SEQUENCE LISTING

<110> Glaxo Group Limited
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<120> Anti-SAP mab

<130> PB63944 WO

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<151> 2010-03-03

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Thr Tyr Asn Met His
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Tyr Ile Tyr Pro Gly Asp Gly Asn Ala Asn Tyr Asn Gln Gln Phe Lys
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Gly Asp Phe Asp Tyr Asp Gly Gly Tyr Tyr Phe Asp Ser
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Arg Ala Ser Glu Asn Ile Tyr Ser Tyr Leu Ala
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Asn Ala Lys Thr Leu Ala Glu
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Gln His His Tyr Gly Ala Pro Leu Thr
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<400> 7
Gln Ala Ser Leu Gln Gln Ser Gly Thr Glu Leu Val Arg Ser Gly Ala
 1   5   10   15
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Phe Thr Phe Ala Thr Tyr
            20   25   30
Asn Met His Trp Ile Lys Gln Thr Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45
Gly Tyr Ile Tyr Pro Gly Asp Gly Asn Ala Asn Tyr Asn Gln Gln Phe
    50   55   60
Lys Gly Lys Ala Thr Leu Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr
65   70   75   80
Met Gln Ile Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
                85   90   95
Arg Asp Phe Asp Tyr Asp Gly Gly Tyr Tyr Phe Asp Ser Trp Gly Gln
            100   105   110
Gly Thr Thr Leu Thr Val Ser Ser
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cccggacagg gcctggaatg gattgggtat atttatcctg gagatggtaa tgctaactac 180
aatcagcagt tcaagggcaa ggccacattg actgcagaca catcctccaa cacagcctac 240
atgcagatca gcagcctgac atctgaagac tctgcggtct atttctgtgc aagaggggac 300
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<223> SAP-E VL amino acid sequence

<400> 9
Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Val Gly
 1   5   10   15
Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Glu Asn Ile Tyr Ser Tyr
            20   25   30
Leu Ala Trp Tyr Gln Gln Lys Gln Gly Arg Ser Pro Gln Leu Leu Val
        35   40   45
His Asn Ala Lys Thr Leu Ala Glu Gly Val Pro Ser Arg Val Ser Gly
    50   55   60
Ser Gly Ser Gly Thr His Phe Ser Leu Lys Ile Asn Gly Leu Gln Pro
65   70   75   80
Glu Asp Phe Gly Asn Tyr Tyr Cys Gln His His Tyr Gly Ala Pro Leu
                85   90   95
Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
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ggaagatccc ctcagctcct ggtccataat gcaaaaacct tagcagaagg tgtgccatca 180
agggtcagtg gcagtggatc aggcacacac ttttctctga agatcaacgg cctgcagcct 240
gaagattttg ggaattatta ctgtcaacat cattatggtg ctccgctcac gttcggtgct 300
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<400> 11
Ser Tyr Trp Met His
 1   5

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<212> PRT

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<220>
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<400> 12
Met Ile His Pro Asn Ser Val Asn Thr Asn Tyr Asn Glu Lys Phe Lys
 1   5   10   15
Ser

<210> 13
<211> 10
<212> PRT
<213> Mus musculus sequence

<220>
<223> SAP-K CDRH3 amino acid sequence

<400> 13
Arg Asn Asp Tyr Tyr Trp Tyr Phe Asp Val
 1   5   10

<210> 14
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<212> PRT
<213> Mus musculus sequence

<220>
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<400> 14
Lys Ala Ser Gln Asn Val Asn Ser Asn Val Ala
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<220>
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<400> 15
Ser Ala Ser Tyr Arg Tyr Ser
 1   5

<210> 16
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<212> PRT
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<220>
<223> SAP-K CDRL3 amino acid sequence

<400> 16
Gln Gln Cys Asn Asn Tyr Pro Phe Thr
 1   5

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<220>
<223> SAP-K VH amino acid sequence

<400> 17
Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Ile Lys Pro Gly Ala
 1   5   10   15
Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20   25   30
Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45
Gly Met Ile His Pro Asn Ser Val Asn Thr Asn Tyr Asn Glu Lys Phe
    50   55   60
Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65   70   75   80
Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Arg Asn Asp Tyr Tyr Trp Tyr Phe Asp Val Trp Gly Thr Gly
            100   105   110
Thr Thr Val Thr Val Ser Ser
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<212> DNA
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cctggacaag gccttgagtg gattggaatg attcatccta atagtgttaa tactaactac 180
aatgagaagt tcaagagtaa ggccacactg actgtagaca aatcctccag cacagcctac 240
atgcaactca acagcctgac atctgaggac tctgcggtct attactgtgc aagacggaat 300
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<223> SAP-K VL amino acid sequence

<400> 19
Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Ser Val Gly
 1   5   10   15
Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val Asn Ser Asn
            20   25   30
Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Ala Leu Ile
        35   40   45
Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Asp Arg Phe Thr Gly
    50   55   60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Asn Val Gln Ser
65   70   75   80
Glu Asp Leu Ala Glu Tyr Phe Cys Gln Gln Cys Asn Asn Tyr Pro Phe
                85   90   95
Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
            100   105

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gggcaatctc ctaaagcact gatttactcg gcttcctacc ggtacagtgg agtccctgat 180
cgcttcacag gcagtggatc tgggacagat ttcactctca ccatcaccaa tgtgcagtct 240
gaagacttgg cagagtattt ctgtcagcaa tgtaacaact atccattcac gttcggctcg 300
gggacaaagt tggaaataaa a 321

<210> 21
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<223> SAP-E VH chimera amino acid sequence

<400> 21
Gln Ala Ser Leu Gln Gln Ser Gly Thr Glu Leu Val Arg Ser Gly Ala
1 5 10 15
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Phe Thr Phe Ala Thr Tyr
20 25 30
Asn Met His Trp Ile Lys Gln Thr Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45
Gly Tyr Ile Tyr Pro Gly Asp Gly Asn Ala Asn Tyr Asn Gln Gln Phe
50 55 60
Lys Gly Lys Ala Thr Leu Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr
65 70 75 80
Met Gln Ile Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95
Arg Asp Phe Asp Tyr Asp Gly Gly Tyr Tyr Phe Asp Ser Trp Gly Gln
100 105 110
Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125
Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175
Leu Gln Ser Ser Gly Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190
Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205
Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220
His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
225 230 235 240
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
245 250 255
Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
260 265 270
Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
275 280 285
Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Tyr Val Val Ser Val
290 295 300
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305 310 315 320
Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
325 330 335
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
340 345 350
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
355 360 365
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly

370 375 380
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
385 390 395 400
Gly Ser Phe Phe Lys Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
405 410 415
Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
420 425 430
Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440

<210> 22
<211> 214
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<223> SAP-E VL chimera amino acid sequence

<400> 22
Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Glu Asn Ile Tyr Ser Tyr
20 25 30
Leu Ala Trp Tyr Gln Gln Lys Gln Gly Arg Ser Pro Gln Leu Leu Val
35 40 45
His Asn Ala Lys Thr Leu Ala Glu Gly Val Pro Ser Arg Val Ser Gly
50 55 60
Ser Gly Ser Gly Thr His Phe Ser Leu Lys Ile Asn Gly Leu Gln Pro
65 70 75 80
Glu Asp Phe Gly Asn Tyr Tyr Cys Gln His His Tyr Gly Ala Pro Leu
85 90 95
Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Thr Val Ala Ala
100 105 110
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205
Phe Asn Arg Gly Glu Cys
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<210> 23
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<223> SAP-K VH chimera amino acid sequence

<400> 23
Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Ile Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30
Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45
Gly Met Ile His Pro Asn Ser Val Asn Thr Asn Tyr Asn Glu Lys Phe
50 55 60
Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr

65 70 75 80
Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Arg Asn Asp Tyr Tyr Trp Tyr Phe Asp Val Trp Gly Thr Gly
100 105 110
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
130 135 140
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145 150 155 160
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
165 170 175
Gln Ser Ser Gly Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
180 185 190
Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
195 200 205
Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
210 215 220
Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
225 230 235 240
Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
245 250 255
Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
260 265 270
Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
275 280 285
Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Tyr Val Val Ser Val Leu
290 295 300
Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305 310 315 320
Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
325 330 335
Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
340 345 350
Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
355 360 365
Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
370 375 380
Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
385 390 395 400
Ser Phe Phe Lys Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
405 410 415
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
420 425 430
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440

<210> 24
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> SAP-K VL chimera amino acid sequence

<400> 24
Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Ser Val Gly
1 5 10 15
Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val Asn Ser Asn
20 25 30
Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Ala Leu Ile
35 40 45
Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Asp Arg Phe Thr Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Asn Val Gln Ser
65 70 75 80

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Glu Asp Leu Ala Glu Tyr Phe Cys Gln Gln Cys Asn Asn Tyr Pro Phe
                85                  90                  95
Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205
Phe Asn Arg Gly Glu Cys
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<210> 25
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<213> Homo sapiens sequence

<220>
<223> IGHV1-69 human variable heavy chain germline acceptor amino acid sequence

<400> 25

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Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1               5                  10                  15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
            20                  25                  30
Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45
Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60
Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr 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
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<210> 26
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<213> Homo sapiens sequence

<220>
<223> JH1 minigene

<400> 26

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Ala Glu Tyr Phe Gln His Trp Gly Gln Gly Thr Leu Val Thr Val Ser
 1               5                  10                  15
Ser
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<210> 27
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> SAP-E humanised VH variant H0 amino acid sequence

<400> 27
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Thr Tyr
20 25 30
Asn Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Tyr Ile Tyr Pro Gly Asp Gly Asn Ala Asn Tyr Asn Gln Gln Phe
50 55 60
Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr 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
Arg Asp Phe Asp Tyr Asp Gly Gly Tyr Tyr Phe Asp Ser Trp Gly Gln
100 105 110
Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 28
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> SAP-E humanised VH variant H1 amino acid sequence

<400> 28
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe Ala Thr Tyr
20 25 30
Asn Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Tyr Ile Tyr Pro Gly Asp Gly Asn Ala Asn Tyr Asn Gln Gln Phe
50 55 60
Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr 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
Arg Asp Phe Asp Tyr Asp Gly Gly Tyr Tyr Phe Asp Ser Trp Gly Gln
100 105 110
Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 29
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> SAP-E humanised VH variant H2 amino acid sequence

<400> 29
Gln Ala Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe Ala Thr Tyr
20 25 30
Asn Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Tyr Ile Tyr Pro Gly Asp Gly Asn Ala Asn Tyr Asn Gln Gln Phe
50 55 60
Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr 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

Arg Asp Phe Asp Tyr Asp Gly Gly Tyr Tyr Phe Asp Ser Trp Gly Gln
100 105 110
Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 30
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> SAP-E humanised VH variant H3 amino acid sequence

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

<210> 31
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> SAP-E humanised VH variant H4 amino acid sequence

<400> 31
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe Ala Thr Tyr
20 25 30
Asn Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45
Gly Tyr Ile Tyr Pro Gly Asp Gly Asn Ala Asn Tyr Asn Gln Gln Phe
50 55 60
Lys Gly Arg Ala Thr Leu Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe Cys
85 90 95
Arg Asp Phe Asp Tyr Asp Gly Gly Tyr Tyr Phe Asp Ser Trp Gly Gln
100 105 110
Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 32
<211> 95
<212> PRT
<213> Homo sapiens sequence

<220>
<223> IGKV1-39 human variable light chain germline
acceptor amino acid sequence

<400> 32
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
            20   25   30
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro
                85   90   95

<210> 33
<211> 12
<212> PRT
<213> Homo sapiens sequence

<220>
<223> JK2 minigene

<400> 33
Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 1   5   10

<210> 34
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> SAP-E humanised VL variant L0 amino acid sequence

<400> 34
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Asn Ile Tyr Ser Tyr
            20   25   30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45
Tyr Asn Ala Lys Thr Leu Ala Glu Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His His Tyr Gly Ala Pro Leu
                85   90   95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100   105

<210> 35
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> SAP-E humanised VL variant L1 amino acid sequence

<400> 35
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Asn Ile Tyr Ser Tyr
            20   25   30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

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        35                  40                  45
His Asn Ala Lys Thr Leu Ala Glu Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His His Tyr Gly Ala Pro Leu
                85                  90                  95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105
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<210> 36
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> SAP-E humanised VL variant L2 amino acid sequence

<400> 36

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Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1               5                  10                  15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Asn Ile Tyr Ser Tyr
            20                  25                  30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Val
        35                  40                  45
His Asn Ala Lys Thr Leu Ala Glu Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His His Tyr Gly Ala Pro Leu
                85                  90                  95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105
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<210> 37
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> SAP-K humanised VH variant H0 amino acid sequence

<400> 37

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Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1               5                  10                  15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
            20                  25                  30
Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45
Gly Met Ile His Pro Asn Ser Val Asn Thr Asn Tyr Asn Glu Lys Phe
    50                  55                  60
Lys Ser Arg Val Thr Ile Thr Ala Asp Lys Ser Thr 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 Asn Asp Tyr Tyr Trp Tyr Phe Asp Val Trp Gly Gln Gly
            100                 105                 110
Thr Leu Val Thr Val Ser Ser
        115
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<210> 38
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> SAP-K humanised VH variant H1 amino acid sequence

<400> 38
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30
Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Met Ile His Pro Asn Ser Val Asn Thr Asn Tyr Asn Glu Lys Phe
50 55 60
Lys Ser Arg Val Thr Ile Thr Ala Asp Lys Ser Thr 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 Asn Asp Tyr Tyr Trp Tyr Phe Asp Val Trp Gly Gln Gly
100 105 110
Thr Leu Val Thr Val Ser Ser
115

<210> 39
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> SAP-K humanised VH variant H2 amino acid sequence

<400> 39
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30
Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45
Gly Met Ile His Pro Asn Ser Val Asn Thr Asn Tyr Asn Glu Lys Phe
50 55 60
Lys Ser Arg Ala Thr Ile Thr Ala Asp Lys Ser Thr 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 Asn Asp Tyr Tyr Trp Tyr Phe Asp Val Trp Gly Gln Gly
100 105 110
Thr Leu Val Thr Val Ser Ser
115

<210> 40
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> SAP-K humanised VH variant H3 amino acid sequence

<400> 40
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30
Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45
Gly Met Ile His Pro Asn Ser Val Asn Thr Asn Tyr Asn Glu Lys Phe
50 55 60
Lys Ser Arg Ala Thr Leu Thr Val Asp Lys Ser Thr 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 Asn Asp Tyr Tyr Trp Tyr Phe Asp Val Trp Gly Gln Gly
100 105 110
Thr Leu Val Thr Val Ser Ser
115

<210> 41
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> SAP-K humanised VL variant L0 amino acid sequence

<400> 41
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Asn Ser Asn
20 25 30
Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45
Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Cys Asn Asn Tyr Pro Phe
85 90 95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 42
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> SAP-K humanised VL variant L1 amino acid sequence

<400> 42
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Asn Ser Asn
20 25 30
Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile
35 40 45
Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Cys Asn Asn Tyr Pro Phe
85 90 95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 43
<211> 204
<212> PRT
<213> Homo sapiens sequence

<220>
<223> Homo sapiens SAP amino acid sequence

<400> 43
His Thr Asp Leu Ser Gly Lys Val Phe Val Phe Pro Arg Glu Ser Val

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


<210> 44
<211> 203
<212> PRT
<213> Mus musculus sequence

<220>
<223> Mus musculus SAP amino acid sequence

<400> 44
Gln Thr Asp Leu Lys Arg Lys Val Phe Val Phe Pro Arg Glu Ser Glu
 1               5                  10                  15
Thr Asp His Val Lys Leu Ile Pro His Leu Glu Lys Pro Leu Gln Asn
            20                  25                  30
Phe Thr Leu Cys Phe Arg Thr Tyr Ser Asp Leu Ser Arg Ser Gln Ser
        35                  40                  45
Leu Phe Ser Tyr Ser Val Lys Gly Arg Asp Asn Glu Leu Leu Ile Tyr
    50                  55                  60
Lys Glu Lys Val Gly Glu Tyr Ser Leu Tyr Ile Gly Gln Ser Lys Val
65                  70                  75                  80
Thr Val Arg Gly Met Glu Glu Tyr Leu Ser Pro Val His Leu Cys Thr
                85                  90                  95
Thr Trp Glu Ser Ser Ser Gly Ile Val Glu Phe Trp Val Asn Gly Lys
            100                 105                 110
Pro Trp Val Lys Lys Ser Leu Gln Arg Glu Tyr Thr Val Lys Ala Pro
        115                 120                 125
Pro Ser Ile Val Leu Gly Gln Glu Gln Asp Asn Tyr Gly Gly Gly Phe
    130                 135                 140
Gln Arg Ser Gln Ser Phe Val Gly Glu Phe Ser Asp Leu Tyr Met Trp
145                 150                 155                 160
Asp Tyr Val Leu Thr Pro Gln Asp Ile Leu Phe Val Tyr Arg Asp Ser
                165                 170                 175
Pro Val Asn Pro Asn Ile Leu Asn Trp Gln Ala Leu Asn Tyr Glu Ile
            180                 185                 190
Asn Gly Tyr Val Val Ile Arg Pro Arg Val Trp
        195                 200


<210> 45
<211> 1356
<212> DNA
<213> Artificial Sequence
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<220>
<223> SAP-E VH chimera nucleotide sequence

<400> 45
caggcttctc tacagcagtc tgggactgag ctggtgaggt ctggggcctc agtgaagatg 60
tcctgcaagg cttctggctt cacatttgcc acttacaata tgcactggat taagcagaca 120
cccggacagg gcctggaatg gattgggtat atttatcctg gagatggtaa tgctaactac 180
aatcagcagt tcaagggcaa ggccacattg actgcagaca catcctccaa cacagcctac 240
atgcagatca gcagcctgac atctgaagac tctgcggtct atttctgtgc aagaggggac 300
tttgattacg acggagggta ctactttgac tcctggggcc agggcacact agtgaccgtg 360
tccagcgcca gcaccaaggg ccccagcgtg ttccccctgg cccccagcag caagagcacc 420
agcggcggca cagccgccct gggctgcctg gtgaaggact acttccccga accggtgacc 480
gtgtcctgga acagcggagc cctgaccagc ggcgtgcaca ccttccccgc cgtgctgcag 540
agcagcggcc tgtacagcct gagcagcgtg gtgaccgtgc ccagcagcag cctgggcacc 600
cagacctaca tctgtaacgt gaaccacaag cccagcaaca ccaaggtgga caagaaggtg 660
gagcccaaga gctgtgacaa gacccacacc tgccccccct gccctgcccc cgagctgctg 720
ggaggcccca gcgtgttcct gttcccccca aagcctaagg acaccctgat gatcagcaga 780
acccccgagg tgacctgtgt ggtggtggat gtgagccacg aggaccctga ggtgaagttc 840
aactggtacg tggacggcgt ggaggtgcac aatgccaaga ccaagcccag ggaggagcag 900
tacaacagca cctaccgggt ggtgtccgtg ctgaccgtgc tgcaccagga ttggctgaac 960
ggcaaggagt acaagtgtaa ggtgtccaac aaggccctgc ctgccctat cgagaaaacc 1020
atcagcaagg ccaagggcca gcccagagag ccccaggtgt acaccctgcc ccctagcaga 1080
gatgagctga ccaagaacca ggtgtccctg acctgcctgg tgaagggctt ctaccccagc 1140
gacatcgccg tggagtggga gagcaacggc cagcccgaga acaactacaa gaccaccccc 1200
cctgtgctgg acagcgatgg cagcttcttc ctgtacagca agctgaccgt ggacaagagc 1260
agatggcagc agggcaacgt gttcagctgc tccgtgatgc acgaggccct gcacaatcac 1320
tacacccaga agagcctgag cctgtccct ggcaag 1356

<210> 46
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> SAP-E VL chimera nucleotide sequence

<400> 46
gacatccaga tgactcagtc tccagcctcc ctatctgcat ctgtgggaga aactgtcacc 60
atcacatgtc gagcaagtga gaatatttac agttatttag catggtatca gcagaaacag 120
ggaagatccc ctcagctcct ggtccataat gcaaaaacct tagcagaagg tgtgccatca 180
agggtcagtg gcagtggatc aggcacacac ttttctctga agatcaacgg cctgcagcct 240
gaagattttg ggaattatta ctgtcaacat cattatggtg ctccgctcac gttcggtgct 300
gggaccaagc tggaactgaa acgtacggtg gccgccccca gcgtgttcat cttcccccc 360
agcgatgagc agctgaagag cggcaccgcc agcgtggtgt gtctgctgaa caacttctac 420
ccccgggagg ccaaggtgca gtggaaggtg gacaatgccc tgcagagcgg caacagccag 480
gagagcgtga ccgagcagga cagcaaggac tccacctaca gcctgagcag caccctgacc 540
ctgagcaagg ccgactacga gaagcacaag gtgtacgcct gtgaggtgac ccaccagggc 600
ctgtccagcc ccgtgaccaa gagcttcaac cggggcgagt gc 642

<210> 47
<211> 1347
<212> DNA
<213> Artificial Sequence

<220>
<223> SAP-K VH chimera nucleotide sequence

<400> 47
caggtccaac tgcagcagcc tggggctgag ctgataaagc ctggggcttc agtgaagttg 60
tcctgcaagg cttctggcta cactttcacc agctactgga tgcactgggt gaagcagagg 120
cctggacaag gccttgagtg gattggaatg attcatccta atagtgttaa tactaactac 180
aatgagaagt tcaagagtaa ggccacactg actgtagaca aatcctccag cacagcctac 240
atgcaactca acagcctgac atctgaggac tctgcggtct attactgtgc aagacggaat 300
gattactact ggtacttcga tgtctggggc acagggacac tagtgaccgt gtccagcgcc 360
agcaccaagg gccccagcgt gttccccctg gccccagca gcaagagcac cagcggcggc 420
acagccgccc tgggctgcct ggtgaaggac tacttccccg aaccggtgac cgtgtcctgg 480
aacagcggag ccctgaccag cggcgtgcac accttccccg ccgtgctgca gagcagcggc 540

ctgtacagcc tgagcagcgt ggtgaccgtg cccagcagca gcctgggcac ccagacctac 600
atctgtaacg tgaaccacaa gcccagcaac accaaggtgg acaagaaggt ggagcccaag 660
agctgtgaca agacccacac ctgccccccc tgccctgccc ccgagctgct gggaggcccc 720
agcgtgttcc tgttcccccc caagcctaag gacaccctga tgatcagcag aacccccgag 780
gtgacctgtg tggtggtgga tgtgagccac gaggaccctg aggtgaagtt caactggtac 840
gtggacggcg tggaggtgca caatgccaag accaagccca gggaggagca gtacaacagc 900
acctaccggg tggtgtccgt gctgaccgtg ctgcaccagg attggctgaa cggcaaggag 960
tacaagtgta aggtgtccaa caaggccctg cctgccccta tcgagaaaac catcagcaag 1020
gccaagggcc agcccagaga gccccaggtg tacaccctgc cccctagcag agatgagctg 1080
accaagaacc aggtgtccct gacctgcctg gtgaagggct tctaccccag cgacatcgcc 1140
gtggagtggg agagcaacgg ccagcccgag aacaactaca agaccacccc ccctgtgctg 1200
gacagcgatg gcagcttctt cctgtacagc aagctgaccg tggacaagag cagatggcag 1260
cagggcaacg tgttcagctg ctccgtgatg cacgaggccc tgcacaatca ctacacccag 1320
aagagcctga gcctgtcccc tggcaag 1347

<210> 48
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> SAP-K VL chimera nucleotide sequence

<400> 48
gacattgtga tgacccagtc tcaaaaattc atgtccacat cagtaggaga cagggtcagc 60
gtcacctgca aggccagtca gaatgtgaac tctaatgtag cctggtatca acagaaacca 120
gggcaatctc ctaaagcact gatttactcg gcttcctacc ggtacagtgg agtccctgat 180
cgcttcacag gcagtggatc tgggacagat ttcactctca ccatcaccaa tgtgcagtct 240
gaagacttgg cagagtattt ctgtcagcaa tgtaacaact atccattcac gttcggctcg 300
gggacaaagt tggaaataaa acgtacggtg gccgccccca gcgtgttcat cttccccccc 360
agcgatgagc agctgaagag cggcaccgcc agcgtggtgt gtctgctgaa caacttctac 420
ccccgggagg ccaaggtgca gtggaaggtg gacaatgccc tgcagagcgg caacagccag 480
gagagcgtga ccgagcagga cagcaaggac tccacctaca gcctgagcag caccctgacc 540
ctgagcaagg ccgactacga gaagcacaag gtgtacgcct gtgaggtgac ccaccagggc 600
ctgtccagcc ccgtgaccaa gagcttcaac cggggcgagt gc 642

<210> 49
<211> 294
<212> DNA
<213> Homo sapiens sequence

<220>
<223> IGHV1-69 human variable heavy chain germline
acceptor nucleotide sequence

<400> 49
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60
tcctgcaagg cttctggagg caccttcagc agctatgcta tcagctgggt gcgacaggcc 120
cctggacaag ggcttgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180
gcacagaagt tccagggcag agtcacgatt accgcggaca aatccacgag cacagcctac 240
atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gaga 294

<210> 50
<211> 285
<212> DNA
<213> Homo sapiens sequence

<220>
<223> IGHV1-39 human variable heavy chain germline
acceptor nucleotide sequence

<400> 50
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 120
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg caacttacta ctgtcaacag agttacagta cccct 285

<210> 51
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> SAP-E humanised heavy chain V region variant H0
nucleotide sequence non-codon optimised

<400> 51
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60
tcctgcaagg cttctggagg caccttcagc acttacaata tgcactgggt gcgacaggcc 120
cctggacaag ggcttgagtg gatgggatat atttatcctg gagatggtaa tgctaactac 180
aatcagcagt tcaagggcag agtcacgatt accgcggaca aatccacgag cacagcctac 240
atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagaggggac 300
tttgattacg acggagggta ctactttgac tcctggggcc agggcaccct ggtcaccgtc 360
tcctca 366

<210> 52
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> SAP-E humanised light chain V region variant L0
nucleotide sequence non-codon optimised

<400> 52
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gagcaagtga gaatatttac agttatttag catggtatca gcagaaacca 120
gggaaagccc ctaagctcct gatctataat gcaaaaacct tagcagaagg ggtcccatca 180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg caacttacta ctgtcaacat cattatggtg ctccgctcac gtttggccag 300
gggaccaagc tggagatcaa a 321

<210> 53
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> SAP-E humanised heavy chain V region variant H0
nucleotide sequence (codon optimised)

<400> 53
caggtgcagc tggtgcagag cggcgccgag gtgaagaaac ccggcagcag cgtgaaggtg 60
agctgcaagg ctagcggggg caccttctcc acctacaaca tgcactgggt caggcaggca 120
cccggccagg gcctggagtg gatgggctat atctaccccg gcgacggcaa cgccaactac 180
aaccagcagt tcaagggcag ggtgaccatc accgccgaca agagcaccag caccgcctac 240
atggaactga gcagcctgag gagcgaggat accgccgtgt actactgcgc caggggcgac 300
ttcgactacg acggcggcta ctacttcgac agctggggac agggcacact agtgaccgtg 360
tccagc 366

<210> 54
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> SAP-E humanised heavy chain V region variant H1
nucleotide sequence (codon optimised)

<400> 54
caggtgcagc tggtgcagag cggcgccgag gtgaagaaac ccggcagcag cgtgaaggtg 60
agctgcaagg ctagcgggtt caccttcgcc acctacaaca tgcactgggt caggcaggca 120
cccggccagg gcctggagtg gatgggctat atctaccccg gcgacggcaa cgccaactac 180
aaccagcagt tcaagggcag ggtgaccatc accgccgaca agagcaccag caccgcctac 240
atggaactga gcagcctgag gagcgaggat accgccgtgt actactgcgc caggggcgac 300

ttcgactacg acggcggcta ctacttcgac agctggggac agggcacact agtgaccgtg 360
tccagc 366

<210> 55
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> SAP-E humanised heavy chain V region variant H2
nucleotide sequence (codon optimised)

<400> 55
caggcgcagc tggtgcagag cggcgccgag gtgaagaaac ccggcagcag cgtgaaggtg 60
agctgcaagg ctagcgggtt caccttcgcc acctacaaca tgcactgggt caggcaggca 120
cccggccagg gcctggagtg gatgggctat atctaccccg gcgacggcaa cgccaactac 180
aaccagcagt tcaagggcag ggtgaccatc accgccgaca agagcaccag caccgcctac 240
atggaactga gcagcctgag gagcgaggat accgccgtgt actactgcgc caggggcgac 300
ttcgactacg acggcggcta ctacttcgac agctggggac agggcacact agtgaccgtg 360
tccagc 366

<210> 56
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> SAP-E humanised heavy chain V region variant H3
nucleotide sequence (codon optimised)

<400> 56
caggtgcagc tggtgcagag cggcgccgag gtgaagaaac ccggcagcag cgtgaaggtg 60
agctgcaagg ctagcgggtt caccttcgcc acctacaaca tgcactgggt caggcaggca 120
cccggccagg gcctggagtg gatcggctat atctaccccg gcgacggcaa cgccaactac 180
aaccagcagt tcaagggcag ggccaccatc accgccgaca agagcaccag caccgcctac 240
atggaactga gcagcctgag gagcgaggat accgccgtgt actactgcgc caggggcgac 300
ttcgactacg acggcggcta ctacttcgac agctggggac agggcacact agtgaccgtg 360
tccagc 366

<210> 57
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> SAP-E humanised heavy chain V region variant H4
nucleotide sequence (codon optimised)

<400> 57
caggtgcagc tggtgcagag cggcgccgag gtgaagaaac ccggcagcag cgtgaaggtg 60
agctgcaagg ctagcgggtt caccttcgcc acctacaaca tgcactgggt caggcaggca 120
cccggccagg gcctggagtg gatcggctat atctaccccg gcgacggcaa cgccaactac 180
aaccagcagt tcaagggcag ggccaccctg accgccgaca ccagcaccag caccgcctac 240
atggaactga gcagcctgag gagcgaggat accgccgtgt acttctgcgc caggggcgac 300
ttcgactacg acggcggcta ctacttcgac agctggggac agggcacact agtgaccgtg 360
tccagc 366

<210> 58
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> SAP-E humanised light chain V region variant L0
nucleotide sequence (codon optimised)

<400> 58
gacatccaga tgacccagag ccccagctca ctgagcgcca gcgtgggcga cagggtgacc 60

attacctgca gggcctccga gaacatctac agctacctgg cctggtacca gcagaagccc 120
ggcaaggccc ccaagctgct gatctacaac gccaagaccc tcgccgaggg cgtccctagc 180
aggttctctg gaagcggcag cggcaccgac ttcaccctga ccatcagcag cctgcagccc 240
gaggacttcg ccacctatta ctgccagcac cactacggcg ccccccctgac ctttggccag 300
ggcaccaaac tggagatcaa g 321

<210> 59
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> SAP-E humanised light chain V region variant L1
nucleotide sequence (codon optimised)

<400> 59
gacatccaga tgacccagag ccccagctca ctgagcgcca gcgtgggcga cagggtgacc 60
attacctgca gggcctccga gaacatctac agctacctgg cctggtacca gcagaagccc 120
ggcaaggccc ccaagctgct gatccacaac gccaagaccc tcgccgaggg cgtccctagc 180
aggttctctg gaagcggcag cggcaccgac ttcaccctga ccatcagcag cctgcagccc 240
gaggacttcg ccacctatta ctgccagcac cactacggcg ccccccctgac ctttggccag 300
ggcaccaaac tggagatcaa g 321

<210> 60
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> SAP-E humanised light chain V region variant L2
nucleotide sequence (codon optimised)

<400> 60
gacatccaga tgacccagag ccccagctca ctgagcgcca gcgtgggcga cagggtgacc 60
attacctgca gggcctccga gaacatctac agctacctgg cctggtacca gcagaagccc 120
ggcaaggccc ccaagctgct ggtgcacaac gccaagaccc tcgccgaggg cgtccctagc 180
aggttctctg gaagcggcag cggcaccgac ttcaccctga ccatcagcag cctgcagccc 240
gaggacttcg ccacctatta ctgccagcac cactacggcg ccccccctgac ctttggccag 300
ggcaccaaac tggagatcaa g 321

<210> 61
<211> 1356
<212> DNA
<213> Artificial Sequence

<220>
<223> SAP-E humanised heavy chain H1 full mature
nucleotide sequence (codon optimised)

<400> 61
caggtgcagc tggtgcagag cggcgccgag gtgaagaaac ccggcagcag cgtgaaggtg 60
agctgcaagg ctagcgggtt caccttcgcc acctacaaca tgcactgggt caggcaggca 120
cccggccagg gcctggagtg gatgggctat atctaccccg gcgacggcaa cgccaactac 180
aaccagcagt tcaagggcag ggtgaccatc accgccgaca agagcaccag caccgcctac 240
atggaactga gcagcctgag gagcgaggat accgccgtgt actactgcgc caggggcgac 300
ttcgactacg acggcggcta ctacttcgac agctggggac agggcacact agtgaccgtg 360
tccagcgcca gcaccaaggg ccccagcgtg ttccccctgg cccccagcag caagagcacc 420
agcggcggca cagccgccct gggctgcctg gtgaaggact acttccccga accggtgacc 480
gtgtcctgga acagcggagc cctgaccagc ggcgtgcaca ccttccccgc cgtgctgcag 540
agcagcggcc tgtacagcct gagcagcgtg gtgaccgtgc ccagcagcag cctgggcacc 600
cagacctaca tctgtaacgt gaaccacaag cccagcaaca ccaaggtgga caagaaggtg 660
gagcccaaga gctgtgacaa gacccacacc tgccccccct gccctgcccc cgagctgctg 720
ggaggcccca gcgtgttcct gttcccccccc aagcctaagg acaccctgat gatcagcaga 780
acccccgagg tgacctgtgt ggtggtggat gtgagccacg aggaccctga ggtgaagttc 840
aactggtacg tggacggcgt ggaggtgcac aatgccaaga ccaagcccag ggaggagcag 900
tacaacagca cctaccgggt ggtgtccgtg ctgaccgtgc tgcaccagga ttggctgaac 960
ggcaaggagt acaagtgtaa ggtgtccaac aaggccctgc ctgccctat cgagaaaacc 1020
atcagcaagg ccaagggcca gcccagagag ccccaggtgt acaccctgcc ccctagcaga 1080

gatgagctga ccaagaacca ggtgtccctg acctgcctgg tgaagggctt ctaccccagc 1140
gacatcgccg tggagtggga gagcaacggc cagcccgaga acaactacaa gaccaccccc 1200
cctgtgctgg acagcgatgg cagcttcttc ctgtacagca agctgaccgt ggacaagagc 1260
agatggcagc agggcaacgt gttcagctgc tccgtgatgc acgaggccct gcacaatcac 1320
tacacccaga agagcctgag cctgtccccc ggcaag 1356

<210> 62
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<223> SAP-E humanised heavy chain H1 full mature amino acid sequence

<400> 62

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ser
1				5				10						15	
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Phe	Thr	Phe	Ala	Thr	Tyr
			20					25					30		
Asn	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met
		35					40					45			
Gly	Tyr	Ile	Tyr	Pro	Gly	Asp	Gly	Asn	Ala	Asn	Tyr	Asn	Gln	Gln	Phe
	50					55					60				
Lys	Gly	Arg	Val	Thr	Ile	Thr	Ala	Asp	Lys	Ser	Thr	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	
Arg	Asp	Phe	Asp	Tyr	Asp	Gly	Gly	Tyr	Tyr	Phe	Asp	Ser	Trp	Gly	Gln
			100					105					110		
Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val
		115					120					125			
Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala
	130					135					140				
Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser
145					150					155					160
Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val
				165					170					175	
Leu	Gln	Ser	Ser	Gly	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser
			180					185					190		
Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser
		195					200					205			
Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr
	210					215					220				
His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser
225					230					235					240
Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg
				245					250					255	
Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro
			260					265					270		
Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala
		275					280					285			
Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Tyr	Val	Val	Ser	Val
	290					295					300				
Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys
305					310					315					320
Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser
				325					330					335	
Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro
			340					345					350		
Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val
		355					360					365			
Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly
	370					375					380				
Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp
385					390					395					400
Gly	Ser	Phe	Phe	Lys	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln
				405					410					415	

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Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
            420                 425                 430
Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440
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<210> 63
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> SAP-E humanised light chain L1 full mature nucleotide sequence (codon optimised)

<400> 63

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gacatccaga tgacccagag ccccagctca ctgagcgcca gcgtgggcga cagggtgacc 60
attacctgca gggcctccga gaacatctac agctacctgg cctggtacca gcagaagccc 120
ggcaaggccc ccaagctgct gatccacaac gccaagaccc tcgccgaggg cgtccctagc 180
aggttctctg gaagcggcag cggcaccgac ttcaccctga ccatcagcag cctgcagccc 240
gaggacttcg ccacctatta ctgccagcac cactacggcg ccccccctgac ctttggccag 300
ggcaccaaac tggagatcaa gcgtacggtg gccgccccca gcgtgttcat cttcccccccc 360
agcgatgagc agctgaagag cggcaccgcc agcgtggtgt gtctgctgaa caacttctac 420
ccccgggagg ccaaggtgca gtggaaggtg gacaatgccc tgcagagcgg caacagccag 480
gagagcgtga ccgagcagga cagcaaggac tccacctaca gcctgagcag caccctgacc 540
ctgagcaagg ccgactacga gaagcacaag gtgtacgcct gtgaggtgac ccaccagggc 600
ctgtccagcc ccgtgaccaa gagcttcaac cggggcgagt gc                    642
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<210> 64
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> SAP-E humanised light chain L1 full mature amino acid sequence

<400> 64

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Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1               5                  10                  15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Asn Ile Tyr Ser Tyr
            20                  25                  30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45
His Asn Ala Lys Thr Leu Ala Glu Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His His Tyr Gly Ala Pro Leu
                85                  90                  95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205
Phe Asn Arg Gly Glu Cys
    210
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<210> 65
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> SAP-K humanised heavy chain V region variant H0
nucleotide sequence non-codon optimised

<400> 65
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60
tcctgcaagg cttctggagg caccttcagc agctactgga tgcactgggt gcgacaggcc 120
cctggacaag ggcttgagtg gatgggaatg attcatccta atagtgttaa tactaactac 180
aatgagaagt tcaagagtag agtcacgatt accgcggaca aatccacgag cacagcctac 240
atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagacggaat 300
gattactact ggtacttcga tgtctggggc cagggcaccc tggtcaccgt ctcctca 357

<210> 66
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> SAP-K humanised light chain V region variant L0
nucleotide sequence non-codon optimised

<400> 66
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgca aggccagtca gaatgtgaac tctaatgtag cctggtatca gcagaaacca 120
gggaaagccc ctaagctcct gatctattcg gcttcctacc ggtacagtgg ggtcccatca 180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg caacttacta ctgtcagcaa tgtaacaact atccattcac gtttggccag 300
gggaccaagc tggagatcaa a 321

<210> 67
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> SAP-K humanised heavy chain V region variant H0
nucleotide sequence (codon optimised)

<400> 67
caggtgcagc tggtgcagag cggcgccgaa gtgaagaagc ccggcagcag cgtgaaagtg 60
agctgcaagg ccagcggcgg aaccttcagc agctactgga tgcactgggt gaggcaggca 120
cccggccagg gcctggagtg gatgggcatg atccacccca acagcgtgaa caccaactac 180
aacgagaagt tcaagagcag agtgaccatc accgccgaca agagcaccag caccgcctat 240
atggagctga gctctctgag gagcgaggat accgccgtgt actactgcgc caggaggaac 300
gactactact ggtacttcga cgtctggggc cagggcacac tagtgaccgt gtccagc 357

<210> 68
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> SAP-K humanised heavy chain V region variant H1
nucleotide sequence (codon optimised)

<400> 68
caggtgcagc tggtgcagag cggcgccgaa gtgaagaagc ccggcagcag cgtgaaagtg 60
agctgcaagg ccagcggcta caccttcacc agctactgga tgcactgggt gaggcaggca 120
cccggccagg gcctggagtg gatgggcatg atccacccca acagcgtgaa caccaactac 180
aacgagaagt tcaagagcag agtgaccatc accgccgaca agagcaccag caccgcctat 240
atggagctga gctctctgag gagcgaggat accgccgtgt actactgcgc caggaggaac 300

gactactact ggtacttcga cgtctggggc cagggcacac tagtgaccgt gtccagc 357

<210> 69
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> SAP-K humanised heavy chain V region variant H2
nucleotide sequence (codon optimised)

<400> 69
caggtgcagc tggtgcagag cggcgccgaa gtgaagaagc ccggcagcag cgtgaaagtg 60
agctgcaagg ccagcggcta caccttcacc agctactgga tgcactgggt gaggcaggca 120
cccggccagg gcctggagtg gatcggcatg atccacccca acagcgtgaa caccaactac 180
aacgagaagt tcaagagcag agccaccatc accgccgaca agagcaccag caccgcctat 240
atggagctga gctctctgag gagcgaggat accgccgtgt actactgcgc caggaggaac 300
gactactact ggtacttcga cgtctggggc cagggcacac tagtgaccgt gtccagc 357

<210> 70
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> SAP-K humanised heavy chain V region variant H3
nucleotide sequence (codon optimised)

<400> 70
caggtgcagc tggtgcagag cggcgccgaa gtgaagaagc ccggcagcag cgtgaaagtg 60
agctgcaagg ccagcggcta caccttcacc agctactgga tgcactgggt gaggcaggca 120
cccggccagg gcctggagtg gatcggcatg atccacccca acagcgtgaa caccaactac 180
aacgagaagt tcaagagcag agccaccctg accgtggaca agagcaccag caccgcctat 240
atggagctga gctctctgag gagcgaggat accgccgtgt actactgcgc caggaggaac 300
gactactact ggtacttcga cgtctggggc cagggcacac tagtgaccgt gtccagc 357

<210> 71
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> SAP-K humanised light chain V region variant L0
nucleotide sequence (codon optimised)

<400> 71
gacatccaga tgacccagag cccctcttca ctgagcgcta gcgtgggcga cagggtgacc 60
atcacctgca aggccagcca gaacgtgaac agcaacgtgg cctggtacca gcagaagccc 120
ggcaaagccc ccaagctcct gatctacagc gccagctaca gatatagcgg cgtgcctagc 180
aggtttagcg gcagcggaag cgggaccgat ttcaccctga ccatcagcag cctgcagccc 240
gaggacttcg ccacttacta ctgccagcag tgcaacaact acccccttcac cttcggccag 300
ggcaccaagc tggagatcaa g 321

<210> 72
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> SAP-K humanised light chain V region variant L1
nucleotide sequence (codon optimised)

<400> 72
gacatccaga tgacccagag cccctcttca ctgagcgcta gcgtgggcga cagggtgacc 60
atcacctgca aggccagcca gaacgtgaac agcaacgtgg cctggtacca gcagaagccc 120
ggcaaagccc ccaaggccct gatctacagc gccagctaca gatatagcgg cgtgcctagc 180
aggtttagcg gcagcggaag cgggaccgat ttcaccctga ccatcagcag cctgcagccc 240
gaggacttcg ccacttacta ctgccagcag tgcaacaact acccccttcac cttcggccag 300

ggcaccaagc tggagatcaa g 321

<210> 73
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> SAP-K humanised light chain V region variant L0
91A nucleotide sequence (codon optimised)

<400> 73
gacatccaga tgacccagag cccctcttca ctgagcgcta gcgtgggcga cagggtgacc 60
atcacctgca aggccagcca gaacgtgaac agcaacgtgg cctggtacca gcagaagccc 120
ggcaaagccc ccaagctcct gatctacagc gccagctaca gatatagcgg cgtgcctagc 180
aggtttagcg gcagcggaag cgggaccgat ttcaccctga ccatcagcag cctgcagccc 240
gaggacttcg ccacttacta ctgccagcag gcgaacaact acccccttcac cttcggccag 300
ggcaccaagc tggagatcaa g 321

<210> 74
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> SAP-K humanised light chain V region variant L0
91A amino acid sequence

<400> 74
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Asn Ser Asn
20 25 30
Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45
Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Asn Tyr Pro Phe
85 90 95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 75
<211> 1347
<212> DNA
<213> Artificial Sequence

<220>
<223> SAP-K humanised H3 heavy chain nucleotide sequence
(codon optimised)

<400> 75
caggtgcagc tggtgcagag cggcgccgaa gtgaagaagc ccggcagcag cgtgaaagtg 60
agctgcaagg ccagcggcta caccttcacc agctactgga tgcactgggt gaggcaggca 120
cccggccagg gcctggagtg gatcggcatg atccacccca acagcgtgaa caccaactac 180
aacgagaagt tcaagagcag agccaccctg accgtggaca agagcaccag caccgcctat 240
atggagctga gctctctgag gagcgaggat accgccgtgt actactgcgc caggaggaac 300
gactactact ggtacttcga cgtctggggc cagggcacac tagtgaccgt gtccagcgcc 360
agcaccaagg gccccagcgt gttccccctg gccccccagca gcaagagcac cagcggcggc 420
acagccgccc tgggctgcct ggtgaaggac tacttccccg aaccggtgac cgtgtcctgg 480
aacagcggag ccctgaccag cggcgtgcac accttccccg ccgtgctgca gagcagcggc 540
ctgtacagcc tgagcagcgt ggtgaccgtg cccagcagca gcctgggcac ccagacctac 600
atctgtaacg tgaaccacaa gcccagcaac accaaggtgg acaagaaggt ggagcccaag 660
agctgtgaca agacccacac ctgccccccc tgccctgccc ccgagctgct gggaggcccc 720
agcgtgttcc tgttcccccc caagcctaag gacaccctga tgatcagcag aacccccgag 780

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gtgacctgtg tggtggtgga tgtgagccac gaggaccctg aggtgaagtt caactggtac 840
gtggacggcg tggaggtgca caatgccaag accaagccca gggaggagca gtacaacagc 900
acctaccggg tggtgtccgt gctgaccgtg ctgcaccagg attggctgaa cggcaaggag 960
tacaagtgta aggtgtccaa caaggccctg cctgccccta tcgagaaaac catcagcaag 1020
gccaagggcc agcccagaga gccccaggtg tacaccctgc cccctagcag agatgagctg 1080
accaagaacc aggtgtccct gacctgcctg gtgaagggct tctaccccag cgacatcgcc 1140
gtggagtggg agagcaacgg ccagcccgag aacaactaca agaccacccc ccctgtgctg 1200
gacagcgatg gcagcttctt cctgtacagc aagctgaccg tggacaagag cagatggcag 1260
cagggcaacg tgttcagctg ctccgtgatg cacgaggccc tgcacaatca ctacacccag 1320
aagagcctga gcctgtcccc tggcaag                                      1347

<210> 76
<211> 443
<212> PRT
<213> Artificial Sequence

<220>
<223> SAP-K humanised H3 heavy chain amino acid sequence

<400> 76
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1               5                  10                  15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20                  25                  30
Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45
Gly Met Ile His Pro Asn Ser Val Asn Thr Asn Tyr Asn Glu Lys Phe
    50                  55                  60
Lys Ser Arg Ala Thr Leu Thr Val Asp Lys Ser Thr 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 Asn Asp Tyr Tyr Trp Tyr Phe Asp Val Trp Gly Gln Gly
            100                 105                 110
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115                 120                 125
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130                 135                 140
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145                 150                 155                 160
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175
Gln Ser Ser Gly Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
            180                 185                 190
Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
        195                 200                 205
Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
    210                 215                 220
Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
225                 230                 235                 240
Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
                245                 250                 255
Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
            260                 265                 270
Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
        275                 280                 285
Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Tyr Val Val Ser Val Leu
    290                 295                 300
Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305                 310                 315                 320
Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
                325                 330                 335
Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
            340                 345                 350
Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
        355                 360                 365
Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
    370                 375                 380
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Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
385                 390                 395                 400
Ser Phe Phe Lys Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
                405                 410                 415
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
            420                 425                 430
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440
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<210> 77
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> SAP-K humanised L0 light chain nucleotide sequence
(codon optimised)

<400> 77

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gacatccaga tgacccagag cccctcttca ctgagcgcta gcgtgggcga cagggtgacc 60
atcacctgca aggccagcca gaacgtgaac agcaacgtgg cctggtacca gcagaagccc 120
ggcaaagccc ccaagctcct gatctacagc gccagctaca gatatagcgg cgtgcctagc 180
aggtttagcg gcagcggaag cgggaccgat ttcaccctga ccatcagcag cctgcagccc 240
gaggacttcg ccacttacta ctgccagcag tgcaacaact acccccttcac cttcggccag 300
ggcaccaagc tggagatcaa gcgtacggtg gccgccccca gcgtgttcat cttcccccccc 360
agcgatgagc agctgaagag cggcaccgcc agcgtggtgt gtctgctgaa caacttctac 420
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gagagcgtga ccgagcagga cagcaaggac tccacctaca gcctgagcag caccctgacc 540
ctgagcaagg ccgactacga gaagcacaag gtgtacgcct gtgaggtgac ccaccagggc 600
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<210> 78
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> SAP-K humanised L0 light chain amino acid sequence

<400> 78

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Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Asn Ser Asn
            20                  25                  30
Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45
Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Cys Asn Asn Tyr Pro Phe
                85                  90                  95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205
Phe Asn Arg Gly Glu Cys
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210

<210> 79
<211> 19
<212> PRT
<213> Mus musculus

<220>
<223> Signal sequence for immunoglobulin chains

<400> 79
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
 1   5   10   15
Val His Ser