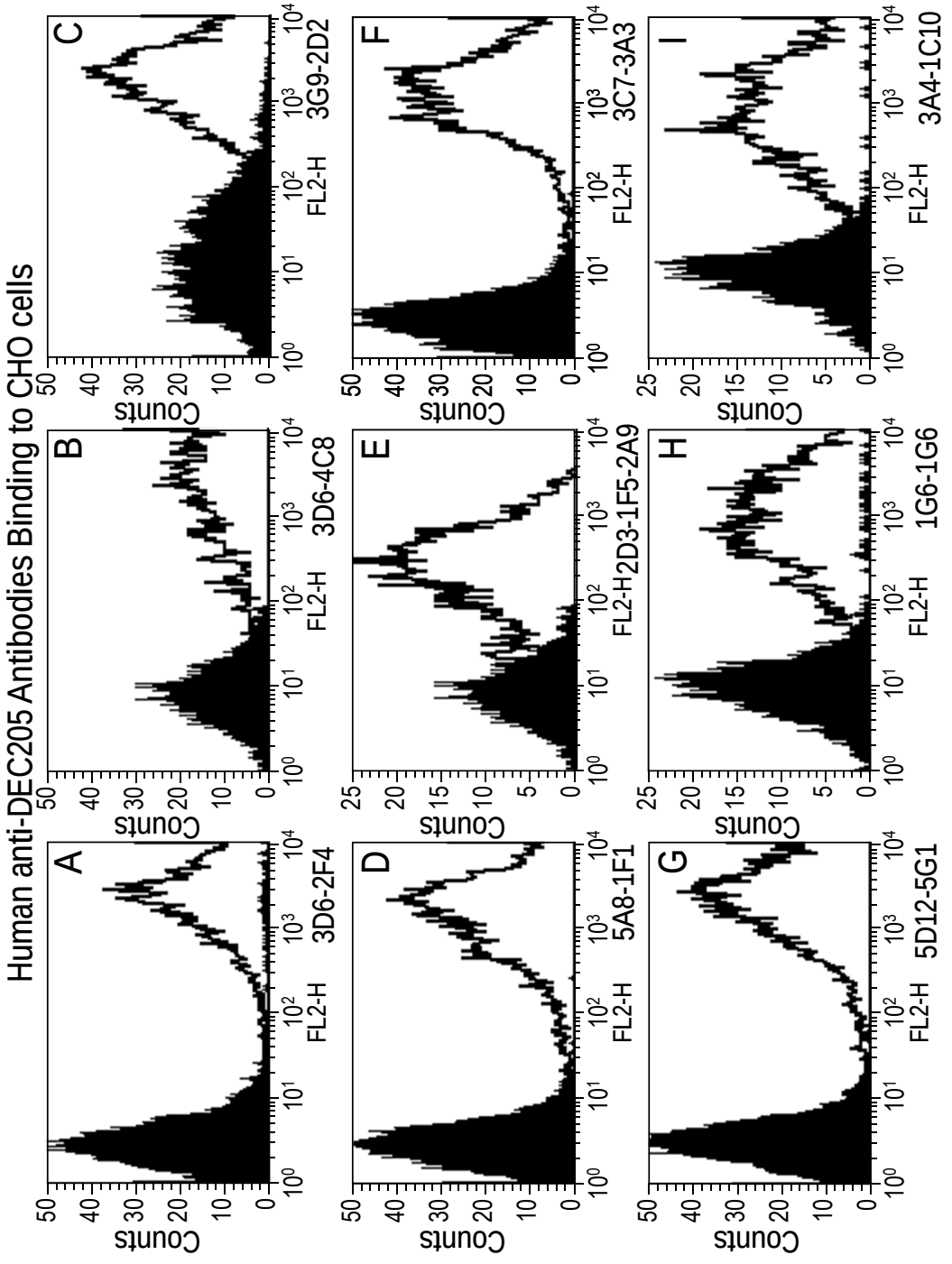

Human anti-DEC205 Antibodies Binding to CHO cells
Filled histogram = control CHO-S cells
Open histograms = CHO-S cells expressing huDEC-205
All antibodies used at saturating concentrations
A
B
C
D
E
F
G
H
I
Counts
FL2-H
3D6-2F4
3D6-4C8
3G9-2D2
5A8-1F1
2D3-1F5-2A9
3C7-3A3
5D12-5G1
1G6-1G6
3A4-1C10

*Fig. 1*

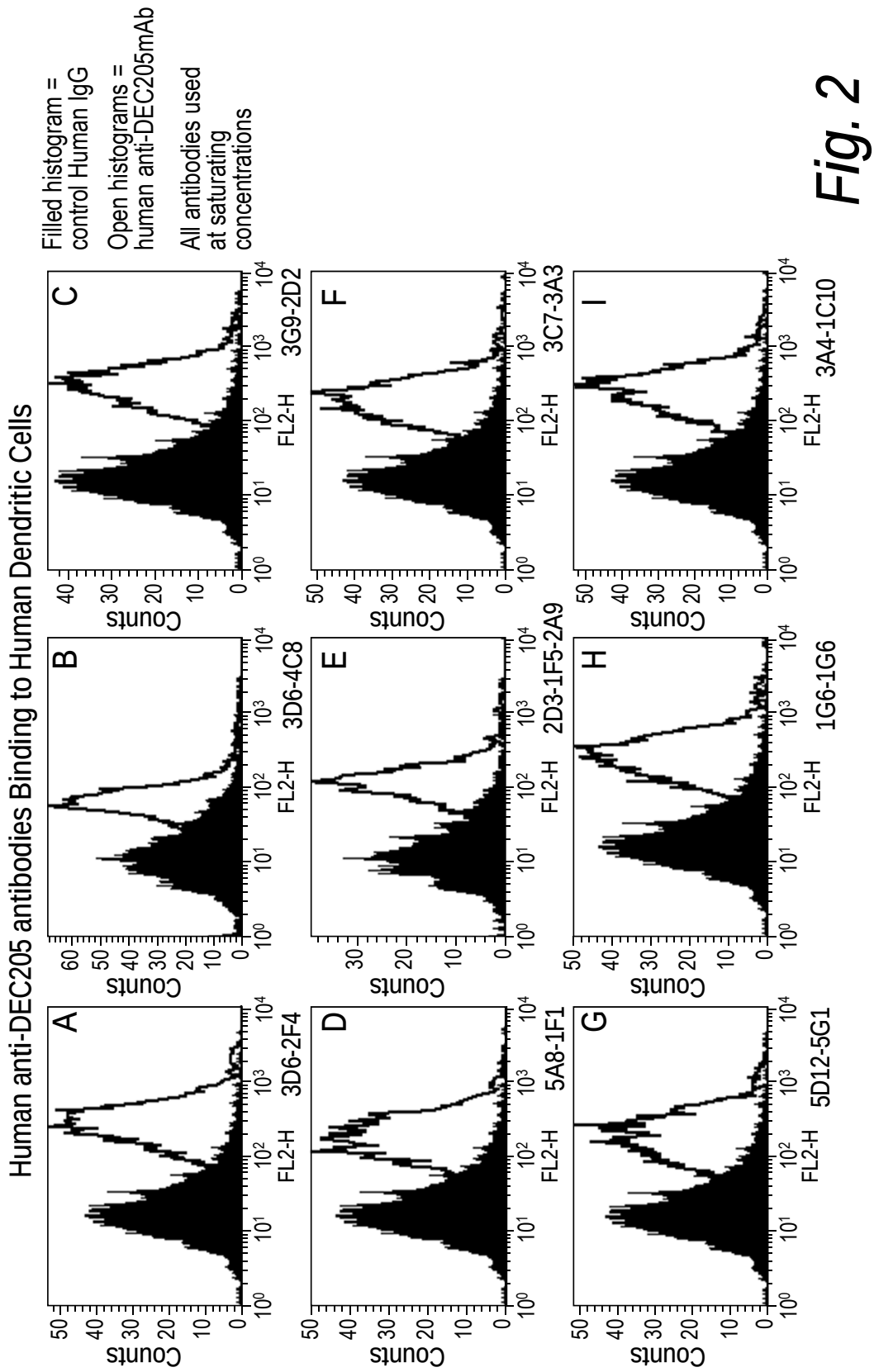

Human anti-DEC205 antibodies Binding to Human Dendritic Cells
Filled histogram = control Human IgG
Open histograms = human anti-DEC205mAb
All antibodies used at saturating concentrations
A
B
C
D
E
F
G
H
I
Counts
FL2-H
5D12-5G1
3D6-2F4
5A8-1F1
3D6-4C8
2D3-1F5-2A9
1G6-1G6
3G9-2D2
3C7-3A3
3A4-1C10

*Fig. 2*

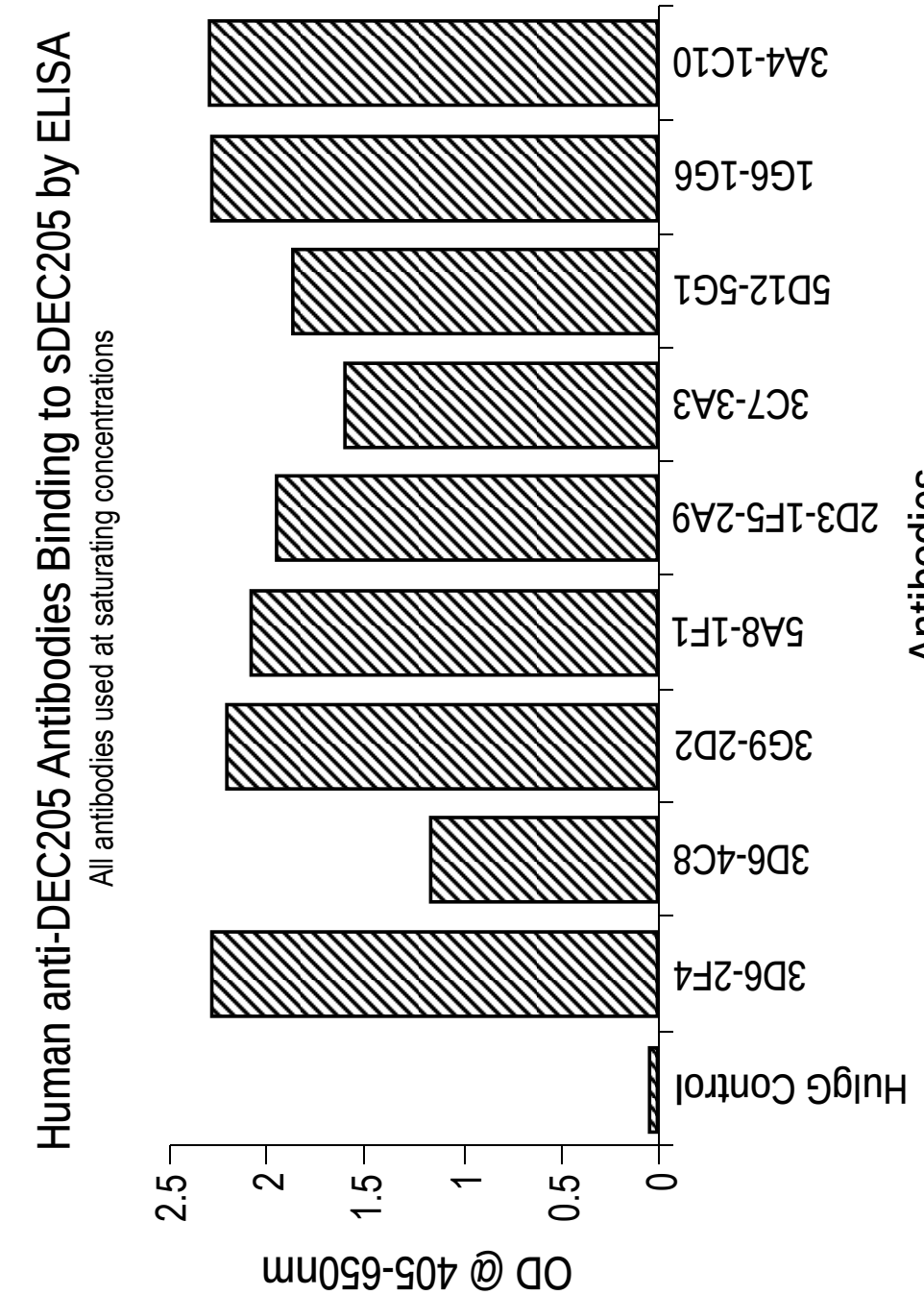
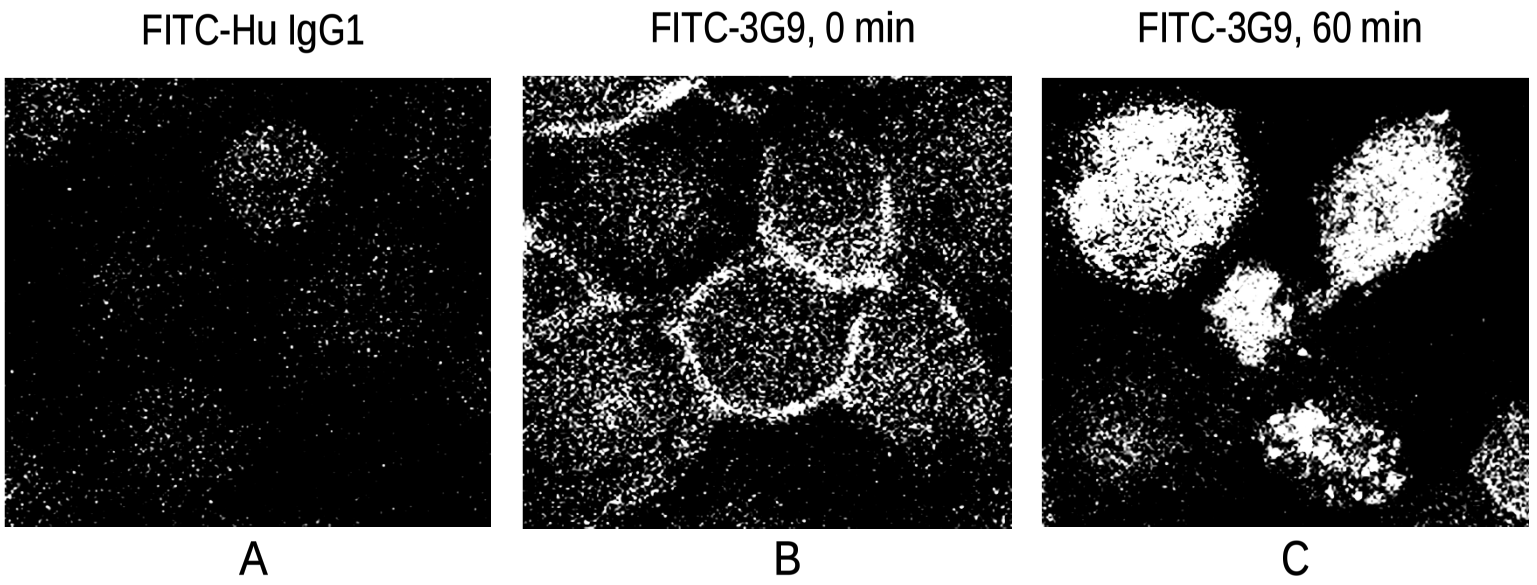

Human anti-DEC205 Antibodies Binding to sDEC205 by ELISA
All antibodies used at saturating concentrations
OD @ 405-650nm
2.5
2
1.5
1
0.5
0
HuIgG Control
3D6-2F4
3D6-4C8
3G9-2D2
5A8-1F1
2D3-1F5-2A9
3C7-3A3
5D12-5G1
1G6-1G6
3A4-1C10
Antibodies

*Fig. 3*

## Dec205 mAb Binding and Internalization in Dendritic Cells

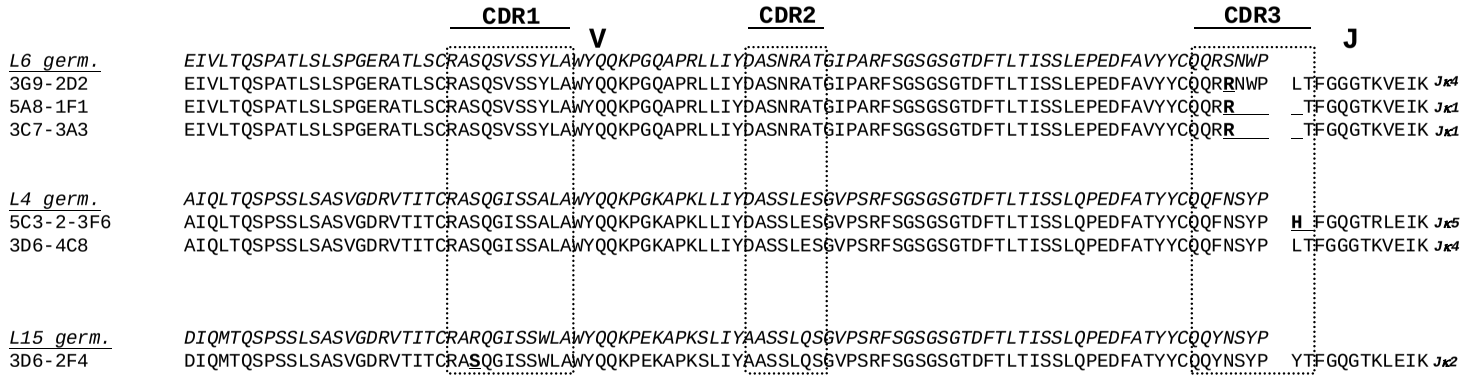



Monocyte-derived human DCs were pulsed with FITC-3G9-2D2 or FITC-human IgG1 for 30 minutes on ice. Cells were then incubated at 37°C for the indicated periods to allow for internalization. Images were captured by confocal microscopy, and green staining revealed the presence of FITC-labeled molecules.

*Fig. 4*

# Human $V_H$ and $V_K$ Alignments and Germline Sequences

## Vκ Alignments




## VH Alignments

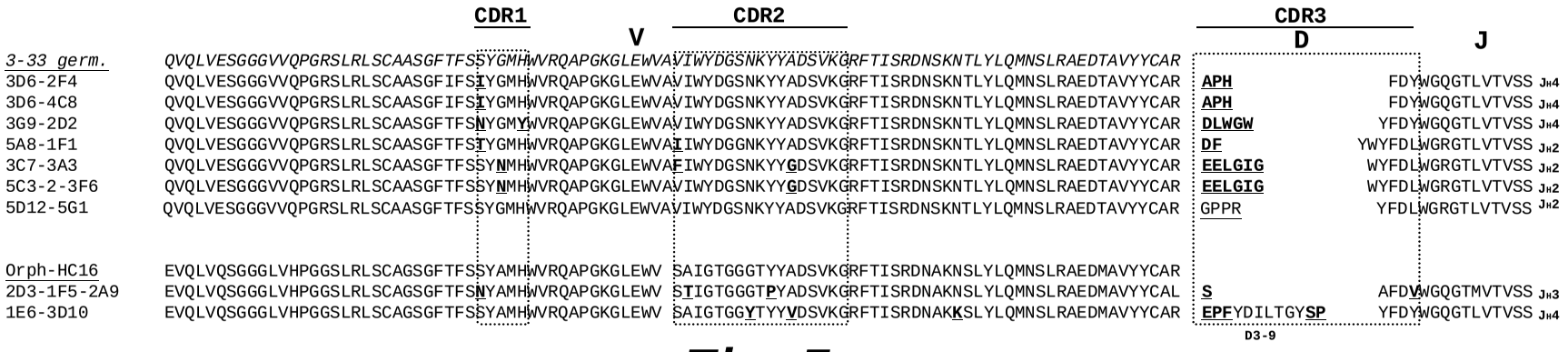



*Fig. 5*

# Human $V_H$ CDR Consensus Sequences

3D6-2F4 VH CDR1 (SEQ ID NO:5): IYGMH
3D6-4C8 VH CDR1 (SEQ ID NO:17): IYGMH
3G9-2D2 VH CDR1 (SEQ ID NO: 29): NYGMY
5A8-1F1 VH CDR1 (SEQ ID NO: 41): TYGMH
3C7-3A3, VH CDR1 (SEQ ID NO: 53): SYNMH
2D3-1F5-2A9, VH CDR1 (SEQ ID NO: 65): NYAMH
1E6-3D10 VH CDR1: (SEQ ID NO: 71): SYAMH
5C3-2-3F6 VH CDR1 (SEQ ID NO: 77): SYNMH
5D12-5G1 VH CDR1 (SEQ ID NO: 89): SYGMH

**VH CDR1 CONSENSUS (SEQ ID NO: 97): (I,N,T,S) Y (G,N,A) M (H,Y)**

3D6-2F4 VH CDR2 (SEQ ID NO: 6): VIWYDGSNKYYADSVKG
3D6-4C8 VH CDR2 (SEQ ID NO: 18): VIWYDGSNKYYADSVKG
3G9-2D2, VH CDR2 (SEQ ID NO: 30): VIWYDGSNKYYADSVKG
5A8-1F1, VH CDR2 (SEQ ID NO: 42): IIWYDGGNKYYADSVKG
3C7-3A3, VH CDR2 (SEQ ID NO: 54): FIWYDGSNKYYGDSVKG
2D3-1F5-2A9, VH CDR2 (SEQ ID NO: 66): TIGTGGGTPYA-DSVKG
1E6-3D10 VH CDR2 (SEQ ID NO: 72): AIGTGGYTYYV-DSVKG
5C3-2-3F6 VH CDR2 (SEQ ID NO: 78): VIWYDGSNKYYGDSVKG
5D12-5G1 VH CDR2 (SEQ ID NO: 90): VIWYDGSNKYYADSVKG

**VH CDR2 CONSENSUS (SEQ ID NO: 98): (V,I,F,T,A) I (W,G) (Y,T) (D,G) G (S,G,Y) (N,T) (K,P) Y (Y,A,V) (A,G,-) D S V K G**

3D6-2F4 VH CDR3 (SEQ ID NO: 7): APHFDY
3D6-4C8 VH CDR3 (SEQ ID NO: 19): APHFDY
3G9-2D2, VH CDR3 (SEQ ID NO: 31): DLWGWYFDY
5A8-1F1, VH CDR3 (SEQ ID NO: 43): DFYWYFDL
3C7-3A3, VH CDR3 (SEQ ID NO: 55): EELGIGWYFDL
2D3-1F5-2A9, VH CDR3 (SEQ ID NO: 67): SAFDV
1E6-3D10 VH CDR3 (SEQ ID NO: 73): EPFYDILTGYSPYFDY
5C3-2-3F6 VH CDR3 (SEQ ID NO: 79): EELGIGWYFDL
5D12-5G1 VH CDR3 (SEQ ID NO: 91): GPPRYFDL

**VH CDR3 (CORE) CONSENSUS (SEQ ID NO: 99): (A,G,Y,S,P,-) (P,W,S,R) (Y,A,H) F D (Y,L,V)**
*(Where "-" denotes option of no amino acid residue present at that position)*

*Fig. 6*

# Human $V_L$ CDR Consensus Sequences

3D6-2F4 VL CDR1 (SEQ ID NO: 11): RASQGISSWLA
3D6-4C8 VL CDR1 (SEQ ID NO: 23): RASQGISSALA
3G9-2D2, VL CDR1 (SEQ ID NO: 35): RASQSVSSYLA
5A8-1F1, VL CDR1 (SEQ ID NO: 47): RASQSVSSYLA
3C7-3A3, VL CDR1 (SEQ ID NO: 59): RASQSVSSYLA
5C3-2-3F6 VL CDR1 (SEQ ID NO: 83): RASQGISSALA

**VL CDR1 CONSENSUS (SEQ ID NO: 100): R A S Q (S,G) (I,V) S S (Y,W,A) L A**

3D6-2F4 VL CDR2 (SEQ ID NO: 12): AASSLQS
3D6-4C8 VL CDR2 (SEQ ID NO: 24): DASSLES
3G9-2D2, VL CDR2 (SEQ ID NO: 36): DASNRAT
5A8-1F1, VL CDR2 (SEQ ID NO: 48): DASNRAT
3C7-3A3, VL CDR2 (SEQ ID NO: 60): DASNRAT
5C3-2-3F6 VL CDR2 (SEQ ID NO: 84): DASSLES

**VL CDR2 CONSENSUS (SEQ ID NO: 101): (D,A) A S (N,S) (R,L) (A,Q,E) (T,S)**

3D6-2F4 VL CDR3 (SEQ ID NO: 13): QQYNSYPYT
3D6-4C8 VL CDR3 (SEQ ID NO: 25): QQFNSYPLT
3G9-2D2, VL CDR3 (SEQ ID NO: 37): QQRRNWPLT
5A8-1F1, VL CDR3 (SEQ ID NO: 49): QQRRT----
3C7-3A3, VL CDR3 (SEQ ID NO: 61): QQRRT----
5C3-2-3F6 VL CDR3 (SEQ ID NO: 85): QQFNSYPH-

**VL CDR3 CONSENSUS (SEQ ID NO: 102): Q Q (R,Y,F) (R,N) (T,S,N) (Y,W,-) (P,-) (Y,L,H,-) (T,-)**

*(Where "-" denotes option of no amino acid residue present at that position)*

*Fig. 7*

Example of anti-DEC-205/antigen fusion
APC targeted vaccine construct (schematic representation)

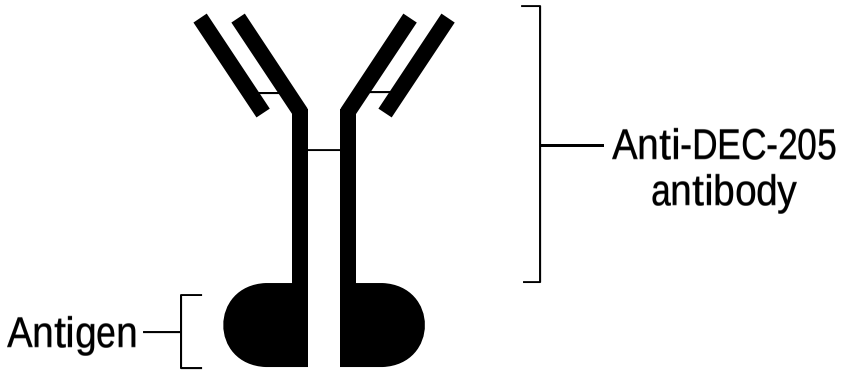



*Fig. 8*

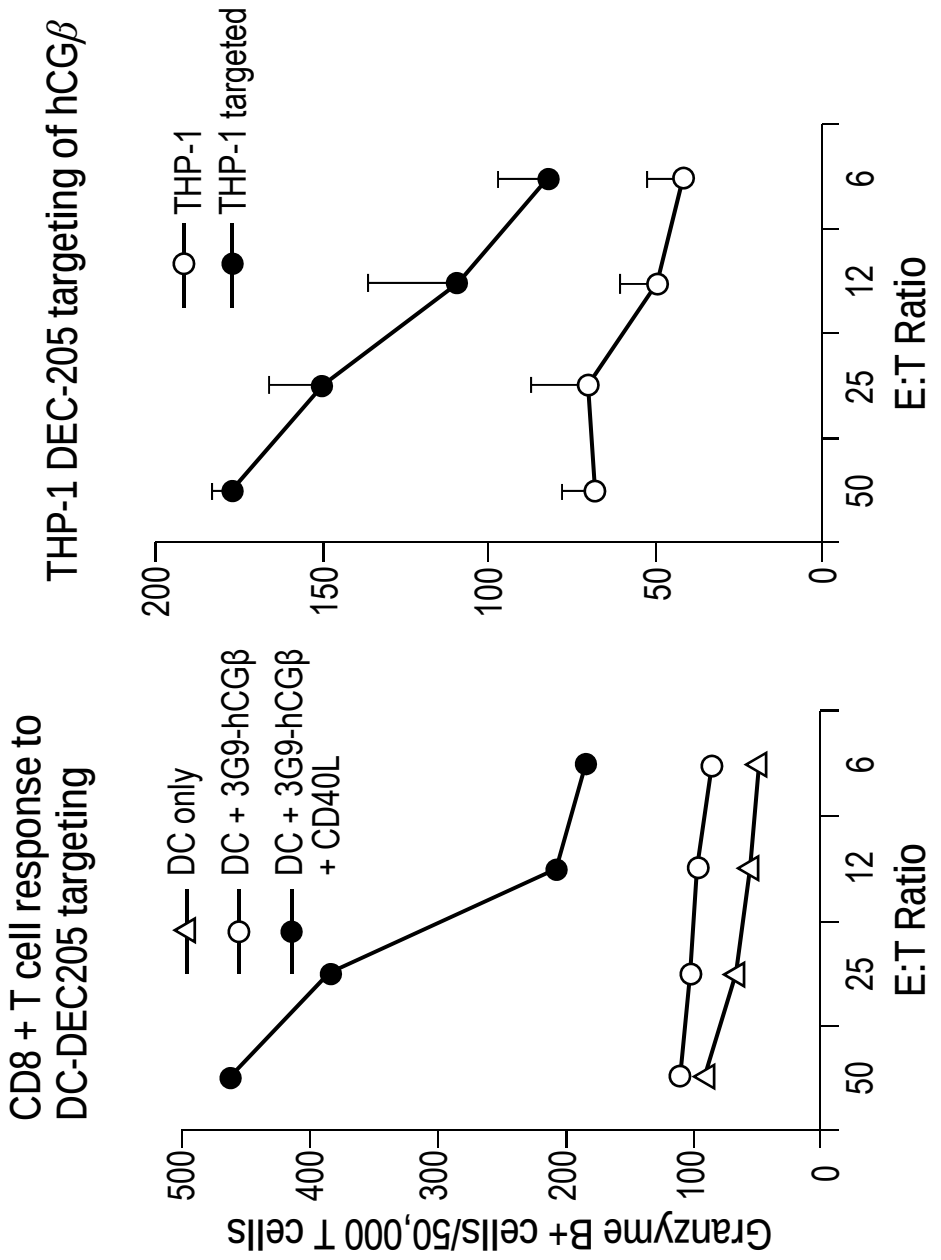

CD8 + T cell response to
DC-DEC205 targeting
DC only
DC + 3G9-hCGβ
DC + 3G9-hCGβ
+ CD40L
Granzyme B+ cells/50,000 T cells
500
400
300
200
100
0
50
25
12
6
E:T Ratio
THP-1 DEC-205 targeting of hCGβ
THP-1
THP-1 targeted
200
150
100
50
0
50
25
12
6
E:T Ratio

*Fig. 9A*

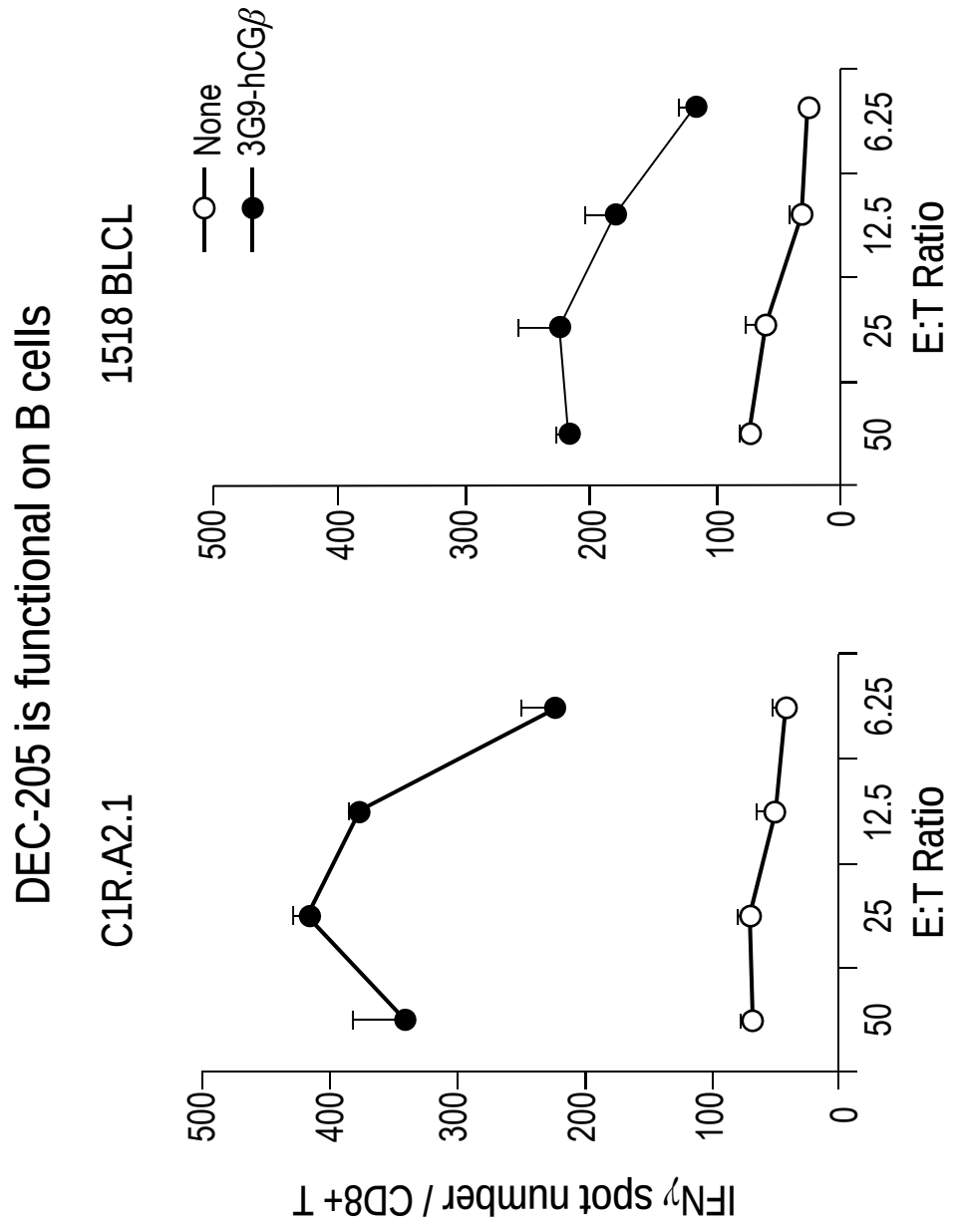

DEC-205 is functional on B cells
C1R.A2.1
1518 BLCL
None
3G9-hCGβ
IFNγ spot number / CD8+ T
500
400
300
200
100
0
50
25
12.5
6.25
E:T Ratio

*Fig. 9B*

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Asn Asp Pro Phe Thr Ile Val His Gly Asn Thr Gly Lys Cys Ile Lys
        35                  40                  45

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

Lys Leu Trp Lys Trp Val Ser Gln His Arg Leu Phe His Leu His Ser
65                  70                  75                  80

Gln Lys Cys Leu Gly Leu Asp Ile Thr Lys Ser Val Asn Glu Leu Arg
                85                  90                  95

Met Phe Ser Cys Asp Ser Ser Ala Met Leu Trp Trp Lys Cys Glu His
            100                 105                 110

His Ser Leu Tyr Gly Ala Ala Arg Tyr Arg Leu Ala Leu Lys Asp Gly
        115                 120                 125

His Gly Thr Ala Ile Ser Asn Ala Ser Asp Val Trp Lys Lys Gly Gly
    130                 135                 140

Ser Glu Glu Ser Leu Cys Asp Gln Pro Tyr His Glu Ile Tyr Thr Arg
145                 150                 155                 160

Asp Gly Asn Ser Tyr Gly Arg Pro Cys Glu Phe Pro Phe Leu Ile Asp
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Gly Thr Trp His His Asp Cys Ile Leu Asp Glu Asp His Ser Gly Pro
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        195                 200                 205

Cys Leu Lys Pro Glu Asn Gly Cys Glu Asp Asn Trp Glu Lys Asn Glu
    210                 215                 220

Gln Phe Gly Ser Cys Tyr Gln Phe Asn Thr Gln Thr Ala Leu Ser Trp
225                 230                 235                 240

Lys Glu Ala Tyr Val Ser Cys Gln Asn Gln Gly Ala Asp Leu Leu Ser
                245                 250                 255

Ile Asn Ser Ala Ala Glu Leu Thr Tyr Leu Lys Glu Lys Glu Gly Ile
            260                 265                 270

Ala Lys Ile Phe Trp Ile Gly Leu Asn Gln Leu Tyr Ser Ala Arg Gly
        275                 280                 285

Trp Glu Trp Ser Asp His Lys Pro Leu Asn Phe Leu Asn Trp Asp Pro
    290                 295                 300

Asp Arg Pro Ser Ala Pro Thr Ile Gly Gly Ser Ser Cys Ala Arg Met
305                 310                 315                 320

Asp Ala Glu Ser Gly Leu Trp Gln Ser Phe Ser Cys Glu Ala Gln Leu
                325                 330                 335

Pro Tyr Val Cys Arg Lys Pro Leu Asn Asn Thr Val Glu Leu Thr Asp
            340                 345                 350

Val Trp Thr Tyr Ser Asp Thr Arg Cys Asp Ala Gly Trp Leu Pro Asn
        355                 360                 365

Asn Gly Phe Cys Tyr Leu Leu Val Asn Glu Ser Asn Ser Trp Asp Lys
    370                 375                 380

Ala His Ala Lys Cys Lys Ala Phe Ser Ser Asp Leu Ile Ser Ile His
385                 390                 395                 400

Ser Leu Ala Asp Val Glu Val Val Val Thr Lys Leu His Asn Glu Asp
                405                 410                 415

Ile Lys Glu Glu Val Trp Ile Gly Leu Lys Asn Ile Asn Ile Pro Thr
            420                 425                 430

Leu Phe Gln Trp Ser Asp Gly Thr Glu Val Thr Leu Thr Tyr Trp Asp
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Glu Asn Glu Pro Asn Val Pro Tyr Asn Lys Thr Pro Asn Cys Val Ser
    450                 455                 460

Tyr Leu Gly Glu Leu Gly Gln Trp Lys Val Gln Ser Cys Glu Glu Lys
465                 470                 475                 480

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

Ser Asp Lys Met Cys Pro Pro Asp Glu Gly Trp Lys Arg His Gly Glu
            500                 505                 510

Thr Cys Tyr Lys Ile Tyr Glu Asp Glu Val Pro Phe Gly Thr Asn Cys
        515                 520                 525

Asn Leu Thr Ile Thr Ser Arg Phe Glu Gln Glu Tyr Leu Asn Asp Leu
    530                 535                 540

Met Lys Lys Tyr Asp Lys Ser Leu Arg Lys Tyr Phe Trp Thr Gly Leu
545                 550                 555                 560

Arg Asp Val Asp Ser Cys Gly Glu Tyr Asn Trp Ala Thr Val Gly Gly
                565                 570                 575

Arg Arg Arg Ala Val Thr Phe Ser Asn Trp Asn Phe Leu Glu Pro Ala
            580                 585                 590

Ser Pro Gly Gly Cys Val Ala Met Ser Thr Gly Lys Ser Val Gly Lys
        595                 600                 605

Trp Glu Val Lys Asp Cys Arg Ser Phe Lys Ala Leu Ser Ile Cys Lys
    610                 615                 620

Lys Met Ser Gly Pro Leu Gly Pro Glu Glu Ala Ser Pro Lys Pro Asp
625                 630                 635                 640

Asp Pro Cys Pro Glu Gly Trp Gln Ser Phe Pro Ala Ser Leu Ser Cys
                645                 650                 655

Tyr Lys Val Phe His Ala Glu Arg Ile Val Arg Lys Arg Asn Trp Glu
            660                 665                 670

Glu Ala Glu Arg Phe Cys Gln Ala Leu Gly Ala His Leu Ser Ser Phe
        675                 680                 685

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

Phe Ser Gly Gln His Trp Leu Trp Ile Gly Leu Asn Lys Arg Ser Pro
705                 710                 715                 720
```

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Asp Leu Gln Gly Ser Trp Gln Trp Ser Asp Arg Thr Pro Val Ser Thr
                725                 730                 735

Ile Ile Met Pro Asn Glu Phe Gln Gln Asp Tyr Asp Ile Arg Asp Cys
            740                 745                 750

Ala Ala Val Lys Val Phe His Arg Pro Trp Arg Arg Gly Trp His Phe
        755                 760                 765

Tyr Asp Asp Arg Glu Phe Ile Tyr Leu Arg Pro Phe Ala Cys Asp Thr
    770                 775                 780

Lys Leu Glu Trp Val Cys Gln Ile Pro Lys Gly Arg Thr Pro Lys Thr
785                 790                 795                 800

Pro Asp Trp Tyr Asn Pro Asp Arg Ala Gly Ile His Gly Pro Pro Leu
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Ile Ile Glu Gly Ser Glu Tyr Trp Phe Val Ala Asp Leu His Leu Asn
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Tyr Glu Glu Ala Val Leu Tyr Cys Ala Ser Asn His Ser Phe Leu Ala
        835                 840                 845

Thr Ile Thr Ser Phe Val Gly Leu Lys Ala Ile Lys Asn Lys Ile Ala
    850                 855                 860

Asn Ile Ser Gly Asp Gly Gln Lys Trp Trp Ile Arg Ile Ser Glu Trp
865                 870                 875                 880

Pro Ile Asp Asp His Phe Thr Tyr Ser Arg Tyr Pro Trp His Arg Phe
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Pro Val Thr Phe Gly Glu Glu Cys Leu Tyr Met Ser Ala Lys Thr Trp
            900                 905                 910

Leu Ile Asp Leu Gly Lys Pro Thr Asp Cys Ser Thr Lys Leu Pro Phe
        915                 920                 925

Ile Cys Glu Lys Tyr Asn Val Ser Ser Leu Glu Lys Tyr Ser Pro Asp
    930                 935                 940

Ser Ala Ala Lys Val Gln Cys Ser Glu Gln Trp Ile Pro Phe Gln Asn
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Glu Thr  Asn Gly Gln Leu Glu  Asp Cys Val Val Leu  Asp Thr Asp
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Gly Phe  Trp Lys Thr Val Asp  Cys Asn Asp Asn Gln  Pro Gly Ala
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Ile Cys  Tyr Tyr Ser Gly Asn  Glu Thr Glu Lys Glu  Val Lys Pro
    1220                 1225                 1230

Val Asp  Ser Val Lys Cys Pro  Ser Pro Val Leu Asn  Thr Pro Trp
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Met Val  Asp Tyr Lys Glu Glu  His Asn Thr Thr Leu  Pro Gln Phe
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Met Pro  Tyr Glu Asp Gly Ile  Tyr Ser Val Ile Gln  Lys Lys Val
    1400                1405                1410

Thr Trp  Tyr Glu Ala Leu Asn  Met Cys Ser Gln Ser  Gly Gly His
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Ile Val  Lys Arg Asp Gly Phe  Pro Leu Trp Val Gly  Leu Ser Ser
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Gly Gly  Leu Ile Trp Phe Leu  Phe Gln Arg His Arg  Leu His Leu
    1685                1690                1695

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Ser Ile Tyr Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
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Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
85 90 95

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

Tyr Tyr Cys Ala Arg Ala Pro His Phe Asp Tyr Trp Gly Gln Gly Thr
115 120 125

Leu Val Thr Val Ser Ser
130

<210> 4
<211> 115
<212> PRT
<213> Homo sapiens

<400> 4
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

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

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

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

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

Val Ser Ser
115

<210> 5
<211> 5
<212> PRT
<213> Homo sapiens

<400> 5
Ile Tyr Gly Met His
1 5

<210> 6
<211> 17
<212> PRT
<213> Homo sapiens

<400> 6
Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 7
<211> 6
<212> PRT
<213> Homo sapiens

<400> 7
Ala Pro His Phe Asp Tyr
1 5

<210> 8
<211> 384
<212> DNA
<213> Homo sapiens

<400> 8
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atccagatga cccagtctcc atcctcactg tctgcatctg ttggagacag agtcaccatc 120

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aaagccccta agtccctgat ctatgctgca tccagtttgc aaagtggggt cccatcaagg 240

ttcagcggca gtggatctgg gacagatttc actctcacca tcagcagcct gcagcctgaa 300

gattttgcaa cttattactg ccaacagtat aatagttacc cgtacacttt tggccagggg 360

accaagctgg agatcaaacg tacg 384

<210> 9
<211> 129
<212> PRT
<213> Homo sapiens

<400> 9
Met Asp Met Arg Val Leu Ala Gln Leu Leu Gly Leu Leu Leu Leu Cys
1 5 10 15

Phe Pro Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
20 25 30

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

Gln Gly Ile Ser Ser Trp Leu Ala Trp Tyr Gln Gln Lys Pro Glu Lys
50 55 60

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

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

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

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

Lys

<210> 10
<211> 107
<212> PRT
<213> Homo sapiens

<400> 10
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

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

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

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

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

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

<210> 11
<211> 11
<212> PRT
<213> Homo sapiens

<400> 11
Arg Ala Ser Gln Gly Ile Ser Ser Trp Leu Ala
1 5 10

<210> 12
<211> 7
<212> PRT
<213> Homo sapiens

<400> 12
Ala Ala Ser Ser Leu Gln Ser
1 5

<210> 13
<211> 9
<212> PRT
<213> Homo sapiens

<400> 13
Gln Gln Tyr Asn Ser Tyr Pro Tyr Thr
1 5

<210> 14
<211> 439
<212> DNA
<213> Homo sapiens

<400> 14
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gtgcagctgg tggagtctgg gggaggcgtg gtccagcctg ggaggtccct gagactctcc 120

tgtgcagcgt ctggattcat cttcagtatc tatggcatgc actgggtccg ccaggctcca 180

ggcaaggggc tggagtgggt ggcagttata tggtatgatg gaagtaataa atactatgca 240

gactccgtga agggccgatt caccatctcc agagacaatt ccaagaacac gctgtatctg 300

caaatgaaca gcctgagagc cgaggacacg gctgtgtatt actgtgcgag agctcctcac 360

tttgactact ggggccaggg aaccctggtc accgtctcct cagcctccac caagggccca 420

tcggtcttcc ccctggcac 439

<210> 15
<211> 134

<212> PRT
<213> Homo sapiens

<400> 15
Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Leu Leu Arg Gly
1 5 10 15

Val Gln Cys Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln
20 25 30

Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ile Phe
35 40 45

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

Glu Trp Val Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala
65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
85 90 95

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

Tyr Tyr Cys Ala Arg Ala Pro His Phe Asp Tyr Trp Gly Gln Gly Thr
115 120 125

Leu Val Thr Val Ser Ser
130

<210> 16
<211> 115
<212> PRT
<213> Homo sapiens

<400> 16
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

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

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

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

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

Val Ser Ser
115

<210> 17
<211> 5
<212> PRT
<213> Homo sapiens

<400> 17
Ile Tyr Gly Met His
1 5

<210> 18
<211> 17
<212> PRT
<213> Homo sapiens

<400> 18
Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 19
<211> 6
<212> PRT
<213> Homo sapiens

<400> 19
Ala Pro His Phe Asp Tyr
1 5

<210> 20
<211> 387
<212> DNA
<213> Homo sapiens

<400> 20
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agatgtgcca tccagttgac ccagtctcca tcctccctgt ctgcatctgt aggagacaga 120

gtcaccatca cttgccgggc aagtcagggc attagcagtg ctttagcctg gtatcagcag 180

aaaccaggga aagctcctaa gctcctgatc tatgatgcct ccagtttgga aagtggggtc 240

ccatcaaggt tcagcggcag tggatctggg acagatttca ctctcaccat cagcagcctg 300

cagcctgaag attttgcaac ttattactgt caacagttta atagttaccc tctcactttc 360

ggcggaggga ccaaggtgga gatcaaa 387

<210> 21
<211> 129
<212> PRT
<213> Homo sapiens

<400> 21
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

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

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

Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
50 55 60

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

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

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

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

Lys

<210> 22
<211> 107
<212> PRT
<213> Homo sapiens

<400> 22
Ala Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

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

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

Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

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

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

<210> 23
<211> 11
<212> PRT
<213> Homo sapiens

<400> 23
Arg Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala
1 5 10

<210> 24
<211> 7
<212> PRT
<213> Homo sapiens

<400> 24
Asp Ala Ser Ser Leu Glu Ser
1 5

<210> 25
<211> 9
<212> PRT
<213> Homo sapiens

<400> 25
Gln Gln Phe Asn Ser Tyr Pro Leu Thr
1 5

<210> 26
<211> 417
<212> DNA
<213> Homo sapiens

<400> 26
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gtgcagctgg tggagtctgg gggaggcgtg gtccagcctg ggaggtccct gagactctcc 120

tgtgcagcgt ctggattcac cttcagtaat tatggcatgt actgggtccg ccaggctcca 180

ggcaaggggc tggagtgggt ggcagttata tggtatgatg gaagtaataa atactatgca 240

gactccgtga agggccgatt caccatctcc agagacaatt ccaagaacac gctgtatctg 300

caaatgaaca gcctgagagc cgaggacacg gctgtgtatt actgtgcgag agatctctgg 360

ggatggtact ttgactattg gggccaggga accctggtca ccgtctcctc agctagc 417

<210> 27
<211> 149
<212> PRT
<213> Homo sapiens

<400> 27
Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Leu Leu Arg Gly
1 5 10 15

Val Gln Cys Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln
20 25 30

Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

```
Ser Asn Tyr Gly Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
    50                  55                  60

Glu Trp Val Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala
65                  70                  75                  80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
                85                  90                  95

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

Tyr Tyr Cys Ala Arg Asp Leu Trp Gly Trp Tyr Phe Asp Tyr Trp Gly
        115                 120                 125

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

Val Phe Pro Leu Ala
145
```

<210> 28
<211> 130
<212> PRT
<213> Homo sapiens

<400> 28

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

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

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

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

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

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

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

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
        115                 120                 125

Leu Ala
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130

<210> 29
<211> 5
<212> PRT
<213> Homo sapiens

<400> 29
Asn Tyr Gly Met Tyr
1 5

<210> 30
<211> 17
<212> PRT
<213> Homo sapiens

<400> 30
Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 31
<211> 9
<212> PRT
<213> Homo sapiens

<400> 31
Asp Leu Trp Gly Trp Tyr Phe Asp Tyr
1 5

<210> 32
<211> 384
<212> DNA
<213> Homo sapiens

<400> 32
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attgtgttga cacagtctcc agccaccctg tctttgtctc caggggaaag agccaccctc 120

tcctgcaggg ccagtcagag tgttagcagc tacttagcct ggtaccaaca gaaacctggc 180

caggctccca ggctcctcat ctatgatgca tccaacaggg ccactggcat cccagccagg 240

ttcagtggca gtgggtctgg gacagacttc actctcacca tcagcagcct agagcctgaa 300

gattttgcag tttattactg tcagcagcgt cgcaactggc cgctcacttt cggcggaggg 360

accaaggtgg agatcaaacg tacg 384

<210> 33
<211> 127
<212> PRT
<213> Homo sapiens

<400> 33
Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

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

```
            20                  25                  30

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

Val Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
    50                  55                  60

Arg Leu Leu Ile Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala
65                  70                  75                  80

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

Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Arg
            100                 105                 110

Asn Trp Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
        115                 120                 125


<210> 34
<211> 107
<212> PRT
<213> Homo sapiens

<400> 34
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1               5                   10                  15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
            20                  25                  30

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

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
    50                  55                  60

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

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Arg Asn Trp Pro Leu
                85                  90                  95

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


<210> 35
<211> 11
<212> PRT
<213> Homo sapiens

<400> 35
Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala
1               5                   10
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<210> 36
<211> 7
<212> PRT
<213> Homo sapiens

<400> 36
Asp Ala Ser Asn Arg Ala Thr
1 5

<210> 37
<211> 9
<212> PRT
<213> Homo sapiens

<400> 37
Gln Gln Arg Arg Asn Trp Pro Leu Thr
1 5

<210> 38
<211> 447
<212> DNA
<213> Homo sapiens

<400> 38
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gtgcagctgg tggagtctgg gggaggcgtg gtccagcctg ggaggtccct gagactctcc 120

tgtgcagcgt ctggattcac cttcagtacc tatggcatgc actgggtccg ccaggctcca 180

ggcaaggggc tggagtgggt ggcaattata tggtatgatg gaggtaataa atactatgca 240

gactccgtga agggccgatt caccatctcc agagacaatt ccaagaacac gctgtatctg 300

caaatgaaca gcctgagagc cgaggacacg gctgtgtatt actgtgcgag agacttctac 360

tggtacttcg atctctgggg ccgtggcacc ctggtcactg tctcctcagc ctccaccaag 420

ggcccatcgg tcttccccct ggcaagg 447

<210> 39
<211> 148
<212> PRT
<213> Homo sapiens

<400> 39
Met Glu Phe Gly Leu Thr Trp Val Phe Leu Val Ala Leu Leu Arg Gly
1 5 10 15

Val Gln Cys Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln
20 25 30

Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

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

Glu Trp Val Ala Ile Ile Trp Tyr Asp Gly Gly Asn Lys Tyr Tyr Ala
65 70 75 80

```
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
                85                  90                  95

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

Tyr Tyr Cys Ala Arg Asp Phe Tyr Trp Tyr Phe Asp Leu Trp Gly Arg
        115                 120                 125

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

Phe Pro Leu Ala
145
```

<210> 40
<211> 129
<212> PRT
<213> Homo sapiens

<400> 40

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

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

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

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

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

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

Ala Arg Asp Phe Tyr Trp Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu
            100                 105                 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
        115                 120                 125

Ala
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<210> 41
<211> 5
<212> PRT
<213> Homo sapiens

<400> 41
Thr Tyr Gly Met His
1 5

<210> 42
<211> 17
<212> PRT
<213> Homo sapiens

<400> 42
Ile Ile Trp Tyr Asp Gly Gly Asn Lys Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 43
<211> 8
<212> PRT
<213> Homo sapiens

<400> 43
Asp Phe Tyr Trp Tyr Phe Asp Leu
1 5

<210> 44
<211> 372
<212> DNA
<213> Homo sapiens

<400> 44
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gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 120

ctctcctgca gggccagtca gagtgttagc agctacttag cctggtacca acagaaacct 180

ggccaggctc ccaggctcct catctatgat gcatccaaca gggccactgg catcccagcc 240

aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag cctagagcct 300

gaagattttg cagtttatta ctgtcagcag cgtaggacgt tcggccaagg gaccaaggtg 360

gaaatcaaac ga 372

<210> 45
<211> 123
<212> PRT
<213> Homo sapiens

<400> 45
Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

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

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

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

```
    50                  55                  60

Arg Leu Leu Ile Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala
65                  70                  75                  80

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

Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Arg
            100                 105                 110

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
        115                 120


<210> 46
<211> 103
<212> PRT
<213> Homo sapiens

<400> 46
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1               5                   10                  15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
            20                  25                  30

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

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
    50                  55                  60

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

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Arg Thr Phe Gly Gln
                85                  90                  95

Gly Thr Lys Val Glu Ile Lys
            100


<210> 47
<211> 11
<212> PRT
<213> Homo sapiens

<400> 47
Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala
1               5                   10


<210> 48
<211> 7
<212> PRT
<213> Homo sapiens

<400> 48
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Asp Ala Ser Asn Arg Ala Thr
1 5

<210> 49
<211> 5
<212> PRT
<213> Homo sapiens

<400> 49
Gln Gln Arg Arg Thr
1 5

<210> 50
<211> 454
<212> DNA
<213> Homo sapiens

<400> 50
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gtgcagctgg tggagtctgg gggaggcgtg gtccagcctg ggaggtccct gagactctcc 120

tgtgcagcgt ctggattcac cttcagtagc tataacatgc actgggtccg ccaggctcca 180

ggcaaggggc tggagtgggt ggcatttata tggtatgatg gaagtaataa atactatgga 240

gactccgtga agggccgatt caccatctcc agagacaatt ccaaaaacac gctgtatctg 300

caaatgaaca gcctgagagc cgaggacacg gctgtgtatt actgtgcgag agaagagctg 360

gggatcgggt ggtacttcga tctctggggc cgtggcaccc tggtcactgt ctcctcagcc 420

tccaccaagg gcccatcggt cttccccctg gcac 454

<210> 51
<211> 151
<212> PRT
<213> Homo sapiens

<400> 51
Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Leu Leu Arg Gly
1 5 10 15

Val Gln Cys Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln
20 25 30

Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

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

Glu Trp Val Ala Phe Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Gly
65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
85 90 95

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

```
Tyr Tyr Cys Ala Arg Glu Glu Leu Gly Ile Gly Trp Tyr Phe Asp Leu
        115                 120                 125


Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
    130                 135                 140


Pro Ser Val Phe Pro Leu Ala
145                 150


<210> 52
<211> 132
<212> PRT
<213> Homo sapiens

<400> 52
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1               5                   10                  15


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


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


Ala Phe Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Gly Asp Ser Val
    50                  55                  60


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


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


Ala Arg Glu Glu Leu Gly Ile Gly Trp Tyr Phe Asp Leu Trp Gly Arg
            100                 105                 110


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


Phe Pro Leu Ala
    130


<210> 53
<211> 5
<212> PRT
<213> Homo sapiens

<400> 53
Ser Tyr Asn Met His
1               5


<210> 54
<211> 17
<212> PRT
```

<213> Homo sapiens

<400> 54
Phe Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Gly Asp Ser Val Lys
1               5                   10                  15

Gly

<210> 55
<211> 11
<212> PRT
<213> Homo sapiens

<400> 55
Glu Glu Leu Gly Ile Gly Trp Tyr Phe Asp Leu
1               5                   10

<210> 56
<211> 454
<212> DNA
<213> Homo sapiens

<400> 56
atggaagccc cagctcagct tctcttcctc ctgctactct ggctcccaga taccaccgga 60

gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 120

ctctcctgca gggccagtca gagtgttagc agctacttag cctggtacca acagaaacct 180

ggccaggctc ccaggctcct catctatgat gcatccaaca gggccactgg catcccagcc 240

aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag cctagagcct 300

gaagattttg cagtttatta ctgtcagcag cgtaggacgt tcggccaagg gaccaaggtg 360

gaaatcaaac gaactgtggc tgcaccatct gtcttcatct tcccgccatc tgatgagcag 420

ttgaaatctg gaactgcctc tgttgtgtgc ctgc 454

<210> 57
<211> 123
<212> PRT
<213> Homo sapiens

<400> 57
Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1               5                   10                  15

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

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

Val Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
    50                  55                  60

Arg Leu Leu Ile Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala
65                  70                  75                  80

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

Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Arg
            100                 105                 110

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
        115                 120
```

<210> 58
<211> 103
<212> PRT
<213> Homo sapiens

<400> 58

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
            20                  25                  30

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

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
    50                  55                  60

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

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Arg Thr Phe Gly Gln
                85                  90                  95

Gly Thr Lys Val Glu Ile Lys
            100
```

<210> 59
<211> 11
<212> PRT
<213> Homo sapiens

<400> 59

```
Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala
1               5                   10
```

<210> 60
<211> 7
<212> PRT
<213> Homo sapiens

<400> 60

```
Asp Ala Ser Asn Arg Ala Thr
1               5
```

<210> 61
<211> 5

<212> PRT
<213> Homo sapiens

<400> 61
Gln Gln Arg Arg Thr
1 5

<210> 62
<211> 433
<212> DNA
<213> Homo sapiens

<400> 62
atggagtttg tgctgagctg ggttctcctt gttgctatat taaaaggtgt ccagtgtgag 60

gttcagctgg tgcagtctgg gggaggcttg gtacatcctg gggggtccct gagactctcc 120

tgtgcaggct ctggattcac cttcagtaac tatgctatgc actgggttcg ccaggctcca 180

ggaaaaggtc tggagtgggt atcaactatt ggtactggtg gtggcacacc ctatgcagac 240

tccgtgaagg gccgcttcac catctccaga gacaatgcca agaactcctt gtatcttcaa 300

atgaacagcc tgagagccga ggacatggct gtgtattact gtgcattaag tgcttttgat 360

gtctggggcc aagggacaat ggtcaccgtc tcttcagcct ccaccaaggg cccatcggtc 420

ttcccccctgg cac 433

<210> 63
<211> 144
<212> PRT
<213> Homo sapiens

<400> 63
Met Glu Phe Val Leu Ser Trp Val Leu Leu Val Ala Ile Leu Lys Gly
1 5 10 15

Val Gln Cys Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His
20 25 30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe
35 40 45

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

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

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser
85 90 95

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

Tyr Cys Ala Leu Ser Ala Phe Asp Val Trp Gly Gln Gly Thr Met Val
115 120 125

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

<210> 64
<211> 125
<212> PRT
<213> Homo sapiens

<400> 64
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
1 5 10 15

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

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

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

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
65 70 75 80

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

Leu Ser Ala Phe Asp Val Trp Gly Gln Gly Thr Met Val Thr Val Ser
100 105 110

Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
115 120 125

<210> 65
<211> 5
<212> PRT
<213> Homo sapiens

<400> 65
Asn Tyr Ala Met His
1 5

<210> 66
<211> 16
<212> PRT
<213> Homo sapiens

<400> 66
Thr Ile Gly Thr Gly Gly Gly Thr Pro Tyr Ala Asp Ser Val Lys Gly
1 5 10 15

<210> 67
<211> 5
<212> PRT
<213> Homo sapiens

<400> 67
Ser Ala Phe Asp Val

1 5

<210> 68
<211> 466
<212> DNA
<213> Homo sapiens

<400> 68
atggagtttg tgctgagctg ggttttcctt gttgctatat taaaaggtgt ccagtgtgag 60

gttcagctgg tgcagtctgg gggaggcttg gtacatcctg gggggtccct gagactctcc 120

tgtgcaggct ctggattcac cttcagtagc tatgctatgc actgggttcg ccaggctcca 180

ggaaaaggtc tggagtgggt atcagctatt ggtactggtg gttacacata ctatgtagac 240

tccgtgaagg gccgattcac catctccaga gacaatgcca agaagtcctt gtatcttcaa 300

atgaacagcc tgagagccga ggacatggct gtgtattact gtgcaagaga gccgttttac 360

gatattttga ctggttattc cccatacttt gactactggg gccagggaac cctggtcacc 420

gtctcctcag cctccaccaa gggcccatcg gtcttccccc tggcac 466

<210> 69
<211> 143
<212> PRT
<213> Homo sapiens

<400> 69
Met Glu Phe Val Leu Ser Trp Val Phe Leu Val Ala Ile Leu Lys Gly
1 5 10 15

Val Gln Cys Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His
20 25 30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe
35 40 45

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

Glu Trp Val Ser Ala Ile Gly Thr Gly Gly Tyr Thr Tyr Tyr Val Asp
65 70 75 80

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Lys Ser
85 90 95

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

Tyr Cys Ala Arg Glu Pro Phe Tyr Asp Ile Leu Thr Gly Tyr Ser Pro
115 120 125

Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
130 135 140

<210> 70

<211> 124
<212> PRT
<213> Homo sapiens

<400> 70
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
1 5 10 15

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

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

Ser Ala Ile Gly Thr Gly Gly Tyr Thr Tyr Tyr Val Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Lys Ser Leu Tyr Leu
65 70 75 80

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

Arg Glu Pro Phe Tyr Asp Ile Leu Thr Gly Tyr Ser Pro Tyr Phe Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 71
<211> 5
<212> PRT
<213> Homo sapiens

<400> 71
Ser Tyr Ala Met His
1 5

<210> 72
<211> 16
<212> PRT
<213> Homo sapiens

<400> 72
Ala Ile Gly Thr Gly Gly Tyr Thr Tyr Tyr Val Asp Ser Val Lys Gly
1 5 10 15

<210> 73
<211> 16
<212> PRT
<213> Homo sapiens

<400> 73
Glu Pro Phe Tyr Asp Ile Leu Thr Gly Tyr Ser Pro Tyr Phe Asp Tyr
1 5 10 15

<210> 74
<211> 454

<212> DNA
<213> Homo sapiens

<400> 74
atggagtttg ggctgagctg ggttttcctc gttgctcttt taagaggtgt ccagtgtcag 60

gtgcagctgg tggagtctgg gggaggcgtg gtccagcctg ggaggtccct gagactctcc 120

tgtgcagcgt ctggattcac cttcagtagc tataacatgc actgggtccg ccaggctcca 180

ggcaaggggc tggagtgggt ggcagttata tggtatgatg gaagtaataa atactatgga 240

gactccgtga agggccgatt caccatctcc agagacaatt ccaagaacac gctgtatctg 300

caaatgaaca gcctgagagc cgaggacacg gctgtgtatt actgtgcgag agaagagctg 360

gggatcgggt ggtacttcga tctctggggc cgtggcaccc tggtcactgt ctcctcagcc 420

tccaccaagg gcccatcggt cttccccctg gcac 454

<210> 75
<211> 139
<212> PRT
<213> Homo sapiens

<400> 75
Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Leu Leu Arg Gly
1 5 10 15

Val Gln Cys Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln
20 25 30

Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

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

Glu Trp Val Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Gly
65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
85 90 95

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

Tyr Tyr Cys Ala Arg Glu Glu Leu Gly Ile Gly Trp Tyr Phe Asp Leu
115 120 125

Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser
130 135

<210> 76
<211> 120
<212> PRT
<213> Homo sapiens

<400> 76

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

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

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

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

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

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

Ala Arg Glu Glu Leu Gly Ile Gly Trp Tyr Phe Asp Leu Trp Gly Arg
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 77
<211> 5
<212> PRT
<213> Homo sapiens

<400> 77
```
Ser Tyr Asn Met His
1               5
```

<210> 78
<211> 17
<212> PRT
<213> Homo sapiens

<400> 78
```
Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Gly Asp Ser Val Lys
1               5                   10                  15

Gly
```

<210> 79
<211> 11
<212> PRT
<213> Homo sapiens

<400> 79
```
Glu Glu Leu Gly Ile Gly Trp Tyr Phe Asp Leu
1               5                   10
```

<210> 80
<211> 475
<212> DNA

<213> Homo sapiens

<400> 80
atggacatga gggtccccgc tcagctcctg gggcttctgc tgctctggct cccaggtgcc 60

agatgtgcca tccagttgac ccagtctcca tcctccctgt ctgcatctgt aggagacaga 120

gtcaccatca cttgccgggc aagtcagggc attagcagtg ctttagcctg gtatcagcag 180

aaaccaggga aagctcctaa gctcctgatc tatgatgcct ccagtttgga aagtggggtc 240

ccatcaaggt tcagcggcag tggatctggg acagatttca ctctcaccat cagcagcctg 300

cagcctgaag attttgcaac ttattactgt caacagttta atagttaccc tcacttcggc 360

caagggacac gactggagat taaacgaact gtggctgcac catctgtctt catcttcccg 420

ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgca agggc 475

<210> 81
<211> 128
<212> PRT
<213> Homo sapiens

<400> 81
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

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

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

Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
50 55 60

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

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

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

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

<210> 82
<211> 106
<212> PRT
<213> Homo sapiens

<400> 82
Ala Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

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

20 25 30

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

Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

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

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

<210> 83
<211> 11
<212> PRT
<213> Homo sapiens

<400> 83
Arg Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala
1 5 10

<210> 84
<211> 7
<212> PRT
<213> Homo sapiens

<400> 84
Asp Ala Ser Ser Leu Glu Ser
1 5

<210> 85
<211> 8
<212> PRT
<213> Homo sapiens

<400> 85
Gln Gln Phe Asn Ser Tyr Pro His
1 5

<210> 86
<211> 445
<212> DNA
<213> Homo sapiens

<400> 86
atggagtttg ggctgagctg ggttttcctc gttgctcttt taagaggtgt ccagtgtcag 60

gtgcagctgg tggagtctgg gggaggcgtg gtccagcctg ggaggtccct gagactctcc 120

tgtgcagcgt ctggattcac cttcagtagc tatggcatgc actgggtccg ccaggctcca 180

ggcaaggggc tggagtgggt ggcagttata tggtatgatg gaagtaataa atactatgca 240

gactccgtga agggccgatt caccatctcc agagacaatt ccaagaacac gctgtatctg 300

caaatgaaca gcctgagagc cgaggacacg gctgtgtatt actgtgcgag aggccccccct 360

cggtacttcg atctctgggg ccgtggcacc ctggtcactg tctcctcagc ctccaccaag 420

ggcccatcgg tcttcccccct ggcac 445

<210> 87
<211> 136
<212> PRT
<213> Homo sapiens

<400> 87
Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Leu Leu Arg Gly
1 5 10 15

Val Gln Cys Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln
20 25 30

Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

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

Glu Trp Val Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala
65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
85 90 95

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

Tyr Tyr Cys Ala Arg Gly Pro Pro Arg Tyr Phe Asp Leu Trp Gly Arg
115 120 125

Gly Thr Leu Val Thr Val Ser Ser
130 135

<210> 88
<211> 117
<212> PRT
<213> Homo sapiens

<400> 88
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

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

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

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

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

Val Thr Val Ser Ser
115

<210> 89
<211> 5
<212> PRT
<213> Homo sapiens

<400> 89
Ser Tyr Gly Met His
1 5

<210> 90
<211> 17
<212> PRT
<213> Homo sapiens

<400> 90
Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 91
<211> 8
<212> PRT
<213> Homo sapiens

<400> 91
Gly Pro Pro Arg Tyr Phe Asp Leu
1 5

<210> 92
<211> 95
<212> PRT
<213> Homo sapiens

<400> 92
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
20 25 30

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

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

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

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro
85 90 95

<210> 93
<211> 95
<212> PRT
<213> Homo sapiens

<400> 93
Ala Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

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

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

Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

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

<210> 94
<211> 95
<212> PRT
<213> Homo sapiens

<400> 94
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 Arg Gln Gly Ile Ser Ser Trp
20 25 30

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

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

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

<210> 95
<211> 98
<212> PRT
<213> Homo sapiens

<400> 95
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu 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

<210> 96
<211> 97
<212> PRT
<213> Homo sapiens

<400> 96
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
1 5 10 15

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

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

Ser Ala Ile Gly Thr Gly Gly Gly Thr Tyr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
65 70 75 80

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

Arg

<210> 97
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<221> source
<223> /note="Description of artificial sequence: Synthetic
consensus sequence"

<220>
<221> VARIANT
<222> (1)..(1)
<223> /replace="Asn" or "Thr" or "Ser"

<220>
<221> misc_feature
<222> (1)..(1)
<223> /note="Residue given in the sequence has no preference
with respect to those in the annotation for said position"

<220>
<221> VARIANT
<222> (3)..(3)
<223> /replace="Asn" or "Ala"

<220>
<221> misc_feature
<222> (3)..(3)
<223> /note="Residue given in the sequence has no preference
with respect to those in the annotation for said position"

<220>
<221> VARIANT
<222> (5)..(5)
<223> /replace="Tyr"

<220>
<221> misc_feature
<222> (5)..(5)
<223> /note="Residue given in the sequence has no preference
with respect to those in the annotation for said position"

<400> 97
Ile Tyr Gly Met His
1 5

<210> 98
<211> 17
<212> PRT
<213> Artificial sequence

<220>
<221> source
<223> /note="Description of artificial sequence: Synthetic
consensus sequence"

<220>
<221> VARIANT
<222> (1)..(1)
<223> /replace="Ile" or "Phe" or "Thr" or "Ala"

<220>

<221> misc_feature
<222> (1)..(1)
<223> /note="Residue given in the sequence has no preference
with respect to those in the annotation for said position"

<220>
<221> VARIANT
<222> (3)..(3)
<223> /replace="Gly"

<220>
<221> VARIANT
<222> (4)..(4)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (5)..(5)
<223> /replace="Gly"

<220>
<221> misc_feature
<222> (3)..(5)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (7)..(7)
<223> /replace="Gly" or "Tyr"

<220>
<221> VARIANT
<222> (8)..(8)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (9)..(9)
<223> /replace="Pro"

<220>
<221> misc_feature
<222> (7)..(9)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (11)..(11)
<223> /replace="Ala" or "Val"

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Gly" or " "

<220>
<221> misc_feature
<222> (11)..(12)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<400> 98
Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 99
<211> 6
<212> PRT
<213> Artificial sequence

<220>
<221> source
<223> /note="Description of artificial sequence: Synthetic
consensus sequence"

<220>
<221> VARIANT
<222> (1)..(1)
<223> /replace="Gly" or "Tyr" or "Ser" or "Pro" or " "

<220>
<221> VARIANT
<222> (2)..(2)
<223> /replace="Trp" or "Ser" or "Arg"

<220>
<221> VARIANT
<222> (3)..(3)
<223> /replace="Ala" or "His"

<220>
<221> misc_feature
<222> (1)..(3)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (6)..(6)
<223> /replace="Leu" or "Val"

<220>
<221> misc_feature
<222> (6)..(6)
<223> /note="Residue given in the sequence has no preference
with respect to those in the annotation for said position"

<400> 99
Ala Pro Tyr Phe Asp Tyr
1 5

<210> 100
<211> 11
<212> PRT
<213> Artificial sequence

<220>
<221> source
<223> /note="Description of artificial sequence: Synthetic
consensus sequence"

<220>
<221> VARIANT
<222> (5)..(5)
<223> /replace="Gly"

<220>
<221> VARIANT

<222> (6)..(6)
<223> /replace="Val"

<220>
<221> misc_feature
<222> (5)..(6)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (9)..(9)
<223> /replace="Trp" or "Ala"

<220>
<221> misc_feature
<222> (9)..(9)
<223> /note="Residue given in the sequence has no preference
with respect to those in the annotation for said position"

<400> 100
Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Ala
1 5 10

<210> 101
<211> 7
<212> PRT
<213> Artificial sequence

<220>
<221> source
<223> /note="Description of artificial sequence: Synthetic
consensus sequence"

<220>
<221> VARIANT
<222> (1)..(1)
<223> /replace="Ala"

<220>
<221> misc_feature
<222> (1)..(1)
<223> /note="Residue given in the sequence has no preference
with respect to those in the annotation for said position"

<220>
<221> VARIANT
<222> (4)..(4)
<223> /replace="Ser"

<220>
<221> VARIANT
<222> (5)..(5)
<223> /replace="Leu"

<220>
<221> VARIANT
<222> (6)..(6)
<223> /replace="Gln" or "Glu"

<220>
<221> VARIANT
<222> (7)..(7)
<223> /replace="Ser"

<220>
<221> misc_feature

<222> (4)..(7)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<400> 101
Asp Ala Ser Asn Arg Ala Thr
1 5

<210> 102
<211> 9
<212> PRT
<213> Artificial sequence

<220>
<221> source
<223> /note="Description of artificial sequence: Synthetic
consensus sequence"

<220>
<221> VARIANT
<222> (3)..(3)
<223> /replace="Tyr" or "Phe"

<220>
<221> VARIANT
<222> (4)..(4)
<223> /replace="Asn"

<220>
<221> VARIANT
<222> (5)..(5)
<223> /replace="Ser" or "Asn"

<220>
<221> VARIANT
<222> (6)..(6)
<223> /replace="Trp" or " "

<220>
<221> VARIANT
<222> (7)..(7)
<223> /replace=" "

<220>
<221> VARIANT
<222> (8)..(8)
<223> /replace="Leu" or "His" or " "

<220>
<221> VARIANT
<222> (9)..(9)
<223> /replace=" "

<220>
<221> misc_feature
<222> (3)..(9)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<400> 102
Gln Gln Arg Arg Thr Tyr Pro Tyr Thr
1 5

<210> 103
<211> 118
<212> PRT

<213> Homo sapiens

<400> 103
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1               5                  10                  15

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

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

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

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

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

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

Leu Val Thr Val Ser Ser
        115

<210> 104
<211> 117
<212> PRT
<213> Homo sapiens

<400> 104
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1               5                  10                  15

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

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

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

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

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

Ala Arg Asp Phe Tyr Trp Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu
            100                 105                 110

Val Thr Val Ser Ser
115

<210> 105
<211> 120
<212> PRT
<213> Homo sapiens

<400> 105
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

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

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

Ala Phe Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Gly Asp Ser Val
50 55 60

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

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

Ala Arg Glu Glu Leu Gly Ile Gly Trp Tyr Phe Asp Leu Trp Gly Arg
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 106
<211> 113
<212> PRT
<213> Homo sapiens

<400> 106
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
1 5 10 15

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

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

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

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala

85 90 95

Leu Ser Ala Phe Asp Val Trp Gly Gln Gly Thr Met Val Thr Val Ser
100 105 110

Ser