

G0157 WO_ST25
SEQUENCE LISTING

<110> UCB Pharma, S.A.
<120> BACTERIAL HOST STRAIN EXPRESSING RECOMBINANT ANTIBODY FRAGMENT
<130> G0157 WO
<150> EP11173880.3
<151> 2011-07-13
<160> 52

<170> PatentIn version 3.5

<210> 1
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 342 CDR-H1

<400> 1

Gly Phe Ser Ser Thr Asn Tyr His Val His
1 5 10

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

<220>
<223> Description of Artificial Sequence: 342 CDR-H2

<400> 2

Val Ile Trp Gly Asp Gly Asp Thr Ser Tyr Asn Ser Val Leu Lys Ser
1 5 10 15

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

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<223> Description of Artificial Sequence: 342 CDR-H3

<400> 3

Gln Leu Thr His Tyr Tyr Val Leu Ala Ala
1 5 10

<210> 4
<211> 11
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: 342 CDR-L1

<400> 4

Arg Ala Ser Glu Asp Leu Tyr Tyr Asn Leu Ala
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<210> 5

<211> 7

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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: 342 CDR-L2

<400> 5

Asp Thr Tyr Arg Leu Ala Asp
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<210> 6

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: 342 CDR-L3

<400> 6

Gln Gln Tyr Tyr Lys Phe Pro Phe Thr
1 5

<210> 7

<211> 384

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: 342 variable light chain (gL4)

<220>

<221> sig_peptide

<222> (1)..(63)

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<221> CDS

<222> (64)..(384)

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gct gat atc cag atg acc cag agt cca agc agt ctc tcc gcc agc gta 108
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
1 5 10 15

ggc gat cgt gtg act att acc tgt cgt gcc agt gag gac ctc tat tac 156
Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Asp Leu Tyr Tyr
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20	25	30	
aac ctg gcc tgg tat cag cgt aaa ccg ggc aaa gcc ccg aag ctg ctc			204
Asn Leu Ala Trp Tyr Gln Arg Lys Pro Gly Lys Ala Pro Lys Leu Leu			
	35	40	
atc tat gat acg tac cgc ctg gct gac ggt gtg cca agc cgt ttc agt			252
Ile Tyr Asp Thr Tyr Arg Leu Ala Asp Gly Val Pro Ser Arg Phe Ser			
	50	55	
ggc agt ggc agc ggt act gac tat acc ctc aca att tcg tct ctc cag			300
Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln			
	65	70	
ccg gaa gat ttc gcc tct tac tat tgt cag caa tat tac aag ttc cct			348
Pro Glu Asp Phe Ala Ser Tyr Tyr Cys Gln Gln Tyr Tyr Lys Phe Pro			
	80	85	
ttc acc ttc ggt cag ggc act aaa gta gaa atc aaa			384
Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys			
	100	105	

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

<220>
 <223> Synthetic Construct

<400> 8

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

<210> 9
 <211> 351

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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 342 variable heavy chain (gH1)

<220>
<221> CDS
<222> (1)..(351)

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<400> 9
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1          5          10          15

agc ctg cgt ctc tct tgt gca gtg agc ggc ttc agc tct acc aat tac      96
Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Ser Ser Thr Asn Tyr
          20          25          30

cat gtg cac tgg gtg cgt cag gca cct ggg aag ggc ctg gag tgg atg      144
His Val His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met
          35          40          45

ggt gtt att tgg ggc gac ggc gat aca tcc tac aac tcc gtc ctg aag      192
Gly Val Ile Trp Gly Asp Gly Asp Thr Ser Tyr Asn Ser Val Leu Lys
          50          55          60

agc cgt ttc acc att tcc cgt gac acc tca aag aat acc gtt tac ctc      240
Ser Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Val Tyr Leu
65          70          75          80

cag atg aac tct ctc cgc gca gag gac aca gca gtc tat tac tgt gca      288
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
          85          90          95

cgt caa ctg acc cac tat tac gtt ttg gca gcc tgg ggt caa ggg act      336
Arg Gln Leu Thr His Tyr Tyr Val Leu Ala Ala Trp Gly Gln Gly Thr
          100          105          110

ctg gtc aca gtc tcg
Leu Val Thr Val Ser
          115

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<210> 10
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

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<400> 10
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1          5          10          15

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

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

Gly Val Ile Trp Gly Asp Gly Asp Thr Ser Tyr Asn Ser Val Leu Lys
50 55 60

Ser Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Gln Leu Thr His Tyr Tyr Val Leu Ala Ala Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser
115

<210> 11
<211> 705
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 342 gL4 (V+C)

<220>
<221> CDS
<222> (64)..(705)

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Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val 15
1 5 10
ggc gat cgt gtg act att acc tgt cgt gcc agt gag gac ctc tat tac 156
Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Asp Leu Tyr Tyr 20 25 30
aac ctg gcc tgg tat cag cgt aaa ccg ggc aaa gcc ccg aag ctg ctc 204
Asn Leu Ala Trp Tyr Gln Arg Lys Pro Gly Lys Ala Pro Lys Leu Leu 35 40 45
atc tat gat acg tac cgc ctg gct gac ggt gtg cca agc cgt ttc agt 252
Ile Tyr Asp Thr Tyr Arg Leu Ala Asp Gly Val Pro Ser Arg Phe Ser 50 55 60
ggc agt ggc agc ggt act gac tat acc ctc aca att tcg tct ctc cag 300
Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln 65 70 75
ccg gaa gat ttc gcc tct tac tat tgt cag caa tat tac aag ttc cct 348
Pro Glu Asp Phe Ala Ser Tyr Tyr Cys Gln Gln Tyr Tyr Lys Phe Pro
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90																		
ttc acc ttc ggt cag ggc act aaa gta gaa atc aaa cgt acg gta gcg	396																	
Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala																		
	100	105	110															
gcc cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa tct	444																	
Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser																		
	115	120	125															
gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga gag	492																	
Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu																		
	130	135	140															
gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc	540																	
Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser																		
	145	150	155															
cag gag agt gtc aca gag cag gac agc aag gac agc acc tac agc ctc	588																	
Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu																		
	160	165	170	175														
agc agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa gtc	636																	
Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val																		
	180	185	190															
tac gcc tgc gaa gtc acc cat cag ggc ctg agc tca cca gta aca aaa	684																	
Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys																		
	195	200	205															
agt ttt aat aga ggg gag tgt	705																	
Ser Phe Asn Arg Gly Glu Cys																		
	210																	

<210> 12
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 <223> Synthetic Construct
 <400> 12

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

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

<210> 13
<211> 726
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 342 gH1 Fab (no hinge) HC
with constant region

<220>
<221> CDS
<222> (64)..(726)

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gct gag gtt cag ctg gtc gag tct gga ggc ggg ctt gtc cag cct ggt 108
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
1 5 10 15
ggg agc ctg cgt ctc tct tgt gca gtg agc ggc ttc agc tct acc aat 156
Gly Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Ser Ser Thr Asn
20 25 30

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tac	cat	gtg	cac	tgg	gtg	cgt	cag	gca	cct	ggg	aag	ggc	ctg	gag	tgg	204
Tyr	His	Val	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	
			35					40					45			
atg	ggt	gtt	att	tgg	ggc	gac	ggc	gat	aca	tcc	tac	aac	tcc	gtc	ctg	252
Met	Gly	Val	Ile	Trp	Gly	Asp	Gly	Asp	Thr	Ser	Tyr	Asn	Ser	Val	Leu	
		50					55					60				
aag	agc	cgt	ttc	acc	att	tcc	cgt	gac	acc	tca	aag	aat	acc	gtt	tac	300
Lys	Ser	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Thr	Ser	Lys	Asn	Thr	Val	Tyr	
		65				70					75					
ctc	cag	atg	aac	tct	ctc	cgc	gca	gag	gac	aca	gca	gtc	tat	tac	tgt	348
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
					85					90					95	
gca	cgt	caa	ctg	acc	cac	tat	tac	gtt	ttg	gca	gcc	tgg	ggt	caa	ggg	396
Ala	Arg	Gln	Leu	Thr	His	Tyr	Tyr	Val	Leu	Ala	Ala	Trp	Gly	Gln	Gly	
				100					105					110		
act	ctg	gtc	aca	gtc	tcg	agc	gct	tct	aca	aag	ggc	cca	tcg	gtc	ttc	444
Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	
			115					120					125			
ccc	ctg	gca	ccc	tcc	tcc	aag	agc	acc	tct	ggg	ggc	aca	gcg	gcc	ctg	492
Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	
		130					135					140				
ggc	tgc	ctg	gtc	aag	gac	tac	ttc	ccc	gaa	ccg	gtg	acg	gtg	tcg	tgg	540
Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	
	145					150					155					
aac	tca	ggc	gcc	ctg	acc	agc	ggc	gtg	cac	acc	ttc	ccg	gct	gtc	cta	588
Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	
					165					170					175	
cag	tcc	tca	gga	ctc	tac	tcc	ctc	agc	agc	gtg	gtg	acc	gtg	ccc	tcc	636
Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	
				180					185					190		
agc	agc	ttg	ggc	acc	cag	acc	tac	atc	tgc	aac	gtg	aat	cac	aag	ccc	684
Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	
			195					200					205			
agc	aac	acc	aag	gtc	gac	aag	aaa	gtt	gag	ccc	aaa	tct	tgt			726
Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys			
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<210> 14
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 14

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

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Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Ser Ser Thr Asn Tyr
20 25 30
His Val His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met
35 40 45
Gly Val Ile Trp Gly Asp Gly Asp Thr Ser Tyr Asn Ser Val Leu Lys
50 55 60
Ser Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Val Tyr Leu
65 70 75 80
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95
Arg Gln Leu Thr His Tyr Tyr Val Leu Ala Ala Trp Gly Gln Gly Thr
100 105 110
Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125
Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140
Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160
Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175
Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190
Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205
Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
210 215 220

<210> 15

<211> 750

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: 342 gH1 Fab' HC with constant region

<220>

G0157 WO_ST25

<221> CDS

<222> (64)..(750)

<400> 15

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	Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	
1					5					10					15	
ggg	agc	ctg	cgt	ctc	tct	tgt	gca	gtg	agc	ggc	ttc	agc	tct	acc	aat	156
Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Val	Ser	Gly	Phe	Ser	Ser	Thr	Asn	
				20					25					30		
tac	cat	gtg	cac	tgg	gtg	cgt	cag	gca	cct	ggg	aag	ggc	ctg	gag	tgg	204
Tyr	His	Val	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	
			35					40					45			
atg	ggt	gtt	att	tgg	ggc	gac	ggc	gat	aca	tcc	tac	aac	tcc	gtc	ctg	252
Met	Gly	Val	Ile	Trp	Gly	Asp	Gly	Asp	Thr	Ser	Tyr	Asn	Ser	Val	Leu	
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aag	agc	cgt	ttc	acc	att	tcc	cgt	gac	acc	tca	aag	aat	acc	gtt	tac	300
Lys	Ser	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Thr	Ser	Lys	Asn	Thr	Val	Tyr	
	65					70					75					
ctc	cag	atg	aac	tct	ctc	cgc	gca	gag	gac	aca	gca	gtc	tat	tac	tgt	348
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
80					85					90					95	
gca	cgt	caa	ctg	acc	cac	tat	tac	gtt	ttg	gca	gcc	tgg	ggt	caa	ggg	396
Ala	Arg	Gln	Leu	Thr	His	Tyr	Tyr	Val	Leu	Ala	Ala	Trp	Gly	Gln	Gly	
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act	ctg	gtc	aca	gtc	tcg	agc	gct	tct	aca	aag	ggc	cca	tcg	gtc	ttc	444
Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	
			115					120					125			
ccc	ctg	gca	ccc	tcc	tcc	aag	agc	acc	tct	ggg	ggc	aca	gcg	gcc	ctg	492
Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	
		130					135					140				
ggc	tgc	ctg	gtc	aag	gac	tac	ttc	ccc	gaa	ccg	gtg	acg	gtg	tcg	tgg	540
Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	
	145				150						155					
aac	tca	ggc	gcc	ctg	acc	agc	ggc	gtg	cac	acc	ttc	ccg	gct	gtc	cta	588
Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	
160					165					170					175	
cag	tcc	tca	gga	ctc	tac	tcc	ctc	agc	agc	gtg	gtg	acc	gtg	ccc	tcc	636
Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	
				180					185					190		
agc	agc	ttg	ggc	acc	cag	acc	tac	atc	tgc	aac	gtg	aat	cac	aag	ccc	684
Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	
			195					200					205			
agc	aac	acc	aag	gtc	gac	aag	aaa	gtt	gag	ccc	aaa	tct	tgt	gac	aaa	732
Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	
		210					215					220				
act	cac	aca	tgc	gcc	gcg											750

Thr His Thr Cys Ala Ala
225

<210> 16
<211> 229
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 16

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

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

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

Gly Val Ile Trp Gly Asp Gly Asp Thr Ser Tyr Asn Ser Val Leu Lys
50 55 60

Ser Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Gln Leu Thr His Tyr Tyr Val Leu Ala Ala Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
Page 11

195

200

205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
 210 215 220

His Thr Cys Ala Ala
 225

<210> 17
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<220>
 <223> Description of Artificial Sequence: hu342 kappa LC

<220>
 <221> CDS
 <222> (1)..(711)

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 ctc cga ggt gcc aga tgt gat atc cag atg acc cag agt cca agc agt 96
 Leu Arg Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
 20 25 30
 ctc tcc gcc agc gta ggc gat cgt gtg act att acc tgt cgt gcc agt 144
 Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
 35 40 45
 gag gac ctc tat tac aac ctg gcc tgg tat cag cgt aaa ccg ggc aaa 192
 Glu Asp Leu Tyr Tyr Asn Leu Ala Trp Tyr Gln Arg Lys Pro Gly Lys
 50 55 60
 gcc ccg aag ctg ctc atc tat gat acg tac cgc ctg gct gac ggt gtg 240
 Ala Pro Lys Leu Leu Ile Tyr Asp Thr Tyr Arg Leu Ala Asp Gly Val
 65 70 75 80
 cca agc cgt ttc agt ggc agt ggc agc ggt act gac tat acc ctc aca 288
 Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr
 85 90 95
 att tcg tct ctc cag ccg gaa gat ttc gcc tct tac tat tgt cag caa 336
 Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Ser Tyr Tyr Cys Gln Gln
 100 105 110
 tat tac aag ttc cct ttc acc ttc ggt cag ggc act aaa gta gaa atc 384
 Tyr Tyr Lys Phe Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
 115 120 125
 aaa cgt acg gtg gct gca cca tct gtc ttc atc ttc ccg cca tct gat 432
 Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
 130 135 140
 gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg aat aac 480
 Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn

145	G0157 WO_ST25										155	160					
ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc	528																
Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu																	
	165	170	175														
caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac agc aag gac	576																
Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp																	
	180	185	190														
agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa gca gac tac	624																
Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr																	
	195	200	205														
gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc	672																
Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser																	
	210	215	220														
tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tag	711																
Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys																	
	225	230	235														

<210> 18
 <211> 236
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 18

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

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Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
130 135 140

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
145 150 155 160

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
165 170 175

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
180 185 190

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
195 200 205

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
210 215 220

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 19
<211> 1392
<212> DNA
<213> Artificial Sequence

<220>
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<220>
<221> CDS
<222> (1)..(1392)

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gcc cac tcc gaa gta caa ttg gtc gag tct gga ggc ggg ctt gtc cag	96
Ala His Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln	
20 25 30	
cct ggt ggg agc ctg cgt ctc tct tgt gca gtg agc ggc ttc agc tct	144
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Ser Ser	
35 40 45	
acc aat tac cat gtg cac tgg gtg cgt cag gca cct ggg aag ggc ctg	192
Thr Asn Tyr His Val His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu	
50 55 60	
gag tgg atg ggt gtt att tgg ggc gac ggc gat aca tcc tac aac tcc	240
Glu Trp Met Gly Val Ile Trp Gly Asp Gly Asp Thr Ser Tyr Asn Ser	
65 70 75 80	

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gtc	ctg	aag	agc	cgt	ttc	acc	att	tcc	cgt	gac	acc	tca	aag	aat	acc	288
Val	Leu	Lys	Ser	Arg 85	Phe	Thr	Ile	Ser	Arg 90	Asp	Thr	Ser	Lys	Asn 95	Thr	
gtt	tac	ctc	cag	atg	aac	tct	ctc	cgc	gca	gag	gac	aca	gca	gtc	tat	336
Val	Tyr	Leu	Gln 100	Met	Asn	Ser	Leu	Arg 105	Ala	Glu	Asp	Thr	Ala 110	Val	Tyr	
tac	tgt	gca	cgt	caa	ctg	acc	cac	tat	tac	gtt	ttg	gca	gcc	tggt	ggg	384
Tyr	Cys	Ala 115	Arg	Gln	Leu	Thr	His 120	Tyr	Tyr	Val	Leu	Ala 125	Ala	Trp	Gly	
caa	ggg	act	ctg	gtc	aca	gtc	tcg	agc	gct	tca	acc	aag	ggc	cca	tcc	432
Gln	Gly 130	Thr	Leu	Val	Thr	Val 135	Ser	Ser	Ala	Ser	Thr 140	Lys	Gly	Pro	Ser	
gtc	ttc	ccc	ctg	gcg	ccc	tgc	tcc	aga	tct	acc	tcc	gag	agc	aca	gcc	480
Val	Phe	Pro	Leu	Ala	Pro 150	Cys	Ser	Arg	Ser	Thr 155	Ser	Glu	Ser	Thr	Ala 160	
gcc	ctg	ggc	tgc	ctg	gtc	aag	gac	tac	ttc	ccc	gaa	ccg	gtg	acg	gtg	528
Ala	Leu	Gly	Cys	Leu 165	Val	Lys	Asp	Tyr	Phe 170	Pro	Glu	Pro	Val	Thr 175	Val	
tcg	tgg	aac	tca	ggc	gcc	ctg	acc	agc	ggc	gtg	cac	acc	ttc	ccg	gct	576
Ser	Trp	Asn	Ser 180	Gly	Ala	Leu	Thr	Ser 185	Gly	Val	His	Thr	Phe 190	Pro	Ala	
gtc	cta	cag	tcc	tca	gga	ctc	tac	tcc	ctc	agc	agc	gtg	gtg	acc	gtg	624
Val	Leu	Gln 195	Ser	Ser	Gly	Leu	Tyr 200	Ser	Leu	Ser	Ser	Val 205	Val	Thr	Val	
ccc	tcc	agc	agc	ttg	ggc	acg	aag	acc	tac	acc	tgc	aac	gta	gat	cac	672
Pro	Ser 210	Ser	Ser	Leu	Gly	Thr 215	Lys	Thr	Tyr	Thr	Cys 220	Asn	Val	Asp	His	
aag	ccc	agc	aac	acc	aag	gtg	gac	aag	aga	gtt	gag	tcc	aaa	tat	ggg	720
Lys 225	Pro	Ser	Asn	Thr	Lys 230	Val	Asp	Lys	Arg	Val 235	Glu	Ser	Lys	Tyr	Gly 240	
ccc	cca	tgc	cca	ccg	tgc	cca	gca	cct	gag	ttc	ctg	ggg	gga	cca	tca	768
Pro	Pro	Cys	Pro	Pro 245	Cys	Pro	Ala	Pro	Glu 250	Phe	Leu	Gly	Gly	Pro 255	Ser	
gtc	ttc	ctg	ttc	ccc	cca	aaa	ccc	aag	gac	act	ctc	atg	atc	tcc	cgg	816
Val	Phe	Leu	Phe 260	Pro	Pro	Lys	Pro	Lys 265	Asp	Thr	Leu	Met	Ile 270	Ser	Arg	
acc	cct	gag	gtc	acg	tgc	gtg	gtg	gtg	gac	gtg	agc	cag	gaa	gac	ccc	864
Thr	Pro	Glu 275	Val	Thr	Cys	Val	Val 280	Val	Asp	Val	Ser	Gln 285	Glu	Asp	Pro	
gag	gtc	cag	ttc	aac	tgg	tac	gtg	gat	ggc	gtg	gag	gtg	cat	aat	gcc	912
Glu	Val 290	Gln	Phe	Asn	Trp	Tyr 295	Val	Asp	Gly	Val	Glu 300	Val	His	Asn	Ala	
aag	aca	aag	ccg	cgg	gag	gag	cag	ttc	aac	agc	gcg	tac	cgt	gtg	gtc	960
Lys 305	Thr	Lys	Pro	Arg	Glu 310	Glu	Gln	Phe	Asn	Ser 315	Ala	Tyr	Arg	Val	Val 320	
agc	gtc	ctc	acc	gtc	ctg	cac	cag	gac	tgg	ctg	aac	ggc	aag	gag	tac	1008
Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	

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330

325

335

aag tgc aag gtc tcc aac aaa ggc ctc ccg tcc tcc atc gag aaa acc	1056
Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr	
340 345 350	
atc tcc aaa gcc aaa ggg cag ccc cga gag cca caa gtg tac acc ctg	1104
Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu	
355 360 365	
ccc cca tcc cag gag gag atg acc aag aac cag gtc agc ctg acc tgc	1152
Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys	
370 375 380	
ctg gtc aaa ggc ttc tac ccc agc gac atc gcc gtg gag tgg gag agc	1200
Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser	
385 390 395 400	
aat ggg cag ccg gag aac aac tac aag acc acg cct ccc gtc ctc gat	1248
Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp	
405 410 415	
tcc gac ggc tcc ttc ttc ctc tac agc agg cta acc gtg gac aag agc	1296
Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser	
420 425 430	
agg tgg cag gag ggg aat gtc ttc tca tgc tcc gtg atg cat gag gct	1344
Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala	
435 440 445	
ctg cac aac cac tac aca cag aag agc ctc tcc ctg tct ctg ggt tga	1392
Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly	
450 455 460	

<210> 20
 <211> 463
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Synthetic Construct
 <400> 20

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

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Val Leu Lys Ser Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr
85 90 95

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

Tyr Cys Ala Arg Gln Leu Thr His Tyr Tyr Val Leu Ala Ala Trp Gly
115 120 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
130 135 140

Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala
145 150 155 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
165 170 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
195 200 205

Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His
210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly
225 230 235 240

Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser
245 250 255

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
260 265 270

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro
275 280 285

Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
290 295 300

Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Ala Tyr Arg Val Val
305 310 315 320

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr

325 G0157 WO_ST25 335
330

Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr
340 345 350

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
355 360 365

Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
370 375 380

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
385 390 395 400

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
405 410 415

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser
420 425 430

Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
435 440 445

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<210> 21
<211> 1438
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 342 gL4gH1 VH3 (V+C) Fab (no hinge) vector DNA

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gctgatatcc agatgaccca gagtccaagc agtctctccg ccagcgtagg cgatcgtgtg 120
actattacct gtcgtgccag tgaggacctc tattacaacc tggcctggta tcagcgtaaa 180
ccgggcaaag ccccgaaagt gctcatctat gatacgtacc gcctggctga cgggtgtgcca 240
agccgtttca gtggcagtg cagcgggtact gactataccc tcacaatttc gtctctccag 300
ccggaagatt tcgcctctta ctattgtcag caatattaca agttcccttt caccttcggt 360
cagggcacta aagtagaaat caaacgtacg gtagcggccc catctgtctt catcttcccg 420
ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 480
tatcccagag aggccaaagt acagtggaag gtggataacg cctccaatc gggttaactcc 540

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caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcacccctg	600
acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt caccatcag	660
ggcctgagct caccagtaac aaaaagtttt aatagagggg agtggtaaaa tgaagaagac	720
tgctatagca attgcagtgg cgctagctgg ttctgccacc gtggcgcaag ctgaggttca	780
gctggtcgag tctggaggcg ggcttgtcca gcctggtggg agcctgcgtc tctcttgtgc	840
agtgagcggc ttcagctcta ccaattacca tgtgactcgg gtgcgtcagg cacctgggaa	900
gggcctggag tggatgggtg ttatttgggg cgacggcgat acatcctaca actccgtcct	960
gaagagccgt ttcaccattt cccgtgacac ctcaaagaat accgtttacc tccagatgaa	1020
ctctctccgc gcagaggaca cagcagtcta ttactgtgca cgtcaactga cccactatta	1080
cgttttggca gcctggggtc aagggactct ggtcacagtc tcgagcgctt ctacaaaggg	1140
cccatcggtc ttccccctgg caccctcctc caagagcacc tctgggggca cagcggccct	1200
gggctgcctg gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc	1260
cctgaccagc ggcgtgcaca cttccccggc tgtcctacag tcctcaggac tctactcct	1320
cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt	1380
gaatcacaag cccagcaaca ccaaggtcga caagaaagt gagcccaaatt cttgttaa	1438

<210> 22

<211> 1459

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: 342 gL4gH1 VH3 (V+C) Fab' vector DNA

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gctgatatcc agatgaccca gagtccaagc agtctctccg ccagcgtagg cgatcgtgtg	120
actattacct gtcgtgccag tgaggacctc tattacaacc tggcctggta tcagcgtaaa	180
ccgggcaaag ccccgaaagt gctcatctat gatacgtacc gcctggctga cgggtgtgcca	240
agccgtttca gtggcagtgg cagcgggtact gactataccc tcacaatttc gtctctccag	300
ccggaagatt tcgcctctta ctattgtcag caatattaca agttcccttt caccttcggt	360
cagggcacta aagtagaaat caaacgtacg gtagcggccc catctgtctt catcttcccg	420
ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc	480
tatcccagag aggccaaagt acagtggaaag gtggataacg ccctccaatc gggtaaactc	540
caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcacccctg	600
acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt caccatcag	660

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ggcctgagct caccagtaac aaaaagtttt aatagagggg agtggttaaaa tgaagaagac      720
tgctatagca attgcagtgg cgctagctgg ttctgccacc gtggcgcaag ctgaggttca      780
gctggtcgag tctggaggcg ggcttgtcca gcctgggtggg agcctgcgtc tctcttgtagc      840
agtgagcggc ttcagctcta ccaattacca tgtgcactgg gtgcgtcagg cacctgggaa      900
gggcctggag tggatgggtg ttatttgggg cgacggcgat acatcctaca actccgtcct      960
gaagagccgt ttcaccattt cccgtgacac ctcaaagaat accgtttacc tccagatgaa     1020
ctctctccgc gcagaggaca cagcagtcta ttactgtgca cgtcaactga cccactatta     1080
cgttttggca gcctggggtc aagggactct ggctcacagtc tcgagcgctt ctacaaaggg     1140
cccatcggtc ttccccctgg caccctcctc caagagcacc tctgggggca cagcggccct     1200
gggctgcctg gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc     1260
cctgaccagc ggctgacaca ccttccccgc tgtcctacag tcctcaggac tctactccct     1320
cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt     1380
gaatcacaag cccagcaaca ccaaggtcga caagaaagt gagcccaaat cttgtgacaa     1440
aactcacaca tgcgccgcg                                     1459

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<210> 23
<211> 986
<212> DNA
<213> Escherichia coli

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<220>
<221> CDS
<222> (379)..(945)

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<300>
<308> GenBank / D86610
<309> 2009-01-10
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ccgcttatta actttctgta tcactttttc ttataaaaaa tcatgtaaaa ccgctcgcca     180
agaccgcacc aatcgggtaa tctcgaactc gttttgcctc ggcggtagat tatcctcaca     240
gcatataatt ttgtgcgtta gtccacagat ttggccttaa ggaattgttt caacatgccc     300
aggtaattag tctcgtgtcg cttggcattt ttttataacg atatttgtcg ttaaggactt     360
caagggaaaa caaacaac  atg gtc aaa tct caa ccg att ttg aga tat atc      411
                      Met Val Lys Ser  Gln Pro Ile Leu Arg Tyr Ile
                      1          5          10

ttg cgc ggg att ccc gcg att gca gta gcg gtt ctg ctt tct gca tgt      459
Leu Arg Gly Ile Pro Ala Ile Ala Val Ala Val Leu Leu Ser Ala Cys

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agt gca aat aac acc gca aag aat atg cat cct gag aca cgt gca gtg Ser Ala Asn Asn Thr Ala Lys Asn Met His Pro Glu Thr Arg Ala Val	30	35	40 507
ggt agt gaa aca tca tca ctg caa gct tct cag gat gaa ttt gaa aac Gly Ser Glu Thr Ser Ser Leu Gln Ala Ser Gln Asp Glu Phe Glu Asn	45	50	55 555
ctg gtt cgt aat gtc gac gta aaa tcg cga att atg gat cag tat gct Leu Val Arg Asn Val Asp Val Lys Ser Arg Ile Met Asp Gln Tyr Ala	60	65	70 603
gac tgg aaa ggc gta cgt tat cgt ctg ggc ggc agc act aaa aaa ggt Asp Trp Lys Gly Val Arg Tyr Arg Leu Gly Gly Ser Thr Lys Lys Gly	80	85	90 651
atc gat tgt tct ggt ttc gta cag cgt aca ttc cgt gag caa ttt ggc Ile Asp Cys Ser Gly Phe Val Gln Arg Thr Phe Arg Glu Gln Phe Gly	95	100	105 699
tta gaa ctt ccg cgt tcg act tac gaa cag cag gaa atg ggt aaa tct Leu Glu Leu Pro Arg Ser Thr Tyr Glu Gln Gln Glu Met Gly Lys Ser	110	115	120 747
gtt tcc cgc agt aat ttg cgt acg ggt gat tta gtt ctg ttc cgt gcc Val Ser Arg Ser Asn Leu Arg Thr Gly Asp Leu Val Leu Phe Arg Ala	125	130	135 795
ggt tca acg gga cgc cat gtc ggt att tat atc ggc aac aat cag ttt Gly Ser Thr Gly Arg His Val Gly Ile Tyr Ile Gly Asn Asn Gln Phe	140	145	150 843
gtc cat gct tcc acc agc agt ggt gtt att att tcc agc atg aat gaa Val His Ala Ser Thr Ser Ser Gly Val Ile Ile Ser Ser Met Asn Glu	160	165	170 891
ccg tac tgg aag aag cgt tac aac gaa gca cgc cgg gtt ctc agc cgc Pro Tyr Trp Lys Lys Arg Tyr Asn Glu Ala Arg Arg Val Leu Ser Arg	175	180	185 939
agc taa taaaccgttt ggatgcaatc ccttggctat cctgacgagt t Ser			986

<210> 24
 <211> 188
 <212> PRT
 <213> Escherichia coli
 <400> 24

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

Ala Ile Ala Val Ala Val Leu Leu Ser Ala Cys Ser Ala Asn Asn Thr
 20 25 30

Ala Lys Asn Met His Pro Glu Thr Arg Ala Val Gly Ser Glu Thr Ser
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35

40

45

Ser Leu Gln Ala Ser Gln Asp Glu Phe Glu Asn Leu Val Arg Asn Val
50 55 60

Asp Val Lys Ser Arg Ile Met Asp Gln Tyr Ala Asp Trp Lys Gly Val
65 70 75 80

Arg Tyr Arg Leu Gly Gly Ser Thr Lys Lys Gly Ile Asp Cys Ser Gly
85 90 95

Phe Val Gln Arg Thr Phe Arg Glu Gln Phe Gly Leu Glu Leu Pro Arg
100 105 110

Ser Thr Tyr Glu Gln Gln Glu Met Gly Lys Ser Val Ser Arg Ser Asn
115 120 125

Leu Arg Thr Gly Asp Leu Val Leu Phe Arg Ala Gly Ser Thr Gly Arg
130 135 140

His Val Gly Ile Tyr Ile Gly Asn Asn Gln Phe Val His Ala Ser Thr
145 150 155 160

Ser Ser Gly Val Ile Ile Ser Ser Met Asn Glu Pro Tyr Trp Lys Lys
165 170 175

Arg Tyr Asn Glu Ala Arg Arg Val Leu Ser Arg Ser
180 185

<210> 25
<211> 2196
<212> DNA
<213> Escherichia coli

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<221> CDS
<222> (69)..(2117)

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<221> sig_peptide
<222> (69)..(134)

<300>
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<309> 1993-04-26
<313> (1)..(2196)

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ggccaggc atg aac atg ttt ttt agg ctt acc gcg tta gct ggc ctg ctt 110
Met Asn Met Phe Phe Arg Leu Thr Ala Leu Ala Gly Leu Leu

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10

1	5	
gca Ala 15	ata Ile	gca Ala 15
ggc Gly	cag Gln	acc Thr 20
ttc Phe	gct Ala	gta Val
gaa Glu	gat Asp 25	atc Ile
acg Thr	cgt Arg	gct Ala 30
gat Asp 30		
158		
caa Gln	att Ile	ccg Pro
gta Val	tta Leu 35	aag Lys
gaa Glu	gag Glu	acg Thr
cag Gln 40	cat His	gcg Ala
acg Thr	gta Val	agt Ser 45
gag Glu		
206		
cgc Arg	gta Val	acg Thr
tcg Ser 50	cgc Arg	ttc Phe 60
ttc Phe	acc Thr	cgt Arg 55
atc Ile 70	ttt Phe	gac Asp 75
ctg Leu 75	aat Asn	ctg Leu
ctc Leu		
302		
gat Asp	tac Tyr 80	agc Ser
cac His	aac Asn	gtg Val 85
ctg Leu 85	ctg Leu	gca Ala
agc Ser	gat Asp	ggt Val 90
gaa Glu	cag Gln	ttc Phe
gcg Ala		
350		
aaa Lys 95	aag Lys	aaa Lys
acc Thr	gag Glu	tta Leu 100
ggc Gly	gat Asp	gaa Glu
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Met Ser Leu Ser Leu Glu Gly Ile Gly Ala Val Leu Gln Met Asp Asp
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540

530

535

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 Gly Asp Ser Thr Ile Tyr Leu Leu Met Gln 1425
 465 470

<210> 30
 <211> 474
 <212> PRT
 <213> Escherichia coli

<400> 30

Met Lys Lys Thr Thr Leu Ala Leu Ser Ala Leu Ala Leu Ser Leu Gly
 1 5 10 15

Leu Ala Leu Ser Pro Leu Ser Ala Thr Ala Ala Glu Thr Ser Ser Ala
 20 25 30

Thr Thr Ala Gln Gln Met Pro Ser Leu Ala Pro Met Leu Glu Lys Val
 35 40 45

Met Pro Ser Val Val Ser Ile Asn Val Glu Gly Ser Thr Thr Val Asn
 50 55 60

Thr Pro Arg Met Pro Arg Asn Phe Gln Gln Phe Phe Gly Asp Asp Ser
 65 70 75 80

Pro Phe Cys Gln Glu Gly Ser Pro Phe Gln Ser Ser Pro Phe Cys Gln
 85 90 95

Gly Gly Gln Gly Gly Asn Gly Gly Gly Gln Gln Gln Lys Phe Met Ala
 100 105 110

Leu Gly Ser Gly Val Ile Ile Asp Ala Asp Lys Gly Tyr Val Val Thr
 115 120 125

Asn Asn His Val Val Asp Asn Ala Thr Val Ile Lys Val Gln Leu Ser
 130 135 140

Asp Gly Arg Lys Phe Asp Ala Lys Met Val Gly Lys Asp Pro Arg Ser
 145 150 155 160

Asp Ile Ala Leu Ile Gln Ile Gln Asn Pro Lys Asn Leu Thr Ala Ile
 165 170 175

Lys Met Ala Asp Ser Asp Ala Leu Arg Val Gly Asp Tyr Thr Val Ala
 180 185 190

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Ile Gly Asn Pro Phe Gly Leu Gly Glu Thr Val Thr Ser Gly Ile Val
 195 200 205

Ser Ala Leu Gly Arg Ser Gly Leu Asn Ala Glu Asn Tyr Glu Asn Phe
 210 215 220

Ile Gln Thr Asp Ala Ala Ile Asn Arg Gly Asn Ser Gly Gly Ala Leu
 225 230 235 240

Val Asn Leu Asn Gly Glu Leu Ile Gly Ile Asn Thr Ala Ile Leu Ala
 245 250 255

Pro Asp Gly Gly Asn Ile Gly Ile Gly Phe Ala Ile Pro Ser Asn Met
 260 265 270

Val Lys Asn Leu Thr Ser Gln Met Val Glu Tyr Gly Gln Val Lys Arg
 275 280 285

Gly Glu Leu Gly Ile Met Gly Thr Glu Leu Asn Ser Glu Leu Ala Lys
 290 295 300

Ala Met Lys Val Asp Ala Gln Arg Gly Ala Phe Val Ser Gln Val Leu
 305 310 315 320

Pro Asn Ser Ser Ala Ala Lys Ala Gly Ile Lys Ala Gly Asp Val Ile
 325 330 335

Thr Ser Leu Asn Gly Lys Pro Ile Ser Ser Phe Ala Ala Leu Arg Ala
 340 345 350

Gln Val Gly Thr Met Pro Val Gly Ser Lys Leu Thr Leu Gly Leu Leu
 355 360 365

Arg Asp Gly Lys Gln Val Asn Val Asn Leu Glu Leu Gln Gln Ser Ser
 370 375 380

Gln Asn Gln Val Asp Ser Ser Ser Ile Phe Asn Gly Ile Glu Gly Ala
 385 390 395 400

Glu Met Ser Asn Lys Gly Lys Asp Gln Gly Val Val Val Asn Asn Val
 405 410 415

Lys Thr Gly Thr Pro Ala Ala Gln Ile Gly Leu Lys Lys Gly Asp Val
 420 425 430

Ile Ile Gly Ala Asn Gln Gln Ala Val Lys Asn Ile Ala Glu Leu Arg
 435 440 445

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Lys Val Leu Asp Ser Lys Pro Ser Val Leu Ala Leu Asn Ile Gln Arg
450 455 460

Gly Asp Ser Thr Ile Tyr Leu Leu Met Gln
465 470

<210> 31
<211> 1425
<212> DNA
<213> Artificial Sequence

<220>
<223> mutated DegP gene comprising the mutation S210A and an Ase I restriction marker

<220>
<221> CDS
<222> (1)..(1425)

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Met Lys Lys Thr Thr Leu Ala Leu Ser Ala Leu Ala Leu Ser Leu Gly	
1 5 10 15	
ttg gcg tta tct ccg ctc tct gca acg gcg gct gag act tct tca gca	96
Leu Ala Leu Ser Pro Leu Ser Ala Thr Ala Ala Glu Thr Ser Ser Ala	
20 25 30	
acg aca gcc cag cag atg cca agc ctt gca ccg atg ctc gaa aag gtg	144
Thr Thr Ala Gln Gln Met Pro Ser Leu Ala Pro Met Leu Glu Lys Val	
35 40 45	
atg cct tca gtg gtc agc att aac gta gaa ggt agc aca acc gtt aat	192
Met Pro Ser Val Val Ser Ile Asn Val Glu Gly Ser Thr Thr Val Asn	
50 55 60	
acg ccg cgt atg ccg cgt aat ttc cag cag ttc ttc ggt gat gat tct	240
Thr Pro Arg Met Pro Arg Asn Phe Gln Gln Phe Phe Gly Asp Asp Ser	
65 70 75 80	
ccg ttc tgc cag gaa ggt tct ccg ttc cag agc tct ccg ttc tgc cag	288
Pro Phe Cys Gln Glu Gly Ser Pro Phe Gln Ser Ser Pro Phe Cys Gln	
85 90 95	
ggt ggc cag ggc ggt aat ggt ggc ggc cag caa cag aaa ttc atg gcg	336
Gly Gly Gln Gly Gly Asn Gly Gly Gly Gln Gln Gln Lys Phe Met Ala	
100 105 110	
ctg ggt tcc ggc gtc atc att gat gcc gat aaa ggc tat gtc gtc acc	384
Leu Gly Ser Gly Val Ile Ile Asp Ala Asp Lys Gly Tyr Val Val Thr	
115 120 125	
aac aac cac gtt gtt gat aac gcg acg gtc att aaa gtt caa ctg agc	432
Asn Asn His Val Val Asp Asn Ala Thr Val Ile Lys Val Gln Leu Ser	
130 135 140	
gat ggc cgt aag ttc gac gcg aag atg gtt ggc aaa gat ccg cgc tct	480
Asp Gly Arg Lys Phe Asp Ala Lys Met Val Gly Lys Asp Pro Arg Ser	
145 150 155 160	

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gat atc gcg ctg atc caa atc cag aac ccg aaa aac ctg acc gca att Asp Ile Ala Leu Ile Gln Ile Gln Asn Pro Lys Asn Leu Thr Ala Ile 165 170 175	528
aag atg gcg gat tct gat gca ctg cgc gtg ggt gat tac acc gta gcg Lys Met Ala Asp Ser Asp Ala Leu Arg Val Gly Asp Tyr Thr Val Ala 180 185 190	576
att ggt aac ccg ttt ggt ctg ggc gag acg gta act tcc ggg att gtc Ile Gly Asn Pro Phe Gly Leu Gly Glu Thr Val Thr Ser Gly Ile Val 195 200 205	624
tct gcg ctg ggg cgt agc ggc ctg aat gcc gaa aac tac gaa aac ttc Ser Ala Leu Gly Arg Ser Gly Leu Asn Ala Glu Asn Tyr Glu Asn Phe 210 215 220	672
atc cag acc gat gca gcg att aat cgt ggt aac gcc ggt ggt gcg ctg Ile Gln Thr Asp Ala Ala Ile Asn Arg Gly Asn Ala Gly Gly Ala Leu 225 230 235 240	720
gtt aac ctg aac ggc gaa ctg atc ggt atc aac acc gcg atc ctc gca Val Asn Leu Asn Gly Glu Leu Ile Gly Ile Asn Thr Ala Ile Leu Ala 245 250 255	768
ccg gac ggc ggc aac atc ggt atc ggt ttt gct atc ccg agt aac atg Pro Asp Gly Gly Asn Ile Gly Ile Gly Phe Ala Ile Pro Ser Asn Met 260 265 270	816
gtg aaa aac ctg acc tcg cag atg gtg gaa tac ggc cag gtg aaa cgc Val Lys Asn Leu Thr Ser Gln Met Val Glu Tyr Gly Gln Val Lys Arg 275 280 285	864
ggt gag ctg ggt att atg ggg act gag ctg aac tcc gaa ctg gcg aaa Gly Glu Leu Gly Ile Met Gly Thr Glu Leu Asn Ser Gly Leu Ala Lys 290 295 300	912
gcg atg aaa gtt gac gcc cag cgc ggt gct ttc gta agc cag gtt ctg Ala Met Lys Val Asp Ala Gln Arg Gly Ala Phe Val Ser Gln Val Leu 305 310 315 320	960
cct aat tcc tcc gct gca aaa gcg ggc att aaa gcg ggt gat gtg atc Pro Asn Ser Ser Ala Ala Lys Ala Gly Ile Lys Ala Gly Asp Val Ile 325 330 335	1008
acc tca ctg aac ggt aag ccg atc agc agc ttt gcc gca ctg cgt gct Thr Ser Leu Asn Gly Lys Pro Ile Ser Ser Phe Ala Ala Leu Arg Ala 340 345 350	1056
cag gtg ggt act atg ccg gta ggc agc aaa ctg acc ctg ggc tta ctg Gln Val Gly Thr Met Pro Val Gly Ser Lys Leu Thr Leu Gly Leu Leu 355 360 365	1104
cgc gac ggt aag cag gtt aac gtg aac ctg gaa ctg cag cag agc agc Arg Asp Gly Lys Gln Val Asn Val Asn Leu Glu Leu Gln Gln Ser Ser 370 375 380	1152
cag aat cag gtt gat tcc agc tcc atc ttc aac ggc att gaa ggc gct Gln Asn Gln Val Asp Ser Ser Ser Ile Phe Asn Gly Ile Glu Gly Ala 385 390 400	1200
gag atg agc aac aaa ggc aaa gat cag ggc gtg gta gtg aac aac gtg Glu Met Ser Asn Lys Gly Lys Asp Gln Gly Val Val Val Asn Asn Val 405 410 415 420	1248

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410

405

415

aaa acg ggc act ccg gct gcg cag atc ggc ctg aag aaa ggt gat gtg	1296
Lys Thr Gly Thr 420 Pro Ala Ala Gln 425 Ile Gly Leu Lys Lys 430 Gly Asp Val	
att att ggc gcg aac cag cag gca gtg aaa aac atc gct gaa ctg cgt	1344
Ile Ile Gly 435 Ala Asn Gln Gln 440 Ala Val Lys Asn Ile 445 Ala Glu Leu Arg	
aaa gtt ctc gac agc aaa ccg tct gtg ctg gca ctc aac att cag cgc	1392
Lys Val 450 Leu Asp Ser Lys 455 Pro Ser Val Leu Ala Leu 460 Asn Ile Gln Arg	
ggc gac agc acc atc tac ctg tta atg cag taa	1425
Gly Asp Ser Thr Ile Tyr 470 Leu Leu Met Gln	
465	

<210> 32
 <211> 474
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 32

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

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Asp Gly Arg Lys Phe Asp Ala Lys Met Val Gly Lys Asp Pro Arg Ser
145 150 155 160

Asp Ile Ala Leu Ile Gln Ile Gln Asn Pro Lys Asn Leu Thr Ala Ile
165 170 175

Lys Met Ala Asp Ser Asp Ala Leu Arg Val Gly Asp Tyr Thr Val Ala
180 185 190

Ile Gly Asn Pro Phe Gly Leu Gly Glu Thr Val Thr Ser Gly Ile Val
195 200 205

Ser Ala Leu Gly Arg Ser Gly Leu Asn Ala Glu Asn Tyr Glu Asn Phe
210 215 220

Ile Gln Thr Asp Ala Ala Ile Asn Arg Gly Asn Ala Gly Gly Ala Leu
225 230 235 240

Val Asn Leu Asn Gly Glu Leu Ile Gly Ile Asn Thr Ala Ile Leu Ala
245 250 255

Pro Asp Gly Gly Asn Ile Gly Ile Gly Phe Ala Ile Pro Ser Asn Met
260 265 270

Val Lys Asn Leu Thr Ser Gln Met Val Glu Tyr Gly Gln Val Lys Arg
275 280 285

Gly Glu Leu Gly Ile Met Gly Thr Glu Leu Asn Ser Glu Leu Ala Lys
290 295 300

Ala Met Lys Val Asp Ala Gln Arg Gly Ala Phe Val Ser Gln Val Leu
305 310 315 320

Pro Asn Ser Ser Ala Ala Lys Ala Gly Ile Lys Ala Gly Asp Val Ile
325 330 335

Thr Ser Leu Asn Gly Lys Pro Ile Ser Ser Phe Ala Ala Leu Arg Ala
340 345 350

Gln Val Gly Thr Met Pro Val Gly Ser Lys Leu Thr Leu Gly Leu Leu
355 360 365

Arg Asp Gly Lys Gln Val Asn Val Asn Leu Glu Leu Gln Gln Ser Ser
370 375 380

Gln Asn Gln Val Asp Ser Ser Ser Ile Phe Asn Gly Ile Glu Gly Ala
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<210> 36
 <211> 81
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> IGS cassette-4

<400> 36
 gagctcacca gtaacaaaaa gttttaatag aggagagtgt tgacgaggat tatataatga 60
 agaaaactgc tatagcaatt g 81

<210> 37
 <211> 954
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)..(954)

<400> 37
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 Met Arg Ala Lys Leu Leu Gly Ile Val Leu Thr Thr Pro Ile Ala Ile
 1 5 10 15
 agc tct ttt gct tct acc gag act tta tcg ttt act cct gac aac ata 96
 Ser Ser Phe Ala Ser Thr Glu Thr Leu Ser Phe Thr Pro Asp Asn Ile
 20 25 30
 aat gcg gac att agt ctt gga act ctg agc gga aaa aca aaa gag cgt 144
 Asn Ala Asp Ile Ser Leu Gly Thr Leu Ser Gly Lys Thr Lys Glu Arg
 35 40 45
 gtt tat cta gcc gaa gaa gga ggc cga aaa gtc agt caa ctc gac tgg 192
 Val Tyr Leu Ala Glu Glu Gly Gly Arg Lys Val Ser Gln Leu Asp Trp
 50 55 60
 aaa ttc aat aac gct gca att att aaa ggt gca att aat tgg gat ttg 240
 Lys Phe Asn Asn Ala Ala Ile Ile Lys Gly Ala Ile Asn Trp Asp Leu
 65 70 75 80
 atg ccc cag ata tct atc ggg gct gct ggc tgg aca act ctc ggc agc 288
 Met Pro Gln Ile Ser Ile Gly Ala Ala Gly Trp Thr Thr Leu Gly Ser
 85 90 95
 cga ggt ggc aat atg gtc gat cag gac tgg atg gat tcc agt aac ccc 336
 Arg Gly Gly Asn Met Val Asp Gln Asp Trp Met Asp Ser Ser Asn Pro
 100 105 110
 gga acc tgg acg gat gaa agt aga cac cct gat aca caa ctc aat tat 384
 Gly Thr Trp Thr Asp Glu Ser Arg His Pro Asp Thr Gln Leu Asn Tyr
 115 120 125
 gcc aac gaa ttt gat ctg aat atc aaa ggc tgg ctc ctc aac gaa ccc 432
 Ala Asn Glu Phe Asp Leu Asn Ile Lys Gly Trp Leu Leu Asn Glu Pro
 130 135 140

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aat	tac	cgc	ctg	gga	ctc	atg	gcc	gga	tat	cag	gaa	agc	cgt	tat	agc	480
Asn	Tyr	Arg	Leu	Gly	Leu	Met	Ala	Gly	Tyr	Gln	Glu	Ser	Arg	Tyr	Ser	
145				150						155					160	
ttt	aca	gcc	aga	ggt	ggt	tcc	tat	atc	tac	agt	tct	gag	gag	gga	ttc	528
Phe	Thr	Ala	Arg	Gly	Gly	Ser	Tyr	Ile	Tyr	Ser	Ser	Glu	Glu	Gly	Phe	
				165					170					175		
aga	gat	gat	atc	ggc	tcc	ttc	ccg	aat	gga	gaa	aga	gca	atc	ggc	tac	576
Arg	Asp	Asp	Ile	Gly	Ser	Phe	Pro	Asn	Gly	Glu	Arg	Ala	Ile	Gly	Tyr	
			180					185					190			
aaa	caa	cgt	ttt	aaa	atg	ccc	tac	att	ggc	ttg	act	gga	agt	tat	cgt	624
Lys	Gln	Arg	Phe	Lys	Met	Pro	Tyr	Ile	Gly	Leu	Thr	Gly	Ser	Tyr	Arg	
		195					200					205				
tat	gaa	gat	ttt	gaa	ctc	ggt	ggc	aca	ttt	aaa	tac	agc	ggc	tgg	gtg	672
Tyr	Glu	Asp	Phe	Glu	Leu	Gly	Gly	Thr	Phe	Lys	Tyr	Ser	Gly	Trp	Val	
	210					215					220					
gaa	tca	tct	gat	aac	gat	gaa	cac	tat	gac	ccg	gga	aaa	aga	atc	act	720
Glu	Ser	Ser	Asp	Asn	Asp	Glu	His	Tyr	Asp	Pro	Gly	Lys	Arg	Ile	Thr	
					230					235					240	
tat	cgc	agt	aag	gtc	aaa	gac	caa	aat	tac	tat	tct	gtt	gca	gtc	aat	768
Tyr	Arg	Ser	Lys	Val	Lys	Asp	Gln	Asn	Tyr	Tyr	Ser	Val	Ala	Val	Asn	
				245					250					255		
gca	ggt	tat	tac	gtc	aca	cct	aac	gca	aaa	gtt	tat	gtt	gaa	ggc	gca	816
Ala	Gly	Tyr	Tyr	Val	Thr	Pro	Asn	Ala	Lys	Val	Tyr	Val	Glu	Gly	Ala	
			260					265					270			
tgg	aat	cgg	gtt	acg	aat	aaa	aaa	ggt	aat	act	tca	ctt	tat	gat	cac	864
Trp	Asn	Arg	Val	Thr	Asn	Lys	Lys	Gly	Asn	Thr	Ser	Leu	Tyr	Asp	His	
		275					280					285				
aat	aat	aac	act	tca	gac	tac	agc	aaa	aat	gga	gca	ggt	ata	gaa	aac	912
Asn	Asn	Asn	Thr	Ser	Asp	Tyr	Ser	Lys	Asn	Gly	Ala	Gly	Ile	Glu	Asn	
		290				295					300					
tat	aac	ttc	atc	act	act	gct	ggt	ctt	aag	tac	aca	ttt	taa			954
Tyr	Asn	Phe	Ile	Thr	Thr	Ala	Gly	Leu	Lys	Tyr	Thr	Phe				
					310					315						

<210> 38
 <211> 317
 <212> PRT
 <213> Escherichia coli

<400> 38

Met Arg Ala Lys Leu Leu Gly Ile Val Leu Thr Thr Pro Ile Ala Ile
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Ser Ser Phe Ala Ser Thr Glu Thr Leu Ser Phe Thr Pro Asp Asn Ile
 20 25 30

Asn Ala Asp Ile Ser Leu Gly Thr Leu Ser Gly Lys Thr Lys Glu Arg
 35 40 45

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

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Tyr Asn Phe Ile Thr Thr Ala Gly Leu Lys Tyr Thr Phe
305 310 315

<210> 39
<211> 954
<212> DNA
<213> Artificial Sequence

<220>
<223> knock-out mutant OmpT gene

<220>
<221> CDS
<222> (1)..(954)

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Ile Arg Ala Lys Leu Leu Gly Ile Val Leu Thr Thr Pro Ile Ala Ile		
1 5 10 15		
agc tct ttt gct tct acc gag act tta tcg ttt act cct gac aac ata		96
Ser Ser Phe Ala Ser Thr Glu Thr Leu Ser Phe Thr Pro Asp Asn Ile		
20 25 30		
aat gcg gac att agt ctt gga act ctg agc gga aaa aca aaa gag cgt		144
Asn Ala Asp Ile Ser Leu Gly Thr Leu Ser Gly Lys Thr Lys Glu Arg		
35 40 45		
gtt tat cta gcc gaa gaa gga ggc cga aaa gtc agt caa ctc gac tgg		192
Val Tyr Leu Ala Glu Glu Gly Gly Arg Lys Val Ser Gln Leu Asp Trp		
50 55 60		
aaa ttc aat aac gct gca att att aaa ggt gca att aat tgg gat ttg		240
Lys Phe Asn Asn Ala Ala Ile Ile Lys Gly Ala Ile Asn Trp Asp Leu		
65 70 75 80		
atg ccc cag ata tct atc ggg gct gct ggc tgg aca act ctc ggc agc		288
Met Pro Gln Ile Ser Ile Gly Ala Ala Gly Trp Thr Thr Leu Gly Ser		
85 90 95		
cga ggt ggc aat atg gtc gat cag gac tgg atg gat tcc agt aac ccc		336
Arg Gly Gly Asn Met Val Asp Gln Asp Trp Met Asp Ser Ser Asn Pro		
100 105 110		
gga acc tgg acg gat gaa agt aga cac cct gat aca caa ctc aat tat		384
Gly Thr Trp Thr Asp Glu Ser Arg His Pro Asp Thr Gln Leu Asn Tyr		
115 120 125		
gcc aac gaa ttt gat ctg aat atc aaa ggc tgg ctc ctc aac gaa ccc		432
Ala Asn Glu Phe Asp Leu Asn Ile Lys Gly Trp Leu Leu Asn Glu Pro		
130 135 140		
aat tac cgc ctg gga ctc atg gcc gga tat cag gaa agc cgt tat agc		480
Asn Tyr Arg Leu Gly Leu Met Ala Gly Tyr Gln Glu Ser Arg Tyr Ser		
145 150 155 160		
ttt aca gcc aga ggt ggt tcc tat atc tac agt tct gag gag gga ttc		528
Phe Thr Ala Arg Gly Gly Ser Tyr Ile Tyr Ser Ser Glu Glu Gly Phe		
165 170 175		

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aga gat gat atc ggc tcc ttc ccg aat gga gaa aga gca atc ggc tac	576
Arg Asp Asp Ile Gly Ser Phe Pro Asn Gly Glu Arg Ala Ile Gly Tyr	
180 185 190	
aaa caa cgt ttt aaa atg ccc tac att ggc ttg act gga agt tat cgt	624
Lys Gln Arg Phe Lys Met Pro Tyr Ile Gly Leu Thr Gly Ser Tyr Arg	
195 200 205	
tat gaa gat ttt gaa ctc ggt ggc aca ttt aaa tac agc ggc tgg gtg	672
Tyr Glu Asp Phe Glu Leu Gly Gly Thr Phe Lys Tyr Ser Gly Trp Val	
210 215 220	
gaa tca tct gat aac gat gaa cac tat gac ccg gga aaa aga atc act	720
Glu Ser Ser Asp Asn Asp Glu His Tyr Asp Pro Gly Lys Arg Ile Thr	
225 230 235 240	
tat cgc agt aag gtc aaa gac caa aat tac tat tct gtt gca gtc aat	768
Tyr Arg Ser Lys Val Lys Asp Gln Asn Tyr Tyr Ser Val Ala Val Asn	
245 250 255	
gca ggt tat tac gtc aca cct aac gca aaa gtt tat gtt gaa ggc gca	816
Ala Gly Tyr Tyr Val Thr Pro Asn Ala Lys Val Tyr Val Glu Gly Ala	
260 265 270	
tgg aat cgg gtt acg aat aaa aaa ggt aat act tca ctt tat gat cac	864
Trp Asn Arg Val Thr Asn Lys Lys Gly Asn Thr Ser Leu Tyr Asp His	
275 280 285	
aat aat aac act tca gac tac agc aaa aat gga gca ggt ata gaa aac	912
Asn Asn Asn Thr Ser Asp Tyr Ser Lys Asn Gly Ala Gly Ile Glu Asn	
290 295 300	
tat aac ttc atc act act gct ggt ctt aag tac aca ttt taa	954
Tyr Asn Phe Ile Thr Thr Ala Gly Leu Lys Tyr Thr Phe	
305 310 315	

<210> 40
 <211> 317
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 40

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

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

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<210> 41
 <211> 954
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> mutated OmpT gene encoding the protein with the point mutations
 D210A and H212A

<220>
 <221> CDS
 <222> (1)..(954)

<400> 41
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 Met Arg Ala Lys Leu Leu Gly Ile Val Leu Thr Thr Pro Ile Ala Ile
 1 5 10 15
 agc tct ttt gct tct acc gag act tta tcg ttt act cct gac aac ata 96
 Ser Ser Phe Ala Ser Thr Glu Thr Leu Ser Phe Thr Pro Asp Asn Ile
 20 25 30
 aat gcg gac att agt ctt gga act ctg agc gga aaa aca aaa gag cgt 144
 Asn Ala Asp Ile Ser Leu Gly Thr Leu Ser Gly Lys Thr Lys Glu Arg
 35 40 45
 gtt tat cta gcc gaa gaa gga ggc cga aaa gtc agt caa ctc gac tgg 192
 Val Tyr Leu Ala Glu Glu Gly Gly Arg Lys Val Ser Gln Leu Asp Trp
 50 55 60
 aaa ttc aat aac gct gca att att aaa ggt gca att aat tgg gat ttg 240
 Lys Phe Asn Asn Ala Ala Ile Ile Lys Gly Ala Ile Asn Trp Asp Leu
 65 70 75 80
 atg ccc cag ata tct atc ggg gct gct ggc tgg aca act ctc ggc agc 288
 Met Pro Gln Ile Ser Ile Gly Ala Ala Gly Trp Thr Thr Leu Gly Ser
 85 90 95
 cga ggt ggc aat atg gtc gat cag gac tgg atg gat tcc agt aac ccc 336
 Arg Gly Gly Asn Met Val Asp Gln Asp Trp Met Asp Ser Ser Asn Pro
 100 105 110
 gga acc tgg acg gat gaa agt aga cac cct gat aca caa ctc aat tat 384
 Gly Thr Trp Thr Asp Glu Ser Arg His Pro Asp Thr Gln Leu Asn Tyr
 115 120 125
 gcc aac gaa ttt gat ctg aat atc aaa ggc tgg ctc ctc aac gaa ccc 432
 Ala Asn Glu Phe Asp Leu Asn Ile Lys Gly Trp Leu Leu Asn Glu Pro
 130 135 140
 aat tac cgc ctg gga ctc atg gcc gga tat cag gaa agc cgt tat agc 480
 Asn Tyr Arg Leu Gly Leu Met Ala Gly Tyr Gln Glu Ser Arg Tyr Ser
 145 150 155 160
 ttt aca gcc aga ggt ggt tcc tat atc tac agt tct gag gag gga ttc 528
 Phe Thr Ala Arg Gly Gly Ser Tyr Ile Tyr Ser Ser Glu Glu Gly Phe
 165 170 175
 aga gat gat atc ggc tcc ttc ccg aat gga gaa aga gca atc ggc tac 576
 Arg Asp Asp Ile Gly Ser Phe Pro Asn Gly Glu Arg Ala Ile Gly Tyr
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180	185	190	
aaa caa cgt ttt aaa atg ccc tac att ggc ttg act gga agt tat cgt Lys Gln Arg Phe Lys Met Pro Tyr Ile Gly Leu Thr Gly Ser Tyr Arg	195	200	205 624
tat gaa gat ttt gaa ctc ggt ggc aca ttt aaa tac agc ggc tgg gtg Tyr Glu Asp Phe Glu Leu Gly Gly Thr Phe Lys Tyr Ser Gly Trp Val	210	215	220 672
gaa tca tct gat aac gct gaa gct tat gac ccg gga aaa aga atc act Glu Ser Ser Asp Asn Ala Glu Ala Tyr Asp Pro Gly Lys Arg Ile Thr	225	230	235 720
tat cgc agt aag gtc aaa gac caa aat tac tat tct gtt gca gtc aat Tyr Arg Ser Lys Val Lys Asp Gln Asn Tyr Tyr Ser Val Ala Val Asn	245	250	255 768
gca ggt tat tac gtc aca cct aac gca aaa gtt tat gtt gaa ggc gca Ala Gly Tyr Tyr Val Thr Pro Asn Ala Lys Val Tyr Val Glu Gly Ala	260	265	270 816
tgg aat cgg gtt acg aat aaa aaa ggt aat act tca ctt tat gat cac Trp Asn Arg Val Thr Asn Lys Lys Gly Asn Thr Ser Leu Tyr Asp His	275	280	285 864
aat aat aac act tca gac tac agc aaa aat gga gca ggt ata gaa aac Asn Asn Asn Thr Ser Asp Tyr Ser Lys Asn Gly Ala Gly Ile Glu Asn	290	295	300 912
tat aac ttc atc act act gct ggt ctt aag tac aca ttt taa Tyr Asn Phe Ile Thr Thr Ala Gly Leu Lys Tyr Thr Phe	305	310	315 954

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

<220>
 <223> Synthetic Construct

<400> 42

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Ser Ser Phe Ala Ser Thr Glu Thr Leu Ser Phe Thr Pro Asp Asn Ile
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Asn Ala Asp Ile Ser Leu Gly Thr Leu Ser Gly Lys Thr Lys Glu Arg
 35 40 45

Val Tyr Leu Ala Glu Glu Gly Gly Arg Lys Val Ser Gln Leu Asp Trp
 50 55 60

Lys Phe Asn Asn Ala Ala Ile Ile Lys Gly Ala Ile Asn Trp Asp Leu
 65 70 75 80

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Met Pro Gln Ile Ser Ile Gly Ala Ala Gly Trp Thr Thr Leu Gly Ser
85 90 95

Arg Gly Gly Asn Met Val Asp Gln Asp Trp Met Asp Ser Ser Asn Pro
100 105 110

Gly Thr Trp Thr Asp Glu Ser Arg His Pro Asp Thr Gln Leu Asn Tyr
115 120 125

Ala Asn Glu Phe Asp Leu Asn Ile Lys Gly Trp Leu Leu Asn Glu Pro
130 135 140

Asn Tyr Arg Leu Gly Leu Met Ala Gly Tyr Gln Glu Ser Arg Tyr Ser
145 150 155 160

Phe Thr Ala Arg Gly Gly Ser Tyr Ile Tyr Ser Ser Glu Glu Gly Phe
165 170 175

Arg Asp Asp Ile Gly Ser Phe Pro Asn Gly Glu Arg Ala Ile Gly Tyr
180 185 190

Lys Gln Arg Phe Lys Met Pro Tyr Ile Gly Leu Thr Gly Ser Tyr Arg
195 200 205

Tyr Glu Asp Phe Glu Leu Gly Gly Thr Phe Lys Tyr Ser Gly Trp Val
210 215 220

Glu Ser Ser Asp Asn Ala Glu Ala Tyr Asp Pro Gly Lys Arg Ile Thr
225 230 235 240

Tyr Arg Ser Lys Val Lys Asp Gln Asn Tyr Tyr Ser Val Ala Val Asn
245 250 255

Ala Gly Tyr Tyr Val Thr Pro Asn Ala Lys Val Tyr Val Glu Gly Ala
260 265 270

Trp Asn Arg Val Thr Asn Lys Lys Gly Asn Thr Ser Leu Tyr Asp His
275 280 285

Asn Asn Asn Thr Ser Asp Tyr Ser Lys Asn Gly Ala Gly Ile Glu Asn
290 295 300

Tyr Asn Phe Ile Thr Thr Ala Gly Leu Lys Tyr Thr Phe
305 310 315

<210> 43

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<211> 711
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)..(711)

<400> 43

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ttt gct cag gct gat gac gcg gca att caa caa acg tta gcc aaa atg	96
Phe Ala Gln Ala Asp Asp Ala Ala Ile Gln Gln Thr Leu Ala Lys Met	
20 25 30	
ggc atc aaa agc agc gat att cag ccc gcg cct gta gct ggc atg aag	144
Gly Ile Lys Ser Ser Asp Ile Gln Pro Ala Pro Val Ala Gly Met Lys	
35 40 45	
aca gtt ctg act aac agc ggc gtg ttg tac atc acc gat gat ggt aaa	192
Thr Val Leu Thr Asn Ser Gly Val Leu Tyr Ile Thr Asp Asp Gly Lys	
50 55 60	
cat atc att cag ggg cca atg tat gac gtt agt ggc acg gct ccg gtc	240
His Ile Ile Gln Gly Pro Met Tyr Asp Val Ser Gly Thr Ala Pro Val	
65 70 75 80	
aat gtc acc aat aag atg ctg tta aag cag ttg aat gcg ctt gaa aaa	288
Asn Val Thr Asn Lys Met Leu Leu Lys Gln Leu Asn Ala Leu Glu Lys	
85 90 95	
gag atg atc gtt tat aaa gcg ccg cag gaa aaa cac gtc atc acc gtg	336
Glu Met Ile Val Tyr Lys Ala Pro Gln Glu Lys His Val Ile Thr Val	
100 105 110	
ttt act gat att acc tgt ggt tac tgc cac aaa ctg cat gag caa atg	384
Phe Thr Asp Ile Thr Cys Gly Tyr Cys His Lys Leu His Glu Gln Met	
115 120 125	
gca gac tac aac gcg ctg ggg atc acc gtg cgt tat ctt gct ttc ccg	432
Ala Asp Tyr Asn Ala Leu Gly Ile Thr Val Arg Tyr Leu Ala Phe Pro	
130 135 140	
cgc cag ggg ctg gac agc gat gca gag aaa gaa atg aaa gct atc tgg	480
Arg Gln Gly Leu Asp Ser Asp Ala Glu Lys Glu Met Lys Ala Ile Trp	
145 150 155 160	
tgt gcg aaa gat aaa aac aaa gcg ttt gat gat gtg atg gca ggt aaa	528
Cys Ala Lys Asp Lys Asn Lys Ala Phe Asp Asp Val Met Ala Gly Lys	
165 170 175	
agc gtc gca cca gcc agt tgc gac gtg gat att gcc gac cat tac gca	576
Ser Val Ala Pro Ala Ser Cys Asp Val Asp Ile Ala Asp His Tyr Ala	
180 185 190	
ctt ggc gtc cag ctt ggc gtt agc ggt act ccg gca gtt gtg ctg agc	624
Leu Gly Val Gln Leu Gly Val Ser Gly Thr Pro Ala Val Val Leu Ser	
195 200 205	
aat ggc aca ctt gtt ccg ggt tac cag ccg ccg aaa gag atg aaa gaa	672

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Asn Gly Thr Leu Val Pro Gly Tyr Gln Pro Pro Lys Glu Met Lys Glu
 210 215 220

ttt ctc gac gaa cac caa aaa atg acc agc ggt aaa taa 711
 Phe Leu Asp Glu His Gln Lys Met Thr Ser Gly Lys
 225 230 235

<210> 44
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 <212> PRT
 <213> Escherichia coli

<400> 44

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 20 25 30

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 35 40 45

Thr Val Leu Thr Asn Ser Gly Val Leu Tyr Ile Thr Asp Asp Gly Lys
 50 55 60

His Ile Ile Gln Gly Pro Met Tyr Asp Val Ser Gly Thr Ala Pro Val
 65 70 75 80

Asn Val Thr Asn Lys Met Leu Leu Lys Gln Leu Asn Ala Leu Glu Lys
 85 90 95

Glu Met Ile Val Tyr Lys Ala Pro Gln Glu Lys His Val Ile Thr Val
 100 105 110

Phe Thr Asp Ile Thr Cys Gly Tyr Cys His Lys Leu His Glu Gln Met
 115 120 125

Ala Asp Tyr Asn Ala Leu Gly Ile Thr Val Arg Tyr Leu Ala Phe Pro
 130 135 140

Arg Gln Gly Leu Asp Ser Asp Ala Glu Lys Glu Met Lys Ala Ile Trp
 145 150 155 160

Cys Ala Lys Asp Lys Asn Lys Ala Phe Asp Asp Val Met Ala Gly Lys
 165 170 175

Ser Val Ala Pro Ala Ser Cys Asp Val Asp Ile Ala Asp His Tyr Ala
 180 185 190

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Leu Gly Val Gln Leu Gly Val Ser Gly Thr Pro Ala Val Val Leu Ser
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Asn Gly Thr Leu Val Pro Gly Tyr Gln Pro Pro Lys Glu Met Lys Glu
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 225 230 235

<210> 45
 <211> 729
 <212> DNA
 <213> Artificial Sequence

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 <222> (1)..(729)

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ttt gct cag gct gat gac gcg gca att caa caa acg tta gcc aaa atg	96
Phe Ala Gln Ala Asp Asp Ala Ala Ile Gln Gln Thr Leu Ala Lys Met	
20 25 30	
ggc atc aaa agc agc gat att cag ccc gcg cct gta gct ggc atg aag	144
Gly Ile Lys Ser Ser Asp Ile Gln Pro Ala Pro Val Ala Gly Met Lys	
35 40 45	
aca gtt ctg act aac agc ggc gtg ttg tac atc acc gat gat ggt aaa	192
Thr Val Leu Thr Asn Ser Gly Val Leu Tyr Ile Thr Asp Asp Gly Lys	
50 55 60	
cat atc att cag ggg cca atg tat gac gtt agt ggc acg gct ccg gtc	240
His Ile Ile Gln Gly Pro Met Tyr Asp Val Ser Gly Thr Ala Pro Val	
65 70 75 80	
aat gtc acc aat aag atg ctg tta aag cag ttg aat gcg ctt gaa aaa	288
Asn Val Thr Asn Lys Met Leu Leu Lys Gln Leu Asn Ala Leu Glu Lys	
85 90 95	
gag atg atc gtt tat aaa gcg ccg cag gaa aaa cac gtc atc acc gtg	336
Glu Met Ile Val Tyr Lys Ala Pro Gln Glu Lys His Val Ile Thr Val	
100 105 110	
ttt act gat att acc tgt ggt tac tgc cac aaa ctg cat gag caa atg	384
Phe Thr Asp Ile Thr Cys Gly Tyr Cys His Lys Leu His Glu Gln Met	
115 120 125	
gca gac tac aac gcg ctg ggg atc acc gtg cgt tat ctt gct ttc ccg	432
Ala Asp Tyr Asn Ala Leu Gly Ile Thr Val Arg Tyr Leu Ala Phe Pro	
130 135 140	
cgc cag ggg ctg gac agc gat gca gag aaa gaa atg aaa gct atc tgg	480

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Arg	Gln	Gly	Leu	Asp	Ser	Asp	Ala	Glu	Lys	Glu	Met	Lys	Ala	Ile	Trp	
145					150					155					160	
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Cys	Ala	Lys	Asp	Lys	Asn	Lys	Ala	Phe	Asp	Asp	Val	Met	Ala	Gly	Lys	
				165					170					175		
agc	gtc	gca	cca	gcc	agt	tgc	gac	gtg	gat	att	gcc	gac	cat	tac	gca	576
Ser	Val	Ala	Pro	Ala	Ser	Cys	Asp	Val	Asp	Ile	Ala	Asp	His	Tyr	Ala	
			180					185					190			
ctt	ggc	gtc	cag	ctt	ggc	gtt	agc	ggg	act	ccg	gca	gtt	gtg	ctg	agc	624
Leu	Gly	Val	Gln	Leu	Gly	Val	Ser	Gly	Thr	Pro	Ala	Val	Val	Leu	Ser	
		195					200					205				
aat	ggc	aca	ctt	gtt	ccg	ggg	tac	cag	ccg	ccg	aaa	gag	atg	aaa	gaa	672
Asn	Gly	Thr	Leu	Val	Pro	Gly	Tyr	Gln	Pro	Pro	Lys	Glu	Met	Lys	Glu	
	210					215					220					
ttt	ctc	gac	gaa	cac	caa	aaa	atg	acc	agc	ggg	aaa	cac	cat	cac	cat	720
Phe	Leu	Asp	Glu	His	Gln	Lys	Met	Thr	Ser	Gly	Lys	His	His	His	His	
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cac	cac	taa														729
His	His															

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Gly	Ile	Lys	Ser	Ser	Asp	Ile	Gln	Pro	Ala	Pro	Val	Ala	Gly	Met	Lys	
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Thr	Val	Leu	Thr	Asn	Ser	Gly	Val	Leu	Tyr	Ile	Thr	Asp	Asp	Gly	Lys	
	50					55					60					
His	Ile	Ile	Gln	Gly	Pro	Met	Tyr	Asp	Val	Ser	Gly	Thr	Ala	Pro	Val	
65					70					75					80	
Asn	Val	Thr	Asn	Lys	Met	Leu	Leu	Lys	Gln	Leu	Asn	Ala	Leu	Glu	Lys	
			85						90					95		
Glu	Met	Ile	Val	Tyr	Lys	Ala	Pro	Gln	Glu	Lys	His	Val	Ile	Thr	Val	

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100

105

110

Phe Thr Asp Ile Thr Cys Gly Tyr Cys His Lys Leu His Glu Gln Met
 115 120 125

Ala Asp Tyr Asn Ala Leu Gly Ile Thr Val Arg Tyr Leu Ala Phe Pro
 130 135 140

Arg Gln Gly Leu Asp Ser Asp Ala Glu Lys Glu Met Lys Ala Ile Trp
 145 150 155 160

Cys Ala Lys Asp Lys Asn Lys Ala Phe Asp Asp Val Met Ala Gly Lys
 165 170 175

Ser Val Ala Pro Ala Ser Cys Asp Val Asp Ile Ala Asp His Tyr Ala
 180 185 190

Leu Gly Val Gln Leu Gly Val Ser Gly Thr Pro Ala Val Val Leu Ser
 195 200 205

Asn Gly Thr Leu Val Pro Gly Tyr Gln Pro Pro Lys Glu Met Lys Glu
 210 215 220

Phe Leu Asp Glu His Gln Lys Met Thr Ser Gly Lys His His His His
 225 230 235 240

His His

<210> 47
 <211> 24
 <212> DNA
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<220>
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24

<210> 48
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 <212> DNA
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<220>
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24

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<213> Escherichia coli

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<223> preprotease III (AA -23 to 939)

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<222> (275)..(3091)
<223> protease III (AA 1 - 939)

<300>
<308> GenBank / x06227
<309> 2005-04-18
<313> (1)..(3120)

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gcagcacaag attaaattct ggcagatgat ttgcgttaac gtgttgaatc tggacagaaa      180
attaagttga ttatgaggtc cgtga  atg ccc cgc agc acc tgg ttc aaa gca      232
                        Met Pro Arg Ser Thr Trp Phe Lys Ala
                        -20                      -15

tta ttg ttg tta gtt gcc ctt tgg gca ccc tta agt cag gca gaa acg      280
Leu Leu Leu Leu Val Ala Leu Trp Ala Pro Leu Ser Gln Ala Glu Thr
                        -10                      -5                      -1  1

gga tgg cag ccg att cag gaa acc atc cgt aaa agt gat aaa gat aac      328
Gly Trp Gln Pro Ile Gln Glu Thr Ile Arg Lys Ser Asp Lys Asp Asn
                        5                      10                      15

cgc cag tat cag gct ata cgt ctg gat aac ggt atg gtg gtc ttg ctg      376
Arg Gln Tyr Gln Ala Ile Arg Leu Asp Asn Gly Met Val Val Leu Leu
                        20                      25                      30

gtt tct gat ccg cag gca gtt aaa tcg ctc tcg gcg ctg gtg gtg ccc      424
Val Ser Asp Pro Gln Ala Val Lys Ser Leu Ser Ala Leu Val Val Pro
35                      40                      45                      50

gtt ggg tcg ctg gaa gat ccc gag gcg tac cag ggg ctg gca cat tac      472
Val Gly Ser Leu Glu Asp Pro Glu Ala Tyr Gln Gly Leu Ala His Tyr
55                      60                      65

ctt gaa cat atg agt ctg atg ggg tcg aaa aag tac ccg cag gct gac      520
Leu Glu His Met Ser Leu Met Gly Ser Lys Lys Tyr Pro Gln Ala Asp
70                      75                      80

agt ctg gcc gaa tat ctc aaa atg cac ggc ggt agt cac aat gcc agc      568
Ser Leu Ala Glu Tyr Leu Lys Met His Gly Gly Ser His Asn Ala Ser
85                      90                      95

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ctc Leu	gac Asp	aag Lys	aaa Lys	tat Tyr 135	gcc Ala	gaa Glu	cgt Arg	gag Glu	cgt Arg 140	aat Asn	gcg Ala	gtg Val	aac Asn	gct Ala 145	gaa Glu	712
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gca Ala	gaa Glu	acc Thr 165	att Ile	aac Asn	ccg Pro	gca Ala	cac His 170	ccc Pro	ggt Gly	tca Ser	aag Lys	ttt Phe 175	tct Ser	ggt Gly	ggt Gly	808
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ctg Leu 195	aaa Lys	gat Asp	ttc Phe	cac His	gag Glu 200	aag Lys	tac Tyr	tat Tyr	tcc Ser	gcc Ala 205	aat Asn	ttg Leu	atg Met	aag Lys	gcg Ala 210	904
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gac Asp	acc Thr	ttt Phe	ggt Gly 230	cgc Arg	gtg Val	ccg Pro	aac Asn	aaa Lys 235	gag Glu	agc Ser	aaa Lys	aaa Lys	ccg Pro 240	gaa Glu	atc Ile	1000
acc Thr	gtg Val	ccg Pro 245	gta Val	gtc Val	acc Thr	gac Asp	gcg Ala 250	caa Gln	aag Lys	ggc Gly	att Ile	atc Ile 255	att Ile	cat His	tac Tyr	1048
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ctg Leu	att Ile	ggc Gly	aat Asn	cgc Arg 295	agc Ser	cca Pro	ggt Gly	aca Thr	ctt Leu 300	tct Ser	gac Asp	tgg Trp	ctg Leu	caa Gln 305	aag Lys	1192
cag Gln	gga Gly	tta Leu	gtt Val 310	gag Glu	ggc Gly	att Ile	agc Ser	gcc Ala 315	aac Asn	tcc Ser	gat Asp	cct Pro	atc Ile 320	gtc Val	aac Asn	1240
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ctg Leu	gct Ala	aat Asn	cgc Arg	gat Asp	cag Gln	gtt Val	gtg Val	gcg Ala	gca Ala	att Ile	ttt Phe	agc Ser	tat Tyr	ctc Leu	aat Asn	1336

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355					360					365					370	
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Asn	Val	Leu	Asp	Ile	Asp	Phe	Arg	Tyr	Pro	Ser	Ile	Thr	Arg	Asp	Met	
				375					380					385		
gat	tac	gtc	gaa	tgg	ctg	gca	gat	acc	atg	att	cgc	gtt	cct	gtt	gag	1480
Asp	Tyr	Val	Glu	Trp	Leu	Ala	Asp	Thr	Met	Ile	Arg	Val	Pro	Val	Glu	
			390					395					400			
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His	Thr	Leu	Asp	Ala	Val	Asn	Ile	Ala	Asp	Arg	Tyr	Asp	Ala	Lys	Ala	
		405					410					415				
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Val	Lys	Glu	Arg	Leu	Ala	Met	Met	Thr	Pro	Gln	Asn	Ala	Arg	Ile	Trp	
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tat	atc	agc	ccg	aaa	gag	ccg	cac	aac	aaa	acg	gct	tac	ttt	gtc	gat	1624
Tyr	Ile	Ser	Pro	Lys	Glu	Pro	His	Asn	Lys	Thr	Ala	Tyr	Phe	Val	Asp	
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Ala	Pro	Tyr	Gln	Val	Asp	Lys	Ile	Ser	Ala	Gln	Thr	Phe	Ala	Asp	Trp	
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Gln	Lys	Lys	Ala	Ala	Asp	Ile	Ala	Leu	Ser	Leu	Pro	Glu	Leu	Asn	Pro	
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Tyr	Ile	Pro	Asp	Asp	Phe	Ser	Leu	Ile	Lys	Ser	Glu	Lys	Lys	Tyr	Asp	
		485					490					495				
cat	cca	gag	ctg	att	gtt	gat	gag	tcg	aat	ctg	cgc	gtg	gtg	tat	gcg	1816
His	Pro	Glu	Leu	Ile	Val	Asp	Glu	Ser	Asn	Leu	Arg	Val	Val	Tyr	Ala	
	500					505					510					
cca	agc	cgt	tat	ttt	gcc	agc	gag	ccc	aaa	gct	gat	gtc	agc	ctg	att	1864
Pro	Ser	Arg	Tyr	Phe	Ala	Ser	Glu	Pro	Lys	Ala	Asp	Val	Ser	Leu	Ile	
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Leu	Arg	Asn	Pro	Lys	Ala	Met	Asp	Ser	Ala	Arg	Asn	Gln	Val	Met	Phe	
				535					540					545		
gcg	ctc	aat	gat	tat	ctc	gca	ggg	ctg	gcg	ctt	gat	cag	tta	agc	aac	1960
Ala	Leu	Asn	Asp	Tyr	Leu	Ala	Gly	Leu	Ala	Leu	Asp	Gln	Leu	Ser	Asn	
			550					555					560			
cag	gcg	tcg	gtt	ggt	ggc	ata	agt	ttt	tcc	acc	aac	gct	aac	aac	ggc	2008
Gln	Ala	Ser	Val	Gly	Gly	Ile	Ser	Phe	Ser	Thr	Asn	Ala	Asn	Asn	Gly	
		565					570					575				
ctt	atg	gtt	aat	gct	aat	ggt	tac	acc	cag	cgt	ctg	ccg	cag	ctg	ttc	2056
Leu	Met	Val	Asn	Ala	Asn	Gly	Tyr	Thr	Gln	Arg	Leu	Pro	Gln	Leu	Phe	
	580					585					590					
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Gln 595	Ala	Leu	Leu	Glu	Gly 600	Tyr	Phe	Ser	Tyr	Thr 605	Ala	Thr	Glu	Asp	Gln 610	
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aag Lys	ggt Gly	aaa Lys	gcg Ala 630	ttt Phe	gag Glu	cag Gln	gcg Ala	att Ile 635	atg Met	ccc Pro	gcg Ala	cag Gln	atg Met 640	ctc Leu	tcg Ser	2200
caa Gln	gtg Val 645	ccg Pro	tac Tyr	ttc Phe	tcg Ser	cga Arg	gat Asp 650	gaa Glu	cgg Arg	cgt Arg	aaa Lys	att Ile 655	ttg Leu	ccc Pro	tcc Ser	2248
att Ile 660	acg Thr	ttg Leu	aaa Lys	gag Glu	gtg Val 665	ctg Leu	gcc Ala	tat Tyr	cgc Arg	gac Asp	gcc Ala 670	tta Leu	aaa Lys	tca Ser	ggg Gly	2296
gct Ala 675	cga Arg	cca Pro	gag Glu	ttt Phe	atg Met 680	gtt Val	atc Ile	ggc Gly	aac Asn	atg Met 685	acc Thr	gag Glu	gcc Ala	cag Gln	gca Ala 690	2344
aca Thr	acg Thr	ctg Leu	gca Ala	cgc Arg 695	gat Asp	gtg Val	caa Gln	aaa Lys	cag Gln 700	ttg Leu	ggc Gly	gct Ala	gat Asp	ggt Gly 705	tca Ser	2392
gag Glu	tgg Trp	tgt Cys	cga Arg 710	aac Asn	aaa Lys	gat Asp	gta Val	gtg Val 715	gtc Val	gat Asp	aaa Lys	aaa Lys	caa Gln 720	tcc Ser	gtc Val	2440
atc Ile	ttt Phe	gaa Glu 725	aaa Lys	gcc Ala	ggt Gly	aac Asn	agc Ser 730	acc Thr	gac Asp	tcc Ser	gca Ala	ctg Leu 735	gca Ala	gcg Ala	gta Val	2488
ttt Phe 740	gta Val	ccg Pro	act Thr	ggc Gly	tac Tyr	gat Asp 745	gaa Glu	tac Tyr	acc Thr	agc Ser	tca Ser 750	gcc Ala	tat Tyr	agc Ser	tct Ser	2536
ctg Leu 755	ttg Leu	ggg Gly	cag Gln	atc Ile	gta Val 760	cag Gln	ccg Pro	tgg Trp	ttc Phe	tac Tyr 765	aat Asn	cag Gln	ttg Leu	cgt Arg	acc Thr 770	2584
gaa Glu	gaa Glu	caa Gln	ttg Leu	ggc Gly 775	tat Tyr	gcc Ala	gtg Val	ttt Phe	gcg Ala 780	ttt Phe	cca Pro	atg Met	agc Ser	gtg Val 785	ggg Gly	2632
cgt Arg	cag Gln	tgg Trp	ggc Gly 790	atg Met	ggc Gly	ttc Phe	ctt Leu	ttg Leu 795	caa Gln	agc Ser	aat Asn	gat Asp	aaa Lys 800	cag Gln	cct Pro	2680
tca Ser	ttc Phe 805	ttg Leu	tgg Trp	gag Glu	cgt Arg	tac Tyr	aag Lys 810	gcg Ala	ttt Phe	ttc Phe	cca Pro	acc Thr 815	gca Ala	gag Glu	gca Ala	2728
aaa Lys 820	ttg Leu	cga Arg	gcg Ala	atg Met	aag Lys	cca Pro 825	gat Asp	gag Glu	ttt Phe	gcg Ala	caa Gln 830	atc Ile	cag Gln	cag Gln	gcg Ala	2776
gta Val 835	att Ile	acc Thr	cag Gln	atg Met	ctg Leu 840	cag Gln	gca Ala	ccg Pro	caa Gln	acg Thr 845	ctc Leu	ggc Gly	gaa Glu	gaa Glu	gca Ala 850	2824

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tcg aag tta agt aaa gat ttc gat cgc ggc aat atg cgc ttc gat tcg 2872
 Ser Lys Leu Ser Lys Asp Phe Asp Arg Gly Asn Met Arg Phe Asp Ser
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cgt gat aaa atc gtg gcc cag ata aaa ctg ctg acg ccg caa aaa ctt 2920
 Arg Asp Lys Ile Val Ala Gln Ile Lys Leu Leu Thr Pro Gln Lys Leu
 870 875 880

gct gat ttc ttc cat cag gcg gtg gtc gag ccg caa ggc atg gct att 2968
 Ala Asp Phe Phe His Gln Ala Val Val Glu Pro Gln Gly Met Ala Ile
 885 890 895

ctg tcg cag att tcc ggc agc cag aac ggg aaa gcc gaa tat gta cac 3016
 Leu Ser Gln Ile Ser Gly Ser Gln Asn Gly Lys Ala Glu Tyr Val His
 900 905 910

cct gaa ggc tgg aaa gtg tgg gag aac gtc agc gcg ttg cag caa aca 3064
 Pro Glu Gly Trp Lys Val Trp Glu Asn Val Ser Ala Leu Gln Gln Thr
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atcctttgc 3120

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Thr Ile Arg Lys Ser Asp Lys Asp Asn Arg Gln Tyr Gln Ala Ile Arg
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Leu Asp Asn Gly Met Val Val Leu Leu Val Ser Asp Pro Gln Ala Val
 30 35 40

Lys Ser Leu Ser Ala Leu Val Val Pro Val Gly Ser Leu Glu Asp Pro
 45 50 55

Glu Ala Tyr Gln Gly Leu Ala His Tyr Leu Glu His Met Ser Leu Met
 60 65 70

Gly Ser Lys Lys Tyr Pro Gln Ala Asp Ser Leu Ala Glu Tyr Leu Lys
 75 80 85

Met His Gly Gly Ser His Asn Ala Ser Thr Ala Pro Tyr Arg Thr Ala
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Phe	Tyr	Leu	Glu	Val	Glu	Asn
			110			Asp
				115		120
Leu	Ala	Asp	Ala	Ile	Ala	Glu
			125			130
						135
Arg	Glu	Arg	Asn	Ala	Val	Asn
			140			145
						150
Asp	Gly	Met	Arg	Met	Ala	Gln
						160
						165
His	Pro	Gly	Ser	Lys	Phe	Ser
170						175
						180
Lys	Pro	Gly	Asn	Pro	Val	Gln
						190
						195
Tyr	Tyr	Ser	Ala	Asn	Leu	Met
			205			210
						215
Leu	Pro	Glu	Leu	Ala	Lys	Met
			220			225
						230
Asn	Lys	Glu	Ser	Lys	Lys	Pro
						240
						245
Ala	Gln	Lys	Gly	Ile	Ile	Ile
250						255
						260
Val	Leu	Arg	Val	Glu	Phe	Arg
						270
						275
Ser	Lys	Thr	Asp	Glu	Leu	Ile
			285			290
						295
Gly	Thr	Leu	Ser	Asp	Trp	Leu
						300
						305
Ser	Ala	Asn	Ser	Asp	Pro	Ile
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						320
Ile	Ser	Ala	Ser	Leu	Thr	Asp
330						335
						340
						345

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Val Ala Ala Ile Phe Ser Tyr Leu Asn Leu Leu Arg Glu Lys Gly Ile
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Asp Lys Gln Tyr Phe Asp Glu Leu Ala Asn Val Leu Asp Ile Asp Phe
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Arg Tyr Pro Ser Ile Thr Arg Asp Met Asp Tyr Val Glu Trp Leu Ala
 380 385 390

Asp Thr Met Ile Arg Val Pro Val Glu His Thr Leu Asp Ala Val Asn
 395 400 405

Ile Ala Asp Arg Tyr Asp Ala Lys Ala Val Lys Glu Arg Leu Ala Met
 410 415 420 425

Met Thr Pro Gln Asn Ala Arg Ile Trp Tyr Ile Ser Pro Lys Glu Pro
 430 435 440

His Asn Lys Thr Ala Tyr Phe Val Asp Ala Pro Tyr Gln Val Asp Lys
 445 450 455

Ile Ser Ala Gln Thr Phe Ala Asp Trp Gln Lys Lys Ala Ala Asp Ile
 460 465 470

Ala Leu Ser Leu Pro Glu Leu Asn Pro Tyr Ile Pro Asp Asp Phe Ser
 475 480 485

Leu Ile Lys Ser Glu Lys Lys Tyr Asp His Pro Glu Leu Ile Val Asp
 490 495 500 505

Glu Ser Asn Leu Arg Val Val Tyr Ala Pro Ser Arg Tyr Phe Ala Ser
 510 515 520

Glu Pro Lys Ala Asp Val Ser Leu Ile Leu Arg Asn Pro Lys Ala Met
 525 530 535

Asp Ser Ala Arg Asn Gln Val Met Phe Ala Leu Asn Asp Tyr Leu Ala
 540 545 550

Gly Leu Ala Leu Asp Gln Leu Ser Asn Gln Ala Ser Val Gly Gly Ile
 555 560 565

Ser Phe Ser Thr Asn Ala Asn Asn Gly Leu Met Val Asn Ala Asn Gly
 570 575 580 585

Tyr Thr Gln Arg Leu Pro Gln Leu Phe Gln Ala Leu Leu Glu Gly Tyr
 590 595 600

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Phe Ser Tyr Thr Ala Thr Glu Asp Gln Leu Glu Gln Ala Lys Ser Trp
 605 610 615
 Tyr Asn Gln Met Met Asp Ser Ala Glu Lys Gly Lys Ala Phe Glu Gln
 620 625 630
 Ala Ile Met Pro Ala Gln Met Leu Ser Gln Val Pro Tyr Phe Ser Arg
 635 640 645
 Asp Glu Arg Arg Lys Ile Leu Pro Ser Ile Thr Leu Lys Glu Val Leu
 650 655 660 665
 Ala Tyr Arg Asp Ala Leu Lys Ser Gly Ala Arg Pro Glu Phe Met Val
 670 675 680
 Ile Gly Asn Met Thr Glu Ala Gln Ala Thr Thr Leu Ala Arg Asp Val
 685 690 695
 Gln Lys Gln Leu Gly Ala Asp Gly Ser Glu Trp Cys Arg Asn Lys Asp
 700 705 710
 Val Val Val Asp Lys Lys Gln Ser Val Ile Phe Glu Lys Ala Gly Asn
 715 720 725
 Ser Thr Asp Ser Ala Leu Ala Ala Val Phe Val Pro Thr Gly Tyr Asp
 730 735 740 745
 Glu Tyr Thr Ser Ser Ala Tyr Ser Ser Leu Leu Gly Gln Ile Val Gln
 750 755 760
 Pro Trp Phe Tyr Asn Gln Leu Arg Thr Glu Glu Gln Leu Gly Tyr Ala
 765 770 775
 Val Phe Ala Phe Pro Met Ser Val Gly Arg Gln Trp Gly Met Gly Phe
 780 785 790
 Leu Leu Gln Ser Asn Asp Lys Gln Pro Ser Phe Leu Trp Glu Arg Tyr
 795 800 805
 Lys Ala Phe Phe Pro Thr Ala Glu Ala Lys Leu Arg Ala Met Lys Pro
 810 815 820 825
 Asp Glu Phe Ala Gln Ile Gln Gln Ala Val Ile Thr Gln Met Leu Gln
 830 835 840
 Ala Pro Gln Thr Leu Gly Glu Glu Ala Ser Lys Leu Ser Lys Asp Phe
 845 850 855

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Asp Arg Gly Asn Met Arg Phe Asp Ser Arg Asp Lys Ile Val Ala Gln
860 865 870

Ile Lys Leu Leu Thr Pro Gln Lys Leu Ala Asp Phe Phe His Gln Ala
875 880 885

Val Val Glu Pro Gln Gly Met Ala Ile Leu Ser Gln Ile Ser Gly Ser
890 895 900 905

Gln Asn Gly Lys Ala Glu Tyr Val His Pro Glu Gly Trp Lys Val Trp
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Asn Glu

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Phe Ala Gln Ala Asp Asp Ala Ala Ile Gln Gln Thr Leu Ala Lys Met	
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Gly Ile Lys Ser Ser Asp Ile Gln Pro Ala Pro Val Ala Gly Met Lys	
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aca gtt ctg act aac agc ggc gtg ttg tac atc acc gat gat ggt aaa	192
Thr Val Leu Thr Asn Ser Gly Val Leu Tyr Ile Thr Asp Asp Gly Lys	
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His Ile Ile Gln Gly Pro Met Tyr Asp Val Ser Gly Thr Ala Pro Val	
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Asn Val Thr Asn Lys Met Leu Leu Lys Gln Leu Asn Ala Leu Glu Lys	
85 90 95	

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Glu Met Ile Val Tyr Lys Ala Pro Gln Glu Lys His Val Ile Thr Val	
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Phe Thr Asp Ile Thr Cys Gly Tyr Cys His Lys Leu His Glu Gln Met	
115 120 125	
gca gac tac aac gcg ctg ggg atc acc gtg cgt tat ctt gct ttc ccg	432
Ala Asp Tyr Asn Ala Leu Gly Ile Thr Val Arg Tyr Leu Ala Phe Pro	
130 135 140	
cgc cag ggg ctg gac agc gat gca gag aaa gaa atg aaa gct atc tgg	480
Arg Gln Gly Leu Asp Ser Asp Ala Glu Lys Glu Met Lys Ala Ile Trp	
145 150 155 160	
tgt gcg aaa gat aaa aac aaa gcg ttt gat gat gtg atg gca ggt aaa	528
Cys Ala Lys Asp Lys Asn Lys Ala Phe Asp Asp Val Met Ala Gly Lys	
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Ser Val Ala Pro Ala Ser Cys Asp Val Asp Ile Ala Asp His Tyr Ala	
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ctt ggc gtc cag ctt ggc gtt agc ggt act ccg gca gtt gtg ctg agc	624
Leu Gly Val Gln Leu Gly Val Ser Gly Thr Pro Ala Val Val Leu Ser	
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Asn Gly Thr Leu Val Pro Gly Tyr Gln Pro Pro Lys Glu Met Lys Glu	
210 215 220	
ttc ctc gac gaa cac caa aaa atg acc agc ggt aaa cac cat cac cat	720
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His His	

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35 40 45

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Thr Val Leu Thr Asn Ser Gly Val Leu Tyr Ile Thr Asp Asp Gly Lys
 50 55 60
 His Ile Ile Gln Gly Pro Met Tyr Asp Val Ser Gly Thr Ala Pro Val
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 Asn Val Thr Asn Lys Met Leu Leu Lys Gln Leu Asn Ala Leu Glu Lys
 85 90 95
 Glu Met Ile Val Tyr Lys Ala Pro Gln Glu Lys His Val Ile Thr Val
 100 105 110
 Phe Thr Asp Ile Thr Cys Gly Tyr Cys His Lys Leu His Glu Gln Met
 115 120 125
 Ala Asp Tyr Asn Ala Leu Gly Ile Thr Val Arg Tyr Leu Ala Phe Pro
 130 135 140
 Arg Gln Gly Leu Asp Ser Asp Ala Glu Lys Glu Met Lys Ala Ile Trp
 145 150 155 160
 Cys Ala Lys Asp Lys Asn Lys Ala Phe Asp Asp Val Met Ala Gly Lys
 165 170 175
 Ser Val Ala Pro Ala Ser Cys Asp Val Asp Ile Ala Asp His Tyr Ala
 180 185 190
 Leu Gly Val Gln Leu Gly Val Ser Gly Thr Pro Ala Val Val Leu Ser
 195 200 205
 Asn Gly Thr Leu Val Pro Gly Tyr Gln Pro Pro Lys Glu Met Lys Glu
 210 215 220
 Phe Leu Asp Glu His Gln Lys Met Thr Ser Gly Lys His His His His
 225 230 235 240
 His His