

sequence listing ST25.txt
SEQUENCE LISTING

<110> INTREXON CORPORATION
BEECH, Robert P.
REED, Thomas D.

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<150> US 61/103,810
<151> 2008-10-08

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sequence listing ST25.txt

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sequence listing ST25.txt
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sequence listing ST25.txt

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<220>
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<220>
 <221> CDS
 <222> (1)..(489)

<400> 9
 atg aag atc ctg aag ccc tac atg agg aac acc agc atc agc tgt tac 48
 Met Lys Ile Leu Lys Pro Tyr Met Arg Asn Thr Ser Ile Ser Cys Tyr
 1 5 10 15
 ctg tgc ttc ctg ctg aac agc cac ttc ctg acc gag gcc gga atc cac 96
 Leu Cys Phe Leu Leu Asn Ser His Phe Leu Thr Glu Ala Gly Ile His
 20 25 30
 gtc ttc atc ctg ggc tgc gtg agc gtg ggc ctg ccc aag acc gag gcc 144
 Val Phe Ile Leu Gly Cys Val Ser Val Gly Leu Pro Lys Thr Glu Ala
 35 40 45
 aac tgg atc gac gtg agg tac gac ctg gag aag atc gag agc ctg atc 192
 Asn Trp Ile Asp Val Arg Tyr Asp Leu Glu Lys Ile Glu Ser Leu Ile
 50 55 60
 cag agc atc cac atc gac acc acc ctg tac acc gag agc gac ttc cac 240
 Gln Ser Ile His Ile Asp Thr Thr Leu Tyr Thr Asp Ser Asp Phe His
 65 70 75 80
 ccc agc tgc aag gtg acc gcc atg aac tgc ttc ctg ctg gag ctg caa 288
 Pro Ser Cys Lys Val Thr Ala Met Asn Cys Phe Leu Leu Glu Leu Gln
 85 90 95
 gtg atc ctg cac gag tac agc aac atg acc ctg aac gag acc gtg agg 336
 Val Ile Leu His Glu Tyr Ser Asn Met Thr Leu Asn Glu Thr Val Arg
 100 105 110
 aac gtg ctg tac ctg gct aac agc acc ctg agc agc aac aag aac gtg 384
 Asn Val Leu Tyr Leu Ala Asn Ser Thr Leu Ser Ser Asn Lys Asn Val
 115 120 125
 gcc gag agc ggc tgc aag gag tgt gag gag ctg gag gag aag acc ttc 432
 Ala Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Thr Phe
 130 135 140
 acc gag ttc ctc cag agc ttc atc agg atc gtg cag atg ttc atc aac 480
 Thr Glu Phe Leu Gln Ser Phe Ile Arg Ile Val Gln Met Phe Ile Asn
 145 150 155 160
 acc agc tga 489
 Thr Ser

sequence listing ST25.txt

<210> 10
 <211> 162
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 10

Met Lys Ile Leu Lys Pro Tyr Met Arg Asn Thr Ser Ile Ser Cys Tyr
 1 5 10 15

Leu Cys Phe Leu Leu Asn Ser His Phe Leu Thr Glu Ala Gly Ile His
 20 25 30

Val Phe Ile Leu Gly Cys Val Ser Val Gly Leu Pro Lys Thr Glu Ala
 35 40 45

Asn Trp Ile Asp Val Arg Tyr Asp Leu Glu Lys Ile Glu Ser Leu Ile
 50 55 60

Gln Ser Ile His Ile Asp Thr Thr Leu Tyr Thr Asp Ser Asp Phe His
 65 70 75 80

Pro Ser Cys Lys Val Thr Ala Met Asn Cys Phe Leu Leu Glu Leu Gln
 85 90 95

Val Ile Leu His Glu Tyr Ser Asn Met Thr Leu Asn Glu Thr Val Arg
 100 105 110

Asn Val Leu Tyr Leu Ala Asn Ser Thr Leu Ser Ser Asn Lys Asn Val
 115 120 125

Ala Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Thr Phe
 130 135 140

Thr Glu Phe Leu Gln Ser Phe Ile Arg Ile Val Gln Met Phe Ile Asn
 145 150 155 160

Thr Ser

<210> 11
 <211> 489
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic mIL-15

sequence listing ST25.txt

<220>

<221> CDS

<222> (1)..(489)

<400> 11

atg	aag	atc	ctg	aag	ccc	tac	atg	agg	aac	acc	agc	atc	agc	tgt	tac	48
Met	Lys	Ile	Leu	Lys	Pro	Tyr	Met	Arg	Asn	Thr	Ser	Ile	Ser	Cys	Tyr	
1				5					10					15		

ctg	tgc	ttc	ctg	ctg	aac	agc	cac	ttc	ctg	acc	gag	gcc	gga	atc	cac	96
Leu	Cys	Phe	Leu	Leu	Asn	Ser	His	Phe	Leu	Thr	Glu	Ala	Gly	Ile	His	
			20					25					30			

gtc	ttc	atc	ctg	ggc	tgc	gtg	agc	gtg	ggc	ctg	ccc	aag	acc	gag	gcc	144
Val	Phe	Ile	Leu	Gly	Cys	Val	Ser	Val	Gly	Leu	Pro	Lys	Thr	Glu	Ala	
		35					40					45				

aac	tgg	atc	gac	gtg	agg	tac	gac	ctg	gag	aag	atc	gag	agc	ctg	atc	192
Asn	Trp	Ile	Asp	Val	Arg	Tyr	Asp	Leu	Glu	Lys	Ile	Glu	Ser	Leu	Ile	
	50					55					60					

cag	agc	atc	cac	atc	gac	acc	acc	ctg	tac	acc	gac	agc	gac	ttc	cac	240
Gln	Ser	Ile	His	Ile	Asp	Thr	Thr	Leu	Tyr	Thr	Asp	Ser	Asp	Phe	His	
65					70					75					80	

ccc	agc	tgc	aag	gtg	acc	gcc	atg	aac	tgc	ttc	ctg	ctg	gag	ctg	caa	288
Pro	Ser	Cys	Lys	Val	Thr	Ala	Met	Asn	Cys	Phe	Leu	Leu	Glu	Leu	Gln	
				85					90					95		

gtg	atc	ctg	cac	gag	tac	agc	aac	atg	acc	ctg	aac	gag	acc	gtg	agg	336
Val	Ile	Leu	His	Glu	Tyr	Ser	Asn	Met	Thr	Leu	Asn	Glu	Thr	Val	Arg	
			100					105					110			

aac	gtg	ctg	tac	ctg	gct	aac	agc	acc	ctg	agc	agc	aac	aag	aac	gtg	384
Asn	Val	Leu	Tyr	Leu	Ala	Asn	Ser	Thr	Leu	Ser	Ser	Asn	Lys	Asn	Val	
		115					120					125				

gcc	gag	agc	ggc	tgc	aag	gag	tgt	gag	gag	ctg	gag	gag	aag	acc	ttc	432
Ala	Glu	Ser	Gly	Cys	Lys	Glu	Cys	Glu	Glu	Leu	Glu	Glu	Lys	Thr	Phe	
	130					135					140					

acc	gag	ttc	ctc	cag	agc	ttc	atc	agg	atc	gtg	cag	atg	ttc	atc	aac	480
Thr	Glu	Phe	Leu	Gln	Ser	Phe	Ile	Arg	Ile	Val	Gln	Met	Phe	Ile	Asn	
145					150					155					160	

acc	agc	tga														489
Thr	Ser															

<210> 12

<211> 162

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 12

Met	Lys	Ile	Leu	Lys	Pro	Tyr	Met	Arg	Asn	Thr	Ser	Ile	Ser	Cys	Tyr
1				5					10					15	

sequence listing ST25.txt

Leu Cys Phe Leu Leu Asn Ser His Phe Leu Thr Glu Ala Gly Ile His
20 25 30

Val Phe Ile Leu Gly Cys Val Ser Val Gly Leu Pro Lys Thr Glu Ala
35 40 45

Asn Trp Ile Asp Val Arg Tyr Asp Leu Glu Lys Ile Glu Ser Leu Ile
50 55 60

Gln Ser Ile His Ile Asp Thr Thr Leu Tyr Thr Asp Ser Asp Phe His
65 70 75 80

Pro Ser Cys Lys Val Thr Ala Met Asn Cys Phe Leu Leu Glu Leu Gln
85 90 95

Val Ile Leu His Glu Tyr Ser Asn Met Thr Leu Asn Glu Thr Val Arg
100 105 110

Asn Val Leu Tyr Leu Ala Asn Ser Thr Leu Ser Ser Asn Lys Asn Val
115 120 125

Ala Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Thr Phe
130 135 140

Thr Glu Phe Leu Gln Ser Phe Ile Arg Ile Val Gln Met Phe Ile Asn
145 150 155 160

Thr Ser

<210> 13
<211> 1008
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic mIL-12, mp40

<220>
<221> CDS
<222> (1)..(1008)

<400> 13	
atg tgc ccc cag aag ctg acc atc agc tgg ttc gcc atc gtg ctg ctg	48
Met Cys Pro Gln Lys Leu Thr Ile Ser Trp Phe Ala Ile Val Leu Leu	
1 5 10 15	
gtg agc ccc ctg atg gcc atg tgg gag ctg gag aag gac gtg tac gtg	96
Val Ser Pro Leu Met Ala Met Trp Glu Leu Glu Lys Asp Val Tyr Val	
20 25 30	

sequence listing ST25.txt																
gtg	gag	gtg	gac	tgg	acc	ccc	gac	gcc	ccc	ggc	gag	acc	gtg	aac	ctg	
Val	Glu	Val	Asp	Trp	Thr	Pro	Asp	Ala	Pro	Gly	Glu	Thr	Val	Asn	Leu	144
		35					40					45				
act	tgc	gac	acc	ccc	gag	gag	gac	gac	atc	acc	tgg	acc	agc	gac	cag	192
Thr	Cys	Asp	Thr	Pro	Glu	Glu	Asp	Asp	Ile	Thr	Trp	Thr	Ser	Asp	Gln	
	50					55					60					
aga	cac	ggc	gtc	atc	ggc	agc	ggc	aag	acc	ctg	acc	atc	acc	gtg	aag	240
Arg	His	Gly	Val	Ile	Gly	Ser	Gly	Lys	Thr	Leu	Thr	Ile	Thr	Val	Lys	
65					70					75					80	
gag	ttc	ctg	gac	gcc	gga	cag	tac	acc	tgt	cac	aag	ggc	ggc	gag	acc	288
Glu	Phe	Leu	Asp	Ala	Gly	Gln	Tyr	Thr	Cys	His	Lys	Gly	Gly	Glu	Thr	
				85					90					95		
ctg	agc	cac	agc	cac	ctg	ttg	ctg	cac	aag	aag	gag	aac	ggc	atc	tgg	336
Leu	Ser	His	Ser	His	Leu	Leu	Leu	His	Lys	Lys	Glu	Asn	Gly	Ile	Trp	
			100					105					110			
agc	acc	gag	atc	ctg	aag	aac	ttc	aag	aac	aag	acc	ttc	ctg	aag	tgc	384
Ser	Thr	Glu	Ile	Leu	Lys	Asn	Phe	Lys	Asn	Lys	Thr	Phe	Leu	Lys	Cys	
		115					120					125				
gag	gcc	ccc	aac	tac	agc	ggc	aga	ttc	acc	tgt	agc	tgg	ctg	gtg	cag	432
Glu	Ala	Pro	Asn	Tyr	Ser	Gly	Arg	Phe	Thr	Cys	Ser	Trp	Leu	Val	Gln	
	130					135					140					
aga	aac	atg	gac	ctg	aag	ttc	aac	atc	aag	agc	agc	agc	agc	agc	ccc	480
Arg	Asn	Met	Asp	Leu	Lys	Phe	Asn	Ile	Lys	Ser	Ser	Ser	Ser	Ser	Pro	
145					150					155					160	
gac	agc	aga	gcc	gtg	aca	tgc	ggc	atg	gcc	agc	ctg	agc	gcc	gag	aag	528
Asp	Ser	Arg	Ala	Val	Thr	Cys	Gly	Met	Ala	Ser	Leu	Ser	Ala	Glu	Lys	
			165						170					175		
gtg	acc	ctg	gac	cag	aga	gac	tac	gag	aag	tac	agc	gtg	agc	tgc	cag	576
Val	Thr	Leu	Asp	Gln	Arg	Asp	Tyr	Glu	Lys	Tyr	Ser	Val	Ser	Cys	Gln	
			180					185					190			
gag	gac	gtg	acc	tgt	ccc	acc	gcc	gag	gag	acc	ctg	ccc	atc	gag	ctt	624
Glu	Asp	Val	Thr	Cys	Pro	Thr	Ala	Glu	Glu	Thr	Leu	Pro	Ile	Glu	Leu	
		195				200						205				
gcc	ctg	gaa	gcc	aga	cag	cag	aac	aag	tac	gag	aac	tac	agc	acc	agc	672
Ala	Leu	Glu	Ala	Arg	Gln	Gln	Asn	Lys	Tyr	Glu	Asn	Tyr	Ser	Thr	Ser	
	210					215					220					
ttc	ttc	atc	aga	gac	atc	atc	aag	ccc	gac	ccc	ccc	aag	aac	ctc	cag	720
Phe	Phe	Ile	Arg	Asp	Ile	Ile	Lys	Pro	Asp	Pro	Pro	Lys	Asn	Leu	Gln	
225					230					235					240	
atg	aag	ccc	ctg	aag	aac	agc	cag	gtg	gag	gtg	tcc	tgg	gag	tac	ccc	768
Met	Lys	Pro	Leu	Lys	Asn	Ser	Gln	Val	Glu	Val	Ser	Trp	Glu	Tyr	Pro	
				245					250					255		
gac	agc	tgg	agc	acc	ccc	cac	agc	tac	ttc	agc	ctg	aag	ttc	ttc	gtg	816
Asp	Ser	Trp	Ser	Thr	Pro	His	Ser	Tyr	Phe	Ser	Leu	Lys	Phe	Phe	Val	
			260					265					270			
aga	atc	cag	aga	aag	aag	gag	aag	atg	aag	gag	acc	gag	gag	ggc	tgc	864
Arg	Ile	Gln	Arg	Lys	Lys	Glu	Lys	Met	Lys	Glu	Thr	Glu	Glu	Gly	Cys	
		275					280					285				

sequence listing ST25.txt

aac	cag	aag	ggc	gct	ttc	ctg	gtg	gag	aaa	acc	agc	acc	gag	gtg	cag	912
Asn	Gln	Lys	Gly	Ala	Phe	Leu	Val	Glu	Lys	Thr	Ser	Thr	Glu	Val	Gln	
	290					295					300					
tgc	aag	ggc	ggc	aac	gtg	tgt	gtg	cag	gcc	cag	gac	aga	tac	tac	aac	960
Cys	Lys	Gly	Gly	Asn	Val	Cys	Val	Gln	Ala	Gln	Asp	Arg	Tyr	Tyr	Asn	
305					310					315					320	
agc	agc	tgc	tcc	aag	tgg	gcc	tgc	gtg	ccc	tgc	cgc	gtg	aga	agc	tga	1008
Ser	Ser	Cys	Ser	Lys	Trp	Ala	Cys	Val	Pro	Cys	Arg	Val	Arg	Ser		
				325					330					335		

<210> 14
 <211> 335
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<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	

sequence listing ST25.txt

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 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
325 330 335

<210> 15
<211> 648
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic mIL-12, mp35

<220>
<221> CDS
<222> (1)..(648)

<400> 15
atg tgc cag agc aga tac ctg ttg ttc ctg gct acc ctg gcc ctg ctg
Met Cys Gln Ser Arg Tyr Leu Leu Phe Leu Ala Thr Leu Ala Leu Leu
1 5 10 15

48

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sequence listing ST25.txt
aac cac ctg agc ctg gcc cgc gtg atc ccc gtg agc ggc ccc gcc aga    96
Asn His Leu Ser Leu Ala Arg Val Ile Pro Val Ser Gly Pro Ala Arg
20 25 30

tgc ctg agc cag agc aga aac ctg ttg aaa aca acc gac gac atg gtg    144
Cys Leu Ser Gln Ser Arg Asn Leu Leu Lys Thr Thr Asp Asp Met Val
35 40 45

aaa acc gcc aga gag aag ctg aag cac tac agc tgc acc gcc gag gac    192
Lys Thr Ala Arg Glu Lys Leu Lys His Tyr Ser Cys Thr Ala Glu Asp
50 55 60

atc gac cac gag gac atc acc aga gac cag acc agc acc ctg aaa acc    240
Ile Asp His Glu Asp Ile Thr Arg Asp Gln Thr Ser Thr Leu Lys Thr
65 70 75 80

tgt ctg ccc ctg gag ctg cac aag aac gag agc tgc ctg gct acc aga    288
Cys Leu Pro Leu Glu Leu His Lys Asn Glu Ser Cys Leu Ala Thr Arg
85 90 95

gag acc agc agc acc acc aga ggc agc tgc ctg ccc ccc cag aaa acc    336
Glu Thr Ser Ser Thr Thr Arg Gly Ser Cys Leu Pro Pro Gln Lys Thr
100 105 110

agc ctg atg atg acc ctg tgc ctg ggc agc atc tac gag gac ctg aag    384
Ser Leu Met Met Thr Leu Cys Leu Gly Ser Ile Tyr Glu Asp Leu Lys
115 120 125

atg tac cag acc gag ttc cag gcc atc aac gcc gcc ctg caa aac cac    432
Met Tyr Gln Thr Glu Phe Gln Ala Ile Asn Ala Ala Leu Gln Asn His
130 135 140

aac cac cag cag atc atc ctg gac aag ggc atg ttg gtg gcc atc gac    480
Asn His Gln Gln Ile Ile Leu Asp Lys Gly Met Leu Val Ala Ile Asp
145 150 155 160

gag ctg atg cag agc ctg aac cac aac ggc gag acc ctg aga cag aag    528
Glu Leu Met Gln Ser Leu Asn His Asn Gly Glu Thr Leu Arg Gln Lys
165 170 175

ccc ccc gtg ggc gag gcc gac ccc tac aga gtg aag atg aag ctg tgc    576
Pro Pro Val Gly Glu Ala Asp Pro Tyr Arg Val Lys Met Lys Leu Cys
180 185 190

atc ctg ctg cac gcc ttc agc acc aga gtg gtg acc atc aac aga gtg    624
Ile Leu Leu His Ala Phe Ser Thr Arg Val Val Thr Ile Asn Arg Val
195 200 205

atg ggc tac ctg agc agc gcc tga    648
Met Gly Tyr Leu Ser Ser Ala
210 215

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<210> 16
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 16

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sequence listing ST25.txt

Met Cys Gln Ser Arg Tyr Leu Leu Phe Leu Ala Thr Leu Ala Leu Leu
1 5 10 15

Asn His Leu Ser Leu Ala Arg Val Ile Pro Val Ser Gly Pro Ala Arg
20 25 30

Cys Leu Ser Gln Ser Arg Asn Leu Leu Lys Thr Thr Asp Asp Met Val
35 40 45

Lys Thr Ala Arg Glu Lys Leu Lys His Tyr Ser Cys Thr Ala Glu Asp
50 55 60

Ile Asp His Glu Asp Ile Thr Arg Asp Gln Thr Ser Thr Leu Lys Thr
65 70 75 80

Cys Leu Pro Leu Glu Leu His Lys Asn Glu Ser Cys Leu Ala Thr Arg
85 90 95

Glu Thr Ser Ser Thr Thr Arg Gly Ser Cys Leu Pro Pro Gln Lys Thr
100 105 110

Ser Leu Met Met Thr Leu Cys Leu Gly Ser Ile Tyr Glu Asp Leu Lys
115 120 125

Met Tyr Gln Thr Glu Phe Gln Ala Ile Asn Ala Ala Leu Gln Asn His
130 135 140

Asn His Gln Gln Ile Ile Leu Asp Lys Gly Met Leu Val Ala Ile Asp
145 150 155 160

Glu Leu Met Gln Ser Leu Asn His Asn Gly Glu Thr Leu Arg Gln Lys
165 170 175

Pro Pro Val Gly Glu Ala Asp Pro Tyr Arg Val Lys Met Lys Leu Cys
180 185 190

Ile Leu Leu His Ala Phe Ser Thr Arg Val Val Thr Ile Asn Arg Val
195 200 205

Met Gly Tyr Leu Ser Ser Ala
210 215

<210> 17
<211> 489
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic hIL-21

sequence listing ST25.txt

<220>
 <221> CDS
 <222> (1)..(489)

<400> 17
 atg aga agc agc ccc ggc aac atg gag aga atc gtg atc tgc ctg atg 48
 Met Arg Ser Ser Pro Gly Asn Met Glu Arg Ile Val Ile Cys Leu Met
 1 5 10 15
 gtg atc ttc ctg ggc acc ctg gtg cat aag agc agc agc cag ggc cag 96
 Val Ile Phe Leu Gly Thr Leu Val His Lys Ser Ser Ser Gln Gly Gln
 20 25 30
 gac aga cac atg atc cgc atg aga cag ctg atc gac atc gtg gac cag 144
 Asp Arg His Met Ile Arg Met Arg Gln Leu Ile Asp Ile Val Asp Gln
 35 40 45
 ctg aag aac tac gtg aac gac ctg gtg ccc gag ttc ctg ccc gcc ccc 192
 Leu Lys Asn Tyr Val Asn Asp Leu Val Pro Glu Phe Leu Pro Ala Pro
 50 55 60
 gag gac gtg gag acc aac tgc gag tgg agc gcc ttc agc tgc ttc cag 240
 Glu Asp Val Glu Thr Asn Cys Glu Trp Ser Ala Phe Ser Cys Phe Gln
 65 70 75 80
 aag gcc cag ctg aag tcc gcc aac acc ggc aac aac gag aga atc atc 288
 Lys Ala Gln Leu Lys Ser Ala Asn Thr Gly Asn Asn Glu Arg Ile Ile
 85 90 95
 aac gtg agc atc aag aag ctg aag cgg aag ccc ccc agc acc aac gcc 336
 Asn Val Ser Ile Lys Lys Leu Lys Arg Lys Pro Pro Ser Thr Asn Ala
 100 105 110
 gga aga aga cag aag cac aga ctg acc tgt ccc agc tgc gac agc tac 384
 Gly Arg Arg Gln Lys His Arg Leu Thr Cys Pro Ser Cys Asp Ser Tyr
 115 120 125
 gag aag aag ccc ccc aag gag ttc ctg gag aga ttc aag agc ctg ctg 432
 Glu Lys Lys Pro Pro Lys Glu Phe Leu Glu Arg Phe Lys Ser Leu Leu
 130 135 140
 caa aag atg atc cac cag cac ctg agc agc aga acc cac ggc agc gag 480
 Gln Lys Met Ile His Gln His Leu Ser Ser Arg Thr His Gly Ser Glu
 145 150 155 160
 gac agc tga 489
 Asp Ser

<210> 18
 <211> 162
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 18

Met Arg Ser Ser Pro Gly Asn Met Glu Arg Ile Val Ile Cys Leu Met
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sequence listing ST25.txt

1 5 10 15

Val Ile Phe Leu Gly Thr Leu Val His Lys Ser Ser Ser Gln Gly Gln
20 25 30

Asp Arg His Met Ile Arg Met Arg Gln Leu Ile Asp Ile Val Asp Gln
35 40 45

Leu Lys Asn Tyr Val Asn Asp Leu Val Pro Glu Phe Leu Pro Ala Pro
50 55 60

Glu Asp Val Glu Thr Asn Cys Glu Trp Ser Ala Phe Ser Cys Phe Gln
65 70 75 80

Lys Ala Gln Leu Lys Ser Ala Asn Thr Gly Asn Asn Glu Arg Ile Ile
85 90 95

Asn Val Ser Ile Lys Lys Leu Lys Arg Lys Pro Pro Ser Thr Asn Ala
100 105 110

Gly Arg Arg Gln Lys His Arg Leu Thr Cys Pro Ser Cys Asp Ser Tyr
115 120 125

Glu Lys Lys Pro Pro Lys Glu Phe Leu Glu Arg Phe Lys Ser Leu Leu
130 135 140

Gln Lys Met Ile His Gln His Leu Ser Ser Arg Thr His Gly Ser Glu
145 150 155 160

Asp Ser

<210> 19
<211> 489
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic hIL-15

<220>
<221> CDS
<222> (1)..(489)

<400> 19
atg aga atc agc aag ccc cac ctg aga agc atc agc atc cag tgt tac 48
Met Arg Ile Ser Lys Pro His Leu Arg Ser Ile Ser Ile Gln Cys Tyr
1 5 10 15

ctg tgc ctg ctg ctg aac agc cac ttc ctg acc gag gcc ggt atc cac 96
Leu Cys Leu Leu Leu Asn Ser His Phe Leu Thr Glu Ala Gly Ile His
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sequence listing ST25.txt

20	25	30			
gtc ttc atc ctg ggc tgc ttc agc gcc gga ctg ccc aag acc gag gcc Val Phe Ile Leu Gly Cys Phe Ser Ala Gly Leu Pro Lys Thr Glu Ala	35	40	45	144	
aac tgg gtg aac gtg atc tct gac ctg aag aag atc gag gac ctg atc Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile	50	55	60	192	
cag tcc atg cac atc gac gcc acc ctg tac acc gag agc gac gtt cat Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His	65	70	75	80	240
ccc agc tgc aag gtg acc gcc atg aag tgc ttc ctg ctg gag ctg caa Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln	85	90	95	288	
gtg atc tcc ctg gag agc ggc gac gcc agc atc cac gac acc gtg gag Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu	100	105	110	336	
aac ctg att atc ctg gct aac aac agc ctg agc agc aac ggc aac gtg Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val	115	120	125	384	
acc gag agc ggc tgc aag gag tgt gag gag ctg gag gag aag aac atc Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile	130	135	140	432	
aag gag ttc ctc cag agc ttc gtg cat atc gtc cag atg ttc atc aac Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn	145	150	155	160	480
acc agc tga Thr Ser				489	

<210> 20
 <211> 162
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 20

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

sequence listing ST25.txt

Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His
65 70 75 80

Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln
85 90 95

Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu
100 105 110

Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val
115 120 125

Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile
130 135 140

Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn
145 150 155 160

Thr Ser

<210> 21
<211> 987
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic hIL-12, p40

<220>
<221> CDS
<222> (1)..(987)

<400> 21	
atg ggt cac cag cag ttg gtc atc tct tgg ttt tcc ctg gtt ttt ctg	48
Met Gly His Gln Gln Leu Val Ile Ser Trp Phe Ser Leu Val Phe Leu	
1 5 10 15	
gca tct ccc ctc gtg gcc ata tgg gaa ctg aag aaa gat gtt tat gtc	96
Ala Ser Pro Leu Val Ala Ile Trp Glu Leu Lys Lys Asp Val Tyr Val	
20 25 30	
gta gaa ttg gat tgg tat ccg gat gcc cct gga gaa atg gtg gtc ctc	144
Val Glu Leu Asp Trp Tyr Pro Asp Ala Pro Gly Glu Met Val Val Leu	
35 40 45	
acc tgt gac acc cct gaa gaa gat ggt atc acc tgg acc ttg gac cag	192
Thr Cys Asp Thr Pro Glu Glu Asp Gly Ile Thr Trp Thr Leu Asp Gln	
50 55 60	
agc agt gag gtc tta ggc tct ggc aaa acc ctg acc atc caa gtc aaa	240
Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys	
65 70 75 80	

sequence listing ST25.txt

gag ttt gga gat gct ggc cag tac acc tgt cac aaa gga ggc gag gtt Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val 85 90 95	288
cta agc cat tcg ctc ctg ctg ctt cac aaa aag gaa gat gga att tgg Leu Ser His Ser Leu Leu Leu Leu His Lys Lys Glu Asp Gly Ile Trp 100 105 110	336
tcc act gat att tta aag gac cag aaa gaa ccc aaa aat aag acc ttt Ser Thr Asp Ile Leu Lys Asp Gln Lys Glu Pro Lys Asn Lys Thr Phe 115 120 125	384
cta aga tgc gag gcc aag aat tat tct gga cgt ttc acc tgc tgg tgg Leu Arg Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp 130 135 140	432
ctg acg aca atc agt act gat ttg aca ttc agt gtc aaa agc agc aga Leu Thr Thr Ile Ser Thr Asp Leu Thr Phe Ser Val Lys Ser Ser Arg 145 150 155 160	480
ggc tct tct gac ccc caa ggg gtg acg tgc gga gct gct aca ctc tct Gly Ser Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Ala Thr Leu Ser 165 170 175	528
gca gag aga gtc aga ggg gac aac aag gag tat gag tac tca gtg gag Ala Glu Arg Val Arg Gly Asp Asn Lys Glu Tyr Glu Tyr Ser Val Glu 180 185 190	576
tgc cag gag gac agt gcc tgc cca gct gct gag gag agt ctg ccc att Cys Gln Glu Asp Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile 195 200 205	624
gag gtc atg gtg gat gcc gtt cac aag ctc aag tat gaa aac tac acc Glu Val Met Val Asp Ala Val His Lys Leu Lys Tyr Glu Asn Tyr Thr 210 215 220	672
agc agc ttc ttc atc agg gac atc atc aaa cct gac cca ccc aag aac Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn 225 230 235 240	720
ttg cag ctg aag cca tta aag aat tct cgg cag gtg gag gtc agc tgg Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg Gln Val Glu Val Ser Trp 245 250 255	768
gag tac cct gac acc tgg agt act cca cat tcc tac ttc tcc ctg aca Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr 260 265 270	816
ttc tgc gtt cag gtc cag ggc aag agc aag aga gaa aag aaa gat aga Phe Cys Val Gln Val Gln Gly Lys Ser Lys Arg Glu Lys Lys Asp Arg 275 280 285	864
gtc ttc acg gac aag acc tca gcc acg gtc atc tgc cgc aaa aat gcc Val Phe Thr Asp Lys Thr Ser Ala Thr Val Ile Cys Arg Lys Asn Ala 290 295 300	912
agc att agc gtg cgg gcc cag gac cgc tac tat agc tca tct tgg agc Ser Ile Ser Val Arg Ala Gln Asp Arg Tyr Tyr Ser Ser Ser Trp Ser 305 310 315 320	960
gaa tgg gca tct gtg ccc tgc agt tag Glu Trp Ala Ser Val Pro Cys Ser	987

sequence listing ST25.txt

325

<210> 22
 <211> 328
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 22

Met Gly His Gln Gln Leu Val Ile Ser Trp Phe Ser Leu Val Phe Leu
 1 5 10 15

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

sequence listing ST25.txt

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> 23
<211> 660
<212> DNA
<213> Artificial sequence

<220>
<223> synthetic hIL-12, p35

<220>
<221> CDS
<222> (1)..(660)

<400> 23
atg ggt cca gcg cgc agc ctc ctc ctt gtg gct acc ctg gtc ctc ctg 48
Met Gly Pro Ala Arg Ser Leu Leu Leu Val Ala Thr Leu Val Leu Leu
1 5 10 15
gac cac ctc agt ttg gcc aga aac ctc ccc gtg gcc act cca gac cca 96
Asp His Leu Ser Leu Ala Arg Asn Leu Pro Val Ala Thr Pro Asp Pro
20 25 30
gga atg ttc cca tgc ctt cac cac tcc caa aac ctg ctg agg gcc gtc 144
Gly Met Phe Pro Cys Leu His His Ser Gln Asn Leu Leu Arg Ala Val
35 40 45
agc aac atg ctc cag aag gcc aga caa act cta gaa ttt tac cct tgc 192
Ser Asn Met Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe Tyr Pro Cys
50 55 60

sequence listing ST25.txt

act tct gaa gag att gat cat gaa gat atc aca aaa gat aaa acc agc	240
Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp Lys Thr Ser	
65 70 75 80	
aca gtg gag gcc tgt tta cca ttg gaa tta acc aag aat gag agt tgc	288
Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Lys Asn Glu Ser Cys	
85 90 95	
cta aat tcc aga gag acc tct ttc ata act aat ggg agt tgc ctg gcc	336
Leu Asn Ser Arg Glu Thr Ser Phe Ile Thr Asn Gly Ser Cys Leu Ala	
100 105 110	
tcc aga aag acc tct ttt atg atg gcc ctg tgc ctt agt agt att tat	384
Ser Arg Lys Thr Ser Phe Met Met Ala Leu Cys Leu Ser Ser Ile Tyr	
115 120 125	
gaa gac ttg aag atg tac cag gtg gag ttc aag acc atg aat gca aag	432
Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Thr Met Asn Ala Lys	
130 135 140	
ctt ctg atg gat cct aag agg cag atc ttt cta gat caa aac atg ctg	480
Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln Asn Met Leu	
145 150 155 160	
gca gtt att gat gag ctg atg cag gcc ctg aat ttc aac agt gag act	528
Ala Val Ile Asp Glu Leu Met Gln Ala Leu Asn Phe Asn Ser Glu Thr	
165 170 175	
gtg cca caa aaa tcc tcc ctt gaa gaa ccg gat ttt tat aaa act aaa	576
Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys	
180 185 190	
atc aag ctc tgc ata ctt ctt cat gct ttc aga att cgg gca gtg act	624
Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg Ala Val Thr	
195 200 205	
att gat aga gtg atg agc tat ctg aat gct tcc taa	660
Ile Asp Arg Val Met Ser Tyr Leu Asn Ala Ser	
210 215	

<210> 24
 <211> 219
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 24

Met Gly Pro Ala Arg Ser Leu Leu Leu Val Ala Thr Leu Val Leu Leu
1 5 10 15
Asp His Leu Ser Leu Ala Arg Asn Leu Pro Val Ala Thr Pro Asp Pro
20 25 30
Gly Met Phe Pro Cys Leu His His Ser Gln Asn Leu Leu Arg Ala Val
35 40 45

sequence listing ST25.txt

Ser Asn Met Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe Tyr Pro Cys
50 55 60

Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp Lys Thr Ser
65 70 75 80

Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Lys Asn Glu Ser Cys
85 90 95

Leu Asn Ser Arg Glu Thr Ser Phe Ile Thr Asn Gly Ser Cys Leu Ala
100 105 110

Ser Arg Lys Thr Ser Phe Met Met Ala Leu Cys Leu Ser Ser Ile Tyr
115 120 125

Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Thr Met Asn Ala Lys
130 135 140

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

Ala Val Ile Asp Glu Leu Met Gln Ala Leu Asn Phe Asn Ser Glu Thr
165 170 175

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

Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg Ala Val Thr
195 200 205

Ile Asp Arg Val Met Ser Tyr Leu Asn Ala Ser
210 215

<210> 25
<211> 17
<212> PRT
<213> Drosophila melanogaster

<400> 25

Arg Arg Gly Gly Thr Thr Cys Ala Asn Thr Gly Ala Cys Ala Cys Tyr
1 5 10 15

Tyr

<210> 26
<211> 13
<212> DNA

sequence listing ST25.txt

<213> Drosophila melanogaster

<220>
 <221> misc_feature
 <222> (7)..(7)
 <223> n is a, c, g, or t

<400> 26
 aggtcanagg tca 13

<210> 27
 <211> 15
 <212> DNA
 <213> Drosophila melanogaster

<400> 27
 gggttgaatg aattt 15

<210> 28
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic homing endonuclease (HE) enzyme (I-SceI)

<400> 28
 tagggataac agggtaat 18

<210> 29
 <211> 37323
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Ad-RTS-hIL-12 (SP1-RheoIL-12)

<400> 29
 catcatcaat aatatacctt attttggatt gaagccaata tgataatgag ggggtggagt 60
 ttgtgacgtg gcgcggggcg tgggaacggg gcgggtgacg tagtagtgtg gcggaagtgt 120
 gatgttgcaa gtgtggcgga acacatgtaa gcgacggatg tggcaaaagt gacgtttttg 180
 gtgtgcgccg gtgtacacag gaagtgacaa ttttcgcgcg gttttaggcg gatgtttag 240
 taaatttggg cgtaaccgag taagatttgg ccattttcgc gggaaaactg aataagagga 300
 agtgaaatct gaataatttt gtgttactca tagcgcgtaa tatttgtcta gggagatccg 360
 gtaccggcgc gcgcgccgtt tggccgcctc gagtctagag atccggtgag tattaggcgc 420
 gcaccagggtg ccgcaataaa atatctttat tttcattaca tctgtgtgtt ggttttttgt 480
 gtgaatcgat agtactaaca tacgctctcc atcaaaacaa aacgaaacaa aacaaactag 540
 caaaataggc tgtccccagt gcaagtgcag gtgccagaac atttctctat cgataatgca 600
 ggtcggagta ctgtcctccg agcggagtac tgtcctccga gcggagtact gtcctccgag 660

cgagatcttg tccctccgagc ggagtaactgt cctccgagcg gagtactgtc ctcgagcgcg 720
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2580	ccagcgcgca gccctccctcct tgtgtctacc ctgttccctc tggaccacct cagtttggcc
2640	agaaaccctc ccgttggccac tccagaccac ggaatgttcc catgtccctca ccactcccaa
2700	aacctgttga gggccgttcag caaatgtctc cagaaggcca gacaacctc agaattttac
2760	ccctgcactt ctgaagagat tgcatagaa gatacaca aagataaaac cagcacagt
2820	gaggccctgt taccatttga attaaccaag aatgagagt gcctaaatc cagagagacc
2880	tcctttcataa ctaattggag ttgacctggc tccagaaga cctctttat gatggccctg
2940	tgccttagta gtatttatga agacttgaag atgtaccagg ttgagttcaa gaccatgaa
3000	gcaagcttc tgaatgatcc taaggagcag atctttctag atcaaaacat gcttggcagt
3060	atgatgagc tgaatgcagg cctgaattc aacagttaga ctgtgccaca aaaaacctc
3120	cttgaagaac cggattttta taaaactaaa atcaagctc gcatacttc tcatgtcttc
3180	agaattcggg cagtgaactat tgatagagt atgaactatc tgaatgtctc ctaacgtacg
3240	tcgacatcga gaaacttgtt attgagctt ataattgtta caaataaagc aatagcatca
3300	caaatctcac aaataaagca tttttttcac tgcattctag ttgtgtttg tccaactca
3360	tcaatgtatc ttatcatgtc ttggcgcgcg ggcctccgcg ccggttttg gcgcctcccg
3420	cgggcgcctc cctccctcac gcgagcgctg ccacgtcaga cgaaggcgag agcgagcgctc
3480	ctgatctctc cgcctccgacg ctacgagcag cggcccgctg ctcatagagc tcggcccttag
3540	aaaccagta tcagcagaag gacattttag gacgggactt ggttgactc agggcacttg
3600	ttttctctcc agagagcgga acagcggaag aaaagtatc ccttccgcg gatcttgcg
3660	aggatctcc gtggggcggt gaacgcgat gattatataa ggaacgcgcg ggtgtggcac
3720	agctagtcc gtccgacgcg ggaattgggt cgggttctt gtttggat cgtgtgatc
3780	gtcaattgtt gagttagcgg ctgttgggt ggtacgtgc gctcgggtt ggcgagtgtg
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3900	cagtgttaga ctagtaaat gtccgctaaa ttctggcgtt ttgtgcttt ttgttagac
3960	gagctagcgc cgcacacatg ggccttaaaa agaagcgtaa agtcgcccc cgaaccgatg
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4140	ccccccacga ctccgcccc taccggctc tgatatggc cgaactcga tttagcaga
4200	tgtttaccga tgccttttga attgacgagt accgttggga attcgagatg cctgtggaca
4260	ggaaccttga ggcagagctt gctgttgaac agaagagtga ccaaggcggt gaggttccctg
4320	ggggaacgg ggttagcgcg agcagcccaa atgacctgt gactaaacatc tgtcaggcag
4380	ctgaacaaca gctattcacg ctgtttgagt gggcggaagag gatcccaac ttttccctc
4440	tgcctcttga tgcacagctc atatgtctgc gggcaggtcg gaatgaactc ctcatgtcct

4500 cctttcaca cggatccatt gatgttcgag atggcatcct ccttgcaca ggtcttcag
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4620 agctagtgtc caaaatgctg gacatgagg tggacaagac agagcttggc tgcctgaggg
4680 caatcatctt gtttaattca gaggtgaggg gtttgaatc cgccaggaa gttgaattc
4740 tacgtgaaaa agtatatgcc gcttggag aatatactag aacaacacat ccggtgaac
4800 caggaaagt tgcataaatt ttgcttcgtc tgccctctt acgttccata ggccttaagt
4860 gtttgagca ttgtttttc ttgcctta ttgagatgt tccaattgat acgttctga
4920 tggagatgt tgaatcacct tctgattcat aatctagcct agcccccct tccctcccc
4980 cccctaag ttactggccg aagccgctg gaataaggcc ggtgtgctgt tgtctatatg
5040 ttattttcca ccatatigcc gtcttttggc aatgtgagg ccggaacc tggccctgtc
5100 ttcttgaca gcatctctag ggtctttcc cctctcgca aagaaatgca agtctgttg
5160 aatgtctgta aggaagcagt tctcttgaa gctcttgaa gacaacaac gtcgttagcg
5220 acccttga ggcagcgga ccccccct ggcgacagt gcccttgcgg ccaaaagcca
5280 cgtgtataag ataccctgc aagcgcca caaccaggt gccagttgt gatttgata
5340 gttgtgaaa gagtcaaatg gctctctca agcgtatca acaagggt gaagtatgcc
5400 cagaagtac cccattgtat gggatctgat ctgggccc ggtgcacatg cttacatgt
5460 gtttagtga gtttaaaaaa cgtctagcc cccgaaacca cgggacgtg gtttcttt
5520 gaaaaacag atctctagc gccaccatga agctactgtc ttctatgaa caagcatgcg
5580 atatitgccg acttaaaaag ctcaagtgt ccaagaaaa accgaagtgc gccaaagtgc
5640 tgaagaacaa ctgggagtgt cgtactctc ccaaaacca aagttctccg ctgactaggg
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5760 ttctctgaga agaccctgac atgatttga aaatggatc tttaaggat ataagaacat
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aggccccgct	aaccgtgcac	gactccaaac	ttagcattgc	caccaagga	cccctcacag	32880
tgtcagaagg	aaagctagcc	ctgcaaacat	caggccccct	caccaccacc	gatagcagta	32940
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tgaaagagcc	catttataca	caaaatggaa	aactaggact	aaagtacggg	gctcctttgc	33060
atgtaacaga	cgacctaaac	actttgaccg	tagcaactgg	tccaggtgtg	actattaata	33120
atacttcctt	gcaaactaaa	gttactggag	ccttgggttt	tgattcacia	ggcaatatgc	33180
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tcctggaccc	agaatattgg	aactttagaa	atggagatct	tactgaaggc	acagcctata	33900
caaacgctgt	tggattttatg	cctaacctat	cagcttatcc	aaaatctcac	ggtaaaactg	33960
ccaaaagtaa	cattgtcagt	caagtttact	taaacggaga	caaaactaaa	cctgtaacac	34020
taaccattac	actaaacggt	acacaggaaa	caggagacac	aactccaagt	gcatactcta	34080
tgtcattttc	atgggactgg	tctggccaca	actacattaa	tgaaatattt	gccacatcct	34140
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tcgctgtcca	gctgctgagc	cacaggctgc	tgtccaactt	gcggttgctt	aacgggcggc	34560
gaaggagaag	tccacgccta	catgggggta	gagtcataat	cgtgcatcag	gatagggcgg	34620
tggtgctgca	gcagcgcgcg	aataaaactgc	tgccgccgcc	gctccgtcct	gcaggaatac	34680

34740 aacatggcag tggctctc aggatgat cgaccggcc gcagcataag gcgcccctgtc
34800 ctccggcac agcagcgac cctgctca ctaaatcag cacgtaac gcagcacagc
34860 acccaatat tgttcaaat ccacagtc aagcgctgt atccaagct catggcggg
34920 accacagaac ccagctggcc atcatccac aagcgcaggt agattaatg gcgacccctc
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35040 taccatataa acctctgatt aaacatggcg ccatccaca ccatccta aaacgctggcc
35100 aaaaacctgc cgccggctat acatgcagg gaaccgggac tggacaatg acagtggaga
35160 gccaggact cgtaaccatg gatcatcatg ctgctcatga tatcaatgtt ggacaacaac
35220 aggcacagt gcatacatt cctcaggatt acaagctct ccgcgttag aacatatcc
35280 cagggaacaa cccattcctg aatcagcgt aatcccacac tgcagggaag acctcgcacg
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35580 ccgcttagat cgctctgtgt agtagttgta gtatatccac tctctcaag catccaggcg
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35820 cctcaaatg aagatctatt aagtgaacgc gctccctcc ggtggcgttg tcaaatcta
35880 cagccaaga acagataatg gcatltgtaa gatgtgcac aatgcttcc aaaaagcaaa
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36120 ccaacttcag cctcaagcag cgaatcatga tggcaaaaat tcaggttctc cacagacctg
36180 tataagattc aaaaagcgaa cattaacaa aataccgga tcccgtagt ccttcgcag
36240 ggccagctga acataatcgt gcaggtctgc acggaacgac gcygccact cccgcgacgg
36300 aacatgaca aaagaaccca cactgatat gcacgcgata ctggagcta tgcataacag
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36420 aaaaatcagc aaagcctcgc gcaaaaaaga aagcacatcg tagtcatgt catgcagata
36480 aagcgagta agctccgaa ccaacacaga aaaagacac atttttctc caaacatgtc
36540 tggggttct tgcataaaca caaataaaa taacaaaaa acatttaaac attagaagcc

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tgtcttaca	caggaaaaac	aacccttata	agcataagac	ggactacggc	catgccggcg	36600
tgaccgtaaa	aaaactggtc	accgtgatta	aaaagcacca	ccgacagctc	ctcggtcatg	36660
tccggagtca	taatgtaaga	ctcggtaa	acatcagggt	gattcacatc	ggtcagtgct	36720
aaaaagcgac	cgaaatagcc	cgggggaata	catacccgca	ggcgtagaga	caacattaca	36780
gcccccatag	gaggtataac	aaaattaata	ggagagaaaa	acacataaac	acctgaaaaa	36840
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tcgacacggc	accagctcaa	tcagtcacag	tgtaaaaaag	ggccaagtgc	agagcgagta	37020
tatataggac	taaaaaatga	cgtaacgggt	aaagtccaca	aaaaacaccc	agaaaaccgc	37080
acgcgaacct	acgcccagaa	acgaaagcca	aaaaacccac	aacttcctca	aatcgtcact	37140
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caaactccac	cccctcatta	tcattattggc	ttcaatccaa	aataaggtat	attattgatg	37320
atg						37323