

SEQUENCE LISTING

<110> Oncorus, Inc.
Evnin, Luke

<120> PSEUDOTYPED ONCOLYTIC VIRAL DELIVERY OF THERAPEUTIC POLYPEPTIDES

<130> ONCR-004/02WO 324865-2063

<150> US 62/357,195

<151> 2016-06-30

<160> 70

<170> PatentIn version 3.5

<210> 1

<211> 57

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesized polynucleotide encoding signal peptide

<400> 1

atggagttcg gcctgagctg ggtgttcctg gtggccctgt tcaggggcgt gcagtgc 57

<210> 2

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized signal peptide sequence

<400> 2

Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Leu Phe Arg Gly

1 5 10 15

Val Gln Cys Asp

20

<210> 3

<400> 3

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<210> 4

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized signal peptide sequence

<400> 4

Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Leu Phe Arg Gly
1 5 10 15

Val Gln Cys Asp
20

<210> 5

<211> 15

<212> DNA

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<223> Synthesized polynucleotide encoding GlySer linker peptide

<400> 5

ggcggcggcg gcagc 15

<210> 6

<211> 5

<212> PRT

<213> Artificial Sequence

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<223> Synthesized GlySer linker peptide sequence

<400> 6

Gly Gly Gly Gly Ser
1 5

<210> 7

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesized polynucleotide encoding GlySer linker peptide

<400> 7

ggcggcggcg gcagcggcgg cggcggcagc ggcggcggcg gcagc 45

<210> 8

<211> 15

<212> PRT

<213> Artificial Sequence

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<223> Synthesized GlySer linker peptide sequence

<400> 8

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

<210> 9

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesized polynucleotide encoding GlySer linker peptide

<400> 9

gtggagggcg gcagcggcgg cagcggcggc agcggcggca gcggcggcgt ggac 54

<210> 10

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized GlySer linker peptide sequence

<400> 10

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

<210> 11

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesized polynucleotide encoding 6-His tag

<400> 11

caccaccacc accaccac 18

<210> 12

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized 6-His tag sequence

<400> 12

His His His His His His
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<210> 13

<211> 66

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesized polynucleotide encoding T2A linker

<400> 13

cgaagaaaac gcgaggggag gggctccctg ctcacctgtg gtgatgtcga agagaaccct 60

gggcccg 66

<210> 14

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized T2A linker linker sequence

<400> 14

Arg Arg Lys Arg Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val
1 5 10 15

Glu Glu Asn Pro Gly Pro
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<210> 15

<211> 333

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesized polynucleotide encoding anti-CD19 light chain
sequence

<400> 15

gacatccagc tgaccagag ccccgccagc ctggccgtga gcctgggccca gagggccacc 60

atcagctgca aggccagcca gagcgtggac tacgacggcg acagctacct gaactgttac 120

cagcagatcc ccggccagcc cccaagctg ctgatctacg acgccagcaa cctggtgagc 180

ggcatccccc ccaggttcag cggcagcggc agcggcaccg acttcaccct gaacatccac 240
cccgtggaga aggtggacgc cgccacctac cactgccagc agagcaccga ggaccctgg 300
accttcggcg gcggcaccaa gctggagatc aag 333

<210> 16
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized anti-CD19 light chain sequence

<400> 16

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

Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
20 25 30

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

Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65 70 75 80

Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr
85 90 95

Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 17
<211> 372
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized polynucleotide encoding anti-CD19 heavy chain
sequence

<400> 17
caggtgcagc tgcagcagag cggcgccgag ctggtgaggc ccggcagcag cgtgaagatc 60
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cccggccagg gcctggagtg gatcggccag atctggcccg gcgacggcga caccaactac 180
aacggcaagt tcaagggcaa ggccaccctg accgccgacg agagcagcag caccgcctac 240
atgcagctga gcagcctggc cagcgaggac agcgccgtgt acttctgcgc caggagggag 300
accaccaccg tgggcaggtg ctactacgcc atggactact ggggccaggg caccaccgtg 360
accgtgagca gc 372

<210> 18
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized anti-CD19 heavy chain sequence

<400> 18

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

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

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

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

Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Ala Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser

115

120

<210> 19

<211> 318

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesized polynucleotide encoding anti-CD3 light chain sequence

<400> 19

gacatccagc tgaccagag ccccgccatc atgagcgcca gccccggcga gaaggtgacc 60

atgacctgca gggccagcag cagcgtgagc tacatgaact ggtaccagca gaagagcggc 120

accagcccca agaggtggat ctacgacacc agcaaggtgg ccagcggcgt gccctacagg 180

ttcagcggca gcggcagcgg caccagctac agcctgacca tcagcagcat ggaggccgag 240

gacgccgcca cctactactg ccagcagtgg agcagcaacc cctgacctt cggcgccggc 300

accaagctgg agctgaag 318

<210> 20

<211> 106

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized anti-CD3 light chain sequence

<400> 20

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

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
85 90 95

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

<210> 21

<211> 357

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesized polynucleotide encoding anti-CD3 heavy chain sequence

<400> 21

gacatcaagc tgcagcagag cggcgccgag ctggccaggc ccggcgccag cgtgaagatg 60

agctgcaaga ccagcggcta caccttcacc aggtacacca tgcactgggt gaagcagagg 120

cccgccagg gcctggagtg gatcggtac atcaaccca gcaggggcta caccaactac 180

aaccagaagt tcaaggacaa ggccaccctg accaccgaca agagcagcag caccgcctac 240

atgcagctga gcagcctgac cagcaggac agcgccgtgt actactgcgc caggtactac 300

gacgaccact actgcctgga ctactggggc cagggcacca ccctgaccgt gagcagc 357

<210> 22

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized anti-CD3 heavy chain sequence

<400> 22

Asp Ile Lys Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala
1 5 10 15

Ser Val Lys Met Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Arg Tyr
20 25 30

Thr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

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

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

Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile
50 55 60

Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His
65 70 75 80

Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln
85 90 95

Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu
100 105 110

Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val
115 120 125

Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile
130 135 140

Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn
145 150 155 160

Thr Ser

<210> 25

<211> 987

<212> DNA

<213> Homo sapiens

<400> 25

atgtgtcacc agcagttggc catctcttgg tttccctgg ttttctggc atctcccctc 60

gtggccatat gggaactgaa gaaagatgtt tatgtcgtag aattggattg gtatccggat 120

gccctggag aaatgggtgt cctcacctgt gacaccctg aagaagatgg tatcacctgg 180

acctggacc agagcagtga ggtcttaggc tctggcaaaa ccctgaccat ccaagtcaaa 240

gagtttggag atgctggcca gtacacctgt cacaaggag gcgaggttct aagccattcg 300

ctcctgctgc ttcaaaaaa ggaagatgga attgggtcca ctgatatttt aaaggaccag 360

aaagaaccca aaaataagac ctttctaaga tgcgaggcca agaattattc tggacgtttc 420
 acctgctggg ggctgacgac aatcagtact gatttgacat tcagtgtaa aagcagcaga 480
 ggctcttctg accccaagg ggtgacgtgc ggagctgcta cactctctgc agagagagtc 540
 agaggggaca acaaggagta tgagtactca gtggagtgcc aggaggacag tgcctgcca 600
 gctgctgagg agagtctgcc cattgaggtc atggtgatg ccgttcacaa gctcaagtat 660
 gaaaactaca ccagcagctt ctcatcagg gacatcatca aacctgacc acccaagaac 720
 ttgcagctga agccattaaa gaattctcgg caggtggagg tcagctggga gtaccctgac 780
 acctggagta ctccacattc ctactctcc ctgacattct gcgttcaggt ccagggaag 840
 agcaagagag aaaagaaaga tagagtcttc acggacaaga cctcagccac ggtcatctgc 900
 cgcaaaaatg ccagcattag cgtgcgggcc caggaccgct actatagctc atcttgagc 960
 gaatgggcat ctgtgccctg cagttag 987

<210> 26
 <211> 329
 <212> PRT
 <213> Homo sapiens
 <400> 26

Pro Met Cys His Gln Gln Leu Val Ile Ser Trp Phe Ser Leu Val Phe
 1 5 10 15

Leu Ala Ser Pro Leu Val Ala Ile Trp Glu Leu Lys Lys Asp Val Tyr
 20 25 30

Val Val Glu Leu Asp Trp Tyr Pro Asp Ala Pro Gly Glu Met Val Val
 35 40 45

Leu Thr Cys Asp Thr Pro Glu Glu Asp Gly Ile Thr Trp Thr Leu Asp
 50 55 60

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

Lys Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu
 85 90 95

Val Leu Ser His Ser Leu Leu Leu Leu His Lys Lys Glu Asp Gly Ile
100 105 110

Trp Ser Thr Asp Ile Leu Lys Asp Gln Lys Glu Pro Lys Asn Lys Thr
115 120 125

Phe Leu Arg Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp
130 135 140

Trp Leu Thr Thr Ile Ser Thr Asp Leu Thr Phe Ser Val Lys Ser Ser
145 150 155 160

Arg Gly Ser Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Ala Thr Leu
165 170 175

Ser Ala Glu Arg Val Arg Gly Asp Asn Lys Glu Tyr Glu Tyr Ser Val
180 185 190

Glu Cys Gln Glu Asp Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro
195 200 205

Ile Glu Val Met Val Asp Ala Val His Lys Leu Lys Tyr Glu Asn Tyr
210 215 220

Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys
225 230 235 240

Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg Gln Val Glu Val Ser
245 250 255

Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu
260 265 270

Thr Phe Cys Val Gln Val Gln Gly Lys Ser Lys Arg Glu Lys Lys Asp
275 280 285

Arg Val Phe Thr Asp Lys Thr Ser Ala Thr Val Ile Cys Arg Lys Asn
290 295 300

Ala Ser Ile Ser Val Arg Ala Gln Asp Arg Tyr Tyr Ser Ser Ser Trp
305 310 315 320

Ser Glu Trp Ala Ser Val Pro Cys Ser
325

<210> 27
<211> 762
<212> DNA
<213> Homo sapiens

<400> 27
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ctctccttg tggtacctt ggtcctctg gaccacctca gttggccag aaacctcccc 180
gtggccactc cagaccagg aatgttcca tgccttacc actcccaaaa cctgctgagg 240
gccgtcagca acatgtcca gaaggccaga caaactctag aattttacc ttgcattct 300
gaagagattg atcatgaaga taccacaaa gataaaacca gcacagtga ggctgttta 360
ccattggaat taaccaagaa tgagagtgc ctaaattcca gagagacctc tttcataact 420
aatgggagtt gcctggcctc cagaaagacc tctttatga tggccctgtg ccttagtagt 480
atttatgaag actgaagat gtaccagggt gagttcaaga ccatgaatgc aaagcttctg 540
atggatccta agaggcagat cttctagat caaaacatgc tggcagttat tgatgagctg 600
atgcaggccc tgaattcaa cagtgaagct gtgccacaaa aatctcctt tgaagaaccg 660
gattttata aaactaaaat caagctctgc atactcttc atgctttcag aatcgggca 720
gtgactattg atagagtgt gagctatctg aatgcttct ag 762

<210> 28
<211> 253
<212> PRT
<213> Homo sapiens

<400> 28

Met Trp Pro Pro Gly Ser Ala Ser Gln Pro Pro Pro Ser Pro Ala Ala
1 5 10 15

Ala Thr Gly Leu His Pro Ala Ala Arg Pro Val Ser Leu Gln Cys Arg
20 25 30

Leu Ser Met Cys Pro Ala Arg Ser Leu Leu Leu Val Ala Thr Leu Val
35 40 45

Leu Leu Asp His Leu Ser Leu Ala Arg Asn Leu Pro Val Ala Thr Pro
50 55 60

Asp Pro Gly Met Phe Pro Cys Leu His His Ser Gln Asn Leu Leu Arg
65 70 75 80

Ala Val Ser Asn Met Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe Tyr
85 90 95

Pro Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp Lys
100 105 110

Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Lys Asn Glu
115 120 125

Ser Cys Leu Asn Ser Arg Glu Thr Ser Phe Ile Thr Asn Gly Ser Cys
130 135 140

Leu Ala Ser Arg Lys Thr Ser Phe Met Met Ala Leu Cys Leu Ser Ser
145 150 155 160

Ile Tyr Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Thr Met Asn
165 170 175

Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln Asn
180 185 190

Met Leu Ala Val Ile Asp Glu Leu Met Gln Ala Leu Asn Phe Asn Ser
195 200 205

Glu Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr Lys
210 215 220

Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg Ala
225 230 235 240

Val Thr Ile Asp Arg Val Met Ser Tyr Leu Asn Ala Ser
245 250

<210> 29

<211> 297
<212> DNA
<213> Homo sapiens

<400> 29
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aatccaaggt ctttagaaaa acttgaaatt attcctgcaa gccaatcttg tccacgtgtt 180
gagatcattg ctacaatgaa aaagaagggt gagaagagat gtctgaatcc agaatcgaag 240
gccatcaaga atttactgaa agcagtttagc aaggaaagggt ctaaaagatc tccttag 297

<210> 30
<211> 98
<212> PRT
<213> Homo sapiens

<400> 30

Met Asn Gln Thr Ala Ile Leu Ile Cys Cys Leu Ile Phe Leu Thr Leu
1 5 10 15

Ser Gly Ile Gln Gly Val Pro Leu Ser Arg Thr Val Arg Cys Thr Cys
20 25 30

Ile Ser Ile Ser Asn Gln Pro Val Asn Pro Arg Ser Leu Glu Lys Leu
35 40 45

Glu Ile Ile Pro Ala Ser Gln Phe Cys Pro Arg Val Glu Ile Ile Ala
50 55 60

Thr Met Lys Lys Lys Gly Glu Lys Arg Cys Leu Asn Pro Glu Ser Lys
65 70 75 80

Ala Ile Lys Asn Leu Leu Lys Ala Val Ser Lys Glu Arg Ser Lys Arg
85 90 95

Ser Pro

<210> 31
<211> 426
<212> DNA
<213> Homo sapiens

<400> 31
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 accgctaccc tcagatgtac catcacttct ctctcccccg ttggcccat ccagtgggtt 180
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 aacataacac ccgctgacgc cggtacatac tattgtatta aatttcgaaa gggctcacca 360
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 gctagc 426

<210> 32
 <211> 142
 <212> PRT
 <213> Homo sapiens

<400> 32
 Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
 1 5 10 15
 Gly Ser Thr Gly Asp Glu Glu Glu Leu Gln Ile Ile Gln Pro Asp Lys
 20 25 30
 Ser Val Leu Val Ala Ala Gly Glu Thr Ala Thr Leu Arg Cys Thr Ile
 35 40 45
 Thr Ser Leu Phe Pro Val Gly Pro Ile Gln Trp Phe Arg Gly Ala Gly
 50 55 60
 Pro Gly Arg Val Leu Ile Tyr Asn Gln Arg Gln Gly Pro Phe Pro Arg
 65 70 75 80
 Val Thr Thr Val Ser Asp Thr Thr Lys Arg Asn Asn Met Asp Phe Ser
 85 90 95
 Ile Arg Ile Gly Asn Ile Thr Pro Ala Asp Ala Gly Thr Tyr Tyr Cys
 100 105 110
 Ile Lys Phe Arg Lys Gly Ser Pro Asp Asp Val Glu Phe Lys Ser Gly

115

120

125

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

<210> 33

<211> 2124

<212> DNA

<213> Homo sapiens

<400> 33

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 gacaggcagc tggcagagga atacctgtac cgctatgggt acactcgggt ggcagagatg 180
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acgcacgacg tcttcagta ccgagagaaa gcctatttct gccaggaccg cttctactgg 2040
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<210> 34
<211> 707
<212> PRT
<213> Homo sapiens

<400> 34

Met Ser Leu Trp Gln Pro Leu Val Leu Val Leu Leu Val Leu Gly Cys
1 5 10 15

Cys Phe Ala Ala Pro Arg Gln Arg Gln Ser Thr Leu Val Leu Phe Pro
20 25 30

Gly Asp Leu Arg Thr Asn Leu Thr Asp Arg Gln Leu Ala Glu Glu Tyr
35 40 45

Leu Tyr Arg Tyr Gly Tyr Thr Arg Val Ala Glu Met Arg Gly Glu Ser
50 55 60

Lys Ser Leu Gly Pro Ala Leu Leu Leu Leu Gln Lys Gln Leu Ser Leu

65

70

75

80

Pro Glu Thr Gly Glu Leu Asp Ser Ala Thr Leu Lys Ala Met Arg Thr
85 90 95

Pro Arg Cys Gly Val Pro Asp Leu Gly Arg Phe Gln Thr Phe Glu Gly
100 105 110

Asp Leu Lys Trp His His His Asn Ile Thr Tyr Trp Ile Gln Asn Tyr
115 120 125

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

Phe Ala Leu Trp Ser Ala Val Thr Pro Leu Thr Phe Thr Arg Val Tyr
145 150 155 160

Ser Arg Asp Ala Asp Ile Val Ile Gln Phe Gly Val Ala Glu His Gly
165 170 175

Asp Gly Tyr Pro Phe Asp Gly Lys Asp Gly Leu Leu Ala His Ala Phe
180 185 190

Pro Pro Gly Pro Gly Ile Gln Gly Asp Ala His Phe Asp Asp Asp Glu
195 200 205

Leu Trp Ser Leu Gly Lys Gly Val Val Val Pro Thr Arg Phe Gly Asn
210 215 220

Ala Asp Gly Ala Ala Cys His Phe Pro Phe Ile Phe Glu Gly Arg Ser
225 230 235 240

Tyr Ser Ala Cys Thr Thr Asp Gly Arg Ser Asp Gly Leu Pro Trp Cys
245 250 255

Ser Thr Thr Ala Asn Tyr Asp Thr Asp Asp Arg Phe Gly Phe Cys Pro
260 265 270

Ser Glu Arg Leu Tyr Thr Arg Asp Gly Asn Ala Asp Gly Lys Pro Cys
275 280 285

Gln Phe Pro Phe Ile Phe Gln Gly Gln Ser Tyr Ser Ala Cys Thr Thr
290 295 300

Asp Gly Arg Ser Asp Gly Tyr Arg Trp Cys Ala Thr Thr Ala Asn Tyr
305 310 315 320

Asp Arg Asp Lys Leu Phe Gly Phe Cys Pro Thr Arg Ala Asp Ser Thr
325 330 335

Val Met Gly Gly Asn Ser Ala Gly Glu Leu Cys Val Phe Pro Phe Thr
340 345 350

Phe Leu Gly Lys Glu Tyr Ser Thr Cys Thr Ser Glu Gly Arg Gly Asp
355 360 365

Gly Arg Leu Trp Cys Ala Thr Thr Ser Asn Phe Asp Ser Asp Lys Lys
370 375 380

Trp Gly Phe Cys Pro Asp Gln Gly Tyr Ser Leu Phe Leu Val Ala Ala
385 390 395 400

His Glu Phe Gly His Ala Leu Gly Leu Asp His Ser Ser Val Pro Glu
405 410 415

Ala Leu Met Tyr Pro Met Tyr Arg Phe Thr Glu Gly Pro Pro Leu His
420 425 430

Lys Asp Asp Val Asn Gly Ile Arg His Leu Tyr Gly Pro Arg Pro Glu
435 440 445

Pro Glu Pro Arg Pro Pro Thr Thr Thr Thr Pro Gln Pro Thr Ala Pro
450 455 460

Pro Thr Val Cys Pro Thr Gly Pro Pro Thr Val His Pro Ser Glu Arg
465 470 475 480

Pro Thr Ala Gly Pro Thr Gly Pro Pro Ser Ala Gly Pro Thr Gly Pro
485 490 495

Pro Thr Ala Gly Pro Ser Thr Ala Thr Thr Val Pro Leu Ser Pro Val
500 505 510

Asp Asp Ala Cys Asn Val Asn Ile Phe Asp Ala Ile Ala Glu Ile Gly
515 520 525

Asn Gln Leu Tyr Leu Phe Lys Asp Gly Lys Tyr Trp Arg Phe Ser Glu
530 535 540

Gly Arg Gly Ser Arg Pro Gln Gly Pro Phe Leu Ile Ala Asp Lys Trp
545 550 555 560

Pro Ala Leu Pro Arg Lys Leu Asp Ser Val Phe Glu Glu Pro Leu Ser
565 570 575

Lys Lys Leu Phe Phe Phe Ser Gly Arg Gln Val Trp Val Tyr Thr Gly
580 585 590

Ala Ser Val Leu Gly Pro Arg Arg Leu Asp Lys Leu Gly Leu Gly Ala
595 600 605

Asp Val Ala Gln Val Thr Gly Ala Leu Arg Ser Gly Arg Gly Lys Met
610 615 620

Leu Leu Phe Ser Gly Arg Arg Leu Trp Arg Phe Asp Val Lys Ala Gln
625 630 635 640

Met Val Asp Pro Arg Ser Ala Ser Glu Val Asp Arg Met Phe Pro Gly
645 650 655

Val Pro Leu Asp Thr His Asp Val Phe Gln Tyr Arg Glu Lys Ala Tyr
660 665 670

Phe Cys Gln Asp Arg Phe Tyr Trp Arg Val Ser Ser Arg Ser Glu Leu
675 680 685

Asn Gln Val Asp Gln Val Gly Tyr Val Thr Tyr Asp Ile Leu Gln Cys
690 695 700

Pro Glu Asp
705

<210> 35
<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesized polynucleotide encoding PD-L1 light chain Fv

<400> 35

gataaccaga tgacacagag cccatcatct ctgtctgcaa gcgtaggaga ccgagtcacc 60

attacatgca gagcctccca agacgtttcc acagcagtgg cctggatatca gcaaaaacct 120

ggtaaggcgc ccaagcttct catctattca gccagttttc tgtatagcgg cgttcccagc 180

cgattctctg gctctggatc cggcacggac ttactttga caatttctc tcttcagccc 240

gaagattttg caacctacta ctgtcagcaa tatctctacc atccagccac attcggacag 300

ggcaccaaag tcgaaatcaa aaga 324

<210> 36

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized PD-L1 light chain Fv sequence

<400> 36

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

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Ser Thr Ala

20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

Tyr Ser Ala Ser Phe Leu Tyr 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 Tyr Leu Tyr His Pro Ala

85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg

100

105

<210> 37

<211> 354

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesized polynucleotide encoding PD-L1 heavy chain Fv

<400> 37

gaagtgaac tcgtgaaag cggaggaggg ctgtccaac ctggcgggtc actgcggtg 60

agctgcgccg caagcggatt caccttctca gactcttga tccattgggt gcgccaggct 120

cccggaaaag gcttggaatg ggttgcttgg attcaccgt atggcgggtc cacatactac 180

gctgacagcg ttaagggtcg attcaccatc tctgcagata ctcaaaaaa cacagcctac 240

cttcagatga atagtttgcg cgccgaggac acagcggttt attattgtgc ccgaagacat 300

tggcccggcg gtttcgacta ctgggggcaa ggtacgttgg tgactgtgag cgcc 354

<210> 38

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized PD-L1 heavy chain Fv sequence

<400> 38

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 Asp Ser
 20 25 30

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

Ala Trp Ile Ser Pro Tyr Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala 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 Arg His Trp Pro Gly Gly Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ala
115

<210> 39
<211> 699
<212> DNA
<213> Homo sapiens

<400> 39
gtagatgaag caaaatcttg tgacaaaacc catactgcc caccatgccc agccccagaa 60
cttcttggcg gaccctctgt cttccttttc cctccgaagc ccaaggatac cctgatgatc 120
agccgaaccc cggaggtaac atgtgtggtg gtcgatgta gccatgagga tctgaagtc 180
aaatttaact ggtatgtaga cgggtgtgag gtgcacaacg ctaaaactaa gcccaggag 240
gagcagtaca actcaaccta tcgctgcgta tctgtgctta ccgtcctgca tcaagactgg 300
ctcaatggta aggaatataa atgtaaagt agtaacaagg cactgccagc acctatcgaa 360
aaaaccatct caaaggcgaa gggacagccc agggaacccc aggtctatac tctgccacct 420
tctcgggatg aattgaccaa gaaccaagtt agcctgacat gtctggtgaa aggtttctat 480
ccaagcgata tagctgtcga gtgggagtc aatggccaac ctgagaacaa ttataagacc 540
acccccccg ttctggacag cgacggatcc ttttctctgt actcaaaact cactgtcgat 600
aatcaagat ggcaacaagg caacgtttt agctgtagcg tgatgcacga agcactcat 660
aatcactata cacagaagtc actctctctt tctccagga 699

<210> 40
<211> 233
<212> PRT
<213> Homo sapiens

<400> 40

Val Asp Glu Ala Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
1 5 10 15

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

20 25 30

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
35 40 45

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
50 55 60

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
65 70 75 80

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
85 90 95

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
100 105 110

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
115 120 125

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
130 135 140

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

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

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
180 185 190

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
195 200 205

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
210 215 220

Gln Lys Ser Leu Ser Leu Ser Pro Gly
225 230

<210> 41
<211> 69
<212> DNA
<213> Homo sapiens

<400> 41
gtagatgaag caaaatcttg tgacaaaacc catacctgcc caccatgccc agccccagaa 60
cttcttggc 69

<210> 42
<211> 23
<212> PRT
<213> Homo sapiens

<400> 42
Val Asp Glu Ala Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
1 5 10 15

Pro Ala Pro Glu Leu Leu Gly
20

<210> 43
<211> 1572
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized polynucleotide encoding CD19-CD3 bi-specific T-cell
engager construct

<400> 43
atggagttcg gcctgagctg ggtgttctg gtggccctgt tcaggggctg gcagtgcgac 60
atccagctga cccagagccc cgccagcctg gccgtgagcc tgggccagag ggccaccatc 120
agctgcaagg ccagccagag cgtggactac gacggcgaca gctacctgaa ctggtaccag 180
cagatccccg gccagcccc caagctgctg atctacgacg ccagcaacct ggtgagcggc 240
atcccccca ggttcagcgg cagcggcagc ggcaccgact tcacctgaa catccacccc 300
gtggagaagg tggacgccgc cacctaccac tgccagcaga gcaccgagga cccctggacc 360
ttcggcggcg gcaccaagct ggagatcaag ggcggcggcg gcagcggcgg cggcggcagc 420
ggcggcggcg gcagccaggt gcagctgcag cagagcggcg ccgagctggt gaggcccggc 480
agcagcgtga agatcagctg caaggccagc ggctacgcct tcagcagcta ctggatgaac 540
tgggtgaagc agaggcccg ccagggcctg gagggtgatc gccagatctg gcccggcgac 600

ggcgacacca actacaacgg caagttcaag ggcaaggcca ccctgaccgc cgacgagagc 660
 agcagcaccg cctacatgca gctgagcagc ctggccagcg aggacagcgc cgtgtacttc 720
 tgcgccagga gggagaccac caccgtgggc aggtactact acgccatgga ctactggggc 780
 cagggcacca ccgtgaccgt gagcagcggc ggcggcggca gcgacatcaa gctgcagcag 840
 agcggcgccg agctggccag gcccggcgcc agcgtgaaga tgagctgcaa gaccagcggc 900
 tacacctca ccaggtacac catgcactgg gtgaagcaga ggcccggcca gggcctggag 960
 tggatcggct acatcaaccc cagcaggggc tacaccaact acaaccagaa gttcaaggac 1020
 aaggccacc tgaccaccga caagagcagc agcaccgcct acatgcagct gagcagcctg 1080
 accagcagg acagcgccgt gtactactgc gccaggtact acgacgacca ctactgcctg 1140
 gactactggg gccagggcac caccctgacc gtgagcagcg tggagggcgg cagcggcggc 1200
 agcggcggca gcggcggcag cggcggcgtg gacgacatcc agctgacca gagccccgcc 1260
 atcatgagcg ccagccccgg cgagaagggtg accatgacct gcagggccag cagcagcgtg 1320
 agctacatga actggtacca gcagaagagc ggcaccagcc ccaagagggtg gatctacgac 1380
 accagcaagg tggccagcgg cgtgcctac aggttcagcg gcagcggcag cggcaccagc 1440
 tacagcctga ccatcagcag catggaggcc gaggacgccg ccacctacta ctgccagcag 1500
 tggagcagca accccctgac cttcggcgcc ggcaccaagc tggagctgaa gcaccaccac 1560
 caccaccact ag 1572

<210> 44

<211> 523

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized CD19-CD3 bi-specific T-cell engager construct

<400> 44

Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Leu Phe Arg Gly
 1 5 10 15

Val Gln Cys Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val
 20 25 30

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

35

40

45

Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly
 50 55 60

Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly
 65 70 75 80

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

Asn Ile His Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln
 100 105 110

Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu
 115 120 125

Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 130 135 140

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

Ser Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser
 165 170 175

Tyr Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp
 180 185 190

Ile Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys
 195 200 205

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala
 210 215 220

Tyr Met Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe
 225 230 235 240

Cys Ala Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met
 245 250 255

Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
260 265 270

Gly Ser Asp Ile Lys Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro
275 280 285

Gly Ala Ser Val Lys Met Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr
290 295 300

Arg Tyr Thr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu
305 310 315 320

Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln
325 330 335

Lys Phe Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr
340 345 350

Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr
355 360 365

Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly
370 375 380

Gln Gly Thr Thr Leu Thr Val Ser Ser Val Glu Gly Gly Ser Gly Gly
385 390 395 400

Ser Gly Gly Ser Gly Gly Ser Gly Gly Val Asp Asp Ile Gln Leu Thr
405 410 415

Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met
420 425 430

Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln
435 440 445

Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val
450 455 460

Ala Ser Gly Val Pro Tyr Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser
465 470 475 480

Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr Tyr
485 490 495

Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Ala Gly Thr
500 505 510

Lys Leu Glu Leu Lys His His His His His
515 520

<210> 45

<211> 1177

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesized polynucleotide encoding SIRP1alpha-CD3-SL bi-specific
T-cell engager construct

<400> 45

atggagaccg ataccctgct cttgtgggtt ttgcttcttt gggtgccagg atctacaggt 60

gatgaagaag aattgcagat catccaacca gacaaatccg tactcgtggc cgcaggagag 120

accgctaccc tcagatgtac catcacttct ctcttccccg ttggcccat ccagtgggtt 180

cgaggcgcag gaccaggacg agtgcttatt tacaatcaac gacagggccc attccaaga 240

gtgacaacag tatccgatac caccaagcgc aataatatgg actttagcat tagaatcggc 300

aacataacac ccgctgacgc cggtagacac tattgtatta aatttcgaaa gggtcacca 360

gacgacgtgg aatttaagtc aggggccgga accgaactct cagttagagc aaaaccttct 420

gctagcgaca tcaagctgca gcagagcggc gccgagctgg ccaggcccgg cgccagcgtg 480

aagatgagct gcaagaccag cggctacacc ttaccaggt acaccatgca ctgggtgaag 540

cagaggcccg gccagggcct ggagtggatc ggctacatca accccagcag gggctacacc 600

aactacaacc agaagttaa ggacaaggcc accctgacca ccgacaagag cagcagcacc 660

gcctacatgc agctgagcag cctgaccagc gaggacagcg ccgtgtacta ctgcgccagg 720

tactacgacg accactactg cctggactac tggggccagg gcaccacct gaccgtgagc 780

agcgtggagg gcggcagcgg cggcagcggc ggagcggcg gcagcggcgg cgtggacgac 840

atccagctga cccagagccc cgccatcatg agcgcagcc ccggcgagaa ggtgaccatg 900

acctgcaggg ccagcagcag cgtgagctac atgaactggt accagcagaa gagcggcacc 960

agccccaaga ggtggatcta cgacaccagc aaggtggcca gcggcgtgcc ctacaggttc 1020
agcggcagcg gcagcggcac cagctacagc ctgacatca gcagcatgga ggccgaggac 1080
gccgccacct actactgccca gcagtggagc agcaaccccc tgaccttcgg cgccggcacc 1140
aagctggagc tgaagcacca ccatcatcac cactgag 1177

<210> 46
<211> 391
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized SIRP1alpha-CD3-SL bi-specific T-cell engager
construct

<400> 46

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

Gly Ser Thr Gly Asp Glu Glu Glu Leu Gln Ile Ile Gln Pro Asp Lys
20 25 30

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

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

Pro Gly Arg Val Leu Ile Tyr Asn Gln Arg Gln Gly Pro Phe Pro Arg
65 70 75 80

Val Thr Thr Val Ser Asp Thr Thr Lys Arg Asn Asn Met Asp Phe Ser
85 90 95

Ile Arg Ile Gly Asn Ile Thr Pro Ala Asp Ala Gly Thr Tyr Tyr Cys
100 105 110

Ile Lys Phe Arg Lys Gly Ser Pro Asp Asp Val Glu Phe Lys Ser Gly
115 120 125

Ala Gly Thr Glu Leu Ser Val Arg Ala Lys Pro Ser Ala Ser Asp Ile
130 135 140

Lys Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val
145 150 155 160

Lys Met Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met
 165 170 175

His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr
 180 185 190

Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp
 195 200 205

Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln
 210 215 220

Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg
225 230 235 240

Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr
 245 250 255

Leu Thr Val Ser Ser Val Glu Gly Gly Ser Gly Gly Ser Gly Gly Ser
 260 265 270

Gly Gly Ser Gly Gly Val Asp Asp Ile Gln Leu Thr Gln Ser Pro Ala
 275 280 285

Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala
 290 295 300

Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Ser Gly Thr
305 310 315 320

Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly Val
 325 330 335

Pro Tyr Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr
 340 345 350

Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln
 355 360 365

Trp Ser Ser Asn Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu
370 375 380

Lys His His His His His His
385 390

<210> 47

<211> 1191

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesized polynucleotide encoding SIRP1alpha-CD3-LL bi-specific
T-cell engager construct

<400> 47

atggagaccg ataccctgct cttgtgggtt ttgcttcttt gggtgccagg atctacaggt 60
gatgaagaag aattgcagat catccaacca gacaaatccg tactcgtggc cgcaggagag 120
accgtaccc tcagatgtac catcacttct ctcttccccg ttggcccat ccagtgggtt 180
cgaggcgag gaccaggacg agtgcttatt tacaatcaac gacagggccc attccaaga 240
gtgacaacag tatccgatac caccaagcgc aataatatgg actttagcat tagaatcggc 300
aacataacac ccgctgacgc cggtacatac tattgtatta aatttcgaaa gggctcacca 360
gacgacgtgg aatttaagtc aggggccgga accgaactct cagttagagc aaaaccttct 420
gctagcggcg gcggcgagcag cgacatcaag ctgcagcaga gcggcgccga gctggccagg 480
cccggcgcca gcgtaagat gagctgcaag accagcggct acaccttcac caggtacacc 540
atgcactggg tgaagcagag gcccgccag ggcctggagt ggatcggcta catcaacccc 600
agcaggggct acaccaacta caaccagaag ttcaaggaca aggccaccct gaccaccgac 660
aagagcagca gcaccgccta catgcagctg agcagcctga ccagcgagga cagcgccgtg 720
tactactgcg ccaggtacta cgacgaccac tactgcctgg actactgggg ccagggcacc 780
accctgaccg tgagcagcgt ggagggcggc agcggcggca gcggcgccag cggcggcagc 840
ggcgcggtgg acgacatcca gctgaccag agcccccca tcatgagcgc cagccccggc 900
gagaaggtga ccatgacctg cagggccagc agcagcgtga gctacatgaa ctggtaccag 960
cagaagagcg gcaccagccc caagaggtgg atctacgaca ccagcaaggt ggccagcggc 1020
gtgcctaca ggttcagcgg cagcggcagc ggcaccagct acagcctgac catcagcagc 1080

atggaggccg aggacgccgc cacctactac tgccagcagt ggagcagcaa cccctgacc 1140

ttcggcgccg gcaccaagct ggagctgaag caccaccacc accaccacta g 1191

<210> 48

<211> 396

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized SIRP1alpha-CD3-LL bi-specific T-cell engager
construct

<400> 48

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

Gly Ser Thr Gly Asp Glu Glu Glu Leu Gln Ile Ile Gln Pro Asp Lys
20 25 30

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

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

Pro Gly Arg Val Leu Ile Tyr Asn Gln Arg Gln Gly Pro Phe Pro Arg
65 70 75 80

Val Thr Thr Val Ser Asp Thr Thr Lys Arg Asn Asn Met Asp Phe Ser
85 90 95

Ile Arg Ile Gly Asn Ile Thr Pro Ala Asp Ala Gly Thr Tyr Tyr Cys
100 105 110

Ile Lys Phe Arg Lys Gly Ser Pro Asp Asp Val Glu Phe Lys Ser Gly
115 120 125

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

Gly Gly Ser Asp Ile Lys Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg
145 150 155 160

Pro Gly Ala Ser Val Lys Met Ser Cys Lys Thr Ser Gly Tyr Thr Phe
165 170 175

Thr Arg Tyr Thr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
180 185 190

Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn
195 200 205

Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser
210 215 220

Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
225 230 235 240

Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp
245 250 255

Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Val Glu Gly Gly Ser Gly
260 265 270

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Val Asp Asp Ile Gln Leu
275 280 285

Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr
290 295 300

Met Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln
305 310 315 320

Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys
325 330 335

Val Ala Ser Gly Val Pro Tyr Arg Phe Ser Gly Ser Gly Ser Gly Thr
340 345 350

Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr
355 360 365

Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Ala Gly

370 375 380

Thr Lys Leu Glu Leu Lys His His His His His His
385 390 395

<210> 49

<211> 1545

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesized polynucleotide encoding PDL1-CD3 bi-specific T-cell
engager construct

<400> 49

```
atggagttcg gcctgagctg ggtgttctg gtggccctgt tcaggggctg gcagtgcgac    60
atcaagctgc agcagagcgg cgccgagctg gccaggcccg gcgccagcgt gaagatgagc    120
tgcaagacca gcggctacac cttcaccagg tacacatgc actgggtgaa gcagaggccc    180
ggccagggcc tggagtggat cggctacatc aacccagca ggggctacac caactacaac    240
cagaagtcca aggacaaggc caccctgacc accgacaaga gcagcagcac cgcctacatg    300
cagctgagca gcctgaccag cgaggacagc gccgtgtact actgcgccag gtactacgac    360
gaccactact gcctggacta ctggggccag ggcaccaccc tgaccgtgag cagcgtggag    420
ggcggcagcg gcggcagcgg cggcagcggc ggcagcggcg gcgtggacga catccagctg    480
accagagcc ccgccatcat gagcgccagc cccggcgaga aggtgacat gacctgcagg    540
gccagcagca gcgtgagcta catgaactgg taccagcaga agagcggcac cagccccaag    600
aggtggatct acgacaccag caaggtggcc agcggcgtgc cctacaggtt cagcggcagc    660
ggcagcggca ccagctacag cctgaccatc agcagcatgg aggccgagga cgccgccacc    720
tactactgcc agcagtggag cagcaacccc ctgacctcg gcgccggcac caagctggag    780
ctgaagggcg gcggcggcag cgatatccag atgacacaga gcccatcatt tctgtctgca    840
agcgtaggag accgagtcac cattacatgc agagcctccc aagacgtttc cacagcagtg    900
gcctggtatc agcaaaaacc tggtaaggcg cccaagcttc tcatctattc agccagtttt    960
ctgtatagcg gcgttcccag ccgattctct ggctctggat ccggcacgga ctttactttg   1020
acaatttctt ctcttcagcc cgaagatttt gcaacctact actgtcagca atatctctac   1080
catccagcca cattcggaca gggcaccaaa gtcgaaatca aaagaggcgg cggcggcagt   1140
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ggcgccgggg gttcaggagg cgggggttct gaagtgaac tcgttgaaag cggaggaggg 1200
 cttgtccaac ctggcgggtc actgcggttg agctgcgccg caagcggatt caccttctca 1260
 gactcttgga tccattgggt gcgccagget cccggaaaag gcttggaatg ggttgcttgg 1320
 atttcaccgt atggcgggtc cacatactac gctgacagcg ttaagggtcg attcaccatc 1380
 tctgcagata ctcaaaaaa cacagcctac cttcagatga atagtttgcg cgccgaggac 1440
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<210> 50

<211> 514

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized PDL1-CD3 bi-specific T-cell engager construct

<400> 50

Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Leu Phe Arg Gly
 1 5 10 15

Val Gln Cys Asp Ile Lys Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg
 20 25 30

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

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

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

Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser
 85 90 95

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

Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp
 115 120 125

Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Val Glu Gly Gly Ser Gly
130 135 140

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Val Asp Asp Ile Gln Leu
145 150 155 160

Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr
165 170 175

Met Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln
180 185 190

Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys
195 200 205

Val Ala Ser Gly Val Pro Tyr Arg Phe Ser Gly Ser Gly Ser Gly Thr
210 215 220

Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr
225 230 235 240

Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Ala Gly
245 250 255

Thr Lys Leu Glu Leu Lys Gly Gly Gly Gly Ser Asp Ile Gln Met Thr
260 265 270

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
275 280 285

Thr Cys Arg Ala Ser Gln Asp Val Ser Thr Ala Val Ala Trp Tyr Gln
290 295 300

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ser Ala Ser Phe
305 310 315 320

Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
325 330 335

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr

340 345 350

Tyr Tyr Cys Gln Gln Tyr Leu Tyr His Pro Ala Thr Phe Gly Gln Gly
355 360 365

Thr Lys Val Glu Ile Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly
370 375 380

Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly
385 390 395 400

Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
405 410 415

Phe Thr Phe Ser Asp Ser Trp Ile His Trp Val Arg Gln Ala Pro Gly
420 425 430

Lys Gly Leu Glu Trp Val Ala Trp Ile Ser Pro Tyr Gly Gly Ser Thr
435 440 445

Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr
450 455 460

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
465 470 475 480

Thr Ala Val Tyr Tyr Cys Ala Arg Arg His Trp Pro Gly Gly Phe Asp
485 490 495

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala His His His His
500 505 510

His His

<210> 51

<211> 2244

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesized polynucleotide encoding PDL1-CD3-Fc bi-specific
T-cell engager construct

<400> 51

atggagttcg gcctgagctg ggtgttctg gtggccctgt tcaggggcgt gcagtgcgac 60
atcaagctgc agcagagcgg cgccgagctg gccaggcccc gcgccagcgt gaagatgagc 120
tgcaagacca gcggctacac cttcaccagg tacacatgc actgggtgaa gcagaggccc 180
ggccagggcc tggagtggat cggctacatc aaccccagca ggggctacac caactaac 240
cagaagtta aggacaaggc caccctgacc accgacaaga gcagcagcac cgctacatg 300
cagctgagca gcctgaccag cgaggacagc gccgtgtact actgcgccag gtactacgac 360
gaccactact gcctggacta ctggggccag ggcaccaccc tgaccgtgag cagcgtggag 420
ggcggcagcg gcggcagcgg cggcagcggc ggcagcggcg gcgtggacga catccagctg 480
accagagcc ccgccatcat gagcgccagc cccggcgaga aggtgacat gacctgcagg 540
gccagcagca gcgtgagcta catgaactgg taccagcaga agagcggcac cagcccaag 600
aggtggatct acgacaccag caaggtggcc agcggcgtgc cctacagggt cagcggcagc 660
ggcagcggca ccagctacag cctgaccatc agcagcatgg aggccgagga cgccgccacc 720
tactactgcc agcagtggag cagcaacccc ctgaccttcg gcgccggcac caagctggag 780
ctgaaggcg gcggcggcag cgatatccag atgacacaga gccatcatc tctgtctgca 840
agcgtaggag accgagtcac cattacatgc agagcctccc aagacgttc cacagcagt 900
gcctggtatc agcaaaaacc tggtaggcg cccaagcttc tcattcttc agccagtttt 960
ctgtatagcg gcgtccag ccgattctct ggctctggat ccggcacgga ctttactttg 1020
acaatttct ctcttcagcc cgaagatttt gcaacctact actgtcagca atatctctac 1080
catccagcca cattcggaca gggcaccaa gtcgaaatca aaagaggcgg cggcggcagt 1140
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ctgtccaac ctggcgggtc actgcggtg agctgcgcc caagcggatt caccttctca 1260
gactcttga tccattgggt gcgccaggct cccggaaaag gcttggaatg ggttgcttg 1320
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tctgcagata ctcaaaaaa cacagcctac cttcagatga atagtttgcg cgccaggac 1440
acagcggttt attattgtc ccgaagacat tggcccggcg gtttcgacta ctgggggcaa 1500
ggtacgttg tgactgtgag cgccgtagat gaagcaaat cttgtgaaa aaccataacc 1560
tgcccacat gccagcccc agaacttctt ggcggaccct ctgtcttct tttcctccg 1620

aagcccaagg ataccctgat gatcagccga accccggagg taacatgtgt ggtggtcgat 1680
gttagccatg aggatcctga agtcaaattt aactggtatg tagacggtgt tgaggtgcac 1740
aacgctaaaa ctaagcccag ggaggagcag tacaactcaa cctatcgcgt cgtatctgtg 1800
cttaccgtcc tgcatcaaga ctggctcaat ggtaaggaat ataatgtaa agtgagtaac 1860
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acatgtctgg tgaaaggitt ctatccaagc gatatagctg tcgagtggga gtccaatggc 2040
caacctgaga acaattataa gaccacccca cccgttctgg acagcgacgg atcctttttc 2100
ctgtactcaa aactcactgt cgataaatca agatggcaac aaggcaacgt ttttagctgt 2160
agcgtgatgc acgaagcact tcataatcac tatacacaga agtcactctc tcttttcca 2220
ggacaccacc atcatcacca ctga 2244

<210> 52

<211> 747

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized PDL1-CD3-Fc bi-specific T-cell engager construct

<400> 52

Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Leu Phe Arg Gly
1 5 10 15

Val Gln Cys Asp Ile Lys Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg
20 25 30

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

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

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

Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser

85

90

95

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

Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp
115 120 125

Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Val Glu Gly Gly Ser Gly
130 135 140

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Val Asp Asp Ile Gln Leu
145 150 155 160

Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr
165 170 175

Met Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln
180 185 190

Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys
195 200 205

Val Ala Ser Gly Val Pro Tyr Arg Phe Ser Gly Ser Gly Ser Gly Thr
210 215 220

Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr
225 230 235 240

Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Ala Gly
245 250 255

Thr Lys Leu Glu Leu Lys Gly Gly Gly Gly Ser Asp Ile Gln Met Thr
260 265 270

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
275 280 285

Thr Cys Arg Ala Ser Gln Asp Val Ser Thr Ala Val Ala Trp Tyr Gln
290 295 300

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ser Ala Ser Phe
305 310 315 320

Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
325 330 335

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
340 345 350

Tyr Tyr Cys Gln Gln Tyr Leu Tyr His Pro Ala Thr Phe Gly Gln Gly
355 360 365

Thr Lys Val Glu Ile Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly
370 375 380

Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly
385 390 395 400

Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
405 410 415

Phe Thr Phe Ser Asp Ser Trp Ile His Trp Val Arg Gln Ala Pro Gly
420 425 430

Lys Gly Leu Glu Trp Val Ala Trp Ile Ser Pro Tyr Gly Gly Ser Thr
435 440 445

Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr
450 455 460

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
465 470 475 480

Thr Ala Val Tyr Tyr Cys Ala Arg Arg His Trp Pro Gly Gly Phe Asp
485 490 495

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Val Asp Glu Ala
500 505 510

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
515 520 525

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
530 535 540

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
545 550 555 560

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
565 570 575

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
580 585 590

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
595 600 605

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
610 615 620

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
625 630 635 640

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
645 650 655

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
660 665 670

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
675 680 685

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
690 695 700

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
705 710 715 720

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
725 730 735

Ser Leu Ser Pro Gly His His His His His His
740 745

<210> 53

<211> 707

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized CD19-IL15 bi-specific T-cell engager construct

<400> 53

Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Leu Phe Arg Gly
1 5 10 15

Val Gln Cys Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val
20 25 30

Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val
35 40 45

Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly
50 55 60

Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly
65 70 75 80

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

Asn Ile His Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln
100 105 110

Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu
115 120 125

Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
130 135 140

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

Ser Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser
165 170 175

Tyr Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp
180 185 190

Ile Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys
195 200 205

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala
210 215 220

Tyr Met Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe
225 230 235 240

Cys Ala Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met
245 250 255

Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
260 265 270

Gly Ser Asp Ile Lys Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro
275 280 285

Gly Ala Ser Val Lys Met Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr
290 295 300

Arg Tyr Thr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu
305 310 315 320

Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln
325 330 335

Lys Phe Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr
340 345 350

Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr
355 360 365

Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly
370 375 380

Gln Gly Thr Thr Leu Thr Val Ser Ser Val Glu Gly Gly Ser Gly Gly
385 390 395 400

Ser Gly Gly Ser Gly Gly Ser Gly Gly Val Asp Asp Ile Gln Leu Thr
405 410 415

Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met
420 425 430

Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln
435 440 445

Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val
450 455 460

Ala Ser Gly Val Pro Tyr Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser
465 470 475 480

Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr Tyr
485 490 495

Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Ala Gly Thr
500 505 510

Lys Leu Glu Leu Lys His His His His His His Arg Arg Lys Arg Glu
515 520 525

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

Pro Met Arg Ile Ser Lys Pro His Leu Arg Ser Ile Ser Ile Gln Cys
545 550 555 560

Tyr Leu Cys Leu Leu Leu Asn Ser His Phe Leu Thr Glu Ala Gly Ile
565 570 575

His Val Phe Ile Leu Gly Cys Phe Ser Ala Gly Leu Pro Lys Thr Glu
580 585 590

Ala Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu
595 600 605

Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val

610 615 620

His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu
625 630 635 640

Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val
645 650 655

Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn
660 665 670

Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn
675 680 685

Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile
690 695 700

Asn Thr Ser
705

<210> 54

<211> 1149

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized CD19-IL12 bi-specific T-cell engager construct

<400> 54

Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Leu Phe Arg Gly
1 5 10 15

Val Gln Cys Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val
20 25 30

Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val
35 40 45

Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly
50 55 60

Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly
65 70 75 80

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

Asn Ile His Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln
100 105 110

Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu
115 120 125

Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
130 135 140

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

Ser Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser
165 170 175

Tyr Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp
180 185 190

Ile Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys
195 200 205

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala
210 215 220

Tyr Met Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe
225 230 235 240

Cys Ala Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met
245 250 255

Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
260 265 270

Gly Ser Asp Ile Lys Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro
275 280 285

Gly Ala Ser Val Lys Met Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr

290 295 300

Arg Tyr Thr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu
305 310 315 320

Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln
325 330 335

Lys Phe Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr
340 345 350

Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr
355 360 365

Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly
370 375 380

Gln Gly Thr Thr Leu Thr Val Ser Ser Val Glu Gly Gly Ser Gly Gly
385 390 395 400

Ser Gly Gly Ser Gly Gly Ser Gly Gly Val Asp Asp Ile Gln Leu Thr
405 410 415

Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met
420 425 430

Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln
435 440 445

Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val
450 455 460

Ala Ser Gly Val Pro Tyr Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser
465 470 475 480

Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr Tyr
485 490 495

Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Ala Gly Thr
500 505 510

Lys Leu Glu Leu Lys His His His His His His Arg Arg Lys Arg Glu
515 520 525

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

Pro Met Trp Pro Pro Gly Ser Ala Ser Gln Pro Pro Pro Ser Pro Ala
545 550 555 560

Ala Ala Thr Gly Leu His Pro Ala Ala Arg Pro Val Ser Leu Gln Cys
565 570 575

Arg Leu Ser Met Cys Pro Ala Arg Ser Leu Leu Leu Val Ala Thr Leu
580 585 590

Val Leu Leu Asp His Leu Ser Leu Ala Arg Asn Leu Pro Val Ala Thr
595 600 605

Pro Asp Pro Gly Met Phe Pro Cys Leu His His Ser Gln Asn Leu Leu
610 615 620

Arg Ala Val Ser Asn Met Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe
625 630 635 640

Tyr Pro Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp
645 650 655

Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Lys Asn
660 665 670

Glu Ser Cys Leu Asn Ser Arg Glu Thr Ser Phe Ile Thr Asn Gly Ser
675 680 685

Cys Leu Ala Ser Arg Lys Thr Ser Phe Met Met Ala Leu Cys Leu Ser
690 695 700

Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Thr Met
705 710 715 720

Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln
725 730 735

Asn Met Leu Ala Val Ile Asp Glu Leu Met Gln Ala Leu Asn Phe Asn
740 745 750

Ser Glu Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr
755 760 765

Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg
770 775 780

Ala Val Thr Ile Asp Arg Val Met Ser Tyr Leu Asn Ala Ser Arg Arg
785 790 795 800

Lys Arg Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu
805 810 815

Asn Pro Gly Pro Pro Met Cys His Gln Gln Leu Val Ile Ser Trp Phe
820 825 830

Ser Leu Val Phe Leu Ala Ser Pro Leu Val Ala Ile Trp Glu Leu Lys
835 840 845

Lys Asp Val Tyr Val Val Glu Leu Asp Trp Tyr Pro Asp Ala Pro Gly
850 855 860

Glu Met Val Val Leu Thr Cys Asp Thr Pro Glu Glu Asp Gly Ile Thr
865 870 875 880

Trp Thr Leu Asp Gln Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu
885 890 895

Thr Ile Gln Val Lys Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His
900 905 910

Lys Gly Gly Glu Val Leu Ser His Ser Leu Leu Leu Leu His Lys Lys
915 920 925

Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Lys Asp Gln Lys Glu Pro
930 935 940

Lys Asn Lys Thr Phe Leu Arg Cys Glu Ala Lys Asn Tyr Ser Gly Arg
945 950 955 960

Phe Thr Cys Trp Trp Leu Thr Thr Ile Ser Thr Asp Leu Thr Phe Ser
965 970 975

Val Lys Ser Ser Arg Gly Ser Ser Asp Pro Gln Gly Val Thr Cys Gly
980 985 990

Ala Ala Thr Leu Ser Ala Glu Arg Val Arg Gly Asp Asn Lys Glu Tyr
995 1000 1005

Glu Tyr Ser Val Glu Cys Gln Glu Asp Ser Ala Cys Pro Ala Ala
1010 1015 1020

Glu Glu Ser Leu Pro Ile Glu Val Met Val Asp Ala Val His Lys
1025 1030 1035

Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile Arg Asp Ile
1040 1045 1050

Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln Leu Lys Pro Leu Lys
1055 1060 1065

Asn Ser Arg Gln Val Glu Val Ser Trp Glu Tyr Pro Asp Thr Trp
1070 1075 1080

Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Cys Val Gln Val
1085 1090 1095

Gln Gly Lys Ser Lys Arg Glu Lys Lys Asp Arg Val Phe Thr Asp
1100 1105 1110

Lys Thr Ser Ala Thr Val Ile Cys Arg Lys Asn Ala Ser Ile Ser
1115 1120 1125

Val Arg Ala Gln Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Glu Trp
1130 1135 1140

Ala Ser Val Pro Cys Ser
1145

<210> 55

<211> 643

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized CD19-CXCL10 bi-specific T-cell engager construct

<400> 55

Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Leu Phe Arg Gly
1 5 10 15

Val Gln Cys Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val
20 25 30

Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val
35 40 45

Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly
50 55 60

Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly
65 70 75 80

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

Asn Ile His Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln
100 105 110

Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu
115 120 125

Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
130 135 140

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

Ser Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser
165 170 175

Tyr Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp
180 185 190

Ile Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys
195 200 205

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala
210 215 220

Tyr Met Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe
225 230 235 240

Cys Ala Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met
245 250 255

Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
260 265 270

Gly Ser Asp Ile Lys Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro
275 280 285

Gly Ala Ser Val Lys Met Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr
290 295 300

Arg Tyr Thr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu
305 310 315 320

Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln
325 330 335

Lys Phe Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr
340 345 350

Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr
355 360 365

Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly
370 375 380

Gln Gly Thr Thr Leu Thr Val Ser Ser Val Glu Gly Gly Ser Gly Gly
385 390 395 400

Ser Gly Gly Ser Gly Gly Ser Gly Gly Val Asp Asp Ile Gln Leu Thr

405 410 415

Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met
420 425 430

Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln
435 440 445

Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val
450 455 460

Ala Ser Gly Val Pro Tyr Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser
465 470 475 480

Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr Tyr
485 490 495

Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Ala Gly Thr
500 505 510

Lys Leu Glu Leu Lys His His His His His His Arg Arg Lys Arg Glu
515 520 525

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

Pro Met Asn Gln Thr Ala Ile Leu Ile Cys Cys Leu Ile Phe Leu Thr
545 550 555 560

Leu Ser Gly Ile Gln Gly Val Pro Leu Ser Arg Thr Val Arg Cys Thr
565 570 575

Cys Ile Ser Ile Ser Asn Gln Pro Val Asn Pro Arg Ser Leu Glu Lys
580 585 590

Leu Glu Ile Ile Pro Ala Ser Gln Phe Cys Pro Arg Val Glu Ile Ile
595 600 605

Ala Thr Met Lys Lys Lys Gly Glu Lys Arg Cys Leu Asn Pro Glu Ser
610 615 620

Lys Ala Ile Lys Asn Leu Leu Lys Ala Val Ser Lys Glu Arg Ser Lys
625 630 635 640

Arg Ser Pro

<210> 56

<211> 575

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized SIRP1alpha-IL15-SL bi-specific T-cell engager
construct

<400> 56

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

Gly Ser Thr Gly Asp Glu Glu Glu Leu Gln Ile Ile Gln Pro Asp Lys
20 25 30

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

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

Pro Gly Arg Val Leu Ile Tyr Asn Gln Arg Gln Gly Pro Phe Pro Arg
65 70 75 80

Val Thr Thr Val Ser Asp Thr Thr Lys Arg Asn Asn Met Asp Phe Ser
85 90 95

Ile Arg Ile Gly Asn Ile Thr Pro Ala Asp Ala Gly Thr Tyr Tyr Cys
100 105 110

Ile Lys Phe Arg Lys Gly Ser Pro Asp Asp Val Glu Phe Lys Ser Gly
115 120 125

Ala Gly Thr Glu Leu Ser Val Arg Ala Lys Pro Ser Ala Ser Asp Ile
130 135 140

Lys Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val
145 150 155 160

Lys Met Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met
 165 170 175

His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr
 180 185 190

Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp
 195 200 205

Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln
 210 215 220

Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg
225 230 235 240

Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr
 245 250 255

Leu Thr Val Ser Ser Val Glu Gly Gly Ser Gly Gly Ser Gly Gly Ser
 260 265 270

Gly Gly Ser Gly Gly Val Asp Asp Ile Gln Leu Thr Gln Ser Pro Ala
 275 280 285

Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala
 290 295 300

Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Ser Gly Thr
305 310 315 320

Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly Val
 325 330 335

Pro Tyr Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr
 340 345 350

Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln
 355 360 365

Trp Ser Ser Asn Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu
370 375 380

Lys His His His His His His Arg Arg Lys Arg Glu Gly Arg Gly Ser
385 390 395 400

Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Arg Ile
405 410 415

Ser Lys Pro His Leu Arg Ser Ile Ser Ile Gln Cys Tyr Leu Cys Leu
420 425 430

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

Leu Gly Cys Phe Ser Ala Gly Leu Pro Lys Thr Glu Ala Asn Trp Val
450 455 460

Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met
465 470 475 480

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

Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser
500 505 510

Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile
515 520 525

Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser
530 535 540

Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe
545 550 555 560

Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser
565 570 575

<210> 57
<211> 580

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized SIRP1alpha-IL15-LL bi-specific T-cell engager construct

<400> 57

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

Gly Ser Thr Gly Asp Glu Glu Glu Leu Gln Ile Ile Gln Pro Asp Lys
20 25 30

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

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

Pro Gly Arg Val Leu Ile Tyr Asn Gln Arg Gln Gly Pro Phe Pro Arg
65 70 75 80

Val Thr Thr Val Ser Asp Thr Thr Lys Arg Asn Asn Met Asp Phe Ser
85 90 95

Ile Arg Ile Gly Asn Ile Thr Pro Ala Asp Ala Gly Thr Tyr Tyr Cys
100 105 110

Ile Lys Phe Arg Lys Gly Ser Pro Asp Asp Val Glu Phe Lys Ser Gly
115 120 125

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

Gly Gly Ser Asp Ile Lys Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg
145 150 155 160

Pro Gly Ala Ser Val Lys Met Ser Cys Lys Thr Ser Gly Tyr Thr Phe
165 170 175

Thr Arg Tyr Thr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
180 185 190

Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn
195 200 205

Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser
210 215 220

Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
225 230 235 240

Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp
245 250 255

Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Val Glu Gly Gly Ser Gly
260 265 270

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Val Asp Asp Ile Gln Leu
275 280 285

Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr
290 295 300

Met Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln
305 310 315 320

Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys
325 330 335

Val Ala Ser Gly Val Pro Tyr Arg Phe Ser Gly Ser Gly Ser Gly Thr
340 345 350

Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr
355 360 365

Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Ala Gly
370 375 380

Thr Lys Leu Glu Leu Lys His His His His His Arg Arg Lys Arg
385 390 395 400

Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro

405 410 415

Gly Pro Met Arg Ile Ser Lys Pro His Leu Arg Ser Ile Ser Ile Gln
420 425 430

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

Ile His Val Phe Ile Leu Gly Cys Phe Ser Ala Gly Leu Pro Lys Thr
450 455 460

Glu Ala Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp
465 470 475 480

Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp
485 490 495

Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu
500 505 510

Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr
515 520 525

Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly
530 535 540

Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys
545 550 555 560

Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe
565 570 575

Ile Asn Thr Ser
580

<210> 58

<211> 1017

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized SIRP1alpha-IL12-SL bi-specific T-cell engager
construct

<400> 58

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

Gly Ser Thr Gly Asp Glu Glu Glu Leu Gln Ile Ile Gln Pro Asp Lys
20 25 30

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

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

Pro Gly Arg Val Leu Ile Tyr Asn Gln Arg Gln Gly Pro Phe Pro Arg
65 70 75 80

Val Thr Thr Val Ser Asp Thr Thr Lys Arg Asn Asn Met Asp Phe Ser
85 90 95

Ile Arg Ile Gly Asn Ile Thr Pro Ala Asp Ala Gly Thr Tyr Tyr Cys
100 105 110

Ile Lys Phe Arg Lys Gly Ser Pro Asp Asp Val Glu Phe Lys Ser Gly
115 120 125

Ala Gly Thr Glu Leu Ser Val Arg Ala Lys Pro Ser Ala Ser Asp Ile
130 135 140

Lys Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val
145 150 155 160

Lys Met Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met
165 170 175

His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr
180 185 190

Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp
195 200 205

Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln
210 215 220

Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg
225 230 235 240

Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr
245 250 255

Leu Thr Val Ser Ser Val Glu Gly Gly Ser Gly Gly Ser Gly Gly Ser
260 265 270

Gly Gly Ser Gly Gly Val Asp Asp Ile Gln Leu Thr Gln Ser Pro Ala
275 280 285

Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala
290 295 300

Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Ser Gly Thr
305 310 315 320

Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly Val
325 330 335

Pro Tyr Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr
340 345 350

Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln
355 360 365

Trp Ser Ser Asn Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu
370 375 380

Lys His His His His His His Arg Arg Lys Arg Glu Gly Arg Gly Ser
385 390 395 400

Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Trp Pro
405 410 415

Pro Gly Ser Ala Ser Gln Pro Pro Pro Ser Pro Ala Ala Ala Thr Gly
420 425 430

Leu His Pro Ala Ala Arg Pro Val Ser Leu Gln Cys Arg Leu Ser Met
435 440 445

Cys Pro Ala Arg Ser Leu Leu Leu Val Ala Thr Leu Val Leu Leu Asp
450 455 460

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

Met Phe Pro Cys Leu His His Ser Gln Asn Leu Leu Arg Ala Val Ser
485 490 495

Asn Met Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe Tyr Pro Cys Thr
500 505 510

Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr
515 520 525

Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Lys Asn Glu Ser Cys Leu
530 535 540

Asn Ser Arg Glu Thr Ser Phe Ile Thr Asn Gly Ser Cys Leu Ala Ser
545 550 555 560

Arg Lys Thr Ser Phe Met Met Ala Leu Cys Leu Ser Ser Ile Tyr Glu
565 570 575

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

Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Ala
595 600 605

Val Ile Asp Glu Leu Met Gln Ala Leu Asn Phe Asn Ser Glu Thr Val
610 615 620

Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile
625 630 635 640

Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile
645 650 655

Asp Arg Val Met Ser Tyr Leu Asn Ala Ser Arg Arg Lys Arg Glu Gly
660 665 670

Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro
675 680 685

Pro Met Cys His Gln Gln Leu Val Ile Ser Trp Phe Ser Leu Val Phe
690 695 700

Leu Ala Ser Pro Leu Val Ala Ile Trp Glu Leu Lys Lys Asp Val Tyr
705 710 715 720

Val Val Glu Leu Asp Trp Tyr Pro Asp Ala Pro Gly Glu Met Val Val
725 730 735

Leu Thr Cys Asp Thr Pro Glu Glu Asp Gly Ile Thr Trp Thr Leu Asp
740 745 750

Gln Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val
755 760 765

Lys Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu
770 775 780

Val Leu Ser His Ser Leu Leu Leu Leu His Lys Lys Glu Asp Gly Ile
785 790 795 800

Trp Ser Thr Asp Ile Leu Lys Asp Gln Lys Glu Pro Lys Asn Lys Thr
805 810 815

Phe Leu Arg Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp
820 825 830

Trp Leu Thr Thr Ile Ser Thr Asp Leu Thr Phe Ser Val Lys Ser Ser
835 840 845

Arg Gly Ser Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Ala Thr Leu
850 855 860

Ser Ala Glu Arg Val Arg Gly Asp Asn Lys Glu Tyr Glu Tyr Ser Val

865 870 875 880

Glu Cys Gln Glu Asp Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro
 885 890 895

Ile Glu Val Met Val Asp Ala Val His Lys Leu Lys Tyr Glu Asn Tyr
 900 905 910

Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys
 915 920 925

Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg Gln Val Glu Val Ser
 930 935 940

Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu
945 950 955 960

Thr Phe Cys Val Gln Val Gln Gly Lys Ser Lys Arg Glu Lys Lys Asp
 965 970 975

Arg Val Phe Thr Asp Lys Thr Ser Ala Thr Val Ile Cys Arg Lys Asn
 980 985 990

Ala Ser Ile Ser Val Arg Ala Gln Asp Arg Tyr Tyr Ser Ser Ser Trp
 995 1000 1005

Ser Glu Trp Ala Ser Val Pro Cys Ser
 1010 1015

<210> 59

<211> 1022

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized SIRP1alpha-IL12-LL bi-specific T-cell engager
construct

<400> 59

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

Gly Ser Thr Gly Asp Glu Glu Glu Leu Gln Ile Ile Gln Pro Asp Lys

20

25

30

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

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

Pro Gly Arg Val Leu Ile Tyr Asn Gln Arg Gln Gly Pro Phe Pro Arg
65 70 75 80

Val Thr Thr Val Ser Asp Thr Thr Lys Arg Asn Asn Met Asp Phe Ser
85 90 95

Ile Arg Ile Gly Asn Ile Thr Pro Ala Asp Ala Gly Thr Tyr Tyr Cys
100 105 110

Ile Lys Phe Arg Lys Gly Ser Pro Asp Asp Val Glu Phe Lys Ser Gly
115 120 125

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

Gly Gly Ser Asp Ile Lys Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg
145 150 155 160

Pro Gly Ala Ser Val Lys Met Ser Cys Lys Thr Ser Gly Tyr Thr Phe
165 170 175

Thr Arg Tyr Thr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
180 185 190

Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn
195 200 205

Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser
210 215 220

Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
225 230 235 240

Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp
245 250 255

Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Val Glu Gly Gly Ser Gly
260 265 270

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Val Asp Asp Ile Gln Leu
275 280 285

Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr
290 295 300

Met Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln
305 310 315 320

Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys
325 330 335

Val Ala Ser Gly Val Pro Tyr Arg Phe Ser Gly Ser Gly Ser Gly Thr
340 345 350

Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr
355 360 365

Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Ala Gly
370 375 380

Thr Lys Leu Glu Leu Lys His His His His His Arg Arg Lys Arg
385 390 395 400

Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro
405 410 415

Gly Pro Met Trp Pro Pro Gly Ser Ala Ser Gln Pro Pro Pro Ser Pro
420 425 430

Ala Ala Ala Thr Gly Leu His Pro Ala Ala Arg Pro Val Ser Leu Gln
435 440 445

Cys Arg Leu Ser Met Cys Pro Ala Arg Ser Leu Leu Leu Val Ala Thr
450 455 460

Leu Val Leu Leu Asp His Leu Ser Leu Ala Arg Asn Leu Pro Val Ala
465 470 475 480

Thr Pro Asp Pro Gly Met Phe Pro Cys Leu His His Ser Gln Asn Leu
485 490 495

Leu Arg Ala Val Ser Asn Met Leu Gln Lys Ala Arg Gln Thr Leu Glu
500 505 510

Phe Tyr Pro Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys
515 520 525

Asp Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Lys
530 535 540

Asn Glu Ser Cys Leu Asn Ser Arg Glu Thr Ser Phe Ile Thr Asn Gly
545 550 555 560

Ser Cys Leu Ala Ser Arg Lys Thr Ser Phe Met Met Ala Leu Cys Leu
565 570 575

Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Thr
580 585 590

Met Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp
595 600 605

Gln Asn Met Leu Ala Val Ile Asp Glu Leu Met Gln Ala Leu Asn Phe
610 615 620

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

Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile
645 650 655

Arg Ala Val Thr Ile Asp Arg Val Met Ser Tyr Leu Asn Ala Ser Arg
660 665 670

Arg Lys Arg Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu
675 680 685

Glu Asn Pro Gly Pro Pro Met Cys His Gln Gln Leu Val Ile Ser Trp
690 695 700

Phe Ser Leu Val Phe Leu Ala Ser Pro Leu Val Ala Ile Trp Glu Leu
705 710 715 720

Lys Lys Asp Val Tyr Val Val Glu Leu Asp Trp Tyr Pro Asp Ala Pro
725 730 735

Gly Glu Met Val Val Leu Thr Cys Asp Thr Pro Glu Glu Asp Gly Ile
740 745 750

Thr Trp Thr Leu Asp Gln Ser Ser Glu Val Leu Gly Ser Gly Lys Thr
755 760 765

Leu Thr Ile Gln Val Lys Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys
770 775 780

His Lys Gly Gly Glu Val Leu Ser His Ser Leu Leu Leu His Lys
785 790 795 800

Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Lys Asp Gln Lys Glu
805 810 815

Pro Lys Asn Lys Thr Phe Leu Arg Cys Glu Ala Lys Asn Tyr Ser Gly
820 825 830

Arg Phe Thr Cys Trp Trp Leu Thr Thr Ile Ser Thr Asp Leu Thr Phe
835 840 845

Ser Val Lys Ser Ser Arg Gly Ser Ser Asp Pro Gln Gly Val Thr Cys
850 855 860

Gly Ala Ala Thr Leu Ser Ala Glu Arg Val Arg Gly Asp Asn Lys Glu
865 870 875 880

Tyr Glu Tyr Ser Val Glu Cys Gln Glu Asp Ser Ala Cys Pro Ala Ala
885 890 895

Glu Glu Ser Leu Pro Ile Glu Val Met Val Asp Ala Val His Lys Leu

900 905 910

Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys
915 920 925

Pro Asp Pro Pro Lys Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg
930 935 940

Gln Val Glu Val Ser Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His
945 950 955 960

Ser Tyr Phe Ser Leu Thr Phe Cys Val Gln Val Gln Gly Lys Ser Lys
965 970 975

Arg Glu Lys Lys Asp Arg Val Phe Thr Asp Lys Thr Ser Ala Thr Val
980 985 990

Ile Cys Arg Lys Asn Ala Ser Ile Ser Val Arg Ala Gln Asp Arg Tyr
995 1000 1005

Tyr Ser Ser Ser Trp Ser Glu Trp Ala Ser Val Pro Cys Ser
1010 1015 1020

<210> 60

<211> 511

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized SIRP1alpha-CXCL10-SL bi-specific T-cell engager
construct

<400> 60

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

Gly Ser Thr Gly Asp Glu Glu Glu Leu Gln Ile Ile Gln Pro Asp Lys
20 25 30

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

Thr Ser Leu Phe Pro Val Gly Pro Ile Gln Trp Phe Arg Gly Ala Gly

50 55 60

Pro Gly Arg Val Leu Ile Tyr Asn Gln Arg Gln Gly Pro Phe Pro Arg
65 70 75 80

Val Thr Thr Val Ser Asp Thr Thr Lys Arg Asn Asn Met Asp Phe Ser
85 90 95

Ile Arg Ile Gly Asn Ile Thr Pro Ala Asp Ala Gly Thr Tyr Tyr Cys
100 105 110

Ile Lys Phe Arg Lys Gly Ser Pro Asp Asp Val Glu Phe Lys Ser Gly
115 120 125

Ala Gly Thr Glu Leu Ser Val Arg Ala Lys Pro Ser Ala Ser Asp Ile
130 135 140

Lys Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val
145 150 155 160

Lys Met Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met
165 170 175

His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr
180 185 190

Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp
195 200 205

Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln
210 215 220

Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg
225 230 235 240

Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr
245 250 255

Leu Thr Val Ser Ser Val Glu Gly Gly Ser Gly Gly Ser Gly Gly Ser
260 265 270

Gly Gly Ser Gly Gly Val Asp Asp Ile Gln Leu Thr Gln Ser Pro Ala
275 280 285

Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala
290 295 300

Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Ser Gly Thr
305 310 315 320

Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly Val
325 330 335

Pro Tyr Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr
340 345 350

Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln
355 360 365

Trp Ser Ser Asn Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu
370 375 380

Lys His His His His His His Arg Arg Lys Arg Glu Gly Arg Gly Ser
385 390 395 400

Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Asn Gln
405 410 415

Thr Ala Ile Leu Ile Cys Cys Leu Ile Phe Leu Thr Leu Ser Gly Ile
420 425 430

Gln Gly Val Pro Leu Ser Arg Thr Val Arg Cys Thr Cys Ile Ser Ile
435 440 445

Ser Asn Gln Pro Val Asn Pro Arg Ser Leu Glu Lys Leu Glu Ile Ile
450 455 460

Pro Ala Ser Gln Phe Cys Pro Arg Val Glu Ile Ile Ala Thr Met Lys
465 470 475 480

Lys Lys Gly Glu Lys Arg Cys Leu Asn Pro Glu Ser Lys Ala Ile Lys
485 490 495

Asn Leu Leu Lys Ala Val Ser Lys Glu Arg Ser Lys Arg Ser Pro
500 505 510

<210> 61

<211> 516

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized SIRP1alpha-CXCL10-LL bi-specific T-cell engager
construct

<400> 61

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

Gly Ser Thr Gly Asp Glu Glu Glu Leu Gln Ile Ile Gln Pro Asp Lys
20 25 30

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

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

Pro Gly Arg Val Leu Ile Tyr Asn Gln Arg Gln Gly Pro Phe Pro Arg
65 70 75 80

Val Thr Thr Val Ser Asp Thr Thr Lys Arg Asn Asn Met Asp Phe Ser
85 90 95

Ile Arg Ile Gly Asn Ile Thr Pro Ala Asp Ala Gly Thr Tyr Tyr Cys
100 105 110

Ile Lys Phe Arg Lys Gly Ser Pro Asp Asp Val Glu Phe Lys Ser Gly
115 120 125

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

Gly Gly Ser Asp Ile Lys Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg
145 150 155 160

Pro Gly Ala Ser Val Lys Met Ser Cys Lys Thr Ser Gly Tyr Thr Phe
165 170 175

Thr Arg Tyr Thr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
180 185 190

Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn
195 200 205

Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser
210 215 220

Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
225 230 235 240

Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp
245 250 255

Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Val Glu Gly Gly Ser Gly
260 265 270

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Val Asp Asp Ile Gln Leu
275 280 285

Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr
290 295 300

Met Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln
305 310 315 320

Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys
325 330 335

Val Ala Ser Gly Val Pro Tyr Arg Phe Ser Gly Ser Gly Ser Gly Thr
340 345 350

Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr
355 360 365

Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Ala Gly
370 375 380

Thr Lys Leu Glu Leu Lys His His His His His Arg Arg Lys Arg
385 390 395 400

Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro
405 410 415

Gly Pro Met Asn Gln Thr Ala Ile Leu Ile Cys Cys Leu Ile Phe Leu
420 425 430

Thr Leu Ser Gly Ile Gln Gly Val Pro Leu Ser Arg Thr Val Arg Cys
435 440 445

Thr Cys Ile Ser Ile Ser Asn Gln Pro Val Asn Pro Arg Ser Leu Glu
450 455 460

Lys Leu Glu Ile Ile Pro Ala Ser Gln Phe Cys Pro Arg Val Glu Ile
465 470 475 480

Ile Ala Thr Met Lys Lys Lys Gly Glu Lys Arg Cys Leu Asn Pro Glu
485 490 495

Ser Lys Ala Ile Lys Asn Leu Leu Lys Ala Val Ser Lys Glu Arg Ser
500 505 510

Lys Arg Ser Pro
515

<210> 62

<211> 698

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized PDL1-CD3-IL15 bi-specific T-cell engager construct

<400> 62

Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Leu Phe Arg Gly
1 5 10 15

Val Gln Cys Asp Ile Lys Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg
20 25 30

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

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

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

Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser
85 90 95

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

Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp
115 120 125

Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Val Glu Gly Gly Ser Gly
130 135 140

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Val Asp Asp Ile Gln Leu
145 150 155 160

Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr
165 170 175

Met Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln
180 185 190

Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys
195 200 205

Val Ala Ser Gly Val Pro Tyr Arg Phe Ser Gly Ser Gly Ser Gly Thr
210 215 220

Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr
225 230 235 240

Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Ala Gly
245 250 255

Thr Lys Leu Glu Leu Lys Gly Gly Gly Gly Ser Asp Ile Gln Met Thr
260 265 270

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
275 280 285

Thr Cys Arg Ala Ser Gln Asp Val Ser Thr Ala Val Ala Trp Tyr Gln
290 295 300

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ser Ala Ser Phe
305 310 315 320

Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
325 330 335

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
340 345 350

Tyr Tyr Cys Gln Gln Tyr Leu Tyr His Pro Ala Thr Phe Gly Gln Gly
355 360 365

Thr Lys Val Glu Ile Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly
370 375 380

Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly
385 390 395 400

Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
405 410 415

Phe Thr Phe Ser Asp Ser Trp Ile His Trp Val Arg Gln Ala Pro Gly
420 425 430

Lys Gly Leu Glu Trp Val Ala Trp Ile Ser Pro Tyr Gly Gly Ser Thr
435 440 445

Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr
450 455 460

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp

465

470

475

480

Thr Ala Val Tyr Tyr Cys Ala Arg Arg His Trp Pro Gly Gly Phe Asp
485 490 495

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala His His His His
500 505 510

His His Arg Arg Lys Arg Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly
515 520 525

Asp Val Glu Glu Asn Pro Gly Pro Met Arg Ile Ser Lys Pro His Leu
530 535 540

Arg Ser Ile Ser Ile Gln Cys Tyr Leu Cys Leu Leu Leu Asn Ser His
545 550 555 560

Phe Leu Thr Glu Ala Gly Ile His Val Phe Ile Leu Gly Cys Phe Ser
565 570 575

Ala Gly Leu Pro Lys Thr Glu Ala Asn Trp Val Asn Val Ile Ser Asp
580 585 590

Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr
595 600 605

Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met
610 615 620

Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp
625 630 635 640

Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn
645 650 655

Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys
660 665 670

Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val
675 680 685

His Ile Val Gln Met Phe Ile Asn Thr Ser
690 695

<210> 63

<211> 1140

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized PDL1-CD3-IL12 bi-specific T-cell engager construct

<400> 63

Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Leu Phe Arg Gly
1 5 10 15

Val Gln Cys Asp Ile Lys Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg
20 25 30

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

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

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

Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser
85 90 95

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

Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp
115 120 125

Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Val Glu Gly Gly Ser Gly
130 135 140

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Val Asp Asp Ile Gln Leu
145 150 155 160

Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr

165 170 175

Met Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln
180 185 190

Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys
195 200 205

Val Ala Ser Gly Val Pro Tyr Arg Phe Ser Gly Ser Gly Ser Gly Thr
210 215 220

Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr
225 230 235 240

Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Ala Gly
245 250 255

Thr Lys Leu Glu Leu Lys Gly Gly Gly Gly Ser Asp Ile Gln Met Thr
260 265 270

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
275 280 285

Thr Cys Arg Ala Ser Gln Asp Val Ser Thr Ala Val Ala Trp Tyr Gln
290 295 300

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ser Ala Ser Phe
305 310 315 320

Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
325 330 335

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
340 345 350

Tyr Tyr Cys Gln Gln Tyr Leu Tyr His Pro Ala Thr Phe Gly Gln Gly
355 360 365

Thr Lys Val Glu Ile Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly
370 375 380

Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly
385 390 395 400

Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
405 410 415

Phe Thr Phe Ser Asp Ser Trp Ile His Trp Val Arg Gln Ala Pro Gly
420 425 430

Lys Gly Leu Glu Trp Val Ala Trp Ile Ser Pro Tyr Gly Gly Ser Thr
435 440 445

Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr
450 455 460

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
465 470 475 480

Thr Ala Val Tyr Tyr Cys Ala Arg Arg His Trp Pro Gly Gly Phe Asp
485 490 495

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala His His His His
500 505 510

His His Arg Arg Lys Arg Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly
515 520 525

Asp Val Glu Glu Asn Pro Gly Pro Met Trp Pro Pro Gly Ser Ala Ser
530 535 540

Gln Pro Pro Pro Ser Pro Ala Ala Ala Thr Gly Leu His Pro Ala Ala
545 550 555 560

Arg Pro Val Ser Leu Gln Cys Arg Leu Ser Met Cys Pro Ala Arg Ser
565 570 575

Leu Leu Leu Val Ala Thr Leu Val Leu Leu Asp His Leu Ser Leu Ala
580 585 590

Arg Asn Leu Pro Val Ala Thr Pro Asp Pro Gly Met Phe Pro Cys Leu
595 600 605

His His Ser Gln Asn Leu Leu Arg Ala Val Ser Asn Met Leu Gln Lys
610 615 620

Ala Arg Gln Thr Leu Glu Phe Tyr Pro Cys Thr Ser Glu Glu Ile Asp
625 630 635 640

His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu
645 650 655

Pro Leu Glu Leu Thr Lys Asn Glu Ser Cys Leu Asn Ser Arg Glu Thr
660 665 670

Ser Phe Ile Thr Asn Gly Ser Cys Leu Ala Ser Arg Lys Thr Ser Phe
675 680 685

Met Met Ala Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr
690 695 700

Gln Val Glu Phe Lys Thr Met Asn Ala Lys Leu Leu Met Asp Pro Lys
705 710 715 720

Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Ala Val Ile Asp Glu Leu
725 730 735

Met Gln Ala Leu Asn Phe Asn Ser Glu Thr Val Pro Gln Lys Ser Ser
740 745 750

Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu
755 760 765

Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asp Arg Val Met Ser
770 775 780

Tyr Leu Asn Ala Ser Arg Arg Lys Arg Glu Gly Arg Gly Ser Leu Leu
785 790 795 800

Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Pro Met Cys His Gln
805 810 815

Gln Leu Val Ile Ser Trp Phe Ser Leu Val Phe Leu Ala Ser Pro Leu
820 825 830

Val Ala Ile Trp Glu Leu Lys Lys Asp Val Tyr Val Val Glu Leu Asp
835 840 845

Trp Tyr Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys Asp Thr
850 855 860

Pro Glu Glu Asp Gly Ile Thr Trp Thr Leu Asp Gln Ser Ser Glu Val
865 870 875 880

Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Gly Asp
885 890 895

Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val Leu Ser His Ser
900 905 910

Leu Leu Leu Leu His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile
915 920 925

Leu Lys Asp Gln Lys Glu Pro Lys Asn Lys Thr Phe Leu Arg Cys Glu
930 935 940

Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Thr Ile
945 950 955 960

Ser Thr Asp Leu Thr Phe Ser Val Lys Ser Ser Arg Gly Ser Ser Asp
965 970 975

Pro Gln Gly Val Thr Cys Gly Ala Ala Thr Leu Ser Ala Glu Arg Val
980 985 990

Arg Gly Asp Asn Lys Glu Tyr Glu Tyr Ser Val Glu Cys Gln Glu Asp
995 1000 1005

Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile Glu Val Met
1010 1015 1020

Val Asp Ala Val His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser
1025 1030 1035

Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu

1040 1045 1050

Gln Leu Lys Pro Leu Lys Asn Ser Arg Gln Val Glu Val Ser Trp
1055 1060 1065

Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu
1070 1075 1080

Thr Phe Cys Val Gln Val Gln Gly Lys Ser Lys Arg Glu Lys Lys
1085 1090 1095

Asp Arg Val Phe Thr Asp Lys Thr Ser Ala Thr Val Ile Cys Arg
1100 1105 1110

Lys Asn Ala Ser Ile Ser Val Arg Ala Gln Asp Arg Tyr Tyr Ser
1115 1120 1125

Ser Ser Trp Ser Glu Trp Ala Ser Val Pro Cys Ser
1130 1135 1140

<210> 64

<211> 634

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized PDL1-CD3-CXCL10 bi-specific T-cell engager construct

<400> 64

Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Leu Phe Arg Gly
1 5 10 15

Val Gln Cys Asp Ile Lys Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg
20 25 30

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

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

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

Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser
85 90 95

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

Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp
115 120 125

Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Val Glu Gly Gly Ser Gly
130 135 140

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Val Asp Asp Ile Gln Leu
145 150 155 160

Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr
165 170 175

Met Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln
180 185 190

Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys
195 200 205

Val Ala Ser Gly Val Pro Tyr Arg Phe Ser Gly Ser Gly Ser Gly Thr
210 215 220

Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr
225 230 235 240

Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Ala Gly
245 250 255

Thr Lys Leu Glu Leu Lys Gly Gly Gly Gly Ser Asp Ile Gln Met Thr
260 265 270

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
275 280 285

Thr Cys Arg Ala Ser Gln Asp Val Ser Thr Ala Val Ala Trp Tyr Gln

290 295 300

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ser Ala Ser Phe
305 310 315 320

Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
325 330 335

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
340 345 350

Tyr Tyr Cys Gln Gln Tyr Leu Tyr His Pro Ala Thr Phe Gly Gln Gly
355 360 365

Thr Lys Val Glu Ile Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly
370 375 380

Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly
385 390 395 400

Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
405 410 415

Phe Thr Phe Ser Asp Ser Trp Ile His Trp Val Arg Gln Ala Pro Gly
420 425 430

Lys Gly Leu Glu Trp Val Ala Trp Ile Ser Pro Tyr Gly Gly Ser Thr
435 440 445

Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr
450 455 460

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
465 470 475 480

Thr Ala Val Tyr Tyr Cys Ala Arg Arg His Trp Pro Gly Gly Phe Asp
485 490 495

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala His His His His
500 505 510

His His Arg Arg Lys Arg Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly
515 520 525

Asp Val Glu Glu Asn Pro Gly Pro Met Asn Gln Thr Ala Ile Leu Ile
530 535 540

Cys Cys Leu Ile Phe Leu Thr Leu Ser Gly Ile Gln Gly Val Pro Leu
545 550 555 560

Ser Arg Thr Val Arg Cys Thr Cys Ile Ser Ile Ser Asn Gln Pro Val
565 570 575

Asn Pro Arg Ser Leu Glu Lys Leu Glu Ile Ile Pro Ala Ser Gln Phe
580 585 590

Cys Pro Arg Val Glu Ile Ile Ala Thr Met Lys Lys Lys Gly Glu Lys
595 600 605

Arg Cys Leu Asn Pro Glu Ser Lys Ala Ile Lys Asn Leu Leu Lys Ala
610 615 620

Val Ser Lys Glu Arg Ser Lys Arg Ser Pro
625 630

<210> 65

<211> 1120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized SIRP1alpha-MMP9-SL bi-specific T-cell engager
construct

<400> 65

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

Gly Ser Thr Gly Asp Glu Glu Glu Leu Gln Ile Ile Gln Pro Asp Lys
20 25 30

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

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

Pro Gly Arg Val Leu Ile Tyr Asn Gln Arg Gln Gly Pro Phe Pro Arg
65 70 75 80

Val Thr Thr Val Ser Asp Thr Thr Lys Arg Asn Asn Met Asp Phe Ser
85 90 95

Ile Arg Ile Gly Asn Ile Thr Pro Ala Asp Ala Gly Thr Tyr Tyr Cys
100 105 110

Ile Lys Phe Arg Lys Gly Ser Pro Asp Asp Val Glu Phe Lys Ser Gly
115 120 125

Ala Gly Thr Glu Leu Ser Val Arg Ala Lys Pro Ser Ala Ser Asp Ile
130 135 140

Lys Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val
145 150 155 160

Lys Met Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met
165 170 175

His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr
180 185 190

Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp
195 200 205

Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln
210 215 220

Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg
225 230 235 240

Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr
245 250 255

Leu Thr Val Ser Ser Val Glu Gly Gly Ser Gly Gly Ser Gly Gly Ser
260 265 270

Gly Gly Ser Gly Gly Val Asp Asp Ile Gln Leu Thr Gln Ser Pro Ala
275 280 285

Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala
290 295 300

Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Ser Gly Thr
305 310 315 320

Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly Val
325 330 335

Pro Tyr Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr
340 345 350

Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln
355 360 365

Trp Ser Ser Asn Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu
370 375 380

Lys His His His His His His Arg Arg Lys Arg Glu Gly Arg Gly Ser
385 390 395 400

Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ser Leu
405 410 415

Trp Gln Pro Leu Val Leu Val Leu Leu Val Leu Gly Cys Cys Phe Ala
420 425 430

Ala Pro Arg Gln Arg Gln Ser Thr Leu Val Leu Phe Pro Gly Asp Leu
435 440 445

Arg Thr Asn Leu Thr Asp Arg Gln Leu Ala Glu Glu Tyr Leu Tyr Arg
450 455 460

Tyr Gly Tyr Thr Arg Val Ala Glu Met Arg Gly Glu Ser Lys Ser Leu
465 470 475 480

Gly Pro Ala Leu Leu Leu Leu Gln Lys Gln Leu Ser Leu Pro Glu Thr
485 490 495

Gly Glu Leu Asp Ser Ala Thr Leu Lys Ala Met Arg Thr Pro Arg Cys
500 505 510

Gly Val Pro Asp Leu Gly Arg Phe Gln Thr Phe Glu Gly Asp Leu Lys
515 520 525

Trp His His His Asn Ile Thr Tyr Trp Ile Gln Asn Tyr Ser Glu Asp
530 535 540

Leu Pro Arg Ala Val Ile Asp Asp Ala Phe Ala Arg Ala Phe Ala Leu
545 550 555 560

Trp Ser Ala Val Thr Pro Leu Thr Phe Thr Arg Val Tyr Ser Arg Asp
565 570 575

Ala Asp Ile Val Ile Gln Phe Gly Val Ala Glu His Gly Asp Gly Tyr
580 585 590

Pro Phe Asp Gly Lys Asp Gly Leu Leu Ala His Ala Phe Pro Pro Gly
595 600 605

Pro Gly Ile Gln Gly Asp Ala His Phe Asp Asp Asp Glu Leu Trp Ser
610 615 620

Leu Gly Lys Gly Val Val Val Pro Thr Arg Phe Gly Asn Ala Asp Gly
625 630 635 640

Ala Ala Cys His Phe Pro Phe Ile Phe Glu Gly Arg Ser Tyr Ser Ala
645 650 655

Cys Thr Thr Asp Gly Arg Ser Asp Gly Leu Pro Trp Cys Ser Thr Thr
660 665 670

Ala Asn Tyr Asp Thr Asp Asp Arg Phe Gly Phe Cys Pro Ser Glu Arg
675 680 685

Leu Tyr Thr Arg Asp Gly Asn Ala Asp Gly Lys Pro Cys Gln Phe Pro
690 695 700

Phe Ile Phe Gln Gly Gln Ser Tyr Ser Ala Cys Thr Thr Asp Gly Arg

705 710 715 720

Ser Asp Gly Tyr Arg Trp Cys Ala Thr Thr Ala Asn Tyr Asp Arg Asp
725 730 735

Lys Leu Phe Gly Phe Cys Pro Thr Arg Ala Asp Ser Thr Val Met Gly
740 745 750

Gly Asn Ser Ala Gly Glu Leu Cys Val Phe Pro Phe Thr Phe Leu Gly
755 760 765

Lys Glu Tyr Ser Thr Cys Thr Ser Glu Gly Arg Gly Asp Gly Arg Leu
770 775 780

Trp Cys Ala Thr Thr Ser Asn Phe Asp Ser Asp Lys Lys Trp Gly Phe
785 790 795 800

Cys Pro Asp Gln Gly Tyr Ser Leu Phe Leu Val Ala Ala His Glu Phe
805 810 815

Gly His Ala Leu Gly Leu Asp His Ser Ser Val Pro Glu Ala Leu Met
820 825 830

Tyr Pro Met Tyr Arg Phe Thr Glu Gly Pro Pro Leu His Lys Asp Asp
835 840 845

Val Asn Gly Ile Arg His Leu Tyr Gly Pro Arg Pro Glu Pro Glu Pro
850 855 860

Arg Pro Pro Thr Thr Thr Thr Pro Gln Pro Thr Ala Pro Pro Thr Val
865 870 875 880

Cys Pro Thr Gly Pro Pro Thr Val His Pro Ser Glu Arg Pro Thr Ala
885 890 895

Gly Pro Thr Gly Pro Pro Ser Ala Gly Pro Thr Gly Pro Pro Thr Ala
900 905 910

Gly Pro Ser Thr Ala Thr Thr Val Pro Leu Ser Pro Val Asp Asp Ala
915 920 925

Cys Asn Val Asn Ile Phe Asp Ala Ile Ala Glu Ile Gly Asn Gln Leu
930 935 940

Tyr Leu Phe Lys Asp Gly Lys Tyr Trp Arg Phe Ser Glu Gly Arg Gly
945 950 955 960

Ser Arg Pro Gln Gly Pro Phe Leu Ile Ala Asp Lys Trp Pro Ala Leu
965 970 975

Pro Arg Lys Leu Asp Ser Val Phe Glu Glu Pro Leu Ser Lys Lys Leu
980 985 990

Phe Phe Phe Ser Gly Arg Gln Val Trp Val Tyr Thr Gly Ala Ser Val
995 1000 1005

Leu Gly Pro Arg Arg Leu Asp Lys Leu Gly Leu Gly Ala Asp Val
1010 1015 1020

Ala Gln Val Thr Gly Ala Leu Arg Ser Gly Arg Gly Lys Met Leu
1025 1030 1035

Leu Phe Ser Gly Arg Arg Leu Trp Arg Phe Asp Val Lys Ala Gln
1040 1045 1050

Met Val Asp Pro Arg Ser Ala Ser Glu Val Asp Arg Met Phe Pro
1055 1060 1065

Gly Val Pro Leu Asp Thr His Asp Val Phe Gln Tyr Arg Glu Lys
1070 1075 1080

Ala Tyr Phe Cys Gln Asp Arg Phe Tyr Trp Arg Val Ser Ser Arg
1085 1090 1095

Ser Glu Leu Asn Gln Val Asp Gln Val Gly Tyr Val Thr Tyr Asp
1100 1105 1110

Ile Leu Gln Cys Pro Glu Asp
1115 1120

<210> 66

<211> 1125

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized SIRP1alpha-MMP9-LL bi-specific T-cell engager
construct

<400> 66

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

Gly Ser Thr Gly Asp Glu Glu Glu Leu Gln Ile Ile Gln Pro Asp Lys
20 25 30

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

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

Pro Gly Arg Val Leu Ile Tyr Asn Gln Arg Gln Gly Pro Phe Pro Arg
65 70 75 80

Val Thr Thr Val Ser Asp Thr Thr Lys Arg Asn Asn Met Asp Phe Ser
85 90 95

Ile Arg Ile Gly Asn Ile Thr Pro Ala Asp Ala Gly Thr Tyr Tyr Cys
100 105 110

Ile Lys Phe Arg Lys Gly Ser Pro Asp Asp Val Glu Phe Lys Ser Gly
115 120 125

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

Gly Gly Ser Asp Ile Lys Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg
145 150 155 160

Pro Gly Ala Ser Val Lys Met Ser Cys Lys Thr Ser Gly Tyr Thr Phe
165 170 175

Thr Arg Tyr Thr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
180 185 190

Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn
195 200 205

Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser
210 215 220

Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
225 230 235 240

Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp
245 250 255

Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Val Glu Gly Gly Ser Gly
260 265 270

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Val Asp Asp Ile Gln Leu
275 280 285

Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr
290 295 300

Met Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln
305 310 315 320

Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys
325 330 335

Val Ala Ser Gly Val Pro Tyr Arg Phe Ser Gly Ser Gly Ser Gly Thr
340 345 350

Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr
355 360 365

Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Ala Gly
370 375 380

Thr Lys Leu Glu Leu Lys His His His His His His Arg Arg Lys Arg
385 390 395 400

Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro
405 410 415

Gly Pro Met Ser Leu Trp Gln Pro Leu Val Leu Val Leu Leu Val Leu
420 425 430

Gly Cys Cys Phe Ala Ala Pro Arg Gln Arg Gln Ser Thr Leu Val Leu
435 440 445

Phe Pro Gly Asp Leu Arg Thr Asn Leu Thr Asp Arg Gln Leu Ala Glu
450 455 460

Glu Tyr Leu Tyr Arg Tyr Gly Tyr Thr Arg Val Ala Glu Met Arg Gly
465 470 475 480

Glu Ser Lys Ser Leu Gly Pro Ala Leu Leu Leu Leu Gln Lys Gln Leu
485 490 495

Ser Leu Pro Glu Thr Gly Glu Leu Asp Ser Ala Thr Leu Lys Ala Met
500 505 510

Arg Thr Pro Arg Cys Gly Val Pro Asp Leu Gly Arg Phe Gln Thr Phe
515 520 525

Glu Gly Asp Leu Lys Trp His His His Asn Ile Thr Tyr Trp Ile Gln
530 535 540

Asn Tyr Ser Glu Asp Leu Pro Arg Ala Val Ile Asp Asp Ala Phe Ala
545 550 555 560

Arg Ala Phe Ala Leu Trp Ser Ala Val Thr Pro Leu Thr Phe Thr Arg
565 570 575

Val Tyr Ser Arg Asp Ala Asp Ile Val Ile Gln Phe Gly Val Ala Glu
580 585 590

His Gly Asp Gly Tyr Pro Phe Asp Gly Lys Asp Gly Leu Leu Ala His
595 600 605

Ala Phe Pro Pro Gly Pro Gly Ile Gln Gly Asp Ala His Phe Asp Asp
610 615 620

Asp Glu Leu Trp Ser Leu Gly Lys Gly Val Val Val Pro Thr Arg Phe

625 630 635 640

Gly Asn Ala Asp Gly Ala Ala Cys His Phe Pro Phe Ile Phe Glu Gly
645 650 655

Arg Ser Tyr Ser Ala Cys Thr Thr Asp Gly Arg Ser Asp Gly Leu Pro
660 665 670

Trp Cys Ser Thr Thr Ala Asn Tyr Asp Thr Asp Asp Arg Phe Gly Phe
675 680 685

Cys Pro Ser Glu Arg Leu Tyr Thr Arg Asp Gly Asn Ala Asp Gly Lys
690 695 700

Pro Cys Gln Phe Pro Phe Ile Phe Gln Gly Gln Ser Tyr Ser Ala Cys
705 710 715 720

Thr Thr Asp Gly Arg Ser Asp Gly Tyr Arg Trp Cys Ala Thr Thr Ala
725 730 735

Asn Tyr Asp Arg Asp Lys Leu Phe Gly Phe Cys Pro Thr Arg Ala Asp
740 745 750

Ser Thr Val Met Gly Gly Asn Ser Ala Gly Glu Leu Cys Val Phe Pro
755 760 765

Phe Thr Phe Leu Gly Lys Glu Tyr Ser Thr Cys Thr Ser Glu Gly Arg
770 775 780

Gly Asp Gly Arg Leu Trp Cys Ala Thr Thr Ser Asn Phe Asp Ser Asp
785 790 795 800

Lys Lys Trp Gly Phe Cys Pro Asp Gln Gly Tyr Ser Leu Phe Leu Val
805 810 815

Ala Ala His Glu Phe Gly His Ala Leu Gly Leu Asp His Ser Ser Val
820 825 830

Pro Glu Ala Leu Met Tyr Pro Met Tyr Arg Phe Thr Glu Gly Pro Pro
835 840 845

Leu His Lys Asp Asp Val Asn Gly Ile Arg His Leu Tyr Gly Pro Arg
850 855 860

Pro Glu Pro Glu Pro Arg Pro Pro Thr Thr Thr Thr Pro Gln Pro Thr
865 870 875 880

Ala Pro Pro Thr Val Cys Pro Thr Gly Pro Pro Thr Val His Pro Ser
885 890 895

Glu Arg Pro Thr Ala Gly Pro Thr Gly Pro Pro Ser Ala Gly Pro Thr
900 905 910

Gly Pro Pro Thr Ala Gly Pro Ser Thr Ala Thr Thr Val Pro Leu Ser
915 920 925

Pro Val Asp Asp Ala Cys Asn Val Asn Ile Phe Asp Ala Ile Ala Glu
930 935 940

Ile Gly Asn Gln Leu Tyr Leu Phe Lys Asp Gly Lys Tyr Trp Arg Phe
945 950 955 960

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

Lys Trp Pro Ala Leu Pro Arg Lys Leu Asp Ser Val Phe Glu Glu Pro
980 985 990

Leu Ser Lys Lys Leu Phe Phe Phe Ser Gly Arg Gln Val Trp Val Tyr
995 1000 1005

Thr Gly Ala Ser Val Leu Gly Pro Arg Arg Leu Asp Lys Leu Gly
1010 1015 1020

Leu Gly Ala Asp Val Ala Gln Val Thr Gly Ala Leu Arg Ser Gly
1025 1030 1035

Arg Gly Lys Met Leu Leu Phe Ser Gly Arg Arg Leu Trp Arg Phe
1040 1045 1050

Asp Val Lys Ala Gln Met Val Asp Pro Arg Ser Ala Ser Glu Val
1055 1060 1065

Asp Arg Met Phe Pro Gly Val Pro Leu Asp Thr His Asp Val Phe
1070 1075 1080

Gln Tyr Arg Glu Lys Ala Tyr Phe Cys Gln Asp Arg Phe Tyr Trp
1085 1090 1095

Arg Val Ser Ser Arg Ser Glu Leu Asn Gln Val Asp Gln Val Gly
1100 1105 1110

Tyr Val Thr Tyr Asp Ile Leu Gln Cys Pro Glu Asp
1115 1120 1125

<210> 67

<211> 2814

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesized polynucleotide encoding SIRP1alpha-PDL1-CD3-Fc-SL
bi-specific T-cell engager construct

<400> 67

atggaaaccg atacacttct gttgtgggtg ctgctgctgt gggtccttgg ttcaacaggc 60
gattatccct acgatgtgcc cgactacgca ggcgctcagc cagctgatga tatccagatg 120
acacagagcc catcatctct gtctgcaagc gtaggagacc gagtcacat tacatgcaga 180
gcctccaag acgtttccac agcagtggcc tggatcagc aaaaacctgg taaggcgccc 240
aagcttctca tctattcagc cagttttctg tatagcggcg ttccagccg attctctggc 300
tctggatccg gcacggactt tactttgaca atttctctc ttcagcccga agattttgca 360
acctactact gtcagcaata tcttaccat ccagccacat tcggacaggg caccaaagtc 420
gaaatcaaaa gaggcggcgg cggcagtggc ggcgggggtt caggaggcgg gggttctgaa 480
gtgcaactcg ttgaaagcgt aggagggtt gtccaacctg gcgggtcact gcggttgagc 540
tgcgccgcaa gcggattcac cttctcagac tcttgatcc attgggtgcg ccaggctccc 600
ggaaaaggct tggaatgggt tgcttgatt tcaccgatg gcggttccac atactacgt 660
gacagcgta agggctgatt caccatctct gcagatactt caaaaaacac agcctacctt 720
cagatgaata gtttgcgcgc cgaggacaca gcggtttatt attgtgcctt aagacattgg 780
cccggcggtt tcgactactg ggggcaaggc acgttggtga ctgtgagcgc cgtagatgaa 840

gcaaaatctt gtgacaaaac ccatacctgc ccaccatgcc cagccccaga acttcttggc 900
gtaccctctg tcttcctttt cctccgaag cccaaggata ccctgatgat cagccgaacc 960
ccggaggtaa catgtgtggt ggtcgatgtt agccatgagg atcctgaagt caaatTTAAC 1020
tggtatgtag acggtgttga ggtgcacaac gctaaaacta agcccaggga ggagcagtac 1080
aactcaacct atcgcgtcgt atctgtgctt accgtcctgc atcaagactg gctcaatggt 1140
aaggaatata aatgtaaagt gagtaacaag gcactgccag cacctatcga aaaaaccatc 1200
tcaaaggcga agggacagcc cagggaaccc cagggtctata ctctgcaacc ttctcgggat 1260
gaattgacca agaaccaagt tagcctgaca tgtctggtga aaggTTtcta tccaagcgat 1320
atagctgtcg agtgggagtc caatggccaa cctgagaaca attataagac caccCCacc 1380
gttctggaca gcgacggatc cttttcctg tactcaaaac tcactgtcga taaatcaaga 1440
tggcaacaag gcaacgtttt tagctgtagc gtgatgcacg aagcacttca taatcactat 1500
acacagaagt cactctctct ttctccagga aaggttgacg aacagaaatt gatatccgag 1560
gaagatctca ataggaggaa gagagaaggc agggggagcc ttctcacttg cggcgatgtc 1620
gaggaaaatc cggggcctat ggagaccgat accctgctct tgtgggtttt gcttctttgg 1680
gtgccaggat ctacaggtga tgaagaagaa ttgcagatca tccaaccaga caaatccgta 1740
ctcgtggccg caggagagac cgctaccctc agatgtacca tcacttctct cttccccgtt 1800
ggccccatcc agtggtttcg aggcgcagga ccaggacgag tgcttattta caatcaacga 1860
cagggcccat tccaagagt gacaacagta tccgatacca ccaagcgcaa taatatggac 1920
tttagcatta gaatcgga cataacaccc gctgacgccg gtacatacta ttgtattaaa 1980
tttcgaaagg gctcaccaga cgacgtggaa tttaagttag gggccggaac cgaacttca 2040
gttagagcaa aaccttctgc tagcgacatc aagctgcagc agagcggcgc cgagctggcc 2100
aggcccggcg ccagcgtgaa gatgagctgc aagaccagcg gctacacctt caccaggtac 2160
accatgcact gggTgaagca gagggccggc cagggcctgg agtggatcgg ctacatcaac 2220
cccagcaggg gctacaccaa ctacaaccag aagTtcaagg acaaggccac cctgaccacc 2280
gacaagagca gcagcaccgc ctacatgcag ctgagcagcc tgaccagcga ggacagcgcc 2340
gtgtactact gcgccaggta ctacgacgac cactactgcc tggactactg gggccagggc 2400
accacctga ccgtgagcag cgtggagggc ggcagcggcg gcagcggcgg cagcggcggc 2460
agcggcggcg tggacgacat ccagctgacc cagagccccg ccatcatgag cgccagcccc 2520

ggcgagaagg tgacatgac ctgcagggcc agcagcagcg tgagctacat gaactggtac 2580
cagcagaaga gcggcaccag cccaagagg tggatctacg acaccagcaa ggtggccagc 2640
ggcgtgccct acaggttcag cggcagcggc agcggcacca gctacagcct gaccatcagc 2700
agcatggagg ccgaggacgc cgccacctac tactgccagc agtggagcag caaccccctg 2760
acctccggcg ccggcaccaa gctggagctg aagcaccacc atcatcacca ctga 2814

<210> 68

<211> 937

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized SIRP1alpha-PDL1-CD3-Fc-SL bi-specific T-cell engager
construct

<400> 68

Met Glu Thr Asp Arg Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

Gly Ser Thr Gly Asp Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Ala
20 25 30

Gln Pro Ala Asp Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
35 40 45

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

Val Ser Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
65 70 75 80

Lys Leu Leu Ile Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser
85 90 95

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
100 105 110

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Leu
115 120 125

Tyr His Pro Ala Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
130 135 140

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
145 150 155 160

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
165 170 175

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Ser Trp
180 185 190

Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala
195 200 205

Trp Ile Ser Pro Tyr Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
210 215 220

Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr Leu
225 230 235 240

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
245 250 255

Arg Arg His Trp Pro Gly Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu
260 265 270

Val Thr Val Ser Ala Val Asp Glu Ala Lys Ser Cys Asp Lys Thr His
275 280 285

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
290 295 300

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
305 310 315 320

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
325 330 335

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
340 345 350

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
355 360 365

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
370 375 380

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
385 390 395 400

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
405 410 415

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
420 425 430

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
435 440 445

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
450 455 460

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
465 470 475 480

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
485 490 495

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

Asp Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Arg Arg Lys Arg
515 520 525

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

Gly Pro Met Glu Thr Asp Arg Leu Leu Leu Trp Val Leu Leu Leu Trp
545 550 555 560

Val Pro Gly Ser Thr Gly Asp Glu Glu Glu Leu Gln Ile Ile Gln Pro
565 570 575

Asp Lys Ser Val Leu Val Ala Ala Gly Glu Thr Ala Thr Leu Arg Cys
580 585 590

Thr Ile Thr Ser Leu Phe Pro Val Gly Pro Ile Gln Trp Phe Arg Gly
595 600 605

Ala Gly Pro Gly Arg Val Leu Ile Tyr Asn Gln Arg Gln Gly Pro Phe
610 615 620

Pro Arg Val Thr Thr Val Ser Asp Thr Thr Lys Arg Asn Asn Met Asp
625 630 635 640

Phe Ser Ile Arg Ile Gly Asn Ile Thr Pro Ala Asp Ala Gly Thr Tyr
645 650 655

Tyr Cys Ile Lys Phe Arg Lys Gly Ser Pro Asp Asp Val Glu Phe Lys
660 665 670

Ser Gly Ala Gly Thr Glu Leu Ser Val Arg Ala Lys Pro Ser Ala Ser
675 680 685

Asp Ile Lys Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala
690 695 700

Ser Val Lys Met Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Arg Tyr
705 710 715 720

Thr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
725 730 735

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe
740 745 750

Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr Ala Tyr
755 760 765

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
770 775 780

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly

785 790 795 800
 Thr Thr Leu Thr Val Ser Ser Val Glu Gly Gly Ser Gly Gly Ser Gly
 805 810 815
 Gly Ser Gly Gly Ser Gly Gly Val Asp Asp Ile Gln Leu Thr Gln Ser
 820 825 830
 Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys
 835 840 845
 Arg Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Ser
 850 855 860
 Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
 865 870 875 880
 Gly Val Pro Tyr Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser
 885 890 895
 Leu Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
 900 905 910
 Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu
 915 920 925
 Glu Leu Lys His His His His His His
 930 935

<210> 69
 <211> 2829
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthesized polynucleotide encoding SIRP1alpha-PDL1-CD3-Fc-LL
 bi-specific T-cell engager construct

<400> 69
 atggaaccg atacacttct gttgtgggtg ctgctgctgt gggtccttg ttcaacaggc 60
 gattatccct acgatgtgcc cgactacgca ggcgctcagc cagctgatga tatccagatg 120
 acacagagcc catcatctct gtctgcaagc gtaggagacc gattcacat tacatgcaga 180

gcctccaag acgtttccac agcagtggcc tggatcagc aaaaacctgg taaggcgccc 240
aagcttctca tctattcagc cagttttctg tatagcggcg ttcccagccg attctctggc 300
tctggatccg gcacggactt tactttgaca atttctctc ttacagcccga agattttgca 360
acctactact gtcagcaata tctctacat ccagccacat tcggacaggg caccaaagtc 420
gaaatcaaaa gaggcggcgg cggcagtggc ggcgggggtt caggagggcg gggttctgaa 480
gtgcaactcg ttgaaagcgt aggagggctt gtccaacctg gcgggtcact gcggttgagc 540
tgcgccgcaa gcggttcac cttctcagac tcttgatcc attgggtgcg ccaggtctcc 600
ggaaaaggct tggaatgggt tgcttgatt tcaccgatg gcggttcac atactacgt 660
gacagcgta agggtcgatt caccatctct gcagatactt caaaaaacac agcctacctt 720
cagatgaata gtttgcgcg cgaggacaca gcggtttatt attgtgccct aagacattgg 780
cccggcggtt tcgactactg ggggcaaggc acgttggtga ctgtgagcgc cgtagatgaa 840
gcaaaatctt gtgacaaaac ccatactgc ccacatgcc cagccccaga acttcttggc 900
gtacctctg tcttctttt cctccgaag cccaaggata ccctgatgat cagccgaacc 960
ccggaggtaa catgtgtgtt ggtcgatgtt agccatgagg atcctgaagt caaatttaac 1020
tggtatgtag acggtgttga ggtgcacaac gctaaaacta agcccaggga ggagcagtac 1080
aactcaacct atcgcgtcgt atctgtgctt accgtctgc atcaagactg gctcaatggt 1140
aaggaatata aatgtaaagt gagtaacaag gcactgccag cacctatcga aaaaaccatc 1200
tcaaaggcga agggacagcc cagggaaccc cagggtctata ctctgcaacc ttctcgggat 1260
gaattgacca agaaccaagt tagcctgaca tgtctggtga aaggtttcta tccaagcgat 1320
atagctgtcg agtgggagtc caatggccaa cctgagaaca attataagac caccacacc 1380
gttctggaca gcgacggatc cttttctg tactcaaac tctctgca taaatcaaga 1440
tggcaacaag gcaacgttt tagctgtagc gtgatgcacg aagcacttca taatcactat 1500
acacagaagt cactctctt ttctccagga aaggttgacg aacagaaatt gatatccgag 1560
gaagatctca ataggaggaa gagagaaggc agggggagcc ttctcacttg cggcgatgtc 1620
gaggaaaatc cggggcctat ggagaccgat accctgctct tgtgggtttt gcttcttgg 1680
gtgccaggat ctacaggtga tgaagaaga ttgcagatca tccaaccaga caaatccgta 1740
ctcgtggccg caggagagac cgctaccctc agatgtacca tcttctctt cttccccgtt 1800
ggccccatcc agtggtttcg aggcgcagga ccaggacgag tgcttattta caatcaacga 1860

cagggcccat tccaagagt gacaacagta tccgatacca ccaagcgcaa taatatggac 1920
tttagcatta gaatcggcaa cataacaccc gctgacgccg gtacatacta ttgtattaaa 1980
tttcgaaagg gctcaccaga cgacgtggaa ttaagtcag gggccggaac cgaactctca 2040
gttagagcaa aaccttctgc tagcggcggc ggcggcagcg acatcaagct gcagcagagc 2100
ggcgccgagc tggccaggcc cggcgccagc gtgaagatga gctgcaagac cagcggctac 2160
acctcacca ggtacacat gcactgggtg aagcagaggc ccggccaggc cctggagtgg 2220
atcggtaca tcaacccag caggggctac accaactaca accagaagtt caaggacaag 2280
gccacctga ccaccgaaa gagcagcagc accgcctaca tgcagctgag cagcctgacc 2340
agcgaggaca gcgccgtgta ctactgcgc accgtactacg acgaccacta ctgcctggac 2400
tactggggcc agggcaccac cctgaccgtg agcagcgtgg agggcggcag cggcggcagc 2460
ggcggcagcg gcggcagcgg cggcgtggac gacatccagc tgaccagag ccccgccatc 2520
atgagcgcca gccccggcga gaaggtgacc atgacctgca gggccagcag cagcgtgagc 2580
tacatgaact ggtaccagca gaagagcggc accagcccca agaggtggat ctacgacacc 2640
agcaaggtgg ccagcggcgt gccctacagg ttcagcggca gcggcagcgg caccagctac 2700
agcctgacca tcagcagcat ggaggccgag gacgccgcca cctactactg ccagcagtgg 2760
agcagcaacc cctgacctt cggcgccggc accaagctgg agctgaagca ccaccaccac 2820
caccactag 2829

<210> 70

<211> 942

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized SIRP1alpha-PDL1-CD3-Fc-LL bi-specific T-cell engager construct

<400> 70

Met Glu Thr Asp Arg Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

Gly Ser Thr Gly Asp Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Ala
20 25 30

Gln Pro Ala Asp Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
35 40 45

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

Val Ser Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
65 70 75 80

Lys Leu Leu Ile Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser
85 90 95

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
100 105 110

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Leu
115 120 125

Tyr His Pro Ala Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
130 135 140

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
145 150 155 160

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
165 170 175

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Ser Trp
180 185 190

Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala
195 200 205

Trp Ile Ser Pro Tyr Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
210 215 220

Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr Leu
225 230 235 240

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
245 250 255

Arg Arg His Trp Pro Gly Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu
260 265 270

Val Thr Val Ser Ala Val Asp Glu Ala Lys Ser Cys Asp Lys Thr His
275 280 285

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
290 295 300

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
305 310 315 320

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
325 330 335

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
340 345 350

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
355 360 365

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
370 375 380

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
385 390 395 400

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
405 410 415

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
420 425 430

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
435 440 445

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
450 455 460

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
465 470 475 480

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
485 490 495

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

Asp Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Arg Arg Lys Arg
515 520 525

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

Gly Pro Met Glu Thr Asp Arg Leu Leu Leu Trp Val Leu Leu Leu Trp
545 550 555 560

Val Pro Gly Ser Thr Gly Asp Glu Glu Glu Leu Gln Ile Ile Gln Pro
565 570 575

Asp Lys Ser Val Leu Val Ala Ala Gly Glu Thr Ala Thr Leu Arg Cys
580 585 590

Thr Ile Thr Ser Leu Phe Pro Val Gly Pro Ile Gln Trp Phe Arg Gly
595 600 605

Ala Gly Pro Gly Arg Val Leu Ile Tyr Asn Gln Arg Gln Gly Pro Phe
610 615 620

Pro Arg Val Thr Thr Val Ser Asp Thr Thr Lys Arg Asn Asn Met Asp
625 630 635 640

Phe Ser Ile Arg Ile Gly Asn Ile Thr Pro Ala Asp Ala Gly Thr Tyr
645 650 655

Tyr Cys Ile Lys Phe Arg Lys Gly Ser Pro Asp Asp Val Glu Phe Lys
660 665 670

Ser Gly Ala Gly Thr Glu Leu Ser Val Arg Ala Lys Pro Ser Ala Ser
675 680 685

Gly Gly Gly Gly Ser Asp Ile Lys Leu Gln Gln Ser Gly Ala Glu Leu

690 695 700

Ala Arg Pro Gly Ala Ser Val Lys Met Ser Cys Lys Thr Ser Gly Tyr
705 710 715 720

Thr Phe Thr Arg Tyr Thr Met His Trp Val Lys Gln Arg Pro Gly Gln
725 730 735

Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn
740 745 750

Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys Ser
755 760 765

Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser
770 775 780

Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp
785 790 795 800

Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Val Glu Gly Gly
805 810 815

Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Val Asp Asp Ile
820 825 830

Gln Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys
835 840 845

Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met Asn Trp
850 855 860

Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr
865 870 875 880

Ser Lys Val Ala Ser Gly Val Pro Tyr Arg Phe Ser Gly Ser Gly Ser
885 890 895

Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu Asp Ala
900 905 910

Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly
915 920 925

Ala Gly Thr Lys Leu Glu Leu Lys His His His His His His
930 935 940