

SEQUENCE LISTING

<110> PsiOxus Therapeutics Limited

<120> Adenovirus armed with bispecific T cell engager (BiTE)

<130> P000192_WO2

<150> GB1614607.8

<151> 2016-08-29

<160> 297

<170> PatentIn version 3.5

<210> 1

<211> 1578

<212> DNA

<213> Artificial Sequence

<220>

<223> Anti-EpCAM BiTE DNA coding sequence, with N-terminal signal sequence and C-terminal deca-His affinity tag

<400> 1

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tcgggggtgc cagaccggtt caccggctcc gggtcaggaa ctgatttcac cctaaccatc    300
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ccagggagcg gcaacatcca ctacaacgag aagttcaagg ggaaagcgac tctgactgcc    660
gacaaatcat ccagcaccgc ctacatgcag ctgtctgc tcactttcga agacagcgcg    720
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 caccaccatc accattag 1578

<210> 2

<211> 525

<212> PRT

<213> Artificial Sequence

<220>

<223> Anti-EpCAM BiTE protein sequence, with N-terminal signal sequence
and C-terminal deca-His affinity tag

<400> 2

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

Val His Ser Glu Leu Val Met Thr Gln Ser Pro Ser Ser Leu Thr Val

20 25 30

Thr Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu
35 40 45

Leu Asn Ser Gly Asn Gln Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys
50 55 60

Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu
65 70 75 80

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

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

Cys Gln Asn Asp Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys
115 120 125

Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
130 135 140

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

Arg Pro Gly Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala
165 170 175

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

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

Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser

210 215 220

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

Val Tyr Phe Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr
245 250 255

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

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

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

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
305 310 315 320

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

Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
340 345 350

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

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

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

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

405 410 415

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
420 425 430

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
435 440 445

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

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

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
485 490 495

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
500 505 510

Glu Ile Lys His His His His His His His His His His His
515 520 525

<210> 3

<211> 1590

<212> DNA

<213> Artificial Sequence

<220>

<223> Anti-FAP BiTE DNA coding sequence, with N-terminal signal
sequence and C-terminal deca-His affinity tag

<400> 3

atgggctgga gctgcatcat ctgttcctg gtcgcaactg ctaccggagt ccattcggac 60

atcgtcatga cccaaagccc tgactcgctc gctgtgtcac tgggagagcg ggcgactatc 120

aactgcaaat catcccagag cctgctgtat tcacgcaatc agaaaaacta cctggcctgg 180

tatcagcaga agccggggcca gcctcccaag ctgctgatct tctgggcctc caccgcgaa 240

agcggcgtgc cggaccgctt cagcgaagc ggattcgaa ctgactttac tctgaccatt 300
 agctccttgc aggcggagga cgtggccgtc tactactgcc agcagtattt ctctatccg 360
 ctcacctttg ggcaaggcac caaggtggag attaaggag ggggcggcag cgggggaggc 420
 ggcagcggcg gcgggggatc gcaggtccag ctctccaat ccggagccga agtcaagaag 480
 ccgggagcgt cggtaaggc cagctgcaaa acttcgcgt acaccttcac tgagtacacg 540
 atccactggg tccgccaggc gcccgccag cggctggagt ggatcggcgg gatcaacca 600
 aacaacggaa tcccaaatta caatcagaaa tttaaaggc ggggtgactat caccgtggat 660
 acctggcct ccacggcgta catggagctc tcactactca gatcggagga caccgcggtc 720
 tattactgcg cccgcccg cgtcgttat ggatacgtg aaggacatgc gatggattac 780
 tggggccagg gcaccctcgt caggtgtcg tcaggaggcg gcggttcaga tgtgcaactc 840
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 caccatcacc atcaccacca tcaccattag 1590

<210> 4

<211> 529

<212> PRT

<213> Artificial Sequence

<220>

<223> Anti-FAP BiTE amino acid sequence, with N-terminal signal sequence and C-terminal deca-His affinity tag

<400> 4

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

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

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

Leu Tyr Ser Arg Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys
50 55 60

Pro Gly Gln Pro Pro Lys Leu Leu Ile Phe Trp Ala Ser Thr Arg Glu
65 70 75 80

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

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

Cys Gln Gln Tyr Phe Ser Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys
115 120 125

Val Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
130 135 140

Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys

145 150 155 160

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

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

Glu Trp Ile Gly Gly Ile Asn Pro Asn Asn Gly Ile Pro Asn Tyr Asn
 195 200 205

Gln Lys Phe Lys Gly Arg Val Thr Ile Thr Val Asp Thr Ser Ala Ser
 210 215 220

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

Tyr Tyr Cys Ala Arg Arg Arg Ile Ala Tyr Gly Tyr Asp Glu Gly His
 245 250 255

Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
 260 265 270

Gly Gly Gly Ser Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys
 275 280 285

Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr
 290 295 300

Phe Thr Arg Tyr Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly
305 310 315 320

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

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr

340

345

350

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

Thr Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr
370 375 380

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

Thr Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val
405 410 415

Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
420 425 430

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

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

Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
465 470 475 480

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

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

Gly Thr Lys Val Glu Ile Lys His His His His His His His His
515 520 525

His

<210> 5
<211> 1629
<212> DNA
<213> Artificial Sequence

<220>
<223> Control (Anti-FHA) BiTE DNA coding sequence, with N-terminal
signal sequence and C-terminal deca-His affinity tag

<400> 5
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ctggacatcg tgatgacca ggcacctgca tctctggcag tgaccctggg acagagagcc 120

accatttcat gccgggccag caagagcgtg tcgtcatccg gatacaatta tctgcactgg 180

tatcagcaga aaccaggaca acctccaaag ctactcatct acctggcgtc gaacctcgaa 240

tcgggcgtcc cagctagatt ctcagggagc gggttcgggaa ccgatttcac cctgaacatc 300

cacctgtgg aggaggaaga gcgggcaacg tactattgcc agcattcccg cgagttccct 360

ctcactttcg gtgcgggaac taagctggag atcaagtcca gcggcggcgg aggtagcgg 420

ggaggtggcg gaggaagctc ccggtcgtcg ctggagggtc agctgcaaca atccggccc 480

gaactggtca agccaggcgc atccgtcaag atttcatgca agacctcggg gtacaccttc 540

accgggtaca cgatgcattg ggtcaggcag agccacggca agtccctgga atggatcgga 600

ggaatcaacc caaaaaacgg cggcattcatc tacaacaaa agttccaggg aaaagccact 660

ctgaccgtgg acaagtcgtc gagcacggcc agcatggagc tgcggtccct cacttccgac 720

gactcagccg tgtattactg cgcgagacgg gtctacgatg actaccata ctactacgt 780

atggactact ggggacaagg aaccagcgtg accgttcat cggcgaaaac tactccgccg 840

tcggtgacgt cgggaggtgg tggaagcgac gtgcagctcg tccagtcggg tgccgaggtg 900

aagaagccag gagcctccgt gaaggtctcg tgcaaagcca gcggctacac tttactagg 960

tacatatgc actgggtgcg gcaagcgccg ggacaaggtc tggagtggat cggatacatc 1020

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aatagcctgg aggccgagga cgctgcaact tactactgcc agcagtggtc ctccaaccct 1560
ctcaccttcg gaggcgggac caaggtggaa atcaaacatc accatcacca tcaccacat 1620
caccattag 1629

<210> 6

<211> 542

<212> PRT

<213> Artificial Sequence

<220>

<223> Control (Anti-FHA) BiTE amino acid sequence with N-terminal
signal sequence and C-terminal deca-His affinity tag

<400> 6

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

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

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

Ser Val Ser Ser Ser Gly Tyr Asn Tyr Leu His Trp Tyr Gln Gln Lys
50 55 60

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

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

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

Cys Gln His Ser Arg Glu Phe Pro Leu Thr Phe Gly Ala Gly Thr Lys
 115 120 125

Leu Glu Ile Lys Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Gly
 130 135 140

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

Glu Leu Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Thr Ser
 165 170 175

Gly Tyr Thr Phe Thr Gly Tyr Thr Met His Trp Val Arg Gln Ser His
 180 185 190

Gly Lys Ser Leu Glu Trp Ile Gly Gly Ile Asn Pro Lys Asn Gly Gly
 195 200 205

Ile Ile Tyr Asn Gln Lys Phe Gln Gly Lys Ala Thr Leu Thr Val Asp
 210 215 220

Lys Ser Ser Ser Thr Ala Ser Met Glu Leu Arg Ser Leu Thr Ser Asp
225 230 235 240

Asp Ser Ala Val Tyr Tyr Cys Ala Arg Arg Val Tyr Asp Asp Tyr Pro
 245 250 255

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

Ser Ser Ala Lys Thr Thr Pro Pro Ser Val Thr Ser Gly Gly Gly Gly
275 280 285

Ser Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly
290 295 300

Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg
305 310 315 320

Tyr Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp
325 330 335

Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser
340 345 350

Val Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala
355 360 365

Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr
370 375 380

Cys Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln
385 390 395 400

Gly Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser
405 410 415

Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln
420 425 430

Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser
435 440 445

Cys Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys
450 455 460

Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala
465 470 475 480

Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr
485 490 495

Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr
500 505 510

Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys
515 520 525

Val Glu Ile Lys His His His His His His His His His His
530 535 540

<210> 7

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Anti-CD3 ScFv amino acid sequence

<400> 7

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

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

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

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val

50 55 60

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

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

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
145 150 155 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225 230 235 240

Glu Ile Lys

<210> 8
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-CD3 VH

<400> 8

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

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

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

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

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

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

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser
115

<210> 9
<211> 106
<212> PRT

<213> Artificial Sequence

<220>

<223> Anti-CD3 VL

<400> 9

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

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

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

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60

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

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

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

<210> 10

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Anti-CD3 ScFv linker sequence

<400> 10

Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly
1 5 10 15

Ala Asp

<210> 11

<211> 252

<212> PRT

<213> Artificial Sequence

<220>

<223> Anti-FAP ScFv

<400> 11

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

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Tyr Ser
20 25 30

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

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

Pro Asp Arg Phe Ser Gly Ser Gly Phe Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

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

Tyr Phe Ser Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala

130 135 140

Ser Val Lys Val Ser Cys Lys Thr Ser Arg Tyr Thr Phe Thr Glu Tyr
145 150 155 160

Thr Ile His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Ile
165 170 175

Gly Gly Ile Asn Pro Asn Asn Gly Ile Pro Asn Tyr Asn Gln Lys Phe
180 185 190

Lys Gly Arg Val Thr Ile Thr Val Asp Thr Ser Ala Ser Thr Ala Tyr
195 200 205

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
210 215 220

Ala Arg Arg Arg Ile Ala Tyr Gly Tyr Asp Glu Gly His Ala Met Asp
225 230 235 240

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
245 250

<210> 12

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<223> Anti-FAP VL domain

<400> 12

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

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Tyr Ser
20 25 30

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

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

Pro Asp Arg Phe Ser Gly Ser Gly Phe Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

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

Tyr Phe Ser Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

Lys

<210> 13

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> Anti-FAP VH domain

<400> 13

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

Ser Val Lys Val Ser Cys Lys Thr Ser Arg Tyr Thr Phe Thr Glu Tyr
20 25 30

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

Gly Gly Ile Asn Pro Asn Asn Gly Ile Pro Asn Tyr Asn Gln Lys Phe

50 55 60

Lys Gly Arg Val Thr Ile Thr Val Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

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

Ala Arg Arg Arg Ile Ala Tyr Gly Tyr Asp Glu Gly His Ala Met Asp
 100 105 110

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

<210> 14

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Anti-FAP and Anti-EpCAM linker sequence

<400> 14

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

<210> 15

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> BiTe leader sequence

<400> 15

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

Val His Ser

<210> 16
<211> 248
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-EpCAM ScFv

<400> 16

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

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Gly Asn Gln Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

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

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

Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
130 135 140

Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
145 150 155 160

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
 165 170 175

Ile Gly Asp Ile Phe Pro Gly Ser Gly Asn Ile His Tyr Asn Glu Lys
 180 185 190

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
 195 200 205

Tyr Met Gln Leu Ser Ser Leu Thr Phe Glu Asp Ser Ala Val Tyr Phe
 210 215 220

Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr Trp Gly Gln
225 230 235 240

Gly Thr Thr Val Thr Val Ser Ser
 245

<210> 17

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<223> Anti-EpCAM VL

<400> 17

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

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
 20 25 30

Gly Asn Gln Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln

35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

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

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

Lys

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

<220>
<223> Anti-EpCAM VH

<400> 18

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

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

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

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

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
65 70 75 80

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

Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 19

<211> 542

<212> PRT

<213> Artificial Sequence

<220>

<223> Control BiTe (Anti-FHA)

<400> 19

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

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

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

Ser Val Ser Ser Ser Gly Tyr Asn Tyr Leu His Trp Tyr Gln Gln Lys
 50 55 60

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

Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe

85

90

95

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

Cys Gln His Ser Arg Glu Phe Pro Leu Thr Phe Gly Ala Gly Thr Lys
115 120 125

Leu Glu Ile Lys Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Gly
130 135 140

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

Glu Leu Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Thr Ser
165 170 175

Gly Tyr Thr Phe Thr Gly Tyr Thr Met His Trp Val Arg Gln Ser His
180 185 190

Gly Lys Ser Leu Glu Trp Ile Gly Gly Ile Asn Pro Lys Asn Gly Gly
195 200 205

Ile Ile Tyr Asn Gln Lys Phe Gln Gly Lys Ala Thr Leu Thr Val Asp
210 215 220

Lys Ser Ser Ser Thr Ala Ser Met Glu Leu Arg Ser Leu Thr Ser Asp
225 230 235 240

Asp Ser Ala Val Tyr Tyr Cys Ala Arg Arg Val Tyr Asp Asp Tyr Pro
245 250 255

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

Ser Ser Ala Lys Thr Thr Pro Pro Ser Val Thr Ser Gly Gly Gly Gly

275 280 285

Ser Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly
290 295 300

Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg
305 310 315 320

Tyr Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp
325 330 335

Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser
340 345 350

Val Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala
355 360 365

Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr
370 375 380

Cys Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln
385 390 395 400

Gly Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser
405 410 415

Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln
420 425 430

Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser
435 440 445

Cys Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys
450 455 460

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

465 470 475 480

Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr
 485 490 495

Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr
 500 505 510

Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys
 515 520 525

Val Glu Ile Lys His His His His His His His His His His
 530 535 540

<210> 20

<211> 265

<212> PRT

<213> Artificial Sequence

<220>

<223> Control (Anti-FHA) ScFv

<400> 20

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

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

Ser Ser Gly Tyr Asn Tyr Leu His Trp Tyr Gln Gln Lys Pro Gly Gln
 35 40 45

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

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

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

Ser Arg Glu Phe Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile
100 105 110

Lys Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Gly Gly Ser Ser
115 120 125

Arg Ser Ser Leu Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val
130 135 140

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

Phe Thr Gly Tyr Thr Met His Trp Val Arg Gln Ser His Gly Lys Ser
165 170 175

Leu Glu Trp Ile Gly Gly Ile Asn Pro Lys Asn Gly Gly Ile Ile Tyr
180 185 190

Asn Gln Lys Phe Gln Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser
195 200 205

Ser Thr Ala Ser Met Glu Leu Arg Ser Leu Thr Ser Asp Asp Ser Ala
210 215 220

Val Tyr Tyr Cys Ala Arg Arg Val Tyr Asp Asp Tyr Pro Tyr Tyr Tyr
225 230 235 240

Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala
245 250 255

Lys Thr Thr Pro Pro Ser Val Thr Ser
260 265

<210> 21
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> Control (Anti-FHA) VL

<400> 21

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

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

Ser Ser Gly Tyr Asn Tyr Leu His Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

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

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

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

Ser Arg Glu Phe Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile
100 105 110

Lys

<210> 22
<211> 133
<212> PRT
<213> Artificial Sequence

<220>

<223> Control (Anti-FHA) VH

<400> 22

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

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

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

Gly Gly Ile Asn Pro Lys Asn Gly Gly Ile Ile Tyr Asn Gln Lys Phe
50 55 60

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

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

Ala Arg Arg Val Tyr Asp Asp Tyr Pro Tyr Tyr Tyr Ala Met Asp Tyr
100 105 110

Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro
115 120 125

Pro Ser Val Thr Ser
130

<210> 23

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Control (Anti-FHA) ScFv linker sequence

<400> 23

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

Ser Ser Leu

<210> 24

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Deca-His Tag sequence

<400> 24

His His His His His His His His His His
1 5 10

<210> 25

<211> 786

<212> PRT

<213> Artificial Sequence

<220>

<223> FAP BiTE-P2A-RFP

<400> 25

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

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

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

Leu Tyr Ser Arg Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys

50 55 60

Pro Gly Gln Pro Pro Lys Leu Leu Ile Phe Trp Ala Ser Thr Arg Glu
65 70 75 80

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

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

Cys Gln Gln Tyr Phe Ser Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys
115 120 125

Val Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
130 135 140

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

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

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

Glu Trp Ile Gly Gly Ile Asn Pro Asn Asn Gly Ile Pro Asn Tyr Asn
195 200 205

Gln Lys Phe Lys Gly Arg Val Thr Ile Thr Val Asp Thr Ser Ala Ser
210 215 220

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

Tyr Tyr Cys Ala Arg Arg Arg Ile Ala Tyr Gly Tyr Asp Glu Gly His

245 250 255

Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
260 265 270

Gly Gly Gly Ser Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys
275 280 285

Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr
290 295 300

Phe Thr Arg Tyr Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly
305 310 315 320

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

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr
340 345 350

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

Thr Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr
370 375 380

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

Thr Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val
405 410 415

Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
420 425 430

Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr

435

440

445

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

Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
465 470 475 480

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

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

Gly Thr Lys Val Glu Ile Lys His His His His His His His His His
515 520 525

His Arg Arg Lys Arg Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys
530 535 540

Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ser Glu Leu Ile
545 550 555 560

Lys Glu Asn Met His Met Lys Leu Tyr Met Glu Gly Thr Val Asn Asn
565 570 575

His His Phe Lys Cys Thr Ser Glu Gly Glu Gly Lys Pro Tyr Glu Gly
580 585 590

Thr Gln Thr Met Lys Ile Lys Val Val Glu Gly Gly Pro Leu Pro Phe
595 600 605

Ala Phe Asp Ile Leu Ala Thr Ser Phe Met Tyr Gly Ser Lys Ala Phe
610 615 620

Ile Asn His Thr Gln Gly Ile Pro Asp Phe Phe Lys Gln Ser Phe Pro

625 630 635 640

Glu Gly Phe Thr Trp Glu Arg Ile Thr Thr Tyr Glu Asp Gly Gly Val
 645 650 655

Leu Thr Ala Thr Gln Asp Thr Ser Phe Gln Asn Gly Cys Ile Ile Tyr
 660 665 670

Asn Val Lys Ile Asn Gly Val Asn Phe Pro Ser Asn Gly Pro Val Met
 675 680 685

Gln Lys Lys Thr Arg Gly Trp Glu Ala Asn Thr Glu Met Leu Tyr Pro
 690 695 700

Ala Asp Gly Gly Leu Arg Gly His Ser Gln Met Ala Leu Lys Leu Val
705 710 715 720

Gly Gly Gly Tyr Leu His Cys Ser Phe Lys Thr Thr Tyr Arg Ser Lys
 725 730 735

Lys Pro Ala Lys Asn Leu Lys Met Pro Gly Phe His Phe Val Asp His
 740 745 750

Arg Leu Glu Arg Ile Lys Glu Ala Asp Lys Glu Thr Tyr Val Glu Gln
 755 760 765

His Glu Met Ala Val Ala Lys Tyr Cys Asp Leu Pro Ser Lys Leu Gly
 770 775 780

His Arg
785

<210> 26

<211> 799

<212> PRT

<213> Artificial Sequence

<220>

<223> Control (Anti-FHA) BiTE-P2A-RFP

<400> 26

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

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

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

Ser Val Ser Ser Ser Gly Tyr Asn Tyr Leu His Trp Tyr Gln Gln Lys
50 55 60

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

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

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

Cys Gln His Ser Arg Glu Phe Pro Leu Thr Phe Gly Ala Gly Thr Lys
115 120 125

Leu Glu Ile Lys Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Gly
130 135 140

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

Glu Leu Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Thr Ser
165 170 175

Gly Tyr Thr Phe Thr Gly Tyr Thr Met His Trp Val Arg Gln Ser His
180 185 190

Gly Lys Ser Leu Glu Trp Ile Gly Gly Ile Asn Pro Lys Asn Gly Gly
195 200 205

Ile Ile Tyr Asn Gln Lys Phe Gln Gly Lys Ala Thr Leu Thr Val Asp
210 215 220

Lys Ser Ser Ser Thr Ala Ser Met Glu Leu Arg Ser Leu Thr Ser Asp
225 230 235 240

Asp Ser Ala Val Tyr Tyr Cys Ala Arg Arg Val Tyr Asp Asp Tyr Pro
245 250 255

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

Ser Ser Ala Lys Thr Thr Pro Pro Ser Val Thr Ser Gly Gly Gly Gly
275 280 285

Ser Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly
290 295 300

Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg
305 310 315 320

Tyr Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp
325 330 335

Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser
340 345 350

Val Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala
355 360 365

Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr
370 375 380

Cys Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln
385 390 395 400

Gly Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser
405 410 415

Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln
420 425 430

Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser
435 440 445

Cys Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys
450 455 460

Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala
465 470 475 480

Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr
485 490 495

Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr
500 505 510

Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys
515 520 525

Val Glu Ile Lys His His His His His His His His Arg Arg
530 535 540

Lys Arg Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly
545 550 555 560

Asp Val Glu Glu Asn Pro Gly Pro Met Ser Glu Leu Ile Lys Glu Asn
565 570 575

Met His Met Lys Leu Tyr Met Glu Gly Thr Val Asn Asn His His Phe
580 585 590

Lys Cys Thr Ser Glu Gly Glu Gly Lys Pro Tyr Glu Gly Thr Gln Thr
595 600 605

Met Lys Ile Lys Val Val Glu Gly Gly Pro Leu Pro Phe Ala Phe Asp
610 615 620

Ile Leu Ala Thr Ser Phe Met Tyr Gly Ser Lys Ala Phe Ile Asn His
625 630 635 640

Thr Gln Gly Ile Pro Asp Phe Phe Lys Gln Ser Phe Pro Glu Gly Phe
645 650 655

Thr Trp Glu Arg Ile Thr Thr Tyr Glu Asp Gly Gly Val Leu Thr Ala
660 665 670

Thr Gln Asp Thr Ser Phe Gln Asn Gly Cys Ile Ile Tyr Asn Val Lys
675 680 685

Ile Asn Gly Val Asn Phe Pro Ser Asn Gly Pro Val Met Gln Lys Lys
690 695 700

Thr Arg Gly Trp Glu Ala Asn Thr Glu Met Leu Tyr Pro Ala Asp Gly
705 710 715 720

Gly Leu Arg Gly His Ser Gln Met Ala Leu Lys Leu Val Gly Gly Gly
725 730 735

Tyr Leu His Cys Ser Phe Lys Thr Thr Tyr Arg Ser Lys Lys Pro Ala
740 745 750

Lys Asn Leu Lys Met Pro Gly Phe His Phe Val Asp His Arg Leu Glu
755 760 765

Arg Ile Lys Glu Ala Asp Lys Glu Thr Tyr Val Glu Gln His Glu Met
770 775 780

Ala Val Ala Lys Tyr Cys Asp Leu Pro Ser Lys Leu Gly His Arg
785 790 795

<210> 27

<211> 945

<212> DNA

<213> Artificial Sequence

<220>

<223> Human EpCAM DNA coding sequence

<400> 27

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aacaataacc gccaatgcca gtgcaccagc gtgggcgcgc agaacactgt catctgcagc 180

aagctggccg caaaatgcct ggtcatgaaa gcggagatga acggatcgaa gctgggtcgg 240

cgcgctaagc cggaaggagc gctacaaaat aacgacgggc tgtacgatcc ggattgcgac 300

gaaagcggtc tgtttaaggc aaagcagtgt aatgggacca gcatgtgttg gtgcgtgaac 360

actgccggag tgcgccgcac tgacaaggat accgaaatta cgtgctcgga gcgcgtgaga 420

acgtattgga tcatcatcga gttgaagcat aaagctagag agaagccgta cgatagcaag 480

tccctgcgca ccgctctcca aaaagaaatt accactagat accaactcga cccgaaattc 540

atcacttcaa tcctgtacga aaacaacgtg attacgatcg acctgggtga gaactccagc 600

caaaagacgc agaacgacgt ggacattgca gacgtggctt actactttga aaaggacgtg 660

aagggggaat cactatttca ttcaagaaa atggacctga ccgtcaacgg agagcagctc 720

gacctggacc caggtcagac tctgatctac tacgtggacg agaaggcacc ggagttttcg 780

atgcagggcc tgaaagccgg agtcatcgcc gtgatcgtgg tggtggtgat tgccgtcgtc 840
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<210> 28

<211> 314

<212> PRT

<213> Artificial Sequence

<220>

<223> Human EpCAM amino acid sequence

<400> 28

Met Ala Pro Pro Gln Val Leu Ala Phe Gly Leu Leu Leu Ala Ala Ala
1 5 10 15

Thr Ala Thr Phe Ala Ala Ala Gln Glu Glu Cys Val Cys Glu Asn Tyr
20 25 30

Lys Leu Ala Val Asn Cys Phe Val Asn Asn Asn Arg Gln Cys Gln Cys
35 40 45

Thr Ser Val Gly Ala Gln Asn Thr Val Ile Cys Ser Lys Leu Ala Ala
50 55 60

Lys Cys Leu Val Met Lys Ala Glu Met Asn Gly Ser Lys Leu Gly Arg
65 70 75 80

Arg Ala Lys Pro Glu Gly Ala Leu Gln Asn Asn Asp Gly Leu Tyr Asp
85 90 95

Pro Asp Cys Asp Glu Ser Gly Leu Phe Lys Ala Lys Gln Cys Asn Gly
100 105 110

Thr Ser Met Cys Trp Cys Val Asn Thr Ala Gly Val Arg Arg Thr Asp
115 120 125

Lys Asp Thr Glu Ile Thr Cys Ser Glu Arg Val Arg Thr Tyr Trp Ile
130 135 140

Ile Ile Glu Leu Lys His Lys Ala Arg Glu Lys Pro Tyr Asp Ser Lys
145 150 155 160

Ser Leu Arg Thr Ala Leu Gln Lys Glu Ile Thr Thr Arg Tyr Gln Leu
165 170 175

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

Ile Asp Leu Val Gln Asn Ser Ser Gln Lys Thr Gln Asn Asp Val Asp
195 200 205

Ile Ala Asp Val Ala Tyr Tyr Phe Glu Lys Asp Val Lys Gly Glu Ser
210 215 220

Leu Phe His Ser Lys Lys Met Asp Leu Thr Val Asn Gly Glu Gln Leu
225 230 235 240

Asp Leu Asp Pro Gly Gln Thr Leu Ile Tyr Tyr Val Asp Glu Lys Ala
245 250 255

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

Val Val Val Val Ile Ala Val Val Ala Gly Ile Val Val Leu Val Ile
275 280 285

Ser Arg Lys Lys Arg Met Ala Lys Tyr Glu Lys Ala Glu Ile Lys Glu
290 295 300

Met Gly Glu Met His Arg Glu Leu Asn Ala
305 310

<210> 29

<211> 2283

<212> DNA

<213> Artificial Sequence

<220>

<223> Human FAP DNA coding sequence

<400> 29

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atcgaaactg gccagagcta caccatcctg tcgaatagaa ctatgaaatc ggtgaatgcg    300
tcgaactacg gacttagccc ggaccgccag ttcgtgtacc tagaatcgga ctacagcaag    360
ctgtggcggg acagctacac tgctacgtac tacatctacg acctgtcgaa tggcgagttc    420
gtgagaggaa acgaactccc ccgcccgatc caatacctgt gctggagccc tgtgggaagc    480
aagctggcgt acgtgtatca gaacaacatc tacctcaagc agaggccggg cgaccacct    540
ttccagatca cttttaacgg tcgggagaac aagattttca atggaatccc ggattgggtg    600
tacgaagaag agatgctggc gaccaaatat gcgctctggt ggtcgccaaa cggaataatt    660
ctagcatacg ccgagttcaa tgacaccgac atccccgtca tcgcctacag ctactacgga    720
gatgagcaat acccacgcac tattaatatc ccgtaccgga aagccggcgc taaaaatccg    780
gtcgtgcgga ttttcatcat cgacactacc tatccagctt acgtgggacc gcaagaggtc    840
cctgtgccag ccatgatcgc cagcagcgat tactacttct cctggctgac ttgggtcact    900
gacgagaggg tgtgcctcca atggctcaag cgcgtgcaga acgtgagcgt gctgtccatc    960
tgcgacttca gagaagattg gcaaactggg gactgtccga aaactcaaga gcatatcgag   1020
gagagcagaa ccggatgggc agggggggtc ttcgtgtcca ccccgtgtt cagctacgat   1080
gcgatctcgt actacaagat ttttccgat aaggacgggt acaaacatat ccactacatc   1140
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Asn Gly Thr Phe Ser Tyr Lys Thr Phe Phe Pro Asn Trp Ile Ser Gly
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Gln Glu Tyr Leu His Gln Ser Ala Asp Asn Asn Ile Val Leu Tyr Asn
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Ile Glu Thr Gly Gln Ser Tyr Thr Ile Leu Ser Asn Arg Thr Met Lys
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Ser Val Asn Ala Ser Asn Tyr Gly Leu Ser Pro Asp Arg Gln Phe Val
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Tyr Leu Glu Ser Asp Tyr Ser Lys Leu Trp Arg Tyr Ser Tyr Thr Ala
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Lys Leu Ala Tyr Val Tyr Gln Asn Asn Ile Tyr Leu Lys Gln Arg Pro
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Gly Asp Pro Pro Phe Gln Ile Thr Phe Asn Gly Arg Glu Asn Lys Ile

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185

190

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Cys Leu Gln Trp Leu Lys Arg Val Gln Asn Val Ser Val Leu Ser Ile
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Cys Asp Phe Arg Glu Asp Trp Gln Thr Trp Asp Cys Pro Lys Thr Gln
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Glu His Ile Glu Glu Ser Arg Thr Gly Trp Ala Gly Gly Phe Phe Val
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Gln Val Asp Phe Gln Ala Met Trp Tyr Ser Asp Gln Asn His Gly Leu
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<211> 201

<212> DNA

<213> Artificial Sequence

<220>

<223> Bx DNA sequence corresponding to and including bp 28166-28366 of
the EnAd genome

<400> 39

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<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> By DNA sequence corresponding to and including bp 29345-29379 of
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<400> 40

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<210> 41

<211> 6

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<213> Artificial Sequence

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<223> His Tag

<400> 41

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<210> 42

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Splice acceptor

<400> 42

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<210> 43

<211> 192

<212> DNA

<213> Artificial Sequence

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<223> SV40 poly Adenylation sequence

<400> 43

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gggaggtttt tt 192

<210> 44

<211> 1539

<212> DNA

<213> Artificial Sequence

<220>

<223> EpCam BiTE nucleic acid sequence (OKT3)

<400> 44

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<210> 45

<211> 1551

<212> DNA

<213> Artificial Sequence

<220>

<223> FAP BiTE nucleic acid sequence (OKT3)

<400> 45

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<210> 46

<211> 1557

<212> DNA

<213> Artificial Sequence

<220>

<223> FAP BiTE nucleic acid sequence (aCD3)

<400> 46

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<210> 47

<211> 1856

<212> DNA

<213> Artificial Sequence

<220>

<223> NG-611 Transgene cassette

<400> 47

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cacagacatg ataagataca ttgatgagtt tggacaaacc acaactagaa tgcagtgaaa 1680

aaaatgcttt atttgtgaaa tttgtgatgc tattgcttta tttgtaacca ttataagctg 1740

caataaacia gttacaaca acaattgcat tcattttatg tttcaggttc agggggaggt 1800

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<210> 48

<211> 1868

<212> DNA

<213> Artificial Sequence

<220>

<223> NG-612 Transgene cassette

<400> 48

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ggcgactatc aactgcaaat catccagag cctgctgtat tcacgcaatc agaaaaacta 180

cctggcctgg tatcagcaga agccgggcca gcctccaag ctgctgatct tctgggcctc 240

cacccgcgaa agcggcgtgc cggaccgctt cagcggaagc ggattcggaa ctgactttac 300

tctgaccatt agtccttgc aggcggagga cgtggccgtc tactactgcc agcagtattt 360

ctcctatccg ctacaccttg ggcaaggcac caagtgaggag attaaggag ggggcggcag 420

cgggggaggc ggcagcggcg gcgggggatc gcaggtccag ctctccaat ccggagccga 480

agtcaagaag ccgggagcgt cggtaaggt cagctgcaaa acttcgcgt acaccttac 540

ttagtacacg atccactggg tccgccaggc gcccgccag cggctggagt ggatcggcgg 600

gatcaacca aacaacggaa tccaaatta caatcagaaa tttaaaggc ggggtgactat 660

caccgtgat acctcgcct ccacggcgta catggagctc tcactactca gatcggagga 720

caccgcgtc tattactgcg cccgccgccg gatcgcttat ggatacgtg aaggacatgc 780

gatggattac tggggccagg gcaccctcgt cacggtgtcg tcaggaggcg gcggttcaca 840

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 cattataagc tgcaataaac aagttaacaa caacaattgc attcatttta tgttcaggt 1800
 tcagggggag gtgtgggagg tttttaag caagtaaac ctctacaaat gtggtagtcg 1860
 tcagctat 1868

<210> 49

<211> 1878

<212> DNA

<213> Artificial Sequence

<220>

<223> NG-613 Transgene cassette

<400> 49

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ctaccggagt ccattcggac atcgtcatga cccaaagccc tgactcgctc gctgtgtcac 120

tgggagagcg ggcgactatc aactgcaa at catcccagag cctgctgtat tcacgcaatc 180
 agaaaaacta cctggcctgg tatcagcaga agccgggccca gcctccaag ctgctgatct 240
 tctgggcctc caccgcgaa agcggcgctgc cggaccgctt cagcggaagc ggattcggaa 300
 ctgactttac tctgaccatt agctccttgc aggcggagga cgtggccgtc tactactgcc 360
 agcagtattt ctctatccg ctacaccttg ggcaaggcac caaggtggag attaagggag 420
 ggggcggcag cggggggaggc ggcagcggcg gcgggggatc gcaggtccag ctgtccaat 480
 ccggagccga agtcaagaag ccgggagcgt cggtaagggt cagctgcaa acttcgcgt 540
 acaccttac tgagtacacg atccactggg tccgccaggc gcccgccag cggctggagt 600
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 gggtgactat caccgtggat acctcggcct ccacggcgta catggagctc tcactactca 720
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 ccacaactag aatgcagtga aaaaaatgct ttatttga aatttggat gctattgctt 1740
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 tgtttcaggt tcagggggag gtgtgggagg tttttaag caagtaaac ctctacaaat 1860
 gtggtagtcg tcagctat 1878

<210> 50
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Restriction site insert (Bx)

<400> 50
 gcggccgcta tggccggcc 19

<210> 51
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Restriction site insert (By)

<400> 51
 gcgatcgcta ccctgcagg 19

<210> 52
 <211> 572
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> CMV promoter sequence

<400> 52
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ttacggtaaa tggcccgct ggctgaccgc ccaacgaccc ccgcccattg acgtcaataa 120
 tgacgtatgt tcccatagta acgccaatag ggactttcca ttgacgtcaa tgggtggagt 180
 atttacggta aactgccac ttggcagtac atcaagtga tcatatgcca agtaccccc 240
 ctattgacgt caatgacggt aaatggcccg cctggcatta tgcccagtac atgaccttat 300
 gggactttcc tacttggcag tacatctacg tattagtcac cgctattacc atgctgatgc 360
 ggttttggca gtacatcaat gggcgtggat agcggtttga ctcacgggga ttccaagtc 420
 tccaccccat tgacgtcaat gggagtttgt ttggcacca aaatcaacgg gactttcaa 480
 aatgtcgtaa caactccgcc ccattgacgc aaatgggcgg taggcgtgta cgggtggagg 540
 tctatataag cagagctggt ttagtgaacc gt 572

<210> 53

<211> 505

<212> DNA

<213> Artificial Sequence

<220>

<223> PGK promoter sequence

<400> 53

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 taggcgcaa ccggctccgt tcttgggtgg ccccttcgcg ccacattcta ccctcccct 180
 agtcaggaag ttccccccg cccgcagct cgcgtcatgc aggacgtgac aaatggaagt 240
 agcacgtctc actagtctcg tgcaaatgga cagcacgct gagcaatgga agcgggtagg 300
 cccttggggc agcggccaat agcagctttg ctcttcgct ttctgggctc agaggctggg 360
 aaggggtggg tccgggggcg ggctcagggg cgggctcagg ggcggggcgg gcgcccgaag 420
 gtctccgga ggcccggcat tccgcagct tcaaaagcgc acgtctgccg cgctgttctc 480
 ttcttctca tctccgggcc ttctg 505

<210> 54
<211> 367
<212> DNA
<213> Artificial Sequence

<220>
<223> CBA promoter sequence

<400> 54
gtcgaggtga gccccacgtt ctgcttact ctcccatct cccccctc cccacccca 60

at ttgtatt tttttttt ttaattatt tatgcagcga tgggggcggg gggggggggg 120

gcgcgcgcca ggcggggcgg ggcggggcga ggggcggggc ggggcgaggc ggagaggtgc 180

ggcggcagcc aatcagagcg gcgcgctccg aaagtcttct tttatggcga ggcggcggcg 240

gcggcgggcc tataaaaagc gaagcgcgcg gcggcgggga gtcgctcgt tgccttcgcc 300

ccgtgccccg ctccgcgcg cctcgcgcg cccgccccgg ctctgactga ccgcttact 360

cccacag 367

<210> 55

<400> 55
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<210> 56
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> splice acceptor (SA) DNA sequence

<400> 56
ccttctctc ttcagg 16

<210> 57
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> branched splice acceptor (bSA) DNA sequence

<400> 57

tgctaatacct ttctctcttc agg

23

<210> 58

<400> 58

000

<210> 59

<211> 13

<212> RNA

<213> Artificial Sequence

<220>

<223> Example of start codon

<220>

<221> misc_feature

<222> (11)..(11)

<223> R is adenine or guanine

<400> 59

gccgccrcca ugg

13

<210> 60

<211> 551

<212> DNA

<213> Artificial Sequence

<220>

<223> Internal Ribosome Entry Sequence (IRES)

<400> 60

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gagcattcct aggggtcttt ccctctcgc caaaggaatg caaggtctgt tgaatgtcgt 180

gaaggaagca gttcctctgg aagcttcttg aagacaaaca acgtctgtag cgaccctttg 240

caggcagcgg aacccccac ctggcgacag gtgcctctgc ggccaaaagc cacgtgtata 300

agatacacct gcaaaggcgg cacaacccca gtgccacgtt gtgagttgga tagttgtgga 360

aagagtcaaa tggctcccct caagcgtatt caacaagggg ctgaaggatg cccagaaggt 420

acccattgt atgggatctg atctggggcc tcggtgcaca tgctttcat gtgttagtc 480

gaggtaaaa aacgtctagg cccccgaac cacggggacg tggtttcct ttgaaaaaca 540

cgatgataat a 551

<210> 61

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<223> P2A peptide

<400> 61

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

1 5 10 15

Glu Glu Asn Pro Gly Pro

20

<210> 62

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> F2A peptide

<400> 62

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

1 5 10 15

Glu Asn Pro Gly Pro

20

<210> 63

<211> 23

<212> PRT
<213> Artificial Sequence

<220>
<223> E2A peptide

<400> 63

Gly Ser Gly Gln Cys Thr Asn Tyr Ala Leu Leu Lys Leu Ala Gly Asp
1 5 10 15

Val Glu Ser Asn Pro Gly Pro
20

<210> 64
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> T2A peptide

<400> 64

Gly Ser Gly Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala
1 5 10 15

Gly Asp Val Glu Ser Asn Pro Gly Pro
20 25

<210> 65
<211> 192
<212> DNA
<213> Artificial Sequence

<220>
<223> polyadenylation (polyA) sequence

<400> 65
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aatgctttat ttgtgaaatt tgtgatgcta ttgctttatt tgtaaccatt ataagctgca 120

ataaacaagt taacaacaac aattgcattc attttatggt tcagggtcag ggggaggtgt 180

gggaggtttt tt

192

<210> 66

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Leader sequence

<400> 66

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

Val His Ser

<210> 67

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Leader sequence

<400> 67

Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala Val Ala Pro Gly
1 5 10 15

Ala His Ser

<210> 68

<211> 166

<212> PRT

<213> Artificial Sequence

<220>

<223> IFN gamma amino acid sequence

<400> 68

Met Lys Tyr Thr Ser Tyr Ile Leu Ala Phe Gln Leu Cys Ile Val Leu
1 5 10 15

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

Asn Leu Lys Lys Tyr Phe Asn Ala Gly His Ser Asp Val Ala Asp Asn
 35 40 45

Gly Thr Leu Phe Leu Gly Ile Leu Lys Asn Trp Lys Glu Glu Ser Asp
 50 55 60

Arg Lys Ile Met Gln Ser Gln Ile Val Ser Phe Tyr Phe Lys Leu Phe
65 70 75 80

Lys Asn Phe Lys Asp Asp Gln Ser Ile Gln Lys Ser Val Glu Thr Ile
 85 90 95

Lys Glu Asp Met Asn Val Lys Phe Phe Asn Ser Asn Lys Lys Lys Arg
 100 105 110

Asp Asp Phe Glu Lys Leu Thr Asn Tyr Ser Val Thr Asp Leu Asn Val
 115 120 125

Gln Arg Lys Ala Ile His Glu Leu Ile Gln Val Met Ala Glu Leu Ser
 130 135 140

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

Gly Arg Arg Ala Ser Gln
 165

<210> 69

<211> 188

<212> PRT

<213> Artificial Sequence

<220>

<223> IFN alpha amino acid sequence

<400> 69

Met Ala Leu Thr Phe Ala Leu Leu Val Ala Leu Leu Val Leu Ser Cys
1 5 10 15

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

Gly Ser Arg Arg Thr Leu Met Leu Leu Ala Gln Met Arg Arg Ile Ser
35 40 45

Leu Phe Ser Cys Leu Lys Asp Arg His Asp Phe Gly Phe Pro Gln Glu
50 55 60

Glu Phe Gly Asn Gln Phe Gln Lys Ala Glu Thr Ile Pro Val Leu His
65 70 75 80

Glu Met Ile Gln Gln Ile Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser
85 90 95

Ala Ala Trp Asp Glu Thr Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr
100 105 110

Gln Gln Leu Asn Asp Leu Glu Ala Cys Val Ile Gln Gly Val Gly Val
115 120 125

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

Tyr Phe Gln Arg Ile Thr Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro
145 150 155 160

Cys Ala Trp Glu Val Val Arg Ala Glu Ile Met Arg Ser Phe Ser Leu
165 170 175

Ser Thr Asn Leu Gln Glu Ser Leu Arg Ser Lys Glu
180 185

<210> 70

<211> 233

<212> PRT

<213> Artificial Sequence

<220>

<223> TNF alpha amino acid sequence

<400> 70

Met Ser Thr Glu Ser Met Ile Arg Asp Val Glu Leu Ala Glu Glu Ala
1 5 10 15

Leu Pro Lys Lys Thr Gly Gly Pro Gln Gly Ser Arg Arg Cys Leu Phe
20 25 30

Leu Ser Leu Phe Ser Phe Leu Ile Val Ala Gly Ala Thr Thr Leu Phe
35 40 45

Cys Leu Leu His Phe Gly Val Ile Gly Pro Gln Arg Glu Glu Phe Pro
50 55 60

Arg Asp Leu Ser Leu Ile Ser Pro Leu Ala Gln Ala Val Arg Ser Ser
65 70 75 80

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

Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu
100 105 110

Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser
115 120 125

Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly
130 135 140

Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala
145 150 155 160

Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro
165 170 175

Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu
180 185 190

Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu
195 200 205

Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly
210 215 220

Gln Val Tyr Phe Gly Ile Ile Ala Leu
225 230

<210> 71

<211> 5288

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA sequence corresponding to E2B region of the EnAd genome (bp
10355-5068)

<400> 71

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tcgagtcagg gttgtttccg tcacagtga ggggtgtgcg cctgcttggg cgcttgccag 180

ggtgcgcttc agactcatcc tgctggtcga aaacttctgt cgcttggcgc cctgtatgtc 240

ggccaagtag cagtttacca tgagttcgta gttgagcgcc tcggctgcgt ggcctttggc 300
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 caacttgggc gcaaggaaaa cggattctgg ggagtatgca tctgcgccgc aggaggcgca 420
 aacagtttca cattccacca gccaggttaa atccggttca ttgggggtcaa aaacaagttt 480
 tccgcatat tttttagtc gtttcttacc ttggtctcc atgagttcgt gtcctcgttg 540
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 agtgctcgg tcttctcgt acaggaactc tgaccactct gatacaaagg cgcgcgtcca 660
 ggccagcaca aaggaggcta tgtgggaggg gtagcgatcg ttgtcaacca ggggggtccac 720
 cttttcaaa gtagcaaac acatgtcacc ctctcaaca tccaggaatg tgattggctt 780
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 taaaagttg gcaatggatc gcatggttg gttctttcc ttgtccgcgc gctctttggc 1140
 ggcgatgttg agttggacat actcgcgtgc caggcacttc cattcgggga agatagttgt 1200
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gatctgatcg tgtcaagatc cacgggatct gaaaacctt cgacgaaagc gtctaaccag 4500
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 gtgtcaaaga tgtaatcgtt gcagggtgac accagatact ggtaccctat aaaaaatgc 5100
 ggcggtggtt ggcggtagag aggccatcgt tctgtagctg gagcgccagg ggcgaggtct 5160
 tccaacataa ggcggtgata gccgtagatg tacctggaca tccaggtgat tctgcggcg 5220
 gtagtagaag cccgaggaaa ctgcgtacg cggttcaaaa tgttcgtag cggcatgaag 5280
 tagttcat 5288

<210> 72

<211> 1548

<212> DNA

<213> Artificial Sequence

<220>

<223> Anti-EpCAM BiTE DNA coding sequence, with N-terminal signal sequence and C-terminal deca-His affinity tag

<400> 72

atgggatgga gctgcatcat cctattcctc gtggcgacgg ccaactggagt gcatagcgaa 60
 ctggtgatga ctcagtcctc gtcacccctg acggtgaccg ccggcgagaa ggtcacatg 120
 tcgtgcaagt cctcgcaaag cctgcttaac agcggcaacc agaaaaacta cctcacgtgg 180
 tatcagcaaa agccagggtca acccccaaaa ctgctcatct actgggagag caccgcgag 240
 tcgggggtgc cagaccggtt caccggctcc gggtcaggaa ctgatttcac ctaaccatc 300
 agctcgggtc aagcggagga cctggccgtg tactactgcc aaaatgatta ctcgtaccct 360

ctgacctttg gagcgggcac caagctcgaa atcaagggcg gtggaggaag cggcggggga 420
 ggctcaggtg ggggaggatc agaagtcaa ctgctggagc agtcaggagc cgaactggtc 480
 cgcccgggaa cctccgtcaa gatttcctgt aaggcttccg gctacgcttt taccaattac 540
 tggctgggct gggtaagca aagaccgggg catggcctgg agtggatcgg cgacatcttc 600
 ccaggagcgc gcaacatcca ctacaacgag aagtcaagg ggaaagcgac tctgactgcc 660
 gacaaatcat ccagcaccgc ctacatgcag ctgtcgtcgc tcactttcga agacagcgcg 720
 gtgtactttt gtgctcggct ccggaactgg gatgaacaa tggactactg gggacaagga 780
 actaccgtga ccgtctctc cggcggcggg ggaagcgatg tgcaactcgt gcagtccggt 840
 gcggaagtga aaaagccggg cgcgagcgtc aaagtgtcat gcaaggcgtc aggatatacg 900
 tttagtagat acactatgca ctgggtcgc caggcacctg gtcagggcct tgaatggatc 960
 ggctacatca atccgtcgag aggctacact aattacgcgg actcagtcaa agggcgcttc 1020
 acgattacga ccgacaagtc cacctcgact gcatacatgg aactgtcctc gctgagaagc 1080
 gaggacaccg ctacttacta ctgcgctaga tactacgatg atcactactg cctcgattac 1140
 tggggccagg gaaccactgt cacggtgtca tcgggagagg gcacctcaac cggatcaggg 1200
 ggatcgggag gctcgggcgg cgcagacgac atcgtcctga cccagtcgcc cgccaccttg 1260
 tcgctgtccc caggagaaag agcgaccctg tcatgccggg cgtcgcaaag cgtgagctat 1320
 atgaattggt atcagcagaa gccaggaaag gcgccgaaga gatggatcta cgacacctcc 1380
 aaggtcgctt caggtgtccc ggctagattc tcaggatcgg gatcaggaac ggactactcc 1440
 ctgaccatca attcactgga agcagaagat gcggccacct actactgtca gcagtgttcc 1500
 tccaacccgc tgactttcgg aggcggaact aaggtcgaga tcaagtag 1548

<210> 73

<211> 515

<212> PRT

<213> Artificial Sequence

<220>

<223> Anti-EpCAM BiTE protein sequence, with N-terminal signal sequence
without C-terminal deca-His affinity tag

<400> 73

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

Val His Ser Glu Leu Val Met Thr Gln Ser Pro Ser Ser Leu Thr Val
20 25 30

Thr Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu
35 40 45

Leu Asn Ser Gly Asn Gln Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys
50 55 60

Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu
65 70 75 80

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

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

Cys Gln Asn Asp Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys
115 120 125

Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
130 135 140

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

Arg Pro Gly Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala
165 170 175

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

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

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

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

Val Tyr Phe Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr
245 250 255

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

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

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

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
305 310 315 320

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

Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
340 345 350

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

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

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

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

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
420 425 430

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
435 440 445

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

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

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
485 490 495

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
500 505 510

Glu Ile Lys
515

<210> 74

<211> 1560

<212> DNA

<213> Artificial Sequence

<220>

<223> Anti-FAP BiTE DNA coding sequence, with N-terminal signal

sequence without C-terminal deca-His affinity tag

<400> 74

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atgggctgga gctgcatcat ctgttctg gtcgcaactg ctaccggagt ccattcggac    60
atcgtcatga cccaaagccc tgactgctc gctgtgtcac tgggagagcg ggcgactatc    120
aactgcaaat catccagag cctgtgtat tcacgcaatc agaaaaacta cctggcctgg    180
tatcagcaga agccgggcca gcctccaag ctgctgatct tctgggcctc caccgcgaa    240
agcggcgtgc cggaccgctt cagcgggaagc ggattcggaa ctgactttac tctgaccatt    300
agctccttgc aggcggagga cgtggccgtc tactactgcc agcagtattt ctctatccg    360
ctcacctttg ggcaaggcac caaggtggag attaaggagc ggggcggcag cgggggaggc    420
ggcagcggcg gcgggggata gcaggtccag ctgtccaat ccggagccga agtcaagaag    480
ccgggagcgt cggtaaggt cagctgcaaa acttcgcgt acacctcac tgagtacacg    540
atccactggg tccgccaggc gcccgccag cggctggagt ggatcggcgg gatcaacca    600
aacaacggaa tccaaatta caatcagaaa tttaaaggc ggggtgactat caccgtggat    660
acctggcct ccacggcgta catggagctc tcactactca gatcggagga caccgcggtc    720
tattactgcg cccgcccg gatcgcttat ggatacatg aaggacatgc gatggattac    780
tggggccagg gcaccctcgt cacggtgtcg tcaggaggcg gcggttcaga tgtgcaactc    840
gtgcagtccg gtgcggaagt gaaaaagccg ggcgcgagcg tcaaagtgtc atgcaaggcg    900
tcaggatata cgtttactag atacactatg cactgggtgc gccaggcacc tggtcagggc    960
cttgaatgga tcggctacat caatccgtcg agaggctaca ctaattacgc ggactcagtc   1020
aaagggcgct tcacgattac gaccgacaag tccacctga ctgcatacat ggaactgtcc   1080
tcgctgagaa gcgaggacac cgctacttac tactgcgcta gatactacga tgatcactac   1140
tgcctcgatt actggggcca gggaaccact gtcacggtgt catcgggaga gggcacctca   1200
accggatcag ggggatcggg aggctcgggc ggcgcagacg acatcgtcct gaccagtcg    1260
cccgccacct tgcgtgtgc ccaggagaa agagcgaccc tgtcatgccg ggcgtcgaa    1320
agcgtgagct atatgaattg gtatcagcag aagccaggaa aggcgccgaa gagatggatc   1380
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tacgacacct ccaaggtcgc ttcaggtgtc ccggctagat tctcaggatc gggatcagga 1440

acggactact ccctgaccat caattcactg gaagcagaag atgcggccac ctactactgt 1500

cagcagtggc cctccaaccc gctgactttc ggaggcggaa ctaaggtcga gatcaagtag 1560

<210> 75

<211> 519

<212> PRT

<213> Artificial Sequence

<220>

<223> Anti-FAP BiTE amino acid sequence, with N-terminal signal
sequence without C-terminal deca-His affinity tag

<400> 75

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

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

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

Leu Tyr Ser Arg Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys
50 55 60

Pro Gly Gln Pro Pro Lys Leu Leu Ile Phe Trp Ala Ser Thr Arg Glu
65 70 75 80

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

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

Cys Gln Gln Tyr Phe Ser Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys

115

120

125

Val Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
130 135 140

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

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

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

Glu Trp Ile Gly Gly Ile Asn Pro Asn Asn Gly Ile Pro Asn Tyr Asn
195 200 205

Gln Lys Phe Lys Gly Arg Val Thr Ile Thr Val Asp Thr Ser Ala Ser
210 215 220

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

Tyr Tyr Cys Ala Arg Arg Arg Ile Ala Tyr Gly Tyr Asp Glu Gly His
245 250 255

Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
260 265 270

Gly Gly Gly Ser Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys
275 280 285

Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr
290 295 300

Phe Thr Arg Tyr Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly

305 310 315 320

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

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr
 340 345 350

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

Thr Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr
 370 375 380

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

Thr Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val
 405 410 415

Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
 420 425 430

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

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

Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
465 470 475 480

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

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

500

505

510

Gly Thr Lys Val Glu Ile Lys
515

<210> 76

<211> 1599

<212> DNA

<213> Artificial Sequence

<220>

<223> Control (Anti-FHA) BiTE DNA coding sequence, with N-terminal
signal sequence without C-terminal deca-His affinity tag

<400> 76

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ctggacatcg tgatgacca ggcacgtgca tctctggcag tgagcctggg acagagagcc    120
accatttcat gccgggccag caagagcgtg tcgtcatccg gatacaatta tctgcactgg    180
tatcagcaga aaccaggaca acctccaaag ctactcatct acctggcgtc gaacctcgaa    240
tcgggcgtcc cagctagatt ctcaggagc ggttcgggaa ccgatttcac cctgaacatc    300
caccctgtgg aggaggaaga cgcggcaacg tactattgcc agcattcccg cgagttccct    360
ctcactttcg gtgcgggaac taagctggag atcaagtcca gcggcggcgg aggtagcggg    420
ggaggtggcg gaggaagctc ccggtcgtcg ctggaggtgc agctgcaaca atccggcccc    480
gaactgtgta agccaggcgc atccgtcaag atttcatgca agacctcggg gtacaccttc    540
accgggtaca cgatgcattg ggtcaggcag agccacggca agtccctgga atggatcgga    600
ggaatcaacc ccaaaaacgg cggcatcatc tacaacaaa agttccaggg aaaagccact    660
ctgaccgtgg acaagtcgtc gagcacggcc agcatggagc tgcggtccct cacttccgac    720
gactcagccg tgtattactg cgcgagacgg gtctacgatg actaccata ctactacgct    780
atggactact ggggacaagg aaccagcgtg accgtctcat cggcgaaaac tactccgccg    840
tcggtgacgt cgggaggtgg tggaagcgac gtgcagctcg tccagtcggg tgccgaggtg    900
aagaagccag gagcctccgt gaaggtctcg tgcaaagcca gcggctacac ttctactagg    960

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 aatccgtcgc ggggatacac taattacgcg gactccgtca agggacgggt tactatcact 1080
 acggataagt ccactagcac cgcctacatg gaactgtcct cgctcggtc ggaagacact 1140
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 ggactacagg tcaccgtctc gtcgggagaa ggaacctcaa ctggatcggg cggatcggga 1260
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 tatcaacaaa aacccggcaa ggccccgaaa cgctggatct acgatacttc aaaggtggcc 1440
 agcgggtgtc ctgcccgtt ctccgggtcg gggccggca ccgattactc gttgactatc 1500
 aatagcctgg aggccgagga cgctgcaact tactactgcc agcagtggtc ctccaaccct 1560
 ctcaccttcg gaggcgggac caaggtggaa atcaaatag 1599

<210> 77

<211> 532

<212> PRT

<213> Artificial Sequence

<220>

<223> Control (Anti-FHA) BiTE amino acid sequence with N-terminal
 signal sequence without C-terminal deca-His tag

<400> 77

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

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

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

Ser Val Ser Ser Ser Gly Tyr Asn Tyr Leu His Trp Tyr Gln Gln Lys

50 55 60

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

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

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

Cys Gln His Ser Arg Glu Phe Pro Leu Thr Phe Gly Ala Gly Thr Lys
115 120 125

Leu Glu Ile Lys Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Gly
130 135 140

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

Glu Leu Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Thr Ser
165 170 175

Gly Tyr Thr Phe Thr Gly Tyr Thr Met His Trp Val Arg Gln Ser His
180 185 190

Gly Lys Ser Leu Glu Trp Ile Gly Gly Ile Asn Pro Lys Asn Gly Gly
195 200 205

Ile Ile Tyr Asn Gln Lys Phe Gln Gly Lys Ala Thr Leu Thr Val Asp
210 215 220

Lys Ser Ser Ser Thr Ala Ser Met Glu Leu Arg Ser Leu Thr Ser Asp
225 230 235 240

Asp Ser Ala Val Tyr Tyr Cys Ala Arg Arg Val Tyr Asp Asp Tyr Pro

245 250 255

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

Ser Ser Ala Lys Thr Thr Pro Pro Ser Val Thr Ser Gly Gly Gly Gly
275 280 285

Ser Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly
290 295 300

Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg
305 310 315 320

Tyr Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp
325 330 335

Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser
340 345 350

Val Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala
355 360 365

Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr
370 375 380

Cys Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln
385 390 395 400

Gly Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser
405 410 415

Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln
420 425 430

Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser

435 440 445

Cys Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys
450 455 460

Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala
465 470 475 480

Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr
485 490 495

Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr
500 505 510

Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys
515 520 525

Val Glu Ile Lys
530

<210> 78

<211> 532

<212> PRT

<213> Artificial Sequence

<220>

<223> Control BiTe (Anti-FHA) without C-terminal deca-His tag

<400> 78

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

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

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

Ser Val Ser Ser Ser Gly Tyr Asn Tyr Leu His Trp Tyr Gln Gln Lys
50 55 60

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

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

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

Cys Gln His Ser Arg Glu Phe Pro Leu Thr Phe Gly Ala Gly Thr Lys
115 120 125

Leu Glu Ile Lys Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Gly
130 135 140

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

Glu Leu Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Thr Ser
165 170 175

Gly Tyr Thr Phe Thr Gly Tyr Thr Met His Trp Val Arg Gln Ser His
180 185 190

Gly Lys Ser Leu Glu Trp Ile Gly Gly Ile Asn Pro Lys Asn Gly Gly
195 200 205

Ile Ile Tyr Asn Gln Lys Phe Gln Gly Lys Ala Thr Leu Thr Val Asp
210 215 220

Lys Ser Ser Ser Thr Ala Ser Met Glu Leu Arg Ser Leu Thr Ser Asp
225 230 235 240

Asp Ser Ala Val Tyr Tyr Cys Ala Arg Arg Val Tyr Asp Asp Tyr Pro
245 250 255

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

Ser Ser Ala Lys Thr Thr Pro Pro Ser Val Thr Ser Gly Gly Gly Gly
275 280 285

Ser Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly
290 295 300

Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg
305 310 315 320

Tyr Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp
325 330 335

Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser
340 345 350

Val Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala
355 360 365

Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr
370 375 380

Cys Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln
385 390 395 400

Gly Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser
405 410 415

Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln
420 425 430

Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser
435 440 445

Cys Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys
450 455 460

Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala
465 470 475 480

Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr
485 490 495

Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr
500 505 510

Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys
515 520 525

Val Glu Ile Lys
530

<210> 79

<400> 79
000

<210> 80

<400> 80
000

<210> 81

<400> 81
000

<210> 82

<400> 82
000

<210> 83
<211> 1539
<212> DNA
<213> Artificial Sequence

<220>
<223> EpCam BiTE nucleic acid sequence (OKT3)

<400> 83
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tcgtgcaagt cctcgcaaag cctgcttaac agcggcaacc agaaaaacta cctcacgtgg 180
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tcgggggtgc cagaccggtt caccggctcc gggtcaggaa ctgatttcac cctaaccatc 300
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ctgaccttg gagcgggcac caagctcgaa atcaaggcg gtggaggaag cggcggggga 420
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tggctgggct gggtaagca aagaccggg catggcctgg agtggatcg cgacatcttc 600
ccaggagcg gcaacatcca ctacaacag aagttcaagg ggaaagcgac tctgactgcc 660
gacaaatcat ccagcaccgc ctacatgcag ctgtcgtgc tcacttcga agacagcgcg 720
gtgtacttt gtgctcggct ccggaactgg gatgaacaa tggactactg gggacaagga 780
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 ttcacgttcg gctcggggac aaagttgaa ataaaccgg 1539

<210> 84

<400> 84
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<210> 85

<211> 1551

<212> DNA

<213> Artificial Sequence

<220>

<223> FAP BiTE nucleic acid sequence (OKT3)

<400> 85

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 atcgtcatga ccaaagccc tgactcgtc gctgtgtcac tgggagagcg ggcgactatc 120
 aactgcaaat catccagag cctgtgtat tcacgcaatc agaaaaacta cctggcctgg 180
 tatcagcaga agccgggcca gcctcccaag ctgctgatct tctgggcctc caccgcgaa 240
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 ctcacctttg ggcaaggcac caaggtggag attaaggag ggggcggcag cgggggaggc 420
 ggcagcggcg gcgggggatc gcaggtccag ctctccaat ccggagccga agtcaagaag 480
 ccgggagcgt cggtaaggt cagctgcaaa acttcgcgct acaccttcac tgagtacag 540
 atccactggg tccgccaggc gcccgccag cggctggagt ggatcggcgg gatcaacca 600

aacaacggaa tcccaaatta caatcagaaa tttaaagggc gggtgactat caccgtggat 660
acctcggcct ccacggcgta catggagctc tcactactca gatcggagga caccgcggtc 720
tattactgcg cccgccgccc gatcgcttat ggatacgaag aaggacatgc gatggattac 780
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tctctcaca tcagcggcat ggaggctgaa gatgctgcca cttattactg ccagcagtgg 1500
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<210> 86

<400> 86

000

<210> 87

<211> 1557

<212> DNA

<213> Artificial Sequence

<220>

<223> FAP BiTE nucleic acid sequence (aCD3)

<400> 87

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 aactgcaa at catccagag cctgctgtat tcacgcaatc agaaaaacta cctggcctgg 180
 tatcagcaga agccgggccca gcctcccaag ctgctgatct tctgggcctc caccgcgaa 240
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 ctcacctttg ggcaaggcac caaggtggag attaaggag ggggcggcag cgggggaggc 420
 ggcagcggcg gcgggggatc gcaggtccag ctgtccaat ccggagccga agtcaagaag 480
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 aacaacgaa tcccaaatta caatcagaaa tttaaaggc ggggtgactat caccgtggat 660
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acggactact ccttgaccat caattcactg gaagcagaag atgcggccac ctactactgt 1500

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<210> 88

<211> 1856

<212> DNA

<213> Artificial Sequence

<220>

<223> NG-611 Transgene cassette

<400> 88

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ggtcaccatg tcgtgcaagt cctcgaaag cctgcttaac agcggcaacc agaaaaacta 180

cctcacgtgg tatcagcaaa agccaggtca acccccaaaa ctgctcatct actgggcgag 240

caccgcgag tcgggggtgc cagaccggtt caccggctcc gggtcaggaa ctgattcac 300

cctaaccatc agctcgggtc aagcggagga cctggccgtg tactactgcc aaaatgatta 360

ctcgtaccct ctgaccttg gagcgggcac caagctcgaa atcaaggcg gtggaggaag 420

cggcggggga ggctcagggt ggggaggatc agaagtcaa ctgctggagc agtcaggagc 480

cgaactggc cggcgggaa cctccgtcaa gatttctgt aaggcttcc gctacgctt 540

taccaattac tggctgggt gggtaagca aagaccggg catggcctgg agtggatcgg 600

cgacatctc ccaggagcg gcaacatca ctacaacgag aagttcaagg ggaaagcgac 660

tctgactgcc gacaaatcat ccagaccgc ctacatgcag ctgtcgtcg tcactttcga 720

agacagcgc gtgtacttt gtgctcggt ccggaactgg gatgaacaa tggactactg 780

gggacaagga actaccgtga ccgtctctc cggcggcgt ggaagccagg tgcagctgca 840

gcagtctgg gctgaactgg caagacctgg ggcctcagt aagatgtct gcaaggcttc 900

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 caataaaciaa gtaacaaca acaattgcat tcattttatg tttcaggttc agggggaggt 1800
 gtgggaggtt ttttaaagca agtaaaacct ctacaaatgt ggtagtcgtc agctat 1856

<210> 89

<211> 1868

<212> DNA

<213> Artificial Sequence

<220>

<223> NG-612 Transgene cassette

<400> 89

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ggcgactatc aactgcaaat catccagag cctgctgtat tcacgcaatc agaaaaacta 180

cctggcctgg tatcagcaga agccgggcca gcctccaag ctgctgatct tctgggcctc 240

caccgcgaa agcggcgtgc cggaccgctt cagcggaagc ggattcggaa ctgactttac 300

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cattataagc tgcaataaac aagttaacaa caacaattgc attcatttta tgtttcaggt 1800
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tcagctat 1868

<210> 90

<211> 1878

<212> DNA

<213> Artificial Sequence

<220>

<223> NG-613 Transgene cassette

<400> 90

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 gtggtagtcg tcagctat 1878

<210> 91

<211> 1884

<212> DNA

<213> Artificial Sequence

<220>

<223> NG-614 Transgene cassette

<400> 91

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<210> 92

<211> 1838

<212> DNA

<213> Artificial Sequence

<220>

<223> NG-617 Transgene cassette

<400> 92

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<210> 93

<211> 513

<212> PRT

<213> Artificial Sequence

<220>

<223> EpCam BiTE amino acid sequence (OKT3)

<400> 93

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly

1 5 10 15

Val His Ser Glu Leu Val Met Thr Gln Ser Pro Ser Ser Leu Thr Val
20 25 30

Thr Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu
35 40 45

Leu Asn Ser Gly Asn Gln Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys
50 55 60

Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu
65 70 75 80

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

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

Cys Gln Asn Asp Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys
115 120 125

Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
130 135 140

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

Arg Pro Gly Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala
165 170 175

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

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

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

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

Val Tyr Phe Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr
245 250 255

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

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

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

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

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

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

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

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

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

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

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

Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Ser Gly Thr Ser
435 440 445

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

Ala His Phe Arg Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
465 470 475 480

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

Ser Ser Asn Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Asn
500 505 510

Arg

<210> 94

<211> 517

<212> PRT

<213> Artificial Sequence

<220>

<223> FAP BiTE amino acid sequence (OKT3)

<400> 94

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

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

20 25 30

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

Leu Tyr Ser Arg Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys
50 55 60

Pro Gly Gln Pro Pro Lys Leu Leu Ile Phe Trp Ala Ser Thr Arg Glu
65 70 75 80

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

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

Cys Gln Gln Tyr Phe Ser Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys
115 120 125

Val Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
130 135 140

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

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

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

Glu Trp Ile Gly Gly Ile Asn Pro Asn Asn Gly Ile Pro Asn Tyr Asn
195 200 205

Gln Lys Phe Lys Gly Arg Val Thr Ile Thr Val Asp Thr Ser Ala Ser

210 215 220

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

Tyr Tyr Cys Ala Arg Arg Arg Ile Ala Tyr Gly Tyr Asp Glu Gly His
 245 250 255

Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
 260 265 270

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

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

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

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

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

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

Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr
 370 375 380

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

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

405 410 415

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

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

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

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

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

Cys Gln Gln Trp Ser Ser Asn Pro Phe Thr Phe Gly Ser Gly Thr Lys
500 505 510

Leu Glu Ile Asn Arg
515

<210> 95

<211> 519

<212> PRT

<213> Artificial Sequence

<220>

<223> FAP BiTE amino acid sequence (aCD3)

<400> 95

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

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

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

Leu Tyr Ser Arg Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys
50 55 60

Pro Gly Gln Pro Pro Lys Leu Leu Ile Phe Trp Ala Ser Thr Arg Glu
65 70 75 80

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

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

Cys Gln Gln Tyr Phe Ser Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys
115 120 125

Val Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
130 135 140

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

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

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

Glu Trp Ile Gly Gly Ile Asn Pro Asn Asn Gly Ile Pro Asn Tyr Asn
195 200 205

Gln Lys Phe Lys Gly Arg Val Thr Ile Thr Val Asp Thr Ser Ala Ser
210 215 220

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

Tyr Tyr Cys Ala Arg Arg Arg Ile Ala Tyr Gly Tyr Asp Glu Gly His
 245 250 255

Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
 260 265 270

Gly Gly Gly Ser Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys
 275 280 285

Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr
 290 295 300

Phe Thr Arg Tyr Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly
305 310 315 320

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

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr
 340 345 350

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

Thr Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr
 370 375 380

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

Thr Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val
 405 410 415

Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
420 425 430

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

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

Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
465 470 475 480

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

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

Gly Thr Lys Val Glu Ile Lys
515

<210> 96

<400> 96
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<210> 97

<400> 97
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<210> 98

<400> 98
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<210> 99

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<210> 102

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<210> 103

<400> 103
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<210> 104

<400> 104
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<210> 105

<211> 537

<212> DNA

<213> Artificial Sequence

<220>

<223> Flt3L nucleic acid sequence

<400> 105

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agctcgggac tcagtgggac ccaggactgc tcctccaac acagcccat ctctccgac 120

ttcgctgtca aaatccgtga gctgtctgac tacctgcttc aagattacc agtcaccgtg 180

gcctccaacc tccaggacga ggagctctgc gggggcctct ggcggtggt cctggcacag 240

cgctggatgg agcggctcaa gactgtcgct gggccaaga tgcaaggctt gctggagcgc 300

gtgaacacgg agatacactt tgtcacaaa tgtgccttc agccccccc cagctgtctt 360

cgcttcgtcc agaccaacat ctccgcctc ctacaggaga cctccgagca gctggaggcg 420

ctgaagccct ggatcactcg ccagaacttc tcccgggtgcc tggagctgca gtgtcagccc 480

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<210> 106

<400> 106

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<210> 107

<211> 279

<212> DNA

<213> Artificial Sequence

<220>

<223> MIP1 alpha nucleic acid sequence

<400> 107

atgcaggctc cactgctgc cctgccgtc ctctctgca ccatggctct ctgcaaccag 60

gtcctctctg caccactgc tgctgacacg cgcaccgcct gctgctcag ctacacctcc 120

cgacagattc cacagaattt catagctgac tactttgaga cgagcagcca gtgtccaag 180

cccagtgtca tcttctaac caagagaggc cggcaggctc gtgctgaccc cagtgaggag 240

tgggtccaga aatacgtcag tgacctggag ctgagtgcc 279

<210> 108

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Flexible linker sequence

<400> 108

Ser Pro Gln Tyr Pro Ser Pro Leu Thr Leu Thr Leu Pro Pro His Pro

1 5 10 15

Ser Leu

<210> 109
<211> 564
<212> DNA
<213> Artificial Sequence

<220>
<223> IFN alpha nucleic acid sequence

<400> 109
atggccttga cctttgctt actggtggcc ctctggtgc tcagctgcaa gtcaagctgc 60
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ctggcacaga tgaggagaat ctctctttc tcctgcttga aggacagaca tgactttgga 180
ttccccagg aggagtttgg caaccagttc caaaaggctg aaaccatccc tgcctccat 240
gagatgatcc agcagatctt caatctctc agcaciaagg actcatctgc tgcttgggat 300
gagaccctcc tagacaaatt ctactgaa ctctaccagc agctgaatga cctggaagcc 360
tgtgtgatac aggggggtggg ggtgacagag actccctga tgaaggagga ctccattctg 420
gctgtgagga aatacttcca aagaatcact ctctatctga aagagaagaa atacagcct 480
tgtgcctggg aggttgtcag agcagaaatc atgagatctt tttcttgtc acaaacttg 540
caagaaagt taagaagta ggaa 564

<210> 110
<211> 294
<212> DNA
<213> Artificial Sequence

<220>
<223> CXCL10 nucleic acid sequence

<400> 110
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aatccaaggt cttagaaaa acttgaaatt attcctgcaa gccaatattg tccacgtgtt 180
gagatcattg ctacaatgaa aaagaagggt gagaagagat gtctgaatcc agaatcgaag 240

gccatcaaga atttactgaa agcagttagc aaggaaaggt ctaaaagatc tcct 294

<210> 111

<211> 372

<212> DNA

<213> Artificial Sequence

<220>

<223> CXCL9 nucleic acid sequence

<400> 111

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cacctacaat ccttgaaaga ccttaacaa ttgccccaa gcccttcctg cgagaaaatt 180

gaaatcattg ctacactgaa gaatggagtt caaacatgtc taaaccaga ttcagcagat 240

gtgaaggaac tgattaaaaa gtgggagaaa caggtcagcc aaaagaaaaa gcaaaagaat 300

gggaaaaaac atcaaaaaaa gaaagtctg aaagttcgaa aatctcaacg ttctcgtaa 360

aagaagacta ca 372

<210> 112

<211> 3407

<212> DNA

<213> Artificial Sequence

<220>

<223> NG-615 Transgene cassette

<400> 112

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ccattcggac atcgatga ccaaagccc tgactcgctc gctgtgtcac tgggagagcg 120

ggcgactatc aactgcaaat catccagag cctgctgtat tcacgcaatc agaaaaacta 180

cctggcctgg tatcagcaga agccgggccca gcctccaag ctgctgatct tctgggcctc 240

caccgcgaa agcggcgtgc cggaccgctt cagcggaagc ggattcggaa ctgactttac 300

tctgaccatt agtccttgc aggcggagga cgtggccgtc tactactgcc agcagtattt 360

ctctatccg ctacaccttg ggcaaggcac caagtgagag attaaggag ggggcggcag 420
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<212> DNA
<213> Artificial Sequence

<220>
<223> NG-640 Transgene cassette

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<211> 3260

<212> DNA

<213> Artificial Sequence

<220>

<223> NG-641 Transgene cassette

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<211> 154

<212> PRT

<213> Artificial Sequence

<220>

<223> FLT3L amino acid sequence

<400> 115

Met Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe

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Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro

20 25 30

Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly Leu
35 40 45

Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr Val
50 55 60

Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile
65 70 75 80

His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu Arg
85 90 95

Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln
100 105 110

Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg Cys
115 120 125

Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Pro Pro Pro Trp
130 135 140

Ser Pro Arg Pro Leu Glu Ala Thr Ala Pro
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<210> 116

<211> 93

<212> PRT

<213> Artificial Sequence

<220>

<223> MIP1 alpha amino acid sequence

<400> 116

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

Ala Cys Cys Phe Ser Tyr Thr Ser Arg Gln Ile Pro Gln Asn Phe Ile
35 40 45

Ala Asp Tyr Phe Glu Thr Ser Ser Gln Cys Ser Lys Pro Ser Val Ile
50 55 60

Phe Leu Thr Lys Arg Gly Arg Gln Val Cys Ala Asp Pro Ser Glu Glu
65 70 75 80

Trp Val Gln Lys Tyr Val Ser Asp Leu Glu Leu Ser Ala
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<210> 117

<211> 188

<212> PRT

<213> Artificial Sequence

<220>

<223> IFN alpha amino acid sequence

<400> 117

Met Ala Leu Thr Phe Ala Leu Leu Val Ala Leu Leu Val Leu Ser Cys
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Lys Ser Ser Cys Ser Val Gly Cys Asp Leu Pro Gln Thr His Ser Leu
20 25 30

Gly Ser Arg Arg Thr Leu Met Leu Leu Ala Gln Met Arg Arg Ile Ser
35 40 45

Leu Phe Ser Cys Leu Lys Asp Arg His Asp Phe Gly Phe Pro Gln Glu
50 55 60

Glu Phe Gly Asn Gln Phe Gln Lys Ala Glu Thr Ile Pro Val Leu His

65 70 75 80

Glu Met Ile Gln Gln Ile Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser
 85 90 95

Ala Ala Trp Asp Glu Thr Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr
 100 105 110

Gln Gln Leu Asn Asp Leu Glu Ala Cys Val Ile Gln Gly Val Gly Val
 115 120 125

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

Tyr Phe Gln Arg Ile Thr Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro
145 150 155 160

Cys Ala Trp Glu Val Val Arg Ala Glu Ile Met Arg Ser Phe Ser Leu
 165 170 175

Ser Thr Asn Leu Gln Glu Ser Leu Arg Ser Lys Glu
 180 185

<210> 118

<211> 125

<212> PRT

<213> Artificial Sequence

<220>

<223> CXCL9 amino acid sequence

<400> 118

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

Cys Ile Ser Thr Asn Gln Gly Thr Ile His Leu Gln Ser Leu Lys Asp
35 40 45

Leu Lys Gln Phe Ala Pro Ser Pro Ser Cys Glu Lys Ile Glu Ile Ile
50 55 60

Ala Thr Leu Lys Asn Gly Val Gln Thr Cys Leu Asn Pro Asp Ser Ala
65 70 75 80

Asp Val Lys Glu Leu Ile Lys Lys Trp Glu Lys Gln Val Ser Gln Lys
85 90 95

Lys Lys Gln Lys Asn Gly Lys Lys His Gln Lys Lys Lys Val Leu Lys
100 105 110

Val Arg Lys Ser Gln Arg Ser Arg Gln Lys Lys Thr Thr
115 120 125

<210> 119

<211> 98

<212> PRT

<213> Artificial Sequence

<220>

<223> CXCL10 amino acid sequence

<400> 119

Met Asn Gln Thr Ala Ile Leu Ile Cys Cys Leu Ile Phe Leu Thr Leu
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Ser Gly Ile Gln Gly Val Pro Leu Ser Arg Thr Val Arg Cys Thr Cys
20 25 30

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

Glu Ile Ile Pro Ala Ser Gln Phe Cys Pro Arg Val Glu Ile Ile Ala

50 55 60

Thr Met Lys Lys Lys Gly Glu Lys Arg Cys Leu Asn Pro Glu Ser Lys
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Ala Ile Lys Asn Leu Leu Lys Ala Val Ser Lys Glu Arg Ser Lys Arg
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Ser Pro

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<211> 1557

<212> DNA

<213> Artificial Sequence

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<223> NG-618 FAP BiTE nucleic acid sequence

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<213> Artificial Sequence

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<223> NG-618 Transgene cassette

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<223> Ser is optional

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<400> 136

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Asp Leu

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Arg Pro Leu Ser Tyr Arg Pro Pro Phe Pro Phe Gly Phe Pro Ser Val
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Arg Pro Val Ser Pro Phe Thr Phe Pro Arg Leu Ser Asn Ser Trp Leu
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Ser Pro Ala Ala His Phe Pro Arg Ser Ile Pro Arg Pro Gly Pro Ile
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Val Pro Pro Ala Pro Val Val Ser Leu Arg Ser Ala His Ala Arg Pro
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Leu Arg Pro Thr Pro Pro Arg Val Arg Ser Tyr Thr Cys Cys Pro Thr
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Pro

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Pro Asn Val Ala His Val Leu Pro Leu Leu Thr Val Pro Trp Asp Asn
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Leu Arg

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Val Asn Val Ser Val Val Met Ala Glu Val Asp Gly Thr Cys Tyr
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Pro Ala Thr Cys Pro Pro Ser Pro Ala
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Pro Ala Thr Cys Pro Pro Cys Pro Ala
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Pro Ala Thr Cys Pro Pro Cys Pro Ala
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Val Asn Val Ser Val Val Met Ala Glu Val Asp Gly Thr Ser Tyr
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Val Asn Val Ser Val Val Met Ala Glu Val Asp Gly Thr Ser Tyr
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Thr Pro Pro Pro Ser Pro Arg Ser Pro Ala
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