SEQUENCE LISTING

<110> Daiichi Sankyo Company, Limited
Mie University

<120> Bispecific Antibodies

<130> PH-8759-PCT

<150> JP 2020-061476
<151> 2020-03-30

<160> 198

<170> PatentIn version 3.5

<210> 1
<211> 9
<212> PRT
<213> Artificial

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<223> Peptide sequence of NY-ESO

<400> 1

Ser Leu Leu Met Trp Ile Thr Gln Cys
1 5

<210> 2
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<220>
<223> Peptide sequence of MAGEC-1

<400> 2

Ile Leu Phe Gly Ile Ser Leu Arg Glu Val
1 5 10

<210> 3
<211> 26
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<220>
<223> Primer for analyzing scFv sequence

<400> 3
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<210> 4
<211> 30
<212> DNA
<213> Artificial

<220>
<223> Primer for analyzing scFv sequence

<400> 4
ataacaattt cacacaggaa acagctatga 30

<210> 5
<211> 360
<212> DNA
<213> Artificial

<220>
<223> Nucleotide sequence of a heavy chain variable region of NYA-0001

<400> 5
gaggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgacaccc 60

tcctgttcag cgtctggatt ctccatccgt agttatgata tacactgggt ccgccaggct 120

ccaggcaagg ggctagagtg ggtggccact atatcatatg atggaagtca gaagtacttc 180

gcagactccg tgaagggccg atttaccatc ttcagagacg aatcggagaa catggtgtat 240

ctgcaaatga gcggcctgag agttgaggac acggctgttt atcactgtgc gagagggagt 300

agtggtcatt atgaggcttt tgatatctgg ggccaaggga caatggtcac cgtctcttca 360

<210> 6
<211> 120
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of a heavy chain variable region of NYA-0001

<400> 6

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

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

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

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

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

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

Ala Arg Gly Ser Ser Gly His Tyr Glu Ala Phe Asp Ile Trp Gly Gln
100 105 110

Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 7
<211> 333
<212> DNA
<213> Artificial

<220>
<223> Nucleotide sequence of a light chain variable region of NYA-0001

<400> 7
cagtctgtgt tgacgcagcc gccctcagtg tctgcggccc caggacagaa ggtcaccatc 60

tcctgctctg gaagcagctc caacattggg aataattatg tatcctggta ccagcagctc 120

ccaggaacag cccccaaact cctcatttat gacaataata agcgaccctc agggattcct 180

gaccgattct ctggctccaa gtctggcacg tcagccaccc tgggcatcac cggactccag 240

actggggacg aggccgatta ttactgcgga acatgggata gcagcctgag tgccccttgg 300

gtgttcggcg gagggaccaa ggtcaccgtc cta 333

<210> 8
<211> 111
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of a light chain variable region of NYA-0001

<400> 8

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

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Lys Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn
            20                  25                  30

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

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

Gly Ser Lys Ser Gly Thr Ser Ala Thr Leu Gly Ile Thr Gly Leu Gln
65                  70                  75                  80

Thr Gly Asp Glu Ala Asp Tyr Tyr Cys Gly Thr Trp Asp Ser Ser Leu
                85                  90                  95

Ser Ala Pro Trp Val Phe Gly Gly Gly Thr Lys Val Thr Val Leu
            100                 105                 110
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<210> 9
<211> 360
<212> DNA
<213> Artificial

<220>
<223> Nucleotide sequence of a heavy chain variable region of NYA-0060

<400> 9

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gaggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgacaccc       60

tcctgttcag cgtctggatt ctccatccgt agctatgata tacactgggt ccgcctggct      120

ccaggcaagg ggctagagtg ggtggccact atatcatatg atggaagtca gaagtacttc      180

gcagactccg tgaagggccg atttaccatc ttcagagacg aatcggagaa catggtgtat      240

ctgcaaatga gcggcctgag agttgaggac acggctgttt atcactgtgc gagagggagt      300
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agtggtcatt atgaggcttt tgatatctgg ggccaaggga caatggtcac cgtctcttca 360

<210> 10
<211> 120
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of a heavy chain variable region of NYA-0060

<400> 10

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

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

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

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

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

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

Ala Arg Gly Ser Ser Gly His Tyr Glu Ala Phe Asp Ile Trp Gly Gln
100 105 110

Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 11
<211> 333
<212> DNA
<213> Artificial

<220>
<223> Nucleotide sequence of a light chain variable region of NYA-0060

<400> 11
cagtctgtgt tgacgcagcc gccctcagtg tctgcggccc caggacagaa ggtcaccatc 60

tcctgctctg gaagcagctc caacattggg aataattatg tatcctggta ccagcagctc 120

ccaggaacag cccccaaact cctcatttat gacaataata agcgaccctc agggattcct 180

gaccgattct ctggctccaa gtctggcacg tcagccaccc tgggcatcac cggactccag 240

actggggacg aggccgatta ttactgcgga acatgggata gcagcctgag tgccccttgg 300

gtgttcggcg gagggaccaa ggtcaccgtc cta 333

<210> 12
<211> 111
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of a light chain variable region of NYA-0060

<400> 12

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

Lys Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn
20 25 30

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

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

Gly Ser Lys Ser Gly Thr Ser Ala Thr Leu Gly Ile Thr Gly Leu Gln
65 70 75 80

Thr Gly Asp Glu Ala Asp Tyr Tyr Cys Gly Thr Trp Asp Ser Ser Leu
85 90 95

Ser Ala Pro Trp Val Phe Gly Gly Gly Thr Lys Val Thr Val Leu
100 105 110

<210> 13
<211> 360
<212> DNA
<213> Artificial

<220>
<223> Nucleotide sequence of a heavy chain variable region of NYA-0068

<400> 13
gaggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgacaccc 60

tcctgttcag cgtctggatt ctccatccgt agttatgata tacactgggt ccgccaggct 120

ccaggcaagg ggctagagtg ggtggccact atatcatatg atggaagtca gaagtacttc 180

gcagactccg tgaagggccg atttaccatc ttcagagacg aatcggagaa catggtgtat 240

ctgcaaatga gcggcctgag agttgaggac acggctgttt atcactgtgc gagagggagt 300

agtggtcatt atgaggcttt tgatatctgg ggccaaggga caatggtcac cgtctcttca 360

<210> 14
<211> 120
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of a heavy chain variable region of NYA-0068

<400> 14

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

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

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

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

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

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

Ala Arg Gly Ser Ser Gly His Tyr Glu Ala Phe Asp Ile Trp Gly Gln
100 105 110

Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 15
<211> 333
<212> DNA
<213> Artificial

<220>
<223> Nucleotide sequence of a light chain variable region of NYA-0068

<400> 15
cagtctgtgt tgacgcagcc gccctcagtg tctgcggccc caggacagaa ggtcaccatc 60

tcctgctctg gaagcagctc caacattggg aattggtatg tatcctggta ccagcagctc 120

ccaggaacag cccccaaact cctcatttat gacaataata agcgaccctc agggattcct 180

gaccgattct ctggctccaa gtctggcacg tcagccaccc tgggcatcac cggactccag 240

actggggacg aggccgatta ttactgcgga acatgggata gcagcctgag tgccccttgg 300

gtgttcggcg gagggaccaa ggtcaccgtc cta 333

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

<220>
<223> Amino acid sequence of a light chain variable region of NYA-0068

<400> 16

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

Lys Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Trp
20 25 30

```
Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
        35                  40                  45

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

Gly Ser Lys Ser Gly Thr Ser Ala Thr Leu Gly Ile Thr Gly Leu Gln
65                  70                  75                  80

Thr Gly Asp Glu Ala Asp Tyr Tyr Cys Gly Thr Trp Asp Ser Ser Leu
                85                  90                  95

Ser Ala Pro Trp Val Phe Gly Gly Gly Thr Lys Val Thr Val Leu
            100                 105                 110
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<210> 17
<211> 360
<212> DNA
<213> Artificial

<220>
<223> Nucleotide sequence of a heavy chain variable region of NYA-0082

<400> 17

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gaggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgacaccc       60

tcctgttcag cgtctggatt ctccatccgt agttatgata tacactgggt ccgccaggct      120

ccaggcaagg ggctagagtg ggtggccact atatcatatg atggaagtca gaagtacttc      180

gcagactccg tgaagggccg atttaccatc ttcagagacg aatcggagaa catggtgtat      240

ctgcaaatga gcggcctgag agttgaggac acggctgttt atcactgtgc gagagggagt      300

agtggtcatt atgaggcttt tgatatctgg ggccaaggga caatggtcac cgtctcttca      360
```

<210> 18
<211> 120
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of a heavy chain variable region of NYA-0082

<400> 18

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


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


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


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


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


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


Ala Arg Gly Ser Ser Gly His Tyr Glu Ala Phe Asp Ile Trp Gly Gln
            100                 105                 110


Gly Thr Met Val Thr Val Ser Ser
        115                 120
```

<210> 19
<211> 333
<212> DNA
<213> Artificial

<220>
<223> Nucleotide sequence of a light chain variable region of NYA-0082

<400> 19
cagtctgtgt tgacgcagcc gccctcagtg tctgcggccc caggacagaa ggtcaccatc 60

tcctgctctg gaagcagctc caacattggg aataattatg tatcctggta ccagcggctc 120

ccaggaacag cccccaaact cctcatttat gacaataata agcgaccctc agggattcct 180

gaccgattct ctggctccaa gtctggcacg tcagccaccc tgggcatcac cggactccag 240

actggggacg aggccgatta ttactgcgga tcatgggata gcagcctgag tgccccttgg 300

gtgttcggcg gagggaccaa ggtcaccgtc cta 333

<210> 20
<211> 111
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of a light chain variable region of NYA-0082

<400> 20

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

Lys Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn
20 25 30

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

```
Ile Tyr Asp Asn Asn Lys Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60

Gly Ser Lys Ser Gly Thr Ser Ala Thr Leu Gly Ile Thr Gly Leu Gln
65                  70                  75                  80

Thr Gly Asp Glu Ala Asp Tyr Tyr Cys Gly Ser Trp Asp Ser Ser Leu
                85                  90                  95

Ser Ala Pro Trp Val Phe Gly Gly Gly Thr Lys Val Thr Val Leu
            100                 105                 110
```

<210> 21
<211> 876
<212> DNA
<213> Artificial

<220>
<223> Full-length nucleotide sequence of NYA-1163

<400> 21

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atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagcgga       60

gaggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgacaccc      120

tcctgttcag cgtctggatt ctccatccgt agctatgata tacactgggt ccgcctggct      180

ccaggcaagg ggctagagtg ggtggccact atatcatatg atggaagtca gaagtacttc      240

gcagactccg tgaagggccg atttaccatc ttcagagacg aatcggagaa catggtgtat      300

ctgcaaatga gcggcctgag agttgaggac acggctgttt atcactgtgc gagagggagt      360

agtggtcatt atgaggcttt tgatatctgg ggccaaggga caatggtcac cgtctcttca      420

ggtggaggcg gttcaggcgg aggtggcagc ggcggtggcg ggagtcagtc tgtgttgacg      480
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cagccgccct cagtgtctgc ggccccagga cagaaggtca ccatctcctg ctctggaagc 540

agctccaaca ttgggaataa ttatgtatcc tggtaccagc agctcccagg aacagccccc 600

aaactcctca tttatgacaa taataagcga ccctcaggga ttcctgaccg attctctggc 660

tccaagtctg gcacgtcagc caccctgggc atcaccggac tccagactgg ggacgaggcc 720

gattattact gcggaacatg ggatagcagc ctgagtgccc cttgggtgtt cggcggaggg 780

accaaggtca ccgtcctagg cgcggccgca ggtgcaggtg gtgattacaa agatgatgac 840

gataaaggtg cagcggcgca tcaccatcat caccac 876

<210> 22
<211> 876
<212> DNA
<213> Artificial

<220>
<223> Full-length nucleotide sequence of NYA-2023

<400> 22
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gaggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgacaccc 120

tcctgttcag cgtctggatt ctccatccgt agttatgata tacactgggt ccgccaggct 180

ccaggcaagg ggctagagtg ggtggccact atatcatatg atggaagtca gaagtacttc 240

gcagactccg tgaagggccg atttaccatc ttcagagacg aatcggagaa catggtgtat 300

ctgcaaatga gcggcctgag agttgaggac acggctgttt atcactgtgc gagagggagt 360

agtggtcatt atgaggcttt tgatatctgg ggccaaggga caatggtcac cgtctcttca 420

ggtggaggcg gttcaggcgg aggtggcagc ggcggtggcg ggagtcagtc tgtgttgacg 480

cagccgccct cagtgtctgc ggccccagga cagaaggtca ccatctcctg ctctggaagc 540

agctccaaca ttgggaattg gtatgtatcc tggtaccagc agctcccagg aacagccccc 600

aaactcctca tttatgacaa taataagcga ccctcaggga ttcctgaccg attctctggc 660

tccaagtctg gcacgtcagc caccctgggc atcaccggac tccagactgg ggacgaggcc 720

gattattact gcggaacatg ggatagcagc ctgagtgccc cttgggtgtt cggcggaggg 780

accaaggtca ccgtcctagg cgcggccgca ggtgcaggtg gtgattacaa agatgatgac 840

gataaaggtg cagcggcgca tcaccatcat caccac 876

<210> 23
<211> 876
<212> DNA
<213> Artificial

<220>
<223> Full-length nucleotide sequence of NYA-2027

<400> 23
atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagcgga 60

gaggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgacaccc 120

tcctgttcag cgtctggatt ctccatccgt agttatgata tacactgggt ccgccaggct 180

ccaggcaagg ggctagagtg ggtggccact atatcatatg atggaagtca gaagtacttc 240

gcagactccg tgaagggccg atttaccatc ttcagagacg aatcggagaa catggtgtat 300

ctgcaaatga gcggcctgag agttgaggac acggctgttt atcactgtgc gagagggagt 360

agtggtcatt atgaggcttt tgatatctgg ggccaaggga caatggtcac cgtctcttca 420

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cagccgccct cagtgtctgc ggccccagga cagaaggtca ccatctcctg ctctggaagc 540

agctccaaca ttgggaataa ttatgtatcc tggtaccagc agctcccagg aacagccccc 600

aaactcctca tttatgacaa taataagcga ccctcaggga ttcctgaccg attctctggc 660

tccaagtctg gcacgtcagc caccctgggc atcaccggac tccagactgg ggacgaggcc 720

gattattact gcggatcatg ggatagcagc ctgagtgccc cttgggtgtt cggcggaggg 780

accaaggtca ccgtcctagg cgcggccgca ggtgcaggtg gtgattacaa agatgatgac 840

gataaaggtg cagcggcgca tcaccatcat caccac 876

<210> 24
<211> 876
<212> DNA
<213> Artificial

<220>
<223> Full-length nucleotide sequence of NYA-1143

<400> 24
atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagcgga 60

gaggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgacaccc 120

tcctgttcag cgtctggatt ctccatccgt agctatgata tacactgggt ccgcctggct 180

ccaggcaagg ggctagagtg ggtggccact atatcatatg atggaagtca gaagtacttc 240

gcagactccg tgaagggccg atttaccatc ttcagagacg aatcggagaa catggtgtat 300

ctgcaaatga gcggcctgag agttgaggac acggctgttt atcactgtgc gagagggagt 360

agtggtcatt atgaggcttt tgatatctgg ggccaaggga caatggtcac cgtctcttca 420

ggtggaggcg gttcaggcgg aggtggcagc ggcggtggcg ggagtcagtc tgtgttgacg 480

cagccgccct cagtgtctgc ggccccagga cagaaggtca ccatctcctg ctctggaagc 540

agctccaaca ttgggaattg gtatgtatcc tggtaccagc agctcccagg aacagccccc 600

aaactcctca tttatgacaa taataagcga ccctcaggga ttcctgaccg attctctggc 660

tccaagtctg gcacgtcagc caccctgggc atcaccggac tccagactgg ggacgaggcc 720

gattattact gcggaacatg ggatagcagc ctgagtgccc cttgggtgtt cggcggaggg 780

accaaggtca ccgtcctagg cgcggccgca ggtgcaggtg gtgattacaa agatgatgac 840

gataaaggtg cagcggcgca tcaccatcat caccac 876

<210> 25
<211> 876
<212> DNA
<213> Artificial

<220>
<223> Full-length nucleotide sequence of NYA-2143

<400> 25
atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagcgga 60

gaggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgacaccc 120

tcctgttcag cgtctggatt ctccatccgt agctatgata tacactgggt ccgcctggct 180

ccaggcaagg ggctagagtg ggtggccact atatcatatg atggaagtca gaagtacttc 240

gcagactccg tgaagggccg atttaccatc ttcagagacg aatcggagaa catggtgtat 300

ctgcaaatga gcggcctgag agttgaggac acggctgttt atcactgtgc gagagggagt 360

agtggtcatt atgaggcttt tgatatctgg ggccaaggga caatggtcac cgtctcttca 420

ggtggaggcg gttcaggcgg aggtggcagc ggcggtggcg ggagtcagtc tgtgttgacg 480

cagccgccct cagtgtctgc ggccccagga cagaaggtca ccatctcctg ctctggaagc 540

agctccaaca ttgggaattg gtatgtatcc tggtaccagc ggctcccagg aacagccccc 600

aaactcctca tttatgacaa taataagcga ccctcaggga ttcctgaccg attctctggc 660

tccaagtctg gcacgtcagc caccctgggc atcaccggac tccagactgg ggacgaggcc 720

gattattact gcggaacatg ggatagcagc ctgagtgccc cttgggtgtt cggcggaggg 780

accaaggtca ccgtcctagg cgcggccgca ggtgcaggtg gtgattacaa agatgatgac 840

gataaaggtg cagcggcgca tcaccatcat caccac 876

<210> 26
<211> 292
<212> PRT
<213> Artificial

<220>
<223> Full-length amino acid sequence of NYA-1163

<400> 26

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

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

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

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

Leu Glu Trp Val Ala Thr Ile Ser Tyr Asp Gly Ser Gln Lys Tyr Phe
65 70 75 80

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

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

Val Tyr His Cys Ala Arg Gly Ser Ser Gly His Tyr Glu Ala Phe Asp
        115                 120                 125

Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr
145                 150                 155                 160

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

Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn Tyr Val Ser Trp Tyr
            180                 185                 190

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

Lys Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly
    210                 215                 220

Thr Ser Ala Thr Leu Gly Ile Thr Gly Leu Gln Thr Gly Asp Glu Ala
225                 230                 235                 240

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

Phe Gly Gly Gly Thr Lys Val Thr Val Leu Gly Ala Ala Ala Gly Ala
            260                 265                 270
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Gly Gly Asp Tyr Lys Asp Asp Asp Asp Lys Gly Ala Ala Ala His His
275 280 285

His His His His
290

<210> 27
<211> 292
<212> PRT
<213> Artificial

<220>
<223> Full-length amino acid sequence of NYA-2023

<400> 27

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

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

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

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

Leu Glu Trp Val Ala Thr Ile Ser Tyr Asp Gly Ser Gln Lys Tyr Phe
65 70 75 80

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

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

Val Tyr His Cys Ala Arg Gly Ser Ser Gly His Tyr Glu Ala Phe Asp
        115                 120                 125

Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr
145                 150                 155                 160

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

Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Trp Tyr Val Ser Trp Tyr
            180                 185                 190

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

Lys Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly
    210                 215                 220

Thr Ser Ala Thr Leu Gly Ile Thr Gly Leu Gln Thr Gly Asp Glu Ala
225                 230                 235                 240

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

```
Phe Gly Gly Gly Thr Lys Val Thr Val Leu Gly Ala Ala Ala Gly Ala
            260                 265                 270


Gly Gly Asp Tyr Lys Asp Asp Asp Asp Lys Gly Ala Ala Ala His His
        275                 280                 285


His His His His
    290


<210>  28
<211>  292
<212>  PRT
<213>  Artificial

<220>
<223>  Full-length amino acid sequence of NYA-2027

<400>  28

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                   10                  15


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


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


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


Leu Glu Trp Val Ala Thr Ile Ser Tyr Asp Gly Ser Gln Lys Tyr Phe
65                  70                  75                  80
```

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

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

Val Tyr His Cys Ala Arg Gly Ser Ser Gly His Tyr Glu Ala Phe Asp
        115                 120                 125

Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr
145                 150                 155                 160

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

Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn Tyr Val Ser Trp Tyr
            180                 185                 190

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

Lys Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly
    210                 215                 220

Thr Ser Ala Thr Leu Gly Ile Thr Gly Leu Gln Thr Gly Asp Glu Ala
225                 230                 235                 240

Asp Tyr Tyr Cys Gly Ser Trp Asp Ser Ser Leu Ser Ala Pro Trp Val
                245                 250                 255
```

Phe Gly Gly Gly Thr Lys Val Thr Val Leu Gly Ala Ala Ala Gly Ala
260 265 270

Gly Gly Asp Tyr Lys Asp Asp Asp Asp Lys Gly Ala Ala Ala His His
275 280 285

His His His His
290

<210> 29
<211> 292
<212> PRT
<213> Artificial

<220>
<223> Full-length amino acid sequence of NYA-1143

<400> 29

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

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

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

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

Leu Glu Trp Val Ala Thr Ile Ser Tyr Asp Gly Ser Gln Lys Tyr Phe
65 70 75 80

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

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

Val Tyr His Cys Ala Arg Gly Ser Ser Gly His Tyr Glu Ala Phe Asp
        115                 120                 125

Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr
145                 150                 155                 160

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

Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Trp Tyr Val Ser Trp Tyr
            180                 185                 190

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

Lys Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly
    210                 215                 220

Thr Ser Ala Thr Leu Gly Ile Thr Gly Leu Gln Thr Gly Asp Glu Ala
225                 230                 235                 240
```

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

Phe Gly Gly Gly Thr Lys Val Thr Val Leu Gly Ala Ala Ala Gly Ala
            260                 265                 270

Gly Gly Asp Tyr Lys Asp Asp Asp Asp Lys Gly Ala Ala Ala His His
        275                 280                 285

His His His His
    290
```

<210> 30
<211> 292
<212> PRT
<213> Artificial

<220>
<223> Full-length amino acid sequence of NYA-2143

<400> 30

```
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                   10                  15

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

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

Ile Arg Ser Tyr Asp Ile His Trp Val Arg Leu Ala Pro Gly Lys Gly
    50                  55                  60
```

```
Leu Glu Trp Val Ala Thr Ile Ser Tyr Asp Gly Ser Gln Lys Tyr Phe
65                  70                  75                  80

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

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

Val Tyr His Cys Ala Arg Gly Ser Ser Gly His Tyr Glu Ala Phe Asp
        115                 120                 125

Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr
145                 150                 155                 160

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

Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Trp Tyr Val Ser Trp Tyr
            180                 185                 190

Gln Arg Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Asp Asn Asn
        195                 200                 205

Lys Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly
    210                 215                 220

Thr Ser Ala Thr Leu Gly Ile Thr Gly Leu Gln Thr Gly Asp Glu Ala
225                 230                 235                 240
```

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

Phe Gly Gly Gly Thr Lys Val Thr Val Leu Gly Ala Ala Ala Gly Ala
            260                 265                 270

Gly Gly Asp Tyr Lys Asp Asp Asp Asp Lys Gly Ala Ala Ala His His
        275                 280                 285

His His His His
    290
```

<210> 31
<211> 876
<212> DNA
<213> Artificial

<220>
<223> Full-length nucleotide sequence of NYA-1154

<400> 31

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atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagcgga       60

gaggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgacaccc      120

tcctgttcag cgtctggatt ctccatccgt agttatgata tgcactgggt ccgccaggct      180

ccaggcaagg ggctagagtg ggtggccact atatcatatg atggaagtca gaagtacttc      240

gcagactccg tgaagggccg atttaccatc ttcagagacg aatcggagaa catggtgtat      300

ctgcaaatga gcggcctgag agttgaggac acggccgttt atcactgtgc gagagggagt      360

agtaatcatt atgaggcttt tgatatctgg ggccaaggga caatggtcac cgtctcttca      420

ggtggaggcg gttcaggcgg aggtggcagc ggcggtggcg ggagtcagtc tgtgttgacg      480
```

cagccgccct cagtgtctgc ggccccagga cagaaggtca ccatctcctg ctctggaagc 540

agctccaaca ttgggaataa ttatgtatcc tggtaccagc ggctcccagg aacagccccc 600

aaactcctca tttatgacaa taataagcga ccctcaggga ttcctgaccg attctctggc 660

tccaagtctg gcacgtcagc caccctgggc atcaccggac tccagactgg ggacgaggcc 720

gattactact gcggagcatg ggatagcagc ctgagtgccc cttgggtgtt cggcggaggg 780

accaaggtca ccgtcctagg cgcggccgca ggtgcaggtg gtgattacaa agatgatgac 840

gataaaggtg cagcggcgca tcaccatcat caccac 876

<210> 32
<211> 292
<212> PRT
<213> Artificial

<220>
<223> Full-length amino acid sequence of NYA-1154

<400> 32

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

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

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

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

```
Leu Glu Trp Val Ala Thr Ile Ser Tyr Asp Gly Ser Gln Lys Tyr Phe
65                  70                  75                  80

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

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

Val Tyr His Cys Ala Arg Gly Ser Ser Asn His Tyr Glu Ala Phe Asp
        115                 120                 125

Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr
145                 150                 155                 160

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

Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn Tyr Val Ser Trp Tyr
            180                 185                 190

Gln Arg Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Asp Asn Asn
        195                 200                 205

Lys Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly
    210                 215                 220

Thr Ser Ala Thr Leu Gly Ile Thr Gly Leu Gln Thr Gly Asp Glu Ala
225                 230                 235                 240
```

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

Phe Gly Gly Gly Thr Lys Val Thr Val Leu Gly Ala Ala Ala Gly Ala
260 265 270

Gly Gly Asp Tyr Lys Asp Asp Asp Asp Lys Gly Ala Ala Ala His His
275 280 285

His His His His
290

<210> 33
<211> 290
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of truncated form of
HLA-A*0201(UniProtKB-P01892)

<400> 33

Met Ser His Ser Met Arg Tyr Phe Phe Thr Ser Val Ser Arg Pro Gly
1 5 10 15

Arg Gly Glu Pro Arg Phe Ile Ala Val Gly Tyr Val Asp Asp Thr Gln
20 25 30

Phe Val Arg Phe Asp Ser Asp Ala Ala Ser Gln Arg Met Glu Pro Arg
35 40 45

Ala Pro Trp Ile Glu Gln Glu Gly Pro Glu Tyr Trp Asp Gly Glu Thr

```
    50                  55                  60

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

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

Arg Met Tyr Gly Cys Asp Val Gly Ser Asp Trp Arg Phe Leu Arg Gly
            100                 105                 110

Tyr His Gln Tyr Ala Tyr Asp Gly Lys Asp Tyr Ile Ala Leu Lys Glu
        115                 120                 125

Asp Leu Arg Ser Trp Thr Ala Ala Asp Met Ala Ala Gln Thr Thr Lys
    130                 135                 140

His Lys Trp Glu Ala Ala His Val Ala Glu Gln Leu Arg Ala Tyr Leu
145                 150                 155                 160

Glu Gly Thr Cys Val Glu Trp Leu Arg Arg Tyr Leu Glu Asn Gly Lys
                165                 170                 175

Glu Thr Leu Gln Arg Thr Asp Ala Pro Lys Thr His Met Thr His His
            180                 185                 190

Ala Val Ser Asp His Glu Ala Thr Leu Arg Cys Trp Ala Leu Ser Phe
        195                 200                 205

Tyr Pro Ala Glu Ile Thr Leu Thr Trp Gln Arg Asp Gly Glu Asp Gln
    210                 215                 220
```

```
Thr Gln Asp Thr Glu Leu Val Glu Thr Arg Pro Ala Gly Asp Gly Thr
225                 230                 235                 240

Phe Gln Lys Trp Ala Ala Val Val Val Pro Ser Gly Gln Glu Gln Arg
                245                 250                 255

Tyr Thr Cys His Val Gln His Glu Gly Leu Pro Lys Pro Leu Thr Leu
            260                 265                 270

Arg Trp Glu Gly Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp
        275                 280                 285

His Glu
    290
```

<210> 34
<211> 100
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of beta 2-microglobin

<400> 34

```
Met Ile Gln Arg Thr Pro Lys Ile Gln Val Tyr Ser Arg His Pro Ala
1               5                   10                  15

Glu Asn Gly Lys Ser Asn Phe Leu Asn Cys Tyr Val Ser Gly Phe His
            20                  25                  30

Pro Ser Asp Ile Glu Val Asp Leu Leu Lys Asn Gly Glu Arg Ile Glu
        35                  40                  45
```

Lys Val Glu His Ser Asp Leu Ser Phe Ser Lys Asp Trp Ser Phe Tyr
    50   55   60

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

Cys Arg Val Asn His Val Thr Leu Ser Gln Pro Lys Ile Val Lys Trp
                85   90   95

Asp Arg Asp Met
            100

<210> 35
<211> 876
<212> DNA
<213> Artificial

<220>
<223> Full-length nucleotide sequence of NYA-2035

<400> 35
atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagcgga   60

gaggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgacaccc   120

tcctgttcag cgtctggatt ctccatccgt agctatgata tacactgggt ccgcctggct   180

ccaggcaagg ggctagagtg ggtggccact atatcatatg atggaagtca gaagtacttc   240

gcagactccg tgaagggccg atttaccatc ttcagagacg aatcggagaa catggtgtat   300

ctgcaaatga gcggcctgag agttgaggac acggctgttt atcactgtgc gagagggagt   360

agtggtcatt atgaggcttt tgatatctgg ggccaaggga caatggtcac cgtctcttca   420

ggtggaggcg gttcaggcgg aggtggcagc ggcggtggcg ggagtcagtc tgtgttgacg   480

cagccgccct cagtgtctgc ggccccagga cagaaggtca ccatctcctg ctctggaagc 540

agctccaaca ttgggaattg gaaggtatcc tggtaccagc agctcccagg aacagccccc 600

aaactcctca tttatgacaa taataagcga ccctcaggga ttcctgaccg attctctggc 660

tccaagtctg gcacgtcagc caccctgggc atcaccggac tccagactgg ggacgaggcc 720

gattattact gcggaacatg ggatagcagc ctgagtgccc cttgggtgtt cggcggaggg 780

accaaggtca ccgtcctagg cgcggccgca ggtgcaggtg gtgattacaa agatgatgac 840

gataaaggtg cagcggcgca tcaccatcat caccac 876

<210> 36
<211> 292
<212> PRT
<213> Artificial

<220>
<223> Full-length amino acid sequence of NYA-2035

<400> 36

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

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

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

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

Leu Glu Trp Val Ala Thr Ile Ser Tyr Asp Gly Ser Gln Lys Tyr Phe

```
65                  70                  75                  80

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

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

Val Tyr His Cys Ala Arg Gly Ser Ser Gly His Tyr Glu Ala Phe Asp
        115                 120                 125

Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr
145                 150                 155                 160

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

Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Trp Lys Val Ser Trp Tyr
            180                 185                 190

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

Lys Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly
    210                 215                 220

Thr Ser Ala Thr Leu Gly Ile Thr Gly Leu Gln Thr Gly Asp Glu Ala
225                 230                 235                 240
```

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


Phe Gly Gly Gly Thr Lys Val Thr Val Leu Gly Ala Ala Ala Gly Ala
            260                 265                 270


Gly Gly Asp Tyr Lys Asp Asp Asp Asp Lys Gly Ala Ala Ala His His
        275                 280                 285


His His His His
    290


<210>  37
<211>  120
<212>  PRT
<213>  Artificial

<220>
<223>  Amino acid sequence of NYA-1143-VH01

<400>  37

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 Ser Ile Arg Ser Tyr
            20                  25                  30


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


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

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

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

Ala Arg Gly Ser Ser Gly His Tyr Glu Ala Phe Asp Ile Trp Gly Gln
            100                 105                 110

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

<210> 38
<211> 120
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of NYA-1143-VH02

<400> 38

```
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 Ser Ile Arg Ser Tyr
            20                  25                  30

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

Ala Thr Ile Ser Tyr Asp Gly Ser Gln 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 Ser Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr His Cys
                85                  90                  95

Ala Arg Gly Ser Ser Gly His Tyr Glu Ala Phe Asp Ile Trp Gly Gln
            100                 105                 110

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

<210> 39
<211> 120
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of NYA-1143-VH03

<400> 39

```
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 Ser Ile Arg Ser Tyr
            20                  25                  30

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

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

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

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

Ala Arg Gly Ser Ser Gly His Tyr Glu Ala Phe Asp Ile Trp Gly Gln
            100                 105                 110

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

<210> 40
<211> 111
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of NYA-1143-VL01

<400> 40

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

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Trp
            20                  25                  30

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

Ile Tyr Asp Asn Asn Lys Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50                  55                  60
```

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gly Thr Trp Asp Ser Ser Leu
85 90 95

Ser Ala Pro Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 41
<211> 876
<212> DNA
<213> Artificial

<220>
<223> Full-length nucleotide sequence of NYA-2044

<400> 41
atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagcggt 60

gaggtacagc tggtggaatc cggtggaggc cttgtgcaac cgggaggctc cctgcgactc 120

tcttgcgccg catctggctt ttccatacga tcctacgata ttcattgggt ccgactcgcc 180

cctggcaaag gtcttgaatg ggttgccact atctcctacg acgggtctca gaaatattat 240

gcggattcag tgaaggggcg gttcacaatt tcacgagacg agtcaaagaa tacactgtac 300

ctccaaatga attcactgag agccgaggat actgcagtct atcattgtgc aagagggtcc 360

tcaggccact acgaggcctt tgatatatgg ggccaaggca ccttggtaac cgttagtagc 420

ggaggtggag gaagcggagg cggcggttcc ggaggaggtg gaagtcaatc cgttctgact 480

cagccaccct ccgtgagtgc agcgcctgga cagaaggtca caatatcatg ttctggctct 540

tcaagcaaca tcggaaactg gtacgtgagc tggtaccagc agctccccgg cacggcgccc 600

aagcttctga tatatgacaa caacaaacgg cccagtggaa tccctgacag attcagtggg 660

tctaaaagtg gtacaagcgc taccctgggt atcaccggat tgcagaccgg agatgaggcg 720

gactattatt gcggaacctg ggactccagc ctgagcgctc cctgggtttt cggcggaggt 780

actaaggtta ccgtcttggg cgcggccgca ggtgcaggtg gtgattacaa agatgatgac 840

gataaaggtg cagcggcgca tcaccatcat caccac 876

<210> 42
<211> 876
<212> DNA
<213> Artificial

<220>
<223> Full-length nucleotide sequence of NYA-2045

<400> 42
atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagcggt 60

gaggtacagc tggtggaatc cggtggaggc cttgtgcaac cgggaggctc cctgcgactc 120

tcttgcgccg catctggctt ttccatacga tcctacgata ttcattgggt ccgactcgcc 180

cctggcaaag gtcttgaatg ggttgccact atctcctacg acgggtctca gaaatattat 240

gcggattcag tgaaggggcg gttcacaatt tcacgagacg agtcaaagaa tacactgtac 300

ctccaaatga attcactgag agccgaggat actgcagtct atcattgtgc aagagggtcc 360

tcaggccact acgaggcctt tgatatatgg ggccaaggca ccttggtaac cgttagtagc 420

ggaggtggag gaagcggagg cggcggttcc ggaggaggtg gaagtcaatc cgttctgact 480

cagccaccct ccgcctctgg caccccgggc caacgggtca caatatcatg ttctggctct 540

tcaagcaaca tcggaaactg gtacgtgagc tggtaccagc agctccccgg cacggcgccc 600

aagcttctga tatatgacaa caacaaacgg cccagtggag ttcctgacag attcagtggg 660

tctaaaagtg gtacaagcgc tagcctggcc ataagtggtc tgcagagtga agatgaggcg 720

gactattatt gcggaacctg ggactccagc ctgagcgctc cctgggtttt cggcggaggt 780

actaagctga ccgtcttggg cgcggccgca ggtgcaggtg gtgattacaa agatgatgac 840

gataaaggtg cagcggcgca tcaccatcat caccac 876

<210> 43
<211> 876
<212> DNA
<213> Artificial

<220>
<223> Full-length nucleotide sequence of NYA-2047

<400> 43
atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagcggt 60

caagtacagc tggtggaatc cggtggaggc gtggtccagc cgggacgcag cttgagactg 120

tcctgcgctg catctggctt ttccatacga tcctacgata tgcactgggt tcgccaagcc 180

cctggcaaag gtcttgaatg ggttgccact atctcctacg acgggtctca gaaatattac 240

gcggattcag tgaaggggcg gttcacaatt tcacgggaca attcaaagaa taccttgtat 300

ctccagatgt cttcactgag agccgaggat actgcagtct atcattgtgc aagagggtcc 360

tcaggccact acgaggcctt tgatatatgg ggccaaggca ccttggtaac cgttagtagc 420

ggaggtggag gaagcggagg cggcggttcc ggaggaggtg gaagtcaatc cgttctgact 480

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aagcttctga tatatgacaa caacaaacgg cccagtggaa tccctgacag attcagtggg 660

tctaaaagtg gtacaagcgc taccctgggt atcaccggat tgcagaccgg agatgaggcg 720

gactattatt gcggaacctg ggactccagc ctgagcgctc cctgggtttt cggcggaggt 780

actaaggtta ccgtcttggg cgcggccgca ggtgcaggtg gtgattacaa agatgatgac 840

gataaaggtg cagcggcgca tcaccatcat caccac 876

<210> 44
<211> 876
<212> DNA
<213> Artificial

<220>
<223> Full-length nucleotide sequence of NYA-2048

<400> 44
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cccggaaagg gtttggaatg ggtggctacg atctcctacg atggatccca gaagtattac 240

gccgacagcg tcaagggccg atttacaata tcacgggaca attcaaagaa taccttgtat 300

ctccagatgt cttcactgag agccgaggat actgcagtct atcattgtgc aagagggtcc 360

tcaggccact acgaggcctt tgatatatgg ggccaaggca ccttggtaac cgttagtagc 420

ggaggtggag gaagcggagg cggcggttcc ggaggaggtg gaagtcaatc cgttctgact 480

cagccaccct ccgcctctgg caccccgggc caacgggtca caatatcatg ttctggctct 540

tcaagcaaca tcggaaactg gtacgtgagc tggtaccagc agctccccgg cacggcgccc 600

aagcttctga tatatgacaa caacaaacgg cccagtggag ttcctgacag attcagtggg 660

tctaaaagtg gtacaagcgc tagcctggcc ataagtggtc tgcagagtga agatgaggcg 720

gactattatt gcggaacctg ggactccagc ctgagcgctc cctgggtttt cggcggaggt 780

actaagctga ccgtcttggg cgcggccgca ggtgcaggtg gtgattacaa agatgatgac 840

gataaaggtg cagcggcgca tcaccatcat caccac 876

<210> 45
<211> 876
<212> DNA
<213> Artificial

<220>
<223> Full-length nucleotide sequence of NYA-2060

<400> 45
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cctggcaaag gtcttgaatg ggttgccact atctcctacg acgggtctca gaaatattat 240

gcggattcag tgaaggggcg gttcacaatt tcacgagacg agtcaaagaa tacactgtac 300

ctccaaatga attcactgag agccgaggat actgcagtct atcattgtgc aagagggtcc 360

tcaggccact acgaggcctt tgatatatgg ggccaaggca ccttggtaac cgttagtagc 420

ggaggtggag gaagcggagg cggcggttcc ggaggaggtg gaagtcaatc cgttctgact 480

cagccaccct ccgtgagtgc agcgcctgga cagaaggtca caatatcatg ttctggctct 540

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aagcttctga tatatgacaa caacaaacgg cccagtggaa tccctgacag attcagtggg 660

tctaaaagtg gtacaagcgc taccctgggt atcaccggat tgcagaccgg agatgaggcg 720

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gataaaggtg cagcggcgca tcaccatcat caccac 876

<210> 46
<211> 876
<212> DNA
<213> Artificial

<220>
<223> Full-length nucleotide sequence of NYA-2061

<400> 46
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gaggtacagc tggtggaatc cggtggaggc cttgtgcaac cgggaggctc cctgcgactc 120

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cctggcaaag gtcttgaatg ggttgccact atctcctacg acgggtctca gaaatattat 240

gcggattcag tgaaggggcg gttcacaatt tcacgagacg agtcaaagaa tacactgtac 300

ctccaaatga attcactgag agccgaggat actgcagtct atcattgtgc aagagggtcc 360

tcaggccact acgaggcctt tgatatatgg ggccaaggca ccttggtaac cgttagtagc 420

ggaggtggag gaagcggagg cggcggttcc ggaggaggtg gaagtcaatc cgttctgact 480

cagccaccct ccgcctctgg caccccgggc caacgggtca caatatcatg ttctggctct 540

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aagcttctga tatatgacaa caacaaacgg cccagtggag ttcctgacag attcagtggg 660

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gataaaggtg cagcggcgca tcaccatcat caccac 876

<210> 47
<211> 292
<212> PRT
<213> Artificial

<220>
<223> Full-length amino acid sequence of NYA-2044

<400> 47

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

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

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

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

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

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

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

Val Tyr His Cys Ala Arg Gly Ser Ser Gly His Tyr Glu Ala Phe Asp
115 120 125

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Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr
145                 150                 155                 160

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

Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Trp Tyr Val Ser Trp Tyr
            180                 185                 190

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

Lys Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly
    210                 215                 220

Thr Ser Ala Thr Leu Gly Ile Thr Gly Leu Gln Thr Gly Asp Glu Ala
225                 230                 235                 240

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

Phe Gly Gly Gly Thr Lys Val Thr Val Leu Gly Ala Ala Ala Gly Ala
            260                 265                 270

Gly Gly Asp Tyr Lys Asp Asp Asp Asp Lys Gly Ala Ala Ala His His
        275                 280                 285

His His His His
```

290

<210> 48
<211> 292
<212> PRT
<213> Artificial

<220>
<223> Full-length amino acid sequence of NYA-2045

<400> 48

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

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

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

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

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

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

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

Val Tyr His Cys Ala Arg Gly Ser Ser Gly His Tyr Glu Ala Phe Asp

```
        115                 120                 125

Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr
145                 150                 155                 160

Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln Arg Val Thr Ile Ser
                165                 170                 175

Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Trp Tyr Val Ser Trp Tyr
            180                 185                 190

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

Lys Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly
    210                 215                 220

Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln Ser Glu Asp Glu Ala
225                 230                 235                 240

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

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ala Ala Ala Gly Ala
            260                 265                 270

Gly Gly Asp Tyr Lys Asp Asp Asp Asp Lys Gly Ala Ala Ala His His
        275                 280                 285
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His His His His
290

<210> 49
<211> 246
<212> PRT
<213> Artificial

<220>
<223> Full-length amino acid sequence of NYA-0082

<400> 49

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

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

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

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

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

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

Ala Arg Gly Ser Ser Gly His Tyr Glu Ala Phe Asp Ile Trp Gly Gln
100 105 110

```
Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
        115                 120                 125

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

Val Ser Ala Ala Pro Gly Gln Lys Val Thr Ile Ser Cys Ser Gly Ser
145                 150                 155                 160

Ser Ser Asn Ile Gly Asn Asn Tyr Val Ser Trp Tyr Gln Arg Leu Pro
                165                 170                 175

Gly Thr Ala Pro Lys Leu Leu Ile Tyr Asp Asn Asn Lys Arg Pro Ser
            180                 185                 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Thr
        195                 200                 205

Leu Gly Ile Thr Gly Leu Gln Thr Gly Asp Glu Ala Asp Tyr Tyr Cys
    210                 215                 220

Gly Ser Trp Asp Ser Ser Leu Ser Ala Pro Trp Val Phe Gly Gly Gly
225                 230                 235                 240

Thr Lys Val Thr Val Leu
                245
```

<210> 50
<211> 292
<212> PRT
<213> Artificial

<220>
<223> Full-length amino acid sequence of NYA-2047

<400> 50

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1   5   10   15

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

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

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

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

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

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

Val Tyr His Cys Ala Arg Gly Ser Ser Gly His Tyr Glu Ala Phe Asp
        115   120   125

Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
    130   135   140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr

145 150 155 160

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

Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Trp Tyr Val Ser Trp Tyr
180 185 190

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

Lys Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly
210 215 220

Thr Ser Ala Thr Leu Gly Ile Thr Gly Leu Gln Thr Gly Asp Glu Ala
225 230 235 240

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

Phe Gly Gly Gly Thr Lys Val Thr Val Leu Gly Ala Ala Ala Gly Ala
260 265 270

Gly Gly Asp Tyr Lys Asp Asp Asp Asp Lys Gly Ala Ala Ala His His
275 280 285

His His His His
290

<210> 51
<211> 292
<212> PRT

<213> Artificial

<220>
<223> Full-length amino acid sequence of NYA-2048

<400> 51

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Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                  10                  15


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


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


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


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


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


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


Val Tyr His Cys Ala Arg Gly Ser Ser Gly His Tyr Glu Ala Phe Asp
        115                 120                 125


Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
    130                 135                 140
```

```
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr
145                 150                 155                 160

Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln Arg Val Thr Ile Ser
                165                 170                 175

Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Trp Tyr Val Ser Trp Tyr
            180                 185                 190

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

Lys Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly
    210                 215                 220

Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln Ser Glu Asp Glu Ala
225                 230                 235                 240

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

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ala Ala Ala Gly Ala
            260                 265                 270

Gly Gly Asp Tyr Lys Asp Asp Asp Asp Lys Gly Ala Ala Ala His His
        275                 280                 285

His His His His
    290
```

<210> 52

<211> 292
<212> PRT
<213> Artificial

<220>
<223> Full-length amino acid sequence of NYA-2060

<400> 52

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

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

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

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

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

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

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

Val Tyr His Cys Ala Arg Gly Ser Ser Gly His Tyr Glu Ala Phe Asp
115 120 125

Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly

```
    130                 135                 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr
145                 150                 155                 160

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

Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Trp Tyr Val Ser Trp Tyr
            180                 185                 190

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

Lys Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly
    210                 215                 220

Thr Ser Ala Thr Leu Gly Ile Thr Gly Leu Gln Thr Gly Asp Glu Ala
225                 230                 235                 240

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

Phe Gly Gly Gly Thr Lys Val Thr Val Leu Gly Ala Ala Ala Gly Ala
            260                 265                 270

Gly Gly Asp Tyr Lys Asp Asp Asp Asp Lys Gly Ala Ala Ala His His
        275                 280                 285

His His His His
    290
```

<210> 53
<211> 292
<212> PRT
<213> Artificial

<220>
<223> Full-length amino acid sequence of NYA-2061

<400> 53

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

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

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

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

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

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

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

Val Tyr His Cys Ala Arg Gly Ser Ser Gly His Tyr Glu Ala Phe Asp
115 120 125

```
Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr
145                 150                 155                 160

Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln Arg Val Thr Ile Ser
                165                 170                 175

Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Trp Tyr Val Ser Trp Tyr
            180                 185                 190

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

Lys Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly
    210                 215                 220

Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln Ser Glu Asp Glu Ala
225                 230                 235                 240

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

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ala Ala Ala Gly Ala
            260                 265                 270

Gly Gly Asp Tyr Lys Asp Asp Asp Asp Lys Gly Ala Ala Ala His His
        275                 280                 285

His His His His
```

290

<210> 54
<211> 8
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of NYA-0001-CDRH1

<400> 54

Gly Phe Ser Ile Arg Ser Tyr Asp
1 5

<210> 55
<211> 8
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of NYA-0001-CDRH2

<400> 55

Ile Ser Tyr Asp Gly Ser Gln Lys
1 5

<210> 56
<211> 13
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of NYA-0001-CDRH3

<400> 56

Ala Arg Gly Ser Ser Gly His Tyr Glu Ala Phe Asp Ile

1 5 10

<210> 57
<211> 8
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of NYA-0001-CDRL1

<400> 57

Ser Ser Asn Ile Gly Asn Asn Tyr
1 5

<210> 58
<211> 3
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of NYA-0001-CDRL2

<400> 58

Asp Asn Asn
1

<210> 59
<211> 12
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of NYA-0001-CDRL3

<400> 59

Gly Thr Trp Asp Ser Ser Leu Ser Ala Pro Trp Val

1 5 10

<210> 60
<211> 8
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of NYA-2023-CDRL1

<400> 60

Ser Ser Asn Ile Gly Asn Trp Tyr
1 5

<210> 61
<211> 12
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of NYA-2027-CDRL3

<400> 61

Gly Ser Trp Asp Ser Ser Leu Ser Ala Pro Trp Val
1 5 10

<210> 62
<211> 13
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of NYA-1154-CDRH3

<400> 62

Ala Arg Gly Ser Ser Asn His Tyr Glu Ala Phe Asp Ile

1 5 10

<210> 63
<211> 12
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of NYA-1154-CDRL3

<400> 63

Gly Ala Trp Asp Ser Ser Leu Ser Ala Pro Trp Val
1 5 10

<210> 64
<211> 8
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of NYA-0035-CDRL1

<400> 64

Ser Ser Asn Ile Gly Asn Trp Lys
1 5

<210> 65
<211> 867
<212> DNA
<213> Artificial

<220>
<223> Full-length nucleotide sequence of NYC-0003

<400> 65
atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagcggc 60

gaagtccagc tgttggagtc aggtggcgga ttggtgcaac ctggcgggtc actgaggctg 120

agttgtgcag ctagcggctt cacattctct acgtatcaga tgagctgggt gagacaggct 180

ccaggaaagg gtctggaatg ggtcagcggg attgtgtcta gcggtggctc cactgcctat 240

gccgatagcg taaaaggccg ctttacgatc tctcgggaca actctaagaa cacactctat 300

ctgcagatga attcccttag agccgaagat accgccgtgt actactgtgc tggggaactg 360

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cgagatgtcg gcggatacaa ctacgtgtct tggtatcagc agcatcccgg caaagcgccc 600

aaactcatca tacacgacgt gattgagcgg tccagtgggg ttcccgatcg tttcagcggg 660

tcaaagtccg gaaataccgc aagcctgacc atttctgggc ttcaggcaga ggatgaggct 720

gactactact gctggtcctt tgccgggagc tattacgtgt ttgggacagg gactgacgtg 780

actgttctgg gcgcggccgc aggtgcaggt ggtgattaca aagatgatga cgataaaggt 840

gcagcggcgc atcaccatca tcaccac 867

<210> 66
<211> 867
<212> DNA
<213> Artificial

<220>
<223> Full-length nucleotide sequence of NYC-0004

<400> 66
atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagcggc 60

gaagtccagc tgttggagtc aggtggcgga ttggtgcaac ctggcgggtc actgaggctg 120

agttgtgcag ctagcggctt cacattctct acgtatcaga tgagctgggt gagacaggct 180

ccaggaaagg gtctggaatg ggtcagcggg attgtgtcta gcggtggctc cactgcctat 240

gccgatagcg taaaaggccg ctttacgatc tctcgggaca actctaagaa cacactctat 300

ctgcagatga attcccttag agccgaagat accgccgtgt actactgtgc tggggaactg 360

ctcccgtatt acggtatgga cgtttggggc caaggcacca ctgtcacagt gagttccggt 420

ggaggcgggt caggcggagg cggtagtgga ggtggaggat cacaaagcga gctgacacag 480

cctaggtccg tatccggaag tccagggcag agcgtcacca tcagctgcac tggcaccgag 540

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aaactcatca tacacgacgt gattgagcgg tccagtgggg ttcccgatcg tttcagcggg 660

tcaaagtccg gaaataccgc aagcctgacc atttctgggc ttcaggcaga ggatgaggct 720

gactactact gctggtcctt tgccgggggc tattacgtgt ttgggacagg gactgacgtg 780

actgttctgg gcgcggccgc aggtgcaggt ggtgattaca aagatgatga cgataaaggt 840

gcagcggcgc atcaccatca tcaccac 867

<210> 67
<211> 289
<212> PRT
<213> Artificial

<220>
<223> Full-length amino acid sequence of NYC-0003

<400> 67

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Gly Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val

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

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

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

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

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

Val Tyr Tyr Cys Ala Gly Glu Leu Leu Pro Tyr Tyr Gly Met Asp Val
        115                 120                 125

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
    130                 135                 140

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Glu Leu Thr Gln
145                 150                 155                 160

Pro Arg Ser Val Ser Gly Ser Pro Gly Gln Ser Val Thr Ile Ser Cys
                165                 170                 175

Thr Gly Thr Ser Arg Asp Val Gly Gly Tyr Asn Tyr Val Ser Trp Tyr
            180                 185                 190
```

```
Gln Gln His Pro Gly Lys Ala Pro Lys Leu Ile Ile His Asp Val Ile
        195                 200                 205

Glu Arg Ser Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly
    210                 215                 220

Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu Gln Ala Glu Asp Glu Ala
225                 230                 235                 240

Asp Tyr Tyr Cys Trp Ser Phe Ala Gly Ser Tyr Tyr Val Phe Gly Thr
                245                 250                 255

Gly Thr Asp Val Thr Val Leu Gly Ala Ala Ala Gly Ala Gly Gly Asp
            260                 265                 270

Tyr Lys Asp Asp Asp Asp Lys Gly Ala Ala Ala His His His His His
        275                 280                 285

His
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<210> 68
<211> 289
<212> PRT
<213> Artificial

<220>
<223> Full-length amino acid sequence of NYC-0004

<400> 68

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Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                   10                  15
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Val Leu Ser Gly Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val
            20                  25                  30

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

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

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

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

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

Val Tyr Tyr Cys Ala Gly Glu Leu Leu Pro Tyr Tyr Gly Met Asp Val
        115                 120                 125

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
    130                 135                 140

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Glu Leu Thr Gln
145                 150                 155                 160

Pro Arg Ser Val Ser Gly Ser Pro Gly Gln Ser Val Thr Ile Ser Cys
                165                 170                 175

Thr Gly Thr Glu Arg Asp Val Gly Gly Tyr Asn Tyr Val Ser Trp Tyr
```

```
            180                 185                 190

Gln Gln His Pro Gly Lys Ala Pro Lys Leu Ile Ile His Asp Val Ile
        195                 200                 205

Glu Arg Ser Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly
    210                 215                 220

Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu Gln Ala Glu Asp Glu Ala
225                 230                 235                 240

Asp Tyr Tyr Cys Trp Ser Phe Ala Gly Gly Tyr Tyr Val Phe Gly Thr
                245                 250                 255

Gly Thr Asp Val Thr Val Leu Gly Ala Ala Ala Gly Ala Gly Gly Asp
            260                 265                 270

Tyr Lys Asp Asp Asp Asp Lys Gly Ala Ala Ala His His His His His
        275                 280                 285

His
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<210> 69
<211> 876
<212> DNA
<213> Artificial

<220>
<223> Full-length nucleotide sequence of NYA-0001

<400> 69
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ccaggcaagg ggctagagtg ggtggccact atatcatatg atggaagtca gaagtacttc 240

gcagactccg tgaagggccg atttaccatc ttcagagacg aatcggagaa catggtgtat 300

ctgcaaatga gcggcctgag agttgaggac acggctgttt atcactgtgc gagagggagt 360

agtggtcatt atgaggcttt tgatatctgg ggccaaggga caatggtcac cgtctcttca 420

ggtggaggcg gttcaggcgg aggtggcagc ggcggtggcg ggagtcagtc tgtgttgacg 480

cagccgccct cagtgtctgc ggccccagga cagaaggtca ccatctcctg ctctggaagc 540

agctccaaca ttgggaataa ttatgtatcc tggtaccagc agctcccagg aacagccccc 600

aaactcctca tttatgacaa taataagcga ccctcaggga ttcctgaccg attctctggc 660

tccaagtctg gcacgtcagc caccctgggc atcaccggac tccagactgg ggacgaggcc 720

gattattact gcggaacatg ggatagcagc ctgagtgccc cttgggtgtt cggcggaggg 780

accaaggtca ccgtcctagg cgcggccgca ggtgcaggtg gtgattacaa agatgatgac 840

gataaaggtg cagcggcgca tcaccatcat caccac 876

<210> 70
<211> 292
<212> PRT
<213> Artificial

<220>
<223> Full-length amino acid sequence of NYA-0001

<400> 70

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

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

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

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

Leu Glu Trp Val Ala Thr Ile Ser Tyr Asp Gly Ser Gln Lys Tyr Phe
65                  70                  75                  80

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

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

Val Tyr His Cys Ala Arg Gly Ser Ser Gly His Tyr Glu Ala Phe Asp
        115                 120                 125

Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr
145                 150                 155                 160

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

Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn Tyr Val Ser Trp Tyr
```

```
            180                 185                 190

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

Lys Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly
    210                 215                 220

Thr Ser Ala Thr Leu Gly Ile Thr Gly Leu Gln Thr Gly Asp Glu Ala
225                 230                 235                 240

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

Phe Gly Gly Gly Thr Lys Val Thr Val Leu Gly Ala Ala Ala Gly Ala
            260                 265                 270

Gly Gly Asp Tyr Lys Asp Asp Asp Asp Lys Gly Ala Ala Ala His His
        275                 280                 285

His His His His
    290
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<210> 71
<211> 738
<212> DNA
<213> Artificial

<220>
<223> Full-length nucleotide sequence of HC1

<400> 71
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aaaactcaca catgcccacc ctgcccagca cctgaagccg cagggggacc ctcagtcttc 120

ctcttccccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc 180

gtggtggtgt cagtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 240

gtggaggtgc ataatgccaa gacaaagccc cgggaggagc agtacaacag cacgtaccgg 300

gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 360

aaggtctcca acaaagccct cccagccccc atcgagaaaa ccatctccaa agccaaaggc 420

cagccccggg aaccacaggt gtacgtgctg cccccatccc gggacgagct gaccaagaac 480

caggtcagcc tgctgtgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 540

gagagcaatg gccagcccga gaacaactac ctgacctggc ctcccgtgct ggactccgac 600

ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcagggcaac 660

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tccctgtctc ccggcaag 738

<210> 72
<211> 2235
<212> DNA
<213> Artificial

<220>
<223> Full-length nucleotide sequence of NYF-0016-HC2

<400> 72
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tcctgttcag cgtctggatt ctccatccgt agctatgata tacactgggt ccgcctggct 180

ccaggcaagg ggctagagtg ggtggccact atatcatatg atggaagtca gaagtacttc 240

gcagactccg tgaagggccg atttaccatc ttcagagacg aatcggagaa catggtgtat 300

ctgcaaatga gcggcctgag agttgaggac acggctgttt atcactgtgc gagagggagt 360

agtggtcatt atgaggcttt tgatatctgg ggccaaggga caatggtcac cgtctcttca 420

ggtggaggcg gttcaggcgg aggtggcagc ggcggtggcg ggagtcagtc tgtgttgacg 480

cagccgccct cagtgtctgc ggccccagga cagaaggtca ccatctcctg ctctggaagc 540

agctccaaca ttgggaattg gtatgtatcc tggtaccagc agctcccagg aacagccccc 600

aaactcctca tttatgacaa taataagcga ccctcaggga ttcctgaccg attctctggc 660

tccaagtctg gcacgtcagc caccctgggc atcaccggac tccagactgg ggacgaggcc 720

gattattact gcggaacatg ggatagcagc ctgagtgccc cttgggtgtt cggcggaggg 780

accaaggtca ccgtcctagg gggaggcggt tcagaagtgc agctggtgga atccgggggg 840

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aactactatg gcatgtcttg gatccgccag gcacctggaa agggcctgga gtgggtggcc 960

agcatcacta ggtccggcgg gcgaatctac tatcccgaca gcgtcaaggg caggttcaca 1020

atttcccgcg agaacacaca gaaaactctg tacctgcaga tgaatagcct gagagccgaa 1080

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tatcagcagc ttccagggac agctcccaag ttgctgatct atcgcgacga caaaagaccc 1380

tcaggggtcc ctgaccgatt tagtggcagc aaaagcggta cttccgcttc cctggcgata 1440

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atcttcggag gcggaactaa gctgacagtg ttggcagccg agcccaaatc ttctgacaaa 1560

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ttccccccaa aacccaagga caccctcatg atctcccgga cccctgaggt cacatgcgtg 1680

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gtctccaaca aagccctccc agcccccatc gagaaaacca tctccaaagc caaaggccag 1920

ccccgggaac cacaggtgta cgtgtacccc ccatcccggg acgagctgac caagaaccag 1980

gtcagcctga cctgcctggt caaaggcttc tatcccagcg acatcgccgt ggagtgggag 2040

agcaatggcc agcccgagaa caactacaag accacccctc ccgtgctgga ctccgacggc 2100

tccttcgccc tcgtgagcaa gctcaccgtg gacaagagca ggtggcagca gggcaacgtc 2160

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ctgtctcccg gcaag 2235

<210> 73
<211> 2235
<212> DNA
<213> Artificial

<220>
<223> Full-length nucleotide sequence of NYF-0019-HC2

<400> 73
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tcctgttcag cgtctggatt ctccatccgt agctatgata tacactgggt ccgcctggct 180

ccaggcaagg ggctagagtg ggtggccact atatcatatg atggaagtca gaagtacttc 240

gcagactccg tgaagggccg atttaccatc ttcagagacg aatcggagaa catggtgtat 300

ctgcaaatga gcggcctgag agttgaggac acggctgttt atcactgtgc gagagggagt 360

agtggtcatt atgaggcttt tgatatctgg ggccaaggga caatggtcac cgtctcttca 420

ggtggaggcg gttcaggcgg aggtggcagc ggcggtggcg ggagtcagtc tgtgttgacg 480

cagccgccct cagtgtctgc ggccccagga cagaaggtca ccatctcctg ctctggaagc 540

agctccaaca ttgggaattg gtatgtatcc tggtaccagc ggctcccagg aacagccccc 600

aaactcctca tttatgacaa taataagcga ccctcaggga ttcctgaccg attctctggc 660

tccaagtctg gcacgtcagc caccctgggc atcaccggac tccagactgg ggacgaggcc 720

gattattact gcggaacatg ggatagcagc ctgagtgccc cttgggtgtt cggcggaggg 780

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tatcagcagc ttccagggac agctcccaag ttgctgatct atcgcgacga caaaagaccc 1380

tcaggggtcc ctgaccgatt tagtggcagc aaaagcggta cttccgcttc cctggcgata 1440

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gtggtgtcag tgagccacga agaccctgag gtcaagttca actggtacgt ggacggcgtg 1740

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gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgcaag 1860

gtctccaaca aagccctccc agcccccatc gagaaaacca tctccaaagc caaaggccag 1920

ccccgggaac cacaggtgta cgtgtacccc ccatcccggg acgagctgac caagaaccag 1980

gtcagcctga cctgcctggt caaaggcttc tatcccagcg acatcgccgt ggagtgggag 2040

agcaatggcc agcccgagaa caactacaag accacccctc ccgtgctgga ctccgacggc 2100

tccttcgccc tcgtgagcaa gctcaccgtg gacaagagca ggtggcagca gggcaacgtc 2160

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ctgtctcccg gcaag 2235

<210> 74
<211> 2235
<212> DNA
<213> Artificial

<220>
<223> Full-length nucleotide sequence of NYF-0022-HC2

<400> 74
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ccaggcaagg ggctagagtg ggtggccact atatcatatg atggaagtca gaagtacttc 240

gcagactccg tgaagggccg atttaccatc ttcagagacg aatcggagaa catggtgtat 300

ctgcaaatga gcggcctgag agttgaggac acggctgttt atcactgtgc gagagggagt 360

agtggtcatt atgaggcttt tgatatctgg ggccaaggga caatggtcac cgtctcttca 420

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cagccgccct cagtgtctgc ggccccagga cagaaggtca ccatctcctg ctctggaagc 540

agctccaaca ttgggaataa ttatgtatcc tggtaccagc agctcccagg aacagccccc 600

aaactcctca tttatgacaa taataagcga ccctcaggga ttcctgaccg attctctggc 660

tccaagtctg gcacgtcagc caccctgggc atcaccggac tccagactgg ggacgaggcc 720

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cgggtgacca ttagctgtac gggtaatacc gggaatatcg ggtctaacta cgtgaactgg 1320

tatcagcagc ttccagggac agctcccaag ttgctgatct atcgcgacga caaaagaccc 1380

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accggctttc aggccgaaga tgaggcagac tactattgcc agtcatattc cagcggcttc 1500

atcttcggag gcggaactaa gctgacagtg ttggcagccg agcccaaatc ttctgacaaa 1560

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ttcccccaa aacccaagga caccctcatg atctcccgga cccctgaggt cacatgcgtg 1680

gtggtgtcag tgagccacga agaccctgag gtcaagttca actggtacgt ggacggcgtg 1740

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gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgcaag 1860

gtctccaaca aagccctccc agcccccatc gagaaaacca tctccaaagc caaaggccag 1920

ccccgggaac cacaggtgta cgtgtacccc ccatcccggg acgagctgac caagaaccag 1980

gtcagcctga cctgcctggt caaaggcttc tatcccagcg acatcgccgt ggagtgggag 2040

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tccttcgccc tcgtgagcaa gctcaccgtg gacaagagca ggtggcagca gggcaacgtc 2160

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ctgtctcccg gcaag 2235

<210> 75
<211> 2235
<212> DNA
<213> Artificial

<220>
<223> Full-length nucleotide sequence of NYF-0023-HC2

<400> 75
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ccaggcaagg ggctagagtg ggtggccact atatcatatg atggaagtca gaagtacttc 240

gcagactccg tgaagggccg atttaccatc ttcagagacg aatcggagaa catggtgtat 300

ctgcaaatga gcggcctgag agttgaggac acggctgttt atcactgtgc gagagggagt 360

agtggtcatt atgaggcttt tgatatctgg ggccaaggga caatggtcac cgtctcttca 420

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cagccgccct cagtgtctgc ggccccagga cagaaggtca ccatctcctg ctctggaagc 540

agctccaaca ttgggaattg gtatgtatcc tggtaccagc agctcccagg aacagccccc 600

aaactcctca tttatgacaa taataagcga ccctcaggga ttcctgaccg attctctggc 660

tccaagtctg gcacgtcagc caccctgggc atcaccggac tccagactgg ggacgaggcc 720

gattattact gcggaacatg ggatagcagc ctgagtgccc cttgggtgtt cggcggaggg 780

accaaggtca ccgtcctagg gggaggcggt tcagaagtgc agctggtgga atccgggggg 840

ggcctggtgc agcctggggg gagcctgaga ctgagttgtg ccgcctctgg ggtgacattt 900

aactactatg gcatgtcttg gatccgccag gcacctggaa agggcctgga gtgggtggcc 960

agcatcacta ggtccggcgg gcgaatctac tatcccgaca gcgtcaaggg caggttcaca 1020

atttcccgcg agaacacaca gaaaactctg tacctgcaga tgaatagcct gagagccgaa 1080

gatacagctg tgtactattg cactctggac ggcagggatg ggtgggtcgc ctattggggg 1140

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tatcagcagc ttccagggac agctcccaag ttgctgatct atcgcgacga caaaagaccc 1380

tcaggggtcc ctgaccgatt tagtggcagc aaaagcggta cttccgcttc cctggcgata 1440

accggctttc aggccgaaga tgaggcagac tactattgcc agtcatattc cagcggcttc 1500

atcttcggag gcggaactaa gctgacagtg ttggcagccg agcccaaatc ttctgacaaa 1560

actcacacat gcccaccctg cccagcacct gaagccgcag ggggaccctc agtcttcctc 1620

ttcccccaa aacccaagga caccctcatg atctcccgga cccctgaggt cacatgcgtg 1680

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tatcagcagc ttccagggac agctcccaag ttgctgatct atcgcgacga caaaagaccc 1380

tcaggggtcc ctgaccgatt tagtggcagc aaaagcggta cttccgcttc cctggcgata 1440

accggctttc aggccgaaga tgaggcagac tactattgcc agtcatattc cagcggcttc 1500

atcttcggag gcggaactaa gctgacagtg ttggcagccg agcccaaatc ttctgacaaa 1560

actcacacat gcccaccctg cccagcacct gaagccgcag ggggaccctc agtcttcctc 1620

ttcccccaa aacccaagga caccctcatg atctcccgga cccctgaggt cacatgcgtg 1680

gtggtgtcag tgagccacga agaccctgag gtcaagttca actggtacgt ggacggcgtg 1740

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gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgcaag 1860

gtctccaaca aagccctccc agcccccatc gagaaaacca tctccaaagc caaaggccag 1920

ccccgggaac cacaggtgta cgtgtacccc ccatcccggg acgagctgac caagaaccag 1980

gtcagcctga cctgcctggt caaaggcttc tatcccagcg acatcgccgt ggagtgggag 2040

agcaatggcc agcccgagaa caactacaag accacccctc ccgtgctgga ctccgacggc 2100

tccttcgccc tcgtgagcaa gctcaccgtg gacaagagca ggtggcagca gggcaacgtc 2160

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<213> Artificial

<220>
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tcttgcgccg catctggctt ttccatacga tcctacgata ttcattgggt ccgacaagcc 180

cctggcaaag gtcttgaatg ggttgccact atctcctacg acgggtctca gaaatattat 240

gcggattcag tgaaggggcg gttcacaatt tcacgagacg agtcaaagaa tacactgtac 300

ctccaaatga attcactgag agccgaggat actgcagtct atcattgtgc aagagggtcc 360

tcaggccact acgaggcctt tgatatatgg ggccaaggca ccttggtaac cgttagtagc 420

ggaggtggag gaagcggagg cggcggttcc ggaggaggtg gaagtcaatc cgttctgact 480

cagccaccct ccgtgagtgc agcgcctgga cagaaggtca caatatcatg ttctggctct 540

tcaagcaaca tcggaaactg gtacgtgagc tggtaccagc agctccccgg cacggcgccc 600

aagcttctga tatatgacaa caacaaacgg cccagtggaa tccctgacag attcagtggg 660

tctaaaagtg gtacaagcgc taccctgggt atcaccggat tgcagaccgg agatgaggcg 720

gactattatt gcggaacctg ggactccagc ctgagcgctc cctgggtttt cggcggaggt 780

actaaggtta ccgtcttggg aggaggcggt tcagaagtgc agctggtgga atccgggggg 840

ggcctggtgc agcctggggg gagcctgaga ctgagttgtg ccgcctctgg ggtgacattt 900

aactactatg gcatgtcttg gatccgccag gcacctggaa agggcctgga gtgggtggcc 960

agcatcacta ggtccggcgg gcgaatctac tatcccgaca gcgtcaaggg caggttcaca 1020

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gatacagctg tgtactattg cactctggac ggcagggatg ggtgggtcgc ctattggggg 1140

cagggaaccc tggtgacagt cagctccgga ggaggaggat ctggcggagg aggcagtggg 1200

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tatcagcagc ttccagggac agctcccaag ttgctgatct atcgcgacga caaaagaccc 1380

tcaggggtcc ctgaccgatt tagtggcagc aaaagcggta cttccgcttc cctggcgata 1440

accggctttc aggccgaaga tgaggcagac tactattgcc agtcatattc cagcggcttc 1500

atcttcggag gcggaactaa gctgacagtg ttggcagccg agcccaaatc ttctgacaaa 1560

actcacacat gcccaccctg cccagcacct gaagccgcag ggggaccctc agtcttcctc 1620

ttcccccaa aacccaagga caccctcatg atctcccgga cccctgaggt cacatgcgtg 1680

gtggtgtcag tgagccacga agaccctgag gtcaagttca actggtacgt ggacggcgtg 1740

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gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgcaag 1860

gtctccaaca aagccctccc agcccccatc gagaaaacca tctccaaagc caaaggccag 1920

ccccgggaac cacaggtgta cgtgtacccc ccatcccggg acgagctgac caagaaccag 1980

gtcagcctga cctgcctggt caaaggcttc tatcccagcg acatcgccgt ggagtgggag 2040

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tccttcgccc tcgtgagcaa gctcaccgtg gacaagagca ggtggcagca gggcaacgtc 2160

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ctgtctcccg gcaag 2235

<210> 83
<211> 2235
<212> DNA
<213> Artificial

<220>
<223> Full-length nucleotide sequence of NYF-0061-HC2

<400> 83
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cctggcaaag gtcttgaatg ggttgccact atctcctacg acgggtctca gaaatattat 240

gcggattcag tgaaggggcg gttcacaatt tcacgagacg agtcaaagaa tacactgtac 300

ctccaaatga attcactgag agccgaggat actgcagtct atcattgtgc aagagggtcc 360

tcaggccact acgaggcctt tgatatatgg ggccaaggca ccttggtaac cgttagtagc 420

ggaggtggag gaagcggagg cggcggttcc ggaggaggtg gaagtcaatc cgttctgact 480

cagccaccct ccgcctctgg caccccgggc caacgggtca caatatcatg ttctggctct 540

tcaagcaaca tcggaaactg gtacgtgagc tggtaccagc agctccccgg cacggcgccc 600

aagcttctga tatatgacaa caacaaacgg cccagtggag ttcctgacag attcagtggg 660

tctaaaagtg gtacaagcgc tagcctggcc ataagtggtc tgcagagtga agatgaggcg 720

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ggcctggtgc agcctggggg gagcctgaga ctgagttgtg ccgcctctgg ggtgacattt 900

aactactatg gcatgtcttg gatccgccag gcacctggaa agggcctgga gtgggtggcc 960

agcatcacta ggtccggcgg gcgaatctac tatcccgaca gcgtcaaggg caggttcaca 1020

atttcccgcg agaacacaca gaaaactctg tacctgcaga tgaatagcct gagagccgaa 1080

gatacagctg tgtactattg cactctggac ggcagggatg ggtgggtcgc ctattggggg 1140

cagggaaccc tggtgacagt cagctccgga ggaggaggat ctggcggagg aggcagtggg 1200

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cgggtgacca ttagctgtac gggtaatacc gggaatatcg ggtctaacta cgtgaactgg 1320

tatcagcagc ttccagggac agctcccaag ttgctgatct atcgcgacga caaaagaccc 1380

tcaggggtcc ctgaccgatt tagtggcagc aaaagcggta cttccgcttc cctggcgata 1440

accggctttc aggccgaaga tgaggcagac tactattgcc agtcatattc cagcggcttc 1500

atcttcggag gcggaactaa gctgacagtg ttggcagccg agcccaaatc ttctgacaaa 1560

actcacacat gcccaccctg cccagcacct gaagccgcag ggggaccctc agtcttcctc 1620

ttcccccaa aacccaagga caccctcatg atctcccgga cccctgaggt cacatgcgtg 1680

gtggtgtcag tgagccacga agaccctgag gtcaagttca actggtacgt ggacggcgtg 1740

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gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgcaag 1860

gtctccaaca aagccctccc agcccccatc gagaaaacca tctccaaagc caaaggccag 1920

ccccgggaac cacaggtgta cgtgtacccc ccatcccggg acgagctgac caagaaccag 1980

gtcagcctga cctgcctggt caaaggcttc tatcccagcg acatcgccgt ggagtgggag 2040

agcaatggcc agcccgagaa caactacaag accacccctc ccgtgctgga ctccgacggc 2100

tccttcgccc tcgtgagcaa gctcaccgtg gacaagagca ggtggcagca gggcaacgtc 2160

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ctgtctcccg gcaag 2235

<210> 84
<211> 246
<212> PRT
<213> Artificial

<220>
<223> Full-length amino acid sequence of HC1

<400> 84

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
20 25 30

Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
35 40 45

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Ser
50 55 60

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
65 70 75 80

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
85 90 95

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp

```
            100                 105                 110

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

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
    130                 135                 140

Pro Gln Val Tyr Val Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
145                 150                 155                 160

Gln Val Ser Leu Leu Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
                165                 170                 175

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Leu Thr
            180                 185                 190

Trp Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
        195                 200                 205

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
    210                 215                 220

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
225                 230                 235                 240

Ser Leu Ser Pro Gly Lys
                245
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<210> 85
<211> 745
<212> PRT

<213> Artificial

<220>
<223> Full-length amino acid sequence of NYF-0016-HC

<400> 85

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Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                  10                  15


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


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


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


Leu Glu Trp Val Ala Thr Ile Ser Tyr Asp Gly Ser Gln Lys Tyr Phe
65                  70                  75                  80


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


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


Val Tyr His Cys Ala Arg Gly Ser Ser Gly His Tyr Glu Ala Phe Asp
        115                 120                 125


Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly
    130                 135                 140
```

```
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr
145                 150                 155                 160

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

Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Trp Tyr Val Ser Trp Tyr
            180                 185                 190

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

Lys Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly
    210                 215                 220

Thr Ser Ala Thr Leu Gly Ile Thr Gly Leu Gln Thr Gly Asp Glu Ala
225                 230                 235                 240

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

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

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        275                 280                 285

Leu Arg Leu Ser Cys Ala Ala Ser Gly Val Thr Phe Asn Tyr Tyr Gly
    290                 295                 300

Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala
```

```
305                 310                 315                 320

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

Gly Arg Phe Thr Ile Ser Arg Glu Asn Thr Gln Lys Thr Leu Tyr Leu
            340                 345                 350

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

Leu Asp Gly Arg Asp Gly Trp Val Ala Tyr Trp Gly Gln Gly Thr Leu
    370                 375                 380

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
385                 390                 395                 400

Gly Gly Gly Ser Asn Phe Met Leu Thr Gln Pro Ser Ser Val Ser Gly
                405                 410                 415

Val Pro Gly Gln Arg Val Thr Ile Ser Cys Thr Gly Asn Thr Gly Asn
            420                 425                 430

Ile Gly Ser Asn Tyr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala
        435                 440                 445

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

Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile
465                 470                 475                 480
```

```
Thr Gly Phe Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr
                485                 490                 495

Ser Ser Gly Phe Ile Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ala
            500                 505                 510

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

Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
    530                 535                 540

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

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

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
            580                 585                 590

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
        595                 600                 605

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
    610                 615                 620

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

Pro Arg Glu Pro Gln Val Tyr Val Tyr Pro Pro Ser Arg Asp Glu Leu
```

645 650 655

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

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
675 680 685

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

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

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

Lys Ser Leu Ser Leu Ser Pro Gly Lys
740 745

<210> 86
<211> 745
<212> PRT
<213> Artificial

<220>
<223> Full-length amino acid sequence of NYF-0019-HC2

<400> 86

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Gly Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val

```
            20                  25                  30

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

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

Leu Glu Trp Val Ala Thr Ile Ser Tyr Asp Gly Ser Gln Lys Tyr Phe
65                  70                  75                  80

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

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

Val Tyr His Cys Ala Arg Gly Ser Ser Gly His Tyr Glu Ala Phe Asp
        115                 120                 125

Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr
145                 150                 155                 160

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

Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Trp Tyr Val Ser Trp Tyr
            180                 185                 190
```

```
Gln Arg Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Asp Asn Asn
        195                 200                 205

Lys Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly
    210                 215                 220

Thr Ser Ala Thr Leu Gly Ile Thr Gly Leu Gln Thr Gly Asp Glu Ala
225                 230                 235                 240

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

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

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        275                 280                 285

Leu Arg Leu Ser Cys Ala Ala Ser Gly Val Thr Phe Asn Tyr Tyr Gly
    290                 295                 300

Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala
305                 310                 315                 320

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

Gly Arg Phe Thr Ile Ser Arg Glu Asn Thr Gln Lys Thr Leu Tyr Leu
            340                 345                 350

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

```
        355                 360                 365

Leu Asp Gly Arg Asp Gly Trp Val Ala Tyr Trp Gly Gln Gly Thr Leu
    370                 375                 380

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
385                 390                 395                 400

Gly Gly Gly Ser Asn Phe Met Leu Thr Gln Pro Ser Ser Val Ser Gly
                405                 410                 415

Val Pro Gly Gln Arg Val Thr Ile Ser Cys Thr Gly Asn Thr Gly Asn
            420                 425                 430

Ile Gly Ser Asn Tyr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala
        435                 440                 445

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

Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile
465                 470                 475                 480

Thr Gly Phe Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr
                485                 490                 495

Ser Ser Gly Phe Ile Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ala
            500                 505                 510

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

```
Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
    530                 535                 540

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

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

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
            580                 585                 590

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
        595                 600                 605

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
    610                 615                 620

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

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

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

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
        675                 680                 685

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Ala Leu
```

```
    690                 695                 700

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

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

Lys Ser Leu Ser Leu Ser Pro Gly Lys
            740                 745
```

<210> 87
<211> 745
<212> PRT
<213> Artificial

<220>
<223> Full-length amino acid sequence of NYF-0022-HC2

<400> 87

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Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                   10                  15

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

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

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

Leu Glu Trp Val Ala Thr Ile Ser Tyr Asp Gly Ser Gln Lys Tyr Phe
```

```
65                  70                  75                  80

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

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

Val Tyr His Cys Ala Arg Gly Ser Ser Gly His Tyr Glu Ala Phe Asp
        115                 120                 125

Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr
145                 150                 155                 160

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

Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn Tyr Val Ser Trp Tyr
            180                 185                 190

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

Lys Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly
    210                 215                 220

Thr Ser Ala Thr Leu Gly Ile Thr Gly Leu Gln Thr Gly Asp Glu Ala
225                 230                 235                 240
```

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

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

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        275                 280                 285

Leu Arg Leu Ser Cys Ala Ala Ser Gly Val Thr Phe Asn Tyr Tyr Gly
    290                 295                 300

Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala
305                 310                 315                 320

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

Gly Arg Phe Thr Ile Ser Arg Glu Asn Thr Gln Lys Thr Leu Tyr Leu
            340                 345                 350

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

Leu Asp Gly Arg Asp Gly Trp Val Ala Tyr Trp Gly Gln Gly Thr Leu
    370                 375                 380

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
385                 390                 395                 400

Gly Gly Gly Ser Asn Phe Met Leu Thr Gln Pro Ser Ser Val Ser Gly
```

```
                405                 410                 415

Val Pro Gly Gln Arg Val Thr Ile Ser Cys Thr Gly Asn Thr Gly Asn
            420                 425                 430

Ile Gly Ser Asn Tyr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala
        435                 440                 445

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

Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile
465                 470                 475                 480

Thr Gly Phe Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr
                485                 490                 495

Ser Ser Gly Phe Ile Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ala
            500                 505                 510

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

Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
    530                 535                 540

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

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

```
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
            580                 585                 590

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
        595                 600                 605

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
    610                 615                 620

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

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

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

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
        675                 680                 685

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

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

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

Lys Ser Leu Ser Leu Ser Pro Gly Lys
```

740 745

<210> 88
<211> 745
<212> PRT
<213> Artificial

<220>
<223> Full-length amino acid sequence of NYF-0023-HC2

<400> 88

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

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

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

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

Leu Glu Trp Val Ala Thr Ile Ser Tyr Asp Gly Ser Gln Lys Tyr Phe
65 70 75 80

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

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

Val Tyr His Cys Ala Arg Gly Ser Ser Gly His Tyr Glu Ala Phe Asp

```
        115                 120                 125

Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr
145                 150                 155                 160

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

Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Trp Tyr Val Ser Trp Tyr
            180                 185                 190

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

Lys Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly
    210                 215                 220

Thr Ser Ala Thr Leu Gly Ile Thr Gly Leu Gln Thr Gly Asp Glu Ala
225                 230                 235                 240

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

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

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        275                 280                 285
```

```
Leu Arg Leu Ser Cys Ala Ala Ser Gly Val Thr Phe Asn Tyr Tyr Gly
    290                 295                 300

Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala
305                 310                 315                 320

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

Gly Arg Phe Thr Ile Ser Arg Glu Asn Thr Gln Lys Thr Leu Tyr Leu
            340                 345                 350

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

Leu Asp Gly Arg Asp Gly Trp Val Ala Tyr Trp Gly Gln Gly Thr Leu
    370                 375                 380

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
385                 390                 395                 400

Gly Gly Gly Ser Asn Phe Met Leu Thr Gln Pro Ser Ser Val Ser Gly
                405                 410                 415

Val Pro Gly Gln Arg Val Thr Ile Ser Cys Thr Gly Asn Thr Gly Asn
            420                 425                 430

Ile Gly Ser Asn Tyr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala
        435                 440                 445

Pro Lys Leu Leu Ile Tyr Arg Asp Asp Lys Arg Pro Ser Gly Val Pro
```

```
    450                 455                 460

Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile
465                 470                 475                 480

Thr Gly Phe Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr
                485                 490                 495

Ser Ser Gly Phe Ile Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ala
            500                 505                 510

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

Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
    530                 535                 540

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

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

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
            580                 585                 590

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
        595                 600                 605

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
    610                 615                 620
```

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

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

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

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
        675                 680                 685

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

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

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

Lys Ser Leu Ser Leu Ser Pro Gly Lys
            740                 745
```

<210> 89
<211> 745
<212> PRT
<213> Artificial

<220>
<223> Full-length amino acid sequence of NYF-0027-HC2

<400> 89

```
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                  10                  15

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

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

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

Leu Glu Trp Val Ala Thr Ile Ser Tyr Asp Gly Ser Gln Lys Tyr Phe
65                  70                  75                  80

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

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

Val Tyr His Cys Ala Arg Gly Ser Ser Gly His Tyr Glu Ala Phe Asp
        115                 120                 125

Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr
145                 150                 155                 160

Gln Pro Pro Ser Val Ser Ala Ala Pro Gly Gln Lys Val Thr Ile Ser
```

```
                165                 170                 175

Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn Tyr Val Ser Trp Tyr
            180                 185                 190

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

Lys Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly
    210                 215                 220

Thr Ser Ala Thr Leu Gly Ile Thr Gly Leu Gln Thr Gly Asp Glu Ala
225                 230                 235                 240

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

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

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        275                 280                 285

Leu Arg Leu Ser Cys Ala Ala Ser Gly Val Thr Phe Asn Tyr Tyr Gly
    290                 295                 300

Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala
305                 310                 315                 320

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

```
Gly Arg Phe Thr Ile Ser Arg Glu Asn Thr Gln Lys Thr Leu Tyr Leu
            340                 345                 350

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

Leu Asp Gly Arg Asp Gly Trp Val Ala Tyr Trp Gly Gln Gly Thr Leu
    370                 375                 380

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
385                 390                 395                 400

Gly Gly Gly Ser Asn Phe Met Leu Thr Gln Pro Ser Ser Val Ser Gly
                405                 410                 415

Val Pro Gly Gln Arg Val Thr Ile Ser Cys Thr Gly Asn Thr Gly Asn
            420                 425                 430

Ile Gly Ser Asn Tyr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala
        435                 440                 445

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

Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile
465                 470                 475                 480

Thr Gly Phe Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr
                485                 490                 495

Ser Ser Gly Phe Ile Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ala
```

```
            500                 505                 510

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

Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
    530                 535                 540

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

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

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
            580                 585                 590

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
        595                 600                 605

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
    610                 615                 620

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

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

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
            660                 665                 670
```

```
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
        675                 680                 685

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

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

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

Lys Ser Leu Ser Leu Ser Pro Gly Lys
            740                 745
```

<210> 90
<211> 745
<212> PRT
<213> Artificial

<220>
<223> Full-length amino acid sequence of NYF-0035-HC2

<400> 90

```
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                   10                  15

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

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

```
Ile Arg Ser Tyr Asp Ile His Trp Val Arg Leu Ala Pro Gly Lys Gly
    50                  55                  60

Leu Glu Trp Val Ala Thr Ile Ser Tyr Asp Gly Ser Gln Lys Tyr Phe
65                  70                  75                  80

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

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

Val Tyr His Cys Ala Arg Gly Ser Ser Gly His Tyr Glu Ala Phe Asp
        115                 120                 125

Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr
145                 150                 155                 160

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

Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Trp Lys Val Ser Trp Tyr
            180                 185                 190

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

Lys Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly
```

```
    210                 215                 220

Thr Ser Ala Thr Leu Gly Ile Thr Gly Leu Gln Thr Gly Asp Glu Ala
225                 230                 235                 240

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

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

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        275                 280                 285

Leu Arg Leu Ser Cys Ala Ala Ser Gly Val Thr Phe Asn Tyr Tyr Gly
    290                 295                 300

Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala
305                 310                 315                 320

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

Gly Arg Phe Thr Ile Ser Arg Glu Asn Thr Gln Lys Thr Leu Tyr Leu
            340                 345                 350

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

Leu Asp Gly Arg Asp Gly Trp Val Ala Tyr Trp Gly Gln Gly Thr Leu
    370                 375                 380
```

```
Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
385                 390                 395                 400

Gly Gly Gly Ser Asn Phe Met Leu Thr Gln Pro Ser Ser Val Ser Gly
                405                 410                 415

Val Pro Gly Gln Arg Val Thr Ile Ser Cys Thr Gly Asn Thr Gly Asn
            420                 425                 430

Ile Gly Ser Asn Tyr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala
        435                 440                 445

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

Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile
465                 470                 475                 480

Thr Gly Phe Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr
                485                 490                 495

Ser Ser Gly Phe Ile Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ala
            500                 505                 510

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

Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
    530                 535                 540

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
```

```
545                 550                 555                 560

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

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
            580                 585                 590

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
        595                 600                 605

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
    610                 615                 620

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

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

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

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
        675                 680                 685

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

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

```
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
                725                 730                 735


Lys Ser Leu Ser Leu Ser Pro Gly Lys
            740                 745


<210>  91
<211>  745
<212>  PRT
<213>  Artificial

<220>
<223>  Full-length amino acid sequence of NYF-0044-HC2

<400>  91

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                   10                  15


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


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


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


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


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

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

Val Tyr His Cys Ala Arg Gly Ser Ser Gly His Tyr Glu Ala Phe Asp
        115                 120                 125

Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr
145                 150                 155                 160

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

Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Trp Tyr Val Ser Trp Tyr
            180                 185                 190

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

Lys Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly
    210                 215                 220

Thr Ser Ala Thr Leu Gly Ile Thr Gly Leu Gln Thr Gly Asp Glu Ala
225                 230                 235                 240

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

Phe Gly Gly Gly Thr Lys Val Thr Val Leu Gly Gly Gly Gly Ser Glu
```

```
            260                 265                 270

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        275                 280                 285

Leu Arg Leu Ser Cys Ala Ala Ser Gly Val Thr Phe Asn Tyr Tyr Gly
    290                 295                 300

Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala
305                 310                 315                 320

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

Gly Arg Phe Thr Ile Ser Arg Glu Asn Thr Gln Lys Thr Leu Tyr Leu
            340                 345                 350

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

Leu Asp Gly Arg Asp Gly Trp Val Ala Tyr Trp Gly Gln Gly Thr Leu
    370                 375                 380

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
385                 390                 395                 400

Gly Gly Gly Ser Asn Phe Met Leu Thr Gln Pro Ser Ser Val Ser Gly
                405                 410                 415

Val Pro Gly Gln Arg Val Thr Ile Ser Cys Thr Gly Asn Thr Gly Asn
            420                 425                 430
```

```
Ile Gly Ser Asn Tyr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala
        435                 440                 445

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

Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile
465                 470                 475                 480

Thr Gly Phe Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr
                485                 490                 495

Ser Ser Gly Phe Ile Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ala
            500                 505                 510

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

Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
    530                 535                 540

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

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

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
            580                 585                 590

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
```

595 600 605

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
610 615 620

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

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

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

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
675 680 685

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

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

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

Lys Ser Leu Ser Leu Ser Pro Gly Lys
740 745

<210> 92
<211> 745
<212> PRT

<213> Artificial

<220>
<223> Full-length amino acid sequence of NYF-0045-HC2

<400> 92

```
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                  10                  15


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


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


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


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


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


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


Val Tyr His Cys Ala Arg Gly Ser Ser Gly His Tyr Glu Ala Phe Asp
        115                 120                 125


Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
    130                 135                 140
```

```
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr
145                 150                 155                 160

Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln Arg Val Thr Ile Ser
                165                 170                 175

Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Trp Tyr Val Ser Trp Tyr
            180                 185                 190

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

Lys Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly
    210                 215                 220

Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln Ser Glu Asp Glu Ala
225                 230                 235                 240

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

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

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        275                 280                 285

Leu Arg Leu Ser Cys Ala Ala Ser Gly Val Thr Phe Asn Tyr Tyr Gly
    290                 295                 300

Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala
```

```
305                 310                 315                 320

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

Gly Arg Phe Thr Ile Ser Arg Glu Asn Thr Gln Lys Thr Leu Tyr Leu
            340                 345                 350

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

Leu Asp Gly Arg Asp Gly Trp Val Ala Tyr Trp Gly Gln Gly Thr Leu
    370                 375                 380

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
385                 390                 395                 400

Gly Gly Gly Ser Asn Phe Met Leu Thr Gln Pro Ser Ser Val Ser Gly
                405                 410                 415

Val Pro Gly Gln Arg Val Thr Ile Ser Cys Thr Gly Asn Thr Gly Asn
            420                 425                 430

Ile Gly Ser Asn Tyr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala
        435                 440                 445

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

Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile
465                 470                 475                 480
```

```
Thr Gly Phe Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr
                485                 490                 495

Ser Ser Gly Phe Ile Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ala
            500                 505                 510

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

Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
    530                 535                 540

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

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

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
            580                 585                 590

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
        595                 600                 605

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
    610                 615                 620

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

Pro Arg Glu Pro Gln Val Tyr Val Tyr Pro Pro Ser Arg Asp Glu Leu
```

645 650 655

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

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
675 680 685

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

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

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

Lys Ser Leu Ser Leu Ser Pro Gly Lys
740 745

<210> 93
<211> 745
<212> PRT
<213> Artificial

<220>
<223> Full-length amino acid sequence of NYF-0047-HC2

<400> 93

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Gly Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val

```
            20                  25                  30

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

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

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

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

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

Val Tyr His Cys Ala Arg Gly Ser Ser Gly His Tyr Glu Ala Phe Asp
        115                 120                 125

Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr
145                 150                 155                 160

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

Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Trp Tyr Val Ser Trp Tyr
            180                 185                 190
```

```
Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Asp Asn Asn
        195                 200                 205

Lys Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly
    210                 215                 220

Thr Ser Ala Thr Leu Gly Ile Thr Gly Leu Gln Thr Gly Asp Glu Ala
225                 230                 235                 240

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

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

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        275                 280                 285

Leu Arg Leu Ser Cys Ala Ala Ser Gly Val Thr Phe Asn Tyr Tyr Gly
    290                 295                 300

Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala
305                 310                 315                 320

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

Gly Arg Phe Thr Ile Ser Arg Glu Asn Thr Gln Lys Thr Leu Tyr Leu
            340                 345                 350

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

```
        355                 360                 365

Leu Asp Gly Arg Asp Gly Trp Val Ala Tyr Trp Gly Gln Gly Thr Leu
    370                 375                 380

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
385                 390                 395                 400

Gly Gly Gly Ser Asn Phe Met Leu Thr Gln Pro Ser Ser Val Ser Gly
                405                 410                 415

Val Pro Gly Gln Arg Val Thr Ile Ser Cys Thr Gly Asn Thr Gly Asn
            420                 425                 430

Ile Gly Ser Asn Tyr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala
        435                 440                 445

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

Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile
465                 470                 475                 480

Thr Gly Phe Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr
                485                 490                 495

Ser Ser Gly Phe Ile Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ala
            500                 505                 510

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

```
Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
    530                 535                 540

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

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

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
            580                 585                 590

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
        595                 600                 605

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
    610                 615                 620

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

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

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

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
        675                 680                 685

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Ala Leu
```

```
    690                 695                 700

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

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

Lys Ser Leu Ser Leu Ser Pro Gly Lys
            740                 745
```

<210> 94
<211> 745
<212> PRT
<213> Artificial

<220>
<223> Full-length amino acid sequence of NYF-0048-HC2

<400> 94

```
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                   10                  15

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

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

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

Leu Glu Trp Val Ala Thr Ile Ser Tyr Asp Gly Ser Gln Lys Tyr Tyr
```

```
65                  70                  75                  80

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

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

Val Tyr His Cys Ala Arg Gly Ser Ser Gly His Tyr Glu Ala Phe Asp
        115                 120                 125

Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr
145                 150                 155                 160

Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln Arg Val Thr Ile Ser
                165                 170                 175

Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Trp Tyr Val Ser Trp Tyr
            180                 185                 190

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

Lys Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly
    210                 215                 220

Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln Ser Glu Asp Glu Ala
225                 230                 235                 240
```

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

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

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        275                 280                 285

Leu Arg Leu Ser Cys Ala Ala Ser Gly Val Thr Phe Asn Tyr Tyr Gly
    290                 295                 300

Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala
305                 310                 315                 320

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

Gly Arg Phe Thr Ile Ser Arg Glu Asn Thr Gln Lys Thr Leu Tyr Leu
            340                 345                 350

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

Leu Asp Gly Arg Asp Gly Trp Val Ala Tyr Trp Gly Gln Gly Thr Leu
    370                 375                 380

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
385                 390                 395                 400

Gly Gly Gly Ser Asn Phe Met Leu Thr Gln Pro Ser Ser Val Ser Gly
```

```
                405                 410                 415

Val Pro Gly Gln Arg Val Thr Ile Ser Cys Thr Gly Asn Thr Gly Asn
            420                 425                 430

Ile Gly Ser Asn Tyr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala
        435                 440                 445

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

Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile
465                 470                 475                 480

Thr Gly Phe Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr
                485                 490                 495

Ser Ser Gly Phe Ile Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ala
            500                 505                 510

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

Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
    530                 535                 540

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

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

```
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
            580                 585                 590

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
        595                 600                 605

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
    610                 615                 620

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

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

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

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
        675                 680                 685

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

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

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

Lys Ser Leu Ser Leu Ser Pro Gly Lys
```

740 745

<210> 95
<211> 745
<212> PRT
<213> Artificial

<220>
<223> Full-length amino acid sequence of NYF-0060-HC2

<400> 95

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

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

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

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

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

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

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

Val Tyr His Cys Ala Arg Gly Ser Ser Gly His Tyr Glu Ala Phe Asp

```
        115                 120                 125

Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr
145                 150                 155                 160

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

Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Trp Tyr Val Ser Trp Tyr
            180                 185                 190

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

Lys Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly
    210                 215                 220

Thr Ser Ala Thr Leu Gly Ile Thr Gly Leu Gln Thr Gly Asp Glu Ala
225                 230                 235                 240

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

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

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        275                 280                 285
```

```
Leu Arg Leu Ser Cys Ala Ala Ser Gly Val Thr Phe Asn Tyr Tyr Gly
    290                 295                 300

Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala
305                 310                 315                 320

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

Gly Arg Phe Thr Ile Ser Arg Glu Asn Thr Gln Lys Thr Leu Tyr Leu
            340                 345                 350

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

Leu Asp Gly Arg Asp Gly Trp Val Ala Tyr Trp Gly Gln Gly Thr Leu
    370                 375                 380

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
385                 390                 395                 400

Gly Gly Gly Ser Asn Phe Met Leu Thr Gln Pro Ser Ser Val Ser Gly
                405                 410                 415

Val Pro Gly Gln Arg Val Thr Ile Ser Cys Thr Gly Asn Thr Gly Asn
            420                 425                 430

Ile Gly Ser Asn Tyr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala
        435                 440                 445

Pro Lys Leu Leu Ile Tyr Arg Asp Asp Lys Arg Pro Ser Gly Val Pro
```

```
    450                 455                 460

Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile
465                 470                 475                 480

Thr Gly Phe Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr
                485                 490                 495

Ser Ser Gly Phe Ile Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ala
            500                 505                 510

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

Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
    530                 535                 540

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

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

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
            580                 585                 590

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
        595                 600                 605

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
    610                 615                 620
```

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

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

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

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
        675                 680                 685

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

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

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

Lys Ser Leu Ser Leu Ser Pro Gly Lys
            740                 745
```

<210> 96
<211> 745
<212> PRT
<213> Artificial

<220>
<223> Full-length amino acid sequence of NYF-0061-HC2

<400> 96

```
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                  10                  15

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

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

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

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

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

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

Val Tyr His Cys Ala Arg Gly Ser Ser Gly His Tyr Glu Ala Phe Asp
        115                 120                 125

Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr
145                 150                 155                 160

Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln Arg Val Thr Ile Ser
```

```
                165                 170                 175

Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Trp Tyr Val Ser Trp Tyr
            180                 185                 190

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

Lys Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly
    210                 215                 220

Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln Ser Glu Asp Glu Ala
225                 230                 235                 240

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

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

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        275                 280                 285

Leu Arg Leu Ser Cys Ala Ala Ser Gly Val Thr Phe Asn Tyr Tyr Gly
    290                 295                 300

Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala
305                 310                 315                 320

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

```
Gly Arg Phe Thr Ile Ser Arg Glu Asn Thr Gln Lys Thr Leu Tyr Leu
            340                 345                 350

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

Leu Asp Gly Arg Asp Gly Trp Val Ala Tyr Trp Gly Gln Gly Thr Leu
    370                 375                 380

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
385                 390                 395                 400

Gly Gly Gly Ser Asn Phe Met Leu Thr Gln Pro Ser Ser Val Ser Gly
                405                 410                 415

Val Pro Gly Gln Arg Val Thr Ile Ser Cys Thr Gly Asn Thr Gly Asn
            420                 425                 430

Ile Gly Ser Asn Tyr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala
        435                 440                 445

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

Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile
465                 470                 475                 480

Thr Gly Phe Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr
                485                 490                 495

Ser Ser Gly Phe Ile Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ala
```

```
            500                 505                 510

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

Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
    530                 535                 540

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

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

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
            580                 585                 590

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
        595                 600                 605

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
    610                 615                 620

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

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

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
            660                 665                 670
```

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
        675   680   685

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

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

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

Lys Ser Leu Ser Leu Ser Pro Gly Lys
            740   745

<210> 97
<211> 1404
<212> DNA
<213> Artificial

<220>
<223> Full-length nucleotide sequence of NYA-0001-Fab-HC1-k delete

<400> 97
atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagcgag   60

gtgcagctgg tggagtctgg gggaggcgtg gtccagcctg ggaggtccct gacaccctcc   120

tgttcagcgt ctggattctc catccgtagt tatgatatac actgggtccg ccaggctcca   180

ggcaaggggc tagagtgggt ggccactata tcatatgatg gaagtcagaa gtacttcgca   240

gactccgtga agggccgatt taccatcttc agagacgaat cggagaacat ggtgtatctg   300

caaatgagcg gcctgagagt tgaggacacg gctgtttatc actgtgcgag agggagtagt   360

ggtcattatg aggcttttga tatctggggc caagggacaa tggtcaccgt ctcttcagcc 420

tccaccaagg gcccaagcgt cttccccctg gcaccctcct ccaagagcac ctctggcggc 480

acagccgccc tgggctgcct ggtcaaggac tacttccccg aacccgtgac cgtgagctgg 540

aactcaggcg ccctgaccag cggcgtgcac accttccccg ctgtcctgca gtcctcagga 600

ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 660

atctgcaacg tgaatcacaa gcccagcaac accaaggtgg acaagagagt tgagcccaaa 720

tcttgtgaca aaactcacac atgcccaccc tgcccagcac ctgaagccgc agggggaccc 780

tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gaccctgag 840

gtcacatgcg tggtggtgtc agtgagccac gaagaccctg aggtcaagtt caactggtac 900

gtggacggcg tggaggtgca taatgccaag acaaagcccc gggaggagca gtacaacagc 960

acgtaccggg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 1020

tacaagtgca aggtctccaa caaagccctc ccagccccca tcgagaaaac catctccaaa 1080

gccaaaggcc agccccggga accacaggtg tacgtgctgc ccccatcccg ggacgagctg 1140

accaagaacc aggtcagcct gctgtgcctg gtcaaaggct tctatcccag cgacatcgcc 1200

gtggagtggg agagcaatgg ccagcccgag aacaactacc tgacctggcc tcccgtgctg 1260

gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1320

cagggcaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacccag 1380

aagagcctct ccctgtctcc cggc 1404

<210> 98
<211> 711
<212> DNA
<213> Artificial

<220>
<223> Full-length nucleotide sequence of NYA-0001-LC

<400> 98
atggtgctgc agacccaggt gttcatctcc ctgctgctgt ggatctccgg cgcgtacggc 60

cagtctgtgt tgacgcagcc gccctcagtg tctgcggccc caggacagaa ggtcaccatc 120

tcctgctctg gaagcagctc caacattggg aataattatg tatcctggta ccagcagctc 180

ccaggaacag cccccaaact cctcatttat gacaataata agcgaccctc agggattcct 240

gaccgattct ctggctccaa gtctggcacg tcagccaccc tgggcatcac cggactccag 300

actggggacg aggccgatta ttactgcgga acatgggata gcagcctgag tgccccttgg 360

gtgttcggcg gagggaccaa ggtcaccgtc ctaggccagc ctaaggctgc ccctagcgtg 420

accctgttcc ctccttccag cgaggagctt caagctaaca aggccaccct ggtgtgtctt 480

atctctgact tctaccctgg cgctgtgacc gtggcctgga aggctgacag ctcccctgtg 540

aaggccggag tggagaccac cacacctagc aagcagtcta acaacaagta cgctgccagc 600

tcctacctga gccttacccc tgagcagtgg aagtctcaca gaagctactc ctgtcaagtg 660

acccacgagg gcagcaccgt ggagaagacc gtggctccta ccgagtgttc c 711

<210> 99
<211> 468
<212> PRT
<213> Artificial

<220>
<223> Full-length amino acid sequence of NYA-0001-Fab-HC1-k delete

<400> 99

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1   5   10   15

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

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

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

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

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

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

Tyr His Cys Ala Arg Gly Ser Ser Gly His Tyr Glu Ala Phe Asp Ile
        115                 120                 125

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
    130                 135                 140

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
145                 150                 155                 160

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

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
```

```
            180                 185                 190

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
        195                 200                 205

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
    210                 215                 220

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys
225                 230                 235                 240

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
                245                 250                 255

Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
            260                 265                 270

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Ser Val
        275                 280                 285

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
    290                 295                 300

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
305                 310                 315                 320

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
                325                 330                 335

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
            340                 345                 350
```

```
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
        355                 360                 365

Gln Val Tyr Val Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
    370                 375                 380

Val Ser Leu Leu Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
385                 390                 395                 400

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Leu Thr Trp
                405                 410                 415

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
            420                 425                 430

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
        435                 440                 445

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
    450                 455                 460

Leu Ser Pro Gly
465
```

<210> 100
<211> 237
<212> PRT
<213> Artificial

<220>
<223> Full-length amino acid sequence of NYA-0001-LC

<400> 100

```
Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1               5                  10                  15

Gly Ala Tyr Gly Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Ala
            20                  25                  30

Ala Pro Gly Gln Lys Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn
        35                  40                  45

Ile Gly Asn Asn Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala
    50                  55                  60

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

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

Thr Gly Leu Gln Thr Gly Asp Glu Ala Asp Tyr Tyr Cys Gly Thr Trp
            100                 105                 110

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

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

Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu
145                 150                 155                 160

Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp
```

```
                165                 170                 175

Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln
            180                 185                 190

Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu
        195                 200                 205

Gln Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly
    210                 215                 220

Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
225                 230                 235
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<210> 101
<211> 1404
<212> DNA
<213> Artificial

<220>
<223> Full-length nucleotide sequence of NYA-1143-Fab-HC1-k delete

<400> 101

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atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagcgag       60

gtgcagctgg tggagtctgg gggaggcgtg gtccagcctg ggaggtccct gacaccctcc      120

tgttcagcgt ctggattctc catccgtagc tatgatatac actgggtccg cctggctcca      180

ggcaaggggc tagagtgggt ggccactata tcatatgatg gaagtcagaa gtacttcgca      240

gactccgtga agggccgatt taccatcttc agagacgaat cggagaacat ggtgtatctg      300

caaatgagcg gcctgagagt tgaggacacg gctgtttatc actgtgcgag agggagtagt      360

ggtcattatg aggcttttga tatctggggc caagggacaa tggtcaccgt ctcttcagcc      420
```

tccaccaagg gcccaagcgt cttccccctg gcaccctcct ccaagagcac ctctggcggc 480

acagccgccc tgggctgcct ggtcaaggac tacttccccg aacccgtgac cgtgagctgg 540

aactcaggcg ccctgaccag cggcgtgcac accttccccg ctgtcctgca gtcctcagga 600

ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 660

atctgcaacg tgaatcacaa gcccagcaac accaaggtgg acaagagagt tgagcccaaa 720

tcttgtgaca aaactcacac atgcccaccc tgcccagcac ctgaagccgc aggggaccc 780

tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gaccctgag 840

gtcacatgcg tggtggtgtc agtgagccac gaagaccctg aggtcaagtt caactggtac 900

gtggacggcg tggaggtgca taatgccaag acaaagcccc gggaggagca gtacaacagc 960

acgtaccggg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 1020

tacaagtgca aggtctccaa caaagccctc ccagccccca tcgagaaaac catctccaaa 1080

gccaaaggcc agccccggga accacaggtg tacgtgctgc ccccatcccg ggacgagctg 1140

accaagaacc aggtcagcct gctgtgcctg gtcaaaggct tctatcccag cgacatcgcc 1200

gtggagtggg agagcaatgg ccagcccgag aacaactacc tgacctggcc tcccgtgctg 1260

gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1320

cagggcaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacccag 1380

aagagcctct ccctgtctcc cggc 1404

<210> 102
<211> 711
<212> DNA
<213> Artificial

<220>
<223> Full-length nucleotide sequence of NYA-1143-LC

<400> 102
atggtgctgc agacccaggt gttcatctcc ctgctgctgt ggatctccgg cgcgtacggc 60

cagtctgtgt tgacgcagcc gccctcagtg tctgcggccc caggacagaa ggtcaccatc 120

tcctgctctg gaagcagctc caacattggg aattggtatg tatcctggta ccagcagctc 180

ccaggaacag cccccaaact cctcatttat gacaataata agcgaccctc agggattcct 240

gaccgattct ctggctccaa gtctggcacg tcagccaccc tgggcatcac cggactccag 300

actggggacg aggccgatta ttactgcgga acatgggata gcagcctgag tgccccttgg 360

gtgttcggcg gagggaccaa ggtcaccgtc ctaggccagc ctaaggctgc ccctagcgtg 420

accctgttcc ctccttccag cgaggagctt caagctaaca aggccaccct ggtgtgtctt 480

atctctgact tctaccctgg cgctgtgacc gtggcctgga aggctgacag ctcccctgtg 540

aaggccggag tggagaccac cacacctagc aagcagtcta acaacaagta cgctgccagc 600

tcctacctga gccttacccc tgagcagtgg aagtctcaca gaagctactc ctgtcaagtg 660

acccacgagg gcagcaccgt ggagaagacc gtggctccta ccgagtgttc c 711

<210> 103
<211> 1476
<212> DNA
<213> Artificial

<220>
<223> Full-length nucleotide sequence of C3E-7085-HC2-k delete

<400> 103
atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagcgga 60

gaagtgcagc tggtggaatc cgggggggc ctggtgcagc ctgggggag cctgagactg 120

agttgtgccg cctctggggt gacatttaac tactatggca tgtcttggat ccgccaggca 180

cctggaaagg gcctggagtg ggtggccagc atcactaggt ccggcgggcg aatctactat 240

cccgacagcg tcaagggcag gttcacaatt tcccgcgaga acacacagaa aactctgtac 300

ctgcagatga atagcctgag agccgaagat acagctgtgt actattgcac tctggacggc 360

agggatgggt gggtcgccta ttgggggcag ggaaccctgg tgacagtcag ctccggagga 420

ggaggatctg gcggaggagg cagtgggggа ggcgggtcaa actttatgct cactcagccg 480

tcctctgttt ctggcgtacc tggccaacgg gtgaccatta gctgtacggg taataccggg 540

aatatcgggt ctaactacgt gaactggtat cagcagcttc cagggacagc tcccaagttg 600

ctgatctatc gcgacgacaa aagaccctca ggggtccctg accgatttag tggcagcaaa 660

agcggtactt ccgcttccct ggcgataacc ggctttcagg ccgaagatga ggcagactac 720

tattgccagt catattccag cggcttcatc ttcggaggcg gaactaagct gacagtgttg 780

gcagccgagc ccaaatcttc tgacaaaact cacacatgcc caccctgccc agcacctgaa 840

gccgcagggg gaccctcagt cttcctcttc cccccaaaac ccaaggacac cctcatgatc 900

tcccggaccc ctgaggtcac atgcgtggtg gtgtcagtga gccacgaaga ccctgaggtc 960

aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccccgggag 1020

gagcagtaca acagcacgta ccgggtggtc agcgtcctca ccgtcctgca ccaggactgg 1080

ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag ccctcccagc ccccatcgag 1140

aaaaccatct ccaaagccaa aggccagccc cgggaaccac aggtgtacgt gtaccccccа 1200

tcccgggacg agctgaccaa gaaccaggtc agcctgacct gcctggtcaa aggcttctat 1260

cccagcgaca tcgccgtgga gtgggagagc aatggccagc ccgagaacaa ctacaagacc 1320

acccctcccg tgctggactc cgacggctcc ttcgccctcg tgagcaagct caccgtggac 1380

aagagcaggt ggcagcaggg caacgtcttc tcatgctccg tgatgcatga ggctctgcac 1440

aaccactaca cccagaagag cctctccctg tctccc 1476

<210> 104
<211> 468
<212> PRT
<213> Artificial

<220>
<223> Full-length amino acid sequence of NYA-1143-Fab-HC1-k delete

<400> 104

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

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

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

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

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

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

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

Tyr His Cys Ala Arg Gly Ser Ser Gly His Tyr Glu Ala Phe Asp Ile

```
        115                 120                 125

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
    130                 135                 140

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
145                 150                 155                 160

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

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

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
        195                 200                 205

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
    210                 215                 220

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys
225                 230                 235                 240

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
                245                 250                 255

Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
            260                 265                 270

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Ser Val
        275                 280                 285
```

```
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
    290                 295                 300

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
305                 310                 315                 320

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
                325                 330                 335

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
            340                 345                 350

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
        355                 360                 365

Gln Val Tyr Val Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
    370                 375                 380

Val Ser Leu Leu Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
385                 390                 395                 400

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Leu Thr Trp
                405                 410                 415

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
            420                 425                 430

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
        435                 440                 445

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
```

450 455 460

Leu Ser Pro Gly
465

<210> 105
<211> 237
<212> PRT
<213> Artificial

<220>
<223> Full-length amino acid sequence of NYA-1143-LC

<400> 105

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

Gly Ala Tyr Gly Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Ala
20 25 30

Ala Pro Gly Gln Lys Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn
35 40 45

Ile Gly Asn Trp Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala
50 55 60

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

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

Thr Gly Leu Gln Thr Gly Asp Glu Ala Asp Tyr Tyr Cys Gly Thr Trp

100 105 110

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

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

Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu
145 150 155 160

Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp
165 170 175

Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln
180 185 190

Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu
195 200 205

Gln Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly
210 215 220

Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
225 230 235

<210> 106
<211> 493
<212> PRT
<213> Artificial

<220>
<223> Full-length amino acid sequence of C3E-7085-HC2-k delete

<400> 106

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Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                  10                  15

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

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

Phe Asn Tyr Tyr Gly Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly
    50                  55                  60

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

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

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

Val Tyr Tyr Cys Thr Leu Asp Gly Arg Asp Gly Trp Val Ala Tyr Trp
        115                 120                 125

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

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asn Phe Met Leu Thr Gln Pro
145                 150                 155                 160
```

```
Ser Ser Val Ser Gly Val Pro Gly Gln Arg Val Thr Ile Ser Cys Thr
                165                 170                 175

Gly Asn Thr Gly Asn Ile Gly Ser Asn Tyr Val Asn Trp Tyr Gln Gln
            180                 185                 190

Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Arg Asp Asp Lys Arg
        195                 200                 205

Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser
    210                 215                 220

Ala Ser Leu Ala Ile Thr Gly Phe Gln Ala Glu Asp Glu Ala Asp Tyr
225                 230                 235                 240

Tyr Cys Gln Ser Tyr Ser Ser Gly Phe Ile Phe Gly Gly Gly Thr Lys
                245                 250                 255

Leu Thr Val Leu Ala Ala Glu Pro Lys Ser Ser Asp Lys Thr His Thr
            260                 265                 270

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
        275                 280                 285

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
    290                 295                 300

Glu Val Thr Cys Val Val Val Ser Val Ser His Glu Asp Pro Glu Val
305                 310                 315                 320

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
```

```
                325                 330                 335

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
            340                 345                 350

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
        355                 360                 365

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
    370                 375                 380

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Val Tyr Pro Pro
385                 390                 395                 400

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
                405                 410                 415

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
            420                 425                 430

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
        435                 440                 445

Gly Ser Phe Ala Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
    450                 455                 460

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
465                 470                 475                 480

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
                485                 490
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<210> 107
<211> 1497
<212> DNA
<213> Artificial

<220>
<223> Full-length nucleotide sequence of NYA-1143-HC1-k delete

<400> 107
atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagcgga 60

gaggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgacaccc 120

tcctgttcag cgtctggatt ctccatccgt agctatgata tacactgggt ccgcctggct 180

ccaggcaagg ggctagagtg ggtggccact atatcatatg atggaagtca gaagtacttc 240

gcagactccg tgaagggccg atttaccatc ttcagagacg aatcggagaa catggtgtat 300

ctgcaaatga gcggcctgag agttgaggac acggctgttt atcactgtgc gagagggagt 360

agtggtcatt atgaggcttt tgatatctgg ggccaaggga caatggtcac cgtctcttca 420

ggtggaggcg gttcaggcgg aggtggcagc ggcggtggcg ggagtcagtc tgtgttgacg 480

cagccgccct cagtgtctgc ggccccagga cagaaggtca ccatctcctg ctctggaagc 540

agctccaaca ttgggaattg gtatgtatcc tggtaccagc agctcccagg aacagccccc 600

aaactcctca tttatgacaa taataagcga ccctcaggga ttcctgaccg attctctggc 660

tccaagtctg gcacgtcagc caccctgggc atcaccggac tccagactgg ggacgaggcc 720

gattattact gcggaacatg ggatagcagc ctgagtgccc cttgggtgtt cggcggaggg 780

accaaggtca ccgtcctagc agccgagccc aaatcttctg acaaaactca cacatgccca 840

ccctgcccag cacctgaagc cgcaggggga ccctcagtct tcctcttccc cccaaaaccc 900

aaggacaccc tcatgatctc ccggacccct gaggtcacat gcgtggtggt gtcagtgagc 960

cacgaagacc ctgaggtcaa gttcaactgg tacgtggacg gcgtggaggt gcataatgcc 1020

aagacaaagc cccgggagga gcagtacaac agcacgtacc gggtggtcag cgtcctcacc 1080

gtcctgcacc aggactggct gaatggcaag gagtacaagt gcaaggtctc caacaaagcc 1140

ctcccagccc ccatcgagaa aaccatctcc aaagccaaag gccagccccg ggaaccacag 1200

gtgtacgtgc tgcccccatc ccgggacgag ctgaccaaga accaggtcag cctgctgtgc 1260

ctggtcaaag gcttctatcc cagcgacatc gccgtggagt gggagagcaa tggccagccc 1320

gagaacaact acctgacctg gcctcccgtg ctggactccg acggctcctt cttcctctac 1380

agcaagctca ccgtggacaa gagcaggtgg cagcagggca acgtcttctc atgctccgtg 1440

atgcatgagg ctctgcacaa ccactacacc cagaagagcc tctccctgtc tcccggc 1497

<210> 108
<211> 499
<212> PRT
<213> Artificial

<220>
<223> Full-length amino acid sequence of NYA-1143-HC1-k delete

<400> 108

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

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

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

Ile Arg Ser Tyr Asp Ile His Trp Val Arg Leu Ala Pro Gly Lys Gly

```
    50                  55                  60

Leu Glu Trp Val Ala Thr Ile Ser Tyr Asp Gly Ser Gln Lys Tyr Phe
65                  70                  75                  80

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

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

Val Tyr His Cys Ala Arg Gly Ser Ser Gly His Tyr Glu Ala Phe Asp
        115                 120                 125

Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr
145                 150                 155                 160

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

Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Trp Tyr Val Ser Trp Tyr
            180                 185                 190

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

Lys Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly
    210                 215                 220
```

```
Thr Ser Ala Thr Leu Gly Ile Thr Gly Leu Gln Thr Gly Asp Glu Ala
225                 230                 235                 240

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

Phe Gly Gly Gly Thr Lys Val Thr Val Leu Ala Ala Glu Pro Lys Ser
            260                 265                 270

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala
        275                 280                 285

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
    290                 295                 300

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Ser Val Ser
305                 310                 315                 320

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
                325                 330                 335

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
            340                 345                 350

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
        355                 360                 365

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
    370                 375                 380

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
```

385 390 395 400

Val Tyr Val Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
405 410 415

Ser Leu Leu Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
420 425 430

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Leu Thr Trp Pro
435 440 445

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
450 455 460

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
465 470 475 480

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
485 490 495

Ser Pro Gly

<210> 109
<211> 2142
<212> DNA
<213> Artificial

<220>
<223> Full-length nucleotide sequence of C3E-7085-NYA-1154-Fab-HC2-k delete

<400> 109
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gaagtgcagc tggtggaatc cgggggggc ctggtgcagc ctgggggag cctgagactg 120

agttgtgccg cctctggggt gacatttaac tactatggca tgtcttggat ccgccaggca 180

cctggaaagg gcctggagtg ggtggccagc atcactaggt ccggcgggcg aatctactat 240

cccgacagcg tcaagggcag gttcacaatt tcccgcgaga acacacagaa aactctgtac 300

ctgcagatga atagcctgag agccgaagat acagctgtgt actattgcac tctggacggc 360

agggatgggt gggtcgccta ttgggggcag ggaaccctgg tgacagtcag ctccggagga 420

ggaggatctg gcggaggagg cagtggggga ggcgggtcaa actttatgct cactcagccg 480

tcctctgttt ctggcgtacc tggccaacgg gtgaccatta gctgtacggg taataccggg 540

aatatcgggt ctaactacgt gaactggtat cagcagcttc cagggacagc tcccaagttg 600

ctgatctatc gcgacgacaa aagaccctca ggggtccctg accgatttag tggcagcaaa 660

agcggtactt ccgcttccct ggcgataacc ggctttcagg ccgaagatga ggcagactac 720

tattgccagt catattccag cggcttcatc ttcggaggcg gaactaagct gacagtgttg 780

gggggaggcg gttcagaggt gcagctggtg gagtctgggg gaggcgtggt ccagcctggg 840

aggtccctga caccctcctg ttcagcgtct ggattctcca tccgtagtta tgatatgcac 900

tgggtccgcc aggctccagg caaggggcta gagtgggtgg ccactatatc atatgatgga 960

agtcagaagt acttcgcaga ctccgtgaag ggccgattta ccatcttcag agacgaatcg 1020

gagaacatgg tgtatctgca aatgagcggc ctgagagttg aggacacggc cgtttatcac 1080

tgtgcgagag ggagtagtaa tcattatgag gcttttgata tctggggcca agggacaatg 1140

gtcaccgtct cttcagcctc caccaagggc ccaagcgtct tccccctggc accctcctcc 1200

aagagcacct ctggcggcac agccgccctg ggctgcctgg tcaaggacta cttccccgaa 1260

cccgtgaccg tgagctggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttccccgct 1320

gtcctgcagt cctcaggact ctactccctc agcagcgtgg tgaccgtgcc ctccagcagc 1380

ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac caaggtggac 1440

aagagagttg agcccaaatc ttgtgacaaa actcacacat gcccaccctg cccagcacct 1500

gaagccgcag ggggaccctc agtcttcctc ttcccccaa aacccaagga caccctcatg 1560

atctcccgga cccctgaggt cacatgcgtg gtggtgtcag tgagccacga agaccctgag 1620

gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccccgg 1680

gaggagcagt acaacagcac gtaccgggtg gtcagcgtcc tcaccgtcct gcaccaggac 1740

tggctgaatg gcaaggagta caagtgcaag gtctccaaca aagccctccc agcccccatc 1800

gagaaaacca tctccaaagc caaaggccag ccccgggaac cacaggtgta cgtgtacccc 1860

ccatcccggg acgagctgac caagaaccag gtcagcctga cctgcctggt caaaggcttc 1920

tatcccagcg acatcgccgt ggagtgggag agcaatggcc agcccgagaa caactacaag 1980

accacccctc ccgtgctgga ctccgacggc tccttcgccc tcgtgagcaa gctcaccgtg 2040

gacaagagca ggtggcagca gggcaacgtc ttctcatgct ccgtgatgca tgaggctctg 2100

cacaaccact acacccagaa gagcctctcc ctgtctcccg gc 2142

<210> 110
<211> 711
<212> DNA
<213> Artificial

<220>
<223> Full-length nucleotide sequence of NYA-1154-LC

<400> 110
atggtgctgc agacccaggt gttcatctcc ctgctgctgt ggatctccgg cgcgtacggc 60

cagtctgtgt tgacgcagcc gccctcagtg tctgcggccc caggacagaa ggtcaccatc 120

tcctgctctg gaagcagctc caacattggg aataattatg tatcctggta ccagcggctc 180

ccaggaacag cccccaaact cctcatttat gacaataata agcgaccctc agggattcct 240

gaccgattct ctggctccaa gtctggcacg tcagccaccc tgggcatcac cggactccag 300

actggggacg aggccgatta ctactgcgga gcatgggata gcagcctgag tgccccttgg 360

gtgttcggcg gagggaccaa ggtcaccgtc ctaggccagc ctaaggctgc ccctagcgtg 420

accctgttcc ctccttccag cgaggagctt caagctaaca aggccaccct ggtgtgtctt 480

atctctgact tctaccctgg cgctgtgacc gtggcctgga aggctgacag ctcccctgtg 540

aaggccggag tggagaccac cacacctagc aagcagtcta acaacaagta cgctgccagc 600

tcctacctga gccttacccc tgagcagtgg aagtctcaca gaagctactc ctgtcaagtg 660

acccacgagg gcagcaccgt ggagaagacc gtggctccta ccgagtgttc c 711

<210> 111
<211> 735
<212> DNA
<213> Artificial

<220>
<223> Full-length nucleotide sequence of OAA-HC1-k delete

<400> 111
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aaaactcaca catgcccacc ctgcccagca cctgaagccg caggggggacc ctcagtcttc 120

ctcttccccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc 180

gtggtggtgt cagtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 240

gtggaggtgc ataatgccaa gacaaagccc cgggaggagc agtacaacag cacgtaccgg 300

gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 360

aaggtctcca acaaagccct cccagccccc atcgagaaaa ccatctccaa agccaaaggc 420

cagccccggg aaccacaggt gtacgtgctg cccccatccc gggacgagct gaccaagaac 480

caggtcagcc tgctgtgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 540

gagagcaatg gccagcccga gaacaactac ctgacctggc ctcccgtgct ggactccgac 600

ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcagggcaac 660

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tccctgtctc ccggc 735

<210> 112
<211> 714
<212> PRT
<213> Artificial

<220>
<223> Full-length amino acid sequence of C3E-7085-NYA-1154-Fab-HC2-k delete

<400> 112

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

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

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

Phe Asn Tyr Tyr Gly Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly
50 55 60

```
Leu Glu Trp Val Ala Ser Ile Thr Arg Ser Gly Gly Arg Ile Tyr Tyr
65                  70                  75                  80

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

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

Val Tyr Tyr Cys Thr Leu Asp Gly Arg Asp Gly Trp Val Ala Tyr Trp
        115                 120                 125

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

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asn Phe Met Leu Thr Gln Pro
145                 150                 155                 160

Ser Ser Val Ser Gly Val Pro Gly Gln Arg Val Thr Ile Ser Cys Thr
                165                 170                 175

Gly Asn Thr Gly Asn Ile Gly Ser Asn Tyr Val Asn Trp Tyr Gln Gln
            180                 185                 190

Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Arg Asp Asp Lys Arg
        195                 200                 205

Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser
    210                 215                 220

Ala Ser Leu Ala Ile Thr Gly Phe Gln Ala Glu Asp Glu Ala Asp Tyr
```

```
225                 230                 235                 240

Tyr Cys Gln Ser Tyr Ser Ser Gly Phe Ile Phe Gly Gly Gly Thr Lys
                245                 250                 255

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

Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu Thr Pro Ser Cys Ser
        275                 280                 285

Ala Ser Gly Phe Ser Ile Arg Ser Tyr Asp Met His Trp Val Arg Gln
    290                 295                 300

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Thr Ile Ser Tyr Asp Gly
305                 310                 315                 320

Ser Gln Lys Tyr Phe Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Phe
                325                 330                 335

Arg Asp Glu Ser Glu Asn Met Val Tyr Leu Gln Met Ser Gly Leu Arg
            340                 345                 350

Val Glu Asp Thr Ala Val Tyr His Cys Ala Arg Gly Ser Ser Asn His
        355                 360                 365

Tyr Glu Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser
    370                 375                 380

Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser
385                 390                 395                 400
```

```
Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
                405                 410                 415

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
            420                 425                 430

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

Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
    450                 455                 460

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
465                 470                 475                 480

Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
                485                 490                 495

Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro
            500                 505                 510

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
        515                 520                 525

Cys Val Val Val Ser Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
    530                 535                 540

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
545                 550                 555                 560

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
```

565 570 575

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
580 585 590

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
595 600 605

Gly Gln Pro Arg Glu Pro Gln Val Tyr Val Tyr Pro Pro Ser Arg Asp
610 615 620

Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
625 630 635 640

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
645 650 655

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
660 665 670

Ala Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
675 680 685

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
690 695 700

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
705 710

<210> 113
<211> 237
<212> PRT

<213> Artificial

<220>
<223> Full-length amino acid sequence of NYA-1154-LC

<400> 113

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Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1               5                  10                  15


Gly Ala Tyr Gly Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Ala
            20                  25                  30


Ala Pro Gly Gln Lys Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn
        35                  40                  45


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


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


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


Thr Gly Leu Gln Thr Gly Asp Glu Ala Asp Tyr Tyr Cys Gly Ala Trp
            100                 105                 110


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


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

```
Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu
145                 150                 155                 160

Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp
                165                 170                 175

Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln
            180                 185                 190

Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu
        195                 200                 205

Gln Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly
    210                 215                 220

Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
225                 230                 235


<210>  114
<211>  245
<212>  PRT
<213>  Artificial

<220>
<223>  Full-length amino acid sequence of OAA-HC1-k delete

<400>  114

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                   10                  15

Val Leu Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
            20                  25                  30
```

```
Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
        35                  40                  45

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Ser
    50                  55                  60

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
65                  70                  75                  80

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
                85                  90                  95

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
            100                 105                 110

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

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
    130                 135                 140

Pro Gln Val Tyr Val Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
145                 150                 155                 160

Gln Val Ser Leu Leu Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
                165                 170                 175

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Leu Thr
            180                 185                 190

Trp Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
```

195 200 205

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
210 215 220

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
225 230 235 240

Ser Leu Ser Pro Gly
245

<210> 115
<211> 2232
<212> DNA
<213> Artificial

<220>
<223> Full-length nucleotide sequence of NYF-0010-HC2-k delete

<400> 115
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gaggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgacaccc 120

tcctgttcag cgtctggatt ctccatccgt agttatgata tgcactgggt ccgccaggct 180

ccaggcaagg ggctagagtg ggtggccact atatcatatg atggaagtca gaagtacttc 240

gcagactccg tgaagggccg atttaccatc ttcagagacg aatcggagaa catggtgtat 300

ctgcaaatga gcggcctgag agttgaggac acggccgttt atcactgtgc gagagggagt 360

agtaatcatt atgaggcttt tgatatctgg ggccaaggga caatggtcac cgtctcttca 420

ggtggaggcg gttcaggcgg aggtggcagc ggcggtggcg ggagtcagtc tgtgttgacg 480

cagccgccct cagtgtctgc ggccccagga cagaaggtca ccatctcctg ctctggaagc 540

agctccaaca ttgggaataa ttatgtatcc tggtaccagc ggctcccagg aacagccccc 600

aaactcctca tttatgacaa taataagcga ccctcaggga ttcctgaccg attctctggc 660

tccaagtctg gcacgtcagc caccctgggc atcaccggac tccagactgg ggacgaggcc 720

gattactact gcggagcatg ggatagcagc ctgagtgccc cttgggtgtt cggcggaggg 780

accaaggtca ccgtcctagg gggaggcggt tcagaagtgc agctggtgga atccgggggg 840

ggcctggtgc agcctggggg gagcctgaga ctgagttgtg ccgcctctgg ggtgacattt 900

aactactatg gcatgtcttg gatccgccag gcacctggaa agggcctgga gtgggtggcc 960

agcatcacta ggtccggcgg gcgaatctac tatcccgaca gcgtcaaggg caggttcaca 1020

atttcccgcg agaacacaca gaaaactctg tacctgcaga tgaatagcct gagagccgaa 1080

gatacagctg tgtactattg cactctggac ggcagggatg ggtgggtcgc ctattggggg 1140

cagggaaccc tggtgacagt cagctccgga ggaggaggat ctggcggagg aggcagtggg 1200

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cgggtgacca ttagctgtac gggtaatacc gggaatatcg ggtctaacta cgtgaactgg 1320

tatcagcagc ttccagggac agctcccaag ttgctgatct atcgcgacga caaaagaccc 1380

tcaggggtcc ctgaccgatt tagtggcagc aaaagcggta cttccgcttc cctggcgata 1440

accggctttc aggccgaaga tgaggcagac tactattgcc agtcatattc cagcggcttc 1500

atcttcggag gcggaactaa gctgacagtg ttggcagccg agcccaaatc ttctgacaaa 1560

actcacacat gcccaccctg cccagcacct gaagccgcag ggggaccctc agtcttcctc 1620

ttcccccaa aacccaagga caccctcatg atctcccgga cccctgaggt cacatgcgtg 1680

gtggtgtcag tgagccacga agaccctgag gtcaagttca actggtacgt ggacggcgtg 1740

gaggtgcata atgccaagac aaagccccgg gaggagcagt acaacagcac gtaccgggtg 1800

gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgcaag 1860

gtctccaaca aagccctccc agcccccatc gagaaaacca tctccaaagc caaaggccag 1920

ccccgggaac cacaggtgta cgtgtacccc ccatcccggg acgagctgac caagaaccag 1980

gtcagcctga cctgcctggt caaaggcttc tatcccagcg acatcgccgt ggagtgggag 2040

agcaatggcc agcccgagaa caactacaag accacccctc ccgtgctgga ctccgacggc 2100

tccttcgccc tcgtgagcaa gctcaccgtg gacaagagca ggtggcagca gggcaacgtc 2160

ttctcatgct ccgtgatgca tgaggctctg cacaaccact acacccagaa gagcctctcc 2220

ctgtctcccg gc 2232

<210> 116
<211> 2232
<212> DNA
<213> Artificial

<220>
<223> Full-length nucleotide sequence of NYF-0004-HC2-k delete

<400> 116
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agttgtgccg cctctggggt gacatttaac tactatggca tgtcttggat ccgccaggca 180

cctggaaagg gcctggagtg ggtggccagc atcactaggt ccggcgggcg aatctactat 240

cccgacagcg tcaagggcag gttcacaatt tcccgcgaga acacacagaa aactctgtac 300

ctgcagatga atagcctgag agccgaagat acagctgtgt actattgcac tctggacggc 360

agggatgggt gggtcgccta ttgggggcag ggaaccctgg tgacagtcag ctccggagga 420

ggaggatctg gcggaggagg cagtgggggga ggcgggtcaa actttatgct cactcagccg 480

tcctctgttt ctggcgtacc tggccaacgg gtgaccatta gctgtacggg taataccggg 540

aatatcgggt ctaactacgt gaactggtat cagcagcttc cagggacagc tcccaagttg 600

ctgatctatc gcgacgacaa aagaccctca ggggtccctg accgatttag tggcagcaaa 660

agcggtactt ccgcttccct ggcgataacc ggctttcagg ccgaagatga ggcagactac 720

tattgccagt catattccag cggcttcatc ttcggaggcg gaactaagct gacagtgttg 780

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agtcagaagt acttcgcaga ctccgtgaag ggccgattta ccatcttcag agacgaatcg 1020

gagaacatgg tgtatctgca aatgagcggc ctgagagttg aggacacggc cgtttatcac 1080

tgtgcgagag ggagtagtaa tcattatgag gcttttgata tctggggcca agggacaatg 1140

gtcaccgtct cttcaggtgg aggcggttca ggcggaggtg gcagcggcgg tggcgggagt 1200

cagtctgtgt tgacgcagcc gccctcagtg tctgcggccc caggacagaa ggtcaccatc 1260

tcctgctctg gaagcagctc caacattggg aataattatg tatcctggta ccagcggctc 1320

ccaggaacag cccccaaact cctcatttat gacaataata agcgaccctc agggattcct 1380

gaccgattct ctggctccaa gtctggcacg tcagccaccc tgggcatcac cggactccag 1440

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actcacacat gcccaccctg cccagcacct gaagccgcag ggggaccctc agtcttcctc 1620

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gtggtgtcag tgagccacga agaccctgag gtcaagttca actggtacgt ggacggcgtg 1740

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gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgcaag 1860

gtctccaaca aagccctccc agcccccatc gagaaaacca tctccaaagc caaaggccag 1920

ccccgggaac cacaggtgta cgtgtacccc ccatcccggg acgagctgac caagaaccag 1980

gtcagcctga cctgcctggt caaaggcttc tatcccagcg acatcgccgt ggagtgggag 2040

agcaatggcc agcccgagaa caactacaag accacccctc ccgtgctgga ctccgacggc 2100

tccttcgccc tcgtgagcaa gctcaccgtg gacaagagca ggtggcagca gggcaacgtc 2160

ttctcatgct ccgtgatgca tgaggctctg cacaaccact acacccagaa gagcctctcc 2220

ctgtctcccg gc 2232

<210> 117
<211> 2232
<212> DNA
<213> Artificial

<220>
<223> Full-length nucleotide sequence of NYF-0011-HC2-k delete

<400> 117
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tcctgttcag cgtctggatt ctccatccgt agctatgata tacactgggt ccgcctggct 180

ccaggcaagg ggctagagtg ggtggccact atatcatatg atggaagtca gaagtacttc 240

gcagactccg tgaagggccg atttaccatc ttcagagacg aatcggagaa catggtgtat 300

ctgcaaatga gcggcctgag agttgaggac acggctgttt atcactgtgc gagagggagt 360

agtggtcatt atgaggcttt tgatatctgg ggccaaggga caatggtcac cgtctcttca 420

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cagccgccct cagtgtctgc ggccccagga cagaaggtca ccatctcctg ctctggaagc 540

agctccaaca ttgggaattg gtatgtatcc tggtaccagc agctcccagg aacagccccc 600

aaactcctca tttatgacaa taataagcga ccctcaggga ttcctgaccg attctctggc 660

tccaagtctg gcacgtcagc caccctgggc atcaccggac tccagactgg ggacgaggcc 720

gattattact gcggaacatg ggatagcagc ctgagtgccc cttgggtgtt cggcggaggg 780

accaaggtca ccgtcctagg gggaggcggt tcagaagtgc agctggtgga atccgggggg 840

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agcatcacta ggtccggcgg gcgaatctac tatcccgaca gcgtcaaggg caggttcaca 1020

atttcccgcg agaacacaca gaaaactctg tacctgcaga tgaatagcct gagagccgaa 1080

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tatcagcagc ttccagggac agctcccaag ttgctgatct atcgcgacga caaaagaccc 1380

tcaggggtcc ctgaccgatt tagtggcagc aaaagcggta cttccgcttc cctggcgata 1440

accggctttc aggccgaaga tgaggcagac tactattgcc agtcatattc cagcggcttc 1500

atcttcggag gcggaactaa gctgacagtg ttggcagccg agcccaaatc ttctgacaaa 1560

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ttcccccaa aacccaagga caccctcatg atctcccgga cccctgaggt cacatgcgtg 1680

gtggtgtcag tgagccacga agaccctgag gtcaagttca actggtacgt ggacggcgtg 1740

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gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgcaag 1860

gtctccaaca aagccctccc agcccccatc gagaaaacca tctccaaagc caaaggccag 1920

ccccgggaac cacaggtgta cgtgtacccc ccatcccggg acgagctgac caagaaccag 1980

gtcagcctga cctgcctggt caaaggcttc tatcccagcg acatcgccgt ggagtgggag 2040

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ctgtctcccg gc 2232

<210> 118
<211> 744
<212> PRT
<213> Artificial

<220>
<223> Full-length amino acid sequence of NYF-0010-HC2-k delete

<400> 118

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

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

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

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

Leu Glu Trp Val Ala Thr Ile Ser Tyr Asp Gly Ser Gln Lys Tyr Phe
65                  70                  75                  80

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

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

Val Tyr His Cys Ala Arg Gly Ser Ser Asn His Tyr Glu Ala Phe Asp
        115                 120                 125

Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr
145                 150                 155                 160

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

Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn Tyr Val Ser Trp Tyr
            180                 185                 190

Gln Arg Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Asp Asn Asn
        195                 200                 205

Lys Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly
```

```
    210                 215                 220

Thr Ser Ala Thr Leu Gly Ile Thr Gly Leu Gln Thr Gly Asp Glu Ala
225                 230                 235                 240

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

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

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        275                 280                 285

Leu Arg Leu Ser Cys Ala Ala Ser Gly Val Thr Phe Asn Tyr Tyr Gly
    290                 295                 300

Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala
305                 310                 315                 320

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

Gly Arg Phe Thr Ile Ser Arg Glu Asn Thr Gln Lys Thr Leu Tyr Leu
            340                 345                 350

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

Leu Asp Gly Arg Asp Gly Trp Val Ala Tyr Trp Gly Gln Gly Thr Leu
    370                 375                 380
```

```
Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
385                 390                 395                 400

Gly Gly Gly Ser Asn Phe Met Leu Thr Gln Pro Ser Ser Val Ser Gly
                405                 410                 415

Val Pro Gly Gln Arg Val Thr Ile Ser Cys Thr Gly Asn Thr Gly Asn
            420                 425                 430

Ile Gly Ser Asn Tyr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala
        435                 440                 445

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

Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile
465                 470                 475                 480

Thr Gly Phe Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr
                485                 490                 495

Ser Ser Gly Phe Ile Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ala
            500                 505                 510

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

Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
    530                 535                 540

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
```

```
545                 550                 555                 560

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

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
            580                 585                 590

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
        595                 600                 605

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
    610                 615                 620

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

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

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

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
        675                 680                 685

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

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

```
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
                725                 730                 735


Lys Ser Leu Ser Leu Ser Pro Gly
            740
```

<210> 119
<211> 744
<212> PRT
<213> Artificial

<220>
<223> Full-length amino acid sequence of NYF-0004-HC2-k delete

<400> 119

```
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                   10                  15


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


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


Phe Asn Tyr Tyr Gly Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly
    50                  55                  60


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


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

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

Val Tyr Tyr Cys Thr Leu Asp Gly Arg Asp Gly Trp Val Ala Tyr Trp
        115                 120                 125

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

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asn Phe Met Leu Thr Gln Pro
145                 150                 155                 160

Ser Ser Val Ser Gly Val Pro Gly Gln Arg Val Thr Ile Ser Cys Thr
                165                 170                 175

Gly Asn Thr Gly Asn Ile Gly Ser Asn Tyr Val Asn Trp Tyr Gln Gln
            180                 185                 190

Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Arg Asp Asp Lys Arg
        195                 200                 205

Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser
    210                 215                 220

Ala Ser Leu Ala Ile Thr Gly Phe Gln Ala Glu Asp Glu Ala Asp Tyr
225                 230                 235                 240

Tyr Cys Gln Ser Tyr Ser Ser Gly Phe Ile Phe Gly Gly Gly Thr Lys
                245                 250                 255

Leu Thr Val Leu Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
```

```
            260                 265                 270

Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu Thr Pro Ser Cys Ser
        275                 280                 285

Ala Ser Gly Phe Ser Ile Arg Ser Tyr Asp Met His Trp Val Arg Gln
    290                 295                 300

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Thr Ile Ser Tyr Asp Gly
305                 310                 315                 320

Ser Gln Lys Tyr Phe Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Phe
                325                 330                 335

Arg Asp Glu Ser Glu Asn Met Val Tyr Leu Gln Met Ser Gly Leu Arg
            340                 345                 350

Val Glu Asp Thr Ala Val Tyr His Cys Ala Arg Gly Ser Ser Asn His
        355                 360                 365

Tyr Glu Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser
    370                 375                 380

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
385                 390                 395                 400

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Ala Ala Pro Gly Gln
                405                 410                 415

Lys Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn
            420                 425                 430
```

```
Tyr Val Ser Trp Tyr Gln Arg Leu Pro Gly Thr Ala Pro Lys Leu Leu
        435                 440                 445

Ile Tyr Asp Asn Asn Lys Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser
    450                 455                 460

Gly Ser Lys Ser Gly Thr Ser Ala Thr Leu Gly Ile Thr Gly Leu Gln
465                 470                 475                 480

Thr Gly Asp Glu Ala Asp Tyr Tyr Cys Gly Ala Trp Asp Ser Ser Leu
                485                 490                 495

Ser Ala Pro Trp Val Phe Gly Gly Gly Thr Lys Val Thr Val Leu Ala
            500                 505                 510

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

Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
    530                 535                 540

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

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

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
            580                 585                 590

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
```

595 600 605

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
610 615 620

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

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

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

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
675 680 685

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

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

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

Lys Ser Leu Ser Leu Ser Pro Gly
740

<210> 120
<211> 744
<212> PRT

<213> Artificial

<220>
<223> Full-length amino acid sequence of NYF-0011-HC2-k delete

<400> 120

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

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

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

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

Leu Glu Trp Val Ala Thr Ile Ser Tyr Asp Gly Ser Gln Lys Tyr Phe
65 70 75 80

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

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

Val Tyr His Cys Ala Arg Gly Ser Ser Gly His Tyr Glu Ala Phe Asp
115 120 125

Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly
130 135 140

```
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr
145                 150                 155                 160

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

Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Trp Tyr Val Ser Trp Tyr
            180                 185                 190

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

Lys Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly
    210                 215                 220

Thr Ser Ala Thr Leu Gly Ile Thr Gly Leu Gln Thr Gly Asp Glu Ala
225                 230                 235                 240

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

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

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        275                 280                 285

Leu Arg Leu Ser Cys Ala Ala Ser Gly Val Thr Phe Asn Tyr Tyr Gly
    290                 295                 300

Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala
```

```
305                 310                 315                 320

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

Gly Arg Phe Thr Ile Ser Arg Glu Asn Thr Gln Lys Thr Leu Tyr Leu
            340                 345                 350

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

Leu Asp Gly Arg Asp Gly Trp Val Ala Tyr Trp Gly Gln Gly Thr Leu
    370                 375                 380

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
385                 390                 395                 400

Gly Gly Gly Ser Asn Phe Met Leu Thr Gln Pro Ser Ser Val Ser Gly
                405                 410                 415

Val Pro Gly Gln Arg Val Thr Ile Ser Cys Thr Gly Asn Thr Gly Asn
            420                 425                 430

Ile Gly Ser Asn Tyr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala
        435                 440                 445

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

Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile
465                 470                 475                 480
```

```
Thr Gly Phe Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr
                485                 490                 495

Ser Ser Gly Phe Ile Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ala
            500                 505                 510

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

Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
    530                 535                 540

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

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

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
            580                 585                 590

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
        595                 600                 605

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
    610                 615                 620

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

Pro Arg Glu Pro Gln Val Tyr Val Tyr Pro Pro Ser Arg Asp Glu Leu
```

645 650 655

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

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
675 680 685

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

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

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

Lys Ser Leu Ser Leu Ser Pro Gly
740

<210> 121
<211> 9
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of point mutated NY-ESO peptide 1F

<400> 121

Phe Leu Leu Met Trp Ile Thr Gln Cys
1 5

<210> 122

<211> 9
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of point mutated NY-ESO peptide 2M

<400> 122

Ser Met Leu Met Trp Ile Thr Gln Cys
1 5

<210> 123
<211> 9
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of point mutated NY-ESO peptide 3A

<400> 123

Ser Leu Ala Met Trp Ile Thr Gln Cys
1 5

<210> 124
<211> 9
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of point mutated NY-ESO peptide 4A

<400> 124

Ser Leu Leu Ala Trp Ile Thr Gln Cys
1 5

<210> 125

<211> 9
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of point mutated NY-ESO peptide 5A

<400> 125

Ser Leu Leu Met Ala Ile Thr Gln Cys
1 5

<210> 126
<211> 9
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of point mutated NY-ESO peptide 6L

<400> 126

Ser Leu Leu Met Trp Leu Thr Gln Cys
1 5

<210> 127
<211> 9
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of point mutated NY-ESO peptide 7F

<400> 127

Ser Leu Leu Met Trp Ile Phe Gln Cys
1 5

<210> 128

<211> 9
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of point mutated NY-ESO peptide 8A

<400> 128

Ser Leu Leu Met Trp Ile Thr Ala Cys
1 5

<210> 129
<211> 9
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of point mutated NY-ESO peptide 9A

<400> 129

Ser Leu Leu Met Trp Ile Thr Gln Ala
1 5

<210> 130
<211> 9
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of gp100 peptide

<400> 130

Ile Met Asp Gln Val Pro Phe Ser Val
1 5

<210> 131

<211> 9
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of homologous peptide DOLPP1

<400> 131

Ser Gln Phe Met Trp Phe Phe Ser Val
1 5

<210> 132
<211> 9
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of homologous peptide IL20RB

<400> 132

Ser Leu Phe Met Trp Phe Phe Tyr Ala
1 5

<210> 133
<211> 9
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of homologous peptide PRKD2

<400> 133

Ser Leu Asp Met Trp Ser Val Gly Val
1 5

<210> 134

<211> 9
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of homologous peptide CD163

<400> 134

Ser Ile Pro Met Trp Val Asp Asn Val
1 5

<210> 135
<211> 9
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of homologous peptide P2RY8

<400> 135

Ser Val Ala Met Trp Ala Val Phe Leu
1 5

<210> 136
<211> 269
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of C3E-7034

<400> 136

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

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Val Thr Phe Asn Tyr

```
            20                  25                  30

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

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

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

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

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

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125

Ser Gly Gly Gly Gly Ser Asn Phe Met Leu Thr Gln Pro His Ser Val
    130                 135                 140

Ser Glu Ser Pro Gly Lys Thr Val Thr Ile Ser Cys Lys Arg Asn Thr
145                 150                 155                 160

Gly Asn Ile Gly Ser Asn Tyr Val Asn Trp Tyr Gln Gln His Glu Gly
                165                 170                 175

Ser Ser Pro Thr Thr Ile Ile Tyr Arg Asp Asp Lys Arg Pro Asp Gly
            180                 185                 190
```

```
Val Ser Asp Arg Phe Ser Gly Ser Ile Asp Arg Ser Ser Lys Ser Ala
        195                 200                 205

Ser Leu Thr Ile Ser Asn Leu Lys Thr Glu Asp Glu Ala Asp Tyr Phe
    210                 215                 220

Cys Gln Ser Tyr Ser Ser Gly Phe Ile Phe Gly Gly Gly Thr Lys Leu
225                 230                 235                 240

Thr Val Leu Gly Ala Ala Ala Gly Ala Gly Gly Asp Tyr Lys Asp Asp
                245                 250                 255

Asp Asp Lys Gly Ala Ala Ala His His His His His His
            260                 265
```

<210> 137
<211> 267
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of C3E-7036

<400> 137

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

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

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

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

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

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

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

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125

Ser Gly Gly Gly Gly Ser Asn Phe Met Leu Thr Gln Pro Ser Ser Val
    130                 135                 140

Ser Gly Val Pro Gly Gln Arg Val Thr Ile Ser Cys Thr Gly Asn Thr
145                 150                 155                 160

Gly Asn Ile Gly Ser Asn Tyr Val Asn Trp Tyr Gln Gln Leu Pro Gly
                165                 170                 175

Thr Ala Pro Lys Leu Leu Ile Tyr Arg Asp Asp Lys Arg Pro Ser Gly
            180                 185                 190

Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu
        195                 200                 205

Ala Ile Thr Gly Phe Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln
```

```
    210                 215                 220

Ser Tyr Ser Ser Gly Phe Ile Phe Gly Gly Gly Thr Lys Leu Thr Val
225                 230                 235                 240

Leu Gly Ala Ala Ala Gly Ala Gly Gly Asp Tyr Lys Asp Asp Asp Asp
                245                 250                 255

Lys Gly Ala Ala Ala His His His His His His
            260                 265
```

<210> 138
<211> 267
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of C3E-7085

<400> 138

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

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

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

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

Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Thr Gln Lys Thr Leu
```

```
65                  70                  75                  80

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

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

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125

Ser Gly Gly Gly Gly Ser Asn Phe Met Leu Thr Gln Pro Ser Ser Val
    130                 135                 140

Ser Gly Val Pro Gly Gln Arg Val Thr Ile Ser Cys Thr Gly Asn Thr
145                 150                 155                 160

Gly Asn Ile Gly Ser Asn Tyr Val Asn Trp Tyr Gln Gln Leu Pro Gly
                165                 170                 175

Thr Ala Pro Lys Leu Leu Ile Tyr Arg Asp Asp Lys Arg Pro Ser Gly
            180                 185                 190

Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu
        195                 200                 205

Ala Ile Thr Gly Phe Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln
    210                 215                 220

Ser Tyr Ser Ser Gly Phe Ile Phe Gly Gly Gly Thr Lys Leu Thr Val
225                 230                 235                 240
```

```
Leu Gly Ala Ala Ala Gly Ala Gly Gly Asp Tyr Lys Asp Asp Asp Asp
                245                 250                 255


Lys Gly Ala Ala Ala His His His His His His
            260                 265


<210>  139
<211>  269
<212>  PRT
<213>  Artificial

<220>
<223>  Amino acid sequence of C3E-7088

<400>  139

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


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


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


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


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


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

```
Cys Thr Leu Asp Gly Arg Asp Gly Trp Val Ala Tyr Trp Gly Gln Gly
            100                 105                 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125

Ser Gly Gly Gly Gly Ser Asn Phe Met Leu Thr Gln Pro His Ser Val
    130                 135                 140

Ser Glu Ser Pro Gly Lys Thr Val Thr Ile Ser Cys Lys Arg Asn Thr
145                 150                 155                 160

Gly Asn Ile Gly Ser Asn Tyr Val Asn Trp Tyr Gln Gln His Glu Gly
                165                 170                 175

Ser Ser Pro Thr Thr Ile Ile Tyr Arg Asn Asp Lys Arg Pro Asp Gly
            180                 185                 190

Val Ser Asp Arg Phe Ser Gly Ser Ile Asp Arg Ser Ser Lys Ser Ala
        195                 200                 205

Ser Leu Thr Ile Ser Asn Leu Lys Thr Glu Asp Glu Ala Asp Tyr Phe
    210                 215                 220

Cys Gln Ser Tyr Ser Ser Gly Phe Ile Phe Gly Gly Gly Thr Lys Leu
225                 230                 235                 240

Thr Val Leu Gly Ala Ala Ala Gly Ala Gly Gly Asp Tyr Lys Asp Asp
                245                 250                 255

Asp Asp Lys Gly Ala Ala Ala His His His His His His
```

260 265

<210> 140
<211> 269
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of C3E-7093

<400> 140

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

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

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

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

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

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

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

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly

```
        115                 120                 125

Ser Gly Gly Gly Gly Ser Asn Phe Met Leu Thr Gln Pro His Ser Val
    130                 135                 140

Ser Glu Ser Pro Gly Lys Thr Val Thr Ile Ser Cys Lys Arg Asn Thr
145                 150                 155                 160

Gly Asn Ile Gly Ser Asn Tyr Val Asn Trp Tyr Gln Gln His Glu Gly
                165                 170                 175

Ser Ser Pro Thr Thr Ile Ile Tyr Arg Asn Asp Lys Arg Pro Asp Gly
            180                 185                 190

Val Ser Asp Arg Phe Ser Gly Ser Ile Asp Arg Ser Ser Lys Ser Ala
        195                 200                 205

Ser Leu Thr Ile Ser Asn Leu Lys Thr Glu Asp Glu Ala Asp Tyr Phe
    210                 215                 220

Cys Gln Ser Tyr Ser Ser Gly Phe Ile Phe Gly Gly Gly Thr Lys Leu
225                 230                 235                 240

Thr Val Leu Gly Ala Ala Ala Gly Ala Gly Gly Asp Tyr Lys Asp Asp
                245                 250                 255

Asp Asp Lys Gly Ala Ala Ala His His His His His His
            260                 265
```

<210> 141
<211> 8
<212> PRT

<213> Artificial

<220>
<223> Amino acid sequence of heavy chain CDR1 of C3E-7085

<400> 141

Gly Val Thr Phe Asn Tyr Tyr Gly
1 5

<210> 142
<211> 8
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of heavy chain CDR2 of C3E-7085

<400> 142

Ile Thr Arg Ser Gly Gly Arg Ile
1 5

<210> 143
<211> 11
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of heavy chain CDR3 of C3E-7085

<400> 143

Thr Leu Asp Gly Arg Asp Gly Trp Val Ala Tyr
1 5 10

<210> 144
<211> 8
<212> PRT

<213> Artificial

<220>
<223> Amino acid sequence of light chain CDR1 of C3E-7085

<400> 144

Thr Gly Asn Ile Gly Ser Asn Tyr
1 5

<210> 145
<211> 3
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of light chain CDR2 of C3E-7085

<400> 145

Arg Asp Asp
1

<210> 146
<211> 8
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of light chain CDR3 of C3E-7085

<400> 146

Gln Ser Tyr Ser Ser Gly Phe Ile
1 5

<210> 147
<211> 269
<212> PRT

<213> Artificial

<220>
<223> Amino acid sequence of C3E-7078

<400> 147

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


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


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


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


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


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


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


Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125


Ser Gly Gly Gly Gly Ser Asn Phe Met Leu Thr Gln Pro His Ser Val
    130                 135                 140
```

```
Ser Glu Ser Pro Gly Lys Thr Val Thr Ile Ser Cys Lys Arg Asn Thr
145                 150                 155                 160

Gly Asn Ile Gly Ser Asn Tyr Val Asn Trp Tyr Gln Gln His Glu Gly
                165                 170                 175

Ser Ser Pro Thr Thr Ile Ile Tyr Arg Asp Asp Lys Arg Pro Asp Gly
            180                 185                 190

Val Ser Asp Arg Phe Ser Gly Ser Ile Asp Arg Ser Ser Lys Ser Ala
        195                 200                 205

Ser Leu Thr Ile Ser Asn Leu Lys Thr Glu Asp Glu Ala Asp Tyr Phe
    210                 215                 220

Cys Gln Ser Tyr Ser Ser Gly Phe Ile Phe Gly Gly Gly Thr Lys Leu
225                 230                 235                 240

Thr Val Leu Gly Ala Ala Ala Gly Ala Gly Gly Asp Tyr Lys Asp Asp
                245                 250                 255

Asp Asp Lys Gly Ala Ala Ala His His His His His His
            260                 265
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<210> 148
<211> 2235
<212> DNA
<213> Artificial

<220>
<223> Full-length nucleotide sequence of NYF-0014-HC2

<400> 148

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tcctgttcag cgtctggatt ctccatccgt agttatgata tacactgggt ccgccaggct 180

ccaggcaagg ggctagagtg ggtggccact atatcatatg atggaagtca gaagtacttc 240

gcagactccg tgaagggccg atttaccatc ttcagagacg aatcggagaa catggtgtat 300

ctgcaaatga gcggcctgag agttgaggac acggctgttt atcactgtgc gagagggagt 360

agtggtcatt atgaggcttt tgatatctgg ggccaaggga caatggtcac cgtctcttca 420

ggtggaggcg gttcaggcgg aggtggcagc ggcggtggcg ggagtcagtc tgtgttgacg 480

cagccgccct cagtgtctgc ggccccagga cagaaggtca ccatctcctg ctctggaagc 540

agctccaaca ttgggaataa ttatgtatcc tggtaccagc agctcccagg aacagccccc 600

aaactcctca tttatgacaa taataagcga ccctcaggga ttcctgaccg attctctggc 660

tccaagtctg gcacgtcagc caccctgggc atcaccggac tccagactgg ggacgaggcc 720

gattattact gcggaacatg ggatagcagc ctgagtgccc cttgggtgtt cggcggaggg 780

accaaggtca ccgtcctagg gggaggcggt tcagaagtgc agctggtgga atccgggggg 840

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aactactatg gcatgtcttg gatccgccag gcacctggaa agggcctgga gtgggtggcc 960

agcatcacta ggtccggcgg gcgaatctac tatcccgaca gcgtcaaggg caggttcaca 1020

atttcccgcg agaacacaca gaaaactctg tacctgcaga tgaatagcct gagagccgaa 1080

gatacagctg tgtactattg cactctggac ggcagggatg ggtgggtcgc ctattggggg 1140

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cgggtgacca ttagctgtac gggtaatacc gggaatatcg ggtctaacta cgtgaactgg 1320

tatcagcagc ttccagggac agctcccaag ttgctgatct atcgcgacga caaaagaccc 1380

tcaggggtcc ctgaccgatt tagtggcagc aaaagcggta cttccgcttc cctggcgata 1440

accggctttc aggccgaaga tgaggcagac tactattgcc agtcatattc cagcggcttc 1500

atcttcggag gcggaactaa gctgacagtg ttggcagccg agcccaaatc ttctgacaaa 1560

actcacacat gcccaccctg cccagcacct gaagccgcag ggggaccctc agtcttcctc 1620

ttccccccaa aacccaagga caccctcatg atctcccgga cccctgaggt cacatgcgtg 1680

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gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgcaag 1860

gtctccaaca aagccctccc agcccccatc gagaaaacca tctccaaagc caaaggccag 1920

ccccgggaac cacaggtgta cgtgtacccc ccatcccggg acgagctgac caagaaccag 1980

gtcagcctga cctgcctggt caaaggcttc tatcccagcg acatcgccgt ggagtgggag 2040

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tccttcgccc tcgtgagcaa gctcaccgtg gacaagagca ggtggcagca gggcaacgtc 2160

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ctgtctcccg gcaag 2235

<210> 149
<211> 745
<212> PRT
<213> Artificial

<220>
<223> Full-length amino acid sequence of NYF-0014-HC2

<400> 149

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Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                  10                  15

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

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

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

Leu Glu Trp Val Ala Thr Ile Ser Tyr Asp Gly Ser Gln Lys Tyr Phe
65                  70                  75                  80

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

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

Val Tyr His Cys Ala Arg Gly Ser Ser Gly His Tyr Glu Ala Phe Asp
        115                 120                 125

Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr
145                 150                 155                 160
```

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

Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn Tyr Val Ser Trp Tyr
            180                 185                 190

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

Lys Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly
    210                 215                 220

Thr Ser Ala Thr Leu Gly Ile Thr Gly Leu Gln Thr Gly Asp Glu Ala
225                 230                 235                 240

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

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

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        275                 280                 285

Leu Arg Leu Ser Cys Ala Ala Ser Gly Val Thr Phe Asn Tyr Tyr Gly
    290                 295                 300

Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala
305                 310                 315                 320

Ser Ile Thr Arg Ser Gly Gly Arg Ile Tyr Tyr Pro Asp Ser Val Lys
```

```
                325                 330                 335

Gly Arg Phe Thr Ile Ser Arg Glu Asn Thr Gln Lys Thr Leu Tyr Leu
            340                 345                 350

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

Leu Asp Gly Arg Asp Gly Trp Val Ala Tyr Trp Gly Gln Gly Thr Leu
    370                 375                 380

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
385                 390                 395                 400

Gly Gly Gly Ser Asn Phe Met Leu Thr Gln Pro Ser Ser Val Ser Gly
                405                 410                 415

Val Pro Gly Gln Arg Val Thr Ile Ser Cys Thr Gly Asn Thr Gly Asn
            420                 425                 430

Ile Gly Ser Asn Tyr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala
        435                 440                 445

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

Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile
465                 470                 475                 480

Thr Gly Phe Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr
                485                 490                 495
```

```
Ser Ser Gly Phe Ile Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ala
            500                 505                 510

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

Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
    530                 535                 540

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

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

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
            580                 585                 590

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
        595                 600                 605

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
    610                 615                 620

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

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

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
```

660 665 670

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
675 680 685

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

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

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

Lys Ser Leu Ser Leu Ser Pro Gly Lys
740 745

<210> 150
<211> 745
<212> PRT
<213> Artificial

<220>
<223> Full-length amino acid sequence of NYF-0082-HC2

<400> 150

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

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

Gln Pro Gly Arg Ser Leu Thr Pro Ser Cys Ser Ala Ser Gly Phe Ser

```
        35                  40                  45

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

Leu Glu Trp Val Ala Thr Ile Ser Tyr Asp Gly Ser Gln Lys Tyr Phe
65                  70                  75                  80

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

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

Val Tyr His Cys Ala Arg Gly Ser Ser Gly His Tyr Glu Ala Phe Asp
        115                 120                 125

Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr
145                 150                 155                 160

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

Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn Tyr Val Ser Trp Tyr
            180                 185                 190

Gln Arg Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Asp Asn Asn
        195                 200                 205
```

```
Lys Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly
    210                 215                 220

Thr Ser Ala Thr Leu Gly Ile Thr Gly Leu Gln Thr Gly Asp Glu Ala
225                 230                 235                 240

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

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

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        275                 280                 285

Leu Arg Leu Ser Cys Ala Ala Ser Gly Val Thr Phe Asn Tyr Tyr Gly
    290                 295                 300

Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala
305                 310                 315                 320

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

Gly Arg Phe Thr Ile Ser Arg Glu Asn Thr Gln Lys Thr Leu Tyr Leu
            340                 345                 350

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

Leu Asp Gly Arg Asp Gly Trp Val Ala Tyr Trp Gly Gln Gly Thr Leu
```

```
    370                 375                 380

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
385                 390                 395                 400

Gly Gly Gly Ser Asn Phe Met Leu Thr Gln Pro Ser Ser Val Ser Gly
                405                 410                 415

Val Pro Gly Gln Arg Val Thr Ile Ser Cys Thr Gly Asn Thr Gly Asn
            420                 425                 430

Ile Gly Ser Asn Tyr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala
        435                 440                 445

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

Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile
465                 470                 475                 480

Thr Gly Phe Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr
                485                 490                 495

Ser Ser Gly Phe Ile Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ala
            500                 505                 510

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

Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
    530                 535                 540
```

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

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

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
            580                 585                 590

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
        595                 600                 605

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
    610                 615                 620

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

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

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

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
        675                 680                 685

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

Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
```

705 710 715 720

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

Lys Ser Leu Ser Leu Ser Pro Gly Lys
740 745

<210> 151
<211> 207
<212> PRT
<213> Homo sapiens

<400> 151

Met Gln Ser Gly Thr His Trp Arg Val Leu Gly Leu Cys Leu Leu Ser
1 5 10 15

Val Gly Val Trp Gly Gln Asp Gly Asn Glu Glu Met Gly Gly Ile Thr
20 25 30

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

Cys Pro Gln Tyr Pro Gly Ser Glu Ile Leu Trp Gln His Asn Asp Lys
50 55 60

Asn Ile Gly Gly Asp Glu Asp Asp Lys Asn Ile Gly Ser Asp Glu Asp
65 70 75 80

His Leu Ser Leu Lys Glu Phe Ser Glu Leu Glu Gln Ser Gly Tyr Tyr
85 90 95

```
Val Cys Tyr Pro Arg Gly Ser Lys Pro Glu Asp Ala Asn Phe Tyr Leu
            100                 105                 110

Tyr Leu Arg Ala Arg Val Cys Glu Asn Cys Met Glu Met Asp Val Met
        115                 120                 125

Ser Val Ala Thr Ile Val Ile Val Asp Ile Cys Ile Thr Gly Gly Leu
    130                 135                 140

Leu Leu Leu Val Tyr Tyr Trp Ser Lys Asn Arg Lys Ala Lys Ala Lys
145                 150                 155                 160

Pro Val Thr Arg Gly Ala Gly Ala Gly Gly Arg Gln Arg Gly Gln Asn
                165                 170                 175

Lys Glu Arg Pro Pro Pro Val Pro Asn Pro Asp Tyr Glu Pro Ile Arg
            180                 185                 190

Lys Gly Gln Arg Asp Leu Tyr Ser Gly Leu Asn Gln Arg Arg Ile
        195                 200                 205
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<210> 152
<211> 2235
<212> DNA
<213> Artificial

<220>
<223> Full-length nucleotide sequence of NYZ-0038-HC2

<400> 152
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cctggcaaag gtcttgaatg ggttgccact atctcctacg acgggtctca gaaatattat 240

gcggattcag tgaaggggcg gttcacaatt tcacgagacg agtcaaagaa tacactgtac 300

ctccaaatga attcactgag agccgaggat actgcagtct atcattgtgc aagagggtcc 360

tcaggccact acgaggcctt tgatatatgg ggccaaggca ccttggtaac cgttagtagc 420

ggaggtggag gaagcggagg cggcggttcc ggaggaggtg gaagtcaatc cgttctgact 480

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tcaggggtcc ctgaccgatt tagtggcagc aaaagcggta cttccgcttc cctggcgata 1440

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atcttcggag gcggaactaa gctgacagtg ttggcagccg agcccaaatc ttctgacaaa 1560

actcacacat gcccaccctg cccagcacct gaagccgcag ggggaccctc agtcttcctc 1620

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gtggtgtcag tgagccacga agaccctgag gtcaagttca actggtacgt ggacggcgtg 1740

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gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgcaag 1860

gtctccaaca aagccctccc agcccccatc gagaaaacca tctccaaagc caaaggccag 1920

ccccgggaac cacaggtgta cgtgtacccc ccatcccggg acgagctgac caagaaccag 1980

gtcagcctga cctgcctggt caaaggcttc tatcccagcg acatcgccgt ggagtgggag 2040

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tccttcgccc tcgtgagcaa gctcaccgtg gacaagagca ggtggcagca gggcaacgtc 2160

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<210> 153
<211> 2250
<212> DNA
<213> Artificial

<220>
<223> Full-length nucleotide sequence of NYZ-0082-HC2

<400> 153
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cctggcaaag gtcttgaatg ggttgccact atctcctacg acgggtctca gaaatattat 240

gcggattcag tgaaggggcg gttcacaatt tcacgagacg agtcaaagaa tacactgtac 300

ctccaaatga attcactgag agccgaggat actgcagtct atcattgtgc aagagggtcc 360

tcaggccact acgaggcctt tgatatatgg ggccaaggca ccttggtaac cgttagtagc 420

ggaggtggag gaagcggagg cggcggttcc ggaggaggtg gaagtggagg aggtggatct 480

caatccgttc tgactcagcc accctccgcc tctggcaccc cgggccaacg ggtcacaata 540

tcatgttctg gctcttcaag caacatcgga aactggtacg tgagctggta ccagcagctc 600

cccggcacgg cgcccaagct tctgatatat gacaacaaca aacggcccag tggagttcct 660

gacagattca gtgggtctaa aagtggtaca agcgctagcc tggccataag tggtctgcag 720

agtgaagatg aggcggacta ttattgcgga acctgggact ccagcctgag cgctccctgg 780

gttttcggcg gaggtactaa gctgaccgtc ttgggaggag gcggttcaga agtgcagctg 840

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agcctgagag ccgaagatac agctgtgtac tattgcactc tggacggcag ggatgggtgg 1140

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ggaggaggca gtgggggagg cgggtcaaac tttatgctca ctcagccgtc ctctgtttct 1260

ggcgtacctg gccaacgggt gaccattagc tgtacgggta ataccgggaa tatcgggtct 1320

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aaatcttctg acaaaactca cacatgccca ccctgcccag cacctgaagc cgcaggggga 1620

ccctcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccccct 1680

gaggtcacat gcgtggtggt gtcagtgagc cacgaagacc ctgaggtcaa gttcaactgg 1740

tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cccgggagga gcagtacaac 1800

agcacgtacc gggtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 1860

gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1920

aaagccaaag gccagccccg ggaaccacag gtgtacgtgt acccccccatc ccgggacgag 1980

ctgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc 2040

gccgtggagt gggagagcaa tggccagccc gagaacaact acaagaccac ccctcccgtg 2100

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cagaagagcc tctccctgtc tcccggcaag 2250

<210> 154
<211> 2250
<212> DNA
<213> Artificial

<220>
<223> Full-length nucleotide sequence of NYZ-0083-HC2

<400> 154
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gaggtacagc tggtggaatc cggtggaggc cttgtgcaac cgggaggctc cctgcgactc 120

tcttgcgccg catctggctt ttccatacga tcctacgata ttcattgggt ccgacaagcc 180

cctggcaaag gtcttgaatg ggttgccact atctcctacg acgggtctca gaaatattat 240

gcggattcag tgaaggggcg gttcacaatt tcacgagacg agtcaaagaa tacactgtac 300

ctccaaatga attcactgag agccgaggat actgcagtct atcattgtgc aagagggtcc 360

tcaggccact acgaggcctt tgatatatgg ggccaaggca ccttggtaac cgttagtagc 420

ggaggtggag gaagcggagg cggcggttcc ggaggaggtg gaagtggagg aggtggatct 480

caatccgttc tgactcagcc accctccgcc tctggcaccc cgggccaacg ggtcacaata 540

tcatgttctg gctcttcaag caacatcgga aactggtacg tgagctggta ccagcagctc 600

cccggcacgg cgcccaagct tctgatatat gacaacaaca aacggcccag tggagttcct 660

gacagattca gtgggtctaa aagtggtaca agcgctagcc tggccataag tggtctgcag 720

agtgaagatg aggcggacta ttattgcgga acctgggact ccagcctgag cgctccctgg 780

gttttcggcg gaggtactaa gctgaccgtc ttgggaggag gcggttcaga agtgcagctg 840

gtggaatccg gggggggcct ggtgcagcct gggggggagcc tgagactgag ttgtgccgcc 900

tctggggtga catttaacta ctatggcatg tcttggatcc gccaggcacc tggaaagtgt 960

ctggagtggg tggccagcat cactaggtcc ggcgggcgaa tctactatcc cgacagcgtc 1020

aagggcaggt tcacaatttc ccgcgagaac acacagaaaa ctctgtacct gcagatgaat 1080

agcctgagag ccgaagatac agctgtgtac tattgcactc tggacggcag ggatgggtgg 1140

gtcgcctatt gggggcaggg aaccctggtg acagtcagct ccggaggagg aggatctggc 1200

ggaggaggca gtgggggagg cgggtcaaac tttatgctca ctcagccgtc ctctgtttct 1260

ggcgtacctg gccaacgggt gaccattagc tgtacgggta ataccgggaa tatcgggtct 1320

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tattccagcg gcttcatctt cggatgtgga actaagctga cagtgttggc agccgagccc 1560

aaatcttctg acaaaactca cacatgccca ccctgcccag cacctgaagc cgcaggggga 1620

ccctcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggacccct 1680

gaggtcacat gcgtggtggt gtcagtgagc cacgaagacc ctgaggtcaa gttcaactgg 1740

tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cccgggagga gcagtacaac 1800

agcacgtacc gggtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 1860

gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1920

aaagccaaag gccagccccg ggaaccacag gtgtacgtgt acccccccatc ccgggacgag 1980

ctgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc 2040

gccgtggagt gggagagcaa tggccagccc gagaacaact acaagaccac ccctcccgtg 2100

ctggactccg acggctcctt cgccctcgtg agcaagctca ccgtggacaa gagcaggtgg 2160

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cagaagagcc tctccctgtc tcccggcaag 2250

<210> 155
<211> 745
<212> PRT
<213> Artificial

<220>
<223> Full-length amino acid sequence of NYZ-0038-HC2

<400> 155

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Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                  10                  15

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

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

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

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

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

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

Val Tyr His Cys Ala Arg Gly Ser Ser Gly His Tyr Glu Ala Phe Asp
        115                 120                 125

Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr
145                 150                 155                 160
```

```
Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln Arg Val Thr Ile Ser
                165                 170                 175

Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Trp Tyr Val Ser Trp Tyr
            180                 185                 190

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

Lys Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly
    210                 215                 220

Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln Ser Glu Asp Glu Ala
225                 230                 235                 240

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

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

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        275                 280                 285

Leu Arg Leu Ser Cys Ala Ala Ser Gly Val Thr Phe Asn Tyr Tyr Gly
    290                 295                 300

Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala
305                 310                 315                 320

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

```
Gly Arg Phe Thr Ile Ser Arg Glu Asn Thr Gln Lys Thr Leu Tyr Leu
            340                 345                 350

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

Leu Asp Gly Arg Asp Gly Trp Val Ala Tyr Trp Gly Cys Gly Thr Leu
    370                 375                 380

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
385                 390                 395                 400

Gly Gly Gly Ser Asn Phe Met Leu Thr Gln Pro Ser Ser Val Ser Gly
                405                 410                 415

Val Pro Gly Gln Arg Val Thr Ile Ser Cys Thr Gly Asn Thr Gly Asn
            420                 425                 430

Ile Gly Ser Asn Tyr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Cys
        435                 440                 445

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

Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile
465                 470                 475                 480

Thr Gly Phe Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr
                485                 490                 495
```

```
Ser Ser Gly Phe Ile Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ala
            500                 505                 510

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

Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
    530                 535                 540

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

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

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
            580                 585                 590

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
        595                 600                 605

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
    610                 615                 620

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

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

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
            660                 665                 670
```

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
675 680 685

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

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

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

Lys Ser Leu Ser Leu Ser Pro Gly Lys
740 745

<210> 156
<211> 750
<212> PRT
<213> Artificial

<220>
<223> Full-length amino acid sequence of NYZ-0082-HC2

<400> 156

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

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

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

```
Ile Arg Ser Tyr Asp Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly
    50                  55                  60

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

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

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

Val Tyr His Cys Ala Arg Gly Ser Ser Gly His Tyr Glu Ala Phe Asp
        115                 120                 125

Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
145                 150                 155                 160

Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
                165                 170                 175

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Trp
            180                 185                 190

Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
        195                 200                 205
```

```
Ile Tyr Asp Asn Asn Lys Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    210                 215                 220

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
225                 230                 235                 240

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

Ser Ala Pro Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            260                 265                 270

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
        275                 280                 285

Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Val Thr
    290                 295                 300

Phe Asn Tyr Tyr Gly Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly
305                 310                 315                 320

Leu Glu Trp Val Ala Ser Ile Thr Arg Ser Gly Gly Arg Ile Tyr Tyr
                325                 330                 335

Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Thr Gln
            340                 345                 350

Lys Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
        355                 360                 365

Val Tyr Tyr Cys Thr Leu Asp Gly Arg Asp Gly Trp Val Ala Tyr Trp
    370                 375                 380
```

```
Gly Cys Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
385                 390                 395                 400

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asn Phe Met Leu Thr Gln Pro
                405                 410                 415

Ser Ser Val Ser Gly Val Pro Gly Gln Arg Val Thr Ile Ser Cys Thr
            420                 425                 430

Gly Asn Thr Gly Asn Ile Gly Ser Asn Tyr Val Asn Trp Tyr Gln Gln
        435                 440                 445

Leu Pro Gly Thr Cys Pro Lys Leu Leu Ile Tyr Arg Asp Asp Lys Arg
    450                 455                 460

Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser
465                 470                 475                 480

Ala Ser Leu Ala Ile Thr Gly Phe Gln Ala Glu Asp Glu Ala Asp Tyr
                485                 490                 495

Tyr Cys Gln Ser Tyr Ser Ser Gly Phe Ile Phe Gly Gly Gly Thr Lys
            500                 505                 510

Leu Thr Val Leu Ala Ala Glu Pro Lys Ser Ser Asp Lys Thr His Thr
        515                 520                 525

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
    530                 535                 540
```

```
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
545                 550                 555                 560

Glu Val Thr Cys Val Val Val Ser Val Ser His Glu Asp Pro Glu Val
                565                 570                 575

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
            580                 585                 590

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
        595                 600                 605

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
    610                 615                 620

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

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Val Tyr Pro Pro
                645                 650                 655

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
            660                 665                 670

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
        675                 680                 685

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
    690                 695                 700

Gly Ser Phe Ala Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
705                 710                 715                 720
```

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
725 730 735

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
740 745 750

<210> 157
<211> 750
<212> PRT
<213> Artificial

<220>
<223> Full-length amino acid sequence of NYZ-0083-HC2

<400> 157

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

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

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

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

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

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

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

Val Tyr His Cys Ala Arg Gly Ser Ser Gly His Tyr Glu Ala Phe Asp
        115                 120                 125

Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
145                 150                 155                 160

Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
                165                 170                 175

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Trp
            180                 185                 190

Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
        195                 200                 205

Ile Tyr Asp Asn Asn Lys Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    210                 215                 220

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
225                 230                 235                 240

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gly Thr Trp Asp Ser Ser Leu
                245                 250                 255
```

```
Ser Ala Pro Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            260                 265                 270

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
        275                 280                 285

Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Val Thr
    290                 295                 300

Phe Asn Tyr Tyr Gly Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Cys
305                 310                 315                 320

Leu Glu Trp Val Ala Ser Ile Thr Arg Ser Gly Gly Arg Ile Tyr Tyr
                325                 330                 335

Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Thr Gln
            340                 345                 350

Lys Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
        355                 360                 365

Val Tyr Tyr Cys Thr Leu Asp Gly Arg Asp Gly Trp Val Ala Tyr Trp
    370                 375                 380

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

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asn Phe Met Leu Thr Gln Pro
                405                 410                 415

Ser Ser Val Ser Gly Val Pro Gly Gln Arg Val Thr Ile Ser Cys Thr
            420                 425                 430
```

```
Gly Asn Thr Gly Asn Ile Gly Ser Asn Tyr Val Asn Trp Tyr Gln Gln
        435                 440                 445

Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Arg Asp Asp Lys Arg
    450                 455                 460

Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser
465                 470                 475                 480

Ala Ser Leu Ala Ile Thr Gly Phe Gln Ala Glu Asp Glu Ala Asp Tyr
                485                 490                 495

Tyr Cys Gln Ser Tyr Ser Ser Gly Phe Ile Phe Gly Cys Gly Thr Lys
            500                 505                 510

Leu Thr Val Leu Ala Ala Glu Pro Lys Ser Ser Asp Lys Thr His Thr
        515                 520                 525

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
    530                 535                 540

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
545                 550                 555                 560

Glu Val Thr Cys Val Val Val Ser Val Ser His Glu Asp Pro Glu Val
                565                 570                 575

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
            580                 585                 590
```

```
Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
        595                 600                 605

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
    610                 615                 620

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

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Val Tyr Pro Pro
                645                 650                 655

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
            660                 665                 670

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
        675                 680                 685

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
    690                 695                 700

Gly Ser Phe Ala Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
705                 710                 715                 720

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
                725                 730                 735

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
            740                 745                 750
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<210> 158
<211> 2172

<212> DNA
<213> Artificial

<220>
<223> Full-length nucleotide sequence of NYZ-1010-HC2

<400> 158
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tcttgcgccg catctggctt ttccatacga tcctacgata ttcattgggt ccgacaagcc 180

cctggcaaag gtcttgaatg ggttgccact atctcctacg acgggtctca gaaatattat 240

gcggattcag tgaaggggcg gttcacaatt tcacgagacg agtcaaagaa tacactgtac 300

ctccaaatga attcactgag agccgaggat actgcagtct atcattgtgc aagagggtcc 360

tcaggccact acgaggcctt tgatatatgg ggccaaggca ccttggtaac cgttagtagc 420

ggaggtggag gaagcggagg cggcggttcc ggaggaggtg gaagtggagg aggtggatct 480

caatccgttc tgactcagcc accctccgcc tctggcaccc cgggccaacg ggtcacaata 540

tcatgttctg gctcttcaag caacatcgga aactggtacg tgagctggta ccagcagctc 600

cccggcacgg cgcccaagct tctgatatat gacaacaaca aacggcccag tggagttcct 660

gacagattca gtgggtctaa aagtggtaca agcgctagcc tggccataag tggtctgcag 720

agtgaagatg aggcggacta ttattgcgga acctgggact ccagcctgag cgctccctgg 780

gttttcggcg gaggtactaa gctgaccgtc ttgggaggag gcggttcaga agtgcagctg 840

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ctggagtggg tggccagcat cactaggtcc ggcgggcgaa tctactatcc cgacagcgtc 1020

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agcctgagag ccgaagatac agctgtgtac tattgcactc tggacggcag ggatgggtgg 1140

gtcgcctatt ggggtcaggg aaccctggtg acagtcagct ccgcctccac caagggccca 1200

agcgtcttcc ccctggcacc ctcctccaag agcacctctg gcggcacagc cgccctgggc 1260

tgcctggtca aggactactt ccccgaaccc gtgaccgtga gctggaactc aggcgccctg 1320

accagcggcg tgcacacctt ccccgctgtc ctgcagtcct caggactcta ctccctcagc 1380

agcgtggtga ccgtgccctc cagcagcttg ggcacccaga cctacatctg caacgtgaat 1440

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cacacatgcc caccctgccc agcacctgaa gccgcagggg gaccctcagt cttcctcttc 1560

cccccaaaac ccaaggacac cctcatgatc tcccggaccc ctgaggtcac atgcgtggtg 1620

gtgtcagtga gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag 1680

gtgcataatg ccaagacaaa gccccgggag gagcagtaca acagcacgta ccgggtggtc 1740

agcgtcctca ctgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc 1800

tccaacaaag ccctcccagc ccccatcgag aaaaccatct ccaaagccaa aggccagccc 1860

cgggaaccac aggtgtacgt gtacccccca tcccgggacg agctgaccaa gaaccaggtc 1920

agcctgacct gcctggtcaa aggcttctat cccagcgaca tcgccgtgga gtgggagagc 1980

aatggccagc ccgagaacaa ctacaagacc acccctcccg tgctggactc cgacggctcc 2040

ttcgccctcg tgagcaagct caccgtggac aagagcaggt ggcagcaggg caacgtcttc 2100

tcatgctccg tgatgcatga ggctctgcac aaccactaca cccagaagag cctctccctg 2160

tctcccggca ag 2172

<210> 159
<211> 699

<212> DNA
<213> Artificial

<220>
<223> Full-length nucleotide sequence of C3E-7085-LC

<400> 159
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agctgtacgg gtaataccgg gaatatcggg tctaactacg tgaactggta tcagcagctt 180

ccagggacag ctcccaagtt gctgatctat cgcgacgaca aaagaccctc aggggtccct 240

gaccgattta gtggcagcaa aagcggtact tccgcttccc tggcgataac cggctttcag 300

gccgaagatg aggcagacta ctattgccag tcatattcca gcggcttcat cttcggaggc 360

ggaactaagc tgacagtgct gggccagcct aaggctgccc ctagcgtgac cctgttccct 420

ccttccagcg aggagcttca agctaacaag gccaccctgg tgtgtcttat ctctgacttc 480

taccctggcg ctgtgaccgt ggcctggaag gctgacagct cccctgtgaa ggccggagtg 540

gagaccacca cacctagcaa gcagtctaac aacaagtacg ctgccagctc ctacctgagc 600

cttacccctg agcagtggaa gtctcacaga agctactcct gtcaagtgac ccacgagggc 660

agcaccgtgg agaagaccgt ggctcctacc gagtgttcc 699

<210> 160
<211> 724
<212> PRT
<213> Artificial

<220>
<223> Full-length amino acid sequence of NYZ-1010-HC2

<400> 160

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Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                  10                  15

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

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

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

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

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

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

Val Tyr His Cys Ala Arg Gly Ser Ser Gly His Tyr Glu Ala Phe Asp
        115                 120                 125

Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
145                 150                 155                 160

Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
                165                 170                 175
```

```
Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Trp
            180                 185                 190

Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
        195                 200                 205

Ile Tyr Asp Asn Asn Lys Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    210                 215                 220

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
225                 230                 235                 240

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

Ser Ala Pro Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            260                 265                 270

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
        275                 280                 285

Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Val Thr
    290                 295                 300

Phe Asn Tyr Tyr Gly Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly
305                 310                 315                 320

Leu Glu Trp Val Ala Ser Ile Thr Arg Ser Gly Gly Arg Ile Tyr Tyr
                325                 330                 335
```

```
Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Thr Gln
            340                 345                 350

Lys Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
        355                 360                 365

Val Tyr Tyr Cys Thr Leu Asp Gly Arg Asp Gly Trp Val Ala Tyr Trp
    370                 375                 380

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
385                 390                 395                 400

Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
                405                 410                 415

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
            420                 425                 430

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
        435                 440                 445

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
    450                 455                 460

Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
465                 470                 475                 480

His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser
                485                 490                 495

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala
            500                 505                 510
```

```
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
        515                 520                 525

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Ser Val Ser
    530                 535                 540

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
545                 550                 555                 560

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
                565                 570                 575

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
            580                 585                 590

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
        595                 600                 605

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
    610                 615                 620

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

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
                645                 650                 655

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
            660                 665                 670
```

```
Pro Val Leu Asp Ser Asp Gly Ser Phe Ala Leu Val Ser Lys Leu Thr
        675                 680                 685

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
    690                 695                 700

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
705                 710                 715                 720

Ser Pro Gly Lys
```

<210> 161
<211> 233
<212> PRT
<213> Artificial

<220>
<223> Full-length amino acid sequence of C3E-7085-LC

<400> 161

```
Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1               5                   10                  15

Gly Ala Tyr Gly Asn Phe Met Leu Thr Gln Pro Ser Ser Val Ser Gly
            20                  25                  30

Val Pro Gly Gln Arg Val Thr Ile Ser Cys Thr Gly Asn Thr Gly Asn
        35                  40                  45

Ile Gly Ser Asn Tyr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala
    50                  55                  60
```

```
Pro Lys Leu Leu Ile Tyr Arg Asp Asp Lys Arg Pro Ser Gly Val Pro
65                  70                  75                  80

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

Thr Gly Phe Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr
            100                 105                 110

Ser Ser Gly Phe Ile Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
        115                 120                 125

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu
    130                 135                 140

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe
145                 150                 155                 160

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val
                165                 170                 175

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys
            180                 185                 190

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
        195                 200                 205

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu
    210                 215                 220

Lys Thr Val Ala Pro Thr Glu Cys Ser
225                 230
```

<210> 162
<211> 5
<212> PRT
<213> Artificial

<220>
<223> Peptide linker

<400> 162

Gly Gly Gly Gly Ser
1 5

<210> 163
<211> 891
<212> DNA
<213> Artificial

<220>
<223> Full-length nucleotide sequence of NYA-3061

<400> 163
atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagcggt 60

gaggtacagc tggtggaatc cggtggaggc cttgtgcaac cgggaggctc cctgcgactc 120

tcttgcgccg catctggctt ttccatacga tcctacgata ttcattgggt ccgacaagcc 180

cctggcaaag gtcttgaatg ggttgccact atctcctacg acgggtctca gaaatattat 240

gcggattcag tgaaggggcg gttcacaatt tcacgagacg agtcaaagaa tacactgtac 300

ctccaaatga attcactgag agccgaggat actgcagtct atcattgtgc aagagggtcc 360

tcaggccact acgaggcctt tgatatatgg ggccaaggca ccttggtaac cgttagtagc 420

ggaggtggag gaagcggagg cggcggttcc ggaggaggtg gaagtggagg aggtggatct 480

caatccgttc tgactcagcc accctccgcc tctggcaccc cgggccaacg ggtcacaata 540

tcatgttctg gctcttcaag caacatcgga aactggtacg tgagctggta ccagcagctc 600

cccggcacgg cgcccaagct tctgatatat gacaacaaca aacggcccag tggagttcct 660

gacagattca gtgggtctaa aagtggtaca agcgctagcc tggccataag tggtctgcag 720

agtgaagatg aggcggacta ttattgcgga acctgggact ccagcctgag cgctccctgg 780

gttttcggcg gaggtactaa gctgaccgtc ttgggcgcgg ccgcaggtgc aggtggtgat 840

tacaaagatg atgacgataa aggtgcagcg gcgcatcacc atcatcacca c 891

<210> 164
<211> 297
<212> PRT
<213> Artificial

<220>
<223> Full-length amino acid sequence of NYA-3061

<400> 164

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

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

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

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

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

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

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

Val Tyr His Cys Ala Arg Gly Ser Ser Gly His Tyr Glu Ala Phe Asp
        115                 120                 125

Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
145                 150                 155                 160

Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
                165                 170                 175

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Trp
            180                 185                 190

Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
        195                 200                 205

Ile Tyr Asp Asn Asn Lys Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    210                 215                 220

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
225                 230                 235                 240
```

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

Ser Ala Pro Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
260 265 270

Ala Ala Ala Gly Ala Gly Gly Asp Tyr Lys Asp Asp Asp Asp Lys Gly
275 280 285

Ala Ala Ala His His His His His His
290 295

<210> 165
<211> 903
<212> DNA
<213> Artificial

<220>
<223> Full-length nucleotide sequence of NYC-0005

<400> 165
atgaagcacc tgtggttctt tctgctgctg gtggccgctc ctagatgggt gttgtctggc 60

gaagtgcagc tggtggaatc tggtggcgga gttgttcagc ctggcggctc tctgagactg 120

agctgtgtgg ccagcggctt caccttcgac gactacgcca tgtactgggt ccgacaggtg 180

ccaggcaagg acctggaatg ggtgtccctg atttctggcg acggcgacat cacctactac 240

gtggactctg tgaagggcag attcaccgtg tccagagaca acaacaagaa cagcctgtac 300

ctgcagatga agtccctgcg cgtggaagat acagccctgt actactgcgc caaggacatg 360

atctactacg cctcttggag cggctacggc agcagcgatt actactacta tgtgatggac 420

gtgtggggcc agggcaccac cgttacagtt tctagcggag gcggaggaag tggcggcgga 480

ggatctggcg gtggtggttc tgatatccag atgacacaga gccccagcag cctgtctgcc 540

tctgtgggag acagagtgac catcacctgt agagccagcc agagcatcag cagctacctg 600

aactggtatc agcagaagcc cggcaaggcc cctaaactgc tgatctatgc cgcctccagt 660

ctgcagagcg gagtgcctag cagattttct ggcagcggct ccggcaccga tttcaccctg 720

accatatcta gcctgcagcc tgaggacttc gccacctact attgccagca gagctacagc 780

acccctccta tcacctttgg ccagggaacc agactggaaa tcaaaggcgc tgctgcaggc 840

gctggcggcg actacaaaga cgatgatgat aagggcgctg ccgctcacca ccaccatcac 900

cat 903

<210> 166
<211> 301
<212> PRT
<213> Artificial

<220>
<223> Full-length amino acid sequence of NYC-0005

<400> 166

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

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

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

Phe Asp Asp Tyr Ala Met Tyr Trp Val Arg Gln Val Pro Gly Lys Asp
50 55 60

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

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

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

Leu Tyr Tyr Cys Ala Lys Asp Met Ile Tyr Tyr Ala Ser Trp Ser Gly
        115                 120                 125

Tyr Gly Ser Ser Asp Tyr Tyr Tyr Tyr Val Met Asp Val Trp Gly Gln
    130                 135                 140

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
145                 150                 155                 160

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser
                165                 170                 175

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
            180                 185                 190

Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly
        195                 200                 205

Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly
    210                 215                 220

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
225                 230                 235                 240
```

```
Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
                245                 250                 255

Gln Ser Tyr Ser Thr Pro Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu
            260                 265                 270

Glu Ile Lys Gly Ala Ala Ala Gly Ala Gly Gly Asp Tyr Lys Asp Asp
        275                 280                 285

Asp Asp Lys Gly Ala Ala Ala His His His His His His
    290                 295                 300
```

<210> 167
<211> 903
<212> DNA
<213> Artificial

<220>
<223> Full-length nucleotide sequence of NYC-0006

<400> 167

```
atgaagcacc tgtggttctt tctgctgctg gtggccgctc ctagatgggt gttgtctggc       60

gaagtgcagc tggtggaatc tggtggcgga gttgttcagc ctggcggctc tctgagactg      120

tcttgtgccg ccagcggctt caccttcgac gactacgcca tgtactgggt ccgacaggcc      180

cctggcaaag gccttgaatg ggtgtccctg atcagcggag atggcggcag catgtactac      240

gccgatagcg tgaagggcag attcaccatc agccgggaca acagcaagaa cagcctgtac      300

ctgcagatga actccctgcg gaccgaggac acagccctgt actactgcgc caaggatatg      360

atcttctacg ccttttggag cggctacggc agcagcgatt actactacta cgtgatggac      420

gtgtggggcc agggcaccac agtgacagtt tattctggcg gcggaggatc tggcggaggt      480
```

ggaagcggag gcggtggatc tgatatccag atgacacaga gccccagcag cctgtctgcc 540

tctgtgggag acagagtgac catcacctgt cgggccagcc agagaatcag cacctacctg 600

aactggtatc agcagaagcc cggcaaggcc cctaagctgc tgatctatgc tgcctccagt 660

ctgcagagcg gcgtgccaag cagattttct ggcagcggct ctggcaccga cttcaccctg 720

accatatcta gcctgcagcc tgaggacttc gccacctact actgccagca gagctacagc 780

acccctccta tcacctttgg ccagggaacc agactggaaa tcaaaggcgc tgctgcaggc 840

gcaggcggcg actacaaaga cgatgatgat aagggcgctg ccgctcacca ccaccatcac 900

cat 903

<210> 168
<211> 301
<212> PRT
<213> Artificial

<220>
<223> Full-length amino acid sequence of NYC-0006

<400> 168

Met Lys His Leu Trp Phe Phe Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

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

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

Phe Asp Asp Tyr Ala Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly
50 55 60

```
Leu Glu Trp Val Ser Leu Ile Ser Gly Asp Gly Gly Ser Met Tyr Tyr
65                  70                  75                  80

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

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

Leu Tyr Tyr Cys Ala Lys Asp Met Ile Phe Tyr Ala Phe Trp Ser Gly
        115                 120                 125

Tyr Gly Ser Ser Asp Tyr Tyr Tyr Tyr Val Met Asp Val Trp Gly Gln
    130                 135                 140

Gly Thr Thr Val Thr Val Tyr Ser Gly Gly Gly Gly Ser Gly Gly Gly
145                 150                 155                 160

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser
                165                 170                 175

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
            180                 185                 190

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

Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly
    210                 215                 220
```

```
Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
225                 230                 235                 240

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
                245                 250                 255

Gln Ser Tyr Ser Thr Pro Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu
            260                 265                 270

Glu Ile Lys Gly Ala Ala Ala Gly Ala Gly Gly Asp Tyr Lys Asp Asp
        275                 280                 285

Asp Asp Lys Gly Ala Ala Ala His His His His His His
    290                 295                 300
```

<210> 169
<211> 888
<212> DNA
<213> Artificial

<220>
<223> Full-length nucleotide sequence of NYC-0007

<400> 169

```
atgaagcacc tgtggttctt tctgctgctg gtggccgctc ctagatgggt gttgtctggc       60

gaagtgcagc tggtggaatc tggtggcgga gttgttcagc ctggcggctc tctgagactg      120

tcttgtgccg ccagcggctt caccttcgac gattatgcca tgcactgggt ccgacaggcc      180

cctggcaaag gacttgaatg ggtgtccctg atcagcggcg acggcgacaa tacctactac      240

gccgatagcg tgaagggcag attcaccatc agccgggaca acaacaagaa cagcctgtac      300

ctgcagatga actccctgcg gaccgaggac accgccttct actactgtgc caaagagctg      360

atcttcggca aggtgctgca cgacttttac tactacgtga tggacgtgtg gggccagggc      420
```

accacagtga cagtttctag cggaggcgga ggaagtggcg gcggaggatc tggcggtggt 480

ggttctgata tccagatgac acagagcccc agcagcctgt ctgcctctgt gggagacaga 540

gtgaccatca cctgtagagc cagccagagc atcagcagct acctgaactg gtatcagcag 600

aagcccggca aggcccctaa actgctgatc tatgccgcct ccagtctgca gagcggagtg 660

cctagcagat tttctggcag cggctccggc accgatttca ccctgaccat atctagcctg 720

cagcctgagg acttcgccac ctactactgc cagcagagct acagcacccc tcctatcacc 780

tttggccagg gaaccagact ggaaatcaaa ggcgctgctg caggcgcagg cggcgactac 840

aaagacgatg atgataaggg cgctgccgct caccaccacc atcaccat 888

<210> 170
<211> 296
<212> PRT
<213> Artificial

<220>
<223> Full-length amino acid sequence of NYC-0007

<400> 170

Met Lys His Leu Trp Phe Phe Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

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

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

Phe Asp Asp Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly
50 55 60

```
Leu Glu Trp Val Ser Leu Ile Ser Gly Asp Gly Asp Asn Thr Tyr Tyr
65                  70                  75                  80

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

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

Phe Tyr Tyr Cys Ala Lys Glu Leu Ile Phe Gly Lys Val Leu His Asp
        115                 120                 125

Phe Tyr Tyr Tyr Val Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr
    130                 135                 140

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
145                 150                 155                 160

Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
                165                 170                 175

Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser
            180                 185                 190

Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
        195                 200                 205

Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe
    210                 215                 220
```

```
Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu
225                 230                 235                 240

Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr
                245                 250                 255

Pro Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Gly Ala
            260                 265                 270

Ala Ala Gly Ala Gly Gly Asp Tyr Lys Asp Asp Asp Asp Lys Gly Ala
        275                 280                 285

Ala Ala His His His His His His
    290                 295
```

<210> 171
<211> 888
<212> DNA
<213> Artificial

<220>
<223> Full-length nucleotide sequence of NYC-0008

<400> 171

```
atgaagcacc tgtggttctt tctgctgctg gtggccgctc ctagatgggt gttgtctggc       60

gaagtgcagc tggtggaatc tggtggcgga gttgttcagc ctggcggctc tctgagactg      120

agctgtgaag cctccggctt catcttcgac gactacgcca tgcactgggt ccgacaggca      180

cctggcaaag gccttgaatg ggtgtccctg atctctggcg acggcgacat catctactac      240

gccgactctg tgaagggcag attcaccatc agccgggaca acagcaagaa cagcctgtac      300

ctgcagatga actccctgat catcgaggac acagccctgt actactgcgc caaggattgg      360

gtgttcggcg tcgtgatgac ccactactgg tacttcggcc tggatgtgtg gggccaggga      420
```

accacagtga cagtttctag cggaggcgga ggaagtggcg gcggaggatc tggcggtggt 480

ggttctgata tccagatgac acagagcccc agcagcctgt ctgcctctga aggcgacaga 540

gtgaccatca cctgtagagc cagccagagc atcagcacct acctgaactg gtatcagcag 600

aagcccggca aggcccctaa gctgctgatc tatggtgcct ccagtctgca gagcggcgtg 660

ccaagcagat tttctggcag cggctctggc accgacttca ccctgaccat atctagcctg 720

cagcctgagg acttcgccac ctactactgc cagcagtcct acagcacccc tcctatcaca 780

tttggccagg gcaccaaggt ggaaatcaaa ggcgctgctg caggcgctgg cggcgactac 840

aaagacgatg atgataaggg cgctgccgct caccaccacc atcaccat 888

<210> 172
<211> 296
<212> PRT
<213> Artificial

<220>
<223> Full-length amino acid sequence of NYC-0008

<400> 172

Met Lys His Leu Trp Phe Phe Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

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

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

Phe Asp Asp Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly
50 55 60

```
Leu Glu Trp Val Ser Leu Ile Ser Gly Asp Gly Asp Ile Ile Tyr Tyr
65                  70                  75                  80

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

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

Leu Tyr Tyr Cys Ala Lys Asp Trp Val Phe Gly Val Val Met Thr His
        115                 120                 125

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

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
145                 150                 155                 160

Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
                165                 170                 175

Glu Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser
            180                 185                 190

Thr Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
        195                 200                 205

Leu Ile Tyr Gly Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe
    210                 215                 220
```

```
Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu
225                 230                 235                 240

Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr
                245                 250                 255

Pro Pro Ile Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly Ala
            260                 265                 270

Ala Ala Gly Ala Gly Gly Asp Tyr Lys Asp Asp Asp Asp Lys Gly Ala
        275                 280                 285

Ala Ala His His His His His His
    290                 295
```

<210> 173
<211> 885
<212> DNA
<213> Artificial

<220>
<223> Full-length nucleotide sequence of NYC-0009

<400> 173

```
atgaagcacc tgtggttctt tctgctgctg gtggccgctc ctagatgggt gttgtctggc       60

gaagtgcagc tggtggaatc tggtggcgga gttgttcagc ctggcggctc tctgagactg      120

tcttgtgccg ccagcggctt caccttcgac gattatgcca tgcactgggt ccgacaggcc      180

cctggcaaag gacttgaatg ggtgtccctg atctctggcg gaggcggcgg aacctactac      240

agcgattctg tgaagggcag attcaccatc agccgggaca ccagcaagga cagcctgtac      300

ctgcagatga acagcctgcg gaccgaggac acagccctgt actactgcgc caaggacatg      360

gtgttcggcg tggtcacccc ttactactac ttcgccctgg atgtgtgggg ccagggcaca      420
```

acagtgacag tctcttctgg cggcggagga agcggaggcg gaggatccgg tggtggtgga 480

tctgacatcc agatgacaca gagccccagc agcctgtctg cctctgtggg agacagagtg 540

accatcacct gtagagccag ccagagcatc aacagctacc tgaactggta tcagcagaag 600

cccggcaagg cccctaagct gctgatctat gctgcctcca gtctgcagag cggcgtgcca 660

agcagatttt ctggcagcgg ctctggcacc gacttcaccc tgaccatatc tagcctgcag 720

cctgaggact tcgccaccta ctactgccag cagagctaca gcgcccctcc tatcacattt 780

ggccagggaa ccagactgga aatcaaaggc gctgctgcag gcgcaggcgg cgactacaaa 840

gacgatgatg ataagggcgc tgccgctcac caccatcacc atcat 885

<210> 174
<211> 295
<212> PRT
<213> Artificial

<220>
<223> Full-length amino acid sequence of NYC-0009

<400> 174

Met Lys His Leu Trp Phe Phe Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

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

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

Phe Asp Asp Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly
50 55 60

```
Leu Glu Trp Val Ser Leu Ile Ser Gly Gly Gly Gly Gly Thr Tyr Tyr
65                  70                  75                  80

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

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

Leu Tyr Tyr Cys Ala Lys Asp Met Val Phe Gly Val Val Thr Pro Tyr
        115                 120                 125

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

Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
145                 150                 155                 160

Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
                165                 170                 175

Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Asn Ser
            180                 185                 190

Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
        195                 200                 205

Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser
    210                 215                 220
```

```
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln
225                 230                 235                 240

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Ala Pro
                245                 250                 255

Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Gly Ala Ala
            260                 265                 270

Ala Gly Ala Gly Gly Asp Tyr Lys Asp Asp Asp Asp Lys Gly Ala Ala
        275                 280                 285

Ala His His His His His His
    290                 295
```

<210> 175
<211> 888
<212> DNA
<213> Artificial

<220>
<223> Full-length nucleotide sequence of NYC-0010

<400> 175

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atgaagcacc tgtggttctt tctgctgctg gtggccgctc ctagatgggt gttgtctggc       60

gaagtgcagc tggtggaatc tggtggcgga gttgttcagc ctggcggctc tctgagactg      120

agctgtgctg tgtccggctt caccttcgac gactacgcca tgcactgggt ccgacaggca      180

cctggcaaag gccttgaatg ggtgtccctg atcagcggag atggcggcag cacacactac      240

gccgattctg tgaagggcag attcaccatc agccgggaca acagcaagaa cagcctgtac      300

ctgcagatga actccctgcg gacaggcgac acagccctgt actactgcgc caaggacatg      360

atcttcgccg tggtcatcac cgactaccac tactacggca tggacgtgtg gggccaggga      420
```

accacagtga cagtttctag cggaggcgga ggaagtggcg gcggaggatc tggcggtggt 480

ggttctgata tccagatgac acagagcccc agcagcctgt ctgcctctgt gggagacaga 540

gtgaccatca cctgtagagc cagccagagc atcagcagct acctgaactg gtatcagcag 600

aagcccggca aggcccctaa actgctgatc tatgccgcct ccagtctgca gagcggagtg 660

cctagcagat tttctggcag cggctccggc accgatttca ccctgaccat atctagcctg 720

cagcctgagg acttcgccac ctactactgc cagcagagct acagcacccc tcctatcacc 780

tttggccagg gcaccagact ggaaatcaaa ggcgctgctg caggcgctgg cggcgactac 840

aaagacgatg atgataaggg cgctgccgct caccaccacc atcaccat 888

<210> 176
<211> 296
<212> PRT
<213> Artificial

<220>
<223> Full-length amino acid sequence of NYC-0010

<400> 176

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

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

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

Phe Asp Asp Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly
50 55 60

```
Leu Glu Trp Val Ser Leu Ile Ser Gly Asp Gly Gly Ser Thr His Tyr
65                  70                  75                  80

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

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

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

Tyr His Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr
    130                 135                 140

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
145                 150                 155                 160

Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
                165                 170                 175

Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser
            180                 185                 190

Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
        195                 200                 205

Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe
    210                 215                 220
```

```
Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu
225                 230                 235                 240

Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr
                245                 250                 255

Pro Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Gly Ala
            260                 265                 270

Ala Ala Gly Ala Gly Gly Asp Tyr Lys Asp Asp Asp Asp Lys Gly Ala
        275                 280                 285

Ala Ala His His His His His His
    290                 295
```

<210> 177
<211> 738
<212> DNA
<213> Artificial

<220>
<223> Full-length nucleotide sequence of HC-h

<400> 177

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atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagcgac       60

aaaactcaca catgcccacc ctgcccagca cctgaagccg ccggcggacc ctcagtcttc      120

ctcttccccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc      180

gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc      240

gtggaggtgc ataatgccaa gaccaagcct agagaggaac agtacaacag cacctaccgg      300

gtggtgtccg tgctgacagt gctgcaccag gactggctga acggcaaaga gtacaagtgc      360

aaggtgtcca acaaggccct gcctgccccc atcgagaaaa ccatcagcaa ggccaagggc      420
```

cagccccgcg aacctcaagt gtgcaccctg ccaccctccc gggatgagct gaccaagaac 480

caggtgtccc tgagctgtgc cgtgaagggc ttctacccct ccgatatcgc cgtggaatgg 540

gagagcaacg gccagcccga gaacaactac aagaccaccc cccctgtgct ggacagcgac 600

ggctcattct tcctggtgtc caagctgacc gtggacaagt ccagatggca gcagggcaac 660

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacaccca gaagagcctc 720

tccctgtctc ccggcaaa 738

<210> 178
<211> 246
<212> PRT
<213> Artificial

<220>
<223> Full-length amino acid sequence of HC-h

<400> 178

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
20 25 30

Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
35 40 45

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
50 55 60

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
65 70 75 80

```
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
                85                  90                  95

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
            100                 105                 110

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

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
    130                 135                 140

Pro Gln Val Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
145                 150                 155                 160

Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile
                165                 170                 175

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
            180                 185                 190

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys
        195                 200                 205

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
    210                 215                 220

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
225                 230                 235                 240
```

Ser Leu Ser Pro Gly Lys
245

<210> 179
<211> 1500
<212> DNA
<213> Artificial

<220>
<223> Full-length nucleotide sequence of NYD-2047-HC-k

<400> 179
atgaagcacc tgtggttctt tctgctgctg gtggccgctc ctagatgggt gctgtctggt 60

caagtacagc tggtggaatc cggtggaggc gtggtccagc cgggacgcag cttgagactg 120

tcctgcgctg catctggctt ttccatacga tcctacgata tgcactgggt tcgccaagcc 180

cctggcaaag gtcttgaatg ggttgccact atctcctacg acgggtctca gaaatattac 240

gcggattcag tgaaggggcg gttcacaatt tcacgggaca attcaaagaa taccttgtat 300

ctccagatgt cttcactgag agccgaggat actgcagtct atcattgtgc aagagggtcc 360

tcaggccact acgaggcctt tgatatatgg ggccaaggca ccttggtaac cgttagtagc 420

ggaggtggag gaagcggagg cggcggttcc ggaggaggtg gaagtcaatc cgttctgact 480

cagccaccct ccgtgagtgc agcgcctgga cagaaggtca caatatcatg ttctggctct 540

tcaagcaaca tcggaaactg gtacgtgagc tggtaccagc agctccccgg cacggcgccc 600

aagcttctga tatatgacaa caacaaacgg cccagtggaa tccctgacag attcagtggg 660

tctaaaagtg gtacaagcgc taccctgggt atcaccggat tgcagaccgg agatgaggcg 720

gactattatt gcggaacctg ggactccagc ctgagcgctc cctgggtttt cggcggaggt 780

actaaggtta ccgtcttggg cggagaaccc aagagcgcag acaagaccca cacctgtcct 840

ccatgtcctg ctccagaagc tgcaggcggc ccttccgtgt ttctgttccc tccaaagcct 900

aaggacaccc tgatgatcag ccggacacct gaagtgacct gcgtggtggt ggatgtgtcc 960

cacgaggatc ccgaagtgaa gttcaattgg tacgtggacg gcgtggaagt gcacaacgcc 1020

aagaccaagc ctagagagga acagtacaac agcacctaca gagtggtgtc tgtgctgaca 1080

gtgctgcacc aggactggct gaacggcaaa gagtacaagt gcaaggtgtc caacaaggcc 1140

ctgcctgctc ctatcgagaa aaccatcagc aaggccaagg gccagcctag ggaaccccag 1200

gtttacaccc tgcctccatg cagggatgag ctgaccaaga accaggtgtc cctgtggtgc 1260

ctggttaagg gcttctaccc ctccgatatc gccgtggaat gggagagcaa tggccagcca 1320

gagaacaact acaagacaac ccctcctgtg ctggactccg acggctcatt cttcctgtac 1380

agcaagctga ccgtggacaa gagcagatgg cagcagggca acgtgttcag ctgcagcgtg 1440

atgcacgagg ccctgcacaa ccactacaca cagaagtccc tgtctctgag ccccggcaaa 1500

<210> 180
<211> 500
<212> PRT
<213> Artificial

<220>
<223> Full-length amino acid sequence of NYD-2047-HC-k

<400> 180

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

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

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

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

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

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

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

Val Tyr His Cys Ala Arg Gly Ser Ser Gly His Tyr Glu Ala Phe Asp
        115                 120                 125

Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr
145                 150                 155                 160

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

Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Trp Tyr Val Ser Trp Tyr
            180                 185                 190

Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Asp Asn Asn
        195                 200                 205
```

```
Lys Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly
    210                 215                 220

Thr Ser Ala Thr Leu Gly Ile Thr Gly Leu Gln Thr Gly Asp Glu Ala
225                 230                 235                 240

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

Phe Gly Gly Gly Thr Lys Val Thr Val Leu Gly Gly Glu Pro Lys Ser
            260                 265                 270

Ala Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala
        275                 280                 285

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
    290                 295                 300

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
305                 310                 315                 320

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
                325                 330                 335

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
            340                 345                 350

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
        355                 360                 365

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
    370                 375                 380
```

```
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
385                 390                 395                 400

Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val
                405                 410                 415

Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
            420                 425                 430

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
        435                 440                 445

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
    450                 455                 460

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
465                 470                 475                 480

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
                485                 490                 495

Ser Pro Gly Lys
            500
```

<210> 181
<211> 1500
<212> DNA
<213> Artificial

<220>
<223> Full-length nucleotide sequence of NYD-2061-HC-k

<400> 181
atgaagcacc tgtggttctt tctgctgctg gtggccgctc ctagatgggt gctgtctggt 60

gaggtacagc tggtggaatc cggtggaggc cttgtgcaac cgggaggctc cctgcgactc 120

tcttgcgccg catctggctt ttccatacga tcctacgata ttcattgggt ccgacaagcc 180

cctggcaaag gtcttgaatg ggttgccact atctcctacg acgggtctca gaaatattat 240

gcggattcag tgaaggggcg gttcacaatt tcacgagacg agtcaaagaa tacactgtac 300

ctccaaatga attcactgag agccgaggat actgcagtct atcattgtgc aagagggtcc 360

tcaggccact acgaggcctt tgatatatgg ggccaaggca ccttggtaac cgttagtagc 420

ggaggtggag gaagcggagg cggcggttcc ggaggaggtg gaagtcaatc cgttctgact 480

cagccaccct ccgcctctgg caccccgggc caacgggtca caatatcatg ttctggctct 540

tcaagcaaca tcggaaactg gtacgtgagc tggtaccagc agctccccgg cacggcgccc 600

aagcttctga tatatgacaa caacaaacgg cccagtggag ttcctgacag attcagtggg 660

tctaaaagtg gtacaagcgc tagcctggcc ataagtggtc tgcagagtga agatgaggcg 720

gactattatt gcggaacctg ggactccagc ctgagcgctc cctgggtttt cggcggaggt 780

actaagctga ccgtcttggg cggagaaccc aagagcgcag acaagaccca cacctgtcct 840

ccatgtcctg ctccagaagc tgcaggcggc ccttccgtgt ttctgttccc tccaaagcct 900

aaggacaccc tgatgatcag ccggacacct gaagtgacct gcgtggtggt ggatgtgtcc 960

cacgaggatc ccgaagtgaa gttcaattgg tacgtggacg gcgtggaagt gcacaacgcc 1020

aagaccaagc ctagagagga acagtacaac agcacctaca gagtggtgtc tgtgctgaca 1080

gtgctgcacc aggactggct gaacggcaaa gagtacaagt gcaaggtgtc caacaaggcc 1140

ctgcctgctc ctatcgagaa aaccatcagc aaggccaagg gccagcctag ggaaccccag 1200

gtttacaccc tgcctccatg cagggatgag ctgaccaaga accaggtgtc cctgtggtgc 1260

ctggttaagg gcttctaccc ctccgatatc gccgtggaat gggagagcaa tggccagcca 1320

gagaacaact acaagacaac ccctcctgtg ctggactccg acggctcatt cttcctgtac 1380

agcaagctga ccgtggacaa gagcagatgg cagcagggca acgtgttcag ctgcagcgtg 1440

atgcacgagg ccctgcacaa ccactacaca cagaagtccc tgtctctgag ccccggcaaa 1500

<210> 182
<211> 500
<212> PRT
<213> Artificial

<220>
<223> Full-length amino acid sequence of NYD-2061-HC-k

<400> 182

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

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

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

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

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

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

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

Val Tyr His Cys Ala Arg Gly Ser Ser Gly His Tyr Glu Ala Phe Asp
        115                 120                 125

Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr
145                 150                 155                 160

Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln Arg Val Thr Ile Ser
                165                 170                 175

Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Trp Tyr Val Ser Trp Tyr
            180                 185                 190

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

Lys Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly
    210                 215                 220

Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln Ser Glu Asp Glu Ala
225                 230                 235                 240

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

```
Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Glu Pro Lys Ser
            260                 265                 270

Ala Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala
        275                 280                 285

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
    290                 295                 300

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
305                 310                 315                 320

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
                325                 330                 335

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
            340                 345                 350

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
        355                 360                 365

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
    370                 375                 380

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
385                 390                 395                 400

Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val
                405                 410                 415

Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
            420                 425                 430
```

```
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
        435                 440                 445

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
    450                 455                 460

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
465                 470                 475                 480

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
                485                 490                 495

Ser Pro Gly Lys
            500
```

<210> 183
<211> 1515
<212> DNA
<213> Artificial

<220>
<223> Full-length nucleotide sequence of NYD-3061-HC-k

<400> 183

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atgaagcacc tgtggttctt tctgctgctg gtggccgctc ctagatgggt gctgtctggt       60

gaggtacagc tggtggaatc cggtggaggc cttgtgcaac cgggaggctc cctgcgactc      120

tcttgcgccg catctggctt ttccatacga tcctacgata ttcattgggt ccgacaagcc      180

cctggcaaag gtcttgaatg ggttgccact atctcctacg acgggtctca gaaatattat      240

gcggattcag tgaaggggcg gttcacaatt tcacgagacg agtcaaagaa tacactgtac      300

ctccaaatga attcactgag agccgaggat actgcagtct atcattgtgc aagagggtcc      360
```

tcaggccact acgaggcctt tgatatatgg ggccaaggca ccttggtaac cgttagtagc 420

ggaggtggag gaagcggagg cggcggttcc ggaggaggtg gaagtggagg aggtggatct 480

caatccgttc tgactcagcc accctccgcc tctggcaccc cgggccaacg ggtcacaata 540

tcatgttctg gctcttcaag caacatcgga aactggtacg tgagctggta ccagcagctc 600

cccggcacgg cgcccaagct tctgatatat gacaacaaca aacggcccag tggagttcct 660

gacagattca gtgggtctaa aagtggtaca agcgctagcc tggccataag tggtctgcag 720

agtgaagatg aggcggacta ttattgcgga acctgggact ccagcctgag cgctccctgg 780

gttttcggcg gaggtactaa gctgaccgtc ttgggcggag aacccaagag cgcagacaag 840

acccacacct gtcctccatg tcctgctcca gaagctgcag gcggcccttc cgtgtttctg 900

ttccctccaa agcctaagga caccctgatg atcagccgga cacctgaagt gacctgcgtg 960

gtggtggatg tgtcccacga ggatcccgaa gtgaagttca attggtacgt ggacggcgtg 1020

gaagtgcaca acgccaagac caagcctaga gaggaacagt acaacagcac ctacagagtg 1080

gtgtctgtgc tgacagtgct gcaccaggac tggctgaacg gcaaagagta caagtgcaag 1140

gtgtccaaca aggccctgcc tgctcctatc gagaaaacca tcagcaaggc caagggccag 1200

cctagggaac cccaggttta caccctgcct ccatgcaggg atgagctgac caagaaccag 1260

gtgtccctgt ggtgcctggt taagggcttc taccctccg atatcgccgt ggaatgggag 1320

agcaatggcc agccagagaa caactacaag acaacccctc ctgtgctgga ctccgacggc 1380

tcattcttcc tgtacagcaa gctgaccgtg gacaagagca gatggcagca gggcaacgtg 1440

ttcagctgca gcgtgatgca cgaggccctg cacaaccact acacacagaa gtccctgtct 1500

ctgagccccg gcaaa 1515

<210> 184
<211> 505
<212> PRT
<213> Artificial

<220>
<223> Full-length amino acid sequence of NYD-3061-HC-k

<400> 184

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

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

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

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

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

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

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

Val Tyr His Cys Ala Arg Gly Ser Ser Gly His Tyr Glu Ala Phe Asp
115 120 125

```
Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
145                 150                 155                 160

Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
                165                 170                 175

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Trp
            180                 185                 190

Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
        195                 200                 205

Ile Tyr Asp Asn Asn Lys Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    210                 215                 220

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
225                 230                 235                 240

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

Ser Ala Pro Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            260                 265                 270

Gly Glu Pro Lys Ser Ala Asp Lys Thr His Thr Cys Pro Pro Cys Pro
        275                 280                 285

Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
    290                 295                 300
```

```
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
305                 310                 315                 320

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
                325                 330                 335

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
            340                 345                 350

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
        355                 360                 365

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

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
385                 390                 395                 400

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu
                405                 410                 415

Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro
            420                 425                 430

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
        435                 440                 445

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
    450                 455                 460
```

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
465 470 475 480

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
485 490 495

Lys Ser Leu Ser Leu Ser Pro Gly Lys
500 505

<210> 185
<211> 1527
<212> DNA
<213> Artificial

<220>
<223> Full-length nucleotide sequence of NYC-0011-HC-k

<400> 185
atgaagcacc tgtggttctt tctgctgctg gtggccgctc ctagatgggt gctgtctggc 60

gaagtgcagc tggtggaatc tggtggcgga gttgttcagc ctggcggctc tctgagactg 120

agctgtgtgg ccagcggctt caccttcgac gactacgcca tgtactgggt ccgacaggtg 180

ccaggcaagg acctggaatg ggtgtccctg atttctggcg acggcgacat cacctactac 240

gtggactctg tgaagggcag attcaccgtg tccagagaca acaacaagaa cagcctgtac 300

ctgcagatga agtccctgcg cgtggaagat acagccctgt actactgcgc caaggacatg 360

atctactacg cctcttggag cggctacggc agcagcgatt actactacta tgtgatggac 420

gtgtggggcc agggcaccac cgttacagtt tctagcggag gcggaggaag tggcggcgga 480

ggatctggcg gtggtggttc tgatatccag atgacacaga gccccagcag cctgtctgcc 540

tctgtgggag acagagtgac catcacctgt agagccagcc agagcatcag cagctacctg 600

aactggtatc agcagaagcc cggcaaggcc cctaaactgc tgatctatgc cgcctccagt 660

ctgcagagcg gagtgcctag cagattttct ggcagcggct ccggcaccga tttcaccctg 720

accatatcta gcctgcagcc tgaggacttc gccacctact attgccagca gagctacagc 780

acccctccta tcacctttgg ccagggaacc agactggaaa tcaaaggcgg agaacccaag 840

agcgcagaca agacccacac ctgtcctcca tgtcctgctc cagaagctgc aggcggccct 900

tccgtgtttc tgttccctcc aaagcctaag gacaccctga tgatcagccg gacacctgaa 960

gtgacctgcg tggtggtgga tgtgtcccac gaggatcccg aagtgaagtt caattggtac 1020

gtggacggcg tggaagtgca caacgccaag accaagccta gagaggaaca gtacaacagc 1080

acctacagag tggtgtctgt gctgacagtg ctgcaccagg actggctgaa cggcaaagag 1140

tacaagtgca aggtgtccaa caaggccctg cctgctccta tcgagaaaac catcagcaag 1200

gccaagggcc agcctaggga accccaggtt tacaccctgc ctccatgcag ggatgagctg 1260

accaagaacc aggtgtccct gtggtgcctg gttaagggct tctacccctc cgatatcgcc 1320

gtggaatggg agagcaatgg ccagccagag aacaactaca agacaacccc tcctgtgctg 1380

gactccgacg gctcattctt cctgtacagc aagctgaccg tggacaagag cagatggcag 1440

cagggcaacg tgttcagctg cagcgtgatg cacgaggccc tgcacaacca ctacacacag 1500

aagtccctgt ctctgagccc cggcaaa 1527

<210> 186
<211> 509
<212> PRT
<213> Artificial

<220>
<223> Full-length amino acid sequence of NYC-0011-HC-k

<400> 186

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Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                  10                  15

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

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

Phe Asp Asp Tyr Ala Met Tyr Trp Val Arg Gln Val Pro Gly Lys Asp
    50                  55                  60

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

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

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

Leu Tyr Tyr Cys Ala Lys Asp Met Ile Tyr Tyr Ala Ser Trp Ser Gly
        115                 120                 125

Tyr Gly Ser Ser Asp Tyr Tyr Tyr Tyr Val Met Asp Val Trp Gly Gln
    130                 135                 140

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
145                 150                 155                 160

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser
                165                 170                 175
```

```
Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
            180                 185                 190

Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly
        195                 200                 205

Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly
    210                 215                 220

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
225                 230                 235                 240

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
                245                 250                 255

Gln Ser Tyr Ser Thr Pro Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu
            260                 265                 270

Glu Ile Lys Gly Gly Glu Pro Lys Ser Ala Asp Lys Thr His Thr Cys
        275                 280                 285

Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu
    290                 295                 300

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
305                 310                 315                 320

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
                325                 330                 335
```

```
Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
            340                 345                 350

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
        355                 360                 365

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
    370                 375                 380

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
385                 390                 395                 400

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys
                405                 410                 415

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys
            420                 425                 430

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
        435                 440                 445

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
    450                 455                 460

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
465                 470                 475                 480

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
                485                 490                 495

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
            500                 505
```

<210> 187
<211> 1527
<212> DNA
<213> Artificial

<220>
<223> Full-length nucleotide sequence of NYC-0012-HC-k

<400> 187
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gaagtgcagc tggtggaatc tggtggcgga gttgttcagc ctggcggctc tctgagactg 120

tcttgtgccg ccagcggctt caccttcgac gactacgcca tgtactgggt ccgacaggcc 180

cctggcaaag gccttgaatg ggtgtccctg atcagcggag atggcggcag catgtactac 240

gccgatagcg tgaagggcag attcaccatc agccgggaca acagcaagaa cagcctgtac 300

ctgcagatga actccctgcg gaccgaggac acagccctgt actactgcgc caaggatatg 360

atcttctacg ccttttggag cggctacggc agcagcgatt actactacta cgtgatggac 420

gtgtggggcc agggcaccac agtgacagtt tattctggcg gcggaggatc tggcggaggt 480

ggaagcggag gcggtggatc tgatatccag atgacacaga gccccagcag cctgtctgcc 540

tctgtgggag acagagtgac catcacctgt cgggccagcc agagaatcag cacctacctg 600

aactggtatc agcagaagcc cggcaaggcc cctaagctgc tgatctatgc tgcctccagt 660

ctgcagagcg gcgtgccaag cagattttct ggcagcggct ctggcaccga cttcaccctg 720

accatatcta gcctgcagcc tgaggacttc gccacctact actgccagca gagctacagc 780

acccctccta tcacctttgg ccagggaacc agactggaaa tcaaaggcgg agaacccaag 840

agcgcagaca agacccacac ctgtcctcca tgtcctgctc cagaagctgc aggcggccct 900

tccgtgtttc tgttccctcc aaagcctaag gacaccctga tgatcagccg gacacctgaa 960

gtgacctgcg tggtggtgga tgtgtcccac gaggatcccg aagtgaagtt caattggtac 1020

gtggacggcg tggaagtgca caacgccaag accaagccta gagaggaaca gtacaacagc 1080

acctacagag tggtgtctgt gctgacagtg ctgcaccagg actggctgaa cggcaaagag 1140

tacaagtgca aggtgtccaa caaggccctg cctgctccta tcgagaaaac catcagcaag 1200

gccaagggcc agcctaggga accccaggtt tacaccctgc ctccatgcag ggatgagctg 1260

accaagaacc aggtgtccct gtggtgcctg gttaagggct tctacccctc cgatatcgcc 1320

gtggaatggg agagcaatgg ccagccagag aacaactaca agacaacccc tcctgtgctg 1380

gactccgacg gctcattctt cctgtacagc aagctgaccg tggacaagag cagatggcag 1440

cagggcaacg tgttcagctg cagcgtgatg cacgaggccc tgcacaacca ctacacacag 1500

aagtccctgt ctctgagccc cggcaaa 1527

<210> 188
<211> 509
<212> PRT
<213> Artificial

<220>
<223> Full-length amino acid sequence of NYC-0012-HC-k

<400> 188

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

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

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

```
Phe Asp Asp Tyr Ala Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly
    50                  55                  60

Leu Glu Trp Val Ser Leu Ile Ser Gly Asp Gly Gly Ser Met Tyr Tyr
65                  70                  75                  80

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

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

Leu Tyr Tyr Cys Ala Lys Asp Met Ile Phe Tyr Ala Phe Trp Ser Gly
        115                 120                 125

Tyr Gly Ser Ser Asp Tyr Tyr Tyr Tyr Val Met Asp Val Trp Gly Gln
    130                 135                 140

Gly Thr Thr Val Thr Val Tyr Ser Gly Gly Gly Gly Ser Gly Gly Gly
145                 150                 155                 160

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser
                165                 170                 175

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
            180                 185                 190

Ser Gln Arg Ile Ser Thr Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly
        195                 200                 205
```

```
Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly
    210                 215                 220

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
225                 230                 235                 240

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
                245                 250                 255

Gln Ser Tyr Ser Thr Pro Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu
            260                 265                 270

Glu Ile Lys Gly Gly Glu Pro Lys Ser Ala Asp Lys Thr His Thr Cys
        275                 280                 285

Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu
    290                 295                 300

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
305                 310                 315                 320

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
                325                 330                 335

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
            340                 345                 350

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
        355                 360                 365

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
    370                 375                 380
```

```
Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
385                 390                 395                 400

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys
                405                 410                 415

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys
            420                 425                 430

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
        435                 440                 445

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
    450                 455                 460

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
465                 470                 475                 480

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
                485                 490                 495

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
            500                 505
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<210> 189
<211> 1512
<212> DNA
<213> Artificial

<220>
<223> Full-length nucleotide sequence of NYC-0013-HC-k

<400> 189
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gaagtgcagc tggtggaatc tggtggcgga gttgttcagc ctggcggctc tctgagactg 120

tcttgtgccg ccagcggctt caccttcgac gattatgcca tgcactgggt ccgacaggcc 180

cctggcaaag gacttgaatg ggtgtccctg atcagcggcg acggcgacaa tacctactac 240

gccgatagcg tgaagggcag attcaccatc agccgggaca acaacaagaa cagcctgtac 300

ctgcagatga actccctgcg gaccgaggac accgccttct actactgtgc caaagagctg 360

atcttcggca aggtgctgca cgacttttac tactacgtga tggacgtgtg gggccagggc 420

accacagtga cagtttctag cggaggcgga ggaagtggcg gcggaggatc tggcggtggt 480

ggttctgata tccagatgac acagagcccc agcagcctgt ctgcctctgt gggagacaga 540

gtgaccatca cctgtagagc cagccagagc atcagcagct acctgaactg gtatcagcag 600

aagcccggca aggcccctaa actgctgatc tatgccgcct ccagtctgca gagcggagtg 660

cctagcagat tttctggcag cggctccggc accgatttca ccctgaccat atctagcctg 720

cagcctgagg acttcgccac ctactactgc cagcagagct acagcacccc tcctatcacc 780

tttggccagg gaaccagact ggaaatcaaa ggcggagaac ccaagagcgc agacaagacc 840

cacacctgtc ctccatgtcc tgctccagaa gctgcaggcg gcccttccgt gtttctgttc 900

cctccaaagc ctaaggacac cctgatgatc agccggacac ctgaagtgac ctgcgtggtg 960

gtggatgtgt cccacgagga tcccgaagtg aagttcaatt ggtacgtgga cggcgtggaa 1020

gtgcacaacg ccaagaccaa gcctagagag gaacagtaca acagcaccta cagagtggtg 1080

tctgtgctga cagtgctgca ccaggactgg ctgaacggca aagagtacaa gtgcaaggtg 1140

tccaacaagg ccctgcctgc tcctatcgag aaaaccatca gcaaggccaa gggccagcct 1200

agggaacccc aggtttacac cctgcctcca tgcagggatg agctgaccaa gaaccaggtg 1260

tccctgtggt gcctggttaa gggcttctac ccctccgata tcgccgtgga atgggagagc 1320

aatggccagc cagagaacaa ctacaagaca acccctcctg tgctggactc cgacggctca 1380

ttcttcctgt acagcaagct gaccgtggac aagagcagat ggcagcaggg caacgtgttc 1440

agctgcagcg tgatgcacga ggccctgcac aaccactaca cacagaagtc cctgtctctg 1500

agccccggca aa 1512

<210> 190
<211> 504
<212> PRT
<213> Artificial

<220>
<223> Full-length amino acid sequence of NYC-0013-HC-k

<400> 190

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

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

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

Phe Asp Asp Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly
50 55 60

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

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

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

Phe Tyr Tyr Cys Ala Lys Glu Leu Ile Phe Gly Lys Val Leu His Asp
        115                 120                 125

Phe Tyr Tyr Tyr Val Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr
    130                 135                 140

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
145                 150                 155                 160

Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
                165                 170                 175

Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser
            180                 185                 190

Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
        195                 200                 205

Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe
    210                 215                 220

Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu
225                 230                 235                 240

Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr
                245                 250                 255
```

```
Pro Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Gly Gly
            260                 265                 270

Glu Pro Lys Ser Ala Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
        275                 280                 285

Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
    290                 295                 300

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
305                 310                 315                 320

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
                325                 330                 335

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
            340                 345                 350

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
        355                 360                 365

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

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
385                 390                 395                 400

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr
                405                 410                 415
```

```
Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser
            420                 425                 430

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
        435                 440                 445

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
    450                 455                 460

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
465                 470                 475                 480

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
                485                 490                 495

Ser Leu Ser Leu Ser Pro Gly Lys
            500
```

<210> 191
<211> 1512
<212> DNA
<213> Artificial

<220>
<223> Full-length nucleotide sequence of NYC-0014-HC-k

<400> 191

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gaagtgcagc tggtggaatc tggtggcgga gttgttcagc ctggcggctc tctgagactg      120

agctgtgaag cctccggctt catcttcgac gactacgcca tgcactgggt ccgacaggca      180

cctggcaaag gccttgaatg ggtgtccctg atctctggcg acggcgacat catctactac      240

gccgactctg tgaagggcag attcaccatc agccgggaca acagcaagaa cagcctgtac      300
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ctgcagatga actccctgat catcgaggac acagccctgt actactgcgc caaggattgg 360

gtgttcggcg tcgtgatgac ccactactgg tacttcggcc tggatgtgtg gggccaggga 420

accacagtga cagtttctag cggaggcgga ggaagtggcg gcggaggatc tggcggtggt 480

ggttctgata tccagatgac acagagcccc agcagcctgt ctgcctctga aggcgacaga 540

gtgaccatca cctgtagagc cagccagagc atcagcacct acctgaactg gtatcagcag 600

aagcccggca aggcccctaa gctgctgatc tatggtgcct ccagtctgca gagcggcgtg 660

ccaagcagat tttctggcag cggctctggc accgacttca ccctgaccat atctagcctg 720

cagcctgagg acttcgccac ctactactgc cagcagtcct acagcacccc tcctatcaca 780

tttggccagg gcaccaaggt ggaaatcaaa ggcggagaac ccaagagcgc agacaagacc 840

cacacctgtc ctccatgtcc tgctccagaa gctgcaggcg gcccttccgt gtttctgttc 900

cctccaaagc ctaaggacac cctgatgatc agccggacac ctgaagtgac ctgcgtggtg 960

gtggatgtgt cccacgagga tcccgaagtg aagttcaatt ggtacgtgga cggcgtggaa 1020

gtgcacaacg ccaagaccaa gcctagagag gaacagtaca acagcaccta cagagtggtg 1080

tctgtgctga cagtgctgca ccaggactgg ctgaacggca aagagtacaa gtgcaaggtg 1140

tccaacaagg ccctgcctgc tcctatcgag aaaaccatca gcaaggccaa gggccagcct 1200

agggaacccc aggtttacac cctgcctcca tgcagggatg agctgaccaa gaaccaggtg 1260

tccctgtggt gcctggttaa gggcttctac ccctccgata tcgccgtgga atgggagagc 1320

aatggccagc cagagaacaa ctacaagaca acccctcctg tgctggactc cgacggctca 1380

ttcttcctgt acagcaagct gaccgtggac aagagcagat ggcagcaggg caacgtgttc 1440

agctgcagcg tgatgcacga ggccctgcac aaccactaca cacagaagtc cctgtctctg 1500

agccccggca aa 1512

<210> 192
<211> 504
<212> PRT
<213> Artificial

<220>
<223> Full-length amino acid sequence of NYC-0014-HC-k

<400> 192

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

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

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

Phe Asp Asp Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly
50 55 60

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

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

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

Leu Tyr Tyr Cys Ala Lys Asp Trp Val Phe Gly Val Val Met Thr His
115 120 125

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

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
145                 150                 155                 160

Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
                165                 170                 175

Glu Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser
            180                 185                 190

Thr Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
        195                 200                 205

Leu Ile Tyr Gly Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe
    210                 215                 220

Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu
225                 230                 235                 240

Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr
                245                 250                 255

Pro Pro Ile Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly Gly
            260                 265                 270

Glu Pro Lys Ser Ala Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
        275                 280                 285
```

```
Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
    290                 295                 300

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
305                 310                 315                 320

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
                325                 330                 335

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
            340                 345                 350

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
        355                 360                 365

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

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
385                 390                 395                 400

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr
                405                 410                 415

Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser
            420                 425                 430

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
        435                 440                 445

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
    450                 455                 460
```

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
465 470 475 480

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
485 490 495

Ser Leu Ser Leu Ser Pro Gly Lys
500

<210> 193
<211> 1509
<212> DNA
<213> Artificial

<220>
<223> Full-length nucleotide sequence of NYC-0015-HC-k

<400> 193
atgaagcacc tgtggttctt tctgctgctg gtggccgctc ctagatgggt gctgtctggc 60

gaagtgcagc tggtggaatc tggtggcgga gttgttcagc ctggcggctc tctgagactg 120

tcttgtgccg ccagcggctt caccttcgac gattatgcca tgcactgggt ccgacaggcc 180

cctggcaaag gacttgaatg ggtgtccctg atctctggcg gaggcggcgg aacctactac 240

agcgattctg tgaagggcag attcaccatc agccgggaca ccagcaagga cagcctgtac 300

ctgcagatga acagcctgcg gaccgaggac acagccctgt actactgcgc caaggacatg 360

gtgttcggcg tggtcacccc ttactactac ttcgccctgg atgtgtgggg ccagggcaca 420

acagtgacag tctcttctgg cggcggagga agcggaggcg gaggatccgg tggtggtgga 480

tctgacatcc agatgacaca gagccccagc agcctgtctg cctctgtggg agacagagtg 540

accatcacct gtagagccag ccagagcatc aacagctacc tgaactggta tcagcagaag 600

cccggcaagg cccctaagct gctgatctat gctgcctcca gtctgcagag cggcgtgcca 660

agcagatttt ctggcagcgg ctctggcacc gacttcaccc tgaccatatc tagcctgcag 720

cctgaggact tcgccaccta ctactgccag cagagctaca gcgcccctcc tatcacattt 780

ggccagggaa ccagactgga aatcaaaggc ggagaaccca agagcgcaga caagacccac 840

acctgtcctc catgtcctgc tccagaagct gcaggcggcc cttccgtgtt tctgttccct 900

ccaaagccta aggacaccct gatgatcagc cggacacctg aagtgacctg cgtggtggtg 960

gatgtgtccc acgaggatcc cgaagtgaag ttcaattggt acgtggacgg cgtggaagtg 1020

cacaacgcca agaccaagcc tagagaggaa cagtacaaca gcacctacag agtggtgtct 1080

gtgctgacag tgctgcacca ggactggctg aacggcaaag agtacaagtg caaggtgtcc 1140

aacaaggccc tgcctgctcc tatcgagaaa accatcagca aggccaaggg ccagcctagg 1200

gaaccccagg tttacaccct gcctccatgc agggatgagc tgaccaagaa ccaggtgtcc 1260

ctgtggtgcc tggttaaggg cttctacccc tccgatatcg ccgtggaatg ggagagcaat 1320

ggccagccag agaacaacta caagacaacc cctcctgtgc tggactccga cggctcattc 1380

ttcctgtaca gcaagctgac cgtggacaag agcagatggc agcagggcaa cgtgttcagc 1440

tgcagcgtga tgcacgaggc cctgcacaac cactacacac agaagtccct gtctctgagc 1500

cccggcaaa 1509

<210> 194
<211> 503
<212> PRT
<213> Artificial

<220>
<223> Full-length amino acid sequence of NYC-0015-HC-k

<400> 194

```
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                  10                  15

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

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

Phe Asp Asp Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly
    50                  55                  60

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

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

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

Leu Tyr Tyr Cys Ala Lys Asp Met Val Phe Gly Val Val Thr Pro Tyr
        115                 120                 125

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

Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
145                 150                 155                 160
```

```
Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
                165                 170                 175

Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Asn Ser
            180                 185                 190

Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
        195                 200                 205

Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser
    210                 215                 220

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln
225                 230                 235                 240

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Ala Pro
                245                 250                 255

Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Gly Gly Glu
            260                 265                 270

Pro Lys Ser Ala Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
        275                 280                 285

Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
    290                 295                 300

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
305                 310                 315                 320

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
                325                 330                 335
```

```
Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
            340                 345                 350

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
        355                 360                 365

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

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
385                 390                 395                 400

Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys
                405                 410                 415

Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
            420                 425                 430

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
        435                 440                 445

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
    450                 455                 460

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
465                 470                 475                 480

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
                485                 490                 495
```

Leu Ser Leu Ser Pro Gly Lys
500

<210> 195
<211> 1512
<212> DNA
<213> Artificial

<220>
<223> Full-length nucleotide sequence of NYC-0016-HC-k

<400> 195
atgaagcacc tgtggttctt tctgctgctg gtggccgctc ctagatgggt gctgtctggc 60

gaagtgcagc tggtggaatc tggtggcgga gttgttcagc ctggcggctc tctgagactg 120

agctgtgctg tgtccggctt caccttcgac gactacgcca tgcactgggt ccgacaggca 180

cctggcaaag gccttgaatg ggtgtccctg atcagcggag atggcggcag cacacactac 240

gccgattctg tgaagggcag attcaccatc agccgggaca acagcaagaa cagcctgtac 300

ctgcagatga actccctgcg gacaggcgac acagccctgt actactgcgc caaggacatg 360

atcttcgccg tggtcatcac cgactaccac tactacggca tggacgtgtg gggccaggga 420

accacagtga cagtttctag cggaggcgga ggaagtggcg gcggaggatc tggcggtggt 480

ggttctgata tccagatgac acagagcccc agcagcctgt ctgcctctgt gggagacaga 540

gtgaccatca cctgtagagc cagccagagc atcagcagct acctgaactg gtatcagcag 600

aagcccggca aggcccctaa actgctgatc tatgccgcct ccagtctgca gagcggagtg 660

cctagcagat tttctggcag cggctccggc accgatttca ccctgaccat atctagcctg 720

cagcctgagg acttcgccac ctactactgc cagcagagct acagcacccc tcctatcacc 780

tttggccagg gcaccagact ggaaatcaaa ggcggagaac ccaagagcgc agacaagacc 840

cacacctgtc ctccatgtcc tgctccagaa gctgcaggcg gcccttccgt gtttctgttc 900

cctccaaagc ctaaggacac cctgatgatc agccggacac ctgaagtgac ctgcgtggtg 960

gtggatgtgt cccacgagga tcccgaagtg aagttcaatt ggtacgtgga cggcgtggaa 1020

gtgcacaacg ccaagaccaa gcctagagag gaacagtaca acagcaccta cagagtggtg 1080

tctgtgctga cagtgctgca ccaggactgg ctgaacggca aagagtacaa gtgcaaggtg 1140

tccaacaagg ccctgcctgc tcctatcgag aaaaccatca gcaaggccaa gggccagcct 1200

agggaacccc aggtttacac cctgcctcca tgcagggatg agctgaccaa gaaccaggtg 1260

tccctgtggt gcctggttaa gggcttctac ccctccgata tcgccgtgga atgggagagc 1320

aatggccagc cagagaacaa ctacaagaca acccctcctg tgctggactc cgacggctca 1380

ttcttcctgt acagcaagct gaccgtggac aagagcagat ggcagcaggg caacgtgttc 1440

agctgcagcg tgatgcacga ggccctgcac aaccactaca cacagaagtc cctgtctctg 1500

agccccggca aa 1512

<210> 196
<211> 504
<212> PRT
<213> Artificial

<220>
<223> Full-length amino acid sequence of NYC-0016-HC-k

<400> 196

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

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

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

Phe Asp Asp Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly
    50                  55                  60

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

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

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

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

Tyr His Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr
    130                 135                 140

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
145                 150                 155                 160

Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
                165                 170                 175

Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser
            180                 185                 190

Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
        195                 200                 205
```

```
Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe
    210                 215                 220

Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu
225                 230                 235                 240

Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr
                245                 250                 255

Pro Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Gly Gly
            260                 265                 270

Glu Pro Lys Ser Ala Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
        275                 280                 285

Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
    290                 295                 300

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
305                 310                 315                 320

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
                325                 330                 335

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
            340                 345                 350

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
        355                 360                 365
```

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

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
385                 390                 395                 400

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr
                405                 410                 415

Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser
            420                 425                 430

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
        435                 440                 445

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
    450                 455                 460

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
465                 470                 475                 480

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
                485                 490                 495

Ser Leu Ser Leu Ser Pro Gly Lys
            500
```

<210> 197
<211> 719
<212> PRT
<213> Artificial

<220>

<223> Full-length amino acid sequence of NYZ-1007-HC2

<400> 197

```
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                  10                  15

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

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

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

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

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

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

Val Tyr His Cys Ala Arg Gly Ser Ser Gly His Tyr Glu Ala Phe Asp
        115                 120                 125

Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr
145                 150                 155                 160
```

```
Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln Arg Val Thr Ile Ser
                165                 170                 175

Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Trp Tyr Val Ser Trp Tyr
            180                 185                 190

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

Lys Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly
    210                 215                 220

Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln Ser Glu Asp Glu Ala
225                 230                 235                 240

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

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

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        275                 280                 285

Leu Arg Leu Ser Cys Ala Ala Ser Gly Val Thr Phe Asn Tyr Tyr Gly
    290                 295                 300

Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala
305                 310                 315                 320
```

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

Gly Arg Phe Thr Ile Ser Arg Glu Asn Thr Gln Lys Thr Leu Tyr Leu
            340                 345                 350

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

Leu Asp Gly Arg Asp Gly Trp Val Ala Tyr Trp Gly Gln Gly Thr Leu
    370                 375                 380

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
385                 390                 395                 400

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
                405                 410                 415

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
            420                 425                 430

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

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
    450                 455                 460

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
465                 470                 475                 480

Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His
                485                 490                 495
```

```
Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
            500                 505                 510

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

Pro Glu Val Thr Cys Val Val Val Ser Val Ser His Glu Asp Pro Glu
    530                 535                 540

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
545                 550                 555                 560

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
                565                 570                 575

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
            580                 585                 590

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
        595                 600                 605

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Val Tyr Pro
    610                 615                 620

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

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
                645                 650                 655
```

```
Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
            660                 665                 670

Asp Gly Ser Phe Ala Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg
        675                 680                 685

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
    690                 695                 700

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
705                 710                 715
```

<210> 198
<211> 719
<212> PRT
<213> Artificial

<220>
<223> Full-length amino acid sequence of NYZ-1017-HC2

<400> 198

```
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                   10                  15

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

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

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

```
Leu Glu Trp Val Ala Thr Ile Ser Tyr Asp Gly Ser Gln Lys Tyr Tyr
65                  70                  75                  80

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

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

Val Tyr His Cys Ala Arg Gly Ser Ser Gly His Tyr Glu Ala Phe Asp
        115                 120                 125

Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr
145                 150                 155                 160

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

Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Trp Tyr Val Ser Trp Tyr
            180                 185                 190

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

Lys Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly
    210                 215                 220

Thr Ser Ala Thr Leu Gly Ile Thr Gly Leu Gln Thr Gly Asp Glu Ala
225                 230                 235                 240
```

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

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

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        275                 280                 285

Leu Arg Leu Ser Cys Ala Ala Ser Gly Val Thr Phe Asn Tyr Tyr Gly
    290                 295                 300

Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala
305                 310                 315                 320

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

Gly Arg Phe Thr Ile Ser Arg Glu Asn Thr Gln Lys Thr Leu Tyr Leu
            340                 345                 350

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

Leu Asp Gly Arg Asp Gly Trp Val Ala Tyr Trp Gly Gln Gly Thr Leu
    370                 375                 380

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
385                 390                 395                 400
```

```
Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
                405                 410                 415

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
            420                 425                 430

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

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
    450                 455                 460

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
465                 470                 475                 480

Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His
                485                 490                 495

Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
            500                 505                 510

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

Pro Glu Val Thr Cys Val Val Val Ser Val Ser His Glu Asp Pro Glu
    530                 535                 540

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
545                 550                 555                 560

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
                565                 570                 575
```

```
Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
            580                 585                 590

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
        595                 600                 605

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Val Tyr Pro
    610                 615                 620

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

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
                645                 650                 655

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
            660                 665                 670

Asp Gly Ser Phe Ala Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg
        675                 680                 685

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
    690                 695                 700

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
705                 710                 715
```