

<110> 重庆精准生物技术有限公司
<120> 抗人CD19抗原的嵌合抗原受体及其应用
<160> 59

<170> PatentIn version 3.3

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Gly Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro	160
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Pro Gly Lys Ala Leu Glu Trp Leu Gly Val Ile Trp Gly Ser Glu	175
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Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Thr Arg Leu Thr Ile Ser	190
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Lys Asp Asn Ser Lys Asn Gln Val Val Leu Thr Met Thr Asn Met	205
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Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile	65	70
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Gly Ser Thr Lys Gly Gln Val Gln Leu Gln Glu Ser Gly Pro Gly	125	130
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Gly Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro	155	160
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Thr Thr Tyr Tyr Ser Thr Ser Leu Lys Thr Arg Leu Thr Ile Ser	185	190
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Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser	50	55
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Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile	65	70
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Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln	80	85
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Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gly Gly Thr Arg Leu Glu	95	100
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Ile Lys Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu	110	115
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Gly Ser Thr Lys Gly Gln Val Gln Leu Gln Glu Ser Gly Pro Gly	125	130
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Leu Val Lys Pro Ser Gln Thr Leu Ser Val Thr Cys Thr Val Ser	140	145

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Gly Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro	155	160
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Pro Gly Lys Ala Leu Glu Trp Leu Gly Val Ile Trp Gly Ser Glu	170	175
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Thr Thr Tyr Tyr Asn Ser Ser Leu Lys Thr Arg Leu Thr Ile Ser	185	190
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Lys Asp Asn Ser Lys Asn Gln Val Val Leu Thr Met Thr Asn Leu	200	205
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Asp Pro Val Asp Thr Ala Thr Tyr Tyr Cys Ala Lys His Tyr Tyr	215	220
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Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg	35	40
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Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly	35	40
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Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu	50	55
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Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met	65	70
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Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln	80	85
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Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met	95	100
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Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser	50	55
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Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile	65	70
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Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln	80	85
	90	
Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gly Gly Thr Arg Leu Glu	95	100

Ile Lys Gly Ser Thr Ser	105	Gly Ser Gly Lys Pro Gly Ser Gly Glu	
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Gly Ser Thr Lys Gly Gln Val Gln	120	Leu Gln Glu Ser Gly Pro Gly	
	125		130
Leu Val Lys Pro Ser Gln Thr Leu	135	Ser Leu Thr Cys Thr Val Ser	
	140		145
Gly Val Ser Leu Pro Asp Tyr Gly	150	Val Ser Trp Ile Arg Gln Pro	
	155		160
Pro Gly Lys Ala Leu Glu Trp Leu	165	Gly Val Ile Trp Gly Ser Glu	
	170		175
Thr Thr Tyr Tyr Asn Ser Ala Leu	180	Lys Thr Arg Leu Thr Ile Ser	
	185		190
Lys Asp Asn Ser Lys Asn Gln Val	195	Val Leu Thr Met Thr Asn Met	
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Asp Pro Val Asp Thr Ala Thr Tyr	210	Tyr Cys Ala Lys His Tyr Tyr	
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Tyr Gly Gly Ser Tyr Ala Met Asp	225	Tyr Trp Gly Gln Gly Ser Ser	
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Val Thr Val Ser Ser Lys Pro Thr	240	Thr Thr Pro Ala Pro Arg Pro	
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Pro Thr Pro Ala Pro Thr Ile Ala	255	Ser Gln Pro Leu Ser Leu Arg	
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Pro Glu Ala Cys Arg Pro Ala Ala	270	Gly Gly Ala Val His Thr Arg	
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Gly Val Leu Ala Cys Tyr Ser Leu	300	Leu Val Thr Val Ala Phe Ile	
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Ile Phe Trp Val Arg Ser Lys Arg	315	Ser Arg Leu Leu His Ser Asp	
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Tyr Met Asn Met Thr Pro Arg Arg	330	Pro Gly Pro Thr Arg Lys His	
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Tyr Gln Pro Tyr Ala Pro Pro Arg	345	Asp Phe Ala Ala Tyr Arg Ser	
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Val Lys Phe Ser Arg Ser Ala Asp	360	Ala Pro Ala Tyr Gln Gln Gly	
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Gln Asn Gln Leu Tyr Asn	375	
Glu Leu Asn Leu Gly Arg Arg Glu Glu	380	385
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Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly	395	400
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Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu	410	415
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Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met	425	430
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Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln	440	445
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Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met	455	460
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Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser	50	55
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Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile	65	70
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Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln	80	85
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Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gly Gly Thr Arg Leu Glu	95	100
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Ile Lys Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu	110	115
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Gly Ser Thr Lys Gly Gln Val Gln Leu Gln Glu Ser Gly Pro Gly		

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Leu Val Lys Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser	140	145
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Gly Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro	155	160
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Pro Gly Lys Ala Leu Glu Trp Leu Gly Val Ile Trp Gly Ser Glu	170	175
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Thr Thr Tyr Tyr Asn Thr Ser Leu Lys Thr Arg Leu Thr Ile Ser	185	190
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Lys Asp Asn Ser Lys Asn Gln Val Val Leu Thr Met Thr Asn Met	200	205
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Asp Pro Val Asp Thr Ala Thr Tyr Tyr Cys Ala Lys His Tyr Tyr	215	220
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Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Ser Ser	230	235
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Val Thr Val Ser Ser Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro	245	250
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Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg	260	265
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Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg	275	280
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Gly Leu Asp Phe Ala Cys Asp Phe Trp Val Leu Val Val Val Gly	290	295
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Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile	305	310
	315	
Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp	320	325
	330	
Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His	335	340
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Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser	350	355
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Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly	365	370
	375	
Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu	380	385
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Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly		

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Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu	410	415
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Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met	425	430
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Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln	440	445
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Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met	455	460
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Gln Ala Leu Pro Pro Arg	470	
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Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg	35	40
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Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser	50	55
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Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile	65	70
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Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln	80	85
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Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gly Gly Thr Arg Leu Glu	95	100
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Ile Lys Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu	110	115
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Gly Ser Thr Lys Gly Gln Val Gln Leu Gln Glu Ser Gly Pro Gly	125	130
	135	
Leu Val Lys Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser	140	145
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Gly Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro	155	160
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Pro Gly Lys Ala Leu Glu Trp Leu Gly Val Ile Trp Gly Ser Glu	170	175
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Thr Thr Tyr Tyr Ser Thr Ser Leu Lys Thr Arg Leu Thr Ile Ser	185	190
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Lys Asp Asn Ser Lys Asn Gln Val Val Leu Thr Met Thr Asn Met	200	205
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Asp Pro Val Asp Thr Ala Thr Tyr Tyr Cys Ala Lys His Tyr Tyr	215	220
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Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Ser Ser	230	235
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Val Thr Val Ser Ser Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro	245	250
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Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg	260	265
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Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg	275	280
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Gly Leu Asp Phe Ala Cys Asp Phe Trp Val Leu Val Val Val Gly	290	295
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Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile	305	310
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Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp	320	325
	330	
Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His	335	340
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Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser	350	355
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Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly	365	370
	375	
Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu	380	385
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Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly	395	400
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Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu	410	415
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Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met	425	430
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Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln	440	445
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Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg	35	40
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Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser	50	55
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Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile	65	70
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Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln	80	85
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Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gly Gly Thr Arg Leu Glu	95	100
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Ile Lys Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu	110	115
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Gly Ser Thr Lys Gly Gln Val Gln Leu Gln Glu Ser Gly Pro Gly	125	130
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Leu Val Lys Pro Ser Gln Thr Leu Ser Val Thr Cys Thr Val Ser	140	145
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Gly Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro	155	160
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Pro Gly Lys Ala Leu Glu Trp Leu Gly Val Ile Trp Gly Ser Glu	170	175

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

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Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg		
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	45	
Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser		
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Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile		
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	75	
Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln		
	80	85
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Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gly Gly Thr Arg Leu Glu		
	95	100
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Ile Lys Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu		
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Gly Ser Thr Lys Gly Gln Val Gln Leu Gln Glu Ser Gly Pro Gly		
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Leu Val Lys Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser		
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Gly Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro		
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Pro Gly Lys Ala Leu Glu Trp Leu Gly Val Ile Trp Gly Ser Glu		
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	180	
Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Thr Arg Leu Thr Ile Ser		
	185	190
	195	

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

205

220

	225	
Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Ser Ser	230	235
	240	
Val Thr Val Ser Ser Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro	245	250
	255	
Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg	260	265
	270	
Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg	275	280
	285	
Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala	290	295
	300	
Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr	305	310
	315	
Cys Val Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln	320	325
	330	
Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys	335	340
	345	
Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg	350	355
	360	
Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly	365	370
	375	
Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu	380	385
	390	
Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly	395	400
	405	
Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu	410	415
	420	
Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met	425	430
	435	
Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln	440	445
	450	
Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met	455	460
	465	
Gln Ala Leu Pro Pro Arg	470	

<210>17

<211>471

<212> PRT
 <213> Artificial
 <220>
 <223> PCAR 025
 <400>17

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

	245	250
	255	
Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg	260	265
	270	
Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg	275	280
	285	
Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala	290	295
	300	
Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr	305	310
	315	
Cys Val Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln	320	325
	330	
Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys	335	340
	345	
Ser Cys Arg Phe Pro Glu Glu Glu Gly Gly Cys Glu Leu Arg	350	355
	360	
Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly	365	370
	375	
Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu	380	385
	390	
Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly	395	400
	405	
Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu	410	415
	420	
Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met	425	430
	435	
Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln	440	445
	450	
Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met	455	460
	465	
Gln Ala Leu Pro Pro Arg	470	

<210>18

<211> 471

<212> PRT

<213> Artificial

<220>

<223> PCAR 026

<400>18

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

Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg	275	280
	285	
Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala	290	295
	300	
Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr	305	310
	315	
Cys Val Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln	320	325
	330	
Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys	335	340
	345	
Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg	350	355
	360	
Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly	365	370
	375	
Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu	380	385
	390	
Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly	395	400
	405	
Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu	410	415
	420	
Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met	425	430
	435	
Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln	440	445
	450	
Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met	455	460
	465	
Gln Ala Leu Pro Pro Arg	470	

<210> 19

<211> 735

<212>DNA

<213> Artificial

<220>

<223> ScFv-humanized4

<400> 19

gatattcaga tgaccagag cccgagcagc ctgagcgcga gcgtgggcga tcgcgtgacc	60
attacctgcc gcgcgagcca ggatattagc aaatatctga actggtatca gcagaaaccg	120
ggcaaagcgc cgcgcctgct gatttatcat accagccgcc tgcatagcgg cgtgccgagc	180
cgcttttagcg gcagcggcag cggcaccgat tataccctga ccattagcag cctgcagccg	240
gaagattttg cgacctatta ttgccagcag ggcaacaccc tgccgtatac ctttggcggc	300

ggcaccgcc	tggaattaa	aggcagcacc	agcggcagcg	gcaaaccggg	cagcggcgaa	360
ggcagcacca	aaggccaggt	gcagctgcag	gaaagcggcc	cgggcctggt	gaaaccgagc	420
cagaccctga	gcctgacctg	caccgtgagc	ggcgtgagcc	tgccggatta	tggcgtgagc	480
tggattcgcc	agccgccggg	caaagcgctg	gaatggctgg	gcgtgatttg	gggcagcgaa	540
accacctatt	ataacagcgc	gctgaaaacc	cgcctgacca	ttagcaaaga	taacagcaaa	600
aaccaggtgg	tgctgacctg	gaccaacatg	gatccggtgg	ataccgcgac	ctattattgc	660
gcgaaacatt	attattatgg	cggcagctat	gcgatggatt	attggggcca	gggcagcagc	720
gtgaccgtga	gcagc					735

<210>20

<211> 735

<212> DNA

<213> Artificial

<220>

<223> ScFv-humanized5

<400> 20

gatattcaga	tgaccagag	cccagcagc	ctgagcgcga	gcgtgggcga	tcgcgtgacc	60
attacctgcc	gcgcgagcca	ggatattagc	aaatatctga	actggtatca	gcagaaaccg	120
ggcaaagcgc	cggcctgct	gatttatcat	accagccgcc	tgcatagcgg	cgtgccgagc	180
cgctttagcg	gcagcggcag	cggcaccgat	tataccctga	ccattagcag	cctgcagccg	240
gaagattttg	cgacctatta	ttgccagcag	ggcaacaccc	tgccgtatac	ctttggcggc	300
ggcaccgcc	tggaattaa	aggcagcacc	agcggcagcg	gcaaaccggg	cagcggcgaa	360
ggcagcacca	aaggccaggt	gcagctgcag	gaaagcggcc	cgggcctggt	gaaaccgagc	420
cagaccctga	gcctgacctg	caccgtgagc	ggcgtgagcc	tgccggatta	tggcgtgagc	480
tggattcgcc	agccgccggg	caaagcgctg	gaatggctgg	gcgtgatttg	gggcagcgaa	540
accacctatt	ataacaccag	cctgaaaacc	cgcctgacca	ttagcaaaga	taacagcaaa	600
aaccaggtgg	tgctgacctg	gaccaacatg	gatccggtgg	ataccgcgac	ctattattgc	660
gcgaaacatt	attattatgg	cggcagctat	gcgatggatt	attggggcca	gggcagcagc	720
gtgaccgtga	gcagc					735

<210> 21

<211> 735

<212> DNA

<213> Artificial

<220>

<223> ScFv-humanized9

<400> 21

gatattcaga	tgaccagag	cccagcagc	ctgagcgcga	gcgtgggcga	tcgcgtgacc	60
attacctgcc	gcgcgagcca	ggatattagc	aaatatctga	actggtatca	gcagaaaccg	120
ggcaaagcgc	cggcctgct	gatttatcat	accagccgcc	tgcatagcgg	cgtgccgagc	180
cgctttagcg	gcagcggcag	cggcaccgat	tataccctga	ccattagcag	cctgcagccg	240
gaagattttg	cgacctatta	ttgccagcag	ggcaacaccc	tgccgtatac	ctttggcggc	300
ggcaccgcc	tggaattaa	aggcagcacc	agcggcagcg	gcaaaccggg	cagcggcgaa	360
ggcagcacca	aaggccaggt	gcagctgcag	gaaagcggcc	cgggcctggt	gaaaccgagc	420
cagaccctga	gcctgacctg	caccgtgagc	ggcgtgagcc	tgccggatta	tggcgtgagc	480
tggattcgcc	agccgccggg	caaagcgctg	gaatggctgg	gcgtgatttg	gggcagcgaa	540
accacctatt	atagcaccag	cctgaaaacc	cgcctgacca	ttagcaaaga	taacagcaaa	600
aaccaggtgg	tgctgacctg	gaccaacatg	gatccggtgg	ataccgcgac	ctattattgc	660
gcgaaacatt	attattatgg	cggcagctat	gcgatggatt	attggggcca	gggcagcagc	720
gtgaccgtga	gcagc					735

<210> 22
 <211> 735
 <212> DNA
 <213> Artificial
 <220>
 <223> ScFv-humanized11
 <400> 22

gatattcaga	tgaccagag	cccagcagc	ctgagcgcga	gcgtgggcga	tcgcgtgacc	60
attacctgcc	gcgcgagcca	ggatattagc	aaatatctga	actggtatca	gcagaaaccg	120
ggcaaagcgc	cgcgctgct	gatttatcat	accagccgcc	tgcatagcgg	cgtgccgagc	180
cgcttttagcg	gcagcggcag	cggcaccgat	tataccctga	ccattagcag	cctgcagccg	240
gaagattttg	cgacctattt	ttgccagcag	ggcaacaccc	tgccgtatac	ctttggcggc	300
ggcacccgcc	tggaaattaa	aggcagcacc	agcggcagcg	gcaaaccggg	cagcggcgaa	360
ggcagcacca	aaggccaggt	gcagctgcag	gaaagcggcc	cgggcctggt	gaaaccgagc	420
cagaccctga	gcgtgacctg	caccgtgagc	ggcgtgagcc	tgccggatta	tggcgtgagc	480
tggattcgcc	agccgccggg	caaagcgctg	gaatggctgg	gcgtgatttg	gggcagcgaa	540
accacctatt	ataacagcag	cctgaaaacc	cgctgacca	ttagcaaaga	taacagcaaa	600
aaccaggtgg	tgctgaccat	gaccaacctg	gatccggtgg	ataccgcgac	ctattattgc	660
gcgaaacatt	attattatgg	cggcagctat	gcgatggatt	attggggcca	gggcagcagc	720
gtgaccgtga	gcagc					735

<210> 23
 <211>1413
 <212> DNA
 <213> Artificial
 <220>
 <223> PCAR 019
 <400> 23

gatattcaga	tgaccagag	cccagcagc	ctgagcgcga	gcgtgggcga	tcgcgtgacc	60
attacctgcc	gcgcgagcca	ggatattagc	aaatatctga	actggtatca	gcagaaaccg	120
ggcaaagcgc	cgcgctgct	gatttatcat	accagccgcc	tgcatagcgg	cgtgccgagc	180
cgcttttagcg	gcagcggcag	cggcaccgat	tataccctga	ccattagcag	cctgcagccg	240
gaagattttg	cgacctatta	ttgccagcag	ggcaacaccc	tgccgtatac	ctttggcggc	300
ggcacccgcc	tggaaattaa	aggcagcacc	agcggcagcg	gcaaaccggg	cagcggcgaa	360
ggcagcacca	aaggccaggt	gcagctgcag	gaaagcggcc	cgggcctggt	gaaaccgagc	420
cagaccctga	gcctgacctg	caccgtgagc	ggcgtgagcc	tgccggatta	tggcgtgagc	480
tggattcgcc	agccgccggg	caaagcgctg	gaatggctgg	gcgtgatttg	gggcagcgaa	540
accacctatt	ataacagcgc	gctgaaaacc	cgctgacca	ttagcaaaga	taacagcaaa	600
aaccaggtgg	tgctgaccat	gaccaacatg	gatccggtgg	ataccgcgac	ctattattgc	660
gcgaaacatt	attattatgg	cggcagctat	gcgatggatt	attggggcca	gggcagcagc	720
gtgaccgtga	gcagcaaacc	gaccaccacc	ccggcgccgc	gcccgccgac	cccggcgccg	780
accattgcga	gccagccgct	gagcctgcgc	ccggaagcgt	gccgcccggc	ggcgggcggc	840
gcggtgcata	cccgcggcct	ggattttgcg	tgcgattttt	gggtgctggt	ggtggtgggc	900
ggcgtgctgg	cgtgctatag	cctgctggtg	accgtggcgt	ttattatttt	ttgggtgcgc	960
agcaaacgca	gccgcctgct	gcatagcgat	tatatgaaca	tgaccccgcg	ccgccggggc	1020
ccgacccgca	aacattatca	gccgtatgcg	ccgccgcgcg	atthttgcggc	gtatcgcagc	1080
gtgaaattta	gccgcagcgc	ggatgcgccg	gcgtatcagc	agggccagaa	ccagctgtat	1140
aacgaactga	acctggggccg	ccgcgaagaa	tatgatgtgc	tggataaacg	ccgcggccgc	1200
gatccggaaa	tgggcggcaa	accgcgccgc	aaaaaccgcg	aggaaggcct	gtataacgaa	1260
ctgcagaaaag	ataaaaatggc	ggaagcgtat	agcgaaattg	gcatgaaagg	cgaacgccgc	1320
cgcgggcaaaag	gccatgatgg	cctgtatcag	ggcctgagca	ccgcgaccaa	agatacctat	1380
gatgcgctgc	atatgcaggc	gctgccgccg	cgc			1413

<210> 24
 <211>1413
 <212> DNA
 <213> Artificial
 <220>

<223>PCAR 020

<400> 24

gatattcaga	tgaccagag	cccgagcagc	ctgagcgcg	gcgtgggcga	tcgcgtgacc	60
attacctgcc	gcgcgagcca	ggatattagc	aaatatctga	actggtatca	gcagaaaccg	120
ggcaaagcgc	cgcgccctgct	gatttatcat	accagccgcc	tgcatagcgg	cgtgccgagc	180
cgcttttagcg	gcagcggcag	cggcaccgat	tataccctga	ccattagcag	cctgcagccg	240
gaagattttg	cgacctatta	ttgccagcag	ggcaacaccc	tgccgtatac	ctttggcggc	300
ggcaccgcc	tggaattaa	aggcagcacc	agcggcagcg	gcaaaccggg	cagcggcgaa	360
ggcagcacca	aaggccaggt	gcagctgcag	gaaagcggcc	cgggcctggt	gaaaccgagc	420
cagaccctga	gcctgacctg	caccgtgagc	ggcgtgagcc	tgccggatta	tggcgtgagc	480
tggattcgcc	agccgccggg	caaagcgctg	gaatggctgg	gcgtgatttg	gggcagcgaa	540
accacctatt	ataacaccag	cctgaaaacc	cgctgacca	ttagcaaaga	taacagcaaa	600
aaccaggtgg	tgctgacat	gaccaacatg	gatccggtgg	ataccgcgac	ctattattgc	660
gcgaaacatt	attattatgg	cggcagctat	gcgatggatt	attggggcca	gggcagcagc	720
gtgaccgtga	gcagcaaacc	gaccaccacc	ccggcgccgc	gcccgccgac	cccggcgccg	780
accattgcga	gccagccgct	gagcctgcgc	ccggaagcgt	gccgcccggc	ggcgggcggc	840
gcggtgcata	cccgcggcct	ggattttgcg	tgcgattttt	gggtgctggt	ggtggtgggc	900
ggcgtgctgg	cgtgctatag	cctgctggtg	accgtggcgt	ttattatttt	ttgggtgcgc	960
agcaaacgca	gccgcctgct	gcatagcgat	tatatgaaca	tgaccccgcg	ccgcccgggc	1020
ccgacccgca	aacattatca	gccgtatgcg	ccgccgcgcg	atatttgcggc	gtatcgcagc	1080
gtgaaattta	gccgcagcgc	ggatgcgcgc	gcgtatcagc	agggccagaa	ccagctgtat	1140
aacgaactga	acctggggccg	ccgcgaagaa	tatgatgtgc	tggataaacg	ccgcggccgc	1200
gatccggaag	tgggcggcaa	accgcgccgc	aaaaacccgc	aggaaggcct	gtataacgaa	1260
ctgcagaaag	ataaaatggc	ggaagcgtat	agcgaaattg	gcatgaaagg	cgaacgccgc	1320
cgcggcaaag	gccatgatgg	cctgtatcag	ggcctgagca	ccgcgaccaa	agatacctat	1380
gatgcgctgc	atatgcaggc	gctgccgccg	cgc			1413

<210> 25
 <211>1413
 <212> DNA
 <213> Artificial
 <220>

<223> PCAR 021

<400>25

gatattcaga	tgaccagag	cccgagcagc	ctgagcgcg	gcgtgggcga	tcgcgtgacc	60
attacctgcc	gcgcgagcca	ggatattagc	aaatatctga	actggtatca	gcagaaaccg	120
ggcaaagcgc	cgcgccctgct	gatttatcat	accagccgcc	tgcatagcgg	cgtgccgagc	180
cgcttttagcg	gcagcggcag	cggcaccgat	tataccctga	ccattagcag	cctgcagccg	240
gaagattttg	cgacctatta	ttgccagcag	ggcaacaccc	tgccgtatac	ctttggcggc	300
ggcaccgcc	tggaattaa	aggcagcacc	agcggcagcg	gcaaaccggg	cagcggcgaa	360
ggcagcacca	aaggccaggt	gcagctgcag	gaaagcggcc	cgggcctggt	gaaaccgagc	420
cagaccctga	gcctgacctg	caccgtgagc	ggcgtgagcc	tgccggatta	tggcgtgagc	480
tggattcgcc	agccgccggg	caaagcgctg	gaatggctgg	gcgtgatttg	gggcagcgaa	540
accacctatt	atagcaccag	cctgaaaacc	cgctgacca	ttagcaaaga	taacagcaaa	600
aaccaggtgg	tgctgacat	gaccaacatg	gatccggtgg	ataccgcgac	ctattattgc	660
gcgaaacatt	attattatgg	cggcagctat	gcgatggatt	attggggcca	gggcagcagc	720
gtgaccgtga	gcagcaaacc	gaccaccacc	ccggcgccgc	gcccgccgac	cccggcgccg	780
accattgcga	gccagccgct	gagcctgcgc	ccggaagcgt	gccgcccggc	ggcgggcggc	840

gcggtgcata	cccgcggcct	ggatTTTTgcg	tgcgattttt	gggtgctggt	ggtggtgggc	900
ggcgtgctgg	cgtgctatag	cctgctggtg	accgtggcgt	ttattatttt	ttgggtgcgc	960
agcaaacgca	gccgcctgct	gcatagcgat	tatatgaaca	tgaccccgcg	ccgcccgggc	1020
ccgacccgca	aacattatca	gccgtatgcg	ccgccgcgcg	atTTTgcggc	gtatcgcagc	1080
gtgaaattta	gccgcagcgc	ggatgcgccg	gcgtatcagc	agggccagaa	ccagctgtat	1140
aacgaactga	acctggggccg	ccgcgaagaa	tatgatgtgc	tggataaacg	ccgcggccgc	1200
gatccggaaa	tgggcgggcaa	accgcgccgc	aaaaacccgc	aggaaggcct	gtataacgaa	1260
ctgcagaaaag	ataaaatggc	ggaagcgtat	agcgaaattg	gcatgaaagg	cgaacgccgc	1320
cgcggcaaag	gccatgatgg	cctgtatcag	ggcctgagca	ccgcgaccaa	agatacctat	1380
gatgcgctgc	atatgcaggc	gctgccgccg	cgc			1413

<210> 26

<211>1413

<212>DNA

<213> Artificial

<220>

<223> PCAR 022

<400>26

gatattcaga	tgaccagag	cccgagcagc	ctgagcgcga	gcgtgggcga	tcgcgtgacc	60
attacctgcc	gcgcgagcca	ggatattagc	aaatatctga	actggtatca	gcagaaaccg	120
ggcaaagcgc	cgcgcctgct	gatttatcat	accagccgcc	tgcatagcgg	cgtgccgagc	180
cgcttttagcg	gcagcggcag	cggcaccgat	tataccctga	ccattagcag	cctgcagccg	240
gaagattttg	cgacctatTT	ttgccagcag	ggcaacaccc	tgccgtatac	ctttggcggc	300
ggcacccgcc	tggaaattaa	aggcagcacc	agcggcagcg	gcaaaccggg	cagcggcgaa	360
ggcagcacca	aaggccaggt	gcagctgcag	gaaagcggcc	cgggcctggt	gaaaccgagc	420
cagaccctga	gcgtgacctg	caccgtgagc	ggcgtgagcc	tgccggatta	tggcgtgagc	480
tggattcgcc	agccgccggg	caaagcgctg	gaatggctgg	gcgtgatttg	gggcagcgaa	540
accacctatt	ataacagcag	cctgaaaacc	cgcctgacca	ttagcaaaga	taacagcaaa	600
aaccaggtgg	tgctgaccat	gaccaacctg	gatccggtgg	ataccgcgac	ctattattgc	660
gcgaaacatt	attattatgg	cggcagctat	gcgatggatt	attggggcca	gggcagcagc	720
gtgaccgtga	gcagcaaacc	gaccaccacc	ccggcgccgc	gcccgccgac	cccggcgccg	780
accattgcga	gccagccgct	gagcctgcgc	ccggaagcgt	gcccggcggc	ggcgggcggc	840
gcggtgcata	cccgcggcct	ggatTTTTgcg	tgcgattttt	gggtgctggt	ggtggtgggc	900
ggcgtgctgg	cgtgctatag	cctgctggtg	accgtggcgt	ttattatttt	ttgggtgcgc	960
agcaaacgca	gccgcctgct	gcatagcgat	tatatgaaca	tgaccccgcg	ccgcccgggc	1020
ccgacccgca	aacattatca	gccgtatgcg	ccgccgcgcg	atTTTgcggc	gtatcgcagc	1080
gtgaaattta	gccgcagcgc	ggatgcgccg	gcgtatcagc	agggccagaa	ccagctgtat	1140
aacgaactga	acctggggccg	ccgcgaagaa	tatgatgtgc	tggataaacg	ccgcggccgc	1200
gatccggaaa	tgggcgggcaa	accgcgccgc	aaaaacccgc	aggaaggcct	gtataacgaa	1260
ctgcagaaaag	ataaaatggc	ggaagcgtat	agcgaaattg	gcatgaaagg	cgaacgccgc	1320
cgcggcaaag	gccatgatgg	cctgtatcag	ggcctgagca	ccgcgaccaa	agatacctat	1380
gatgcgctgc	atatgcaggc	gctgccgccg	cgc			1413

<210> 27

<211>1413

<212> DNA

<213> Artificial

<220>

<223> PCAR 023

<400>27

gatattcaga	tgaccagag	cccgagcagc	ctgagcgcga	gcgtgggcga	tcgcgtgacc	60
attacctgcc	gcgcgagcca	ggatattagc	aaatatctga	actggtatca	gcagaaaccg	120

ggcaaagcgc	cgcgccctgct	gatttatcat	accagccgcc	tgcatagcgg	cgtgccgagc	180
cgcttttagcg	gcagcggcag	cggcaccgat	tataccctga	ccattagcag	cctgcagccg	240
gaagattttg	cgacctatta	ttgccagcag	ggcaacaccc	tgccgtatac	ctttggcggc	300
ggcaccgcc	tggaaattaa	aggcagcacc	agcggcagcg	gcaaaccggg	cagcggcgaa	360
ggcagcacca	aaggccaggt	gcagctgcag	gaaagcggcc	cgggcctggt	gaaaccgagc	420
cagaccctga	gcctgacctg	caccgtgagc	ggcgtgagcc	tgccggatta	tggcgtgagc	480
tggattcgcc	agccgccggg	caaagcgctg	gaatggctgg	gcgtgatttg	gggcagcgaa	540
accacctatt	ataacagcgc	gctgaaaacc	cgcttgacca	ttagcaaaga	taacagcaaa	600
aaccaggtgg	tgctgaccat	gaccaacatg	gatccggtgg	ataccgcgac	ctattattgc	660
gcgaaacatt	attattatgg	cggcagctat	gcgatggatt	attggggcca	gggcagcagc	720
gtgaccgtga	gcagcaaacc	gaccaccacc	ccggcgccgc	gcccgccgac	cccggcgccg	780
accattgcga	gccagccgct	gagcctgcgc	ccggaagcgt	gccgcccggc	ggcgggcggc	840
gcggtgcata	cccgcggcct	ggattttgcg	tgcatatatt	atatttgggc	gccgctggcg	900
ggcacctgcg	gcgtgctgct	gctgagcctg	gtgattaccc	tgtattgcgt	gaaacgcggc	960
cgcaaaaaac	tgctgtatat	ttttaaacag	ccgtttatgc	gcccgggtgca	gaccaccag	1020
gaagaagatg	gctgcagctg	ccgctttccg	gaagaagaag	aaggcggctg	cgaactgcgc	1080
gtgaaattta	gccgcagcgc	ggatgcgccg	gcgtatcagc	agggccagaa	ccagctgtat	1140
aacgaactga	acctgggccg	ccgcgaagaa	tatgatgtgc	tgataaacg	ccgcggccgc	1200
gatccggaaa	tgggcggcaa	accgcgccgc	aaaaaccgc	aggaaggcct	gtataacgaa	1260
ctgcagaaaag	ataaaatggc	ggaagcgtat	agcgaaattg	gcatgaaagg	cgaacgccgc	1320
cgcggcaaaag	gccatgatgg	cctgtatcag	ggcctgagca	ccgcgaccaa	agatacctat	1380
gatgcgctgc	atatgcaggc	gctgccgccg	cgc			1413

<210>28

<211> 1413

<212> DNA

<213> Artificial

<220>

<223> PCAR 024

<400> 28

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attacctgcc	gcgcgagcca	ggatattagc	aaatatctga	actggtatca	gcagaaaccg	120
ggcaaagcgc	cgcgccctgct	gatttatcat	accagccgcc	tgcatagcgg	cgtgccgagc	180
cgcttttagcg	gcagcggcag	cggcaccgat	tataccctga	ccattagcag	cctgcagccg	240
gaagattttg	cgacctatta	ttgccagcag	ggcaacaccc	tgccgtatac	ctttggcggc	300
ggcaccgcc	tggaaattaa	aggcagcacc	agcggcagcg	gcaaaccggg	cagcggcgaa	360
ggcagcacca	aaggccaggt	gcagctgcag	gaaagcggcc	cgggcctggt	gaaaccgagc	420
cagaccctga	gcctgacctg	caccgtgagc	ggcgtgagcc	tgccggatta	tggcgtgagc	480
tggattcgcc	agccgccggg	caaagcgctg	gaatggctgg	gcgtgatttg	gggcagcgaa	540
accacctatt	ataacaccag	cctgaaaacc	cgcttgacca	ttagcaaaga	taacagcaaa	600
aaccaggtgg	tgctgaccat	gaccaacatg	gatccggtgg	ataccgcgac	ctattattgc	660
gcgaaacatt	attattatgg	cggcagctat	gcgatggatt	attggggcca	gggcagcagc	720
gtgaccgtga	gcagcaaacc	gaccaccacc	ccggcgccgc	gcccgccgac	cccggcgccg	780
accattgcga	gccagccgct	gagcctgcgc	ccggaagcgt	gccgcccggc	ggcgggcggc	840
gcggtgcata	cccgcggcct	ggattttgcg	tgcatatatt	atatttgggc	gccgctggcg	900
ggcacctgcg	gcgtgctgct	gctgagcctg	gtgattaccc	tgtattgcgt	gaaacgcggc	960
cgcaaaaaac	tgctgtatat	ttttaaacag	ccgtttatgc	gcccgggtgca	gaccaccag	1020
gaagaagatg	gctgcagctg	ccgctttccg	gaagaagaag	aaggcggctg	cgaactgcgc	1080
gtgaaattta	gccgcagcgc	ggatgcgccg	gcgtatcagc	agggccagaa	ccagctgtat	1140
aacgaactga	acctgggccg	ccgcgaagaa	tatgatgtgc	tgataaacg	ccgcggccgc	1200
gatccggaaa	tgggcggcaa	accgcgccgc	aaaaaccgc	aggaaggcct	gtataacgaa	1260
ctgcagaaaag	ataaaatggc	ggaagcgtat	agcgaaattg	gcatgaaagg	cgaacgccgc	1320
cgcggcaaaag	gccatgatgg	cctgtatcag	ggcctgagca	ccgcgaccaa	agatacctat	1380

gatgcgctgc atatgcaggc gctgccgccg cgc

1413

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<211>1413

<212> DNA

<213> Artificial

<220>

<223> PCAR 025

<400>29

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ggcaaagcgc	cgcgctgct	gatttatcat	accagccgcc	tgcatagcgg	cgtgccgagc	180
cgctttagcg	gcagcggcag	cggcaccgat	tataccctga	ccattagcag	cctgcagccg	240
gaagattttg	cgacctatta	ttgccagcag	ggcaacaccc	tgccgtatac	ctttggcggc	300
ggcacccgcc	tggaaattaa	aggcagcacc	agcggcagcg	gcaaaccggg	cagcggcgaa	360
ggcagcacca	aaggccaggt	gcagctgcag	gaaagcggcc	cgggcctggt	gaaaccgagc	420
cagaccctga	gcctgacctg	caccgtgagc	ggcgtgagcc	tgccggatta	tggcgtgagc	480
tggattcgcc	agccgccggg	caaagcgctg	gaatggctgg	gcgtgatttg	gggcagcgaa	540
accacctatt	atagcaccag	cctgaaaacc	cgcttgacca	ttagcaaaga	taacagcaaa	600
aaccaggtgg	tgctgaccat	gaccaacatg	gatccggtgg	ataccgcgac	ctattattgc	660
gcgaaacatt	attattatgg	cggcagctat	gcgatggatt	attggggcca	gggcagcagc	720
gtgacctga	gcagcaaacc	gaccaccacc	ccggcgccgc	gcccgccgac	cccggcgccg	780
accattgcga	gccagccgct	gagcctgcgc	ccggaagcgt	gccgcccggc	ggcgggcggc	840
gcggtgcata	cccgcggcct	ggattttgcg	tgcatatatt	atatttgggc	gccgctggcg	900
ggcacctgcg	gcgtgctgct	gctgagcctg	gtgattacc	tgtattgcgt	gaaacgcggc	960
cgcaaaaaac	tgctgtatat	ttttaaacag	ccgtttatgc	gcccgggtga	gaccaccag	1020
gaagaagatg	gctgcagctg	ccgctttccg	gaagaagaag	aaggcggctg	cgaactgcgc	1080
gtgaaattta	gccgcagcgc	ggatgcgccg	gcgtatcagc	agggccagaa	ccagctgtat	1140
aacgaactga	acctgggccg	ccgcgaagaa	tatgatgtgc	tggataaacg	ccgcggccgc	1200
gatccggaag	tgggcggcaa	accgcgccgc	aaaaaccgc	aggaaggcct	gtataacgaa	1260
ctgcagaaag	ataaaatggc	ggaagcgtat	agcgaaattg	gcatgaaagg	cgaacgccgc	1320
cgcggcaaag	gccatgatgg	cctgtatcag	ggcctgagca	ccgcgaccaa	agatacctat	1380
gatgcgctgc	atatgcaggc	gctgccgccg	cgc			1413

<210> 30

<211> 1413

<212>DNA

<213> Artificial

<220>

<223> PCAR 026

<400> 30

gatattcaga	tgaccagag	cccgagcagc	ctgagcgcg	gcgtgggcga	tcgctgacc	60
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ggcaaagcgc	cgcgctgct	gatttatcat	accagccgcc	tgcatagcgg	cgtgccgagc	180
cgctttagcg	gcagcggcag	cggcaccgat	tataccctga	ccattagcag	cctgcagccg	240
gaagattttg	cgacctattt	ttgccagcag	ggcaacaccc	tgccgtatac	ctttggcggc	300
ggcacccgcc	tggaaattaa	aggcagcacc	agcggcagcg	gcaaaccggg	cagcggcgaa	360
ggcagcacca	aaggccaggt	gcagctgcag	gaaagcggcc	cgggcctggt	gaaaccgagc	420
cagaccctga	gcgtgacctg	caccgtgagc	ggcgtgagcc	tgccggatta	tggcgtgagc	480
tggattcgcc	agccgccggg	caaagcgctg	gaatggctgg	gcgtgatttg	gggcagcgaa	540
accacctatt	ataacagcag	cctgaaaacc	cgcttgacca	ttagcaaaga	taacagcaaa	600
aaccaggtgg	tgctgaccat	gaccaacctg	gatccggtgg	ataccgcgac	ctattattgc	660

gcgaaacatt	attattatgg	cggcagctat	gcgatggatt	attggggcca	gggcagcagc	720
gtgaccgtga	gcagcaaacc	gaccaccacc	ccggcgccgc	gcccgcgcac	cccggcgccg	780
accattgcga	gccagccgct	gagcctgcgc	ccggaagcgt	gccgccgggc	ggcgggcggc	840
gcggtgcata	cccgcggcct	ggatttttgcg	tgcgatattt	atattttgggc	gccgctggcg	900
ggcacctgcg	gcgtgctgct	gctgagcctg	gtgattacc	tgtattgcgt	gaaacgcggc	960
cgcaaaaaac	tgctgtatat	ttttaaacag	ccgtttatgc	gcccgggtgca	gaccaccag	1020
gaagaagatg	gctgcagctg	ccgctttccg	gaagaagaag	aaggcggctg	cgaactgcgc	1080
gtgaaattta	gccgcagcgc	ggatgcgccg	gcgtatcagc	agggccagaa	ccagctgtat	1140
aacgaactga	acctgggccg	ccgcgaagaa	tatgatgtgc	tggataaacg	ccgcggccgc	1200
gatccggaaa	tgggcggcaa	accgcgccgc	aaaaacccgc	aggaaggcct	gtataacgaa	1260
ctgcagaaa	ataaaatggc	ggaagcgtat	agcgaattt	gcatgaaagg	cgaacgccgc	1320
cgcgggcaa	gccatgatgg	cctgtatcag	ggcctgagca	ccgcgaccaa	agatacctat	1380
gatgcgctgc	atatgcaggc	gctgccgccg	cgc			1413

<210>	32	
<211>	492	
<212>	PRT	
<213>	Artificial	
<220>		
<223>	PCAR 003	
<400>	32	
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu	5	10
	15	
Leu His Ala Ala Arg Pro Asp Ile Gln Met Thr Gln Ser Pro Ser	20	25
	30	
Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg	35	40
	45	
Ala Ser Gln Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys	50	55
	60	
Pro Gly Lys Ala Pro Arg Leu Leu Ile Tyr His Thr Ser Arg Leu	65	70
	75	
His Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr	80	85
	90	
Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala	95	100
	105	
Thr Tyr Tyr Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly	110	115

	120	
Gly Gly Thr Arg Leu Glu Ile Lys Gly Ser Thr Ser Gly Ser Gly	125	130
	135	
Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Gln Val Gln Leu	140	145
	150	
Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln Thr Leu Ser	155	160
	165	
Leu Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val	170	175
	180	
Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu Trp Leu Gly	185	190
	195	
Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ser Leu Lys	200	205
	210	
Thr Arg Leu Thr Ile Ser Lys Asp Asn Ser Lys Asn Gln Val Val	215	220
	225	
Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr	230	235
	240	
Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr	245	250
	255	
Trp Gly Gln Gly Ser Ser Val Thr Val Ser Ser Lys Pro Thr Thr	260	265
	270	
Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser	275	280
	285	
Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly	290	295
	300	
Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr	305	310
	315	
Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser	320	325
	330	
Leu Val Ile Thr Leu Tyr Cys Val Lys Arg Gly Arg Lys Lys Leu	335	340
	345	
Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr	350	355
	360	
Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu	365	370
	375	
Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala	380	385

	390	
Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn	395	400
	405	
Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly	410	415
	420	
Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln	425	430
	435	
Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala	440	445
	450	
Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly	455	460
	465	
His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr	470	475
	480	
Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg	485	490

<210> 33
 <211> 28
 <212>DNA
 <213> Artificial

<220>

<223> 正向引物

<400> 33

aggctagcat gggatggagc tgtatcat 28

<210> 34

<211> 38

<212> DNA

<213> Artificial

<220>

<223> 反向引物

<400> 34

gattgtcgac ttagcgaggg ggcagggcct gcatgtga 38

<210> 35

<211> 245

<212> PRT

<213> Artificial

<220>

<223>

<400> 35

Asp Ile Gln Met Thr Gln Ser Thr Ser Ser Leu Ser Ala Ser Val	5	10
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15

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

<210> 36

<211> 245

<212> PRT

<213> Artificial

<220>

<223>

<400> 36

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val

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

<210> 37

<211> 245

<212> PRT

<213> Artificial

<220>
 <223>
 <400> 37
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
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 15
 Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser
 20 25
 30
 Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
 35 40
 45
 Leu Leu Ile Tyr His Thr Ser Ser Leu Gln Ser Gly Val Pro Ser
 50 55
 60
 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
 65 70
 75
 Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
 80 85
 90
 Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gly Gly Thr Arg Leu Glu
 95 100
 105
 Ile Lys Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu
 110 115
 120
 Gly Ser Thr Lys Gly Gln Val Gln Leu Gln Glu Ser Gly Pro Gly
 125 130
 135
 Leu Val Lys Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser
 140 145
 150
 Gly Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro
 155 160
 165
 Pro Gly Lys Ala Leu Glu Trp Leu Ala Leu Ile Trp Gly Ser Glu
 170 175
 180
 Thr Thr Tyr Tyr Ser Thr Ser Leu Lys Thr Arg Leu Thr Ile Ser
 185 190
 195
 Lys Asp Thr Ser Lys Asn Gln Val Val Leu Thr Met Thr Asn Met
 200 205
 210
 Asp Pro Val Asp Thr Ala Thr Tyr Tyr Cys Ala Lys His Tyr Tyr
 215 220
 225
 Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Ser Ser
 230 235
 240
 Val Thr Val Ser Ser
 245

<210>	38	
<211>	120	
<212>	PRT	
<213>	Artificial	
<220>		
<223>		
<400>	38	
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser	5	10
	15	
Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Val Ser Leu Pro	20	25
	30	
Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Arg Lys Ala Leu	35	40
	45	
Glu Trp Leu Ala Leu Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Asn	50	55
	60	
Thr Ser Leu Lys Ser Arg Leu Thr Ile Ile Lys Asp Thr Ser Lys	65	70
	75	
Asn Gln Val Val Leu Lys Met Thr Asn Met Gln Thr Asp Asp Thr	80	85
	90	
Ala Val Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr	95	100
	105	
Ala Met Asp Tyr Trp Gly Gln Gly Ser Ser Val Thr Val Ser Ser	110	115
	120	

<210>	39	
<211>	120	
<212>	PRT	
<213>	Artificial	
<220>		
<223>		
<400>	39	
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser		
	5	10
	15	
Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Val Ser Leu Pro		
	20	25
	30	
Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu		
	35	40
	45	
Glu Trp Leu Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Asn		
	50	55
	60	
Ser Ser Leu Lys Thr Arg Leu Thr Ile Ser Lys Asp Asn Ser Lys		
	65	70
	75	

Asn Gln Val Val Leu Thr Met Thr	Asn Met Asp Pro Val Asp Thr	85
	80	
	90	
Ala Thr Tyr Tyr Cys Ala Lys His	Tyr Tyr Tyr Gly Gly Ser Tyr	100
	95	
	105	
Ala Met Asp Tyr Trp Gly Gln Gly	Ser Ser Val Thr Val Ser Ser	115
	110	
	120	
<210> 40		
<211> 120		
<212> PRT		
<213> Artificial		
<220>		
<223>		
<400> 40		
Gln Val Gln Leu Gln Glu Ser Gly	Pro Gly Leu Val Lys Pro Ser	10
	5	
	15	
Gln Thr Leu Ser Leu Thr Cys Thr	Val Ser Gly Val Ser Leu Pro	25
	20	
	30	
Asp Tyr Gly Val Ser Trp Ile Arg	Gln Pro Pro Gly Lys Ala Leu	40
	35	
	45	
Glu Trp Leu Ala Leu Ile Trp Gly	Ser Glu Thr Thr Tyr Tyr Ser	55
	50	
	60	
Thr Ser Leu Lys Thr Arg Leu Thr	Ile Ser Lys Asp Thr Ser Lys	70
	65	
	75	
Asn Gln Val Val Leu Thr Met Thr	Asn Met Asp Pro Val Asp Thr	85
	80	
	90	
Ala Thr Tyr Tyr Cys Ala Lys His	Tyr Tyr Tyr Gly Gly Ser Tyr	100
	95	
	105	
Ala Met Asp Tyr Trp Gly Gln Gly	Ser Ser Val Thr Val Ser Ser	115
	110	
	120	
<210> 41		
<211> 107		
<212> PRT		
<213> Artificial		
<220>		
<223>		
<400> 41		
Asp Ile Gln Met Thr Gln Ser Thr	Ser Ser Leu Ser Ala Ser Val	10
	5	
	15	
Gly Asp Arg Val Thr Ile Thr Cys	Arg Ala Ser Gln Asp Ile Ser	25
	20	

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

<210> 42
 <211> 107
 <212> PRT
 <213> Artificial
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 <400> 42

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

<210> 43
 <211> 107
 <212> PRT

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile	105	
	110	115
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln	120	
	125	130
Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln	135	
	140	145
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile	150	
	155	160
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys	165	
	170	175
Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr	180	
	185	190
Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val	195	
	200	205
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr	210	
	215	220
Gln Lys Ser Leu Ser Leu Ser Pro Gly	225	
	230	
<210> 45		
<211> 497		
<212> PRT		
<213> Artificial		
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Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu		
	5	10
Leu His Ala Ala Arg Pro Asp Ile Gln Met Thr Gln Ser Thr Ser	15	
	20	25
Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg	30	
	35	40
Ala Ser Gln Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys	45	
	50	55
Pro Asp Gly Thr Pro Lys Leu Leu Ile Tyr His Thr Ser Arg Leu	60	
	65	70
His Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr	75	
	80	85
Asp Tyr Thr Leu Thr Ile Ser Ser Leu Glu Gln Glu Asp Phe Ala	90	

	95	100
	105	
Thr Tyr Tyr Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly	110	115
	120	
Gly Gly Thr Arg Leu Glu Ile Lys Gly Ser Thr Ser Gly Ser Gly	125	130
	135	
Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Gln Val Gln Leu	140	145
	150	
Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Thr Leu Ser	155	160
	165	
Leu Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val	170	175
	180	
Ser Trp Ile Arg Gln Pro Pro Arg Lys Ala Leu Glu Trp Leu Ala	185	190
	195	
Leu Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Thr Ser Leu Lys	200	205
	210	
Ser Arg Leu Thr Ile Ile Lys Asp Thr Ser Lys Asn Gln Val Val	215	220
	225	
Leu Lys Met Thr Asn Met Gln Thr Asp Asp Thr Ala Val Tyr Tyr	230	235
	240	
Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr	245	250
	255	
Trp Gly Gln Gly Ser Ser Val Thr Val Ser Ser Leu Glu Lys Pro	260	265
	270	
Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile	275	280
	285	
Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala	290	295
	300	
Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp	305	310
	315	
Glu Phe Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys	320	325
	330	
Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg	335	340
	345	
Ser Lys Arg Ser Arg Gly Gly His Ser Asp Tyr Met Asn Met Thr	350	355
	360	
Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala		

	365	370
	375	
Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser	380	385
	390	
Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu	395	400
	405	
Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu	410	415
	420	
Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg	425	430
	435	
Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp	440	445
	450	
Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg	455	460
	465	
Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr	470	475
	480	
Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro	485	490
	495	
Pro Arg		
<210> 46		
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<400> 46		
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu	5	10
	15	
Leu His Ala Ala Arg Pro Asp Ile Gln Met Thr Gln Ser Pro Ser	20	25
	30	
Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg	35	40
	45	
Ala Ser Gln Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys	50	55
	60	
Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr His Thr Ser Ser Leu	65	70
	75	
Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr	80	85
	90	

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala	95	100
	105	
Thr Tyr Tyr Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly	110	115
	120	
Gly Gly Thr Arg Leu Glu Ile Lys Gly Ser Thr Ser Gly Ser Gly	125	130
	135	
Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Gln Val Gln Leu	140	145
	150	
Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln Thr Leu Ser	155	160
	165	
Leu Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val	170	175
	180	
Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu Trp Leu Ala	185	190
	195	
Leu Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Ser Thr Ser Leu Lys	200	205
	210	
Thr Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val Val	215	220
	225	
Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr	230	235
	240	
Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr	245	250
	255	
Trp Gly Gln Gly Ser Ser Val Thr Val Ser Ser Leu Glu Lys Pro	260	265
	270	
Thr Thr Thr Pro Ala Pro Arg Pro Thr Pro Ala Pro Thr Ile	275	280
	285	
Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala	290	295
	300	
Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp	305	310
	315	
Glu Phe Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys	320	325
	330	
Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg	335	340
	345	
Ser Lys Arg Ser Arg Gly Gly His Ser Asp Tyr Met Asn Met Thr	350	355
	360	

Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala	365	370
	375	
Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser	380	385
	390	
Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu	395	400
	405	
Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu	410	415
	420	
Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg	425	430
	435	
Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp	440	445
	450	
Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg	455	460
	465	
Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr	470	475
	480	
Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro	485	490
	495	
Pro Arg		
<210> 47		
<211> 497		
<212> PRT		
<213> Artificial		
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<223>		
<400> 47		
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu	5	10
	15	
Leu His Ala Ala Arg Pro Asp Ile Gln Met Thr Gln Ser Pro Ser	20	25
	30	
Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg	35	40
	45	
Ala Ser Gln Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys	50	55
	60	
Pro Gly Lys Ala Pro Arg Leu Leu Ile Tyr His Thr Ser Arg Leu	65	70
	75	
His Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr	80	85
	90	

Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala	95	100
	105	
Thr Tyr Tyr Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly	110	115
	120	
Gly Gly Thr Arg Leu Glu Ile Lys Gly Ser Thr Ser Gly Ser Gly	125	130
	135	
Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Gln Val Gln Leu	140	145
	150	
Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln Thr Leu Ser	155	160
	165	
Leu Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val	170	175
	180	
Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu Trp Leu Gly	185	190
	195	
Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ser Leu Lys	200	205
	210	
Thr Arg Leu Thr Ile Ser Lys Asp Asn Ser Lys Asn Gln Val Val	215	220
	225	
Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr	230	235
	240	
Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr	245	250
	255	
Trp Gly Gln Gly Ser Ser Val Thr Val Ser Ser Leu Glu Lys Pro	260	265
	270	
Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile	275	280
	285	
Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala	290	295
	300	
Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp	305	310
	315	
Glu Phe Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys	320	325
	330	
Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg	335	340
	345	
Ser Lys Arg Ser Arg Gly Gly His Ser Asp Tyr Met Asn Met Thr	350	355
	360	

Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala	365	370
	375	
Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser	380	385
	390	
Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu	395	400
	405	
Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu	410	415
	420	
Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg	425	430
	435	
Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp	440	445
	450	
Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg	455	460
	465	
Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr	470	475
	480	
Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro	485	490
	495	

Pro Arg

<210> 48

<211> 1494

<212> DNA

<213> Artificial

<220>

<223>

<400> 48

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cccgacatcc	agatgacca	gagcacaagc	tctctgagcg	ccagcgtggg	agacagagtg	120
accatcactt	gcagggccag	ccaggacatc	agcaagtacc	tgaattggta	ccagcagaag	180
cccgacggca	cacctaagct	gctgatctac	cacacaagca	gactgcacag	cggagtgcct	240
agcagattca	gcggcagcgg	aagcggaacc	gactacaccc	tgaccatcag	cagcctggag	300
caggaggact	tcgccaccta	ctactgccag	cagggcaaca	cactgcctta	caccttcggc	360
ggaggcacia	gactggagat	caagggcagc	acaagcggaa	gcggcaaacc	aggaagcgga	420
gaaggaagca	ccaagggaca	ggtgcagctg	caggaatcag	gaccaggact	ggtggctcct	480
tctcagaccc	tgagcctgac	ttgcaccgtg	tcaggagtgt	ccctgccaga	ttacggcgtg	540
tcttgatca	gacagcccc	cagaaaggcc	ctggagtggc	tggtctctgat	ttggggaagc	600
gagaccacct	actacaacac	cagcctgaag	agccggctga	ccatcatcaa	ggacaccagc	660
aagaaccagg	tggtgctgaa	gatgaccaac	atgcagaccg	acgacaccgc	cgtgtactat	720
tgcgccaagc	actactacta	cggcggaagc	tacgccatgg	actattgggg	ccagggaagc	780
agcgtgaccg	tgtctagcct	cgagaagccc	accacgacgc	cagcgccgcg	accaccaaca	840
ccggcgcca	ccatcgctc	gcagcccctg	tccctgcgcc	cagaggcgtg	ccggccagcg	900
gcggggggcg	cagtgcacac	gagggggctg	gacttcgcct	gcgacgaatt	cttctgggtg	960
ctggctgtgg	tgggtggcgt	gctggcctgc	tacagcctgc	tggtgacagt	ggccttcac	1020
atcttttggg	tgaggagcaa	gcggagcaga	ggcggccaca	gcgactacat	gaacatgact	1080

ccccgccgcc	ccggggccac	ccgcaagcat	taccagccct	atgccccacc	acgcgacttc	1140
gcagcctatc	gctccagagt	gaagttcagc	aggagcgag	acgccccgc	gtaccagcag	1200
ggccagaacc	agctctataa	cgagctcaat	ctaggacgaa	gagaggagta	cgatgttttg	1260
gacaagagac	gtggccggga	ccctgagatg	gggggaaagc	cgagaaggaa	gaaccctcag	1320
gaaggcctgt	acaatgaact	gcagaaaagat	aagatggcgg	aggcctacag	tgagattggg	1380
atgaaaggcg	agcgccggag	gggcaagggg	cacgatggcc	tttaccaggg	tctcagtaca	1440
gccaccaagg	acacctacga	cgcccttcac	atgcaggccc	tgccccctcg	ctaa	1494

<210> 49

<211> 1494

<212> DNA

<213> Artificial

<220>

<223>

<400> 49

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cccgacatcc	agatgaccca	gagcccttct	tctctgagcg	ccagcgtggg	agacagagtg	120
accatcactt	gcagggccag	ccaggacatc	agcaagtacc	tgaattggta	ccagcagaag	180
ccaggcaagg	cccctaagct	gctgatctac	cacacatcta	gcctgcagag	cggagtgcct	240
agcagattca	gcggcagcgg	aagcggaacc	gacttcaccc	tgaccatcag	cagcctgcag	300
ccagaggact	tcgccaccta	ctactgccag	cagggaaca	cactgcctta	caccttcggc	360
ggaggcacia	gactggagat	caagggcagc	acaagcggaa	gcggcaaacc	aggaagcgga	420
gaaggaaagca	ccaaggga	ggtgcagctg	caggaaagcg	gaccaggact	ggtgaagcct	480
tctcagaccc	tgagcctgac	ttgcaccgtg	tcaggagtgt	ccctgccaga	ttacggcgtg	540
tcttggatca	gacagcccc	aggaaaggcc	ctggagtggc	tggtctctgat	ttggggaagc	600
gagaccacct	actacagcac	cagcctgaag	acccggctga	caatcagcaa	ggacaccagc	660
aagaaccagg	tggtgctgac	catgaccaac	atggaccccg	tggacaccgc	cacctactat	720
tgcgccaagc	actactacta	cggcggaagc	tacgccatgg	actattgggg	ccagggaagc	780
agcgtgaccg	tgtctagcct	cgagaagccc	accacgacgc	cagcgccgcg	accaccaaca	840
ccggcgccca	ccatcgctgc	gcagcccctg	tccctgcgcc	cagaggcgtg	ccggccagcg	900
gcggggggcg	cagtgcacac	gagggggctg	gacttcgcct	gcgacgaatt	cttctgggtg	960
ctggtcgtgg	tgggtggcgt	gctggcctgc	tacagcctgc	tggtgacagt	ggccttcac	1020
atcttttggg	tgaggagcaa	gcggagcaga	ggcggccaca	gcgactacat	gaacatgact	1080
ccccgccgcc	ccggggccac	ccgcaagcat	taccagccct	atgccccacc	acgcgacttc	1140
gcagcctatc	gctccagagt	gaagttcagc	aggagcgag	acgccccgc	gtaccagcag	1200
ggccagaacc	agctctataa	cgagctcaat	ctaggacgaa	gagaggagta	cgatgttttg	1260
gacaagagac	gtggccggga	ccctgagatg	gggggaaagc	cgagaaggaa	gaaccctcag	1320
gaaggcctgt	acaatgaact	gcagaaaagat	aagatggcgg	aggcctacag	tgagattggg	1380
atgaaaggcg	agcgccggag	gggcaagggg	cacgatggcc	tttaccaggg	tctcagtaca	1440
gccaccaagg	acacctacga	cgcccttcac	atgcaggccc	tgccccctcg	ctaa	1494

<210> 50

<211> 1494

<212> DNA

<213> Artificial

<220>

<223>

<400> 50

atggctctgc	cagtgcagc	tctgctgctg	cctctggctc	tgctgctgca	cgagctaga	60
cccgacatcc	agatgaccca	gagcccttct	tctctgagcg	ccagcgtggg	agacagagtg	120
accatcactt	gcagggccag	ccaggacatc	agcaagtacc	tgaattggta	ccagcagaag	180
ccaggcaagg	cccctagact	gctgatctac	cacacaagca	gactgcacag	cggagtgcct	240
agcagattca	gcggcagcgg	aagcggaacc	gactacaccc	tgaccatcag	cagcctgcag	300
ccagaggact	tcgccaccta	ctactgccag	cagggaaca	cactgcctta	caccttcggc	360

ggaggcacia	gactggagat	caagggcagc	acaagcggaa	gcggcaaacc	aggaagcggg	420
gaaggaagca	ccaagggaca	ggtgcagctg	caggaaagcg	gaccaggact	ggtgaagcct	480
tctcagaccc	tgagcctgac	ttgcaccgtg	tcaggagtgt	ccctgccaga	ttacggcgtg	540
tcttggatca	gacagccccc	aggaaaggcc	ctggagtggc	tgggagtgat	ttggggaagc	600
gagaccacct	actacaacag	cagcctgaag	acccggctga	ccatcagcaa	ggacaacagc	660
aagaaccagg	tggtgctgac	catgaccaac	atggaccccg	tggacaccgc	cacctactat	720
tgcgccaagc	actactacta	cggcggaagc	tacgccatgg	actattgggg	ccagggaagc	780
agcgtgaccg	tgtctagcct	cgagaagccc	accacgacgc	cagcgccgcg	accaccaaca	840
ccggcgccca	ccatcgctc	gcagcccctg	tccctgcgcc	cagaggcgtg	ccggccagcg	900
gcggggggcg	cagtgcacac	gagggggctg	gacttcgcct	gcgacgaatt	cttctgggtg	960
ctggctcgtg	tggttggtg	gctggcctgc	tacagcctgc	tggtgacagt	ggccttcac	1020
atcttttggg	tgaggagcaa	gcggagcaga	ggcgccaca	gcgactacat	gaacatgact	1080
ccccgccgcc	ccggggccac	ccgcaagcat	taccagccct	atgccccacc	acgcgacttc	1140
gcagcctatc	gctccagagt	gaagttcagc	aggagcgcag	acgccccgcg	gtaccagcag	1200
ggccagaacc	agctctataa	cgagctcaat	ctaggacgaa	gagaggagta	cgatgttttg	1260
gacaagagac	gtggccggga	ccctgagatg	gggggaaagc	cgagaaggaa	gaaccctcag	1320
gaaggcctgt	acaatgaact	gcagaaagat	aagatggcgg	aggcctacag	tgagattggg	1380
atgaaaggcg	agcgccggag	gggcaagggg	cacgatggcc	tttaccaggg	tctcagtaca	1440
gccaccaagg	acacctacga	cgcccttcac	atgcaggccc	tgccccctcg	ctaa	1494

<210> 51

<211> 735

<212> DNA

<213> Artificial

<220>

<223>

<400> 51

gacatccaga	tgaccagag	cacaagctct	ctgagcgcca	gcgtgggaga	cagagtgacc	60
atcacttgca	gggccagcca	ggacatcagc	aagtacctga	attggtacca	gcagaagccc	120
gacggcacac	ctaagctgct	gatctaccac	acaagcagac	tgcacagcgg	agtgccctagc	180
agattcagcg	gcagcggaag	cggaaccgac	tacaccctga	ccatcagcag	cctggagcag	240
gaggacttcg	ccacctacta	ctgccagcag	ggcaacacac	tgcccttacac	cttcggcgga	300
ggcacaagac	tggagatcaa	gggcagcaca	agcggaagcg	gcaaaccagg	aagcggagaa	360
ggaagcacca	agggacaggt	gcagctgcag	gaatcaggac	caggactggt	ggctccttct	420
cagaccctga	gcctgacttg	caccgtgtca	ggagtgtccc	tgccagatta	cggcgtgtct	480
tggatcagac	agccccccag	aaaggccctg	gagtggctgg	ctctgatttg	gggaagcgag	540
accacctact	acaacaccag	cctgaagagc	cggctgacca	tcacaaagga	caccagcaag	600
aaccaggtgg	tgctgaagat	gaccaacatg	cagaccgacg	acaccgccgt	gtactattgc	660
gccaaagcact	actactacgg	cggaagctac	gccatggact	attggggcca	gggaagcagc	720
gtgaccgtgt	ctagc					735

<210> 52

<211> 735

<212> DNA

<213> Artificial

<220>

<223>

<400> 52

gacatccaga	tgaccagag	cccttcttct	ctgagcgcca	gcgtgggaga	cagagtgacc	60
atcacttgca	gggccagcca	ggacatcagc	aagtacctga	attggtacca	gcagaagcca	120
ggcaaggccc	ctaagctgct	gatctaccac	acatctagcc	tgcagagcgg	agtgccctagc	180
agattcagcg	gcagcggaag	cggaaccgac	ttcaccctga	ccatcagcag	cctgcagcca	240
gaggacttcg	ccacctacta	ctgccagcag	ggcaacacac	tgcccttacac	cttcggcgga	300
ggcacaagac	tggagatcaa	gggcagcaca	agcggaagcg	gcaaaccagg	aagcggagaa	360

ggaagcacca	agggacaggt	gcagctgcag	gaaagcggac	caggactggt	gaagccttct	420
cagaccctga	gcctgacttg	caccgtgtca	ggagtgtccc	tgccagatta	cggcgtgtct	480
tggatcagac	agccccagg	aaaggccctg	gagtggctgg	ctctgatttg	gggaagcgag	540
accacctact	acagcaccag	cctgaagacc	cggctgacaa	tcagcaagga	caccagcaag	600
aaccaggtgg	tgctgaccat	gaccaacatg	gaccccgtgg	acaccgccac	ctactattgc	660
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<211> 735

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<400> 53

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<212> DNA

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