

<110> GI Innovation, Inc.
 <120> PHARMACEUTICAL COMPOSITION FOR TREATING CANCER COMPRISING FUSION
 PROTEIN COMPRISING IL-2 PROTEIN AND CD80 PROTEIN AND ANTICANCER DRUG
 <130> POPB214532PCT
 <150> KR 10-2020-0033233
 <151> 2020-03-18
 <150> KR 10-2021-0020708
 <151> 2021-02-16
 <160> 39
 <170> KopatentIn 3.0
 <210> 1
 <211> 25
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> signal peptide (TPA)
 <400> 1
 Met Asp Ala Met Leu Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
 1 5 10 15
 Ala Val Phe Val Ser Pro Ser His Ala
 20 25
 <210> 2
 <211> 208
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> hB7-1:35-242
 <400> 2
 Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
 1 5 10 15
 Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
 20 25 30
 Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
 35 40 45
 Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn

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

<210> 3
 <211> 30
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hinge

<400> 3
 Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 1 5 10 15
 Ser Ala Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro
 20 25 30

<210> 4
 <211> 216
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> immunoglobulin fc

<400> 4
 Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 1 5 10 15
 Pro Lys Asp Gln Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 20 25 30
 Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
 35 40 45
 Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 50 55 60
 Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 65 70 75 80
 Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 85 90 95
 Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 100 105 110
 Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met
 115 120 125
 Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 130 135 140
 Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 145 150 155 160
 Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 165 170 175
 Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val
 180 185 190
 Phe Ser Cys Ser Val Leu His Glu Ala Leu His Asn His Tyr Thr Gln
 195 200 205
 Lys Ser Leu Ser Leu Ser Leu Gly
 210 215

<210> 5
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>

<223> linker

<400> 5
Gly Gly Gly Gly Ser
1 5

<210> 6
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> hIL-2M

<400> 6
Ala Pro Thr Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
1 5 10 15
Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
20 25 30
Asn Pro Lys Leu Thr Ala Met Leu Thr Ala Lys Phe Tyr Met Pro Lys
35 40 45
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
50 55 60
Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
65 70 75 80
Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
85 90 95
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
100 105 110
Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser Ile
115 120 125
Ile Ser Thr Leu Thr
130

<210> 7
<211> 617
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein comprising variants of IL-2 and fragments of CD80

<400> 7
 Met Asp Ala Met Leu Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
 1 5 10 15
 Ala Val Phe Val Ser Pro Ser His Ala Val Ile His Val Thr Lys Glu
 20 25 30
 Val Lys Glu Val Ala Thr Leu Ser Cys Gly His Asn Val Ser Val Glu
 35 40 45
 Glu Leu Ala Gln Thr Arg Ile Tyr Trp Gln Lys Glu Lys Lys Met Val
 50 55 60
 Leu Thr Met Met Ser Gly Asp Met Asn Ile Trp Pro Glu Tyr Lys Asn
 65 70 75 80
 Arg Thr Ile Phe Asp Ile Thr Asn Asn Leu Ser Ile Val Ile Leu Ala
 85 90 95
 Leu Arg Pro Ser Asp Glu Gly Thr Tyr Glu Cys Val Val Leu Lys Tyr
 100 105 110
 Glu Lys Asp Ala Phe Lys Arg Glu His Leu Ala Glu Val Thr Leu Ser
 115 120 125
 Val Lys Ala Asp Phe Pro Thr Pro Ser Ile Ser Asp Phe Glu Ile Pro
 130 135 140
 Thr Ser Asn Ile Arg Arg Ile Ile Cys Ser Thr Ser Gly Gly Phe Pro
 145 150 155 160
 Glu Pro His Leu Ser Trp Leu Glu Asn Gly Glu Glu Leu Asn Ala Ile
 165 170 175
 Asn Thr Thr Val Ser Gln Asp Pro Glu Thr Glu Leu Tyr Ala Val Ser
 180 185 190
 Ser Lys Leu Asp Phe Asn Met Thr Thr Asn His Ser Phe Met Cys Leu
 195 200 205
 Ile Lys Tyr Gly His Leu Arg Val Asn Gln Thr Phe Asn Trp Asn Thr
 210 215 220
 Thr Lys Gln Glu His Phe Pro Asp Asn Gly Ser Gly Gly Gly Gly Ser
 225 230 235 240
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Glu Ser Lys Tyr Gly
 245 250 255
 Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser
 260 265 270
 Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Gln Leu Met Ile Ser Arg

275					280					285					
Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro
	290					295					300				
Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala
305					310					315					320
Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val
				325					330					335	
Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr
			340					345					350		
Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr
		355					360					365			
Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu
	370					375					380				
Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys
385					390					395					400
Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser
				405					410					415	
Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp
			420					425					430		
Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser
		435					440					445			
Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Leu	His	Glu	Ala
	450					455					460				
Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Gly
465					470					475					480
Gly	Gly	Gly	Ser	Ala	Pro	Thr	Ser	Ser	Ser	Thr	Lys	Lys	Thr	Gln	Leu
				485					490					495	
Gln	Leu	Glu	His	Leu	Leu	Leu	Asp	Leu	Gln	Met	Ile	Leu	Asn	Gly	Ile
			500					505					510		
Asn	Asn	Tyr	Lys	Asn	Pro	Lys	Leu	Thr	Ala	Met	Leu	Thr	Ala	Lys	Phe
		515					520					525			
Tyr	Met	Pro	Lys	Lys	Ala	Thr	Glu	Leu	Lys	His	Leu	Gln	Cys	Leu	Glu
	530					535					540				
Glu	Glu	Leu	Lys	Pro	Leu	Glu	Glu	Val	Leu	Asn	Leu	Ala	Gln	Ser	Lys
545					550					555					560
Asn	Phe	His	Leu	Arg	Pro	Arg	Asp	Leu	Ile	Ser	Asn	Ile	Asn	Val	Ile

	565		570		575										
Val	Leu	Glu	Leu	Lys	Gly	Ser	Glu	Thr	Thr	Phe	Met	Cys	Glu	Tyr	Ala
	580						585					590			
Asp	Glu	Thr	Ala	Thr	Ile	Val	Glu	Phe	Leu	Asn	Arg	Trp	Ile	Thr	Phe
	595						600					605			
Cys	Gln	Ser	Ile	Ile	Ser	Thr	Leu	Thr							
	610					615									

<210> 8
 <211> 1857
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> nucleotides coding fusion protein (GI101)

<400> 8
 atggatgcta tgctgagagg cctgtgttgc gtgctgctgc tgtgtggcgc tgtgttcgtg 60
 tctccttctc acgctgtgat ccacgtgacc aaagaagtga aagaggctgc cacactgtcc 120
 tgcggccaca acgtttcagt ggaagaactg gcccagacca ggatctactg gcagaaagaa 180
 aagaaaatgg tgctgaccat gatgtccggc gacatgaaca tctggcctga gtacaagaac 240
 cggaccatct tcgacatcac caacaacctg tccatcgtga ttctggccct gaggccttct 300
 gatgagggca cctatgagtg cgtgggtgctg aagtacgaga aggacgcctt caagcgcgag 360
 cacctggctg aagtgacact gtccgtgaag gccgactttc ccacaccttc catctccgac 420
 ttcgagatcc ctacctcaa catccggcgg atcatctgtt ctacctctgg cggctttcct 480
 gagcctcacc tgtcttggct ggaaaacggc gaggaactga acgccatcaa caccaccgtg 540
 tctcaggacc ccgaaaccga gctgtacgct gtgtcctcca agctggactt caacatgacc 600
 accaaccaca gcttcatgtg cctgattaag tacggccacc tgagagtga ccagaccttc 660
 aactggaaca ccaccaagca agagcacttc cctgacaatg gatctggcgg cggaggttct 720
 ggcgagggtg gaagcggagg cggaggatct gctgagtcta agtatggccc tccttgtcct 780
 ccatgtcctg ctccagaagc tgctggcgga ccctctgtgt tcctgtttcc tccaaagcct 840
 aaggaccagc tcatgatctc tcggacaccc gaagtgacct gcgtgggtgt ggatgtgtct 900
 caagaggacc ctgagggtgca gttcaattgg tacgtggacg gcgtggaagt gcacaacgcc 960

aagaccaagc ctagagagga acagttcaac tccacctaca gagtggtgtc cgtgctgacc 1020
gtgctgcacc aggattggct gaacggcaaa gagtacaagt gcaaggtgtc caacaagggc 1080
ctgccttcca gcatcgaaaa gaccatctcc aaggctaagg gccagcctag ggaacccag 1140
gtttacaccc tgcctccaag ccaagaggaa atgaccaaga accaggtgtc cctgacctgc 1200
ctgggtcaagg gcttctaccc ttccgacatt gccgtggaat gggagtccaa tggccagcct 1260
gagaacaact acaagaccac acctcctgtg ctggactccg acggctcctt ctttctgtac 1320
tctcgcctga ccgtggacaa gtctagatgg caagagggca acgtgttctc ctgctctgtg 1380
ctgcacgagg ccctgcacaa tcactacacc cagaagtccc tgtctctgtc tcttgagggt 1440
ggtggcggtt ctgcccctac cagctcctct accaagaaaa cccagctcca gttggagcat 1500
ctgctgctgg acctccagat gattctgaac gggatcaaca actataagaa cccaagctg 1560
accgccatgc tgaccgctaa gttctacatg cccaagaagg ccaccgagct gaagcacctc 1620
cagtgcctgg aagaagaact gaagcccctg gaagaggtgc tgaatctggc ccagtccaag 1680
aacttccacc tgaggccacg ggacctgac agcaacatca acgtgatcgt gctggaactg 1740
aagggtccg agacaacctt tatgtgcgag tacgccgacg agacagccac catcgtggaa 1800
tttctgaacc ggtggatcac cttctgccag agcatcatct ccacactgac ctgatga 1857

<210> 9
<211> 592
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein (GI101)

<400> 9
Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15
Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30
Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45
Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60
Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr

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

355	360	365
Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp		
370	375	380
Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys		
385	390	395
Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser		
405	410	415
Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser		
420	425	430
Cys Ser Val Leu His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser		
435	440	445
Leu Ser Leu Ser Leu Gly Gly Gly Gly Gly Ser Ala Pro Thr Ser Ser		
450	455	460
Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu		
465	470	475
Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr		
485	490	495
Ala Met Leu Thr Ala Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu		
500	505	510
Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val		
515	520	525
Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu		
530	535	540
Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr		
545	550	555
Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe		
565	570	575
Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr		
580	585	590

<210> 10
 <211> 133
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hIL-2

<400> 10
Ala Pro Thr Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
1 5 10 15
Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
20 25 30
Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys
35 40 45
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
50 55 60
Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
65 70 75 80
Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
85 90 95
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
100 105 110
Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser Ile
115 120 125
Ile Ser Thr Leu Thr
130

<210> 11
<211> 288
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80

<400> 11
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
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
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
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
Glu Arg Arg Arg	Asn Glu Arg Leu	Arg Arg Glu Ser	Val Arg Pro Val
	275	280	285

<210> 12
 <211> 215
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> modified Fc

<400> 12

Ser His Thr Gln Pro Leu Gly Val Phe Leu Phe Pro Pro Lys Pro Lys
 1 5 10 15
 Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
 20 25 30
 Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
 35 40 45
 Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
 50 55 60
 Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
 65 70 75 80
 Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
 85 90 95
 Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
 100 105 110
 Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
 115 120 125
 Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
 130 135 140
 Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
 145 150 155 160
 Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
 165 170 175
 Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
 180 185 190
 Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
 195 200 205
 Leu Ser Leu Ser Leu Gly Lys
 210 215

<210> 13
 <211> 306
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> mCD80

<400> 13
 Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu Lys Phe

1	5	10	15
Pro Cys Pro Arg	Leu Ile Leu Leu Phe Val Leu Leu Ile Arg Leu Ser		
	20	25	30
Gln Val Ser Ser Asp Val Asp Glu Gln Leu Ser Lys Ser Val Lys Asp			
	35	40	45
Lys Val Leu Leu Pro Cys Arg Tyr Asn Ser Pro His Glu Asp Glu Ser			
	50	55	60
Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val Val Leu Ser Val			
	65	70	75
Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys Asn Arg Thr Leu			
	85	90	95
Tyr Asp Asn Thr Thr Tyr Ser Leu Ile Ile Leu Gly Leu Val Leu Ser			
	100	105	110
Asp Arg Gly Thr Tyr Ser Cys Val Val Gln Lys Lys Glu Arg Gly Thr			
	115	120	125
Tyr Glu Val Lys His Leu Ala Leu Val Lys Leu Ser Ile Lys Ala Asp			
	130	135	140
Phe Ser Thr Pro Asn Ile Thr Glu Ser Gly Asn Pro Ser Ala Asp Thr			
	145	150	155
Lys Arg Ile Thr Cys Phe Ala Ser Gly Gly Phe Pro Lys Pro Arg Phe			
	165	170	175
Ser Trp Leu Glu Asn Gly Arg Glu Leu Pro Gly Ile Asn Thr Thr Ile			
	180	185	190
Ser Gln Asp Pro Glu Ser Glu Leu Tyr Thr Ile Ser Ser Gln Leu Asp			
	195	200	205
Phe Asn Thr Thr Arg Asn His Thr Ile Lys Cys Leu Ile Lys Tyr Gly			
	210	215	220
Asp Ala His Val Ser Glu Asp Phe Thr Trp Glu Lys Pro Pro Glu Asp			
	225	230	235
Pro Pro Asp Ser Lys Asn Thr Leu Val Leu Phe Gly Ala Gly Phe Gly			
	245	250	255
Ala Val Ile Thr Val Val Val Ile Val Val Ile Ile Lys Cys Phe Cys			
	260	265	270
Lys His Arg Ser Cys Phe Arg Arg Asn Glu Ala Ser Arg Glu Thr Asn			
	275	280	285
Asn Ser Leu Thr Phe Gly Pro Glu Glu Ala Leu Ala Glu Gln Thr Val			

290	295	300	
Phe Leu			
305			
<210>	14		
<211>	1848		
<212>	DNA		
<213>	Artificial Sequence		
<220>			
<223>	nucleotides coding fusion protein (mGI101)		
<400>	14		
atggatgcta tgctgagagg cctgtgttgc gtgctgctgc tgtgtggcgc tgtgttcgtg		60	
tctccttctc acgctgtgga cgagcagctc tccaagtccg tgaaggataa ggtcctgctg		120	
ccttgccggt acaactctcc tcacaggagc gagtctgagg accggatcta ctggcagaaa		180	
cacgacaagg tgggtgctgtc cgtgatcgcc ggaaagctga aagtgtggcc tgagtacaag		240	
aacaggaccc tgtacgacaa caccacctac agcctgatca tcctgggcct cgtgctgagc		300	
gatagaggca cctattcttg cgtgggtgcag aagaaagagc ggggcaccta cgaagtgaag		360	
cacctggctc tgggtcaagct gtccatcaag gccgacttca gcaccctaa catcaccgag		420	
tctggcaacc cttccgccga caccaagaga atcacctgtt tcgcctctgg cggcttcctt		480	
aagcctcggc tctcttggct ggaaaacggc agagagctgc ccggcatcaa taccaccatt		540	
tctcaggacc cagagtccga gctgtacacc atctccagcc agctcgactt taacaccacc		600	
agaaaccaca ccatcaagtg cctgattaag tacggcgacg cccacgtgtc cgaggacttt		660	
acttgggaga aacctcctga ggacctcct gactctggat ctggcggcgg aggttctggc		720	
ggaggtggaa gcggaggcgg aggatctgct gagtctaagt atggccctcc ttgtcctcca		780	
tgtcctgctc cagaagctgc tggcggaccc tctgtgttcc tgtttcctcc aaagcctaag		840	
gaccagctca tgatctctcg gaccttgaa gtgacctgcg tgggtggtgga tgtgtctcaa		900	
gaggaccctg aggtgcagtt caattggtac gtggacggcg tggaaagtga caacgccaaag		960	
accaagccta gagaggaaca gttcaactcc acctatagag tgggtgtccgt gctgaccgtg		1020	
ctgcaccagg attggctgaa cggcaaagag tacaagtga aggtgtccaa caagggcctg		1080	
ccttcagca tcgaaaagac catcagcaag gctaagggcc agcctaggga accccaggtt		1140	

tacaccctgc ctccaagcca agaggaaatg accaagaacc aggtgtccct gacctgcctg	1200
gtcaagggct tctacccttc cgacattgcc gtggaatggg agtccaatgg ccagcctgag	1260
aacaactaca agaccacacc tcctgtgctg gactccgacg gtccttctt tctgtactct	1320
cgcctgaccg tggacaagtc taggtggcaa gagggcaacg tgttctcctg ctctgtgctg	1380
cacgaggctc tgcacaacca ctacaccag aagtcctgt ctctgtctct tggagggtgt	1440
ggcggttctg cccctacctc cagctctacc aagaaaacc agctccagtt ggagcatctg	1500
ctgctggacc tccagatgat cctgaatggc atcaacaatt acaagaacc caagctgacc	1560
gccatgctga ccgctaagtt ctacatgccc aagaaggcca ccgagctgaa gcacttgacg	1620
tgcttgaag aggaactgaa gcccctggaa gaagtgtga atctggcca gtccaagaac	1680
ttccacctga ggcctaggga cctgatctcc aacatcaacg tgatcgtgct ggaactgaaa	1740
ggctccgaga caaccttcat gtgcgagtac gccgacgaga cagccaccat cgtggaattt	1800
ctgaaccggt ggatcacctt ctgccagagc atcatctcca cactgacc	1848

<210> 15
 <211> 616
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fusion protein (mGI101)

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

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

385		390		395		400									
Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn
			405						410					415	
Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser
			420					425					430		
Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg
		435					440					445			
Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Leu	His	Glu	Ala	Leu
	450					455					460				
His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Gly	Gly
465					470					475					480
Gly	Gly	Ser	Ala	Pro	Thr	Ser	Ser	Ser	Thr	Lys	Lys	Thr	Gln	Leu	Gln
				485					490					495	
Leu	Glu	His	Leu	Leu	Leu	Asp	Leu	Gln	Met	Ile	Leu	Asn	Gly	Ile	Asn
			500					505					510		
Asn	Tyr	Lys	Asn	Pro	Lys	Leu	Thr	Ala	Met	Leu	Thr	Ala	Lys	Phe	Tyr
		515					520					525			
Met	Pro	Lys	Lys	Ala	Thr	Glu	Leu	Lys	His	Leu	Gln	Cys	Leu	Glu	Glu
	530					535					540				
Glu	Leu	Lys	Pro	Leu	Glu	Glu	Val	Leu	Asn	Leu	Ala	Gln	Ser	Lys	Asn
545					550					555					560
Phe	His	Leu	Arg	Pro	Arg	Asp	Leu	Ile	Ser	Asn	Ile	Asn	Val	Ile	Val
				565					570					575	
Leu	Glu	Leu	Lys	Gly	Ser	Glu	Thr	Thr	Phe	Met	Cys	Glu	Tyr	Ala	Asp
			580					585					590		
Glu	Thr	Ala	Thr	Ile	Val	Glu	Phe	Leu	Asn	Arg	Trp	Ile	Thr	Phe	Cys
		595					600					605			
Gln	Ser	Ile	Ile	Ser	Thr	Leu	Thr								
	610					615									

<210> 16
 <211> 1437
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> nucleotides coding fusion protein (GI101C1)

<400> 16
atggatgcta tgctgagagg cctgtgttgc gtgctgctgc tgtgtggcgc tgtgttcgtg 60
tctccttctc acgctgtgat ccacgtgacc aaagaagtga aagaggtcgc cacactgtcc 120
tgccggccaca acgtttcagt ggaagaactg gcccagacca ggatctactg gcagaaagaa 180
aagaaaatgg tgctgaccat gatgtccggc gacatgaaca tctggcctga gtacaagaac 240
cggaccatct tcgacatcac caacaacctg tccatcgtga ttctggccct gaggccttct 300
gatgagggca cctatgagtg cgtggtgctg aagtacgaga aggacgcctt caagcgcgag 360
cacctggctg aagtgacact gtccgtgaag gccgactttc ccacaccttc catctccgac 420
ttcgagatcc ctacctcaa catccggcgg atcatctgtt ctacctctgg cggctttcct 480
gagcctcacc tgtcttggct ggaaaacggc gaggaactga acgccatcaa caccaccgtg 540
tctcaggacc ccgaaaccga gctgtacgct gtgtcctcca agctggactt caacatgacc 600
accaaccaca gcttcatgtg cctgattaag tacggccacc tgagagtga ccagaccttc 660
aactggaaca ccaccaagca agagcacttc cctgacaatg gatctggcgg cggagggttct 720
ggcggagggtg gaagcggagg cggaggatct gctgagtcta agtatggccc tccttgcctt 780
ccatgtcctg ctccagaagc tgctggcggg ccctctgtgt tcctgtttcc tccaaagcct 840
aaggaccagc tcatgatctc tcggacacc gaagtgacct gcgtgggtgg ggatgtgtct 900
caagaggacc ctgagggtgca gttcaattgg tacgtggacg gcgtggaagt gcacaacgcc 960
aagaccaagc ctagagagga acagttcaac tccacctaca gagtgggtgtc cgtgctgacc 1020
gtgctgcacc aggattggct gaacggcaaa gagtacaagt gcaagggtgtc caacaagggc 1080
ctgccttcca gcatcga aaa gaccatctcc aaggctaagg gccagcctag ggaacccag 1140
gtttacaccc tgctccaag ccaagaggaa atgaccaaga accagggtgtc cctgacctgc 1200
ctgggtcaagg gcttctaccc ttccgacatt gccgtggaat gggagtccaa tggccagcct 1260
gagaacaact acaagaccac acctcctgtg ctggactccg acggctcctt ctttctgtac 1320
tctcgcctga ccgtggacaa gtctagggtg caagagggca acgtgttctc ctgctctgtg 1380
ctgcacgagg ccctgcacaa tcactacacc cagaagtccc tgtctctgtc cctgggc 1437

<210> 17
<211> 454
<212> PRT
<213> Artificial Sequence

<220>

<223> fusion protein (GI101C1)

<400> 17

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

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

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
100 105 110

Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
115 120 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
130 135 140

Gly Glu Glu Leu Asn Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145 150 155 160

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
165 170 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
180 185 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
195 200 205

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
210 215 220

Ser Ala Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro
225 230 235 240

Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
245 250 255

Asp Gln Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
 260 265 270
 Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
 275 280 285
 Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
 290 295 300
 Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
 305 310 315 320
 Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
 325 330 335
 Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
 340 345 350
 Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
 355 360 365
 Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
 370 375 380
 Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
 385 390 395 400
 Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
 405 410 415
 Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
 420 425 430
 Cys Ser Val Leu His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
 435 440 445
 Leu Ser Leu Ser Leu Gly
 450

<210> 18
 <211> 1176
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> nucleotides coding fusion protein (GI101C2)

<400> 18
 atggatgcta tgctgagagg cctgtgttgc gtgctgctgc tgtgtggcgc tgtgttcgtg 60
 tctccatctc acgccgtga gtctaagtac ggccctcctt gtcctccatg tcctgctcca 120

gaagctgctg gcggaacctc tgtgttcctg tttcctccaa agcctaagga ccagctcatg	180
atctctcgga cccctgaagt gacctgcgtg gtggtggatg tgtctcaaga ggacctgag	240
gtgcagttca attggtacgt ggacggcgtg gaagtgcaca acgccaagac caagcctaga	300
gaggaacagt tcaactccac ctacagagtg gtgtccgtgc tgaccgtgct gcaccaggat	360
tggctgaacg gcaaagagta caagtgcaag gtgtccaaca agggcctgcc ttccagcatc	420
gaaaagacca tctccaaggc taagggccag cctaggggaac cccaggttta caccctgcct	480
ccaagccaag aggaaatgac caagaaccag gtgtccctga cctgcctggt caagggcttc	540
tacccttccg acattgccgt ggaatgggag tccaatggcc agcctgagaa caactacaag	600
accacacctc ctgtgctgga ctccgacggc tccttctttc tgtactctcg cctgaccgtg	660
gacaagtcta ggtggcaaga gggcaacgtg ttctcctgct ctgtgctgca cgaggccctg	720
cacaatcact acaccagaa gtccctgtct ctgtctcttg gcggaggcgg aggatctgct	780
cctacctcca gtcaccacaa gaaaaccag ctccagttgg agcatctgct gctggacctc	840
cagatgatcc tgaatggcat caacaattac aagaaccca agctgaccgc catgctgacc	900
gctaagttct acatgcccaa gaaggccacc gagctgaagc acctccagtg cctggaagag	960
gaactgaagc ccctggaaga agtgctgaat ctggcccagt ccaagaactt ccacctgagg	1020
cctagggacc tgatctccaa catcaacgtg atcgtgctgg aactgaaagg ctccgagaca	1080
accttcatgt gcgagtacgc cgacgagaca gccaccatcg tggaatttct gaaccggtgg	1140
atcaccttct gccagtccat catctccaca ctgacc	1176

<210> 19
 <211> 367
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> fusion protein (GI101C2)

<400> 19
 Ala Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu
 1 5 10 15

 Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
 20 25 30

 Gln Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp

35	40	45															
Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly		
50						55					60						
Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn		
65					70					75					80		
Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp		
				85					90					95			
Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro		
			100					105					110				
Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu		
		115					120					125					
Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn		
		130				135					140						
Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile		
145					150					155					160		
Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr		
				165					170					175			
Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg		
			180					185					190				
Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys		
		195					200					205					
Ser	Val	Leu	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu		
		210				215					220						
Ser	Leu	Ser	Leu	Gly	Gly	Gly	Gly	Gly	Ser	Ala	Pro	Thr	Ser	Ser	Ser		
225					230					235					240		
Thr	Lys	Lys	Thr	Gln	Leu	Gln	Leu	Glu	His	Leu	Leu	Leu	Asp	Leu	Gln		
				245				250						255			
Met	Ile	Leu	Asn	Gly	Ile	Asn	Asn	Tyr	Lys	Asn	Pro	Lys	Leu	Thr	Ala		
			260					265					270				
Met	Leu	Thr	Ala	Lys	Phe	Tyr	Met	Pro	Lys	Lys	Ala	Thr	Glu	Leu	Lys		
		275					280					285					
His	Leu	Gln	Cys	Leu	Glu	Glu	Glu	Leu	Lys	Pro	Leu	Glu	Glu	Val	Leu		
		290				295					300						
Asn	Leu	Ala	Gln	Ser	Lys	Asn	Phe	His	Leu	Arg	Pro	Arg	Asp	Leu	Ile		
305					310					315					320		
Ser	Asn	Ile	Asn	Val	Ile	Val	Leu	Glu	Leu	Lys	Gly	Ser	Glu	Thr	Thr		

	325		330		335
Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu					
	340		345		350
Asn Arg Trp Ile Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr					
	355		360		365

<210> 20
 <211> 1434
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> nucleotiedes coding fusion protein (mGI101C1)

<400> 20
 atggatgcta tgctgagagg cctgtgttgc gtgctgctgc tgtgtggcgc tgtgttcgtg 60
 tctccttctc acgctgtgga cgagcagctc tccaagtccg tgaaggataa ggtcctgctg 120
 ccttgccggt acaactctcc tcacaggagc gagtctgagg accggatcta ctggcagaaa 180
 cacgacaagg tgggtgctgtc cgtgatcgcc ggaaagctga aagtgtggcc tgagtacaag 240
 aacaggaccc tgtacgacaa caccacctac agcctgatca tcctgggcct cgtgctgagc 300
 gatagaggca cctattcttg cgtgggtgcag aagaaagagc ggggcaccta cgaagtgaag 360
 cacctggctc tgggtcaagct gtccatcaag gccgacttca gcacccctaa catcaccgag 420
 tctggcaacc cttccgccga caccaagaga atcacctgtt tcgcctctgg cggcttcctt 480
 aagcctcggc tctcttggct ggaaaacggc agagagctgc ccggcatcaa taccaccatt 540
 tctcaggacc cagagtccga gctgtacacc atctccagcc agctcgactt taacaccacc 600
 agaaaccaca ccatcaagtg cctgattaag tacggcgacg cccacgtgtc cgaggacttt 660
 acttgggaga aacctcctga ggaccctcct gactctggat ctggcggcgg aggttctggc 720
 ggaggtggaa gcggaggcgg aggatctgct gagtctaagt atggccctcc ttgtcctcca 780
 tgtcctgctc cagaagctgc tggcggaccc tctgtgttcc tgtttcctcc aaagcctaag 840
 gaccagctca tgatctctcg gaccctgaa gtgacctgcg tgggtggtgga tgtgtctcaa 900
 gaggaccctg aggtgcagtt caattggtac gtggacggcg tggaaagtga caacgccaag 960
 accaagccta gagaggaaca gttcaactcc acctatagag tgggtgtccgt gctgaccgtg 1020

ctgcaccagg attggctgaa cggcaaagag tacaagtgca aggtgtccaa caagggcctg 1080
ccttccagca tcgaaaagac catcagcaag gctaagggcc agcctaggga accccaggtt 1140
tacaccctgc ctccaagcca agaggaaatg accaagaacc aggtgtccct gacctgcctg 1200
gtcaagggct tctacccttc cgacattgcc gtggaatggg agtccaatgg ccagcctgag 1260
aacaactaca agaccacacc tcctgtgctg gactccgacg gctccttctt tctgtactct 1320
cgcctgaccg tggacaagtc taggtggcaa gagggcaacg tgttctcctg ctctgtgctg 1380
cacgaggctc tgcacaacca ctacaccag aagtcctgt ctctgtccct gggc 1434

<210> 21
<211> 478
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein (mGI101C1)

<400> 21
Met Asp Ala Met Leu Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
1 5 10 15
Ala Val Phe Val Ser Pro Ser His Ala Val Asp Glu Gln Leu Ser Lys
20 25 30
Ser Val Lys Asp Lys Val Leu Leu Pro Cys Arg Tyr Asn Ser Pro His
35 40 45
Glu Asp Glu Ser Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val
50 55 60
Val Leu Ser Val Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys
65 70 75 80
Asn Arg Thr Leu Tyr Asp Asn Thr Thr Tyr Ser Leu Ile Ile Leu Gly
85 90 95
Leu Val Leu Ser Asp Arg Gly Thr Tyr Ser Cys Val Val Gln Lys Lys
100 105 110
Glu Arg Gly Thr Tyr Glu Val Lys His Leu Ala Leu Val Lys Leu Ser
115 120 125
Ile Lys Ala Asp Phe Ser Thr Pro Asn Ile Thr Glu Ser Gly Asn Pro
130 135 140
Ser Ala Asp Thr Lys Arg Ile Thr Cys Phe Ala Ser Gly Gly Phe Pro

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

435 440 445
 Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Leu His Glu Ala Leu
 450 455 460

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly
 465 470 475

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

<220>
 <223> variants of IL-2 (3M, M45)

<400> 22
 Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
 1 5 10 15

Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
 20 25 30

Asn Pro Lys Leu Thr Ala Met Leu Thr Ala Lys Phe Ala Met Pro Lys
 35 40 45

Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
 50 55 60

Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
 65 70 75 80

Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
 85 90 95

Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
 100 105 110

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

Ile Ser Thr Leu Thr
 130

<210> 23
 <211> 133
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> variants of IL-2 (3M, M61)

<400> 23
Ala Pro Thr Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
1 5 10 15
Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
20 25 30
Asn Pro Lys Leu Thr Ala Met Leu Thr Ala Lys Phe Tyr Met Pro Lys
35 40 45
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Arg Glu Leu Lys
50 55 60
Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
65 70 75 80
Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
85 90 95
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
100 105 110
Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser Ile
115 120 125
Ile Ser Thr Leu Thr
130

<210> 24
<211> 133
<212> PRT
<213> Artificial Sequence
<220>
<223> variants of IL-2 (3M, M72)

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

65		70		75		80									
Arg	Pro	Arg	Asp	Leu	Ile	Ser	Asn	Ile	Asn	Val	Ile	Val	Leu	Glu	Leu
				85					90					95	
Lys	Gly	Ser	Glu	Thr	Thr	Phe	Met	Cys	Glu	Tyr	Ala	Asp	Glu	Thr	Ala
			100					105					110		
Thr	Ile	Val	Glu	Phe	Leu	Asn	Arg	Trp	Ile	Thr	Phe	Cys	Gln	Ser	Ile
		115					120					125			
Ile	Ser	Thr	Leu	Thr											
		130													

<210> 25
 <211> 1851
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> nucleotides coding fusion protein (GI102-M45)

<400> 25	
atggatgcta tgctgagagg cctgtgttgc gtgctgctgc tgtgtggcgc tgtgttcgtg	60
tctccttctc acgctgtgat ccacgtgacc aaagaagtga aagaggctgc cacactgtcc	120
tgcggccaca acgtttcagt ggaagaactg gccagacca ggatctactg gcagaaagaa	180
aagaaaatgg tgctgacat gatgtccggc gacatgaaca tctggcctga gtacaagaac	240
cggaccatct tcgacatcac caacaacctg tccatcgtga ttctggccct gaggccttct	300
gatgagggca cctatgagtg cgtgggtgctg aagtacgaga aggacgcctt caagcgcgag	360
cacctggctg aagtgacact gtccgtgaag gccgactttc ccacaccttc catctccgac	420
ttcgagatcc ctacctcaa catccggcgg atcatctgtt ctacctctgg cggctttcct	480
gagcctcacc tgtcttggct ggaaaacggc gaggaactga acgccatcaa caccaccgtg	540
tctcaggacc ccgaaaccga gctgtacgct gtgtcctcca agctggactt caacatgacc	600
accaaccaca gcttcatgtg cctgattaag tacggccacc tgagagtga ccagaccttc	660
aactggaaca ccaccaagca agagcacttc cctgacaatg gatctggcgg cggaggttct	720
ggcggagggtg gaagcggagg cggaggatct gctgagtcta agtatggccc tcctgtcct	780
ccatgtcctg ctccagaagc tgctggcgga ccctctgtgt tcctgtttcc tccaaagcct	840
aaggaccagc tcatgatctc tcggacaccc gaagtgacct gcgtggtggt ggatgtgtct	900

caagaggacc ctgagggtgca gttcaattgg tacgtggacg gcgtggaagt gcacaacgcc 960
 aagaccaagc ctagagagga acagttcaac tccacctaca gagtggtgtc cgtgctgacc 1020
 gtgctgcacc aggattggct gaacggcaaa gagtacaagt gcaaggtgtc caacaagggc 1080
 ctgccttcca gcatcgaaaa gaccatctcc aaggctaagg gccagcctag ggaaccccag 1140
 gtttacaccc tgcctccaag ccaagaggaa atgaccaaga accaggtgtc cctgacctgc 1200
 ctgggtcaagg gcttctaccc ttccgacatt gccgtggaat gggagtccaa tggccagcct 1260
 gagaacaact acaagaccac acctcctgtg ctggactccg acggctcctt ctttctgtac 1320
 tctcgctga ccgtggacaa gtctagatgg caagagggca acgtgttctc ctgctctgtg 1380
 ctgcacgagg ccctgcacaa tcactacacc cagaagtccc tgtctctgtc tcttgagggt 1440
 ggtggcggtt ctgcccctac cagctcctct accaagaaaa cccagctcca gttggagcat 1500
 ctgctgctgg acctccagat gattctgaac gggatcaaca actataagaa cccaagctg 1560
 accgccatgc tgaccgctaa gttcgccatg cccaagaagg ccaccgagct gaagcacctc 1620
 cagtgcctgg aagaagaact gaagcccctg gaagaggtgc tgaatctggc ccagtccaag 1680
 aacttccacc tgaggccacg ggacctgatc agcaacatca acgtgatcgt gctggaactg 1740
 aagggtccg agacaacctt tatgtgcgag tacgccgacg agacagccac catcgtggaa 1800
 tttctgaacc ggtggatcac cttctgccag agcatcatct ccacactgac c 1851

<210> 26
 <211> 592
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> fusion protein (GI102-M45)

<400> 26
 Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
 1 5 10 15
 Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
 20 25 30
 Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
 35 40 45
 Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn

50	55	60																	
Leu	Ser	Ile	Val	Ile	Leu	Ala	Leu	Arg	Pro	Ser	Asp	Glu	Gly	Thr	Tyr				
65					70					75					80				
Glu	Cys	Val	Val	Leu	Lys	Tyr	Glu	Lys	Asp	Ala	Phe	Lys	Arg	Glu	His				
				85					90					95					
Leu	Ala	Glu	Val	Thr	Leu	Ser	Val	Lys	Ala	Asp	Phe	Pro	Thr	Pro	Ser				
			100					105					110						
Ile	Ser	Asp	Phe	Glu	Ile	Pro	Thr	Ser	Asn	Ile	Arg	Arg	Ile	Ile	Cys				
		115					120					125							
Ser	Thr	Ser	Gly	Gly	Phe	Pro	Glu	Pro	His	Leu	Ser	Trp	Leu	Glu	Asn				
	130					135					140								
Gly	Glu	Glu	Leu	Asn	Ala	Ile	Asn	Thr	Thr	Val	Ser	Gln	Asp	Pro	Glu				
145					150					155					160				
Thr	Glu	Leu	Tyr	Ala	Val	Ser	Ser	Lys	Leu	Asp	Phe	Asn	Met	Thr	Thr				
				165					170					175					
Asn	His	Ser	Phe	Met	Cys	Leu	Ile	Lys	Tyr	Gly	His	Leu	Arg	Val	Asn				
			180					185					190						
Gln	Thr	Phe	Asn	Trp	Asn	Thr	Thr	Lys	Gln	Glu	His	Phe	Pro	Asp	Asn				
		195					200					205							
Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly				
210						215					220								
Ser	Ala	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro				
225					230					235					240				
Glu	Ala	Ala	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys				
				245					250					255					
Asp	Gln	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val				
			260					265					270						
Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp				
		275					280					285							
Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe				
290					295						300								
Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp				
305					310				315						320				
Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu				
				325					330					335					
Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg				

	340		345		350										
Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys
	355						360					365			
Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp
	370					375					380				
Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys
385					390					395					400
Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser
				405					410					415	
Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser
			420					425					430		
Cys	Ser	Val	Leu	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser
		435					440					445			
Leu	Ser	Leu	Ser	Leu	Gly	Gly	Gly	Gly	Gly	Ser	Ala	Pro	Thr	Ser	Ser
	450					455					460				
Ser	Thr	Lys	Lys	Thr	Gln	Leu	Gln	Leu	Glu	His	Leu	Leu	Leu	Asp	Leu
465					470				475						480
Gln	Met	Ile	Leu	Asn	Gly	Ile	Asn	Asn	Tyr	Lys	Asn	Pro	Lys	Leu	Thr
				485					490					495	
Ala	Met	Leu	Thr	Ala	Lys	Phe	Ala	Met	Pro	Lys	Lys	Ala	Thr	Glu	Leu
			500					505					510		
Lys	His	Leu	Gln	Cys	Leu	Glu	Glu	Glu	Leu	Lys	Pro	Leu	Glu	Glu	Val
	515						520					525			
Leu	Asn	Leu	Ala	Gln	Ser	Lys	Asn	Phe	His	Leu	Arg	Pro	Arg	Asp	Leu
	530					535					540				
Ile	Ser	Asn	Ile	Asn	Val	Ile	Val	Leu	Glu	Leu	Lys	Gly	Ser	Glu	Thr
545					550				555						560
Thr	Phe	Met	Cys	Glu	Tyr	Ala	Asp	Glu	Thr	Ala	Thr	Ile	Val	Glu	Phe
				565				570						575	
Leu	Asn	Arg	Trp	Ile	Thr	Phe	Cys	Gln	Ser	Ile	Ile	Ser	Thr	Leu	Thr
			580					585					590		

<210> 27
 <211> 1851
 <212> DNA
 <213> Artificial Sequence

<220>

<223> nucleotides coding fusion protein (GI102-M61)

<400> 27

atggatgcta tgctgagagg cctgtgttgc gtgctgctgc tgtgtggcgc tgtgttcgtg	60
tctccttctc acgctgtgat ccacgtgacc aaagaagtga aagaggtcgc cacactgtcc	120
tgcgccaca acgtttcagt ggaagaactg gcccagacca ggatctactg gcagaaagaa	180
aagaaaatgg tgctgaccat gatgtccggc gacatgaaca tctggcctga gtacaagaac	240
cggaccatct tcgacatcac caacaacctg tccatcgtga ttctggccct gaggccttct	300
gatgagggca cctatgagtg cgtgggtgctg aagtacgaga aggacgcctt caagcgcgag	360
cacctggctg aagtgacact gtccgtgaag gccgactttc ccacaccttc catctccgac	420
ttcgagatcc ctacctcaa catccggcgg atcatctgtt ctacctctgg cggctttcct	480
gagcctcacc tgtcttggct ggaaaacggc gaggaactga acgccatcaa caccaccgtg	540
tctcaggacc ccgaaaccga gctgtacgct gtgtcctcca agctggactt caacatgacc	600
accaaccaca gttcatgtg cctgattaag tacggccacc tgagagtga ccagaccttc	660
aactggaaca ccaccaagca agagcacttc cctgacaatg gatctggcgg cggaggttct	720
ggcggagggtg gaagcggagg cggaggatct gctgagtcta agtatggccc tccttgcct	780
ccatgtcctg ctccagaagc tgctggcggg ccctctgtgt tcctgtttcc tcaaagcct	840
aaggaccagc tcatgatctc tcggacacc gaagtgacct gcgtgggtgt ggatgtgtct	900
caagaggacc ctgagggtgca gttcaattgg tacgtggacg gcgtggaagt gcacaacgcc	960
aagaccaagc ctagagagga acagttcaac tccacctaca gagtgggtgtc cgtgctgacc	1020
gtgctgcacc aggattggct gaacggcaaa gagtacaagt gcaagggtgtc caacaagggc	1080
ctgccttcca gcatcgaaaa gaccatctcc aaggctaagg gccagcctag ggaacccag	1140
gtttacaccc tgctccaag ccaagaggaa atgaccaaga accagggtgtc cctgacctgc	1200
ctgggtcaagg gcttctaccc ttccgacatt gccgtggaat gggagtccaa tggccagcct	1260
gagaacaact acaagaccac acctcctgtg ctggactccg acggctcctt ctttctgtac	1320
tctcgcctga ccgtggacaa gtctagatgg caagagggca acgtgttctc ctgctctgtg	1380
ctgcacgagg ccctgcacaa tcactacacc cagaagtccc tgtctctgtc tcttgagggt	1440

ggtggcggtt ctgcccctac cagctcctct accaagaaaa cccagctcca gttggagcat 1500
 ctgctgctgg acctccagat gattctgaac gggatcaaca actataagaa cccaagctg 1560
 accgccatgc tgaccgctaa gttctacatg cccaagaagg ccaccgagct gaagcacctc 1620
 cagtgcctgg aaagggaact gaagcccctg gaagaggtgc tgaatctggc ccagtccaag 1680
 aatttccacc tgaggccacg ggacctgac agcaacatca acgtgacgt gctggaactg 1740
 aagggtccg agacaacctt tatgtgcgag tacgccgacg agacagccac catcgtggaa 1800
 tttctgaacc ggtggatcac cttctgccag agcatcatct ccacactgac c 1851

<210> 28
 <211> 592
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> fusion protein (GI102-M61)

<400> 28
 Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
 1 5 10 15
 Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
 20 25 30
 Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
 35 40 45
 Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
 50 55 60
 Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
 65 70 75 80
 Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
 85 90 95
 Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
 100 105 110
 Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
 115 120 125
 Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
 130 135 140
 Gly Glu Glu Leu Asn Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
 145 150 155 160

Thr	Glu	Leu	Tyr	Ala	Val	Ser	Ser	Lys	Leu	Asp	Phe	Asn	Met	Thr	Thr	
				165					170					175		
Asn	His	Ser	Phe	Met	Cys	Leu	Ile	Lys	Tyr	Gly	His	Leu	Arg	Val	Asn	
			180					185					190			
Gln	Thr	Phe	Asn	Trp	Asn	Thr	Thr	Lys	Gln	Glu	His	Phe	Pro	Asp	Asn	
		195					200					205				
Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	
	210					215					220					
Ser	Ala	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	
225					230				235						240	
Glu	Ala	Ala	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	
				245					250					255		
Asp	Gln	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	
			260					265					270			
Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	
		275					280					285				
Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	
	290					295					300					
Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	
305					310					315					320	
Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	
				325					330					335		
Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	
			340					345					350			
Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	
		355					360				365					
Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	
		370				375					380					
Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	
385					390					395					400	
Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	
				405					410					415		
Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	
			420					425					430			
Cys	Ser	Val	Leu	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	
		435					440					445				

Leu Ser Leu Ser Leu Gly Gly Gly Gly Ser Ala Pro Thr Ser Ser
 450 455 460
 Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu
 465 470 475 480
 Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr
 485 490 495
 Ala Met Leu Thr Ala Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu
 500 505 510
 Lys His Leu Gln Cys Leu Glu Arg Glu Leu Lys Pro Leu Glu Glu Val
 515 520 525
 Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu
 530 535 540
 Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr
 545 550 555 560
 Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe
 565 570 575
 Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr
 580 585 590

<210> 29
 <211> 1857
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> nucleotides coding fusion protein (GI102-M72)

<400> 29
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 tctccttctc acgctgtgat ccacgtgacc aaagaagtga aagaggtcgc cacactgtcc 120
 tgcggccaca acgtttcagt ggaagaactg gcccagacca ggatctactg gcagaaagaa 180
 aagaaaatgg tgctgaccat gatgtccggc gacatgaaca tctggcctga gtacaagaac 240
 cggaccatct tcgacatcac caacaacctg tccatcgtga ttctggccct gaggccttct 300
 gatgagggca cctatgagtg cgtgggtgctg aagtacgaga aggacgcctt caagcgcgag 360
 cacctggctg aagtgacact gtccgtgaag gccgactttc ccacaccttc catctccgac 420

ttcgagatcc ctacctcaa catccggcgg atcatctgtt ctacctctgg cggctttcct	480
gagcctcacc tgtcttggct ggaaaacggc gaggaactga acgccatcaa caccaccgtg	540
tctcaggacc ccgaaaccga gctgtacgct gtgtcctcca agctggactt caacatgacc	600
accaaccaca gcttcatgtg cctgattaag tacggccacc tgagagtga ccagaccttc	660
aactggaaca ccaccaagca agagcacttc cctgacaatg gatctggcgg cggagggttct	720
ggcggaggtg gaagcggagg cggaggatct gctgagtcta agtatggccc tccttgcct	780
ccatgtcctg ctccagaagc tgctggcggg ccctctgtgt tcctgtttcc tccaaagcct	840
aaggaccagc tcatgatctc tcggacaccc gaagtgcct gcgtgggtgt ggatgtgtct	900
caagaggacc ctgaggtgca gttcaattgg tacgtggacg gcgtggaagt gcacaacgcc	960
aagaccaagc ctagagagga acagttcaac tccacctaca gagtggtgtc cgtgctgacc	1020
gtgctgcacc aggattggct gaacggcaaa gagtacaagt gcaagggtgtc caacaagggc	1080
ctgccttcca gcatcgaaaa gaccatctcc aaggctaagg gccagcctag ggaacccag	1140
gtttacaccc tgcctccaag ccaagaggaa atgaccaaga accaggtgtc cctgacctgc	1200
ctgggtcaagg gcttctaccc ttccgacatt gccgtggaat gggagtccaa tggccagcct	1260
gagaacaact acaagaccac acctctgtg ctggactccg acggctcctt ctttctgtac	1320
tctcgctga ccgtggacaa gtctagatgg caagagggca acgtgttctc ctgctctgtg	1380
ctgcacgagg ccctgcacaa tcactacacc cagaagtccc tgtctctgtc tcttggaggt	1440
ggtggcgggt ctgcccctac cagctcctct accaagaaaa cccagctcca gttggagcat	1500
ctgctgctgg acctccagat gattctgaac gggatcaaca actataagaa cccaagctg	1560
accgccatgc tgaccgctaa gttctacatg cccaagaagg ccaccgagct gaagcacctc	1620
cagtgcctgg aagaagaact gaagcccctg gaagaggtgc tgaatggggc ccagtccaag	1680
aacttccacc tgaggccacg ggacctgatc agcaacatca acgtgatcgt gctggaactg	1740
aagggtccg agacaacctt tatgtgcgag tacgccgacg agacagccac catcgtggaa	1800
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<210> 30
 <211> 592
 <212> PRT
 <213> Artificial Sequence

<220>

<223> fusion protein (GI102-M72)

<400> 30

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

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

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
100 105 110

Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
115 120 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
130 135 140

Gly Glu Glu Leu Asn Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145 150 155 160

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
165 170 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
180 185 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
195 200 205

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
210 215 220

Ser Ala Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro
225 230 235 240

Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
245 250 255

Asp	Gln	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	
			260					265					270			
Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	
		275					280					285				
Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	
	290					295					300					
Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	
305					310					315					320	
Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	
				325					330					335		
Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	
			340					345					350			
Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	
		355					360					365				
Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	
	370					375					380					
Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	
385					390					395					400	
Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	
				405					410					415		
Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	
			420					425					430			
Cys	Ser	Val	Leu	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	
		435					440					445				
Leu	Ser	Leu	Ser	Leu	Gly	Gly	Gly	Gly	Gly	Ser	Ala	Pro	Thr	Ser	Ser	
	450					455					460					
Ser	Thr	Lys	Lys	Thr	Gln	Leu	Gln	Leu	Glu	His	Leu	Leu	Leu	Asp	Leu	
465					470				475						480	
Gln	Met	Ile	Leu	Asn	Gly	Ile	Asn	Asn	Tyr	Lys	Asn	Pro	Lys	Leu	Thr	
				485					490					495		
Ala	Met	Leu	Thr	Ala	Lys	Phe	Tyr	Met	Pro	Lys	Lys	Ala	Thr	Glu	Leu	
			500					505					510			
Lys	His	Leu	Gln	Cys	Leu	Glu	Glu	Glu	Leu	Lys	Pro	Leu	Glu	Glu	Val	
		515					520					525				
Leu	Asn	Gly	Ala	Gln	Ser	Lys	Asn	Phe	His	Leu	Arg	Pro	Arg	Asp	Leu	
	530					535					540					

Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr
545 550 555 560

Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe
565 570 575

Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr
580 585 590

<210> 31
<211> 1851
<212> DNA
<213> Artificial Sequence

<220>
<223> nucleotides coding fusion protein (GI101w)

<400> 31
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tctccttctc acgctgtgat ccacgtgacc aaagaagtga aagaggctgc cacactgtcc 120
tgcggccaca acgtttcagt ggaagaactg gcccagacca ggatctactg gcagaaagaa 180
aagaaaatgg tgctgaccat gatgtccggc gacatgaaca tctggcctga gtacaagaac 240
cggaccatct tcgacatcac caacaacctg tccatcgtga ttctggccct gaggccttct 300
gatgagggca cctatgagtg cgtgggtgctg aagtacgaga aggacgcctt caagcgcgag 360
cacctggctg aagtgacact gtccgtgaag gccgactttc ccacaccttc catctccgac 420
ttcgagatcc ctacctcaa catccggcgg atcatctgtt ctacctctgg cggctttcct 480
gagcctcacc tgtcttggct ggaaaacggc gaggaactga acgccatcaa caccaccgtg 540
tctcaggacc ccgaaaccga gctgtacgct gtgtcctcca agctggactt caacatgacc 600
accaaccaca gcttcatgtg cctgattaag tacggccacc tgagagtga ccagaccttc 660
aactggaaca ccaccaagca agagcacttc cctgacaatg gatctggcgg cggaggttct 720
ggcggagggtg gaagcggagg cggaggatct gctgagtcta agtatggccc tccttgcctt 780
ccatgtcctg ctccagaagc tgctggcgga ccctctgtgt tcctgtttcc tccaaagcct 840
aaggaccagc tcatgatctc tcggacaccc gaagtgacct gcgtgggtgt ggatgtgtct 900
caagaggacc ctgagggtgca gttcaattgg tacgtggacg gcgtggaagt gcacaacgcc 960

aagaccaagc ctagagagga acagttcaac tccacctaca gagtggtgtc cgtgctgacc 1020
gtgctgcacc aggattggct gaacggcaaa gagtacaagt gcaaggtgtc caacaagggc 1080
ctgccttcca gcatcgaana gaccatctcc aaggctaagg gccagcctag ggaacccag 1140
gtttacaccc tgcctccaag ccaagaggaa atgaccaaga accaggtgtc cctgacctgc 1200
ctgggtcaagg gcttctaccc ttccgacatt gccgtggaat gggagtccaa tggccagcct 1260
gagaacaact acaagaccac acctcctgtg ctggactccg acggctcctt ctttctgtac 1320
tctcgcctga ccgtggacaa gtctagatgg caagagggca acgtgttctc ctgctctgtg 1380
ctgcacgagg ccctgcacaa tcactacacc cagaagtccc tgtctctgtc tcttgagggt 1440
ggtggcggtt ctgcccctac cagctcctct accaagaaaa cccagctcca gttggagcat 1500
ctgctgctgg acctccagat gattctgaac gggatcaaca actataagaa cccaagctg 1560
acccgcatgc tgacctttaa gttctacatg cccaagaagg ccaccgagct gaagcacctc 1620
cagtgcctgg aagaagaact gaagcccctg gaagaggtgc tgaatctggc ccagtccaag 1680
aacttccacc tgaggccacg ggacctgac agcaacatca acgtgatcgt gctggaactg 1740
aagggtccg agacaacctt tatgtgcgag tacgccgacg agacagccac catcgtggaa 1800
tttctgaacc ggtggatcac cttctgccag agcatcatct ccacactgac c 1851

<210> 32
<211> 592
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein (GI101w)

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

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

355	360	365
Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp		
370	375	380
Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys		
385	390	395
Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser		
405	410	415
Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser		
420	425	430
Cys Ser Val Leu His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser		
435	440	445
Leu Ser Leu Ser Leu Gly Gly Gly Gly Gly Ser Ala Pro Thr Ser Ser		
450	455	460
Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu		
465	470	475
Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr		
485	490	495
Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu		
500	505	510
Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val		
515	520	525
Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu		
530	535	540
Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr		
545	550	555
Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe		
565	570	575
Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr		
580	585	590

<210> 33
 <211> 1848
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> nucleotiedes coding fusion protein (mGI102-M61)

<400> 33

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ccttgccggt acaactctcc tcacgaggac gagtctgagg accggatcta ctggcagaaa	180
cacgacaagg tgggtgctgtc cgtgatcgcc ggaaagctga aagtgtggcc tgagtacaag	240
aacaggaccc tgtacgacaa caccacctac agcctgatca tcctgggcct cgtgctgagc	300
gatagaggca cctattcttg cgtggtgcag aagaaagagc ggggcaccta cgaagtgaag	360
cacctggctc tggtaagct gtccatcaag gccgacttca gcaccctaata catcaccgag	420
tctggcaacc cttccgccga caccaagaga atcacctgtt tcgcctctgg cggcttccct	480
aagcctcggc tctcttggct ggaaaacggc agagagctgc ccggcatcaa taccaccatt	540
tctcaggacc cagagtccga gctgtacacc atctccagcc agctcgactt taacaccacc	600
agaaaccaca ccatcaagtg cctgattaag tacggcgacg cccacgtgtc cgaggacttt	660
acttgggaga aacctcctga ggacctcct gactctggat ctggcggcgg aggttctggc	720
ggaggtggaa gcggaggcgg aggatctgct gagtctaagt atggccctcc ttgtcctcca	780
tgtcctgctc cagaagctgc tggcggaccc tctgtgttcc tgtttcctcc aaagcctaag	840
gaccagctca tgatctctcg gaccttgaa gtgacctgcg tgggtggtgga tgtgtctcaa	900
gaggaccctg aggtgcagtt caattggtac gtggacggcg tggaaagtga caacgccaag	960
accaagccta gagaggaaca gttcaactcc acctatagag tgggtgtccgt gctgaccgtg	1020
ctgcaccagg attggctgaa cggcaaagag tacaagtga aggtgtccaa caagggcctg	1080
ccttccagca tcgaaaagac catcagcaag gctaagggcc agcctaggga accccaggtt	1140
tacaccctgc ctccaagcca agaggaaatg accaagaacc aggtgtccct gacctgcctg	1200
gtcaagggtc tctacccttc cgacattgcc gtggaatggg agtccaatgg ccagcctgag	1260
aacaactaca agaccacacc tcctgtgctg gactccgacg gctccttctt tctgtactct	1320
cgctgaccg tggacaagtc taggtggcaa gagggcaacg tgttctcctg ctctgtgctg	1380
cacgaggctc tgcacaacca ctacaccag aagtccctgt ctctgtctct tggaggtggt	1440
ggcggttctg cccctacctc cagctctacc aagaaaaccc agctccagtt ggagcatctg	1500
ctgctggacc tccagatgat cctgaatggc atcaacaatt acaagaaccc caagctgacc	1560

gccatgctga ccgctaagtt ctacatgccc aagaaggcca ccgagctgaa gcacttgtag 1620
 tgcctggaaa gggaactgaa gcccctggaa gaagtgtgta atctggccca gtccaagaac 1680
 ttccacctga ggcctaggga cctgatctcc aacatcaacg tgatcgtgct ggaactgaaa 1740
 ggctccgaga caaccttcat gtgcgagtac gccgacgaga cagccaccat cgtggaattt 1800
 ctgaaccggt ggatcacctt ctgccagagc atcatctcca cactgacc 1848

<210> 34
 <211> 616
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> fusion protein (mGI102-M61)

<400> 34
 Met Asp Ala Met Leu Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
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 Ala Val Phe Val Ser Pro Ser His Ala Val Asp Glu Gln Leu Ser Lys
 20 25 30
 Ser Val Lys Asp Lys Val Leu Leu Pro Cys Arg Tyr Asn Ser Pro His
 35 40 45
 Glu Asp Glu Ser Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val
 50 55 60
 Val Leu Ser Val Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys
 65 70 75 80
 Asn Arg Thr Leu Tyr Asp Asn Thr Thr Tyr Ser Leu Ile Ile Leu Gly
 85 90 95
 Leu Val Leu Ser Asp Arg Gly Thr Tyr Ser Cys Val Val Gln Lys Lys
 100 105 110
 Glu Arg Gly Thr Tyr Glu Val Lys His Leu Ala Leu Val Lys Leu Ser
 115 120 125
 Ile Lys Ala Asp Phe Ser Thr Pro Asn Ile Thr Glu Ser Gly Asn Pro
 130 135 140
 Ser Ala Asp Thr Lys Arg Ile Thr Cys Phe Ala Ser Gly Gly Phe Pro
 145 150 155 160
 Lys Pro Arg Phe Ser Trp Leu Glu Asn Gly Arg Glu Leu Pro Gly Ile
 165 170 175

Asn	Thr	Thr	Ile	Ser	Gln	Asp	Pro	Glu	Ser	Glu	Leu	Tyr	Thr	Ile	Ser		
			180					185						190			
Ser	Gln	Leu	Asp	Phe	Asn	Thr	Thr	Arg	Asn	His	Thr	Ile	Lys	Cys	Leu		
		195					200					205					
Ile	Lys	Tyr	Gly	Asp	Ala	His	Val	Ser	Glu	Asp	Phe	Thr	Trp	Glu	Lys		
	210					215					220						
Pro	Pro	Glu	Asp	Pro	Pro	Asp	Ser	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly		
225					230					235					240		
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Ala	Glu	Ser	Lys	Tyr	Gly	Pro		
				245					250					255			
Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Ala	Ala	Gly	Gly	Pro	Ser	Val		
			260					265					270				
Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Gln	Leu	Met	Ile	Ser	Arg	Thr		
		275					280					285					
Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu		
	290					295					300						
Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys		
305					310					315					320		
Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser		
				325					330					335			
Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys		
			340					345					350				
Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile		
		355					360					365					
Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro		
	370					375					380						
Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu		
385					390					395					400		
Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn		
			405						410					415			
Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser		
			420					425					430				
Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg		
		435					440					445					
Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Leu	His	Glu	Ala	Leu		
	450					455					460						

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Gly Gly
 465 470 475 480
 Gly Gly Ser Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln
 485 490 495
 Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn
 500 505 510
 Asn Tyr Lys Asn Pro Lys Leu Thr Ala Met Leu Thr Ala Lys Phe Tyr
 515 520 525
 Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Arg
 530 535 540
 Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn
 545 550 555 560
 Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val
 565 570 575
 Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp
 580 585 590
 Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys
 595 600 605
 Gln Ser Ile Ile Ser Thr Leu Thr
 610 615

<210> 35
 <211> 153
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> wild type hIL-2

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

Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu
 65 70 75 80
 Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys
 85 90 95
 Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile
 100 105 110
 Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala
 115 120 125
 Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe
 130 135 140
 Cys Gln Ser Ile Ile Ser Thr Leu Thr
 145 150

<210> 36
 <211> 158
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> IL-2 with signal sequence

<400> 36
 Met Asp Ala Met Leu Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
 1 5 10 15
 Ala Val Phe Val Ser Pro Ser His Ala Ala Pro Thr Ser Ser Ser Thr
 20 25 30
 Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met
 35 40 45
 Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met
 50 55 60
 Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His
 65 70 75 80
 Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn
 85 90 95
 Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser
 100 105 110
 Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe
 115 120 125
 Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn

130	135	140
Arg Trp Ile Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr		
145	150	155

<210> 37
 <211> 474
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> nucleotide sequence coding IL-2 with signal sequence

<400> 37
 atggatgcta tgctgagagg cctgtgttgc gtgctgctgc tgtgtggcgc tgtgttcgtg 60
 tctccttctc acgctgcccc taccagctcc tctaccaaga aaaccagct ccagttggag 120
 catctgctgc tggacctcca gatgattctg aacgggatca acaactataa gaacccaag 180
 ctgacccgca tgctgacctt taagttctac atgcccaaga aggccaccga gctgaagcac 240
 ctccagtgcc tggaagaaga actgaagccc ctggaagagg tgctgaatct ggcccagtcc 300
 aagaacttcc acctgaggcc acgggacctg atcagcaaca tcaacgtgat cgtgctggaa 360
 ctgaagggct ccgagacaac ctttatgtgc gagtacgccg acgagacagc caccatcgtg 420
 gaatttctga accggtggat caccttctgc cagagcatca tctccacact gacc 474

<210> 38
 <211> 591
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> mGI-101

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

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

Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	
		355					360					365				
Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	
	370					375					380					
Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	
385					390					395					400	
Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	
			405					410						415		
Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	
		420						425					430			
Ser	Val	Leu	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	
	435						440					445				
Ser	Leu	Ser	Leu	Gly	Gly	Gly	Gly	Gly	Ser	Ala	Pro	Thr	Ser	Ser	Ser	
	450					455					460					
Thr	Lys	Lys	Thr	Gln	Leu	Gln	Leu	Glu	His	Leu	Leu	Leu	Asp	Leu	Gln	
465					470			475							480	
Met	Ile	Leu	Asn	Gly	Ile	Asn	Asn	Tyr	Lys	Asn	Pro	Lys	Leu	Thr	Ala	
			485					490						495		
Met	Leu	Thr	Ala	Lys	Phe	Tyr	Met	Pro	Lys	Lys	Ala	Thr	Glu	Leu	Lys	
			500					505					510			
His	Leu	Gln	Cys	Leu	Glu	Glu	Glu	Leu	Lys	Pro	Leu	Glu	Glu	Val	Leu	
	515					520						525				
Asn	Leu	Ala	Gln	Ser	Lys	Asn	Phe	His	Leu	Arg	Pro	Arg	Asp	Leu	Ile	
	530					535					540					
Ser	Asn	Ile	Asn	Val	Ile	Val	Leu	Glu	Leu	Lys	Gly	Ser	Glu	Thr	Thr	
545				550				555							560	
Phe	Met	Cys	Glu	Tyr	Ala	Asp	Glu	Thr	Ala	Thr	Ile	Val	Glu	Phe	Leu	
			565					570					575			
Asn	Arg	Trp	Ile	Thr	Phe	Cys	Gln	Ser	Ile	Ile	Ser	Thr	Leu	Thr		
		580						585					590			

<210> 39
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>

<223> TIGIT ECD

<400> 39

Met Met Thr Gly Thr Ile Glu Thr Thr Gly Asn Ile Ser Ala Glu Lys
1 5 10 15

Gly Gly Ser Ile Ile Leu Gln Cys His Leu Ser Ser Thr Thr Ala Gln
20 25 30

Val Thr Gln Val Asn Trp Glu Gln Gln Asp Gln Leu Leu Ala Ile Cys
35 40 45

Asn Ala Asp Leu Gly Trp His Ile Ser Pro Ser Phe Lys Asp Arg Val
50 55 60

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

Asp Thr Gly Glu Tyr Phe Cys Ile Tyr His Thr Tyr Pro Asp Gly Thr
85 90 95

Tyr Thr Gly Arg Ile Phe Leu Glu Val Leu Glu Ser Ser Val Ala Glu
100 105 110

His Gly Ala Arg Phe Gln Ile Pro
115 120