

eolf-seql (3)
SEQUENCE LISTING

<110> PsiOxus Therapeutics Limited
<120> Virus Encoding An Anti-TCR-Complex Antibody or Fragment
<130> P000208W0
<150> GB1522334.0
<151> 2015-12-17
<150> GB1607463.5
<151> 2016-04-29
<150> GB1617207.4
<151> 2016-10-10
<150> GB1617206.6
<151> 2016-10-10
<160> 119
<170> PatentIn version 3.5
<210> 1
<211> 119
<212> PRT
<213> Artificial Sequence
<220>
<223> Muromonab-CD3 (OKT3) VH
<400> 1

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

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

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

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

eolf-seql (3)

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

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val 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 Leu Thr Val Ser Ser
115

<210> 2
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Muromonab-CD3 (OKT3) VL

<400> 2

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

Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
20 25 30

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

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

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

eolf-seql (3)

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

Phe Gly Ser Gly Thr Lys Leu Glu Ile Asn Arg
100 105

<210> 3
<211> 241
<212> PRT
<213> Artificial Sequence

<220>
<223> Muromonab -CD3 (OKT3) single chain Fv

<400> 3

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

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

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

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

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

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val 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 Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

eolf-seql (3)

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

Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Ser Ala Ser
145 150 155 160

Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Ser Gly Thr Ser
165 170 175

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

Ala His Phe Arg Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
195 200 205

Ser Gly Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
210 215 220

Ser Ser Asn Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Asn
225 230 235 240

Arg

<210> 4

<211> 322

<212> PRT

<213> Artificial Sequence

<220>

<223> Membrane anchored form of the anti-human CD3 single chain Fv

<400> 4

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

eolf-seql (3)

Val His Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg
20 25 30

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

Thr Arg Tyr Thr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
50 55 60

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

Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser
85 90 95

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

Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp
115 120 125

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

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

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

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Ser
180 185 190

Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser
195 200 205

eolf-seql (3)

Gly Val Pro Ala His Phe Arg Gly Ser Gly Ser Gly Thr Ser Tyr Ser
210 215 220

Leu Thr Ile Ser Gly Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
225 230 235 240

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

Glu Ile Asn Arg Gly Ser Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
260 265 270

Asn Ala Val Gly Gln Asp Thr Gln Glu Val Ile Val Val Pro His Ser
275 280 285

Leu Pro Phe Lys Val Val Val Ile Ser Ala Ile Leu Ala Leu Val Val
290 295 300

Leu Thr Ile Ile Ser Leu Ile Ile Leu Ile Met Leu Trp Gln Lys Lys
305 310 315 320

Pro Arg

<210> 5

<211> 333

<212> PRT

<213> Artificial Sequence

<220>

<223> Membrane anchored form of anti-human CD3 single chain Fv with
C-terminal V5 tag

<400> 5

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

Val His Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg

eolf-seql (3)

20

25

30

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

Thr Arg Tyr Thr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
50 55 60

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

Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser
85 90 95

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

Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp
115 120 125

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

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

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

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Ser
180 185 190

Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser
195 200 205

Gly Val Pro Ala His Phe Arg Gly Ser Gly Ser Gly Thr Ser Tyr Ser

eolf-seql (3)

210

215

220

Leu Thr Ile Ser Gly Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
225 230 235 240

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

Glu Ile Asn Arg Gly Ser Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
260 265 270

Asn Ala Val Gly Gln Asp Thr Gln Glu Val Ile Val Val Pro His Ser
275 280 285

Leu Pro Phe Lys Val Val Val Ile Ser Ala Ile Leu Ala Leu Val Val
290 295 300

Leu Thr Ile Ile Ser Leu Ile Ile Leu Ile Met Leu Trp Gln Lys Lys
305 310 315 320

Pro Arg Gly Ser Ile Pro Asn Pro Leu Leu Gly Leu Asp
325 330

<210> 6

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Teplizumab VH sequence

<400> 6

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

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

eolf-seql (3)

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

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Val
 50 55 60

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

Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys
 85 90 95

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

Thr Pro Val Thr Val Ser Ser
 115

<210> 7
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Teplizumab VL sequence

<400> 7

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 Ser Ala Ser Ser Ser Val Ser Tyr Met
 20 25 30

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

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

eolf-seql (3)

50

55

60

Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu
65 70 75 80

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

Phe Gly Gln Gly Thr Lys Leu Gln Ile Thr Arg
100 105

<210> 8

<211> 449

<212> PRT

<213> Artificial Sequence

<220>

<223> Teplizumab Heavy chain sequence

<400> 8

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

Ser Leu Arg Leu 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 Lys Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Val
50 55 60

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

Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys
85 90 95

eolf-seql (3)

Ala	Arg	Tyr	Tyr	Asp	Asp	His	Tyr	Cys	Leu	Asp	Tyr	Trp	Gly	Gln	Gly	100	105	110	
Thr	Pro	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	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	180	185	190	
Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	195	200	205	
Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	210	215	220	
Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Ala	Ala	Gly	Gly	Pro	225	230	235	240
Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	245	250	255	
Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	260	265	270	
Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	275	280	285	

eolf-seql (3)

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
290 295 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305 310 315 320

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
325 330 335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
340 345 350

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
355 360 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
370 375 380

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

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
405 410 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
420 425 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
435 440 445

Lys

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

eolf-seql (3)

<213> Artificial Sequence

<220>

<223> Teplizumab Light Chain Sequence

<400> 9

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 Ser Ala Ser Ser Ser Val Ser Tyr Met
20 25 30

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

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

Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu
65 70 75 80

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

Phe Gly Gln Gly Thr Lys Leu Gln Ile Thr Arg Thr Val Ala Ala Pro
100 105 110

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

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
130 135 140

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

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser

eolf-seql (3)

165

170

175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
180 185 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
195 200 205

Asn Arg Gly Glu Cys
210

<210> 10
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> PDGFR Receptor A

<400> 10

Ala Val Leu Val Leu Leu Val Ile Val Ile Ile Ser Leu Ile Val Leu
1 5 10 15

Val Val Ile Trp
20

<210> 11
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> PDGFR Receptor B

<400> 11

Val Val Ile Ser Ala Ile Leu Ala Leu Val Val Leu Thr Ile Ile Ser
1 5 10 15

Leu Ile Ile Leu Ile

20

<210> 12
 <211> 24
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Insulin-Like growth factor 1

<400> 12

Ile Ile Ile Gly Pro Pro Leu Ile Phe Val Phe Leu Phe Ser Val Val
 1 5 10 15

Ile Gly Ser Ile Tyr Leu Phe Leu
 20

<210> 13
 <211> 28
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> IL6-R

<400> 13

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

Ala Phe Gly Thr Leu Leu Cys Ile Ala Ile Val Leu
 20 25

<210> 14
 <211> 27
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD28

<400> 14

eolf-seql (3)

Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu
1 5 10 15

Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val
20 25

<210> 15
<211> 49
<212> PRT
<213> Artificial Sequence

<220>
<223> PDGFR TM Domain

<400> 15

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

Pro Phe Lys Val Val Val Ile Ser Ala Ile Leu Ala Leu Val Val Leu
20 25 30

Thr Ile Ile Ser Leu Ile Ile Leu Ile Met Leu Trp Gln Lys Lys Pro
35 40 45

Arg

<210> 16
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> c-myc tag

<400> 16

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
1 5 10

eolf-seql (3)

<210> 17
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> c-myc tag with spacers

<400> 17

Gly Ser Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn
 1 5 10

<210> 18
 <211> 62
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PDGFR TM Domain with N-terminal c-myc tag

<400> 18

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

Gln Asp Thr Gln Glu Val Ile Val Val Pro His Ser Leu Pro Phe Lys
 20 25 30

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

Ser Leu Ile Ile Leu Ile Met Leu Trp Gln Lys Lys Pro Arg
 50 55 60

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

<220>
 <223> HuVH human VH leader sequence

eolf-seql (3)

<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

<210> 20

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker

<400> 20

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

<210> 21

<211> 32326

<212> DNA

<213> Artificial Sequence

<220>

<223> EnAd Genome

<400> 21

tctatctata taatataacct tatagatgga atggtgccaa tatgtaaatg aggtgatttt	60
aaaaagtgtg gatcgtgtgg tgattggctg tggggttaac ggctaaaagg ggcggtgcga	120
ccgtgggaaa atgacgtttt gtgggggtgg agtttttttg caagttgtcg cgggaaatgt	180
gacgcataaaa aaggcttttt tctcacggaa ctacttagtt ttcccacggt atttaacagg	240
aaatgaggta gttttgaccg gatgcaagtg aaaattgttg attttcgcgc gaaaactgaa	300
tgaggaagtg tttttctgaa taatgtggta tttatggcag ggtggagtat ttgttcaggg	360
ccaggtagac tttgacccat tacgtggagg tttcgattac cgtgtttttt acctgaattt	420

eolf-seql (3)

ccgcgtaccg tgtcaaagtc ttctgttttt acgtagggtg cagctgatcg ctaggggtatt	480
tataacctcag ggtttgtgtc aagaggccac tcttgagtgc cagcgagaag agttttctcc	540
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aatctctgct gagactggaa atgaaatatt ggagcttgtg gtgcacgccc tgatgggaga	660
cgatccggag ccacctgtgc agctttttga gcctcctacg cttcaggaac tgtatgattt	720
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tatgctttta gctgctaata aagggttaga attagatccg cttttggaca cttttgatac	840
tccaggggta attgtggaaa gcggtacagg tgtaagaaaa ttacctgatt tgagttccgt	900
ggactgtgat ttgcactgct atgaagacgg gtttcctccg agtgatgagg aggaccatga	960
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tcagttggat tgcccgagc ttcctggaca tggctgtaag tcttgatgaat ttcacaggaa	1080
aaatactgga gtaaaggaac tgttatgttc gctttgttat atgagaacgc actgccactt	1140
tatttacagt aagtgtgttt aagttaaaat ttaaaggaat atgctgtttt tcacatgtat	1200
attgagtgtg agttttgtgc ttcttattat aggtcctgtg tctgatgctg atgaatcacc	1260
atctcctgat tctactacct cacctcctga gattcaagca cctgttcctg tggacgtgcg	1320
caagcccatt cctgtgaagc ttaagcctgg gaaacgtcca gcagtggaaa aacttgagga	1380
cttgttacag ggtggggacg gacctttgga cttgagtaca cggaacgtc caagacaata	1440
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tctccggttt ttggagattc tggttcgcta gtgaattagc tagggtagtt tttaggataa	1740
aacaggacta taaacaagaa tttgaaaagt tgttggtaga ttgccaggga ctttttgaag	1800
ctcttaattt gggccatcag gttcacttta aagaaaaagt tttatcagtt ttagactttt	1860

eolf-seql (3)

caaccccagg tagaactgct gctgctgtgg cttttcttac ttttatatta gataaatgga	1920
tcccgagac tcatttcagc aggggatacg ttttgattt catagccaca gcattgtgga	1980
gaacatggaa ggttcgcaag atgaggacaa tcttaggtta ctggccagtg cagcctttgg	2040
gtgtagcggg aatcctgagg catccaccgg tcatgccagc ggttctggag gaggaacagc	2100
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acagtataag attactagac ggattaatat ccggaatgct tgttacatat ctggaaatgg	2520
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gcattgtaat atgctggcta ctgtgcatat tgtttcccat caacgcaaaa aatggcctgt	3060
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tatgccttac cagtgaaca tgaatcatgt gaaagtgtt ttggaaccag atgccttttc	3180
cagaatgagc ctaacaggaa tttttgacat gaacatgcaa atctggaaga tcctgaggta	3240
tgatgatacg agatcgaggg tacgcgcatg cgaatgcgga ggcaagcatg ccaggttcca	3300

eolf-seql (3)

gccggtgtgt gtagatgtga ctgaagatct cagaccggat catttggtta ttgcccgcac	3360
tggagcagag ttcggatcca gtggagaaga aactgactaa ggtgagtatt gggaaaactt	3420
tgggggtggga ttttcagatg gacagattga gtaaaaaattt gttttttctg tcttgcagct	3480
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ctcccatcct gggcaggagt tcgtcagaat gttatgggat ctactgtgga tggaagaccc	3600
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gcagctgcag ctgccgccgc cgcttctgtt gccgctaaca ctgtgcttgg aatgggttac	3720
tatggaagca tcatggctaa ttccacttcc tctaataacc cttctaccct gactcaggac	3780
aagttacttg tccttttggc ccagctggag gctttgaccc aacgtctggg tgaactttct	3840
cagcaggtgg tcgagttgcg agtacaaact gagtctgctg tcggcacggc aaagtctaaa	3900
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gaacgatggg aatcataatc cgaaaacggg atcggacgat tgtgtctcat caaaccaca	29700
agcagccgct gtctgcgtcg ctccgtgcga ctgctgttta tgggatcagg gtccacagtg	29760
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cgcattctga tttcactcaa atctttgcag taggtacaac acattattac aatattgttt	29880
aataaaccat aattaaagc gctccagcca aaactcatat ctgatataat cgcccctgca	29940
tgaccatcat accaaagttt aatataaatt aaatgacgtt cctcaaaaa cactacccc	30000
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gccatgcatt gaagtgaacc ctgctgatta caatgacaat gaagaacca attctctcga	30180
ccgtgaatca cttgagaatg aaaaatatct atagtggcac aacatagaca taaatgcatg	30240
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atagcaaaac gcggccctgg cagaacacac tcttcttcgc cttctatcct gccgcttagc	30600
gtgttccgtg tgatagttca agtacaacca cactcttaag ttgggtcaaaa gaatgctggc	30660

eolf-seql (3)

ttcagttgta atcaaaaactc catcgcatct aatcgttctg aggaaatcat ccaagcaatg	30720
caactggatt gtgtttcaag caggagagga gaggggaagag acggaagaac catgttaatt	30780
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caagctctaa agtgactctc caacctctcc acaatatata tatacacaag ccctaaactg	32040
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eolf-seql (3)

tcaccaggga aaagtacagt ttcacttccg caatcccaac aggcgtaact tcctctttct 32160
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<210> 22
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<213> Artificial Sequence

<220>
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<400> 22

Asp Lys Thr His Thr Cys Ala Ala
1 5

<210> 23
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> hinge linker sequence

<400> 23

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10

<210> 24
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> hinge linker sequence

<400> 24

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Thr Cys Pro Pro Cys

eolf-seql (3)

1 5 10 15

Pro Ala

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

<220>
 <223> hinge linker sequence

<400> 25

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Thr Cys Pro Pro Cys
 1 5 10 15

Pro Ala Thr Cys Pro Pro Cys Pro Ala
 20 25

<210> 26
 <211> 30
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hinge linker sequence

<400> 26

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Gly Lys Pro Thr Leu
 1 5 10 15

Tyr Asn Ser Leu Val Met Ser Asp Thr Ala Gly Thr Cys Tyr
 20 25 30

<210> 27
 <211> 31
 <212> PRT
 <213> Artificial Sequence

eolf-seql (3)

<220>

<223> hinge linker sequence

<400> 27

Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Gly	Lys	Pro	Thr	His
1				5				10						15	

Val	Asn	Val	Ser	Val	Val	Met	Ala	Glu	Val	Asp	Gly	Thr	Cys	Tyr
			20					25					30	

<210> 28

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> hinge linker sequence

<400> 28

Asp	Lys	Thr	His	Thr	Cys	Cys	Val	Glu	Cys	Pro	Pro	Cys	Pro	Ala
1				5				10						15

<210> 29

<211> 26

<212> PRT

<213> Artificial Sequence

<220>

<223> hinge linker sequence

<400> 29

Asp	Lys	Thr	His	Thr	Cys	Pro	Arg	Cys	Pro	Glu	Pro	Lys	Ser	Cys	Asp
1				5				10						15	

Thr	Pro	Pro	Pro	Cys	Pro	Arg	Cys	Pro	Ala
			20				25		

<210> 30

<211> 11

<212> PRT

eolf-seql (3)

<213> Artificial Sequence

<220>

<223> hinge linker sequence

<400> 30

Asp	Lys	Thr	His	Thr	Cys	Pro	Ser	Cys	Pro	Ala
1				5					10	

<210> 31

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> flexible linker sequence

<400> 31

Ser	Gly	Gly	Gly	Gly	Ser	Glu
1				5		

<210> 32

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> flexible linker sequence

<400> 32

Asp	Lys	Thr	His	Thr	Ser
1				5	

<210> 33

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> flexible linker sequence

eolf-seql (3)

<220>
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 <222> (1)..(1)
 <223> Xaa is absent or S

<400> 33

Xaa Gly Gly Gly Gly Ser
 1 5

<210> 34
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> flexible linker sequence

<220>
 <221> misc_feature
 <222> (1)..(1)
 <223> Xaa is absent or S

<400> 34

Xaa Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1 5 10

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

<220>
 <223> flexible linker sequence

<220>
 <221> misc_feature
 <222> (1)..(1)
 <223> Xaa is absent or S

<400> 35

Xaa Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

		eolf-seql (3)	
1	5	10	15

<210> 36
 <211> 21
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> flexible linker sequence

<220>
 <221> misc_feature
 <222> (1)..(1)
 <223> Xaa is absent or S

<400> 36

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

Gly	Gly	Gly	Gly	Ser
				20

<210> 37
 <211> 26
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> flexible linker sequence

<220>
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 <222> (1)..(1)
 <223> Xaa is absent or S

<400> 37

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

Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

20

25

<210> 38
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> flexible linker sequence

<400> 38

Ala Ala Ala Gly Ser Gly Gly Ala Ser Ala Ser
 1 5 10

<210> 39
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> flexible linker sequence

<220>
 <221> misc_feature
 <222> (7)..(7)
 <223> X represents an amino acid

<400> 39

Ala Ala Ala Gly Ser Gly Xaa Gly Gly Gly Ser Gly Ala Ser Ala Ser
 1 5 10 15

<210> 40
 <211> 21
 <212> PRT
 <213> Artificial Sequence

<220>
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<220>
 <221> misc_feature

eolf-seql (3)

<222> (7)..(7)

<223> X represents an amino acid

<220>

<221> misc_feature

<222> (12)..(12)

<223> X represents an amino acid

<400> 40

Ala Ala Ala Gly Ser Gly Xaa Gly Gly Gly Ser Xaa Gly Gly Gly Ser
1 5 10 15

Gly Ala Ser Ala Ser
20

<210> 41

<211> 26

<212> PRT

<213> Artificial Sequence

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<221> misc_feature

<222> (7)..(7)

<223> X represents an amino acid

<220>

<221> misc_feature

<222> (12)..(12)

<223> X represents an amino acid

<220>

<221> misc_feature

<222> (17)..(17)

<223> X represents an amino acid

<400> 41

Ala Ala Ala Gly Ser Gly Xaa Gly Gly Gly Ser Xaa Gly Gly Gly Ser
1 5 10 15

eolf-seql (3)

Xaa Gly Gly Gly Ser Gly Ala Ser Ala Ser
20 25

<210> 42
<211> 31
<212> PRT
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<220>
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<223> X represents an amino acid

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<223> X represents an amino acid

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<222> (17)..(17)
<223> X represents an amino acid

<220>
<221> misc_feature
<222> (22)..(22)
<223> X represents an amino acid

<400> 42

Ala Ala Ala Gly Ser Gly Xaa Gly Gly Gly Ser Xaa Gly Gly Gly Ser
1 5 10 15

Xaa Gly Gly Gly Ser Xaa Gly Gly Gly Ser Gly Ala Ser Ala Ser
20 25 30

<210> 43
<211> 13
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<213> Artificial Sequence

eolf-seql (3)

<220>

<223> flexible linker sequence

<220>

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<222> (7)..(7)

<223> X represents an amino acid

<400> 43

Ala Ala Ala Gly Ser Gly Xaa Ser Gly Ala Ser Ala Ser
1 5 10

<210> 44

<211> 28

<212> PRT

<213> Artificial Sequence

<220>

<223> flexible linker sequence

<400> 44

Pro Gly Gly Asn Arg Gly Thr Thr Thr Thr Arg Arg Pro Ala Thr Thr
1 5 10 15

Thr Gly Ser Ser Pro Gly Pro Thr Gln Ser His Tyr
20 25

<210> 45

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> flexible linker sequence

<400> 45

Ala Thr Thr Thr Gly Ser Ser Pro Gly Pro Thr
1 5 10

<210> 46

eolf-seql (3)

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

<220>
 <223> flexible linker sequence

<400> 46

Ala Thr Thr Thr Gly Ser
 1 5

<210> 47
 <211> 21
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 47

Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Ser Pro Pro Ser Lys Glu
 1 5 10 15

Ser His Lys Ser Pro
 20

<210> 48
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Flexible linker sequence

<400> 48

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

<210> 49
 <211> 15
 <212> PRT

eolf-seql (3)

<213> Artificial Sequence

<220>

<223> Flexible linker sequence

<400> 49

Gly	Gly	Gly	Gly	Ile	Ala	Pro	Ser	Met	Val	Gly	Gly	Gly	Gly	Ser
1				5					10					15

<210> 50

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Flexible linker sequence

<400> 50

Gly	Gly	Gly	Gly	Lys	Val	Glu	Gly	Ala	Gly	Gly	Gly	Gly	Gly	Ser
1				5					10					15

<210> 51

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Flexible linker sequence

<400> 51

Gly	Gly	Gly	Gly	Ser	Met	Lys	Ser	His	Asp	Gly	Gly	Gly	Gly	Ser
1				5					10					15

<210> 52

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Flexible linker sequence

<400> 52

eolf-seql (3)

Gly Gly Gly Gly Asn Leu Ile Thr Ile Val Gly Gly Gly Gly Ser
1 5 10 15

<210> 53
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Flexible linker sequence

<400> 53

Gly Gly Gly Gly Val Val Pro Ser Leu Pro Gly Gly Gly Gly Ser
1 5 10 15

<210> 54
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Flexible linker sequence

<400> 54

Gly Gly Glu Lys Ser Ile Pro Gly Gly Gly Gly Ser
1 5 10

<210> 55
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Flexible linker sequence

<400> 55

Arg Pro Leu Ser Tyr Arg Pro Pro Phe Pro Phe Gly Phe Pro Ser Val
1 5 10 15

Arg Pro

eolf-seql (3)

<210> 56
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Flexible linker sequence

<400> 56

Tyr Pro Arg Ser Ile Tyr Ile Arg Arg Arg His Pro Ser Pro Ser Leu
1 5 10 15

Thr Thr

<210> 57
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Flexible linker sequence

<400> 57

Thr Pro Ser His Leu Ser His Ile Leu Pro Ser Phe Gly Leu Pro Thr
1 5 10 15

Phe Asn

<210> 58
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Flexible linker sequence

<400> 58

eolf-seql (3)

Arg Pro Val Ser Pro Phe Thr Phe Pro Arg Leu Ser Asn Ser Trp Leu
1 5 10 15

Pro Ala

<210> 59
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Flexible linker sequence

<400> 59

Ser Pro Ala Ala His Phe Pro Arg Ser Ile Pro Arg Pro Gly Pro Ile
1 5 10 15

Arg Thr

<210> 60
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Flexible linker sequence

<400> 60

Ala Pro Gly Pro Ser Ala Pro Ser His Arg Ser Leu Pro Ser Arg Ala
1 5 10 15

Phe Gly

<210> 61
<211> 18
<212> PRT

eolf-seql (3)

<213> Artificial Sequence

<220>

<223> Flexible linker sequence

<400> 61

Pro	Arg	Asn	Ser	Ile	His	Phe	Leu	His	Pro	Leu	Leu	Val	Ala	Pro	Leu
1				5				10						15	

Gly Ala

<210> 62

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Flexible linker sequence

<400> 62

Met	Pro	Ser	Leu	Ser	Gly	Val	Leu	Gln	Val	Arg	Tyr	Leu	Ser	Pro	Pro
1				5				10						15	

Asp Leu

<210> 63

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Flexible linker sequence

<400> 63

Ser	Pro	Gln	Tyr	Pro	Ser	Pro	Leu	Thr	Leu	Thr	Leu	Pro	Pro	His	Pro
1				5				10						15	

Ser Leu

eolf-seql (3)

<210> 64
<211> 18
<212> PRT
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<220>
<223> Flexible linker sequence

<400> 64

Asn Pro Ser Leu Asn Pro Pro Ser Tyr Leu His Arg Ala Pro Ser Arg
1 5 10 15

Ile Ser

<210> 65
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Flexible linker sequence

<400> 65

Leu Pro Trp Arg Thr Ser Leu Leu Pro Ser Leu Pro Leu Arg Arg Arg
1 5 10 15

Pro

<210> 66
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Flexible linker sequence

<400> 66

eolf-seql (3)

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

Pro Pro

<210> 67
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Flexible linker sequence

<400> 67

Val Pro Pro Ala Pro Val Val Ser Leu Arg Ser Ala His Ala Arg Pro
1 5 10 15

Pro Tyr

<210> 68
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
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<400> 68

Leu Arg Pro Thr Pro Pro Arg Val Arg Ser Tyr Thr Cys Cys Pro Thr
1 5 10 15

Pro

<210> 69
<211> 18
<212> PRT

eolf-seql (3)

<213> Artificial Sequence

<220>

<223> Flexible linker sequence

<400> 69

Pro	Asn	Val	Ala	His	Val	Leu	Pro	Leu	Leu	Thr	Val	Pro	Trp	Asp	Asn
1				5					10					15	

Leu Arg

<210> 70

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Flexible linker sequence

<400> 70

Cys	Asn	Pro	Leu	Leu	Pro	Leu	Cys	Ala	Arg	Ser	Pro	Ala	Val	Arg	Thr
1				5					10					15	

Phe Pro

<210> 71

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> linker sequence

<400> 71

Gly	Ala	Pro	Ala	Pro	Ala	Ala	Pro	Ala	Pro	Ala
1				5				10		

<210> 72

eolf-seql (3)

<211> 4
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<220>
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<400> 72

Pro Pro Pro Pro
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<210> 73
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
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<400> 73

Asp Leu Cys Leu Arg Asp Trp Gly Cys Leu Trp
1 5 10

<210> 74
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker sequence

<400> 74

Asp Ile Cys Leu Pro Arg Trp Gly Cys Leu Trp
1 5 10

<210> 75
<211> 15
<212> PRT
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<220>
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eolf-seql (3)

<400> 75

Met	Glu	Asp	Ile	Cys	Leu	Pro	Arg	Trp	Gly	Cys	Leu	Trp	Gly	Asp
1				5					10					15

<210> 76

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker sequence

<400> 76

Gln	Arg	Leu	Met	Glu	Asp	Ile	Cys	Leu	Pro	Arg	Trp	Gly	Cys	Leu	Trp
1				5					10					15	

Glu	Asp	Asp	Glu
			20

<210> 77

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker sequence

<400> 77

Gln	Gly	Leu	Ile	Gly	Asp	Ile	Cys	Leu	Pro	Arg	Trp	Gly	Cys	Leu	Trp
1				5					10					15	

Gly	Arg	Ser	Val
			20

<210> 78

<211> 21

<212> PRT

<213> Artificial Sequence

eolf-seql (3)

<220>

<223> Linker sequence

<400> 78

Gln Gly Leu Ile Gly Asp Ile Cys Leu Pro Arg Trp Gly Cys Leu Trp
1 5 10 15

Gly Arg Ser Val Lys
20

<210> 79

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker sequence

<400> 79

Glu Asp Ile Cys Leu Pro Arg Trp Gly Cys Leu Trp Glu Asp Asp
1 5 10 15

<210> 80

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker sequence

<400> 80

Arg Leu Met Glu Asp Ile Cys Leu Pro Arg Trp Gly Cys Leu Trp Glu
1 5 10 15

Asp Asp

<210> 81

<211> 16

<212> PRT

eolf-seql (3)

<213> Artificial Sequence

<220>

<223> Linker sequence

<400> 81

Met	Glu	Asp	Ile	Cys	Leu	Pro	Arg	Trp	Gly	Cys	Leu	Trp	Glu	Asp	Asp
1				5					10					15	

<210> 82

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker sequence

<400> 82

Met	Glu	Asp	Ile	Cys	Leu	Pro	Arg	Trp	Gly	Cys	Leu	Trp	Glu	Asp
1				5					10					15

<210> 83

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

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<400> 83

Arg	Leu	Met	Glu	Asp	Ile	Cys	Leu	Ala	Arg	Trp	Gly	Cys	Leu	Trp	Glu
1				5					10					15	

Asp Asp

<210> 84

<211> 20

<212> PRT

<213> Artificial Sequence

eolf-seql (3)

<220>

<223> Linker sequence

<400> 84

Glu	Val	Arg	Ser	Phe	Cys	Thr	Arg	Trp	Pro	Ala	Glu	Lys	Ser	Cys	Lys
1				5				10						15	

Pro	Leu	Arg	Gly
			20

<210> 85

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker sequence

<400> 85

Arg	Ala	Pro	Glu	Ser	Phe	Val	Cys	Tyr	Trp	Glu	Thr	Ile	Cys	Phe	Glu
1				5				10						15	

Arg	Ser	Glu	Gln
			20

<210> 86

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

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<400> 86

Glu	Met	Cys	Tyr	Phe	Pro	Gly	Ile	Cys	Trp	Met
1				5				10		

<210> 87

<211> 5288

<212> DNA

eolf-seql (3)

<213> Artificial Sequence

<220>

<223> DNA sequence corresponding to E2B region of the ENAD GENOME (BP
10355-5068)

<400> 87

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eolf-seql (3)

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catgggatgg gtgagtgcag aggcatacat gccacagatg tcatagacgt agatgggatc	1560
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eolf-seql (3)

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eolf-seql (3)

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tccaacataa ggcggtgata gccgtagatg tacctggaca tccagggtgat tcctgcggcg	5220
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tagttcat	5288

<210> 88
 <211> 201
 <212> DNA
 <213> Artificial Sequence

eolf-seql (3)

<220>

<223> A non-coding sequence suitable for inclusion into BX

<400> 88

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catactttct ccatacttta aaggggatgt caaatTTtag ctctctcct gtaccacaa 180

tcttcatgtc tttcttccca g 201

<210> 89

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> A non-coding sequence suitable for inclusion into BY

<400> 89

caaataaagt ttaacttggt tatttgaaaa tcaa 34

<210> 90

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Splice acceptor sequence

<400> 90

tttctctctt cagg 14

<210> 91

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Splice acceptor sequence

<400> 91

tgctaattctt cctttctctc ttcagg 26

eolf-seql (3)

<210> 92
 <211> 13
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> sequence comprising a start codon

<400> 92
 gccgccrcca ugg 13

<210> 93
 <211> 550
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Internal Ribosome Entry Sequence (IRES)

<400> 93
 gttactggcc gaagccgctt ggaataaggc cgggtgtcgt ttgtctatat gttatittcc 60
 accatattgc cgtcttttgg caatgtgagg gcccggaaac ctggccctgt cttcttgacg 120
 agcattccta ggggtctttc ccctctcgcc aaaggaatgc aaggctctgtt gaatgtcgtg 180
 aaggaagcag ttcctctgga agcttcttga agacaaacaa cgtctgtagc gaccctttgc 240
 aggcagcggg accccccacc tggcgacagg tgcctctgcg gccaaaagcc acgtgtataa 300
 gatacacctg caaaggcggc acaaccccag tgccacgttg tgagttggat agttgtggaa 360
 agagtcaa at ggctcccctc aagcgtattc aacaaggggc tgaaggatgc ccagaaggta 420
 ccccatgtga tgggatctga tctggggcct cgggtgcacat gcttttcatg tgtttagtcg 480
 aggttaaaaa acgtctaggc cccccgaacc acggggacgt ggttttcctt tgaaaaacac 540
 gatgataata 550

<210> 94
 <211> 22
 <212> PRT
 <213> Artificial Sequence

eolf-seql (3)

<220>

<223> High efficiency self-cleavable P2A peptide sequence

<400> 94

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> 95

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> High efficiency self-cleavable F2A peptide sequence

<400> 95

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> 96

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> High efficiency self-cleavable E2A peptide sequence

<400> 96

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

eolf-seql (3)

<210> 97
 <211> 25
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> High efficiency self-cleavable T2A peptide sequence

<400> 97

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> 98
 <211> 288
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Human CD80 amino acid sequence

<400> 98

Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser Lys Cys Pro Tyr
 1 5 10 15

Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu Ser His Phe Cys
 20 25 30

Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu
 35 40 45

Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile
 50 55 60

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

eolf-seql (3)

Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr
85 90 95

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

Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg
115 120 125

Glu His Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr
130 135 140

Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn Ile Arg Arg Ile
145 150 155 160

Ile Cys Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu
165 170 175

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

Pro Glu Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met
195 200 205

Thr Thr Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg
210 215 220

Val Asn Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro
225 230 235 240

Asp Asn Leu Leu Pro Ser Trp Ala Ile Thr Leu Ile Ser Val Asn Gly
245 250 255

Ile Phe Val Ile Cys Cys Leu Thr Tyr Cys Phe Ala Pro Arg Cys Arg
260 265 270

eolf-seql (3)

Glu Arg Arg Arg Asn Glu Arg Leu Arg Arg Glu Ser Val Arg Pro Val
 275 280 285

<210> 99
 <211> 192
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> poly adenylation sequence (SV40 late polyA sequence)

<400> 99
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 aatgctttat ttgtgaaatt tgtgatgcta ttgctttatt tgtaaccatt ataagctgca 120
 ataaacaagt taacaacaac aattgcattc attttatgtt tcaggttcag ggggaggtgt 180
 gggaggtttt tt 192

<210> 100
 <211> 34522
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> NG-348 virus genome sequence comprising the EnAd genome with a transgene cassette that encodes a membrane-anchored chimeric form of the single chain Fv anti-human CD3e and the T lymphocyte activation antigen, CD80 inserted in the region BY.

<400> 100
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 aaaaagtgtg gatcgtgtgg tgattggctg tgggggtaac ggctaaaagg ggcgggtcga 120
 ccgtgggaaa atgacgtttt gtgggggtgg agtttttttg caagttgtcg cgggaaatgt 180
 gacgcataaa aaggcttttt tctcacggaa ctacttagtt ttcccacggt atttaacagg 240
 aaatgaggta gttttgaccg gatgcaagtg aaaattgttg attttcgcgc gaaaactgaa 300
 tgaggaagtg tttttctgaa taatgtggta tttatggcag ggtggagtat ttgttcaggg 360
 ccaggtagac tttgacccat tacgtggagg tttcgattac cgtgtttttt acctgaattt 420

eolf-seql (3)

ccgcgtaccg tgtcaaagtc ttctgttttt acgtagggtgt cagctgatcg ctaggggtatt	480
tataacctcag ggttttgtgtc aagaggccac tcttgagtgc cagcgagaag agttttctcc	540
tctgcgccgg cagtttaata ataaaaaaat gagagatttg cgatttctgc ctcaggaaat	600
aatctctgct gagactggaa atgaaatatt ggagcttggt gtgcacgccc tgatgggaga	660
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eolf-seql (3)

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eolf-seql (3)

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eolf-seql (3)

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eolf-seql (3)

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eolf-seql (3)

<210> 102
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 <213> Artificial Sequence

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 <223> NG-348A virus genome sequence comprising the EnAd genome with a transgene cassette that encodes a membrane-anchored chimeric form of the single chain Fv anti-human CD3e with C-terminal V5 tag and the T lymphocyte activation antigen, CD80 inserted in region BY

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eolf-seql (3)

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<211> 33595

<212> DNA

<213> Artificial Sequence

<220>

<223> NG-420 virus genome sequence comprising the EnAd genome with a transgene cassette that encodes a membrane-anchored chimeric form of the single chain Fv anti-human CD3e inserted in the region BY.

<400> 103

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eolf-seql (3)

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eolf-seql (3)

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<212> DNA

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eolf-seql (3)

<220>

<223> NG-420A virus genome sequence comprising the EnAd genome with a transgene cassette that encodes a membrane-anchored chimeric form of the single chain Fv anti-human CD3e and a C-terminal V5 tag, inserted in the region BY

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eolf-seql (3)

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eolf-seql (3)

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eolf-seql (3)

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eolf-seql (3)

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eolf-seql (3)

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eolf-seql (3)

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eolf-seql (3)

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eolf-seql (3)

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eolf-seql (3)

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eolf-seql (3)

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eolf-seql (3)

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eolf-seql (3)

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eolf-seql (3)

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<210> 105

<211> 188

<212> PRT

<213> Artificial Sequence

<220>

<223> Human Interferona amino acid sequence

<400> 105

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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

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eolf-seql (3)

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> 106

<211> 179

<212> PRT

<213> Artificial Sequence

<220>

<223> Human soluble Flt3 ligand amino acid sequence

<400> 106

eolf-seql (3)

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20 25 30

Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu
35 40 45

Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
50 55 60

Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
65 70 75 80

Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly
85 90 95

Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala
100 105 110

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

Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp
130 135 140

Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro
145 150 155 160

Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala
165 170 175

Thr Ala Pro

eolf-seql (3)

<210> 107

<211> 93

<212> PRT

<213> Artificial Sequence

<220>

<223> Human Macrophage Inflammatory protein 1a amino acid sequence
(LD78b isoform)

<400> 107

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1 5 10 15

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
85 90

<210> 108

<211> 322

<212> PRT

<213> Artificial Sequence

<220>

<223> Membrane anchored form of the anti-human CD3 single chain Fv

<400> 108

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eolf-seql (3)

Val His Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg
20 25 30

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

Thr Arg Tyr Thr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
50 55 60

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

Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser
85 90 95

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

Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp
115 120 125

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

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

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

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Ser
180 185 190

Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser
195 200 205

eolf-seql (3)

Gly Val Pro Ala His Phe Arg Gly Ser Gly Ser Gly Thr Ser Tyr Ser
 210 215 220

Leu Thr Ile Ser Gly Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
 225 230 235 240

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

Glu Ile Asn Arg Gly Ser Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
 260 265 270

Asn Ala Val Gly Gln Asp Thr Gln Glu Val Ile Val Val Pro His Ser
 275 280 285

Leu Pro Phe Lys Val Val Val Ile Ser Ala Ile Leu Ala Leu Val Val
 290 295 300

Leu Thr Ile Ile Ser Leu Ile Ile Leu Ile Met Leu Trp Gln Lys Lys
 305 310 315 320

Pro Arg

- <210> 109
- <211> 33493
- <212> DNA
- <213> Artificial Sequence

- <220>
- <223> NG-330 virus genome sequence comprising the EnAd genome with a transgene cassette that encodes the T lymphocyte activation antigen, CD80, inserted in the region By. The transgene cassette contains a 5' SSA, human CD80 cDNA sequence and a 3' poly(A)

<400> 109
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eolf-seql (3)

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ccgtgggaaa atgacgtttt gtgggggtgg agtttttttg caagttgtcg cgggaaatgt	180
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ccaggtagac tttgacccat tacgtggagg tttcgattac cgtgtttttt acctgaattt	420
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eolf-seql (3)

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eolf-seql (3)

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eolf-seql (3)

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eolf-seql (3)

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eolf-seql (3)

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eolf-seql (3)

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 <213> Artificial Sequence

<220>
 <223> NG-343 virus genome sequence comprising the EnAd genome with a transgene cassette that encodes IFNa, and CD80, inserted in the region By. The transgene cassette contains a 5' SSA, IFNa cDNA sequence, P2A peptide, CD80 cDNA sequence and a 3' poly(A)

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 <213> Artificial Sequence

<220>
 <223> NG-345 virus genome sequence comprising the EnAd genome with a transgene cassette that encodes Flt3 Ligand, MIP1a and IFNa, inserted in the region BY. The transgene cassette contains a 5' SSA, Flt3 Ligand cDNA , P2A peptide sequence, MIP1a cDNA sequence

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eolf-seql (3)

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eolf-seql (3)

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 <211> 34432
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> NG-346 virus genome sequence comprising a transgene cassette that encodes Flt3 Ligand, MIP1a and CD80, employing SSA and P2A sequence, inserted in the region BY

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eolf-seql (3)

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eolf-seql (3)

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eolf-seql (3)

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eolf-seql (3)

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 <212> DNA
 <213> Artificial Sequence

<220>
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eolf-seql (3)

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eolf-seql (3)

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eolf-seql (3)

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eolf-seql (3)

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eolf-seql (3)

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eolf-seql (3)

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eolf-seql (3)

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eolf-seql (3)

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eolf-seql (3)

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eolf-seql (3)

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eolf-seql (3)

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eolf-seql (3)

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 <211> 981
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> E3 REGION FROM ENAD

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eolf-seql (3)

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<210> 115
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> A NON-CODING SEQUENCE SUITABLE FOR INCLUSION INTO BY

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<210> 116
 <211> 34522

eolf-seql (3)

<212> DNA

<213> Artificial Sequence

<220>

<223> NG-348 virus genome sequence comprising a transgene cassette that encoding a membrane-anchored chimeric form an anti-human CD3e scFv, and CD80 inserted in the region BY

<400> 116

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eolf-seql (3)

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eolf-seql (3)

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eolf-seql (3)

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eolf-seql (3)

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eolf-seql (3)

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eolf-seql (3)

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eolf-seql (3)

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eolf-seql (3)

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eolf-seql (3)

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 <211> 966
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> MEMBRANE TETHERED OKT3-SCFV NUCLEIC ACID SEQUENCE

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eolf-seql (3)

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gccctgggtgg tgctcaccat catctccctt atcatcctca tcatgctttg gcagaagaag	960
ccacgt	966

<210> 118
 <211> 2196
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Transgene Cassette sequence - NG-348

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eolf-seql (3)

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<210> 119

<211> 32345

eolf-seql (3)

<212> DNA

<213> Artificial Sequence

<220>

<223> Fully synthetic EnAd genome with incorporated cloning site for transgene cassette insertion as in plasmid pEnAd2.4

<400> 119

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eolf-seql (3)

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eolf-seql (3)

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eolf-seql (3)

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eolf-seql (3)

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eolf-seql (3)

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eolf-seql (3)

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eolf-seql (3)

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eolf-seql (3)

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eolf-seql (3)

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eolf-seql (3)