SEQUENCE LISTING

<110> Seattle Children's Hospital
(DBA) Seattle Children's Research Institute

<120> TRANSGENE GENETIC TAGS AND METHODS OF USE

<130> SP100132SGA

<150> 62/058,973
<151> 2014-10-02

<150> 61/977,751
<151> 2014-04-10

<150> 61/986,479
<151> 2014-04-30

<150> 62/089,730
<151> 2014-12-09

<150> 62/090,845
<151> 2014-12-11

<150> 62/088,363
<151> 2014-12-05

<160> 50

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> CD19CAR DNA encoding a portion of modified IgG4 hinge region

<400> 1
gacgtggagg agaatcccgg ccctagg 27

<210> 2
<211> 476
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 CAR

<400> 2
Met Leu Leu Leu Val Thr Ser Leu Leu Leu Cys Glu Leu Pro His Pro
1 5 10 15
Ala Phe Leu Leu Ile Pro Asp Ile Gln Met Thr Gln Thr Thr Ser Ser
20 25 30
Leu Ser Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser
35 40 45
Gln Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly
50 55 60
Thr Val Lys Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Val
65 70 75 80
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr
85 90 95
Ile Ser Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln

```
            100                 105                 110
Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
        115                 120                 125
Thr Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser
    130                 135                 140
Thr Lys Gly Glu Val Lys Leu Gln Glu Ser Gly Pro Gly Leu Val Ala
145                 150                 155                 160
Pro Ser Gln Ser Leu Ser Val Thr Cys Thr Val Ser Gly Val Ser Leu
                165                 170                 175
Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu
            180                 185                 190
Glu Trp Leu Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser
        195                 200                 205
Ala Leu Lys Ser Arg Leu Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln
    210                 215                 220
Val Phe Leu Lys Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr
225                 230                 235                 240
Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr
                245                 250                 255
Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Glu Ser Lys Tyr Gly
            260                 265                 270
Pro Pro Cys Pro Pro Cys Pro Met Phe Trp Val Leu Val Val Val Gly
        275                 280                 285
Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile
    290                 295                 300
Phe Trp Val Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
305                 310                 315                 320
Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser
                325                 330                 335
Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys
            340                 345                 350
Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln
        355                 360                 365
Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
    370                 375                 380
Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
385                 390                 395                 400
Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
                405                 410                 415
Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
            420                 425                 430
Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
        435                 440                 445
Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Leu Glu Gly
    450                 455                 460
Gly Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly
465                 470                 475


<210> 3
<211> 180
<212> PRT
<213> Artificial Sequence

<220>
<223> CD28 domain

<400> 3
Met Leu Arg Leu Leu Leu Ala Leu Asn Leu Phe Pro Ser Ile Gln Val
 1               5                  10                  15
Thr Gly Asn Lys Ile Leu Val Lys Gln Ser Pro Met Leu Val Ala Tyr
            20                  25                  30
Asp Asn Ala Val Asn Leu Ser Cys Lys Tyr Ser Tyr Asn Leu Phe Ser
        35                  40                  45
Arg Glu Phe Arg Ala Ser Leu His Lys Gly Leu Asp Ser Ala Val Glu
    50                  55                  60
Val Cys Val Val Tyr Gly Asn Tyr Ser Gln Gln Leu Gln Val Tyr Ser
65                  70                  75                  80
Lys Thr Gly Phe Asn Cys Asp Gly Lys Leu Gly Asn Glu Ser Val Thr
```

```
                85                  90                  95
Phe Tyr Leu Gln Asn Leu Tyr Val Asn Gln Thr Asp Ile Tyr Phe Cys
            100                 105                 110
Lys Ile Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys Ser
        115                 120                 125
Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro
    130                 135                 140
Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly
145                 150                 155                 160
Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile
                165                 170                 175
Phe Trp Val Arg
            180


<210> 4
<211> 240
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-1BB domain

<400> 4
Met Gly Asn Ser Cys Tyr Asn Ile Val Ala Thr Leu Leu Leu Val Leu
 1                5                  10                  15
Asn Phe Glu Arg Thr Arg Ser Leu Gln Asp Pro Cys Ser Asn Cys Pro
            20                  25                  30
Ala Gly Thr Phe Cys Asp Asn Asn Arg Asn Gln Ile Cys Ser Pro Cys
        35                  40                  45
Pro Pro Asn Ser Phe Ser Ser Ala Gly Gly Gln Arg Thr Cys Asp Ile
    50                  55                  60
Cys Arg Gln Cys Lys Gly Val Phe Arg Thr Arg Lys Glu Cys Ser Ser
65                  70                  75                  80
Thr Ser Asn Ala Glu Cys Asp Cys Thr Pro Gly Phe His Cys Leu Gly
                85                  90                  95
Ala Gly Cys Ser Met Cys Glu Gln Asp Cys Lys Gln Gly Gln Glu Leu
            100                 105                 110
Thr Lys Lys Gly Cys Lys Asp Cys Cys Phe Gly Thr Phe Asn Asp Gln
        115                 120                 125
Lys Arg Gly Ile Cys Arg Pro Trp Thr Asn Cys Ser Leu Asp Gly Lys
    130                 135                 140
Ser Val Leu Val Asn Gly Thr Lys Glu Arg Asp Val Val Cys Gly Pro
145                 150                 155                 160
Ser Pro Ala Asp Leu Ser Pro Gly Ala Ser Ser Val Thr Pro Pro Ala
                165                 170                 175
Pro Ala Arg Glu Pro Gly His Ser Pro Gln Ile Ile Ser Phe Phe Leu
            180                 185                 190
Ala Leu Thr Ser Thr Ala Leu Leu Phe Leu Leu Phe Phe Leu Thr Leu
        195                 200                 205
Arg Phe Ser Val Val Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe
    210                 215                 220
Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly
225                 230                 235                 240


<210> 5
<211> 164
<212> PRT
<213> Artificial Sequence

<220>
<223> Human CD3 Zeta isoform 3

<400> 5
Met Lys Trp Lys Ala Leu Phe Thr Ala Ala Ile Leu Gln Ala Gln Leu
 1                5                  10                  15
Pro Ile Thr Glu Ala Gln Ser Phe Gly Leu Leu Asp Pro Lys Leu Cys
            20                  25                  30
```

```
Tyr Leu Leu Asp Gly Ile Leu Phe Ile Tyr Gly Val Ile Leu Thr Ala
        35                  40                  45
Leu Phe Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr
    50                  55                  60
Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
65                  70                  75                  80
Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
                85                  90                  95
Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn
            100                 105                 110
Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met
        115                 120                 125
Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly
    130                 135                 140
Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala
145                 150                 155                 160
Leu Pro Pro Arg
```

<210> 6
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Human IgG1 hinge region

<400> 6
```
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 1               5                  10                  15
```

<210> 7
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Human IgG2 hinge region

<400> 7
```
Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro
 1               5                  10
```

<210> 8
<211> 61
<212> PRT
<213> Artificial Sequence

<220>
<223> Human IgG3 hinge region

<400> 8
```
Glu Leu Lys Thr Pro Leu Gly Asp Thr His Thr Cys Pro Arg Cys Pro
 1               5                  10                  15
Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro Glu
            20                  25                  30
Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro Glu Pro
        35                  40                  45
Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro
    50                  55                  60
```

<210> 9
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Human IgG4 hinge region

<400> 9
Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro
 1   5   10

<210> 10
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Modified Human IgG4 hinge region

<400> 10
Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro
 1   5   10

<210> 11
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Modified Human IgG4 hinge region

<400> 11
Tyr Gly Pro Pro Cys Pro Pro Cys Pro
 1   5

<210> 12
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Modified Human IgG4 hinge region

<400> 12
Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro
 1   5   10

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

<220>
<223> Modified Human IgG4 hinge region

<400> 13
Glu Val Val Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro
 1   5   10

<210> 14
<211> 408
<212> DNA
<213> Artificial Sequence

<220>
<223> Her2t (truncated Her2 protein)

<400> 14
atgcttctcc tggtgacaag ccttctgctc tgtgagttac cacacccagc attcctcctg 60
atcccatgcc accctgagtg tcagccccag aatggctcag tgacctgttt tggaccggag 120
gctgaccagt gtgtggcctg tgcccactat aaggaccctc ccttctgcgt ggcccgctgc 180
cccagcggtg tgaaacctga cctctcctac atgcccatct ggaagtttcc agatgaggag 240
ggcgcatgcc agccttgccc catcaactgc acccactcct gtgtggacct ggatgacaag 300
ggctgccccg ccgagcagag agccagccct ctgacgtcca tcatctctgc ggtggttggc 360
attctgctgg tcgtggtctt gggggtggtc tttgggatcc tcatctga 408

<210> 15
<211> 135
<212> PRT
<213> Artificial Sequence

<220>
<223> Her2t (truncated Her2 protein)

<400> 15
Met Leu Leu Leu Val Thr Ser Leu Leu Leu Cys Glu Leu Pro His Pro
 1   5   10   15
Ala Phe Leu Leu Ile Pro Cys His Pro Glu Cys Gln Pro Gln Asn Gly
            20   25   30
Ser Val Thr Cys Phe Gly Pro Glu Ala Asp Gln Cys Val Ala Cys Ala
        35   40   45
His Tyr Lys Asp Pro Pro Phe Cys Val Ala Arg Cys Pro Ser Gly Val
    50   55   60
Lys Pro Asp Leu Ser Tyr Met Pro Ile Trp Lys Phe Pro Asp Glu Glu
65   70   75   80
Gly Ala Cys Gln Pro Cys Pro Ile Asn Cys Thr His Ser Cys Val Asp
                85   90   95
Leu Asp Asp Lys Gly Cys Pro Ala Glu Gln Arg Ala Ser Pro Leu Thr
            100   105   110
Ser Ile Ile Ser Ala Val Val Gly Ile Leu Leu Val Val Val Leu Gly
        115   120   125
Val Val Phe Gly Ile Leu Ile
    130   135

<210> 16
<211> 35
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic genetic tag

<400> 16
Met Leu Leu Leu Val Thr Ser Leu Leu Leu Cys Glu Leu Pro His Pro
 1   5   10   15
Ala Phe Leu Leu Ile Pro Cys His Pro Glu Cys Gln Pro Gln Asn Gly
            20   25   30
Ser Val Thr
        35

<210> 17
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Leader sequence for protein localization

<400> 17
Met Leu Leu Leu Val Thr Ser Leu Leu Leu Cys Glu Leu Pro His Pro
 1   5   10   15
Ala Phe Leu Leu Ile Pro
            20

<210> 18
<211> 90
<212> PRT
<213> Artificial Sequence

<220>
<223> Fragment of Her2 protein recognized by an antiHer2 antibody

<400> 18
Cys His Pro Glu Cys Gln Pro Gln Asn Gly Ser Val Thr Cys Phe Gly
 1   5   10   15
Pro Glu Ala Asp Gln Cys Val Ala Cys Ala His Tyr Lys Asp Pro Pro
            20   25   30
Phe Cys Val Ala Arg Cys Pro Ser Gly Val Lys Pro Asp Leu Ser Tyr
        35   40   45
Met Pro Ile Trp Lys Phe Pro Asp Glu Glu Gly Ala Cys Gln Pro Cys
    50   55   60
Pro Ile Asn Cys Thr His Ser Cys Val Asp Leu Asp Asp Lys Gly Cys
65   70   75   80
Pro Ala Glu Gln Arg Ala Ser Pro Leu Thr
                85   90

<210> 19
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Fragment of Her2 transmembrane domain, the transmembrane domain of Her2

<400> 19
Ser Ile Ile Ser Ala Val Val Gly Ile Leu Leu Val Val Val Leu Gly
 1   5   10   15
Val Val Phe Gly Ile Leu Ile Ile
            20

<210> 20
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> Her2 transmembrane domain as amino acids 653-675

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

<210> 21

<211> 1074
<212> DNA
<213> Artificial Sequence

<220>
<223> Encoding a truncated epidermal growth factor receptor

<400> 21
atgcttctcc tggtgacaag ccttctgctc tgtgagttac cacacccagc attcctcctg 60
atcccacgca aagtgtgtaa cggaataggt attggtgaat ttaaagactc actctccata 120
aatgctacga atattaaaca cttcaaaaac tgcacctcca tcagtggcga tctccacatc 180
ctgccggtgg catttagggg tgactccttc acacatactc ctcctctgga tccacaggaa 240
ctggatattc tgaaaaccgt aaaggaaatc acagggtttt tgctgattca ggcttggcct 300
gaaaacagga cggacctcca tgcctttgag aacctagaaa tcatacgcgg caggaccaag 360
caacatggtc agttttctct tgcagtcgtc agcctgaaca taacatcctt gggattacgc 420
tccctcaagg agataagtga tggagatgtg ataatttcag gaaacaaaaa tttgtgctat 480
gcaaatacaa taaactggaa aaaactgttt gggacctccg gtcagaaaac caaaattata 540
agcaacagag gtgaaaacag ctgcaaggcc acaggccagg tctgccatgc cttgtgctcc 600
cccgagggct gctggggccc ggagcccagg gactgcgtct cttgccggaa tgtcagccga 660
ggcagggaat gcgtggacaa gtgcaacctt ctggagggtg agccaaggga gtttgtggag 720
aactctgagt gcatacagtg ccacccagag tgcctgcctc aggccatgaa catcacctgc 780
acaggacggg gaccagacaa ctgtatccag tgtgcccact acattgacgg cccccactgc 840
gtcaagacct gcccggcagg agtcatggga gaaaacaaca ccctggtctg gaagtacgca 900
gacgccggcc atgtgtgcca cctgtgccat ccaaactgca cctacggatg cactgggcca 960
ggtcttgaag gctgtccaac gaatgggcct aagatcccgt ccatcgccac tgggatggtg 1020
ggggccctcc tcttgctgct ggtggtggcc ctggggatcg gcctcttcat gtga 1074

<210> 22
<211> 357
<212> PRT
<213> Artificial Sequence

<220>
<223> Truncated epidermal growth factor receptor

<400> 22
Met Leu Leu Leu Val Thr Ser Leu Leu Leu Cys Glu Leu Pro His Pro
 1   5   10   15
Ala Phe Leu Leu Ile Pro Arg Lys Val Cys Asn Gly Ile Gly Ile Gly
            20   25   30
Glu Phe Lys Asp Ser Leu Ser Ile Asn Ala Thr Asn Ile Lys His Phe
        35   40   45
Lys Asn Cys Thr Ser Ile Ser Gly Asp Leu His Ile Leu Pro Val Ala
    50   55   60
Phe Arg Gly Asp Ser Phe Thr His Thr Pro Pro Leu Asp Pro Gln Glu
65   70   75   80
Leu Asp Ile Leu Lys Thr Val Lys Glu Ile Thr Gly Phe Leu Leu Ile
                85   90   95
Gln Ala Trp Pro Glu Asn Arg Thr Asp Leu His Ala Phe Glu Asn Leu
            100   105   110
Glu Ile Ile Arg Gly Arg Thr Lys Gln His Gly Gln Phe Ser Leu Ala
        115   120   125
Val Val Ser Leu Asn Ile Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu
    130   135   140
Ile Ser Asp Gly Asp Val Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr
145   150   155   160
Ala Asn Thr Ile Asn Trp Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys
                165   170   175
Thr Lys Ile Ile Ser Asn Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly
            180   185   190
Gln Val Cys His Ala Leu Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu
        195   200   205
Pro Arg Asp Cys Val Ser Cys Arg Asn Val Ser Arg Gly Arg Glu Cys
    210   215   220
Val Asp Lys Cys Asn Leu Leu Glu Gly Glu Pro Arg Glu Phe Val Glu
225   230   235   240
Asn Ser Glu Cys Ile Gln Cys His Pro Glu Cys Leu Pro Gln Ala Met
                245   250   255

```
Asn Ile Thr Cys Thr Gly Arg Gly Pro Asp Asn Cys Ile Gln Cys Ala
            260                 265                 270
His Tyr Ile Asp Gly Pro His Cys Val Lys Thr Cys Pro Ala Gly Val
        275                 280                 285
Met Gly Glu Asn Asn Thr Leu Val Trp Lys Tyr Ala Asp Ala Gly His
    290                 295                 300
Val Cys His Leu Cys His Pro Asn Cys Thr Tyr Gly Cys Thr Gly Pro
305                 310                 315                 320
Gly Leu Glu Gly Cys Pro Thr Asn Gly Pro Lys Ile Pro Ser Ile Ala
                325                 330                 335
Thr Gly Met Val Gly Ala Leu Leu Leu Leu Leu Val Val Ala Leu Gly
            340                 345                 350
Ile Gly Leu Phe Met
        355


<210> 23
<211> 1255
<212> PRT
<213> Artificial Sequence

<220>
<223> Full length Her2 isoform 1 human

<400> 23
Met Glu Leu Ala Ala Leu Cys Arg Trp Gly Leu Leu Leu Ala Leu Leu
 1                  5                  10                  15
Pro Pro Gly Ala Ala Ser Thr Gln Val Cys Thr Gly Thr Asp Met Lys
            20                  25                  30
Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met Leu Arg His
        35                  40                  45
Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu Leu Thr Tyr
    50                  55                  60
Leu Pro Thr Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile Gln Glu Val
65                  70                  75                  80
Gln Gly Tyr Val Leu Ile Ala His Asn Gln Val Arg Gln Val Pro Leu
                85                  90                  95
Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu Asp Asn Tyr
            100                 105                 110
Ala Leu Ala Val Leu Asp Asn Gly Asp Pro Leu Asn Asn Thr Thr Pro
        115                 120                 125
Val Thr Gly Ala Ser Pro Gly Gly Leu Arg Glu Leu Gln Leu Arg Ser
    130                 135                 140
Leu Thr Glu Ile Leu Lys Gly Gly Val Leu Ile Gln Arg Asn Pro Gln
145                 150                 155                 160
Leu Cys Tyr Gln Asp Thr Ile Leu Trp Lys Asp Ile Phe His Lys Asn
                165                 170                 175
Asn Gln Leu Ala Leu Thr Leu Ile Asp Thr Asn Arg Ser Arg Ala Cys
            180                 185                 190
His Pro Cys Ser Pro Met Cys Lys Gly Ser Arg Cys Trp Gly Glu Ser
        195                 200                 205
Ser Glu Asp Cys Gln Ser Leu Thr Arg Thr Val Cys Ala Gly Gly Cys
    210                 215                 220
Ala Arg Cys Lys Gly Pro Leu Pro Thr Asp Cys Cys His Glu Gln Cys
225                 230                 235                 240
Ala Ala Gly Cys Thr Gly Pro Lys His Ser Asp Cys Leu Ala Cys Leu
                245                 250                 255
His Phe Asn His Ser Gly Ile Cys Glu Leu His Cys Pro Ala Leu Val
            260                 265                 270
Thr Tyr Asn Thr Asp Thr Phe Glu Ser Met Pro Asn Pro Glu Gly Arg
        275                 280                 285
Tyr Thr Phe Gly Ala Ser Cys Val Thr Ala Cys Pro Tyr Asn Tyr Leu
    290                 295                 300
Ser Thr Asp Val Gly Ser Cys Thr Leu Val Cys Pro Leu His Asn Gln
305                 310                 315                 320
Glu Val Thr Ala Glu Asp Gly Thr Gln Arg Cys Glu Lys Cys Ser Lys
                325                 330                 335
Pro Cys Ala Arg Val Cys Tyr Gly Leu Gly Met Glu His Leu Arg Glu
            340                 345                 350
```

```
Val Arg Ala Val Thr Ser Ala Asn Ile Gln Glu Phe Ala Gly Cys Lys
        355                 360                 365
Lys Ile Phe Gly Ser Leu Ala Phe Leu Pro Glu Ser Phe Asp Gly Asp
    370                 375                 380
Pro Ala Ser Asn Thr Ala Pro Leu Gln Pro Glu Gln Leu Gln Val Phe
385                 390                 395                 400
Glu Thr Leu Glu Glu Ile Thr Gly Tyr Leu Tyr Ile Ser Ala Trp Pro
                405                 410                 415
Asp Ser Leu Pro Asp Leu Ser Val Phe Gln Asn Leu Gln Val Ile Arg
            420                 425                 430
Gly Arg Ile Leu His Asn Gly Ala Tyr Ser Leu Thr Leu Gln Gly Leu
        435                 440                 445
Gly Ile Ser Trp Leu Gly Leu Arg Ser Leu Arg Glu Leu Gly Ser Gly
    450                 455                 460
Leu Ala Leu Ile His His Asn Thr His Leu Cys Phe Val His Thr Val
465                 470                 475                 480
Pro Trp Asp Gln Leu Phe Arg Asn Pro His Gln Ala Leu Leu His Thr
                485                 490                 495
Ala Asn Arg Pro Glu Asp Glu Cys Val Gly Glu Gly Leu Ala Cys His
            500                 505                 510
Gln Leu Cys Ala Arg Gly His Cys Trp Gly Pro Gly Pro Thr Gln Cys
        515                 520                 525
Val Asn Cys Ser Gln Phe Leu Arg Gly Gln Glu Cys Val Glu Glu Cys
    530                 535                 540
Arg Val Leu Gln Gly Leu Pro Arg Glu Tyr Val Asn Ala Arg His Cys
545                 550                 555                 560
Leu Pro Cys His Pro Glu Cys Gln Pro Gln Asn Gly Ser Val Thr Cys
                565                 570                 575
Phe Gly Pro Glu Ala Asp Gln Cys Val Ala Cys Ala His Tyr Lys Asp
            580                 585                 590
Pro Pro Phe Cys Val Ala Arg Cys Pro Ser Gly Val Lys Pro Asp Leu
        595                 600                 605
Ser Tyr Met Pro Ile Trp Lys Phe Pro Asp Glu Glu Gly Ala Cys Gln
    610                 615                 620
Pro Cys Pro Ile Asn Cys Thr His Ser Cys Val Asp Leu Asp Asp Lys
625                 630                 635                 640
Gly Cys Pro Ala Glu Gln Arg Ala Ser Pro Leu Thr Ser Ile Ile Ser
                645                 650                 655
Ala Val Val Gly Ile Leu Leu Val Val Val Leu Gly Val Val Phe Gly
            660                 665                 670
Ile Leu Ile Lys Arg Arg Gln Gln Lys Ile Arg Lys Tyr Thr Met Arg
        675                 680                 685
Arg Leu Leu Gln Glu Thr Glu Leu Val Glu Pro Leu Thr Pro Ser Gly
    690                 695                 700
Ala Met Pro Asn Gln Ala Gln Met Arg Ile Leu Lys Glu Thr Glu Leu
705                 710                 715                 720
Arg Lys Val Lys Val Leu Gly Ser Gly Ala Phe Gly Thr Val Tyr Lys
                725                 730                 735
Gly Ile Trp Ile Pro Asp Gly Glu Asn Val Lys Ile Pro Val Ala Ile
            740                 745                 750
Lys Val Leu Arg Glu Asn Thr Ser Pro Lys Ala Asn Lys Glu Ile Leu
        755                 760                 765
Asp Glu Ala Tyr Val Met Ala Gly Val Gly Ser Pro Tyr Val Ser Arg
    770                 775                 780
Leu Leu Gly Ile Cys Leu Thr Ser Thr Val Gln Leu Val Thr Gln Leu
785                 790                 795                 800
Met Pro Tyr Gly Cys Leu Leu Asp His Val Arg Glu Asn Arg Gly Arg
                805                 810                 815
Leu Gly Ser Gln Asp Leu Leu Asn Trp Cys Met Gln Ile Ala Lys Gly
            820                 825                 830
Met Ser Tyr Leu Glu Asp Val Arg Leu Val His Arg Asp Leu Ala Ala
        835                 840                 845
Arg Asn Val Leu Val Lys Ser Pro Asn His Val Lys Ile Thr Asp Phe
    850                 855                 860
Gly Leu Ala Arg Leu Leu Asp Ile Asp Glu Thr Glu Tyr His Ala Asp
865                 870                 875                 880
Gly Gly Lys Val Pro Ile Lys Trp Met Ala Leu Glu Ser Ile Leu Arg
                885                 890                 895
Arg Arg Phe Thr His Gln Ser Asp Val Trp Ser Tyr Gly Val Thr Val
```

```
            900                 905                 910
Trp Glu Leu Met Thr Phe Gly Ala Lys Pro Tyr Asp Gly Ile Pro Ala
        915                 920                 925
Arg Glu Ile Pro Asp Leu Leu Glu Lys Gly Glu Arg Leu Pro Gln Pro
    930                 935                 940
Pro Ile Cys Thr Ile Asp Val Tyr Met Ile Met Val Lys Cys Trp Met
945                 950                 955                 960
Ile Asp Ser Glu Cys Arg Pro Arg Phe Arg Glu Leu Val Ser Glu Phe
                965                 970                 975
Ser Arg Met Ala Arg Asp Pro Gln Arg Phe Val Val Ile Gln Asn Glu
            980                 985                 990
Asp Leu Gly Pro Ala Ser Pro Leu Asp Ser Thr Phe Tyr Arg Ser Leu
        995                 1000                1005
Leu Glu Asp Asp Asp Met Gly Asp Leu Val Asp Ala Glu Glu Tyr Leu
    1010                1015                1020
Val Pro Gln Gln Gly Phe Phe Cys Pro Asp Pro Ala Pro Gly Ala Gly
1025                1030                1035                1040
Gly Met Val His His Arg His Arg Ser Ser Ser Thr Arg Ser Gly Gly
                1045                1050                1055
Gly Asp Leu Thr Leu Gly Leu Glu Pro Ser Glu Glu Glu Ala Pro Arg
            1060                1065                1070
Ser Pro Leu Ala Pro Ser Glu Gly Ala Gly Ser Asp Val Phe Asp Gly
        1075                1080                1085
Asp Leu Gly Met Gly Ala Ala Lys Gly Leu Gln Ser Leu Pro Thr His
    1090                1095                1100
Asp Pro Ser Pro Leu Gln Arg Tyr Ser Glu Asp Pro Thr Val Pro Leu
1105                1110                1115                1120
Pro Ser Glu Thr Asp Gly Tyr Val Ala Pro Leu Thr Cys Ser Pro Gln
                1125                1130                1135
Pro Glu Tyr Val Asn Gln Pro Asp Val Arg Pro Gln Pro Pro Ser Pro
            1140                1145                1150
Arg Glu Gly Pro Leu Pro Ala Ala Arg Pro Ala Gly Ala Thr Leu Glu
        1155                1160                1165
Arg Pro Lys Thr Leu Ser Pro Gly Lys Asn Gly Val Val Lys Asp Val
    1170                1175                1180
Phe Ala Phe Gly Gly Ala Val Glu Asn Pro Glu Tyr Leu Thr Pro Gln
1185                1190                1195                1200
Gly Gly Ala Ala Pro Gln Pro His Pro Pro Pro Ala Phe Ser Pro Ala
                1205                1210                1215
Phe Asp Asn Leu Tyr Tyr Trp Asp Gln Asp Pro Pro Glu Arg Gly Ala
            1220                1225                1230
Pro Pro Ser Thr Phe Lys Gly Thr Pro Thr Ala Glu Asn Pro Glu Tyr
        1235                1240                1245
Leu Gly Leu Asp Val Pro Val
    1250                1255
```

<210> 24
<211> 798
<212> DNA
<213> Artificial Sequence

<220>
<223> CD20CAR DNA chimeric antigen receptor

<400> 24
```
atggagacag acacactcct gctatgggtg ctgctgctct gggttccagg ttccacaggt 60
gacattgtgc tgacccaatc tccagctatc ctgtctgcat ctccagggga gaaggtcaca 120
atgacttgca gggccagctc aagtgtaaat tacatggact ggtaccagaa gaagccagga 180
tcctccccca aaccctggat ttatgccaca tccaacctgg cttctggagt ccctgctcgc 240
ttcagtggca gtgggtctgg gacctcttac tctctcacaa tcagcagagt ggaggctgaa 300
gatgctgcca cttattactg ccagcagtgg agttttaatc cacccacgtt cggaggggga 360
accaagctgg aaataaaagg cagtactagc ggtggtggct ccgggggcgg ttccggtggg 420
ggcggcagca gcgaggtgca gctgcagcag tctggggctg agctggtgaa gcctggggcc 480
tcagtgaaga tgtcctgcaa ggcttctggc tacacattta ccagttacaa tatgcactgg 540
gtaaagcaga cacctggaca gggcctggaa tggattggag ctatttatcc aggaaatggt 600
gatacttcct acaatcagaa gttcaaaggc aaggccacat tgactgcaga caaatcctcc 660
agcacagcct acatgcagct cagcagcctg acatctgagg actctgcgga ctattactgt 720
gcaagatcta attattacgg tagtagctac tggttcttcg atgtctgggg cgcagggacc 780
```

acggtcaccg tctcctca 798

<210> 25
<211> 266
<212> PRT
<213> Artificial Sequence

<220>
<223> CD20CAR sythetic construct

<400> 25
Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
 1   5   10   15
Gly Ser Thr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Ile Leu Ser
            20   25   30
Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser
        35   40   45
Val Asn Tyr Met Asp Trp Tyr Gln Lys Lys Pro Gly Ser Ser Pro Lys
    50   55   60
Pro Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg
65   70   75   80
Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg
                85   90   95
Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Phe
            100   105   110
Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Ser
        115   120   125
Thr Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser
    130   135   140
Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
145   150   155   160
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
                165   170   175
Asn Met His Trp Val Lys Gln Thr Pro Gly Gln Gly Leu Glu Trp Ile
            180   185   190
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
        195   200   205
Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
    210   215   220
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Asp Tyr Tyr Cys
225   230   235   240
Ala Arg Ser Asn Tyr Tyr Gly Ser Ser Tyr Trp Phe Phe Asp Val Trp
                245   250   255
Gly Ala Gly Thr Thr Val Thr Val Ser Ser
            260   265

<210> 26
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Self-cleaving linker T2A

<400> 26
Leu Glu Gly Gly Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly
 1   5   10   15

<210> 27
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable light chain comprising a CDRL1

<400> 27

Arg Ala Ser Gln Asp Ile Ser Lys Tyr Leu Asn
1 5 10

<210> 28
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable light chain comprising CDRL2

<400> 28
Ser Arg Leu His Ser Gly Val
1 5

<210> 29
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable light chain comprising CDRL3

<400> 29
Gly Asn Thr Leu Pro Tyr Thr Phe Gly
1 5

<210> 30
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable heavy chain comprising CDRH1

<400> 30
Asp Tyr Gly Val Ser
1 5

<210> 31
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable heavy chain comprising CDRH2

<400> 31
Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser
1 5 10 15

<210> 32
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable heavy chain comprising CDRH3

<400> 32
Tyr Ala Met Asp Tyr
1 5

<210> 33
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable light chain comprising CDRL1

<400> 33
Arg Ala Ser Ser Ser Val Asn Tyr Met Asp
 1   5   10

<210> 34
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable light chain comprising CDRL2

<400> 34
Ala Thr Ser Asn Leu Ala Ser
 1   5

<210> 35
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable light chain comprising CDRL3

<400> 35
Gln Gln Trp Ser Phe Asn Pro Pro Thr
 1   5

<210> 36
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable heavy chain comprising CDRH1 sequence, a
      synthetic humanized or human sequence

<400> 36
Ser Tyr Asn Met His
 1   5

<210> 37
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRH2, variable heavy chain comprising a synthetic
      humanized or human sequence

<400> 37
Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe Lys
 1   5   10   15
Gly

<210> 38
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable heavy chain comprising CDRH3, a synthetic
humanized or human sequence

<400> 38
Ser Asn Tyr Tyr Gly Ser Ser Tyr Trp Phe Phe Asp Val
1 5 10

<210> 39
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Flexible linker amino acids

<400> 39
Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr
1 5 10 15
Lys Gly

<210> 40
<211> 429
<212> DNA
<213> Artificial Sequence

<220>
<223> Her2Domain IV and 7 amino acid linker

<400> 40
atgcttctcc tggtgacaag ccttctgctc tgtgagttac cacacccagc attcctcctg 60
atcccatgcc accctgagtg tcagccccag aatggctcag tgacctgttt tggaccggag 120
gctgaccagt gtgtggcctg tgcccactat aaggaccctc ccttctgcgt ggcccgctgc 180
cccagcggtg tgaaacctga cctctcctac atgcccatct ggaagtttcc agatgaggag 240
ggcgcatgcc agccttgccc catcaactgc acccactcct gtgtggacct ggatgacaag 300
ggctgccccg ccgagcagag agccagcccg ttaacgggtg gaggcagcgg aggtggctcc 360
atcatctctg cggtggttgg cattctgctg gtcgtggtct tgggggtggt ctttgggatc 420
ctcatctga 429

<210> 41
<211> 142
<212> PRT
<213> Artificial Sequence

<220>
<223> Her2Domain IV and 7 amino acid linker

<400> 41
Met Leu Leu Leu Val Thr Ser Leu Leu Leu Cys Glu Leu Pro His Pro
1 5 10 15
Ala Phe Leu Leu Ile Pro Cys His Pro Glu Cys Gln Pro Gln Asn Gly
20 25 30
Ser Val Thr Cys Phe Gly Pro Glu Ala Asp Gln Cys Val Ala Cys Ala
35 40 45
His Tyr Lys Asp Pro Pro Phe Cys Val Ala Arg Cys Pro Ser Gly Val
50 55 60
Lys Pro Asp Leu Ser Tyr Met Pro Ile Trp Lys Phe Pro Asp Glu Glu
65 70 75 80
Gly Ala Cys Gln Pro Cys Pro Ile Asn Cys Thr His Ser Cys Val Asp
85 90 95
Leu Asp Asp Lys Gly Cys Pro Ala Glu Gln Arg Ala Ser Pro Leu Thr

```
            100                 105                 110
Gly Gly Gly Ser Gly Gly Gly Ser Ile Ile Ser Ala Val Val Gly Ile
        115                 120                 125
Leu Leu Val Val Val Leu Gly Val Val Phe Gly Ile Leu Ile
    130                 135                 140
```

<210> 42
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Loop 1 of Her2 protein, protein region, human protein

<400> 42
Glu Ala Asp Gln Cys
1 5

<210> 43
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Loop 2 of Her2 protein, protein region, human protein

<400> 43
Asp Pro Pro Phe
1

<210> 44
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Loop 3 of Her2 protein, protein region, human protein

<400> 44
Phe Pro Asp Glu Glu Gly Ala Cys Gln Pro
1 5 10

<210> 45
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic linker

<400> 45
Gly Gly Gly Ser Gly Gly Gly Ser
1 5

<210> 46
<211> 1428
<212> DNA
<213> Artificial Sequence

<220>
<223> CD19 CAR

<400> 46
atgctgctgc tggtgaccag cctgctgctg tgcgagctgc cccaccccgc ctttctgctg 60
atccccgaca tccagatgac ccagaccacc tccagcctga gcgccagcct gggcgaccgg 120
gtgaccatca gctgccgggc cagccaggac atcagcaagt acctgaactg gtatcagcag 180
aagcccgacg gcaccgtcaa gctgctgatc taccacacca gccggctgca cagcggcgtg 240
cccagccggt ttagcggcag cggctccggc accgactaca gcctgaccat ctccaacctg 300
gaacaggaag atatcgccac ctacttttgc cagcagggca acacactgcc ctacaccttt 360
ggcggcggaa caaagctgga aatcaccggc agcacctccg gcagcggcaa gcctggcagc 420
ggcgagggca gcaccaaggg cgaggtgaag ctgcaggaaa gcggccctgg cctggtggcc 480
cccagccaga gcctgagcgt gacctgcacc gtgagcggcg tgagcctgcc cgactacggc 540
gtgagctgga tccggcagcc ccccaggaag ggcctggaat ggctgggcgt gatctggggc 600
agcgagacca cctactacaa cagcgccctg aagagccggc tgaccatcat caaggacaac 660
agcaagagcc aggtgttcct gaagatgaac agcctgcaga ccgacgacac cgccatctac 720
tactgcgcca agcactacta ctacggcggc agctacgcca tggactactg gggccagggc 780
accagcgtga ccgtgagcag cgagagcaag tacggaccgc cctgcccccc ttgccctatg 840
ttctgggtgc tggtggtggt cggaggcgtg ctggcctgct acagcctgct ggtcaccgtg 900
gccttcatca tcttttgggt gaaacggggc agaaagaaac tcctgtatat attcaaacaa 960
ccatttatga gaccagtaca aactactcaa gaggaagatg gctgtagctg ccgatttcca 1020
gaagaagaag aaggaggatg tgaactgcgg gtgaagttca gcagaagcgc cgacgccccc 1080
gcctaccagc agggccagaa tcagctgtac aacgagctga acctgggcag aagggaagag 1140
tacgacgtcc tggataagcg gagaggccgg gaccctgaga tgggcggcaa gcctcggcgg 1200
aagaaccccc aggaaggcct gtataacgaa ctgcagaaag acaagatggc cgaggcctac 1260
agcgagatcg gcatgaaggg cgagcggagg cggggcaagg gccacgacgg cctgtatcag 1320
ggcctgtcca ccgccaccaa ggatacctac gacgccctgc acatgcaggc cctgccccca 1380
aggctcgagg gcggcggaga gggcagagga agtcttctaa catgcggt 1428

<210> 47
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> IgG4-Hinge

<400> 47
gagagcaagt acggaccgcc ctgccccccc tgccct 36

<210> 48
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> CH3 hinge region

<400> 48
ggccagcctc gcgagcccca ggtgtacacc ctgcctccct cccaggaaga gatgaccaag 60
aaccaggtgt ccctgacctg cctggtgaag ggcttctacc ccagcgacat cgccgtggag 120
tgggagagca acggccagcc tgagaacaac tacaagacca cccctcccgt gctggacagc 180
gacggcagct tcttcctgta cagccggctg accgtggaca agagccggtg gcaggaaggc 240
aacgtcttta gctgcagcgt gatgcacgag gccctgcaca accactacac ccagaagagc 300
ctgagcctgt ccctgggcaa g 321

<210> 49
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG4-Hinge

<400> 49
Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro
 1   5   10

<210> 50
<211> 107

<212> PRT
<213> Artificial Sequence

<220>
<223> CH3 hinge region

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