

Phe Ile Ser Thr Trp Trp Lys Glu Pro Leu Asn Ile Val Ser Phe Leu
        755                 760                 765

Phe Cys Phe Ala Ser Gly Gly Ser Thr Ile Thr Gly Val Gly Lys Asn
    770                 775                 780

Leu Asn Ser Val Ser Val Pro Arg Met Val Ile Asn Val His Glu Ala
785                 790                 795                 800

Gly Arg Asn Phe Thr Val Ala Cys Gln His Arg Ser Asn Ser Glu Ile
                805                 810                 815

Ile Cys Cys Thr Thr Pro Ser Leu Gln Gln Leu Asn Leu Gln Leu Pro
            820                 825                 830

Leu Lys Thr Lys Ala Phe Phe Met Leu Asp Gly Ile Leu Ser Lys Tyr
        835                 840                 845

Phe Asp Leu Ile Tyr Val His Asn Pro Val Phe Lys Pro Phe Glu Lys
    850                 855                 860

Pro Val Met Ile Ser Met Gly Asn Glu Asn Val Leu Glu Ile Lys Gly
865                 870                 875                 880

Asn Asp Ile Asp Pro Glu Ala Val Lys Gly Glu Val Leu Lys Val Gly
                885                 890                 895

Asn Lys Ser Cys Glu Asn Ile His Leu His Ser Glu Ala Val Leu Cys
            900                 905                 910

Thr Val Pro Asn Asp Leu Leu Lys Leu Asn Ser Glu Leu Asn Ile Glu
        915                 920                 925

Trp Lys Gln Ala Ile Ser Ser Thr Val Leu Gly Lys Val Ile Val Gln
    930                 935                 940

Pro Asp Gln Asn Phe Thr Gly Leu Ile Ala Gly Val Val Ser Ile Ser
945                 950                 955                 960

Thr Ala Leu Leu Leu Leu Leu Gly Phe Phe Leu Trp Leu Lys Lys Arg
                965                 970                 975
```

```
Lys Gln Ile Lys Asp Leu Gly Ser Glu Leu Val Arg Tyr Asp Ala Arg
            980                 985                 990

Val His Thr Pro His Leu Asp Arg  Leu Val Ser Ala Arg  Ser Val Ser
        995                 1000                1005

Pro Thr  Thr Glu Met Val Ser  Asn Glu Ser Val Asp  Tyr Arg Ala
    1010                1015                1020

Thr Phe  Pro Glu Asp Gln Phe  Pro Asn Ser Ser Gln  Asn Gly Ser
    1025                1030                1035

Cys Arg  Gln Val Gln Tyr Pro  Leu Thr Asp Met Ser  Pro Ile Leu
    1040                1045                1050

Thr Ser  Gly Asp Ser Asp Ile  Ser Ser Pro Leu Leu  Gln Asn Thr
    1055                1060                1065

Val His  Ile Asp Leu Ser Ala  Leu Asn Pro Glu Leu  Val Gln Ala
    1070                1075                1080

Val Gln  His Val Val Ile Gly  Pro Ser Ser Leu Ile  Val His Phe
    1085                1090                1095

Asn Glu  Val Ile Gly Arg Gly  His Phe Gly Cys Val  Tyr His Gly
    1100                1105                1110

Thr Leu  Leu Asp Asn Asp Gly  Lys Lys Ile His Cys  Ala Val Lys
    1115                1120                1125

Ser Leu  Asn Arg Ile Thr Asp  Ile Gly Glu Val Ser  Gln Phe Leu
    1130                1135                1140

Thr Glu  Gly Ile Ile Met Lys  Asp Phe Ser His Pro  Asn Val Leu
    1145                1150                1155

Ser Leu  Leu Gly Ile Cys Leu  Arg Ser Glu Gly Ser  Pro Leu Val
    1160                1165                1170

Val Leu  Pro Tyr Met Lys His  Gly Asp Leu Arg Asn  Phe Ile Arg
    1175                1180                1185

Asn Glu  Thr His Asn Pro Thr  Val Lys Asp Leu Ile  Gly Phe Gly
    1190                1195                1200

Leu Gln  Val Ala Lys Gly Met  Lys Tyr Leu Ala Ser  Lys Lys Phe
    1205                1210                1215

Val His  Arg Asp Leu Ala Ala  Arg Asn Cys Met Leu  Asp Glu Lys
    1220                1225                1230
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```
Phe Thr  Val Lys Val Ala Asp  Phe Gly Leu Ala Arg  Asp Met Tyr
    1235                 1240                 1245


Asp Lys  Glu Tyr Tyr Ser Val  His Asn Lys Thr Gly  Ala Lys Leu
    1250                 1255                 1260


Pro Val  Lys Trp Met Ala Leu  Glu Ser Leu Gln Thr  Gln Lys Phe
    1265                 1270                 1275


Thr Thr  Lys Ser Asp Val Trp  Ser Phe Gly Val Leu  Leu Trp Glu
    1280                 1285                 1290


Leu Met  Thr Arg Gly Ala Pro  Pro Tyr Pro Asp Val  Asn Thr Phe
    1295                 1300                 1305


Asp Ile  Thr Val Tyr Leu Leu  Gln Gly Arg Arg Leu  Leu Gln Pro
    1310                 1315                 1320


Glu Tyr  Cys Pro Asp Pro Leu  Tyr Glu Val Met Leu  Lys Cys Trp
    1325                 1330                 1335


His Pro  Lys Ala Glu Met Arg  Pro Ser Phe Ser Glu  Leu Val Ser
    1340                 1345                 1350


Arg Ile  Ser Ala Ile Phe Ser  Thr Phe Ile Gly Glu  His Tyr Val
    1355                 1360                 1365


His Val  Asn Ala Thr Tyr Val  Asn Val Lys Cys Val  Ala Pro Tyr
    1370                 1375                 1380


Pro Ser  Leu Leu Ser Ser Glu  Asp Asn Ala Asp Asp  Glu Val Asp
    1385                 1390                 1395


Thr Arg  Pro Ala Ser Phe Trp  Glu Thr Ser
    1400                 1405


<210>  102
<211>  697
<212>  PRT
<213>  HOMO SAPIENS

<400>  102

Gln Arg Lys Arg Arg Asn Thr Ile His Glu Phe Lys Lys Ser Ala Lys
1               5                  10                  15


Thr Thr Leu Ile Lys Ile Asp Pro Ala Leu Lys Ile Lys Thr Lys Lys
            20                  25                  30


Val Asn Thr Ala Asp Gln Cys Ala Asn Arg Cys Thr Arg Asn Lys Gly
        35                  40                  45
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Leu Pro Phe Thr Cys Lys Ala Phe Val Phe Asp Lys Ala Arg Lys Gln
    50                  55                  60

Cys Leu Trp Phe Pro Phe Asn Ser Met Ser Ser Gly Val Lys Lys Glu
65                  70                  75                  80

Phe Gly His Glu Phe Asp Leu Tyr Glu Asn Lys Asp Tyr Ile Arg Asn
                85                  90                  95

Cys Ile Ile Gly Lys Gly Arg Ser Tyr Lys Gly Thr Val Ser Ile Thr
            100                 105                 110

Lys Ser Gly Ile Lys Cys Gln Pro Trp Ser Ser Met Ile Pro His Glu
        115                 120                 125

His Ser Phe Leu Pro Ser Ser Tyr Arg Gly Lys Asp Leu Gln Glu Asn
    130                 135                 140

Tyr Cys Arg Asn Pro Arg Gly Glu Glu Gly Gly Pro Trp Cys Phe Thr
145                 150                 155                 160

Ser Asn Pro Glu Val Arg Tyr Glu Val Cys Asp Ile Pro Gln Cys Ser
                165                 170                 175

Glu Val Glu Cys Met Thr Cys Asn Gly Glu Ser Tyr Arg Gly Leu Met
            180                 185                 190

Asp His Thr Glu Ser Gly Lys Ile Cys Gln Arg Trp Asp His Gln Thr
        195                 200                 205

Pro His Arg His Lys Phe Leu Pro Glu Arg Tyr Pro Asp Lys Gly Phe
    210                 215                 220

Asp Asp Asn Tyr Cys Arg Asn Pro Asp Gly Gln Pro Arg Pro Trp Cys
225                 230                 235                 240

Tyr Thr Leu Asp Pro His Thr Arg Trp Glu Tyr Cys Ala Ile Lys Thr
                245                 250                 255

Cys Ala Asp Asn Thr Met Asn Asp Thr Asp Val Pro Leu Glu Thr Thr
            260                 265                 270

Glu Cys Ile Gln Gly Gln Gly Glu Gly Tyr Arg Gly Thr Val Asn Thr
        275                 280                 285

Ile Trp Asn Gly Ile Pro Cys Gln Arg Trp Asp Ser Gln Tyr Pro His
    290                 295                 300

Glu His Asp Met Thr Pro Glu Asn Phe Lys Cys Lys Asp Leu Arg Glu
305                 310                 315                 320
```

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Asn Tyr Cys Arg Asn Pro Asp Gly Ser Glu Ser Pro Trp Cys Phe Thr
                325                 330                 335

Thr Asp Pro Asn Ile Arg Val Gly Tyr Cys Ser Gln Ile Pro Asn Cys
            340                 345                 350

Asp Met Ser His Gly Gln Asp Cys Tyr Arg Gly Asn Gly Lys Asn Tyr
        355                 360                 365

Met Gly Asn Leu Ser Gln Thr Arg Ser Gly Leu Thr Cys Ser Met Trp
    370                 375                 380

Asp Lys Asn Met Glu Asp Leu His Arg His Ile Phe Trp Glu Pro Asp
385                 390                 395                 400

Ala Ser Lys Leu Asn Glu Asn Tyr Cys Arg Asn Pro Asp Asp Asp Ala
                405                 410                 415

His Gly Pro Trp Cys Tyr Thr Gly Asn Pro Leu Ile Pro Trp Asp Tyr
            420                 425                 430

Cys Pro Ile Ser Arg Cys Glu Gly Asp Thr Thr Pro Thr Ile Val Asn
        435                 440                 445

Leu Asp His Pro Val Ile Ser Cys Ala Lys Thr Lys Gln Leu Arg Val
    450                 455                 460

Val Asn Gly Ile Pro Thr Arg Thr Asn Ile Gly Trp Met Val Ser Leu
465                 470                 475                 480

Arg Tyr Arg Asn Lys His Ile Cys Gly Gly Ser Leu Ile Lys Glu Ser
                485                 490                 495

Trp Val Leu Thr Ala Arg Gln Cys Phe Pro Ser Arg Asp Leu Lys Asp
            500                 505                 510

Tyr Glu Ala Trp Leu Gly Ile His Asp Val His Gly Arg Gly Asp Glu
        515                 520                 525

Lys Cys Lys Gln Val Leu Asn Val Ser Gln Leu Val Tyr Gly Pro Glu
    530                 535                 540

Gly Ser Asp Leu Val Leu Met Lys Leu Ala Arg Pro Ala Val Leu Asp
545                 550                 555                 560

Asp Phe Val Ser Thr Ile Asp Leu Pro Asn Tyr Gly Cys Thr Ile Pro
                565                 570                 575

Glu Lys Thr Ser Cys Ser Val Tyr Gly Trp Gly Tyr Thr Gly Leu Ile
            580                 585                 590
```

Asn Tyr Asp Gly Leu Leu Arg Val Ala His Leu Tyr Ile Met Gly Asn
595 600 605

Glu Lys Cys Ser Gln His His Arg Gly Lys Val Thr Leu Asn Glu Ser
610 615 620

Glu Ile Cys Ala Gly Ala Glu Lys Ile Gly Ser Gly Pro Cys Glu Gly
625 630 635 640

Asp Tyr Gly Gly Pro Leu Val Cys Glu Gln His Lys Met Arg Met Val
645 650 655

Leu Gly Val Ile Val Pro Gly Arg Gly Cys Ala Ile Pro Asn Arg Pro
660 665 670

Gly Ile Phe Val Arg Val Ala Tyr Tyr Ala Lys Trp Ile His Lys Ile
675 680 685

Ile Leu Thr Tyr Lys Val Pro Gln Ser
690 695

<210> 103
<211> 276
<212> DNA
<213> Artificial Sequence

<220>
<223> c-Met binding FN3 domain

<400> 103
ctgccggctc cgaagaactt ggtggtgagc cgtgttaccg aagatagcgc acgcctgagc 60

tggacggcac cggatgcggc gttcgatagc ttctggattc gctattttga gtttctgggt 120

agcggtgagg caattgttct gacggtgccg ggctctgaac gctcctacga tttgaccggt 180

ctgaaaccgg gcaccgagta tgtggtgaac attctgagcg ttaagggcgg tagcatcagc 240

ccaccgctga gcgcgatctt cacgactggt ggttgc 276

<210> 104
<211> 267
<212> DNA
<213> Artificial Sequence

<220>
<223> c-Met binding FN3 domain

<400> 104
ctgccggcac cgaagaacct ggttgtcagc cgtgtgaccg aggatagcgc acgtttgagc 60

tggaccgctc cggatgcagc ctttgacagc ttctggattc gttactttga atttctgggt 120

agcggtgagg cgatcgttct gacggtgccg ggctctgaac gcagctatga tttgacgggc 180

ctgaagccgg gtactgagta cgtggttaac atcatgggcg ttaagggtgg taaaatcagc 240

ccgccattgt ccgcgatctt taccacg 267

<210> 105
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<400> 105

Gly Gly Gly Gly Ser
1 5

<210> 106
<211> 194
<212> PRT
<213> Artificial Sequence

<220>
<223> Bispecific EGFR/c-Met binding molecule

<400> 106

Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Glu Val Thr Glu Asp
1 5 10 15

Ser Ala Arg Leu Ser Trp Asp Asp Pro Trp Ala Phe Tyr Glu Ser Phe
20 25 30

Leu Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu
35 40 45

Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro
50 55 60

Gly Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys
65 70 75 80

Asp Thr Asn Ile Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Ala
85 90 95

Pro Ala Pro Ala Pro Ala Pro Ala Pro Leu Pro Ala Pro Lys Asn Leu
100 105 110

Val Val Ser Arg Val Thr Glu Asp Ser Ala Arg Leu Ser Trp Thr Ala
115 120 125

Pro Asp Ala Ala Phe Asp Ser Phe Trp Ile Arg Tyr Phe Glu Phe Leu
130 135 140

Gly Ser Gly Glu Ala Ile Val Leu Thr Val Pro Gly Ser Glu Arg Ser
145 150 155 160

Tyr Asp Leu Thr Gly Leu Lys Pro Gly Thr Glu Tyr Val Val Asn Ile
165 170 175

Leu Ser Val Lys Gly Gly Ser Ile Ser Pro Pro Leu Ser Ala Ile Phe
180 185 190

Thr Thr

<210> 107
<211> 94
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR binding FN3 domain

<400> 107

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

Ala Arg Leu Ser Trp Ala Asp Pro His Gly Phe Tyr Asp Ser Phe Leu
20 25 30

Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu Thr
35 40 45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
50 55 60

Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys Asp
65 70 75 80

Thr Asn Met Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr
85 90

<210> 108
<211> 94
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR binding FN3 domain

<400> 108

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

Ala Arg Leu Ser Trp Asp Asp Pro Trp Ala Phe Tyr Glu Ser Phe Leu
20 25 30

Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu Thr
35 40 45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
50 55 60

Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys Asp
65 70 75 80

Thr Asn Ile Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr
85 90

<210> 109
<211> 94
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR binding FN3 domain

<400> 109

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

Ala Arg Leu Ser Trp Asp Asp Pro His Ala Phe Tyr Glu Ser Phe Leu
20 25 30

Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu Thr
35 40 45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
50 55 60

Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys Asp
65 70 75 80

Thr Asn Ile Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr
85 90

<210> 110
<211> 94
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR binding FN3 domain

<400> 110

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

Ala Arg Leu Ser Trp Ala Asp Pro His Gly Phe Tyr Asp Ser Phe Leu
20 25 30

Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu Thr
35 40 45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
50 55 60

Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys Asp
65 70 75 80

Thr Asn Ile Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr
85 90

<210> 111
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> c-Met binding FN3 domain

<400> 111

Leu Pro Ala Pro Lys Asn Leu Val Val Ser Arg Val Thr Glu Asp Ser
1 5 10 15

Ala Arg Leu Ser Trp Thr Ala Pro Asp Ala Ala Phe Asp Ser Phe Trp
20 25 30

Ile Arg Tyr Phe Glu Phe Leu Gly Ser Gly Glu Ala Ile Val Leu Thr
35 40 45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
50 55 60

Thr Glu Tyr Val Val Asn Ile Leu Gly Val Lys Gly Gly Lys Ile Ser
65 70 75 80

Pro Pro Leu Ser Ala Ile Phe Thr Thr
85

<210> 112
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> c-Met binding FN3 domain

<400> 112

Leu Pro Ala Pro Lys Asn Leu Val Val Ser Arg Val Thr Glu Asp Ser
1 5 10 15

Ala Arg Leu Ser Trp Thr Ala Pro Asp Ala Ala Phe Asp Ser Phe Trp
20 25 30

Ile Arg Tyr Phe Glu Phe Val Gly Ser Gly Glu Ala Ile Val Leu Thr
35 40 45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
50 55 60

Thr Glu Tyr Val Val Asn Ile Leu Gly Val Lys Gly Gly Ser Ile Ser
65 70 75 80

Pro Pro Leu Ser Ala Ile Phe Thr Thr
85

<210> 113
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> c-Met binding FN3 domain

<400> 113

Leu Pro Ala Pro Lys Asn Leu Val Val Ser Arg Val Thr Glu Asp Ser
1 5 10 15

Ala Arg Leu Ser Trp Thr Ala Pro Asp Ala Ala Phe Asp Ser Phe Trp
20 25 30

Ile Arg Tyr Phe Glu Phe Val Ser Lys Gly Asp Ala Ile Val Leu Thr
35 40 45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
50 55 60

Thr Glu Tyr Val Val Asn Ile Leu Gly Val Lys Gly Gly Ser Ile Ser
65 70 75 80

Pro Pro Leu Ser Ala Ile Phe Thr Thr
85

<210> 114
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> c-Met binding FN3 domain

<400> 114

Leu Pro Ala Pro Lys Asn Leu Val Val Ser Arg Val Thr Glu Asp Ser
1 5 10 15

Ala Arg Leu Ser Trp Thr Ala Pro Asp Ala Ala Phe Asp Ser Phe Trp
20 25 30

Ile Arg Tyr Phe Glu Phe Leu Gly Ser Gly Glu Ala Ile Val Leu Thr
35 40 45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
50 55 60

Thr Glu Tyr Val Val Asn Ile Leu Ser Val Lys Gly Gly Ser Ile Ser
65 70 75 80

Pro Pro Leu Ser Ala Ile Phe Thr Thr
85

<210> 115
<211> 591
<212> DNA
<213> Artificial Sequence

<220>
<223> Bispecific EGFR/c-Met binding molecule

<400> 115
atgttgccag cgccgaagaa cctggtagtt agcgaggtta ctgaggacag cgcgcgtctg 60

agctgggacg atccgtgggc gttctacgag agctttctga tccagtatca agagagcgag 120

aaagtcggtg aagcgattgt gctgaccgtc ccgggctccg agcgttccta cgacctgacc 180

ggtttgaagc cgggtaccga gtatacggtg agcatctacg gtgttcacaa tgtctataag 240

gacactaata tccgcggtct gcctctgagc gccattttca ccaccgcacc ggcaccggct 300

ccggctcctg ccccgctgcc ggctccgaag aacttggtgg tgagccgtgt taccgaagat 360

agcgcacgcc tgagctggac ggcaccggat gcggcgttcg atagcttctg gattcgctat 420

tttgagtttc tgggtagcgg tgaggcaatt gttctgacgg tgccgggctc tgaacgctcc 480

tacgatttga ccggtctgaa accgggcacc gagtatgtgg tgaacattct gagcgttaag 540

ggcggtagca tcagcccacc gctgagcgcg atcttcacga ctggtggttg c 591

<210> 116
<211> 582
<212> DNA
<213> Artificial Sequence

<220>
<223> Bispecific EGFR/c-Met binding molecule

<400> 116
atgctgccag cccctaagaa tctggtcgtg agcgaagtaa ccgaggacag cgcccgcctg 60

agctgggacg acccgtgggc gttctatgag tctttcctga ttcagtatca agaaagcgaa 120

aaagttggcg aagcgatcgt cctgaccgtc ccgggtagcg agcgctccta cgatctgacc 180

ggcctgaaac cgggtacgga gtacacggtg tccatttacg gtgttcacaa tgtgtataaa 240

gacaccaaca tgcgtggcct gccgctgtcg gcgattttca ccaccgcgcc tgcgccagcg 300

cctgcaccgg ctccgctgcc ggcaccgaag aacctggttg tcagccgtgt gaccgaggat 360

agcgcacgtt tgagctggac cgctccggat gcagcctttg acagcttctg gattcgttac 420

tttgaatttc tgggtagcgg tgaggcgatc gttctgacgg tgccgggctc tgaacgcagc 480

tatgatttga cgggcctgaa gccgggtact gagtacgtgg ttaacatcat gggcgttaag 540

ggtggtaaaa tcagcccgcc attgtccgcg atctttacca cg 582

<210> 117
<211> 51
<212> PRT
<213> Artificial Sequence

<220>
<223> albumin binding domain

<400> 117

Thr Ile Asp Glu Trp Leu Leu Lys Glu Ala Lys Glu Lys Ala Ile Glu
1 5 10 15

Glu Leu Lys Lys Ala Gly Ile Thr Ser Asp Tyr Tyr Phe Asp Leu Ile
20 25 30

Asn Lys Ala Lys Thr Val Glu Gly Val Asn Ala Leu Lys Asp Glu Ile
35 40 45

Leu Lys Ala
50

<210> 118
<211> 250
<212> PRT
<213> Artificial Sequence

<220>
<223> Bispecific EGFR/c-Met binding molecule

<400> 118

Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Glu Val Thr Glu Asp
1 5 10 15

Ser Ala Arg Leu Ser Trp Asp Asp Pro Trp Ala Phe Tyr Glu Ser Phe
20 25 30

Leu Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu
35 40 45

Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro
50 55 60

Gly Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys
65 70 75 80

Asp Thr Asn Met Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Ala
85 90 95

Pro Ala Pro Ala Pro Ala Pro Ala Pro Leu Pro Ala Pro Lys Asn Leu
100 105 110

Val Val Ser Arg Val Thr Glu Asp Ser Ala Arg Leu Ser Trp Thr Ala
115 120 125

Pro Asp Ala Ala Phe Asp Ser Phe Trp Ile Arg Tyr Asp Glu Val Val
130 135 140

Val Gly Gly Glu Ala Ile Val Leu Thr Val Pro Gly Ser Glu Arg Ser
145 150 155 160

Tyr Asp Leu Thr Gly Leu Lys Pro Gly Thr Glu Tyr Tyr Val Asn Ile
165 170 175

Leu Gly Val Lys Gly Gly Ser Ile Ser Val Pro Leu Ser Ala Ile Phe
180 185 190

Thr Thr Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Leu Ala Glu Ala
195 200 205

Lys Val Leu Ala Asn Arg Glu Leu Asp Lys Tyr Gly Val Ser Asp Tyr
210 215 220

Tyr Lys Asn Leu Ile Asn Asn Ala Lys Thr Val Glu Gly Val Lys Ala
225 230 235 240

Leu Leu Asp Glu Ile Leu Ala Ala Leu Pro
245 250

<210> 119
<211> 250
<212> PRT
<213> Artificial Sequence

<220>
<223> Bispecific EGFR/c-Met binding molecule

<400> 119

Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Glu Val Thr Glu Asp
1 5 10 15

Ser Ala Arg Leu Ser Trp Ala Asp Pro His Gly Phe Tyr Asp Ser Phe
20 25 30

Leu Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu
35 40 45

Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro
50 55 60

Gly Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys
65 70 75 80

Asp Thr Asn Met Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Ala
85 90 95

Pro Ala Pro Ala Pro Ala Pro Ala Pro Leu Pro Ala Pro Lys Asn Leu
100 105 110

```
Val Val Ser Arg Val Thr Glu Asp Ser Ala Arg Leu Ser Trp Thr Ala
        115                 120                 125

Pro Asp Ala Ala Phe Asp Ser Phe Trp Ile Arg Tyr Asp Glu Val Val
    130                 135                 140

Val Gly Gly Glu Ala Ile Val Leu Thr Val Pro Gly Ser Glu Arg Ser
145                 150                 155                 160

Tyr Asp Leu Thr Gly Leu Lys Pro Gly Thr Glu Tyr Tyr Val Asn Ile
                165                 170                 175

Leu Gly Val Lys Gly Gly Ser Ile Ser Val Pro Leu Ser Ala Ile Phe
            180                 185                 190

Thr Thr Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Leu Ala Glu Ala
        195                 200                 205

Lys Val Leu Ala Asn Arg Glu Leu Asp Lys Tyr Gly Val Ser Asp Tyr
    210                 215                 220

Tyr Lys Asn Leu Ile Asn Asn Ala Lys Thr Val Glu Gly Val Lys Ala
225                 230                 235                 240

Leu Leu Asp Glu Ile Leu Ala Ala Leu Pro
                245                 250
```

<210> 120
<211> 250
<212> PRT
<213> Artificial Sequence

<220>
<223> Bispecific EGFR/c-Met binding molecule

<400> 120

```
Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Glu Val Thr Glu Asp
1               5                   10                  15

Ser Ala Arg Leu Ser Trp Asp Asp Pro Trp Ala Phe Tyr Glu Ser Phe
            20                  25                  30

Leu Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu
        35                  40                  45

Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro
    50                  55                  60

Gly Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys
65                  70                  75                  80
```

Asp Thr Asn Met Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Ala
85 90 95

Pro Ala Pro Ala Pro Ala Pro Ala Pro Leu Pro Ala Pro Lys Asn Leu
100 105 110

Val Val Ser Arg Val Thr Glu Asp Ser Ala Arg Leu Ser Trp Thr Ala
115 120 125

Pro Asp Ala Ala Phe Asp Ser Phe Trp Ile Arg Tyr Phe Glu Phe Leu
130 135 140

Gly Ser Gly Glu Ala Ile Val Leu Thr Val Pro Gly Ser Glu Arg Ser
145 150 155 160

Tyr Asp Leu Thr Gly Leu Lys Pro Gly Thr Glu Tyr Val Val Asn Ile
165 170 175

Met Gly Val Lys Gly Gly Lys Ile Ser Pro Pro Leu Ser Ala Ile Phe
180 185 190

Thr Thr Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Leu Ala Glu Ala
195 200 205

Lys Val Leu Ala Asn Arg Glu Leu Asp Lys Tyr Gly Val Ser Asp Tyr
210 215 220

Tyr Lys Asn Leu Ile Asn Asn Ala Lys Thr Val Glu Gly Val Lys Ala
225 230 235 240

Leu Leu Asp Glu Ile Leu Ala Ala Leu Pro
245 250

<210> 121
<211> 250
<212> PRT
<213> Artificial Sequence

<220>
<223> Bispecific EGFR/c-Met binding molecule

<400> 121

Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Glu Val Thr Glu Asp
1 5 10 15

Ser Ala Arg Leu Ser Trp Ala Asp Pro His Gly Phe Tyr Asp Ser Phe
20 25 30

Leu Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu
35 40 45

Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro
50 55 60

```
Gly Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys
65                  70                  75                  80

Asp Thr Asn Met Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Ala
                85                  90                  95

Pro Ala Pro Ala Pro Ala Pro Ala Pro Leu Pro Ala Pro Lys Asn Leu
            100                 105                 110

Val Val Ser Arg Val Thr Glu Asp Ser Ala Arg Leu Ser Trp Thr Ala
        115                 120                 125

Pro Asp Ala Ala Phe Asp Ser Phe Trp Ile Arg Tyr Phe Glu Phe Leu
    130                 135                 140

Gly Ser Gly Glu Ala Ile Val Leu Thr Val Pro Gly Ser Glu Arg Ser
145                 150                 155                 160

Tyr Asp Leu Thr Gly Leu Lys Pro Gly Thr Glu Tyr Val Val Asn Ile
                165                 170                 175

Met Gly Val Lys Gly Gly Lys Ile Ser Pro Pro Leu Ser Ala Ile Phe
            180                 185                 190

Thr Thr Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Leu Ala Glu Ala
        195                 200                 205

Lys Val Leu Ala Asn Arg Glu Leu Asp Lys Tyr Gly Val Ser Asp Tyr
    210                 215                 220

Tyr Lys Asn Leu Ile Asn Asn Ala Lys Thr Val Glu Gly Val Lys Ala
225                 230                 235                 240

Leu Leu Asp Glu Ile Leu Ala Ala Leu Pro
                245                 250
```

<210> 122
<211> 95
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR binding FN3 domain

<400> 122

```
Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Glu Val Thr Glu Asp
1               5                   10                  15

Ser Leu Arg Leu Ser Trp Ala Asp Pro His Gly Phe Tyr Asp Ser Phe
            20                  25                  30
```

Leu Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Asn Leu
35 40 45

Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro
50 55 60

Gly Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys
65 70 75 80

Asp Thr Asn Met Arg Gly Leu Pro Leu Ser Ala Glu Phe Thr Thr
85 90 95

<210> 123
<211> 95
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR binding FN3 domain

<400> 123

Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Glu Val Thr Glu Asp
1 5 10 15

Ser Leu Arg Leu Ser Trp Thr Tyr Asp Arg Asp Gly Tyr Asp Ser Phe
20 25 30

Leu Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Asn Leu
35 40 45

Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro
50 55 60

Gly Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys
65 70 75 80

Asp Thr Asn Met Arg Gly Leu Pro Leu Ser Ala Glu Phe Thr Thr
85 90 95

<210> 124
<211> 95
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR binding FN3 domain

<400> 124

Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Glu Val Thr Glu Asp
1 5 10 15

Ser Leu Arg Leu Ser Trp Gly Tyr Asn Gly Asp His Phe Asp Ser Phe
20 25 30

Leu Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Asn Leu
35 40 45

Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro
50 55 60

Gly Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys
65 70 75 80

Asp Thr Asn Met Arg Gly Leu Pro Leu Ser Ala Glu Phe Thr Thr
85 90 95

<210> 125
<211> 95
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR binding FN3 domain

<400> 125

Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Glu Val Thr Glu Asp
1 5 10 15

Ser Leu Arg Leu Ser Trp Asp Asp Pro Arg Gly Phe Tyr Glu Ser Phe
20 25 30

Leu Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Asn Leu
35 40 45

Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro
50 55 60

Gly Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys
65 70 75 80

Asp Thr Asn Met Arg Gly Leu Pro Leu Ser Ala Glu Phe Thr Thr
85 90 95

<210> 126
<211> 95
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR binding FN3 domain

<400> 126

Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Glu Val Thr Glu Asp
1 5 10 15

Ser Leu Arg Leu Ser Trp Thr Trp Pro Tyr Ala Asp Leu Asp Ser Phe
20 25 30

Leu Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Asn Leu
35 40 45

Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro
50 55 60

Gly Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys
65 70 75 80

Asp Thr Asn Met Arg Gly Leu Pro Leu Ser Ala Glu Phe Thr Thr
85 90 95

<210> 127
<211> 95
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR binding FN3 domain

<400> 127

Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Glu Val Thr Glu Asp
1 5 10 15

Ser Leu Arg Leu Ser Trp Gly Tyr Asn Gly Asp His Phe Asp Ser Phe
20 25 30

Leu Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Asn Leu
35 40 45

Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro
50 55 60

Gly Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys
65 70 75 80

Asp Thr Asn Met Arg Gly Leu Pro Leu Ser Ala Glu Phe Thr Thr
85 90 95

<210> 128
<211> 96
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR binding FN3 domain

<400> 128

Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Glu Val Thr Glu Asp
1 5 10 15

Ser Leu Arg Leu Ser Trp Asp Tyr Asp Leu Gly Val Tyr Phe Asp Ser
20 25 30

Phe Leu Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Asn
35 40 45

Leu Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys
50 55 60

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

Lys Asp Thr Asn Met Arg Gly Leu Pro Leu Ser Ala Glu Phe Thr Thr
85 90 95

<210> 129
<211> 95
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR binding FN3 domain

<400> 129

Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Glu Val Thr Glu Asp
1 5 10 15

Ser Leu Arg Leu Ser Trp Asp Asp Pro Trp Ala Phe Tyr Glu Ser Phe
20 25 30

Leu Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Asn Leu
35 40 45

Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro
50 55 60

Gly Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys
65 70 75 80

Asp Thr Asn Met Arg Gly Leu Pro Leu Ser Ala Glu Phe Thr Thr
85 90 95

<210> 130
<211> 95
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR binding FN3 domain

<400> 130

Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Glu Val Thr Glu Asp
1 5 10 15

Ser Leu Arg Leu Ser Trp Thr Ala Pro Asp Ala Ala Phe Asp Ser Phe
20 25 30

```
Leu Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Asn Leu
        35                  40                  45

Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro
    50                  55                  60

Gly Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val Leu Gly Ser Tyr Val
65                  70                  75                  80

Phe Glu His Asp Val Met Leu Pro Leu Ser Ala Glu Phe Thr Thr
                85                  90                  95


<210>  131
<211>  95
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  EGFR binding FN3 domain

<400>  131

Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Glu Val Thr Glu Asp
1               5                   10                  15

Ser Ala Arg Leu Ser Trp Asp Asp Pro Trp Ala Phe Tyr Glu Ser Phe
            20                  25                  30

Leu Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu
        35                  40                  45

Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro
    50                  55                  60

Gly Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys
65                  70                  75                  80

Asp Thr Asn Met Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr
                85                  90                  95


<210>  132
<211>  95
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  EGFR binding FN3 domain

<400>  132

Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Glu Val Thr Glu Asp
1               5                   10                  15

Ser Ala Arg Leu Ser Trp Thr Ala Pro Asp Ala Ala Phe Asp Ser Phe
            20                  25                  30
```

Leu Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu
35 40 45

Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro
50 55 60

Gly Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val Leu Gly Ser Tyr Val
65 70 75 80

Phe Glu His Asp Val Met Leu Pro Leu Ser Ala Ile Phe Thr Thr
85 90 95

<210> 133
<211> 95
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR binding FN3 domain

<400> 133

Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Glu Val Thr Glu Asp
1 5 10 15

Ser Leu Arg Leu Ser Trp Thr Trp Pro Tyr Ala Asp Leu Asp Ser Phe
20 25 30

Leu Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Asn Leu
35 40 45

Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro
50 55 60

Gly Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys
65 70 75 80

Asp Thr Asn Met Arg Gly Leu Pro Leu Ser Ala Glu Phe Thr Thr
85 90 95

<210> 134
<211> 95
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR binding FN3 domain

<400> 134

Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Glu Val Thr Glu Asp
1 5 10 15

Ser Ala Arg Leu Ser Trp Ala Asp Pro His Gly Phe Tyr Asp Ser Phe
20 25 30

Leu Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu
35 40 45

Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro
50 55 60

Gly Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys
65 70 75 80

Asp Thr Asn Met Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr
85 90 95

<210> 135
<211> 95
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR binding FN3 domain

<400> 135

Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Glu Val Thr Glu Asp
1 5 10 15

Ser Ala Arg Leu Ser Trp Asp Asp Pro Trp Ala Phe Tyr Glu Ser Phe
20 25 30

Leu Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu
35 40 45

Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro
50 55 60

Gly Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys
65 70 75 80

Asp Thr Asn Ile Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr
85 90 95

<210> 136
<211> 95
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR binding FN3 domain

<400> 136

Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Glu Val Thr Glu Asp
1 5 10 15

Ser Ala Arg Leu Ser Trp Asp Asp Pro His Ala Phe Tyr Glu Ser Phe
20 25 30

Leu Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu
35 40 45

Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro
50 55 60

Gly Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys
65 70 75 80

Asp Thr Asn Ile Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr
85 90 95

<210> 137
<211> 95
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR binding FN3 domain

<400> 137

Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Glu Val Thr Glu Asp
1 5 10 15

Ser Ala Arg Leu Ser Trp Ala Asp Pro His Gly Phe Tyr Asp Ser Phe
20 25 30

Leu Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu
35 40 45

Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro
50 55 60

Gly Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys
65 70 75 80

Asp Thr Asn Ile Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr
85 90 95

<210> 138
<211> 204
<212> PRT
<213> Artificial Sequence

<220>
<223> Bispecific EGFR/c-Met binding domain

<400> 138

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

Ala Arg Leu Ser Trp Asp Asp Pro Trp Ala Phe Tyr Glu Ser Phe Leu
20 25 30

Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu Thr
35 40 45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
50 55 60

Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys Asp
65 70 75 80

Thr Asn Met Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Gly Gly
85 90 95

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
100 105 110

Gly Ser Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Arg Val Thr
115 120 125

Glu Asp Ser Ala Arg Leu Ser Trp Thr Ala Pro Asp Ala Ala Phe Asp
130 135 140

Ser Phe Trp Ile Arg Tyr Asp Glu Val Val Val Gly Gly Glu Ala Ile
145 150 155 160

Val Leu Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu
165 170 175

Lys Pro Gly Thr Glu Tyr Tyr Val Asn Ile Leu Gly Val Lys Gly Gly
180 185 190

Ser Ile Ser Val Pro Leu Ser Ala Ile Phe Thr Thr
195 200

<210> 139
<211> 203
<212> PRT
<213> Artificial Sequence

<220>
<223> Bispecific EGFR/c-Met binding domain

<400> 139

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

Ala Arg Leu Ser Trp Asp Asp Pro Trp Ala Phe Tyr Glu Ser Phe Leu
20 25 30

Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu Thr
35 40 45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
50 55 60

```
Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys Asp
65                  70                  75                  80

Thr Asn Met Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Gly Gly
                85                  90                  95

Gly Gly Ser Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
            100                 105                 110

Gly Ser Leu Pro Ala Pro Lys Asn Leu Val Val Ser Arg Val Thr Glu
        115                 120                 125

Asp Ser Ala Arg Leu Ser Trp Thr Ala Pro Asp Ala Ala Phe Asp Ser
    130                 135                 140

Phe Trp Ile Arg Tyr Phe Glu Phe Leu Gly Ser Gly Glu Ala Ile Val
145                 150                 155                 160

Leu Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys
                165                 170                 175

Pro Gly Thr Glu Tyr Val Val Asn Ile Met Gly Val Lys Gly Gly Lys
            180                 185                 190

Ile Ser Pro Pro Leu Ser Ala Ile Phe Thr Thr
        195                 200


<210>  140
<211>  204
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Bispecific EGFR/c-Met binding domain

<400>  140

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

Ala Arg Leu Ser Trp Asp Asp Pro Trp Ala Phe Tyr Glu Ser Phe Leu
            20                  25                  30

Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu Thr
        35                  40                  45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
    50                  55                  60

Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys Asp
65                  70                  75                  80
```

```
Thr Asn Met Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Gly Gly
                85                  90                  95

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
            100                 105                 110

Gly Ser Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Arg Val Thr
        115                 120                 125

Glu Asp Ser Ala Arg Leu Ser Trp Thr Ala Pro Asp Ala Ala Phe Asp
    130                 135                 140

Ser Phe Trp Ile Arg Tyr Phe Glu Phe Leu Gly Ser Gly Glu Ala Ile
145                 150                 155                 160

Val Leu Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu
                165                 170                 175

Lys Pro Gly Thr Glu Tyr Val Val Gln Ile Ile Gly Val Lys Gly Gly
            180                 185                 190

His Ile Ser Leu Pro Leu Ser Ala Ile Phe Thr Thr
        195                 200
```

<210> 141
<211> 204
<212> PRT
<213> Artificial Sequence

<220>
<223> Bispecific EGFR/c-Met binding domain

<400> 141

```
Leu Pro Ala Pro Lys Asn Leu Val Val Ser Glu Val Thr Glu Asp Ser
1               5                   10                  15

Ala Arg Leu Ser Trp Asp Asp Pro Trp Ala Phe Tyr Glu Ser Phe Leu
            20                  25                  30

Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu Thr
        35                  40                  45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
    50                  55                  60

Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys Asp
65                  70                  75                  80

Thr Asn Met Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Gly Gly
                85                  90                  95

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
            100                 105                 110
```

```
Gly Ser Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Arg Val Thr
        115                 120                 125


Glu Asp Ser Ala Arg Leu Ser Trp Thr Ala Pro Asp Ala Ala Phe Asp
    130                 135                 140


Ser Phe Phe Ile Arg Tyr Asp Glu Phe Leu Arg Ser Gly Glu Ala Ile
145                 150                 155                 160


Val Leu Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu
                165                 170                 175


Lys Pro Gly Thr Glu Tyr Trp Val Thr Ile Leu Gly Val Lys Gly Gly
            180                 185                 190


Leu Val Ser Thr Pro Leu Ser Ala Ile Phe Thr Thr
        195                 200


<210>  142
<211>  204
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Bispecific EGFR/c-Met binding domain

<400>  142

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


Ala Arg Leu Ser Trp Ala Asp Pro His Gly Phe Tyr Asp Ser Phe Leu
            20                  25                  30


Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu Thr
        35                  40                  45


Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
    50                  55                  60


Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys Asp
65                  70                  75                  80


Thr Asn Met Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Gly Gly
                85                  90                  95


Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
            100                 105                 110


Gly Ser Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Arg Val Thr
        115                 120                 125
```

```
Glu Asp Ser Ala Arg Leu Ser Trp Thr Ala Pro Asp Ala Ala Phe Asp
    130                 135                 140

Ser Phe Trp Ile Arg Tyr Phe Glu Phe Leu Gly Ser Gly Glu Ala Ile
145                 150                 155                 160

Val Leu Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu
                165                 170                 175

Lys Pro Gly Thr Glu Tyr Val Val Asn Ile Met Gly Val Lys Gly Gly
            180                 185                 190

Lys Ile Ser Pro Pro Leu Ser Ala Ile Phe Thr Thr
        195                 200
```

<210> 143
<211> 204
<212> PRT
<213> Artificial Sequence

<220>
<223> Bispecific EGFR/c-Met binding domain

<400> 143

```
Leu Pro Ala Pro Lys Asn Leu Val Val Ser Glu Val Thr Glu Asp Ser
1               5                   10                  15

Ala Arg Leu Ser Trp Ala Asp Pro His Gly Phe Tyr Asp Ser Phe Leu
            20                  25                  30

Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu Thr
        35                  40                  45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
    50                  55                  60

Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys Asp
65                  70                  75                  80

Thr Asn Met Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Gly Gly
                85                  90                  95

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
            100                 105                 110

Gly Ser Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Arg Val Thr
        115                 120                 125

Glu Asp Ser Ala Arg Leu Ser Trp Thr Ala Pro Asp Ala Ala Phe Asp
    130                 135                 140

Ser Phe Trp Ile Arg Tyr Phe Glu Phe Leu Gly Ser Gly Glu Ala Ile
145                 150                 155                 160
```

Val Leu Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu
165 170 175

Lys Pro Gly Thr Glu Tyr Val Val Gln Ile Ile Gly Val Lys Gly Gly
180 185 190

His Ile Ser Leu Pro Leu Ser Ala Ile Phe Thr Thr
195 200

<210> 144
<211> 204
<212> PRT
<213> Artificial Sequence

<220>
<223> Bispecific EGFR/c-Met binding domain

<400> 144

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

Ala Arg Leu Ser Trp Ala Asp Pro His Gly Phe Tyr Asp Ser Phe Leu
20 25 30

Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu Thr
35 40 45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
50 55 60

Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys Asp
65 70 75 80

Thr Asn Met Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Gly Gly
85 90 95

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
100 105 110

Gly Ser Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Arg Val Thr
115 120 125

Glu Asp Ser Ala Arg Leu Ser Trp Thr Ala Pro Asp Ala Ala Phe Asp
130 135 140

Ser Phe Trp Ile Arg Tyr Phe Glu Phe Leu Gly Ser Gly Glu Ala Ile
145 150 155 160

Val Leu Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu
165 170 175

Lys Pro Gly Thr Glu Tyr Val Val Gln Ile Ile Gly Val Lys Gly Gly
180 185 190

His Ile Ser Leu Pro Leu Ser Ala Ile Phe Thr Thr
195 200

<210> 145
<211> 193
<212> PRT
<213> Artificial Sequence

<220>
<223> Bispecific EGFR/c-Met binding domain

<400> 145

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

Ala Arg Leu Ser Trp Asp Asp Pro Trp Ala Phe Tyr Glu Ser Phe Leu
20 25 30

Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu Thr
35 40 45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
50 55 60

Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys Asp
65 70 75 80

Thr Asn Met Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Ala Pro
85 90 95

Ala Pro Ala Pro Ala Pro Ala Pro Leu Pro Ala Pro Lys Asn Leu Val
100 105 110

Val Ser Arg Val Thr Glu Asp Ser Ala Arg Leu Ser Trp Thr Ala Pro
115 120 125

Asp Ala Ala Phe Asp Ser Phe Trp Ile Arg Tyr Phe Glu Phe Leu Gly
130 135 140

Ser Gly Glu Ala Ile Val Leu Thr Val Pro Gly Ser Glu Arg Ser Tyr
145 150 155 160

Asp Leu Thr Gly Leu Lys Pro Gly Thr Glu Tyr Val Val Asn Ile Met
165 170 175

Gly Val Lys Gly Gly Lys Ile Ser Pro Pro Leu Ser Ala Ile Phe Thr
180 185 190

Thr

<210> 146
<211> 193
<212> PRT
<213> Artificial Sequence

<220>
<223> Bispecific EGFR/c-Met binding domain

<400> 146

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

Ala Arg Leu Ser Trp Asp Asp Pro Trp Ala Phe Tyr Glu Ser Phe Leu
20 25 30

Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu Thr
35 40 45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
50 55 60

Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys Asp
65 70 75 80

Thr Asn Met Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Ala Pro
85 90 95

Ala Pro Ala Pro Ala Pro Ala Pro Leu Pro Ala Pro Lys Asn Leu Val
100 105 110

Val Ser Arg Val Thr Glu Asp Ser Ala Arg Leu Ser Trp Thr Ala Pro
115 120 125

Asp Ala Ala Phe Asp Ser Phe Trp Ile Arg Tyr Asp Glu Val Val Val
130 135 140

Gly Gly Glu Ala Ile Val Leu Thr Val Pro Gly Ser Glu Arg Ser Tyr
145 150 155 160

Asp Leu Thr Gly Leu Lys Pro Gly Thr Glu Tyr Tyr Val Asn Ile Leu
165 170 175

Gly Val Lys Gly Gly Ser Ile Ser Val Pro Leu Ser Ala Ile Phe Thr
180 185 190

Thr

<210> 147
<211> 194
<212> PRT
<213> Artificial Sequence

<220>
<223> Bispecific EGFR/c-Met binding domain

<400> 147

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

Ala Arg Leu Ser Trp Ala Asp Pro His Gly Phe Tyr Asp Ser Phe Leu
20 25 30

Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu Thr
35 40 45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
50 55 60

Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys Asp
65 70 75 80

Thr Asn Met Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Ala Pro
85 90 95

Ala Pro Ala Pro Ala Pro Ala Pro Met Leu Pro Ala Pro Lys Asn Leu
100 105 110

Val Val Ser Arg Val Thr Glu Asp Ser Ala Arg Leu Ser Trp Thr Ala
115 120 125

Pro Asp Ala Ala Phe Asp Ser Phe Trp Ile Arg Tyr Phe Glu Phe Leu
130 135 140

Gly Ser Gly Glu Ala Ile Val Leu Thr Val Pro Gly Ser Glu Arg Ser
145 150 155 160

Tyr Asp Leu Thr Gly Leu Lys Pro Gly Thr Glu Tyr Val Val Asn Ile
165 170 175

Met Gly Val Lys Gly Gly Lys Ile Ser Pro Pro Leu Ser Ala Ile Phe
180 185 190

Thr Thr

<210> 148
<211> 193
<212> PRT
<213> Artificial Sequence

<220>
<223> Bispecific EGFR/c-Met binding domain

<400> 148

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

Ala Arg Leu Ser Trp Ala Asp Pro His Gly Phe Tyr Asp Ser Phe Leu
20 25 30

Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu Thr
35 40 45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
50 55 60

Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys Asp
65 70 75 80

Thr Asn Met Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Ala Pro
85 90 95

Ala Pro Ala Pro Ala Pro Ala Pro Leu Pro Ala Pro Lys Asn Leu Val
100 105 110

Val Ser Arg Val Thr Glu Asp Ser Ala Arg Leu Ser Trp Thr Ala Pro
115 120 125

Asp Ala Ala Phe Asp Ser Phe Trp Ile Arg Tyr Asp Glu Val Val Val
130 135 140

Gly Gly Glu Ala Ile Val Leu Thr Val Pro Gly Ser Glu Arg Ser Tyr
145 150 155 160

Asp Leu Thr Gly Leu Lys Pro Gly Thr Glu Tyr Tyr Val Asn Ile Leu
165 170 175

Gly Val Lys Gly Gly Ser Ile Ser Val Pro Leu Ser Ala Ile Phe Thr
180 185 190

Thr

<210> 149
<211> 193
<212> PRT
<213> Artificial Sequence

<220>
<223> Bispecific EGFR/c-Met binding domain

<400> 149

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

Ala Arg Leu Ser Trp Asp Asp Pro Trp Ala Phe Tyr Glu Ser Phe Leu
20 25 30

```
Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu Thr
        35                  40                  45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
    50                  55                  60

Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys Asp
65                  70                  75                  80

Thr Asn Ile Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Ala Pro
                85                  90                  95

Ala Pro Ala Pro Ala Pro Ala Pro Leu Pro Ala Pro Lys Asn Leu Val
            100                 105                 110

Val Ser Arg Val Thr Glu Asp Ser Ala Arg Leu Ser Trp Thr Ala Pro
        115                 120                 125

Asp Ala Ala Phe Asp Ser Phe Trp Ile Arg Tyr Phe Glu Phe Leu Gly
    130                 135                 140

Ser Gly Glu Ala Ile Val Leu Thr Val Pro Gly Ser Glu Arg Ser Tyr
145                 150                 155                 160

Asp Leu Thr Gly Leu Lys Pro Gly Thr Glu Tyr Val Val Asn Ile Leu
                165                 170                 175

Gly Val Lys Gly Gly Lys Ile Ser Pro Pro Leu Ser Ala Ile Phe Thr
            180                 185                 190

Thr
```

<210> 150
<211> 193
<212> PRT
<213> Artificial Sequence

<220>
<223> Bispecific EGFR/c-Met binding domain

<400> 150

```
Leu Pro Ala Pro Lys Asn Leu Val Val Ser Glu Val Thr Glu Asp Ser
1               5                   10                  15

Ala Arg Leu Ser Trp Asp Asp Pro Trp Ala Phe Tyr Glu Ser Phe Leu
            20                  25                  30

Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu Thr
        35                  40                  45
```

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
50 55 60

Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys Asp
65 70 75 80

Thr Asn Ile Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Ala Pro
85 90 95

Ala Pro Ala Pro Ala Pro Ala Pro Leu Pro Ala Pro Lys Asn Leu Val
100 105 110

Val Ser Arg Val Thr Glu Asp Ser Ala Arg Leu Ser Trp Thr Ala Pro
115 120 125

Asp Ala Ala Phe Asp Ser Phe Trp Ile Arg Tyr Phe Glu Phe Val Gly
130 135 140

Ser Gly Glu Ala Ile Val Leu Thr Val Pro Gly Ser Glu Arg Ser Tyr
145 150 155 160

Asp Leu Thr Gly Leu Lys Pro Gly Thr Glu Tyr Val Val Asn Ile Leu
165 170 175

Gly Val Lys Gly Gly Ser Ile Ser Pro Pro Leu Ser Ala Ile Phe Thr
180 185 190

Thr

<210> 151
<211> 193
<212> PRT
<213> Artificial Sequence

<220>
<223> Bispecific EGFR/c-Met binding domain

<400> 151

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

Ala Arg Leu Ser Trp Asp Asp Pro Trp Ala Phe Tyr Glu Ser Phe Leu
20 25 30

Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu Thr
35 40 45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
50 55 60

Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys Asp
65 70 75 80

Thr Asn Ile Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Ala Pro
85 90 95

Ala Pro Ala Pro Ala Pro Ala Pro Leu Pro Ala Pro Lys Asn Leu Val
100 105 110

Val Ser Arg Val Thr Glu Asp Ser Ala Arg Leu Ser Trp Thr Ala Pro
115 120 125

Asp Ala Ala Phe Asp Ser Phe Trp Ile Arg Tyr Phe Glu Phe Val Ser
130 135 140

Lys Gly Asp Ala Ile Val Leu Thr Val Pro Gly Ser Glu Arg Ser Tyr
145 150 155 160

Asp Leu Thr Gly Leu Lys Pro Gly Thr Glu Tyr Val Val Asn Ile Leu
165 170 175

Gly Val Lys Gly Gly Ser Ile Ser Pro Pro Leu Ser Ala Ile Phe Thr
180 185 190

Thr

<210> 152
<211> 193
<212> PRT
<213> Artificial Sequence

<220>
<223> Bispecific EGFR/c-Met binding domain

<400> 152

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

Ala Arg Leu Ser Trp Asp Asp Pro Trp Ala Phe Tyr Glu Ser Phe Leu
20 25 30

Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu Thr
35 40 45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
50 55 60

Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys Asp
65 70 75 80

Thr Asn Ile Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Ala Pro
85 90 95

Ala Pro Ala Pro Ala Pro Ala Pro Leu Pro Ala Pro Lys Asn Leu Val
100 105 110

Val Ser Arg Val Thr Glu Asp Ser Ala Arg Leu Ser Trp Thr Ala Pro
115 120 125

Asp Ala Ala Phe Asp Ser Phe Trp Ile Arg Tyr Phe Glu Phe Leu Gly
130 135 140

Ser Gly Glu Ala Ile Val Leu Thr Val Pro Gly Ser Glu Arg Ser Tyr
145 150 155 160

Asp Leu Thr Gly Leu Lys Pro Gly Thr Glu Tyr Val Val Asn Ile Leu
165 170 175

Ser Val Lys Gly Gly Ser Ile Ser Pro Pro Leu Ser Ala Ile Phe Thr
180 185 190

Thr

<210> 153
<211> 193
<212> PRT
<213> Artificial Sequence

<220>
<223> Bispecific EGFR/c-Met binding domain

<400> 153

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

Ala Arg Leu Ser Trp Asp Asp Pro His Ala Phe Tyr Glu Ser Phe Leu
20 25 30

Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu Thr
35 40 45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
50 55 60

Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys Asp
65 70 75 80

Thr Asn Ile Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Ala Pro
85 90 95

Ala Pro Ala Pro Ala Pro Ala Pro Leu Pro Ala Pro Lys Asn Leu Val
100 105 110

Val Ser Arg Val Thr Glu Asp Ser Ala Arg Leu Ser Trp Thr Ala Pro
115 120 125

```
Asp Ala Ala Phe Asp Ser Phe Trp Ile Arg Tyr Phe Glu Phe Leu Gly
    130                 135                 140

Ser Gly Glu Ala Ile Val Leu Thr Val Pro Gly Ser Glu Arg Ser Tyr
145                 150                 155                 160

Asp Leu Thr Gly Leu Lys Pro Gly Thr Glu Tyr Val Val Asn Ile Leu
                165                 170                 175

Gly Val Lys Gly Gly Lys Ile Ser Pro Pro Leu Ser Ala Ile Phe Thr
            180                 185                 190

Thr
```

<210> 154
<211> 193
<212> PRT
<213> Artificial Sequence

<220>
<223> Bispecific EGFR/c-Met binding domain

<400> 154

```
Leu Pro Ala Pro Lys Asn Leu Val Val Ser Glu Val Thr Glu Asp Ser
1               5                   10                  15

Ala Arg Leu Ser Trp Asp Asp Pro His Ala Phe Tyr Glu Ser Phe Leu
            20                  25                  30

Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu Thr
        35                  40                  45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
    50                  55                  60

Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys Asp
65                  70                  75                  80

Thr Asn Ile Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Ala Pro
                85                  90                  95

Ala Pro Ala Pro Ala Pro Ala Pro Leu Pro Ala Pro Lys Asn Leu Val
            100                 105                 110

Val Ser Arg Val Thr Glu Asp Ser Ala Arg Leu Ser Trp Thr Ala Pro
        115                 120                 125

Asp Ala Ala Phe Asp Ser Phe Trp Ile Arg Tyr Phe Glu Phe Val Gly
    130                 135                 140
```

Ser Gly Glu Ala Ile Val Leu Thr Val Pro Gly Ser Glu Arg Ser Tyr
145 150 155 160

Asp Leu Thr Gly Leu Lys Pro Gly Thr Glu Tyr Val Val Asn Ile Leu
165 170 175

Gly Val Lys Gly Gly Ser Ile Ser Pro Pro Leu Ser Ala Ile Phe Thr
180 185 190

Thr

<210> 155
<211> 193
<212> PRT
<213> Artificial Sequence

<220>
<223> Bispecific EGFR/c-Met binding domain

<400> 155

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

Ala Arg Leu Ser Trp Asp Asp Pro His Ala Phe Tyr Glu Ser Phe Leu
20 25 30

Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu Thr
35 40 45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
50 55 60

Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys Asp
65 70 75 80

Thr Asn Ile Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Ala Pro
85 90 95

Ala Pro Ala Pro Ala Pro Ala Pro Leu Pro Ala Pro Lys Asn Leu Val
100 105 110

Val Ser Arg Val Thr Glu Asp Ser Ala Arg Leu Ser Trp Thr Ala Pro
115 120 125

Asp Ala Ala Phe Asp Ser Phe Trp Ile Arg Tyr Phe Glu Phe Val Ser
130 135 140

Lys Gly Asp Ala Ile Val Leu Thr Val Pro Gly Ser Glu Arg Ser Tyr
145 150 155 160

Asp Leu Thr Gly Leu Lys Pro Gly Thr Glu Tyr Val Val Asn Ile Leu
165 170 175

Gly Val Lys Gly Gly Ser Ile Ser Pro Pro Leu Ser Ala Ile Phe Thr
180 185 190

Thr

<210> 156
<211> 193
<212> PRT
<213> Artificial Sequence

<220>
<223> Bispecific EGFR/c-Met binding domain

<400> 156

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

Ala Arg Leu Ser Trp Asp Asp Pro His Ala Phe Tyr Glu Ser Phe Leu
20 25 30

Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu Thr
35 40 45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
50 55 60

Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys Asp
65 70 75 80

Thr Asn Ile Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Ala Pro
85 90 95

Ala Pro Ala Pro Ala Pro Ala Pro Leu Pro Ala Pro Lys Asn Leu Val
100 105 110

Val Ser Arg Val Thr Glu Asp Ser Ala Arg Leu Ser Trp Thr Ala Pro
115 120 125

Asp Ala Ala Phe Asp Ser Phe Trp Ile Arg Tyr Phe Glu Phe Leu Gly
130 135 140

Ser Gly Glu Ala Ile Val Leu Thr Val Pro Gly Ser Glu Arg Ser Tyr
145 150 155 160

Asp Leu Thr Gly Leu Lys Pro Gly Thr Glu Tyr Val Val Asn Ile Leu
165 170 175

Ser Val Lys Gly Gly Ser Ile Ser Pro Pro Leu Ser Ala Ile Phe Thr
180 185 190

Thr

<210> 157
<211> 193
<212> PRT
<213> Artificial Sequence

<220>
<223> Bispecific EGFR/c-Met binding domain

<400> 157

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

Ala Arg Leu Ser Trp Ala Asp Pro His Gly Phe Tyr Asp Ser Phe Leu
20 25 30

Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu Thr
35 40 45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
50 55 60

Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys Asp
65 70 75 80

Thr Asn Ile Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Ala Pro
85 90 95

Ala Pro Ala Pro Ala Pro Ala Pro Leu Pro Ala Pro Lys Asn Leu Val
100 105 110

Val Ser Arg Val Thr Glu Asp Ser Ala Arg Leu Ser Trp Thr Ala Pro
115 120 125

Asp Ala Ala Phe Asp Ser Phe Trp Ile Arg Tyr Phe Glu Phe Leu Gly
130 135 140

Ser Gly Glu Ala Ile Val Leu Thr Val Pro Gly Ser Glu Arg Ser Tyr
145 150 155 160

Asp Leu Thr Gly Leu Lys Pro Gly Thr Glu Tyr Val Val Asn Ile Leu
165 170 175

Gly Val Lys Gly Gly Lys Ile Ser Pro Pro Leu Ser Ala Ile Phe Thr
180 185 190

Thr

<210> 158
<211> 193

<212> PRT
<213> Artificial Sequence

<220>
<223> Bispecific EGFR/c-Met binding domain

<400> 158

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

Ala Arg Leu Ser Trp Ala Asp Pro His Gly Phe Tyr Asp Ser Phe Leu
20 25 30

Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu Thr
35 40 45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
50 55 60

Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys Asp
65 70 75 80

Thr Asn Ile Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Ala Pro
85 90 95

Ala Pro Ala Pro Ala Pro Ala Pro Leu Pro Ala Pro Lys Asn Leu Val
100 105 110

Val Ser Arg Val Thr Glu Asp Ser Ala Arg Leu Ser Trp Thr Ala Pro
115 120 125

Asp Ala Ala Phe Asp Ser Phe Trp Ile Arg Tyr Phe Glu Phe Val Gly
130 135 140

Ser Gly Glu Ala Ile Val Leu Thr Val Pro Gly Ser Glu Arg Ser Tyr
145 150 155 160

Asp Leu Thr Gly Leu Lys Pro Gly Thr Glu Tyr Val Val Asn Ile Leu
165 170 175

Gly Val Lys Gly Gly Ser Ile Ser Pro Pro Leu Ser Ala Ile Phe Thr
180 185 190

Thr

<210> 159
<211> 193
<212> PRT
<213> Artificial Sequence

<220>
<223> Bispecific EGFR/c-Met binding domain

<400> 159

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

Ala Arg Leu Ser Trp Ala Asp Pro His Gly Phe Tyr Asp Ser Phe Leu
20 25 30

Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu Thr
35 40 45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
50 55 60

Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys Asp
65 70 75 80

Thr Asn Ile Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Ala Pro
85 90 95

Ala Pro Ala Pro Ala Pro Ala Pro Leu Pro Ala Pro Lys Asn Leu Val
100 105 110

Val Ser Arg Val Thr Glu Asp Ser Ala Arg Leu Ser Trp Thr Ala Pro
115 120 125

Asp Ala Ala Phe Asp Ser Phe Trp Ile Arg Tyr Phe Glu Phe Val Ser
130 135 140

Lys Gly Asp Ala Ile Val Leu Thr Val Pro Gly Ser Glu Arg Ser Tyr
145 150 155 160

Asp Leu Thr Gly Leu Lys Pro Gly Thr Glu Tyr Val Val Asn Ile Leu
165 170 175

Gly Val Lys Gly Gly Ser Ile Ser Pro Pro Leu Ser Ala Ile Phe Thr
180 185 190

Thr

<210> 160
<211> 193
<212> PRT
<213> Artificial Sequence

<220>
<223> Bispecific EGFR/c-Met binding domain

<400> 160

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

Ala Arg Leu Ser Trp Ala Asp Pro His Gly Phe Tyr Asp Ser Phe Leu
20 25 30

Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu Thr
35 40 45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
50 55 60

Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys Asp
65 70 75 80

Thr Asn Ile Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Ala Pro
85 90 95

Ala Pro Ala Pro Ala Pro Ala Pro Leu Pro Ala Pro Lys Asn Leu Val
100 105 110

Val Ser Arg Val Thr Glu Asp Ser Ala Arg Leu Ser Trp Thr Ala Pro
115 120 125

Asp Ala Ala Phe Asp Ser Phe Trp Ile Arg Tyr Phe Glu Phe Leu Gly
130 135 140

Ser Gly Glu Ala Ile Val Leu Thr Val Pro Gly Ser Glu Arg Ser Tyr
145 150 155 160

Asp Leu Thr Gly Leu Lys Pro Gly Thr Glu Tyr Val Val Asn Ile Leu
165 170 175

Ser Val Lys Gly Gly Ser Ile Ser Pro Pro Leu Ser Ala Ile Phe Thr
180 185 190

Thr

<210> 161
<211> 193
<212> PRT
<213> Artificial Sequence

<220>
<223> Bispecific EGFR/c-Met binding domain

<400> 161

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

Ala Arg Leu Ser Trp Asp Asp Pro Trp Ala Phe Tyr Glu Ser Phe Leu
20 25 30

Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu Thr
35 40 45

```
Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
    50                  55                  60

Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys Asp
65                  70                  75                  80

Thr Asn Ile Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Ala Pro
                85                  90                  95

Ala Pro Ala Pro Ala Pro Ala Pro Leu Pro Ala Pro Lys Asn Leu Val
            100                 105                 110

Val Ser Arg Val Thr Glu Asp Ser Ala Arg Leu Ser Trp Thr Ala Pro
        115                 120                 125

Asp Ala Ala Phe Asp Ser Phe Trp Ile Arg Tyr Phe Glu Phe Leu Gly
    130                 135                 140

Ser Gly Glu Ala Ile Val Leu Thr Val Pro Gly Ser Glu Arg Ser Tyr
145                 150                 155                 160

Asp Leu Thr Gly Leu Lys Pro Gly Thr Glu Tyr Val Val Asn Ile Leu
                165                 170                 175

Ser Val Lys Gly Gly Ser Ile Ser Pro Pro Leu Ser Ala Ile Phe Thr
            180                 185                 190

Thr
```

<210> 162
<211> 249
<212> PRT
<213> Artificial Sequence

<220>
<223> Bispecific EGFR/c-Met binding domain

<400> 162

```
Leu Pro Ala Pro Lys Asn Leu Val Val Ser Glu Val Thr Glu Asp Ser
1               5                   10                  15

Ala Arg Leu Ser Trp Asp Asp Pro Trp Ala Phe Tyr Glu Ser Phe Leu
            20                  25                  30

Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu Thr
        35                  40                  45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
    50                  55                  60
```

Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys Asp
65 70 75 80

Thr Asn Met Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Ala Pro
85 90 95

Ala Pro Ala Pro Ala Pro Ala Pro Leu Pro Ala Pro Lys Asn Leu Val
100 105 110

Val Ser Arg Val Thr Glu Asp Ser Ala Arg Leu Ser Trp Thr Ala Pro
115 120 125

Asp Ala Ala Phe Asp Ser Phe Trp Ile Arg Tyr Asp Glu Val Val Val
130 135 140

Gly Gly Glu Ala Ile Val Leu Thr Val Pro Gly Ser Glu Arg Ser Tyr
145 150 155 160

Asp Leu Thr Gly Leu Lys Pro Gly Thr Glu Tyr Tyr Val Asn Ile Leu
165 170 175

Gly Val Lys Gly Gly Ser Ile Ser Val Pro Leu Ser Ala Ile Phe Thr
180 185 190

Thr Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Leu Ala Glu Ala Lys
195 200 205

Val Leu Ala Asn Arg Glu Leu Asp Lys Tyr Gly Val Ser Asp Tyr Tyr
210 215 220

Lys Asn Leu Ile Asn Asn Ala Lys Thr Val Glu Gly Val Lys Ala Leu
225 230 235 240

Leu Asp Glu Ile Leu Ala Ala Leu Pro
245

<210> 163
<211> 249
<212> PRT
<213> Artificial Sequence

<220>
<223> Bispecific EGFR/c-Met binding domain

<400> 163

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

Ala Arg Leu Ser Trp Ala Asp Pro His Gly Phe Tyr Asp Ser Phe Leu
20 25 30

Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu Thr
35 40 45

```
Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
    50                  55                  60

Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys Asp
65                  70                  75                  80

Thr Asn Met Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Ala Pro
                85                  90                  95

Ala Pro Ala Pro Ala Pro Ala Pro Leu Pro Ala Pro Lys Asn Leu Val
            100                 105                 110

Val Ser Arg Val Thr Glu Asp Ser Ala Arg Leu Ser Trp Thr Ala Pro
        115                 120                 125

Asp Ala Ala Phe Asp Ser Phe Trp Ile Arg Tyr Asp Glu Val Val Val
    130                 135                 140

Gly Gly Glu Ala Ile Val Leu Thr Val Pro Gly Ser Glu Arg Ser Tyr
145                 150                 155                 160

Asp Leu Thr Gly Leu Lys Pro Gly Thr Glu Tyr Tyr Val Asn Ile Leu
                165                 170                 175

Gly Val Lys Gly Gly Ser Ile Ser Val Pro Leu Ser Ala Ile Phe Thr
            180                 185                 190

Thr Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Leu Ala Glu Ala Lys
        195                 200                 205

Val Leu Ala Asn Arg Glu Leu Asp Lys Tyr Gly Val Ser Asp Tyr Tyr
    210                 215                 220

Lys Asn Leu Ile Asn Asn Ala Lys Thr Val Glu Gly Val Lys Ala Leu
225                 230                 235                 240

Leu Asp Glu Ile Leu Ala Ala Leu Pro
                245
```

<210> 164
<211> 249
<212> PRT
<213> Artificial Sequence

<220>
<223> Bispecific EGFR/c-Met binding domain

<400> 164

```
Leu Pro Ala Pro Lys Asn Leu Val Val Ser Glu Val Thr Glu Asp Ser
1               5                   10                  15
```

```
Ala Arg Leu Ser Trp Asp Asp Pro Trp Ala Phe Tyr Glu Ser Phe Leu
            20                  25                  30

Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu Thr
        35                  40                  45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
    50                  55                  60

Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys Asp
65                  70                  75                  80

Thr Asn Met Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Ala Pro
                85                  90                  95

Ala Pro Ala Pro Ala Pro Ala Pro Leu Pro Ala Pro Lys Asn Leu Val
            100                 105                 110

Val Ser Arg Val Thr Glu Asp Ser Ala Arg Leu Ser Trp Thr Ala Pro
        115                 120                 125

Asp Ala Ala Phe Asp Ser Phe Trp Ile Arg Tyr Phe Glu Phe Leu Gly
    130                 135                 140

Ser Gly Glu Ala Ile Val Leu Thr Val Pro Gly Ser Glu Arg Ser Tyr
145                 150                 155                 160

Asp Leu Thr Gly Leu Lys Pro Gly Thr Glu Tyr Val Val Asn Ile Met
                165                 170                 175

Gly Val Lys Gly Gly Lys Ile Ser Pro Pro Leu Ser Ala Ile Phe Thr
            180                 185                 190

Thr Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Leu Ala Glu Ala Lys
        195                 200                 205

Val Leu Ala Asn Arg Glu Leu Asp Lys Tyr Gly Val Ser Asp Tyr Tyr
    210                 215                 220

Lys Asn Leu Ile Asn Asn Ala Lys Thr Val Glu Gly Val Lys Ala Leu
225                 230                 235                 240

Leu Asp Glu Ile Leu Ala Ala Leu Pro
                245
```

<210> 165
<211> 249
<212> PRT
<213> Artificial Sequence

<220>
<223> Bispecific EGFR/c-Met binding domain

<400> 165

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

Ala Arg Leu Ser Trp Ala Asp Pro His Gly Phe Tyr Asp Ser Phe Leu
20 25 30

Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu Thr
35 40 45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
50 55 60

Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys Asp
65 70 75 80

Thr Asn Met Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Ala Pro
85 90 95

Ala Pro Ala Pro Ala Pro Ala Pro Leu Pro Ala Pro Lys Asn Leu Val
100 105 110

Val Ser Arg Val Thr Glu Asp Ser Ala Arg Leu Ser Trp Thr Ala Pro
115 120 125

Asp Ala Ala Phe Asp Ser Phe Trp Ile Arg Tyr Phe Glu Phe Leu Gly
130 135 140

Ser Gly Glu Ala Ile Val Leu Thr Val Pro Gly Ser Glu Arg Ser Tyr
145 150 155 160

Asp Leu Thr Gly Leu Lys Pro Gly Thr Glu Tyr Val Val Asn Ile Met
165 170 175

Gly Val Lys Gly Gly Lys Ile Ser Pro Pro Leu Ser Ala Ile Phe Thr
180 185 190

Thr Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Leu Ala Glu Ala Lys
195 200 205

Val Leu Ala Asn Arg Glu Leu Asp Lys Tyr Gly Val Ser Asp Tyr Tyr
210 215 220

Lys Asn Leu Ile Asn Asn Ala Lys Thr Val Glu Gly Val Lys Ala Leu
225 230 235 240

Leu Asp Glu Ile Leu Ala Ala Leu Pro
245

<210> 166
<211> 588

<212> DNA
<213> Artificial Sequence

<220>
<223> Bispecific EGFR/c-Met binding domain

<400> 166
ttgccagcgc cgaagaacct ggtagttagc gaggttactg aggacagcgc gcgtctgagc 60

tgggacgatc cgtgggcgtt ctacgagagc tttctgatcc agtatcaaga gagcgagaaa 120

gtcggtgaag cgattgtgct gaccgtcccg ggctccgagc gttcctacga cctgaccggt 180

ttgaagccgg gtaccgagta tacggtgagc atctacggtg ttcacaatgt ctataaggac 240

actaatatcc gcggtctgcc tctgagcgcc attttcacca ccgcaccggc accggctccg 300

gctcctgccc cgctgccggc tccgaagaac ttggtggtga gccgtgttac cgaagatagc 360

gcacgcctga gctggacggc accggatgcg gcgttcgata gcttctggat tcgctatttt 420

gagtttctgg gtagcggtga ggcaattgtt ctgacggtgc cgggctctga acgctcctac 480

gatttgaccg gtctgaaacc gggcaccgag tatgtggtga acattctgag cgttaagggc 540

ggtagcatca gcccaccgct gagcgcgatc ttcacgactg gtggttgc 588

<210> 167
<211> 579
<212> DNA
<213> Artificial Sequence

<220>
<223> Bispecific EGFR/c-Met binding domain

<400> 167
ctgccagccc ctaagaatct ggtcgtgagc gaagtaaccg aggacagcgc ccgcctgagc 60

tgggacgacc cgtgggcgtt ctatgagtct ttcctgattc agtatcaaga aagcgaaaaa 120

gttggcgaag cgatcgtcct gaccgtcccg ggtagcgagc gctcctacga tctgaccggc 180

ctgaaaccgg gtacggagta cacggtgtcc atttacggtg ttcacaatgt gtataaagac 240

accaacatgc gtggcctgcc gctgtcggcg attttcacca ccgcgcctgc gccagcgcct 300

gcaccggctc cgctgccggc accgaagaac ctggttgtca gccgtgtgac cgaggatagc 360

gcacgtttga gctggaccgc tccggatgca gcctttgaca gcttctggat tcgttacttt 420

gaatttctgg gtagcggtga ggcgatcgtt ctgacggtgc cgggctctga acgcagctat 480

gatttgacgg gcctgaagcc gggtactgag tacgtggtta acatcatggg cgttaagggt 540

ggtaaaatca gcccgccatt gtccgcgatc tttaccacg 579

<210> 168
<211> 282
<212> DNA
<213> Artificial Sequence

<220>
<223> EGFR binding FN3 domain from ECB97

<400> 168
ttgccagcgc cgaagaacct ggtagttagc gaggttactg aggacagcgc gcgtctgagc 60

tgggacgatc cgtgggcgtt ctacgagagc tttctgatcc agtatcaaga gagcgagaaa 120

gtcggtgaag cgattgtgct gaccgtcccg ggctccgagc gttcctacga cctgaccggt 180

ttgaagccgg gtaccgagta tacggtgagc atctacggtg ttcacaatgt ctataaggac 240

actaatatcc gcggtctgcc tctgagcgcc attttcacca cc 282

<210> 169
<211> 282
<212> DNA
<213> Artificial Sequence

<220>
<223> EGFR binding FN3 domain from ECB15

<400> 169
ctgccagccc ctaagaatct ggtcgtgagc gaagtaaccg aggacagcgc ccgcctgagc 60

tgggacgacc cgtgggcgtt ctatgagtct ttcctgattc agtatcaaga aagcgaaaaa 120

gttggcgaag cgatcgtcct gaccgtcccg ggtagcgagc gctcctacga tctgaccggc 180

ctgaaaccgg gtacggagta cacggtgtcc atttacggtg ttcacaatgt gtataaagac 240

accaacatgc gtggcctgcc gctgtcggcg attttcacca cc 282

<210> 170
<211> 195
<212> PRT
<213> Artificial Sequence

<220>
<223> Bispecific EGFR/c-Met binding molecule

<400> 170

Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Glu Val Thr Glu Asp
1 5 10 15

Ser Ala Arg Leu Ser Trp Asp Asp Pro Trp Ala Phe Tyr Glu Ser Phe
20 25 30

Leu Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu
35 40 45

Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro
50 55 60

Gly Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys
65 70 75 80

Asp Thr Asn Ile Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Ala
85 90 95

Pro Ala Pro Ala Pro Ala Pro Ala Pro Leu Pro Ala Pro Lys Asn Leu
100 105 110

Val Val Ser Arg Val Thr Glu Asp Ser Ala Arg Leu Ser Trp Thr Ala
115 120 125

Pro Asp Ala Ala Phe Asp Ser Phe Trp Ile Arg Tyr Phe Glu Phe Leu
130 135 140

Gly Ser Gly Glu Ala Ile Val Leu Thr Val Pro Gly Ser Glu Arg Ser
145 150 155 160

Tyr Asp Leu Thr Gly Leu Lys Pro Gly Thr Glu Tyr Val Val Asn Ile
165 170 175

Leu Gly Val Lys Gly Gly Lys Ile Ser Pro Pro Leu Ser Ala Ile Phe
180 185 190

Thr Thr Cys
195

<210> 171
<211> 195
<212> PRT
<213> Artificial Sequence

<220>
<223> Bispecific EGFR/c-Met binding molecule

<400> 171

Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Glu Val Thr Glu Asp
1 5 10 15

Ser Ala Arg Leu Ser Trp Asp Asp Pro Trp Ala Phe Tyr Glu Ser Phe
20 25 30

Leu Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu
35 40 45

Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro
50 55 60

Gly Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys
65 70 75 80

Asp Thr Asn Ile Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Ala
85 90 95

Pro Ala Pro Ala Pro Ala Pro Ala Pro Leu Pro Ala Pro Lys Asn Leu
100 105 110

Val Val Ser Arg Val Thr Glu Asp Ser Ala Arg Leu Ser Trp Thr Ala
115 120 125

Pro Asp Ala Ala Phe Asp Ser Phe Trp Ile Arg Tyr Phe Glu Phe Val
130 135 140

Gly Ser Gly Glu Ala Ile Val Leu Thr Val Pro Gly Ser Glu Arg Ser
145 150 155 160

Tyr Asp Leu Thr Gly Leu Lys Pro Gly Thr Glu Tyr Val Val Asn Ile
165 170 175

Leu Gly Val Lys Gly Gly Ser Ile Ser Pro Pro Leu Ser Ala Ile Phe
180 185 190

Thr Thr Cys
195

<210> 172
<211> 195
<212> PRT
<213> Artificial Sequence

<220>
<223> Bispecific EGFR/c-Met binding molecule

<400> 172

Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Glu Val Thr Glu Asp
1 5 10 15

Ser Ala Arg Leu Ser Trp Asp Asp Pro Trp Ala Phe Tyr Glu Ser Phe
20 25 30

Leu Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu
35 40 45

Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro
50 55 60

Gly Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys
65 70 75 80

Asp Thr Asn Ile Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Ala
85 90 95

Pro Ala Pro Ala Pro Ala Pro Ala Pro Leu Pro Ala Pro Lys Asn Leu
100 105 110

Val Val Ser Arg Val Thr Glu Asp Ser Ala Arg Leu Ser Trp Thr Ala
115 120 125

Pro Asp Ala Ala Phe Asp Ser Phe Trp Ile Arg Tyr Phe Glu Phe Val
130 135 140

Ser Lys Gly Asp Ala Ile Val Leu Thr Val Pro Gly Ser Glu Arg Ser
145 150 155 160

Tyr Asp Leu Thr Gly Leu Lys Pro Gly Thr Glu Tyr Val Val Asn Ile
165 170 175

Leu Gly Val Lys Gly Gly Ser Ile Ser Pro Pro Leu Ser Ala Ile Phe
180 185 190

Thr Thr Cys
195

<210> 173
<211> 195
<212> PRT
<213> Artificial Sequence

<220>
<223> Bispecific EGFR/c-Met binding molecule

<400> 173

Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Glu Val Thr Glu Asp
1 5 10 15

Ser Ala Arg Leu Ser Trp Asp Asp Pro Trp Ala Phe Tyr Glu Ser Phe
20 25 30

Leu Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu
35 40 45

Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro
50 55 60

Gly Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys
65 70 75 80

Asp Thr Asn Ile Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Ala
85 90 95

Pro Ala Pro Ala Pro Ala Pro Ala Pro Leu Pro Ala Pro Lys Asn Leu
100 105 110

Val Val Ser Arg Val Thr Glu Asp Ser Ala Arg Leu Ser Trp Thr Ala
115 120 125

Pro Asp Ala Ala Phe Asp Ser Phe Trp Ile Arg Tyr Phe Glu Phe Leu
130 135 140

Gly Ser Gly Glu Ala Ile Val Leu Thr Val Pro Gly Ser Glu Arg Ser
145 150 155 160

Tyr Asp Leu Thr Gly Leu Lys Pro Gly Thr Glu Tyr Val Val Asn Ile
165 170 175

Leu Ser Val Lys Gly Gly Ser Ile Ser Pro Pro Leu Ser Ala Ile Phe
180 185 190

Thr Thr Cys
195

<210> 174
<211> 195
<212> PRT
<213> Artificial Sequence

<220>
<223> Bispecific EGFR/c-Met binding molecule

<400> 174

Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Glu Val Thr Glu Asp
1 5 10 15

Ser Ala Arg Leu Ser Trp Asp Asp Pro His Ala Phe Tyr Glu Ser Phe
20 25 30

Leu Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu
35 40 45

Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro
50 55 60

Gly Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys
65 70 75 80

Asp Thr Asn Ile Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Ala
85 90 95

Pro Ala Pro Ala Pro Ala Pro Ala Pro Leu Pro Ala Pro Lys Asn Leu
100 105 110

Val Val Ser Arg Val Thr Glu Asp Ser Ala Arg Leu Ser Trp Thr Ala
115 120 125

Pro Asp Ala Ala Phe Asp Ser Phe Trp Ile Arg Tyr Phe Glu Phe Leu
130 135 140

Gly Ser Gly Glu Ala Ile Val Leu Thr Val Pro Gly Ser Glu Arg Ser
145 150 155 160

Tyr Asp Leu Thr Gly Leu Lys Pro Gly Thr Glu Tyr Val Val Asn Ile
165 170 175

Leu Gly Val Lys Gly Gly Lys Ile Ser Pro Pro Leu Ser Ala Ile Phe
180 185 190

Thr Thr Cys
195

<210> 175
<211> 195
<212> PRT
<213> Artificial Sequence

<220>
<223> Bispecific EGFR/c-Met binding molecule

<400> 175

Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Glu Val Thr Glu Asp
1 5 10 15

Ser Ala Arg Leu Ser Trp Asp Asp Pro His Ala Phe Tyr Glu Ser Phe
20 25 30

Leu Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu
35 40 45

Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro
50 55 60

Gly Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys
65 70 75 80

Asp Thr Asn Ile Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Ala
85 90 95

Pro Ala Pro Ala Pro Ala Pro Ala Pro Leu Pro Ala Pro Lys Asn Leu
100 105 110

Val Val Ser Arg Val Thr Glu Asp Ser Ala Arg Leu Ser Trp Thr Ala
115 120 125

Pro Asp Ala Ala Phe Asp Ser Phe Trp Ile Arg Tyr Phe Glu Phe Val
130 135 140

Gly Ser Gly Glu Ala Ile Val Leu Thr Val Pro Gly Ser Glu Arg Ser
145 150 155 160

Tyr Asp Leu Thr Gly Leu Lys Pro Gly Thr Glu Tyr Val Val Asn Ile
165 170 175

Leu Gly Val Lys Gly Gly Ser Ile Ser Pro Pro Leu Ser Ala Ile Phe
180 185 190

Thr Thr Cys
195

<210> 176
<211> 195
<212> PRT
<213> Artificial Sequence

<220>

<223> Bispecific EGFR/c-Met binding molecule

<400> 176

```
Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Glu Val Thr Glu Asp
1               5                  10                  15

Ser Ala Arg Leu Ser Trp Asp Asp Pro His Ala Phe Tyr Glu Ser Phe
            20                  25                  30

Leu Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu
        35                  40                  45

Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro
    50                  55                  60

Gly Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys
65                  70                  75                  80

Asp Thr Asn Ile Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Ala
                85                  90                  95

Pro Ala Pro Ala Pro Ala Pro Ala Pro Leu Pro Ala Pro Lys Asn Leu
            100                 105                 110

Val Val Ser Arg Val Thr Glu Asp Ser Ala Arg Leu Ser Trp Thr Ala
        115                 120                 125

Pro Asp Ala Ala Phe Asp Ser Phe Trp Ile Arg Tyr Phe Glu Phe Val
    130                 135                 140

Ser Lys Gly Asp Ala Ile Val Leu Thr Val Pro Gly Ser Glu Arg Ser
145                 150                 155                 160

Tyr Asp Leu Thr Gly Leu Lys Pro Gly Thr Glu Tyr Val Val Asn Ile
                165                 170                 175

Leu Gly Val Lys Gly Gly Ser Ile Ser Pro Pro Leu Ser Ala Ile Phe
            180                 185                 190

Thr Thr Cys
        195
```

<210> 177
<211> 195
<212> PRT
<213> Artificial Sequence

<220>
<223> Bispecific EGFR/c-Met binding molecule

<400> 177

```
Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Glu Val Thr Glu Asp
1               5                  10                  15
```

```
Ser Ala Arg Leu Ser Trp Asp Asp Pro His Ala Phe Tyr Glu Ser Phe
            20                  25                  30

Leu Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu
        35                  40                  45

Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro
    50                  55                  60

Gly Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys
65                  70                  75                  80

Asp Thr Asn Ile Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Ala
                85                  90                  95

Pro Ala Pro Ala Pro Ala Pro Ala Pro Leu Pro Ala Pro Lys Asn Leu
            100                 105                 110

Val Val Ser Arg Val Thr Glu Asp Ser Ala Arg Leu Ser Trp Thr Ala
        115                 120                 125

Pro Asp Ala Ala Phe Asp Ser Phe Trp Ile Arg Tyr Phe Glu Phe Leu
    130                 135                 140

Gly Ser Gly Glu Ala Ile Val Leu Thr Val Pro Gly Ser Glu Arg Ser
145                 150                 155                 160

Tyr Asp Leu Thr Gly Leu Lys Pro Gly Thr Glu Tyr Val Val Asn Ile
                165                 170                 175

Leu Ser Val Lys Gly Gly Ser Ile Ser Pro Pro Leu Ser Ala Ile Phe
            180                 185                 190

Thr Thr Cys
        195


<210>  178
<211>  195
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Bispecific EGFR/c-Met binding molecule

<400>  178

Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Glu Val Thr Glu Asp
1               5                   10                  15

Ser Ala Arg Leu Ser Trp Asp Asp Pro Trp Ala Phe Tyr Glu Ser Phe
            20                  25                  30
```

Leu Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Val Leu
35 40 45

Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro
50 55 60

Gly Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys
65 70 75 80

Asp Thr Asn Ile Arg Gly Leu Pro Leu Ser Ala Ile Phe Thr Thr Ala
85 90 95

Pro Ala Pro Ala Pro Ala Pro Ala Pro Leu Pro Ala Pro Lys Asn Leu
100 105 110

Val Val Ser Arg Val Thr Glu Asp Ser Ala Arg Leu Ser Trp Thr Ala
115 120 125

Pro Asp Ala Ala Phe Asp Ser Phe Trp Ile Arg Tyr Phe Glu Phe Leu
130 135 140

Gly Ser Gly Glu Ala Ile Val Leu Thr Val Pro Gly Ser Glu Arg Ser
145 150 155 160

Tyr Asp Leu Thr Gly Leu Lys Pro Gly Thr Glu Tyr Val Val Asn Ile
165 170 175

Leu Ser Val Lys Gly Gly Ser Ile Ser Pro Pro Leu Ser Ala Ile Phe
180 185 190

Thr Thr Cys
195

<210> 179
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus FG loop of EGFR bindiing FN3 domain

<220>
<221> VARIANT
<222> (9)..(9)
<223> Xaa may be Met or Ile

<400> 179

His Asn Val Tyr Lys Asp Thr Asn Xaa Arg Gly Leu
1 5 10

<210> 180
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> GF loop of EGFR binding FN3 domain

<400> 180

Leu Gly Ser Tyr Val Phe Glu His Asp Val Met Leu
1 5 10

<210> 181
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus BC loop of EGFR binding FN3 domain

<220>
<221> VARIANT
<222> (1)..(1)
<223> Xaa may be Ala, Thr, Gly or Asp

<220>
<221> VARIANT
<222> (2)..(2)
<223> Xaa may be Ala, Asp, Tyr or Trp

<220>
<221> VARIANT
<222> (3)..(3)
<223> Xaa may be Pro, Asp or Asn

<220>
<221> VARIANT
<222> (4)..(4)
<223> Xaa may be Leu or absent

<220>
<221> VARIANT
<222> (5)..(5)
<223> Xaa may be Asp, His, Arg, Gly, Tyr or Trp

<220>
<221> VARIANT
<222> (6)..(6)
<223> Xaa may be Glu, Asp or Ala

<220>
<221> VARIANT
<222> (7)..(7)
<223> Xaa may be Ala, Phe, Gly, His or Asp

<220>
<221> VARIANT
<222> (8)..(8)
<223> Xaa may be Tyr, Phe or Leu

<400> 181

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

<210> 182
<211> 95
<212> PRT

<213> Artificial Sequence

<220>
<223> EGFR binding FN3 domain consensus sequence

<220>
<221> VARIANT
<222> (22)..(22)
<223> Xaa may be Ala, Thr, Gly or Asp

<220>
<221> VARIANT
<222> (23)..(23)
<223> Xaa may be Ala, Asp, Tyr or Trp

<220>
<221> VARIANT
<222> (24)..(24)
<223> Xaa may be Pro, Asp or Asn

<220>
<221> VARIANT
<222> (25)..(25)
<223> Xaa may be Leu or absent

<220>
<221> VARIANT
<222> (26)..(26)
<223> Xaa may be Asp, His, Arg, Gly, Tyr or Trp

<220>
<221> VARIANT
<222> (27)..(27)
<223> Xaa may be Gly, Asp or Ala

<220>
<221> VARIANT
<222> (28)..(28)
<223> Xaa may be Ala, Phe, Gly, His or Asp

<220>
<221> VARIANT
<222> (29)..(29)
<223> Xaa may be Tyr, Phe or Leu

<220>
<221> VARIANT
<222> (84)..(84)
<223> Xaa may be Met or Ile

<400> 182

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

Leu Arg Leu Ser Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asp Ser Phe
            20                  25                  30

Leu Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Asn Leu
        35                  40                  45

Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro
    50                  55                  60
```

Gly Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val His Asn Val Tyr Lys
65 70 75 80

Asp Thr Asn Xaa Arg Gly Leu Pro Leu Ser Ala Glu Phe Thr Thr
85 90 95

<210> 183
<211> 95
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR binding FN3 domain consensus sequence

<220>
<221> VARIANT
<222> (22)..(22)
<223> Xaa may be Ala, Thr, Gly or Asp

<220>
<221> VARIANT
<222> (23)..(23)
<223> Xaa may be Ala, Asp, Tyr or Trp

<220>
<221> VARIANT
<222> (24)..(24)
<223> Xaa may be Pro, Asp or Asn

<220>
<221> VARIANT
<222> (25)..(25)
<223> Xaa may be Leu or absent

<220>
<221> VARIANT
<222> (26)..(26)
<223> Xaa may be Asp, His, Arg, Gly, Tyr or Trp

<220>
<221> VARIANT
<222> (27)..(27)
<223> Xaa may be Gly, Asp or Ala

<220>
<221> VARIANT
<222> (28)..(28)
<223> Xaa may be Ala, Phe, Gly, His or Asp

<220>
<221> VARIANT
<222> (29)..(29)
<223> Xaa may be Tyr, Phe or Leu

<400> 183

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

Leu Arg Leu Ser Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asp Ser Phe
20 25 30

Leu Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Asn Leu
35 40 45

Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro
50 55 60

Gly Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val Leu Gly Ser Tyr Val
65 70 75 80

Phe Glu His Asp Val Met Leu Pro Leu Ser Ala Glu Phe Thr Thr
85 90 95

<210> 184
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> c-Met binding FN3 domain C strand and CD loop consensus sequence

<220>
<221> VARIANT
<222> (4)..(4)
<223> Xaa is Trp, Phe or Val

<220>
<221> VARIANT
<222> (8)..(8)
<223> Xaa is Asp, Phe or Leu

<220>
<221> VARIANT
<222> (10)..(10)
<223> Xaa is Val, Phe or Leu

<220>
<221> VARIANT
<222> (11)..(11)
<223> Xaa is Val, Leu or Thr

<220>
<221> VARIANT
<222> (12)..(12)
<223> Xaa is Val, Arg, Gly, Leu, Thr or Ser

<220>
<221> VARIANT
<222> (13)..(13)
<223> Xaa is Gly, Ser, Ala, Thr or Lys

<220>
<221> VARIANT
<222> (15)..(15)
<223> Xaa is Glu or Asp

<400> 184

Asp Ser Phe Xaa Ile Arg Tyr Xaa Glu Xaa Xaa Xaa Xaa Gly Xaa
1 5 10 15

<210> 185
<211> 17

<212> PRT
<213> Artificial Sequence

<220>
<223> c-Met binding FN3 domain F strand and FG loop consensus sequence

<220>
<221> VARIANT
<222> (4)..(4)
<223> Xaa is Tyr, Trp, Ile, Val, Gly or Ala

<220>
<221> VARIANT
<222> (6)..(6)
<223> Xaa is Asn, Thr, Qln or Gly

<220>
<221> VARIANT
<222> (8)..(8)
<223> Xaa is Leu, Met, Asn or Ile

<220>
<221> VARIANT
<222> (9)..(9)
<223> Xaa is Gly or Ser

<220>
<221> VARIANT
<222> (14)..(14)
<223> Xaa is Ser, Leu, Gly, Tyr, Thr, Arg, His or Lys

<220>
<221> VARIANT
<222> (15)..(15)
<223> Xaa is Ile, Val or Leu

<220>
<221> VARIANT
<222> (17)..(17)
<223> Xaa is Val, Thr, His, Ile, Pro, Tyr or Leu

<400> 185

Thr Glu Tyr Xaa Val Xaa Ile Xaa Xaa Val Lys Gly Gly Xaa Xaa Ser
1 5 10 15

Xaa

<210> 186
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> c-Met binding FN3 domain consensus sequence

<220>
<221> VARIANT
<222> (32)..(32)
<223> Xaa is Trp, Phe or Val

<220>
<221> VARIANT

<222> (36)..(36)
<223> Xaa is Asp, Phe or Leu

<220>
<221> VARIANT
<222> (38)..(38)
<223> Xaa is Val, Phe or Leu

<220>
<221> VARIANT
<222> (39)..(39)
<223> Xaa is Val, Leu or Thr

<220>
<221> VARIANT
<222> (40)..(40)
<223> Xaa is Val, Arg, Gly, Leu, Thr or Ser

<220>
<221> VARIANT
<222> (41)..(41)
<223> Xaa is Gly, Ser, Ala, Thr or Lys

<220>
<221> VARIANT
<222> (43)..(43)
<223> Xaa is Glu or Asp

<220>
<221> VARIANT
<222> (68)..(68)
<223> Xaa is Tyr, Trp, Ile, Val, Gly or Ala

<220>
<221> VARIANT
<222> (70)..(70)
<223> Xaa is Asn, Thr, Qln or Gly

<220>
<221> VARIANT
<222> (72)..(72)
<223> Xaa is Leu, Met, Asn or Ile

<220>
<221> VARIANT
<222> (73)..(73)
<223> Xaa is Gly or Ser

<220>
<221> VARIANT
<222> (78)..(78)
<223> Xaa is Ser, Leu, Gly, Tyr, Thr, Arg, His or Lys

<220>
<221> VARIANT
<222> (79)..(79)
<223> Xaa is Ile, Val or Leu

<220>
<221> VARIANT
<222> (81)..(81)
<223> Xaa is Val, Thr, His, Ile, Pro, Tyr or Leu

<400> 186

Leu Pro Ala Pro Lys Asn Leu Val Val Ser Arg Val Thr Glu Asp Ser
1 5 10 15

Ala Arg Leu Ser Trp Thr Ala Pro Asp Ala Ala Phe Asp Ser Phe Xaa
            20   25   30

Ile Arg Tyr Xaa Glu Xaa Xaa Xaa Xaa Gly Xaa Ala Ile Val Leu Thr
        35   40   45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
    50   55   60

Thr Glu Tyr Xaa Val Xaa Ile Xaa Xaa Val Lys Gly Gly Xaa Xaa Ser
65   70   75   80

Xaa Pro Leu Ser Ala Glu Phe Thr Thr
                85

<210> 187
<211> 94
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR consensus FN3 domain of bispecific EGFR/c-Met molecule

<220>
<221> VARIANT
<222> (11)..(11)
<223> Xaa is Glu, Asn or Arg

<220>
<221> VARIANT
<222> (14)..(14)
<223> Xaa is Glu or Pro

<220>
<221> VARIANT
<222> (17)..(17)
<223> Xaa is Leu or Ala

<220>
<221> VARIANT
<222> (25)..(25)
<223> Xaa is His or Trp

<220>
<221> VARIANT
<222> (29)..(29)
<223> Xaa is Glu or Asp

<220>
<221> VARIANT
<222> (37)..(37)
<223> Xaa is Glu or Pro

<220>
<221> VARIANT
<222> (46)..(46)
<223> Xaa is Asn or Val

<220>
<221> VARIANT
<222> (73)..(73)

<223> Xaa is Gly or Tyr

<220>
<221> VARIANT
<222> (83)..(83)
<223> Xaa is Met or Ile

<220>
<221> VARIANT
<222> (91)..(91)
<223> Xaa is Glu or Ile

<400> 187

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

Xaa Arg Leu Ser Trp Asp Asp Pro Xaa Ala Phe Tyr Xaa Ser Phe Leu
20 25 30

Ile Gln Tyr Gln Xaa Ser Glu Lys Val Gly Glu Ala Ile Xaa Leu Thr
35 40 45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
50 55 60

Thr Glu Tyr Thr Val Ser Ile Tyr Xaa Val His Asn Val Tyr Lys Asp
65 70 75 80

Thr Asn Xaa Arg Gly Leu Pro Leu Ser Ala Xaa Phe Thr Thr
85 90

<210> 188
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> c-Met consensus FN3 domain of bispecific EGFR/c-Met molecule

<220>
<221> VARIANT
<222> (11)..(11)
<223> Xaa is Glu, Asn or Arg

<220>
<221> VARIANT
<222> (14)..(14)
<223> Xaa is Glu or Pro

<220>
<221> VARIANT
<222> (17)..(17)
<223> Xaa is Leu or Ala

<220>
<221> VARIANT
<222> (37)..(37)
<223> Xaa is Glu or Pro

<220>

<221> VARIANT
<222> (39)..(39)
<223> Xaa is Val or Leu

<220>
<221> VARIANT
<222> (40)..(40)
<223> Xaa is Gly or Ser

<220>
<221> VARIANT
<222> (41)..(41)
<223> Xaa is Ser or Lys

<220>
<221> VARIANT
<222> (43)..(43)
<223> Xaa is Glu or Asp

<220>
<221> VARIANT
<222> (46)..(46)
<223> Xaa is Asn or Val

<220>
<221> VARIANT
<222> (72)..(72)
<223> Xaa is Leu or Met

<220>
<221> VARIANT
<222> (73)..(73)
<223> Xaa is Gly or Ser

<220>
<221> VARIANT
<222> (78)..(78)
<223> Xaa is Ser or Lys

<220>
<221> VARIANT
<222> (86)..(86)
<223> Xaa is Glu or Ile

<400> 188

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

Xaa Arg Leu Ser Trp Thr Ala Pro Asp Ala Ala Phe Asp Ser Phe Trp
20 25 30

Ile Arg Tyr Phe Xaa Phe Xaa Xaa Xaa Gly Xaa Ala Ile Xaa Leu Thr
35 40 45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
50 55 60

Thr Glu Tyr Val Val Asn Ile Xaa Xaa Val Lys Gly Gly Xaa Ile Ser
65 70 75 80

Pro Pro Leu Ser Ala Xaa Phe Thr Thr
85

<210> 189
<211> 125
<212> PRT
<213> Homo Sapiens

<400> 189

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

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

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

Ala Val Ile Trp Asp Asp Gly Ser Tyr Lys Tyr Tyr Gly Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

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

Ala Arg Asp Gly Ile Thr Met Val Arg Gly Val Met Lys Asp Tyr Phe
            100                 105                 110

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125
```

<210> 190
<211> 107
<212> PRT
<213> Homo Sapiens

<400> 190

```
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 Asp Ile Ser Ser Ala
            20                  25                  30

Leu Val 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 Glu 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> 191
<211> 121
<212> PRT
<213> Homo Sapiens

<400> 191

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 Phe Ser Ser Tyr
20 25 30

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

Ala Asn Ile Lys Lys Asp Gly Ser Glu Lys Tyr Tyr Val 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 Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Leu Gly Trp Gly Trp Gly Trp Tyr Phe Asp Leu Trp Gly
100 105 110

Arg Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 192
<211> 107
<212> PRT
<213> Homo Sapiens

<400> 192

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
20 25 30

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

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

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


Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100                 105


<210>  193
<211>  119
<212>  PRT
<213>  Homo Sapiens

<400>  193

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 Glu Thr Ser Gly Tyr Thr Phe Thr Ser Tyr
            20                  25                  30


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


Gly Trp Ile Ser Ala Tyr Asn Gly Tyr Thr Asn Tyr Ala Gln Lys Leu
    50                  55                  60


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


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


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


Thr Leu Val Thr Val Ser Ser
        115


<210>  194
<211>  107
<212>  PRT
<213>  Homo Sapiens

<400>  194

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 Asn Trp
            20                  25                  30
```

Leu Ala Trp Phe Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu Leu 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 Ile
85 90 95

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

<210> 195
<211> 125
<212> PRT
<213> Homo Sapiens

<400> 195

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

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

Tyr Met Tyr Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
35 40 45

Ala Thr Ile Ser Asp Asp Gly Ser Tyr Thr Tyr Tyr Pro Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Asn Leu Tyr
65 70 75 80

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

Ala Arg Glu Gly Leu Tyr Tyr Tyr Gly Ser Gly Ser Tyr Tyr Asn Gln
100 105 110

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 196
<211> 106
<212> PRT
<213> Homo Sapiens

<400> 196

Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
1 5 10 15

```
Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Leu Ser Ser Ala Leu Ala
            20                  25                  30

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

Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
    50                  55                  60

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

Phe Ala Thr Tyr Tyr Cys Gln Gln Phe Thr Ser Tyr Pro Gln Ile Thr
                85                  90                  95

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


<210>  197
<211>  457
<212>  PRT
<213>  Homo Sapiens

<400>  197

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 Gln Ala Ser Gly Tyr Arg Phe Ser Asn Phe
            20                  25                  30

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

Gly Trp Ile Asn Pro Tyr Asn Gly Asn Lys Glu Phe Ser Ala Lys Phe
    50                  55                  60

Gln Asp Arg Val Thr Phe Thr Ala Asp Thr Ser Ala Asn Thr Ala Tyr
65                  70                  75                  80

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

Ala Arg Val Gly Pro Tyr Ser Trp Asp Asp Ser Pro Gln Asp Asn Tyr
            100                 105                 110

Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Ile Val Ser Ser Ala
        115                 120                 125

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

```
Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
145                 150                 155                 160

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
                165                 170                 175

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
            180                 185                 190

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

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

Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
225                 230                 235                 240

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                245                 250                 255

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            260                 265                 270

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        275                 280                 285

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    290                 295                 300

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
305                 310                 315                 320

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                325                 330                 335

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            340                 345                 350

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
        355                 360                 365

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    370                 375                 380

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
385                 390                 395                 400

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Leu Leu
                405                 410                 415
```

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
420 425 430

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

Lys Ser Leu Ser Leu Ser Pro Gly Lys
450 455

<210> 198
<211> 457
<212> PRT
<213> Homo Sapiens

<400> 198

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 Gln Ala Ser Gly Tyr Arg Phe Ser Asn Phe
20 25 30

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

Gly Trp Ile Asn Pro Tyr Asn Gly Asn Lys Glu Phe Ser Ala Lys Phe
50 55 60

Gln Asp Arg Val Thr Phe Thr Ala Asp Thr Ser Ala Asn Thr Ala Tyr
65 70 75 80

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

Ala Arg Val Gly Pro Tyr Ser Trp Asp Asp Ser Pro Gln Asp Asn Tyr
100 105 110

Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Ile Val Ser Ser Ala
115 120 125

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

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

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
165 170 175

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
180 185 190

```
Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
        195                 200                 205

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

Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
225                 230                 235                 240

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                245                 250                 255

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            260                 265                 270

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        275                 280                 285

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    290                 295                 300

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
305                 310                 315                 320

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                325                 330                 335

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            340                 345                 350

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
        355                 360                 365

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    370                 375                 380

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
385                 390                 395                 400

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                405                 410                 415

Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            420                 425                 430

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

Lys Ser Leu Ser Leu Ser Pro Gly Lys
    450                 455
```

<210> 199
<211> 455
<212> PRT
<213> Homo Sapiens

<400> 199

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

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

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

Ala Val Ile Trp Asp Asp Gly Ser Tyr Lys Tyr Tyr Gly Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

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

Ala Arg Asp Gly Ile Thr Met Val Arg Gly Val Met Lys Asp Tyr Phe
100 105 110

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr
115 120 125

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

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

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

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

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
195 200 205

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

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
225 230 235 240

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys

245 250 255

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
260 265 270

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
275 280 285

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
290 295 300

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
305 310 315 320

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
325 330 335

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
340 345 350

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
355 360 365

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
370 375 380

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
385 390 395 400

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Leu Leu Tyr Ser
405 410 415

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
420 425 430

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

Leu Ser Leu Ser Pro Gly Lys
450 455

<210> 200
<211> 214
<212> PRT
<213> Homo Sapiens

<400> 200

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 Asp Ile Ser Ser Ala
20 25 30

```
Leu Val 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 Glu 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 Arg Thr Val Ala Ala
            100                 105                 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125

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

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205

Phe Asn Arg Gly Glu Cys
    210
```

<210> 201
<211> 449
<212> PRT
<213> Homo Sapiens

<400> 201

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

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

```
Gly Trp Ile Ser Ala Tyr Asn Gly Tyr Thr Asn Tyr Ala Gln Lys Leu
    50                  55                  60

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

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

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

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115                 120                 125

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

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

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

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

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

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

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240

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

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320
```

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
325 330 335

Thr Ile Ser Lys Ala 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 Val Leu
385 390 395 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg 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> 202
<211> 214
<212> PRT
<213> Homo Sapiens

<400> 202

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 Asn Trp
20 25 30

Leu Ala Trp Phe Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu Leu 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 Ile
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

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

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 203
<211> 330
<212> PRT
<213> Homo Sapiens

<400> 203

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
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 Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Arg 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
145 150 155 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
165 170 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
180 185 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
195 200 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
210 215 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
225 230 235 240

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
245 250 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
260 265 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
275 280 285

Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
290 295 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 204
<211> 330
<212> PRT
<213> Homo Sapiens

<400> 204

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
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 Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95

Arg 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
145                 150                 155                 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
                165                 170                 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
            180                 185                 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
        195                 200                 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
    210                 215                 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
225                 230                 235                 240

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
                245                 250                 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
            260                 265                 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Leu
        275                 280                 285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
    290                 295                 300
```

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 205
<211> 1368
<212> DNA
<213> Homo Sapiens

<400> 205
caggtgcagc tggtcgagag cggcggaggg gtggtgcagc ccggcagaag cctgaggctg 60

tcctgcgccg ccagcggctt caccttcagc acctacggca tgcactgggt gcggcaggcc 120

ccaggcaagg gcctggagtg ggtggccgtg atctgggacg acggcagcta caagtactac 180

ggcgacagcg tgaagggcag gttcaccatc agcagggaca acagcaagaa caccctgtac 240

ctgcagatga acagcctgag ggccgaggac accgccgtgt actactgcgc cagggacggc 300

atcaccatgg tgcggggcgt gatgaaggac tacttcgact actggggcca gggcaccctg 360

gtgaccgtga gcagcgccag caccaagggc ccaagcgtgt tcccccctggc ccccagcagc 420

aagagcacca gcggcggcac agccgccctg ggctgcctgg tgaaggacta cttccccgag 480

ccagtgaccg tgtcctggaa ctctggcgcc ctgacctccg gcgtgcacac cttccccgcc 540

gtgctgcaga gcagcggcct gtacagcctg agcagcgtgg tgaccgtgcc cagcagcagc 600

ctgggcaccc agacctacat ctgcaacgtg aaccacaagc ccagcaacac caaggtggac 660

aagagagtgg agcccaagag ctgcgacaag acccacacct gccccccctg cccagcccca 720

gagctgctgg gcggacccag cgtgttcctg ttcccccca agcccaagga caccctgatg 780

atcagcagga cccccgaggt gacctgcgtg gtggtggacg tgagccacga ggacccagag 840

gtgaagttca actggtacgt ggacggcgtg gaggtgcaca acgccaagac caagcccaga 900

gaggagcagt acaacagcac ctacagggtg gtgtccgtgc tgaccgtgct gcaccaggac 960

tggctgaacg gcaaggaata caagtgcaag gtctccaaca aggccctgcc agcccccatc 1020

gaaaagacca tcagcaaggc caagggccag ccacgggagc cccaggtgta caccctgccc 1080

cccagccggg aggagatgac caagaaccag gtgtccctga cctgtctggt gaagggcttc 1140

taccccagcg acatcgccgt ggagtgggag agcaacggcc agcccgagaa caactacaag 1200

accacccccc cagtgctgga cagcgacggc agcttcctcc tgtacagcaa gctgaccgtg 1260

gacaagtcca ggtggcagca gggcaacgtg ttcagctgca gcgtgatgca cgaggccctg 1320

cacaaccact acacccagaa gtccctgagc ctgagccccg gcaaatga 1368

<210> 206
<211> 642
<212> DNA
<213> Homo Sapiens

<400> 206
atccagctga cccagagccc cagcagcctg agcgccagcg tgggcgaccg ggtgaccatc 60

acctgccggg ccagccagga catcagcagc gccctggtct ggtatcagca gaagcccggc 120

aaggccccca agctgctgat ctacgacgcc agctccctgg aaagcggcgt gcccagccgg 180

ttcagcggca gcgagagcgg caccgacttc accctgacca tcagcagcct gcagcccgag 240

gacttcgcca cctactactg ccagcagttc aacagctacc ccctgacctt tggcggcgga 300

acaaaggtgg agatcaagcg tacggtggcc gctcccagcg tgttcatctt cccccccagc 360

gacgagcagc tgaagagcgg caccgccagc gtggtgtgcc tgctgaacaa cttctacccc 420

cgggaggcca aggtgcagtg gaaggtggac aacgccctgc agagcggcaa cagccaggag 480

agcgtcaccg agcaggacag caaggactcc acctacagcc tgagcagcac cctgaccctg 540

tccaaggccg actacgagaa gcacaaggtg tacgcctgcg aggtgaccca ccagggcctg 600

tccagccccg tgaccaagag cttcaacagg ggcgagtgct ga 642

<210> 207
<211> 1350
<212> DNA
<213> Homo Sapiens

<400> 207
caggttcagc tggtgcagtc tggagctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcgaga cttctggtta cacctttacc agctatggta tcagctgggt gcgacaggcc 120

cctggacacg ggcttgagtg gatgggatgg atcagcgctt acaatggtta cacaaactat 180

gcacagaagc tccagggcag ggtcaccatg accacagaca catccacgag cacagcctac 240

atggagctga ggagcctgag atctgacgac acggccgtgt attactgtgc gagagatctg 300

agaggaacta actactttga ctactggggc cagggaaccc tggtcaccgt ctcctcagcc 360

tccaccaagg gcccaagcgt gttccctctg gcccccagca gcaagagcac atctggcgga 420

acagccgccc tgggctgcct ggtgaaagac tacttccccg agcccgtgac cgtgtcctgg 480

aactctggcg ccctgaccag cggcgtgcac acctttccag ccgtgctgca gagcagcggc 540

ctgtacagcc tgtccagcgt ggtgaccgtg cccagcagct ccctgggcac ccagacctac 600

atctgcaacg tgaaccacaa gcccagcaac accaaggtgg acaagcgggt ggaacccaag 660

agctgcgaca agacccacac ctgtcccccc tgccctgccc ctgaactgct gggcggaccc 720

tccgtgttcc tgttcccccc aaagcccaag gacaccctga tgatcagccg gacccccgaa 780

gtgacctgcg tggtggtgga cgtgtcccac gaggaccctg aagtgaagtt caattggtac 840

gtggacggcg tggaagtgca caacgccaag accaagccca gagaggaaca gtacaacagc 900

acctaccggg tggtgtccgt gctgacagtg ctgcaccagg actggctgaa cggcaaagag 960

tacaagtgca aggtctccaa caaggccctg cctgctccca tcgagaaaac catcagcaag 1020

gccaagggcc agccccgcga gcctcaggtg tacacactgc ctcccagccg ggaagagatg 1080

accaagaacc aggtgtccct gacctgtctg gtgaaaggct tctaccccag cgatatcgcc 1140

gtggaatggg agagcaacgg acagcccgag aacaactaca agaccacccc ccctgtgctg 1200

gacagcgacg gctccttctt cctgtactct cggctgaccg tggacaagag ccggtggcag 1260

cagggaaacg tgttcagctg cagcgtgatg cacgaggccc tgcacaacca ctacacccag 1320

aagtccctga gcctgagccc cgggaagtga 1350

<210> 208
<211> 645
<212> DNA
<213> Homo Sapiens

<400> 208
gacatccaga tgacccagtc cccctcctcc gtgtccgcct ctgtgggcga cagagtgacc 60

atcacctgtc gggcctccca gggcatctcc aactggctgg cctggttcca gcacaagccc 120

ggcaaggccc ccaagctgct gatctacgcc gcctcctccc tgctgtccgg cgtgccctcc 180

agattctccg gctctggctc cggcaccgac ttcaccctga ccatctccag cctgcagccc 240

gaggacttcg ccacctacta ctgccagcag gccaactcct tccccatcac cttcggccag 300

ggcacccggc tggaaatcaa gcgtacggtg gccgctccca gcgtgttcat cttccccccc 360

agcgacgagc agctgaagag cggcaccgcc agcgtggtgt gcctgctgaa caacttctac 420

ccccgggagg ccaaggtgca gtggaaggtg gacaacgccc tgcagagcgg caacagccag 480

gagagcgtca ccgagcagga cagcaaggac tccacctaca gcctgagcag caccctgacc 540

ctgtccaagg ccgactacga gaagcacaag gtgtacgcct gcgaggtgac ccaccagggc 600

ctgtccagcc ccgtgaccaa gagcttcaac aggggcgagt gctga 645

<210> 209
<211> 215
<212> PRT
<213> Homo Sapiens

<400> 209

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

Glu Arg Ala Thr Phe Ser Cys Arg Ser Ser His Ser Ile Arg Ser Arg
20 25 30

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

Ile His Gly Val Ser Asn Arg Ala Ser Gly Ile Ser Asp Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Arg Val Glu
65 70 75 80

Pro Glu Asp Phe Ala Leu Tyr Tyr Cys Gln Val Tyr Gly Ala Ser Ser
85 90 95

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Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Arg Lys Arg Thr Val Ala
            100                 105                 110


Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
        115                 120                 125


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


Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145                 150                 155                 160


Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
                165                 170                 175


Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
            180                 185                 190


Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
        195                 200                 205


Ser Phe Asn Arg Gly Glu Cys
    210                 215


<210>  210
<211>  5
<212>  PRT
<213>  Homo Sapiens

<400>  210

Thr Tyr Gly Met His
1               5


<210>  211
<211>  17
<212>  PRT
<213>  Homo Sapiens

<400>  211

Val Ile Trp Asp Asp Gly Ser Tyr Lys Tyr Tyr Gly Asp Ser Val Lys
1               5                   10                  15


Gly



<210>  212
<211>  16
<212>  PRT
<213>  Homo Sapiens

<400>  212

Asp Gly Ile Thr Met Val Arg Gly Val Met Lys Asp Tyr Phe Asp Tyr
1               5                   10                  15
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<210> 213
<211> 11
<212> PRT
<213> Homo Sapiens

<400> 213

Arg Ala Ser Gln Asp Ile Ser Ser Ala Leu Val
1 5 10

<210> 214
<211> 7
<212> PRT
<213> Homo Sapiens

<400> 214

Asp Ala Ser Ser Leu Glu Ser
1 5

<210> 215
<211> 9
<212> PRT
<213> Homo Sapiens

<400> 215

Gln Gln Phe Asn Ser Tyr Pro Leu Thr
1 5

<210> 216
<211> 5
<212> PRT
<213> Homo Sapiens

<400> 216

Ser Tyr Gly Ile Ser
1 5

<210> 217
<211> 17
<212> PRT
<213> Homo Sapiens

<400> 217

Trp Ile Ser Ala Tyr Asn Gly Tyr Thr Asn Tyr Ala Gln Lys Leu Gln
1 5 10 15

Gly

<210> 218
<211> 10
<212> PRT
<213> Homo Sapiens

<400> 218

Asp Leu Arg Gly Thr Asn Tyr Phe Asp Tyr
1 5 10

<210> 219
<211> 11
<212> PRT
<213> Homo Sapiens

<400> 219

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

<210> 220
<211> 7
<212> PRT
<213> Homo Sapiens

<400> 220

Ala Ala Ser Ser Leu Leu Ser
1 5

<210> 221
<211> 9
<212> PRT
<213> Homo Sapiens

<400> 221

Gln Gln Ala Asn Ser Phe Pro Ile Thr
1 5

<210> 222
<211> 5
<212> PRT
<213> Homo Sapiens

<400> 222

Ser Tyr Trp Met Asn
1 5

<210> 223
<211> 17
<212> PRT
<213> Homo Sapiens

<400> 223

Asn Ile Lys Lys Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val Lys
1 5 10 15

Gly

<210> 224
<211> 12
<212> PRT
<213> Homo Sapiens

<400> 224

Asp Leu Gly Trp Gly Trp Gly Trp Tyr Phe Asp Leu
1 5 10

<210> 225
<211> 11
<212> PRT
<213> Homo Sapiens

<400> 225

Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala
1 5 10

<210> 226
<211> 7
<212> PRT
<213> Homo Sapiens

<400> 226

Asp Ala Ser Asn Arg Ala Thr
1 5

<210> 227
<211> 9
<212> PRT
<213> Homo Sapiens

<400> 227

Gln Gln Arg Ser Asn Trp Pro Pro Thr
1 5

<210> 228
<211> 5
<212> PRT
<213> Homo Sapiens

<400> 228

Asp Tyr Tyr Met Tyr
1 5

<210> 229
<211> 17
<212> PRT
<213> Homo Sapiens

<400> 229

Thr Ile Ser Asp Asp Gly Ser Tyr Thr Tyr Tyr Pro Asp Ser Val Lys
1 5 10 15

Gly

<210> 230
<211> 16
<212> PRT

<213> Homo Sapiens

<400> 230

Glu Gly Leu Tyr Tyr Tyr Gly Ser Gly Ser Tyr Tyr Asn Gln Asp Tyr
1 5 10 15

<210> 231
<211> 11
<212> PRT
<213> Homo Sapiens

<400> 231

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

<210> 232
<211> 7
<212> PRT
<213> Homo Sapiens

<400> 232

Asp Ala Ser Ser Leu Glu Ser
1 5

<210> 233
<211> 10
<212> PRT
<213> Homo Sapiens

<400> 233

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

<210> 234
<211> 451
<212> PRT
<213> Homo Sapiens

<400> 234

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 Phe Ser Ser Tyr
20 25 30

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

Ala Asn Ile Lys Lys Asp Gly Ser Glu Lys Tyr Tyr Val 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

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

Ala Arg Asp Leu Gly Trp Gly Trp Gly Trp Tyr Phe Asp Leu Trp Gly
            100                 105                 110

Arg Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
        115                 120                 125

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

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

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

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
            180                 185                 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
        195                 200                 205

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

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
225                 230                 235                 240

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

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
            260                 265                 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
        275                 280                 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
    290                 295                 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
                325                 330                 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
            340                 345                 350
```

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Leu Leu Tyr Ser Lys Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

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

Pro Gly Lys
450

<210> 235
<211> 214
<212> PRT
<213> Homo Sapiens

<400> 235

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
20 25 30

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

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

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

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala

130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 236
<211> 455
<212> PRT
<213> Homo Sapiens

<400> 236

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

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

Tyr Met Tyr Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
35 40 45

Ala Thr Ile Ser Asp Asp Gly Ser Tyr Thr Tyr Tyr Pro Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Asn Leu Tyr
65 70 75 80

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

Ala Arg Glu Gly Leu Tyr Tyr Tyr Gly Ser Gly Ser Tyr Tyr Asn Gln
100 105 110

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr
115 120 125

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

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

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

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

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
        195                 200                 205

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

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
225                 230                 235                 240

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
                245                 250                 255

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
            260                 265                 270

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
        275                 280                 285

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
    290                 295                 300

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
305                 310                 315                 320

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
                325                 330                 335

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
            340                 345                 350

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
        355                 360                 365

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
    370                 375                 380

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
385                 390                 395                 400

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
                405                 410                 415

Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
            420                 425                 430
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Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
435 440 445

Leu Ser Leu Ser Pro Gly Lys
450 455

<210> 237
<211> 213
<212> PRT
<213> Homo Sapiens

<400> 237

Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
1 5 10 15

Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Leu Ser Ser Ala Leu Ala
20 25 30

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

Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
50 55 60

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

Phe Ala Thr Tyr Tyr Cys Gln Gln Phe Thr Ser Tyr Pro Gln Ile Thr
85 90 95

Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala Pro
100 105 110

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
115 120 125

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
130 135 140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145 150 155 160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
165 170 175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
180 185 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
195 200 205

Asn Arg Gly Glu Cys
    210

<210> 238
<211> 15
<212> PRT
<213> Homo Sapiens

<400> 238

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

<210> 239
<211> 16
<212> PRT
<213> Homo Sapiens

<400> 239

Phe Ala Gln Ser Lys Pro Asp Ser Ala Glu Pro Met Asp Arg Ser Ala
1   5   10   15

<210> 240
<211> 16
<212> PRT
<213> Homo Sapiens

<400> 240

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