SEQUENCE LISTING

<110> NBE Therapeutics

<120> Method of producing an immunoligand/payload conjugate

<130> ND40306

<160> 58

<170> PatentIn version 3.5

<210> 1
<211> 417
<212> DNA
<213> Artificial Sequence

<220>
<223> VH coding region of humanized anti-human CD19 antibody hBU12

<400> 1
atgggatgga gctggatctt tcttttcctc ctgtcaggaa ctgcaggtgt ccattgtcag 60

gttcagctgc aagagtctgg ccctgggttg gttaagccct cccagaccct cagtctgact 120

tgtactgtgt ctgggggttc aatcagcact tctggtatgg gtgtaggctg gattaggcag 180

cacccaggga agggtctgga gtggattgga cacatttggt gggatgatga caagagatat 240

aacccagccc tgaagagcag agtgacaatc tctgtggata cctccaagaa ccagtttagc 300

ctcaagctgt ccagtgtgac agctgcagat actgctgtct actactgtgc tagaatggaa 360

ctttggtcct actattttga ctactggggc caaggcaccc ttgtcacagt ctcctca 417

<210> 2
<211> 139
<212> PRT
<213> Artificial Sequence

<220>
<223> amino acid sequence of VH region of humanized anti-human CD19 antibody hBU12

<400> 2

Met Gly Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly
1 5 10 15

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

Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile
35 40 45

Ser Thr Ser Gly Met Gly Val Gly Trp Ile Arg Gln His Pro Gly Lys
50 55 60

Gly Leu Glu Trp Ile Gly His Ile Trp Trp Asp Asp Asp Lys Arg Tyr
65 70 75 80

Asn Pro Ala Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys

85 90 95

Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala
100 105 110

Val Tyr Tyr Cys Ala Arg Met Glu Leu Trp Ser Tyr Tyr Phe Asp Tyr
115 120 125

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

<210> 3
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> VL coding region of humanized anti-human CD19 antibody hBU12

<400> 3
atgaagttgc ctgttaggct gttggtgctg atgttctgga ttcctgcttc cagcagtgaa 60

attgttctca cccagtctcc agcaaccctg tctctctctc caggggaaag ggctaccctg 120

agctgcagtg ccagctcaag tgtaagttac atgcactggt accagcagaa gccagggcag 180

gctcccagac tcctgattta tgacacatcc aaactggctt ctggtattcc agcaaggttc 240

agtggcagtg ggtctggaac agattttaca ctcacaatca gcagcctgga gccagaggat 300

gttgctgtct attactgttt tcaggggagt gtatacccat tcacttttgg ccaagggaca 360

aagttggaaa tcaaa 375

<210> 4
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> amino acid sequence of VL region of humanized anti-human CD19 antibody hBU12

<400> 4

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

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

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

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

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

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

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

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

<210> 5
<211> 1083
<212> DNA
<213> Artificial Sequence

<220>
<223> human IgG1 heavy chain constant coding region with in-frame 3' extension encoding an LPETG sortase tag, an 6xHis tag and a strepII tag

<400> 5
agcaccaagg gcccatctgt cttccccctg gcaccctcct ccaagagcac ctctgggggc 60

acagctgccc tgggctgcct ggtcaaggac tacttccctg aacctgtgac agtgtcctgg 120

aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 180

ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 240

atctgcaacg tgaatcacaa gcccagcaac accaaggtgg acaagaaagt tgagcccaaa 300

tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaactcct gggggggaccg 360

tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 420

gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 480

gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 540

acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 600

tacaagtgca aggtctccaa caaagccctc ccagccccca tcgagaaaac catctccaaa 660

gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 720

accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 780

gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 840

gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 900

caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacacag 960

aagagcctct ccctgtctcc gggtaaactg cccgagaccg gccaccacca ccaccaccac 1020

ggcgagcaga agctgatcag cgaggaggac ctgggctgga gccaccccca gttcgagaag 1080

tag 1083

<210> 6
<211> 360
<212> PRT
<213> Artificial Sequence

<220>
<223> amino acid sequence of human IgG1 heavy chain constant region with LPETG sortase tag, an 6xHis tag and a strepII tag

<400> 6

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

Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
            20                  25                  30

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

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

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
65                  70                  75                  80

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
                85                  90                  95

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

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

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
    130                 135                 140

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
145                 150                 155                 160

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
                165                 170                 175

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
            180                 185                 190

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
        195                 200                 205

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
    210                 215                 220

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
225                 230                 235                 240

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
```

245 250 255

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
260 265 270

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
275 280 285

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
290 295 300

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
305 310 315 320

Lys Ser Leu Ser Leu Ser Pro Gly Lys Leu Pro Glu Thr Gly His His
325 330 335

His His His His Gly Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Gly
340 345 350

Trp Ser His Pro Gln Phe Glu Lys
355 360

<210> 7
<211> 414
<212> DNA
<213> Artificial Sequence

<220>
<223> human IgG1 kappa light chain constant coding region with in-frame 3' extension encoding an LPETG sortase tag, an 6xHis tag and a strepII tag.

<400> 7
acggtggctg caccatctgt cttcatcttc ccgccatctg atgagcagtt gaaatctgga 60

actgcctctg ttgtgtgcct gctgaataac ttctatccca gagaggccaa agtacagtgg 120

aaggtggata acgccctcca atcgggtaac tcccaggaga gtgtcacaga gcaggacagc 180

aaggacagca cctacagcct cagcagcacc ctgacgctga gcaaagcaga ctacgagaaa 240

cacaaagtct acgcctgcga agtcacccat cagggcctga gctcgcccgt cacaaagagc 300

ttcaacaggg gagagtgtct gcccgagacc ggccaccacc accaccacca cggcgagcag 360

aagctgatca gcgaggagga cctgggctgg agccaccccc agttcgagaa gtag 414

<210> 8
<211> 137
<212> PRT
<213> Artificial Sequence

<220>
<223> amino acid sequence of human IgG1 kappa light chain constant region with LPETG sortase tag, an 6xHis tag and a strepII tag.

<400> 8

```
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
1               5                   10                  15

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

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
        35                  40                  45

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
    50                  55                  60

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

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

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys Leu Pro Glu Thr Gly His
            100                 105                 110

His His His His His Gly Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
        115                 120                 125

Gly Trp Ser His Pro Gln Phe Glu Lys
    130                 135
```

<210> 9
<211> 1503
<212> DNA
<213> Artificial Sequence

<220>
<223> Complete human IgG1 VH-CH heavy chain coding region for hBU12 with C-terminal LPETG sortase tag, 6xHis tag and a strepII tag

<400> 9

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atgggatgga gctggatctt tcttttcctc ctgtcaggaa ctgcaggtgt ccattgtcag       60

gttcagctgc aagagtctgg ccctgggttg gttaagccct cccagaccct cagtctgact      120

tgtactgtgt ctgggggttc aatcagcact tctggtatgg gtgtaggctg gattaggcag      180

cacccaggga agggtctgga gtggattgga cacatttggt gggatgatga caagagatat      240

aacccagccc tgaagagcag agtgacaatc tctgtggata cctccaagaa ccagtttagc      300

ctcaagctgt ccagtgtgac agctgcagat actgctgtct actactgtgc tagaatggaa      360

ctttggtcct actattttga ctactggggc caaggcaccc ttgtcacagt ctcctcagct      420

agcaccaagg gcccatctgt cttccccctg gcaccctcct ccaagagcac ctctgggggc      480

acagctgccc tgggctgcct ggtcaaggac tacttccctg aacctgtgac agtgtcctgg      540

aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga      600

ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac      660
```

atctgcaacg tgaatcacaa gcccagcaac accaaggtgg acaagaaagt tgagcccaaa 720

tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaactcct gggggggaccg 780

tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 840

gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 900

gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 960

acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 1020

tacaagtgca aggtctccaa caaagccctc ccagccccca tcgagaaaac catctccaaa 1080

gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 1140

accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1200

gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1260

gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1320

caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacacag 1380

aagagcctct ccctgtctcc gggtaaactg cccgagaccg gccaccacca ccaccaccac 1440

ggcgagcaga agctgatcag cgaggaggac ctgggctgga gccaccccca gttcgagaag 1500

tag 1503

<210> 10
<211> 500
<212> PRT
<213> Artificial Sequence

<220>
<223> amino acid sequence of complete human IgG1 VH-CH heavy chain region of hBU12 with C-terminal LPETG sortase tag, 6xHis tag and a strepII tag

<400> 10

Met Gly Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly
1 5 10 15

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

Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile
35 40 45

Ser Thr Ser Gly Met Gly Val Gly Trp Ile Arg Gln His Pro Gly Lys
50 55 60

Gly Leu Glu Trp Ile Gly His Ile Trp Trp Asp Asp Asp Lys Arg Tyr
65 70 75 80

Asn Pro Ala Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys
85 90 95

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

```
            100                 105                 110

Val Tyr Tyr Cys Ala Arg Met Glu Leu Trp Ser Tyr Tyr Phe Asp Tyr
        115                 120                 125

Trp Gly Gln Gly Thr Leu 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 Lys Val Glu Pro Lys
225                 230                 235                 240

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
                245                 250                 255

Leu 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 Asp 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 Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
```

370 375 380

Val Ser Leu Thr 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 Lys Thr Thr
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 Lys Leu Pro Glu Thr Gly His His His His His His
465 470 475 480

Gly Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Gly Trp Ser His Pro
485 490 495

Gln Phe Glu Lys
500

<210> 11
<211> 792
<212> DNA
<213> Artificial Sequence

<220>
<223> Complete human IgG1 VL-CL kappa chain coding region for hBU12 with C-terminal LPETG sortase tag, 6xHis tag and a strepII tag

<400> 11
atgaagttgc ctgttaggct gttggtgctg atgttctgga ttcctgcttc cagcagtgaa 60

attgttctca cccagtctcc agcaaccctg tctctctctc caggggaaag ggctaccctg 120

agctgcagtg ccagctcaag tgtaagttac atgcactggt accagcagaa gccagggcag 180

gctcccagac tcctgattta tgacacatcc aaactggctt ctggtattcc agcaaggttc 240

agtggcagtg ggtctggaac agattttaca ctcacaatca gcagcctgga gccagaggat 300

gttgctgtct attactgttt tcaggggagt gtatacccat tcacttttgg ccaagggaca 360

aagttggaaa tcaaaagaac tgtggctgca ccatctgtct tcatcttccc gccatctgat 420

gagcagttga aatctggaac tgcctctgtt gtgtgcctgc tgaataactt ctatcccaga 480

gaggccaaag tacagtggaa ggtggataac gccctccaat cgggtaactc ccaggagagt 540

gtcacagagc aggacagcaa ggacagcacc tacagcctca gcagcaccct gacgctgagc 600

aaagcagact acgagaaaca caaagtctac gcctgcgaag tcacccatca gggcctgagc 660

tcgcccgtca caaagagctt caacagggga gagtgtctgc ccgagaccgg ccaccaccac 720

caccaccacg gcgagcagaa gctgatcagc gaggaggacc tgggctggag ccacccccag 780

ttcgagaagt ag 792

<210> 12
<211> 263
<212> PRT
<213> Artificial Sequence

<220>
<223> amino acid sequence of complete human IgG1 VL-CL kappa chain region of hBU12 with C-terminal LPETG sortase tag, 6xHis tag and a strepII tag

<400> 12

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

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

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

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

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

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

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

Pro Phe Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val
115 120 125

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

Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
145 150 155 160

Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn
165 170 175

Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser
180 185 190

Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys
195 200 205

Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr
210 215 220

Lys Ser Phe Asn Arg Gly Glu Cys Leu Pro Glu Thr Gly His His His
225 230 235 240

His His His Gly Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Gly Trp
245 250 255

Ser His Pro Gln Phe Glu Lys
260

<210> 13
<211> 7045
<212> DNA
<213> Artificial Sequence

<220>
<223> coding region of human IgG1 VH-CH heavy chain for hBU12 with C-terminal LPETG sortase tag, 6xHis tag and a strepII tag and HindIII and NotI cloning sites

<400> 13
gacggatcgg gagatctccc gatcccctat ggtcgactct cagtacaatc tgctctgatg 60

ccgcatagtt aagccagtat ctgctccctg cttgtgtgtt ggaggtcgct gagtagtgcg 120

cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc 180

ttagggttag gcgttttgcg ctgcttcgcg atgtacgggc cagatatacg cgttgacatt 240

gattattgac tagttattaa tagtaatcaa ttacggggtc attagttcat agcccatata 300

tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaacgacc 360

cccgcccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc 420

attgacgtca atgggtggac tatttacggt aaactgccca cttggcagta catcaagtgt 480

atcatatgcc aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt 540

atgcccagta catgacctta tgggactttc ctacttggca gtacatctac gtattagtca 600

tcgctattac catggtgatg cggttttggc agtacatcaa tgggcgtgga tagcggtttg 660

actcacgggg atttccaagt ctccacccca ttgacgtcaa tgggagtttg ttttggcacc 720

aaaatcaacg ggactttcca aaatgtcgta acaactccgc cccattgacg caaatgggcg 780

gtaggcgtgt acggtgggag gtctatataa gcagagctct ctggctaact agagaaccca 840

ctgcttactg gcttatcgaa attaatacga ctcactatag ggagacccaa gctggctagc 900

gtttaaactt aagcttccat gggatggagc tggatctttc ttttcctcct gtcaggaact 960

gcaggtgtcc attgtcaggt tcagctgcaa gagtctggcc ctgggttggt taagccctcc 1020

cagaccctca gtctgacttg tactgtgtct gggggttcaa tcagcacttc tggtatgggt 1080

gtaggctgga ttaggcagca cccagggaag ggtctggagt ggattggaca catttggtgg 1140

gatgatgaca agagatataa cccagccctg aagagcagag tgacaatctc tgtggatacc 1200

tccaagaacc agtttagcct caagctgtcc agtgtgacag ctgcagatac tgctgtctac 1260

tactgtgcta gaatggaact ttggtcctac tattttgact actggggcca aggcaccctt 1320

gtcacagtct cctcagctag caccaagggc ccatctgtct tccccctggc accctcctcc 1380

aagagcacct ctgggggcac agctgccctg ggctgcctgg tcaaggacta cttccctgaa 1440

cctgtgacag tgtcctggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttcccggct 1500

gtcctacagt cctcaggact ctactccctc agcagcgtgg tgaccgtgcc ctccagcagc 1560

ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac caaggtggac 1620

aagaaagttg agcccaaatc ttgtgacaaa actcacacat gcccaccgtg cccagcacct 1680

gaactcctgg ggggaccgtc agtcttcctc ttcccccaa aacccaagga caccctcatg 1740

atctcccgga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag 1800

gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg 1860

gaggagcagt acaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac 1920

tggctgaatg gcaaggagta caagtgcaag gtctccaaca aagccctccc agcccccatc 1980

gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc 2040

ccatcccggg atgagctgac caagaaccag gtcagcctga cctgcctggt caaaggcttc 2100

tatcccagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag 2160

accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctacagcaa gctcaccgtg 2220

gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 2280

cacaaccact acacacagaa gagcctctcc ctgtctccgg gtaaactgcc cgagaccggc 2340

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atcgcattgt ctgagtaggt gtcattctat tctgggggggt ggggtggggc aggacagcaa 2640

gggggaggat tgggaagaca atagcaggca tgctggggat gcggtgggct ctatggcttc 2700

tgaggcggaa agaaccagct ggggctctag ggggtatccc cacgcgccct gtagcggcgc 2760

attaagcgcg gcgggtgtgg tggttacgcg cagcgtgacc gctacacttg ccagcgccct 2820

agcgcccgct cctttcgctt tcttcccttc ctttctcgcc acgttcgccg gctttccccg 2880

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ccccaaaaaa cttgattagg gtgatggttc acgtagtggg ccatcgccct gatagacggt 3000

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aatactcata ctcttccttt ttcaatatta ttgaagcatt tatcagggtt attgtctcat 6960

gagcggatac atatttgaat gtatttagaa aaataaacaa atagggggttc cgcgcacatt 7020

tccccgaaaa gtgccacctg acgtc 7045

<210> 14
<211> 6334
<212> DNA
<213> Artificial Sequence

<220>

<223> coding region of human IgG1 VL-CL kappa light chain for hBU12 with C-terminal LPETG sortase tag, 6xHis tag and a strepII tag and HindIII and NotI cloning sites

<400> 14

gacggatcgg gagatctccc gatcccctat ggtcgactct cagtacaatc tgctctgatg 60

ccgcatagtt aagccagtat ctgctccctg cttgtgtgtt ggaggtcgct gagtagtgcg 120

cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc 180

ttagggttag gcgttttgcg ctgcttcgcg atgtacgggc cagatatacg cgttgacatt 240

gattattgac tagttattaa tagtaatcaa ttacggggtc attagttcat agcccatata 300

tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaacgacc 360

cccgcccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc 420

attgacgtca atgggtggac tatttacggt aaactgccca cttggcagta catcaagtgt 480

atcatatgcc aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt 540

atgcccagta catgacctta tgggactttc ctacttggca gtacatctac gtattagtca 600

tcgctattac catggtgatg cggttttggc agtacatcaa tgggcgtgga tagcggtttg 660

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aaaatcaacg ggactttcca aaatgtcgta acaactccgc cccattgacg caaatgggcg 780

gtaggcgtgt acggtgggag gtctatataa gcagagctct ctggctaact agagaaccca 840

ctgcttactg gcttatcgaa attaatacga ctcactatag ggagacccaa gctggctagc 900

gtttaaactt aagcttccat gaagttgcct gttaggctgt tggtgctgat gttctggatt 960

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gaaatgttga tactcatac tcttccttt tcaatattat tgaagcattt atcagggtta 6240

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gcgcacattt ccccgaaaag tgccacctga cgtc 6334

<210> 15
<211> 150
<212> PRT
<213> Artificial Sequence

<220>
<223> amino acid sequence of the N-intein domain of Ssp GyrB 11 split-intein

<400> 15

Cys Phe Ser Gly Asp Thr Leu Val Ala Leu Thr Asp Gly Arg Ser Val
1 5 10 15

Ser Phe Glu Gln Leu Val Glu Glu Glu Lys Gln Gly Lys Gln Asn Phe
20 25 30

Cys Tyr Thr Ile Arg His Asp Gly Ser Ile Gly Val Glu Lys Ile Ile
35 40 45

Asn Ala Arg Lys Thr Lys Thr Asn Ala Lys Val Ile Lys Val Thr Leu
50 55 60

Asp Asn Gly Glu Ser Ile Ile Cys Thr Pro Asp His Lys Phe Met Leu
65 70 75 80

Arg Asp Gly Ser Tyr Lys Cys Ala Met Asp Leu Thr Leu Asp Asp Ser
85 90 95

Leu Met Pro Leu His Arg Lys Ile Ser Thr Thr Glu Asp Ser Gly His
100 105 110

Met Glu Ala Val Leu Asn Tyr Asn His Arg Ile Val Asn Ile Glu Ala
115 120 125

Val Ser Glu Thr Ile Asp Val Tyr Asp Ile Glu Val Pro His Thr His
130 135 140

Asn Phe Ala Leu Ala Ser
145 150

<210> 16
<211> 450
<212> DNA

<213> Artificial Sequence

<220>
<223> Reverse translation of SEQ ID NO 15 with mammalian codon usage results in the coding sequence for the N-intein domain of Ssp GyrB 11 split-intein

<400> 16
tgcttcagcg gcgacaccct ggtggccctg accgacggca gaagcgtgag cttcgagcag 60

ctggtggagg aggagaagca gggcaagcag aacttctgct acaccatcag acacgacggc 120

agcatcggcg tggagaagat catcaacgcc agaaagacca agaccaacgc caaggtgatc 180

aaggtgaccc tggacaacgg cgagagcatc atctgcaccc ccgaccacaa gttcatgctg 240

agagacggca gctacaagtg cgccatggac ctgaccctgg acgacagcct gatgcccctg 300

cacagaaaga tcagcaccac cgaggacagc ggccacatgg aggccgtgct gaactacaac 360

cacagaatcg tgaacatcga ggccgtgagc gagaccatcg acgtgtacga catcgaggtg 420

ccccacaccc acaacttcgc cctggccagc 450

<210> 17
<211> 1905
<212> DNA
<213> Artificial Sequence

<220>
<223> complete IgG1 heavy chain coding region for anti-human CD19 antibody hBU12 with C-terminal extension, comprising the N-intein domain of Ssp GyrB 11 split-intein, followed by a 6xHis-tag and a strepII tag

<400> 17
atgaattttg gactgaggct gattttcctg gtgctgaccc tgaaaggcgt ccagtgtcag 60

gttcagctgc aagagtctgg ccctgggttg gttaagccct cccagaccct cagtctgact 120

tgtactgtgt ctgggggttc aatcagcact tctggtatgg gtgtaggctg gattaggcag 180

cacccaggga agggtctgga gtggattgga cacatttggt gggatgatga caagagatat 240

aacccagccc tgaagagcag agtgacaatc tctgtggata cctccaagaa ccagtttagc 300

ctcaagctgt ccagtgtgac agctgcagat actgctgtct actactgtgc tagaatggaa 360

ctttggtcct actattttga ctactggggc caaggcaccc ttgtcacagt ctcctcagct 420

agcaccaagg gcccatctgt cttccccctg gcaccctcct ccaagagcac ctctgggggc 480

acagctgccc tgggctgcct ggtcaaggac tacttccctg aacctgtgac agtgtcctgg 540

aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 600

ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 660

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tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaactcct gggggggaccg 780

tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 840

gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 900

gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 960

acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 1020

tacaagtgca aggtctccaa caaagccctc ccagccccca tcgagaaaac catctccaaa 1080

gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 1140

accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1200

gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1260

gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1320

caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacacag 1380

aagagcctct ccctgtctcc gggtaaatgc ttcagcggcg acaccctggt ggccctgacc 1440

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aagaccaaga ccaacgccaa ggtgatcaag gtgaccctgg acaacggcga gagcatcatc 1620

tgcacccccg accacaagtt catgctgaga gacggcagct acaagtgcgc catggacctg 1680

accctggacg acagcctgat gcccctgcac agaaagatca gcaccaccga ggacagcggc 1740

cacatggagg ccgtgctgaa ctacaaccac agaatcgtga acatcgaggc cgtgagcgag 1800

accatcgacg tgtacgacat cgaggtgccc cacacccaca acttcgccct ggccagccac 1860

catcaccatc accatggctg gagccacccc cagttcgaga agtag 1905

<210> 18
<211> 634
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence translated from SEQ ID NO 17

<400> 18

Met Asn Phe Gly Leu Arg Leu Ile Phe Leu Val Leu Thr Leu Lys Gly
1 5 10 15

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

Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile
35 40 45

Ser Thr Ser Gly Met Gly Val Gly Trp Ile Arg Gln His Pro Gly Lys
50 55 60

Gly Leu Glu Trp Ile Gly His Ile Trp Trp Asp Asp Asp Lys Arg Tyr
65 70 75 80

Asn Pro Ala Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys
85 90 95

```
Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala
            100                 105                 110

Val Tyr Tyr Cys Ala Arg Met Glu Leu Trp Ser Tyr Tyr Phe Asp Tyr
        115                 120                 125

Trp Gly Gln Gly Thr Leu 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 Lys Val Glu Pro Lys
225                 230                 235                 240

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
                245                 250                 255

Leu 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 Asp 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 Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
    370                 375                 380

Val Ser Leu Thr 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 Lys Thr Thr
                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 Lys Cys Phe Ser Gly Asp Thr Leu Val Ala Leu Thr
465                 470                 475                 480

Asp Gly Arg Ser Val Ser Phe Glu Gln Leu Val Glu Glu Glu Lys Gln
                485                 490                 495

Gly Lys Gln Asn Phe Cys Tyr Thr Ile Arg His Asp Gly Ser Ile Gly
            500                 505                 510

Val Glu Lys Ile Ile Asn Ala Arg Lys Thr Lys Thr Asn Ala Lys Val
        515                 520                 525

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

His Lys Phe Met Leu Arg Asp Gly Ser Tyr Lys Cys Ala Met Asp Leu
545                 550                 555                 560

Thr Leu Asp Asp Ser Leu Met Pro Leu His Arg Lys Ile Ser Thr Thr
                565                 570                 575

Glu Asp Ser Gly His Met Glu Ala Val Leu Asn Tyr Asn His Arg Ile
            580                 585                 590

Val Asn Ile Glu Ala Val Ser Glu Thr Ile Asp Val Tyr Asp Ile Glu
        595                 600                 605

Val Pro His Thr His Asn Phe Ala Leu Ala Ser His His His His His
    610                 615                 620

His Gly Trp Ser His Pro Gln Phe Glu Lys
625                 630
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<210> 19
<211> 1206
<212> DNA
<213> Artificial Sequence

<220>
<223> complete IgG1 kappa light chain coding region for anti-human CD19 antibody hBU12 with C-terminal extension, comprising the N-intein domain of Ssp GyrB 11 split-intein, followed by a 6xHis-tag and a strepII tag

<400> 19
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attgtgctga cccaatctcc agcttctttg gctgtgtctc tagggcagag ggccaccatc 120

tcctgcaagg ccagccaaag tgttgatttt gatggtgata gttatatgaa ctggtaccaa 180

cagaaaccag gacagccacc caaagtcctc atctatgctg catccaatct agaatctggg 240

atcccagcca ggtttagtgg cagtgggtct gggacagact tcaccctcaa catccatcct 300

gtggaggagg aggatgctgc aacctattac tgtcagcaaa gtaatgagga tccgtggacg 360

ttcggtggag gcaccaagct ggaaatcaaa cgtacggtgg ctgcaccatc tgtcttcatc 420

ttcccgccat ctgatgagca gttgaaatct ggaactgcct ctgttgtgtg cctgctgaat 480

aacttctatc ccagagaggc caaagtacag tggaaggtgg ataacgccct ccaatcgggt 540

aactcccagg agagtgtcac agagcaggac agcaaggaca gcacctacag cctcagcagc 600

accctgacgc tgagcaaagc agactacgag aaacacaaag tctacgcctg cgaagtcacc 660

catcagggcc tgagctcgcc cgtcacaaag agcttcaaca ggggagagtg cttcagcggc 720

gacaccctgg tggccctgac cgacggcaga agcgtgagct tcgagcagct ggtggaggag 780

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gacaacggcg agagcatcat ctgcaccccc gaccacaagt tcatgctgag agacggcagc 960

tacaagtgcg ccatggacct gaccctggac gacagcctga tgcccctgca cagaaagatc 1020

agcaccaccg aggacagcgg ccacatggag gccgtgctga actacaacca cagaatcgtg 1080

aacatcgagg ccgtgagcga gaccatcgac gtgtacgaca tcgaggtgcc ccacacccac 1140

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aagtag 1206

<210> 20
<211> 401
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence translated from SEQ ID NO 19

<400> 20

Met Asn Phe Gly Leu Arg Leu Ile Phe Leu Val Leu Thr Leu Lys Gly
1 5 10 15

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

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

Asp Phe Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly
    50                  55                  60

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

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

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

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

Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser
    130                 135                 140

Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn
145                 150                 155                 160

Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala
                165                 170                 175

Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys
            180                 185                 190

Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp
        195                 200                 205

Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu
    210                 215                 220

Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys Phe Ser Gly
225                 230                 235                 240

Asp Thr Leu Val Ala Leu Thr Asp Gly Arg Ser Val Ser Phe Glu Gln
                245                 250                 255

Leu Val Glu Glu Glu Lys Gln Gly Lys Gln Asn Phe Cys Tyr Thr Ile
            260                 265                 270

Arg His Asp Gly Ser Ile Gly Val Glu Lys Ile Ile Asn Ala Arg Lys
        275                 280                 285
```

```
Thr Lys Thr Asn Ala Lys Val Ile Lys Val Thr Leu Asp Asn Gly Glu
    290                 295                 300

Ser Ile Ile Cys Thr Pro Asp His Lys Phe Met Leu Arg Asp Gly Ser
305                 310                 315                 320

Tyr Lys Cys Ala Met Asp Leu Thr Leu Asp Asp Ser Leu Met Pro Leu
                325                 330                 335

His Arg Lys Ile Ser Thr Thr Glu Asp Ser Gly His Met Glu Ala Val
            340                 345                 350

Leu Asn Tyr Asn His Arg Ile Val Asn Ile Glu Ala Val Ser Glu Thr
        355                 360                 365

Ile Asp Val Tyr Asp Ile Glu Val Pro His Thr His Asn Phe Ala Leu
    370                 375                 380

Ala Ser His His His His His His Gly Trp Ser His Pro Gln Phe Glu
385                 390                 395                 400

Lys
```

<210> 21
<211> 7447
<212> DNA
<213> Artificial Sequence

<220>
<223> coding region of human IgG1 VH-CH heavy chain for hBU12 with C-terminal N-intein domain of Ssp GyrB S11 split intein, followed by 6xHis tag strepII tag and HindIII and NotI cloning sites

<400> 21

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gacggatcgg gagatctccc gatcccctat ggtcgactct cagtacaatc tgctctgatg       60

ccgcatagtt aagccagtat ctgctccctg cttgtgtgtt ggaggtcgct gagtagtgcg      120

cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc      180

ttagggttag gcgttttgcg ctgcttcgcg atgtacgggc cagatatacg cgttgacatt      240

gattattgac tagttattaa tagtaatcaa ttacggggtc attagttcat agcccatata      300

tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaacgacc      360

cccgcccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc      420

attgacgtca atgggtggac tatttacggt aaactgccca cttggcagta catcaagtgt      480

atcatatgcc aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt      540

atgcccagta catgacctta tgggactttc ctacttggca gtacatctac gtattagtca      600

tcgctattac catggtgatg cggttttggc agtacatcaa tgggcgtgga tagcggtttg      660

actcacgggg atttccaagt ctccacccca ttgacgtcaa tgggagtttg ttttggcacc      720
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aaaatcaacg ggactttcca aaatgtcgta acaactccgc cccattgacg caaatgggcg      780
gtaggcgtgt acggtgggag gtctatataa gcagagctct ctggctaact agagaaccca      840
ctgcttactg gcttatcgaa attaatacga ctcactatag ggagacccaa gctggctagc      900
gtttaaactt aagcttccat gaattttgga ctgaggctga ttttcctggt gctgaccctg      960
aaaggcgtcc agtgtcaggt tcagctgcaa gagtctggcc ctgggttggt taagccctcc     1020
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tccaagaacc agtttagcct caagctgtcc agtgtgacag ctgcagatac tgctgtctac     1260
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gaggagcagt acaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac     1920
tggctgaatg gcaaggagta caagtgcaag gtctccaaca aagccctccc agcccccatc     1980
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cggagccggg actgtcgggc gtacacaaat cgcccgcaga agcgcggccg tctggaccga 4920

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ggagttcttc gcccacccca acttgtttat tgcagcttat aatggttaca aataaagcaa 5160

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caaactcatc aatgtatctt atcatgtctg tataccgtcg acctctagct agagcttggc 5280

gtaatcatgg tcatagctgt ttcctgtgtg aaattgttat ccgctcacaa ttccacacaa 5340

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ttaatgaatc ggccaacgcg cggggagagg cggtttgcgt attgggcgct cttccgcttc 5520

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tgagtccaac ccggtaagac acgacttatc gccactggca gcagccactg gtaacaggat 6060

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aagagttggt agctcttgat ccggcaaaca aaccaccgct ggtagcggtg gtttttttgt 6240

ttgcaagcag cagattacgc gcagaaaaaa aggatctcaa gaagatcctt tgatcttttc 6300

tacggggtct gacgctcagt ggaacgaaaa ctcacgttaa gggattttgg tcatgagatt 6360

atcaaaaagg atcttcacct agatcctttt aaattaaaaa tgaagtttta aatcaatcta 6420

aagtatatat gagtaaactt ggtctgacag ttaccaatgc ttaatcagtg aggcacctat 6480

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ctcaccggct ccagatttat cagcaataaa ccagccagcc ggaagggccg agcgcagaag 6660

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cagaagtaag ttggccgcag tgttatcact catggttatg gcagcactgc ataattctct 6960

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ctgatcttca gcatctttta ctttcaccag cgtttctggg tgagcaaaaa caggaaggca 7260

aaatgccgca aaaaagggaa taagggcgac acggaaatgt tgaatactca tactcttcct 7320

ttttcaatat tattgaagca tttatcaggg ttattgtctc atgagcggat acatatttga 7380

atgtatttag aaaaataaac aaataggggt tccgcgcaca tttccccgaa aagtgccacc 7440

tgacgtc 7447

<210> 22
<211> 6748
<212> DNA
<213> Artificial Sequence

<220>
<223> coding region of human IgG1 VL-CL kappa light chain for hBU12 with C-terminal Ssp GyrB S11 N-intein domain, 6xHis tag and a strepII tag, and HindIII and NotI cloning sites

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ccgcatagtt aagccagtat ctgctccctg cttgtgtgtt ggaggtcgct gagtagtgcg 120

cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc 180

ttagggttag gcgttttgcg ctgcttcgcg atgtacgggc cagatatacg cgttgacatt 240

gattattgac tagttattaa tagtaatcaa ttacggggtc attagttcat agcccatata 300

tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaacgacc 360

cccgcccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc 420

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tcgctattac catggtgatg cggttttggc agtacatcaa tgggcgtgga tagcggtttg 660

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ctgcttactg gcttatcgaa attaatacga ctcactatag ggagacccaa gctggctagc 900

gtttaaactt aagcttccat gaattttgga ctgaggctga ttttcctggt gctgaccctg 960

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atgctgagag acggcagcta caagtgcgcc atggacctga ccctggacga cagcctgatg 1920

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ttgaatactc atactcttcc tttttcaata ttattgaagc atttatcagg gttattgtct 6660

catgagcgga tacatatttg aatgtattta gaaaaataaa caaatagggg ttccgcgcac 6720

atttccccga aaagtgccac ctgacgtc 6748

<210> 23
<211> 206
<212> PRT
<213> Artificial Sequence

<220>
<223> amino acid sequence of sortase A from Staphylococcus aureus

<400> 23

Met Lys Lys Trp Thr Asn Arg Leu Met Thr Ile Ala Gly Val Val Leu

1 5 10 15

Ile Leu Val Ala Ala Tyr Leu Phe Ala Lys Pro His Ile Asp Asn Tyr
20 25 30

Leu His Asp Lys Asp Lys Asp Glu Lys Ile Glu Gln Tyr Asp Lys Asn
35 40 45

Val Lys Glu Gln Ala Ser Lys Asp Lys Lys Gln Gln Ala Lys Pro Gln
50 55 60

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

Ala Asp Ile Lys Glu Pro Val Tyr Pro Gly Pro Ala Thr Pro Glu Gln
85 90 95

Leu Asn Arg Gly Val Ser Phe Ala Glu Glu Asn Glu Ser Leu Asp Asp
100 105 110

Gln Asn Ile Ser Ile Ala Gly His Thr Phe Ile Asp Arg Pro Asn Tyr
115 120 125

Gln Phe Thr Asn Leu Lys Ala Ala Lys Lys Gly Ser Met Val Tyr Phe
130 135 140

Lys Val Gly Asn Glu Thr Arg Lys Tyr Lys Met Thr Ser Ile Arg Asp
145 150 155 160

Val Lys Pro Thr Asp Val Gly Val Leu Asp Glu Gln Lys Gly Lys Asp
165 170 175

Lys Gln Leu Thr Leu Ile Thr Cys Asp Asp Tyr Asn Glu Lys Thr Gly
180 185 190

Val Trp Glu Lys Arg Lys Ile Phe Val Ala Thr Glu Val Lys
195 200 205

<210> 24
<211> 621
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding for SEQ ID NO 23

<400> 24
atgaaaaaat ggacaaatcg attaatgaca atcgctggtg tggtacttat cctagtggca 60

gcatatttgt ttgctaaacc acatatcgat aattatcttc acgataaaga taaagatgaa 120

aagattgaac aatatgataa aaatgtaaaa gaacaggcga gtaaagataa aaagcagcaa 180

gctaaacctc aaattccgaa agataaatcg aaagtggcag gctatattga aattccagat 240

gctgatatta aagaaccagt atatccagga ccagcaacac ctgaacaatt aaatagaggt 300

gtaagctttg cagaagaaaa tgaatcacta gatgatcaaa atatttcaat tgcaggacac 360

actttcattg accgtccgaa ctatcaattt acaaatctta aagcagccaa aaaaggtagt 420

atggtgtact ttaaagttgg taatgaaaca cgtaagtata aaatgacaag tataagagat 480

gttaagccta cagatgtagg agttctagat gaacaaaaag gtaaagataa acaattaaca 540

ttaattactt gtgatgatta caatgaaaag acaggcgttt gggaaaaacg taaaatcttt 600

gtagctacag aagtcaaata a 621

<210> 25
<211> 465
<212> DNA
<213> Artificial Sequence

<220>
<223> coding region for a 6xHis tagged version of Staphylococcus aureus sortase A (aa60-205)

<400> 25
atgcaagcta aacctcaaat tccgaaagat aaatcgaaag tggcaggcta tattgaaatt 60

ccagatgctg atattaaaga accagtatat ccaggaccag caacacctga acaattaaat 120

agaggtgtaa gctttgcaga agaaaatgaa tcactagatg atcaaaatat ttcaattgca 180

ggacacactt tcattgaccg tccgaactat caatttacaa atcttaaagc agccaaaaaa 240

ggtagtatgg tgtactttaa agttggtaat gaaacacgta agtataaaat gacaagtata 300

agagatgtta agcctacaga tgtaggagtt ctagatgaac aaaaaggtaa agataaacaa 360

ttaacattaa ttacttgtga tgattacaat gaaaagacag gcgtttggga aaaacgtaaa 420

atctttgtag ctacagaagt caaacaccat caccatcacc attaa 465

<210> 26
<211> 154
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence translated from SEQ ID NO 25

<400> 26

Met Gln Ala Lys Pro Gln Ile Pro Lys Asp Lys Ser Lys Val Ala Gly
1 5 10 15

Tyr Ile Glu Ile Pro Asp Ala Asp Ile Lys Glu Pro Val Tyr Pro Gly
20 25 30

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

Asn Glu Ser Leu Asp Asp Gln Asn Ile Ser Ile Ala Gly His Thr Phe
50 55 60

Ile Asp Arg Pro Asn Tyr Gln Phe Thr Asn Leu Lys Ala Ala Lys Lys
65 70 75 80

Gly Ser Met Val Tyr Phe Lys Val Gly Asn Glu Thr Arg Lys Tyr Lys
85 90 95

Met Thr Ser Ile Arg Asp Val Lys Pro Thr Asp Val Gly Val Leu Asp
100 105 110

Glu Gln Lys Gly Lys Asp Lys Gln Leu Thr Leu Ile Thr Cys Asp Asp
115 120 125

Tyr Asn Glu Lys Thr Gly Val Trp Glu Lys Arg Lys Ile Phe Val Ala
130 135 140

Thr Glu Val Lys His His His His His His
145 150

<210> 27
<211> 1401
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of mAb Ac10 Heavy Chain

<400> 27
atgaattttg gactgaggct gattttcctg gtgctgaccc tgaaaggcgt ccagtgtcag 60

atccagctgc agcagtctgg ccccgaggtc gtgaaacctg gcgcctccgt gaagatctcc 120

tgcaaggcct ccggctacac cttcaccgac tactacatca cctgggtcaa gcagaagccc 180

ggccagggcc tggaatggat cggctggatc tatcccggct ccggcaacac caagtacaac 240

gagaagttca agggcaaggc caccctgacc gtggacacct cctcttccac cgccttcatg 300

cagctgtcct ccctgacctc cgaggatacc gccgtgtact tctgcgccaa ctacggcaac 360

tattggttcg cctactgggg ccagggcaca caagtgaccg tgtctgctgc tagcaccaag 420

ggcccatcgg tcttcccccct ggcaccctcc tccaagagca cctctggggg cacagcagcc 480

ctgggctgcc tggtcaagga ctacttcccc gaaccggtga cggtgtcgtg gaactcaggc 540

gccctgacca gcggcgtgca caccttcccg gctgtcctac agtcctcagg actctactcc 600

ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 660

gtgaatcaca agcccagcaa caccaaggtg gacaagaaag ttgagcccaa atcttgtgac 720

aaaactcaca catgcccacc gtgcccagca cctgaactcc tgggggggacc gtcagtcttc 780

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aaggtctcca acaaagccct cccagccccc atcgagaaaa ccatctccaa agccaaaggg 1080

cagccccgag aaccacaggt gtacaccctg cccccatccc gggatgagct gaccaagaac 1140

caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1200

gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1260

ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac 1320

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacaca gaagagcctc 1380

tccctgtctc cgggtaaata g 1401

<210> 28
<211> 466
<212> PRT
<213> Artificial Sequence

<220>
<223> AMINO ACID SEQUENCE OF MAB AC10 HEAVY CHAIN

<400> 28

Met Asn Phe Gly Leu Arg Leu Ile Phe Leu Val Leu Thr Leu Lys Gly
1 5 10 15

Val Gln Cys Gln Ile Gln Leu Gln Gln Ser Gly Pro Glu Val Val Lys
20 25 30

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

Thr Asp Tyr Tyr Ile Thr Trp Val Lys Gln Lys Pro Gly Gln Gly Leu
50 55 60

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

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

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

Tyr Phe Cys Ala Asn Tyr Gly Asn Tyr Trp Phe Ala Tyr Trp Gly Gln
115 120 125

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

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
145 150 155 160

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

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Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
            180                 185                 190

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
        195                 200                 205

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
    210                 215                 220

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
225                 230                 235                 240

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
                245                 250                 255

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
            260                 265                 270

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
        275                 280                 285

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
    290                 295                 300

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
305                 310                 315                 320

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
                325                 330                 335

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
            340                 345                 350

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
        355                 360                 365

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
    370                 375                 380

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
385                 390                 395                 400

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
                405                 410                 415

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
            420                 425                 430

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
        435                 440                 445
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Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
450 455 460

Gly Lys
465

<210> 29
<211> 714
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of mAb Ac10 Light Chain

<400> 29
atgaattttg gactgaggct gattttcctg gtgctgaccc tgaaaggcgt ccagtgtgac 60

attgtgctga cccaatctcc agcttctttg gctgtgtctc tagggcagag ggccaccatc 120

tcctgcaagg ccagccaaag tgttgatttt gatggtgata gttatatgaa ctggtaccaa 180

cagaaaccag gacagccacc caaagtcctc atctatgctg catccaatct agaatctggg 240

atcccagcca ggtttagtgg cagtgggtct gggacagact tcaccctcaa catccatcct 300

gtggaggagg aggatgctgc aacctattac tgtcagcaaa gtaatgagga tccgtggacg 360

ttcggtggag gcaccaagct ggaaatcaaa cgtacggtgg ctgcaccatc tgtcttcatc 420

ttcccgccat ctgatgagca gttgaaatct ggaactgcct ctgttgtgtg cctgctgaat 480

aacttctatc ccagagaggc caaagtacag tggaaggtgg ataacgccct ccaatcgggt 540

aactcccagg agagtgtcac agagcaggac agcaaggaca gcacctacag cctcagcagc 600

accctgacgc tgagcaaagc agactacgag aaacacaaag tctacgcctg cgaagtcacc 660

catcagggcc tgagctcgcc cgtcacaaag agcttcaaca ggggagagtg ttag 714

<210> 30
<211> 237
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of mAb Ac10 Light Chain

<400> 30

Met Asn Phe Gly Leu Arg Leu Ile Phe Leu Val Leu Thr Leu Lys Gly
1 5 10 15

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

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

Asp Phe Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly
50 55 60

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

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

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

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

Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser
130 135 140

Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn
145 150 155 160

Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala
165 170 175

Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys
180 185 190

Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp
195 200 205

Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu
210 215 220

Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 31
<211> 1422
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of Trastuzumab Heavy Chain

<400> 31
atgaaaaaaa acattgcctt tctgctggcc tccatgttcg tgttctctat cgccacaaac 60

gcttacgctg aagtccagct ggtcgaatct ggtggtggcc tggtccagcc tggtggatca 120

ctgagactgt cctgtgctgc ttctggtttc aacatcaagg acacctacat ccattgggtc 180

agacaggcac ctggcaaggg actggaatgg gtcgcccgaa tctaccctac aaacggctac 240

actcgctacg ccgactccgt caagggacgc tttaccatct ccgccgacac ctctaaaaac 300

accgcctacc tgcagatgaa tagtctgagg gccgaggata ctgctgtgta ctactgctca 360

cgatggggag gcgacggctt ttacgctatg gattactggg gacagggaac tctggtcact 420

gtgtctagcg ctagcaccaa gggcccatcg gtcttccccc tggcaccctc ctccaagagc 480

acctctgggg gcacagcagc cctgggctgc ctggtcaagg actacttccc cgaaccggtg 540

acggtgtcgt ggaactcagg cgccctgacc agcggcgtgc acaccttccc ggctgtccta 600

cagtcctcag gactctactc cctcagcagc gtggtgaccg tgccctccag cagcttgggc 660

acccagacct acatctgcaa cgtgaatcac aagcccagca acaccaaggt ggacaagaaa 720

gttgagccca aatcttgtga caaaactcac acatgcccac cgtgcccagc acctgaactc 780

ctgggggggac cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc 840

cggaccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagaccc tgaggtcaag 900

ttcaactggt acgtggacgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag 960

cagtacaaca gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg 1020

aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa 1080

accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gcccccatcc 1140

cgggatgagc tgaccaagaa ccaggtcagc ctgacctgcc tggtcaaagg cttctatccc 1200

agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 1260

cctcccgtgc tggactccga cggctccttc ttcctctaca gcaagctcac cgtggacaag 1320

agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac 1380

cactacacac agaagagcct ctccctgtct ccgggtaaat ag 1422

<210> 32
<211> 473
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of Trastuzumab Heavy Chain

<400> 32

Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe Ser
1 5 10 15

Ile Ala Thr Asn Ala Tyr Ala Glu Val Gln Leu Val Glu Ser Gly Gly
20 25 30

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

Gly Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala Pro
50 55 60

Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly Tyr
65 70 75 80

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

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

Asp Thr Ala Val Tyr Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe Tyr
        115                 120                 125

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

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
145                 150                 155                 160

Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
                165                 170                 175

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

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
        195                 200                 205

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
    210                 215                 220

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
225                 230                 235                 240

Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
                245                 250                 255

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
            260                 265                 270

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
        275                 280                 285

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

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
305                 310                 315                 320

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
                325                 330                 335

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
            340                 345                 350

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
        355                 360                 365
```

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
370 375 380

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
385 390 395 400

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
405 410 415

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
420 425 430

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
435 440 445

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
450 455 460

Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470

<210> 33
<211> 1491
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of Trastuzumab Heavy Chain with C-terminal GS peptide spacer, LPETG sortase A recognition motif and additional 6x-His and strep-II affinity purification tags

<400> 33
atgaaaaaaa acattgcctt tctgctggcc tccatgttcg tgttctctat cgccacaaac 60

gcttacgctg aagtccagct ggtcgaatct ggtggtggcc tggtccagcc tggtggatca 120

ctgagactgt cctgtgctgc ttctggtttc aacatcaagg acacctacat ccattgggtc 180

agacaggcac ctggcaaggg actggaatgg gtcgcccgaa tctaccctac aaacggctac 240

actcgctacg ccgactccgt caagggacgc tttaccatct ccgccgacac ctctaaaaac 300

accgcctacc tgcagatgaa tagtctgagg gccgaggata ctgctgtgta ctactgctca 360

cgatggggag gcgacggctt ttacgctatg gattactggg gacagggaac tctggtcact 420

gtgtctagcg ctagcaccaa gggcccatcg gtcttccccc tggcaccctc ctccaagagc 480

acctctgggg gcacagcagc cctgggctgc ctggtcaagg actacttccc cgaaccggtg 540

acggtgtcgt ggaactcagg cgccctgacc agcggcgtgc acaccttccc ggctgtccta 600

cagtcctcag gactctactc cctcagcagc gtggtgaccg tgccctccag cagcttgggc 660

acccagacct acatctgcaa cgtgaatcac aagcccagca acaccaaggt ggacaagaaa 720

gttgagccca aatcttgtga caaaactcac acatgcccac cgtgcccagc acctgaactc 780

ctgggggggac cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc 840

cggacccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagaccc tgaggtcaag 900

ttcaactggt acgtggacgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag 960

cagtacaaca gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg 1020

aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa 1080

accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gcccccatcc 1140

cgggatgagc tgaccaagaa ccaggtcagc ctgacctgcc tggtcaaagg cttctatccc 1200

agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 1260

cctcccgtgc tggactccga cggctccttc ttcctctaca gcaagctcac cgtggacaag 1320

agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac 1380

cactacacac agaagagcct ctccctgtct ccgggtaaag gatccctgcc cgagaccggc 1440

ggacaccatc accatcacca tggctggagc cacccccagt tcgagaagta g 1491

<210> 34
<211> 496
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of Trastuzumab Heavy Chain with C-terminal GS peptide spacer, LPETG sortase A recognition motif and additional 6x-His and strep-II affinity purification tags

<400> 34

Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe Ser
1 5 10 15

Ile Ala Thr Asn Ala Tyr Ala Glu Val Gln Leu Val Glu Ser Gly Gly
20 25 30

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

Gly Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala Pro
50 55 60

Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly Tyr
65 70 75 80

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

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

Asp Thr Ala Val Tyr Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe Tyr
115 120 125

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

```
Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
145                 150                 155                 160

Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
                165                 170                 175

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

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
        195                 200                 205

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
    210                 215                 220

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
225                 230                 235                 240

Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
                245                 250                 255

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
            260                 265                 270

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
        275                 280                 285

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

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
305                 310                 315                 320

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
                325                 330                 335

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
            340                 345                 350

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
        355                 360                 365

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
    370                 375                 380

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
385                 390                 395                 400

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
                405                 410                 415
```

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
420 425 430

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
435 440 445

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
450 455 460

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Ser Leu Pro Glu Thr Gly
465 470 475 480

Gly His His His His His His Gly Trp Ser His Pro Gln Phe Glu Lys
485 490 495

<210> 35
<211> 714
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of Trastuzumab Light Chain

<400> 35
atgaaaaaaa acattgcctt tctgctggcc tccatgttcg tgttctctat cgccacaaat 60

gcttatgccg acatccagat gacacagtct ccctcttccc tgtccgcttc tgtgggcgat 120

cgagtgacaa tcacctgtag ggctagtcag gatgtgaata ctgctgttgc ttggtaccag 180

cagaaaccag gaaaagcccc taaactgctg atctactctg cctcattcct gtactctggg 240

gtgccttctc gattcagtgg ttctagatct ggcaccgatt tcacactgac catttcttca 300

ctgcaacctg aggattttgc cacctactac tgtcagcagc actacacaac acctcccaca 360

tttggccagg gcacaaaagt ggagatcaaa cgtacggtgg ctgcaccatc tgtcttcatc 420

ttcccgccat ctgatgagca gttgaaatct ggaactgcct ctgttgtgtg cctgctgaat 480

aacttctatc ccagagaggc caaagtacag tggaaggtgg ataacgccct ccaatcgggt 540

aactcccagg agagtgtcac agagcaggac agcaaggaca gcacctacag cctcagcagc 600

accctgacgc tgagcaaagc agactacgag aaacacaaag tctacgcctg cgaagtcacc 660

catcagggcc tgagctcgcc cgtcacaaag agcttcaaca ggggagagtg ttag 714

<210> 36
<211> 237
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of Trastuzumab Light Chain

<400> 36

Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe Ser
1 5 10 15

```
Ile Ala Thr Asn Ala Tyr Ala Asp Ile Gln Met Thr Gln Ser Pro Ser
            20                  25                  30

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

Ser Gln Asp Val Asn Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly
    50                  55                  60

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

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

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

Gln His Tyr Thr Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu
        115                 120                 125

Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser
    130                 135                 140

Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn
145                 150                 155                 160

Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala
                165                 170                 175

Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys
            180                 185                 190

Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp
        195                 200                 205

Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu
    210                 215                 220

Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230                 235
```

<210> 37
<211> 783
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of Trastuzumab Light Chain with C-terminal GS peptide spacer, LPETG sortase A recognition motif and additional 6x-His and strep-II affinity purification tags

<400> 37
atgaaaaaaa acattgcctt tctgctggcc tccatgttcg tgttctctat cgccacaaat 60

gcttatgccg acatccagat gacacagtct ccctcttccc tgtccgcttc tgtgggcgat 120

cgagtgacaa tcacctgtag ggctagtcag gatgtgaata ctgctgttgc ttggtaccag 180

cagaaaccag gaaaagcccc taaactgctg atctactctg cctcattcct gtactctggg 240

gtgccttctc gattcagtgg ttctagatct ggcaccgatt tcacactgac catttcttca 300

ctgcaacctg aggattttgc cacctactac tgtcagcagc actacacaac acctcccaca 360

tttggccagg gcacaaaagt ggagatcaaa cgtacggtgg ctgcaccatc tgtcttcatc 420

ttcccgccat ctgatgagca gttgaaatct ggaactgcct ctgttgtgtg cctgctgaat 480

aacttctatc ccagagaggc caaagtacag tggaaggtgg ataacgccct ccaatcgggt 540

aactcccagg agagtgtcac agagcaggac agcaaggaca gcacctacag cctcagcagc 600

accctgacgc tgagcaaagc agactacgag aaacacaaag tctacgcctg cgaagtcacc 660

catcagggcc tgagctcgcc cgtcacaaag agcttcaaca ggggagagtg tggatccctg 720

cccgagaccg gcggacacca tcaccatcac catggctgga gccaccccca gttcgagaag 780

tag 783

<210> 38
<211> 260
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of Trastuzumab Light Chain with C-terminal GS peptide-spacer, LPETG sortase A recognition motif and additional 6x-His and strep-II affinity purification tags

<400> 38

Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe Ser
1 5 10 15

Ile Ala Thr Asn Ala Tyr Ala Asp Ile Gln Met Thr Gln Ser Pro Ser
20 25 30

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

Ser Gln Asp Val Asn Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly
50 55 60

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

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

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

```
Gln His Tyr Thr Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu
        115                 120                 125

Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser
    130                 135                 140

Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn
145                 150                 155                 160

Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala
                165                 170                 175

Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys
            180                 185                 190

Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp
        195                 200                 205

Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu
    210                 215                 220

Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys Gly Ser Leu
225                 230                 235                 240

Pro Glu Thr Gly Gly His His His His His His Gly Trp Ser His Pro
                245                 250                 255

Gln Phe Glu Lys
            260
```

<210> 39
<211> 1470
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of mAb Ac10 Heavy Chain with C-terminal GS peptide-spacer, LPETG sortase A recognition motif and additional 6x-His and strep-II affinity purification tags

<400> 39

```
atgaattttg gactgaggct gattttcctg gtgctgaccc tgaaaggcgt ccagtgtcag       60

atccagctgc agcagtctgg ccccgaggtc gtgaaacctg gcgcctccgt gaagatctcc      120

tgcaaggcct ccggctacac cttcaccgac tactacatca cctgggtcaa gcagaagccc      180

ggccagggcc tggaatggat cggctggatc tatcccggct ccggcaacac caagtacaac      240

gagaagttca agggcaaggc caccctgacc gtggacacct cctcttccac cgccttcatg      300

cagctgtcct ccctgacctc cgaggatacc gccgtgtact tctgcgccaa ctacggcaac      360

tattggttcg cctactgggg ccagggcaca caagtgaccg tgtctgctgc tagcaccaag      420

ggcccatcgg tcttcccccc ggcaccctcc tccaagagca cctctggggg cacagcagcc      480
```

ctgggctgcc tggtcaagga ctacttcccc gaaccggtga cggtgtcgtg gaactcaggc 540

gccctgacca gcggcgtgca caccttcccg gctgtcctac agtcctcagg actctactcc 600

ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 660

gtgaatcaca agcccagcaa caccaaggtg gacaagaaag ttgagcccaa atcttgtgac 720

aaaactcaca catgcccacc gtgcccagca cctgaactcc tgggggggacc gtcagtcttc 780

ctcttccccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc 840

gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 900

gtggaggtgc ataatgccaa gacaaagccg cgggaggagc agtacaacag cacgtaccgt 960

gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 1020

aaggtctcca acaaagccct cccagccccc atcgagaaaa ccatctccaa agccaaaggg 1080

cagccccgag aaccacaggt gtacaccctg cccccatccc gggatgagct gaccaagaac 1140

caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1200

gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1260

ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac 1320

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacaca gaagagcctc 1380

tccctgtctc cgggtaaagg atccctgccc gagaccggcg gacaccatca ccatcaccat 1440

ggctggagcc acccccagtt cgagaagtag 1470

<210> 40
<211> 489
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of mAb Ac10 Heavy Chain with C-terminal GS peptide-spacer, LPETG sortase A recognition motif and additional 6x-His and strep II affinity purification tags

<400> 40

Met Asn Phe Gly Leu Arg Leu Ile Phe Leu Val Leu Thr Leu Lys Gly
1 5 10 15

Val Gln Cys Gln Ile Gln Leu Gln Gln Ser Gly Pro Glu Val Val Lys
20 25 30

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

Thr Asp Tyr Tyr Ile Thr Trp Val Lys Gln Lys Pro Gly Gln Gly Leu
50 55 60

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

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

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

Tyr Phe Cys Ala Asn Tyr Gly Asn Tyr Trp Phe Ala Tyr Trp Gly Gln
        115                 120                 125

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

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
145                 150                 155                 160

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

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
            180                 185                 190

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
        195                 200                 205

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
    210                 215                 220

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
225                 230                 235                 240

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
                245                 250                 255

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
            260                 265                 270

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
        275                 280                 285

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
    290                 295                 300

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
305                 310                 315                 320

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
                325                 330                 335

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
            340                 345                 350
```

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
355 360 365

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
370 375 380

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
385 390 395 400

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
405 410 415

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
420 425 430

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
435 440 445

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
450 455 460

Gly Lys Gly Ser Leu Pro Glu Thr Gly Gly His His His His His His
465 470 475 480

Gly Trp Ser His Pro Gln Phe Glu Lys
485

<210> 41
<211> 783
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of mAb Ac10 Light Chain with C-terminal GS peptide-spacer, LPETG sortase A recognition motif and additional 6x-His and strep II affinity purification tags

<400> 41
atgaattttg gactgaggct gattttcctg gtgctgaccc tgaaaggcgt ccagtgtgac 60

attgtgctga cccaatctcc agcttctttg gctgtgtctc tagggcagag ggccaccatc 120

tcctgcaagg ccagccaaag tgttgatttt gatggtgata gttatatgaa ctggtaccaa 180

cagaaaccag gacagccacc caaagtcctc atctatgctg catccaatct agaatctggg 240

atcccagcca ggtttagtgg cagtgggtct gggacagact tcaccctcaa catccatcct 300

gtggaggagg aggatgctgc aacctattac tgtcagcaaa gtaatgagga tccgtggacg 360

ttcggtggag gcaccaagct ggaaatcaaa cgtacggtgg ctgcaccatc tgtcttcatc 420

ttcccgccat ctgatgagca gttgaaatct ggaactgcct ctgttgtgtg cctgctgaat 480

aacttctatc ccagagaggc caaagtacag tggaaggtgg ataacgccct ccaatcgggt 540

aactcccagg agagtgtcac agagcaggac agcaaggaca gcacctacag cctcagcagc 600

accctgacgc tgagcaaagc agactacgag aaacacaaag tctacgcctg cgaagtcacc 660

catcagggcc tgagctcgcc cgtcacaaag agcttcaaca ggggagagtg tggatccctg 720

cccgagaccg gcggacacca tcaccatcac catggctgga gccaccccca gttcgagaag 780

tag 783

<210> 42
<211> 260
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of mAb Ac10 Light Chain with C-terminal GS peptide-spacer, LPETG sortase A recognition motif and additional 6x-His and strep II affinity purification tags

<400> 42

Met Asn Phe Gly Leu Arg Leu Ile Phe Leu Val Leu Thr Leu Lys Gly
1 5 10 15

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

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

Asp Phe Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly
50 55 60

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

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

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

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

Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser
130 135 140

Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn
145 150 155 160

Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala
165 170 175

Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys
180 185 190

Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp
195 200 205

Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu
210 215 220

Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys Gly Ser Leu
225 230 235 240

Pro Glu Thr Gly Gly His His His His His His Gly Trp Ser His Pro
245 250 255

Gln Phe Glu Lys
260

<210> 43
<211> 1443
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of mAb Ac10 Heavy Chain with C-terminal LPETG sortase A recognition motif and strep II affinity purification tag

<400> 43
atgaattttg gactgaggct gattttcctg gtgctgaccc tgaaaggcgt ccagtgtcag 60

atccagctgc agcagtctgg ccccgaggtc gtgaaacctg gcgcctccgt gaagatctcc 120

tgcaaggcct ccggctacac cttcaccgac tactacatca cctgggtcaa gcagaagccc 180

ggccagggcc tggaatggat cggctggatc tatcccggct ccggcaacac caagtacaac 240

gagaagttca agggcaaggc caccctgacc gtggacacct cctcttccac cgccttcatg 300

cagctgtcct ccctgacctc cgaggatacc gccgtgtact tctgcgccaa ctacggcaac 360

tattggttcg cctactgggg ccagggcaca caagtgaccg tgtctgctgc tagcaccaag 420

ggcccatcgg tcttcccccc ggcaccctcc tccaagagca cctctggggg cacagcagcc 480

ctgggctgcc tggtcaagga ctacttcccc gaaccggtga cggtgtcgtg gaactcaggc 540

gccctgacca gcggcgtgca caccttcccg gctgtcctac agtcctcagg actctactcc 600

ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 660

gtgaatcaca agcccagcaa caccaaggtg gacaagaaag ttgagcccaa atcttgtgac 720

aaaactcaca catgcccacc gtgcccagca cctgaactcc tgggggggacc gtcagtcttc 780

ctcttccccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc 840

gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 900

gtggaggtgc ataatgccaa gacaaagccg cgggaggagc agtacaacag cacgtaccgt 960

gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 1020

aaggtctcca acaaagccct cccagccccc atcgagaaaa ccatctccaa agccaaaggg 1080

cagccccgag aaccacaggt gtacaccctg cccccatccc gggatgagct gaccaagaac 1140

caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1200

gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1260

ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac 1320

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacaca gaagagcctc 1380

tccctgtctc cgggtaaact gcccgagacc ggcggatgga gccaccccca gttcgagaag 1440

tag 1443

<210> 44
<211> 480
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of mAb Ac10 Heavy Chain with C-terminal LPETG sortase A recognition motif and strep-II affinity purification tag

<400> 44

Met Asn Phe Gly Leu Arg Leu Ile Phe Leu Val Leu Thr Leu Lys Gly
1 5 10 15

Val Gln Cys Gln Ile Gln Leu Gln Gln Ser Gly Pro Glu Val Val Lys
20 25 30

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

Thr Asp Tyr Tyr Ile Thr Trp Val Lys Gln Lys Pro Gly Gln Gly Leu
50 55 60

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

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

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

Tyr Phe Cys Ala Asn Tyr Gly Asn Tyr Trp Phe Ala Tyr Trp Gly Gln
115 120 125

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

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
145 150 155 160

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

```
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
            180                 185                 190

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
        195                 200                 205

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
    210                 215                 220

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
225                 230                 235                 240

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
                245                 250                 255

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
            260                 265                 270

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
        275                 280                 285

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
    290                 295                 300

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
305                 310                 315                 320

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
                325                 330                 335

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
            340                 345                 350

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
        355                 360                 365

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
    370                 375                 380

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
385                 390                 395                 400

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
                405                 410                 415

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
            420                 425                 430

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
        435                 440                 445
```

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
450 455 460

Gly Lys Leu Pro Glu Thr Gly Gly Trp Ser His Pro Gln Phe Glu Lys
465 470 475 480

<210> 45
<211> 756
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of mAb Ac10 Light Chain with C-terminal LPETG sortase A recognition motif and strep-II affinity purification tag

<400> 45
atgaattttg gactgaggct gattttcctg gtgctgaccc tgaaaggcgt ccagtgtgac 60

attgtgctga cccaatctcc agcttctttg gctgtgtctc tagggcagag ggccaccatc 120

tcctgcaagg ccagccaaag tgttgatttt gatggtgata gttatatgaa ctggtaccaa 180

cagaaaccag gacagccacc caaagtcctc atctatgctg catccaatct agaatctggg 240

atcccagcca ggtttagtgg cagtgggtct gggacagact tcaccctcaa catccatcct 300

gtggaggagg aggatgctgc aacctattac tgtcagcaaa gtaatgagga tccgtggacg 360

ttcggtggag gcaccaagct ggaaatcaaa cgtacggtgg ctgcaccatc tgtcttcatc 420

ttcccgccat ctgatgagca gttgaaatct ggaactgcct ctgttgtgtg cctgctgaat 480

aacttctatc ccagagaggc caaagtacag tggaaggtgg ataacgccct ccaatcgggt 540

aactcccagg agagtgtcac agagcaggac agcaaggaca gcacctacag cctcagcagc 600

accctgacgc tgagcaaagc agactacgag aaacacaaag tctacgcctg cgaagtcacc 660

catcagggcc tgagctcgcc cgtcacaaag agcttcaaca ggggagagtg tctgcccgag 720

accggcggat ggagccaccc ccagttcgag aagtag 756

<210> 46
<211> 251
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of mAb Ac10 Light Chain with C-terminal LPETG sortase A recognition motif and strep-II affinity purification tag

<400> 46

Met Asn Phe Gly Leu Arg Leu Ile Phe Leu Val Leu Thr Leu Lys Gly
1 5 10 15

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

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

Asp Phe Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly
    50                  55                  60

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

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

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

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

Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser
    130                 135                 140

Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn
145                 150                 155                 160

Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala
                165                 170                 175

Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys
            180                 185                 190

Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp
        195                 200                 205

Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu
    210                 215                 220

Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys Leu Pro Glu
225                 230                 235                 240

Thr Gly Gly Trp Ser His Pro Gln Phe Glu Lys
                245                 250
```

<210> 47
<211> 762
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of mAb Ac10 Light Chain with C-terminal GS peptide-spacer, LPETG sortase A recognition motif and strep II affinity purification tag

<400> 47

```
atgaattttg gactgaggct gattttcctg gtgctgaccc tgaaaggcgt ccagtgtgac       60
```

attgtgctga cccaatctcc agcttctttg gctgtgtctc tagggcagag ggccaccatc 120

tcctgcaagg ccagccaaag tgttgatttt gatggtgata gttatatgaa ctggtaccaa 180

cagaaaccag gacagccacc caaagtcctc atctatgctg catccaatct agaatctggg 240

atcccagcca ggtttagtgg cagtgggtct gggacagact tcaccctcaa catccatcct 300

gtggaggagg aggatgctgc aacctattac tgtcagcaaa gtaatgagga tccgtggacg 360

ttcggtggag gcaccaagct ggaaatcaaa cgtacggtgg ctgcaccatc tgtcttcatc 420

ttcccgccat ctgatgagca gttgaaatct ggaactgcct ctgttgtgtg cctgctgaat 480

aacttctatc ccagagaggc caaagtacag tggaaggtgg ataacgccct ccaatcgggt 540

aactcccagg agagtgtcac agagcaggac agcaaggaca gcacctacag cctcagcagc 600

accctgacgc tgagcaaagc agactacgag aaacacaaag tctacgcctg cgaagtcacc 660

catcagggcc tgagctcgcc cgtcacaaag agcttcaaca ggggagagtg tggatccctg 720

cccgagaccg gcggatggag ccacccccag ttcgagaagt ag 762

<210> 48
<211> 253
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of mAb Ac10 Light Chain with C-terminal GS peptide-spacer, LPETG sortase A recognition motif and strep II affinity purification tag

<400> 48

Met Asn Phe Gly Leu Arg Leu Ile Phe Leu Val Leu Thr Leu Lys Gly
1 5 10 15

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

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

Asp Phe Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly
50 55 60

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

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

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

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

Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser
130 135 140

Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn
145 150 155 160

Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala
165 170 175

Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys
180 185 190

Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp
195 200 205

Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu
210 215 220

Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys Gly Ser Leu
225 230 235 240

Pro Glu Thr Gly Gly Trp Ser His Pro Gln Phe Glu Lys
245 250

<210> 49
<211> 765
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of mAb Ac10 Light Chain with C-terminal GGS peptide-spacer, LPETG sortase A recognition motif and strep II affinity purification tag

<400> 49
atgaattttg gactgaggct gattttcctg gtgctgaccc tgaaaggcgt ccagtgtgac 60

attgtgctga cccaatctcc agcttctttg gctgtgtctc tagggcagag ggccaccatc 120

tcctgcaagg ccagccaaag tgttgatttt gatggtgata gttatatgaa ctggtaccaa 180

cagaaaccag gacagccacc caaagtcctc atctatgctg catccaatct agaatctggg 240

atcccagcca ggtttagtgg cagtgggtct gggacagact tcaccctcaa catccatcct 300

gtggaggagg aggatgctgc aacctattac tgtcagcaaa gtaatgagga tccgtggacg 360

ttcggtggag gcaccaagct ggaaatcaaa cgtacggtgg ctgcaccatc tgtcttcatc 420

ttcccgccat ctgatgagca gttgaaatct ggaactgcct ctgttgtgtg cctgctgaat 480

aacttctatc ccagagaggc caaagtacag tggaaggtgg ataacgccct ccaatcgggt 540

aactcccagg agagtgtcac agagcaggac agcaaggaca gcacctacag cctcagcagc 600

accctgacgc tgagcaaagc agactacgag aaacacaaag tctacgcctg cgaagtcacc 660

catcagggcc tgagctcgcc cgtcacaaag agcttcaaca ggggagagtg tggtggatcc 720

ctgcccgaga ccggcggatg gagccacccc cagttcgaga agtag 765

<210> 50
<211> 254
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of mAb Ac10 Light Chain with C-terminal GGS peptide-spacer, LPETG sortase A recognition motif and strep II affinity purification tag

<400> 50

Met Asn Phe Gly Leu Arg Leu Ile Phe Leu Val Leu Thr Leu Lys Gly
1 5 10 15

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

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

Asp Phe Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly
50 55 60

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

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

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

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

Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser
130 135 140

Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn
145 150 155 160

Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala
165 170 175

Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys
180 185 190

Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp
195 200 205

Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu
210 215 220

Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys Gly Gly Ser
225 230 235 240

Leu Pro Glu Thr Gly Gly Trp Ser His Pro Gln Phe Glu Lys
245 250

<210> 51
<211> 768
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of mAb Ac10 Light Chain with C-terminal GGGS peptide-spacer, LPETG sortase A recognition motif and strep II affinity purification tag

<400> 51
atgaattttg gactgaggct gattttcctg gtgctgaccc tgaaaggcgt ccagtgtgac 60

attgtgctga cccaatctcc agcttctttg gctgtgtctc tagggcagag ggccaccatc 120

tcctgcaagg ccagccaaag tgttgatttt gatggtgata gttatatgaa ctggtaccaa 180

cagaaaccag gacagccacc caaagtcctc atctatgctg catccaatct agaatctggg 240

atcccagcca ggtttagtgg cagtgggtct gggacagact tcaccctcaa catccatcct 300

gtggaggagg aggatgctgc aacctattac tgtcagcaaa gtaatgagga tccgtggacg 360

ttcggtggag gcaccaagct ggaaatcaaa cgtacggtgg ctgcaccatc tgtcttcatc 420

ttcccgccat ctgatgagca gttgaaatct ggaactgcct ctgttgtgtg cctgctgaat 480

aacttctatc ccagagaggc caaagtacag tggaaggtgg ataacgccct ccaatcgggt 540

aactcccagg agagtgtcac agagcaggac agcaaggaca gcacctacag cctcagcagc 600

accctgacgc tgagcaaagc agactacgag aaacacaaag tctacgcctg cgaagtcacc 660

catcagggcc tgagctcgcc cgtcacaaag agcttcaaca ggggagagtg tgggggtgga 720

tccctgcccg agaccggcgg atggagccac ccccagttcg agaagtag 768

<210> 52
<211> 255
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of mAb Ac10 Light Chain with C-terminal GGGS peptide-spacer, LPETG sortase A recognition motif and strep II affinity purification tag

<400> 52

Met Asn Phe Gly Leu Arg Leu Ile Phe Leu Val Leu Thr Leu Lys Gly
1 5 10 15

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

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

Asp Phe Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly
    50                  55                  60

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

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

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

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

Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser
    130                 135                 140

Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn
145                 150                 155                 160

Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala
                165                 170                 175

Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys
            180                 185                 190

Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp
        195                 200                 205

Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu
    210                 215                 220

Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys Gly Gly Gly
225                 230                 235                 240

Ser Leu Pro Glu Thr Gly Gly Trp Ser His Pro Gln Phe Glu Lys
                245                 250                 255
```

<210> 53
<211> 771
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of mAb Ac10 Light Chain with C-terminal GGGGS peptide-spacer, LPETG sortase A recognition motif and strep II affinity purification tag

<400> 53
atgaattttg gactgaggct gattttcctg gtgctgaccc tgaaaggcgt ccagtgtgac 60

attgtgctga cccaatctcc agcttctttg gctgtgtctc tagggcagag ggccaccatc 120

tcctgcaagg ccagccaaag tgttgatttt gatggtgata gttatatgaa ctggtaccaa 180

cagaaaccag gacagccacc caaagtcctc atctatgctg catccaatct agaatctggg 240

atcccagcca ggtttagtgg cagtgggtct gggacagact tcaccctcaa catccatcct 300

gtggaggagg aggatgctgc aacctattac tgtcagcaaa gtaatgagga tccgtggacg 360

ttcggtggag gcaccaagct ggaaatcaaa cgtacggtgg ctgcaccatc tgtcttcatc 420

ttcccgccat ctgatgagca gttgaaatct ggaactgcct ctgttgtgtg cctgctgaat 480

aacttctatc ccagagaggc caaagtacag tggaaggtgg ataacgccct ccaatcgggt 540

aactcccagg agagtgtcac agagcaggac agcaaggaca gcacctacag cctcagcagc 600

accctgacgc tgagcaaagc agactacgag aaacacaaag tctacgcctg cgaagtcacc 660

catcagggcc tgagctcgcc cgtcacaaag agcttcaaca ggggagagtg tggaggggt 720

ggatccctgc ccgagaccgg cggatggagc caccccagt tcgagaagta g 771

<210> 54
<211> 256
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of mAb Ac10 Light Chain with C-terminal GGGGS peptide-spacer, LPETG sortase A recognition motif and strep II affinity purification tag

<400> 54

Met Asn Phe Gly Leu Arg Leu Ile Phe Leu Val Leu Thr Leu Lys Gly
1 5 10 15

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

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

Asp Phe Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly
50 55 60

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

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

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

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

Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser
130 135 140

Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn
145 150 155 160

Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala
165 170 175

Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys
180 185 190

Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp
195 200 205

Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu
210 215 220

Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys Gly Gly Gly
225 230 235 240

Gly Ser Leu Pro Glu Thr Gly Gly Trp Ser His Pro Gln Phe Glu Lys
245 250 255

<210> 55
<211> 1464
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of Trastuzumab Heavy Chain with C-terminal LPETG Sortase tag and strep II affinity purification tag

<400> 55
atgaaaaaaa acattgcctt tctgctggcc tccatgttcg tgttctctat cgccacaaac 60

gcttacgctg aagtccagct ggtcgaatct ggtggtggcc tggtccagcc tggtggatca 120

ctgagactgt cctgtgctgc ttctggtttc aacatcaagg acacctacat ccattgggtc 180

agacaggcac ctggcaaggg actggaatgg gtcgcccgaa tctaccctac aaacggctac 240

actcgctacg ccgactccgt caagggacgc tttaccatct ccgccgacac ctctaaaaac 300

accgcctacc tgcagatgaa tagtctgagg gccgaggata ctgctgtgta ctactgctca 360

cgatggggag gcgacggctt ttacgctatg gattactggg gacagggaac tctggtcact 420

gtgtctagcg ctagcaccaa gggcccatcg gtcttccccc tggcaccctc ctccaagagc 480

acctctgggg gcacagcagc cctgggctgc ctggtcaagg actacttccc cgaaccggtg 540

acggtgtcgt ggaactcagg cgccctgacc agcggcgtgc acaccttccc ggctgtccta 600

cagtcctcag gactctactc cctcagcagc gtggtgaccg tgccctccag cagcttgggc 660

acccagacct acatctgcaa cgtgaatcac aagcccagca acaccaaggt ggacaagaaa 720

gttgagccca aatcttgtga caaaactcac acatgcccac cgtgcccagc acctgaactc 780

ctggggggac cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc 840

cggacccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagaccc tgaggtcaag 900

ttcaactggt acgtggacgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag 960

cagtacaaca gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg 1020

aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa 1080

accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gcccccatcc 1140

cgggatgagc tgaccaagaa ccaggtcagc ctgacctgcc tggtcaaagg cttctatccc 1200

agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 1260

cctcccgtgc tggactccga cggctccttc ttcctctaca gcaagctcac cgtggacaag 1320

agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac 1380

cactacacac agaagagcct ctccctgtct ccgggtaaac tgcccgagac cggcggatgg 1440

agccaccccc agttcgagaa gtag 1464

<210> 56
<211> 487
<212> PRT
<213> Amino acid sequence of mAb Ac10 Heavy Chain with C-terminal LPETG Sortase tag and strep II affinity purification tag

<400> 56

Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe Ser
1 5 10 15

Ile Ala Thr Asn Ala Tyr Ala Glu Val Gln Leu Val Glu Ser Gly Gly
20 25 30

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

Gly Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala Pro
50 55 60

Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly Tyr
65 70 75 80

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

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

Asp Thr Ala Val Tyr Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe Tyr
115 120 125

```
Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala
    130                 135                 140

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
145                 150                 155                 160

Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
                165                 170                 175

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

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
        195                 200                 205

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
    210                 215                 220

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
225                 230                 235                 240

Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
                245                 250                 255

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
            260                 265                 270

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
        275                 280                 285

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

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
305                 310                 315                 320

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
                325                 330                 335

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
            340                 345                 350

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
        355                 360                 365

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
    370                 375                 380

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
385                 390                 395                 400
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Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
405 410 415

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
420 425 430

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
435 440 445

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
450 455 460

Lys Ser Leu Ser Leu Ser Pro Gly Lys Leu Pro Glu Thr Gly Gly Trp
465 470 475 480

Ser His Pro Gln Phe Glu Lys
485

<210> 57
<211> 771
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of Trastuzumab Light Chain with C-terminal GGGGS linker, LPETG Sortase tag and strep II affinity purification tag

<400> 57
atgaaaaaaa acattgcctt tctgctggcc tccatgttcg tgttctctat cgccacaaat 60

gcttatgccg acatccagat gacacagtct ccctcttccc tgtccgcttc tgtgggcgat 120

cgagtgacaa tcacctgtag ggctagtcag gatgtgaata ctgctgttgc ttggtaccag 180

cagaaaccag gaaaagcccc taaactgctg atctactctg cctcattcct gtactctggg 240

gtgccttctc gattcagtgg ttctagatct ggcaccgatt tcacactgac catttcttca 300

ctgcaacctg aggattttgc cacctactac tgtcagcagc actacacaac acctcccaca 360

tttggccagg gcacaaaagt ggagatcaaa cgtacggtgg ctgcaccatc tgtcttcatc 420

ttcccgccat ctgatgagca gttgaaatct ggaactgcct ctgttgtgtg cctgctgaat 480

aacttctatc ccagagaggc caaagtacag tggaaggtgg ataacgccct ccaatcgggt 540

aactcccagg agagtgtcac agagcaggac agcaaggaca gcacctacag cctcagcagc 600

accctgacgc tgagcaaagc agactacgag aaacacaaag tctacgcctg cgaagtcacc 660

catcagggcc tgagctcgcc cgtcacaaag agcttcaaca ggggagagtg tggaggggt 720

ggatccctgc ccgagaccgg cggatggagc caccccagt tcgagaagta g 771

<210> 58
<211> 256
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of mAb Ac10 Light Chain with C-terminal GGGGS linker, LPETG Sortase tag and strep II affinity purification tag

<400> 58

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Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe Ser
1               5                  10                  15

Ile Ala Thr Asn Ala Tyr Ala Asp Ile Gln Met Thr Gln Ser Pro Ser
            20                  25                  30

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

Ser Gln Asp Val Asn Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly
    50                  55                  60

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

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

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

Gln His Tyr Thr Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu
        115                 120                 125

Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser
    130                 135                 140

Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn
145                 150                 155                 160

Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala
                165                 170                 175

Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys
            180                 185                 190

Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp
        195                 200                 205

Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu
    210                 215                 220

Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys Gly Gly Gly
225                 230                 235                 240

Gly Ser Leu Pro Glu Thr Gly Gly Trp Ser His Pro Gln Phe Glu Lys
                245                 250                 255
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