

SEQUENCE LISTING

<110> Jacques-Eric Gottenberg

5 <120> LEVELS OF APRIL IN SERUM AND USE IN
DIAGNOSTIC METHODS

10 <130> 054878/371387

<160> 26

<170> FastSEQ for Windows Version 4.0

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35 gtg gct atg aga tcc tgc ccc gaa gag cag tac tgg gat cct ctg ctg 145
Val Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu
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40 ggt acc tgc atg tcc tgc aaa acc att tgc aac cat cag agc cag cgc 193
Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg
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Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly
65 70 75

45 aag ttc tat gac cat ctc ctg agg gac tgc atc agc tgt gcc tcc atc 289
Lys Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile
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50 tgt gga cag cac cct aag caa tgt gca tac ttc tgt gag aac aag ctc 337
Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu
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55 agg agc cca gtg aac ctt cca cca gag ctc agg aga cag cgg agt gga 385
Arg Ser Pro Val Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly
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60 gaa gtt gaa aac aat tca gac aac tcg gga agg tac caa gga ttg gag 433
Glu Val Glu Asn Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu
125 130 135 140

cac aga ggc tca gaa gca agt cca gct ctc ccg ggg ctg aag ctg agt 481
His Arg Gly Ser Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser
145 150 155

65 gca gat cag gtg gcc ctg gtc tac agc acg ctg ggg ctc tgc ctg tgt 529
Ala Asp Gln Val Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys
160 165 170

gcc gtc ctc tgc tgc ttc ctg gtg ggc gtg gcc tgc ttc ctc aag aag 577
 Ala Val Leu Cys Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys
 175 180 185

5 agg ggg gat ccc tgc tcc tgc cag ccc cgc tca agg ccc cgt caa agt 625
 Arg Gly Asp Pro Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser
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10 ccg gcc aag tct tcc cag gat cac ggc atg gaa gcc ggc agc cct gtg 673
 Pro Ala Lys Ser Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val
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15 agc aca tcc ccc gag cca gtg gag acc tgc agc ttc tgc ttc cct gag 721
 Ser Thr Ser Pro Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu
 225 230 235

20 tgc agg ggc ccc acg cag gag agc gca gtc acg cct ggg acc ccc gac 769
 Cys Arg Ala Pro Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp
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25 ccc act tgt gct gga agg tgg ggg tgc cac acc agg acc aca gtc ctg 817
 Pro Thr Cys Ala Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu
 255 260 265

30 cag cct tgc cca cac atc cca gac agt ggc ctt ggc att gtg tgt gtg 865
 Gln Pro Cys Pro His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val
 270 275 280

35 cct gcc cag gag ggg ggc cca ggt gca taaatggggg tcaggagggg 912
 Pro Ala Gln Glu Gly Gly Pro Gly Ala
 285 290

40 aaaggaggag ggagagagat ggagaggagg ggagagagaa agagaggtgg ggagagggga 972
 gagagatatg aggagagaga gacagaggag gcagaaaggg agagaacag aggagacaga 1032
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 35 40 45
 55 Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg Thr Cys Ala Ala
 50 55 60
 Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp
 65 70 75 80
 His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His
 85 90 95
 60 Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser Pro Val
 100 105 110
 Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val Glu Asn
 115 120 125
 65 Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg Gly Ser
 130 135 140
 Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp Gln Val
 145 150 155 160
 Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys Ala Val Leu Cys

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35		ggc	agg	gac	gag	cca	gcc	ccc	acg	ccc	tgc	gtc	ccg	gcc	gag	tgc	ttc	101
		Gly	Arg	Asp	Ala	Pro	Ala	Pro	Thr	Pro	Cys	Val	Pro	Ala	Gln	Cys	Phe	
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40		gac	ctg	ctg	gtc	cgc	cac	tgc	gtg	gcc	tgc	ggg	ctc	ctg	cgc	acg	ccg	149
		Asp	Leu	Leu	Val	Arg	His	Cys	Val	Ala	Cys	Gly	Leu	Leu	Arg	Thr	Pro	
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45		cgg	ccg	aaa	ccg	gcc	ggg	gcc	agc	agc	cct	gcg	ccc	agg	acg	gcg	ctg	197
		Arg	Pro	Lys	Pro	Ala	Gly	Ala	Ser	Ser	Pro	Ala	Pro	Arg	Thr	Ala	Leu	
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50		cag	ccg	cag	gag	tgc	gtg	ggc	gcg	ggg	gcc	ggc	gag	gcg	gcg	ctg	ccc	245
		Gln	Pro	Gln	Glu	Ser	Val	Gly	Ala	Gly	Ala	Gly	Gln	Ala	Ala	Leu	Pro	
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55		ctg	ccc	ggg	ctg	ctc	ttt	ggc	gcc	ccc	gcg	ctg	ctg	ggc	ctg	gca	ctg	293
		Leu	Pro	Gly	Leu	Leu	Phe	Gly	Ala	Pro	Ala	Leu	Leu	Gly	Leu	Ala	Leu	
			75				80					85						
60		gtc	ctg	gcg	ctg	gtc	ctg	gtg	ggc	ctg	gtg	agc	tgg	agg	cgg	cga	cag	341
		Val	Leu	Ala	Leu	Val	Leu	Val	Gly	Leu	Val	Ser	Trp	Arg	Arg	Arg	Gln	
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65		cgg	cgg	ctt	cgc	ggc	gcg	tcc	tcc	gca	gag	gcc	ccc	gac	gga	gac	aag	389
		Arg	Arg	Leu	Arg	Gly	Ala	Ser	Ser	Ala	Glu	Ala	Pro	Asp	Gly	Asp	Lys	
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		gac	gcc	cca	gag	ccc	ctg	gac	aag	gtc	atc	att	ctg	tct	ccg	gga	atc	437
		Asp	Ala	Pro	Glu	Pro	Leu	Asp	Lys	Val	Ile	Ile	Leu	Ser	Pro	Gly	Ile	
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70		tct	gat	gcc	aca	gct	cct	gcc	tgg	cct	cct	cct	ggg	gaa	gac	cca	gga	485
		Ser	Asp	Ala	Thr	Ala	Pro	Ala	Trp	Pro	Pro	Pro	Gly	Glu	Asp	Pro	Gly	
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acc acc cca cct ggc cac agt gtc cct gtg cca gcc aca gag ctg ggc 533
 Thr Thr Pro Pro Gly His Ser Val Pro Val Pro Ala Thr Glu Leu Gly
 155 160 165

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 tcc act gaa ctg gtg acc acc aag acg gcc ggc cct gag caa caa 578
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 Val Ala Cys Gly Leu Leu Arg Thr Pro Arg Pro Lys Pro Ala Gly Ala
 35 40 45
 Ser Ser Pro Ala Pro Arg Thr Ala Leu Gln Pro Gln Glu Ser Val Gly
 50 55 60
 Ala Gly Ala Gly Glu Ala Ala Leu Pro Leu Pro Gly Leu Leu Phe Gly
 65 70 75 80
 Ala Pro Ala Leu Leu Gly Leu Ala Leu Val Leu Ala Leu Val Leu Val
 85 90 95
 Gly Leu Val Ser Trp Arg Arg Arg Gln Arg Arg Leu Arg Gly Ala Ser
 100 105 110
 Ser Ala Glu Ala Pro Asp Gly Asp Lys Asp Ala Pro Glu Pro Leu Asp
 115 120 125
 Lys Val Ile Ile Leu Ser Pro Gly Ile Ser Asp Ala Thr Ala Pro Ala
 130 135 140
 Trp Pro Pro Pro Gly Glu Asp Pro Gly Thr Thr Pro Pro Gly His Ser
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 agctgctctt gctgcatttg ctctggaatt ctgttagaga tattacttgt ccttcagggc 180
 tgtttcttct gtagctccct tgttttcttt ttgtgac atg ttg cag atg gct ggg 236
 Met Leu Gln Met Ala Gly
 1 5

60
 cag tgc tcc caa aat gaa tat ttt gac agt ttg ttg cat gct tgc ata 284
 Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu Leu His Ala Cys Ile
 10 15 20

65
 cct tgt caa ctt cga tgt tct tct aat act cct cct cta aca tgt cag 332
 Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr Pro Pro Leu Thr Cys Gln
 25 30 35

5 cgt tat tgt aat gca agt gtg acc aat tca gtg aaa gga acg aat gcg 380
 Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val Lys Gly Thr Asn Ala
 40 45 50

10 att ctc tgg acc tgt ttg gga ctg agc tta ata att tct ttg gca gtt 428
 Ile Leu Trp Thr Cys Leu Gly Leu Ser Leu Ile Ile Ser Leu Ala Val
 55 60 65 70

15 ttc gtg cta atg ttt ttg cta agg aag ata agc tct gaa cca tta aag 476
 Phe Val Leu Met Phe Leu Leu Arg Lys Ile Ser Ser Glu Pro Leu Lys
 75 80 85

20 gac gag ttt aaa aac aca gga tca ggt ctc ctg ggc atg gct aac att 524
 Asp Glu Phe Lys Asn Thr Gly Ser Gly Leu Leu Gly Met Ala Asn Ile
 90 95 100

25 gac ctg gaa aag agc agg act ggt gat gaa att att ctt ccg aga ggc 572
 Asp Leu Glu Lys Ser Arg Thr Gly Asp Glu Ile Ile Leu Pro Arg Gly
 105 110 115

30 ctc gag tac acg gtg gaa gaa tgc acc tgt gaa gac tgc atc aag agc 620
 Leu Glu Tyr Thr Val Glu Glu Cys Thr Cys Glu Asp Cys Ile Lys Ser
 120 125 130

35 aaa ccg aag gtc gac tct gac cat tgc ttt cca ctc cca gct atg gag 668
 Lys Pro Lys Val Asp Ser Asp His Cys Phe Pro Leu Pro Ala Met Glu
 135 140 145 150

40 gaa ggc gca acc att ctt gtc acc acg aaa acg aat gac tat tgc aag 716
 Glu Gly Ala Thr Ile Leu Val Thr Thr Lys Thr Asn Asp Tyr Cys Lys
 155 160 165

45 agc ctg cca gct gct ttg agt gct acg gag ata gag aaa tca att tct 764
 Ser Leu Pro Ala Ala Leu Ser Ala Thr Glu Ile Glu Lys Ser Ile Ser
 170 175 180

50 gct agg taattaacca ttctgactcg agcagtgcca ctttaaaaat cttttgtcag 820
 Ala Arg

55 aatagatgat gtgtcagatc tctttaggat gactgtatatt ttcagttgcc gatacagctt 880
 tttgtcctct aactgtggaa actctttatg ttagatatat ttctctaggt tactgttggg 940
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 35 40 45
 Val Lys Gly Thr Asn Ala Ile Leu Trp Thr Cys Leu Gly Leu Ser Leu
 50 55 60
 Ile Ile Ser Leu Ala Val Phe Val Leu Met Phe Leu Leu Arg Lys Ile
 65 70 75 80
 Ser Ser Glu Pro Leu Lys Asp Glu Phe Lys Asn Thr Gly Ser Gly Leu
 85 90 95
 Leu Gly Met Ala Asn Ile Asp Leu Glu Lys Ser Arg Thr Gly Asp Glu
 100 105 110
 Ile Ile Leu Pro Arg Gly Leu Glu Tyr Thr Val Glu Glu Cys Thr Cys
 115 120 125
 Glu Asp Cys Ile Lys Ser Lys Pro Lys Val Asp Ser Asp His Cys Phe
 130 135 140

Pro Leu Pro Ala Met Glu Glu Gly Ala Thr Ile Leu Val Thr Thr Lys
 145 150 155 160
 Thr Asn Asp Tyr Cys Lys Ser Leu Pro Ala Ala Leu Ser Ala Thr Glu
 165 170 175
 5 Ile Glu Lys Ser Ile Ser Ala Arg
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 ccctgtggtc acttattcta aaggcccaaa ccttcaaagt tcaagtagtg at atg gat 178
 Met Asp
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 25 gac tcc aca gaa agg gag cag tca cgc ctt act tct tgc ctt aag aaa 226
 Asp Ser Thr Glu Arg Glu Gln Ser Arg Leu Thr Ser Cys Leu Lys Lys
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 30 aga gaa gaa atg aaa ctg aag gag tgt gtt tcc atc ctc cca cgg aag 274
 Arg Glu Glu Met Lys Leu Lys Glu Cys Val Ser Ile Leu Pro Arg Lys
 20 25 30

 35 gaa agc ccc tct gtc cga tcc tcc aaa gac gga aag ctg ctg gct gca 322
 Glu Ser Pro Ser Val Arg Ser Ser Lys Asp Gly Lys Leu Leu Ala Ala
 35 40 45 50

 40 acc ttg ctg ctg gca ctg ctg tct tgc tgc ctc acg gtg gtg tct ttc 370
 Thr Leu Leu Leu Ala Leu Leu Ser Cys Cys Leu Thr Val Val Ser Phe
 55 60 65

 45 tac cag gtg gcc gcc ctg caa ggg gac ctg gcc agc ctc cgg gca gag 418
 Tyr Gln Val Ala Ala Leu Gln Gly Asp Leu Ala Ser Leu Arg Ala Glu
 70 75 80

 50 ctg cag ggc cac cac ggc gag aag ctg cca gca gga gca gga gcc ccc 466
 Leu Gln Gly His His Ala Glu Lys Leu Pro Ala Gly Ala Gly Ala Pro
 85 90 95

 55 aag gcc ggc ctg gag gaa gct cca gct gtc acc gcg gga ctg aaa atc 514
 Lys Ala Gly Leu Glu Glu Ala Pro Ala Val Thr Ala Gly Leu Lys Ile
 100 105 110

 60 ttt gaa cca cca gct cca gga gaa ggc aac tcc agt cag aac agc aga 562
 Phe Glu Pro Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Asn Ser Arg
 115 120 125 130

 65 aat aag cgt gcc gtt cag ggt cca gaa gaa aca gtc act caa gac tgc 610
 Asn Lys Arg Ala Val Gln Gly Pro Glu Thr Val Thr Gln Asp Cys
 135 140 145

 70 ttg caa ctg att gca gac agt gaa aca cca act ata caa aaa gga tct 658
 Leu Gln Leu Ile Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys Gly Ser
 150 155 160

 75 tac aca ttt gtt cca tgg ctt ctc agc ttt aaa agg gga agt gcc cta 706
 Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser Ala Leu
 165 170 175

gaa gaa aaa gag aat aaa ata ttg gtc aaa gaa act ggt tac ttt ttt 754
 Glu Glu Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr Phe Phe
 180 185 190

5 ata tat ggt cag gtt tta tat act gat aag acc tac gcc atg gga cat 802
 Ile Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met Gly His
 195 200 205 210

10 cta att cag agg aag aag gtc cat gtc ttt ggg gat gaa ttg agt ctg 850
 Leu Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu Ser Leu
 215 220 225

15 gtg act ttg ttt cga tgt att caa aat atg cct gaa aca cta ccc aat 898
 Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu Pro Asn
 230 235 240

20 aat tcc tgc tat tca gct ggc att gca aaa ctg gaa gaa gga gat gaa 946
 Asn Ser Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly Asp Glu
 245 250 255

25 ctc caa ctt gca ata cca aga gaa aat gca caa ata tca ctg gat gga 994
 Leu Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Leu Asp Gly
 260 265 270

30 gat gtc aca ttt ttt ggt gca ttg aaa ct gctgtgacct acttacacca 1043
 Asp Val Thr Phe Phe Gly Ala Leu Lys
 275 280

35 tgtctgtagc tattttcctc cttttctctg tacctctaag aagaagaat ctaactgaaa 1103
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 35 40 45
 Ala Ala Thr Leu Leu Leu Ala Leu Leu Ser Cys Cys Leu Thr Val Val
 50 55 60
 Ser Phe Tyr Gln Val Ala Ala Leu Gln Gly Asp Leu Ala Ser Leu Arg
 65 70 75 80
 Ala Glu Leu Gln Gly His His Ala Glu Lys Leu Pro Ala Gly Ala Gly
 85 90 95
 50 Ala Pro Lys Ala Gly Leu Glu Glu Ala Pro Ala Val Thr Ala Gly Leu
 100 105 110
 Lys Ile Phe Glu Pro Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Asn
 115 120 125
 55 Ser Arg Asn Lys Arg Ala Val Gln Gly Pro Glu Glu Thr Val Thr Gln
 130 135 140
 Asp Cys Leu Gln Leu Ile Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys
 145 150 155 160
 Gly Ser Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser
 165 170 175
 60 Ala Leu Glu Glu Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr
 180 185 190
 Phe Phe Ile Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met
 195 200 205
 65 Gly His Leu Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu
 210 215 220
 Ser Leu Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu
 225 230 235 240
 Pro Asn Asn Ser Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly

5 <210> 15
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 <212> PRT
 <213> Artificial Sequence

 10 <220>
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 1 5 10 15
 15 Arg

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 Leu Leu Cys Gly Ala Val Phe Val Ser Leu Ser Gln Glu Ile His Ala
 15 20 25
 40 gag ttg aga cgc ttc cgt aga gct atg aga tcc tgc ccc gaa gag cag 148
 Glu Leu Arg Arg Phe Arg Arg Ala Met Arg Ser Cys Pro Glu Glu Gln
 30 35 40
 45 tac tgg gat cct ctg ctg ggt acc tgc atg tcc tgc aaa acc att tgc 196
 Tyr Trp Asp Pro Leu Leu Gly Thr Cys Met Ser Cys Lys Thr Ile Cys
 45 50 55 60
 50 aac cat cag agc cag cgc acc tgt gca gcc ttc tgc agg tca ctc agc 244
 Asn His Gln Ser Gln Arg Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser
 65 70 75
 55 tgc cgc aag gag caa ggc aag ttc tat gac cat ctc ctg agg gac tgc 292
 Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp His Leu Leu Arg Asp Cys
 80 85 90
 60 atc agc tgt gcc tcc atc tgt gga cag cac cct aag caa tgt gca tac 340
 Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln Cys Ala Tyr
 95 100 105
 65 ttc tgt gag aac aag ctc agg agc cca gtg aac ctt cca cca gag ctc 388
 Phe Cys Glu Asn Lys Leu Arg Ser Pro Val Asn Leu Pro Pro Glu Leu
 110 115 120
 70 agg aga cag cgg agt gga gaa gtt gaa aac aat tca gac aac tgg gga 436
 Arg Arg Gln Arg Ser Gly Glu Val Glu Asn Asn Ser Asp Asn Ser Gly
 125 130 135 140
 75 agg tac caa gga ttg gag cac aga ggc tca gaa gca agt cca gct ctc 484

	Arg Tyr Gln Gly Leu Glu His Arg Gly Ser Glu Ala Ser Pro Ala Leu	
	145 150 155	
5	cca ggt ctc aag gag ccc aaa tct tca gac aaa act cac aca tgc cca Pro Gly Leu Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro	532
	160 165 170	
10	ccg tgc cca gca cct gaa gcc gag ggg gca ccg tca gtc ttc ctc ttc Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe	580
	175 180 185	
15	ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg acc cct gag gtc Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val	628
	190 195 200	
20	aca tgc gtg gtg gtg gac gtg agc cac gaa gac cct gag gtc aag ttc Thr Cys Val Val Val Val Ser His Glu Asp Pro Glu Val Lys Phe	676
	205 210 215 220	
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70	tac	aag	acc	acg	cct	ccc	gtg	ctg	gac	tcc	gac	ggc	tcc	ttc	ttc	ctc	964
	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	
				305					310					315			
75	tac	agc	aag	ctc	acc	gtg	gac	aag	agc	agg	tgg	cag	cag	ggg	aac	gtc	1012
	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	
				320					325					330			
80	ttc	tca	tgc	tcc	gtg	atg	cat	gag	gct	ctg	cac	aac	cac	tac	acg	cag	1060
	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	
			335					340					345				
85	aag	agc	ctc	tcc	ctg	tct	ccg	ggt	aaa	taa	tctagagggc	cgccaatta					1109

Lys Ser Leu Ser Leu Ser Pro Gly Lys *
 350 355

5 <210> 23
 <211> 357
 <212> PRT
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10 <220>
 <223> TACI-Fc fusion protein

15 <400> 23
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 Phe Arg Arg Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro
 35 40 45
 Leu Leu Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser
 50 55 60
 Gln Arg Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu
 65 70 75 80
 Gln Gly Lys Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala
 85 90 95
 Ser Ile Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn
 100 105 110
 Lys Leu Arg Ser Pro Val Asn Leu Pro Pro Glu Leu Arg Glu Pro Lys
 115 120 125
 Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
 130 135 140
 Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
 145 150 155 160
 Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
 165 170 175
 Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
 180 185 190
 Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
 195 200 205
 Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
 210 215 220
 Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ser
 225 230 235 240
 Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
 245 250 255
 Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
 260 265 270
 Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
 275 280 285
 Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
 290 295 300
 Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
 305 310 315 320
 Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
 325 330 335
 Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
 340 345 350
 Leu Ser Pro Gly Lys
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 <212> PRT
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65 <220>
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 Thr Pro Cys Val Pro Ala Glu Cys Phe Asp Leu Leu Val Arg His Cys
 35 40 45
 10 Val Ala Cys Gly Leu Leu Arg Thr Pro Arg Pro Lys Pro Ala Gly Ala
 50 55 60
 Ser Ser Pro Ala Pro Arg Thr Ala Leu Gln Pro Gln Glu Ser Gln Val
 65 70 75 80
 Thr Asp Lys Ala Ala His Tyr Thr Leu Cys Pro Pro Cys Pro Ala Pro
 85 90 95
 15 Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
 100 105 110
 Asp Thr Leu Met Ile Ser Arg Thr Pro Gln Val Thr Cys Val Val Val
 115 120 125
 20 Ala Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
 130 135 140
 Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
 145 150 155 160
 Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
 165 170 175
 25 Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
 180 185 190
 Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
 195 200 205
 30 Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
 210 215 220
 Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
 225 230 235 240
 Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
 245 250 255
 35 Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
 260 265 270
 Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
 275 280 285
 40 Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
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 Leu Ser Leu Ser Pro Gly Lys
 305 310

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 50 <220>
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 ttgctttcct cctccctcct ttttattttc aagttccttt ttattttctc ttgggtaaca 180
 acctttcttc cttctgcacc actgcccgta cccttaccgg ccccgccacc tccttgctac 240
 cccactcttg aaaccacagc tgttggcagg gtccccagct c atg cca gcc tca tct 296
 Met Pro Ala Ser Ser
 1 5

 60 cct ttc ttg cta gcc ccc aaa ggg cct cca ggc aac atg ggg ggc cca 344
 Pro Phe Leu Leu Ala Pro Lys Gly Pro Pro Gly Asn Met Gly Gly Pro
 10 15 20

 65 gtc aga gag ccg gca ctc tca gtt gcc ctc tgg ttg agt tgg ggg gca 392
 Val Arg Glu Pro Ala Leu Ser Val Ala Leu Trp Leu Ser Trp Gly Ala

	25	30	35	
5	gct ctg ggg gcc gtg gct tgt gcc atg gct ctg ctg acc caa caa aca Ala Leu Gly Ala Val Ala Cys Ala Met Ala Leu Leu Thr Gln Gln Thr	40 45	50	440
10	gag ctg cag agc ctc agg aga gag gtg agc cgg ctg cag ggg aca gga Glu Leu Gln Ser Leu Arg Arg Gln Val Ser Arg Leu Gln Gly Thr Gly	55 60	65	488
15	ggc ccc tcc cag aat ggg gaa ggg tat ccc tgg cag agt ctc ccg gag Gly Pro Ser Gln Asn Gly Glu Gly Tyr Pro Trp Gln Ser Leu Pro Glu	70 75	80	536
20	cag agt tcc gat gcc ctg gaa gcc tgg gag aat ggg gag aga tcc cgg Gln Ser Ser Asp Ala Leu Glu Ala Trp Glu Asn Gly Glu Arg Ser Arg	90 95	100	584
25	aaa agg aga gca gtg ctc acc caa aaa cag aag aag cag cac tct gtc Lys Arg Arg Ala Val Leu Thr Gln Lys Gln Lys Lys Gln His Ser Val	105 110	115	632
30	ctg cac ctg gtt ccc att aac gcc acc tcc aag gat gac tcc gat gtg Leu His Leu Val Pro Ile Asn Ala Thr Ser Lys Asp Asp Ser Asp Val	120 125	130	680
35	aca gag gtg atg tgg caa cca gct ctt agg cgt ggg aga ggc cta cag Thr Glu Val Met Trp Gln Pro Ala Leu Arg Arg Gly Arg Gly Leu Gln	135 140	145	728
40	gcc caa gga tat ggt gtc cga atc cag gat gct gga gtt tat ctg ctg Ala Gln Gly Tyr Gly Val Arg Ile Gln Asp Ala Gly Val Tyr Leu Leu	150 155	160	776
45	tat agc cag gtc ctg ttt caa gac gtg act ttc acc atg ggt cag gtg Tyr Ser Gln Val Leu Phe Gln Asp Val Thr Phe Thr Met Gly Gln Val	170 175	180	824
50	gtg tct cga gaa ggc caa gga agg cag gag act cta ttc cga tgt ata Val Ser Arg Glu Gly Gln Gly Arg Gln Glu Thr Leu Phe Arg Cys Ile	185 190	195	872
55	aga agt atg ccc tcc cac ccg gac cgg gcc tac aac agc tgc tat agc Arg Ser Met Pro Ser His Pro Asp Arg Ala Tyr Asn Ser Cys Tyr Ser	200 205	210	920
60	gca ggt gtc ttc cat tta cac caa ggg gat att ctg agt gtc ata att Ala Gly Val Phe His Leu His Gln Gly Asp Ile Leu Ser Val Ile Ile	215 220	225	968
65	ccc cgg gca agg gcg aaa ctt aac ctc tot cca cat gga acc ttc ctg Pro Arg Ala Arg Ala Lys Leu Asn Leu Ser Pro His Gly Thr Phe Leu	230 235	240	1016
	ggg ttt gtg aaa ctg tga ttgtgttata aaaagtggct cccagcttgg Gly Phe Val Lys Leu *	250		1064
	aagaccaggg tgggtacata ctggagacag ccaagagctg agtatataaa ggagagggaa tgtgcaggaa cagaggcatc ttccctgggtt tggctccccg ttccctcactt ttcccttttc attcccaccc cctagacttt gattttacgg atatcttgct tctgttcccc atggagctcc gaattcttgc gtgtgtgtag atgaggggag ggggacgggc gccaggcatt gttcagacct ggtcgggggc cactggaagc atccagaaca gcaccaccat ctta			1124 1184 1244 1304 1348
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<400> 26

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