

SEQUENCE LISTING

<110> AMGEN INC.

<120> USE OF ONCOLYTIC VIRUSES FOR THE TREATMENT OF CANCER

<130> A-2353-US-PSP

<140> 62/813,961

<141> 2019-03-05

<160> 24

<170> PatentIn version 3.5

<210> 1

<211> 705

<212> DNA

<213> Artificial Sequence

<220>

<223> huFLT3L

<400> 1

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ttcgtgtca aaatccgtga gctgtctgac tacctgcttc aagattacc agtcaccgtg	180
gcctccaacc tgcaggacga ggagctctgc ggtggcctct ggcggctggt cctggcacag	240
cgctggatgg agcggctcaa gactgtcgct ggggtccaaga tgcaaggctt gctggagcgc	300
gtgaacacgg agatacactt tgtcaccaaa tgtgcctttc agccacctcc cagctgtctt	360
cgcttcgtcc agaccaacat ctccgcctc ctgcaggaga cctccgagca gctgggtggcg	420
ctgaagccct ggatcactcg ccagaacttc tcccggtgcc tggagctgca gtgtcaacct	480
gactcctcaa ctctgccacc tccatggagt ccacggcctc tggaggcaac agcgccgaca	540
gctccgcagc cccctctgtt actcctactg ctgctgcccg tgggcctcct actgctggca	600
gctgcctggt gcctgcactg gcagaggacg cggcggagga caccgacc tggggagcag	660
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<210> 2

<211> 235
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<213> Artificial Sequence

<220>
<223> huFLT3L

<400> 2

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Leu Leu Leu Leu Ser Ser Gly Leu Ser Gly Thr Gln Asp Cys Ser Phe
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 Thr Ala Pro Gln Pro Pro Leu Leu Leu Leu Leu Leu Leu
 180 185 190

Pro Val Gly Leu Leu Leu Leu Ala Ala Ala Trp Cys Leu His Trp Gln
 195 200 205

Arg Thr Arg Arg Arg Thr Pro Arg Pro Gly Glu Gln Val Pro Pro Val
 210 215 220

Pro Ser Pro Gln Asp Leu Leu Leu Val Glu His
 225 230 235

<210> 3
 <211> 594
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> huIL12A

<400> 3
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 ccttgcactt ctgaagagat tgatcatgaa gatatcaciaa aagataaaac cagcacagtg 180
 gaggcctgtt taccattgga attaaccaag aatgagagtt gcctaaattc cagagagacc 240
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 tgccttagta gtatttatga agacttgaag atgtaccagg tggagttcaa gaccatgaat 360
 gcaaagcttc tgatggatcc taagaggcag atctttctag atcaaaacat gctggcagtt 420
 attgatgagc tgatgcaggc cctgaatttc aacagtgaga ctgtgccaca aaaatcctcc 480
 cttgaagaac cggattttta taaaactaaa atcaagctct gcatacttct tcatgctttc 540
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<210> 4

<211> 197
<212> PRT
<213> Artificial Sequence

<220>
<223> huIL12A

<400> 4

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1 5 10 15

His His Ser Gln Asn Leu Leu Arg Ala Val Ser Asn Met Leu Gln Lys
20 25 30

Ala Arg Gln Thr Leu Glu Phe Tyr Pro Cys Thr Ser Glu Glu Ile Asp
35 40 45

His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu
50 55 60

Pro Leu Glu Leu Thr Lys Asn Glu Ser Cys Leu Asn Ser Arg Glu Thr
65 70 75 80

Ser Phe Ile Thr Asn Gly Ser Cys Leu Ala Ser Arg Lys Thr Ser Phe
85 90 95

Met Met Ala Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr
100 105 110

Gln Val Glu Phe Lys Thr Met Asn Ala Lys Leu Leu Met Asp Pro Lys
115 120 125

Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Ala Val Ile Asp Glu Leu
130 135 140

Met Gln Ala Leu Asn Phe Asn Ser Glu Thr Val Pro Gln Lys Ser Ser
145 150 155 160

Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu

165

170

175

Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asp Arg Val Met Ser
 180 185 190

Tyr Leu Asn Ala Ser
 195

<210> 5
 <211> 984
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> huIL12B

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 gcccctggag aaatggtggt cctcacctgt gacacccctg aagaagatgg tatcacctgg 180
 accttgacc agagcagtga ggtcttaggc tctggcaaaa ccctgaccat ccaagtcaaa 240
 gagtttggag atgctggcca gtacacctgt cacaaggag gcgaggttct aagccattcg 300
 ctctgtctgc ttcacaaaaa ggaagatgga atttgtcca ctgatatttt aaaggaccag 360
 aaagaaccca aaaataagac ctttctaaga tgcgaggcca agaattattc tggacgtttc 420
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 gctgctgagg agagtctgcc cattgagggtc atggtggatg ccgttcacaa gctcaagtat 660
 gaaaactaca ccagcagctt cttcatcagg gacatcatca aacctgacct acccaagaac 720
 ttgcagctga agccattaaa gaattctcgg cagggtggagg tcagctggga gtacctgac 780
 acctggagta ctccacattc ctacttctcc ctgacattct gcgttcaggt ccagggaag 840
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 gaatgggcat ctgtgccctg cagt 984

<210> 6
 <211> 328
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> huIL12B

<400> 6

Met Cys His Gln Gln Leu Val Ile Ser Trp Phe Ser Leu Val Phe Leu
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Ala Ser Pro Leu Val Ala Ile Trp Glu Leu Lys Lys Asp Val Tyr Val
 20 25 30

Val Glu Leu Asp Trp Tyr Pro Asp Ala Pro Gly Glu Met Val Val Leu
 35 40 45

Thr Cys Asp Thr Pro Glu Glu Asp Gly Ile Thr Trp Thr Leu Asp Gln
 50 55 60

Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
 65 70 75 80

Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val
 85 90 95

Leu Ser His Ser Leu Leu Leu Leu His Lys Lys Glu Asp Gly Ile Trp
 100 105 110

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

Leu Arg Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
 130 135 140

Leu Thr Thr Ile Ser Thr Asp Leu Thr Phe Ser Val Lys Ser Ser Arg
145 150 155 160

Gly Ser Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Ala Thr Leu Ser
165 170 175

Ala Glu Arg Val Arg Gly Asp Asn Lys Glu Tyr Glu Tyr Ser Val Glu
180 185 190

Cys Gln Glu Asp Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile
195 200 205

Glu Val Met Val Asp Ala Val His Lys Leu Lys Tyr Glu Asn Tyr Thr
210 215 220

Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn
225 230 235 240

Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg Gln Val Glu Val Ser Trp
245 250 255

Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr
260 265 270

Phe Cys Val Gln Val Gln Gly Lys Ser Lys Arg Glu Lys Lys Asp Arg
275 280 285

Val Phe Thr Asp Lys Thr Ser Ala Thr Val Ile Cys Arg Lys Asn Ala
290 295 300

Ser Ile Ser Val Arg Ala Gln Asp Arg Tyr Tyr Ser Ser Ser Trp Ser
305 310 315 320

Glu Trp Ala Ser Val Pro Cys Ser
325

<210> 7

<211> 1590
<212> DNA
<213> Artificial Sequence

<220>
<223> human single-chain IL-12 (huIL12B-GGGGS-huIL12A)

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gcccctggag aaatgggtggt cctcacctgt gacacccctg aagaagatgg tatcacctgg 180
accttgacc agagcagtga ggtcttaggc tctggcaaaa ccctgaccat ccaagtcaaa 240
gagtttggag atgtggcca gtacacctgt cacaaaggag gcgagggttct aagccattcg 300
ctcctgctgc ttcacaaaaa ggaagatgga atttggtcca ctgatatttt aaaggaccag 360
aaagaaccca aaaataagac ctttctaaga tgcgaggcca agaattattc tggacgtttc 420
acctgctggt ggctgacgac aatcagtact gatttgacat tcagtgtcaa aagcagcaga 480
ggctcttctg acccccaagg ggtgacgtgc ggagctgcta cactctctgc agagagagtc 540
agaggggaca acaaggagta tgagtactca gtggagtgcc aggaggacag tgcctgcccc 600
gctgctgagg agagtctgcc cattgagggtc atgggtggatg ccgttcacaa gctcaagtat 660
gaaaactaca ccagcagctt cttcatcagg gacatcatca aacctgaccc acccaagaac 720
ttgcagctga agccattaaa gaattctcgg caggtggagg tcagctggga gtaccctgac 780
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aacatgctcc agaaggccag acaaactcta gaattttacc cttgcacttc tgaagagatt 1140
gatcatgaag atatcacaaa agataaaacc agcacagtgg aggctgttt accattggaa 1200
ttaaccaaga atgagagttg cctaaattcc agagagacct ctttcataac taatgggagt 1260

tgcttgccct ccagaaagac ctcttttatg atggccctgt gccttagtag tatttatgaa	1320
gacttgaaga tgtaccaggt ggagttcaag accatgaatg caaagcttct gatggatcct	1380
aagaggcaga tcttttctaga tcaaaacatg ctggcagtta ttgatgagct gatgcaggcc	1440
ctgaatttca acagtgagac tgtgccacaa aaatcctccc ttgaagaacc ggatttttat	1500
aaaactaaaa tcaagctctg catacttctt catgctttca gaattcgggc agtgactatt	1560
gatagagtga tgagctatct gaatgcttcc	1590

<210> 8
 <211> 530
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> human single-chain IL-12 (huIL12B-GGGGS-huIL12A)

<400> 8

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Ala	Ser	Pro	Leu	Val	Ala	Ile	Trp	Glu	Leu	Lys	Lys	Asp	Val	Tyr	Val
			20					25					30		

Val	Glu	Leu	Asp	Trp	Tyr	Pro	Asp	Ala	Pro	Gly	Glu	Met	Val	Val	Leu
		35					40					45			

Thr	Cys	Asp	Thr	Pro	Glu	Glu	Asp	Gly	Ile	Thr	Trp	Thr	Leu	Asp	Gln
	50					55					60				

Ser	Ser	Glu	Val	Leu	Gly	Ser	Gly	Lys	Thr	Leu	Thr	Ile	Gln	Val	Lys
65					70				75					80	

Glu	Phe	Gly	Asp	Ala	Gly	Gln	Tyr	Thr	Cys	His	Lys	Gly	Gly	Glu	Val
				85					90					95	

Leu	Ser	His	Ser	Leu	Leu	Leu	Leu	His	Lys	Lys	Glu	Asp	Gly	Ile	Trp
			100					105					110		

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

Leu Arg Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
130 135 140

Leu Thr Thr Ile Ser Thr Asp Leu Thr Phe Ser Val Lys Ser Ser Arg
145 150 155 160

Gly Ser Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Ala Thr Leu Ser
165 170 175

Ala Glu Arg Val Arg Gly Asp Asn Lys Glu Tyr Glu Tyr Ser Val Glu
180 185 190

Cys Gln Glu Asp Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile
195 200 205

Glu Val Met Val Asp Ala Val His Lys Leu Lys Tyr Glu Asn Tyr Thr
210 215 220

Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn
225 230 235 240

Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg Gln Val Glu Val Ser Trp
245 250 255

Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr
260 265 270

Phe Cys Val Gln Val Gln Gly Lys Ser Lys Arg Glu Lys Lys Asp Arg
275 280 285

Val Phe Thr Asp Lys Thr Ser Ala Thr Val Ile Cys Arg Lys Asn Ala
290 295 300

Ser Ile Ser Val Arg Ala Gln Asp Arg Tyr Tyr Ser Ser Ser Trp Ser

305		310		315		320
Glu Trp Ala Ser Val Pro Cys Ser Gly Gly Gly Gly Ser Arg Asn Leu						
		325		330		335
Pro Val Ala Thr Pro Asp Pro Gly Met Phe Pro Cys Leu His His Ser						
		340		345		350
Gln Asn Leu Leu Arg Ala Val Ser Asn Met Leu Gln Lys Ala Arg Gln						
		355		360		365
Thr Leu Glu Phe Tyr Pro Cys Thr Ser Glu Glu Ile Asp His Glu Asp						
		370		375		380
Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu						
385		390		395		400
Leu Thr Lys Asn Glu Ser Cys Leu Asn Ser Arg Glu Thr Ser Phe Ile						
		405		410		415
Thr Asn Gly Ser Cys Leu Ala Ser Arg Lys Thr Ser Phe Met Met Ala						
		420		425		430
Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Val Glu						
		435		440		445
Phe Lys Thr Met Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile						
		450		455		460
Phe Leu Asp Gln Asn Met Leu Ala Val Ile Asp Glu Leu Met Gln Ala						
465		470		475		480
Leu Asn Phe Asn Ser Glu Thr Val Pro Gln Lys Ser Ser Leu Glu Glu						
		485		490		495
Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala						
		500		505		510

Phe Arg Ile Arg Ala Val Thr Ile Asp Arg Val Met Ser Tyr Leu Asn
515 520 525

Ala Ser
530

<210> 9
<211> 696
<212> DNA
<213> Artificial Sequence

<220>
<223> muF131

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gtggccgtca atcttcagga cgagaagcac tgcaaggcct tgtggagcct cttcctagcc 240
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acactggtgc tgctggcagc cgcctggggc cttcgctggc aaagggaag aaggaggggg 660
gagctccacc ctgggggtgcc cctcccctcc catccc 696

<210> 10
<211> 232
<212> PRT
<213> Artificial Sequence

<220>
<223> muF131

<400> 10

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

Phe Ser His Ser Pro Ile Ser Ser Asn Phe Lys Val Lys Phe Arg Glu
35 40 45

Leu Thr Asp His Leu Leu Lys Asp Tyr Pro Val Thr Val Ala Val Asn
50 55 60

Leu Gln Asp Glu Lys His Cys Lys Ala Leu Trp Ser Leu Phe Leu Ala
65 70 75 80

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

Thr Leu Leu Glu Asp Val Asn Thr Glu Ile His Phe Val Thr Ser Cys
100 105 110

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

Ser His Leu Leu Lys Asp Thr Cys Thr Gln Leu Leu Ala Leu Lys Pro
130 135 140

Cys Ile Gly Lys Ala Cys Gln Asn Phe Ser Arg Cys Leu Glu Val Gln
145 150 155 160

Cys Gln Pro Asp Ser Ser Thr Leu Leu Pro Pro Arg Ser Pro Ile Ala
165 170 175

Leu Glu Ala Thr Glu Leu Pro Glu Pro Arg Pro Arg Gln Leu Leu Leu
180 185 190

Leu Leu Leu Leu Leu Leu Pro Leu Thr Leu Val Leu Leu Ala Ala Ala
195 200 205

Trp Gly Leu Arg Trp Gln Arg Ala Arg Arg Arg Gly Glu Leu His Pro
210 215 220

Gly Val Pro Leu Pro Ser His Pro
225 230

<210> 11
<211> 579
<212> DNA
<213> Artificial Sequence

<220>
<223> muIl12a

<400> 11
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gaagacatcg atcatgaaga catcacacgg gaccaaacca gcacattgaa gacctgttta 180
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<210> 12
<211> 193
<212> PRT
<213> Artificial Sequence

<220>
<223> muIl12a

<400> 12

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

Asn Leu Leu Lys Thr Thr Asp Asp Met Val Lys Thr Ala Arg Glu Lys
20 25 30

Leu Lys His Tyr Ser Cys Thr Ala Glu Asp Ile Asp His Glu Asp Ile
35 40 45

Thr Arg Asp Gln Thr Ser Thr Leu Lys Thr Cys Leu Pro Leu Glu Leu
50 55 60

His Lys Asn Glu Ser Cys Leu Ala Thr Arg Glu Thr Ser Ser Thr Thr
65 70 75 80

Arg Gly Ser Cys Leu Pro Pro Gln Lys Thr Ser Leu Met Met Thr Leu
85 90 95

Cys Leu Gly Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Thr Glu Phe
100 105 110

Gln Ala Ile Asn Ala Ala Leu Gln Asn His Asn His Gln Gln Ile Ile
115 120 125

Leu Asp Lys Gly Met Leu Val Ala Ile Asp Glu Leu Met Gln Ser Leu
130 135 140

Asn His Asn Gly Glu Thr Leu Arg Gln Lys Pro Pro Val Gly Glu Ala
145 150 155 160

Asp Pro Tyr Arg Val Lys Met Lys Leu Cys Ile Leu Leu His Ala Phe
165 170 175

Ser Thr Arg Val Val Thr Ile Asn Arg Val Met Gly Tyr Leu Ser Ser
180 185 190

Ala

<210> 13
<211> 1005
<212> DNA
<213> Artificial Sequence

<220>
<223> muIl12b

<400> 13
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gcccctggag aaacagtga cctcacctgt gacacgcctg aagaagatga catcacctgg 180
acctcagacc agagacatgg agtcataggc tctggaaaga ccctgaccat cactgtcaaa 240
gagtttctag atgctggcca gtacacctgc cacaaggag gcgagactct gagccactca 300
catctgctgc tccacaagaa ggaaaatgga atttggtcca ctgaaatttt aaaaaatttc 360
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caaagggact atgagaagta ttcagtgtcc tgccaggagg atgtcacctg cccaactgcc 600
gaggagaccc tgccattga actggcggtg gaagcacggc agcagaataa atatgagaac 660
tacagacca gcttcttcat caggacatc atcaaaccag acccgccaa gaacttgcag 720
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tcctcatgca gcaagtgggc atgtgttccc tgcagggtcc gatcc 1005

<210> 14

<211> 335
<212> PRT
<213> Artificial Sequence

<220>
<223> muIl12b

<400> 14

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

Val Ser Pro Leu Met Ala Met Trp Glu Leu Glu Lys Asp Val Tyr Val
20 25 30

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

Thr Cys Asp Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln
50 55 60

Arg His Gly Val Ile Gly Ser Gly Lys Thr Leu Thr Ile Thr Val Lys
65 70 75 80

Glu Phe Leu Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Thr
85 90 95

Leu Ser His Ser His Leu Leu Leu His Lys Lys Glu Asn Gly Ile Trp
100 105 110

Ser Thr Glu Ile Leu Lys Asn Phe Lys Asn Lys Thr Phe Leu Lys Cys
115 120 125

Glu Ala Pro Asn Tyr Ser Gly Arg Phe Thr Cys Ser Trp Leu Val Gln
130 135 140

Arg Asn Met Asp Leu Lys Phe Asn Ile Lys Ser Ser Ser Ser Ser Pro
145 150 155 160

Asp Ser Arg Ala Val Thr Cys Gly Met Ala Ser Leu Ser Ala Glu Lys

165

170

175

Val Thr Leu Asp Gln Arg Asp Tyr Glu Lys Tyr Ser Val Ser Cys Gln
 180 185 190

Glu Asp Val Thr Cys Pro Thr Ala Glu Glu Thr Leu Pro Ile Glu Leu
 195 200 205

Ala Leu Glu Ala Arg Gln Gln Asn Lys Tyr Glu Asn Tyr Ser Thr Ser
 210 215 220

Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln
 225 230 235 240

Met Lys Pro Leu Lys Asn Ser Gln Val Glu Val Ser Trp Glu Tyr Pro
 245 250 255

Asp Ser Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Lys Phe Phe Val
 260 265 270

Arg Ile Gln Arg Lys Lys Glu Lys Met Lys Glu Thr Glu Glu Gly Cys
 275 280 285

Asn Gln Lys Gly Ala Phe Leu Val Glu Lys Thr Ser Thr Glu Val Gln
 290 295 300

Cys Lys Gly Gly Asn Val Cys Val Gln Ala Glu Asp Arg Tyr Tyr Asn
 305 310 315 320

Ser Ser Cys Ser Lys Trp Ala Cys Val Pro Cys Arg Val Arg Ser
 325 330 335

<210> 15

<211> 1599

<212> DNA

<213> Artificial Sequence

<220>

<223> murine single-chain IL12 (muIl12b-GGGGS-muIl12a)

<400> 15

atgtgtcctc agaagctaac catctcctgg tttgccatcg ttttgctggg gtctccactc	60
atggccatgt gggagctgga gaaagacgtt tatgtttag aggtggactg gactcccgat	120
gcccctggag aaacagtga cctcacctgt gacacgcctg aagaagatga catcacctgg	180
acctcagacc agagacatgg agtcataggc tctggaaaga ccctgaccat cactgtcaaa	240
gagtttctag atgctggcca gtacacctgc cacaaaggag gcgagactct gagccactca	300
catctgctgc tccacaagaa ggaaaatgga atttgggtcca ctgaaatttt aaaaaatttc	360
aaaaacaaga ctttcctgaa gtgtgaagca ccaaattact ccggacgggt cactgtctca	420
tggctgggtc aaagaaacat ggacttgaag ttcaacatca agagcagtag cagttcccct	480
gactctcggg cagtgcacatg tggaatggcg tctctgtctg cagagaaggc cacactggac	540
caaagggact atgagaagta ttcagtgtcc tgccaggagg atgtcacctg cccaactgcc	600
gaggagaccc tgcccattga actggcggtg gaagcacggc agcagaataa atatgagaac	660
tacagcacca gcttcttcat caggacatc atcaaaccag acccgcccaa gaacttgtag	720
atgaagcctt tgaagaactc acaggtggag gtcagctggg agtaccctga ctctggagc	780
actccccatt cctacttctc cctcaagttc tttgttcgaa tccagcgcaa gaaagaaaag	840
atgaaggaga cagaggagg gtgtaaccag aaagggtcgt tcctcgtaga gaagacatct	900
accgaagtcc aatgcaaagg cgggaatgtc tgcgtgcaag ctccaggatcg ctattacaat	960
tcctcatgca gcaagtgggc atgtgttccc tgcagggtcc gatccggcgg tggagggtcc	1020
agggtcattc cagtctctgg acctgccagg tgtcttagcc agtcccgaag cctgctgaag	1080
accacagatg acatggtgaa gacggccaga gaaaaactga aacattattc ctgcactgct	1140
gaagacatcg atcatgaaga catcacacgg gaccaaacca gcacattgaa gacctgttta	1200
ccactggaac tacacaagaa cgagagttgc ctggctacta gagagacttc ttccacaaca	1260
agagggagct gcctgcccc acagaagacg tctttgatga tgaccctgtg ctttggtagc	1320
atctatgagg acttgaagat gtaccagaca gagttccagg ccatcaacgc agcattcag	1380
aatcacaacc atcagcagat cattctagac aagggcacgc tgggtggccat cgatgagctg	1440

atgcagtctc tgaatcataa tggcgagact ctgcgccaga aacctcctgt gggagaagca 1500
gacccttaca gagtgaaaat gaagctctgc atcctgcttc acgccttcag caccgcgctc 1560
gtgaccatca acaggggtgat gggctatctg agctccgcc 1599

<210> 16
<211> 533
<212> PRT
<213> Artificial Sequence

<220>
<223> murine single-chain IL12 (muIl12b-GGGGS-muIl12a)

<400> 16

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

Val Ser Pro Leu Met Ala Met Trp Glu Leu Glu Lys Asp Val Tyr Val
20 25 30

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

Thr Cys Asp Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln
50 55 60

Arg His Gly Val Ile Gly Ser Gly Lys Thr Leu Thr Ile Thr Val Lys
65 70 75 80

Glu Phe Leu Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Thr
85 90 95

Leu Ser His Ser His Leu Leu Leu His Lys Lys Glu Asn Gly Ile Trp
100 105 110

Ser Thr Glu Ile Leu Lys Asn Phe Lys Asn Lys Thr Phe Leu Lys Cys
115 120 125

Glu Ala Pro Asn Tyr Ser Gly Arg Phe Thr Cys Ser Trp Leu Val Gln

130

135

140

Arg Asn Met Asp Leu Lys Phe Asn Ile Lys Ser Ser Ser Ser Ser Pro
 145 150 155 160

Asp Ser Arg Ala Val Thr Cys Gly Met Ala Ser Leu Ser Ala Glu Lys
 165 170 175

Val Thr Leu Asp Gln Arg Asp Tyr Glu Lys Tyr Ser Val Ser Cys Gln
 180 185 190

Glu Asp Val Thr Cys Pro Thr Ala Glu Glu Thr Leu Pro Ile Glu Leu
 195 200 205

Ala Leu Glu Ala Arg Gln Gln Asn Lys Tyr Glu Asn Tyr Ser Thr Ser
 210 215 220

Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln
 225 230 235 240

Met Lys Pro Leu Lys Asn Ser Gln Val Glu Val Ser Trp Glu Tyr Pro
 245 250 255

Asp Ser Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Lys Phe Phe Val
 260 265 270

Arg Ile Gln Arg Lys Lys Glu Lys Met Lys Glu Thr Glu Glu Gly Cys
 275 280 285

Asn Gln Lys Gly Ala Phe Leu Val Glu Lys Thr Ser Thr Glu Val Gln
 290 295 300

Cys Lys Gly Gly Asn Val Cys Val Gln Ala Gln Asp Arg Tyr Tyr Asn
 305 310 315 320

Ser Ser Cys Ser Lys Trp Ala Cys Val Pro Cys Arg Val Arg Ser Gly
 325 330 335

Gly Gly Gly Ser Arg Val Ile Pro Val Ser Gly Pro Ala Arg Cys Leu
340 345 350

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

Ala Arg Glu Lys Leu Lys His Tyr Ser Cys Thr Ala Glu Asp Ile Asp
370 375 380

His Glu Asp Ile Thr Arg Asp Gln Thr Ser Thr Leu Lys Thr Cys Leu
385 390 395 400

Pro Leu Glu Leu His Lys Asn Glu Ser Cys Leu Ala Thr Arg Glu Thr
405 410 415

Ser Ser Thr Thr Arg Gly Ser Cys Leu Pro Pro Gln Lys Thr Ser Leu
420 425 430

Met Met Thr Leu Cys Leu Gly Ser Ile Tyr Glu Asp Leu Lys Met Tyr
435 440 445

Gln Thr Glu Phe Gln Ala Ile Asn Ala Ala Leu Gln Asn His Asn His
450 455 460

Gln Gln Ile Ile Leu Asp Lys Gly Met Leu Val Ala Ile Asp Glu Leu
465 470 475 480

Met Gln Ser Leu Asn His Asn Gly Glu Thr Leu Arg Gln Lys Pro Pro
485 490 495

Val Gly Glu Ala Asp Pro Tyr Arg Val Lys Met Lys Leu Cys Ile Leu
500 505 510

Leu His Ala Phe Ser Thr Arg Val Val Thr Ile Asn Arg Val Met Gly
515 520 525

Tyr Leu Ser Ser Ala

530

<210> 17
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<223> GSG-P2A

<400> 17
ggatccggtg ccacaaactt ctctttgcta aagcaagcag gagatgttga ggaaaaccct 60
gggccc 66

<210> 18
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> GSG-P2A

<400> 18

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> 19
<211> 587
<212> DNA
<213> Artificial Sequence

<220>
<223> IRES sequence

<400> 19
cccctctccc tccccccccc ctaacgttac tggccgaagc cgcttggaat aaggccggtg 60
tgcgtttgtc tatatgttat tttccaccat attgccgtct tttggcaatg tgagggcccg 120
gaaacctggc cctgtcttct tgacgagcat tcctaggggt ctttcccctc tcgccaaagg 180

aatgcaaggt ctgttgaatg tcgtgaagga agcagttcct ctggaagctt cttgaagaca	240
aacaacgtct gtagcgaccc tttgcaggca gcggaacccc ccacctggcg acaggtgcct	300
ctgcggccaa aagccacgtg tataagatac acctgcaaag gcggcacaac cccagtgcca	360
cgttgtgagt tggatagttg tggaaagagt caaatggctc tcctcaagcg tattcaacaa	420
ggggctgaag gatgcccaga aggtacccca ttgtatggga tctgatctgg ggcctcggta	480
cacatgcttt acatgtgttt agtcgagggt aaaaaaacgt ctaggcccc cgaaccacgg	540
ggacgtgggtt ttcctttgaa aaacacgatg ataatatggc cacaacc	587

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

<220>
 <223> Kozak sequence

<400> 20	
ctaggccacc	10

<210> 21
 <211> 225
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> BGHpA sequence

<400> 21	
ctgtgccttc tagttgccag ccatctgttg tttgcccctc ccccgtcct tccttgaccc	60
tggaaggtgc cactcccact gtcctttcct aataaaatga ggaaattgca tcgcattgtc	120
tgagtaggtg tcattctatt ctgggggggtg ggggtggggca ggacagcaag ggggaggatt	180
gggaagacaa tagcaggcat gctgggggatg cggtgggctc tatgg	225

<210> 22
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Elastin sequence

<400> 22

gttcctggag taggggtacc tggagtgggc ggatct

36

<210> 23

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Elastin sequence

<400> 23

Val Pro Gly Val Gly Val Pro Gly Val Gly Gly Ser
1 5 10

<210> 24

<211> 588

<212> DNA

<213> Artificial Sequence

<220>

<223> CMV sequence

<400> 24

gttgacattg attattgact agttattaat agtaatcaat tacggggtca ttagttcata 60
gcccataatat ggagttccgc gttacataac ttacggtaaa tggcccgctt ggctgaccgc 120
ccaacgaccc ccgcccattg acgtcaataa tgacgtatgt tcccatagta acgccaatag 180
ggactttcca ttgacgtcaa tgggtggact atttacggta aactgcccac ttggcagtac 240
atcaagtgta tcatatgcca agtacgcccc ctattgacgt caatgacggg aaatggcccg 300
cctggcatta tgcccagtac atgaccttat gggactttcc tacttggcag tacatctacg 360
tattagtcac cgctattacc atggtgatgc ggttttggca gtacatcaat gggcgtggat 420
agcggtttga ctcacgggga tttccaagtc tccaccccat tgacgtcaat gggagtttgt 480
tttggcacca aaatcaacgg gactttccaa aatgtcgtaa caactccgcc ccattgacgc 540
aaatgggcgg taggcgtgta cggtgggagg tctatataag cagagctc 588

