

3108SEQPC1

SEQUENCE LISTING

<110> Halozyme, Inc.
 Maneval, Daniel C.
 Shepard, Harold Michael
 Thompson, Curtis B.

<120> Combination Therapy with an anti-Hyaluronan
 Agent and Therapeutic Agent

<130> 033320.03108.W001/3108PC

<140> Not Yet Assigned

<141> Herewith

<150> US 61/686,429

<151> 2012-04-04

<150> US 61/714,719

<151> 2012-10-16

<160> 213

<170> FastSEQ for windows version 4.0

<210> 1

<211> 509

<212> PRT

<213> Homo sapiens

<220>

<223> precursor human PH20

<400> 1

```

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

```

3108SEQPC1

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

<210> 2
 <211> 474
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Mature PH20

<400> 2

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

3108SEQPC1

Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
 210 215 220
 Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
 225 230 235 240
 Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
 245 250 255
 Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
 260 265 270
 Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
 275 280 285
 Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
 290 295 300
 Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
 305 310 315 320
 Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
 325 330 335
 Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
 340 345 350
 Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
 355 360 365
 Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
 370 375 380
 Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
 385 390 395 400
 Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
 405 410 415
 Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala
 420 425 430
 Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile Phe Tyr Asn
 435 440 445
 Ala Ser Pro Ser Thr Leu Ser Ala Thr Met Phe Ile Val Ser Ile Leu
 450 455 460
 Phe Leu Ile Ile Ser Ser Val Ala Ser Leu
 465 470

<210> 3

<211> 482

<212> PRT

<213> Homo sapiens

<220>

<223> precursor PH20 1-482

<400> 3

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

3108SEQPC1

Glu	Lys	Ala	Gly	Lys	Asp	Phe	Leu	Val	Glu	Thr	Ile	Lys	Leu	Gly	Lys
		180					185					190			
Leu	Leu	195	Arg	Pro	Asn	His	Leu	Trp	Gly	Tyr	Tyr	Leu	Phe	Pro	Asp
	210						215					220			Cys
Tyr	Asn	His	His	Tyr	Lys	Lys	Pro	Gly	Tyr	Asn	Gly	Ser	Cys	Phe	Asn
	225				230					235				240	
Val	Glu	Ile	Lys	Arg	Asn	Asp	Asp	Leu	Ser	Trp	Leu	Trp	Asn	Glu	Ser
			245						250				255		
Thr	Ala	Leu	Tyr	Pro	Ser	Ile	Tyr	Leu	Asn	Thr	Gln	Gln	Ser	Pro	Val
		260						265					270		
Ala	Ala	Thr	Leu	Tyr	Val	Arg	Asn	Arg	Val	Arg	Glu	Ala	Ile	Arg	Val
		275					280					285			
Ser	Lys	Ile	Pro	Asp	Ala	Lys	Ser	Pro	Leu	Pro	Val	Phe	Ala	Tyr	Thr
	290					295					300				
Arg	Ile	Val	Phe	Thr	Asp	Gln	Val	Leu	Lys	Phe	Leu	Ser	Gln	Asp	Glu
	305				310					315				320	
Leu	Val	Tyr	Thr	Phe	Gly	Glu	Thr	Val	Ala	Leu	Gly	Ala	Ser	Gly	Ile
				325					330					335	
Val	Ile	Trp	Gly	Thr	Leu	Ser	Ile	Met	Arg	Ser	Met	Lys	Ser	Cys	Leu
		340						345					350		
Leu	Leu	Asp	Asn	Tyr	Met	Glu	Thr	Ile	Leu	Asn	Pro	Tyr	Ile	Ile	Asn
		355					360					365			
Val	Thr	Leu	Ala	Ala	Lys	Met	Cys	Ser	Gln	Val	Leu	Cys	Gln	Glu	Gln
	370					375					380				
Gly	Val	Cys	Ile	Arg	Lys	Asn	Trp	Asn	Ser	Ser	Asp	Tyr	Leu	His	Leu
	385				390					395				400	
Asn	Pro	Asp	Asn	Phe	Ala	Ile	Gln	Leu	Glu	Lys	Gly	Gly	Lys	Phe	Thr
				405					410					415	
Val	Arg	Gly	Lys	Pro	Thr	Leu	Glu	Asp	Leu	Glu	Gln	Phe	Ser	Glu	Lys
			420					425				430			
Phe	Tyr	Cys	Ser	Cys	Tyr	Ser	Thr	Leu	Ser	Cys	Lys	Glu	Lys	Ala	Asp
		435					440					445			
Val	Lys	Asp	Thr	Asp	Ala	Val	Asp	Val	Cys	Ile	Ala	Asp	Gly	Val	Cys
	450					455					460				
Ile	Asp	Ala	Phe	Leu	Lys	Pro	Pro	Met	Glu	Thr	Glu	Glu	Pro	Gln	Ile
	465				470					475				480	
Phe	Tyr														

<210> 4

<211> 447

<212> PRT

<213> Homo sapiens

<220>

<223> PH20 36-482

<400> 4

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

3108SEQPC1

Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
 145 150 155 160
 Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
 165 170 175
 Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
 180 185 190
 His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
 195 200 205
 Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
 210 215 220
 Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
 225 230 235 240
 Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
 245 250 255
 Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
 260 265 270
 Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
 275 280 285
 Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
 290 295 300
 Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
 305 310 315 320
 Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
 325 330 335
 Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
 340 345 350
 Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
 355 360 365
 Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
 370 375 380
 Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
 385 390 395 400
 Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
 405 410 415
 Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala
 420 425 430
 Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile Phe Tyr
 435 440 445

<210> 5
 <211> 446
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PH20 36-481

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

3108SEQPC1

145	Gly	Lys	Asp	Phe	Leu	Val	Glu	Thr	Ile	Lys	Leu	Gly	Lys	Leu	Leu	Arg	160
					165					170						175	
Pro	Asn	His	Leu	Trp	Gly	Tyr	Tyr	Leu	Phe	Pro	Asp	Cys	Tyr	Asn	His		
			180					185					190				
His	Tyr	Lys	Lys	Pro	Gly	Tyr	Asn	Gly	Ser	Cys	Phe	Asn	Val	Glu	Ile		
		195					200					205					
Lys	Arg	Asn	Asp	Asp	Leu	Ser	Trp	Leu	Trp	Asn	Glu	Ser	Thr	Ala	Leu		
	210					215				220							
Tyr	Pro	Ser	Ile	Tyr	Leu	Asn	Thr	Gln	Gln	Ser	Pro	Val	Ala	Ala	Thr		
225					230					235					240		
Leu	Tyr	Val	Arg	Asn	Arg	Val	Arg	Glu	Ala	Ile	Arg	Val	Ser	Lys	Ile		
				245					250					255			
Pro	Asp	Ala	Lys	Ser	Pro	Leu	Pro	Val	Phe	Ala	Tyr	Thr	Arg	Ile	Val		
			260					265					270				
Phe	Thr	Asp	Gln	Val	Leu	Lys	Phe	Leu	Ser	Gln	Asp	Glu	Leu	Val	Tyr		
		275					280					285					
Thr	Phe	Gly	Glu	Thr	Val	Ala	Leu	Gly	Ala	Ser	Gly	Ile	Val	Ile	Trp		
	290					295					300						
Gly	Thr	Leu	Ser	Ile	Met	Arg	Ser	Met	Lys	Ser	Cys	Leu	Leu	Leu	Asp		
305					310					315					320		
Asn	Tyr	Met	Glu	Thr	Ile	Leu	Asn	Pro	Tyr	Ile	Ile	Asn	Val	Thr	Leu		
				325				330						335			
Ala	Ala	Lys	Met	Cys	Ser	Gln	Val	Leu	Cys	Gln	Glu	Gln	Gly	Val	Cys		
		340						345					350				
Ile	Arg	Lys	Asn	Trp	Asn	Ser	Ser	Asp	Tyr	Leu	His	Leu	Asn	Pro	Asp		
		355					360					365					
Asn	Phe	Ala	Ile	Gln	Leu	Glu	Lys	Gly	Gly	Lys	Phe	Thr	Val	Arg	Gly		
	370					375					380						
Lys	Pro	Thr	Leu	Glu	Asp	Leu	Glu	Gln	Phe	Ser	Glu	Lys	Phe	Tyr	Cys		
385					390					395					400		
Ser	Cys	Tyr	Ser	Thr	Leu	Ser	Cys	Lys	Glu	Lys	Ala	Asp	Val	Lys	Asp		
				405					410					415			
Thr	Asp	Ala	Val	Asp	Val	Cys	Ile	Ala	Asp	Gly	Val	Cys	Ile	Asp	Ala		
			420					425					430				
Phe	Leu	Lys	Pro	Pro	Met	Glu	Thr	Glu	Glu	Pro	Gln	Ile	Phe				
		435					440					445					

<210> 6
 <211> 445
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PH20 36-480

<400> 6

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

3108SEQPC1

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

<210> 7
 <211> 444
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PH20 36-479

<400> 7
 Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1 5 10 15
 Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
 20 25 30
 Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
 35 40 45
 Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
 50 55 60
 Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
 65 70 75 80
 Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
 85 90 95
 Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
 100 105 110
 Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
 115 120 125
 Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
 130 135 140
 Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
 145 150 155 160
 Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg

3108SEQPC1

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

<210> 8
 <211> 443
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PH20 36-478

<400> 8

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

3108SEQPC1

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

<210> 9

<211> 442

<212> PRT

<213> Homo sapiens

<220>

<223> PH20 36-477

<400> 9

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

3108SEQPC1

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

<210> 10

<211> 450

<212> PRT

<213> Bos taurus

<220>

<223> hyaluronidase

<400> 10

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

3108SEQPC1

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

<210> 11
 <211> 553
 <212> PRT
 <213> Bos taurus

<220>
 <223> Precursor cow PH20

<400> 11
 Met Arg Met Leu Arg Arg His His Ile Ser Phe Arg Ser Phe Ala Gly
 1 5 10 15
 Ser Ser Gly Thr Pro Gln Ala Val Phe Thr Phe Leu Leu Leu Pro Cys
 20 25 30
 Cys Leu Ala Leu Asp Phe Arg Ala Pro Pro Leu Ile Ser Asn Thr Ser
 35 40 45
 Phe Leu Trp Ala Trp Asn Ala Pro Val Glu Arg Cys Val Asn Arg Arg
 50 55 60
 Phe Gln Leu Pro Pro Asp Leu Arg Leu Phe Ser Val Lys Gly Ser Pro
 65 70 75 80
 Gln Lys Ser Ala Thr Gly Gln Phe Ile Thr Leu Phe Tyr Ala Asp Arg
 85 90 95
 Leu Gly Tyr Tyr Pro His Ile Asp Glu Lys Thr Gly Lys Thr Val Phe
 100 105 110
 Gly Gly Ile Pro Gln Leu Gly Asn Leu Lys Ser His Met Glu Lys Ala
 115 120 125
 Lys Asn Asp Ile Ala Tyr Tyr Ile Pro Asn Asp Ser Val Gly Leu Ala
 130 135 140
 Val Ile Asp Trp Glu Asn Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys
 145 150 155 160
 Pro Lys Asp Val Tyr Arg Asp Glu Ser Val Glu Leu Val Leu Gln Lys
 165 170 175
 Asn Pro Gln Leu Ser Phe Pro Glu Ala Ser Lys Ile Ala Lys Val Asp

3108SEQPC1

Phe	Glu	Thr	180													
		195	Ala	Gly	Lys	Ser	Phe	Met	Gln	Glu	Thr	Leu	Lys	Leu	Gly	
Lys	Leu	Leu	Arg	Pro	Asn	His	200	Trp	Gly	Tyr	Tyr	205	Phe	Pro	Asp	
210						215	Leu					Leu				
Cys	Tyr	Asn	His	Asn	His	230	Gln	Pro	Thr	Tyr	235	Asn	Gly	Asn	Cys	Pro
225																240
Asp	Val	Glu	Lys	Arg	Arg	Asn	Asp	Asp	Leu	Glu	Trp	Leu	Trp	Lys	Glu	
				245					250					255		
Ser	Thr	Ala	Leu	Phe	Pro	Ser	Val	Tyr	Leu	Asn	Ile	Arg	Leu	Lys	Ser	
			260						265					270		
Thr	Gln	Asn	Ala	Ala	Leu	Tyr	Val	Arg	Asn	Arg	Val	Gln	Glu	Ala	Ile	
			275						280					285		
Arg	Leu	Ser	Lys	Ile	Ala	Ser	Val	Glu	Ser	Pro	Leu	Pro	Val	Phe	Val	
						295					300					
Tyr	Ala	Arg	Pro	Val	Phe	Thr	Asp	Gly	Ser	Ser	Thr	Tyr	Leu	Ser	Gln	
305					310					315					320	
Gly	Asp	Leu	Val	Asn	Ser	Val	Gly	Glu	Ile	Val	Ser	Leu	Gly	Ala	Ser	
				325					330					335		
Gly	Ile	Ile	Met	Trp	Gly	Ser	Leu	Asn	Leu	Ser	Leu	Ser	Met	Gln	Ser	
			340						345					350		
Cys	Met	Asn	Leu	Gly	Thr	Tyr	Leu	Asn	Thr	Thr	Leu	Asn	Pro	Tyr	Ile	
			355						360				365			
Ile	Asn	Val	Thr	Leu	Ala	Ala	Lys	Met	Cys	Ser	Gln	Val	Leu	Cys	His	
						375					380					
Asn	Glu	Gly	Val	Cys	Thr	Arg	Lys	His	Trp	Asn	Ser	Ser	Asp	Tyr	Leu	
385					390					395					400	
His	Leu	Asn	Pro	Met	Asn	Phe	Ala	Ile	Gln	Thr	Gly	Glu	Gly	Gly	Lys	
				405					410					415		
Tyr	Thr	Val	Pro	Gly	Thr	Val	Thr	Leu	Glu	Asp	Leu	Gln	Lys	Phe	Ser	
			420						425				430			
Asp	Thr	Phe	Tyr	Cys	Ser	Cys	Tyr	Ala	Asn	Ile	His	Cys	Lys	Lys	Arg	
			435					440				445				
Val	Asp	Ile	Lys	Asn	Val	His	Ser	Val	Asn	Val	Cys	Met	Ala	Glu	Asp	
						455					460					
Ile	Cys	Ile	Asp	Ser	Pro	Val	Lys	Leu	Gln	Pro	Ser	Asp	His	Ser	Ser	
465					470					475					480	
Ser	Gln	Glu	Ala	Ser	Thr	Thr	Thr	Phe	Ser	Ser	Ile	Ser	Pro	Ser	Thr	
				485					490					495		
Thr	Thr	Ala	Thr	Val	Ser	Pro	Cys	Thr	Pro	Glu	Lys	His	Ser	Pro	Glu	
			500					505					510			
Cys	Leu	Lys	Val	Arg	Cys	Ser	Glu	Val	Ile	Pro	Asn	Val	Thr	Gln	Lys	
							520					525				
Ala	Cys	Gln	Ser	Val	Lys	Leu	Lys	Asn	I							

<210> 12

<211> 331

<212> PRT

<213> vespuła vulgaris

 $\langle 220 \rangle$

<223> hyaluronidase A

<400> 12

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

3108SEQPC1

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

<210> 13

<211> 340

<212> PRT

<213> *Vesputula vulgaris*

<220>

<223> hyaluronidase B

<400> 13

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

3108SEQPC1

195 200 205
 Lys Met Ser Trp Leu Phe Asn Asn Gln Asn Val Leu Leu Pro Ser Ile
 210 215 220
 Tyr Leu Lys Asn Val Leu Lys Pro Asp Glu Lys Ile His Leu Val Gln
 225 230 235 240
 Glu Arg Leu Lys Glu Ala Ile Arg Ile Ser Lys Asn Phe Lys His Leu
 245 250 255
 Pro Lys Val Leu Pro Tyr Trp Trp Tyr Thr Tyr Gln Asp Lys Glu Ser
 260 265 270
 Ile Phe Leu Thr Glu Ala Asp Val Lys Asn Thr Phe Lys Glu Ile Leu
 275 280 285
 Thr Asn Gly Ala Asp Gly Ile Ile Ile Trp Gly Val Ser Tyr Glu Leu
 290 295 300
 Thr Asp Arg Lys Arg Cys Glu Lys Leu Lys Glu Tyr Leu Met Lys Ile
 305 310 315 320
 Leu Gly Pro Ile Ala Phe Lys Val Thr Lys Ala Val Lys Glu Asn Thr
 325 330 335
 Pro Leu Asn Phe
 340

<210> 14
 <211> 382
 <212> PRT
 <213> Apis mellifera

<220>
 <223> hyaluronidase

<400> 14
 Met Ser Arg Pro Leu Val Ile Thr Glu Gly Met Met Ile Gly Val Leu
 1 5 10 15
 Leu Met Leu Ala Pro Ile Asn Ala Leu Leu Gly Phe Val Gln Ser
 20 25 30
 Thr Pro Asp Asn Asn Lys Thr Val Arg Glu Phe Asn Val Tyr Trp Asn
 35 40 45
 Val Pro Thr Phe Met Cys His Lys Tyr Gly Leu Arg Phe Glu Glu Val
 50 55 60
 Ser Glu Lys Tyr Gly Ile Leu Gln Asn Trp Met Asp Lys Phe Arg Gly
 65 70 75 80
 Glu Glu Ile Ala Ile Leu Tyr Asp Pro Gly Met Phe Pro Ala Leu Leu
 85 90 95
 Lys Asp Pro Asn Gly Asn Val Val Ala Arg Asn Gly Gly Val Pro Gln
 100 105 110
 Leu Gly Asn Leu Thr Lys His Leu Gln Val Phe Arg Asp His Leu Ile
 115 120 125
 Asn Gln Ile Pro Asp Lys Ser Phe Pro Gly Val Gly Val Ile Asp Phe
 130 135 140
 Glu Ser Trp Arg Pro Ile Phe Arg Gln Asn Trp Ala Ser Leu Gln Pro
 145 150 155 160
 Tyr Lys Lys Leu Ser Val Glu Val Val Arg Arg Glu His Pro Phe Trp
 165 170 175
 Asp Asp Gln Arg Val Glu Gln Glu Ala Lys Arg Arg Phe Glu Lys Tyr
 180 185 190
 Gly Gln Leu Phe Met Glu Glu Thr Leu Lys Ala Ala Lys Arg Met Arg
 195 200 205
 Pro Ala Ala Asn Trp Gly Tyr Tyr Ala Tyr Pro Tyr Cys Tyr Asn Leu
 210 215 220
 Thr Pro Asn Gln Pro Ser Ala Gln Cys Glu Ala Thr Thr Met Gln Glu
 225 230 235 240
 Asn Asp Lys Met Ser Trp Leu Phe Glu Ser Glu Asp Val Leu Leu Pro
 245 250 255
 Ser Val Tyr Leu Arg Trp Asn Leu Thr Ser Gly Glu Arg Val Gly Leu
 260 265 270
 Val Gly Gly Arg Val Lys Glu Ala Leu Arg Ile Ala Arg Gln Met Thr
 275 280 285
 Thr Ser Arg Lys Lys Val Leu Pro Tyr Tyr Trp Tyr Lys Tyr Gln Asp
 290 295 300

3108SEQPC1
 Arg Arg Asp Thr Asp Leu Ser Arg Ala Asp Leu Glu Ala Thr Leu Arg
 305 310 315 320
 Lys Ile Thr Asp Leu Gly Ala Asp Gly Phe Ile Ile Trp Gly Ser Ser
 325 330 335
 Asp Asp Ile Asn Thr Lys Ala Lys Cys Leu Gln Phe Arg Glu Tyr Leu
 340 345 350
 Asn Asn Glu Leu Gly Pro Ala Val Lys Arg Ile Ala Leu Asn Asn Asn
 355 360 365
 Ala Asn Asp Arg Leu Thr Val Asp Val Ser Val Asp Gln Val
 370 375 380

<210> 15
 <211> 331
 <212> PRT
 <213> Dolichovespula maculata

<220>
 <223> hyaluronidase

<400> 15
 Ser Glu Arg Pro Lys Arg Val Phe Asn Ile Tyr Trp Asn Val Pro Thr
 1 5 10 15
 Phe Met Cys His Gln Tyr Gly Leu Tyr Phe Asp Glu Val Thr Asn Phe
 20 25 30
 Asn Ile Lys His Asn Ser Lys Asp Phe Gln Gly Asp Lys Ile Ser
 35 40 45
 Ile Phe Tyr Asp Pro Gly Glu Phe Pro Ala Leu Leu Pro Leu Lys Glu
 50 55 60
 Gly Asn Tyr Lys Ile Arg Asn Gly Gly Val Pro Gln Glu Gly Asn Ile
 65 70 75 80
 Thr Ile His Leu Gln Arg Phe Ile Glu Asn Leu Asp Lys Thr Tyr Pro
 85 90 95
 Asn Arg Asn Phe Asn Gly Ile Gly Val Ile Asp Phe Glu Arg Trp Arg
 100 105 110
 Pro Ile Phe Arg Gln Asn Trp Gly Asn Met Met Ile His Lys Lys Phe
 115 120 125
 Ser Ile Asp Leu Val Arg Asn Glu His Pro Phe Trp Asp Lys Lys Met
 130 135 140
 Ile Glu Leu Glu Ala Ser Lys Arg Phe Glu Lys Tyr Ala Arg Leu Phe
 145 150 155 160
 Met Glu Glu Thr Leu Lys Leu Ala Lys Lys Thr Arg Lys Gln Ala Asp
 165 170 175
 Trp Gly Tyr Tyr Gly Tyr Pro Tyr Cys Phe Asn Met Ser Pro Asn Asn
 180 185 190
 Leu Val Pro Asp Cys Asp Ala Thr Ala Met Leu Glu Asn Asp Lys Met
 195 200 205
 Ser Trp Leu Phe Asn Asn Gln Asn Val Leu Leu Pro Ser Val Tyr Ile
 210 215 220
 Arg His Glu Leu Thr Pro Asp Gln Arg Val Gly Leu Val Gln Gly Arg
 225 230 235 240
 Val Lys Glu Ala Val Arg Ile Ser Asn Asn Leu Lys His Ser Pro Lys
 245 250 255
 Val Leu Ser Tyr Trp Trp Tyr Val Tyr Gln Asp Asp Thr Asn Thr Phe
 260 265 270
 Leu Thr Glu Thr Asp Val Lys Lys Thr Phe Gln Glu Ile Ala Ile Asn
 275 280 285
 Gly Gly Asp Gly Ile Ile Ile Trp Gly Ser Ser Ser Asp Val Asn Ser
 290 295 300
 Leu Ser Lys Cys Lys Arg Leu Arg Glu Tyr Leu Leu Thr Val Leu Gly
 305 310 315 320
 Pro Ile Thr Val Asn Val Thr Glu Thr Val Asn
 325 330

<210> 16
 <211> 367
 <212> PRT

<213> Polistes annularis

<220>

<223> hyaluronidase

<400> 16

```

Tyr Val Ser Leu Ser Pro Asp Ser Val Phe Asn Ile Ile Thr Asp Asp
1      5      10      15
Ile Ser His Gln Ile Leu Ser Arg Ser Asn Cys Glu Arg Ser Lys Arg
20      25      30
Pro Lys Arg Val Phe Ser Ile Tyr Trp Asn Val Pro Thr Phe Met Cys
35      40      45
His Gln Tyr Gly Met Asn Phe Asp Glu Val Thr Asp Phe Asn Ile Lys
50      55      60
His Asn Ser Lys Asp Asn Phe Arg Gly Glu Thr Ile Ser Ile Tyr Tyr
65      70      75      80
Asp Pro Gly Lys Phe Pro Ala Leu Met Pro Leu Lys Asn Gly Asn Tyr
85      90      95
Glu Glu Arg Asn Gly Gly Val Pro Gln Arg Gly Asn Ile Thr Ile His
100     105     110
Leu Gln Gln Phe Asn Glu Asp Leu Asp Lys Met Thr Pro Asp Lys Asn
115     120     125
Phe Gly Gly Ile Gly Val Ile Asp Phe Glu Arg Trp Lys Pro Ile Phe
130     135     140
Arg Gln Asn Trp Gly Asn Thr Glu Ile His Lys Lys Tyr Ser Ile Glu
145     150     155     160
Leu Val Arg Lys Glu His Pro Lys Trp Ser Glu Ser Met Ile Glu Ala
165     170     175
Glu Ala Thr Lys Lys Phe Glu Lys Tyr Ala Arg Tyr Phe Met Glu Glu
180     185     190
Thr Leu Lys Leu Ala Lys Lys Thr Arg Lys Arg Ala Lys Trp Gly Tyr
195     200     205
Tyr Gly Phe Pro Tyr Cys Tyr Asn Val Thr Pro Asn Asn Pro Gly Pro
210     215     220
Asp Cys Asp Ala Lys Ala Thr Ile Glu Asn Asp Arg Leu Ser Trp Met
225     230     235     240
Tyr Asn Asn Gln Glu Ile Leu Phe Pro Ser Val Tyr Val Arg His Glu
245     250     255
Gln Lys Pro Glu Glu Arg Val Tyr Leu Val Gln Gly Arg Ile Lys Glu
260     265     270
Ala Val Arg Ile Ser Asn Asn Leu Glu His Ser Pro Ser Val Leu Ala
275     280     285
Tyr Trp Trp Tyr Val Tyr Gln Asp Lys Met Asp Ile Tyr Leu Ser Glu
290     295     300
Thr Asp Val Glu Lys Thr Phe Gln Glu Ile Val Thr Asn Gly Gly Asp
305     310     315     320
Gly Ile Ile Ile Trp Gly Ser Ser Ser Asp Val Asn Ser Leu Ser Lys
325     330     335
Cys Lys Arg Leu Arg Glu Tyr Leu Leu Asn Thr Leu Gly Pro Phe Ala
340     345     350
Val Asn Val Thr Glu Thr Val Asn Gly Arg Ser Ser Leu Asn Phe
355     360     365

```

<210> 17

<211> 462

<212> PRT

<213> Mus musculus

<220>

<223> hyaluronidase

<400> 17

```

Met Leu Gly Leu Thr Gln His Ala Gln Lys Val Trp Arg Met Lys Pro
1      5      10      15
Phe Ser Pro Glu Val Ser Pro Gly Ser Ser Pro Ala Thr Ala Gly His
20      25      30
Leu Leu Arg Ile Ser Thr Leu Phe Leu Thr Leu Leu Glu Leu Ala Gln

```

3108SEQPC1

```

      35              40              45
Val Cys Arg Gly Ser Val Val Ser Asn Arg Pro Phe Ile Thr Val Trp
  50      55      60
Asn Gly Asp Thr His Trp Cys Leu Thr Glu Tyr Gly Val Asp Val Asp
  65      70      75      80
Val Ser Val Phe Asp Val Val Ala Asn Lys Glu Gln Ser Phe Gln Gly
      85      90      95
Ser Asn Met Thr Ile Phe Tyr Arg Glu Leu Gly Thr Tyr Pro Tyr
      100      105      110
Tyr Thr Pro Thr Gly Glu Pro Val Phe Gly Gly Leu Pro Gln Asn Ala
      115      120      125
Ser Leu Val Thr His Leu Ala His Thr Phe Gln Asp Ile Lys Ala Ala
      130      135      140
Met Pro Glu Pro Asp Phe Ser Gly Leu Ala Val Ile Asp Trp Glu Ala
      145      150      155      160
Trp Arg Pro Arg Trp Ala Phe Asn Trp Asp Ser Lys Asp Ile Tyr Arg
      165      170      175
Gln Arg Ser Met Glu Leu Val Gln Ala Glu His Pro Asp Trp Pro Glu
      180      185      190
Thr Leu Val Glu Ala Ala Ala Lys Asn Gln Phe Gln Glu Ala Ala Glu
      195      200      205
Ala Trp Met Ala Gly Thr Leu Gln Leu Gly Gln Val Leu Arg Pro Arg
      210      215      220
Gly Leu Trp Gly Tyr Tyr Gly Phe Pro Asp Cys Tyr Asn Asn Asp Phe
      225      230      235      240
Leu Ser Leu Asn Tyr Thr Gly Gln Cys Pro Val Phe Val Arg Asp Gln
      245      250      255
Asn Asp Gln Leu Gly Trp Leu Trp Asn Gln Ser Tyr Ala Leu Tyr Pro
      260      265      270
Ser Ile Tyr Leu Pro Ala Ala Leu Met Gly Thr Gly Lys Ser Gln Met
      275      280      285
Tyr Val Arg His Arg Val Gln Glu Ala Leu Arg Val Ala Ile Val Ser
      290      295      300
Arg Asp Pro His Val Pro Val Met Pro Tyr Val Gln Ile Phe Tyr Glu
      305      310      315      320
Met Thr Asp Tyr Leu Leu Pro Leu Glu Glu Leu Glu His Ser Leu Gly
      325      330      335
Glu Ser Ala Ala Gln Gly Val Ala Gly Ala Val Leu Trp Leu Ser Ser
      340      345      350
Asp Lys Thr Ser Thr Lys Glu Ser Cys Gln Ala Ile Lys Ala Tyr Met
      355      360      365
Asp Ser Thr Leu Gly Pro Phe Ile Val Asn Val Thr Ser Ala Ala Leu
      370      375      380
Leu Cys Ser Glu Ala Leu Cys Ser Gly His Gly Arg Cys Val Arg His
      385      390      395      400
Pro Ser Tyr Pro Glu Ala Leu Leu Thr Leu Asn Pro Ala Ser Phe Ser
      405      410      415
Ile Glu Leu Thr His Asp Gly Arg Pro Pro Ser Leu Lys Gly Thr Leu
      420      425      430
Ser Leu Lys Asp Arg Ala Gln Met Ala Met Lys Phe Arg Cys Arg Cys
      435      440      445
Tyr Arg Gly Trp Arg Gly Lys Trp Cys Asp Lys Arg Gly Met
      450      455      460

```

<210> 18

<211> 473

<212> PRT

<213> Mus musculus

<220>

<223> Hyaluronidase 2

<400> 18

```

Met Arg Ala Gly Leu Gly Pro Ile Ile Thr Leu Ala Leu Val Leu Glu
  1      5      10      15
Val Ala Trp Ala Gly Glu Leu Lys Pro Thr Ala Pro Pro Ile Phe Thr
      20      25      30

```

3108SEQPC1

Gly Arg Pro Phe Val Val Ala Trp Asn Val Pro Thr Gln Glu Cys Ala
 35 40 45
 Pro Arg His Lys Val Pro Leu Asp Leu Arg Ala Phe Asp Val Lys Ala
 50 55 60
 Thr Pro Asn Glu Gly Phe Phe Asn Gln Asn Ile Thr Thr Phe Tyr Tyr
 65 70 75 80
 Asp Arg Leu Gly Leu Tyr Pro Arg Phe Asp Ala Ala Gly Thr Ser Val
 85 90 95
 His Gly Gly Val Pro Gln Asn Gly Ser Leu Cys Ala His Leu Pro Met
 100 105 110
 Leu Lys Glu Ser Val Glu Arg Tyr Ile Gln Thr Gln Glu Pro Gly Gly
 115 120 125
 Leu Ala Val Ile Asp Trp Glu Trp Arg Pro Val Trp Val Arg Asn
 130 135 140
 Trp Gln Glu Lys Asp Val Tyr Arg Gln Ser Ser Arg Gln Leu Val Ala
 145 150 155 160
 Ser Arg His Pro Asp Trp Pro Ser Asp Arg Val Met Lys Gln Ala Gln
 165 170 175
 Tyr Glu Phe Glu Phe Ala Ala Arg Gln Phe Met Leu Asn Thr Leu Arg
 180 185 190
 Tyr Val Lys Ala Val Arg Pro Gln His Leu Trp Gly Phe Tyr Leu Phe
 195 200 205
 Pro Asp Cys Tyr Asn His Asp Tyr Val Gln Asn Trp Glu Ser Tyr Thr
 210 215 220
 Gly Arg Cys Pro Asp Val Glu Val Ala Arg Asn Asp Gln Leu Ala Trp
 225 230 235 240
 Leu Trp Ala Glu Ser Thr Ala Leu Phe Pro Ser Val Tyr Leu Asp Glu
 245 250 255
 Thr Leu Ala Ser Ser Val His Ser Arg Asn Phe Val Ser Phe Arg Val
 260 265 270
 Arg Glu Ala Leu Arg Val Ala His Thr His His Ala Asn His Ala Leu
 275 280 285
 Pro Val Tyr Val Phe Thr Arg Pro Thr Tyr Thr Arg Gly Leu Thr Gly
 290 295 300
 Leu Ser Gln Val Asp Leu Ile Ser Thr Ile Gly Glu Ser Ala Ala Leu
 305 310 315 320
 Gly Ser Ala Gly Val Ile Phe Trp Gly Asp Ser Glu Asp Ala Ser Ser
 325 330 335
 Met Glu Thr Cys Gln Tyr Leu Lys Asn Tyr Leu Thr Gln Leu Leu Val
 340 345 350
 Pro Tyr Ile Val Asn Val Ser Trp Ala Thr Gln Tyr Cys Ser Trp Thr
 355 360 365
 Gln Cys His Gly His Gly Arg Cys Val Arg Arg Asn Pro Ser Ala Asn
 370 375 380
 Thr Phe Leu His Leu Asn Ala Ser Ser Phe Arg Leu Val Pro Gly His
 385 390 395 400
 Thr Pro Ser Glu Pro Gln Leu Arg Pro Glu Gly Gln Leu Ser Glu Ala
 405 410 415
 Asp Leu Asn Tyr Leu Gln Lys His Phe Arg Cys Gln Cys Tyr Leu Gly
 420 425 430
 Trp Gly Gly Glu Gln Cys Gln Arg Asn Tyr Lys Gly Ala Ala Gly Asn
 435 440 445
 Ala Ser Arg Ala Trp Ala Gly Ser His Leu Thr Ser Leu Leu Gly Leu
 450 455 460
 Val Ala Val Ala Leu Thr Trp Thr Leu
 465 470

<210> 19

<211> 412

<212> PRT

<213> Mus musculus

<220>

<223> hyaluronidase 3

<400> 19

Met Ile Met His Leu Gly Leu Met Met Val Val Gly Leu Thr Leu Cys
 Page 18

3108SEQPC1

1	5	10	15
Leu Met His Gly Gln Ala Leu Leu Gln Val Pro Glu His Pro Phe Ser			
20	25	30	35
Val Val Trp Asn Val Pro Ser Ala Arg Cys Lys Ala His Phe Gly Val			
40	45	50	55
His Leu Pro Leu Asp Ala Leu Gly Ile Val Ala Asn His Gly Gln His			
60	65	70	75
Phe His Gly Gln Asn Ile Ser Ile Phe Tyr Lys Asn Gln Phe Gly Leu			
80	85	90	95
Tyr Pro Tyr Phe Gly Pro Arg Gly Thr Ala His Asn Gly Gly Ile Pro			
100	105	110	115
Gln Ala Val Ser Leu Asp His His Leu Ala Arg Ala Ala His Gln Ile			
120	125	130	135
Leu His Ser Leu Gly Ser Ser Phe Ala Gly Leu Ala Val Leu Asp Trp			
140	145	150	155
Glu Glu Trp Tyr Pro Leu Trp Ala Gly Asn Trp Gly Pro His Arg Gln			
160	165	170	175
Val Tyr Leu Ala Ala Ser Trp Val Trp Thr Gln Gln Met Phe Pro Gly			
180	185	190	195
Leu Asp Pro Gln Glu Gln Leu His Lys Ala His Thr Ser Phe Glu Gln			
200	205	210	215
Ala Ala Arg Ala Leu Met Glu Tyr Thr Leu Gln Leu Gly Arg Thr Leu			
220	225	230	235
Arg Pro Ser Gly Leu Trp Gly Phe Tyr Arg Tyr Pro Ala Cys Gly Asn			
240	245	250	255
Gly Trp His Lys Met Ala Ser Asn Tyr Thr Gly His Cys His Ala Ala			
260	265	270	275
Ile Thr Thr Gln Asn Thr Gln Leu Arg Trp Leu Trp Ala Ala Ser Ser			
280	285	290	295
Ala Leu Phe Pro Ser Ile Tyr Leu Pro Pro Arg Leu Pro Leu Ala Tyr			
300	305	310	315
Arg Gln Ala Phe Val Arg His Arg Leu Glu Glu Ala Phe Arg Val Ala			
320	325	330	335
Leu Leu Glu His Ser His Pro Leu Pro Val Leu Ala Tyr Ser Arg Leu			
340	345	350	355
Thr His Arg Ser Ser Gly Arg Phe Leu Ser Leu Asp Asp Leu Met Gln			
360	365	370	375
Thr Ile Gly Val Ser Ala Ala Leu Gly Thr Ala Gly Val Val Leu Trp			
380	385	390	395
Gly Asp Leu Ser Phe Ser Ser Ser Glu Glu Lys Cys Trp Arg Leu His			
400	405	410	
Asp Tyr Leu Val Gly Thr Leu Gly Pro Tyr Val Ile Asn Val Thr Lys			
Ala Asp Met Ala Cys Ser His Gln Arg Cys His Gly His Gly Arg Cys			
Ala Arg Lys Asp Pro Gly Gln Met Glu Ala Phe Leu His Leu Gln Pro			
Asp Asp Ser Leu Gly Ala Trp Asn Ser Phe Arg Cys His Cys Tyr Ser			
Gly Trp Ala Gly Pro Thr Cys Leu Glu Pro Lys Pro			

<210> 20
 <211> 435
 <212> PRT
 <213> Sus scrofa

<220>
 <223> hyalauronidase

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

3108SEQPC1

Val Asp Val Asp Val Ser Val Phe Glu Val Val Val Asn Pro Gly Gln
 50 55 60
 Thr Phe Arg Gly Pro Asn Met Thr Ile Phe Tyr Ser Ser Gln Leu Gly
 65 70 75 80
 Thr Tyr Pro Tyr Tyr Thr Ser Ala Gly Glu Pro Val Phe Gly Gly Leu
 85 90 95
 Pro Gln Asn Ala Ser Leu Asp Val His Leu Asn Arg Thr Phe Lys Asp
 100 105 110
 Ile Leu Ala Ala Met Pro Glu Ser Asn Phe Ser Gly Leu Ala Val Ile
 115 120 125
 Asp Trp Glu Ala Trp Arg Pro Arg Trp Ala Phe Asn Trp Asp Ala Lys
 130 135 140
 Asp Ile Tyr Arg Gln Arg Ser Arg Ala Leu Val Gln Lys Gln His Pro
 145 150 155 160
 Asp Trp Pro Ala Pro Trp Val Glu Ala Ala Ala Gln Asp Gln Phe Gln
 165 170 175
 Glu Ala Ala Gln Thr Trp Met Ala Gly Thr Leu Lys Leu Gly Gln Thr
 180 185 190
 Leu Arg Pro His Gly Leu Trp Gly Phe Tyr Gly Phe Pro Asp Cys Tyr
 195 200 205
 Asn Tyr Asp Phe Gln Ser Ser Asn Tyr Thr Gly Gln Cys Pro Pro Gly
 210 215 220
 Val Ser Ala Gln Asn Asp Gln Leu Gly Trp Leu Trp Gly Gln Ser Arg
 225 230 235 240
 Ala Leu Tyr Pro Ser Ile Tyr Leu Pro Ser Ala Leu Glu Gly Thr Asn
 245 250 255
 Lys Thr Gln Leu Tyr Val Gln His Arg Val Asn Glu Ala Phe Arg Val
 260 265 270
 Ala Ala Ala Ala Gly Asp Pro Asn Leu Pro Val Leu Pro Tyr Ala Gln
 275 280 285
 Ile Phe His Asp Met Thr Asn Arg Leu Leu Ser Arg Glu Glu Leu Glu
 290 295 300
 His Ser Leu Gly Glu Ser Ala Ala Gln Gly Ala Ala Gly Val Val Leu
 305 310 315 320
 Trp Val Ser Trp Glu Asn Thr Arg Thr Lys Glu Ser Cys Gln Ser Ile
 325 330 335
 Lys Glu Tyr Val Asp Thr Thr Leu Gly Pro Phe Ile Leu Asn Val Thr
 340 345 350
 Ser Gly Ala Leu Leu Cys Ser Gln Ala Val Cys Ser Gly His Gly Arg
 355 360 365
 Cys Val Arg Arg Pro Ser His Thr Glu Ala Leu Pro Ile Leu Asn Pro
 370 375 380
 Ser Ser Phe Ser Ile Lys Pro Thr Pro Gly Gly Gly Pro Leu Thr Leu
 385 390 395 400
 Gln Gly Ala Leu Ser Leu Lys Asp Arg Val Gln Met Ala Glu Glu Phe
 405 410 415
 Gln Cys Arg Cys Tyr Pro Gly Trp Arg Gly Thr Trp Cys Glu Gln Gln
 420 425 430
 Gly Thr Arg
 435

<210> 21
 <211> 419
 <212> PRT
 <213> Sus scrofa

<220>
 <223> hyaluronidase 3

<400> 21
 Met Thr Met Gln Leu Gly Leu Ala Leu Val Leu Gly Val Ala Met Cys
 1 5 10 15
 Leu Gly Cys Gly Gln Pro Leu Leu Arg Ala Pro Glu Arg Pro Phe Cys
 20 25 30
 Val Leu Trp Asn Val Pro Ser Ala Arg Cys Lys Ala Arg Phe Gly Val
 35 40 45
 His Leu Pro Leu Glu Ala Leu Gly Ile Thr Ala Asn His Gly Gln Arg
 Page 20

3108SEQPC1

50 55 60
 Phe His Gly Gln Asn Ile Thr Ile Phe Tyr Lys Ser Gln Leu Gly Leu
 65 70 75 80
 Tyr Pro Tyr Phe Gly Pro Arg Gly Thr Ala His Asn Gly Gly Ile Pro
 85 90 95
 Gln Ala Val Ser Leu Asp His His Leu Ala Arg Ala Ala Tyr Gln Ile
 100 105 110
 His Arg Ser Leu Arg Pro Gly Phe Thr Gly Leu Ala Val Leu Asp Trp
 115 120 125
 Glu Glu Trp Cys Pro Leu Trp Ala Gly Asn Trp Gly Arg Arg Gln Ala
 130 135 140
 Tyr Gln Ala Ala Ser Cys Ala Trp Ala Gln Arg Val Tyr Pro Asn Leu
 145 150 155 160
 Asp Pro Gln Glu Gln Leu Cys Lys Ala Arg Ala Gly Phe Glu Glu Ala
 165 170 175
 Ala Arg Ala Leu Met Glu Asp Thr Leu Arg Leu Gly Arg Met Leu Arg
 180 185 190
 Pro His Gly Leu Trp Gly Phe Tyr His Tyr Pro Ala Cys Gly Asn Gly
 195 200 205
 Trp His Gly Thr Ala Ser Asn Tyr Thr Gly His Cys His Ala Ala Ala
 210 215 220
 Leu Ala Arg Asn Thr Gln Leu Tyr Trp Leu Trp Ala Ala Ser Ser Ala
 225 230 235 240
 Leu Phe Pro Ser Ile Tyr Leu Pro Pro Gly Leu Pro Pro Ala Tyr His
 245 250 255
 Gln Ala Phe Val Arg Tyr Arg Leu Glu Ala Phe Arg Val Ala Leu
 260 265 270
 Val Gly His Pro His Pro Leu Pro Val Leu Ala Tyr Ala Arg Leu Thr
 275 280 285
 His Arg Asn Ser Gly Arg Phe Leu Ser Gln Asp Glu Leu Val Gln Thr
 290 295 300
 Ile Gly Val Ser Ala Ala Leu Gly Ala Ser Gly Val Val Leu Trp Gly
 305 310 315 320
 Asp Leu Ser Phe Ser Ser Ser Glu Glu Glu Cys Trp His Leu Arg Gly
 325 330 335
 Tyr Leu Val Gly Thr Leu Gly Pro Tyr Val Ile Asn Val Thr Arg Ala
 340 345 350
 Ala Met Ala Cys Ser His Gln Arg Cys His Gly His Gly Arg Cys Ala
 355 360 365
 Trp Gln Asp Pro Gly Gln Leu Lys Val Phe Leu His Leu His Pro Gly
 370 375 380
 Gly Ser Pro Gly Ala Trp Glu Ser Phe Ser Cys Arg Cys Tyr Trp Gly
 385 390 395 400
 Trp Ala Gly Pro Thr Cys Gln Glu Pro Arg Pro Glu Leu Gly Pro Glu
 405 410 415
 Glu Ala Thr

<210> 22

<211> 449

<212> PRT

<213> Rattus norvegicus

<220>

<223> hyaluronidase 1

<400> 22

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

3108SEQPC1

Phe	Gln	Gly	Pro	Asn	Met	Thr	Ile	Phe	Tyr	Arg	Glu	Glu	Leu	Gly	Thr
				85					90					95	
Tyr	Pro	Tyr	Tyr	Thr	Pro	Thr	Gly	Glu	Pro	Val	Phe	Gly	Gly	Leu	Pro
			100					105					110		
Gln	Asn	Ala	Ser	Leu	Val	Thr	His	Leu	Ala	His	Ala	Phe	Gln	Asp	Ile
		115					120					125			
Lys	Ala	Ala	Met	Pro	Glu	Pro	Asp	Phe	Ser	Gly	Leu	Ala	Val	Ile	Asp
	130					135					140				
Trp	Glu	Ala	Trp	Arg	Pro	Arg	Trp	Ala	Phe	Asn	Trp	Asp	Ser	Lys	Asp
145					150					155					160
Ile	Tyr	Gln	Gln	Arg	Ser	Met	Glu	Leu	Val	Arg	Ala	Glu	His	Pro	Asp
				165						170					175
Trp	Pro	Glu	Thr	Leu	Val	Glu	Ala	Glu	Ala	Gln	Gly	Gln	Phe	Gln	Glu
			180					185						190	
Ala	Ala	Glu	Ala	Trp	Met	Ala	Gly	Thr	Leu	Gln	Leu	Gly	Gln	Val	Leu
		195					200					205			
Arg	Pro	Arg	Gly	Leu	Trp	Gly	Tyr	Tyr	Gly	Phe	Pro	Asp	Cys	Tyr	Asn
	210					215					220				
Tyr	Asp	Phe	Leu	Ser	Pro	Asn	Tyr	Thr	Gly	Gln	Cys	Ser	Leu	Ser	Ile
225					230					235					240
His	Asp	Gln	Asn	Asp	Gln	Leu	Gly	Trp	Leu	Trp	Asn	Gln	Ser	Tyr	Ala
			245						250					255	
Leu	Tyr	Pro	Ser	Ile	Tyr	Leu	Pro	Ala	Ala	Leu	Met	Gly	Thr	Gly	Lys
			260					265					270		
Ser	Gln	Met	Tyr	Val	Arg	Tyr	Arg	Val	Gln	Glu	Ala	Phe	Arg	Leu	Ala
		275					280					285			
Leu	Val	Ser	Arg	Asp	Pro	His	Val	Pro	Ile	Met	Pro	Tyr	Val	Gln	Ile
	290					295					300				
Phe	Tyr	Glu	Lys	Thr	Asp	Tyr	Leu	Leu	Pro	Leu	Glu	Glu	Leu	Glu	His
305					310					315					320
Ser	Leu	Gly	Glu	Ser	Ala	Ala	Gln	Gly	Ala	Ala	Gly	Ala	Val	Leu	Trp
				325					330					335	
Ile	Ser	Ser	Glu	Lys	Thr	Ser	Thr	Lys	Glu	Ser	Cys	Gln	Ala	Ile	Lys
			340					345					350		
Ala	Tyr	Met	Asp	Ser	Thr	Leu	Gly	Pro	Phe	Ile	Leu	Asn	Val	Thr	Ser
		355					360					365			
Ala	Ala	Leu	Leu	Cys	Ser	Glu	Ala	Leu	Cys	Ser	Gly	Arg	Gly	Arg	Cys
	370					375					380				
Val	Arg	His	Pro	Ser	Tyr	Pro	Glu	Ala	Leu	Leu	Thr	Leu	Ser	Pro	Ala
385					390					395					400
Ser	Phe	Ser	Ile	Glu	Pro	Thr	His	Asp	Gly	Arg	Pro	Leu	Ser	Leu	Lys
			405						410					415	
Gly	Thr	Leu	Ser	Leu	Lys	Asp	Arg	Ala	Gln	Met	Ala	Met	Lys	Phe	Lys
			420					425					430		
Cys	Arg	Cys	Tyr	Arg	Gly	Trp	Ser	Gly	Glu	Trp	Cys	Lys	Lys	Gln	Asp
		435					440					445			

Met

<210> 23
 <211> 473
 <212> PRT
 <213> Rattus norvegicus

<220>
 <223> hyaluronidase 2

<400> 23

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

Page 22

3108SEQPC1

65	Asp	Arg	Leu	Gly	Leu	Tyr	Pro	Arg	Phe	Asp	Ala	Ala	Gly	Met	Ser	Val	80
					85					90					95		
	His	Gly	Gly	Val	Pro	Gln	Asn	Gly	Ser	Leu	Cys	Ala	His	Leu	Pro	Met	
				100					105					110			
	Leu	Lys	Glu	Ala	Val	Glu	Arg	Tyr	Ile	Gln	Thr	Gln	Glu	Pro	Ala	Gly	
			115					120					125				
	Leu	Ala	Val	Ile	Asp	Trp	Glu	Glu	Trp	Arg	Pro	Val	Trp	Val	Arg	Asn	
			130				135					140					
	Trp	Gln	Glu	Lys	Asp	Val	Tyr	Arg	Gln	Ser	Ser	Arg	Gln	Leu	Val	Ala	
	145				150					155						160	
	Ser	Arg	His	Pro	Asp	Trp	Pro	Ser	Asp	Arg	Ile	Val	Lys	Gln	Ala	Gln	
				165						170					175		
	Tyr	Glu	Phe	Glu	Phe	Ala	Ala	Arg	Gln	Phe	Met	Leu	Asn	Thr	Leu	Arg	
			180						185					190			
	Tyr	Val	Lys	Ala	Val	Arg	Pro	Gln	His	Leu	Trp	Gly	Phe	Tyr	Leu	Phe	
			195					200					205				
	Pro	Asp	Cys	Tyr	Asn	His	Asp	Tyr	Val	Gln	Asn	Trp	Asp	Ser	Tyr	Thr	
		210					215					220					
	Gly	Arg	Cys	Pro	Asp	Val	Glu	Val	Ala	Gln	Asn	Asp	Gln	Leu	Ala	Trp	
	225				230					235						240	
	Leu	Trp	Ala	Glu	Asn	Thr	Ala	Leu	Phe	Pro	Ser	Val	Tyr	Leu	Asp	Lys	
				245						250					255		
	Thr	Leu	Ala	Ser	Ser	Lys	His	Ser	Arg	Asn	Phe	Val	Ser	Phe	Arg	Val	
			260						265					270			
	Gln	Glu	Ala	Leu	Arg	Val	Ala	His	Thr	His	His	Ala	Asn	His	Ala	Leu	
			275					280					285				
	Pro	Val	Tyr	Val	Phe	Thr	Arg	Pro	Thr	Tyr	Thr	Arg	Arg	Leu	Thr	Glu	
			290				295					300					
	Leu	Asn	Gln	Met	Asp	Leu	Ile	Ser	Thr	Ile	Gly	Glu	Ser	Ala	Ala	Leu	
	305				310					315						320	
	Gly	Ser	Ala	Gly	Val	Ile	Phe	Trp	Gly	Asp	Ser	Val	Tyr	Ala	Ser	Ser	
				325						330					335		
	Met	Glu	Asn	Cys	Gln	Asn	Leu	Lys	Lys	Tyr	Leu	Thr	Gln	Thr	Leu	Val	
			340						345					350			
	Pro	Tyr	Ile	Val	Asn	Val	Ser	Trp	Ala	Thr	Gln	Tyr	Cys	Ser	Trp	Thr	
			355					360					365				
	Gln	Cys	His	Gly	His	Gly	Arg	Cys	Val	Arg	Arg	Asn	Pro	Ser	Ala	Ser	
		370					375					380					
	Thr	Phe	Leu	His	Leu	Ser	Pro	Ser	Ser	Phe	Arg	Leu	Val	Pro	Gly	Arg	
	385				390					395						400	
	Thr	Pro	Ser	Glu	Pro	Gln	Leu	Arg	Pro	Glu	Gly	Glu	Leu	Ser	Glu	Asp	
				405						410					415		
	Asp	Leu	Ser	Tyr	Leu	Gln	Met	His	Phe	Arg	Cys	His	Cys	Tyr	Leu	Gly	
			420						425					430			
	Trp	Gly	Gly	Glu	Gln	Cys	Gln	Trp	Asn	His	Lys	Arg	Ala	Ala	Gly	Asp	
			435					440					445				
	Ala	Ser	Arg	Ala	Trp	Ala	Gly	Ala	His	Leu	Ala	Ser	Leu	Leu	Gly	Leu	
			450				455					460					
	Val	Ala	Met	Thr	Leu	Thr	Trp	Thr	Leu								
	465					470											

<210> 24
 <211> 412
 <212> PRT
 <213> Rattus norvegicus

<220>
 <223> hyaluronidase 3

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

3108SEQPC1

His	Leu	Pro	Leu	Asp	Ala	Leu	Gly	Ile	Ile	Ala	Asn	His	Gly	Gln	Arg
50						55				60					
Phe	His	Gly	Gln	Asn	Ile	Thr	Ile	Phe	Tyr	Lys	Asn	Gln	Phe	Gly	Leu
65				70					75						80
Tyr	Pro	Tyr	Phe	Gly	Pro	Arg	Gly	Thr	Ala	His	Asn	Gly	Gly	Ile	Pro
				85				90						95	
Gln	Ala	Val	Ser	Leu	Asp	His	His	Leu	Ala	Gln	Ala	Ala	His	Gln	Ile
			100					105					110		
Leu	His	Asn	Leu	Gly	Ser	Ser	Phe	Ala	Gly	Leu	Ala	Val	Leu	Asp	Trp
		115					120					125			
Glu	Glu	Trp	Tyr	Pro	Leu	Trp	Ala	Gly	Asn	Trp	Gly	Thr	His	Arg	Gln
	130					135					140				
Val	Tyr	Gln	Ala	Ala	Ser	Trp	Ala	Trp	Ala	Gln	Gln	Met	Phe	Pro	Asp
145					150					155					160
Leu	Asn	Pro	Gln	Glu	Gln	Leu	His	Lys	Ala	Gln	Thr	Gly	Phe	Glu	Gln
				165					170					175	
Ala	Ala	Arg	Ala	Leu	Met	Glu	His	Thr	Leu	Arg	Leu	Gly	Gln	Met	Leu
			180					185						190	
Arg	Pro	His	Gly	Leu	Trp	Gly	Phe	Tyr	Arg	Tyr	Pro	Val	Cys	Gly	Asn
		195						200				205			
Gly	Trp	His	Asn	Met	Ala	Ser	Asn	Tyr	Thr	Gly	His	Cys	His	Pro	Ala
	210					215					220				
Ile	Ile	Thr	Arg	Asn	Thr	Gln	Leu	Arg	Trp	Leu	Trp	Ala	Ala	Ser	Ser
225					230					235					240
Ala	Leu	Phe	Pro	Ser	Ile	Tyr	Leu	Pro	Pro	Arg	Leu	Pro	Pro	Ala	Tyr
				245					250					255	
His	Gln	Thr	Phe	Val	Arg	His	Arg	Leu	Glu	Glu	Ala	Phe	Arg	Val	Ala
			260					265					270		
Leu	Thr	Gly	His	Ala	His	Pro	Leu	Pro	Val	Leu	Ala	Tyr	Val	Arg	Leu
		275					280					285			
Thr	His	Arg	Ser	Ser	Gly	Arg	Phe	Leu	Ser	Leu	Asp	Asp	Leu	Met	Gln
	290					295					300				
Thr	Ile	Gly	Val	Ser	Ala	Ala	Leu	Gly	Ala	Ala	Gly	Val	Val	Leu	Trp
305					310					315					320
Gly	Asp	Leu	Ser	Val	Ser	Ser	Ser	Glu	Glu	Glu	Cys	Trp	Arg	Leu	His
				325					330					335	
Asp	Tyr	Leu	Val	Gly	Thr	Leu	Gly	Pro	Tyr	Val	Ile	Asn	Val	Thr	Lys
			340					345					350		
Ala	Ala	Thr	Ala	Cys	Ser	His	Gln	Arg	Cys	His	Gly	His	Gly	Arg	Cys
			355					360				365			
Ser	Trp	Lys	Asp	Pro	Gly	Gln	Met	Glu	Ala	Phe	Leu	His	Leu	Gln	Pro
	370					375					380				
Asp	Asp	Asn	Leu	Gly	Ala	Trp	Lys	Ser	Phe	Arg	Cys	Arg	Cys	Tyr	Leu
385					390					395					400
Gly	Trp	Ser	Gly	Pro	Thr	Cys	Leu	Glu	Pro	Lys	Pro				
				405					410						

<210> 25

<211> 545

<212> PRT

<213> Oryctolagus cuniculus

<220>

<223> Precursor rabbit PH20

<400> 25

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

3108SEQPC1

				85						90				95					
Gly	Tyr	Tyr	Pro	Tyr	Ile	Asp	Pro	His	Thr	Gly	Ala	Ile	Val	His	Gly				
			100					105					110						
Arg	Ile	Pro	Gln	Leu	Gly	Pro	Leu	Gln	Gln	His	Leu	Thr	Lys	Leu	Arg				
		115					120					125							
Gln	Glu	Ile	Leu	Tyr	Tyr	Met	Pro	Lys	Asp	Asn	Val	Gly	Leu	Ala	Val				
	130					135					140								
Ile	Asp	Trp	Glu	Glu	Trp	Leu	Pro	Thr	Trp	Leu	Arg	Asn	Trp	Lys	Pro				
145					150					155					160				
Lys	Asp	Ile	Tyr	Arg	Ile	Lys	Ser	Ile	Glu	Leu	Val	Lys	Ser	Gln	His				
				165					170					175					
Pro	Gln	Tyr	Asn	His	Ser	Tyr	Ala	Thr	Glu	Lys	Ala	Lys	Arg	Asp	Phe				
			180					185					190						
Glu	Lys	Ala	Gly	Lys	Asp	Phe	Met	Glu	Glu	Thr	Leu	Lys	Leu	Gly	Arg				
		195					200					205							
Leu	Leu	Arg	Pro	Asn	His	Leu	Trp	Gly	Tyr	Tyr	Leu	Phe	Pro	Asp	Cys				
	210					215					220								
Tyr	Asn	His	His	Tyr	Asp	Lys	Pro	Asn	Leu	Tyr	Lys	Gly	Ser	Cys	Phe				
225					230					235					240				
Asp	Ile	Glu	Lys	Lys	Arg	Asn	Asp	Asp	Leu	Ser	Trp	Leu	Trp	Lys	Glu				
				245					250					255					
Ser	Thr	Ala	Leu	Phe	Pro	Ser	Val	Tyr	Leu	Thr	Ser	Arg	Ala	Arg	Ser				
		260						265					270						
Ala	Thr	Ala	Leu	Ser	Lys	Leu	Tyr	Val	Val	Arg	Asn	Arg	Val	His	Glu				
		275					280					285							
Ala	Ile	Arg	Val	Ser	Lys	Ile	Pro	Asp	Asp	Lys	Ser	Pro	Leu	Pro	Asn				
	290					295					300								
Phe	Val	Tyr	Thr	Arg	Leu	Val	Phe	Thr	Asp	Gln	Ile	Phe	Gln	Phe	Leu				
305					310					315					320				
Ser	His	His	Asp	Leu	Val	Tyr	Thr	Ile	Gly	Glu	Ile	Val	Ala	Leu	Gly				
				325					330					335					
Ala	Ser	Gly	Ile	Val	Val	Trp	Gly	Ser	Gln	Ser	Leu	Ala	Arg	Ser	Met				
			340					345					350						
Lys	Ser	Cys	Leu	His	Leu	Asp	Asn	Tyr	Met	Lys	Thr	Ile	Leu	Asn	Pro				
		355					360					365							
Tyr	Leu	Ile	Asn	Val	Thr	Leu	Ala	Ala	Lys	Met	Cys	Asn	Gln	Val	Leu				
	370					375					380								
Cys	Gln	Glu	Gln	Gly	Val	Cys	Thr	Arg	Lys	Asn	Trp	Asn	Pro	Asn	Asp				
385					390					395					400				
Tyr	Leu	His	Leu	Asn	Pro	Gly	Asn	Phe	Ala	Ile	Gln	Leu	Gly	Ser	Asn				
				405					410					415					
Gly	Thr	Tyr	Lys	Val	Asp	Gly	Lys	Pro	Thr	Leu	Thr	Asp	Leu	Glu	Gln				
			420					425					430						
Phe	Ser	Lys	Asn	Phe	Gln	Cys	Ser	Cys	Tyr	Thr	Asn	Leu	Asn	Cys	Lys				
		435					440					445							
Glu	Arg	Thr	Asp	Met	Asn	Asn	Val	Arg	Thr	Val	Asn	Val	Cys	Ala	Val				
		450				455					460								
Glu	Asn	Val	Cys	Ile	Asp	Thr	Asn	Val	Gly	Pro	Gln	Ala	Val	Thr	Tyr				
465					470					475					480				
Ala	Pro	Lys	Glu	Lys	Lys	Asp	Val	Ala	His	Ile	Leu	Ser	Asn	Thr	Thr				
				485					490					495					
Ser	Ile	Asn	Ser	Ser	Thr	Thr	Met	Ser	Leu	Pro	Phe	Pro	Arg	Lys	His				
			500					505					510						
Val	Ser	Gly	Cys	Leu	Leu	Val	Leu	Cys	Met	Tyr	Ser	Gln	Tyr	Leu	Asn				
		515					520					525							
Ile	Cys	Tyr	Arg	Leu	Val	Ala	Ile	Gly	Ile	Gln	His	Gly	Tyr	Tyr	Leu				
	530					535					540								

Lys
545

<210> 26
 <211> 476
 <212> PRT
 <213> Ovis aries

<220>
 <223> hyaluronidase 2

3108SEQPC1

<400> 26

```

Met Trp Thr Gly Leu Gly Pro Ala Val Thr Leu Ala Leu Val Leu Val
1      5      10      15
Val Ala Trp Ala Thr Glu Leu Lys Pro Thr Ala Pro Pro Ile Phe Thr
20      25      30
Gly Arg Pro Phe Val Val Ala Trp Asp Val Pro Thr Gln Asp Cys Gly
35      40      45
Pro Arg His Lys Met Pro Leu Asp Pro Lys Asp Met Lys Ala Phe Asp
50      55      60
Val Gln Ala Ser Pro Asn Glu Gly Phe Val Asn Gln Asn Ile Thr Ile
65      70      75      80
Phe Tyr Arg Asp Arg Leu Gly Met Tyr Pro His Phe Asn Ser Val Gly
85      90      95
Arg Ser Val His Gly Gly Val Pro Gln Asn Gly Ser Leu Trp Val His
100     105     110
Leu Glu Met Leu Lys Gly His Val Glu His Tyr Ile Arg Thr Gln Glu
115     120     125
Pro Ala Gly Leu Ala Val Ile Asp Trp Glu Asp Trp Arg Pro Val Trp
130     135     140
Val Arg Asn Trp Gln Asp Lys Asp Val Tyr Arg Arg Leu Ser Arg Gln
145     150     155     160
Leu Val Ala Ser His His Pro Asp Trp Pro Pro Glu Arg Ile Val Lys
165     170     175
Glu Ala Gln Tyr Glu Phe Glu Phe Ala Ala Arg Gln Phe Met Leu Glu
180     185     190
Thr Leu Arg Phe Val Lys Ala Phe Arg Pro Arg His Leu Trp Gly Phe
195     200     205
Tyr Leu Phe Pro Asp Cys Tyr Asn His Asp Tyr Val Gln Asn Trp Glu
210     215     220
Thr Tyr Thr Gly Arg Cys Pro Asp Val Glu Val Ser Arg Asn Asp Gln
225     230     235     240
Leu Ser Trp Leu Trp Ala Glu Ser Thr Ala Leu Phe Pro Ser Val Tyr
245     250     255
Leu Glu Glu Thr Leu Ala Ser Ser Thr His Gly Arg Asn Phe Val Ser
260     265     270
Phe Arg Val Gln Glu Ala Leu Arg Val Ala Asp Val His His Ala Asn
275     280     285
His Ala Leu Pro Val Tyr Val Phe Thr Arg Pro Thr Tyr Ser Arg Gly
290     295     300
Leu Thr Gly Leu Ser Glu Met Asp Leu Ile Ser Thr Ile Gly Glu Ser
305     310     315     320
Ala Ala Leu Gly Ala Ala Gly Val Ile Leu Trp Gly Asp Ala Gly Phe
325     330     335
Thr Thr Ser Asn Glu Thr Cys Arg Arg Leu Lys Asp Tyr Leu Thr Arg
340     345     350
Ser Leu Val Pro Tyr Val Val Asn Val Ser Trp Ala Ala Gln Tyr Cys
355     360     365
Ser Trp Ala Gln Cys His Gly His Gly Arg Cys Val Arg Arg Asp Pro
370     375     380
Asn Ala His Thr Phe Leu His Leu Ser Ala Ser Ser Phe Arg Leu Val
385     390     395     400
Pro Ser His Ala Pro Asp Glu Pro Arg Leu Arg Pro Glu Gly Glu Leu
405     410     415
Ser Trp Ala Asp Arg Asn His Leu Gln Thr His Phe Arg Cys Gln Cys
420     425     430
Tyr Leu Gly Trp Gly Gly Glu Gln Cys Gln Trp Asp Arg Arg Arg Ala
435     440     445
Ala Gly Gly Ala Ser Gly Ala Trp Ala Gly Ser His Leu Thr Gly Leu
450     455     460
Leu Ala Val Ala Val Leu Ala Phe Thr Trp Thr Ser
465     470     475

```

<210> 27

<211> 114

<212> PRT

<213> Ovis aries

3108SEQPC1

<220>

<223> PH20 partial sequence

<400> 27

```

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

```

<210> 28

<211> 414

<212> PRT

<213> Pongo pygmaeus

<220>

<223> hyaluronidase 3

<400> 28

```

Met Thr Thr Arg Leu Gly Pro Ala Leu Val Leu Gly Val Ala Leu Cys
 1           5           10           15
Leu Gly Cys Gly Gln Pro Leu Pro Gln Val Pro Glu Arg Pro Phe Ser
          20           25           30
Val Leu Trp Asn Val Pro Ser Ala His Cys Lys Ser Arg Phe Gly Val
          35           40           45
His Leu Pro Leu Asn Ala Leu Gly Ile Ile Ala Asn Arg Gly Gln His
          50           55           60
Phe His Gly Gln Asn Met Thr Ile Phe Tyr Lys Asn Gln Leu Gly Leu
65           70           75           80
Tyr Pro Tyr Phe Gly Pro Lys Gly Thr Ala His Asn Gly Gly Ile Pro
          85           90           95
Gln Ala Leu Pro Leu Asp Arg His Leu Ala Leu Ala Ala Tyr Gln Ile
          100          105          110
His His Ser Leu Arg Pro Gly Phe Ala Gly Pro Ala Val Leu Asp Trp
          115          120          125
Glu Glu Trp Cys Pro Leu Trp Ala Gly Asn Trp Gly Arg Arg Arg Ala
          130          135          140
Tyr Gln Ala Ala Ser Trp Ala Trp Ala Gln Gln Val Phe Pro Asp Leu
145           150           155           160
Asp Pro Gln Glu Gln Leu Tyr Lys Ala Tyr Thr Gly Phe Glu Gln Ala
          165          170          175
Ala Arg Ala Leu Met Glu Asp Thr Leu Arg Val Ala Gln Ala Leu Arg
          180          185          190
Pro His Gly Leu Trp Gly Phe Tyr His Tyr Pro Ala Cys Gly Asn Gly
          195          200          205
Trp His Ser Met Ala Ser Asn Tyr Thr Gly Arg Cys His Ala Ala Thr
          210          215          220
Leu Ala Arg Asn Thr Gln Leu His Trp Leu Trp Ala Ala Ser Ser Ala
225           230           235           240
Leu Phe Pro Ser Ile Tyr Leu Pro Pro Arg Leu Pro Pro Ala His His
          245          250          255
Gln Ala Phe Val Arg His Arg Leu Glu Glu Ala Phe Arg Val Ala Leu
          260          265          270
Val Gly His Leu Pro Val Leu Ala Tyr Val Arg Leu Thr His Arg Arg
          275          280          285

```

3108SEQPC1

Ser Gly Arg Phe Leu Ser Gln Asp Asp Leu Val Gln Thr Ile Gly Val
 290 295 300
 Ser Ala Ala Leu Gly Ala Ala Gly Val Val Leu Trp Gly Asp Leu Ser
 305 310 315 320
 Leu Ser Ser Ser Glu Glu Glu Cys Trp His Leu His Asp Tyr Leu Val
 325 330 335
 Asp Thr Leu Gly Pro Tyr Gly Ile Asn Val Thr Arg Ala Ala Met Ala
 340 345 350
 Cys Ser His Gln Arg Cys His Gly His Gly Arg Cys Ala Arg Arg Asp
 355 360 365
 Pro Gly Gln Met Glu Ala Phe Leu His Leu Trp Pro Asp Gly Ser Leu
 370 375 380
 Gly Asp Trp Lys Ser Phe Ser Cys His Cys Tyr Trp Gly Trp Ala Gly
 385 390 395 400
 Pro Thr Cys Gln Glu Pro Arg Leu Gly Pro Lys Glu Ala Val
 405 410

<210> 29

<211> 510

<212> PRT

<213> Macaca fascicularis

<220>

<223> Precursor Cynomolgus monkey PH20

<400> 29

Met Gly Val Leu Lys Phe Lys His Ile Phe Phe Arg Ser Phe Val Lys
 1 5 10 15
 Ser Ser Gly Val Ser Gln Ile Val Phe Thr Phe Leu Leu Ile Pro Cys
 20 25 30
 Cys Leu Thr Leu Asn Phe Arg Ala Pro Pro Ile Ile Pro Asn Val Pro
 35 40 45
 Phe Leu Trp Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe
 50 55 60
 Asn Glu Pro Leu Asp Met Ser Leu Phe Thr Leu Met Gly Ser Pro Arg
 65 70 75 80
 Ile Asn Val Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu
 85 90 95
 Gly Tyr Tyr Pro Tyr Ile Asp Leu Thr Thr Gly Val Thr Val His Gly
 100 105 110
 Gly Ile Pro Gln Lys Val Ser Leu Gln Asp His Leu Asp Lys Ser Lys
 115 120 125
 Gln Asp Ile Leu Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val
 130 135 140
 Ile Asp Trp Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro
 145 150 155 160
 Lys Asp Val Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn
 165 170 175
 Val Gln Leu Ser Leu Pro Gln Ala Thr Asp Lys Ala Lys Gln Glu Phe
 180 185 190
 Glu Lys Ala Gly Lys Asp Phe Met Leu Glu Thr Ile Lys Leu Gly Arg
 195 200 205
 Ser Leu Arg Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys
 210 215 220
 Tyr Asn His His Tyr Arg Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asp
 225 230 235 240
 Val Glu Ile Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser
 245 250 255
 Thr Ala Leu Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Val Val
 260 265 270
 Val Ala Thr Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val
 275 280 285
 Ser Lys Ile Pro Asp Ala Lys Asn Pro Leu Pro Val Phe Val Tyr Ala
 290 295 300
 Arg Leu Val Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Arg Glu Glu
 305 310 315 320
 Leu Val Ser Thr Leu Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile

3108SEQPC1

325 330 335
 Val Ile Trp Gly Ser Leu Ser Ile Thr Arg Ser Met Lys Ser Cys Leu
 340 345 350
 Leu Leu Asp Thr Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn
 355 360 365
 Val Thr Leu Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln
 370 375 380
 Gly Val Cys Ile Arg Lys Asp Trp Asn Ser Ser Asp Tyr Leu His Leu
 385 390 395 400
 Asn Pro Asp Asn Phe Asp Ile Arg Leu Glu Lys Gly Gly Lys Phe Thr
 405 410 415
 Val His Gly Lys Pro Thr Val Glu Asp Leu Glu Glu Phe Ser Glu Lys
 420 425 430
 Phe Tyr Cys Ser Cys Tyr Thr Asn Leu Ser Cys Lys Glu Lys Ala Asp
 435 440 445
 Val Lys Asp Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys
 450 455 460
 Ile Asp Ala Ser Leu Lys Pro Pro Val Glu Thr Glu Gly Ser Pro Pro
 465 470 475 480
 Ile Phe Tyr Asn Thr Ser Ser Ser Thr Val Ser Thr Thr Met Phe Ile
 485 490 495
 Val Asn Ile Leu Phe Leu Ile Ile Ser Ser Val Ala Ser Leu
 500 505 510

<210> 30

<211> 529

<212> PRT

<213> *Cavia porcellus*

<220>

<223> Precursor guinea pig PH20

<400> 30

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

3108SEQPC1

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

<210> 31
 <211> 512
 <212> PRT
 <213> Rattus norvegicus

<220>
 <223> Precursor rat PH20

<400> 31
 Met Gly Glu Leu Gln Phe Lys Trp Leu Phe Trp Arg Ser Phe Ala Glu
 1 5 10 15
 Ser Gly Gly Thr Phe Gln Thr Val Leu Ile Phe Leu Phe Ile Pro Tyr
 20 25 30
 Ser Leu Thr Val Asp Tyr Arg Ala Thr Pro Val Leu Ser Asp Thr Thr
 35 40 45
 Phe Val Trp Val Trp Asn Val Pro Thr Glu Ala Cys Val Glu Asn Val
 50 55 60
 Thr Glu Pro Ile Asp Leu Ser Phe Phe Ser Leu Ile Gly Ser Pro Arg
 65 70 75 80
 Lys Thr Ala Ile Gly Gln Pro Val Thr Leu Phe Tyr Val Asp Arg Leu
 85 90 95
 Gly Asn Tyr Pro His Ile Asp Ala Gln Gln Thr Glu His His Gly Gly
 100 105 110
 Ile Pro Gln Lys Gly Asp Leu Thr His Leu Val Lys Ala Lys Glu
 115 120 125
 Asp Val Glu Arg Tyr Ile Pro Thr Asp Lys Leu Gly Leu Ala Ile Ile
 130 135 140
 Asp Trp Glu Glu Trp Arg Pro Thr Trp Met Arg Asn Trp Thr Pro Lys
 145 150 155 160
 Asp Ile Tyr Arg Asn Lys Ser Ile Glu Leu Val Gln Ala Ala Asp Pro
 165 170 175
 Ala Ile Asn Ile Thr Glu Ala Thr Val Arg Ala Lys Ala Gln Phe Glu

3108SEQPC1

Gly	Ala	Ala	180	Lys	Glu	Phe	Met	Glu	185	Gly	Thr	Leu	Lys	Leu	190	Gly	Lys	His
Ile	Arg	Pro	195	Lys	His	Leu	Trp	Gly	200	Phe	Tyr	Leu	Phe	Pro	205	Asp	Cys	Tyr
Asn	Asn	Lys	210	Phe	Gln	Val	Asp	Asn	215	Tyr	Asp	Gly	Gln	Cys	Pro	Asp	Val	
225	Lys	Lys	230	Arg	Asn	Asp	Asp	Leu	235	Trp	Leu	Trp	Lys	Glu	Ser	Thr		
Gly	Leu	Tyr	245	Pro	Ser	Val	Tyr	Leu	250	Lys	Lys	Asp	Leu	Lys	Ser	Ser	Arg	
Lys	Ala	Thr	260	Leu	Tyr	Val	Arg	Tyr	265	Arg	Val	Leu	Glu	Ser	Ile	Arg	Val	
Ser	Lys	Val	275	Ser	Asp	Glu	Ser	Asn	280	Pro	Val	Pro	Ile	Phe	Val	Tyr	Ile	
Arg	Leu	Val	290	Phe	Thr	Asp	His	Val	295	Ser	Glu	Tyr	Leu	Leu	Glu	Asp	Asp	
305	Val	Asn	310	Thr	Ile	Gly	Glu	Ile	315	Val	Ala	Gln	Gly	Thr	Ser	Gly	Ile	
Ile	Ile	Trp	325	Asp	Ala	Met	Ser	Leu	330	Gln	Arg	Ser	Ala	Gly	Cys	Pro		
Ile	Leu	Arg	340	Gln	Tyr	Met	Lys	Thr	345	Thr	Leu	Asn	Pro	Tyr	Ile	Val	Asn	
Val	Thr	Leu	355	Ala	Ala	Lys	Met	Cys	360	Ser	Gln	Thr	Leu	Cys	Lys	Glu	Lys	
Gly	Met	Cys	370	Ser	Arg	Lys	Thr	Glu	375	Ser	Ser	Asp	Ala	Tyr	Leu	His	Leu	
385	Pro	Ser	390	Ser	Phe	Ser	Ile	Asn	395	Val	Thr	Glu	Ala	Gly	Lys	Tyr	Glu	
Val	Leu	Gly	405	Lys	Pro	Glu	Val	Lys	410	Leu	Glu	Tyr	Phe	Ser	Glu	His		
Phe	Lys	Cys	420	Ser	Cys	Phe	Ser	Lys	425	Met	Thr	Cys	Glu	Glu	Thr	Ser	Asp	
Met	Arg	Ser	435	Ile	Gln	Asp	Val	Asn	440	Val	Cys	Met	Gly	Asp	Asn	Val	Cys	
Ile	Lys	Ala	450	Thr	Leu	Gly	Pro	Asn	455	Ser	Ala	Phe	His	Leu	Leu	Pro	Gly	
465	Gly	Leu	470	Leu	Met	Thr	Thr	Leu	475	Ala	His	Ile	Leu	His	His	Leu		
Lys	Gly	Leu	485	Leu	Met	Thr	Thr	Leu	490	Ala	His	Ile	Leu	His	His	Leu		
Pro	His	Asp	500	Ile	Phe	Val	Phe	Pro	505	Trp	Lys	Met	Leu	Val	Ser	Thr	Pro	

<210> 32

<211> 512

<212> PRT

<213> Mus musculus

<220>

<223> Precursor mouse PH20

<400> 32

Met	Gly	Glu	Leu	Arg	Phe	Lys	His	Leu	10	Phe	Trp	Gly	Ser	Phe	Val	Glu		
1	Ser	Gly	Gly	Thr	Phe	Gln	Thr	Val	25	Ile	Phe	Leu	Leu	Ile	Pro	Cys		
Ser	Leu	Thr	Val	Asp	Tyr	Arg	Ala	Ala	40	Pro	Ile	Leu	Ser	Asn	Thr	Thr		
Phe	Leu	Trp	Ile	Trp	Asn	Val	Pro	Thr	55	Glu	Arg	Cys	Val	Gly	Asn	Val		
50	Asn	Asp	Pro	Ile	Asp	Leu	Ser	Phe	60	Ser	Leu	Ile	Gly	Ser	Pro	Arg		
65	Lys	Thr	Ala	Thr	Gly	Gln	Pro	Val	75	Leu	Phe	Tyr	Val	Asp	Arg	Leu		
Gly	Leu	Tyr	Pro	His	Ile	Asp	Ala	Asn	90	Gln	Ala	Glu	His	Tyr	Gly	Gly		
Ile	Pro	Gln	Arg	Gly	Asp	Tyr	Gln	Ala	105	His	Leu	Arg	Lys	Ala	Lys	Thr		
115									120									

3108SEQPC1

Asp Ile Glu His Tyr Ile Pro Asp Asp Lys Leu Gly Leu Ala Ile Ile
 130 135 140
 Asp Trp Glu Glu Trp Arg Pro Thr Trp Leu Arg Asn Trp Lys Pro Lys
 145 150 155 160
 Asp Asn Tyr Arg Asn Lys Ser Ile Glu Leu Val Gln Ser Thr Asn Pro
 165 170 175
 Gly Leu Ser Ile Thr Glu Ala Thr Gln Lys Ala Ile Gln Gln Phe Glu
 180 185 190
 Glu Ala Gly Arg Lys Phe Met Glu Thr Leu His Leu Gly Lys Phe
 195 200 205
 Leu Arg Pro Asn Gln Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr
 210 215 220
 Asn Asn Lys Phe Gln Asp Pro Lys Tyr Asp Gly Gln Cys Pro Ala Val
 225 230 235 240
 Glu Lys Lys Arg Asn Asp Asn Leu Lys Trp Leu Trp Lys Ala Ser Thr
 245 250 255
 Gly Leu Tyr Pro Ser Val Tyr Leu Lys Lys Asp Leu Lys Ser Asn Arg
 260 265 270
 Gln Ala Thr Leu Tyr Val Arg Tyr Arg Val Val Glu Ala Ile Arg Val
 275 280 285
 Ser Lys Val Gly Asn Ala Ser Asp Pro Val Pro Ile Phe Val Tyr Ile
 290 295 300
 Arg Leu Val Phe Thr Asp Arg Thr Ser Glu Tyr Leu Leu Glu Asp Asp
 305 310 315 320
 Leu Val Asn Thr Ile Gly Glu Ile Val Ala Leu Gly Thr Ser Gly Ile
 325 330 335
 Ile Ile Trp Asp Ala Met Ser Leu Ala Gln Arg Ala Ala Gly Cys Pro
 340 345 350
 Ile Leu His Lys Tyr Met Gln Thr Thr Leu Asn Pro Tyr Ile Val Asn
 355 360 365
 Val Thr Leu Ala Ala Lys Met Cys Ser Gln Thr Leu Cys Asn Glu Lys
 370 375 380
 Gly Met Cys Ser Arg Arg Lys Glu Ser Ser Asp Val Tyr Leu His Leu
 385 390 395 400
 Asn Pro Ser His Phe Asp Ile Met Leu Thr Glu Thr Gly Lys Tyr Glu
 405 410 415
 Val Leu Gly Asn Pro Arg Val Gly Asp Leu Glu Tyr Phe Ser Glu His
 420 425 430
 Phe Lys Cys Ser Cys Phe Ser Arg Met Thr Cys Lys Glu Thr Ser Asp
 435 440 445
 Val Lys Asn Val Gln Asp Val Asn Val Cys Val Gly Asp Asn Val Cys
 450 455 460
 Ile Lys Ala Lys Val Glu Pro Asn Pro Ala Phe Tyr Leu Leu Pro Gly
 465 470 475 480
 Lys Ser Leu Leu Phe Met Thr Thr Leu Gly His Val Leu Tyr His Leu
 485 490 495
 Pro Gln Asp Ile Phe Val Phe Pro Arg Lys Thr Leu Val Ser Thr Pro
 500 505 510

<210> 33

<211> 807

<212> PRT

<213> Staphylococcus aureus

<220>

<223> hyaluronidase

<400> 33

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

3108SEQPC1

65	Glu	Lys	Glu	Ala	Thr	70	Asn	Leu	Leu	Lys	75	Glu	Met	Lys	Thr	Glu	80	Ser	Gly
					85						90	Thr	Leu	Glu	Thr		95	Asn	Ser
	Arg	Lys	Tyr	Leu	Trp		Ser	Gly	Ala	Glu									
				100						105							110		
	His	Met	Thr	Arg	Thr		Tyr	Arg	Asn	Ile	Glu	Lys	Ile	Ala	Glu	Ala		Met	
			115						120								125		
	Arg	Asn	Pro	Lys	Thr		Thr	Leu	Asn	Thr	Asp	Glu	Asn		Lys	Lys		Lys	Val
									135					140					
	Lys	Asp	Ala	Leu	Glu		Trp	Leu	His	Lys	Asn	Ala	Tyr	Gly	Lys	Glu		Pro	
									150					155					160
	Asp	Lys	Lys	Val	Lys		Glu	Leu	Ser	Glu	Asn	Phe	Thr	Lys	Thr	Thr		Gly	
																			175
	Lys	Asn	Thr	Asn	Leu		Asn	Trp	Trp	Asp	Tyr	Glu	Ile	Gly	Thr	Pro		Lys	
				180						185									
	Ser	Leu	Thr	Asn	Thr		Leu	Ile	Leu	Leu	Asn	Asp	Gln	Phe	Ser	Asn		Glu	
									200					205					
	Glu	Lys	Lys	Lys	Phe		Thr	Ala	Pro	Ile	Lys	Thr	Phe	Ala	Pro	Asp		Ser	
									215					220					
	Asp	Lys	Ile	Leu	Ser		Ser	Val	Gly	Lys	Ala	Glu	Leu	Ala	Lys	Gly		Gly	
									230					235					240
	Asn	Leu	Val	Asp	Ile		Ser	Lys	Val	Lys	Leu	Leu	Glu	Cys	Ile	Ile		Glu	
									245					250					255
	Glu	Asp	Lys	Asp	Met		Met	Lys	Lys	Ser	Ile	Asp	Ser	Phe	Asn	Lys		Val	
										265					270				
	Phe	Thr	Tyr	Val	Gln		Asp	Ser	Ala	Thr	Gly	Lys	Glu	Arg	Asn	Gly		Phe	
									280					285					
	Tyr	Lys	Asp	Gly	Ser		Tyr	Ile	Asp	His	Gln	Asp	Val	Pro	Tyr	Thr		Gly	
									295					300					
	Ala	Tyr	Gly	Val	Val		Leu	Glu	Gly	Ile	Ser	Gln	Met	Met	Pro	Met			
									310					315					320
	Ile	Lys	Glu	Thr	Pro		Phe	Asn	Asp	Lys	Thr	Gln	Asn	Asp	Thr	Thr		Leu	
									325					330					335
	Lys	Ser	Trp	Ile	Asp		Asp	Gly	Phe	Met	Pro	Leu	Ile	Tyr	Lys	Gly		Glu	
									340					350					
	Met	Met	Asp	Leu	Ser		Arg	Gly	Arg	Ala	Ile	Ser	Arg	Glu	Asn	Glu		Thr	
									360					365					
	Ser	His	Ser	Ala	Ser		Ala	Thr	Val	Met	Lys	Ser	Leu	Leu	Arg	Leu		Ser	
									375					380					
	Asp	Ala	Met	Asp	Asp		Ser	Thr	Lys	Ala	Lys	Tyr	Lys	Lys	Ile	Val		Lys	
									390					395					400
	Ser	Ser	Val	Glu	Ser		Asp	Ser	Ser	Tyr	Lys	Gln	Asn	Asp	Tyr	Leu		Asn	
									405										415
	Ser	Tyr	Ser	Asp	Ile		Asp	Lys	Met	Lys	Ser	Leu	Met	Thr	Asp	Asn		Ser	
									420					430					
	Ile	Ser	Lys	Asn	Gly		Leu	Thr	Gln	Gln	Leu	Lys	Ile	Tyr	Asn	Asp		Met	
									440					445					
	Asp	Arg	Val	Thr	Tyr		His	Asn	Lys	Asp	Leu	Asp	Phe	Ala	Phe	Gly		Leu	
									455					460					
	Ser	Met	Thr	Ser	Lys		Asn	Val	Ala	Arg	Tyr	Glu	Ser	Ile	Asn	Gly		Glu	
									470					475					480
	Asn	Leu	Lys	Gly	Trp		His	Thr	Gly	Ala	Gly	Met	Ser	Tyr	Leu	Tyr		Asn	
									485					490					495
	Ser	Asp	Val	Lys	His		Tyr	His	Asp	Asn	Phe	Trp	Val	Thr	Ala	Asp		Met	
									500					510					
	Lys	Arg	Leu	Ser	Gly		Thr	Thr	Thr	Leu	Asp	Asn	Glu	Ile	Leu	Lys		Asp	
									515					525					
	Thr	Asp	Asp	Lys	Lys		Ser	Ser	Lys	Thr	Phe	Val	Gly	Gly	Thr	Lys		Val	
									535					540					
	Asp	Asp	Gln	His	Ala		Ser	Ile	Gly	Met	Asp	Phe	Glu	Asn	Gln	Asp		Lys	
									550					555					560
	Thr	Leu	Thr	Ala	Lys		Lys	Ser	Tyr	Phe	Ile	Leu	Asn	Asp	Lys	Ile		Val	
									565					570					575
	Phe	Leu	Gly	Thr	Gly		Ile	Lys	Ser	Thr	Asp	Ser	Ser	Lys	Asn	Pro		Val	
									580					590					
	Thr	Thr	Ile	Glu	Asn		Arg	Lys	Ala	Asn	Gly	Tyr	Thr	Leu	Tyr	Thr		Asp	
									595					605					
	Asp	Lys	Gln	Thr	Thr		Asn	Ser	Asp	Asn	Gln	Glu	Asn	Asn	Ser	Val		Phe	
									600										

3108SEQPC1

610	Leu	Glu	Ser	Thr	Asp	Thr	615	Lys	Lys	Asn	Ile	Gly	620	Tyr	His	Phe	Leu	Asn
625	Lys	Pro	Lys	Ile	Thr	Val	630	Lys	Lys	Glu	Ser	635	His	Thr	Gly	Lys	Trp	Lys
							645					650						
	Glu	Ile	Asn	Lys	Ser	Gln	655	Lys	Asp	Thr	Gln	660	Lys	Thr	Asp	Glu	Tyr	Tyr
							665					670						
	Glu	Val	Thr	Gln	Lys	His	680	Ser	Asn	Ser	Asp	685	Asn	Lys	Tyr	Gly	Tyr	Val
							690					695						
	Leu	Tyr	Pro	Gly	Leu	Ser	700	Lys	Asp	Val	Phe	705	Lys	Thr	Lys	Lys	Asp	Glu
							710					715						
	Val	Thr	Val	Val	Lys	Gln	720	Glu	Asp	Asp	Phe	725	His	Val	Val	Lys	Asp	Asn
							730					735						
	Glu	Ser	Val	Trp	Ala	Gly	740	Val	Asn	Tyr	Ser	745	Asn	Ser	Thr	Gln	Thr	Phe
							750					755						
	Asp	Ile	Asn	Asn	Thr	Lys	760	Val	Glu	Val	Lys	765	Ala	Lys	Gly	Met	Phe	Ile
							770					775						
	Leu	Lys	Lys	Lys	Asp	Asp	780	Asn	Thr	Tyr	Glu	785	Cys	Ser	Phe	Tyr	Asn	Pro
							790					795						
	Glu	Ser	Thr	Asn	Ser	Ala	800	Ser	Asp	Ile	Glu		Ser	Lys	Ile	Ser	Met	Thr
	Gly	Tyr	Ser	Ile	Thr	Asn		Lys	Asn	Thr	Ser		Thr	Ser	Asn	Glu	Ser	Gly
	Val	His	Phe	Glu	Leu	Thr		Lys										

<210> 34

<211> 371

<212> PRT

<213> Streptococcus pyogenes bacteriophage H4489A

<220>

<223> hyaluronidase

<400> 34

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

3108SEQPC1

Thr Leu Lys Ile Thr His Glu Asn Pro Asn Val Glu Ala Lys Tyr Asp
 260 265 270
 Glu Asn Ala Ala Leu Ser Ile Asp Ile Val Lys Lys Gln Lys Gly
 275 280 285
 Gly Lys Gly Thr Ala Ala Gln Gly Ile Tyr Ile Asn Ser Thr Ser Gly
 290 295 300
 Thr Ala Gly Lys Met Leu Arg Ile Arg Asn Lys Asn Glu Asp Lys Phe
 305 310 315 320
 Tyr Val Gly Pro Asp Gly Gly Phe His Ser Gly Ala Asn Ser Thr Val
 325 330 335
 Ala Gly Asn Leu Thr Val Lys Asp Pro Thr Ser Gly Lys His Ala Ala
 340 345 350
 Thr Lys Asp Tyr Val Asp Glu Lys Ile Ala Glu Leu Lys Lys Leu Ile
 355 360 365
 Leu Lys Lys
 370

<210> 35

<211> 1628

<212> PRT

<213> Clostridium perfringens

<220>

<223> hyaluronidase

<400> 35

Met Asn Lys Asn Ile Arg Lys Ile Ile Thr Ser Thr Val Leu Ala Ala
 1 5 10 15
 Met Thr Ile Ser Val Leu Pro Ser Asn Leu Val Val Phe Ala Thr Asp
 20 25 30
 Gly Ile Thr Glu Asn Phe Tyr Glu Ile Tyr Pro Lys Pro Gln Glu Ile
 35 40 45
 Ser Tyr Ser Gly Gly Glu Phe Gln Ile Ser Asp Glu Ile Asn Ile Val
 50 55 60
 Tyr Asp Asp Gly Ile Asp Thr Tyr Thr Lys Lys Arg Val Asp Glu Val
 65 70 75 80
 Leu Glu Ala Ser Asn Leu Glu Ala Thr Val Ser Asn Glu Ile Val Pro
 85 90 95
 Gly Lys Thr Asn Phe Leu Val Gly Ile Asn Glu Ser Gly Gly Val Val
 100 105 110
 Asp Asn Tyr Phe Asn Lys Asn Ile Pro His Asp Glu Ser Phe Phe Asp
 115 120 125
 Glu Lys Met Asp Ala Asn Ile Val Ser Val Lys Asp Gly Val Ile Gly
 130 135 140
 Val Ile Gly Glu Asp Thr Asp Ser Ala Phe Tyr Gly Val Thr Thr Leu
 145 150 155 160
 Lys His Val Phe Asn Gln Leu Glu Glu Gly Asn Lys Ile Gln Ser Phe
 165 170 175
 Arg Ala Asp Asp Tyr Ala Glu Val Ala His Arg Gly Phe Ile Glu Gly
 180 185 190
 Tyr Tyr Gly Asn Pro Trp Ser Asn Glu Asp Arg Ala Glu Leu Met Lys
 195 200 205
 Phe Gly Gly Asp Tyr Lys Leu Asn Gln Tyr Val Phe Ala Pro Lys Asp
 210 215 220
 Asp Pro Tyr His Asn Ser Lys Trp Arg Asp Leu Tyr Pro Glu Glu Lys
 225 230 235 240
 Leu Ser Glu Ile Lys Lys Leu Ala Gln Val Gly Asn Glu Thr Lys Asn
 245 250 255
 Arg Tyr Val Tyr Ala Leu His Pro Phe Met Asn Asn Pro Val Arg Phe
 260 265 270
 Asp Thr Glu Asn Tyr Gln Asn Asp Leu Gly Val Ile Lys Ala Lys
 275 280 285
 Phe Thr Gln Leu Leu Glu Asn Asp Val Arg Gln Phe Ala Ile Leu Ala
 290 295 300
 Asp Asp Ala Ser Ala Pro Ala Gln Gly Ala Ser Met Tyr Val Lys Leu
 305 310 315 320
 Leu Thr Asp Leu Thr Arg Trp Leu Glu Glu Gln Gln Ser Thr Tyr Pro

3108SEQPC1

Asp	Leu	Lys	Thr	325	Asp	Leu	Met	Phe	Cys	330	Pro	Ser	Asp	Tyr	Tyr	335	Gly	Asn
Gly	Ser	Ser	Ala	340	Gln	Leu	Lys	Glu	Leu	345	Asn	Lys	Ala	Glu	Asp	350	Asn	Val
Ser	Ile	Val	Met	355	Thr	Gly	Gly	Arg	Ile	360	Trp	Gly	Glu	Val	Asp	365	Glu	Asn
Phe	Ala	Asn	Asn	370	Phe	Met	Asn	Asn	Ile	375	Ser	Thr	Glu	Gly	His	380	Pro	Gly
385	Arg	Ala	Pro	390	Phe	Trp	Ile	Asn	Trp	395	Pro	Cys	Ser	Asp	Asn	400	Ser	Lys
Gln	His	Leu	Ile	405	Met	Gly	Gly	Asn	Asp	410	Thr	Phe	Leu	His	Pro	415	Gly	Val
Asp	Pro	Ser	Lys	420	Ile	Asp	Gly	Ile	Val	425	Leu	Asn	Pro	Met	Gln	430	Gln	Ala
Glu	Ala	Asn	Lys	435	Ser	Ala	Leu	Phe	Ala	440	Ile	Ala	Asp	Tyr	Ala	445	Trp	Asn
Ile	Trp	Asp	Asn	450	Lys	Glu	Glu	Ala	Asp	455	Glu	Asn	Trp	Asn	Asp	460	Ser	Phe
465	Lys	Tyr	Met	470	Asp	His	Gly	Thr	Ala	475	Glu	Thr	Asn	Ser	Ser	480	Leu	Ala
Leu	Arg	Glu	Ile	485	Ser	Lys	His	Met	Ile	490	Asn	Gln	Asn	Met	Asp	495	Gly	Arg
Val	Arg	Pro	Leu	500	Gln	Glu	Ser	Val	Glu	505	Leu	Ala	Pro	Lys	Leu	510	Glu	Ala
Phe	Lys	Gln	Lys	515	Tyr	Asp	Ser	Gly	Ala	520	Ser	Ile	Lys	Glu	Asp	525	Ala	Leu
Glu	Leu	Ile	Ala	530	Glu	Phe	Thr	Asn	Leu	535	Gln	Lys	Ala	Ala	Asp	540	Tyr	Tyr
545	Lys	Asn	Asn	550	Pro	Gly	Asn	Glu	Arg	555	Arg	Asp	Gln	Ile	Ile	560	Tyr	Trp
Leu	Asn	Cys	Trp	565	Glu	Asp	Thr	Met	Asp	570	Ala	Ala	Ile	Gly	Tyr	575	Leu	Lys
Ser	Ala	Ile	Ala	580	Ile	Glu	Glu	Gly	Asp	585	Asp	Glu	Ala	Ala	Trp	590	Ala	Asn
Tyr	Ser	Glu	Ala	595	Gln	Gly	Ala	Phe	Glu	600	Lys	Ser	Lys	Thr	Tyr	605	Gly	Phe
His	Tyr	Val	Asp	610	His	Thr	Glu	Tyr	Ala	615	Glu	Val	Gly	Val	Gln	620	His	Ile
625	Val	Pro	Phe	630	Ile	Lys	Ser	Met	Gly	635	Gln	Asn	Leu	Ser	Val	640	Ile	Gly
Ser	Ile	Val	Asp	645	Pro	Asn	Arg	Ile	Ile	650	Ala	Thr	Tyr	Ile	Ser	655	Asn	Arg
Gln	Asp	Ala	Pro	660	Thr	Gly	Asn	Pro	Asp	665	Asn	Ile	Phe	Asp	Asn	670	Asn	Ala
Ser	Thr	Glu	Leu	675	Val	Tyr	Lys	Asn	Pro	680	Asn	Arg	Ile	Asp	Val	685	Gly	Thr
Tyr	Val	Gly	Val	690	Lys	Tyr	Ser	Asn	Pro	695	Ile	Thr	Leu	Asn	Asn	700	Val	Glu
705	Phe	Leu	Met	710	Gly	Ala	Asn	Ser	Asn	715	Pro	Asp	Thr	Met	Gln	720	Lys	Ala
Lys	Ile	Gln	Tyr	725	Thr	Val	Asp	Gly	Arg	730	Glu	Trp	Ile	Asp	Leu	735	Glu	Glu
Gly	Val	Glu	Tyr	740	Thr	Met	Pro	Gly	Ala	745	Ile	Lys	Val	Glu	Asn	750	Leu	Asp
Leu	Lys	Val	Arg	755	Gly	Val	Arg	Leu	Ile	760	Ala	Thr	Glu	Ala	Arg	765	Glu	Asn
Thr	Trp	Leu	Gly	770	Val	Arg	Asp	Ile	Asn	775	Val	Asn	Lys	Lys	Glu	780	Asp	Ser
785	Asn	Ser	Gly	790	Val	Glu	Phe	Asn	Pro	795	Leu	Ile	Arg	Ser	Glu	800	Ser	Trp
Gln	Val	Tyr	Glu	805	Gly	Asn	Glu	Ala	Asn	810	Leu	Leu	Asp	Gly	Asp	815	Asp	Asn
Thr	Gly	Val	Trp	820	Tyr	Lys	Thr	Leu	Asn	825	Gly	Asp	Thr	Ser	Leu	830	Ala	Gly
Glu	Phe	Ile	Gly	835	Leu	Asp	Leu	Gly	Lys	840	Glu	Ile	Lys	Leu	Asp	845	Gly	Ile
850	Arg	Phe	Val	855	Ile	Gly	Lys	Asn	Gly	860	Gly	Ser	Ser	Asp	Lys	865	Trp	Asn

3108SEQPC1

865 Lys Phe Lys Leu Glu Tyr Ser Leu Asp Asn Glu Ser Trp Thr Thr Ile
 870 875 880
 Lys Glu Tyr Asp Lys Thr Gly Ala Pro Ala Gly Lys Asp Val Ile Glu
 885 890 895
 Glu Ser Phe Glu Thr Pro Ile Ser Ala Lys Tyr Ile Arg Leu Thr Asn
 900 905 910
 Met Glu Asn Ile Asn Lys Trp Leu Thr Phe Ser Glu Phe Ala Ile Ile
 915 920 925
 Ser Asp Glu Leu Glu Asn Ala Gly Asn Lys Glu Asn Val Tyr Thr Asn
 930 935 940
 945 Thr Glu Leu Asp Leu Leu Ser Leu Ala Lys Glu Asp Val Thr Lys Leu
 950 955 960
 Ile Pro Thr Asp Asp Ile Ser Leu Asn His Gly Glu Tyr Ile Gly Val
 965 970 975
 Lys Leu Asn Arg Ile Lys Asp Leu Ser Asn Ile Asn Leu Glu Ile Ser
 980 985 990
 Asn Asp Thr Gly Leu Lys Leu Gln Ser Ser Met Asn Gly Val Glu Trp
 995 1000 1005
 1010 Thr Glu Ile Thr Asp Lys Asn Thr Leu Glu Asp Gly Arg Tyr Val Arg
 1015 1020 1025
 1030 1035 1040
 Leu Ile Asn Thr Ser Asn Glu Ala Val Asn Phe Asn Leu Thr Lys Phe
 1045 1050 1055
 Glu Val Asn Ser Asn Glu Val Tyr Glu Pro Ser Leu Val Asp Ala Tyr
 1060 1065 1070
 Val Gly Asp Asp Gly Ala Lys Lys Ala Val Asp Gly Asp Leu Lys Thr
 1075 1080 1085
 Arg Val Lys Phe Leu Gly Ala Pro Ser Thr Gly Asp Thr Ile Val Tyr
 1090 1095 1100
 Asp Leu Gly Gln Glu Ile Leu Val Asp Asn Leu Lys Tyr Val Val Leu
 1105 1110 1115
 Asp Thr Glu Val Asp His Val Arg Asp Gly Lys Ile Gln Leu Ser Leu
 1125 1130 1135
 Asp Gly Glu Thr Trp Thr Asp Ala Ile Thr Ile Gly Asp Gly Val Glu
 1140 1145 1150
 Asn Gly Val Asp Asp Met Phe Ser Thr Pro Leu Lys Asn Gly Tyr Lys
 1155 1160 1165
 His Gly Asn Gln Ser Gly Gly Ile Val Pro Ile Asp Ser Ala Tyr Val
 1170 1175 1180
 Glu Gly Asp Asn Leu Asn Gln Lys Ala Arg Tyr Val Arg Ile Leu Phe
 1185 1190 1195
 Thr Ala Pro Tyr Arg His Arg Trp Thr Val Ile Asn Glu Leu Met Ile
 1205 1210 1215
 Asn Asn Gly Glu Tyr Ile Ser Thr Val Asn Asp Pro Thr Tyr Ile Ser
 1220 1225 1230
 Asn Pro Ile Glu Glu Arg Gly Phe Ala Pro Ser Asn Leu Arg Asp Gly
 1235 1240 1245
 Asn Leu Thr Thr Ser Tyr Lys Pro Asn Thr Asn Asn Gly Glu Ile Ser
 1250 1255 1260
 Glu Gly Ser Ile Thr Tyr Arg Leu Ser Glu Lys Thr Asp Val Arg Lys
 1265 1270 1275
 Val Thr Ile Val Gln Ser Gly Ser Ser Ile Ser Asn Ala Lys Val Met
 1285 1290 1295
 Ala Arg Val Gly Asp Gly Ser Glu Asn Val Thr Asp Gln Trp Val Gln
 1300 1305 1310
 Leu Gly Thr Leu Ser Asn Ser Leu Asn Glu Phe Ile Asn Arg Asp Tyr
 1315 1320 1325
 Asn Asn Ile Tyr Glu Ile Lys Ile Glu Trp Thr Asp Val Ala Pro Asn
 1330 1335 1340
 Ile Tyr Glu Ile Ile Thr Leu Asn Gln Glu Phe Glu Phe Pro Val Asn
 1345 1350 1355
 Asp Ser Leu Lys Ala Lys Tyr Asp Glu Leu Ile Asn Leu Ser Gly Asp
 1365 1370 1375
 Glu Tyr Thr Leu Ser Ser Phe Glu Thr Leu Lys Glu Ala Leu Asn Glu
 1380 1385 1390
 Ala Lys Ser Ile Leu Asp Asp Ser Asn Ser Ser Gln Lys Lys Ile Asp
 1395 1400 1405
 Lys Ala Leu Glu Lys Leu Asn Lys Ala Glu Glu Arg Leu Asp Leu Arg

3108SEQPC1

1410 1415 1420
 Ala Thr Asp Phe Glu Asp Phe Asn Lys Val Leu Thr Leu Gly Asn Ser
 1425 1430 1435 1440
 Leu Val Glu Glu Glu Tyr Thr Ala Glu Ser Trp Ala Leu Phe Ser Glu
 1445 1450 1455
 Val Leu Glu Ala Ala Asn Glu Ala Asn Lys Asn Lys Ala Asp Tyr Thr
 1460 1465 1470
 Gln Asp Gln Ile Asn Gln Ile Val Ile Asp Leu Asp Ala Ser Ile Lys
 1475 1480 1485
 Ala Leu Val Lys Glu Thr Pro Glu Val Asp Lys Thr Asn Leu Gly Glu
 1490 1495 1500
 Leu Ile Asn Gln Gly Lys Ser Leu Leu Asp Glu Ser Val Glu Gly Phe
 1505 1510 1515 1520
 Asn Val Gly Glu Tyr His Lys Gly Ala Lys Asp Gly Leu Thr Val Glu
 1525 1530 1535
 Ile Asn Lys Ala Glu Glu Val Phe Asn Lys Glu Asp Ala Thr Glu Glu
 1540 1545 1550
 Glu Ile Asn Leu Ala Lys Glu Ser Leu Glu Gly Ala Ile Ala Arg Phe
 1555 1560 1565
 Asn Ser Leu Leu Ile Glu Glu Ser Thr Gly Asp Phe Asn Gly Asn Gly
 1570 1575 1580
 Lys Ile Asp Ile Gly Asp Leu Ala Met Val Ser Lys Asn Ile Gly Ser
 1585 1590 1595 1600
 Thr Thr Asn Thr Ser Leu Asp Leu Asn Lys Asp Gly Ser Ile Asp Glu
 1605 1610 1615
 Tyr Glu Ile Ser Phe Ile Asn His Arg Ile Leu Asn
 1620 1625

<210> 36
 <211> 435
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Hyaluronidase-1 [Precursor]

<400> 36
 Met Ala Ala His Leu Leu Pro Ile Cys Ala Leu Phe Leu Thr Leu Leu
 1 5 10 15
 Asp Met Ala Gln Gly Phe Arg Gly Pro Leu Leu Pro Asn Arg Pro Phe
 20 25 30
 Thr Thr Val Trp Asn Ala Asn Thr Gln Trp Cys Leu Glu Arg His Gly
 35 40 45
 Val Asp Val Asp Val Ser Val Phe Asp Val Val Ala Asn Pro Gly Gln
 50 55 60
 Thr Phe Arg Gly Pro Asp Met Thr Ile Phe Tyr Ser Ser Gln Leu Gly
 65 70 75 80
 Thr Tyr Pro Tyr Tyr Thr Pro Thr Gly Glu Pro Val Phe Gly Gly Leu
 85 90 95
 Pro Gln Asn Ala Ser Leu Ile Ala His Leu Ala Arg Thr Phe Gln Asp
 100 105 110
 Ile Leu Ala Ala Ile Pro Ala Pro Asp Phe Ser Gly Leu Ala Val Ile
 115 120 125
 Asp Trp Glu Ala Trp Arg Pro Arg Trp Ala Phe Asn Trp Asp Thr Lys
 130 135 140
 Asp Ile Tyr Arg Gln Arg Ser Arg Ala Leu Val Gln Ala Gln His Pro
 145 150 155 160
 Asp Trp Pro Ala Pro Gln Val Glu Ala Val Ala Gln Asp Gln Phe Gln
 165 170 175
 Gly Ala Ala Arg Ala Trp Met Ala Gly Thr Leu Gln Leu Gly Arg Ala
 180 185 190
 Leu Arg Pro Arg Gly Leu Trp Gly Phe Tyr Gly Phe Pro Asp Cys Tyr
 195 200 205
 Asn Tyr Asp Phe Leu Ser Pro Asn Tyr Thr Gly Gln Cys Pro Ser Gly
 210 215 220
 Ile Arg Ala Gln Asn Asp Gln Leu Gly Trp Leu Trp Gly Gln Ser Arg
 225 230 235 240

3108SEQPC1

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

<210> 37

<211> 473

<212> PRT

<213> Homo sapiens

<220>

<223> Hyaluronidase-2 [Precursor]

<400> 37

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

3108SEQPC1

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

<210> 38

<211> 417

<212> PRT

<213> Homo sapiens

<220>

<223> Hyaluronidase-3 [Precursor]

<400> 38

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

3108SEQPC1

```

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

```

<210> 39
 <211> 481
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Hyaluronidase-4

```

<400> 39
Met Lys Val Leu Ser Glu Gly Gln Leu Lys Leu Cys Val Val Gln Pro
1      5      10      15
Val His Leu Thr Ser Trp Leu Leu Ile Phe Phe Ile Leu Lys Ser Ile
      20      25      30
Ser Cys Leu Lys Pro Ala Arg Leu Pro Ile Tyr Gln Arg Lys Pro Phe
      35      40      45
Ile Ala Ala Trp Asn Ala Pro Thr Asp Gln Cys Leu Ile Lys Tyr Asn
      50      55      60
Leu Arg Leu Asn Leu Lys Met Phe Pro Val Ile Gly Ser Pro Leu Ala
65      70      75      80
Lys Ala Arg Gly Gln Asn Val Thr Ile Phe Tyr Val Asn Arg Leu Gly
      85      90      95
Tyr Tyr Pro Trp Tyr Thr Ser Gln Gly Val Pro Ile Asn Gly Gly Leu
      100      105      110
Pro Gln Asn Ile Ser Leu Gln Val His Leu Glu Lys Ala Asp Gln Asp
      115      120      125
Ile Asn Tyr Tyr Ile Pro Ala Glu Asp Phe Ser Gly Leu Ala Val Ile
      130      135      140
Asp Trp Glu Tyr Trp Arg Pro Gln Trp Ala Arg Asn Trp Asn Ser Lys
145      150      155      160
Asp Val Tyr Arg Gln Lys Ser Arg Lys Leu Ile Ser Asp Met Gly Lys
      165      170      175
Asn Val Ser Ala Thr Asp Ile Glu Tyr Leu Ala Lys Val Thr Phe Glu
      180      185      190
Glu Ser Ala Lys Ala Phe Met Lys Glu Thr Ile Lys Leu Gly Ile Lys
      195      200      205
Ser Arg Pro Lys Gly Leu Trp Gly Tyr Tyr Leu Tyr Pro Asp Cys His
210      215      220
Asn Tyr Asn Val Tyr Ala Pro Asn Tyr Ser Gly Ser Cys Pro Glu Asp
225      230      235      240
Glu Val Leu Arg Asn Asn Glu Leu Ser Trp Leu Trp Asn Ser Ser Ala
      405      410      415

```

3108SEQPC1

Ala	Leu	Tyr	Pro	Ser	Ile	Gly	Val	Trp	Lys	Ser	Leu	Gly	Asp	Ser	Glu
			245						250					255	
Asn	Ile	Leu	Arg	Phe	Ser	Lys	Phe	Arg	Val	His	Glu	Ser	Met	Arg	Ile
		275					280					285			
Ser	Thr	Met	Thr	Ser	His	Asp	Tyr	Ala	Leu	Pro	Val	Phe	Val	Tyr	Thr
		290				295					300				
Arg	Leu	Gly	Tyr	Arg	Asp	Glu	Pro	Leu	Phe	Phe	Leu	Ser	Lys	Gln	Asp
		305			310					315				320	
Leu	Val	Ser	Thr	Ile	Gly	Glu	Ser	Ala	Ala	Leu	Gly	Ala	Ala	Gly	Ile
				325					330					335	
Val	Ile	Trp	Gly	Asp	Met	Asn	Leu	Thr	Ala	Ser	Lys	Ala	Asn	Cys	Thr
			340					345					350		
Lys	Val	Lys	Gln	Phe	Val	Ser	Ser	Asp	Leu	Gly	Ser	Tyr	Ile	Ala	Asn
		355					360					365			
Val	Thr	Arg	Ala	Ala	Glu	Val	Cys	Ser	Leu	His	Leu	Cys	Arg	Asn	Asn
		370				375					380				
Gly	Arg	Cys	Ile	Arg	Lys	Met	Trp	Asn	Ala	Pro	Ser	Tyr	Leu	His	Leu
		385			390				395					400	
Asn	Pro	Ala	Ser	Tyr	His	Ile	Glu	Ala	Ser	Glu	Asp	Gly	Glu	Phe	Thr
			405						410					415	
Val	Lys	Gly	Lys	Ala	Ser	Asp	Thr	Asp	Leu	Ala	Val	Met	Ala	Asp	Thr
			420					425					430		
Phe	Ser	Cys	His	Cys	Tyr	Gln	Gly	Tyr	Glu	Gly	Ala	Asp	Cys	Arg	Glu
		435					440					445			
Ile	Lys	Thr	Ala	Asp	Gly	Cys	Ser	Gly	Val	Ser	Pro	Ser	Pro	Gly	Ser
		450				455					460				
Leu	Met	Thr	Leu	Cys	Leu	Leu	Leu	Leu	Ala	Ser	Tyr	Arg	Ser	Ile	Gln
		465			470				475					480	
Leu															

<210> 40

<211> 467

<212> PRT

<213> Homo sapiens

<220>

<223> PH20 precursor 1-467

<400> 40

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

3108SEQPC1

Leu Leu Arg Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys
 210 215 220
 Tyr Asn His His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn
 225 230 235 240
 Val Glu Ile Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser
 245 250 255
 Thr Ala Leu Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val
 260 265 270
 Ala Ala Thr Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val
 275 280 285
 Ser Lys Ile Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr
 290 295 300
 Arg Ile Val Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu
 305 310 315 320
 Leu Val Tyr Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile
 325 330 335
 Val Ile Trp Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu
 340 345 350
 Leu Leu Asp Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn
 355 360 365
 Val Thr Leu Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln
 370 375 380
 Gly Val Cys Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu
 385 390 395 400
 Asn Pro Asp Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr
 405 410 415
 Val Arg Gly Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys
 420 425 430
 Phe Tyr Cys Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp
 435 440 445
 Val Lys Asp Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys
 450 455 460
 Ile Asp Ala
 465

<210> 41

<211> 477

<212> PRT

<213> Homo sapiens

<220>

<223> PH20 precursor 1-477

<400> 41

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

3108SEQPC1

Val Gln Leu Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe
 180 185 190
 Glu Lys Ala Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys
 195 200 205
 Leu Leu Arg Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys
 210 215 220
 Tyr Asn His His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn
 225 230 235 240
 Val Glu Ile Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser
 245 250 255
 Thr Ala Leu Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val
 260 265 270
 Ala Ala Thr Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val
 275 280 285
 Ser Lys Ile Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr
 290 295 300
 Arg Ile Val Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu
 305 310 315 320
 Leu Val Tyr Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile
 325 330 335
 Val Ile Trp Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu
 340 345 350
 Leu Leu Asp Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn
 355 360 365
 Val Thr Leu Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln
 370 375 380
 Gly Val Cys Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu
 385 390 395 400
 Asn Pro Asp Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr
 405 410 415
 Val Arg Gly Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys
 420 425 430
 Phe Tyr Cys Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp
 435 440 445
 Val Lys Asp Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys
 450 455 460
 Ile Asp Ala Phe Leu Lys Pro Pro Met Glu Thr Glu Glu
 465 470 475

<210> 42

<211> 478

<212> PRT

<213> Homo sapiens

<220>

<223> PH20 precursor 1-478

<400> 42

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

3108SEQPC1

```

Ile Asp Trp Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro
145      150      155      160
Lys Asp Val Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn
      165      170      175
Val Gln Leu Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe
      180      185      190
Glu Lys Ala Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys
      195      200      205
Leu Leu Arg Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys
      210      215      220
Tyr Asn His His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn
      225      230      235
Val Glu Ile Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser
      245      250      255
Thr Ala Leu Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val
      260      265      270
Ala Ala Thr Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val
      275      280      285
Ser Lys Ile Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr
      290      295      300
Arg Ile Val Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu
      305      310      315
Leu Val Tyr Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile
      325      330      335
Val Ile Trp Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu
      340      345      350
Leu Leu Asp Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn
      355      360      365
Val Thr Leu Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln
      370      375      380
Gly Val Cys Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu
      385      390      395
Asn Pro Asp Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr
      405      410      415
Val Arg Gly Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys
      420      425      430
Phe Tyr Cys Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp
      435      440      445
Val Lys Asp Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys
      450      455      460
Ile Asp Ala Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro
      465      470      475

```

<210> 43

<211> 479

<212> PRT

<213> Homo sapiens

<220>

<223> PH20 precursor 1-479

<400> 43

```

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

```

3108SEQPC1

Gly Ile Pro Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys
115 120 125
Lys Asp Ile Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val
130 135 140
Ile Asp Trp Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro
145 150 155 160
Lys Asp Val Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn
165 170 175
Val Gln Leu Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe
180 185 190
Glu Lys Ala Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys
195 200 205
Leu Leu Arg Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys
210 215 220
Tyr Asn His His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn
225 230 235 240
Val Glu Ile Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser
245 250 255
Thr Ala Leu Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val
260 265 270
Ala Ala Thr Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val
275 280 285
Ser Lys Ile Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr
290 295 300
Arg Ile Val Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu
305 310 315 320
Leu Val Tyr Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile
325 330 335
Val Ile Trp Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu
340 345 350
Leu Leu Asp Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn
355 360 365
Val Thr Leu Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln
370 375 380
Gly Val Cys Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu
385 390 395 400
Asn Pro Asp Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr
405 410 415
Val Arg Gly Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys
420 425 430
Phe Tyr Cys Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp
435 440 445
Val Lys Asp Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys
450 455 460
Ile Asp Ala Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln
465 470 475

<210> 44

<211> 480

<212> PRT

<213> Homo sapiens

<220>

<223> PH20 precursor 1-480

<400> 44

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

3108SEQPC1

Ile	Asn	Ala	Thr	Gly	Gln	Gly	Val	Thr	Ile	Phe	Tyr	Val	Asp	Arg	Leu
				85					90					95	
Gly	Tyr	Tyr	Pro	Tyr	Ile	Asp	Ser	Ile	Thr	Gly	Val	Thr	Val	Asn	Gly
			100					105					110		
Gly	Ile	Pro	Gln	Lys	Ile	Ser	Leu	Gln	Asp	His	Leu	Asp	Lys	Ala	Lys
		115					120					125			
Lys	Asp	Ile	Thr	Phe	Tyr	Met	Pro	Val	Asp	Asn	Leu	Gly	Met	Ala	Val
	130					135					140				
Ile	Asp	Trp	Glu	Glu	Trp	Arg	Pro	Thr	Trp	Ala	Arg	Asn	Trp	Lys	Pro
145					150					155					160
Lys	Asp	Val	Tyr	Lys	Asn	Arg	Ser	Ile	Glu	Leu	Val	Gln	Gln	Gln	Asn
				165					170					175	
Val	Gln	Leu	Ser	Leu	Thr	Glu	Ala	Thr	Glu	Lys	Ala	Lys	Gln	Glu	Phe
			180					185					190		
Glu	Lys	Ala	Gly	Lys	Asp	Phe	Leu	Val	Glu	Thr	Ile	Lys	Leu	Gly	Lys
		195					200					205			
Leu	Leu	Arg	Pro	Asn	His	Leu	Trp	Gly	Tyr	Tyr	Leu	Phe	Pro	Asp	Cys
	210					215					220				
Tyr	Asn	His	His	Tyr	Lys	Lys	Pro	Gly	Tyr	Asn	Gly	Ser	Cys	Phe	Asn
225					230					235					240
Val	Glu	Ile	Lys	Arg	Asn	Asp	Asp	Leu	Ser	Trp	Leu	Trp	Asn	Glu	Ser
				245					250					255	
Thr	Ala	Leu	Tyr	Pro	Ser	Ile	Tyr	Leu	Asn	Thr	Gln	Gln	Ser	Pro	Val
			260					265					270		
Ala	Ala	Thr	Leu	Tyr	Val	Arg	Asn	Arg	Val	Arg	Glu	Ala	Ile	Arg	Val
		275					280					285			
Ser	Lys	Ile	Pro	Asp	Ala	Lys	Ser	Pro	Leu	Pro	Val	Phe	Ala	Tyr	Thr
	290					295					300				
Arg	Ile	Val	Phe	Thr	Asp	Gln	Val	Leu	Lys	Phe	Leu	Ser	Gln	Asp	Glu
305					310					315					320
Leu	Val	Tyr	Thr	Phe	Gly	Glu	Thr	Val	Ala	Leu	Gly	Ala	Ser	Gly	Ile
				325					330					335	
Val	Ile	Trp	Gly	Thr	Leu	Ser	Ile	Met	Arg	Ser	Met	Lys	Ser	Cys	Leu
		340						345					350		
Leu	Leu	Asp	Asn	Tyr	Met	Glu	Thr	Ile	Leu	Asn	Pro	Tyr	Ile	Ile	Asn
		355					360					365			
Val	Thr	Leu	Ala	Ala	Lys	Met	Cys	Ser	Gln	Val	Leu	Cys	Gln	Glu	Gln
	370					375					380				
Gly	Val	Cys	Ile	Arg	Lys	Asn	Trp	Asn	Ser	Ser	Asp	Tyr	Leu	His	Leu
385					390					395					400
Asn	Pro	Asp	Asn	Phe	Ala	Ile	Gln	Leu	Glu	Lys	Gly	Gly	Lys	Phe	Thr
				405					410					415	
Val	Arg	Gly	Lys	Pro	Thr	Leu	Glu	Asp	Leu	Glu	Gln	Phe	Ser	Glu	Lys
				420				425					430		
Phe	Tyr	Cys	Ser	Cys	Tyr	Ser	Thr	Leu	Ser	Cys	Lys	Glu	Lys	Ala	Asp
		435					440					445			
Val	Lys	Asp	Thr	Asp	Ala	Val	Asp	Val	Cys	Ile	Ala	Asp	Gly	Val	Cys
	450					455					460				
Ile	Asp	Ala	Phe	Leu	Lys	Pro	Pro	Met	Glu	Thr	Glu	Glu	Pro	Gln	Ile
465					470					475					480

<210> 45

<211> 481

<212> PRT

<213> Homo sapiens

<220>

<223> PH20 precursor 1-481

<400> 45

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

3108SEQPC1

Phe Leu Trp Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe
 50 55 60
 Asp Glu Pro Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg
 65 70 75 80
 Ile Asn Ala Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu
 85 90 95
 Gly Tyr Tyr Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly
 100 105 110
 Gly Ile Pro Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys
 115 120 125
 Lys Asp Ile Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val
 130 135 140
 Ile Asp Trp Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro
 145 150 155 160
 Lys Asp Val Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn
 165 170 175
 Val Gln Leu Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe
 180 185 190
 Glu Lys Ala Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys
 195 200 205
 Leu Leu Arg Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys
 210 215 220
 Tyr Asn His His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn
 225 230 235 240
 Val Glu Ile Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser
 245 250 255
 Thr Ala Leu Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val
 260 265 270
 Ala Ala Thr Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val
 275 280 285
 Ser Lys Ile Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr
 290 295 300
 Arg Ile Val Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu
 305 310 315 320
 Leu Val Tyr Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile
 325 330 335
 Val Ile Trp Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu
 340 345 350
 Leu Leu Asp Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn
 355 360 365
 Val Thr Leu Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln
 370 375 380
 Gly Val Cys Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu
 385 390 395 400
 Asn Pro Asp Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr
 405 410 415
 Val Arg Gly Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys
 420 425 430
 Phe Tyr Cys Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp
 435 440 445
 Val Lys Asp Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys
 450 455 460
 Ile Asp Ala Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile
 465 470 475 480
 Phe

<210> 46

<211> 483

<212> PRT

<213> Homo sapiens

<220>

<223> PH20 precursor 1-483

<400> 46

3108SEQPC1

Met	Gly	Val	Leu	Lys	Phe	Lys	His	Ile	Phe	Phe	Arg	Ser	Phe	Val	Lys
1				5					10					15	
Ser	Ser	Gly	Val	Ser	Gln	Ile	Val	Phe	Thr	Phe	Leu	Leu	Ile	Pro	Cys
			20					25					30		
Cys	Leu	Thr	Leu	Asn	Phe	Arg	Ala	Pro	Pro	Val	Ile	Pro	Asn	Val	Pro
		35					40					45			
Phe	Leu	Trp	Ala	Trp	Asn	Ala	Pro	Ser	Glu	Phe	Cys	Leu	Gly	Lys	Phe
	50					55					60				
Asp	Glu	Pro	Leu	Asp	Met	Ser	Leu	Phe	Ser	Phe	Ile	Gly	Ser	Pro	Arg
65					70					75					80
Ile	Asn	Ala	Thr	Gly	Gln	Gly	Val	Thr	Ile	Phe	Tyr	Val	Asp	Arg	Leu
			85						90					95	
Gly	Tyr	Tyr	Pro	Tyr	Ile	Asp	Ser	Ile	Thr	Gly	Val	Thr	Val	Asn	Gly
			100					105					110		
Gly	Ile	Pro	Gln	Lys	Ile	Ser	Leu	Gln	Asp	His	Leu	Asp	Lys	Ala	Lys
		115					120					125			
Lys	Asp	Ile	Thr	Phe	Tyr	Met	Pro	Val	Asp	Asn	Leu	Gly	Met	Ala	Val
	130					135					140				
Ile	Asp	Trp	Glu	Glu	Trp	Arg	Pro	Thr	Trp	Ala	Arg	Asn	Trp	Lys	Pro
145					150					155					160
Lys	Asp	Val	Tyr	Lys	Asn	Arg	Ser	Ile	Glu	Leu	Val	Gln	Gln	Gln	Asn
				165					170					175	
Val	Gln	Leu	Ser	Leu	Thr	Glu	Ala	Thr	Glu	Lys	Ala	Lys	Gln	Glu	Phe
		180						185					190		
Glu	Lys	Ala	Gly	Lys	Asp	Phe	Leu	Val	Glu	Thr	Ile	Lys	Leu	Gly	Lys
	195						200					205			
Leu	Leu	Arg	Pro	Asn	His	Leu	Trp	Gly	Tyr	Tyr	Leu	Phe	Pro	Asp	Cys
	210					215					220				
Tyr	Asn	His	His	Tyr	Lys	Lys	Pro	Gly	Tyr	Asn	Gly	Ser	Cys	Phe	Asn
225					230					235					240
Val	Glu	Ile	Lys	Arg	Asn	Asp	Asp	Leu	Ser	Trp	Leu	Trp	Asn	Glu	Ser
			245						250					255	
Thr	Ala	Leu	Tyr	Pro	Ser	Ile	Tyr	Leu	Asn	Thr	Gln	Gln	Ser	Pro	Val
		260						265					270		
Ala	Ala	Thr	Leu	Tyr	Val	Arg	Asn	Arg	Val	Arg	Glu	Ala	Ile	Arg	Val
	275						280					285			
Ser	Lys	Ile	Pro	Asp	Ala	Lys	Ser	Pro	Leu	Pro	Val	Phe	Ala	Tyr	Thr
	290					295					300				
Arg	Ile	Val	Phe	Thr	Asp	Gln	Val	Leu	Lys	Phe	Leu	Ser	Gln	Asp	Glu
305					310					315					320
Leu	Val	Tyr	Thr	Phe	Gly	Glu	Thr	Val	Ala	Leu	Gly	Ala	Ser	Gly	Ile
			325						330					335	
Val	Ile	Trp	Gly	Thr	Leu	Ser	Ile	Met	Arg	Ser	Met	Lys	Ser	Cys	Leu
		340						345					350		
Leu	Leu	Asp	Asn	Tyr	Met	Glu	Thr	Ile	Leu	Asn	Pro	Tyr	Ile	Ile	Asn
	355						360					365			
Val	Thr	Leu	Ala	Ala	Lys	Met	Cys	Ser	Gln	Val	Leu	Cys	Gln	Glu	Gln
	370					375					380				
Gly	Val	Cys	Ile	Arg	Lys	Asn	Trp	Asn	Ser	Ser	Asp	Tyr	Leu	His	Leu
385					390					395					400
Asn	Pro	Asp	Asn	Phe	Ala	Ile	Gln	Leu	Glu	Lys	Gly	Gly	Lys	Phe	Thr
			405						410					415	
Val	Arg	Gly	Lys	Pro	Thr	Leu	Glu	Asp	Leu	Glu	Gln	Phe	Ser	Glu	Lys
		420						425					430		
Phe	Tyr	Cys	Ser	Cys	Tyr	Ser	Thr	Leu	Ser	Cys	Lys	Glu	Lys	Ala	Asp
	435						440					445			
Val	Lys	Asp	Thr	Asp	Ala	Val	Asp	Val	Cys	Ile	Ala	Asp	Gly	Val	Cys
	450					455					460				
Ile	Asp	Ala	Phe	Leu	Lys	Pro	Pro	Met	Glu	Thr	Glu	Glu	Pro	Gln	Ile
465					470					475					480
Phe	Tyr	Asn													

<210> 47
 <211> 432
 <212> PRT
 <213> Homo sapiens

3108SEQPC1

<220>

<223> PH20 mature 36-467

<400> 47

Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1 5 10 15
 Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
 20 25 30
 Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
 35 40 45
 Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
 50 55 60
 Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
 65 70 75 80
 Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
 85 90 95
 Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
 100 105 110
 Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
 115 120 125
 Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
 130 135 140
 Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
 145 150 155 160
 Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
 165 170 175
 Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
 180 185 190
 His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
 195 200 205
 Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
 210 215 220
 Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
 225 230 235 240
 Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
 245 250 255
 Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
 260 265 270
 Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
 275 280 285
 Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
 290 295 300
 Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
 305 310 315 320
 Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
 325 330 335
 Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
 340 345 350
 Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
 355 360 365
 Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
 370 375 380
 Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
 385 390 395 400
 Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
 405 410 415
 Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala
 420 425 430

<210> 48

<211> 448

<212> PRT

<213> Homo sapiens

<220>

3108SEQPC1

<223> PH20 mature 36-483

<400> 48

Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1 5 10 15
 Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
 20 25 30
 Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
 35 40 45
 Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
 50 55 60
 Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
 65 70 75 80
 Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
 85 90 95
 Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
 100 105 110
 Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
 115 120 125
 Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
 130 135 140
 Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
 145 150 155 160
 Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
 165 170 175
 Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
 180 185 190
 His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
 195 200 205
 Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
 210 215 220
 Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
 225 230 235 240
 Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
 245 250 255
 Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
 260 265 270
 Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
 275 280 285
 Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
 290 295 300
 Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
 305 310 315 320
 Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
 325 330 335
 Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
 340 345 350
 Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
 355 360 365
 Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
 370 375 380
 Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
 385 390 395 400
 Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
 405 410 415
 Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala
 420 425 430
 Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile Phe Tyr Asn
 435 440 445

<210> 49

<211> 1446

<212> DNA

<213> Homo sapiens

<220>

<223> DNA encoding soluble rHuPH20 "precursor"

<400> 49

```

atgggagtg taaaattcaa gcacatcttt ttcagaagct ttgttaaatac aagtggagta 60
tcccagatag ttttcacctt ccttctgatt ccatgttgct tgactctgaa tttcagagca 120
cctcctgtta ttccaaatgt gccttttcctc tgggcctgga atgccccaaag tgaattttgt 180
cttgaaaaat ttgatgagcc actagatatg agcctcttct ctttcatagg aagccccga 240
ataaacgcca ccgggcaagg tgttacaata ttttatgttg atagacttgg ctactatcct 300
tacatagatt caatcacagg agtaactgtg aatggaggaa tccccagaa gatttcctta 360
caagaccatc tggacaaagc taagaaagac attacatctt atatgccagt agacaatttg 420
ggaatggctg ttattgactg ggaagaatgg agaccacactt gggcaagaaa ctggaaacct 480
aaagatgttt acaagaatag gtctattgaa ttggttcagc aacaaaatgt acaacttagt 540
ctcacagagg ccactgagaa agcaaaacaa gaatttgaaa aggcaggga ggatttcctg 600
gtagagacta taaaattggg aaaattactt cggccaaatc acttgtgggg ttattatctt 660
tttcgggatt gttacaacca tcactataag aaacccgggtt acaatggaag ttgcttcaat 720
gtagaaataa aaagaaatga tgatctcagc tgggttgaga atgaaagcac tgctctttac 780
ccatccatctt atttgaacac tcagcagctc cctgtagctg ctacactcta tgtgcgcaat 840
cgagttcggg aagccatcag agtttccaaa atacctgatg caaaaagtcc acttccgggtt 900
tttgcatata cccgcatagt ttttactgat caagttttga aattcctttc tcaagatgaa 960
cttggtata catitggcga aactgttgct ctgggtgctt ctggaattgt aatatgggga 1020
accctcagta taatgcgaag tatgaaatct tgcctgctcc tagacaatta catggagact 1080
atactgaatc cttacataat caacgtcaca ctacagcca aaatgtgtag ccaagtgtct 1140
tgccaggagc aaggagtgtg tataaggaaa aactggaatt caagtgacta tcttcacctc 1200
aaccagata attttgcctt tcaacttgag aaagggtgaa agttcacagt acgtggaaaa 1260
ccgacacttg aagacctgga gcaatcttct gaaaaatttt attgcagctg ttatagcacc 1320
ttgagttgta aggagaaagc tgatgtaaaa gacactgatg ctgttgatgt gtgtattgct 1380
gatggtgtct gtatagatgc ttttctaaaa cctcccatgg agacagaaga acctcaaatt 1440
ttctac

```

<210> 50

<211> 509

<212> PRT

<213> Homo sapiens

<220>

<223> PH20 variant P48A

<400> 50

```

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

```

3108SEQPC1

225	Val	Glu	Ile	Lys	Arg	Asn	Asp	Asp	Leu	Ser	Trp	Leu	Trp	Asn	Glu	Ser	240
					245					250						255	
Thr	Ala	Leu	Tyr	Pro	Ser	Ile	Tyr	Leu	Asn	Thr	Gln	Gln	Ser	Pro	Val		
			260					265					270				
Ala	Ala	Thr	Leu	Tyr	Val	Arg	Asn	Arg	Val	Arg	Glu	Ala	Ile	Arg	Val		
		275					280					285					
Ser	Lys	Ile	Pro	Asp	Ala	Lys	Ser	Pro	Leu	Pro	Val	Phe	Ala	Tyr	Thr		
	290					295					300						
Arg	Ile	Val	Phe	Thr	Asp	Gln	Val	Leu	Lys	Phe	Leu	Ser	Gln	Asp	Glu		
305					310					315					320		
Leu	Val	Tyr	Thr	Phe	Gly	Glu	Thr	Val	Ala	Leu	Gly	Ala	Ser	Gly	Ile		
				325					330					335			
Val	Ile	Trp	Gly	Thr	Leu	Ser	Ile	Met	Arg	Ser	Met	Lys	Ser	Cys	Leu		
			340					345					350				
Leu	Leu	Asp	Asn	Tyr	Met	Glu	Thr	Ile	Leu	Asn	Pro	Tyr	Ile	Ile	Asn		
		355				360						365					
Val	Thr	Leu	Ala	Ala	Lys	Met	Cys	Ser	Gln	Val	Leu	Cys	Gln	Glu	Gln		
	370					375					380						
Gly	Val	Cys	Ile	Arg	Lys	Asn	Trp	Asn	Ser	Ser	Asp	Tyr	Leu	His	Leu		
385					390					395					400		
Asn	Pro	Asp	Asn	Phe	Ala	Ile	Gln	Leu	Glu	Lys	Gly	Gly	Lys	Phe	Thr		
				405					410					415			
Val	Arg	Gly	Lys	Pro	Thr	Leu	Glu	Asp	Leu	Glu	Gln	Phe	Ser	Glu	Lys		
			420					425					430				
Phe	Tyr	Cys	Ser	Cys	Tyr	Ser	Thr	Leu	Ser	Cys	Lys	Glu	Lys	Ala	Asp		
		435					440					445					
Val	Lys	Asp	Thr	Asp	Ala	Val	Asp	Val	Cys	Ile	Ala	Asp	Gly	Val	Cys		
	450					455					460						
Ile	Asp	Ala	Phe	Leu	Lys	Pro	Pro	Met	Glu	Thr	Glu	Glu	Pro	Gln	Ile		
465					470					475					480		
Phe	Tyr	Asn	Ala	Ser	Pro	Ser	Thr	Leu	Ser	Ala	Thr	Met	Phe	Ile	Val		
				485					490					495			
Ser	Ile	Leu	Phe	Leu	Ile	Ile	Ser	Ser	Val	Ala	Ser	Leu					
		500						505									

<210> 51
 <211> 509
 <212> PRT
 <213> Homo sapiens

<220>
 <223> precursor PH20 variant L499W

<400> 51

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

[illegible]

3108SEQPC1

```

attgaaaaag gaagagtatg agtattcaac atttccgtgt cgcccttatt ccccttttttg 4980
cggcatttttg ccttcctggt tttgctcacc cagaaacgct ggtgaaagta aaagatgctg 5040
aagatcagtt ggggtgcacga gtgggttaca tcgaactgga tctcaacagc ggtaagatcc 5100
ttgagagttt tcgccccgaa gaacgttttc caatgatgag cactttttaa gttctgctat 5160
gtggcgcggt attatcccggt attgacgccg ggcaagagca actcggtcgc cgcatacact 5220
attctcagaa tgacttgggt gagtactcac cagtcacaga aaagcatctt acggatggca 5280
tgacagtaag agaattatgc agtgctgcca taaccatgag tgataaacact gcggccaact 5340
tacttctgac aacgatcgga ggaccgaagg agctaaccgc ttttttgac aacatggggg 5400
atcatgtaac tcgccttgat cggttgggaac cggagctgaa tgaagccata ccaaacgacg 5460
agcgtgacac cagcatgcct gtagcaatgg caacaacggt gcgcaaacta ttaactggcg 5520
aactacttac tctagcttcc cggcaacaat taatagactg gatggaggcg gataaagttg 5580
caggaccact tctgcgctcg gcccttcccg ctggctggtt tattgctgat aaatctggag 5640
ccggtgagcg tgggtctcgc ggtatcattg cagcactggg gccagatggt aagccctccc 5700
gtatcgtagt tatctacacg acggggagtc aggcactat ggatgaacga aatagacaga 5760
tcgctgagat aggtgcctca ctgattaagc attggtaact gtcagaccaa gtttactcat 5820
atatacttta gattgattta aaacttcatt tttaatttaa aaggatctag gtgaagatcc 5880
tttttgataa tctcatgacc aaaatccctt aacgtgagtt ttcgttcac tgagcgtcag 5940
accccgtaga aaagatcaaa ggatcttctt gagatccttt ttttctgctg gtaatctgct 6000
gcttgcaaac aaaaaaacca ccgctaccag cgggtggttg tttgccgat caagagctac 6060
caactctttt tccgaaggta actggcttca gcagagcgca gataccaaat actgttcttc 6120
tagtgtagcc gtagttaggc caccacttca agaactctgt agcaccgcct acatacctcg 6180
ctctgctaatt cctgttaccg gtggctgctg ccagtggcga taagtcgtgt cttaccgggt 6240
tggaactcaag acgatagtta ccggaataagg cgcagcggtc gggctgaacg gggggttcgt 6300
gcacacagcc cagcttggag cgaacgacct acaccgaact gagataccta cagcgtgagc 6360
tatgagaaaag cgccacgctt cccgaaggga gaaaggcgga caggatatccg gtaagcggca 6420
gggtcgggaac aggagagcgc acgagggagc ttccaggggg aaacgcctgg tatctttata 6480
gtcctgtcgg gtttcgccac ctctgacttg agcgtcgatt tttgtgatgc tcgtcagggg 6540
ggcggagcct atggaaaaac gccagcaacg cggccttttt acggttctct gccttttgct 6600
ggccttttgc tcacatggct cgacagatct 6630

```

<210> 53
 <211> 186
 <212> PRT
 <213> Mus musculus

<220>
 <223> dihydrofolate reductase

```

<400> 53
Val Arg Pro Leu Asn Cys Ile Val Ala Val Ser Gln Asn Met Gly Ile
 1           5           10           15
Gly Lys Asn Gly Asp Leu Pro Trp Pro Pro Leu Arg Asn Glu Phe Lys
 20           25           30
Tyr Phe Gln Arg Met Thr Thr Thr Ser Ser Val Glu Gly Lys Gln Asn
 35           40           45
Leu Val Ile Met Gly Arg Lys Thr Trp Phe Ser Ile Pro Glu Lys Asn
 50           55           60
Arg Pro Leu Lys Asp Arg Ile Asn Ile Val Leu Ser Arg Glu Leu Lys
 65           70           75           80
Glu Pro Pro Arg Gly Ala His Phe Leu Ala Lys Ser Leu Asp Asp Ala
 85           90           95
Leu Arg Leu Ile Glu Gln Pro Glu Leu Ala Ser Lys Val Asp Met Val
100           105           110
Trp Ile Val Gly Gly Ser Ser Val Tyr Gln Glu Ala Met Asn Gln Pro
115           120           125
Gly His Leu Arg Leu Phe Val Thr Arg Ile Met Gln Glu Phe Glu Ser
130           135           140
Asp Thr Phe Phe Pro Glu Ile Asp Leu Gly Lys Tyr Lys Leu Leu Pro
145           150           155           160
Glu Tyr Pro Gly Val Leu Ser Glu Val Gln Glu Glu Lys Gly Ile Lys
165           170           175
Tyr Lys Phe Glu Val Tyr Glu Lys Lys Asp
180           185

```

<210> 54
 <211> 6
 <212> PRT

<213> Artificial Sequence

<220>

<223> His tag

<400> 54

His His His His His
1 5

<210> 55

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Flag tag

<400> 55

Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

<210> 56

<211> 1449

<212> DNA

<213> Homo sapiens

<220>

<223> Gen2 mRNA sequence

<400> 56

```
atggggagtgc taaaattcaa gcacatcttt ttcagaagct ttgttaaadc aagtggagta 60
tcccagatag ttttcacctt ctttctgatt ccatgttgct tgactctgaa tttcagagca 120
cttctgttta ttccaaatgt gcctttcctc tgggcctgga atgcccacag tgaattttgt 180
cttggaaaaat ttgatgagcc actagatatg agcctcttct ctttcatagg aagcccccca 240
ataaacgcca ccgggcaagg tgttacaata ttttatgttg atagacttgg ctactatcct 300
tacatagatt caatcacagg agtaactgtg aatggaggaa tccccagaa gatttcctta 360
caagaccatc tggacaaaagc taagaaaagac attacatttt atatgccagt agacaatttg 420
ggaatggctg ttattgactg ggaagaatgg agaccactt gggcaagaaa ctggaaacct 480
aaagatgttt acaagaatag gtctattgaa ttggttcagc aacaaaatgt acaacttagt 540
ctcacagagg ccactgagaa agcaaaaaca gaatttgaaa aggcagggaa ggatttcctg 600
gtagagacta taaaattggg aaaattactt cggccaaatc acttgtgggg ttattatcct 660
tttccggatt gttacaacca tcactataag aaacccggtt acaatggaag ttgcttcaat 720
gtagaaataa aaagaaatga tgatctcagc tgggttgagg atgaaagcac tgctctttac 780
ccatccattt atttgaacac tcagcagctt cctgtagctg ctacactcta tgtgcgcaat 840
cgagttcggg aagccatcag agtttccaaa atacctgatg caaaaagtcc acttccggtt 900
tttgcatata cccgcatagt ttttactgat caagttttga aattcctttc tcaagatgaa 960
cttgtgtata catttgccga aactgttgct ctgggtgctt ctggaattgt aatatgggga 1020
accctcagta taatgcgaag tatgaaatct tgcttgctcc tagacaatta catggagact 1080
atactgaatc cttacataat caacgtcaca ctagcagcca aaatgtgtag tcaagtgtt 1140
tgccaggagc aaggagtgtg tataaggaaa aactggaatt caagtgacta tcttcacctc 1200
aaccagata attttgctat tcaacttgag aaagggtggaa agttcacagt acgtggaaaa 1260
ccgacacttg aagacctgga gcaattttct gaaaaatttt attgcagctg ttatagcacc 1320
ttgagttgta aggagaaaagc tgatgtaaaa gacactgatg ctgttgatgt gtgtattgct 1380
gatggtgtct gtatagatgc ttttctaaaa cctcccattg agacagaaga acctcaaatt 1440
ttctactga 1449
```

<210> 57

<211> 17

<212> PRT

<213> Homo sapiens

<220>

<223> C-terminal peptide cleaved from soluble rHuPH20 aa
431-447

3108SEQPC1

<400> 57

Asp Ala Phe Lys Leu Pro Pro Met Glu Thr Glu Glu Pro Gln Ile Phe
 1 5 10 15
 Tyr

<210> 58

<211> 16

<212> PRT

<213> Homo sapiens

<220>

<223> C-terminal peptide cleaved from soluble rHuPH20 aa
 431-446

<400> 58

Asp Ala Phe Lys Leu Pro Pro Met Glu Thr Glu Glu Pro Gln Ile Phe
 1 5 10 15

<210> 59

<211> 15

<212> PRT

<213> Homo sapiens

<220>

<223> C-terminal peptide cleaved from soluble rHuPH20 aa
 431-445

<400> 59

Asp Ala Phe Lys Leu Pro Pro Met Glu Thr Glu Glu Pro Gln Ile
 1 5 10 15

<210> 60

<211> 14

<212> PRT

<213> Homo sapiens

<220>

<223> C-terminal peptide cleaved from soluble rHuPH20 aa
 431-444

<400> 60

Asp Ala Phe Lys Leu Pro Pro Met Glu Thr Glu Glu Pro Gln
 1 5 10

<210> 61

<211> 13

<212> PRT

<213> Homo sapiens

<220>

<223> C-terminal peptide cleaved from soluble rHuPH20 aa
 431-443

<400> 61

Asp Ala Phe Lys Leu Pro Pro Met Glu Thr Glu Glu Pro
 1 5 10

3108SEQPC1

<210> 62
 <211> 12
 <212> PRT
 <213> Homo sapiens

<220>
 <223> C-terminal peptide cleaved from soluble rHuPH20 aa
 431-442

<400> 62
 Asp Ala Phe Lys Leu Pro Pro Met Glu Thr Glu Glu
 1 5 10

<210> 63
 <211> 520
 <212> PRT
 <213> Ovis aries

<220>
 <223> PH20

<400> 63
 Leu Asp Phe Pro Ala Pro Pro Leu Ile Ser Asn Thr Ser Phe Leu Trp
 1 5 10 15
 Ala Trp Asn Ala Pro Ala Glu Arg Cys Val Lys Ile Phe Lys Leu Pro
 20 25 30
 Pro Asp Leu Arg Leu Phe Ser Val Lys Gly Ser Pro Gln Lys Ser Ala
 35 40 45
 Thr Gly Gln Phe Ile Thr Leu Phe Tyr Ala Asp Arg Leu Gly Tyr Tyr
 50 55 60
 Pro His Ile Asp Glu Lys Thr Gly Asn Thr Val Tyr Gly Gly Ile Pro
 65 70 75 80
 Gln Leu Gly Asn Leu Lys Asn His Leu Glu Lys Ala Lys Lys Asp Ile
 85 90 95
 Ala Tyr Tyr Ile Pro Asn Asp Ser Val Gly Leu Ala Val Ile Asp Trp
 100 105 110
 Glu Asn Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
 115 120 125
 Tyr Arg Asp Glu Ser Val Glu Leu Val Leu Gln Lys Asn Pro Gln Leu
 130 135 140
 Ser Phe Pro Glu Ala Ser Lys Ile Ala Lys Val Asp Phe Glu Thr Ala
 145 150 155 160
 Gly Lys Ser Phe Met Gln Glu Thr Leu Lys Leu Gly Lys Leu Leu Arg
 165 170 175
 Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
 180 185 190
 Asn Tyr Asn Gln Pro Thr Tyr Asn Gly Asn Cys Ser Asp Leu Glu Lys
 195 200 205
 Arg Arg Asn Asp Asp Leu Asp Trp Leu Trp Lys Glu Ser Thr Ala Leu
 210 215 220
 Phe Pro Ser Val Tyr Leu Asn Ile Lys Leu Lys Ser Thr Pro Lys Ala
 225 230 235 240
 Ala Phe Tyr Val Arg Asn Arg Val Gln Glu Ala Ile Arg Leu Ser Lys
 245 250 255
 Ile Ala Ser Val Glu Ser Pro Leu Pro Val Phe Val Tyr His Arg Pro
 260 265 270
 Val Phe Thr Asp Gly Ser Ser Thr Tyr Leu Ser Gln Gly Asp Leu Val
 275 280 285
 Asn Ser Val Gly Glu Ile Val Ala Leu Gly Ala Ser Gly Ile Ile Met
 290 295 300
 Trp Gly Ser Leu Asn Leu Ser Leu Thr Met Gln Ser Cys Met Asn Leu
 305 310 315 320
 Gly Asn Tyr Asn Thr Thr Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
 325 330 335
 Ala Ala Lys Met Cys Ser Gln Val Leu Cys His Asp Glu Gly Val Cys
 340 345 350

3108SEQPC1

Thr Arg Lys Gln Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Ile
 355 360
 Met Asn Phe Ala Ile Gln Thr Gly Lys Gly Gly Lys Tyr Thr Val Pro
 370 375 380
 Gly Lys Val Thr Leu Glu Asp Leu Gln Thr Phe Ser Asp Lys Phe Tyr
 385 390 395 400
 Cys Ser Cys Tyr Ala Asn Ile Asn Cys Lys Lys Arg Val Asp Ile Lys
 405 410 415
 Asn Val His Ser Val Asn Val Cys Met Ala Glu Asp Ile Cys Ile Glu
 420 425 430
 Gly Pro Val Lys Leu Gln Pro Ser Asp His Ser Ser Ser Gln Asn Glu
 435 440 445
 Ala Ser Thr Thr Thr Val Ser Ile Ser Pro Ser Thr Thr Ala Thr
 450 455 460
 Thr Val Val Ser Pro Cys Thr Pro Glu Lys Gln Ser Pro Glu Cys Leu
 465 470 475 480
 Lys Val Arg Cys Leu Glu Ala Ile Ala Asn Val Thr Gln Thr Gly Cys
 485 490 495
 Gln Gly Val Lys Trp Lys Asn Thr Ser Gln Ser Gln Ser Ser Ile
 500 505 510
 Gln Asn Ile Lys Asn Gln Thr Thr
 515 520

<210> 64

<211> 474

<212> PRT

<213> Bos taurus

<220>

<223> precursor cow PH20

<400> 64

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

3108SEQPC1

```

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

```

<210> 65
 <211> 517
 <212> PRT
 <213> Ovis aries

<220>
 <223> PH20

<400> 65

```

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

```

3108SEQPC1

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

<210> 66

<211> 1620

<212> DNA

<213> Ovis aries

<220>

<223> encoding sheep PH20

<400> 66

```

ttttccgtgt tggttggctc tggacttcag agcaccctc ctcatttcaa acacttcttt 60
cctctgggccc tggaaatgccc cagctgaacg ttgtattaaa atcttttaaac tacctccaga 120
tctgagactc ttctctgtaa aaggaagccc ccaaaaaagt gctacgggac aatttattac 180
attattttat gctgatagac ttggctacta tcctcatata gatgaaaaaa caggcaaac 240
tgtatatgga ggaattcccc agttgggaaa cttaaaaaat catttgga aaagccaaaa 300
agacattgcc tattacatac caaatgacag cgtgggcttg gcggtcattg actgggaaaa 360
ctggaggcct acctgggcaa gaaactggaa acctaaagat gtttacaggg atgagtctgt 420
tgagttgggt ctgcaaaaaa atccacaact cagtttccca gaggcttcca agattgcaaa 480
agtggatttt gagacagcag gaaagagttt catgcaagag actttaaaac tgggaaaatt 540
acttcggcca aatcacttat ggggttatta tcttttccct gattgttaca atcataatta 600
taaccagcct acttacaatg gaaattgctc tgatttagaa aaaaggagaa atgatgatct 660
cgactgggtt tggaggaaaa gcactgccct tttcccttct gtttatttga atatcaagtt 720
aaaatctact ccaaaagctg ctttctatgt tcgtaatcgt gtccaggaag ccattcgggt 780
gtctaaaata gcgagtgttg aaagtccact tcccgttttt gtatatcacc gtccagtttt 840
tactgatggg tcttcaacat acctttctca gggtgacctt gtgaattcgg ttggtgagat 900
cgttgctcta ggtgcctctg ggattataat gtggggcagt ctcaatctaa gcctaactat 960
gcaatcttgc atgaacctag gcaattactt gaacactaca ctgaatcctt acataatcaa 1020
cgtcacccta gcagccaaaa tgtgcagcca agtgccttgc cacgatgaag gagtgtgtac 1080
aaggaaacaa tggaaattcaa gcgactatct tcacctgaac ccaatgaatt ttgctattca 1140
aactgggaaa ggtggaaaat acacagtacc tgggaaaagtc aacttgaag acctgcaaac 1200
gttttctgat aaattttatt gcagttgtta tgccaacatc aactgtaaga agagagttga 1260
tataaaaaat gttcatagtg ttaatgtatg tatggcagaa gacatttgta tagagggccc 1320
tgtgaagtta caaccagtg atcattcctc tagccagaat gaggcattcta ctaccaccgt 1380

```

3108SEQPC1

cagcagtatc tcaccctcta ctacagccac cacagtatct ccatgtactc ctgagaaaca 1440
gtccccctgag tgcctcaaag tcaggtggtt ggaagccatc gccaacgtca cccaaacggg 1500
gtgtcaaggt gttaaatgga agaacacttc cagtcagtca agtattcaaa atattaaaaa 1560
tcaaacaacc tattaataaata taaattcagt gcttataaaa aaaaaaaaaa aaaaaaaaaa 1620

<210> 67

<211> 793

<212> PRT

<213> *Arthrobacter* sp.

<220>

<223> hyaluronan lyase (strain FB24)

<400> 67

Met Thr Arg Glu Phe Ser Arg Arg Thr Ala Leu Lys Gly Ala Ala Leu
1 5 10 15
Ser Gly Leu Leu Leu Ala Met Val His Gly Pro Ala His Ala Ala Ala
20 25 30
Thr Ala Asn Ala Thr Leu Thr Pro Ala Asp Phe Ala Gly Leu Arg Gln
35 40 45
Arg Trp Val Asp Gln Ile Thr Gly Arg Lys Val Leu Val Ala Gly Asp
50 55 60
Asn Asp Phe Val Thr Ala Leu Ala Ala Leu Asp Lys Lys Ala Arg Thr
65 70 75 80
Ala Ile Asp Leu Leu Glu Arg Ser Ala Gly Arg Leu Thr Val Phe Ser
85 90 95
Asp Leu Ser Leu Ala Lys Asp Thr Asp Leu Val Thr Thr His Thr Arg
100 105 110
Leu Ala Thr Met Ala Thr Ala Trp Ala Thr Pro Gly Ser Glu His Phe
115 120 125
Ala Asp Ala Gly Leu Leu Ala Ala Ile Arg Ala Gly Leu Ala Asp Ala
130 135 140
Asn Ser Leu Cys Tyr Asn Ala Ser Lys Glu Glu Gln Gly Asn Trp Trp
145 150 155 160
Ser Trp Glu Ile Gly Thr Pro Lys Ala Leu Ala Asp Thr Met Val Leu
165 170 175
Leu His Ala Glu Leu Thr Ala Ala Glu Arg Ala Ala Tyr Cys Ala Ala
180 185 190
Ile Asp His Phe Val Pro Asp Pro Trp Gln Gln Phe Pro Pro Lys Arg
195 200 205
Gly Lys Ile Thr Ser Val Gly Ala Asn Arg Val Asp Leu Cys Gln Ala
210 215 220
Val Thr Ile Arg Ser Leu Val Asp Glu Asp Ala Glu Lys Leu Thr His
225 230 235 240
Ala Val Ala Gly Leu Ser Glu Val Trp Gln Tyr Val Ser Ala Gly Asn
245 250 255
Gly Phe Phe Thr Asp Gly Ser Phe Ile Gln His Ser Thr Thr Pro Tyr
260 265 270
Thr Gly Ser Tyr Gly Val Val Leu Thr Gly Leu Ser Lys Leu Phe
275 280 285
Ala Leu Leu Gly Gly Thr Gly Ala Glu Val Ser Asp Pro Ser Arg Asp
290 295 300
Ile Leu Phe Lys Thr Val Glu Gly Ser Phe Ala Pro Phe Met Val Ala
305 310 315 320
Gly Ala Met Ala Asp Ser Val Arg Gly Arg Ser Ile Ser Arg Glu Ser
325 330 335
Asn Thr Gly Phe Asp Leu Gly Ala Ser Thr Ile Glu Ser Ile Leu Leu
340 345 350
Leu Ala Arg Ala Val Asp Pro Val Thr Ala Arg Arg Trp Arg Ser Leu
355 360 365
Cys Leu Ala Trp Ile Asn Gln Asn Arg Lys Ala Pro Ile Leu Ala Asp
370 375 380
Ala Gly Val Gly Arg Thr Ala Leu Val Lys Glu Leu Leu Ala Met Gly
385 390 395 400
Leu Thr Glu Thr Asp Leu Pro Gly Gly His Tyr Leu Phe Pro Ala Met
405 410 415
Asp Arg Thr Met His His Ser Gln Gly Trp Thr Leu Ser Thr Ala Met

3108SEQPC1

Ala Ser Ser 420 Arg Ile Ala Trp Tyr 425 Glu Cys Gly Asn Gly 430 Glu Asn Asn
 435 440 445
 Arg Gly Tyr His Thr Gly Ser Gly Met Thr Tyr Val Tyr Asp Gly Asp
 450 455 460
 Leu Gly Gln Tyr Asp Asp Ala Phe Trp Ala Thr Ala Asn His Cys Arg
 465 470 475 480
 Leu Pro Gly Ile Thr Val Asp Thr Ser Ser Leu Pro Asp Lys Val Glu
 485 490 495
 Gly Glu Trp Gly Ala Ala Thr Pro Ala Asn Glu Trp Thr Gly Ser Thr
 500 505 510
 Ala Tyr Gly Asp Val Ala Ala Val Gly Gln His Leu Ile Gly Pro Gly
 515 520 525
 Gly Thr Gly Leu Thr Ala Arg Lys Ser Trp Phe Val Ser Lys Asp Val
 530 535 540
 Ile Val Cys Leu Gly Ala Asp Ile Arg Thr Gly Ser Gly Ser Arg Ile
 545 550 555 560
 Glu Thr Val Val Asp His Arg Asn Leu His Ala Gly Phe Asn Ala Met
 565 570 575
 Gly Thr Ala Ala Gly Thr Val Ala Ala Thr Pro Gly His Pro Glu Val
 580 585 590
 Leu Thr Val Asp Arg Trp Val His Leu Glu Gly Phe Gly Gly Tyr Val
 595 600 605
 Val Leu Asp Ala Ala Pro Leu Gln Val Leu Arg Glu Gln Arg Glu Gly
 610 615 620
 Ser Trp Ser Glu Val Asn Val Lys Gly Ser Ala Ala Arg Gln Thr Arg
 625 630 635 640
 Asn Tyr Ala Thr Leu Tyr Phe Asp His Gly His Glu Pro Glu Ala Ala
 645 650 655
 Ser Tyr Ala Tyr Leu Val Ala Pro Gly Ala Ser Ala Ser Met Thr Ser
 660 665 670
 Ser Leu Ser Gly Gln Ser Phe His Thr Val Leu Arg Asn Asp Glu Val
 675 680 685
 Ala Gln Ala Val Lys Phe Lys Lys Glu Lys Thr Thr Ala Ala Thr Phe
 690 695 700
 Trp Arg Pro Gly Thr Val Gly Asp Leu Ala Leu Ser Gly Pro Ala Cys
 705 710 715 720
 Val Val Val Lys Glu Val Gly Asp Arg Leu Ser Ile Ala Val Ser Asp
 725 730 735
 Pro Thr Gln Asn Ala Ser Thr Leu Thr Leu Arg Leu Lys Thr Lys Arg
 740 745 750
 Phe Phe Arg Ile Ile Glu Gly Gln Gly Ala Ser Leu Ser His Gly Ala
 755 760 765
 Asp Gly Phe Thr Val Leu Glu Val Asp Ile Ala Asn His Ala Gly Arg
 770 775 780
 Thr Lys Gln Ile Glu Leu Ser Ala Glu
 785 790

<210> 68

<211> 557

<212> PRT

<213> Bdellovibrio bacteriovorus

<220>

<223> hyaluronan lyase

<400> 68

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

3108SEQPC1

Asn	Ser	Asn	Pro	Leu	Arg	Lys	Trp	Ile	Gln	Ser	Leu	Met	Lys	Gly	Leu
				85					90					95	
Ser	Gly	Phe	Arg	Ser	Phe	Glu	Asp	Val	Leu	Lys	Asn	Leu	Gly	Leu	His
			100					105					110		
Lys	Tyr	Pro	Leu	Glu	Asn	Glu	Arg	Gly	Val	Tyr	Ala	Val	Pro	Tyr	Pro
		115					120					125			
Asn	Glu	Ile	Arg	Pro	Asp	Thr	Leu	Met	Gly	Phe	Gly	Leu	Ile	Glu	Arg
	130					135					140				
Asn	Gly	Ala	Glu	Gly	Phe	Thr	Phe	Ser	Cys	Ala	Ala	Cys	His	Ser	Ser
145					150					155					160
Asn	Leu	Phe	Gly	Lys	Thr	Val	Leu	Gly	Met	Thr	Asn	Arg	Phe	Pro	Arg
			165						170					175	
Ala	Asn	Glu	Phe	Phe	Ile	Lys	Ala	Lys	Lys	Val	Met	Pro	Leu	Met	Asp
			180					185					190		
Pro	His	Ile	Phe	Gln	Ala	Tyr	Thr	Arg	Ala	Thr	Asp	Ala	Glu	Thr	Ala
		195					200					205			
Leu	Leu	Val	Glu	Ser	Lys	Glu	Arg	Leu	Lys	Ser	Val	Ala	Leu	Lys	Gln
	210					215					220				
Pro	Ile	Ala	Leu	Gly	Leu	Asp	Thr	Ser	Leu	Ala	Gln	Val	Ser	Leu	Ser
225					230					235					240
Leu	Asn	Arg	Arg	Ala	Lys	Asp	Gly	Tyr	Ala	Asn	Tyr	Ser	Asp	Lys	Ala
			245						250					255	
Ala	Arg	Ser	Pro	Arg	Ala	Asp	Ala	Tyr	Leu	Asp	Asn	Lys	Pro	Ala	Asp
			260					265					270		
Ser	Lys	Pro	Ala	Val	Trp	Trp	Asn	Val	Lys	Tyr	Lys	Asn	Arg	Trp	Leu
		275					280						285		
Ser	Asp	Gly	Ser	Val	Leu	Ser	Gly	Asn	Pro	Ile	Phe	Thr	Asn	Leu	Ile
	290					295					300				
Trp	Asn	Glu	Ile	Gly	Arg	Gly	Ala	Asp	Leu	His	Glu	Leu	Glu	Gln	Trp
305					310					315					320
Leu	Ala	Asp	Asn	Asp	His	Ile	Ile	Lys	Glu	Leu	Thr	Thr	Ala	Val	Phe
			325						330					335	
Ala	Ser	Glu	Ala	Pro	His	Ile	Thr	Asp	Phe	Tyr	Pro	Ala	Glu	Lys	Ile
			340					345					350		
Asp	Leu	Gly	Arg	Ala	Lys	Ala	Gly	Glu	Gln	Ile	Phe	Lys	Asn	Thr	Cys
		355					360					365			
Ala	Lys	Cys	His	Gly	His	Tyr	Glu	Lys	Ala	Trp	Asn	Leu	Pro	Gln	Ala
	370					375					380				
Leu	Val	Leu	Ser	Ala	Ala	Glu	Arg	Leu	Lys	Thr	Val	Glu	Val	Arg	Tyr
385					390					395					400
Lys	Glu	Lys	Thr	Pro	Val	Val	Asn	Val	Gly	Thr	Asp	Pro	Phe	Arg	Arg
			405						410					415	
Gln	Gly	Met	Lys	Ser	Leu	Glu	Gln	Leu	Asn	Asp	Leu	Glu	Ile	Ser	Lys
			420					425					430		
Lys	Asn	Gly	Ile	Val	Ile	Lys	Ala	Gln	Glu	Gly	Tyr	Val	Pro	Pro	Pro
		435					440					445			
Leu	Val	Gly	Ile	Trp	Ala	Arg	Trp	Pro	Tyr	Met	His	Asn	Asn	Ser	Ile
	450					455					460				
Pro	Asn	Leu	Cys	Val	Leu	Leu	Thr	Pro	Ala	Lys	Lys	Arg	Pro	Ser	Ile
465					470					475					480
Tyr	Tyr	Ser	Gly	Glu	Ala	Leu	Asn	Lys	Asp	Thr	Asp	Tyr	Asp	Phe	Ser
			485						490					495	
Cys	Gly	Gly	Tyr	Pro	Ile	Gly	Asp	Lys	Thr	Pro	Lys	Ala	Trp	Lys	Thr
			500					505					510		
Arg	Glu	His	Leu	Tyr	Asp	Thr	Arg	Asn	Pro	Gly	Met	Gly	Asn	Met	Gly
		515					520					525			
His	Asp	Glu	Gly	Ile	Phe	Ile	Lys	Asp	Gly	Lys	Glu	Ile	Leu	Ser	Ala
	530					535					540				
Glu	Asp	Lys	Tyr	Asn	Leu	Ile	Gln	Phe	Leu	Gln	Thr	Leu			
545					550					555					

<210> 69
 <211> 813
 <212> PRT
 <213> Propionibacterium acnes

<220>

3108SEQPC1

<223> hyaluronan lyase

<400> 69

Met Phe Gly Thr Pro Ser Arg Arg Thr Phe Leu Thr Ala Ser Ala Leu
 1 5 10 15
 Ser Ala Met Ala Leu Ala Ala Ser Pro Thr Val Thr Asp Ala Ile Ala
 20 25 30
 Ala Pro Gly Pro Asp Ser Trp Ser Ala Leu Cys Glu Arg Trp Ile Asp
 35 40 45
 Ile Ile Thr Gly Arg Arg Ala Arg Thr Ser Asp Pro Arg Ala Arg
 50 55 60
 Ala Ile Ile Ala Lys Thr Asp Arg Lys Val Ala Glu Ile Leu Thr Asp
 65 70 75 80
 Leu Val Ser Gly Ser Ser Arg Gln Thr Val Leu Ile Ser Ala Asp Leu
 85 90 95
 Arg Lys Glu Gln Ser Pro Phe Ile Thr Lys Thr Ala Arg Ala Ile Glu
 100 105 110
 Ser Met Ala Cys Ala Trp Ala Thr Pro Gly Ser Ser Tyr His Lys Asp
 115 120 125
 Pro Glu Ile Leu Ser Ala Cys Ile Glu Gly Leu Arg Asp Phe Cys Arg
 130 135 140
 Leu Arg Tyr Asn Pro Ser Gln Asp Glu Tyr Gly Asn Trp Trp Asp Trp
 145 150 155 160
 Glu Asp Gly Ala Ser Arg Ala Val Ala Asp Val Met Cys Ile Leu His
 165 170 175
 Asp Val Leu Pro Pro Glu Val Met Ser Ala Ala Ala Ala Gly Ile Asp
 180 185 190
 His Phe Ile Pro Asp Pro Trp Phe Gln Gln Pro Ala Ser Val Lys Pro
 195 200 205
 Thr Ala Asn Pro Val Gln Pro Val Val Ser Thr Gly Ala Asn Arg Met
 210 215 220
 Asp Leu Thr Arg Ala Val Met Cys Arg Ser Ile Ala Thr Gly Asp Glu
 225 230 235 240
 Lys Arg Leu Arg His Ala Val Asp Gly Leu Pro Asp Ala Trp Arg Val
 245 250 255
 Thr Thr Glu Gly Asp Gly Phe Arg Ala Asp Gly Gly Phe Ile Gln His
 260 265 270
 Ser His Ile Pro Tyr Thr Gly Gly Tyr Gly Asp Val Leu Phe Ser Gly
 275 280 285
 Leu Ala Met Leu Phe Pro Leu Val Ser Gly Met Arg Phe Asp Ile Val
 290 295 300
 Glu Ser Ala Arg Lys Ala Phe His Asp Gln Val Glu Arg Gly Phe Ile
 305 310 315 320
 Pro Val Met Tyr Asn Gly Gln Ile Leu Asp Asp Val Arg Gly Arg Ser
 325 330 335
 Ile Ser Arg Ile Asn Glu Ser Ala Ala Met His Gly Ile Ser Ile Ala
 340 345 350
 Arg Ala Met Leu Met Met Ala Asp Ala Leu Pro Thr His Arg Ala Glu
 355 360 365
 Gln Trp Arg Gly Ile Val His Gly Trp Met Ala Arg Asn Thr Phe Asp
 370 375 380
 His Leu Ser Glu Pro Ser Thr Leu Val Asp Ile Ser Leu Phe Asp Ala
 385 390 395 400
 Ala Ala Lys Ala Arg Pro Val Pro Glu Ser Ser Thr Pro Ser Tyr Phe
 405 410 415
 Ala Ser Met Asp Arg Leu Val His Arg Thr Ala Asp Trp Leu Ile Thr
 420 425 430
 Val Ser Asn Cys Ser Asp Arg Ile Ala Trp Tyr Glu Tyr Gly Asn Gly
 435 440 445
 Glu Asn Glu Trp Ala Ser Arg Thr Ser Gln Gly Met Arg Tyr Leu Leu
 450 455 460
 Leu Pro Gly Asp Met Gly Gln Tyr Glu Asp Gly Tyr Trp Ala Thr Val
 465 470 475 480
 Asp Tyr Ser Ala Pro Thr Gly Thr Thr Val Asp Ser Thr Pro Leu Lys
 485 490 495
 Arg Ala Val Gly Ala Ser Trp Ala Ala Lys Thr Pro Thr Asn Glu Trp
 500 505 510
 Ser Gly Gly Leu Ala Ser Gly Ser Trp Ser Ala Ala Ala Ser His Ile

3108SEQPC1

515 520 525
 Thr Ser Gln Asp Ser Ala Leu Lys Ala Arg Arg Leu Trp Val Gly Leu
 530 535 540
 Lys Asp Ala Met Val Glu Leu Thr Thr Asp Val Thr Thr Asp Ala Ser
 545 550 555 560
 Arg Ala Ile Thr Val Val Glu His Arg Lys Val Ala Ser Ser Ser Thr
 565 570 575
 Lys Leu Leu Val Asp Gly Asn Arg Val Ser Ser Ala Thr Ser Phe Gln
 580 585 590
 Asn Pro Arg Trp Ala His Leu Asp Gly Val Gly Gly Tyr Val Phe Ala
 595 600 605
 Thr Asp Thr Asp Leu Ser Ala Asp Val Ala Thr Arg Lys Gly Thr Trp
 610 615 620
 Ile Asp Val Asn Pro Ser Arg Lys Val Lys Gly Ala Asp Glu Val Ile
 625 630 635 640
 Glu Arg Ala Tyr Ala Ser Leu His Val Thr His His Asp Arg Pro Val
 645 650 655
 Ala Trp Ala Leu Leu Pro Thr Ala Ser Arg Ser His Thr Met Ala Leu
 660 665 670
 Ala Thr Arg Pro Gly Val Glu Pro Phe Thr Val Leu Arg Asn Asp Ala
 675 680 685
 Thr Val Gln Ala Val Arg Ser Ala Gly Ala Leu Leu Thr Lys Asp Pro
 690 695 700
 Thr Val Val Thr Thr Leu Ala Phe Trp Lys Pro Ala Thr Cys Gly Gly
 705 710 715 720
 Val Ala Val Asn Arg Pro Ala Leu Val Gln Thr Arg Glu Ser Ala Asn
 725 730 735
 Gln Met Glu Val Val Ile Val Glu Pro Thr Gln Lys Arg Gly Ser Leu
 740 745 750
 Thr Val Thr Ile Glu Gly Ser Trp Lys Val Lys Thr Ala Asp Ser His
 755 760 765
 Val Asp Val Ser Cys Glu Asn Ala Ala Gly Thr Leu His Val Asp Thr
 770 775 780
 Ala Gly Leu Gly Gly Gln Ser Val Arg Val Thr Leu Ala Arg Gln Val
 785 790 795 800
 Thr Gln Thr Pro Ser Gly Gly Gly Arg His Asp Arg Ala
 805 810

<210> 70

<211> 1072

<212> PRT

<213> Streptococcus agalactiae

<220>

<223> hyaluronan lyase

<400> 70

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

3108SEQPC1

Ala	Val	Thr	Gln	Lys	Val	Asn	Ile	Asp	Pro	Thr	Lys	Lys	Tyr	Glu	Val
				165					170					175	
Lys	Phe	Asp	Ile	Glu	Thr	Ser	Asn	Lys	Ala	Gly	Gln	Ala	Phe	Leu	Arg
			180					185					190		
Ile	Met	Glu	Lys	Lys	Asp	Asn	Asn	Thr	Arg	Leu	Trp	Leu	Ser	Glu	Met
		195					200					205			
Thr	Ser	Gly	Thr	Thr	Asn	Lys	His	Thr	Leu	Thr	Lys	Ile	Tyr	Asn	Pro
	210					215					220				
Lys	Leu	Asn	Val	Ser	Glu	Val	Thr	Leu	Glu	Leu	Tyr	Tyr	Glu	Lys	Gly
225					230					235					240
Thr	Gly	Ser	Ala	Thr	Phe	Asp	Asn	Ile	Ser	Met	Lys	Ala	Lys	Gly	Pro
			245						250					255	
Lys	Asp	Ser	Glu	His	Pro	Gln	Pro	Val	Thr	Thr	Gln	Ile	Glu	Glu	Ser
			260					265					270		
Val	Asn	Thr	Ala	Leu	Asn	Lys	Asn	Tyr	Val	Phe	Asn	Lys	Ala	Asp	Tyr
		275					280					285			
Gln	Tyr	Thr	Leu	Thr	Asn	Pro	Ser	Leu	Gly	Lys	Ile	Val	Gly	Gly	Ile
	290					295					300				
Leu	Tyr	Pro	Asn	Ala	Thr	Gly	Ser	Thr	Thr	Val	Lys	Ile	Ser	Asp	Lys
305					310					315					320
Ser	Gly	Lys	Ile	Ile	Lys	Glu	Val	Pro	Leu	Ser	Val	Thr	Ala	Ser	Thr
			325						330					335	
Glu	Asp	Lys	Phe	Thr	Lys	Leu	Leu	Asp	Lys	Trp	Asn	Asp	Val	Thr	Ile
			340					345					350		
Gly	Asn	His	Val	Tyr	Asp	Thr	Asn	Asp	Ser	Asn	Met	Gln	Lys	Ile	Asn
		355					360					365			
Gln	Lys	Leu	Asp	Glu	Thr	Asn	Ala	Lys	Asn	Ile	Lys	Thr	Ile	Lys	Leu
	370					375					380				
Asp	Ser	Asn	His	Thr	Phe	Leu	Trp	Lys	Asp	Leu	Asp	Asn	Leu	Asn	Asn
385					390					395					400
Ser	Ala	Gln	Leu	Thr	Ala	Thr	Tyr	Arg	Arg	Leu	Glu	Asp	Leu	Ala	Lys
			405						410					415	
Gln	Ile	Thr	Asn	Pro	His	Ser	Thr	Ile	Tyr	Lys	Asn	Glu	Lys	Ala	Ile
			420					425					430		
Arg	Thr	Val	Lys	Glu	Ser	Leu	Ala	Trp	Leu	His	Gln	Asn	Phe	Tyr	Asn
		435					440					445			
Val	Asn	Lys	Asp	Ile	Glu	Gly	Ser	Ala	Asn	Trp	Trp	Asp	Phe	Glu	Ile
	450					455					460				
Gly	Val	Pro	Arg	Ser	Ile	Thr	Ala	Thr	Leu	Ala	Leu	Met	Asn	Asn	Tyr
465					470				475						480
Phe	Thr	Asp	Ala	Glu	Ile	Lys	Thr	Tyr	Thr	Asp	Pro	Ile	Glu	His	Phe
			485						490					495	
Val	Pro	Asp	Ala	Gly	Tyr	Phe	Arg	Lys	Thr	Leu	Asp	Asn	Pro	Phe	Lys
			500					505					510		
Ala	Leu	Gly	Gly	Asn	Leu	Val	Asp	Met	Gly	Arg	Val	Lys	Ile	Ile	Glu
		515					520					525			
Gly	Leu	Leu	Arg	Lys	Asp	Asn	Thr	Ile	Ile	Glu	Lys	Thr	Ser	His	Ser
	530					535					540				
Leu	Lys	Asn	Leu	Phe	Thr	Ala	Thr	Lys	Ala	Glu	Gly	Phe	Tyr	Ala	
545					550				555						560
Asp	Gly	Ser	Tyr	Ile	Asp	His	Thr	Asn	Val	Ala	Tyr	Thr	Gly	Ala	Tyr
			565						570					575	
Gly	Asn	Val	Leu	Ile	Asp	Gly	Leu	Thr	Gln	Leu	Leu	Pro	Ile	Ile	Gln
		580						585					590		
Glu	Thr	Asp	Tyr	Lys	Ile	Ser	Asn	Gln	Glu	Leu	Asp	Met	Val	Tyr	Lys
		595					600					605			
Trp	Ile	Asn	Gln	Ser	Phe	Leu	Pro	Leu	Ile	Val	Lys	Gly	Glu	Leu	Met
	610					615					620				
Asp	Met	Ser	Arg	Gly	Arg	Ser	Ile	Ser	Arg	Glu	Ala	Ala	Ser	Ser	His
625					630					635					640
Ala	Ala	Ala	Val	Glu	Val	Leu	Arg	Gly	Phe	Leu	Arg	Leu	Ala	Asn	Met
			645						650					655	
Ser	Asn	Glu	Glu	Arg	Asn	Leu	Asp	Leu	Lys	Ser	Thr	Ile	Lys	Thr	Ile
			660					665					670		
Ile	Thr	Ser	Asn	Lys	Phe	Tyr	Asn	Val	Phe	Asn	Asn	Leu	Lys	Ser	Tyr
		675					680					685			
Ser	Asp	Ile	Ala	Asn	Met	Asn	Lys	Met	Leu	Asn	Asp	Ser	Thr	Val	Ala
	690					695					700				

3108SEQPC1

Thr Lys Pro Leu Lys Ser Asn Leu Ser Thr Phe Asn Ser Met Asp Arg
 705 710 715 720
 Leu Ala Tyr Tyr Asn Ala Glu Lys Asp Phe Gly Phe Ala Leu Ser Leu
 725 730 735
 His Ser Lys Arg Thr Leu Asn Tyr Glu Met Asn Asp Glu Asn Thr
 740 745 750
 Arg Gly Trp Tyr Thr Gly Asp Gly Met Phe Tyr Leu Tyr Asn Ser Asp
 755 760 765
 Gln Ser His Tyr Ser Asn His Phe Trp Pro Thr Val Asn Pro Tyr Lys
 770 775 780
 Met Ala Gly Thr Thr Glu Lys Asp Ala Lys Arg Glu Asp Thr Thr Lys
 785 790 795 800
 Glu Phe Met Ser Lys His Ser Lys Asp Ala Lys Glu Lys Thr Gly Gln
 805 810 815
 Val Thr Gly Thr Ser Asp Phe Val Gly Ser Val Lys Leu Asn Asp His
 820 825 830
 Phe Ala Leu Ala Ala Met Asp Phe Thr Asn Trp Asp Arg Thr Leu Thr
 835 840 845
 Ala Gln Lys Gly Trp Val Ile Leu Asn Asp Lys Ile Val Phe Leu Gly
 850 855 860
 Ser Asn Ile Lys Asn Thr Asn Gly Ile Gly Asn Val Ser Thr Thr Ile
 865 870 875 880
 Asp Gln Arg Lys Asp Asp Ser Lys Thr Pro Tyr Thr Thr Tyr Val Asn
 885 890 895
 Gly Lys Thr Ile Asp Leu Lys Gln Ala Ser Ser Gln Gln Phe Thr Asp
 900 905 910
 Thr Lys Ser Val Phe Leu Glu Ser Lys Glu Pro Gly Arg Asn Ile Gly
 915 920 925
 Tyr Ile Phe Phe Lys Asn Ser Thr Ile Asp Ile Glu Arg Lys Glu Gln
 930 935 940
 Thr Gly Thr Trp Asn Ser Ile Asn Arg Thr Ser Lys Asn Thr Ser Ile
 945 950 955 960
 Val Ser Asn Pro Phe Ile Thr Ile Ser Gln Lys His Asp Asn Lys Gly
 965 970 975
 Asp Ser Tyr Gly Tyr Met Met Val Pro Asn Ile Asp Arg Thr Ser Phe
 980 985 990
 Asp Lys Leu Ala Asn Ser Lys Glu Val Glu Leu Leu Glu Asn Ser Ser
 995 1000 1005
 Lys Gln Gln Val Ile Tyr Asp Lys Asn Ser Gln Thr Trp Ala Val Ile
 1010 1015 1020
 Lys His Asp Asn Gln Glu Ser Leu Ile Asn Asn Gln Phe Lys Met Asn
 1025 1030 1035 1040
 Lys Ala Gly Leu Tyr Leu Val Gln Lys Val Gly Asn Asp Tyr Gln Asn
 1045 1050 1055
 Val Tyr Tyr Gln Pro Gln Thr Met Thr Lys Thr Asp Gln Leu Ala Ile
 1060 1065 1070

<210> 71

<211> 1072

<212> PRT

<213> Streptococcus agalactiae 18RS21

<220>

<223> hyaluronan lyase

<400> 71

Met Glu Ile Lys Lys Lys His Arg Ile Met Leu Tyr Ser Ala Leu Ile
 1 5 10 15
 Leu Gly Thr Ile Leu Val Asn Asn Ser Tyr Gln Ala Lys Ala Glu Glu
 20 25 30
 Leu Thr Lys Thr Thr Ser Thr Ser Gln Ile Arg Asp Thr Gln Thr Asn
 35 40 45
 Asn Ile Glu Val Leu Gln Thr Glu Ser Thr Thr Val Lys Glu Thr Ser
 50 55 60
 Thr Thr Thr Thr Gln Gln Asp Leu Ser Asn Pro Thr Ala Ser Thr Ala
 65 70 75 80
 Thr Ala Thr Ala Thr His Ser Thr Met Lys Gln Val Val Asp Asn Gln
 Page 69

3108SEQPC1

Thr	Gln	Asn	Lys	85	Glu	Leu	Val	Lys	Asn	90	Gly	Asp	Phe	Asn	95	Gln	Thr	Asn
Pro	Val	Ser	100	Gly	Ser	Trp	Ser	His	105	Thr	Ser	Ala	Arg	Glu	110	Trp	Ser	Ala
Trp	Ile	115	Asp	Lys	Glu	Asn	Thr	120	Ala	Asp	Lys	Ser	Pro	125	Ile	Ile	Gln	Arg
Thr	Glu	Gln	Gly	Gln	Val	Ser	Leu	Ser	Ser	Asp	Lys	Gly	Phe	Arg	Gly	145	160	
Ala	Val	Thr	Gln	Lys	Val	Asn	Ile	Asp	Pro	155	Thr	Lys	Lys	Tyr	Glu	Val	175	
Lys	Phe	Asp	Ile	165	Glu	Thr	Ser	Asn	Lys	170	Ala	Gly	Gln	Ala	Phe	Leu	Arg	
Ile	Met	Glu	Lys	Lys	Asp	Asn	Asn	Thr	Arg	185	Leu	Trp	Leu	Ser	Glu	Met	190	
Thr	Ser	Gly	Thr	Thr	Asn	Lys	His	Thr	Leu	200	Thr	Lys	Ile	Tyr	Asn	Pro	205	
Lys	Leu	Asn	Val	Ser	Glu	Val	Thr	Leu	Glu	215	Leu	Tyr	Tyr	Glu	Lys	Gly	220	
Thr	Gly	Ser	Ala	Thr	Phe	Asp	Asn	Ile	Ser	225	Met	Lys	Ala	Lys	Gly	Pro	230	
Lys	Asp	Ser	Glu	His	Pro	Gln	Pro	Val	Thr	235	Thr	Gln	Ile	Glu	Glu	Ser	240	
Val	Asn	Thr	Ala	Leu	Asn	Lys	Asn	Tyr	Val	245	Phe	Asn	Lys	Ala	Asp	Tyr	250	
Gln	Tyr	Thr	Leu	Thr	Asn	Pro	Ser	Leu	Gly	255	Lys	Ile	Val	Gly	Gly	Ile	260	
Leu	Tyr	Pro	Asn	Ala	Thr	Gly	Ser	Thr	Thr	265	Val	Lys	Ile	Ser	Asp	Lys	270	
Ser	Gly	Lys	Ile	Ile	Lys	Glu	Val	Pro	Leu	280	Ser	Val	Thr	Ala	Ser	Thr	285	
Glu	Asp	Lys	Phe	Thr	Lys	Leu	Leu	Asp	Lys	290	Trp	Asn	Asp	Val	Thr	Ile	300	
Gly	Asn	His	Val	Tyr	Asp	Thr	Asn	Asp	Ser	305	Asn	Met	Gln	Lys	Ile	Asn	310	
Gln	Lys	Leu	Asp	Glu	Thr	Asn	Ala	Lys	Asn	315	Ile	Lys	Thr	Ile	Lys	Leu	320	
Asp	Ser	Asn	His	Thr	Phe	Leu	Trp	Lys	Asp	325	Leu	Asp	Asn	Leu	Asn	Asn	330	
Ser	Ala	Gln	Leu	Thr	Ala	Thr	Tyr	Arg	Arg	335	Leu	Glu	Asp	Leu	Ala	Lys	340	
Gln	Ile	Thr	Asn	Pro	His	Ser	Thr	Ile	Tyr	345	Lys	Asn	Glu	Lys	Ala	Ile	350	
Arg	Thr	Val	Lys	Glu	Ser	Leu	Ala	Trp	Leu	355	His	Gln	Asn	Phe	Tyr	Asn	360	
Val	Asn	Lys	Asp	Ile	Glu	Gly	Ser	Ala	Asn	365	Trp	Trp	Asp	Phe	Glu	Ile	370	
Gly	Val	Pro	Arg	Ser	Ile	Thr	Ala	Thr	Leu	375	Ala	Leu	Met	Asn	Asn	Tyr	380	
Phe	Thr	Asp	Ala	Glu	Ile	Lys	Thr	Tyr	Thr	385	Asp	Pro	Ile	Glu	His	Phe	390	
Val	Pro	Asp	Ala	Gly	Tyr	Phe	Arg	Lys	Thr	395	Leu	Asp	Asn	Pro	Phe	Lys	400	
Ala	Leu	Gly	Gly	Asn	Leu	Val	Asp	Met	Gly	405	Arg	Val	Lys	Ile	Ile	Glu	410	
Gly	Leu	Leu	Arg	Lys	Asp	Asn	Thr	Ile	Ile	415	Glu	Lys	Thr	Ser	His	Ser	420	
Leu	Lys	Asn	Leu	Phe	Thr	Thr	Ala	Thr	Lys	425	Ala	Glu	Gly	Phe	Tyr	Ala	430	
Asp	Gly	Ser	Tyr	Ile	Asp	His	Thr	Asn	Val	435	Ala	Tyr	Thr	Gly	Ala	Tyr	440	
Gly	Asn	Val	Leu	Ile	Asp	Gly	Leu	Thr	Gln	445	Leu	Leu	Pro	Ile	Ile	Gln	450	
Glu	Thr	Asp	Tyr	Lys	Ile	Ser	Asn	Gln	Glu	455	Leu	Asp	Met	Val	Tyr	Lys	460	
Trp	Ile	Asn	Gln	Ser	Phe	Leu	Pro	Leu	Ile	465	Val	Lys	Gly	Glu	Leu	Met	470	
Asp	Met	Ser	Arg	Gly	Arg	Ser	Ile	Ser	Arg	475	Glu	Ala	Ala	Ser	Ser	His	480	

3108SEQPC1

625 630 635 640
 Ala Ala Ala Val Glu Val Leu Arg Gly Phe Leu Arg Leu Ala Asn Met
 645 650 655
 Ser Asn Glu Glu Arg Asn Leu Asp Leu Ile Ser Thr Ile Lys Thr Ile
 660 665 670
 Ile Thr Ser Asn Lys Phe Tyr Asn Val Phe Asn Asn Leu Lys Ser Tyr
 675 680 685
 Ser Asp Ile Ala Asn Met Asn Lys Met Leu Asn Asp Ser Thr Val Ala
 690 695 700
 Thr Lys Pro Leu Lys Ser Asn Leu Ser Thr Phe Asn Ser Met Asp Arg
 705 710 715 720
 Leu Ala Tyr Tyr Asn Ala Glu Lys Asp Phe Gly Phe Ala Leu Ser Leu
 725 730 735
 His Ser Lys Arg Thr Leu Asn Tyr Glu Gly Met Asn Asp Glu Asn Thr
 740 745 750
 Arg Gly Trp Tyr Thr Gly Asp Gly Met Phe Tyr Leu Tyr Asn Ser Asp
 755 760 765
 Gln Ser His Tyr Ser Asn His Phe Trp Pro Thr Val Asn Pro Tyr Lys
 770 775 780
 Met Ala Gly Thr Thr Glu Lys Asp Ala Lys Arg Glu Asp Thr Thr Lys
 785 790 795 800
 Glu Phe Met Ser Lys His Ser Lys Asp Ala Lys Glu Lys Thr Gly Gln
 805 810 815
 Val Thr Gly Thr Ser Asp Phe Val Gly Ser Val Lys Leu Asn Asp His
 820 825 830
 Phe Ala Leu Ala Ala Met Asp Phe Thr Asn Trp Asp Arg Thr Leu Thr
 835 840 845
 Ala Gln Lys Gly Trp Val Ile Leu Asn Asp Lys Ile Val Phe Leu Gly
 850 855 860
 Ser Asn Ile Lys Asn Thr Asn Gly Ile Gly Asn Val Ser Thr Thr Ile
 865 870 875 880
 Asp Gln Arg Lys Asp Asp Ser Lys Thr Pro Tyr Thr Thr Tyr Val Asn
 885 890 895
 Gly Lys Thr Ile Asp Leu Lys Gln Ala Ser Ser Gln Gln Phe Thr Asp
 900 905 910
 Thr Lys Ser Val Phe Leu Glu Ser Lys Glu Pro Gly Arg Asn Ile Gly
 915 920 925
 Tyr Ile Phe Phe Lys Asn Ser Thr Ile Asp Ile Glu Arg Lys Glu Gln
 930 935 940
 Thr Gly Thr Trp Asn Ser Ile Asn Arg Thr Ser Lys Asn Thr Ser Ile
 945 950 955 960
 Val Ser Asn Pro Phe Ile Thr Ile Ser Gln Lys His Asp Asn Lys Gly
 965 970 975
 Asp Ser Tyr Gly Tyr Met Met Val Pro Asn Ile Asp Arg Thr Ser Phe
 980 985 990
 Asp Lys Leu Ala Asn Ser Lys Glu Val Glu Leu Leu Glu Asn Ser Ser
 995 1000 1005
 Lys Gln Gln Val Ile Tyr Asp Lys Asn Ser Gln Thr Trp Ala Val Ile
 1010 1015 1020
 Lys His Asp Asn Gln Glu Ser Leu Ile Asn Asn Gln Phe Lys Met Asn
 1025 1030 1035 1040
 Lys Ala Gly Leu Tyr Leu Val Gln Lys Val Gly Asn Asp Tyr Gln Asn
 1045 1050 1055
 Val Tyr Tyr Gln Pro Gln Thr Met Thr Lys Thr Asp Gln Leu Ala Ile
 1060 1065 1070

<210> 72

<211> 1081

<212> PRT

<213> Streptococcus agalactiae serotype Ia

<220>

<223> hyaluronan lyase

<400> 72

Met Glu Ile Lys Lys Lys His Arg Ile Met Leu Tyr Ser Ala Leu Ile
 1 5 10 15

3108SEQPC1

Leu Gly Thr Ile Leu Val Asn Asn Ser Tyr Gln Ala Lys Ala Glu Glu
 20 30
 Phe Thr Lys Thr Thr Ser Thr Ser Gln Ile Arg Asp Thr Gln Thr Asn
 35 40 45
 Asn Val Glu Val Pro Gln Thr Glu Ser Thr Thr Val Lys Gly Thr Ser
 50 55 60
 Thr Thr Thr Thr Gln Gln Asp Leu Ser Asn Ser Thr Ala Ser Thr Ala
 65 70 75 80
 Thr Ala Thr Ala Thr His Ser Thr Met Lys Gln Val Val Asp Asn Gln
 85 90 95
 Thr Gln Asn Lys Glu Leu Val Lys Asn Gly Asp Phe Lys Glu Lys Ile
 100 105 110
 Ile Asp Lys Lys Ile Asp Lys Lys Ser Gln Trp Thr Asn Leu Tyr Gly
 115 120 125
 Ala Lys Asp Trp Asn Thr Tyr Ile Asp Gln Thr Lys Ser Val Asn Lys
 130 135 140
 Ser Pro Ile Ile Gln Arg Thr Glu Gln Gly Gln Val Ser Leu Ser Ser
 145 150 155 160
 Asp Lys Gly Phe Arg Gly Ala Val Thr Gln Lys Val Asn Ile Asp Pro
 165 170 175
 Thr Lys Lys Tyr Glu Val Lys Phe Asp Ile Glu Thr Ser Asn Lys Val
 180 185 190
 Gly Gln Ala Phe Leu Arg Ile Met Lys Lys Lys Asp Lys Asn Thr Arg
 195 200 205
 Leu Trp Leu Ser Glu Met Thr Ser Gly Thr Thr Asn Lys His Thr Leu
 210 215 220
 Thr Lys Ile Tyr Asn Pro Lys Leu Asn Val Ser Glu Val Thr Leu Glu
 225 230 235 240
 Leu Tyr Tyr Glu Lys Gly Thr Gly Ser Val Thr Phe Asp Asn Ile Ser
 245 250 255
 Met Lys Ala Lys Gly Pro Lys Asp Ser Glu His Pro Gln Pro Val Thr
 260 265 270
 Thr Gln Ile Glu Glu Ser Val Asn Thr Ala Leu Asn Lys Asn Tyr Val
 275 280 285
 Phe Asn Lys Ala Asp Tyr Gln Tyr Thr Leu Thr Asn Pro Ser Leu Gly
 290 295 300
 Lys Ile Val Gly Gly Ile Leu Tyr Pro Ser Ala Thr Gly Ser Thr Thr
 305 310 315 320
 Val Lys Ile Ser Asp Lys Ser Gly Lys Ile Ile Lys Glu Val Pro Leu
 325 330 335
 Ser Val Thr Ala Ser Thr Glu Asp Asn Phe Thr Lys Leu Leu Asp Lys
 340 345 350
 Trp Asn Asp Val Thr Ile Gly Asn His Val Tyr Asp Thr Asn Asp Ser
 355 360 365
 Asn Met Gln Lys Leu Asn Gln Lys Leu Asp Glu Thr Asn Ala Lys Asn
 370 375 380
 Ile Lys Asp Ile Lys Leu Asp Ser Asn Arg Thr Phe Leu Trp Glu Asp
 385 390 395 400
 Leu Lys Gly Leu Asn Asn Ser Ala Gln Leu Thr Ala Thr Tyr Arg Arg
 405 410 415
 Leu Glu Asp Leu Ala Lys Gln Ile Thr Asn Pro His Ser Thr Ile Tyr
 420 425 430
 Lys Asn Glu Lys Ala Ile Arg Thr Val Lys Glu Ser Leu Ala Trp Leu
 435 440 445
 His Gln Asn Phe Tyr Asn Val Asn Lys Asp Ile Glu Gly Ser Ala Asn
 450 455 460
 Trp Trp Asp Phe Glu Ile Gly Val Pro Arg Ser Ile Thr Ala Thr Leu
 465 470 475 480
 Ala Leu Met Asn Asn Tyr Phe Thr Asp Ala Glu Ile Lys Thr Tyr Thr
 485 490 495
 Asp Pro Ile Glu His Phe Val Pro Asp Ala Gly Tyr Phe Arg Lys Thr
 500 505 510
 Leu Val Asn Pro Phe Lys Ala Leu Gly Gly Asn Leu Val Asp Met Gly
 515 520 525
 Arg Val Lys Ile Ile Glu Gly Leu Leu Arg Lys Asp Asn Thr Ile Ile
 530 535 540
 Lys Lys Thr Ser His Ser Leu Lys Asn Leu Phe Thr Thr Ala Thr Lys
 545 550 555 560

3108SEQPC1

Ala	Glu	Gly	Phe	Tyr	Ala	Asp	Gly	Ser	Tyr	Ile	Asp	His	Thr	Asn	Val
				565					570					575	
Ala	Tyr	Thr	Gly	Ala	Tyr	Gly	Asn	Val	Leu	Ile	Asp	Gly	Leu	Thr	Gln
			580					585					590		
Leu	Leu	Pro	Ile	Ile	Gln	Glu	Thr	Asp	Tyr	Lys	Ile	Ser	Asn	Gln	Glu
		595					600					605			
Leu	Asp	Met	Val	Tyr	Lys	Trp	Ile	Asn	Gln	Ser	Phe	Leu	Pro	Leu	Ile
	610					615					620				
Val	Lys	Gly	Glu	Leu	Met	Asp	Met	Ser	Arg	Gly	Arg	Ser	Ile	Ser	Arg
625					630					635					640
Glu	Ala	Ala	Ser	Ser	His	Ala	Ala	Ala	Val	Glu	Val	Leu	Arg	Gly	Phe
				645					650					655	
Leu	Arg	Leu	Ala	Asn	Met	Ser	Asn	Glu	Glu	Arg	Asn	Leu	Asp	Leu	Lys
			660					665					670		
Ser	Thr	Ile	Lys	Thr	Ile	Ile	Thr	Ser	Asn	Lys	Phe	Tyr	Asn	Val	Phe
		675					680					685			
Asn	Asn	Leu	Lys	Ser	Tyr	Ser	Asp	Ile	Ala	Asn	Met	Asn	Lys	Leu	Leu
		690				695					700				
Asn	Asp	Ser	Thr	Val	Ala	Thr	Lys	Pro	Leu	Lys	Ser	Asn	Leu	Ser	Thr
705					710					715					720
Phe	Asn	Ser	Met	Asp	Arg	Leu	Ala	Tyr	Tyr	Asn	Ala	Glu	Lys	Asp	Phe
			725						730					735	
Gly	Phe	Ala	Leu	Ser	Leu	His	Ser	Lys	Arg	Thr	Leu	Asn	Tyr	Glu	Gly
			740					745					750		
Met	Asn	Asp	Glu	Asn	Thr	Arg	Gly	Trp	Tyr	Thr	Gly	Asp	Gly	Met	Phe
		755					760					765			
Tyr	Leu	Tyr	Asn	Ser	Asp	Gln	Ser	His	Tyr	Ser	Asn	His	Phe	Trp	Pro
	770					775					780				
Thr	Val	Asn	Pro	Tyr	Lys	Met	Ala	Gly	Thr	Thr	Glu	Lys	Asp	Thr	Gly
785					790					795					800
Arg	Glu	Asp	Thr	Ile	Lys	Lys	Leu	Met	Asn	Arg	Tyr	Asp	Lys	Thr	Asn
			805						810					815	
Lys	Asn	Ser	Lys	Val	Met	Thr	Gly	Gln	Val	Thr	Gly	Thr	Ser	Asp	Phe
			820					825					830		
Val	Gly	Ser	Val	Lys	Leu	Asn	Asp	His	Phe	Ala	Leu	Ala	Ala	Met	Asp
		835					840					845			
Phe	Thr	Asn	Trp	Asp	Arg	Thr	Leu	Thr	Ala	Gln	Lys	Gly	Trp	Val	Ile
	850					855					860				
Leu	Asn	Asp	Lys	Ile	Val	Phe	Leu	Gly	Ser	Asn	Ile	Lys	Asn	Thr	Asn
865					870					875					880
Gly	Val	Gly	Asn	Val	Ser	Thr	Thr	Ile	Asp	Gln	Arg	Lys	Asp	Asp	Ser
			885						890					895	
Lys	Thr	Pro	Tyr	Thr	Thr	Tyr	Val	Asn	Gly	Lys	Thr	Val	Asp	Leu	Lys
		900						905					910		
Gln	Ala	Ser	Ser	Gln	Gln	Phe	Thr	Asp	Thr	Lys	Ser	Val	Phe	Leu	Glu
		915					920					925			
Ser	Lys	Glu	Pro	Gly	Arg	Asn	Ile	Gly	Tyr	Ile	Phe	Phe	Lys	Asn	Ser
		930				935					940				
Thr	Ile	Asp	Ile	Glu	Arg	Lys	Glu	Gln	Thr	Gly	Thr	Trp	Asn	Ser	Ile
945					950					955					960
Asn	Arg	Thr	Ser	Lys	Asn	Thr	Ser	Ile	Val	Ser	Asn	Pro	Phe	Ile	Thr
				965					970					975	
Ile	Ser	Gln	Lys	His	Asp	Asn	Lys	Gly	Asp	Ser	Tyr	Gly	Tyr	Met	Met
			980					985					990		
Val	Pro	Asn	Ile	Asp	Arg	Thr	Ser	Phe	Asp	Lys	Leu	Ala	Asn	Ser	Lys
		995					1000					1005			
Glu	Val	Glu	Leu	Leu	Glu	Asn	Ser	Ser	Lys	Gln	Gln	Val	Ile	Tyr	Asp
	1010					1015					1020				
Lys	Asn	Ser	Gln	Thr	Trp	Ala	Val	Ile	Lys	His	Asp	Asn	Gln	Glu	Ser
1025					1030					1035					1040
Leu	Ile	Asn	Asn	Gln	Phe	Lys	Met	Asn	Lys	Ala	Gly	Leu	Tyr	Leu	Val
				1045					1050					1055	
Gln	Lys	Val	Gly	Asn	Asp	Tyr	Gln	Asn	Val	Tyr	Tyr	Gln	Pro	Gln	Thr
			1060					1065					1070		
Met	Thr	Lys	Thr	Asp	Gln	Leu	Ala	Ile							
		1075					1080								

3108SEQPC1

<210> 73
 <211> 984
 <212> PRT
 <213> Streptococcus agalactiae serotype III

<220>
 <223> hyaluronan lyase

<400> 73

Met	Lys	Gln	Val	Val	Asp	Asn	Gln	Thr	Gln	Asn	Lys	Glu	Leu	Val	Lys
1				5					10					15	
Asn	Gly	Asp	Phe	Asn	Gln	Thr	Asn	Pro	Val	Ser	Gly	Ser	Trp	Ser	His
		20					25					30			
Thr	Ser	Ala	Arg	Glu	Trp	Ser	Ala	Trp	Ile	Asp	Lys	Glu	Asn	Thr	Ala
		35					40					45			
Asp	Lys	Ser	Pro	Ile	Ile	Gln	Arg	Thr	Glu	Gln	Gly	Gln	Val	Ser	Leu
	50					55					60				
Ser	Ser	Asp	Lys	Gly	Phe	Arg	Gly	Ala	Val	Thr	Gln	Lys	Val	Asn	Ile
65					70					75				80	
Asp	Pro	Thr	Lys	Lys	Tyr	Glu	Val	Lys	Phe	Asp	Ile	Glu	Thr	Ser	Asn
			85						90					95	
Lys	Ala	Gly	Gln	Ala	Phe	Leu	Arg	Ile	Met	Glu	Lys	Lys	Asp	Asn	Asn
			100					105					110		
Thr	Arg	Leu	Trp	Leu	Ser	Glu	Met	Thr	Ser	Gly	Thr	Thr	Asn	Lys	His
		115					120					125			
Thr	Leu	Thr	Lys	Ile	Tyr	Asn	Pro	Lys	Leu	Asn	Val	Ser	Glu	Val	Thr
	130					135					140				
Leu	Glu	Leu	Tyr	Tyr	Glu	Lys	Gly	Thr	Gly	Ser	Ala	Thr	Phe	Asp	Asn
145					150					155				160	
Ile	Ser	Met	Lys	Ala	Lys	Gly	Pro	Lys	Asp	Ser	Glu	His	Pro	Gln	Pro
			165						170					175	
Val	Thr	Thr	Gln	Ile	Glu	Glu	Ser	Val	Asn	Thr	Ala	Leu	Asn	Lys	Asn
			180					185					190		
Tyr	Val	Phe	Asn	Lys	Ala	Asp	Tyr	Gln	Tyr	Thr	Leu	Thr	Asn	Pro	Ser
		195					200					205			
Leu	Gly	Lys	Ile	Val	Gly	Gly	Ile	Leu	Tyr	Pro	Asn	Ala	Thr	Gly	Ser
	210					215					220				
Thr	Thr	Val	Lys	Ile	Ser	Asp	Lys	Ser	Gly	Lys	Ile	Ile	Lys	Glu	Val
225					230					235				240	
Pro	Leu	Ser	Val	Thr	Ala	Ser	Thr	Glu	Asp	Lys	Phe	Thr	Lys	Leu	Leu
			245						250					255	
Asp	Lys	Trp	Asn	Asp	Val	Thr	Ile	Gly	Asn	His	Val	Tyr	Asp	Thr	Asn
			260					265					270		
Asp	Ser	Asn	Met	Gln	Lys	Ile	Asn	Gln	Lys	Leu	Asp	Glu	Thr	Asn	Ala
		275					280					285			
Lys	Asn	Ile	Lys	Thr	Ile	Lys	Leu	Asp	Ser	Asn	His	Thr	Phe	Leu	Trp
	290					295					300				
Lys	Asp	Leu	Asp	Asn	Leu	Asn	Asn	Ser	Ala	Gln	Leu	Thr	Ala	Thr	Tyr
305					310					315				320	
Arg	Arg	Leu	Glu	Asp	Leu	Ala	Lys	Gln	Ile	Thr	Asn	Pro	His	Ser	Thr
			325					330						335	
Ile	Tyr	Lys	Asn	Glu	Lys	Ala	Ile	Arg	Thr	Val	Lys	Glu	Ser	Leu	Ala
			340					345					350		
Trp	Leu	His	Gln	Asn	Phe	Tyr	Asn	Val	Asn	Lys	Asp	Ile	Glu	Gly	Ser
		355					360					365			
Ala	Asn	Trp	Trp	Asp	Phe	Glu	Ile	Gly	Val	Pro	Arg	Ser	Ile	Thr	Ala
	370					375					380				
Thr	Leu	Ala	Leu	Met	Asn	Asn	Tyr	Phe	Thr	Asp	Ala	Glu	Ile	Lys	Thr
385					390					395				400	
Tyr	Thr	Asp	Pro	Ile	Glu	His	Phe	Val	Pro	Asp	Ala	Gly	Tyr	Phe	Arg
			405						410					415	
Lys	Thr	Leu	Asp	Asn	Pro	Phe	Lys	Ala	Leu	Gly	Gly	Asn	Leu	Val	Asp
			420					425					430		
Met	Gly	Arg	Val	Lys	Ile	Ile	Glu	Gly	Leu	Leu	Arg	Lys	Asp	Asn	Thr
		435					440					445			
Ile	Ile	Glu	Lys	Thr	Ser	His	Ser	Leu	Lys	Asn	Leu	Phe	Thr	Thr	Ala
	450					455					460				
Thr	Lys	Ala	Glu	Gly	Phe	Tyr	Ala	Asp	Gly	Ser	Tyr	Ile	Asp	His	Thr

3108SEQPC1

465	Asn	Val	Ala	Tyr	Thr	470	Gly	Ala	Tyr	Gly	475	Asn	Val	Leu	Ile	Asp	Gly	480	Leu
					485						490						495		
	Thr	Gln	Leu	Leu	Pro	Ile	Ile	Gln	Glu	Thr	Asp	Tyr	Lys	Ile	Ser	Asn			
			500						505					510					
	Gln	Glu	Leu	Asp	Met	Val	Tyr	Lys	Trp	Ile	Asn	Gln	Ser	Phe	Leu	Pro			
			515					520					525						
	Leu	Ile	Val	Lys	Gly	Glu	Leu	Met	Asp	Met	Ser	Arg	Gly	Arg	Ser	Ile			
		530					535					540							
	Ser	Arg	Glu	Ala	Ala	Ser	Ser	His	Ala	Ala	Ala	Val	Glu	Val	Leu	Arg			
545					550					555							560		
	Gly	Phe	Leu	Arg	Leu	Ala	Asn	Met	Ser	Asn	Glu	Glu	Arg	Asn	Leu	Asp			
				565						570					575				
	Leu	Lys	Ser	Thr	Ile	Lys	Thr	Ile	Ile	Thr	Ser	Asn	Lys	Phe	Tyr	Asn			
			580						585					590					
	Val	Phe	Asn	Asn	Leu	Lys	Ser	Tyr	Ser	Asp	Ile	Ala	Asn	Met	Asn	Lys			
			595					600					605						
	Met	Leu	Asn	Asp	Ser	Thr	Val	Ala	Thr	Lys	Pro	Leu	Lys	Ser	Asn	Leu			
			610				615					620							
	Ser	Thr	Phe	Asn	Ser	Met	Asp	Arg	Leu	Ala	Tyr	Tyr	Asn	Ala	Glu	Lys			
625					630					635						640			
	Asp	Phe	Gly	Phe	Ala	Leu	Ser	Leu	His	Ser	Lys	Arg	Thr	Leu	Asn	Tyr			
				645						650					655				
	Glu	Gly	Met	Asn	Asp	Glu	Asn	Thr	Arg	Asp	Trp	Tyr	Thr	Gly	Asp	Gly			
			660						665					670					
	Met	Phe	Tyr	Leu	Tyr	Asn	Ser	Asp	Gln	Ser	His	Tyr	Ser	Asn	His	Phe			
			675					680					685						
	Trp	Pro	Thr	Val	Asn	Pro	Tyr	Lys	Met	Ala	Gly	Thr	Thr	Glu	Lys	Asp			
			690				695					700							
	Ala	Lys	Arg	Glu	Asp	Thr	Thr	Lys	Glu	Phe	Met	Ser	Lys	His	Ser	Lys			
705					710					715						720			
	Asp	Ala	Lys	Glu	Lys	Thr	Gly	Gln	Val	Thr	Gly	Thr	Ser	Asp	Phe	Val			
				725						730					735				
	Gly	Ser	Val	Lys	Leu	Asn	Asp	His	Phe	Ala	Leu	Ala	Ala	Met	Asp	Phe			
			740						745					750					
	Thr	Asn	Trp	Asp	Arg	Thr	Leu	Thr	Ala	Gln	Lys	Gly	Trp	Val	Ile	Leu			
			755					760					765						
	Asn	Asp	Lys	Ile	Val	Phe	Leu	Gly	Ser	Asn	Ile	Lys	Asn	Thr	Asn	Gly			
			770				775					780							
	Ile	Gly	Asn	Val	Ser	Thr	Thr	Ile	Asp	Gln	Arg	Lys	Asp	Asp	Ser	Lys			
785					790					795						800			
	Thr	Pro	Tyr	Thr	Thr	Val	Asn	Gly	Lys	Thr	Ile	Asp	Leu	Lys	Gln				
				805					810					815					
	Ala	Ser	Ser	Gln	Gln	Phe	Thr	Asp	Thr	Lys	Ser	Val	Phe	Leu	Glu	Ser			
			820					825						830					
	Lys	Glu	Pro	Gly	Arg	Asn	Ile	Gly	Tyr	Ile	Phe	Phe	Lys	Asn	Ser	Thr			
			835					840					845						
	Ile	Asp	Ile	Glu	Arg	Lys	Glu	Gln	Thr	Gly	Thr	Trp	Asn	Ser	Ile	Asn			
			850				855					860							
	Arg	Thr	Ser	Lys	Asn	Thr	Ser	Ile	Val	Ser	Asn	Pro	Phe	Ile	Thr	Ile			
865					870					875						880			
	Ser	Gln	Lys	His	Asp	Asn	Lys	Gly	Asp	Ser	Tyr	Gly	Tyr	Met	Met	Val			
				885						890					895				
	Pro	Asn	Ile	Asp	Arg	Thr	Ser	Phe	Asp	Lys	Leu	Ala	Asn	Ser	Lys	Glu			
			900						905					910					
	Val	Glu	Leu	Leu	Glu	Asn	Ser	Ser	Lys	Gln	Gln	Val	Ile	Tyr	Asp	Lys			
			915					920					925						
	Asn	Ser	Gln	Thr	Trp	Ala	Val	Ile	Lys	His	Asp	Asn	Gln	Glu	Ser	Leu			
			930				935					940							
	Ile	Asn	Asn	Gln	Phe	Lys	Met	Asn	Lys	Ala	Gly	Leu	Tyr	Leu	Val	Gln			
945					950					955						960			
	Lys	Val	Gly	Asn	Asp	Tyr	Gln	Asn	Val	Tyr	Tyr	Gln	Pro	Gln	Thr	Met			
				965						970					975				
	Thr	Lys	Thr	Asp	Gln	Leu	Ala	Ile											
			980																

3108SEQPC1

<211> 807

<212> PRT

<213> Staphylococcus aureus (strain COL)

<220>

<223> hyaluronan lyase

<400> 74

```

Met Thr Tyr Arg Ile Lys Lys Trp Gln Lys Leu Ser Thr Ile Thr Leu
 1      5      10      15
Leu Met Ala Gly Val Ile Thr Leu Asn Gly Gly Glu Phe Arg Ser Val
      20      25      30
Asp Lys His Gln Ile Ala Val Ala Asp Thr Asn Val Gln Thr Pro Asp
      35      40      45
Tyr Glu Lys Leu Arg Asn Thr Trp Leu Asp Val Asn Tyr Gly Tyr Asp
      50      55      60
Lys Tyr Asp Glu Asn Asn Pro Asp Met Lys Lys Lys Phe Asp Ala Thr
65      70      75      80
Glu Lys Glu Ala Thr Asn Leu Leu Lys Glu Met Lys Thr Glu Ser Gly
      85      90      95
Arg Lys Tyr Leu Trp Ser Gly Ala Glu Thr Leu Glu Thr Asn Ser Ser
      100      105      110
His Met Thr Arg Thr Tyr Arg Asn Ile Glu Lys Ile Ala Glu Ala Met
      115      120      125
Arg Asn Pro Lys Thr Thr Leu Asn Thr Asp Glu Asn Lys Lys Lys Val
130      135      140
Lys Asp Ala Leu Glu Trp Leu His Lys Asn Ala Tyr Gly Lys Glu Pro
145      150      155      160
Asp Lys Lys Val Lys Glu Leu Ser Glu Asn Phe Thr Lys Thr Thr Gly
      165      170      175
Lys Asn Thr Asn Leu Asn Trp Trp Asp Tyr Glu Ile Gly Thr Pro Lys
      180      185      190
Ser Leu Thr Asn Thr Leu Ile Leu Leu Asn Asp Gln Phe Ser Asn Glu
      195      200      205
Glu Lys Lys Lys Phe Thr Ala Pro Ile Lys Thr Phe Ala Pro Asp Ser
210      215      220
Asp Lys Ile Leu Ser Ser Val Gly Lys Ala Glu Leu Ala Lys Gly Gly
225      230      235      240
Asn Leu Val Asp Ile Ser Lys Val Lys Leu Leu Glu Cys Ile Ile Glu
      245      250      255
Glu Asp Lys Asp Met Met Lys Lys Ser Ile Asp Ser Phe Asn Lys Val
      260      265      270
Phe Thr Tyr Val Gln Asp Ser Ala Thr Gly Lys Glu Arg Asn Gly Phe
      275      280      285
Tyr Lys Asp Gly Ser Tyr Ile Asp His Gln Asp Val Pro Tyr Thr Gly
290      295      300
Ala Tyr Gly Val Val Leu Leu Glu Gly Ile Ser Gln Met Met Pro Met
305      310      315      320
Ile Lys Glu Thr Pro Phe Asn Asp Lys Thr Gln Asn Asp Thr Thr Leu
      325      330      335
Lys Ser Trp Ile Asp Asp Gly Phe Met Pro Leu Ile Tyr Lys Gly Glu
      340      345      350
Met Met Asp Leu Ser Arg Gly Arg Ala Ile Ser Arg Glu Asn Glu Thr
      355      360      365
Ser His Ser Ala Ser Ala Thr Val Met Lys Ser Leu Leu Arg Leu Ser
370      375      380
Asp Ala Met Asp Asp Ser Thr Lys Ala Lys Tyr Lys Lys Ile Val Lys
385      390      395      400
Ser Ser Val Glu Ser Asp Ser Ser Tyr Lys Gln Asn Asp Tyr Leu Asn
      405      410      415
Ser Tyr Ser Asp Ile Asp Lys Met Lys Ser Leu Met Thr Asp Asn Ser
      420      425      430
Ile Ser Lys Asn Gly Leu Thr Gln Gln Leu Lys Ile Tyr Asn Asp Met
435      440      445
Asp Arg Val Thr Tyr His Asn Lys Asp Leu Asp Phe Ala Phe Gly Leu
450      455      460
Ser Met Thr Ser Lys Asn Val Ala Arg Tyr Glu Ser Ile Asn Gly Glu
465      470      475      480

```

3108SEQPC1

Asn Leu Lys Gly Trp His Thr Gly Ala Gly Met Ser Tyr Leu Tyr Asn
 485 490 495
 Ser Asp Val Lys His Tyr His Asp Asn Phe Trp Val Thr Ala Asp Met
 500 505 510
 Lys Arg Leu Ser Gly Thr Thr Thr Leu Asp Asn Glu Ile Leu Lys Asp
 515 520 525
 Thr Asp Asp Lys Lys Ser Ser Lys Thr Phe Val Gly Gly Thr Lys Val
 530 535 540
 Asp Asp Gln His Ala Ser Ile Gly Met Asp Phe Glu Asn Gln Asp Lys
 545 550 555
 Thr Leu Thr Ala Lys Lys Ser Tyr Phe Ile Leu Asn Asp Lys Ile Val
 565 570 575
 Phe Leu Gly Thr Gly Ile Lys Ser Thr Asp Ser Ser Lys Asn Pro Val
 580 585 590
 Thr Thr Ile Glu Asn Arg Lys Ala Asn Gly Tyr Thr Leu Tyr Thr Asp
 595 600 605
 Asp Lys Gln Thr Thr Asn Ser Asp Asn Gln Glu Asn Asn Ser Val Phe
 610 615 620
 Leu Glu Ser Thr Asp Thr Lys Lys Asn Ile Gly Tyr His Phe Leu Asn
 625 630 635
 Lys Pro Lys Ile Thr Val Lys Lys Glu Ser His Thr Gly Lys Trp Lys
 645 650 655
 Glu Ile Asn Lys Ser Gln Lys Asp Thr Gln Lys Thr Asp Glu Tyr Tyr
 660 665 670
 Glu Val Thr Gln Lys His Ser Asn Ser Asp Asn Lys Tyr Gly Tyr Val
 675 680 685
 Leu Tyr Pro Gly Leu Ser Lys Asp Val Phe Lys Thr Lys Lys Asp Glu
 690 695 700
 Val Thr Val Val Lys Gln Glu Asp Asp Phe His Val Val Lys Asp Asn
 705 710 715
 Glu Ser Val Trp Ala Gly Val Asn Tyr Ser Asn Ser Thr Gln Thr Phe
 725 730 735
 Asp Ile Asn Asn Thr Lys Val Glu Val Lys Ala Lys Gly Met Phe Ile
 740 745 750
 Leu Lys Lys Lys Asp Asp Asn Thr Tyr Glu Cys Ser Phe Tyr Asn Pro
 755 760 765
 Glu Ser Thr Asn Ser Ala Ser Asp Ile Glu Ser Lys Ile Ser Met Thr
 770 775 780
 Gly Tyr Ser Ile Thr Asn Lys Asn Thr Ser Thr Ser Asn Glu Ser Gly
 785 790 795 800
 Val His Phe Glu Leu Thr Lys
 805

<210> 75

<211> 420

<212> PRT

<213> Staphylococcus aureus (strain MRSA252)

<220>

<223> hyaluronan lyase

<400> 75

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

3108SEQPC1

115 120 125
 Lys His Lys Asn Thr Lys Leu Lys Thr Asp Glu Asn Lys Thr Lys Val
 130 135 140
 Lys Asp Ala Leu Glu Trp Leu His Lys Asn Ala Tyr Gly Lys Glu Pro
 145 150 155 160
 Asp Lys Lys Val Ala Asp Leu Thr Ser Asn Phe Lys Asn Lys Thr Ser
 165 170 175
 Arg Asn Thr Asn Leu Asn Trp Trp Asp Tyr Glu Ile Gly Thr Pro Arg
 180 185 190
 Ala Leu Thr Asn Thr Leu Ile Leu Leu Gln Glu Asp Phe Thr Asp Glu
 195 200 205
 Glu Lys Lys Lys Tyr Thr Ala Pro Ile Lys Thr Phe Ala Pro Asp Ser
 210 215 220
 Asp Lys Ile Leu Ser Ser Val Gly Lys Ser Glu Pro Ala Lys Gly Gly
 225 230 235 240
 Asn Leu Val Asp Ile Ser Lys Val Lys Leu Leu Glu Ser Ile Ile Glu
 245 250 255
 Glu Asp Lys Asp Met Met Lys Lys Ser Ile Asp Ser Phe Asn Thr Val
 260 265 270
 Phe Thr Tyr Ala Gln Asn Ser Ala Thr Gly Lys Glu Arg Asn Gly Phe
 275 280 285
 Tyr Lys Asp Gly Ser Tyr Ile Asp His Gln Asp Val Pro Tyr Thr Gly
 290 295 300
 Ala Tyr Gly Val Val Leu Leu Glu Gly Ile Ser Gln Met Met Pro Met
 305 310 315 320
 Ile Lys Glu Thr Pro Phe Asn Asp Ser Asn Gln Asn Asp Thr Thr Leu
 325 330 335
 Lys Ser Trp Ile Asp Asp Gly Phe Met Pro Leu Ile Tyr Lys Gly Glu
 340 345 350
 Met Met Asp Leu Ser Arg Gly Arg Ala Ile Ser Arg Glu Asn Glu Thr
 355 360 365
 Ser His Ser Ala Ser Ala Thr Val Met Lys Ser Leu Leu Arg Leu Ser
 370 375 380
 Asp Thr Met Asp Lys Ser Thr Lys Ala Lys Tyr Lys Lys Ile Val Lys
 385 390 395 400
 Thr Ser Val Glu Ser Asp Ser Ser Tyr Lys Gln Thr Asp Tyr Leu Ser
 405 410 415
 Ser Tyr Ser Asp
 420

<210> 76

<211> 806

<212> PRT

<213> Staphylococcus aureus (strain MRSA252)

<220>

<223> hyaluronan lyase

<400> 76

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

3108SEQPC1

Lys Glu Ala Leu Asp Trp Met His Lys Asn Val Tyr Gly Lys Asn Pro
 145 150 155 160
 Ser Gln Lys Val Glu Asp Leu Thr Lys Asn Arg Lys Gly Gln Thr Thr
 165 170 175
 Pro Lys Asn Asn Ser Leu Asn Trp Trp Asp Tyr Glu Ile Gly Thr Pro
 180 185 190
 Arg Ala Leu Thr Asn Thr Leu Leu Leu Met Asp Asp Met Leu Thr Lys
 195 200 205
 Asp Glu Met Lys Asn Tyr Ser Lys Pro Ile Ser Thr Tyr Ala Pro Ser
 210 215 220
 Ser Asp Lys Ile Leu Ser Ser Val Gly Glu Ser Glu Asp Ala Lys Gly
 225 230 235 240
 Gly Asn Leu Val Asp Ile Ser Lys Val Lys Leu Leu Glu Ser Val Ile
 245 250 255
 Glu Glu Asp Val Asp Met Leu Lys Lys Ser Ile Asp Ser Phe Asn Lys
 260 265 270
 Val Phe Thr Tyr Val Gln Asp Ser Ala Thr Gly Lys Gly Arg Asn Gly
 275 280 285
 Phe Tyr Lys Asp Gly Ser Tyr Ile Asp His Gln Asp Val Pro Tyr Thr
 290 295 300
 Gly Ala Tyr Gly Val Val Leu Leu Glu Gly Ile Ser Gln Met Met Pro
 305 310 315 320
 Met Ile Lys Glu Ser Pro Phe Lys Thr Thr Gln Asp Asn Ala Thr Leu
 325 330 335
 Ser Asn Trp Ile Asp Glu Gly Phe Met Pro Leu Ile Tyr Lys Gly Glu
 340 345 350
 Met Met Asp Leu Ser Arg Gly Arg Ala Ile Ser Arg Glu Asn Glu Thr
 355 360 365
 Ser His Thr Ala Ser Ala Thr Val Met Lys Ser Leu Leu Arg Leu Asn
 370 375 380
 Asp Thr Met Asp Asp Ser Thr Lys Thr Arg Tyr Lys Gln Ile Val Lys
 385 390 395 400
 Thr Ser Val Asn Ser Asp Ser Ser Tyr Asn Gln Asn Asn Tyr Leu Asn
 405 410 415
 Ser Tyr Ser Asp Ile Ala Lys Met Lys Lys Leu Met Asn Asp Ser Thr
 420 425 430
 Ile Ser Lys Asn Asp Leu Thr Gln Gln Leu Lys Ile Tyr Asn Asp Met
 435 440 445
 Asp Arg Val Thr Tyr His Asn Lys Asp Leu Asp Phe Ala Phe Gly Leu
 450 455 460
 Ser Met Thr Ser Lys Asn Ile Ala Arg Tyr Glu Asn Ile Asn Gly Glu
 465 470 475 480
 Asn Leu Lys Gly Trp His Thr Gly Ala Gly Met Ser Tyr Leu Tyr Asn
 485 490 495
 Ser Asp Val Lys His Tyr Arg Asp Asn Phe Trp Ala Thr Ala Asp Met
 500 505 510
 Thr Cys Leu Pro Gly Thr Thr Thr Leu Asn Asp Met Pro Ser Thr Asn
 515 520 525
 Thr Lys Asn Asp Lys Ser Phe Val Gly Gly Thr Lys Leu Asn Asn Lys
 530 535 540
 Tyr Ala Ser Ile Gly Met Asp Phe Glu Asn Gln Asp Lys Thr Leu Thr
 545 550 555 560
 Ala Lys Lys Ser Tyr Phe Ile Leu Asn Asp Lys Ile Val Phe Leu Gly
 565 570 575
 Thr Gly Ile Lys Ser Thr Asp Ser Lys Asn Pro Val Thr Ser Val
 580 585 590
 Glu Asn Arg Lys Ala Asn Gly Tyr Lys Leu Phe Lys Asp Asp Ile Glu
 595 600 605
 Ile Thr Thr Ser Asp Val Asn Ala Gln Glu Thr His Ser Val Phe Leu
 610 615 620
 Glu Ser Asn Asp Thr Lys Lys Asn Ile Gly Tyr His Phe Leu Asp Lys
 625 630 635 640
 Pro Lys Ile Thr Val Lys Lys Glu Ser His Thr Gly Lys Trp Ser Glu
 645 650 655
 Ile Asn Lys Ser Gln Lys Lys Asp Asp Lys Lys Asp Glu Tyr Tyr Glu
 660 665 670
 Val Thr Gln Thr His Asn Thr Ser Asp Ser Lys Tyr Ala Tyr Val Leu
 675 680 685

3108SEQPC1

Tyr Pro Gly Leu Ser Lys Ser Asp Phe Lys Ser Lys Asn Asn Asn Val
690 695 700
Ser Ile Val Lys Gln Asp Glu Asp Phe His Val Ile Lys Asp Asn Asp
705 710 715 720
Gly Val Phe Ala Gly Val Asn Tyr Ser Asp Asn Thr Lys Ser Phe Asp
725 730 735
Ile Asn Gly Ile Thr Val Glu Leu Lys Glu Lys Gly Met Phe Val Ile
740 745 750
Lys Lys Lys Asp Asp Lys Ala Tyr Lys Cys Ser Phe Tyr Asn Pro Glu
755 760 765
Thr Thr Asn Thr Ala Ser Asn Ile Glu Ser Lys Ile Phe Ile Lys Gly
770 775 780
Tyr Thr Ile Thr Asn Lys Ser Val Ile Asn Ser Asn Asp Ala Gly Val
785 790 795 800
Asn Phe Glu Leu Thr Lys
805

<210> 77

<211> 815

<212> PRT

<213> Staphylococcus aureus (strain MSSA476)

<220>

<223> hyaluronan lyase

<400> 77

Met Thr Tyr Arg Ile Lys Lys Trp Gln Lys Leu Ser Thr Ile Thr Leu
1 5 10 15
Leu Met Ala Gly Val Ile Thr Leu Asn Gly Gly Glu Phe Arg Ser Ile
20 25 30
Asp Lys Tyr Gln Ile Ala Val Ala Asp Thr Asn Val Gln Thr Pro Asp
35 40 45
Tyr Glu Lys Leu Arg Asn Thr Trp Leu Asp Val Asn Tyr Gly Tyr Asp
50 55 60
Lys Tyr Asp Glu Lys Asn Asp Ala Met Lys Lys Lys Phe Glu Ala Thr
65 70 75 80
Glu Asn Glu Ala Lys Lys Leu Leu Ser Glu Met Lys Thr Glu Ser Asp
85 90 95
Arg Lys Tyr Leu Trp Glu Asn Ser Lys Asp Leu Asp Thr Lys Ser Ala
100 105 110
Asp Met Thr Arg Thr Tyr Arg Asn Ile Glu Lys Ile Ala Glu Ala Met
115 120 125
Lys His Lys Asp Thr Lys Leu Lys Ile Asp Glu Asn Lys Lys Lys Val
130 135 140
Lys Asp Ala Leu Glu Trp Leu His Lys Asn Ala Tyr Gly Lys Glu Pro
145 150 155 160
Asp Lys Lys Val Ala Asp Leu Thr Ser Asn Phe Lys Asn Lys Thr Ser
165 170 175
Arg Asn Thr Asn Leu Asn Trp Trp Asp Tyr Glu Ile Gly Thr Pro Arg
180 185 190
Ala Leu Thr Asn Thr Leu Ile Leu Leu Asn Asp Gln Phe Ser Asn Asp
195 200 205
Glu Lys Lys Lys Tyr Thr Ala Pro Ile Lys Thr Phe Ala Pro Glu Ser
210 215 220
Asp Lys Ile Leu Ser Ser Val Gly Gln Pro Glu Gln Ala Lys Gly Gly
225 230 235 240
Asn Leu Val Asp Ile Ala Lys Val Lys Leu Leu Glu Ser Ile Ile Glu
245 250 255
Glu Asp Lys Asp Ile Thr Lys Asn Ser Ile Asp Ala Phe Asn Lys Val
260 265 270
Phe Thr Tyr Val Gln Ser Asn Ala Thr Gly Lys Glu Arg Asn Gly Phe
275 280 285
Tyr Lys Asp Gly Ser Tyr Ile Asp His Gln Asp Val Pro Tyr Thr Gly
290 295 300
Ala Tyr Gly Val Val Leu Leu Glu Gly Ile Ser Gln Met Met Pro Met
305 310 315 320
Ile Lys Glu Thr Pro Phe Asn Asp Lys Thr Gln Asn Asp Thr Thr Leu

3108SEQPC1

Lys	Ser	Trp	Ile	325	Asp	Asp	Gly	Phe	Met	330	Pro	Leu	Ile	Tyr	Lys	335	Gly	Glu
			340						345						350			
Met	Met	Asp	Leu	Ser	Arg	Gly	Arg	Ala	Ile	Ser	Arg	Glu	Asn	Glu	Thr			
		355					360							365				
Ser	His	Thr	Ala	Ser	Ala	Thr	Val	Met	Lys	Ser	Leu	Leu	Arg	Leu	Ser			
		370					375					380						
Asp	Ala	Met	Asp	Asp	Ser	Thr	Lys	Ala	Lys	Tyr	Lys	Gln	Ile	Val	Lys			
385					390					395					400			
Thr	Ser	Val	Lys	Ser	Asp	Ser	Ser	Tyr	Gly	Gln	Asn	Asp	Thr	Leu	Ser			
				405					410					415				
Ser	Tyr	Ser	Asp	Ile	Ser	Lys	Met	Lys	Ser	Leu	Met	Glu	Asp	Ser	Thr			
			420					425						430				
Ile	Ser	Thr	Asn	Gly	Leu	Thr	Gln	Gln	Leu	Lys	Ile	Tyr	Asn	Asp	Met			
		435					440						445					
Asp	Arg	Val	Thr	Tyr	His	Asn	Lys	Asp	Leu	Asp	Phe	Ala	Phe	Gly	Leu			
		450				455					460							
Ser	Met	Thr	Ser	Lys	Asn	Val	Ala	Arg	Tyr	Glu	Ser	Ile	Asn	Gly	Glu			
465					470					475					480			
Asn	Leu	Lys	Gly	Trp	His	Thr	Gly	Ala	Gly	Met	Ser	Tyr	Leu	Tyr	Asn			
				485					490					495				
Ser	Asp	Val	Lys	His	Tyr	Arg	Asp	Asn	Phe	Trp	Ala	Thr	Ala	Asp	Met			
			500					505					510					
Lys	Arg	Leu	Ala	Gly	Thr	Thr	Thr	Leu	Glu	Asn	Glu	Glu	Pro	Lys	Gly			
		515					520						525					
Thr	Asp	Val	Lys	Lys	Ser	Ser	Lys	Thr	Phe	Val	Gly	Gly	Thr	Lys	Phe			
		530				535					540							
Asp	Asp	Gln	His	Ala	Ser	Ile	Gly	Met	Asp	Phe	Glu	Asn	Gln	Asp	Lys			
545					550					555					560			
Thr	Leu	Thr	Ala	Lys	Ser	Tyr	Phe	Ile	Leu	Asn	Asp	Lys	Ile	Val				
				565				570					575					
Phe	Leu	Gly	Thr	Gly	Ile	Lys	Ser	Thr	Asp	Ser	Ser	Lys	Asn	Pro	Val			
			580					585					590					
Thr	Thr	Ile	Glu	Asn	Arg	Lys	Ala	Asn	Gly	Tyr	Thr	Leu	Tyr	Thr	Asp			
		595					600					605						
Asp	Lys	Gln	Thr	Thr	Ala	Ser	Asp	Asn	Gln	Gly	Thr	Asn	Ser	Val	Phe			
		610				615					620							
Leu	Glu	Ser	Thr	Asn	Lys	Pro	Lys	Asn	Asn	Ile	Gly	Tyr	His	Phe	Leu			
625					630					635					640			
Asn	Glu	Ser	Lys	Ile	Thr	Val	Lys	Lys	Glu	Ser	His	Thr	Gly	Lys	Trp			
				645					650					655				
Ser	Asp	Ile	Asn	Lys	Ser	Gln	Lys	Gln	Asp	Ser	Lys	Thr	Asn	Gln	Tyr			
			660					665					670					
Tyr	Glu	Val	Thr	Gln	Lys	His	Ser	Asn	Thr	Asp	Ser	Lys	Tyr	Ala	Tyr			
			675				680						685					
Val	Leu	Tyr	Pro	Gly	Leu	Ser	Lys	Asp	Asp	Phe	Asn	Thr	Lys	Lys	Asp			
		690				695					700							
Lys	Val	Thr	Val	Val	Lys	Gln	Asp	Asp	Asp	Phe	His	Val	Val	Lys	Asp			
705					710					715					720			
Asn	Glu	Ser	Val	Trp	Ala	Gly	Val	Asn	Tyr	Ser	Asp	Ser	Thr	Gln	Thr			
				725					730					735				
Phe	Ile	Ile	Asn	Asn	Thr	Lys	Val	Glu	Val	Lys	Ala	Lys	Gly	Met	Phe			
			740					745					750					
Ile	Leu	Lys	Lys	Lys	Asp	Asp	Lys	Thr	Tyr	Glu	Cys	Ser	Phe	Tyr	Asn			
		755					760					765						
Pro	Glu	Ser	Thr	Asn	Thr	Ala	Ser	Asp	Ile	Glu	Ser	Lys	Ile	Ser	Met			
			770			775				780								
Thr	Gly	Tyr	Ser	Ile	Thr	Asn	Lys	Asn	Thr	Ser	Thr	Ser	Asn	Glu	Ser			
785					790					795				800				
Gly	Val	Arg	Phe	Glu	Leu	Gln	Gln	Thr	Leu	Asn	Lys	Asp	Asp	Asn				
				805					810					815				

<210> 78
 <211> 807
 <212> PRT
 <213> Staphylococcus aureus (strain NCTC 8325)

3108SEQPC1

<220>

<223> hyaluronan lyase

<400> 78

```

Met Thr Tyr Arg Ile Lys Lys Trp Gln Lys Leu Ser Thr Ile Thr Leu
 1      5      10      15
Leu Met Ala Gly Val Ile Thr Leu Asn Gly Gly Glu Phe Arg Ser Val
 20      25      30
Asp Lys His Gln Ile Ala Val Ala Asp Thr Asn Val Gln Thr Pro Asp
 35      40      45
Tyr Glu Lys Leu Arg Asn Thr Trp Leu Asp Val Asn Tyr Gly Tyr Asp
 50      55      60
Lys Tyr Asp Glu Asn Asn Pro Asp Met Lys Lys Lys Phe Asp Ala Thr
 65      70      75      80
Glu Lys Glu Ala Thr Asn Leu Leu Lys Glu Met Lys Thr Glu Ser Gly
 85      90      95
Arg Lys Tyr Leu Trp Ser Gly Ala Glu Thr Leu Glu Thr Asn Ser Ser
100      105      110
His Met Thr Arg Thr Tyr Arg Asn Ile Glu Lys Ile Ala Glu Ala Met
115      120      125
Arg Asn Pro Lys Thr Thr Leu Asn Thr Asp Glu Asn Lys Lys Lys Val
130      135      140
Lys Asp Ala Leu Glu Trp Leu His Lys Asn Ala Tyr Gly Lys Glu Pro
145      150      155      160
Asp Lys Lys Val Lys Glu Leu Ser Glu Asn Phe Thr Lys Thr Thr Gly
165      170      175
Lys Asn Thr Asn Leu Asn Trp Trp Asp Tyr Glu Ile Gly Thr Pro Lys
180      185      190
Ser Leu Thr Asn Thr Leu Ile Leu Leu Asn Asp Gln Phe Ser Asn Glu
195      200      205
Glu Lys Lys Lys Phe Thr Ala Pro Ile Lys Thr Phe Ala Pro Asp Ser
210      215      220
Asp Lys Ile Leu Ser Ser Val Gly Lys Ala Glu Leu Ala Lys Gly Gly
225      230      235      240
Asn Leu Val Asp Ile Ser Lys Val Lys Leu Leu Glu Cys Ile Ile Glu
245      250      255
Glu Asp Lys Asp Met Met Lys Lys Ser Ile Asp Ser Phe Asn Lys Val
260      265      270
Phe Thr Tyr Val Gln Asp Ser Ala Thr Gly Lys Glu Arg Asn Gly Phe
275      280      285
Tyr Lys Asp Gly Ser Tyr Ile Asp His Gln Asp Val Pro Tyr Thr Gly
290      295      300
Ala Tyr Gly Val Val Leu Leu Glu Gly Ile Ser Gln Met Met Pro Met
305      310      315      320
Ile Lys Glu Thr Pro Phe Asn Asp Lys Thr Gln Asn Asp Thr Thr Leu
325      330      335
Lys Ser Trp Ile Asp Asp Gly Phe Met Pro Leu Ile Tyr Lys Gly Glu
340      345      350
Met Met Asp Leu Ser Arg Gly Arg Ala Ile Ser Arg Glu Asn Glu Thr
355      360      365
Ser His Ser Ala Ser Ala Thr Val Met Lys Ser Leu Leu Arg Leu Ser
370      375      380
Asp Ala Met Asp Asp Ser Thr Lys Ala Lys Tyr Lys Lys Ile Val Lys
385      390      395      400
Ser Ser Val Glu Ser Asp Ser Ser Tyr Lys Gln Asn Asp Tyr Leu Asn
405      410      415
Ser Tyr Ser Asp Ile Asp Lys Met Lys Ser Leu Met Thr Asp Asn Ser
420      425      430
Ile Ser Lys Asn Gly Leu Thr Gln Gln Leu Lys Ile Tyr Asn Asp Met
435      440      445
Asp Arg Val Thr Tyr His Asn Lys Asp Leu Asp Phe Ala Phe Gly Leu
450      455      460
Ser Met Thr Ser Lys Asn Val Ala Arg Tyr Glu Ser Ile Asn Gly Glu
465      470      475      480
Asn Leu Lys Gly Trp His Thr Gly Ala Gly Met Ser Tyr Leu Tyr Asn
485      490      495
Ser Asp Val Lys His Tyr His Asp Asn Phe Trp Val Thr Ala Asp Met
500      505      510

```

3108SEQPC1

Lys Arg Leu Ser Gly Thr Thr Thr Leu Asp Asn Glu Ile Leu Lys Asp
 515 520 525
 Thr Asp Asp Lys Lys Ser Ser Lys Thr Phe Val Gly Gly Thr Lys Val
 530 535 540
 Asp Asp Gln His Ala Ser Ile Gly Met Asp Phe Glu Asn Gln Asp Lys
 545 550 555 560
 Thr Leu Thr Ala Lys Lys Ser Tyr Phe Ile Leu Asn Asp Lys Ile Val
 565 570 575
 Phe Leu Gly Thr Gly Ile Lys Ser Thr Asp Ser Ser Lys Asn Pro Val
 580 585 590
 Thr Thr Ile Glu Asn Arg Lys Ala Asn Gly Tyr Thr Leu Tyr Thr Asp
 595 600 605
 Asp Lys Gln Thr Thr Asn Ser Asp Asn Gln Glu Asn Asn Ser Val Phe
 610 615 620
 Leu Glu Ser Thr Asp Thr Lys Lys Asn Ile Gly Tyr His Phe Leu Asn
 625 630 635 640
 Lys Pro Lys Ile Thr Val Lys Lys Glu Ser His Thr Gly Lys Trp Lys
 645 650 655
 Glu Ile Asn Lys Ser Gln Lys Asp Thr Gln Lys Thr Asp Glu Tyr Tyr
 660 665 670
 Glu Val Thr Gln Lys His Ser Asn Ser Asp Asn Lys Tyr Gly Tyr Val
 675 680 685
 Leu Tyr Pro Gly Leu Ser Lys Asp Val Phe Lys Thr Lys Lys Asp Glu
 690 695 700
 Val Thr Val Val Lys Gln Glu Asp Asp Phe His Val Val Lys Asp Asn
 705 710 715 720
 Glu Ser Val Trp Ala Gly Val Asn Tyr Ser Asn Ser Thr Gln Thr Phe
 725 730 735
 Asp Ile Asn Asn Thr Lys Val Glu Val Lys Ala Lys Gly Met Phe Ile
 740 745 750
 Leu Lys Lys Lys Asp Asp Asn Thr Tyr Glu Cys Ser Phe Tyr Asn Pro
 755 760 765
 Glu Ser Thr Asn Ser Ala Ser Asp Ile Glu Ser Lys Ile Ser Met Thr
 770 775 780
 Gly Tyr Ser Ile Thr Asn Lys Asn Thr Ser Thr Ser Asn Glu Ser Gly
 785 790 795 800
 Val His Phe Glu Leu Thr Lys
 805

<210> 79

<211> 809

<212> PRT

<213> Staphylococcus aureus (strain bovine RF122)

<220>

<223> hyaluronan lyase

<400> 79

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

3108SEQPC1

145	Gly	Lys	Lys	Val	Ala	Asp	Leu	Lys	Thr	Asn	Phe	Ser	Lys	Ser	Ala	Pro
					165					170					175	
Gln	Lys	Asn	Thr	Asn	Leu	Asn	Trp	Trp	Asp	Tyr	Glu	Ile	Gly	Thr	Pro	
			180					185					190			
Arg	Ala	Leu	Thr	Asn	Thr	Leu	Ile	Leu	Leu	Lys	Glu	Asp	Phe	Thr	Asp	
		195					200					205				
Glu	Glu	Lys	Lys	Lys	Tyr	Thr	Ala	Pro	Ile	Lys	Thr	Phe	Ala	Pro	Lys	
	210					215					220					
Ser	Asp	Glu	Ile	Leu	Ser	Ser	Val	Gly	Lys	Ala	Glu	Pro	Ala	Lys	Gly	
225					230					235					240	
Gly	Asn	Leu	Val	Asp	Ile	Ser	Lys	Val	Lys	Leu	Leu	Glu	Ser	Ile	Ile	
				245					250					255		
Glu	Glu	Asp	Lys	Asp	Met	Met	Lys	Asn	Ser	Ile	Asp	Ser	Phe	Asn	Lys	
			260					265					270			
Val	Phe	Thr	Tyr	Val	Gln	Asp	Ser	Ala	Thr	Asp	Lys	Glu	Arg	Asn	Gly	
		275					280					285				
Phe	Tyr	Lys	Asp	Gly	Ser	Tyr	Ile	Asp	His	Lys	Asp	Val	Pro	Tyr	Thr	
	290					295					300					
Gly	Ala	Tyr	Gly	Val	Val	Leu	Leu	Glu	Gly	Ile	Ser	Gln	Met	Met	Pro	
305					310					315					320	
Met	Ile	Lys	Glu	Thr	Pro	Phe	Asn	Asp	Lys	Thr	Gln	Asn	Asn	Thr	Thr	
				325					330					335		
Leu	Thr	Ser	Trp	Ile	Asp	Asp	Gly	Phe	Met	Pro	Leu	Ile	Tyr	Lys	Gly	
			340					345					350			
Glu	Met	Met	Asp	Leu	Ser	Arg	Gly	Arg	Ala	Ile	Ser	Arg	Glu	Asn	Glu	
		355					360					365				
Thr	Ser	His	Ser	Ala	Ser	Ala	Thr	Val	Met	Lys	Ser	Leu	Leu	Arg	Leu	
	370					375					380					
Ser	Asp	Ala	Met	Asp	Glu	Ser	Thr	Lys	Ala	Lys	Tyr	Lys	Gln	Ile	Val	
385					390					395					400	
Lys	Asn	Ser	Val	Lys	Ser	Asp	Ser	Ser	Tyr	Gly	Gln	Asn	Asp	Thr	Leu	
				405					410					415		
Ser	Ser	Tyr	Ser	Asp	Ile	Asp	Lys	Met	Lys	Ser	Leu	Met	Thr	Asp	Ser	
			420					425					430			
Thr	Ile	Ser	Thr	Asn	Gly	Leu	Thr	Gln	Gln	Leu	Lys	Ile	Tyr	Asn	Ala	
	435						440					445				
Met	Asp	Arg	Val	Thr	Tyr	His	Asn	Lys	Asp	Leu	Asp	Phe	Ala	Phe	Gly	
	450					455				460						
Leu	Ser	Met	Thr	Ser	Lys	Asn	Val	Ala	Arg	Tyr	Glu	Asn	Ile	Asn	Gly	
465					470					475					480	
Glu	Asn	Leu	Lys	Gly	Trp	His	Thr	Gly	Ala	Gly	Met	Ser	Tyr	Leu	Tyr	
				485					490					495		
Asn	Ser	Asp	Val	Arg	His	Tyr	Arg	Asp	Asn	Phe	Trp	Ala	Thr	Ala	Asp	
			500					505					510			
Met	Lys	Arg	Leu	Ala	Asp	Thr	Thr	Thr	Leu	Glu	Asn	Glu	Glu	Pro	Lys	
		515					520					525				
Gly	Thr	Asp	Val	Lys	Lys	Ser	Ser	Lys	Thr	Phe	Val	Gly	Gly	Thr	Lys	
	530					535					540					
Phe	Asp	Asp	Gln	His	Ala	Ser	Ile	Gly	Met	Asp	Phe	Glu	Asn	Gln	Asp	
545					550					555					560	
Lys	Thr	Leu	Thr	Ala	Lys	Lys	Ser	Tyr	Phe	Ile	Leu	Asn	Asp	Lys	Ile	
				565					570					575		
Val	Phe	Leu	Gly	Thr	Gly	Ile	Lys	Thr	Thr	Asp	Ser	Ser	Lys	Asn	Pro	
		580						585					590			
Val	Thr	Thr	Ile	Glu	Asn	Arg	Lys	Ala	His	Gly	Tyr	Thr	Leu	Tyr	Thr	
		595					600					605				
Asp	Asp	Lys	Gln	Thr	Thr	Asn	Ser	Asn	Asn	Gln	Glu	Thr	Asn	Ser	Val	
	610					615					620					
Phe	Leu	Glu	Ser	Thr	Asn	Ser	Thr	Gln	Asn	Asn	Ile	Gly	Tyr	His	Phe	
625					630					635					640	
Leu	Asn	Lys	Ser	Lys	Ile	Thr	Val	Lys	Lys	Glu	Ser	His	Thr	Gly	Lys	
				645					650					655		
Trp	Ser	Asp	Ile	Asn	Lys	Ser	Gln	Lys	Asp	Thr	Gln	Lys	Thr	Asp	Glu	
			660					665					670			
Tyr	Tyr	Glu	Val	Thr	Gln	Lys	His	Ser	Asn	Thr	Asp	Asp	Lys	Tyr	Ala	
		675					680					685				
Tyr	Val	Leu	Tyr	Pro	Gly	Ile	Thr	Lys	Asp	Asn	Phe	Lys	Ser	Lys	Ala	

3108SEQPC1

690 695 700
 Ser Gln Val Thr Val Val Lys Gln Asp Asp Asp Phe His Val Val Lys
 705 710 715 720
 Asp Asn Glu Ser Val Trp Ala Gly Val Asn Tyr Ser Asp Ser Thr Gln
 725 730 735
 Thr Phe Asp Ile Asn Gly Thr Lys Val Glu Val Lys Ala Lys Gly Met
 740 745 750
 Phe Ile Leu Lys Lys Lys Asp Asp Asn Thr Tyr Glu Cys Ser Phe Tyr
 755 760 765
 Asn Pro Glu Ser Thr Asn Ser Ala Ser Asp Ile Glu Ser Lys Ile Ser
 770 775 780
 Met Thr Gly Tyr Ser Ile Thr Asn Lys Asn Thr Ser Asn Thr Asn Glu
 785 790 795 800
 Ser Gly Val Arg Phe Glu Leu Thr Lys
 805

<210> 80

<211> 807

<212> PRT

<213> Staphylococcus aureus (strain bovine RF122)

<220>

<223> hyaluronan lyase

<400> 80

Met Thr Tyr Lys Met Lys Lys Trp Gln Lys Leu Ser Thr Ile Thr Leu
 1 5 10 15
 Leu Met Ala Gly Val Ile Thr Leu Asn Asn Gly Glu Phe Arg Asn Val
 20 25 30
 Asp Lys His Gln Ile Ala Val Ala Asp Thr Asn Val Gln Thr Pro Asp
 35 40 45
 Tyr Glu Lys Leu Lys Lys Thr Trp Leu Asp Val Asn Tyr Gly Asn Asp
 50 55 60
 Gln Tyr Asp Glu Asn Asn Gln Asp Met Lys Lys Lys Phe Asp Ala Lys
 65 70 75 80
 Glu Asn Glu Ala Lys Lys Leu Leu Glu Asp Met Lys Thr Asp Thr Asn
 85 90 95
 Arg Thr Tyr Leu Trp Ser Gly Ala Glu Asn Leu Glu Thr Asn Ser Ser
 100 105 110
 His Met Thr Lys Thr Tyr Arg Asn Ile Glu Lys Ile Ala Glu Ala Met
 115 120 125
 Arg His Lys Asn Thr Ser Leu Lys Thr Asp Glu Asn Lys Leu Lys Ile
 130 135 140
 Lys Asp Ala Ile Lys Trp Leu His His Asn Val Tyr Gly Lys Asp Pro
 145 150 155 160
 Asp Lys Lys Val Ala Asp Leu Thr Thr Asn Arg Lys Glu Lys Asp Ser
 165 170 175
 Ser Lys Lys Asn Asn Ser Leu Asn Trp Trp Asp Tyr Glu Ile Gly Thr
 180 185 190
 Pro Arg Ala Leu Thr Asn Thr Leu Leu Leu Met Asp Asn Met Leu Thr
 195 200 205
 Lys Asp Glu Met Lys Asn Tyr Ser Lys Pro Ile Ser Ile Tyr Ser Pro
 210 215 220
 Ser Ser Tyr Lys Ile Leu Ser Ser Val Gly Glu Ser Glu Asp Ala Lys
 225 230 235 240
 Gly Gly Asn Leu Val Asp Ile Ala Lys Val Lys Phe Leu Glu Ser Val
 245 250 255
 Ile Glu Glu Asp Val Asp Met Met Lys Lys Ser Ile Asp Ser Phe Asn
 260 265 270
 Lys Val Phe Thr Tyr Val Gln Asp Ser Ala Thr Gly Lys Ala Arg Asn
 275 280 285
 Gly Phe Tyr Lys Asp Gly Ser Tyr Ile Asp His Gln Asp Val Pro Tyr
 290 295 300
 Thr Gly Ala Tyr Gly Val Val Leu Leu Glu Gly Ile Ser Gln Met Met
 305 310 315 320
 Pro Met Ile Lys Glu Ser Pro Phe Lys His Thr Gln Asp Lys Ala Thr
 325 330 335

3108SEQPC1

Leu	Ser	Asn	Trp	Ile	Asp	Glu	Gly	Phe	Met	Pro	Leu	Ile	Tyr	Lys	Gly
			340					345					350		
Glu	Met	Met	Asp	Leu	Ser	Arg	Gly	Arg	Ala	Ile	Ser	Arg	Glu	Asn	Glu
		355					360					365			
Thr	Ser	His	Thr	Ala	Ser	Ala	Thr	Val	Met	Lys	Ser	Leu	Leu	Arg	Leu
		370				375					380				
Ser	Asp	Thr	Met	Asp	Glu	Ser	Thr	Lys	Thr	Lys	Tyr	Lys	Gln	Ile	Val
385					390					395					400
Lys	Thr	Ser	Val	Lys	Ser	Asp	Ser	Ser	Tyr	Asp	Ser	Asn	Asp	Thr	Leu
			405						410					415	
Asn	Ser	Tyr	Ser	Asp	Ile	Asp	Lys	Met	Lys	Lys	Leu	Met	Asn	Asp	Ser
		420						425					430		
Thr	Ile	Ser	Lys	Asn	Asp	Leu	Thr	Gln	Gln	Leu	Lys	Ile	Tyr	Asn	Asp
		435				440						445			
Met	Asp	Arg	Val	Thr	Tyr	His	Asn	Lys	Glu	Leu	Asp	Phe	Ala	Phe	Gly
	450					455					460				
Leu	Ser	Met	Thr	Ser	Lys	Asn	Ile	Ala	Arg	Tyr	Glu	Asn	Ile	Asn	Gly
465					470					475					480
Glu	Asn	Leu	Lys	Gly	Trp	His	Thr	Gly	Ala	Gly	Met	Ser	Tyr	Leu	Tyr
			485						490						495
Asn	Ser	Asp	Val	Lys	His	Tyr	Arg	Asp	Asn	Phe	Trp	Ala	Thr	Ala	Asp
		500						505					510		
Met	Thr	Arg	Leu	Pro	Gly	Thr	Thr	Thr	Leu	Asn	Asp	Met	Pro	Ser	Thr
		515					520					525			
Asn	Thr	Lys	Asn	Asp	Lys	Ser	Phe	Val	Gly	Gly	Thr	Lys	Leu	Asn	Asn
		530				535					540				
Lys	Tyr	Ala	Ser	Ile	Gly	Met	Asp	Phe	Glu	Asn	Gln	Asp	Lys	Thr	Leu
545					550					555					560
Thr	Ala	Lys	Lys	Ser	Tyr	Phe	Ile	Leu	Asn	Asp	Lys	Ile	Val	Phe	Ile
			565						570					575	
Gly	Thr	Gly	Ile	Lys	Ser	Thr	Asp	Ser	Ser	Lys	Asn	Pro	Val	Thr	Ser
			580					585					590		
Val	Glu	Asn	Arg	Lys	Ala	Asn	Gly	Tyr	Lys	Leu	Phe	Lys	Gly	Asp	Ile
		595					600					605			
Glu	Ile	Thr	Thr	Ser	Asp	Val	Asn	Ala	Gln	Glu	Thr	His	Ser	Val	Phe
	610					615					620				
Leu	Glu	Ser	Asn	Asp	Thr	Lys	Lys	Asn	Ile	Gly	Tyr	His	Phe	Leu	Asp
625					630					635					640
Lys	Pro	Lys	Ile	Thr	Val	Lys	Lys	Glu	Ser	His	Thr	Gly	Lys	Trp	Ser
			645						650					655	
Glu	Ile	Asn	Lys	Ser	Gln	Lys	Thr	Asp	Lys	Lys	Asp	Glu	Tyr	Tyr	
		660						665				670			
Glu	Val	Thr	Gln	Thr	His	Asn	Thr	Ser	Asp	Ser	Lys	Tyr	Ala	Tyr	Val
		675					680					685			
Leu	Tyr	Pro	Gly	Leu	Ser	Lys	Ser	Asp	Phe	Lys	Ser	Lys	Asn	Asn	Asn
	690					695					700				
Val	Ser	Ile	Val	Lys	Gln	Asp	Glu	Asp	Phe	His	Val	Ile	Lys	Asp	Asn
705					710					715					720
Asp	Gly	Val	Phe	Ala	Gly	Val	Asn	Tyr	Ser	Asp	Ser	Thr	Lys	Ser	Phe
			725						730					735	
Asp	Ile	Asn	Gly	Thr	Ile	Val	Glu	Leu	Lys	Glu	Lys	Gly	Met	Phe	Val
			740					745					750		
Ile	Lys	Lys	Lys	Asp	Asp	Asn	Thr	Tyr	Glu	Cys	Ser	Phe	Tyr	Asn	Pro
		755					760					765			
Thr	Ser	Thr	Asn	Ser	Thr	Ser	Asn	Lys	Glu	Ser	Lys	Ile	Ser	Val	Thr
		770				775					780				
Gly	Tyr	Thr	Ile	Thr	Asn	Gln	Ser	Val	Ser	Asn	Phe	Lys	Glu	Ser	Asp
785					790					795					800
Ile	His	Phe	Glu	Leu	Thr	Lys									
			805												

<210> 81

<211> 807

<212> PRT

<213> Staphylococcus aureus (strain USA300)

<220>

3108SEQPC1

<223> hyaluronan lyase

<400> 81

```

Met Thr Tyr Arg Ile Lys Lys Trp Gln Lys Leu Ser Thr Ile Thr Leu
 1      5      10      15
Leu Met Ala Gly Val Ile Thr Leu Asn Gly Gly Glu Phe Arg Ser Val
 20      25      30
Asp Lys His Gln Ile Ala Val Ala Asp Thr Asn Val Gln Thr Pro Asp
 35      40      45
Tyr Glu Lys Leu Arg Asn Thr Trp Leu Asp Val Asn Tyr Gly Tyr Asp
 50      55      60
Lys Tyr Asp Glu Asn Asn Pro Asp Met Lys Lys Lys Phe Asp Ala Thr
 65      70      75      80
Glu Lys Glu Ala Thr Asn Leu Leu Lys Glu Met Lys Thr Glu Ser Gly
 85      90      95
Arg Lys Tyr Leu Trp Ser Gly Ala Glu Thr Leu Glu Thr Asn Ser Ser
100      105      110
His Met Thr Arg Thr Tyr Arg Asn Ile Glu Lys Ile Ala Glu Ala Met
115      120      125
Arg Asn Pro Lys Thr Thr Leu Asn Thr Asp Glu Asn Lys Lys Val
130      135      140
Lys Asp Ala Leu Glu Trp Leu His Lys Asn Ala Tyr Gly Lys Glu Pro
145      150      155      160
Asp Lys Lys Val Lys Glu Leu Ser Glu Asn Phe Thr Lys Thr Thr Gly
165      170      175
Lys Asn Thr Asn Leu Asn Trp Trp Asp Tyr Glu Ile Gly Thr Pro Lys
180      185      190
Ser Leu Thr Asn Thr Leu Ile Leu Leu Asn Asp Gln Phe Ser Asn Glu
195      200      205
Glu Lys Lys Lys Phe Thr Ala Pro Ile Lys Thr Phe Ala Pro Asp Ser
210      215      220
Asp Lys Ile Leu Ser Ser Val Gly Lys Ala Glu Leu Ala Lys Gly Gly
225      230      235      240
Asn Leu Val Asp Ile Ser Lys Val Lys Leu Leu Glu Cys Ile Ile Glu
245      250      255
Glu Asp Lys Asp Met Met Lys Lys Ser Ile Asp Ser Phe Asn Lys Val
260      265      270
Phe Thr Tyr Val Gln Asp Ser Ala Thr Gly Lys Glu Arg Asn Gly Phe
275      280      285
Tyr Lys Asp Gly Ser Tyr Ile Asp His Gln Asp Val Pro Tyr Thr Gly
290      295      300
Ala Tyr Gly Val Val Leu Leu Glu Gly Ile Ser Gln Met Met Pro Met
305      310      315      320
Ile Lys Glu Thr Pro Phe Asn Asp Lys Thr Gln Asn Asp Thr Thr Leu
325      330      335
Lys Ser Trp Ile Asp Asp Gly Phe Met Pro Leu Ile Tyr Lys Gly Glu
340      345      350
Met Met Asp Leu Ser Arg Gly Arg Ala Ile Ser Arg Glu Asn Glu Thr
355      360      365
Ser His Ser Ala Ser Ala Thr Val Met Lys Ser Leu Leu Arg Leu Ser
370      375      380
Asp Ala Met Asp Asp Ser Thr Lys Ala Lys Tyr Lys Lys Ile Val Lys
385      390      395      400
Ser Ser Val Glu Ser Asp Ser Ser Tyr Lys Gln Asn Asp Tyr Leu Asn
405      410      415
Ser Tyr Ser Asp Ile Asp Lys Met Lys Ser Leu Met Thr Asp Asn Ser
420      425      430
Ile Ser Lys Asn Gly Leu Thr Gln Gln Leu Lys Ile Tyr Asn Asp Met
435      440      445
Asp Arg Val Thr Tyr His Asn Lys Asp Leu Asp Phe Ala Phe Gly Leu
450      455      460
Ser Met Thr Ser Lys Asn Val Ala Arg Tyr Glu Ser Ile Asn Gly Glu
465      470      475      480
Asn Leu Lys Gly Trp His Thr Gly Ala Gly Met Ser Tyr Leu Tyr Asn
485      490      495
Ser Asp Val Lys His Tyr His Asp Asn Phe Trp Val Thr Ala Asp Met
500      505      510
Lys Arg Leu Ser Gly Thr Thr Thr Leu Asp Asn Glu Ile Leu Lys Asp

```

3108SEQPC1

515 520 525
 Thr Asp Asp Lys Lys Ser Ser Lys Thr Phe Val Gly Gly Thr Lys Val
 530 535 540
 Asp Asp Gln His Ala Ser Ile Gly Met Asp Phe Glu Asn Gln Asp Lys
 545 550 555 560
 Thr Leu Thr Ala Lys Lys Ser Tyr Phe Ile Leu Asn Asp Lys Ile Val
 565 570 575
 Phe Leu Gly Thr Gly Ile Lys Ser Thr Asp Ser Ser Lys Asn Pro Val
 580 585 590
 Thr Thr Ile Glu Asn Arg Lys Ala Asn Gly Tyr Thr Leu Tyr Thr Asp
 595 600 605
 Asp Lys Gln Thr Thr Asn Ser Asp Asn Gln Glu Asn Asn Ser Val Phe
 610 615 620
 Leu Glu Ser Thr Asp Thr Lys Lys Asn Ile Gly Tyr His Phe Leu Asn
 625 630 635 640
 Lys Pro Lys Ile Thr Val Lys Lys Glu Ser His Thr Gly Lys Trp Lys
 645 650 655
 Glu Ile Asn Lys Ser Gln Lys Asp Thr Gln Lys Thr Asp Glu Tyr Tyr
 660 665 670
 Glu Val Thr Gln Lys His Ser Asn Ser Asp Asn Lys Tyr Gly Tyr Val
 675 680 685
 Leu Tyr Pro Gly Leu Ser Lys Asp Val Phe Lys Thr Lys Lys Asp Glu
 690 695 700
 Val Thr Val Val Lys Gln Glu Asp Asp Phe His Val Val Lys Asp Asn
 705 710 715 720
 Glu Ser Val Trp Ala Gly Val Asn Tyr Ser Asn Ser Thr Gln Thr Phe
 725 730 735
 Asp Ile Asn Asn Thr Lys Val Glu Val Lys Ala Lys Gly Met Phe Ile
 740 745 750
 Leu Lys Lys Lys Asp Asp Asn Thr Tyr Glu Cys Ser Phe Tyr Asn Pro
 755 760 765
 Glu Ser Thr Asn Ser Ala Ser Asp Ile Glu Ser Lys Ile Ser Met Thr
 770 775 780
 Gly Tyr Ser Ile Thr Asn Lys Asn Thr Ser Thr Ser Asn Glu Ser Gly
 785 790 795 800
 Val His Phe Glu Leu Thr Lys
 805

<210> 82

<211> 1066

<212> PRT

<213> Streptococcus pneumoniae

<220>

<223> hyaluronan lyase

<400> 82

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

3108SEQPC1

Thr Thr Ser Gly Thr Lys Asp Trp Gln Thr Ile Glu Ala Asp Tyr Ser
 165 170
 Pro Thr Leu Asp Val Asp Lys Ile Lys Leu Glu Leu Phe Tyr Glu Thr
 180 185 190
 Gly Thr Gly Thr Val Ser Phe Lys Asp Ile Glu Leu Val Glu Val Ala
 195 200 205
 Asp Gln Leu Ser Glu Asp Ser Gln Thr Asp Lys Gln Leu Glu Glu Lys
 210 215 220
 Ile Asp Leu Pro Ile Gly Lys Lys His Val Phe Ser Leu Ala Asp Tyr
 225 230 235 240
 Thr Tyr Lys Val Glu Asn Pro Asp Val Ala Ser Val Lys Asn Gly Ile
 245 250 255
 Leu Glu Pro Leu Lys Glu Gly Thr Thr Asn Val Ile Val Ser Lys Asp
 260 265 270
 Gly Lys Glu Val Lys Lys Ile Pro Leu Lys Ile Leu Ala Ser Val Lys
 275 280 285
 Asp Ala Tyr Thr Asp Arg Leu Asp Asp Trp Asn Gly Ile Ile Ala Gly
 290 295 300
 Asn Gln Tyr Tyr Asp Ser Lys Asn Glu Gln Met Ala Lys Leu Asn Gln
 305 310 315 320
 Glu Leu Glu Gly Lys Val Ala Asp Ser Leu Ser Ser Ile Ser Ser Gln
 325 330 335
 Ala Asp Arg Thr Tyr Leu Trp Glu Lys Phe Ser Asn Tyr Lys Thr Ser
 340 345 350
 Ala Asn Leu Thr Ala Thr Tyr Arg Lys Leu Glu Glu Met Ala Lys Gln
 355 360 365
 Val Thr Asn Pro Ser Ser Arg Tyr Tyr Gln Asp Glu Thr Val Val Arg
 370 375 380
 Thr Val Arg Asp Ser Met Glu Trp Met His Lys His Val Tyr Asn Ser
 385 390 395 400
 Glu Lys Ser Ile Val Gly Asn Trp Trp Asp Tyr Glu Ile Gly Thr Pro
 405 410 415
 Arg Ala Ile Asn Asn Thr Leu Ser Leu Met Lys Glu Tyr Phe Ser Asp
 420 425 430
 Glu Glu Ile Lys Lys Tyr Thr Asp Val Ile Glu Lys Phe Val Pro Asp
 435 440 445
 Pro Glu His Phe Arg Lys Thr Thr Asp Asn Pro Phe Lys Ala Leu Gly
 450 455 460
 Gly Asn Leu Val Asp Met Gly Arg Val Lys Val Ile Ala Gly Leu Leu
 465 470 475 480
 Arg Lys Asp Asp Gln Glu Ile Ser Ser Thr Ile Arg Ser Ile Glu Gln
 485 490 495
 Val Phe Lys Leu Val Asp Gln Gly Glu Gly Phe Tyr Gln Asp Gly Ser
 500 505 510
 Tyr Ile Asp His Thr Asn Val Ala Tyr Thr Gly Ala Tyr Gly Asn Val
 515 520 525
 Leu Ile Asp Gly Leu Ser Gln Leu Leu Pro Val Ile Gln Lys Thr Lys
 530 535 540
 Asn Pro Ile Asp Lys Asp Lys Met Gln Thr Met Tyr His Trp Ile Asp
 545 550 555 560
 Lys Ser Phe Ala Pro Leu Leu Val Asn Gly Glu Leu Met Asp Met Ser
 565 570 575 580
 Arg Gly Arg Ser Ile Ser Arg Ala Asn Ser Glu Gly His Val Ala Ala
 585 590 595
 Val Glu Val Leu Arg Gly Ile His Arg Ile Ala Asp Met Ser Glu Gly
 600 605
 Glu Thr Lys Gln Cys Leu Gln Ser Leu Val Lys Thr Ile Val Gln Ser
 610 615 620
 Asp Ser Tyr Tyr Asp Val Phe Lys Asn Leu Lys Thr Tyr Lys Asp Ile
 625 630 635 640
 Ser Leu Met Gln Ser Leu Leu Ser Asp Ala Gly Val Ala Ser Val Pro
 645 650 655
 Arg Pro Ser Tyr Leu Ser Ala Phe Asn Lys Met Asp Lys Thr Ala Met
 660 665 670
 Tyr Asn Ala Glu Lys Gly Phe Gly Phe Gly Leu Ser Leu Phe Ser Ser
 675 680 685
 Arg Thr Leu Asn Tyr Glu His Met Asn Lys Glu Asn Lys Arg Gly Trp
 690 695 700

3108SEQPC1

Tyr Thr Ser Asp Gly Met Phe Tyr Leu Tyr Asn Gly Asp Leu Ser His
 705 710 715 720
 Tyr Ser Asp Gly Tyr Trp Pro Thr Val Asn Pro Tyr Lys Met Pro Gly
 725 730 735
 Thr Thr Glu Thr Asp Ala Lys Arg Ala Asp Ser Asp Thr Gly Lys Val
 740 745 750
 Leu Pro Ser Ala Phe Val Gly Thr Ser Lys Leu Asp Asp Ala Asn Ala
 755 760 765
 Thr Ala Thr Met Asp Phe Thr Asn Trp Asn Gln Thr Leu Thr Ala His
 770 775 780
 Lys Ser Trp Phe Met Leu Lys Asp Lys Ile Ala Phe Leu Gly Ser Asn
 785 790 795 800
 Ile Gln Asn Thr Ser Thr Asp Thr Ala Ala Thr Thr Ile Asp Gln Arg
 805 810 815
 Lys Leu Glu Ser Gly Asn Pro Tyr Lys Val Tyr Val Asn Asp Lys Glu
 820 825 830
 Ala Ser Leu Thr Glu Gln Glu Lys Asp Tyr Pro Glu Thr Gln Ser Val
 835 840 845
 Phe Leu Glu Ser Phe Asp Ser Lys Lys Asn Ile Gly Tyr Phe Phe Phe
 850 855 860
 Lys Lys Ser Ser Ile Ser Met Ser Lys Ala Leu Gln Lys Gly Ala Trp
 865 870 875 880
 Lys Asp Ile Asn Glu Gly Gln Ser Asp Lys Glu Val Glu Asn Glu Phe
 885 890 895
 Leu Thr Ile Ser Gln Ala His Lys Gln Asn Arg Asp Ser Tyr Gly Tyr
 900 905 910
 Met Leu Ile Pro Asn Val Asp Arg Ala Thr Phe Asn Gln Met Ile Lys
 915 920 925
 Glu Leu Glu Ser Ser Leu Ile Glu Asn Asn Glu Thr Leu Gln Ser Val
 930 935 940
 Tyr Asp Ala Lys Gln Gly Val Trp Gly Ile Val Lys Tyr Asp Asp Ser
 945 950 955 960
 Val Ser Thr Ile Ser Asn Gln Phe Gln Val Leu Lys Arg Gly Val Tyr
 965 970 975
 Thr Ile Arg Lys Glu Gly Asp Glu Tyr Lys Ile Ala Tyr Tyr Asn Pro
 980 985 990
 Glu Thr Gln Glu Ser Ala Pro Asp Gln Glu Val Phe Lys Lys Leu Glu
 995 1000 1005
 Gln Ala Ala Gln Pro Gln Val Gln Asn Ser Lys Glu Lys Glu Lys Ser
 1010 1015 1020
 Glu Glu Glu Lys Asn His Ser Asp Gln Lys Asn Leu Pro Gln Thr Gly
 1025 1030 1035 1040
 Glu Gly Gln Ser Ile Leu Ala Ser Leu Gly Phe Leu Leu Leu Gly Ala
 1045 1050 1055
 Phe Tyr Leu Phe Arg Arg Gly Lys Asn Asn
 1060 1065

<210> 83

<211> 1078

<212> PRT

<213> Streptococcus pneumoniae (strain ATCC BAA-255/R6)

<220>

<223> hyaluronan lyase

<400> 83

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

3108SEQPC1

				85					90					95	
Lys	Asn	Ser	Ser	Ala	Asp	Ala	Ser	Thr	Arg	Val	Ile	Glu	Ala	Lys	Asp
Gly	Ala	Ile	Thr	Ile	Ser	Ser	Pro	Glu	Lys	Leu	Arg	Ala	Ala	Val	His
Arg	Met	Val	Pro	Ile	Glu	Ala	Lys	Lys	Lys	Tyr	Lys	Leu	Arg	Phe	Lys
Ile	Lys	Thr	Asp	Asn	Lys	Val	Gly	Ile	Ala	Lys	Val	Arg	Ile	Ile	Glu
Glu	Ser	Gly	Lys	Asp	Lys	Arg	Leu	Trp	Asn	Ser	Ala	Thr	Thr	Ser	Gly
Thr	Lys	Asp	Trp	Gln	Thr	Ile	Glu	Ala	Asp	Tyr	Ser	Pro	Thr	Leu	Asp
Val	Asp	Lys	Ile	Lys	Leu	Glu	Leu	Phe	Tyr	Glu	Thr	Gly	Thr	Gly	Thr
Val	Ser	Phe	Lys	Asp	Ile	Glu	Leu	Val	Glu	Val	Ala	Asp	Gln	Pro	Ser
Glu	Asp	Ser	Gln	Thr	Asp	Lys	Gln	Leu	Glu	Glu	Lys	Ile	Asp	Leu	Pro
Ile	Gly	Lys	Lys	His	Val	Phe	Ser	Leu	Ala	Asp	Tyr	Thr	Tyr	Lys	Val
Glu	Asn	Pro	Asp	Val	Ala	Ser	Val	Lys	Asn	Gly	Ile	Leu	Glu	Pro	Leu
Lys	Glu	Gly	Thr	Thr	Asn	Val	Ile	Val	Ser	Lys	Asp	Gly	Lys	Glu	Val
Lys	Lys	Ile	Pro	Leu	Lys	Ile	Leu	Ala	Ser	Val	Lys	Asp	Thr	Tyr	Thr
Asp	Arg	Leu	Asp	Asp	Trp	Asn	Gly	Ile	Ile	Ala	Gly	Asn	Gln	Tyr	Tyr
Asp	Ser	Lys	Asn	Glu	Gln	Met	Ala	Lys	Leu	Asn	Gln	Glu	Leu	Glu	Gly
Lys	Val	Ala	Asp	Ser	Leu	Ser	Ser	Ile	Ser	Ser	Gln	Ala	Asp	Arg	Ile
Tyr	Leu	Trp	Glu	Lys	Phe	Ser	Asn	Tyr	Lys	Thr	Ser	Ala	Asn	Leu	Thr
Ala	Thr	Tyr	Arg	Lys	Leu	Glu	Glu	Met	Ala	Lys	Gln	Val	Thr	Asn	Pro
Ser	Ser	Arg	Tyr	Tyr	Gln	Asp	Glu	Thr	Val	Val	Arg	Thr	Val	Arg	Asp
Ser	Met	Glu	Trp	Met	His	Lys	His	Val	Tyr	Asn	Ser	Glu	Lys	Ser	Ile
Val	Gly	Asn	Trp	Trp	Asp	Tyr	Glu	Ile	Gly	Thr	Pro	Arg	Ala	Ile	Asn
Asn	Thr	Leu	Ser	Leu	Met	Lys	Glu	Tyr	Phe	Ser	Asp	Glu	Glu	Ile	Lys
Lys	Tyr	Thr	Asp	Val	Ile	Glu	Lys	Phe	Val	Pro	Asp	Pro	Glu	His	Phe
Arg	Lys	Thr	Thr	Asp	Asn	Pro	Phe	Lys	Ala	Leu	Gly	Gly	Asn	Leu	Val
Asp	Met	Gly	Arg	Val	Lys	Val	Ile	Ala	Gly	Leu	Leu	Arg	Lys	Asp	Asp
Gln	Glu	Ile	Ser	Ser	Thr	Ile	Arg	Ser	Ile	Glu	Gln	Val	Phe	Lys	Leu
Val	Asp	Gln	Gly	Glu	Gly	Phe	Tyr	Gln	Asp	Gly	Ser	Tyr	Ile	Asp	His
Thr	Asn	Val	Ala	Tyr	Thr	Gly	Ala	Tyr	Gly	Asn	Val	Leu	Ile	Asp	Gly
Leu	Ser	Gln	Leu	Leu	Pro	Val	Ile	Gln	Lys	Thr	Lys	Asn	Pro	Ile	Asp
Lys	Asp	Lys	Met	Gln	Thr	Met	Tyr	His	Trp	Ile	Asp	Lys	Ser	Phe	Ala
Pro	Leu	Leu	Val	Asn	Gly	Glu	Leu	Met	Asp	Met	Ser	Arg	Gly	Arg	Ser
Ile	Ser	Arg	Ala	Asn	Ser	Glu	Gly	His	Val	Ala	Ala	Val	Glu	Val	Leu
Arg	Gly	Ile	His	Arg	Ile	Ala	Asp	Met	Ser	Glu	Gly	Glu	Thr	Lys	Gln
Arg	Leu	Gln	Ser	Leu	Val	Lys	Thr	Ile	Val	Gln	Ser	Asp	Ser	Tyr	Tyr

3108SEQPC1

625	Asp	Val	Phe	Lys	Asn	Leu	Lys	Thr	Tyr	Lys	Asp	Ile	Ser	Leu	Met	Gln
					645					650					655	
	Ser	Leu	Leu	Ser	Asp	Ala	Gly	Val	Ala	Ser	Val	Pro	Arg	Thr	Ser	Tyr
				660					665					670		
	Leu	Ser	Ala	Phe	Asn	Lys	Met	Asp	Lys	Thr	Ala	Met	Tyr	Asn	Ala	Glu
			675					680					685			
	Lys	Gly	Phe	Gly	Phe	Gly	Leu	Ser	Leu	Phe	Ser	Ser	Arg	Thr	Leu	Asn
		690					695					700				
	Tyr	Glu	His	Met	Asn	Lys	Glu	Asn	Lys	Arg	Gly	Trp	Tyr	Thr	Ser	Asp
705					710						715					720
	Gly	Met	Phe	Tyr	Leu	Tyr	Asn	Gly	Asp	Leu	Ser	His	Tyr	Ser	Asp	Gly
					725					730					735	
	Tyr	Trp	Pro	Thr	Val	Asn	Pro	Tyr	Lys	Met	Pro	Gly	Thr	Thr	Glu	Thr
				740					745					750		
	Asp	Ala	Lys	Arg	Ala	Asp	Ser	Asp	Thr	Gly	Lys	Val	Leu	Pro	Ser	Ala
			755					760					765			
	Phe	Val	Gly	Thr	Ser	Lys	Leu	Asp	Asp	Ala	Asn	Ala	Thr	Ala	Thr	Met
		770					775					780				
	Asp	Phe	Thr	Asn	Trp	Asn	Gln	Thr	Leu	Thr	Ala	His	Lys	Ser	Trp	Phe
785					790						795					800
	Met	Leu	Lys	Asp	Lys	Ile	Ala	Phe	Leu	Gly	Ser	Asn	Ile	Gln	Asn	Thr
				805						810					815	
	Ser	Thr	Asp	Thr	Ala	Ala	Thr	Thr	Ile	Asp	Gln	Arg	Lys	Leu	Glu	Ser
				820					825					830		
	Ser	Asn	Pro	Tyr	Lys	Val	Tyr	Val	Asn	Asp	Lys	Glu	Ala	Ser	Leu	Thr
			835					840					845			
	Glu	Gln	Glu	Lys	Asp	Tyr	Pro	Glu	Thr	Gln	Ser	Val	Phe	Leu	Glu	Ser
		850					855					860				
	Ser	Asp	Ser	Lys	Lys	Asn	Ile	Gly	Tyr	Phe	Phe	Phe	Lys	Lys	Ser	Ser
865					870					875						880
	Ile	Ser	Met	Ser	Lys	Ala	Leu	Gln	Lys	Gly	Ala	Trp	Lys	Asp	Ile	Asn
				885						890					895	
	Glu	Gly	Gln	Ser	Asp	Lys	Glu	Val	Glu	Asn	Glu	Phe	Leu	Thr	Ile	Ser
			900						905					910		
	Gln	Ala	His	Lys	Gln	Asn	Gly	Asp	Ser	Tyr	Gly	Tyr	Met	Leu	Ile	Pro
		915					920						925			
	Asn	Val	Asp	Arg	Ala	Thr	Phe	Asn	Gln	Met	Ile	Lys	Glu	Leu	Glu	Ser
		930				935						940				
	Ser	Leu	Ile	Glu	Asn	Asn	Glu	Thr	Leu	Gln	Ser	Val	Tyr	Asp	Ala	Lys
945					950						955					960
	Gln	Gly	Val	Trp	Gly	Ile	Val	Lys	Tyr	Asp	Asp	Ser	Val	Ser	Thr	Ile
				965						970					975	
	Ser	Asn	Gln	Phe	Gln	Val	Leu	Lys	Arg	Gly	Val	Tyr	Thr	Ile	Arg	Lys
			980						985					990		
	Glu	Gly	Asp	Glu	Tyr	Lys	Ile	Ala	Tyr	Tyr	Asn	Pro	Glu	Thr	Gln	Glu
		995						1000					1005			
	Ser	Ala	Pro	Asp	Gln	Glu	Val	Phe	Lys	Lys	Leu	Glu	Gln	Ala	Ala	Gln
		1010				1015						1020				
	Pro	Gln	Val	Gln	Asn	Ser	Lys	Glu	Lys	Glu	Lys	Ser	Glu	Glu	Glu	Lys
1025					1030					1035						1040
	Asn	His	Ser	Asp	Gln	Lys	Asn	Leu	Pro	Gln	Thr	Gly	Glu	Gly	Gln	Ser
				1045						1050					1055	
	Ile	Leu	Ala	Ser	Leu	Gly	Phe	Leu	Leu	Gly	Ala	Phe	Tyr	Leu	Phe	
			1060					1065					1070			
	Arg	Arg	Gly	Lys	Asn	Asn										
			1075													

<210> 84

<211> 1067

<212> PRT

<213> Streptococcus pneumoniae serotype 2 (strain D39/N)

<220>

<223> hyaluronan lyase

<400> 84

3108SEQPC1

Met	Gln	Thr	Lys	Thr	Lys	Lys	Leu	Ile	Val	Ser	Leu	Ser	Ser	Leu	Val
1				5					10					15	
Leu	Ser	Gly	Phe	Leu	Leu	Asn	His	Tyr	Met	Thr	Val	Gly	Ala	Glu	Glu
			20					25					30		
Thr	Thr	Thr	Asn	Thr	Ile	Gln	Gln	Ser	Gln	Lys	Glu	Val	Gln	Tyr	Gln
		35				40						45			
Gln	Arg	Asp	Thr	Lys	Asn	Leu	Val	Glu	Asn	Gly	Asp	Phe	Gly	Gln	Thr
	50				55					60					
Glu	Asp	Gly	Ser	Ser	Pro	Trp	Thr	Gly	Ser	Lys	Ala	Gln	Gly	Trp	Ser
65					70					75				80	
Ala	Trp	Val	Asp	Gln	Lys	Asn	Ser	Ser	Ala	Asp	Ala	Ser	Thr	Arg	Val
			85						90					95	
Ile	Glu	Ala	Lys	Asp	Gly	Ala	Ile	Thr	Ile	Ser	Ser	Pro	Glu	Lys	Leu
		100						105					110		
Arg	Ala	Ala	Val	His	Arg	Met	Val	Pro	Ile	Glu	Ala	Lys	Lys	Lys	Tyr
		115				120						125			
Lys	Leu	Arg	Phe	Lys	Ile	Lys	Thr	Asp	Asn	Lys	Val	Gly	Ile	Ala	Lys
	130					135					140				
Val	Arg	Ile	Ile	Glu	Glu	Ser	Gly	Lys	Asp	Lys	Arg	Leu	Trp	Asn	Ser
145					150					155				160	
Ala	Thr	Thr	Ser	Gly	Thr	Lys	Asp	Trp	Gln	Thr	Ile	Glu	Ala	Asp	Tyr
			165					170						175	
Ser	Pro	Thr	Leu	Asp	Val	Asp	Lys	Ile	Lys	Leu	Glu	Leu	Phe	Tyr	Glu
		180						185					190		
Thr	Gly	Thr	Gly	Thr	Val	Ser	Phe	Lys	Asp	Ile	Glu	Leu	Val	Glu	Val
		195					200					205			
Ala	Asp	Gln	Pro	Ser	Glu	Asp	Ser	Gln	Thr	Asp	Lys	Gln	Leu	Glu	Glu
	210					215					220				
Lys	Ile	Asp	Leu	Pro	Ile	Gly	Lys	Lys	His	Val	Phe	Ser	Leu	Ala	Asp
225				230						235				240	
Tyr	Thr	Tyr	Lys	Val	Glu	Asn	Pro	Asp	Val	Ala	Ser	Val	Lys	Asn	Gly
			245						250					255	
Ile	Leu	Glu	Pro	Leu	Lys	Glu	Gly	Thr	Thr	Asn	Val	Ile	Val	Ser	Lys
		260					265						270		
Asp	Gly	Lys	Glu	Val	Lys	Lys	Ile	Pro	Leu	Lys	Ile	Leu	Ala	Ser	Val
	275						280					285			
Lys	Asp	Thr	Tyr	Thr	Asp	Arg	Leu	Asp	Asp	Trp	Asn	Gly	Ile	Ile	Ala
	290					295					300				
Gly	Asn	Gln	Tyr	Tyr	Asp	Ser	Lys	Asn	Glu	Gln	Met	Ala	Lys	Leu	Asn
305					310					315				320	
Gln	Glu	Leu	Glu	Gly	Lys	Val	Ala	Asp	Ser	Leu	Ser	Ser	Ile	Ser	Ser
			325						330					335	
Gln	Ala	Asp	Arg	Ile	Tyr	Leu	Trp	Glu	Lys	Phe	Ser	Asn	Tyr	Lys	Thr
		340						345					350		
Ser	Ala	Asn	Leu	Thr	Ala	Thr	Tyr	Arg	Lys	Leu	Glu	Glu	Met	Ala	Lys
		355					360					365			
Gln	Val	Thr	Asn	Pro	Ser	Ser	Arg	Tyr	Tyr	Gln	Asp	Glu	Thr	Val	Val
	370					375					380				
Arg	Thr	Val	Arg	Asp	Ser	Met	Glu	Trp	Met	His	Lys	His	Val	Tyr	Asn
385					390					395				400	
Ser	Glu	Lys	Ser	Ile	Val	Gly	Asn	Trp	Trp	Asp	Tyr	Glu	Ile	Gly	Thr
			405					410						415	
Pro	Arg	Ala	Ile	Asn	Asn	Thr	Leu	Ser	Leu	Met	Lys	Glu	Tyr	Phe	Ser
		420						425					430		
Asp	Glu	Glu	Ile	Lys	Lys	Tyr	Thr	Asp	Val	Ile	Glu	Lys	Phe	Val	Pro
		435					440					445			
Asp	Pro	Glu	His	Phe	Arg	Lys	Thr	Thr	Asp	Asn	Pro	Phe	Lys	Ala	Leu
	450					455					460				
Gly	Gly	Asn	Leu	Val	Asp	Met	Gly	Arg	Val	Lys	Val	Ile	Ala	Gly	Leu
465					470					475				480	
Leu	Arg	Lys	Asp	Asp	Gln	Glu	Ile	Ser	Ser	Thr	Ile	Arg	Ser	Ile	Glu
			485						490					495	
Gln	Val	Phe	Lys	Leu	Val	Asp	Gln	Gly	Glu	Gly	Phe	Tyr	Gln	Asp	Gly
		500						505					510		
Ser	Tyr	Ile	Asp	His	Thr	Asn	Val	Ala	Tyr	Thr	Gly	Ala	Tyr	Gly	Asn
		515					520					525			
Val	Leu	Ile	Asp	Gly	Leu	Ser	Gln	Leu	Leu	Pro	Val	Ile	Gln	Lys	Thr
	530					535					540				

3108SEQPC1

Lys	Asn	Pro	Ile	Asp	Lys	Asp	Lys	Met	Gln	Thr	Met	Tyr	His	Trp	Ile
545					550					555					560
Asp	Lys	Ser	Phe	Ala	Pro	Leu	Leu	Val	Asn	Gly	Glu	Leu	Met	Asp	Met
				565					570					575	
Ser	Arg	Gly	Arg	Ser	Ile	Ser	Arg	Ala	Asn	Ser	Glu	Gly	His	Val	Ala
			580					585					590		
Ala	Val	Glu	Val	Leu	Arg	Gly	Ile	His	Arg	Ile	Ala	Asp	Met	Ser	Glu
		595					600					605			
Gly	Glu	Thr	Lys	Gln	Arg	Leu	Gln	Ser	Leu	Val	Lys	Thr	Ile	Val	Gln
	610					615					620				
Ser	Asp	Ser	Tyr	Tyr	Asp	Val	Phe	Lys	Asn	Leu	Lys	Thr	Tyr	Lys	Asp
625					630					635					640
Ile	Ser	Leu	Met	Gln	Ser	Leu	Leu	Ser	Asp	Ala	Gly	Val	Ala	Ser	Val
				645					650					655	
Pro	Arg	Thr	Ser	Tyr	Leu	Ser	Ala	Phe	Asn	Lys	Met	Asp	Lys	Thr	Ala
			660					665					670		
Met	Tyr	Asn	Ala	Glu	Lys	Gly	Phe	Gly	Phe	Gly	Leu	Ser	Leu	Phe	Ser
		675					680					685			
Ser	Arg	Thr	Leu	Asn	Tyr	Glu	His	Met	Asn	Lys	Glu	Asn	Lys	Arg	Gly
	690					695					700				
Trp	Tyr	Thr	Ser	Asp	Gly	Met	Phe	Tyr	Leu	Tyr	Asn	Gly	Asp	Leu	Ser
705					710					715					720
His	Tyr	Ser	Asp	Gly	Tyr	Trp	Pro	Thr	Val	Asn	Pro	Tyr	Lys	Met	Pro
				725					730					735	
Gly	Thr	Thr	Glu	Thr	Asp	Ala	Lys	Arg	Ala	Asp	Ser	Asp	Thr	Gly	Lys
			740					745					750		
Val	Leu	Pro	Ser	Ala	Phe	Val	Gly	Thr	Ser	Lys	Leu	Asp	Asp	Ala	Asn
		755					760					765			
Ala	Thr	Ala	Thr	Met	Asp	Phe	Thr	Asn	Trp	Asn	Gln	Thr	Leu	Thr	Ala
	770					775					780				
His	Lys	Ser	Trp	Phe	Met	Leu	Lys	Asp	Lys	Ile	Ala	Phe	Leu	Gly	Ser
785					790					795					800
Asn	Ile	Gln	Asn	Thr	Ser	Thr	Asp	Thr	Ala	Ala	Thr	Thr	Ile	Asp	Gln
				805					810					815	
Arg	Lys	Leu	Glu	Ser	Ser	Asn	Pro	Tyr	Lys	Val	Tyr	Val	Asn	Asp	Lys
			820					825					830		
Glu	Ala	Ser	Leu	Thr	Glu	Gln	Glu	Lys	Asp	Tyr	Pro	Glu	Thr	Gln	Ser
		835					840					845			
Val	Phe	Leu	Glu	Ser	Ser	Asp	Ser	Lys	Lys	Asn	Ile	Gly	Tyr	Phe	Phe
	850					855					860				
Phe	Lys	Lys	Ser	Ser	Ile	Ser	Met	Ser	Lys	Ala	Leu	Gln	Lys	Gly	Ala
865					870					875					880
Trp	Lys	Asp	Ile	Asn	Glu	Gly	Gln	Ser	Asp	Lys	Glu	Val	Glu	Asn	Glu
				885					890					895	
Phe	Leu	Thr	Ile	Ser	Gln	Ala	His	Lys	Gln	Asn	Gly	Asp	Ser	Tyr	Gly
			900					905					910		
Tyr	Met	Leu	Ile	Pro	Asn	Val	Asp	Arg	Ala	Thr	Phe	Asn	Gln	Met	Ile
	915					920						925			
Lys	Glu	Leu	Glu	Ser	Ser	Leu	Ile	Glu	Asn	Asn	Glu	Thr	Leu	Gln	Ser
	930					935					940				
Val	Tyr	Asp	Ala	Lys	Gln	Gly	Val	Trp	Gly	Ile	Val	Lys	Tyr	Asp	Asp
945					950					955					960
Ser	Val	Ser	Thr	Ile	Ser	Asn	Gln	Phe	Gln	Val	Leu	Lys	Arg	Gly	Val
				965					970					975	
Tyr	Thr	Ile	Arg	Lys	Glu	Gly	Asp	Glu	Tyr	Lys	Ile	Ala	Tyr	Tyr	Asn
			980					985					990		
Pro	Glu	Thr	Gln	Glu	Ser	Ala	Pro	Asp	Gln	Glu	Val	Phe	Lys	Lys	Leu
		995					1000					1005			
Glu	Gln	Ala	Ala	Gln	Pro	Gln	Val	Gln	Asn	Ser	Lys	Glu	Lys	Glu	Lys
	1010					1015					1020				
Ser	Glu	Glu	Glu	Lys	Asn	His	Ser	Asp	Gln	Lys	Asn	Leu	Pro	Gln	Thr
1025					1030					1035					1040
Gly	Glu	Gly	Gln	Ser	Ile	Leu	Ala	Ser	Leu	Gly	Phe	Leu	Leu	Leu	Gly
				1045					1050					1055	
Ala	Phe	Tyr	Leu	Phe	Arg	Arg	Gly	Lys	Asn	Asn					
			1060					1065							

3108SEQPC1

<210> 85

<211> 805

<212> PRT

<213> Streptococcus pyogenes serotype M1

<220>

<223> hyaluronan lyase

<400> 85

```

Met Asn Thr Tyr Phe Cys Thr His His Lys Gln Leu Leu Leu Tyr Ser
 1      5      10      15
Asn Leu Phe Leu Ser Phe Ala Met Met Gly Gln Gly Thr Ala Ile Tyr
      20      25      30
Ala Asp Thr Leu Thr Ser Asn Ser Glu Pro Asn Asn Thr Tyr Phe Gln
      35      40      45
Thr Gln Thr Leu Thr Thr Thr Asp Ser Glu Lys Lys Val Val Gln Pro
      50      55      60
Gln Gln Lys Asp Tyr Tyr Thr Glu Leu Leu Asp Gln Trp Asn Ser Ile
65      70      75
Ile Ala Gly Asn Asp Ala Tyr Asp Lys Thr Asn Pro Asp Met Val Thr
      85      90      95
Phe His Asn Lys Ala Glu Lys Asp Ala Gln Asn Ile Ile Lys Ser Tyr
      100      105      110
Gln Gly Pro Asp His Glu Asn Arg Thr Tyr Leu Trp Glu His Ala Lys
      115      120      125
Asp Tyr Ser Ala Ser Ala Asn Ile Thr Lys Thr Tyr Arg Asn Ile Glu
      130      135      140
Lys Ile Ala Lys Gln Ile Thr Asn Pro Glu Ser Cys Tyr Tyr Gln Asp
145      150      155
Ser Lys Ala Ile Ala Ile Val Lys Asp Gly Met Ala Phe Met Tyr Glu
      165      170      175
His Ala Tyr Asn Leu Asp Arg Glu Asn His Gln Thr Thr Gly Lys Glu
      180      185      190
Asn Lys Glu Asn Trp Trp Val Tyr Glu Ile Gly Thr Pro Arg Ala Ile
      195      200      205
Asn Asn Thr Leu Ser Leu Met Tyr Pro Tyr Phe Thr Gln Glu Glu Ile
210      215      220
Leu Lys Tyr Thr Ala Pro Ile Glu Lys Phe Val Pro Asp Pro Thr Arg
225      230      235
Phe Arg Val Arg Ala Ala Asn Phe Ser Pro Phe Glu Ala Asn Ser Gly
      245      250      255
Asn Leu Ile Asp Met Gly Arg Val Lys Leu Ile Ser Gly Ile Leu Arg
260      265      270
Lys Asp Asp Leu Glu Ile Ser Asp Thr Ile Lys Ala Ile Glu Lys Val
275      280      285
Phe Thr Leu Val Asp Glu Gly Asn Gly Phe Tyr Gln Asp Gly Ser Leu
290      295      300
Ile Asp His Val Val Thr Asn Ala Gln Ser Pro Leu Tyr Lys Lys Gly
305      310      315
Ile Ala Tyr Thr Gly Ala Tyr Gly Asn Val Leu Ile Asp Gly Leu Ser
      325      330      335
Gln Leu Ile Pro Ile Ile Gln Lys Thr Lys Ser Pro Ile Lys Ala Asp
      340      345      350
Lys Met Ala Thr Ile Tyr His Trp Ile Asn His Ser Phe Phe Pro Ile
355      360      365
Ile Val Arg Gly Glu Met Met Asp Met Thr Arg Gly Arg Ser Ile Ser
370      375      380
Arg Phe Asn Ala Gln Ser His Val Ala Gly Ile Glu Ala Leu Arg Ala
385      390      395
Ile Leu Arg Ile Ala Asp Met Ser Glu Glu Pro His Arg Leu Ala Leu
      405      410      415
Lys Thr Arg Ile Lys Thr Leu Val Thr Gln Gly Asn Ala Phe Tyr Asn
420      425      430
Val Tyr Asp Asn Leu Lys Thr Tyr His Asp Ile Lys Leu Met Lys Glu
435      440      445
Leu Leu Ser Asp Thr Ser Val Pro Val Gln Lys Leu Asp Ser Tyr Val
450      455      460
Ala Ser Phe Asn Ser Met Asp Lys Leu Ala Leu Tyr Asn Asn Lys His

```

3108SEQPC1

465	Asp	Phe	Ala	Phe	Gly	470	Leu	Ser	Met	Phe	Ser	Asn	Arg	Thr	Gln	Asn	480	Tyr
				485							490					495		
	Glu	Ala	Met	Asn	Asn	Glu	Asn	Leu	His	Gly	Trp	Phe	Thr	Ser	Asp	Gly		
			500						505					510				
	Met	Phe	Tyr	Leu	Tyr	Asn	Asn	Asp	Leu	Gly	His	Tyr	Ser	Glu	Asn	Tyr		
			515					520					525					
	Trp	Ala	Thr	Val	Asn	Pro	Tyr	Arg	Leu	Pro	Gly	Thr	Thr	Glu	Thr	Glu		
		530					535					540						
	Gln	Lys	Pro	Leu	Glu	Gly	Thr	Pro	Glu	Asn	Ile	Lys	Thr	Asn	Tyr	Gln		
545					550						555					560		
	Gln	Val	Gly	Met	Thr	Gly	Leu	Ser	Asp	Asp	Ala	Phe	Val	Ala	Ser	Lys		
				565						570					575			
	Lys	Leu	Asn	Asn	Thr	Ser	Ala	Leu	Ala	Ala	Met	Thr	Phe	Thr	Asn	Trp		
			580						585					590				
	Asn	Lys	Ser	Leu	Thr	Leu	Asn	Lys	Gly	Trp	Phe	Ile	Leu	Gly	Asn	Lys		
			595					600					605					
	Ile	Ile	Phe	Val	Gly	Ser	Asn	Ile	Lys	Asn	Gln	Ser	Ser	His	Lys	Ala		
		610					615					620						
	Tyr	Thr	Thr	Ile	Glu	Gln	Arg	Lys	Glu	Asn	Gln	Lys	Tyr	Pro	Tyr	Cys		
625					630						635					640		
	Ser	Tyr	Val	Asn	Asn	Gln	Pro	Val	Asp	Leu	Asn	Asn	Gln	Leu	Val	Asp		
				645					650					655				
	Phe	Thr	Asn	Thr	Lys	Ser	Ile	Phe	Leu	Glu	Ser	Asp	Asp	Pro	Ala	Gln		
			660						665					670				
	Asn	Ile	Gly	Tyr	Tyr	Phe	Phe	Lys	Pro	Thr	Thr	Leu	Ser	Ile	Ser	Lys		
			675					680					685					
	Ala	Leu	Gln	Thr	Gly	Lys	Trp	Gln	Asn	Ile	Lys	Ala	Asp	Asp	Lys	Ser		
		690					695					700						
	Pro	Glu	Ala	Ile	Lys	Glu	Val	Ser	Asn	Thr	Phe	Ile	Thr	Ile	Met	Gln		
705					710						715					720		
	Asn	His	Thr	Gln	Asp	Gly	Asp	Arg	Tyr	Ala	Tyr	Met	Met	Leu	Pro	Asn		
				725						730					735			
	Met	Thr	Arg	Gln	Glu	Phe	Glu	Thr	Tyr	Ile	Ser	Lys	Leu	Asp	Ile	Asp		
			740						745					750				
	Leu	Leu	Glu	Asn	Asp	Lys	Leu	Ala	Ala	Val	Tyr	Asp	His	Asp	Ser			
			755				760					765						
	Gln	Gln	Met	His	Val	Ile	His	Tyr	Gly	Lys	Lys	Ala	Thr	Met	Phe	Ser		
		770					775					780						
	Asn	His	Asn	Leu	Ser	His	Gln	Gly	Phe	Tyr	Ser	Phe	Pro	His	Pro	Val		
785					790						795					800		
	Arg	Gln	Asn	Gln	Gln													
				805														

<210> 86

<211> 780

<212> PRT

<213> Streptococcus pyogenes serotype M2 (strain MGAS10)

<220>

<223> hyaluronan lyase

<400> 86

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

3108SEQPC1

Thr Asn Pro Asp Met Val Thr Phe His Asn Lys Ala Glu Lys Asp Ala
 115 120 125
 Gln Asn Ile Ile Lys Ser Tyr Gln Gly Pro Asp His Glu Asn Arg Thr
 130 135 140
 Tyr Leu Trp Glu His Ala Lys Asp Tyr Ser Ala Ser Thr Asn Ile Thr
 145 150 155 160
 Lys Thr Tyr Arg Asn Ile Glu Lys Ile Ala Lys Gln Ile Thr Asn Pro
 165 170 175
 Glu Ser Cys Tyr Tyr Gln Asp Ser Lys Ala Ile Ala Ile Val Lys Asp
 180 185 190
 Gly Met Ala Phe Met Tyr Glu His Ala Tyr Asn Leu Asn Arg Glu Asn
 195 200 205
 His Gln Thr Thr Gly Lys Glu Asn Lys Glu Asn Trp Trp Val Tyr Glu
 210 215 220
 Ile Gly Thr Pro Arg Ala Ile Asn Asn Thr Leu Ser Leu Met Tyr Pro
 225 230 235 240
 Tyr Phe Thr Gln Glu Glu Ile Leu Lys Tyr Thr Ala Pro Ile Glu Lys
 245 250 255
 Phe Val Pro Asp Pro Thr Arg Phe Arg Val Arg Ala Ala Asn Phe Ser
 260 265 270
 Pro Phe Glu Ala Asn Ser Gly Asn Leu Ile Asp Met Gly Arg Val Lys
 275 280 285
 Leu Ile Ser Gly Ile Leu Arg Lys Asp Asp Leu Glu Ile Ser Asp Thr
 290 295 300
 Ile Lys Ala Ile Glu Lys Val Phe Thr Leu Val Asp Glu Gly Asn Gly
 305 310 315 320
 Phe Tyr Gln Asp Gly Ser Leu Ile Asp His Val Val Thr Asn Thr Gln
 325 330 335
 Ser Pro Leu Tyr Lys Lys Gly Ile Ala Tyr Thr Gly Ala Tyr Gly Asn
 340 345 350
 Val Leu Ile Asp Gly Leu Ser Gln Leu Ile Pro Ile Ile Gln Lys Thr
 355 360 365
 Lys Ser Pro Ile Glu Ala Asp Lys Met Ala Thr Ile Tyr His Trp Ile
 370 375 380
 Asn His Ser Phe Phe Pro Ile Ile Val Arg Gly Glu Met Met Asp Met
 385 390 395 400
 Thr Arg Gly Arg Ser Ile Ser Arg Phe Asn Ala Gln Ser His Val Ala
 405 410 415
 Gly Ile Glu Ala Leu Arg Ala Ile Leu Arg Ile Ala Asp Met Ser Glu
 420 425 430
 Glu Pro His Arg Leu Glu Leu Lys Thr Arg Ile Lys Thr Leu Val Thr
 435 440 445
 Gln Gly Asn Ala Phe Tyr Asn Val Tyr Asp Asn Leu Lys Thr Tyr His
 450 455 460
 Asp Ile Lys Leu Met Lys Glu Leu Leu Ser Asp Thr Ser Val Pro Val
 465 470 475 480
 Gln Lys Leu Asp Ser Tyr Val Ala Ser Phe Asn Ser Met Asp Lys Leu
 485 490 495
 Ala Leu Tyr Asn Asn Lys His Asp Phe Ala Phe Gly Leu Ser Met Phe
 500 505 510
 Ser Asn Arg Thr Gln Asn Tyr Glu Ala Met Asn Asn Glu Asn Leu His
 515 520 525
 Gly Trp Phe Thr Ser Asp Gly Met Phe Tyr Leu Tyr Asn Asn Asp Leu
 530 535 540
 Gly His Tyr Ser Glu Asn Tyr Trp Ala Thr Val Asn Pro Tyr Arg Leu
 545 550 555 560
 Pro Gly Thr Thr Glu Thr Glu Gln Lys Pro Leu Glu Gly Thr Pro Glu
 565 570 575
 Asn Ile Lys Thr Asn Tyr Gln Gln Val Gly Met Thr Ser Leu Ser Asp
 580 585 590
 Asp Ala Phe Val Ala Ser Lys Lys Leu Asn Asn Thr Ser Ala Leu Ala
 595 600 605
 Ala Met Thr Phe Thr Asn Trp Asn Lys Ser Leu Thr Leu Asn Lys Gly
 610 615 620
 Trp Phe Ile Leu Gly Asn Lys Ile Ile Phe Val Gly Ser Asn Ile Lys
 625 630 635 640
 Asn Gln Ser Ser His Lys Ala Tyr Thr Thr Ile Glu Gln Arg Lys Glu
 645 650 655

3108SEQPC1

Asn Gln Lys His Pro Tyr Cys Ser Tyr Val Asn Asn Gln Pro Val Asp
 660 665 670
 Leu Asn Asn Gln Leu Val Asp Phe Thr Asn Thr Lys Ser Ile Phe Leu
 675 680 685
 Glu Ser Asp Asp Pro Ala Gln Asn Ile Gly Tyr Tyr Phe Phe Lys Pro
 690 695 700
 Arg Thr Leu Ser Ile Ser Lys Ala Leu Gln Thr Gly Lys Trp Gln Asn
 705 710 715 720
 Ile Lys Ala Asp Asp Lys Ser Pro Glu Ala Ile Lys Glu Val Ser Asn
 725 730 735
 Thr Phe Ile Thr Ile Met Gln Asn His Thr Gln Glu Gly Asp Arg Tyr
 740 745 750
 Ala Tyr Met Met Leu Pro Asn Met Thr Arg Gln Glu Phe Glu Thr Tyr
 755 760 765
 Ile Ser Lys Leu Asp Ile Asp Leu Leu Glu Asn Asn
 770 775 780

<210> 87

<211> 868

<212> PRT

<213> Streptococcus pyogenes serotype M4 (strain MGAS10)

<220>

<223> hyaluronan lyase

<400> 87

Met Asn Thr Tyr Phe Cys Thr His His Lys Gln Leu Leu Leu Tyr Ser
 1 5 10 15
 Asn Leu Phe Leu Ser Phe Ala Met Met Gly Gln Gly Thr Ala Ile Tyr
 20 25 30
 Ala Asp Thr Leu Thr Ser Asn Ser Lys Pro Asn Asn Thr Tyr Phe Gln
 35 40 45
 Thr Gln Thr Leu Thr Thr Thr Asp Ser Glu Lys Lys Val Val Gln Pro
 50 55 60
 Gln Gln Lys Asp Tyr Tyr Thr Glu Leu Leu Asp Gln Trp Asn Ser Ile
 65 70 75 80
 Ile Ala Gly Asn Asp Ala Tyr Asp Lys Thr Asn Pro Asp Met Val Thr
 85 90 95
 Phe His Asn Lys Ala Glu Lys Asp Ala Gln Asn Ile Ile Lys Ser Tyr
 100 105 110
 Gln Glu Pro Asp His Glu Asn Arg Thr Tyr Leu Trp Glu His Ala Lys
 115 120 125
 Asp Tyr Ser Ala Ser Ala Asn Ile Thr Lys Thr Tyr Arg Asn Ile Glu
 130 135 140
 Lys Ile Ala Lys Gln Ile Thr Asn Pro Glu Ser Cys Tyr Tyr Gln Asp
 145 150 155 160
 Ser Lys Ala Ile Ala Ile Val Lys Asp Gly Met Ala Phe Met Tyr Glu
 165 170 175
 His Ala Tyr Asn Leu Asp Arg Glu Asn His Gln Thr Thr Gly Lys Glu
 180 185 190
 Asn Lys Glu Asn Trp Trp Asp Tyr Glu Ile Gly Thr Pro Arg Ala Ile
 195 200 205
 Asn Asn Thr Leu Ser Leu Met Tyr Pro Tyr Phe Thr Gln Glu Glu Ile
 210 215 220
 Leu Lys Tyr Thr Ala Pro Ile Glu Lys Phe Val Pro Asp Pro Thr Arg
 225 230 235 240
 Phe Arg Val Arg Ala Ala Asn Phe Pro Pro Phe Glu Ala Asn Ser Gly
 245 250 255
 Asn Leu Ile Asp Met Gly Arg Val Lys Leu Ile Ser Gly Ile Leu Arg
 260 265 270
 Lys Asp Asp Leu Glu Ile Ser Asp Thr Ile Lys Ala Ile Glu Lys Val
 275 280 285
 Phe Thr Leu Val Asp Glu Gly Asn Gly Phe Tyr Gln Asp Gly Ser Leu
 290 295 300
 Ile Asp His Val Val Thr Asn Ala Gln Ser Pro Leu Tyr Lys Lys Gly
 305 310 315 320
 Ile Ala Tyr Thr Gly Ala Tyr Gly Asn Val Leu Ile Asp Gly Leu Ser

3108SEQPC1

Gln	Leu	Ile	Pro	Ile	Ile	Gln	Lys	Thr	Lys	Ser	Pro	Ile	Glu	Ala	Asp
			340					345					350		
Lys	Met	Ala	Thr	Ile	Tyr	His	Trp	Ile	Asn	His	Ser	Phe	Phe	Pro	Ile
		355					360					365			
Ile	Val	Arg	Gly	Glu	Met	Met	Asp	Met	Thr	Arg	Gly	Arg	Ser	Ile	Ser
	370					375					380				
Arg	Phe	Asn	Ala	Gln	Ser	His	Val	Ala	Gly	Ile	Glu	Ala	Leu	Arg	Ala
385					390					395					400
Ile	Leu	Arg	Ile	Ala	Asp	Met	Ser	Glu	Glu	Pro	His	Arg	Leu	Ala	Leu
				405					410					415	
Lys	Thr	Arg	Ile	Lys	Thr	Leu	Val	Thr	Gln	Gly	Asn	Val	Phe	Tyr	Asn
			420					425					430		
Val	Tyr	Asp	Asn	Leu	Lys	Thr	Tyr	His	Asp	Ile	Lys	Leu	Met	Lys	Glu
		435					440					445			
Leu	Leu	Ser	Asp	Thr	Ser	Val	Pro	Val	Gln	Lys	Leu	Asp	Ser	Tyr	Val
	450					455					460				
Ala	Ser	Phe	Asn	Ser	Met	Asp	Lys	Leu	Ala	Leu	Tyr	Asn	Asn	Lys	His
465					470					475					480
Asp	Phe	Ala	Phe	Gly	Leu	Ser	Met	Phe	Ser	Asn	Arg	Thr	Gln	Asn	Tyr
				485					490					495	
Glu	Ala	Met	Asn	Glu	Asn	Leu	His	Gly	Trp	Phe	Thr	Ser	Asp	Gly	
			500					505					510		
Met	Phe	Tyr	Leu	Tyr	Asn	Asn	Asp	Leu	Gly	His	Tyr	Ser	Glu	Asn	Tyr
		515					520					525			
Trp	Ala	Thr	Val	Asn	Pro	Tyr	Arg	Leu	Pro	Gly	Thr	Thr	Glu	Thr	Glu
	530					535					540				
Gln	Lys	Pro	Leu	Glu	Gly	Thr	Pro	Glu	Asn	Ile	Lys	Thr	Asn	Tyr	Gln
545					550					555					560
Gln	Val	Gly	Met	Thr	Ser	Leu	Ser	Asp	Asp	Ala	Phe	Val	Ala	Ser	Lys
				565					570					575	
Lys	Leu	Asn	Asn	Thr	Ser	Ala	Leu	Ala	Ala	Met	Thr	Phe	Thr	Asn	Trp
			580					585					590		
Asn	Lys	Ser	Leu	Thr	Leu	Asn	Lys	Gly	Trp	Phe	Ile	Leu	Gly	Asn	Lys
		595					600					605			
Ile	Ile	Phe	Val	Gly	Ser	Asn	Ile	Lys	Asn	Gln	Ser	Ser	His	Lys	Ala
	610					615					620				
Tyr	Thr	Thr	Ile	Glu	Gln	Arg	Lys	Glu	Asn	Gln	Lys	His	Pro	Tyr	Cys
625					630					635					640
Ser	Tyr	Val	Asn	Asn	Gln	Pro	Val	Asp	Leu	Asn	Asn	Gln	Leu	Val	Asp
				645					650					655	
Phe	Thr	Asn	Thr	Lys	Ser	Ile	Phe	Leu	Glu	Ser	Asp	Asp	Pro	Ala	Gln
			660					665					670		
Asn	Ile	Gly	Tyr	Tyr	Phe	Phe	Lys	Pro	Thr	Thr	Leu	Ser	Ile	Ser	Lys
		675					680					685			
Ala	Leu	Gln	Thr	Gly	Lys	Trp	Gln	Asn	Ile	Lys	Ala	Asp	Asp	Lys	Ser
	690					695					700				
Pro	Glu	Ala	Ile	Lys	Glu	Val	Ser	Asn	Thr	Phe	Ile	Thr	Ile	Met	Gln
705					710					715					720
Asn	His	Thr	Gln	Asp	Gly	Asp	Arg	Tyr	Ala	Tyr	Met	Met	Leu	Pro	Asn
				725					730					735	
Met	Thr	Arg	Gln	Glu	Phe	Glu	Thr	Tyr	Ile	Ser	Lys	Leu	Asp	Ile	Asp
			740					745					750		
Leu	Leu	Glu	Asn	Asn	Asp	Lys	Leu	Ala	Ala	Val	Tyr	Asp	His	Asp	Ser
		755					760					765			
Gln	Gln	Met	His	Val	Ile	His	Tyr	Glu	Lys	Lys	Ala	Thr	Thr	Phe	Ser
	770					775					780				
Asn	His	Asn	Leu	Ser	His	Gln	Gly	Phe	Tyr	Ser	Phe	Pro	His	Pro	Val
785					790					795					800
Lys	Gln	Asn	Gln	Gln	Gln	Lys	Leu	Ala	His	Gln	Gly	Ile	Ala	Ala	Lys
				805					810					815	
Asn	Asn	Ala	Leu	Asn	Ser	His	Lys	Ile	Pro	His	Lys	Arg	Gln	Arg	Arg
			820					825					830		
Leu	Pro	Arg	Thr	Gly	Tyr	Gln	Ser	Ser	Ser	Leu	Glu	Phe	Leu	Gly	Gly
		835					840					845			
Ala	Leu	Val	Ala	Ser	Phe	Asn	His	Ile	Thr	Lys	Pro	Phe	Arg	Lys	Lys
	850					855					860				
Asp	Leu	Arg	Ile												

865

<210> 88

<211> 828

<212> PRT

<213> Streptococcus pyogenes serotype M6

<220>

<223> hyaluronan lyase

<400> 88

```

Met Val Tyr Phe Tyr Leu Val Asp Gln Phe Thr Phe Ile Ile Ser Phe
 1      5      10      15
Leu Tyr Trp Arg Asn Leu Ser Val Asn Thr Tyr Phe Cys Thr His His
 20      25      30
Lys Gln Leu Leu Leu Tyr Ser Asn Leu Phe Leu Ser Phe Ala Met Met
 35      40      45
Gly Gln Gly Thr Ala Ile Tyr Ala Asp Thr Leu Thr Ser Asn Ser Glu
 50      55      60
Pro Asn Asn Thr Tyr Phe Gln Thr Gln Thr Leu Thr Thr Thr Asp Ser
 65      70      75      80
Glu Lys Lys Val Val Gln Pro Gln Gln Lys Asp Tyr Tyr Thr Glu Leu
 85      90      95
Leu Asp Gln Trp Asn Ser Ile Ile Ala Gly Asn Asp Ala Tyr Asp Lys
100      105      110
Thr Asn Pro Asp Met Val Thr Phe His Asn Lys Ala Glu Lys Asp Ala
115      120      125
Gln Asn Ile Ile Lys Ser Tyr Gln Gly Pro Asp His Glu Asn Arg Thr
130      135      140
Tyr Leu Trp Glu His Ala Lys Asp Tyr Ser Ala Ser Thr Asn Ile Thr
145      150      155      160
Lys Thr Tyr Arg Asn Ile Glu Lys Ile Ala Lys Gln Ile Thr Asn Pro
165      170      175
Glu Ser Cys Tyr Tyr Gln Asp Ser Lys Ala Ile Ala Ile Val Lys Asp
180      185      190
Gly Met Ala Phe Met Tyr Glu His Ala Tyr Asn Leu Asp Arg Glu Asn
195      200      205
His Gln Thr Thr Gly Lys Glu Asn Lys Glu Asn Trp Trp Val Tyr Glu
210      215      220
Ile Gly Thr Pro Arg Ala Ile Asn Asn Thr Leu Ser Leu Met Tyr Pro
225      230      235      240
Tyr Phe Thr Gln Glu Glu Ile Leu Lys Tyr Thr Ala Pro Ile Glu Lys
245      250      255
Phe Val Pro Asp Pro Thr Arg Phe Arg Val Arg Ala Ala Asn Phe Ser
260      265      270
Pro Phe Glu Ala Asn Ser Gly Asn Leu Ile Asp Met Gly Arg Val Lys
275      280      285
Leu Ile Ser Gly Ile Leu Arg Lys Asp Asp Leu Glu Ile Ser Asp Thr
290      295      300
Ile Lys Ala Ile Glu Lys Val Phe Thr Leu Val Asp Glu Gly Asn Gly
305      310      315      320
Phe Tyr Gln Asp Gly Ser Leu Ile Asp His Val Val Thr Asn Ala Gln
325      330      335
Ser Pro Leu Tyr Lys Lys Gly Ile Ala Tyr Thr Gly Ala Tyr Gly Asn
340      345      350
Val Leu Ile Asp Gly Leu Ser Gln Leu Ile Pro Ile Ile Gln Lys Thr
355      360      365
Lys Ser Pro Ile Glu Ala Asp Lys Met Ala Thr Ile Tyr His Trp Ile
370      375      380
Asn His Ser Phe Phe Pro Ile Ile Val Arg Gly Glu Met Met Asp Met
385      390      395      400
Thr Arg Gly Arg Ser Ile Ser Arg Phe Asn Ala Gln Ser His Val Ala
405      410      415
Gly Ile Glu Ala Leu Arg Ala Ile Leu Arg Ile Ala Asp Met Ser Glu
420      425      430
Glu Pro His Arg Leu Ala Leu Lys Thr Arg Ile Lys Thr Leu Val Thr
435      440      445

```

3108SEQPC1

Gln Gly Asn Ala Phe Tyr Asn Val Tyr Asp Asn Leu Lys Thr Tyr His
 450 455 460
 Asp Ile Lys Leu Met Lys Glu Leu Leu Ser Asp Thr Phe Val Pro Val
 465 470 475 480
 Gln Lys Leu Asp Ser Tyr Val Ala Ser Phe Asn Ser Met Asp Lys Leu
 485 490 495
 Ala Leu Tyr Asn Asn Lys His Asp Phe Ala Phe Gly Leu Ser Met Phe
 500 505 510
 Ser Asn Arg Thr Gln Asn Tyr Glu Ala Met Asn Asn Glu Asn Leu His
 515 520 525
 Gly Trp Phe Thr Ser Asp Gly Met Phe Tyr Leu Tyr Asn Asn Asp Leu
 530 535 540
 Gly His Tyr Ser Glu Asn Tyr Trp Ala Thr Val Asn Pro Tyr Arg Leu
 545 550 555 560
 Pro Gly Thr Thr Glu Thr Glu Gln Lys Pro Leu Glu Gly Thr Pro Glu
 565 570 575
 Asn Ile Lys Thr Asp Tyr Gln Gln Val Gly Met Thr Ser Leu Ser Asp
 580 585 590
 Asp Ala Phe Val Ala Ser Lys Lys Leu Asn Asn Thr Ser Ala Leu Ala
 595 600 605
 Ala Met Thr Phe Thr Asn Trp Asn Lys Ser Leu Thr Leu Asn Lys Gly
 610 615 620
 Trp Phe Ile Leu Gly Asn Lys Ile Ile Phe Val Gly Ser Asn Ile Lys
 625 630 635 640
 Asn Gln Ser Ser His Lys Ala Tyr Thr Thr Ile Glu Gln Arg Lys Glu
 645 650 655
 Asn Gln Lys His Pro Tyr Cys Ser Tyr Val Asn Asn Gln Pro Val Asp
 660 665 670
 Leu Asn Asn Gln Leu Val Asp Phe Thr Asn Thr Lys Ser Ile Phe Leu
 675 680 685
 Glu Ser Asp Asp Pro Ala Gln Asn Ile Gly Tyr Tyr Phe Phe Lys Pro
 690 695 700
 Thr Thr Leu Ser Ile Ser Lys Ala Leu Gln Thr Gly Lys Trp Gln Asn
 705 710 715 720
 Ile Lys Ala Asp Asp Lys Ser Pro Glu Ala Ile Lys Glu Val Ser Asn
 725 730 735
 Thr Phe Ile Thr Ile Met Gln Asn His Thr Gln Asp Gly Asp Arg Tyr
 740 745 750
 Ala Tyr Met Met Leu Pro Asn Met Thr Arg Gln Glu Phe Glu Thr Tyr
 755 760 765
 Ile Ser Lys Leu Asp Ile Asp Leu Leu Glu Asn Asn Asp Lys Leu Ala
 770 775 780
 Ala Val Tyr Asp His Asp Ser Gln Gln Met His Val Ile His Tyr Glu
 785 790 795 800
 Lys Lys Ala Thr Met Phe Ser Asn His Asn Leu Ser His Gln Gly Phe
 805 810 815
 Tyr Ser Phe Pro His Pro Val Lys Gln Asn Gln Gln
 820 825

<210> 89

<211> 556

<212> PRT

<213> Streptococcus pyogenes serotype M12 (strain MGAS2)

<220>

<223> hyaluronan lyase

<400> 89

Met Val Tyr Phe Tyr Leu Val Asn Gln Ser Thr Phe Ile Ile Ser Phe
 1 5 10 15
 Leu Tyr Trp Arg Asn Leu Ser Val Asn Thr Tyr Phe Cys Thr His His
 20 25 30
 Lys Gln Leu Leu Leu Tyr Ser Asn Leu Phe Leu Ser Phe Ala Met Met
 35 40 45
 Gly Gln Gly Thr Ala Ile Tyr Ala Asp Thr Leu Thr Ser Asn Ser Glu
 50 55 60
 Pro Asn Asn Thr Tyr Phe Gln Thr Gln Thr Leu Thr Thr Asp Ser
 Page 101

3108SEQPC1

65	Glu	Lys	Lys	Val	Val	Gln	Pro	Gln	Gln	Lys	Asp	Tyr	Tyr	Thr	Glu	Leu
				85						90					95	
Leu	Asp	Gln	Trp	Asn	Ser	Ile	Ile	Ala	Gly	Asn	Asp	Ala	Tyr	Asp	Lys	
			100					105					110			
Thr	Asn	Pro	Asp	Met	Val	Thr	Phe	His	Asn	Lys	Ala	Glu	Lys	Asp	Ala	
			115				120					125				
Gln	Asn	Ile	Ile	Lys	Ser	Tyr	Gln	Gly	Pro	Asp	His	Glu	Asn	Arg	Thr	
			130			135					140					
Tyr	Leu	Gly	Asn	Met	Gln	Arg	Ile	Ile	Pro	Leu	Leu	Leu	Ile	Ser	Arg	
145					150					155					160	
Lys	Leu	Thr	Ala	Ile	Leu	Lys	Lys	Ile	Ser	Lys	Met	Lys	Ser	Leu	Met	
				165					170					175		
Glu	Asp	Ser	Thr	Ile	Ser	Thr	Asn	Gly	Leu	Thr	Gln	Gln	Leu	Lys	Ile	
			180					185					190			
Tyr	Asn	Asp	Met	Asp	Arg	Val	Thr	Tyr	His	Asn	Lys	Gly	Leu	Asp	Phe	
			195				200					205				
Ala	Phe	Gly	Leu	Ser	Met	Thr	Ser	Lys	Asn	Val	Ala	Arg	Tyr	Glu	Ser	
			210			215				220						
Ile	Asn	Gly	Glu	Asn	Leu	Lys	Gly	Trp	His	Thr	Gly	Ala	Gly	Met	Ser	
225					230					235					240	
Tyr	Leu	Tyr	Asn	Ser	Asp	Val	Lys	His	Tyr	Arg	Asp	Asn	Phe	Trp	Ala	
				245					250					255		
Thr	Ala	Asp	Met	Lys	Arg	Leu	Ala	Gly	Thr	Thr	Thr	Leu	Asp	Asn	Glu	
			260					265					270			
Glu	Pro	Lys	Ser	Thr	Asp	Val	Lys	Lys	Ser	Ser	Lys	Thr	Phe	Val	Gly	
			275				280					285				
Gly	Thr	Lys	Phe	Asp	Asp	Gln	His	Ala	Ser	Ile	Gly	Met	Asp	Phe	Glu	
			290			295				300						
Asn	Gln	Asp	Lys	Thr	Leu	Thr	Ala	Lys	Lys	Ser	Tyr	Phe	Ile	Leu	Asn	
305					310					315					320	
Asp	Lys	Ile	Val	Phe	Leu	Gly	Thr	Gly	Ile	Lys	Ser	Thr	Asp	Ser	Ser	
				325					330					335		
Lys	Asn	Pro	Val	Thr	Thr	Ile	Glu	Asn	Arg	Lys	Ala	Asn	Asp	Tyr	Lys	
			340					345					350			
Leu	Tyr	Lys	Asp	Asp	Thr	Gln	Thr	Thr	Asn	Ser	Asp	Asn	Gln	Glu	Thr	
			355			360						365				
Asn	Ser	Leu	Phe	Leu	Glu	Ser	Thr	Asn	Ser	Thr	Gln	Asn	Asn	Ile	Gly	
			370			375				380						
Tyr	His	Phe	Leu	Asn	Glu	Ser	Lys	Ile	Thr	Val	Lys	Lys	Glu	Ser	His	
385					390					395					400	
Thr	Gly	Lys	Trp	Ser	Asp	Ile	Asn	Lys	Ser	Gln	Lys	Asp	Ile	Gln	Lys	
				405					410					415		
Thr	Asp	Glu	Tyr	Tyr	Glu	Val	Thr	Gln	Lys	His	Ser	Asn	Thr	Asp	Ser	
			420				425						430			
Lys	Tyr	Ala	Tyr	Val	Leu	Tyr	Pro	Gly	Leu	Ser	Lys	Asp	Val	Phe	Lys	
			435				440					445				
Ser	Lys	Ala	Ser	Lys	Val	Thr	Val	Val	Lys	Gln	Glu	Asp	Asp	Phe	His	
			450			455				460						
Val	Val	Lys	Asp	Asn	Glu	Ser	Val	Trp	Ala	Gly	Ile	Asn	Tyr	Ser	Asp	
465					470					475					480	
Ser	Ala	Lys	Thr	Phe	Glu	Ile	Asn	Asn	Thr	Lys	Val	Glu	Val	Lys	Ala	
				485					490					495		
Lys	Gly	Met	Phe	Ile	Leu	Thr	Lys	Lys	Asp	Asp	Asn	Thr	Tyr	Glu	Cys	
			500					505					510			
Ser	Phe	Tyr	Asn	Pro	Glu	Ser	Thr	Asn	Ser	Val	Ser	Asp	Ile	Glu	Ser	
			515				520					525				
Lys	Ile	Ser	Met	Thr	Gly	Tyr	Ser	Ile	Ile	Asn	Lys	Asn	Thr	Ser	Thr	
			530			535					540					
Ser	Asn	Glu	Ser	Gly	Val	Arg	Phe	Glu	Leu	Thr	Lys					
545					550					555						

<210> 90

<211> 635

<212> PRT

<213> Streptococcus pyogenes serotype M12 (strain MGAS2)

3108SEQPC1

<220>

<223> hyaluronan lyase

<400> 90

```

Met Ala Phe Met Tyr Glu His Ala Tyr Asn Leu Asn Arg Glu Asn His
 1      5      10      15
Gln Thr Thr Gly Lys Glu Asn Lys Glu Asn Trp Trp Val Tyr Glu Ile
 20      25      30
Gly Thr Pro Arg Ala Ile Asn Asn Thr Leu Ser Leu Met Tyr Pro Tyr
 35      40      45
Phe Thr Gln Glu Glu Ile Leu Lys Tyr Thr Ala Pro Ile Glu Lys Phe
 50      55      60
Val Pro Asp Pro Thr Arg Phe Arg Val Arg Ala Ala Asn Phe Ser Pro
 65      70      75      80
Phe Glu Ala Ser Ser Gly Asn Leu Ile Asp Met Gly Arg Val Lys Leu
 85      90      95
Ile Ser Gly Ile Leu Arg Lys Asp Asp Leu Glu Ile Ser Asp Thr Ile
100      105      110
Lys Ala Ile Glu Lys Val Phe Thr Leu Val Asp Glu Gly Asn Gly Phe
115      120      125
Tyr Gln Asp Gly Ser Leu Ile Asp His Val Val Thr Asn Ala Gln Ser
130      135      140
Pro Leu Tyr Lys Lys Gly Ile Ala Tyr Thr Gly Ala Tyr Gly Asn Val
145      150      155      160
Leu Ile Asp Gly Leu Ser Gln Leu Ile Pro Ile Ile Gln Lys Thr Lys
165      170      175
Ser Pro Ile Glu Ala Asp Lys Met Ala Thr Ile Tyr His Trp Ile Asn
180      185      190
His Ser Phe Phe Pro Ile Ile Val Arg Gly Glu Met Met Asp Met Thr
195      200      205
Arg Gly Arg Ser Ile Ser Arg Phe Asn Ala Gln Ser His Val Ala Gly
210      215      220
Ile Glu Ala Leu Arg Ala Ile Leu Arg Ile Ala Asp Met Ser Glu Glu
225      230      235      240
Pro His Arg Leu Ala Leu Lys Thr Arg Ile Lys Thr Leu Val Thr Gln
245      250      255
Gly Asn Ala Phe Tyr Asn Val Tyr Asp Asn Leu Lys Thr Tyr His Asp
260      265      270
Ile Lys Leu Met Lys Glu Leu Leu Ser Asp Thr Ser Val Pro Val Gln
275      280      285
Lys Leu Asp Ser Tyr Val Ala Ser Phe Asn Ser Met Asp Lys Leu Ala
290      295      300
Leu Tyr Asn Asn Lys His Asp Phe Ala Phe Gly Leu Ser Met Phe Ser
305      310      315      320
Asn Arg Thr Gln Asn Tyr Glu Ala Met Asn Asn Glu Asn Leu His Gly
325      330      335
Trp Phe Thr Ser Asp Gly Met Phe Tyr Leu Tyr Asn Asn Asp Leu Gly
340      345      350
His Tyr Ser Glu Asn Tyr Trp Ala Thr Val Asn Pro Tyr Arg Leu Pro
355      360      365
Gly Thr Thr Glu Thr Glu Gln Lys Pro Leu Glu Gly Thr Pro Glu Asn
370      375      380
Ile Lys Thr Asn Tyr Gln Gln Val Gly Met Thr Ser Leu Ser Asp Asp
385      390      395      400
Ala Phe Val Ala Ser Lys Lys Leu Asn Asn Thr Ser Ala Leu Ala Ala
405      410      415
Met Thr Phe Thr Asn Trp Asn Lys Ser Leu Thr Leu Asn Lys Gly Trp
420      425      430
Phe Ile Leu Gly Asn Lys Ile Ile Phe Val Gly Ser Asn Ile Lys Asn
435      440      445
Gln Ser Ser His Lys Ala Tyr Thr Thr Ile Glu Gln Arg Lys Glu Asn
450      455      460
Gln Lys His Pro Tyr Cys Ser Tyr Val Asn Asn Gln Pro Val Asp Leu
465      470      475      480
Asn Asn Gln Leu Val Asp Phe Thr Asn Thr Lys Ser Ile Phe Leu Glu
485      490      495
Ser Asp Asp Pro Ala Gln Asn Ile Gly Tyr Tyr Phe Phe Lys Pro Thr
500      505      510

```

3108SEQPC1

Thr Leu Ser Ile Ser Lys Ala Leu Gln Thr Gly Lys Trp Gln Asn Ile
 515 520 525
 Lys Ala Asp Asp Lys Ser Pro Glu Ala Ile Lys Glu Val Ser Asn Thr
 530 535 540
 Phe Ile Thr Ile Met Gln Asn His Thr Gln Asp Gly Asp Arg Tyr Ala
 545 550 555 560
 Tyr Met Met Leu Pro Asn Met Thr Arg Gln Glu Phe Glu Thr Tyr Ile
 565 570 575
 Ser Lys Leu Asp Ile Asp Leu Leu Glu Asn Asn Asp Lys Leu Ala Ala
 580 585 590
 Val Tyr Asp His Asp Ser Gln Gln Met His Val Ile His Tyr Glu Lys
 595 600 605
 Lys Ala Thr Met Phe Ser Asn His Asn Leu Ser His Gln Gly Phe Tyr
 610 615 620
 Ser Phe Pro His Pro Val Lys Gln Asn Gln Gln
 625 630 635

<210> 91

<211> 828

<212> PRT

<213> Streptococcus pyogenes serotype M12 (strain MGAS9)

<220>

<223> hyaluronan lyase

<400> 91

Met Val Tyr Phe Tyr Leu Val Asn Gln Ser Thr Phe Ile Ile Ser Phe
 1 5 10 15
 Leu Tyr Trp Arg Asn Leu Ser Val Asn Thr Tyr Phe Cys Thr His His
 20 25 30
 Lys Gln Leu Leu Tyr Ser Asn Leu Phe Leu Ser Phe Ala Met Met
 35 40 45
 Gly Gln Gly Thr Ala Ile Tyr Ala Asp Thr Leu Thr Ser Asn Ser Glu
 50 55 60
 Pro Asn Asn Thr Tyr Phe Gln Thr Gln Thr Leu Thr Thr Thr Asp Ser
 65 70 75 80
 Glu Lys Lys Val Val Gln Pro Gln Gln Lys Asp Tyr Tyr Thr Glu Leu
 85 90 95
 Leu Asp Gln Trp Asn Ser Ile Ile Ala Gly Asn Asp Ala Tyr Val Lys
 100 105 110
 Thr Asn Pro Asp Met Val Thr Phe His Asn Lys Ala Glu Lys Asp Ala
 115 120 125
 Gln Asn Ile Ile Lys Ser Tyr Gln Gly Pro Asp His Glu Asn Arg Thr
 130 135 140
 Tyr Leu Trp Glu His Ala Lys Asp Tyr Ser Ala Ser Thr Asn Ile Thr
 145 150 155 160
 Lys Thr Tyr Arg Asn Ile Glu Lys Ile Ala Lys Gln Ile Thr Asn Pro
 165 170 175
 Glu Ser Cys Tyr Tyr Gln Asp Ser Lys Ala Ile Ala Ile Val Lys Asp
 180 185 190
 Gly Met Ala Phe Met Tyr Glu His Ala Tyr Asn Leu Asn Arg Glu Asn
 195 200 205
 His Gln Thr Thr Gly Lys Glu Asn Lys Glu Asn Trp Trp Val Tyr Glu
 210 215 220
 Ile Gly Thr Pro Arg Ala Ile Asn Asn Thr Leu Ser Leu Met Tyr Pro
 225 230 235 240
 Tyr Phe Thr Gln Glu Glu Ile Leu Lys Tyr Thr Ala Pro Ile Glu Lys
 245 250 255
 Phe Val Pro Asp Pro Thr Arg Phe Arg Val Arg Ala Ala Asn Phe Ser
 260 265 270
 Pro Phe Glu Ala Ser Ser Gly Asn Leu Ile Asp Met Gly Arg Val Lys
 275 280 285
 Leu Ile Ser Gly Ile Leu Arg Lys Asp Asp Leu Glu Ile Ser Asp Thr
 290 295 300
 Ile Lys Ala Ile Glu Lys Val Phe Thr Leu Val Asp Glu Gly Asn Gly
 305 310 315 320
 Phe Tyr Gln Asp Gly Ser Leu Ile Asp His Val Val Thr Asn Ala Gln

3108SEQPC1

Ser	Pro	Leu	Tyr	Lys	Lys	Gly	Ile	Ala	Tyr	Thr	Gly	Ala	Tyr	Gly	Asn
			340					345					350		
Val	Leu	Ile	Asp	Gly	Leu	Ser	Gln	Leu	Ile	Pro	Ile	Ile	Gln	Lys	Thr
		355					360					365			
Lys	Ser	Pro	Ile	Glu	Ala	Asp	Lys	Met	Ala	Thr	Ile	Tyr	His	Trp	Ile
	370					375					380				
Asn	His	Ser	Phe	Phe	Pro	Ile	Ile	Val	Arg	Gly	Glu	Met	Met	Asp	Met
385					390					395				400	
Thr	Arg	Gly	Arg	Ser	Ile	Ser	Arg	Phe	Asn	Ala	Gln	Ser	His	Val	Ala
			405						410					415	
Gly	Ile	Glu	Ala	Leu	Arg	Ala	Ile	Leu	Arg	Ile	Ala	Asp	Met	Ser	Glu
			420					425					430		
Glu	Pro	His	Arg	Leu	Ala	Leu	Lys	Thr	Arg	Ile	Lys	Thr	Leu	Val	Thr
		435					440					445			
Gln	Gly	Asn	Ala	Phe	Tyr	Asn	Val	Tyr	Asp	Asn	Leu	Lys	Thr	Tyr	His
	450					455					460				
Asp	Ile	Lys	Leu	Met	Lys	Glu	Leu	Leu	Ser	Asp	Thr	Ser	Val	Pro	Val
465					470					475				480	
Gln	Lys	Leu	Asp	Ser	Tyr	Val	Ala	Ser	Phe	Asn	Ser	Met	Asp	Lys	Leu
			485						490					495	
Ala	Leu	Tyr	Asn	Asn	Lys	His	Asp	Phe	Ala	Phe	Gly	Leu	Ser	Met	Phe
			500					505					510		
Ser	Asn	Arg	Thr	Gln	Asn	Tyr	Glu	Ala	Met	Asn	Asn	Glu	Asn	Leu	His
		515					520					525			
Gly	Trp	Phe	Thr	Ser	Asp	Gly	Met	Phe	Tyr	Leu	Tyr	Asn	Asn	Asp	Leu
	530					535					540				
Gly	His	Tyr	Ser	Glu	Asn	Tyr	Trp	Ala	Thr	Val	Asn	Pro	Tyr	Arg	Leu
545					550					555				560	
Pro	Gly	Thr	Thr	Glu	Thr	Glu	Gln	Lys	Pro	Leu	Glu	Gly	Thr	Pro	Glu
			565						570					575	
Asn	Ile	Lys	Thr	Asn	Tyr	Gln	Gln	Val	Gly	Met	Thr	Ser	Leu	Ser	Asp
			580					585					590		
Asp	Ala	Phe	Val	Ala	Ser	Lys	Lys	Leu	Asn	Asn	Thr	Ser	Ala	Leu	Ala
		595					600					605			
Ala	Met	Thr	Phe	Thr	Asn	Trp	Asn	Lys	Ser	Leu	Thr	Leu	Asn	Lys	Gly
	610					615					620				
Trp	Phe	Ile	Leu	Gly	Asn	Lys	Ile	Ile	Phe	Val	Gly	Ser	Asn	Ile	Lys
625					630					635				640	
Asn	Gln	Ser	Ser	His	Lys	Ala	Tyr	Thr	Thr	Ile	Glu	Gln	Arg	Lys	Glu
				645					650					655	
Asn	Gln	Lys	His	Pro	Tyr	Cys	Ser	Tyr	Val	Asn	Asn	Gln	Pro	Val	Asp
			660					665					670		
Leu	Asn	Asn	Gln	Leu	Val	Asp	Phe	Thr	Asn	Thr	Lys	Ser	Ile	Phe	Leu
		675					680					685			
Glu	Ser	Asp	Asp	Pro	Ala	Gln	Asn	Ile	Gly	Tyr	Tyr	Phe	Phe	Lys	Pro
	690					695					700				
Thr	Thr	Leu	Ser	Ile	Ser	Lys	Ala	Leu	Gln	Thr	Gly	Lys	Trp	Gln	Asn
705					710					715				720	
Ile	Lys	Ala	Asp	Asp	Lys	Ser	Pro	Glu	Ala	Ile	Lys	Glu	Val	Ser	Asn
			725						730					735	
Thr	Phe	Ile	Thr	Ile	Met	Gln	Asn	His	Thr	Gln	Asp	Gly	Asp	Arg	Tyr
			740					745					750		
Ala	Tyr	Met	Met	Leu	Pro	Asn	Met	Thr	Arg	Gln	Glu	Phe	Glu	Thr	Tyr
		755					760					765			
Ile	Ser	Lys	Leu	Asp	Ile	Asp	Leu	Leu	Glu	Asn	Asn	Asp	Lys	Leu	Ala
	770					775					780				
Ala	Val	Tyr	Asp	His	Asp	Ser	Gln	Gln	Met	His	Val	Ile	His	Tyr	Glu
785					790					795				800	
Lys	Lys	Ala	Thr	Met	Phe	Ser	Asn	His	Asn	Leu	Ser	His	Gln	Gly	Phe
			805						810					815	
Tyr	Ser	Phe	Pro	His	Pro	Val	Lys	Gln	Asn	Gln	Gln				
			820					825							

<210> 92
 <211> 828
 <212> PRT

<213> Streptococcus pyogenes serotype M28

<220>

<223> hyaluronan lyase

<400> 92

Met Val Tyr Phe Tyr Leu Val Asn Gln Phe Thr Phe Ile Ile Ser Phe
 1 5 10 15
 Leu Tyr Arg Arg Asn Leu Ser Val Asn Thr Tyr Phe Cys Thr His His
 20 25 30
 Lys Gln Leu Leu Tyr Ser Asn Leu Phe Leu Ser Phe Ala Met Met
 35 40 45
 Gly Gln Gly Thr Ala Ile Tyr Ala Asp Thr Leu Thr Ser Asn Ser Glu
 50 55 60
 Pro Asn Asn Thr Tyr Phe Gln Thr Gln Met Leu Thr Thr Thr Asp Ser
 65 70 75 80
 Glu Lys Lys Val Val Gln Pro Gln Gln Lys Asp Tyr Tyr Thr Glu Leu
 85 90 95
 Leu Asp Gln Trp Asn Ser Ile Ile Ala Gly Asn Asp Ala Tyr Asp Lys
 100 105 110
 Thr Asn Pro Asp Met Val Thr Phe His Asn Lys Ala Glu Lys Asp Ala
 115 120 125
 Gln Asn Ile Ile Lys Ser Tyr Gln Gly Pro Asp His Glu Asn Arg Thr
 130 135 140
 Tyr Leu Trp Glu His Ala Lys Asp Tyr Ser Ala Ser Ala Asn Ile Thr
 145 150 155 160
 Lys Thr Tyr Arg Asn Ile Glu Lys Ile Ala Lys Gln Ile Thr Asn Pro
 165 170 175
 Glu Ser Cys Tyr Tyr Gln Asp Ser Lys Ala Ile Ala Ile Val Lys Asp
 180 185 190
 Gly Met Ala Phe Met Tyr Glu His Ala Tyr Asn Leu Asp Arg Glu Asn
 195 200 205
 His Gln Thr Thr Gly Lys Glu Asn Lys Glu Asn Trp Trp Val Tyr Glu
 210 215 220
 Ile Gly Thr Pro Arg Ala Ile Asn Asn Thr Leu Ser Leu Met Tyr Pro
 225 230 235 240
 Tyr Phe Thr Gln Glu Glu Ile Leu Lys Tyr Thr Ala Pro Ile Glu Lys
 245 250 255
 Phe Val Pro Asp Pro Thr Arg Phe Arg Val Arg Ala Ala Asn Phe Ser
 260 265 270
 Pro Phe Glu Ala Asn Ser Gly Asn Leu Ile Asp Met Gly Arg Val Lys
 275 280 285
 Leu Ile Ser Gly Ile Leu Arg Lys Asp Asp Leu Glu Ile Ser Asp Thr
 290 295 300
 Ile Lys Ala Ile Glu Lys Val Phe Thr Leu Val Asp Glu Gly Asn Gly
 305 310 315 320
 Phe Tyr Gln Asp Gly Ser Leu Ile Asp His Val Val Thr Asn Ala Gln
 325 330 335
 Ser Pro Leu Tyr Lys Lys Gly Ile Ala Tyr Thr Gly Ala Tyr Gly Asn
 340 345 350
 Val Leu Ile Asp Gly Leu Ser Gln Leu Ile Pro Ile Ile Gln Lys Thr
 355 360 365
 Lys Ser Ser Ile Glu Ala Asp Lys Met Ala Thr Ile Tyr His Trp Ile
 370 375 380
 Asn His Ser Phe Phe Pro Ile Ile Val Arg Gly Glu Met Met Asp Met
 385 390 395 400
 Thr Arg Gly Arg Ser Ile Ser Arg Phe Asn Ala Gln Ser His Val Ala
 405 410 415
 Gly Ile Glu Ala Leu Arg Ala Ile Leu Arg Ile Ala Asp Met Ser Glu
 420 425 430
 Glu Pro His Arg Leu Ala Leu Lys Thr Arg Ile Lys Thr Leu Val Thr
 435 440 445
 Gln Gly Asn Ala Phe Tyr Asn Val Tyr Asp Asn Leu Lys Thr Tyr His
 450 455 460
 Asp Ile Lys Leu Met Lys Glu Leu Leu Ser Asp Thr Ser Val Pro Val
 465 470 475 480
 Gln Lys Leu Asp Ser Tyr Val Ala Ser Phe Asn Ser Met Asp Lys Leu
 485 490 495

3108SEQPC1

Ala Leu Tyr Asn Asn Lys His Asp Phe Ala Phe Gly Leu Ser Met Phe
500 505 510
Ser Asn Arg Thr Gln Asn Tyr Glu Ala Met Asn Asn Glu Asn Leu His
515 520 525
Gly Trp Phe Thr Ser Asp Gly Met Phe Tyr Leu Tyr Asn Asn Asp Leu
530 535 540
Gly His Tyr Ser Glu Asn Tyr Trp Ala Thr Val Asn Pro Tyr Arg Leu
545 550 555 560
Pro Gly Thr Thr Glu Thr Glu Gln Lys Pro Leu Glu Gly Thr Pro Glu
565 570 575
Asn Ile Lys Thr Asn Tyr Gln Gln Val Gly Met Thr Ser Leu Ser Asp
580 585 590
Asp Ala Phe Val Ala Ser Lys Lys Leu Asn Asn Thr Ser Ala Leu Ala
595 600 605
Ala Met Thr Phe Thr Asn Trp Asn Lys Ser Leu Thr Leu Asn Lys Gly
610 615 620
Trp Phe Ile Leu Gly Asn Lys Ile Ile Phe Val Gly Ser Asn Ile Lys
625 630 635 640
Asn Gln Ser Ser His Lys Ala Tyr Thr Thr Ile Glu Gln Arg Lys Glu
645 650 655
Asn Gln Lys His Pro Tyr His Ala Tyr Val Asn Asn Gln Pro Val Asp
660 665 670
Leu Asn Asn Gln Leu Val Asp Phe Thr Asn Thr Lys Ser Ile Phe Leu
675 680 685
Glu Ser Asp Asp Ser Ala Gln Asn Ile Gly Tyr Tyr Phe Phe Lys Pro
690 695 700
Thr Thr Leu Ser Ile Ser Lys Ala Leu Gln Thr Gly Lys Trp Gln Asn
705 710 715 720
Ile Lys Ala Asp Asp Lys Ser Pro Glu Ala Ile Lys Glu Val Ser Asn
725 730 735
Thr Phe Ile Thr Ile Met Gln Asn His Thr Gln Asp Gly Asp Arg Tyr
740 745 750
Ala Tyr Met Met Leu Pro Asn Met Thr Arg Gln Glu Phe Glu Thr Tyr
755 760 765
Ile Ser Lys Leu Asp Ile Asp Leu Leu Glu Asn Asn Asp Lys Leu Ala
770 775 780
Ala Val Tyr Asp His Asp Ser Gln Gln Met His Val Ile His Tyr Glu
785 790 795 800
Lys Lys Ala Thr Met Phe Ser Asn His Asn Leu Ser His Gln Gly Phe
805 810 815
Tyr Ser Phe Pro His Pro Val Lys Gln Asn Gln Gln
820 825

<210> 93

<211> 522

<212> PRT

<213> Streptococcus suis

<220>

<223> hyaluronan lyase

<400> 93

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

3108SEQPC1

```

      115      120      125
Asn Trp Ala Asp Pro Ala Ala Thr Asn Trp Glu Thr Trp Ile Pro Ala
      130      135      140
Asn Val Lys Lys Glu Asn Gly Gln Val Arg Ile Asp Glu Gly Arg Leu
145      150      155      160
His Ile Ser Ser Thr Ala Ser Tyr Arg Val Ala Val His Gln Thr Val
      165      170      175
Asp Val Asp Pro Asn Lys Arg Tyr Leu Phe Ser Tyr Asn Val Glu Thr
      180      185      190
Lys Asp Leu Lys Gly Ser Gly Val Arg Val Arg Leu Arg Ser Leu Thr
      195      200      205
Ala Glu Gly Lys Asp Leu Ser Pro Gln Glu Phe Ala Tyr Thr Pro Tyr
      210      215      220
Lys Asn Gly Ser Gln Ala Glu His Ile Glu Gln Ile Leu Thr Val Ser
225      230      235      240
Pro Glu Thr Arg Lys Leu Lys Val Glu Leu Phe Phe Glu Asn Ser Val
      245      250      255
Gly Gln Ala Trp Leu Asp Asn Ile Ser Leu Val Glu Tyr Val Glu Lys
      260      265      270
Thr Pro Glu Thr Pro Glu Pro Ser Leu Glu Leu Val Gln Pro Glu Thr
      275      280      285
Gly Gln Ile Ser Leu Ala Ser Asn Lys Val Tyr Leu Pro Val Arg Pro
      290      295      300
Asp Leu Thr Tyr Arg Ile Ala Asp Ala Ala Val Ala Ile Val Glu Lys
305      310      315      320
Asn Met Ile Arg Pro Leu Ala Ala Gly Lys Thr Gln Val Asp Val Tyr
      325      330      335
Asp Lys Asp Thr Lys Leu Ser Ser Phe Glu Leu Thr Val Thr Glu His
      340      345      350
Gln Ala Thr Val Phe Asp Thr Leu Arg Asn Asn Trp Glu Asp Ile Ser
      355      360      365
Leu Ala Asn Lys Arg Tyr Gln Ser Asn Asp Thr Gln Met Lys Ala Phe
      370      375      380
Leu Gly Arg Leu Asp Ala Gly Val Ala Ser Ser Leu Lys Lys Trp Val
385      390      395      400
Glu Pro Thr Asn Gln Gly Lys Thr Ile Phe Asn Asp Ile Asp Phe Ser
      405      410      415
Lys Ser Ser His Leu Thr Thr Val Tyr Arg Arg Leu Glu Gln Met Ala
      420      425      430
Gln Val Val Glu Asn Pro Asp Ser Ala Tyr Tyr His Asp Arg Ser Leu
      435      440      445
Ile Asp Leu Val Arg Lys Gly Met Asn Trp Leu Tyr Thr Asn Val Tyr
      450      455      460
Asn Glu Asn Lys Ser Ile Asp Gly Asn Trp Trp Asp Tyr Glu Ile Gly
465      470      475      480
Thr Pro Arg Ala Val Val Asn Thr Leu Ile Tyr Met His Pro Tyr Phe
      485      490      495
Ser Gln Glu Glu Ile Leu Thr Tyr Thr Lys Pro Ile Ser Lys Phe Val
      500      505      510
Pro Asp Pro Thr Thr Ile Ser Val Lys His
      515      520

```

<210> 94

<211> 1164

<212> PRT

<213> Streptococcus suis

<220>

<223> hyaluronan lyase

<400> 94

```

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

```

3108SEQPC1

Gln	Ser	Ser	Gln	Leu	Val	Glu	Thr	Thr	Pro	Glu	Thr	Thr	Glu	Ala	Val
50						55				60					
Met	Thr	Ser	Glu	Val	Ser	Ser	Glu	Val	Ser	Pro	Val	Thr	Ser	Thr	Glu
65					70				75						80
Thr	Gln	Pro	Ser	Ser	Thr	Thr	Ala	Glu	Thr	Leu	Ala	Ser	Pro	Gln	Ala
				85					90					95	
Val	Gln	Ala	Thr	Lys	Glu	Glu	Lys	Asn	Leu	Val	Ala	Asn	Gly	Glu	Phe
			100					105					110		
Ile	Ser	Thr	Thr	Ala	Pro	Ser	Gly	Asn	Trp	Lys	Glu	Leu	Ala	Ala	Thr
		115					120					125			
Asn	Trp	Glu	Thr	Trp	Ile	Pro	Ala	Asn	Val	Lys	Lys	Glu	Asn	Gly	Gln
	130					135					140				
Val	Arg	Ile	Asp	Glu	Gly	Arg	Leu	His	Ile	Ser	Ser	Thr	Ala	Ser	Tyr
145					150					155					160
Arg	Val	Ala	Val	His	Gln	Thr	Val	Asp	Val	Asp	Pro	Asn	Lys	Arg	Tyr
				165					170					175	
Leu	Phe	Ser	Tyr	Asp	Val	Glu	Thr	Lys	Asp	Leu	Lys	Gly	Ser	Gly	Val
			180					185					190		
Arg	Val	Arg	Leu	Arg	Ser	Leu	Thr	Ala	Glu	Gly	Lys	Asp	Leu	Ser	Pro
		195					200						205		
Gln	Glu	Phe	Ala	Tyr	Thr	Pro	Tyr	Lys	Asn	Gly	Ser	Gln	Ala	Glu	His
	210					215					220				
Ile	Glu	Gln	Ile	Leu	Thr	Val	Ser	Pro	Glu	Thr	Arg	Lys	Leu	Lys	Val
225					230						235				240
Glu	Leu	Phe	Phe	Glu	Asn	Ser	Val	Gly	Gln	Ala	Trp	Leu	Asp	Asn	Ile
				245					250					255	
Ser	Leu	Val	Glu	Tyr	Val	Glu	Lys	Thr	Pro	Glu	Thr	Pro	Glu	Gln	Ser
			260					265					270		
Pro	Glu	Leu	Val	Gln	Pro	Glu	Thr	Gly	Gln	Ile	Ser	Leu	Ala	Ser	Asn
		275					280					285			
Lys	Val	Tyr	Leu	Pro	Val	Arg	Pro	Asp	Leu	Thr	Tyr	Arg	Ile	Ala	Asp
	290					295					300				
Ala	Ala	Val	Ala	Thr	Val	Glu	Lys	Asn	Met	Ile	Arg	Pro	Leu	Ala	Ala
305					310					315					320
Gly	Lys	Thr	Gln	Val	Asp	Val	Tyr	Asp	Lys	Asp	Thr	Lys	Leu	Ser	Ser
				325					330					335	
Phe	Glu	Leu	Ile	Val	Thr	Glu	His	Gln	Ala	Thr	Val	Phe	Asp	Thr	Leu
			340					345					350		
Arg	Asn	Asn	Trp	Glu	Asp	Ile	Ser	Leu	Ala	Asn	Lys	Arg	Tyr	Gln	Ser
		355					360						365		
Asn	Asp	Ala	Gln	Met	Lys	Ala	Phe	Leu	Gly	Arg	Leu	Asp	Ala	Gly	Val
	370					375					380				
Ala	Ser	Ser	Leu	Glu	Lys	Trp	Val	Glu	Pro	Thr	Glu	Gln	Ser	Lys	Thr
385					390					395					400
Ile	Phe	Asn	Asp	Ile	Asp	Phe	Ser	Lys	Ser	Ser	His	Leu	Thr	Thr	Val
			405						410					415	
Tyr	Arg	Arg	Leu	Glu	Gln	Met	Ala	Gln	Val	Val	Glu	Asn	Pro	Asp	Ser
			420					425					430		
Ala	Tyr	Tyr	His	Asp	Arg	Ser	Leu	Ile	Asp	Leu	Val	Arg	Lys	Gly	Met
		435					440					445			
Asn	Trp	Leu	Tyr	Ala	Asn	Val	Tyr	Asn	Glu	Asn	Lys	Ser	Ile	Asp	Gly
	450					455					460				
Asn	Trp	Trp	Asp	Tyr	Glu	Ile	Gly	Thr	Ser	Arg	Ala	Val	Val	Asn	Thr
465					470					475					480
Leu	Ile	Tyr	Met	His	Pro	Tyr	Phe	Ser	Gln	Glu	Glu	Ile	Leu	Thr	Tyr
				485					490					495	
Thr	Lys	Pro	Ile	Ser	Lys	Phe	Val	Pro	Asp	Pro	Thr	Thr	Ile	Arg	Lys
			500					505					510		
Thr	Leu	Thr	Asn	Pro	Val	Pro	Ala	Val	Gly	Gly	Asn	Gln	Thr	Asp	Leu
		515					520					525			
Ser	Lys	Val	Ala	Ile	Leu	Glu	Gly	Ala	Leu	Arg	Glu	Asp	Ala	Asp	Arg
		530				535					540				
Val	Arg	Ala	Gly	Ala	Gln	Gly	Leu	Thr	Thr	Ile	Met	Lys	Phe	Val	Asp
545					550					555					560
Lys	Gly	Glu	Gly	Phe	Tyr	Arg	Asp	Gly	Ser	Phe	Ile	Asp	His	Thr	Asn
				565					570					575	
Val	Ala	Tyr	Thr	Gly	Ala	Tyr	Gly	Asn	Val	Leu	Ile	Glu	Gly	Phe	Ser
			580					585					590		

3108SEQPC1

Gln Leu Leu Pro Val Ile Gln Pro Thr Glu Phe Ala Leu Lys Glu Glu
 595 600 605
 Gln Thr Asn Ile Leu Tyr Glu Trp Ile Glu Lys Ala Phe Met Pro Ile
 610 615 620
 Leu Val Arg Gly Glu Leu Met Asp Met Thr Arg Gly Arg Ser Ile Ser
 625 630 635 640
 Arg Ala Thr Gly Glu Ser His Val Gln Ala Met Glu Ile Leu Arg Ser
 645 650 655
 Leu Val Arg Ile Ala Glu Ser Ala Gln Pro Glu Gln Lys Thr Lys Leu
 660 665 670
 Leu Ser Phe Val Lys Ala Gln Leu Thr Ser Asp Thr Phe Tyr Asp Ser
 675 680 685
 Tyr Arg Ser Leu Lys Ser Tyr Lys Asp Ile Asp Leu Val Asn Lys Leu
 690 695 700
 Leu Ala Asp Asn Gln Ile Pro Ala Glu Val Asp Lys Asp Tyr Ile Ala
 705 710 715 720
 Ala Phe Asn Asn Met Asp Lys Phe Val Tyr Arg Ser Ala Gln Glu Gly
 725 730 735
 Phe Thr Phe Ala Leu Ser Met Tyr Ser Ser Arg Thr Gln Asn Tyr Glu
 740 745 750
 Asp Met Asn Asn Glu Asn Arg Lys Gly Trp Tyr Thr Ala Asp Gly Met
 755 760 765
 Val Tyr Leu Tyr Asn Asp Asp Leu Ser His Tyr Ser Asn His Tyr Trp
 770 775 780
 Ala Thr Val Asp Pro Tyr Arg Leu Pro Gly Thr Thr Thr Lys Asp
 785 790 795 800
 Lys Arg Glu Asp Gly Ser Gly Glu Val Thr Leu Ala Ser Asp Phe Val
 805 810 815
 Gly Ala Ser Gln Leu Gly Asn Arg Leu Ala Thr Ile Ala Met Asp Phe
 820 825 830
 Asn Asn Trp Asn Asn Ser Leu Thr Ala Arg Lys Ala Trp Ile Val Leu
 835 840 845
 Gly Asn Lys Ile Val Phe Leu Gly Thr Asp Ile Gln His Gln Ser Ala
 850 855 860
 Gln Gly Ala Glu Thr Thr Ile Glu Asn Arg Lys Leu Leu Thr Gly Glu
 865 870 875 880
 Lys Tyr Ser Tyr Tyr Ile Asn Gly Gln Pro Val Asp Leu Ser Lys Glu
 885 890 895
 Val Val Thr Asp Lys Thr Gln Ser Phe Tyr Met Thr Asn Gly Lys Asp
 900 905 910
 Asn Gln Ser Ile Gly Tyr Val Phe Leu Asn Gln Leu Pro Thr His Ala
 915 920 925
 Lys Leu Asp Gln Arg Thr Gly Lys Trp Ser Asp Ile Asn Tyr Asn Gln
 930 935 940
 Ser Lys Glu Glu Val Ser Asn Ser Phe Val Ser Leu Trp His Glu His
 945 950 955 960
 Ala Gln Thr Ser Ser Asn Tyr Ala Tyr Val Leu Val Pro Asn Gln Ser
 965 970 975
 Met Glu Lys Val Asn Gln Ala Ala Ala Ser Val Lys Leu Leu His Gln
 980 985 990
 Asp Arg Asp Leu Gln Val Val Tyr Asp Gln Glu Gln Asn Val Trp Gly
 995 1000 1005
 Val Val Lys Tyr Thr Asp Thr Ala Tyr Lys Leu Thr Asp Asp Ile Thr
 1010 1015 1020
 Leu Thr Asp Ala Gly Leu Tyr Thr Ile Gln Lys Val Glu Gly Gly Tyr
 1025 1030 1035 1040
 Arg Ile Ala Phe Tyr Asn Pro Ser Thr Arg Thr Val Lys Asn Gly Ile
 1045 1050 1055
 Glu Leu Thr Lys Ala Gly Ser Ser Leu Thr Val Glu Met Glu Pro Thr
 1060 1065 1070
 Ala Ala Tyr Pro Ser Thr Val Trp Lys Val Thr Met Pro Glu Gly Ser
 1075 1080 1085
 Asp Lys Gln Thr Gly Ser Val Glu Lys Thr Glu Lys Glu Glu Lys Gln
 1090 1095 1100
 Leu Lys Glu Asn Gln Pro Ser Ser Glu Val Lys Gln Val Val His His
 1105 1110 1115 1120
 Ala Ala Glu Lys Thr Lys Pro Ser Lys Pro Arg Leu Pro Gln Thr Gly
 1125 1130 1135

3108SEQPC1

Glu Glu Ala Ser Leu Gly Leu Gly Phe Leu Gly Leu Leu Thr Leu Gly
 1140 1145 1150
 Ala Val Val Asp Phe Lys Cys Arg Arg Ser His Ser
 1155 1160

<210> 95

<211> 1164

<212> PRT

<213> Streptococcus suis

<220>

<223> hyaluronan lyase

<400> 95

Met Gly Phe Phe Ile Ser Gln Ser Lys Gln His Tyr Gly Ile Arg Lys
 1 5 10 15
 Tyr Lys Val Gly Val Cys Ser Ala Leu Ile Ala Leu Ser Ile Leu Gly
 20 25 30
 Thr Arg Val Ala Ala Asn Gln Leu Pro Ser Thr Glu Thr Ala Ser Pro
 35 40 45
 Gln Ser Ser Gln Leu Val Glu Thr Thr Pro Glu Thr Thr Glu Ala Val
 50 55 60
 Met Thr Ser Glu Val Ser Glu Val Ser Pro Val Thr Ser Thr Glu
 65 70 75 80
 Thr Gln Pro Ser Ser Thr Thr Ala Glu Thr Leu Ala Ser Pro Gln Ala
 85 90 95
 Val Gln Ala Thr Lys Glu Glu Lys Asn Leu Val Ala Asn Gly Glu Phe
 100 105 110
 Ile Ser Thr Thr Ala Pro Ser Gly Asn Trp Lys Glu Leu Ala Ala Thr
 115 120 125
 Asn Trp Glu Thr Trp Ile Pro Ala Asn Val Lys Lys Glu Asn Gly Gln
 130 135 140
 Val Arg Ile Asp Glu Gly Arg Leu His Ile Ser Ser Thr Ala Ser Tyr
 145 150 155 160
 Arg Val Ala Val His Gln Thr Val Asp Val Asp Pro Asn Lys Arg Tyr
 165 170 175
 Leu Phe Ser Tyr Asp Val Glu Thr Lys Asp Leu Lys Gly Ser Gly Val
 180 185 190
 Arg Val Arg Leu Arg Ser Leu Thr Ala Glu Gly Lys Asp Leu Ser Pro
 195 200 205
 Gln Glu Phe Ala Tyr Thr Pro Tyr Lys Asn Gly Ser Gln Ala Glu His
 210 215 220
 Ile Glu Gln Ile Leu Thr Val Ser Pro Glu Thr Arg Lys Leu Lys Val
 225 230 235 240
 Glu Leu Phe Phe Glu Asn Ser Val Gly Gln Ala Trp Leu Asp Asn Ile
 245 250 255
 Ser Leu Val Glu Tyr Val Glu Lys Thr Pro Glu Thr Pro Glu Gln Ser
 260 265 270
 Pro Glu Leu Val Gln Pro Glu Thr Gly Gln Ile Ser Leu Ala Ser Asn
 275 280 285
 Lys Val Tyr Leu Pro Val Arg Pro Asp Leu Thr Tyr Arg Ile Ala Asp
 290 295 300
 Ala Ala Val Ala Thr Val Glu Lys Asn Met Ile Arg Pro Leu Ala Ala
 305 310 315 320
 Gly Lys Thr Gln Val Asp Val Tyr Asp Lys Asp Thr Lys Leu Ser Ser
 325 330 335
 Phe Glu Leu Ile Val Thr Glu His Gln Ala Thr Val Phe Asp Thr Leu
 340 345 350
 Arg Asn Asn Trp Glu Asp Ile Ser Leu Ala Asn Lys Arg Tyr Gln Ser
 355 360 365
 Asn Asp Ala Gln Met Lys Ala Phe Leu Gly Arg Leu Asp Ala Gly Val
 370 375 380
 Ala Ser Ser Leu Glu Lys Trp Val Glu Pro Thr Glu Gln Ser Lys Thr
 385 390 395 400
 Ile Phe Asn Asp Ile Asp Phe Ser Lys Ser Ser His Leu Thr Thr Val
 405 410 415
 Tyr Arg Arg Leu Glu Gln Met Ala Gln Val Val Glu Asn Pro Asp Ser

3108SEQPC1

Ala	Tyr	Tyr	420	His	Asp	Arg	Ser	Leu	425	Ile	Asp	Leu	Val	Arg	430	Lys	Gly	Met
Asn	Trp	435	Leu	Tyr	Thr	Asn	Val	440	Tyr	Asn	Glu	Asn	Lys	445	Ser	Ile	Asp	Gly
Asn	Trp	450	Trp	Asp	Tyr	Glu	Ile	455	Gly	Thr	Pro	Arg	Ala	460	Val	Val	Asn	Thr
465	Ile	Tyr	Met	470	His	Pro	Tyr	475	Phe	Ser	Gln	Glu	Glu	480	Ile	Leu	Thr	Tyr
Thr	Lys	Pro	485	Ile	Ser	Lys	Phe	490	Val	Pro	Asp	Pro	Thr	495	Thr	Ile	Arg	Lys
Thr	Leu	Thr	500	Asn	Pro	Val	Pro	505	Ala	Val	Gly	Gly	Asn	510	Gln	Thr	Asp	Leu
Ser	Lys	Val	515	Ala	Ile	Leu	Glu	520	Gly	Ala	Leu	Arg	Glu	525	Asp	Ala	Asp	Arg
Val	Arg	Ala	530	Gly	Ala	Gln	Gly	535	Leu	Thr	Thr	Ile	Met	540	Lys	Phe	Val	Asp
545	Gly	Glu	Gly	550	Phe	Tyr	Arg	555	Asp	Gly	Ser	Phe	Ile	560	Asp	His	Thr	Asn
Lys	Gly	Glu	Gly	565	Phe	Tyr	Arg	570	Asp	Gly	Ser	Phe	Ile	575	Asp	His	Thr	Asn
Val	Ala	Tyr	Thr	580	Gly	Ala	Tyr	585	Gly	Asn	Val	Leu	Ile	590	Glu	Gly	Phe	Ser
Gln	Leu	Leu	Pro	595	Val	Ile	Gln	600	Thr	Glu	Phe	Ala	Leu	605	Lys	Glu	Glu	Glu
Gln	Thr	Asn	Ile	610	Leu	Tyr	Glu	615	Trp	Ile	Glu	Lys	Ala	620	Phe	Met	Pro	Ile
Leu	Val	Arg	Gly	625	Glu	Leu	Met	630	Asp	Met	Thr	Arg	Gly	635	Arg	Ser	Ile	Ser
Arg	Ala	Thr	Gly	645	Glu	Ser	His	650	Val	Gln	Ala	Met	Glu	655	Ile	Leu	Arg	Ser
Leu	Val	Arg	Ile	660	Ala	Glu	Ser	665	Ala	Gln	Pro	Glu	Gln	670	Lys	Thr	Lys	Leu
Leu	Ser	Phe	Val	675	Lys	Ala	Gln	680	Leu	Thr	Ser	Asp	Thr	685	Phe	Tyr	Asp	Ser
Tyr	Arg	Ser	Leu	690	Lys	Ser	Tyr	695	Lys	Asp	Ile	Asp	Leu	700	Val	Asn	Lys	Leu
Leu	Ala	Asp	Asn	705	Gln	Ile	Pro	710	Ala	Glu	Val	Asp	Lys	715	Asp	Tyr	Ile	Ala
Ala	Phe	Asn	Asn	725	Met	Asp	Lys	730	Phe	Val	Tyr	Arg	Ser	735	Ala	Gln	Glu	Gly
Phe	Thr	Phe	Ala	740	Leu	Ser	Met	745	Tyr	Ser	Ser	Arg	Thr	750	Gln	Asn	Tyr	Glu
Asp	Met	Asn	Asn	755	Glu	Asn	Arg	760	Lys	Gly	Trp	Tyr	Thr	765	Ala	Asp	Gly	Met
Val	Tyr	Leu	Tyr	770	Asn	Asp	Asp	775	Leu	Ser	His	Tyr	Ser	780	Asn	His	Tyr	Trp
Ala	Thr	Val	Asp	785	Pro	Tyr	Arg	790	Leu	Pro	Gly	Thr	Thr	795	Thr	Thr	Lys	Asp
Lys	Arg	Glu	Asp	805	Gly	Ser	Gly	810	Glu	Val	Thr	Leu	Ala	815	Ser	Asp	Phe	Val
Gly	Ala	Ser	Gln	820	Leu	Gly	Asn	825	Arg	Leu	Ala	Thr	Ile	830	Ala	Met	Asp	Phe
Asn	Asn	Trp	Asn	835	Asn	Ser	Leu	840	Thr	Ala	Arg	Lys	Ala	845	Trp	Ile	Val	Leu
Gly	Asn	Lys	Ile	850	Val	Phe	Leu	855	Gly	Thr	Asp	Ile	Gln	860	His	Gln	Ser	Ala
Gln	Gly	Ala	Glu	865	Thr	Thr	Ile	870	Glu	Asn	Arg	Lys	Leu	875	Leu	Leu	Thr	Gly
Lys	Tyr	Ser	Tyr	885	Tyr	Ile	Asn	890	Gly	Gln	Pro	Val	Asp	895	Leu	Ser	Lys	Glu
Val	Val	Thr	Asp	900	Lys	Thr	Gln	905	Ser	Phe	Tyr	Met	Thr	910	Asn	Gly	Lys	Asp
Asn	Gln	Ser	Ile	915	Gly	Tyr	Val	920	Phe	Leu	Asn	Gln	Leu	925	Pro	Thr	His	Ala
Lys	Leu	Asp	Gln	930	Arg	Thr	Gly	935	Lys	Trp	Ser	Asp	Ile	940	Asn	Tyr	Asn	Gln
Ser	Lys	Glu	Glu	945	Val	Ser	Asn	950	Ser	Phe	Val	Ser	Leu	955	Trp	His	Glu	His
Ala	Gln	Thr	Ser	955	Ser	Asn	Tyr	960	Ala	Tyr	Val	Leu	Val	965	Pro	Asn	Gln	Ser

3108SEQPC1

965 970 975
 Met Glu Lys Val Asn Gln Ala Ala Ala Ser Val Lys Leu Leu His Gln
 980 985 990
 Asp Arg Asp Leu Gln Val Val Tyr Asp Gln Glu Gln Asn Val Trp Gly
 995 1000 1005
 Val Val Lys Tyr Thr Asp Thr Ala Tyr Lys Leu Thr Asp Asp Ile Thr
 1010 1015 1020
 Leu Thr Asp Ala Gly Leu Tyr Thr Ile Gln Lys Val Glu Gly Gly Tyr
 1025 1030 1035 1040
 Arg Ile Ala Phe Tyr Asn Pro Ser Thr Arg Thr Val Lys Asn Gly Ile
 1045 1050 1055
 Glu Leu Thr Lys Ala Gly Ser Ser Leu Thr Val Glu Met Glu Pro Thr
 1060 1065 1070
 Ala Ala Tyr Pro Ser Thr Val Trp Lys Val Thr Met Pro Glu Gly Ser
 1075 1080 1085
 Asp Lys Gln Thr Gly Ser Val Glu Lys Thr Glu Lys Glu Lys Gln
 1090 1095 1100
 Leu Lys Glu Asn Gln Pro Ser Ser Glu Val Lys Gln Val Val His His
 1105 1110 1115 1120
 Ala Ala Glu Lys Thr Lys Pro Ser Lys Pro Arg Leu Pro Gln Thr Gly
 1125 1130 1135
 Glu Glu Ala Ser Leu Gly Leu Gly Phe Leu Gly Leu Leu Thr Leu Gly
 1140 1145 1150
 Ala Val Val Asp Phe Lys Cys Arg Arg Ser His Ser
 1155 1160

<210> 96

<211> 802

<212> PRT

<213> *Vibrio fischeri* (strain ATCC 700601 / ES114)

<220>

<223> hyaluronan lyase

<400> 96

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

3108SEQPC1

Pro Ala Val Ile Glu Tyr Val Ser Glu Gly Asp Gly Tyr Tyr Thr Asp
 Gly Ser Phe 260 Leu Gln His Ser Asp 265 Ile Ala Tyr Asn Gly Thr Tyr Gly
 Asn Val 275 Leu Leu Gly Gly Leu Gly Ile Gln Met Asn Ala Val Ala Gly
 Ser Pro Trp Ser Met Asp Asn Gln Thr Ile Ser Asn Val Tyr Asn Ile
 305 310 Ile Asn Gln Ser Tyr Glu Pro Leu Leu Tyr Lys Gly Ala Met Met Asp
 325 Met Val Asn Gly Arg Ser Ile Ser Arg Ser Ala Glu Gln Asn His Asp
 340 Val Gly Leu Asn Ile Val Asn Ser Met Leu Phe Tyr Thr Asn Gly Pro
 355 Asp Ser Asp Lys Asn Lys Gln Leu Ser Ser Leu Ile Lys Thr Gln Ile
 370 Thr Asp Asp Thr Tyr Gln Asn Phe Phe Asp Lys Ile Tyr Tyr Val Ser
 385 390 Thr Tyr Gln Ala Ala Gln His Ile Val Asn Asp Pro Thr Val Ser Leu
 405 Lys Asp Pro Leu Ile Gly Asn Phe Ser Tyr Pro Ser Met Asp Arg Ile
 420 Val His Arg Arg Thr Asp Trp Ala Phe Ala Leu Ala Met His Ser Tyr
 435 Arg Ile Gly Asn Tyr Glu Cys Met Asn Gly Glu Asn Leu Lys Gly Trp
 450 455 Phe Thr Gly Asp Gly Met Ile Tyr Leu Tyr Asn Asp Gln Leu Asp His
 465 470 Tyr Thr Gly Tyr Trp Pro Thr Val Asn Ala Ser Arg Met Pro Gly Thr
 485 490 Thr Val Asp Ser Gln Ile Met Ala Asp Cys Ser Gly Glu Arg Val Gly
 500 Gly Asn Val Asn Thr Asn Met Gln Trp Val Gly Ser Thr Ser Leu Asn
 515 Asn Tyr Gly Ile Ala Gly Met Gln Phe Tyr Asn Trp Ser Asp Thr Leu
 530 535 Ser Ala Tyr Lys Ser Trp Phe Met Phe Asp Asn Glu Val Val Met Leu
 545 550 Gly Ser Asn Ile Lys Asp Gln Ser Asn Ala Asn Asn Ile Thr Thr Ile
 565 570 Glu Asn Arg Lys Arg Leu Ala Glu Thr Lys Leu Phe Ile Asp Gly Thr
 580 585 Glu Gln Ala Ala Leu Pro Tyr Gln Gly Ala Pro Ala Thr Phe Ser Ile
 595 600 Arg Asn Lys Thr Leu Ala Asn Ser Asp Leu Ser Tyr Val Met Leu Thr
 610 615 Pro Lys Thr Ile Ser Ile Ser Gln Asn Asp Val Asp Gly Asn Trp Ser
 625 630 Asp Ile Gly Asn Ser Lys Gly Asp Val Ser Asp Ser Tyr Leu Gln Ala
 645 650 Thr Leu Thr Gln Val Asp Gln Ala Asp Tyr Gln Tyr Ala Leu Leu Pro
 660 665 Asn Gln Asn Asn Asp Thr Val Gln Asn Tyr Ala Gln His Pro Asp Val
 675 680 Thr Val Leu Arg Gln Asp Glu Gln Ala His Ala Val Gln Glu Asn Thr
 690 695 Leu Asn Ile Ile Ala Ala Asn Asn Trp Lys Asn Asn Pro Val Asn Ile
 705 710 Thr Asp Thr Ile Thr Leu Asn Ser Met Met Gly Phe Met Ile Lys Glu
 725 730 Glu Ser Ser Asn Thr Phe Thr Val Ala Val Ser Glu Pro Ile Gln Thr
 740 745 Ile Asp Ser Val Asn Phe Thr Phe Asp Lys Gln Gly Ile Val Ile Lys
 755 760 Glu Asp Ile Glu Asn Arg Val Val Leu Asn Gly Thr Thr Leu Thr Ile
 770 775 Asn Thr Ser Gly Leu Gln Gly Gln Ser Tyr Ser Phe Gln Val Thr Ile
 785 790 795 800

Gln Asp

<210> 97

<211> 517

<212> PRT

<213> Synechococcus sp. (strain RCC307)

<220>

<223> hyaluronan lyase

<400> 97

```

Met Gly Ala Pro Ala Ile Pro Lys Val Pro Arg Ser Pro Ser Lys Ser
 1      5      10      15
Glu His Thr Thr Arg Pro Asn Ser Gly Glu Ser Glu Val Val Arg Gln
 20      25      30
Ala Glu Glu Leu Phe Glu Gln Thr Leu Val Asn Val Arg Gly Gln Leu
 35      40      45
Ala Gly Ala Val Ala Ala Leu Glu Ser Ser Val His Asp Ser Glu Leu
 50      55      60
Asn Tyr Gly Glu Ile Phe Leu Arg Asp Asn Val Pro Val Met Val Tyr
 65      70      75      80
Leu Leu Leu Arg Gly Arg Phe Glu Ile Val Arg His Phe Leu Asp Leu
 85      90      95
Cys Leu Glu Leu Gln Ser Arg Ser Tyr Arg Thr Arg Gly Val Phe Pro
100      105      110
Thr Ser Phe Val Glu Glu Asp Asp Lys Ile Leu Ala Asp Tyr Gly Gln
115      120      125
Arg Ser Ile Gly Arg Ile Thr Ser Val Asp Ala Ser Leu Trp Trp Pro
130      135      140
Val Leu Cys Trp Met Tyr Val Arg Ala Ser Gly Asp Thr Ser Tyr Gly
145      150      155      160
Thr Ser Pro Lys Val Gln Arg Ala Val Gln Leu Leu Leu Asp Leu Val
165      170      175
Leu Gln Pro Ser Phe Tyr Glu Pro Pro Val Leu Phe Val Pro Asp Cys
180      185      190
Ala Phe Met Ile Asp Arg Pro Met Asp Val Trp Gly Ala Pro Leu Glu
195      200      205
Val Glu Val Leu Leu Phe Gly Cys Leu Lys Ser Cys Cys Gln Leu Met
210      215      220
Ser Leu Val Glu Gly Gly Gly His Gly Gly Pro Leu Ile Gln Gln Arg
225      230      235      240
Leu Glu Leu Thr Arg Thr Trp Met Arg Asp Leu Arg Val Tyr Leu Leu
245      250      255
Asn His Tyr Trp Val Thr Ser Lys Thr Met Gln Val Leu Arg Arg Arg
260      265      270
Pro Thr Glu Gln Tyr Gly Asp Tyr Gln Ser Arg Asn Glu Phe Asn Val
275      280      285
Gln Pro Glu Val Ile Pro His Trp Leu Gln Glu Trp Leu Asp Asp Arg
290      295      300
Gly Gly Tyr Leu Ile Gly Asn Met Arg Thr Gly Arg Pro Asp Phe Arg
305      310      315      320
Phe Tyr Ser Leu Gly Asn Ala Leu Gly Ser Leu Phe Gly Leu Leu Thr
325      330      335
Gly Pro Gln Gln Leu Ala Leu Phe Arg Leu Val Ile His Asn Arg Gln
340      345      350
His Leu Met Ala Glu Met Pro Met Arg Ile Cys His Pro Pro Met Asp
355      360      365
Gln Asp Glu Trp Ile Thr Asn Thr Gly Met Asp Pro Lys Asn Trp Pro
370      375      380
Trp Ser Tyr His Asn Gly Gly His Trp Pro Ser Leu Leu Trp Pro Met
385      390      395      400
Ala Ala Ala Val Leu Met His Gln Arg Leu Tyr Pro Asn Asp Asp Leu
405      410      415
Leu Leu Leu Gly Gln Thr Arg Thr Met Leu Glu Glu Cys Tyr Trp Gln
420      425      430
Gln Leu Asn Gln Leu Pro Arg Gln Gln Trp Ala Glu Tyr Phe Asp Gly

```

3108SEQPC1

435 440 445
 Pro Thr Gly Thr Trp Val Gly Gln Gln Ala Arg Ile Asn Gln Thr Trp
 450 455 460
 Thr Ile Val Gly Phe Leu Leu Leu His His Leu Met Arg Lys Ala Pro
 465 470 475 480
 Gln Asp Val Lys Leu Asp Leu Asp Asp Val Gly Pro Leu Arg Leu
 485 490 495
 Ser Phe Gln Asp Gln His Glu Lys Ser Ser Thr Asp Glu Arg Lys Ser
 500 505 510
 Phe Leu Lys Asn Tyr
 515

<210> 98

<211> 1021

<212> PRT

<213> *Proteus vulgaris*

<220>

<223> chondroitin-sulfate-ABC endolyase

<400> 98

Met Pro Ile Phe Arg Phe Thr Ala Leu Ala Met Thr Leu Gly Leu Leu
 1 5 10 15
 Ser Ala Pro Tyr Asn Ala Met Ala Ala Thr Ser Asn Pro Ala Phe Asp
 20 25 30
 Pro Lys Asn Leu Met Gln Ser Glu Ile Tyr His Phe Ala Gln Asn Asn
 35 40 45
 Pro Leu Ala Asp Phe Ser Ser Asp Lys Asn Ser Ile Leu Thr Leu Ser
 50 55 60
 Asp Lys Arg Ser Ile Met Gly Asn Gln Ser Leu Leu Trp Lys Trp Lys
 65 70 75 80
 Gly Gly Ser Ser Phe Thr Leu His Lys Lys Leu Ile Val Pro Thr Asp
 85 90 95
 Lys Glu Ala Ser Lys Ala Trp Gly Arg Ser Ser Thr Pro Val Phe Ser
 100 105 110
 Phe Trp Leu Tyr Asn Glu Lys Pro Ile Asp Gly Tyr Leu Thr Ile Asp
 115 120 125
 Phe Gly Glu Lys Leu Ile Ser Thr Ser Glu Ala Gln Ala Gly Phe Lys
 130 135 140
 Val Lys Leu Asp Phe Thr Gly Trp Arg Ala Val Gly Val Ser Leu Asn
 145 150 155 160
 Asn Asp Leu Glu Asn Arg Glu Met Thr Leu Asn Ala Thr Asn Thr Ser
 165 170 175
 Ser Asp Gly Thr Gln Asp Ser Ile Gly Arg Ser Leu Gly Ala Lys Val
 180 185 190
 Asp Ser Ile Arg Phe Lys Ala Pro Ser Asn Val Ser Gln Gly Glu Ile
 195 200 205
 Tyr Ile Asp Arg Ile Met Phe Ser Val Asp Asp Ala Arg Tyr Gln Trp
 210 215 220
 Ser Asp Tyr Gln Val Lys Thr Arg Leu Ser Glu Pro Glu Ile Gln Phe
 225 230 235 240
 His Asn Val Lys Pro Gln Leu Pro Val Thr Pro Glu Asn Leu Ala Ala
 245 250 255
 Ile Asp Leu Ile Arg Gln Arg Leu Ile Asn Glu Phe Val Gly Gly Glu
 260 265 270
 Lys Glu Thr Asn Leu Ala Leu Glu Glu Asn Ile Ser Lys Leu Lys Ser
 275 280 285
 Asp Phe Asp Ala Leu Asn Ile His Thr Leu Ala Asn Gly Gly Thr Gln
 290 295 300
 Gly Arg His Leu Ile Thr Asp Lys Gln Ile Ile Ile Tyr Gln Pro Glu
 305 310 315 320
 Asn Leu Asn Ser Gln Asp Lys Gln Leu Phe Asp Asn Tyr Val Ile Leu
 325 330 335
 Gly Asn Tyr Thr Thr Leu Met Phe Asn Ile Ser Arg Ala Tyr Val Leu
 340 345 350
 Glu Lys Asp Pro Thr Gln Lys Ala Gln Leu Lys Gln Met Tyr Leu Leu
 355 360 365

3108SEQPC1

Met Thr Lys His Leu Leu Asp Gln Gly Phe Val Lys Gly Ser Ala Leu
 370 375 380
 Val Thr Thr His His Trp Gly Tyr Ser Ser Arg Trp Trp Tyr Ile Ser
 385 390 395 400
 Thr Leu Leu Met Ser Asp Ala Leu Lys Glu Ala Asn Leu Gln Thr Gln
 405 410 415
 Val Tyr Asp Ser Leu Leu Trp Tyr Ser Arg Glu Phe Lys Ser Ser Phe
 420 425 430
 Asp Met Lys Val Ser Ala Asp Ser Asp Leu Asp Tyr Phe Asn Thr
 435 440 445
 Leu Ser Arg Gln His Leu Ala Leu Leu Leu Glu Pro Asp Asp Gln
 450 455 460
 Lys Arg Ile Asn Leu Val Asn Thr Phe Ser His Tyr Ile Thr Gly Ala
 465 470 475 480
 Leu Thr Gln Val Pro Gly Gly Lys Asp Gly Leu Arg Pro Asp Gly
 485 490 495
 Thr Ala Trp Arg His Glu Gly Asn Tyr Pro Gly Tyr Ser Phe Pro Ala
 500 505 510
 Phe Lys Asn Ala Ser Gln Leu Ile Tyr Leu Leu Arg Asp Thr Pro Phe
 515 520 525
 Ser Val Gly Glu Ser Gly Trp Asn Asn Leu Lys Lys Ala Met Val Ser
 530 535 540
 Ala Trp Ile Tyr Ser Asn Pro Glu Val Gly Leu Pro Leu Ala Gly Arg
 545 550 555 560
 His Pro Phe Asn Ser Pro Ser Leu Lys Ser Val Ala Gln Gly Tyr Tyr
 565 570 575
 Trp Leu Ala Met Ser Ala Lys Ser Ser Pro Asp Lys Thr Leu Ala Ser
 580 585 590
 Ile Tyr Leu Ala Ile Ser Asp Lys Thr Gln Asn Glu Ser Thr Ala Ile
 595 600 605
 Phe Gly Glu Thr Ile Thr Pro Ala Ser Leu Pro Gln Gly Phe Tyr Ala
 610 615 620
 Phe Asn Gly Gly Ala Phe Gly Ile His Arg Trp Gln Asp Lys Met Val
 625 630 635 640
 Thr Leu Lys Ala Tyr Asn Thr Asn Val Trp Ser Ser Glu Ile Tyr Asn
 645 650 655
 Lys Asp Asn Arg Tyr Gly Arg Tyr Gln Ser His Gly Val Ala Gln Ile
 660 665 670
 Val Ser Asn Gly Ser Gln Leu Ser Gln Gly Tyr Gln Gln Glu Gly Trp
 675 680 685
 Asp Trp Asn Arg Met Glu Gly Ala Thr Thr Ile His Leu Pro Leu Lys
 690 695 700
 Asp Leu Asp Ser Pro Lys Pro His Thr Leu Met Gln Arg Gly Glu Arg
 705 710 715 720
 Gly Phe Ser Gly Thr Ser Ser Leu Glu Gly Gln Tyr Gly Met Met Ala
 725 730 735
 Phe Asn Leu Ile Tyr Pro Ala Asn Leu Glu Arg Phe Asp Pro Asn Phe
 740 745 750
 Thr Ala Lys Lys Ser Val Leu Ala Ala Asp Asn His Leu Ile Phe Ile
 755 760 765
 Gly Ser Asn Ile Asn Ser Ser Asp Lys Asn Lys Asn Val Glu Thr Thr
 770 775 780
 Leu Phe Gln His Ala Ile Thr Pro Thr Leu Asn Thr Leu Trp Ile Asn
 785 790 795 800
 Gly Gln Lys Ile Glu Asn Met Pro Tyr Gln Thr Thr Leu Gln Gln Gly
 805 810 815
 Asp Trp Leu Ile Asp Ser Asn Gly Asn Gly Tyr Leu Ile Thr Gln Ala
 820 825 830
 Glu Lys Val Asn Val Ser Arg Gln His Gln Val Ser Ala Glu Asn Lys
 835 840 845
 Asn Arg Gln Pro Thr Glu Gly Asn Phe Ser Ser Ala Trp Ile Asp His
 850 855 860
 Ser Thr Arg Pro Lys Asp Ala Ser Tyr Glu Tyr Met Val Phe Leu Asp
 865 870 875 880
 Ala Thr Pro Glu Lys Met Gly Glu Met Ala Gln Lys Phe Arg Glu Asn
 885 890 895
 Asn Gly Leu Tyr Gln Val Leu Arg Lys Asp Lys Asp Val His Ile Ile
 900 905 910

3108SEQPC1

Leu Asp Lys Leu Ser Asn Val Thr Gly Tyr Ala Phe Tyr Gln Pro Ala
 915 920 925
 Ser Ile Glu Asp Lys Trp Ile Lys Lys Val Asn Lys Pro Ala Ile Val
 930 935 940
 Met Thr His Arg Gln Lys Asp Thr Leu Ile Val Ser Ala Val Thr Pro
 945 950 955 960
 Asp Leu Asn Met Thr Arg Gln Lys Ala Ala Thr Pro Val Thr Ile Asn
 965 970 975
 Val Thr Ile Asn Gly Lys Trp Gln Ser Ala Asp Lys Asn Ser Glu Val
 980 985 990
 Lys Tyr Gln Val Ser Gly Asp Asn Thr Glu Leu Thr Phe Thr Ser Tyr
 995 1000 1005
 Phe Gly Ile Pro Gln Glu Ile Lys Leu Ser Pro Leu Pro
 1010 1015 1020

<210> 99

<211> 684

<212> PRT

<213> Pedobacter heparinus

<220>

<223> chondroitin AC lyase

<400> 99

Pro Ala Leu Leu Ile Ala Gln Gln Thr Gly Thr Ala Glu Leu Ile Met
 1 5 10 15
 Lys Arg Val Met Leu Asp Leu Lys Lys Pro Leu Arg Asn Met Asp Lys
 20 25 30
 Val Ala Glu Lys Asn Leu Asn Thr Leu Gln Pro Asp Gly Ser Trp Lys
 35 40 45
 Asp Val Pro Tyr Lys Asp Asp Ala Met Thr Asn Trp Leu Pro Asn Asn
 50 55 60
 His Leu Leu Gln Leu Glu Thr Ile Ile Gln Ala Tyr Ile Glu Lys Asp
 65 70 75 80
 Ser His Tyr Tyr Gly Asp Asp Lys Val Phe Asp Gln Ile Ser Lys Ala
 85 90 95
 Phe Lys Tyr Trp Tyr Asp Ser Asp Pro Lys Ser Arg Asn Trp Trp His
 100 105 110
 Asn Glu Ile Ala Thr Pro Gln Ala Leu Gly Glu Met Leu Ile Leu Met
 115 120 125
 Arg Tyr Gly Lys Lys Pro Leu Asp Glu Ala Leu Val His Lys Leu Thr
 130 135 140
 Glu Arg Met Lys Arg Gly Glu Pro Glu Lys Lys Thr Gly Ala Asn Lys
 145 150 155 160
 Thr Asp Ile Ala Leu His Tyr Phe Tyr Arg Ala Leu Leu Thr Ser Asp
 165 170 175
 Glu Ala Leu Leu Ser Phe Ala Val Lys Glu Leu Phe Tyr Pro Val Gln
 180 185 190
 Phe Val His Tyr Glu Glu Gly Leu Gln Tyr Asp Tyr Ser Tyr Leu Gln
 195 200 205
 His Gly Pro Gln Leu Gln Ile Ser Ser Tyr Gly Ala Val Phe Ile Thr
 210 215 220
 Gly Val Leu Lys Leu Ala Asn Tyr Val Arg Asp Thr Pro Tyr Ala Leu
 225 230 235 240
 Ser Thr Glu Lys Leu Ala Ile Phe Ser Lys Tyr Tyr Arg Asp Ser Tyr
 245 250 255
 Leu Lys Ala Ile Arg Gly Ser Tyr Met Asp Phe Asn Val Glu Gly Arg
 260 265 270
 Gly Val Ser Arg Pro Asp Ile Leu Asn Lys Lys Ala Glu Lys Lys Arg
 275 280 285
 Leu Leu Val Ala Lys Met Ile Asp Leu Lys His Thr Glu Glu Trp Ala
 290 295 300
 Asp Ala Ile Ala Arg Thr Asp Ser Thr Val Ala Ala Gly Tyr Lys Ile
 305 310 315 320
 Glu Pro Tyr His His Gln Phe Trp Asn Gly Asp Tyr Val Gln His Leu
 325 330 335
 Arg Pro Ala Tyr Ser Phe Asn Val Arg Met Val Ser Lys Arg Thr Arg

3108SEQPC1

340 345 350
 Arg Ser Glu Ser Gly Asn Lys Glu Asn Leu Leu Gly Arg Tyr Leu Ser
 355 360 365
 Asp Gly Ala Thr Asn Ile Gln Leu Arg Gly Pro Glu Tyr Tyr Asn Ile
 370 375 380
 Met Pro Val Trp Glu Trp Asp Lys Ile Pro Gly Ile Thr Ser Arg Asp
 385 390 395 400
 Tyr Leu Thr Asp Arg Pro Leu Thr Lys Leu Trp Gly Glu Gln Gly Ser
 405 410 415
 Asn Asp Phe Ala Gly Gly Val Ser Asp Gly Val Tyr Gly Ala Ser Ala
 420 425 430
 Tyr Ala Leu Asp Tyr Asp Ser Leu Gln Ala Lys Lys Ala Trp Phe Phe
 435 440 445
 Phe Asp Lys Glu Ile Val Cys Leu Gly Ala Gly Ile Asn Ser Asn Ala
 450 455 460
 Pro Glu Asn Ile Thr Thr Leu Asn Gln Ser Trp Leu Asn Gly Pro
 465 470 475 480
 Val Ile Ser Thr Ala Gly Lys Thr Gly Arg Gly Lys Ile Thr Thr Phe
 485 490 495
 Lys Ala Gln Gly Gln Phe Trp Leu Leu His Asp Ala Ile Gly Tyr Tyr
 500 505 510
 Phe Pro Glu Gly Ala Asn Leu Ser Leu Ser Thr Gln Ser Gln Lys Gly
 515 520 525
 Asn Trp Phe His Ile Asn Asn Ser His Ser Lys Asp Glu Val Ser Gly
 530 535 540
 Asp Val Phe Lys Leu Trp Ile Asn His Gly Ala Arg Pro Glu Asn Ala
 545 550 555 560
 Gln Tyr Ala Tyr Ile Val Leu Pro Gly Ile Asn Lys Pro Glu Glu Ile
 565 570 575
 Lys Lys Tyr Asn Gly Thr Ala Pro Lys Val Leu Ala Asn Thr Asn Gln
 580 585 590
 Leu Gln Ala Val Tyr His Gln Gln Leu Asp Met Val Gln Ala Ile Phe
 595 600 605
 Tyr Thr Ala Gly Lys Leu Ser Val Ala Gly Ile Glu Ile Glu Thr Asp
 610 615 620
 Lys Pro Cys Ala Val Leu Ile Lys His Ile Asn Gly Lys Gln Val Ile
 625 630 635 640
 Trp Ala Ala Asp Pro Leu Gln Lys Glu Lys Thr Ala Val Leu Ser Ile
 645 650 655
 Arg Asp Leu Lys Thr Gly Lys Thr Asn Arg Val Lys Ile Asp Phe Pro
 660 665 670
 Gln Gln Glu Phe Ala Gly Ala Thr Val Glu Leu Lys
 675 680

<210> 100

<211> 844

<212> PRT

<213> Victivallis vadensis ATCC BAA-548

<220>

<223> chondroitin AC lyase

<400> 100

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

3108SEQPC1

Trp	Thr	Gln	Ala	Glu	Ile	Pro	His	Glu	Pro	Phe	Pro	Trp	Arg	Arg	Phe
		115					120					125			
Arg	Phe	Ser	Glu	Arg	Ile	Pro	Ala	Asp	Ala	Thr	Ser	Gly	Thr	Leu	Arg
	130					135					140				
Leu	Gly	Leu	Gln	Gly	Ser	Ser	Gly	Asn	Val	Glu	Phe	Asp	Leu	Asp	Ser
145					150					155					160
Leu	Gln	Ile	Arg	Pro	Leu	Asp	Pro	Glu	Leu	Ser	Pro	Val	Pro	Pro	Thr
				165					170					175	
Pro	Glu	Gln	Ile	Arg	Glu	Cys	Glu	Leu	Ile	Glu	Ser	Arg	Leu	Arg	Ala
			180					185					190		
Gly	Leu	Pro	Ala	Gln	Gln	Pro	Pro	Pro	Gly	Pro	Glu	Val	Lys	Lys	Leu
		195					200					205			
Leu	Glu	Arg	Gln	Asn	Gly	Asp	Gly	Thr	Phe	Arg	Asp	Leu	Asp	Tyr	Ser
	210					215					220				
Ala	Arg	Asn	Arg	Ser	Ile	Trp	Pro	Ala	Ala	Arg	His	Leu	Lys	Arg	Thr
225					230					235					240
Phe	Glu	Leu	Ala	Leu	Ala	Arg	Ala	Thr	Pro	Gly	His	Ala	Leu	Tyr	Arg
			245						250					255	
Asp	Pro	Ala	Ala	Gly	Glu	Ala	Val	Arg	Lys	Ala	Val	Ala	Trp	Trp	Ala
			260					265					270		
Glu	Arg	Gln	Pro	Gln	Asn	Gly	Asn	Trp	Trp	Trp	Asn	Asp	Met	Tyr	Val
		275					280					285			
Pro	Lys	Ile	Leu	Gly	Asn	Ile	Leu	Leu	Leu	Ser	Pro	Glu	Leu	Phe	Pro
	290					295					300				
Asp	Gly	Pro	Arg	Arg	Arg	Ala	Ala	Leu	Asn	Val	Cys	Arg	Gln	Ala	Cys
305					310					315					320
Phe	Leu	Ser	Arg	Tyr	Thr	Gly	Asn	Asn	Arg	Val	Phe	Ile	Ala	Ala	Asn
			325						330					335	
Ile	Phe	Cys	Arg	Ala	Leu	Leu	Glu	Arg	Asn	Leu	Pro	Val	Met	Asp	Arg
			340					345					350		
Ala	Ala	Ala	Val	Leu	Ser	Glu	Glu	Ile	Arg	Phe	Ala	Pro	Ala	Glu	His
		355					360					365			
Lys	Thr	Ala	Trp	Ser	Phe	Gly	Gly	Ile	Arg	Ala	Asp	Gly	Cys	Tyr	His
	370					375					380				
Gln	His	Gly	Pro	Gln	Ile	Gln	Phe	Gly	Asn	Tyr	Gly	Gly	Glu	Phe	Leu
385					390					395					400
Ala	Asn	Ile	Ala	Tyr	Trp	Ser	Asn	Ile	Leu	Lys	Glu	Thr	His	Trp	Glu
			405						410					415	
Leu	Ser	Pro	Glu	Gln	Trp	Arg	Ile	Met	Arg	His	Leu	Thr	Phe	Asn	Gly
			420					425					430		
Phe	Gln	Trp	Val	Leu	Trp	Arg	Gly	Arg	Met	Asp	Leu	Leu	Ala	Cys	Gly
		435					440					445			
Arg	Gln	Leu	Gly	Arg	Asn	Ala	Ala	Glu	Thr	Lys	Gly	Glu	Arg	Thr	Leu
					455						460				
Asn	Ala	Phe	Ala	Gln	Leu	Arg	Asn	Ala	Asp	Pro	Gly	Asp	Arg	Ala	Pro
465					470					475					480
Tyr	Asp	Ala	Ala	Leu	Arg	Arg	Asn	Arg	Asp	Gly	Glu	Asn	Thr	Leu	Thr
			485						490					495	
Gly	Asn	Arg	His	Phe	Trp	Asn	Ser	Asp	Tyr	Met	Val	His	Arg	Arg	Pro
			500					505					510		
Thr	Trp	Tyr	Ala	Ser	Val	Arg	Met	Asn	Ser	Val	Arg	Val	Arg	Pro	Ile
		515					520					525			
Glu	Asp	Thr	Asn	Trp	Asp	Asn	Ala	Leu	Gly	Arg	Tyr	Phe	Ser	Asp	
	530				535					540					
Gly	Ala	Cys	Leu	Val	Met	Arg	Ser	Gly	Arg	Glu	Tyr	Glu	Asn	Ile	Thr
545					550					555					560
Ala	Cys	Trp	Asp	Trp	Thr	Arg	Leu	Pro	Gly	Thr	Thr	Leu	Pro	Lys	Thr
			565						570					575	
Pro	Val	Tyr	Thr	Gly	Glu	Asp	Ala	Arg	Phe	Gly	Leu	Lys	Ile	Gly	
			580					585					590		
Gly	Gly	Asp	Leu	Pro	Arg	Trp	Thr	His	Ser	Arg	Asn	Trp	Arg	Gln	Leu
		595					600					605			
Gly	Glu	Thr	Gly	Phe	Val	Gly	Gly	Val	Thr	Asp	Gly	Glu	Arg	Gly	Ala
	610					615				620					
Ala	Val	Tyr	Thr	Gln	Asp	Leu	Asp	Gly	Val	Arg	Ala	Arg	Lys	Ala	Trp
625					630					635					640
Phe	Phe	Asp	Arg	Asp	Ala	Ile	Tyr	Cys	Leu	Gly	Ser	Gly	Ile	Thr	Ser
			645						650					655	

3108SEQPC1

Thr Ser Pro Tyr Glu Val Ala Thr Thr Val Asn Ser Cys Leu Arg Asn
 660 665
 Gly Glu Ile Gln Gln Gly Asp Gly Trp Phe Arg His Asp Gly Ile Gly
 675 680 685
 Tyr Arg Gly Glu Asn Leu Lys Leu Thr Ala Gly Pro Arg Thr Gly Asp
 690 695 700
 Trp Arg Tyr Val Glu Gly Leu Thr Arg Pro Val Pro Glu Thr Lys
 705 710 715 720
 Glu Leu Phe Thr Leu Thr Val Glu His Gly Val Lys Pro Arg Asn Ala
 725 730 735
 Ser Tyr Ile Tyr Thr Ile Leu Pro Gly Ala Thr Pro Glu Glu Thr Ala
 740 745 750
 Gly Thr Pro Pro Gly Arg Val Leu Arg Asn Thr Pro Glu Cys Gln Ala
 755 760 765
 Val Glu Phe Ala Asp Gly Val Arg Ala Ala Ile Phe Tyr Glu Pro Gly
 770 775 780
 Arg Leu Asp Asp Phe Glu Thr Asp Thr Pro Gly Val Phe Leu Ile Gly
 785 790 795 800
 Lys Gly Thr Val His Ala Ala Asp Pro Thr Gly Arg His Ser Ser Phe
 805 810 815
 Thr Leu Lys Leu Asn Gly Val Ser Arg Lys Val Pro Leu Pro Ala Gly
 820 825 830
 Glu Phe Ala Gly Gln Ser Val Lys Ile Val Leu Lys
 835 840

<210> 101

<211> 510

<212> PRT

<213> Pan troglodytes

<220>

<223> Chimpanzee PH20

<400> 101

Met Gly Val Leu Lys Phe Lys His Ile Phe Phe Arg Ser Phe Val Lys
 1 5 10 15
 Ser Ser Gly Val Ser Gln Ile Val Phe Thr Phe Leu Leu Ile Pro Cys
 20 25 30
 Cys Leu Thr Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro
 35 40 45
 Phe Leu Trp Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe
 50 55 60
 Asp Glu Pro Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg
 65 70 75 80
 Ile Asn Val Thr Gly Gln Asp Val Thr Ile Phe Tyr Val Asp Arg Leu
 85 90 95
 Gly Tyr Tyr Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly
 100 105 110
 Gly Ile Pro Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys
 115 120 125
 Lys Asp Ile Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val
 130 135 140
 Ile Asp Trp Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro
 145 150 155 160
 Lys Asp Val Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn
 165 170 175
 Val Gln Leu Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe
 180 185 190
 Glu Lys Ala Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys
 195 200 205
 Leu Leu Arg Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys
 210 215 220
 Tyr Asn His His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn
 225 230 235 240
 Val Glu Ile Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser
 245 250 255
 Thr Ala Leu Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val
 Page 121

3108SEQPC1

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

<210> 102
 <211> 512
 <212> PRT
 <213> Macaca mulatta

<220>
 <223> Precursor Rhesus Monkey PH20

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

3108SEQPC1

Ser Leu Arg Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys
 210 215 220
 Tyr Asn His His Tyr Arg Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asp
 225 230 235 240
 Val Glu Ile Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser
 245 250 255
 Thr Ala Leu Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Val Val
 260 265 270
 Val Ala Thr Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val
 275 280 285
 Ser Lys Ile Pro Asp Ala Lys Asn Pro Leu Pro Val Phe Val Tyr Ala
 290 295 300
 Arg Leu Val Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Arg Glu Glu
 305 310 315 320
 Leu Val Ser Thr Leu Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile
 325 330 335
 Val Ile Trp Gly Ser Leu Ser Ile Thr Arg Ser Met Lys Ser Cys Leu
 340 345 350
 Leu Leu Asp Thr Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn
 355 360 365
 Val Thr Leu Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln
 370 375 380
 Gly Val Cys Ile Arg Lys Asp Trp Asn Ser Ser Asp Tyr Leu His Leu
 385 390 395 400
 Asn Pro Asp Asn Phe Asp Ile Arg Leu Glu Lys Gly Gly Lys Phe Thr
 405 410 415
 Val His Gly Lys Pro Thr Val Glu Asp Leu Glu Glu Phe Ser Glu Lys
 420 425 430
 Phe Tyr Cys Ser Cys Tyr Thr Asn Leu Ser Cys Lys Glu Lys Ala Asp
 435 440 445
 Val Lys Asp Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys
 450 455 460
 Ile Asp Ala Ser Leu Lys Pro Pro Val Glu Thr Glu Gly Ser Pro Pro
 465 470 475 480
 Ile Phe Tyr Asn Thr Ser Ser Ser Thr Val Ser Thr Thr Met Phe Ile
 485 490 495
 Trp Arg Leu Glu Val Trp Asp Gln Gly Ile Ser Arg Ile Gly Phe Phe
 500 505 510

<210> 103

<211> 505

<212> PRT

<213> Homo sapiens

<220>

<223> PH20 precursor 1-505

<400> 103

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

3108SEQPC1

145				150				155				160
Lys	Asp	Val	Tyr	Lys	Asn	Arg	Ser	Ile	Glu	Leu	Val	Gln
				165					170			Gln
Val	Gln	Leu	Ser	Leu	Thr	Glu	Ala	Thr	Glu	Lys	Ala	Lys
			180					185				Gln
Glu	Lys	Ala	Gly	Lys	Asp	Phe	Leu	Val	Glu	Thr	Ile	Lys
		195					200					190
Leu	Leu	Arg	Pro	Asn	His	Leu	Trp	Gly	Tyr	Tyr	Leu	Phe
	210					215					220	Pro
Tyr	Asn	His	His	Tyr	Lys	Lys	Pro	Gly	Tyr	Asn	Gly	Ser
225					230					235		Cys
Val	Glu	Ile	Lys	Arg	Asn	Asp	Asp	Leu	Ser	Trp	Leu	Trp
				245					250			Asn
Thr	Ala	Leu	Tyr	Pro	Ser	Ile	Tyr	Leu	Asn	Thr	Gln	Gln
		260						265				270
Ala	Ala	Thr	Leu	Tyr	Val	Arg	Asn	Arg	Val	Arg	Glu	Ala
		275					280					285
Ser	Lys	Ile	Pro	Asp	Ala	Lys	Ser	Pro	Leu	Pro	Val	Phe
	290					295						Ala
Arg	Ile	Val	Phe	Thr	Asp	Gln	Val	Leu	Lys	Phe	Leu	Ser
305					310					315		Gln
Leu	Val	Tyr	Thr	Phe	Gly	Glu	Thr	Val	Ala	Leu	Gly	Ala
				325					330			Ser
Val	Ile	Trp	Gly	Thr	Leu	Ser	Ile	Met	Arg	Ser	Met	Lys
		340						345				Ser
Leu	Leu	Asp	Asn	Tyr	Met	Glu	Thr	Ile	Leu	Asn	Pro	Tyr
	355						360					Ile
Val	Thr	Leu	Ala	Ala	Lys	Met	Cys	Ser	Gln	Val	Leu	Cys
	370					375					380	Gln
Gly	Val	Cys	Ile	Arg	Lys	Asn	Trp	Asn	Ser	Ser	Asp	Tyr
385					390					395		Leu
Asn	Pro	Asp	Asn	Phe	Ala	Ile	Gln	Leu	Glu	Lys	Gly	Gly
				405					410			Lys
Val	Arg	Gly	Lys	Pro	Thr	Leu	Glu	Asp	Leu	Glu	Gln	Phe
				420				425				Ser
Phe	Tyr	Cys	Ser	Cys	Tyr	Ser	Thr	Leu	Ser	Cys	Lys	Glu
	435						440					Lys
Val	Lys	Asp	Thr	Asp	Ala	Val	Asp	Val	Cys	Ile	Ala	Asp
	450					455					460	Gly
Ile	Asp	Ala	Phe	Leu	Lys	Pro	Pro	Met	Glu	Thr	Glu	Glu
465					470					475		Pro
Phe	Tyr	Asn	Ala	Ser	Pro	Ser	Thr	Leu	Ser	Ala	Thr	Met
				485					490			Phe
Ser	Ile	Leu	Phe	Leu	Ile	Ile	Ser	Ser				Ile
		500						505				Val

<210> 104

<211> 503

<212> PRT

<213> Homo sapiens

<220>

<223> PH20 precursor 1-503

<400> 104

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

3108SEQPC1

Gly Tyr Tyr Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly
 100 105
 Gly Ile Pro Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys
 115 120
 Lys Asp Ile Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val
 130 135 140
 Ile Asp Trp Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro
 145 150 155
 Lys Asp Val Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn
 165 170 175
 Val Gln Leu Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe
 180 185 190
 Glu Lys Ala Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys
 195 200 205
 Leu Leu Arg Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys
 210 215 220
 Tyr Asn His His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn
 225 230 235 240
 Val Glu Ile Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser
 245 250 255
 Thr Ala Leu Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val
 260 265 270
 Ala Ala Thr Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val
 275 280 285
 Ser Lys Ile Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr
 290 295 300
 Arg Ile Val Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu
 305 310 315 320
 Leu Val Tyr Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile
 325 330 335
 Val Ile Trp Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu
 340 345 350
 Leu Leu Asp Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn
 355 360 365
 Val Thr Leu Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln
 370 375 380
 Gly Val Cys Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu
 385 390 395 400
 Asn Pro Asp Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr
 405 410 415
 Val Arg Gly Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys
 420 425 430
 Phe Tyr Cys Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp
 435 440 445
 Val Lys Asp Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys
 450 455 460
 Ile Asp Ala Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile
 465 470 475 480
 Phe Tyr Asn Ala Ser Pro Ser Thr Leu Ser Ala Thr Met Phe Ile Val
 485 490 495
 Ser Ile Leu Phe Leu Ile Ile
 500

<210> 105

<211> 501

<212> PRT

<213> Homo sapiens

<220>

<223> PH20 precursor 1-501

<400> 105

Met Gly Val Leu Lys Phe Lys His Ile Phe Phe Arg Ser Phe Val Lys
 1 5 10 15
 Ser Ser Gly Val Ser Gln Ile Val Phe Thr Phe Leu Leu Ile Pro Cys
 20 25 30
 Cys Leu Thr Leu Asn Phe Arg Ala Pro Val Ile Pro Asn Val Pro
 Page 125

3108SEQPC1

			35				40					45			
Phe	Leu	Trp	Ala	Trp	Asn	Ala	Pro	Ser	Glu	Phe	Cys	Leu	Gly	Lys	Phe
50						55					60				
Asp	Glu	Pro	Leu	Asp	Met	Ser	Leu	Phe	Ser	Phe	Ile	Gly	Ser	Pro	Arg
65					70					75					80
Ile	Asn	Ala	Thr	Gly	Gln	Gly	Val	Thr	Ile	Phe	Tyr	Val	Asp	Arg	Leu
				85					90					95	
Gly	Tyr	Tyr	Pro	Tyr	Ile	Asp	Ser	Ile	Thr	Gly	Val	Thr	Val	Asn	Gly
			100					105					110		
Gly	Ile	Pro	Gln	Lys	Ile	Ser	Leu	Gln	Asp	His	Leu	Asp	Lys	Ala	Lys
		115					120					125			
Lys	Asp	Ile	Thr	Phe	Tyr	Met	Pro	Val	Asp	Asn	Leu	Gly	Met	Ala	Val
	130					135					140				
Ile	Asp	Trp	Glu	Glu	Trp	Arg	Pro	Thr	Trp	Ala	Arg	Asn	Trp	Lys	Pro
145					150					155					160
Lys	Asp	Val	Tyr	Lys	Asn	Arg	Ser	Ile	Glu	Leu	Val	Gln	Gln	Gln	Asn
				165					170					175	
Val	Gln	Leu	Ser	Leu	Thr	Glu	Ala	Thr	Glu	Lys	Ala	Lys	Gln	Glu	Phe
			180					185					190		
Glu	Lys	Ala	Gly	Lys	Asp	Phe	Leu	Val	Glu	Thr	Ile	Lys	Leu	Gly	Lys
		195					200					205			
Leu	Leu	Arg	Pro	Asn	His	Leu	Trp	Gly	Tyr	Tyr	Leu	Phe	Pro	Asp	Cys
	210					215					220				
Tyr	Asn	His	His	Tyr	Lys	Lys	Pro	Gly	Tyr	Asn	Gly	Ser	Cys	Phe	Asn
225					230					235					240
Val	Glu	Ile	Lys	Arg	Asn	Asp	Asp	Leu	Ser	Trp	Leu	Trp	Asn	Glu	Ser
				245					250					255	
Thr	Ala	Leu	Tyr	Pro	Ser	Ile	Tyr	Leu	Asn	Thr	Gln	Gln	Ser	Pro	Val
			260					265					270		
Ala	Ala	Thr	Leu	Tyr	Val	Arg	Asn	Arg	Val	Arg	Glu	Ala	Ile	Arg	Val
		275					280					285			
Ser	Lys	Ile	Pro	Asp	Ala	Lys	Ser	Pro	Leu	Pro	Val	Phe	Ala	Tyr	Thr
	290					295					300				
Arg	Ile	Val	Phe	Thr	Asp	Gln	Val	Leu	Lys	Phe	Leu	Ser	Gln	Asp	Glu
305					310					315					320
Leu	Val	Tyr	Thr	Phe	Gly	Glu	Thr	Val	Ala	Leu	Gly	Ala	Ser	Gly	Ile
				325					330					335	
Val	Ile	Trp	Gly	Thr	Leu	Ser	Ile	Met	Arg	Ser	Met	Lys	Ser	Cys	Leu
			340					345					350		
Leu	Leu	Asp	Asn	Tyr	Met	Glu	Thr	Ile	Leu	Asn	Pro	Tyr	Ile	Ile	Asn
		355					360					365			
Val	Thr	Leu	Ala	Ala	Lys	Met	Cys	Ser	Gln	Val	Leu	Cys	Gln	Glu	Gln
						375					380				
Gly	Val	Cys	Ile	Arg	Lys	Asn	Trp	Asn	Ser	Ser	Asp	Tyr	Leu	His	Leu
385					39										

```
<210> 106
<211> 499
<212> PRT
<213> Homo sapiens
```

```
<220>
<223> PH2O precursor 1-499
```

3108SEQPC1

<400> 106

```

Met Gly Val Leu Lys Phe Lys His Ile Phe Phe Arg Ser Phe Val Lys
 1      5      10      15
Ser Ser Gly Val Ser Gln Ile Val Phe Thr Phe Leu Leu Ile Pro Cys
 20      25      30
Cys Leu Thr Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro
 35      40      45
Phe Leu Trp Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe
 50      55      60
Asp Glu Pro Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg
 65      70      75      80
Ile Asn Ala Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu
 85      90      95
Gly Tyr Tyr Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly
100      105      110
Gly Ile Pro Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys
115      120      125
Lys Asp Ile Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val
130      135      140
Ile Asp Trp Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro
145      150      155      160
Lys Asp Val Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn
165      170      175
Val Gln Leu Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe
180      185      190
Glu Lys Ala Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys
195      200      205
Leu Leu Arg Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys
210      215      220
Tyr Asn His His Tyr Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn
225      230      235      240
Val Glu Ile Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser
245      250      255
Thr Ala Leu Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val
260      265      270
Ala Ala Thr Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val
275      280      285
Ser Lys Ile Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr
290      295      300
Arg Ile Val Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu
305      310      315      320
Leu Val Tyr Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile
325      330      335
Val Ile Trp Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu
340      345      350
Leu Leu Asp Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn
355      360      365
Val Thr Leu Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln
370      375      380
Gly Val Cys Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu
385      390      395      400
Asn Pro Asp Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr
405      410      415
Val Arg Gly Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys
420      425      430
Phe Tyr Cys Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp
435      440      445
Val Lys Asp Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys
450      455      460
Ile Asp Ala Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile
465      470      475      480
Phe Tyr Asn Ala Ser Pro Ser Thr Leu Ser Ala Thr Met Phe Ile Val
485      490      495
Ser Ile Leu

```

3108SEQPC1

<210> 107
 <211> 497
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PH20 precursor 1-497

<400> 107

Met	Gly	Val	Leu	Lys	Phe	Lys	His	Ile	Phe	Phe	Arg	Ser	Phe	Val	Lys
1				5					10					15	
Ser	Ser	Gly	Val	Ser	Gln	Ile	Val	Phe	Thr	Phe	Leu	Leu	Ile	Pro	Cys
			20					25					30		
Cys	Leu	Thr	Leu	Asn	Phe	Arg	Ala	Pro	Pro	Val	Ile	Pro	Asn	Val	Pro
		35					40					45			
Phe	Leu	Trp	Ala	Trp	Asn	Ala	Pro	Ser	Glu	Phe	Cys	Leu	Gly	Lys	Phe
	50				55					60					
Asp	Glu	Pro	Leu	Asp	Met	Ser	Leu	Phe	Ser	Phe	Ile	Gly	Ser	Pro	Arg
65					70				75					80	
Ile	Asn	Ala	Thr	Gly	Gln	Gly	Val	Thr	Ile	Phe	Tyr	Val	Asp	Arg	Leu
			85					90					95		
Gly	Tyr	Tyr	Pro	Tyr	Ile	Asp	Ser	Ile	Thr	Gly	Val	Thr	Val	Asn	Gly
			100					105					110		
Gly	Ile	Pro	Gln	Lys	Ile	Ser	Leu	Gln	Asp	His	Leu	Asp	Lys	Ala	Lys
		115					120					125			
Lys	Asp	Ile	Thr	Phe	Tyr	Met	Pro	Val	Asp	Asn	Leu	Gly	Met	Ala	Val
	130					135					140				
Ile	Asp	Trp	Glu	Glu	Trp	Arg	Pro	Thr	Trp	Ala	Arg	Asn	Trp	Lys	Pro
145					150					155				160	
Lys	Asp	Val	Tyr	Lys	Asn	Arg	Ser	Ile	Glu	Leu	Val	Gln	Gln	Gln	Asn
			165						170				175		
Val	Gln	Leu	Ser	Leu	Thr	Glu	Ala	Thr	Glu	Lys	Ala	Lys	Gln	Glu	Phe
		180						185					190		
Glu	Lys	Ala	Gly	Lys	Asp	Phe	Leu	Val	Glu	Thr	Ile	Lys	Leu	Gly	Lys
	195						200					205			
Leu	Leu	Arg	Pro	Asn	His	Leu	Trp	Gly	Tyr	Tyr	Leu	Phe	Pro	Asp	Cys
	210					215					220				
Tyr	Asn	His	His	Tyr	Lys	Lys	Pro	Gly	Tyr	Asn	Gly	Ser	Cys	Phe	Asn
225					230					235				240	
Val	Glu	Ile	Lys	Arg	Asn	Asp	Asp	Leu	Ser	Trp	Leu	Trp	Asn	Glu	Ser
			245						250				255		
Thr	Ala	Leu	Tyr	Pro	Ser	Ile	Tyr	Leu	Asn	Thr	Gln	Gln	Ser	Pro	Val
		260						265					270		
Ala	Ala	Thr	Leu	Tyr	Val	Arg	Asn	Arg	Val	Arg	Glu	Ala	Ile	Arg	Val
		275					280					285			
Ser	Lys	Ile	Pro	Asp	Ala	Lys	Ser	Pro	Leu	Pro	Val	Phe	Ala	Tyr	Thr
	290					295					300				
Arg	Ile	Val	Phe	Thr	Asp	Gln	Val	Leu	Lys	Phe	Leu	Ser	Gln	Asp	Glu
305					310					315				320	
Leu	Val	Tyr	Thr	Phe	Gly	Glu	Thr	Val	Ala	Leu	Gly	Ala	Ser	Gly	Ile
			325						330					335	
Val	Ile	Trp	Gly	Thr	Leu	Ser	Ile	Met	Arg	Ser	Met	Lys	Ser	Cys	Leu
		340						345					350		
Leu	Leu	Asp	Asn	Tyr	Met	Glu	Thr	Ile	Leu	Asn	Pro	Tyr	Ile	Ile	Asn
	355					360						365			
Val	Thr	Leu	Ala	Ala	Lys	Met	Cys	Ser	Gln	Val	Leu	Cys	Gln	Glu	Gln
	370					375					380				
Gly	Val	Cys	Ile	Arg	Lys	Asn	Trp	Asn	Ser	Ser	Asp	Tyr	Leu	His	Leu
385					390					395				400	
Asn	Pro	Asp	Asn	Phe	Ala	Ile	Gln	Leu	Glu	Lys	Gly	Gly	Lys	Phe	Thr
			405						410					415	
Val	Arg	Gly	Lys	Pro	Thr	Leu	Glu	Asp	Leu	Glu	Gln	Phe	Ser	Glu	Lys
			420					425					430		
Phe	Tyr	Cys	Ser	Cys	Tyr	Ser	Thr	Leu	Ser	Cys	Lys	Glu	Lys	Ala	Asp
		435					440					445			
Val	Lys	Asp	Thr	Asp	Ala	Val	Asp	Val	Cys	Ile	Ala	Asp	Gly	Val	Cys
	450					455					460				
Ile	Asp	Ala	Phe	Leu	Lys	Pro	Pro	Met	Glu	Thr	Glu	Glu	Pro	Gln	Ile

3108SEQPC1

465 470 475 480
Phe Tyr Asn Ala Ser Pro Ser Thr Leu Ser Ala Thr Met Phe Ile Val
 485 490 495

Ser

<210> 108
<211> 495
<212> PRT
<213> Homo sapiens

<220>
<223> PH20 precursor 1-495

<400> 108
Met Gly Val Leu Lys Phe Lys His Ile Phe Phe Arg Ser Phe Val Lys
1 5 10 15
Ser Ser Gly Val Ser Gln Ile Val Phe Thr Phe Leu Leu Ile Pro Cys
 20 25 30
Cys Leu Thr Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro
 35 40 45
Phe Leu Trp Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe
50 55 60
Asp Glu Pro Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg
65 70 75 80
Ile Asn Ala Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu
 85 90 95
Gly Tyr Tyr Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly
 100 105 110
Gly Ile Pro Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys
 115 120 125
Lys Asp Ile Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val
130 135 140
Ile Asp Trp Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro
145 150 155
Lys Asp Val Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn
 165 170 175
Val Gln Leu Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe
 180 185 190
Glu Lys Ala Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys
195 200 205
Leu Leu Arg Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys
210 215 220
Tyr Asn His His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn
225 230 235
Val Glu Ile Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser
 245 250 255
Thr Ala Leu Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val
 260 265 270
Ala Ala Thr Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val
275 280 285
Ser Lys Ile Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr
290 295 300
Arg Ile Val Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu
305 310 315
Leu Val Tyr Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile
 325 330 335
Val Ile Trp Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu
340 345
Leu Leu Asp Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn
355 360 365
Val Thr Leu Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln
370 375 380
Gly Val Cys Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu
385 390 395
Asn Pro Asp Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr
 405 410 415

3108SEQPC1

Val Arg Gly Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys
 420 425 430
 Phe Tyr Cys Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp
 435 440 445
 Val Lys Asp Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys
 450 455 460
 Ile Asp Ala Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile
 465 470 475 480
 Phe Tyr Asn Ala Ser Pro Ser Thr Leu Ser Ala Thr Met Phe Ile
 485 490 495

<210> 109

<211> 493

<212> PRT

<213> Homo sapiens

<220>

<223> PH20 precursor 1-493

<400> 109

Met Gly Val Leu Lys Phe Lys His Ile Phe Phe Arg Ser Phe Val Lys
 1 5 10 15
 Ser Ser Gly Val Ser Gln Ile Val Phe Thr Phe Leu Leu Ile Pro Cys
 20 25 30
 Cys Leu Thr Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro
 35 40 45
 Phe Leu Trp Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe
 50 55 60
 Asp Glu Pro Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg
 65 70 75 80
 Ile Asn Ala Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu
 85 90 95
 Gly Tyr Tyr Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly
 100 105 110
 Gly Ile Pro Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys
 115 120 125
 Lys Asp Ile Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val
 130 135 140
 Ile Asp Trp Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro
 145 150 155 160
 Lys Asp Val Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn
 165 170 175
 Val Gln Leu Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe
 180 185 190
 Glu Lys Ala Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys
 195 200 205
 Leu Leu Arg Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys
 210 215 220
 Tyr Asn His His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn
 225 230 235 240
 Val Glu Ile Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser
 245 250 255
 Thr Ala Leu Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val
 260 265 270
 Ala Ala Thr Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val
 275 280 285
 Ser Lys Ile Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr
 290 295 300
 Arg Ile Val Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu
 305 310 315 320
 Leu Val Tyr Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile
 325 330 335
 Val Ile Trp Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu
 340 345 350
 Leu Leu Asp Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn
 355 360 365
 Val Thr Leu Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln
 Page 130

3108SEQPC1

370	Gly Val Cys Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu	380
385	Asn Pro Asp Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr	400
	Val Arg Gly Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys	415
	Phe Tyr Cys Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp	430
	Val Lys Asp Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys	445
	Ile Asp Ala Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile	460
465	Phe Tyr Asn Ala Ser Pro Ser Thr Leu Ser Ala Thr Met	480
		490

<210> 110

<211> 491

<212> PRT

<213> Homo sapiens

<220>

<223> PH20 precursor 1-489

<400> 110

Met Gly Val Leu Lys Phe Lys His Ile Phe Phe Arg Ser Phe Val Lys	1	5	10	15
Ser Ser Gly Val Ser Gln Ile Val Phe Thr Phe Leu Leu Ile Pro Cys	20	25	30	
Cys Leu Thr Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro	35	40	45	
Phe Leu Trp Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe	50	55	60	
Asp Glu Pro Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg	65	70	75	80
Ile Asn Ala Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu	85	90	95	
Gly Tyr Tyr Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly	100	105	110	
Gly Ile Pro Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys	115	120	125	
Lys Asp Ile Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val	130	135	140	
Ile Asp Trp Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro	145	150	155	160
Lys Asp Val Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn	165	170	175	
Val Gln Leu Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe	180	185	190	
Glu Lys Ala Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys	195	200	205	
Leu Leu Arg Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys	210	215	220	
Tyr Asn His His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn	225	230	235	240
Val Glu Ile Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser	245	250	255	
Thr Ala Leu Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val	260	265	270	
Ala Ala Thr Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val	275	280	285	
Ser Lys Ile Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr	290	295	300	
Arg Ile Val Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu	305	310	315	320
Leu Val Tyr Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile	325	330	335	

3108SEQPC1

Val Ile Trp Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu
 340 345
 Leu Leu Asp Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn
 355 360
 Val Thr Leu Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln
 370 375 380
 Gly Val Cys Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu
 385 390 395 400
 Asn Pro Asp Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr
 405 410 415
 Val Arg Gly Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys
 420 425 430
 Phe Tyr Cys Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp
 435 440 445
 Val Lys Asp Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys
 450 455 460
 Ile Asp Ala Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile
 465 470 475 480
 Phe Tyr Asn Ala Ser Pro Ser Thr Leu Ser Ala
 485 490

<210> 111

<211> 489

<212> PRT

<213> Homo sapiens

<220>

<223> PH20 precursor 1-489

<400> 111

Met Gly Val Leu Lys Phe Lys His Ile Phe Phe Arg Ser Phe Val Lys
 1 5 10 15
 Ser Ser Gly Val Ser Gln Ile Val Phe Thr Phe Leu Leu Ile Pro Cys
 20 25 30
 Cys Leu Thr Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro
 35 40 45
 Phe Leu Trp Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe
 50 55 60
 Asp Glu Pro Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg
 65 70 75 80
 Ile Asn Ala Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu
 85 90 95
 Gly Tyr Tyr Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly
 100 105 110
 Gly Ile Pro Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys
 115 120 125
 Lys Asp Ile Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val
 130 135 140
 Ile Asp Trp Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro
 145 150 155 160
 Lys Asp Val Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn
 165 170 175
 Val Gln Leu Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe
 180 185 190
 Glu Lys Ala Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys
 195 200 205
 Leu Leu Arg Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys
 210 215 220
 Tyr Asn His His Tyr Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn
 225 230 235 240
 Val Glu Ile Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser
 245 250 255
 Thr Ala Leu Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val
 260 265 270
 Ala Ala Thr Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val
 275 280 285
 Ser Lys Ile Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr
 290

3108SEQPC1

290 295 300
 Arg Ile Val Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu
 305 310 315 320
 Leu Val Tyr Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile
 325 330 335
 Val Ile Trp Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu
 340 345 350
 Leu Leu Asp Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn
 355 360 365
 Val Thr Leu Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln
 370 375 380
 Gly Val Cys Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu
 385 390 395 400
 Asn Pro Asp Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr
 405 410 415
 Val Arg Gly Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys
 420 425 430
 Phe Tyr Cys Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp
 435 440 445
 Val Lys Asp Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys
 450 455 460
 Ile Asp Ala Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile
 465 470 475 480
 Phe Tyr Asn Ala Ser Pro Ser Thr Leu
 485

<210> 112

<211> 490

<212> PRT

<213> Homo sapiens

<220>

<223> PH20 precursor 1-490

<400> 112

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

3108SEQPC1

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

<210> 113

<211> 487

<212> PRT

<213> Homo sapiens

<220>

<223> PH20 precursor 1-487

<400> 113

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

3108SEQPC1

210	Tyr	Asn	His	His	Tyr	Lys	215	Lys	Pro	Gly	Tyr	Asn	220	Gly	Ser	Cys	Phe	Asn
225	Val	Glu	Ile	Lys	Arg	Asn	230	Asp	Asp	Leu	Ser	Trp	235	Leu	Trp	Asn	Glu	Ser
					245						250						255	
	Thr	Ala	Leu	Tyr	Pro	Ser	Ile	Tyr	Leu	Asn	Thr	Gln	260	Gln	Ser	Pro	Val	
					265								270					
	Ala	Ala	Thr	Leu	Tyr	Val	Arg	Asn	Arg	Val	Arg	Glu	275	Ala	Ile	Arg	Val	
					280								285					
	Ser	Lys	Ile	Pro	Asp	Ala	Lys	Ser	Pro	Leu	Pro	Val	290	Phe	Ala	Tyr	Thr	
					295								300					
	Arg	Ile	Val	Phe	Thr	Asp	Gln	Val	Leu	Lys	Phe	Leu	305	Ser	Gln	Asp	Glu	
					310								315					
	Leu	Val	Tyr	Thr	Phe	Gly	Glu	Thr	Val	Ala	Leu	Gly	320	Ala	Ser	Gly	Ile	
					325								330					
	Val	Ile	Trp	Gly	Thr	Leu	Ser	Ile	Met	Arg	Ser	Met	335	Lys	Ser	Cys	Leu	
					340								345					
	Leu	Leu	Asp	Asn	Tyr	Met	Glu	Thr	Ile	Leu	Asn	Pro	350	Tyr	Ile	Ile	Asn	
					355								360					
	Val	Thr	Leu	Ala	Ala	Lys	Met	Cys	Ser	Gln	Val	Leu	365	Cys	Gln	Glu	Gln	
					370								375					
	Gly	Val	Cys	Ile	Arg	Lys	Asn	Trp	Asn	Ser	Ser	Asp	380	Tyr	Leu	His	Leu	
					385								390					
	Asn	Pro	Asp	Asn	Phe	Ala	Ile	Gln	Leu	Glu	Lys	Gly	395	Gly	Lys	Phe	Thr	
					400								405					
	Val	Arg	Gly	Lys	Pro	Thr	Leu	Glu	Asp	Leu	Glu	Gln	410	Phe	Ser	Glu	Lys	
					415								420					
	Phe	Tyr	Cys	Ser	Cys	Tyr	Ser	Thr	Leu	Ser	Cys	Lys	425	Glu	Lys	Ala	Asp	
					430								435					
	Val	Lys	Asp	Thr	Asp	Ala	Val	Asp	Val	Cys	Ile	Ala	440	Asp	Gly	Val	Cys	
					445								450					
	Ile	Asp	Ala	Phe	Leu	Lys	Pro	Pro	Met	Glu	Thr	Glu	455	Glu	Pro	Gln	Ile	
					460								465					
	Phe	Tyr	Asn	Ala	Ser	Pro	Ser						470					
					475								480					
					485													

<210> 114
 <211> 485
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PH20 precursor 1-485

<400> 114

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

3108SEQPC1

Val Gln Leu Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe
 180 185 190
 Glu Lys Ala Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys
 195 200 205
 Leu Leu Arg Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys
 210 215 220
 Tyr Asn His His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn
 225 230 235 240
 Val Glu Ile Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser
 245 250 255
 Thr Ala Leu Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val
 260 265 270
 Ala Ala Thr Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val
 275 280 285
 Ser Lys Ile Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr
 290 295 300
 Arg Ile Val Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu
 305 310 315 320
 Leu Val Tyr Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile
 325 330 335
 Val Ile Trp Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu
 340 345 350
 Leu Leu Asp Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn
 355 360 365
 Val Thr Leu Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln
 370 375 380
 Gly Val Cys Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu
 385 390 395 400
 Asn Pro Asp Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr
 405 410 415
 Val Arg Gly Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys
 420 425 430
 Phe Tyr Cys Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp
 435 440 445
 Val Lys Asp Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys
 450 455 460
 Ile Asp Ala Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile
 465 470 475 480
 Phe Tyr Asn Ala Ser
 485

<210> 115

<211> 484

<212> PRT

<213> Homo sapiens

<220>

<223> PH20 precursor 1-484

<400> 115

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

3108SEQPC1

130 135 140
 Ile Asp Trp Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro
 145 150 155 160
 Lys Asp Val Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn
 165 170 175
 Val Gln Leu Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe
 180 185 190
 Glu Lys Ala Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys
 195 200 205
 Leu Leu Arg Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys
 210 215 220
 Tyr Asn His His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn
 225 230 235 240
 Val Glu Ile Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser
 245 250 255
 Thr Ala Leu Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val
 260 265 270
 Ala Ala Thr Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val
 275 280 285
 Ser Lys Ile Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr
 290 295 300
 Arg Ile Val Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu
 305 310 315 320
 Leu Val Tyr Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile
 325 330 335
 Val Ile Trp Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu
 340 345 350
 Leu Leu Asp Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn
 355 360 365
 Val Thr Leu Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln
 370 375 380
 Gly Val Cys Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu
 385 390 395 400
 Asn Pro Asp Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr
 405 410 415
 Val Arg Gly Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys
 420 425 430
 Phe Tyr Cys Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp
 435 440 445
 Val Lys Asp Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys
 450 455 460
 Ile Asp Ala Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile
 465 470 475 480
 Phe Tyr Asn Ala

<210> 116

<211> 476

<212> PRT

<213> Homo sapiens

<220>

<223> PH20 precursor 1-476

<400> 116

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

3108SEQPC1

Gly Tyr Tyr Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly
 100 105 110
 Gly Ile Pro Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys
 115 120 125
 Lys Asp Ile Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val
 130 135 140
 Ile Asp Trp Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro
 145 150 155 160
 Lys Asp Val Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn
 165 170 175
 Val Gln Leu Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe
 180 185 190
 Glu Lys Ala Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys
 195 200 205
 Leu Leu Arg Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys
 210 215 220
 Tyr Asn His His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn
 225 230 235 240
 Val Glu Ile Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser
 245 250 255
 Thr Ala Leu Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val
 260 265 270
 Ala Ala Thr Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val
 275 280 285
 Ser Lys Ile Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr
 290 295 300
 Arg Ile Val Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu
 305 310 315 320
 Leu Val Tyr Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile
 325 330 335
 Val Ile Trp Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu
 340 345 350
 Leu Leu Asp Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn
 355 360 365
 Val Thr Leu Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln
 370 375 380
 Gly Val Cys Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu
 385 390 395 400
 Asn Pro Asp Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr
 405 410 415
 Val Arg Gly Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys
 420 425 430
 Phe Tyr Cys Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp
 435 440 445
 Val Lys Asp Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys
 450 455 460
 Ile Asp Ala Phe Leu Lys Pro Pro Met Glu Thr Glu
 465 470 475

<210> 117

<211> 475

<212> PRT

<213> Homo sapiens

<220>

<223> PH20 precursor 1-475

<400> 117

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

3108SEQPC1

```

65      70      75      80
Ile Asn Ala Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu
      85      90      95
Gly Tyr Tyr Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly
      100      105      110
Gly Ile Pro Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys
      115      120      125
Lys Asp Ile Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val
      130      135      140
Ile Asp Trp Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro
      145      150      155
Lys Asp Val Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn
      160      165      170
Val Gln Leu Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe
      175      180      185
Glu Lys Ala Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys
      190      195      200
Leu Leu Arg Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys
      205      210      215
Tyr Asn His His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn
      220      225      230
Val Glu Ile Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser
      235      240      245
Thr Ala Leu Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val
      250      255      260
Ala Ala Thr Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val
      265      270      275
Ser Lys Ile Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr
      280      285      290
Arg Ile Val Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu
      295      300      305
Leu Val Tyr Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile
      310      315      320
Val Ile Trp Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu
      325      330      335
Leu Leu Asp Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn
      340      345      350
Val Thr Leu Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln
      355      360      365
Gly Val Cys Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu
      370      375      380
Asn Pro Asp Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr
      385      390      395
Val Arg Gly Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys
      400      405      410
Phe Tyr Cys Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp
      415      420      425
Val Lys Asp Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys
      430      435      440
Ile Asp Ala Phe Leu Lys Pro Pro Met Glu Thr
      445      450      455
465      470      475

```

<210> 118

<211> 474

<212> PRT

<213> Homo sapiens

<220>

<223> PH20 precursor 1-474

<400> 118

```

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

```

3108SEQPC1

Phe Leu Trp Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe
 50 55 60
 Asp Glu Pro Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg
 65 70 75 80
 Ile Asn Ala Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu
 85 90 95
 Gly Tyr Tyr Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly
 100 105 110
 Gly Ile Pro Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys
 115 120 125
 Lys Asp Ile Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val
 130 135 140
 Ile Asp Trp Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro
 145 150 155 160
 Lys Asp Val Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn
 165 170 175
 Val Gln Leu Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe
 180 185 190
 Glu Lys Ala Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys
 195 200 205
 Leu Leu Arg Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys
 210 215 220
 Tyr Asn His His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn
 225 230 235 240
 Val Glu Ile Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser
 245 250 255
 Thr Ala Leu Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val
 260 265 270
 Ala Ala Thr Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val
 275 280 285
 Ser Lys Ile Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr
 290 295 300
 Arg Ile Val Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu
 305 310 315 320
 Leu Val Tyr Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile
 325 330 335
 Val Ile Trp Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu
 340 345 350
 Leu Leu Asp Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn
 355 360 365
 Val Thr Leu Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln
 370 375 380
 Gly Val Cys Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu
 385 390 395 400
 Asn Pro Asp Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr
 405 410 415
 Val Arg Gly Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys
 420 425 430
 Phe Tyr Cys Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp
 435 440 445
 Val Lys Asp Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys
 450 455 460
 Ile Asp Ala Phe Leu Lys Pro Pro Met Glu
 465 470

<210> 119

<211> 473

<212> PRT

<213> Homo sapiens

<220>

<223> PH20 precursor 1-473

<400> 119

Met Gly Val Leu Lys Phe Lys His Ile Phe Phe Arg Ser Phe Val Lys
 1 5 10 15
 Ser Ser Gly Val Ser Gln Ile Val Phe Thr Phe Leu Leu Ile Pro Cys

			20					25					30			
Cys	Leu	Thr	Leu	Asn	Phe	Arg	Ala	Pro	Pro	Val	Ile	Pro	Asn	Val	Pro	
		35					40					45				
Phe	Leu	Trp	Ala	Trp	Asn	Ala	Pro	Ser	Glu	Phe	Cys	Leu	Gly	Lys	Phe	
	50					55					60					
Asp	Glu	Pro	Leu	Asp	Met	Ser	Leu	Phe	Ser	Phe	Ile	Gly	Ser	Pro	Arg	
65					70					75					80	
Ile	Asn	Ala	Thr	Gly	Gln	Gly	Val	Thr	Ile	Phe	Tyr	Val	Asp	Arg	Leu	
				85					90					95		
Gly	Tyr	Tyr	Pro	Tyr	Ile	Asp	Ser	Ile	Thr	Gly	Val	Thr	Val	Asn	Gly	
			100					105					110			
Gly	Ile	Pro	Gln	Lys	Ile	Ser	Leu	Gln	Asp	His	Leu	Asp	Lys	Ala	Lys	
		115					120					125				
Lys	Asp	Ile	Thr	Phe	Tyr	Met	Pro	Val	Asp	Asn	Leu	Gly	Met	Ala	Val	
	130					135					140					
Ile	Asp	Trp	Glu	Glu	Trp	Arg	Pro	Thr	Trp	Ala	Arg	Asn	Trp	Lys	Pro	
145					150					155					160	
Lys	Asp	Val	Tyr	Lys	Asn	Arg	Ser	Ile	Glu	Leu	Val	Gln	Gln	Gln	Asn	
				165					170				175			
Val	Gln	Leu	Ser	Leu	Thr	Glu	Ala	Thr	Glu	Lys	Ala	Lys	Gln	Glu	Phe	
			180					185					190			
Glu	Lys	Ala	Gly	Lys	Asp	Phe	Leu	Val	Glu	Thr	Ile	Lys	Leu	Gly	Lys	
		195					200					205				
Leu	Leu	Arg	Pro	Asn	His	Leu	Trp	Gly	Tyr	Tyr	Leu	Phe	Pro	Asp	Cys	
	210					215					220					
Tyr	Asn	His	His	Tyr	Lys	Lys	Pro	Gly	Tyr	Asn	Gly	Ser	Cys	Phe	Asn	
225					230					235					240	
Val	Glu	Ile	Lys	Arg	Asn	Asp	Asp	Leu	Ser	Trp	Leu	Trp	Asn	Glu	Ser	
				245					250					255		
Thr	Ala	Leu	Tyr	Pro	Ser	Ile	Tyr	Leu	Asn	Thr	Gln	Gln	Ser	Pro	Val	
			260					265					270			
Ala	Ala	Thr	Leu	Tyr	Val	Arg	Asn	Arg	Val	Arg	Glu	Ala	Ile	Arg	Val	
		275					280					285				
Ser	Lys	Ile	Pro	Asp	Ala	Lys	Ser	Pro	Leu	Pro	Val	Phe	Ala	Tyr	Thr	
	290					295					300					
Arg	Ile	Val	Phe	Thr	Asp	Gln	Val	Leu	Lys	Phe	Leu	Ser	Gln	Asp	Glu	
305					310					315					320	
Leu	Val	Tyr	Thr	Phe	Gly	Glu	Thr	Val	Ala	Leu	Gly	Ala	Ser	Gly	Ile	
				325					330					335		
Val	Ile	Trp	Gly	Thr	Leu	Ser	Ile	Met	Arg	Ser	Met	Lys	Ser	Cys	Leu	
			340					345					350			
Leu	Leu	Asp	Asn	Tyr	Met	Glu	Thr	Ile	Leu	Asn	Pro	Tyr	Ile	Ile	Asn	
		355					360									

<210> 120

<211> 472

<212> PRT

<213> Homo sapiens

 $\langle 220 \rangle$

<223> PH20 precursor 1-472

<400> 120

3108SEQPC1

```

Met Gly Val Leu Lys Phe Lys His Ile Phe Phe Arg Ser Phe Val Lys
 1      5      10      15
Ser Ser Gly Val Ser Gln Ile Val Phe Thr Phe Leu Leu Ile Pro Cys
 20      25      30
Cys Leu Thr Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro
 35      40      45
Phe Leu Trp Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe
 50      55      60
Asp Glu Pro Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg
 65      70      75      80
Ile Asn Ala Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu
 85      90      95
Gly Tyr Tyr Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly
100      105      110
Gly Ile Pro Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys
115      120      125
Lys Asp Ile Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val
130      135      140
Ile Asp Trp Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro
145      150      155      160
Lys Asp Val Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn
165      170      175
Val Gln Leu Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe
180      185      190
Glu Lys Ala Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys
195      200      205
Leu Leu Arg Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys
210      215      220
Tyr Asn His His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn
225      230      235      240
Val Glu Ile Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser
245      250      255
Thr Ala Leu Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val
260      265      270
Ala Ala Thr Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val
275      280      285
Ser Lys Ile Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr
290      295      300
Arg Ile Val Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu
305      310      315      320
Leu Val Tyr Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile
325      330      335
Val Ile Trp Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu
340      345      350
Leu Leu Asp Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn
355      360      365
Val Thr Leu Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln
370      375      380
Gly Val Cys Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu
385      390      395      400
Asn Pro Asp Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr
405      410      415
Val Arg Gly Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys
420      425      430
Phe Tyr Cys Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp
435      440      445
Val Lys Asp Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys
450      455      460
Ile Asp Ala Phe Leu Lys Pro Pro
465      470

```

<210> 121

<211> 471

<212> PRT

<213> Homo sapiens

<220>

<223> PH20 precursor 1-471

<400> 121

```

Met Gly Val Leu Lys Phe Lys His Ile Phe Phe Arg Ser Phe Val Lys
 1      5      10      15
Ser Ser Gly Val Ser Gln Ile Val Phe Thr Phe Leu Leu Ile Pro Cys
      20      25      30
Cys Leu Thr Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro
      35      40      45
Phe Leu Trp Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe
      50      55      60
Asp Glu Pro Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg
      65      70      75      80
Ile Asn Ala Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu
      85      90      95
Gly Tyr Tyr Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly
      100      105      110
Gly Ile Pro Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys
      115      120      125
Lys Asp Ile Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val
      130      135      140
Ile Asp Trp Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro
      145      150      155      160
Lys Asp Val Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn
      165      170      175
Val Gln Leu Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe
      180      185      190
Glu Lys Ala Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys
      195      200      205
Leu Leu Arg Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys
      210      215      220
Tyr Asn His His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn
      225      230      235      240
Val Glu Ile Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser
      245      250      255
Thr Ala Leu Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val
      260      265      270
Ala Ala Thr Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val
      275      280      285
Ser Lys Ile Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr
      290      295      300
Arg Ile Val Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu
      305      310      315      320
Leu Val Tyr Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile
      325      330      335
Val Ile Trp Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu
      340      345      350
Leu Leu Asp Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn
      355      360      365
Val Thr Leu Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln
      370      375      380
Gly Val Cys Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu
      385      390      395      400
Asn Pro Asp Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr
      405      410      415
Val Arg Gly Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys
      420      425      430
Phe Tyr Cys Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp
      435      440      445
Val Lys Asp Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys
      450      455      460
Ile Asp Ala Phe Leu Lys Pro
      465      470

```

<210> 122

<211> 470

<212> PRT

3108SEQPC1

<213> Homo sapiens

<220>

<223> PH20 precursor 1-470

<400> 122

```

Met Gly Val Leu Lys Phe Lys His Ile Phe Phe Arg Ser Phe Val Lys
 1      5      10      15
Ser Ser Gly Val Ser Gln Ile Val Phe Thr Phe Leu Leu Ile Pro Cys
      20      25      30
Cys Leu Thr Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro
      35      40      45
Phe Leu Trp Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe
      50      55      60
Asp Glu Pro Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg
65      70      75      80
Ile Asn Ala Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu
      85      90      95
Gly Tyr Tyr Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly
      100      105      110
Gly Ile Pro Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys
      115      120      125
Lys Asp Ile Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val
      130      135      140
Ile Asp Trp Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro
145      150      155      160
Lys Asp Val Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn
      165      170      175
Val Gln Leu Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe
      180      185      190
Glu Lys Ala Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys
      195      200      205
Leu Leu Arg Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys
      210      215      220
Tyr Asn His His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn
225      230      235      240
Val Glu Ile Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser
      245      250      255
Thr Ala Leu Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val
      260      265      270
Ala Ala Thr Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val
      275      280      285
Ser Lys Ile Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr
      290      295      300
Arg Ile Val Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu
305      310      315      320
Leu Val Tyr Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile
      325      330      335
Val Ile Trp Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu
      340      345      350
Leu Leu Asp Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn
      355      360      365
Val Thr Leu Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln
      370      375      380
Gly Val Cys Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu
385      390      395      400
Asn Pro Asp Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr
      405      410      415
Val Arg Gly Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys
      420      425      430
Phe Tyr Cys Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp
      435      440      445
Val Lys Asp Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys
      450      455      460
Ile Asp Ala Phe Leu Lys
465      470

```

3108SEQPC1

<210> 123
 <211> 469
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PH20 precursor 1-469

<400> 123

Met	Gly	Val	Leu	Lys	Phe	Lys	His	Ile	Phe	Phe	Arg	Ser	Phe	Val	Lys
1				5					10					15	
Ser	Ser	Gly	Val	Ser	Gln	Ile	Val	Phe	Thr	Phe	Leu	Leu	Ile	Pro	Cys
			20					25					30		
Cys	Leu	Thr	Leu	Asn	Phe	Arg	Ala	Pro	Pro	Val	Ile	Pro	Asn	Val	Pro
		35					40					45			
Phe	Leu	Trp	Ala	Trp	Asn	Ala	Pro	Ser	Glu	Phe	Cys	Leu	Gly	Lys	Phe
	50					55					60				
Asp	Glu	Pro	Leu	Asp	Met	Ser	Leu	Phe	Ser	Phe	Ile	Gly	Ser	Pro	Arg
65					70					75					80
Ile	Asn	Ala	Thr	Gly	Gln	Gly	Val	Thr	Ile	Phe	Tyr	Val	Asp	Arg	Leu
			85						90				95		
Gly	Tyr	Tyr	Pro	Tyr	Ile	Asp	Ser	Ile	Thr	Gly	Val	Thr	Val	Asn	Gly
			100					105					110		
Gly	Ile	Pro	Gln	Lys	Ile	Ser	Leu	Gln	Asp	His	Leu	Asp	Lys	Ala	Lys
		115					120					125			
Lys	Asp	Ile	Thr	Phe	Tyr	Met	Pro	Val	Asp	Asn	Leu	Gly	Met	Ala	Val
	130					135					140				
Ile	Asp	Trp	Glu	Glu	Trp	Arg	Pro	Thr	Trp	Ala	Arg	Asn	Trp	Lys	Pro
145					150					155					160
Lys	Asp	Val	Tyr	Lys	Asn	Arg	Ser	Ile	Glu	Leu	Val	Gln	Gln	Gln	Asn
			165						170				175		
Val	Gln	Leu	Ser	Leu	Thr	Glu	Ala	Thr	Glu	Lys	Ala	Lys	Gln	Glu	Phe
		180					185						190		
Glu	Lys	Ala	Gly	Lys	Asp	Phe	Leu	Val	Glu	Thr	Ile	Lys	Leu	Gly	Lys
	195						200					205			
Leu	Leu	Arg	Pro	Asn	His	Leu	Trp	Gly	Tyr	Tyr	Leu	Phe	Pro	Asp	Cys
	210					215					220				
Tyr	Asn	His	His	Tyr	Lys	Lys	Pro	Gly	Tyr	Asn	Gly	Ser	Cys	Phe	Asn
225					230					235					240
Val	Glu	Ile	Lys	Arg	Asn	Asp	Asp	Leu	Ser	Trp	Leu	Trp	Asn	Glu	Ser
			245						250				255		
Thr	Ala	Leu	Tyr	Pro	Ser	Ile	Tyr	Leu	Asn	Thr	Gln	Gln	Ser	Pro	Val
		260						265					270		
Ala	Ala	Thr	Leu	Tyr	Val	Arg	Asn	Arg	Val	Arg	Glu	Ala	Ile	Arg	Val
	275						280					285			
Ser	Lys	Ile	Pro	Asp	Ala	Lys	Ser	Pro	Leu	Pro	Val	Phe	Ala	Tyr	Thr
	290					295					300				
Arg	Ile	Val	Phe	Thr	Asp	Gln	Val	Leu	Lys	Phe	Leu	Ser	Gln	Asp	Glu
305					310					315					320
Leu	Val	Tyr	Thr	Phe	Gly	Glu	Thr	Val	Ala	Leu	Gly	Ala	Ser	Gly	Ile
			325						330				335		
Val	Ile	Trp	Gly	Thr	Leu	Ser	Ile	Met	Arg	Ser	Met	Lys	Ser	Cys	Leu
		340						345					350		
Leu	Leu	Asp	Asn	Tyr	Met	Glu	Thr	Ile	Leu	Asn	Pro	Tyr	Ile	Ile	Asn
	355						360					365			
Val	Thr	Leu	Ala	Ala	Lys	Met	Cys	Ser	Gln	Val	Leu	Cys	Gln	Glu	Gln
	370					375					380				
Gly	Val	Cys	Ile	Arg	Lys	Asn	Trp	Asn	Ser	Ser	Asp	Tyr	Leu	His	Leu
385					390					395					400
Asn	Pro	Asp	Asn	Phe	Ala	Ile	Gln	Leu	Glu	Lys	Gly	Gly	Lys	Phe	Thr
			405						410				415		
Val	Arg	Gly	Lys	Pro	Thr	Leu	Glu	Asp	Leu	Glu	Gln	Phe	Ser	Glu	Lys
		420						425				430			
Phe	Tyr	Cys	Ser	Cys	Tyr	Ser	Thr	Leu	Ser	Cys	Lys	Glu	Lys	Ala	Asp
	435						440					445			
Val	Lys	Asp	Thr	Asp	Ala	Val	Asp	Val	Cys	Ile	Ala	Asp	Gly	Val	Cys
	450					455					460				
Ile	Asp	Ala	Phe	Leu											

465

<210> 124

<211> 468

<212> PRT

<213> Homo sapiens

<220>

<223> PH20 precursor 1-468

<400> 124

```

Met Gly Val Leu Lys Phe Lys His Ile Phe Phe Arg Ser Phe Val Lys
 1      5      10      15
Ser Ser Gly Val Ser Gln Ile Val Phe Thr Phe Leu Leu Ile Pro Cys
      20      25      30
Cys Leu Thr Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro
      35      40      45
Phe Leu Trp Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe
      50      55      60
Asp Glu Pro Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg
65      70      75      80
Ile Asn Ala Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu
      85      90      95
Gly Tyr Tyr Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly
      100      105      110
Gly Ile Pro Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys
      115      120      125
Lys Asp Ile Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val
      130      135      140
Ile Asp Trp Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro
145      150      155      160
Lys Asp Val Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn
      165      170      175
Val Gln Leu Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe
      180      185      190
Glu Lys Ala Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys
      195      200      205
Leu Leu Arg Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys
      210      215      220
Tyr Asn His His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn
225      230      235      240
Val Glu Ile Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser
      245      250      255
Thr Ala Leu Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val
      260      265      270
Ala Ala Thr Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val
      275      280      285
Ser Lys Ile Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr
      290      295      300
Arg Ile Val Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu
305      310      315      320
Leu Val Tyr Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile
      325      330      335
Val Ile Trp Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu
      340      345      350
Leu Leu Asp Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn
      355      360      365
Val Thr Leu Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln
      370      375      380
Gly Val Cys Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu
385      390      395      400
Asn Pro Asp Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr
      405      410      415
Val Arg Gly Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys
      420      425      430
Phe Tyr Cys Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp
      435      440      445

```

3108SEQPC1

Val Lys Asp Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys
 450 455 460
 Ile Asp Ala Phe
 465

<210> 125
 <211> 466
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PH20 precursor 1-466

<400> 125
 Met Gly Val Leu Lys Phe Lys His Ile Phe Phe Arg Ser Phe Val Lys
 1 5 10 15
 Ser Ser Gly Val Ser Gln Ile Val Phe Thr Phe Leu Leu Ile Pro Cys
 20 25 30
 Cys Leu Thr Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro
 35 40 45
 Phe Leu Trp Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe
 50 55 60
 Asp Glu Pro Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg
 65 70 75 80
 Ile Asn Ala Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu
 85 90 95
 Gly Tyr Tyr Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly
 100 105 110
 Gly Ile Pro Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys
 115 120 125
 Lys Asp Ile Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val
 130 135 140
 Ile Asp Trp Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro
 145 150 155 160
 Lys Asp Val Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn
 165 170 175
 Val Gln Leu Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe
 180 185 190
 Glu Lys Ala Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys
 195 200 205
 Leu Leu Arg Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys
 210 215 220
 Tyr Asn His His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn
 225 230 235 240
 Val Glu Ile Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser
 245 250 255
 Thr Ala Leu Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val
 260 265 270
 Ala Ala Thr Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val
 275 280 285
 Ser Lys Ile Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr
 290 295 300
 Arg Ile Val Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu
 305 310 315 320
 Leu Val Tyr Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile
 325 330 335
 Val Ile Trp Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu
 340 345 350
 Leu Leu Asp Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn
 355 360 365
 Val Thr Leu Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln
 370 375 380
 Gly Val Cys Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu
 385 390 395 400
 Asn Pro Asp Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr
 405 410 415
 Val Arg Gly Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys

3108SEQPC1

420 425 430
 Phe Tyr Cys Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp
 435 440 445
 Val Lys Asp Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys
 450 455 460
 Ile Asp
 465

<210> 126
 <211> 465
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PH20 precursor 1-465

<400> 126
 Met Gly Val Leu Lys Phe Lys His Ile Phe Phe Arg Ser Phe Val Lys
 1 5 10 15
 Ser Ser Gly Val Ser Gln Ile Val Phe Thr Phe Leu Leu Ile Pro Cys
 20 25 30
 Cys Leu Thr Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro
 35 40 45
 Phe Leu Trp Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe
 50 55 60
 Asp Glu Pro Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg
 65 70 75 80
 Ile Asn Ala Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu
 85 90 95
 Gly Tyr Tyr Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly
 100 105 110
 Gly Ile Pro Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys
 115 120 125
 Lys Asp Ile Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val
 130 135 140
 Ile Asp Trp Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro
 145 150 155 160
 Lys Asp Val Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn
 165 170 175
 Val Gln Leu Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe
 180 185 190
 Glu Lys Ala Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys
 195 200 205
 Leu Leu Arg Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys
 210 215 220
 Tyr Asn His His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn
 225 230 235 240
 Val Glu Ile Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser
 245 250 255
 Thr Ala Leu Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val
 260 265 270
 Ala Ala Thr Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val
 275 280 285
 Ser Lys Ile Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr
 290 295 300
 Arg Ile Val Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu
 305 310 315 320
 Leu Val Tyr Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile
 325 330 335
 Val Ile Trp Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu
 340 345 350
 Leu Leu Asp Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn
 355 360 365
 Val Thr Leu Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln
 370 375 380
 Gly Val Cys Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu
 385 390 395 400

3108SEQPC1
 Asn Pro Asp Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr
 405 410 415
 Val Arg Gly Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys
 420 425 430
 Phe Tyr Cys Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp
 435 440 445
 Val Lys Asp Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys
 450 455 460
 Ile
 465

<210> 127
 <211> 464
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PH20 precursor 1-464

<400> 127
 Met Gly Val Leu Lys Phe Lys His Ile Phe Phe Arg Ser Phe Val Lys
 1 5 10 15
 Ser Ser Gly Val Ser Gln Ile Val Phe Thr Phe Leu Leu Ile Pro Cys
 20 25 30
 Cys Leu Thr Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro
 35 40 45
 Phe Leu Trp Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe
 50 55 60
 Asp Glu Pro Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg
 65 70 75 80
 Ile Asn Ala Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu
 85 90 95
 Gly Tyr Tyr Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly
 100 105 110
 Gly Ile Pro Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys
 115 120 125
 Lys Asp Ile Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val
 130 135 140
 Ile Asp Trp Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro
 145 150 155 160
 Lys Asp Val Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn
 165 170 175
 Val Gln Leu Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe
 180 185 190
 Glu Lys Ala Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys
 195 200 205
 Leu Leu Arg Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys
 210 215 220
 Tyr Asn His His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn
 225 230 235 240
 Val Glu Ile Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser
 245 250 255
 Thr Ala Leu Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val
 260 265 270
 Ala Ala Thr Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val
 275 280 285
 Ser Lys Ile Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr
 290 295 300
 Arg Ile Val Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu
 305 310 315 320
 Leu Val Tyr Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile
 325 330 335
 Val Ile Trp Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu
 340 345 350
 Leu Leu Asp Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn
 355 360 365
 Val Thr Leu Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln
 Page 149

3108SEQPC1

370	Gly Val Cys Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu	375	380
385	Asn Pro Asp Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr	390	400
	Val Arg Gly Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys	405	415
	Phe Tyr Cys Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp	420	430
	Val Lys Asp Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys	435	445
		450	460

<210> 128

<211> 462

<212> PRT

<213> Homo sapiens

<220>

<223> PH20 precursor 1-462

<400> 128

Met Gly Val Leu Lys Phe Lys His Ile Phe Phe Arg Ser Phe Val Lys	1	5	10	15
Ser Ser Gly Val Ser Gln Ile Val Phe Thr Phe Leu Leu Ile Pro Cys	20	25	30	
Cys Leu Thr Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro	35	40	45	
Phe Leu Trp Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe	50	55	60	
Asp Glu Pro Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg	65	70	75	80
Ile Asn Ala Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu	85	90	95	
Gly Tyr Tyr Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly	100	105	110	
Gly Ile Pro Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys	115	120	125	
Lys Asp Ile Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val	130	135	140	
Ile Asp Trp Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro	145	150	155	160
Lys Asp Val Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn	165	170	175	
Val Gln Leu Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe	180	185	190	
Glu Lys Ala Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys	195	200	205	
Leu Leu Arg Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys	210	215	220	
Tyr Asn His His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn	225	230	235	240
Val Glu Ile Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser	245	250	255	
Thr Ala Leu Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val	260	265	270	
Ala Ala Thr Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val	275	280	285	
Ser Lys Ile Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr	290	295	300	
Arg Ile Val Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu	305	310	315	320
Leu Val Tyr Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile	325	330	335	
Val Ile Trp Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu	340	345	350	
Leu Leu Asp Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn	355	360	365	

3108SEQPC1

Val Thr Leu Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln
 370 375 380
 Gly Val Cys Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu
 385 390 395 400
 Asn Pro Asp Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr
 405 410 415
 Val Arg Gly Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys
 420 425 430
 Phe Tyr Cys Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp
 435 440 445
 Val Lys Asp Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly
 450 455 460

<210> 129

<211> 460

<212> PRT

<213> Homo sapiens

<220>

<223> PH20 precursor 1-460

<400> 129

Met Gly Val Leu Lys Phe Lys His Ile Phe Phe Arg Ser Phe Val Lys
 1 5 10 15
 Ser Ser Gly Val Ser Gln Ile Val Phe Thr Phe Leu Leu Ile Pro Cys
 20 25 30
 Cys Leu Thr Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro
 35 40 45
 Phe Leu Trp Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe
 50 55 60
 Asp Glu Pro Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg
 65 70 75 80
 Ile Asn Ala Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu
 85 90 95
 Gly Tyr Tyr Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly
 100 105 110
 Gly Ile Pro Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys
 115 120 125
 Lys Asp Ile Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val
 130 135 140
 Ile Asp Trp Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro
 145 150 155 160
 Lys Asp Val Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn
 165 170 175
 Val Gln Leu Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe
 180 185 190
 Glu Lys Ala Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys
 195 200 205
 Leu Leu Arg Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys
 210 215 220
 Tyr Asn His His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn
 225 230 235 240
 Val Glu Ile Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser
 245 250 255
 Thr Ala Leu Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val
 260 265 270
 Ala Ala Thr Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val
 275 280 285
 Ser Lys Ile Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr
 290 295 300
 Arg Ile Val Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu
 305 310 315 320
 Leu Val Tyr Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile
 325 330 335
 Val Ile Trp Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu
 340 345 350
 Leu Leu Asp Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn

3108SEQPC1

355 360 365
 Val Thr Leu Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln
 370 375 380
 Gly Val Cys Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu
 385 390 395 400
 Asn Pro Asp Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr
 405 410 415
 Val Arg Gly Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys
 420 425 430
 Phe Tyr Cys Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp
 435 440 445
 Val Lys Asp Thr Asp Ala Val Asp Val Cys Ile Ala
 450 455 460

<210> 130

<211> 458

<212> PRT

<213> Homo sapiens

<220>

<223> PH20 precursor 1-458

<400> 130

Met Gly Val Leu Lys Phe Lys His Ile Phe Phe Arg Ser Phe Val Lys
 1 5 10 15
 Ser Ser Gly Val Ser Gln Ile Val Phe Thr Phe Leu Leu Ile Pro Cys
 20 25 30
 Cys Leu Thr Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro
 35 40 45
 Phe Leu Trp Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe
 50 55 60
 Asp Glu Pro Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg
 65 70 75 80
 Ile Asn Ala Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu
 85 90 95
 Gly Tyr Tyr Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly
 100 105 110
 Gly Ile Pro Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys
 115 120 125
 Lys Asp Ile Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val
 130 135 140
 Ile Asp Trp Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro
 145 150 155 160
 Lys Asp Val Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn
 165 170 175
 Val Gln Leu Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe
 180 185 190
 Glu Lys Ala Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys
 195 200 205
 Leu Leu Arg Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys
 210 215 220
 Tyr Asn His His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn
 225 230 235 240
 Val Glu Ile Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser
 245 250 255
 Thr Ala Leu Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val
 260 265 270
 Ala Ala Thr Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val
 275 280 285
 Ser Lys Ile Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr
 290 295 300
 Arg Ile Val Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu
 305 310 315 320
 Leu Val Tyr Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile
 325 330 335
 Val Ile Trp Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu
 340 345 350

3108SEQPC1

Leu Leu Asp Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn
 355 360
 Val Thr Leu Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln
 370 375 380
 Gly Val Cys Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu
 385 390 395 400
 Asn Pro Asp Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr
 405 410 415
 Val Arg Gly Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys
 420 425 430
 Phe Tyr Cys Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp
 435 440 445
 Val Lys Asp Thr Asp Ala Val Asp Val Cys
 450 455

<210> 131
 <211> 456
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PH20 precursor 1-456

<400> 131
 Met Gly Val Leu Lys Phe Lys His Ile Phe Phe Arg Ser Phe Val Lys
 1 5 10 15
 Ser Ser Gly Val Ser Gln Ile Val Phe Thr Phe Leu Leu Ile Pro Cys
 20 25 30
 Cys Leu Thr Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro
 35 40 45
 Phe Leu Trp Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe
 50 55 60
 Asp Glu Pro Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg
 65 70 75 80
 Ile Asn Ala Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu
 85 90 95
 Gly Tyr Tyr Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly
 100 105 110
 Gly Ile Pro Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys
 115 120 125
 Lys Asp Ile Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val
 130 135 140
 Ile Asp Trp Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro
 145 150 155 160
 Lys Asp Val Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn
 165 170 175
 Val Gln Leu Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe
 180 185 190
 Glu Lys Ala Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys
 195 200 205
 Leu Leu Arg Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys
 210 215 220
 Tyr Asn His His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn
 225 230 235 240
 Val Glu Ile Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser
 245 250 255
 Thr Ala Leu Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val
 260 265 270
 Ala Ala Thr Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val
 275 280 285
 Ser Lys Ile Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr
 290 295 300
 Arg Ile Val Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu
 305 310 315 320
 Leu Val Tyr Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile
 325 330 335
 Val Ile Trp Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu

3108SEQPC1

340 345 350
 Leu Leu Asp Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn
 355 360 365
 Val Thr Leu Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln
 370 375 380
 Gly Val Cys Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu
 385 390 395 400
 Asn Pro Asp Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr
 405 410 415
 Val Arg Gly Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys
 420 425 430
 Phe Tyr Cys Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp
 435 440 445
 Val Lys Asp Thr Asp Ala Val Asp
 450 455

<210> 132

<211> 454

<212> PRT

<213> Homo sapiens

<220>

<223> PH20 precursor 1-454

<400> 132

Met Gly Val Leu Lys Phe Lys His Ile Phe Phe Arg Ser Phe Val Lys
 1 5 10 15
 Ser Ser Gly Val Ser Gln Ile Val Phe Thr Phe Leu Leu Ile Pro Cys
 20 25 30
 Cys Leu Thr Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro
 35 40 45
 Phe Leu Trp Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe
 50 55 60
 Asp Glu Pro Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg
 65 70 75 80
 Ile Asn Ala Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu
 85 90 95
 Gly Tyr Tyr Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly
 100 105 110
 Gly Ile Pro Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys
 115 120 125
 Lys Asp Ile Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val
 130 135 140
 Ile Asp Trp Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro
 145 150 155 160
 Lys Asp Val Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn
 165 170 175
 Val Gln Leu Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe
 180 185 190
 Glu Lys Ala Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys
 195 200 205
 Leu Leu Arg Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys
 210 215 220
 Tyr Asn His His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn
 225 230 235 240
 Val Glu Ile Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser
 245 250 255
 Thr Ala Leu Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val
 260 265 270
 Ala Ala Thr Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val
 275 280 285
 Ser Lys Ile Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr
 290 295 300
 Arg Ile Val Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu
 305 310 315 320
 Leu Val Tyr Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile
 325 330 335

3108SEQPC1

Val Ile Trp Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu
 340 345 350
 Leu Leu Asp Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn
 355 360 365
 Val Thr Leu Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln
 370 375 380
 Gly Val Cys Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu
 385 390 395 400
 Asn Pro Asp Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr
 405 410 415
 Val Arg Gly Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys
 420 425 430
 Phe Tyr Cys Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp
 435 440 445
 Val Lys Asp Thr Asp Ala
 450

<210> 133

<211> 452

<212> PRT

<213> Homo sapiens

<220>

<223> PH20 precursor 1-452

<400> 133

Met Gly Val Leu Lys Phe Lys His Ile Phe Phe Arg Ser Phe Val Lys
 1 5 10 15
 Ser Ser Gly Val Ser Gln Ile Val Phe Thr Phe Leu Leu Ile Pro Cys
 20 25 30
 Cys Leu Thr Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro
 35 40 45
 Phe Leu Trp Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe
 50 55 60
 Asp Glu Pro Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg
 65 70 75 80
 Ile Asn Ala Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu
 85 90 95
 Gly Tyr Tyr Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly
 100 105 110
 Gly Ile Pro Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys
 115 120 125
 Lys Asp Ile Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val
 130 135 140
 Ile Asp Trp Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro
 145 150 155 160
 Lys Asp Val Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn
 165 170 175
 Val Gln Leu Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe
 180 185 190
 Glu Lys Ala Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys
 195 200 205
 Leu Leu Arg Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys
 210 215 220
 Tyr Asn His His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn
 225 230 235 240
 Val Glu Ile Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser
 245 250 255
 Thr Ala Leu Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val
 260 265 270
 Ala Ala Thr Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val
 275 280 285
 Ser Lys Ile Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr
 290 295 300
 Arg Ile Val Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu
 305 310 315 320
 Leu Val Tyr Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile

[illegible]

```
<210> 134
<211> 450
<212> PRT
<213> Homo sapiens
```

<400>	134															
Met	Gly	Val	Leu	Lys	Phe	Lys	His	Ile	Phe	Phe	Arg	Ser	Phe	Val	Lys	
1				5					10					15		
Ser	Ser	Gly	Val	Ser	Gln	Ile	Val	Phe	Thr	Phe	Leu	Leu	Ile	Pro	Cys	
			20					25					30			
Cys	Leu	Thr	Leu	Asn	Phe	Arg	Ala	Pro	Pro	Val	Ile	Pro	Asn	Val	Pro	
		35					40					45				
Phe	Leu	Trp	Ala	Trp	Asn	Ala	Pro	Ser	Glu	Phe	Cys	Leu	Gly	Lys	Phe	
	50				55						60					
Asp	Glu	Pro	Leu	Asp	Met	Ser	Leu	Phe	Ser	Phe	Ile	Gly	Ser	Pro	Arg	
65					70					75					80	
Ile	Asn	Ala	Thr	Gly	Gln	Gly	Val	Thr	Ile	Phe	Tyr	Val	Asp	Arg	Leu	
				85					90					95		
Gly	Tyr	Tyr	Pro	Tyr	Ile	Asp	Ser	Ile	Thr	Gly	Val	Thr	Val	Asn	Gly	
			100					105					110			
Gly	Ile	Pro	Gln	Lys	Ile	Ser	Leu	Gln	Asp	His	Leu	Asp	Lys	Ala	Lys	
		115					120					125				
Lys	Asp	Ile	Thr	Phe	Tyr	Met	Pro	Val	Asp	Asn	Leu	Gly	Met	Ala	Val	
	130					135					140					
Ile	Asp	Trp	Glu	Glu	Trp	Arg	Pro	Thr	Trp	Ala	Arg	Asn	Trp	Lys	Pro	
145					150					155					160	
Lys	Asp	Val	Tyr	Lys	Asn	Arg	Ser	Ile	Glu	Leu	Val	Gln	Gln	Gln	Asn	
				165					170				175			
Val	Gln	Leu	Ser	Leu	Thr	Glu	Ala	Thr	Glu	Lys	Ala	Lys	Gln	Glu	Phe	
			180					185					190			
Glu	Lys	Ala	Gly	Lys	Asp	Phe	Leu	Val	Glu	Thr	Ile	Lys	Leu	Gly	Lys	
		195					200					205				
Leu	Leu	Arg	Pro	Asn	His	Leu	Trp	Gly	Tyr	Tyr	Leu	Phe	Pro	Asp	Cys	
	210					215					220					
Tyr	Asn	His	His	Tyr	Lys	Lys	Pro	Gly	Tyr	Asn	Gly	Ser	Cys	Phe	Asn	
225					230					235					240	
Val	Glu	Ile	Lys	Arg	Asn	Asp	Asp	Leu	Ser	Trp	Leu	Trp	Asn	Glu	Ser	
				245					250					255		
Thr	Ala	Leu	Tyr	Pro	Ser	Ile	Tyr	Leu	Asn	Thr	Gln	Gln	Ser	Pro	Val	
			260					265					270			
Ala	Ala	Thr	Leu	Tyr	Val	Arg	Asn	Arg	Val	Arg	Glu	Ala	Ile	Arg	Val	
		275					280					285				
Ser	Lys	Ile	Pro	Asp	Ala	Lys	Ser	Pro	Leu	Pro	Val	Phe	Ala	Tyr	Thr	
	290					295					300					
Arg	Ile	Val	Phe	Thr	Asp	Gln	Val	Leu	Lys	Phe	Leu	Ser	Gln	Asp	Glu	
305					310					315					320	

3108SEQPC1

Leu Val Tyr Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile
 325 330 335
 Val Ile Trp Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu
 340 345 350
 Leu Leu Asp Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn
 355 360 365
 Val Thr Leu Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln
 370 375 380
 Gly Val Cys Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu
 385 390 395 400
 Asn Pro Asp Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr
 405 410 415
 Val Arg Gly Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys
 420 425 430
 Phe Tyr Cys Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp
 435 440 445
 Val Lys
 450

<210> 135

<211> 508

<212> PRT

<213> Homo sapiens

<220>

<223> PH20 precursor 1-508

<400> 135

Met Gly Val Leu Lys Phe Lys His Ile Phe Phe Arg Ser Phe Val Lys
 1 5 10 15
 Ser Ser Gly Val Ser Gln Ile Val Phe Thr Phe Leu Leu Ile Pro Cys
 20 25 30
 Cys Leu Thr Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro
 35 40 45
 Phe Leu Trp Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe
 50 55 60
 Asp Glu Pro Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg
 65 70 75 80
 Ile Asn Ala Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu
 85 90 95
 Gly Tyr Tyr Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly
 100 105 110
 Gly Ile Pro Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys
 115 120 125
 Lys Asp Ile Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val
 130 135 140
 Ile Asp Trp Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro
 145 150 155 160
 Lys Asp Val Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn
 165 170 175
 Val Gln Leu Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe
 180 185 190
 Glu Lys Ala Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys
 195 200 205
 Leu Leu Arg Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys
 210 215 220
 Tyr Asn His His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn
 225 230 235 240
 Val Glu Ile Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser
 245 250 255
 Thr Ala Leu Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val
 260 265 270
 Ala Ala Thr Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val
 275 280 285
 Ser Lys Ile Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr
 290 295 300
 Arg Ile Val Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu

3108SEQPC1

305	Leu	Val	Tyr	Thr	Phe	Gly	Glu	Thr	Val	Ala	Leu	Gly	Ala	Ser	Gly	Ile
					325					330					335	
	Val	Ile	Trp	Gly	Thr	Leu	Ser	Ile	Met	Arg	Ser	Met	Lys	Ser	Cys	Leu
				340					345					350		
	Leu	Leu	Asp	Asn	Tyr	Met	Glu	Thr	Ile	Leu	Asn	Pro	Tyr	Ile	Ile	Asn
			355					360					365			
	Val	Thr	Leu	Ala	Ala	Lys	Met	Cys	Ser	Gln	Val	Leu	Cys	Gln	Glu	Gln
		370					375					380				
	Gly	Val	Cys	Ile	Arg	Lys	Asn	Trp	Asn	Ser	Ser	Asp	Tyr	Leu	His	Leu
		385				390					395					400
	Asn	Pro	Asp	Asn	Phe	Ala	Ile	Gln	Leu	Glu	Lys	Gly	Gly	Lys	Phe	Thr
				405						410					415	
	Val	Arg	Gly	Lys	Pro	Thr	Leu	Glu	Asp	Leu	Glu	Gln	Phe	Ser	Glu	Lys
			420						425					430		
	Phe	Tyr	Cys	Ser	Cys	Tyr	Ser	Thr	Leu	Ser	Cys	Lys	Glu	Lys	Ala	Asp
			435					440					445			
	Val	Lys	Asp	Thr	Asp	Ala	Val	Asp	Val	Cys	Ile	Ala	Asp	Gly	Val	Cys
		450					455					460				
	Ile	Asp	Ala	Phe	Leu	Lys	Pro	Pro	Met	Glu	Thr	Glu	Glu	Pro	Gln	Ile
		465				470					475					480
	Phe	Tyr	Asn	Ala	Ser	Pro	Ser	Thr	Leu	Ser	Ala	Thr	Met	Phe	Ile	Val
				485						490					495	
	Ser	Ile	Leu	Phe	Leu	Ile	Ile	Ser	Ser	Val	Ala	Ser				
			500						505							

<210> 136
 <211> 506
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PH20 precursor 1-506

<400> 136

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

3108SEQPC1

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

<210> 137

<211> 504

<212> PRT

<213> Homo sapiens

<220>

<223> PH20 precursor 1-504

<400> 137

Met Gly Val Leu Lys Phe Lys His Ile Phe Phe Arg Ser Phe Val Lys
 1 5 10 15
 Ser Ser Gly Val Ser Gln Ile Val Phe Thr Phe Leu Leu Ile Pro Cys
 20 25 30
 Cys Leu Thr Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro
 35 40 45
 Phe Leu Trp Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe
 50 55 60
 Asp Glu Pro Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg
 65 70 75 80
 Ile Asn Ala Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu
 85 90 95
 Gly Tyr Tyr Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly
 100 105 110
 Gly Ile Pro Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys
 115 120 125
 Lys Asp Ile Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val
 130 135 140
 Ile Asp Trp Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro
 145 150 155 160
 Lys Asp Val Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn
 165 170 175
 Val Gln Leu Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe
 180 185 190
 Glu Lys Ala Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys
 Page 159

3108SEQPC1

```

      195              200              205
Leu Leu Arg Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys
 210 215 220
Tyr Asn His His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn
 225 230 235 240
Val Glu Ile Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser
 245 250 255
Thr Ala Leu Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val
 260 265 270
Ala Ala Thr Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val
 275 280 285
Ser Lys Ile Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr
 290 295 300
Arg Ile Val Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu
 305 310 315 320
Leu Val Tyr Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile
 325 330 335
Val Ile Trp Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu
 340 345 350
Leu Leu Asp Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn
 355 360 365
Val Thr Leu Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln
 370 375 380
Gly Val Cys Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu
 385 390 395 400
Asn Pro Asp Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr
 405 410 415
Val Arg Gly Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys
 420 425 430
Phe Tyr Cys Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp
 435 440 445
Val Lys Asp Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys
 450 455 460
Ile Asp Ala Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile
 465 470 475 480
Phe Tyr Asn Ala Ser Pro Ser Thr Leu Ser Ala Thr Met Phe Ile Val
 485 490 495
Ser Ile Leu Phe Leu Ile Ile Ser
      500

```

<210> 138

<211> 502

<212> PRT

<213> Homo sapiens

<220>

<223> PH20 precursor 1-502

<400> 138

```

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

```

3108SEQPC1

Ile Asp Trp Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro
 145 150 155 160
 Lys Asp Val Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn
 165 170 175
 Val Gln Leu Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe
 180 185 190
 Glu Lys Ala Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys
 195 200 205
 Leu Leu Arg Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys
 210 215 220
 Tyr Asn His His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn
 225 230 235 240
 Val Glu Ile Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser
 245 250 255
 Thr Ala Leu Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val
 260 265 270
 Ala Ala Thr Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val
 275 280 285
 Ser Lys Ile Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr
 290 295 300
 Arg Ile Val Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu
 305 310 315 320
 Leu Val Tyr Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile
 325 330 335
 Val Ile Trp Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu
 340 345 350
 Leu Leu Asp Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn
 355 360 365
 Val Thr Leu Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln
 370 375 380
 Gly Val Cys Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu
 385 390 395 400
 Asn Pro Asp Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr
 405 410 415
 Val Arg Gly Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys
 420 425 430
 Phe Tyr Cys Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp
 435 440 445
 Val Lys Asp Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys
 450 455 460
 Ile Asp Ala Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile
 465 470 475 480
 Phe Tyr Asn Ala Ser Pro Ser Thr Leu Ser Ala Thr Met Phe Ile Val
 485 490 495
 Ser Ile Leu Phe Leu Ile
 500

<210> 139

<211> 500

<212> PRT

<213> Homo sapiens

<220>

<223> PH20 precursor 1-500

<400> 139

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

3108SEQPC1

Cys Leu Thr Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro
 35 40 45
 Phe Leu Trp Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe
 50 55 60
 Asp Glu Pro Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg
 65 70 75 80
 Ile Asn Ala Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu
 85 90 95
 Gly Tyr Tyr Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly
 100 105 110
 Gly Ile Pro Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys
 115 120 125
 Lys Asp Ile Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val
 130 135 140
 Ile Asp Trp Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro
 145 150 155 160
 Lys Asp Val Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn
 165 170 175
 Val Gln Leu Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe
 180 185 190
 Glu Lys Ala Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys
 195 200 205
 Leu Leu Arg Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys
 210 215 220
 Tyr Asn His His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn
 225 230 235 240
 Val Glu Ile Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser
 245 250 255
 Thr Ala Leu Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val
 260 265 270
 Ala Ala Thr Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val
 275 280 285
 Ser Lys Ile Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr
 290 295 300
 Arg Ile Val Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu
 305 310 315 320
 Leu Val Tyr Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile
 325 330 335
 Val Ile Trp Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu
 340 345 350
 Leu Leu Asp Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn
 355 360 365
 Val Thr Leu Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln
 370 375 380
 Gly Val Cys Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu
 385 390 395 400
 Asn Pro Asp Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr
 405 410 415
 Val Arg Gly Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys
 420 425 430
 Phe Tyr Cys Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp
 435 440 445
 Val Lys Asp Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys
 450 455 460
 Ile Asp Ala Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile
 465 470 475 480
 Phe Tyr Asn Ala Ser Pro Ser Thr Leu Ser Ala Thr Met Phe Ile Val
 485 490 495
 Ser Ile

<210> 141

<211> 496

<212> PRT

<213> Homo sapiens

<220>

<223> PH20 precursor 1-496

<400> 141

```

Met Gly Val Leu Lys Phe Lys His Ile Phe Phe Arg Ser Phe Val Lys
 1      5      10      15
Ser Ser Gly Val Ser Gln Ile Val Phe Thr Phe Leu Leu Ile Pro Cys
 20      25      30
Cys Leu Thr Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro
 35      40      45
Phe Leu Trp Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe
 50      55      60
Asp Glu Pro Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg
 65      70      75      80
Ile Asn Ala Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu
 85      90      95
Gly Tyr Tyr Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly
100      105      110
Gly Ile Pro Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys
115      120      125
Lys Asp Ile Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val
130      135      140
Ile Asp Trp Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro
145      150      155      160
Lys Asp Val Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn
165      170      175
Val Gln Leu Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe
180      185      190
Glu Lys Ala Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys
195      200      205
Leu Leu Arg Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys
210      215      220
Tyr Asn His His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn
225      230      235      240
Val Glu Ile Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser
245      250      255
Thr Ala Leu Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val
260      265      270
Ala Ala Thr Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val
275      280      285
Ser Lys Ile Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr
290      295      300
Arg Ile Val Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu
305      310      315      320
Leu Val Tyr Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile
325      330      335
Val Ile Trp Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu
340      345      350
Leu Leu Asp Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn
355      360      365
Val Thr Leu Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln
370      375      380
Gly Val Cys Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu
385      390      395      400
Asn Pro Asp Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr
405      410      415
Val Arg Gly Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys
420      425      430
Phe Tyr Cys Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp
435      440      445
Val Lys Asp Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys
450      455      460
Ile Asp Ala Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile
465      470      475      480
Phe Tyr Asn Ala Ser Pro Ser Thr Leu Ser Ala Thr Met Phe Ile Val
485      490      495

```

<210> 142

3108SEQPC1

<211> 494

<212> PRT

<213> Homo sapiens

<220>

<223> PH20 precursor 1-494

<400> 142

```

Met Gly Val Leu Lys Phe Lys His Ile Phe Phe Arg Ser Phe Val Lys
 1      5      10      15
Ser Ser Gly Val Ser Gln Ile Val Phe Thr Phe Leu Leu Ile Pro Cys
      20      25      30
Cys Leu Thr Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro
      35      40      45
Phe Leu Trp Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe
      50      55      60
Asp Glu Pro Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg
65      70      75      80
Ile Asn Ala Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu
      85      90      95
Gly Tyr Tyr Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly
      100      105      110
Gly Ile Pro Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys
      115      120      125
Lys Asp Ile Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val
      130      135      140
Ile Asp Trp Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro
145      150      155      160
Lys Asp Val Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn
      165      170      175
Val Gln Leu Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe
      180      185      190
Glu Lys Ala Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys
      195      200      205
Leu Leu Arg Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys
210      215      220
Tyr Asn His His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn
225      230      235      240
Val Glu Ile Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser
      245      250      255
Thr Ala Leu Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val
      260      265      270
Ala Ala Thr Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val
      275      280      285
Ser Lys Ile Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr
290      295      300
Arg Ile Val Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu
305      310      315      320
Leu Val Tyr Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile
      325      330      335
Val Ile Trp Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu
      340      345      350
Leu Leu Asp Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn
      355      360      365
Val Thr Leu Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln
      370      375      380
Gly Val Cys Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu
385      390      395      400
Asn Pro Asp Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr
      405      410      415
Val Arg Gly Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys
      420      425      430
Phe Tyr Cys Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp
      435      440      445
Val Lys Asp Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys
      450      455      460
Ile Asp Ala Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile
465      470      475      480

```

3108SEQPC1

Phe Tyr Asn Ala Ser Pro Ser Thr Leu Ser Ala Thr Met Phe
485 490

<210> 143

<211> 492

<212> PRT

<213> Homo sapiens

<220>

<223> PH20 precursor 1-492

<400> 143

Met Gly Val Leu Lys Phe Lys His Ile Phe Phe Arg Ser Phe Val Lys
1 5 10 15
Ser Ser Gly Val Ser Gln Ile Val Phe Thr Phe Leu Leu Ile Pro Cys
20 25 30
Cys Leu Thr Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro
35 40 45
Phe Leu Trp Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe
50 55 60
Asp Glu Pro Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg
65 70 75 80
Ile Asn Ala Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu
85 90 95
Gly Tyr Tyr Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly
100 105 110
Gly Ile Pro Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys
115 120 125
Lys Asp Ile Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val
130 135 140
Ile Asp Trp Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro
145 150 155 160
Lys Asp Val Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn
165 170 175
Val Gln Leu Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe
180 185 190
Glu Lys Ala Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys
195 200 205
Leu Leu Arg Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys
210 215 220
Tyr Asn His His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn
225 230 235 240
Val Glu Ile Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser
245 250 255
Thr Ala Leu Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val
260 265 270
Ala Ala Thr Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val
275 280 285
Ser Lys Ile Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr
290 295 300
Arg Ile Val Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu
305 310 315 320
Leu Val Tyr Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile
325 330 335
Val Ile Trp Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu
340 345 350
Leu Leu Asp Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn
355 360 365
Val Thr Leu Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln
370 375 380
Gly Val Cys Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu
385 390 395 400
Asn Pro Asp Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr
405 410 415
Val Arg Gly Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys
420 425 430
Phe Tyr Cys Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp

3108SEQPC1

435 440 445
 Val Lys Asp Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys
 450 455 460
 Ile Asp Ala Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile
 465 470 475 480
 Phe Tyr Asn Ala Ser Pro Ser Thr Leu Ser Ala Thr
 485 490

<210> 144

<211> 488

<212> PRT

<213> Homo sapiens

<220>

<223> PH20 precursor 1-488

<400> 144

Met Gly Val Leu Lys Phe Lys His Ile Phe Phe Arg Ser Phe Val Lys
 1 5 10 15
 Ser Ser Gly Val Ser Gln Ile Val Phe Thr Phe Leu Leu Ile Pro Cys
 20 25 30
 Cys Leu Thr Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro
 35 40 45
 Phe Leu Trp Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe
 50 55 60
 Asp Glu Pro Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg
 65 70 75 80
 Ile Asn Ala Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu
 85 90 95
 Gly Tyr Tyr Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly
 100 105 110
 Gly Ile Pro Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys
 115 120 125
 Lys Asp Ile Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val
 130 135 140
 Ile Asp Trp Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro
 145 150 155 160
 Lys Asp Val Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn
 165 170 175
 Val Gln Leu Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe
 180 185 190
 Glu Lys Ala Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys
 195 200 205
 Leu Leu Arg Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys
 210 215 220
 Tyr Asn His His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn
 225 230 235 240
 Val Glu Ile Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser
 245 250 255
 Thr Ala Leu Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val
 260 265 270
 Ala Ala Thr Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val
 275 280 285
 Ser Lys Ile Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr
 290 295 300
 Arg Ile Val Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu
 305 310 315 320
 Leu Val Tyr Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile
 325 330 335
 Val Ile Trp Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu
 340 345 350
 Leu Leu Asp Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn
 355 360 365
 Val Thr Leu Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln
 370 375 380
 Gly Val Cys Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu
 385 390 395 400

3108SEQPC1

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

<210> 145
 <211> 486
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PH20 precursor 1-486

<400> 145

Met	Gly	Val	Leu	Lys	Phe	Lys	His	Ile	Phe	Phe	Arg	Ser	Phe	Val	Lys
1				5					10					15	
Ser	Ser	Gly	Val	Ser	Gln	Ile	Val	Phe	Thr	Phe	Leu	Leu	Ile	Pro	Cys
			20					25					30		
Cys	Leu	Thr	Leu	Asn	Phe	Arg	Ala	Pro	Pro	Val	Ile	Pro	Asn	Val	Pro
		35					40					45			
Phe	Leu	Trp	Ala	Trp	Asn	Ala	Pro	Ser	Glu	Phe	Cys	Leu	Gly	Lys	Phe
	50				55					60					
Asp	Glu	Pro	Leu	Asp	Met	Ser	Leu	Phe	Ser	Phe	Ile	Gly	Ser	Pro	Arg
65					70					75					80
Ile	Asn	Ala	Thr	Gly	Gln	Gly	Val	Thr	Ile	Phe	Tyr	Val	Asp	Arg	Leu
			85						90				95		
Gly	Tyr	Tyr	Pro	Tyr	Ile	Asp	Ser	Ile	Thr	Gly	Val	Thr	Val	Asn	Gly
			100					105					110		
Gly	Ile	Pro	Gln	Lys	Ile	Ser	Leu	Gln	Asp	His	Leu	Asp	Lys	Ala	Lys
		115					120					125			
Lys	Asp	Ile	Thr	Phe	Tyr	Met	Pro	Val	Asp	Asn	Leu	Gly	Met	Ala	Val
	130					135					140				
Ile	Asp	Trp	Glu	Glu	Trp	Arg	Pro	Thr	Trp	Ala	Arg	Asn	Trp	Lys	Pro
145					150					155					160
Lys	Asp	Val	Tyr	Lys	Asn	Arg	Ser	Ile	Glu	Leu	Val	Gln	Gln	Gln	Asn
				165					170					175	
Val	Gln	Leu	Ser	Leu	Thr	Glu	Ala	Thr	Glu	Lys	Ala	Lys	Gln	Glu	Phe
			180					185					190		
Glu	Lys	Ala	Gly	Lys	Asp	Phe	Leu	Val	Glu	Thr	Ile	Lys	Leu	Gly	Lys
		195					200					205			
Leu	Leu	Arg	Pro	Asn	His	Leu	Trp	Gly	Tyr	Tyr	Leu	Phe	Pro	Asp	Cys
	210					215					220				
Tyr	Asn	His	His	Tyr	Lys	Lys	Pro	Gly	Tyr	Asn	Gly	Ser	Cys	Phe	Asn
225					230					235					240
Val	Glu	Ile	Lys	Arg	Asn	Asp	Asp	Leu	Ser	Trp	Leu	Trp	Asn	Glu	Ser
				245					250					255	
Thr	Ala	Leu	Tyr	Pro	Ser	Ile	Tyr	Leu	Asn	Thr	Gln	Gln	Ser	Pro	Val
			260					265					270		
Ala	Ala	Thr	Leu	Tyr	Val	Arg	Asn	Arg	Val	Arg	Glu	Ala	Ile	Arg	Val
		275					280					285			
Ser	Lys	Ile	Pro	Asp	Ala	Lys	Ser	Pro	Leu	Pro	Val	Phe	Ala	Tyr	Thr
	290					295					300				
Arg	Ile	Val	Phe	Thr	Asp	Gln	Val	Leu	Lys	Phe	Leu	Ser	Gln	Asp	Glu
305					310					315					320
Leu	Val	Tyr	Thr	Phe	Gly	Glu	Thr	Val	Ala	Leu	Gly	Ala	Ser	Gly	Ile
				325					330					335	
Val	Ile	Trp	Gly	Thr	Leu	Ser	Ile	Met	Arg	Ser	Met	Lys	Ser	Cys	Leu
		340						345					350		
Leu	Leu	Asp	Asn	Tyr	Met	Glu	Thr	Ile	Leu	Asn	Pro	Tyr	Ile	Ile	Asn

3108SEQPC1

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

<210> 146

<211> 472

<212> PRT

<213> Homo sapiens

<220>

<223> mature PH20 36-507

<400> 146

Leu	Asn	Phe	Arg	Ala	Pro	Pro	Val	Ile	Pro	Asn	Val	Pro	Phe	Leu	Trp
1				5					10					15	
Ala	Trp	Asn	Ala	Pro	Ser	Glu	Phe	Cys	Leu	Gly	Lys	Phe	Asp	Glu	Pro
			20					25				30			
Leu	Asp	Met	Ser	Leu	Phe	Ser	Phe	Ile	Gly	Ser	Pro	Arg	Ile	Asn	Ala
		35					40					45			
Thr	Gly	Gln	Gly	Val	Thr	Ile	Phe	Tyr	Val	Asp	Arg	Leu	Gly	Tyr	Tyr
	50					55				60					
Pro	Tyr	Ile	Asp	Ser	Ile	Thr	Gly	Val	Thr	Val	Asn	Gly	Gly	Ile	Pro
65					70				75					80	
Gln	Lys	Ile	Ser	Leu	Gln	Asp	His	Leu	Asp	Lys	Ala	Lys	Lys	Asp	Ile
			85						90					95	
Thr	Phe	Tyr	Met	Pro	Val	Asp	Asn	Leu	Gly	Met	Ala	Val	Ile	Asp	Trp
			100					105					110		
Glu	Glu	Trp	Arg	Pro	Thr	Trp	Ala	Arg	Asn	Trp	Lys	Pro	Lys	Asp	Val
		115					120					125			
Tyr	Lys	Asn	Arg	Ser	Ile	Glu	Leu	Val	Gln	Gln	Gln	Asn	Val	Gln	Leu
	130					135				140					
Ser	Leu	Thr	Glu	Ala	Thr	Glu	Lys	Ala	Lys	Gln	Glu	Phe	Glu	Lys	Ala
145					150					155					160
Gly	Lys	Asp	Phe	Leu	Val	Glu	Thr	Ile	Lys	Leu	Gly	Lys	Leu	Leu	Arg
			165						170					175	
Pro	Asn	His	Leu	Trp	Gly	Tyr	Tyr	Leu	Phe	Pro	Asp	Cys	Tyr	Asn	His
			180					185					190		
His	Tyr	Lys	Lys	Pro	Gly	Tyr	Asn	Gly	Ser	Cys	Phe	Asn	Val	Glu	Ile
		195					200					205			
Lys	Arg	Asn	Asp	Asp	Leu	Ser	Trp	Leu	Trp	Asn	Glu	Ser	Thr	Ala	Leu
	210					215					220				
Tyr	Pro	Ser	Ile	Tyr	Leu	Asn	Thr	Gln	Gln	Ser	Pro	Val	Ala	Ala	Thr
225					230					235					240
Leu	Tyr	Val	Arg	Asn	Arg	Val	Arg	Glu	Ala	Ile	Arg	Val	Ser	Lys	Ile
			245						250					255	
Pro	Asp	Ala	Lys	Ser	Pro	Leu	Pro	Val	Phe	Ala	Tyr	Thr	Arg	Ile	Val
		260						265					270		
Phe	Thr	Asp	Gln	Val	Leu	Lys	Phe	Leu	Ser	Gln	Asp	Glu	Leu	Val	Tyr
		275					280					285			
Thr	Phe	Gly	Glu	Thr	Val	Ala	Leu	Gly	Ala	Ser	Gly	Ile	Val	Ile	Trp
	290					295					300				
Gly	Thr	Leu	Ser	Ile	Met	Arg	Ser	Met	Lys	Ser	Cys	Leu	Leu	Leu	Asp
305					310					315					320

3108SEQPC1

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

<210> 147
 <211> 470
 <212> PRT
 <213> Homo sapiens

<220>
 <223> mature PH20 36-505

<400> 147
 Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1 5 10 15
 Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
 20 25 30
 Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
 35 40 45
 Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
 50 55 60
 Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
 65 70 75 80
 Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
 85 90 95
 Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
 100 105 110
 Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
 115 120 125
 Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
 130 135 140
 Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
 145 150 155 160
 Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
 165 170 175
 Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
 180 185 190
 His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
 195 200 205
 Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
 210 215 220
 Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
 225 230 235 240
 Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
 245 250 255
 Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
 260 265 270
 Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
 275 280 285
 Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp

3108SEQPC1

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

<210> 148

<211> 468

<212> PRT

<213> Homo sapiens

<220>

<223> mature PH20 36-503

<400> 148

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

3108SEQPC1

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

<210> 149

<211> 466

<212> PRT

<213> Homo sapiens

<220>

<223> mature PH20 36-501

<400> 149

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

3108SEQPC1

Pro	Asp	Ala	Lys	245	Ser	Pro	Leu	Pro	Val	250	Phe	Ala	Tyr	Thr	Arg	255	Ile	Val
Phe	Thr	Asp	260	Gln	Val	Leu	Lys	265	Phe	Leu	Ser	Gln	Asp	Glu	270	Leu	Val	Tyr
Thr	Phe	Gly	275	Glu	Thr	Val	Ala	280	Leu	Gly	Ala	Ser	Gly	Ile	Val	Ile	Trp	
Gly	Thr	Leu	Ser	Ile	Met	Arg	Ser	Met	Lys	Ser	Cys	Leu	Leu	Leu	Asp	300	320	
Asn	Tyr	Met	Glu	Thr	Ile	Leu	Asn	Pro	Tyr	Ile	Ile	Asn	Val	Thr	Leu	335	335	
Ala	Ala	Lys	Met	Cys	Ser	Gln	Val	Leu	Cys	Gln	Glu	Gln	Gly	Val	Cys	340	350	
Ile	Arg	Lys	Asn	Trp	Asn	Ser	Ser	Asp	Tyr	Leu	His	Leu	Asn	Pro	Asp	355	365	
Asn	Phe	Ala	Ile	Gln	Leu	Glu	Lys	Gly	Gly	Lys	Phe	Thr	Val	Arg	Gly	370	380	
Lys	Pro	Thr	Leu	Glu	Asp	Leu	Glu	Gln	Phe	Ser	Glu	Lys	Phe	Tyr	Cys	385	400	
Ser	Cys	Tyr	Ser	Thr	Leu	Ser	Cys	Lys	Glu	Lys	Ala	Asp	Val	Lys	Asp	405	415	
Thr	Asp	Ala	Val	Asp	Val	Cys	Ile	Ala	Asp	Gly	Val	Cys	Ile	Asp	Ala	420	430	
Phe	Leu	Lys	Pro	Pro	Met	Glu	Thr	Glu	Glu	Pro	Gln	Ile	Phe	Tyr	Asn	435	445	
Ala	Ser	Pro	Ser	Thr	Leu	Ser	Ala	Thr	Met	Phe	Ile	Val	Ser	Ile	Leu	450	460	
Phe	Leu															465		

<210> 150

<211> 464

<212> PRT

<213> Homo sapiens

<220>

<223> mature PH20 36-499

<400> 150

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

3108SEQPC1

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

<210> 151
 <211> 462
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PH20 36-497

<400> 151
 Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1 5 10 15
 Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
 20 25 30
 Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
 35 40 45
 Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
 50 55 60
 Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
 65 70 75 80
 Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
 85 90 95
 Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
 100 105 110
 Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
 115 120 125
 Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
 130 135 140
 Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
 145 150 155 160
 Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
 165 170 175
 Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
 180 185 190
 His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
 195 200 205
 Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu

3108SEQPC1

210	Tyr	Pro	Ser	Ile	Tyr	215	Leu	Asn	Thr	Gln	Gln	220	Ser	Pro	Val	Ala	Ala	Thr
225	Leu	Tyr	Val	Arg	Asn	230	Arg	Val	Arg	Glu	Ala	235	Ile	Arg	Val	Ser	Lys	Ile
					245		Pro	Leu	Pro	Val	Phe	250	Ala	Tyr	Thr	Arg	Ile	Val
	Phe	Thr	Asp	Gln	Val		Leu	Lys	Phe	Leu	Ser	265	Gln	Asp	Glu	Leu	Val	Tyr
	Thr	Phe	Gly	Glu	Thr	275	Val	Ala	Leu	Gly	Ala	280	Ser	Gly	Ile	Val	Ile	Trp
	Gly	Thr	Leu	Ser	Ile	290	Met	Arg	Ser	Met	Lys	300	Ser	Cys	Leu	Leu	Leu	Asp
305	Asn	Tyr	Met	Glu	Thr	310	Ile	Leu	Asn	Pro	Tyr	315	Ile	Ile	Asn	Val	Thr	Leu
	Ala	Ala	Lys	Met	Cys	325	Ser	Gln	Val	Leu	Cys	330	Gln	Glu	Gln	Gly	Val	Cys
	Ile	Arg	Lys	Asn	Trp	340	Asn	Ser	Ser	Asp	Tyr	345	Leu	His	Leu	Asn	Pro	Asp
	Asn	Phe	Ala	Ile	Gln	355	Leu	Glu	Lys	Gly	Gly	360	Lys	Phe	Thr	Val	Arg	Gly
	Lys	Pro	Thr	Leu	Glu	370	Asp	Leu	Glu	Gln	Phe	375	Ser	Glu	Lys	Phe	Tyr	Cys
385	Ser	Cys	Tyr	Ser	Thr	390	Leu	Ser	Cys	Lys	Glu	395	Lys	Ala	Asp	Val	Lys	Asp
	Thr	Asp	Ala	Val	Asp	405	Val	Cys	Ile	Ala	Asp	410	Gly	Val	Cys	Ile	Asp	Ala
	Phe	Leu	Lys	Pro	Pro	420	Met	Glu	Thr	Glu	Glu	425	Pro	Gln	Ile	Phe	Tyr	Asn
	Ala	Ser	Pro	Ser	Thr	435	Leu	Ser	Ala	Thr	Met	440	Phe	Ile	Val	Ser		
450						455						460						

<210> 152
 <211> 460
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PH20 36-495

<400> 152	Leu	Asn	Phe	Arg	Ala	Pro	Pro	Val	Ile	Pro	Asn	Val	Pro	Phe	Leu	Trp
1	Ala	Trp	Asn	Ala	Pro	Ser	Glu	Phe	Cys	Leu	Gly	Lys	Phe	Asp	Glu	Pro
	Leu	Asp	Met	Ser	Leu	Phe	Ser	Phe	Ile	Gly	Ser	Pro	Arg	Ile	Asn	Ala
	Thr	Gly	Gln	Gly	Val	Thr	Ile	Phe	Tyr	Val	Asp	Arg	Leu	Gly	Tyr	Tyr
	Pro	Tyr	Ile	Asp	Ser	Ile	Thr	Gly	Val	Thr	Val	Asn	Gly	Gly	Ile	Pro
65	Gln	Lys	Ile	Ser	Leu	Gln	Asp	His	Leu	Asp	Lys	Ala	Lys	Lys	Asp	Ile
	Thr	Phe	Tyr	Met	Pro	Val	Asp	Asn	Leu	Gly	Met	Ala	Val	Ile	Asp	Trp
	Glu	Glu	Trp	Arg	Pro	Thr	Trp	Ala	Arg	Asn	Trp	Lys	Pro	Lys	Asp	Val
	Tyr	Lys	Asn	Arg	Ser	Ile	Glu	Leu	Val	Gln	Gln	Gln	Asn	Val	Gln	Leu
130	Ser	Leu	Thr	Glu	Ala	Thr	Glu	Lys	Ala	Lys	Gln	Glu	Phe	Glu	Lys	Ala
145	Gly	Lys	Asp	Phe	Leu	Val	Glu	Thr	Ile	Lys	Leu	Gly	Lys	Leu	Leu	Arg
	Pro	Asn	His	Leu	Trp	Gly	Tyr	Tyr	Leu	Phe	Pro	Asp	Cys	Tyr	Asn	His
	His	Tyr	Lys	Lys	Pro	Gly	Tyr	Asn	Gly	Ser	Cys	Phe	Asn	Val	Glu	Ile
195																

3108SEQPC1

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

<210> 153
 <211> 458
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PH20 36-493

<400> 153
 Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1 5 10 15
 Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
 20 25 30
 Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
 35 40 45
 Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
 50 55 60
 Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
 65 70 75 80
 Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
 85 90 95
 Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
 100 105 110
 Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
 115 120 125
 Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
 130 135 140
 Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
 145 150 155 160
 Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
 165 170 175
 Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
 180 185 190
 His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile

3108SEQPC1

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

<210> 154

<211> 456

<212> PRT

<213> Homo sapiens

<220>

<223> PH20 36-491

<400> 154

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

3108SEQPC1

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

<210> 155

<211> 454

<212> PRT

<213> Homo sapiens

<220>

<223> PH20 36-489

<400> 155

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

3108SEQPC1

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

<210> 156

<211> 455

<212> PRT

<213> Homo sapiens

<220>

<223> PH20 36-490

<400> 156

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

3108SEQPC1

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

<210> 157
 <211> 452
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PH20 36-487

<400> 157
 Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1 5 10 15
 Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
 20 25 30
 Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
 35 40 45
 Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
 50 55 60
 Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
 65 70 75 80
 Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
 85 90 95
 Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
 100 105 110
 Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
 115 120 125
 Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
 130 135 140
 Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
 145 150 155 160
 Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg

3108SEQPC1

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

<210> 158
 <211> 450
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PH20 36-485

<400> 158

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

3108SEQPC1

Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
 165 170 175
 Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
 180 185 190
 His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
 195 200 205
 Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
 210 215 220
 Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
 225 230 235 240
 Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
 245 250 255
 Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
 260 265 270
 Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
 275 280 285
 Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
 290 295 300
 Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
 305 310 315 320
 Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
 325 330 335
 Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
 340 345 350
 Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
 355 360 365
 Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
 370 375 380
 Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
 385 390 395 400
 Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
 405 410 415
 Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala
 420 425 430
 Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile Phe Tyr Asn
 435 440 445
 Ala Ser
 450

<210> 159
 <211> 449
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PH20 36-484

<400> 159
 Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1 5 10 15
 Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
 20 25 30
 Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
 35 40 45
 Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
 50 55 60
 Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
 65 70 75 80
 Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
 85 90 95
 Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
 100 105 110
 Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
 115 120 125
 Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
 130 135 140
 Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala

3108SEQPC1

145	Gly	Lys	Asp	Phe	Leu	Val	Glu	Thr	Ile	Lys	Leu	Gly	Lys	Leu	Leu	Arg
	Pro	Asn	His	Leu	Trp	Gly	Tyr	Tyr	Leu	Phe	Pro	Asp	Cys	Tyr	Asn	His
	His	Tyr	Lys	Lys	Pro	Gly	Tyr	Asn	Gly	Ser	Cys	Phe	Asn	Val	Glu	Ile
	Lys	Arg	Asn	Asp	Asp	Leu	Ser	Trp	Leu	Trp	Asn	Glu	Ser	Thr	Ala	Leu
	Tyr	Pro	Ser	Ile	Tyr	Leu	Asn	Thr	Gln	Gln	Ser	Pro	Val	Ala	Ala	Thr
	Leu	Tyr	Val	Arg	Asn	Arg	Val	Arg	Glu	Ala	Ile	Arg	Val	Ser	Lys	Ile
	Pro	Asp	Ala	Lys	Ser	Pro	Leu	Pro	Val	Phe	Ala	Tyr	Thr	Arg	Ile	Val
	Phe	Thr	Asp	Gln	Val	Leu	Lys	Phe	Leu	Ser	Gln	Asp	Glu	Leu	Val	Tyr
	Thr	Phe	Gly	Glu	Thr	Val	Ala	Leu	Gly	Ala	Ser	Gly	Ile	Val	Ile	Trp
	Gly	Thr	Leu	Ser	Ile	Met	Arg	Ser	Met	Lys	Ser	Cys	Leu	Leu	Leu	Asp
	Asn	Tyr	Met	Glu	Thr	Ile	Leu	Asn	Pro	Tyr	Ile	Ile	Asn	Val	Thr	Leu
	Ala	Ala	Lys	Met	Cys	Ser	Gln	Val	Leu	Cys	Gln	Glu	Gln	Gly	Val	Cys
	Ile	Arg	Lys	Asn	Trp	Asn	Ser	Ser	Asp	Tyr	Leu	His	Leu	Asn	Pro	Asp
	Asn	Phe	Ala	Ile	Gln	Leu	Glu	Lys	Gly	Gly	Lys	Phe	Thr	Val	Arg	Gly
	Lys	Pro	Thr	Leu	Glu	Asp	Leu	Glu	Gln	Phe	Ser	Glu	Lys	Phe	Tyr	Cys
	Ser	Cys	Tyr	Ser	Thr	Leu	Ser	Cys	Lys	Glu	Lys	Ala	Asp	Val	Lys	Asp
	Thr	Asp	Ala	Val	Asp	Val	Cys	Ile	Ala	Asp	Gly	Val	Cys	Ile	Asp	Ala
	Phe	Leu	Lys	Pro	Pro	Met	Glu	Thr	Glu	Glu	Pro	Gln	Ile	Phe	Tyr	Asn
	Ala															

<210> 160
 <211> 441
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PH20 36-476

<400> 160

1	Leu	Asn	Phe	Arg	Ala	Pro	Pro	Val	Ile	Pro	Asn	Val	Pro	Phe	Leu	Trp
	Ala	Trp	Asn	Ala	Pro	Ser	Glu	Phe	Cys	Leu	Gly	Lys	Phe	Asp	Glu	Pro
	Leu	Asp	Met	Ser	Leu	Phe	Ser	Phe	Ile	Gly	Ser	Pro	Arg	Ile	Asn	Ala
	Thr	Gly	Gln	Gly	Val	Thr	Ile	Phe	Tyr	Val	Asp	Arg	Leu	Gly	Tyr	Tyr
	Pro	Tyr	Ile	Asp	Ser	Ile	Thr	Gly	Val	Thr	Val	Asn	Gly	Gly	Ile	Pro
	Gln	Lys	Ile	Ser	Leu	Gln	Asp	His	Leu	Asp	Lys	Ala	Lys	Lys	Asp	Ile
	Thr	Phe	Tyr	Met	Pro	Val	Asp	Asn	Leu	Gly	Met	Ala	Val	Ile	Asp	Trp
	Glu	Glu	Trp	Arg	Pro	Thr	Trp	Ala	Arg	Asn	Trp	Lys	Pro	Lys	Asp	Val
	Tyr	Lys	Asn	Arg	Ser	Ile	Glu	Leu	Val	Gln	Gln	Gln	Asn	Val	Gln	Leu

3108SEQPC1

Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
 145 150 155 160
 Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
 165 170 175
 Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
 180 185 190
 His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
 195 200 205
 Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
 210 215 220
 Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
 225 230 235 240
 Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
 245 250 255
 Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
 260 265 270
 Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
 275 280 285
 Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
 290 295 300
 Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
 305 310 315 320
 Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
 325 330 335
 Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
 340 345 350
 Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
 355 360 365
 Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
 370 375 380
 Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
 385 390 395 400
 Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
 405 410 415
 Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala
 420 425 430
 Phe Leu Lys Pro Pro Met Glu Thr Glu
 435 440

<210> 161

<211> 440

<212> PRT

<213> Homo sapiens

<220>

<223> PH20 36-475

<400> 161

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

3108SEQPC1

145				150				155				160	
Gly	Lys	Asp	Phe	Leu	Val	Glu	Thr	Ile	Lys	Leu	Gly	Lys	Leu
				165					170				175
Pro	Asn	His	Leu	Trp	Gly	Tyr	Tyr	Leu	Phe	Pro	Asp	Cys	Tyr
			180					185				190	Asn
His	Tyr	Lys	Lys	Pro	Gly	Tyr	Asn	Gly	Ser	Cys	Phe	Asn	Val
		195					200					205	Glu
Lys	Arg	Asn	Asp	Asp	Leu	Ser	Trp	Leu	Trp	Asn	Glu	Ser	Thr
		210					215				220		Ala
Tyr	Pro	Ser	Ile	Tyr	Leu	Asn	Thr	Gln	Gln	Ser	Pro	Val	Ala
225					230					235			Ala
Leu	Tyr	Val	Arg	Asn	Arg	Val	Arg	Glu	Ala	Ile	Arg	Val	Ser
				245					250				Lys
Pro	Asp	Ala	Lys	Ser	Pro	Leu	Pro	Val	Phe	Ala	Tyr	Thr	Arg
			260					265					Ile
Phe	Thr	Asp	Gln	Val	Leu	Lys	Phe	Leu	Ser	Gln	Asp	Glu	Leu
		275					280					285	Val
Thr	Phe	Gly	Glu	Thr	Val	Ala	Leu	Gly	Ala	Ser	Gly	Ile	Val
		290				295					300		Ile
Gly	Thr	Leu	Ser	Ile	Met	Arg	Ser	Met	Lys	Ser	Cys	Leu	Leu
305					310								Asp
Asn	Tyr	Met	Glu	Thr	Ile	Leu	Asn	Pro	Tyr	Ile	Ile	Asn	Val
				325					330				Thr
Ala	Ala	Lys	Met	Cys	Ser	Gln	Val	Leu	Cys	Gln	Glu	Gln	Gly
			340					345					Val
Ile	Arg	Lys	Asn	Trp	Asn	Ser	Ser	Asp	Tyr	Leu	His	Leu	Asn
		355					360					365	Pro
Asn	Phe	Ala	Ile	Gln	Leu	Glu	Lys	Gly	Gly	Lys	Phe	Thr	Val
		370				375					380		Arg
Lys	Pro	Thr	Leu	Glu	Asp	Leu	Glu	Gln	Phe	Ser	Glu	Lys	Phe
385					390					395			Tyr
Ser	Cys	Tyr	Ser	Thr	Leu	Ser	Cys	Lys	Glu	Lys	Ala	Asp	Val
				405					410				Lys
Thr	Asp	Ala	Val	Asp	Val	Cys	Ile	Ala	Asp	Gly	Val	Cys	Ile
			420					425					Asp
Phe	Leu	Lys	Pro	Pro	Met	Glu	Thr						Ala
		435					440						160

<210> 162
 <211> 439
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PH20 36-474

<400> 162

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

3108SEQPC1

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

<210> 163
 <211> 438
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PH20 36-473

<400> 163

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

3108SEQPC1

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

<210> 164
 <211> 437
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PH20 36-472

<400> 164

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

3108SEQPC1

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

<210> 165
<211> 436
<212> PRT
<213> Homo sapiens

<220>
<223> PH20 36-471

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

3108SEQPC1

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

<210> 166

<211> 435

<212> PRT

<213> Homo sapiens

<220>

<223> PH20 36-470

<400> 166

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

3108SEQPC1

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

<210> 167

<211> 434

<212> PRT

<213> Homo sapiens

<220>

<223> PH20 36-469

<400> 167

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

3108SEQPC1

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

<210> 168

<211> 433

<212> PRT

<213> Homo sapiens

<220>

<223> PH20 36-468

<400> 168

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

3108SEQPC1

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

<210> 169

<211> 431

<212> PRT

<213> Homo sapiens

<220>

<223> PH20 36-466

<400> 169

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

3108SEQPC1

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

<210> 170

<211> 430

<212> PRT

<213> Homo sapiens

<220>

<223> PH20 36-465

<400> 170

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

3108SEQPC1

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

<210> 171
 <211> 429
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PH20 36-464

<400> 171
 Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1 5 10 15
 Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
 20 25 30
 Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
 35 40 45
 Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
 50 55 60
 Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
 65 70 75 80
 Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
 85 90 95
 Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
 100 105 110
 Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
 115 120 125
 Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
 130 135 140
 Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
 145 150 155 160
 Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
 165 170 175
 Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
 180 185 190
 His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
 195 200 205
 Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
 210 215 220
 Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
 225 230 235 240
 Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
 245 250 255
 Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val

3108SEQPC1

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

<210> 172

<211> 427

<212> PRT

<213> Homo sapiens

<220>

<223> PH20 36-462

<400> 172

1 5 10 15
 Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 20 25 30
 Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
 35 40 45
 Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
 50 55 60
 Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
 65 70 75 80
 Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
 85 90 95
 Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
 100 105 110
 Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
 115 120 125
 Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
 130 135 140
 Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
 145 150 155 160
 Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
 165 170 175
 Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
 180 185 190
 Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
 195 200 205
 His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
 210 215 220
 Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
 225 230 235 240
 Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
 245 250 255
 Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
 260 265 270
 Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
 275 280 285
 Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr

3108SEQPC1

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

<210> 173

<211> 425

<212> PRT

<213> Homo sapiens

<220>

<223> PH20 36-460

<400> 173

Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1 5 10 15
 Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
 20 25 30
 Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
 35 40 45
 Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
 50 55 60
 Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
 65 70 75 80
 Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
 85 90 95
 Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
 100 105 110
 Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
 115 120 125
 Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
 130 135 140
 Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
 145 150 155 160
 Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
 165 170 175
 Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
 180 185 190
 His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
 195 200 205
 Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
 210 215 220
 Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
 225 230 235 240
 Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
 245 250 255
 Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
 260 265 270
 Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
 275 280 285
 Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
 290 295 300
 Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp

3108SEQPC1

305	Asn	Tyr	Met	Glu	Thr	Ile	Leu	Asn	Pro	Tyr	Ile	Ile	Asn	Val	Thr	Leu
					325					330					335	
Ala	Ala	Lys	Met	Cys	Ser	Gln	Val	Leu	Cys	Gln	Glu	Gln	Gly	Val	Cys	
			340					345					350			
Ile	Arg	Lys	Asn	Trp	Asn	Ser	Ser	Asp	Tyr	Leu	His	Leu	Asn	Pro	Asp	
		355					360					365				
Asn	Phe	Ala	Ile	Gln	Leu	Glu	Lys	Gly	Gly	Lys	Phe	Thr	Val	Arg	Gly	
	370					375					380					
Lys	Pro	Thr	Leu	Glu	Asp	Leu	Glu	Gln	Phe	Ser	Glu	Lys	Phe	Tyr	Cys	
385					390					395					400	
Ser	Cys	Tyr	Ser	Thr	Leu	Ser	Cys	Lys	Glu	Lys	Ala	Asp	Val	Lys	Asp	
			405						410					415		
Thr	Asp	Ala	Val	Asp	Val	Cys	Ile	Ala								
			420					425								

<210> 174
 <211> 423
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PH20 36-458

<400> 174

Leu	Asn	Phe	Arg	Ala	Pro	Pro	Val	Ile	Pro	Asn	Val	Pro	Phe	Leu	Trp
1				5					10					15	
Ala	Trp	Asn	Ala	Pro	Ser	Glu	Phe	Cys	Leu	Gly	Lys	Phe	Asp	Glu	Pro
			20					25					30		
Leu	Asp	Met	Ser	Leu	Phe	Ser	Phe	Ile	Gly	Ser	Pro	Arg	Ile	Asn	Ala
		35					40					45			
Thr	Gly	Gln	Gly	Val	Thr	Ile	Phe	Tyr	Val	Asp	Arg	Leu	Gly	Tyr	Tyr
	50					55				60					
Pro	Tyr	Ile	Asp	Ser	Ile	Thr	Gly	Val	Thr	Val	Asn	Gly	Gly	Ile	Pro
65					70					75				80	
Gln	Lys	Ile	Ser	Leu	Gln	Asp	His	Leu	Asp	Lys	Ala	Lys	Lys	Asp	Ile
			85						90					95	
Thr	Phe	Tyr	Met	Pro	Val	Asp	Asn	Leu	Gly	Met	Ala	Val	Ile	Asp	Trp
			100					105					110		
Glu	Glu	Trp	Arg	Pro	Thr	Trp	Ala	Arg	Asn	Trp	Lys	Pro	Lys	Asp	Val
		115					120					125			
Tyr	Lys	Asn	Arg	Ser	Ile	Glu	Leu	Val	Gln	Gln	Gln	Asn	Val	Gln	Leu
	130					135				140					
Ser	Leu	Thr	Glu	Ala	Thr	Glu	Lys	Ala	Lys	Gln	Glu	Phe	Glu	Lys	Ala
145					150					155					160
Gly	Lys	Asp	Phe	Leu	Val	Glu	Thr	Ile	Lys	Leu	Gly	Lys	Leu	Leu	Arg
				165					170					175	
Pro	Asn	His	Leu	Trp	Gly	Tyr	Tyr	Leu	Phe	Pro	Asp	Cys	Tyr	Asn	His
			180					185					190		
His	Tyr	Lys	Lys	Pro	Gly	Tyr	Asn	Gly	Ser	Cys	Phe	Asn	Val	Glu	Ile
	195						200					205			
Lys	Arg	Asn	Asp	Asp	Leu	Ser	Trp	Leu	Trp	Asn	Glu	Ser	Thr	Ala	Leu
	210					215					220				
Tyr	Pro	Ser	Ile	Tyr	Leu	Asn	Thr	Gln	Gln	Ser	Pro	Val	Ala	Ala	Thr
225					230				235					240	
Leu	Tyr	Val	Arg	Asn	Arg	Val	Arg	Glu	Ala	Ile	Arg	Val	Ser	Lys	Ile
				245					250					255	
Pro	Asp	Ala	Lys	Ser	Pro	Leu	Pro	Val	Phe	Ala	Tyr	Thr	Arg	Ile	Val
			260					265					270		
Phe	Thr	Asp	Gln	Val	Leu	Lys	Phe	Leu	Ser	Gln	Asp	Glu	Leu	Val	Tyr
		275					280					285			
Thr	Phe	Gly	Glu	Thr	Val	Ala	Leu	Gly	Ala	Ser	Gly	Ile	Val	Ile	Trp
	290					295					300				
Gly	Thr	Leu	Ser	Ile	Met	Arg	Ser	Met	Lys	Ser	Cys	Leu	Leu	Leu	Asp
305					310					315					320
Asn	Tyr	Met	Glu	Thr	Ile	Leu	Asn	Pro	Tyr	Ile	Ile	Asn	Val	Thr	Leu
				325					330					335	

3108SEQPC1

Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
 340 345 350
 Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
 355 360 365
 Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
 370 375 380
 Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
 385 390 395 400
 Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
 405 410 415
 Thr Asp Ala Val Asp Val Cys
 420

<210> 175
 <211> 421
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PH20 36-456

<400> 175
 Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1 5 10 15
 Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
 20 25 30
 Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
 35 40 45
 Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
 50 55 60
 Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
 65 70 75 80
 Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
 85 90 95
 Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
 100 105 110
 Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
 115 120 125
 Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
 130 135 140
 Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
 145 150 155 160
 Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
 165 170 175
 Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
 180 185 190
 His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
 195 200 205
 Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
 210 215 220
 Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
 225 230 235 240
 Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
 245 250 255
 Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
 260 265 270
 Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
 275 280 285
 Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
 290 295 300
 Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
 305 310 315 320
 Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
 325 330 335
 Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
 340 345 350
 Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
 Page 198

3108SEQPC1

355 360 365
 Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
 370 375 380
 Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
 385 390 395 400
 Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
 405 410 415
 Thr Asp Ala Val Asp
 420

<210> 176

<211> 419

<212> PRT

<213> Homo sapiens

<220>

<223> PH20 36-454

<400> 176

Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1 5 10 15
 Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
 20 25 30
 Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
 35 40 45
 Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
 50 55 60
 Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
 65 70 75 80
 Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
 85 90 95
 Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
 100 105 110
 Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
 115 120 125
 Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
 130 135 140
 Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
 145 150 155 160
 Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
 165 170 175
 Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
 180 185 190
 His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
 195 200 205
 Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
 210 215 220
 Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
 225 230 235 240
 Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
 245 250 255
 Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
 260 265 270
 Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
 275 280 285
 Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
 290 295 300
 Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
 305 310 315 320
 Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
 325 330 335
 Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
 340 345 350
 Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
 355 360 365
 Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
 370 375 380

3108SEQPC1

Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
 385 390 395 400
 Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
 405 410 415
 Thr Asp Ala

<210> 177
 <211> 417
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PH20 36-452

<400> 177
 Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1 5 10 15
 Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
 20 25 30
 Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
 35 40 45
 Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
 50 55 60
 Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
 65 70 75 80
 Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
 85 90 95
 Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
 100 105 110
 Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
 115 120 125
 Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
 130 135 140
 Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
 145 150 155 160
 Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
 165 170 175
 Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
 180 185 190
 His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
 195 200 205
 Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
 210 215 220
 Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
 225 230 235 240
 Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
 245 250 255
 Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
 260 265 270
 Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
 275 280 285
 Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
 290 295 300
 Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
 305 310 315 320
 Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
 325 330 335
 Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
 340 345 350
 Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
 355 360 365
 Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
 370 375 380
 Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
 385 390 395 400
 Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp

Thr 405 3108SEQPC1 410 415
 <210> 178
 <211> 415
 <212> PRT
 <213> Homo sapiens
 <220>
 <223> PH20 36-450
 <400> 178
 Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1 5 10 15
 Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
 20 25 30
 Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
 35 40 45
 Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
 50 55 60
 Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
 65 70 75 80
 Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
 85 90 95
 Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
 100 105 110
 Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
 115 120 125
 Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
 130 135 140
 Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
 145 150 155 160
 Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
 165 170 175
 Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
 180 185 190
 His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
 195 200 205
 Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
 210 215 220
 Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
 225 230 235 240
 Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
 245 250 255
 Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
 260 265 270
 Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
 275 280 285
 Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
 290 295 300
 Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
 305 310 315 320
 Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
 325 330 335
 Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
 340 345 350
 Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
 355 360 365
 Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
 370 375 380
 Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
 385 390 395 400
 Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys
 405 410 415

3108SEQPC1

<210> 179
 <211> 473
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PH20 36-508

<400> 179

Leu	Asn	Phe	Arg	Ala	Pro	Pro	Val	Ile	Pro	Asn	Val	Pro	Phe	Leu	Trp
1				5					10					15	
Ala	Trp	Asn	Ala	Pro	Ser	Glu	Phe	Cys	Leu	Gly	Lys	Phe	Asp	Glu	Pro
			20					25					30		
Leu	Asp	Met	Ser	Leu	Phe	Ser	Phe	Ile	Gly	Ser	Pro	Arg	Ile	Asn	Ala
		35					40					45			
Thr	Gly	Gln	Gly	Val	Thr	Ile	Phe	Tyr	Val	Asp	Arg	Leu	Gly	Tyr	Tyr
	50					55					60				
Pro	Tyr	Ile	Asp	Ser	Ile	Thr	Gly	Val	Thr	Val	Asn	Gly	Gly	Ile	Pro
65					70					75					80
Gln	Lys	Ile	Ser	Leu	Gln	Asp	His	Leu	Asp	Lys	Ala	Lys	Lys	Asp	Ile
				85					90					95	
Thr	Phe	Tyr	Met	Pro	Val	Asp	Asn	Leu	Gly	Met	Ala	Val	Ile	Asp	Trp
			100					105					110		
Glu	Glu	Trp	Arg	Pro	Thr	Trp	Ala	Arg	Asn	Trp	Lys	Pro	Lys	Asp	Val
		115					120					125			
Tyr	Lys	Asn	Arg	Ser	Ile	Glu	Leu	Val	Gln	Gln	Gln	Asn	Val	Gln	Leu
	130					135					140				
Ser	Leu	Thr	Glu	Ala	Thr	Glu	Lys	Ala	Lys	Gln	Glu	Phe	Glu	Lys	Ala
145					150					155					160
Gly	Lys	Asp	Phe	Leu	Val	Glu	Thr	Ile	Lys	Leu	Gly	Lys	Leu	Leu	Arg
				165					170					175	
Pro	Asn	His	Leu	Trp	Gly	Tyr	Tyr	Leu	Phe	Pro	Asp	Cys	Tyr	Asn	His
			180					185					190		
His	Tyr	Lys	Lys	Pro	Gly	Tyr	Asn	Gly	Ser	Cys	Phe	Asn	Val	Glu	Ile
	195						200					205			
Lys	Arg	Asn	Asp	Asp	Leu	Ser	Trp	Leu	Trp	Asn	Glu	Ser	Thr	Ala	Leu
	210					215					220				
Tyr	Pro	Ser	Ile	Tyr	Leu	Asn	Thr	Gln	Gln	Ser	Pro	Val	Ala	Ala	Thr
225					230					235					240
Leu	Tyr	Val	Arg	Asn	Arg	Val	Arg	Glu	Ala	Ile	Arg	Val	Ser	Lys	Ile
				245					250					255	
Pro	Asp	Ala	Lys	Ser	Pro	Leu	Pro	Val	Phe	Ala	Tyr	Thr	Arg	Ile	Val
			260					265					270		
Phe	Thr	Asp	Gln	Val	Leu	Lys	Phe	Leu	Ser	Gln	Asp	Glu	Leu	Val	Tyr
		275					280					285			
Thr	Phe	Gly	Glu	Thr	Val	Ala	Leu	Gly	Ala	Ser	Gly	Ile	Val	Ile	Trp
	290					295					300				
Gly	Thr	Leu	Ser	Ile	Met	Arg	Ser	Met	Lys	Ser	Cys	Leu	Leu	Leu	Asp
305					310					315					320
Asn	Tyr	Met	Glu	Thr	Ile	Leu	Asn	Pro	Tyr	Ile	Ile	Asn	Val	Thr	Leu
				325					330					335	
Ala	Ala	Lys	Met	Cys	Ser	Gln	Val	Leu	Cys	Gln	Glu	Gln	Gly	Val	Cys
			340					345					350		
Ile	Arg	Lys	Asn	Trp	Asn	Ser	Ser	Asp	Tyr	Leu	His	Leu	Asn	Pro	Asp
		355					360					365			
Asn	Phe	Ala	Ile	Gln	Leu	Glu	Lys	Gly	Gly	Lys	Phe	Thr	Val	Arg	Gly
	370					375					380				
Lys	Pro	Thr	Leu	Glu	Asp	Leu	Glu	Gln	Phe	Ser	Glu	Lys	Phe	Tyr	Cys
385					390					395					400
Ser	Cys	Tyr	Ser	Thr	Leu	Ser	Cys	Lys	Glu	Lys	Ala	Asp	Val	Lys	Asp
				405					410					415	
Thr	Asp	Ala	Val	Asp	Val	Cys	Ile	Ala	Asp	Gly	Val	Cys	Ile	Asp	Ala
			420					425					430		
Phe	Leu	Lys	Pro	Pro	Met	Glu	Thr	Glu	Glu	Pro	Gln	Ile	Phe	Tyr	Asn
		435					440					445			
Ala	Ser	Pro	Ser	Thr	Leu	Ser	Ala	Thr	Met	Phe	Ile	Val	Ser	Ile	Leu
	450					455					460				
Phe	Leu	Ile	Ile	Ser	Ser	Val	Ala	Ser							

465

470

<210> 180
 <211> 471
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PH20 36-506

<400> 180

```

Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1      5      10      15
Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
 20      25      30
Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
 35      40      45
Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
 50      55      60
Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
 65      70      75      80
Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
 85      90      95
Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
 100     105     110
Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
 115     120     125
Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
 130     135     140
Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
 145     150     155     160
Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
 165     170     175
Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
 180     185     190
His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
 195     200     205
Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
 210     215     220
Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
 225     230     235     240
Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
 245     250     255
Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
 260     265     270
Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
 275     280     285
Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
 290     295     300
Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
 305     310     315     320
Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
 325     330     335
Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
 340     345     350
Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
 355     360     365
Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
 370     375     380
Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
 385     390     395     400
Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
 405     410     415
Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala
 420     425     430
Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile Phe Tyr Asn
 435     440     445

```

3108SEQPC1

Ala Ser Pro Ser Thr Leu Ser Ala Thr Met Phe Ile Val Ser Ile Leu
 450 455 460
 Phe Leu Ile Ile Ser Ser Val
 465 470

<210> 181
 <211> 469
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PH20 36-504

<400> 181
 Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1 5 10 15
 Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
 20 25 30
 Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
 35 40 45
 Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
 50 55 60
 Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
 65 70 75 80
 Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
 85 90 95
 Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
 100 105 110
 Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
 115 120 125
 Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
 130 135 140
 Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
 145 150 155 160
 Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
 165 170 175
 Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
 180 185 190
 His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
 195 200 205
 Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
 210 215 220
 Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
 225 230 235 240
 Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
 245 250 255
 Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
 260 265 270
 Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
 275 280 285
 Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
 290 295 300
 Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
 305 310 315 320
 Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
 325 330 335
 Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
 340 345 350
 Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
 355 360 365
 Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
 370 375 380
 Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
 385 390 395 400
 Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
 405 410 415
 Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala

3108SEQPC1

420 425 430
 Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile Phe Tyr Asn
 435 440 445
 Ala Ser Pro Ser Thr Leu Ser Ala Thr Met Phe Ile Val Ser Ile Leu
 450 455 460
 Phe Leu Ile Ile Ser
 465

<210> 182
 <211> 467
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PH20 36-502

<400> 182
 Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1 5 10 15
 Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
 20 25 30
 Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
 35 40 45
 Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
 50 55 60
 Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
 65 70 75 80
 Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
 85 90 95
 Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
 100 105 110
 Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
 115 120 125
 Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
 130 135 140
 Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
 145 150 155 160
 Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
 165 170 175
 Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
 180 185 190
 His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
 195 200 205
 Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
 210 215 220
 Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
 225 230 235 240
 Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
 245 250 255
 Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
 260 265 270
 Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
 275 280 285
 Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
 290 295 300
 Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
 305 310 315 320
 Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
 325 330 335
 Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
 340 345 350
 Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
 355 360 365
 Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
 370 375 380
 Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
 385 390 395 400

3108SEQPC1

Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
 405 410 415
 Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala
 420 425 430
 Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile Phe Tyr Asn
 435 440 445
 Ala Ser Pro Ser Thr Leu Ser Ala Thr Met Phe Ile Val Ser Ile Leu
 450 455 460
 Phe Leu Ile
 465

<210> 183
 <211> 465
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PH20 36-500

<400> 183
 Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1 5 10 15
 Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
 20 25 30
 Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
 35 40 45
 Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
 50 55 60
 Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
 65 70 75 80
 Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
 85 90 95
 Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
 100 105 110
 Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
 115 120 125
 Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
 130 135 140
 Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
 145 150 155 160
 Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
 165 170 175
 Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
 180 185 190
 His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
 195 200 205
 Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
 210 215 220
 Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
 225 230 235 240
 Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
 245 250 255
 Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
 260 265 270
 Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
 275 280 285
 Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
 290 295 300
 Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
 305 310 315 320
 Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
 325 330 335
 Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
 340 345 350
 Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
 355 360 365
 Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
 Page 206

3108SEQPC1

370 375 380
 Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
 385 390 395 400
 Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
 405 410 415
 Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala
 420 425 430
 Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile Phe Tyr Asn
 435 440 445
 Ala Ser Pro Ser Thr Leu Ser Ala Thr Met Phe Ile Val Ser Ile Leu
 450 455 460
 Phe
 465

<210> 184
 <211> 463
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PH20 36-498

<400> 184
 Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1 5 10 15
 Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
 20 25 30
 Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
 35 40 45
 Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
 50 55 60
 Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
 65 70 75 80
 Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
 85 90 95
 Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
 100 105 110
 Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
 115 120 125
 Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
 130 135 140
 Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
 145 150 155 160
 Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
 165 170 175
 Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
 180 185 190
 His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
 195 200 205
 Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
 210 215 220
 Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
 225 230 235 240
 Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
 245 250 255
 Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
 260 265 270
 Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
 275 280 285
 Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
 290 295 300
 Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
 305 310 315 320
 Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
 325 330 335
 Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
 340 345 350

3108SEQPC1

Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
 355 360 365
 Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
 370 375 380
 Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
 385 390 395 400
 Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
 405 410 415
 Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala
 420 425 430
 Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile Phe Tyr Asn
 435 440 445
 Ala Ser Pro Ser Thr Leu Ser Ala Thr Met Phe Ile Val Ser Ile
 450 455 460

<210> 185
 <211> 461
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PH20 36-496

<400> 185
 Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1 5 10 15
 Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
 20 25 30
 Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
 35 40 45
 Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
 50 55 60
 Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
 65 70 75 80
 Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
 85 90 95
 Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
 100 105 110
 Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
 115 120 125
 Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
 130 135 140
 Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
 145 150 155 160
 Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
 165 170 175
 Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
 180 185 190
 His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
 195 200 205
 Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
 210 215 220
 Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
 225 230 235 240
 Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
 245 250 255
 Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
 260 265 270
 Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
 275 280 285
 Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
 290 295 300
 Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
 305 310 315 320
 Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
 325 330 335
 Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys

3108SEQPC1

Ile	Arg	Lys	340	Asn	Trp	Asn	Ser	Ser	345	Asp	Tyr	Leu	His	Leu	350	Asn	Pro	Asp
Asn	Phe	355	Ala	Ile	Gln	Leu	Glu	360	Lys	Gly	Gly	Lys	Phe	365	Thr	Val	Arg	Gly
Lys	Pro	370	Thr	Leu	Glu	Asp	Leu	375	Glu	Gln	Phe	Ser	Glu	380	Lys	Phe	Tyr	Cys
Ser	Cys	385	Tyr	Ser	Thr	Leu	Ser	390	Cys	Lys	Glu	Lys	Ala	395	Asp	Val	Lys	Asp
Thr	Asp	405	Ala	Val	Asp	Val	Cys	410	Ile	Ala	Asp	Gly	Val	415	Cys	Ile	Asp	Ala
Phe	Leu	420	Lys	Pro	Pro	Met	Glu	425	Thr	Glu	Glu	Pro	Gln	430	Ile	Phe	Tyr	Asn
Ala	Ser	435	Pro	Ser	Thr	Leu	Ser	440	Ala	Thr	Met	Phe	Ile	445	Val			
		450						455						460				

<210> 186

<211> 459

<212> PRT

<213> Homo sapiens

<220>

<223> PH20 36-494

<400> 186

Leu	Asn	Phe	Arg	Ala	Pro	Pro	Val	Ile	Pro	Asn	Val	Pro	Phe	Leu	Trp
1				5					10					15	
Ala	Trp	Asn	Ala	Pro	Ser	Glu	Phe	Cys	Leu	Gly	Lys	Phe	Asp	Glu	Pro
			20					25					30		
Leu	Asp	Met	Ser	Leu	Phe	Ser	Phe	Ile	Gly	Ser	Pro	Arg	Ile	Asn	Ala
		35					40						45		
Thr	Gly	Gln	Gly	Val	Thr	Ile	Phe	Tyr	Val	Asp	Arg	Leu	Gly	Tyr	Tyr
	50					55				60					
Pro	Tyr	Ile	Asp	Ser	Ile	Thr	Gly	Val	Thr	Val	Asn	Gly	Gly	Ile	Pro
65					70				75					80	
Gln	Lys	Ile	Ser	Leu	Gln	Asp	His	Leu	Asp	Lys	Ala	Lys	Lys	Asp	Ile
			85					90						95	
Thr	Phe	Tyr	Met	Pro	Val	Asp	Asn	Leu	Gly	Met	Ala	Val	Ile	Asp	Trp
			100					105					110		
Glu	Glu	Trp	Arg	Pro	Thr	Trp	Ala	Arg	Asn	Trp	Lys	Pro	Lys	Asp	Val
		115					120					125			
Tyr	Lys	Asn	Arg	Ser	Ile	Glu	Leu	Val	Gln	Gln	Gln	Asn	Val	Gln	Leu
	130					135					140				
Ser	Leu	Thr	Glu	Ala	Thr	Glu	Lys	Ala	Lys	Gln	Glu	Phe	Glu	Lys	Ala
145					150				155					160	
Gly	Lys	Asp	Phe	Leu	Val	Glu	Thr	Ile	Lys	Leu	Gly	Lys	Leu	Leu	Arg
			165					170						175	
Pro	Asn	His	Leu	Trp	Gly	Tyr	Tyr	Leu	Phe	Pro	Asp	Cys	Tyr	Asn	His
			180					185					190		
His	Tyr	Lys	Lys	Pro	Gly	Tyr	Asn	Gly	Ser	Cys	Phe	Asn	Val	Glu	Ile
		195					200					205			
Lys	Arg	Asn	Asp	Asp	Leu	Ser	Trp	Leu	Trp	Asn	Glu	Ser	Thr	Ala	Leu
	210					215					220				
Tyr	Pro	Ser	Ile	Tyr	Leu	Asn	Thr	Gln	Gln	Ser	Pro	Val	Ala	Ala	Thr
	225				230				235					240	
Leu	Tyr	Val	Arg	Asn	Arg	Val	Arg	Glu	Ala	Ile	Arg	Val	Ser	Lys	Ile
			245					250						255	
Pro	Asp	Ala	Lys	Ser	Pro	Leu	Pro	Val	Phe	Ala	Tyr	Thr	Arg	Ile	Val
		260						265					270		
Phe	Thr	Asp	Gln	Val	Leu	Lys	Phe	Leu	Ser	Gln	Asp	Glu	Leu	Val	Tyr
		275					280					285			
Thr	Phe	Gly	Glu	Thr	Val	Ala	Leu	Gly	Ala	Ser	Gly	Ile	Val	Ile	Trp
	290					295					300				
Gly	Thr	Leu	Ser	Ile	Met	Arg	Ser	Met	Lys	Ser	Cys	Leu	Leu	Leu	Asp
305					310				315					320	
Asn	Tyr	Met	Glu	Thr	Ile	Leu	Asn	Pro	Tyr	Ile	Ile	Asn	Val	Thr	Leu
			325						330					335	

3108SEQPC1

Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
 340 345 350
 Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
 355 360 365
 Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
 370 375 380
 Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
 385 390 395 400
 Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
 405 410 415
 Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala
 420 425 430
 Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile Phe Tyr Asn
 435 440 445
 Ala Ser Pro Ser Thr Leu Ser Ala Thr Met Phe
 450 455

<210> 187
 <211> 457
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PH20 36-492

<400> 187
 Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1 5 10 15
 Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
 20 25 30
 Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
 35 40 45
 Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
 50 55 60
 Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
 65 70 75 80
 Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
 85 90 95
 Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
 100 105 110
 Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
 115 120 125
 Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
 130 135 140
 Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
 145 150 155 160
 Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
 165 170 175
 Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
 180 185 190
 His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
 195 200 205
 Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
 210 215 220
 Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
 225 230 235 240
 Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
 245 250 255
 Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
 260 265 270
 Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
 275 280 285
 Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
 290 295 300
 Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
 305 310 315 320
 Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu

3108SEQPC1

Ala	Ala	Lys	Met	Cys	Ser	Gln	Val	Leu	Cys	Gln	Glu	Gln	Gly	Val	Cys
			340					345					350		
Ile	Arg	Lys	Asn	Trp	Asn	Ser	Ser	Asp	Tyr	Leu	His	Leu	Asn	Pro	Asp
		355					360					365			
Asn	Phe	Ala	Ile	Gln	Leu	Glu	Lys	Gly	Gly	Lys	Phe	Thr	Val	Arg	Gly
	370					375					380				
Lys	Pro	Thr	Leu	Glu	Asp	Leu	Glu	Gln	Phe	Ser	Glu	Lys	Phe	Tyr	Cys
385					390					395					400
Ser	Cys	Tyr	Ser	Thr	Leu	Ser	Cys	Lys	Glu	Lys	Ala	Asp	Val	Lys	Asp
				405					410					415	
Thr	Asp	Ala	Val	Asp	Val	Cys	Ile	Ala	Asp	Gly	Val	Cys	Ile	Asp	Ala
			420					425					430		
Phe	Leu	Lys	Pro	Pro	Met	Glu	Thr	Glu	Glu	Pro	Gln	Ile	Phe	Tyr	Asn
		435					440					445			
Ala	Ser	Pro	Ser	Thr	Leu	Ser	Ala	Thr							
	450					455									

<210> 188
 <211> 453
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PH20 36-488

<400> 188

Leu	Asn	Phe	Arg	Ala	Pro	Pro	Val	Ile	Pro	Asn	Val	Pro	Phe	Leu	Trp
1				5					10					15	
Ala	Trp	Asn	Ala	Pro	Ser	Glu	Phe	Cys	Leu	Gly	Lys	Phe	Asp	Glu	Pro
			20					25					30		
Leu	Asp	Met	Ser	Leu	Phe	Ser	Phe	Ile	Gly	Ser	Pro	Arg	Ile	Asn	Ala
		35					40					45			
Thr	Gly	Gln	Gly	Val	Thr	Ile	Phe	Tyr	Val	Asp	Arg	Leu	Gly	Tyr	Tyr
	50					55				60					
Pro	Tyr	Ile	Asp	Ser	Ile	Thr	Gly	Val	Thr	Val	Asn	Gly	Gly	Ile	Pro
65					70					75					80
Gln	Lys	Ile	Ser	Leu	Gln	Asp	His	Leu	Asp	Lys	Ala	Lys	Lys	Asp	Ile
			85						90					95	
Thr	Phe	Tyr	Met	Pro	Val	Asp	Asn	Leu	Gly	Met	Ala	Val	Ile	Asp	Trp
			100					105					110		
Glu	Glu	Trp	Arg	Pro	Thr	Trp	Ala	Arg	Asn	Trp	Lys	Pro	Lys	Asp	Val
		115					120					125			
Tyr	Lys	Asn	Arg	Ser	Ile	Glu	Leu	Val	Gln	Gln	Gln	Asn	Val	Gln	Leu
		130				135					140				
Ser	Leu	Thr	Glu	Ala	Thr	Glu	Lys	Ala	Lys	Gln	Glu	Phe	Glu	Lys	Ala
145					150					155					160
Gly	Lys	Asp	Phe	Leu	Val	Glu	Thr	Ile	Lys	Leu	Gly	Lys	Leu	Leu	Arg
			165						170					175	
Pro	Asn	His	Leu	Trp	Gly	Tyr	Tyr	Leu	Phe	Pro	Asp	Cys	Tyr	Asn	His
			180					185					190		
His	Tyr	Lys	Lys	Pro	Gly	Tyr	Asn	Gly	Ser	Cys	Phe	Asn	Val	Glu	Ile
		195					200					205			
Lys	Arg	Asn	Asp	Asp	Leu	Ser	Trp	Leu	Trp	Asn	Glu	Ser	Thr	Ala	Leu
	210					215					220				
Tyr	Pro	Ser	Ile	Tyr	Leu	Asn	Thr	Gln	Gln	Ser	Pro	Val	Ala	Ala	Thr
225					230					235					240
Leu	Tyr	Val	Arg	Asn	Arg	Val	Arg	Glu	Ala	Ile	Arg	Val	Ser	Lys	Ile
			245						250					255	
Pro	Asp	Ala	Lys	Ser	Pro	Leu	Pro	Val	Phe	Ala	Tyr	Thr	Arg	Ile	Val
			260					265					270		
Phe	Thr	Asp	Gln	Val	Leu	Lys	Phe	Leu	Ser	Gln	Asp	Glu	Leu	Val	Tyr
		275					280					285			
Thr	Phe	Gly	Glu	Thr	Val	Ala	Leu	Gly	Ala	Ser	Gly	Ile	Val	Ile	Trp
	290					295					300				
Gly	Thr	Leu	Ser	Ile	Met	Arg	Ser	Met	Lys	Ser	Cys	Leu	Leu	Leu	Asp
305					310					315					320

3108SEQPC1

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

450

<210> 190
 <211> 2105
 <212> DNA
 <213> Bos taurus
 <220>
 <223> PH20 DNA

<400> 190

ggtttatctc tgttcttgtt gagagagacag acagaattga ctgctgtgtc catccgcgag 60
 ggttaaatgtg ctacgctctt tatgagtag tggagacggg cagagatgac aagatgtagc 120
 aacttgcaaa acatcccaa atacggaagg agagaatat atcttgcatc aaatatagg 240
 ttcatittta tccatcaag tggcttcat ctgtgttcat atcttgcatc aaatatagg 240
 tacaccaag cgtgtagag aaaaaagtc ctttcaagt catcgctctt tgtgtagaga 300
 atgcctaggg gcccatat ctcccttcgg agctcttcg tggcttcgag aacacccct 360
 gcatcttgca ccttcctt tgttcctgtc tggacttcag agcaccctc 420
 ctatttcaa acacttctt ccttcggcc tggaaatgcc cagtgtgaag tttgtgtaac 480
 agaagattc aactaccctc agatctgaag ctctctctc taagaaggag cccccagaaa 540
 agtgcaccg gacatttat tacatttat tatgtctgata gacttggcta ctatccctat 600
 atagatgaaa aacaggcaaa aaccgtatc ggaaggaaatc ccagtttggg aaacttaaaa 660
 agtccatagg aagaagcaaa aaatgacat gccatatca taccaaatga cagcgttggc 720
 gatgtttaca gggatgagtc agttgagttg gttctgcgaa aaaaatccgc aactcagttc 780
 ccaagagctt ccaagatgac aaaaagtggat ttgtgagcag caggaagag ttctcagcaa 900
 gagactttaa aacttggaaa attacttcgg ccaatcatc tatgggggtta ttatcttttt 960
 cctgatgtt acaattcataa tcataaacca cctaattaca atggaatatg cccctgattga 1020
 gaaaataagg gaaatgaga tctcggaagg ttgtggaagg aaaagcactg ccttttccct 1080
 tctgtttat tgaatatcag gtttaaatc actcaaaaag ctgcccctgt tgttcgtaat 1140
 cgtgtccagg aagccatccg gttgtcttaa attagcgaagt tcgaaagttc acttccggtt 1200
 ttgttatag cccgtccagt ttltatcgtat ggttcttcaa catatcttct tcagggttag 1260
 ctgttgaaat cgtttgttga gatcgtttct ctatgtgtcct ctgggattat aatgttgggc 1320
 agtcccaatc taagccttat caagctcac caagcggcca aaaatgttcag cttgaaact 1380
 aacttgaaac cttaaatat caagctcac ctgagcacta taggcactta cttgaaact 1440
 tggccaatg aaggaagtgt tacaaggaag cacttgaatt caagcgaacta tcttcaacct 1500
 aacccaatga atttgcctat tcaaacctgg gaaagtggaa aatacacagt accctgggaca 1560
 gtccacactg aagaacttga aaagttrct gatacaattt atgtcagttg ttatgccaac 1620
 atccactgt aagaagagagt tgaatataaa aatgttcatat gttgttaacgt gttgtatgca 1680
 gaggcatcta ctaccacct cagcagtatc tcaaccccca ctgagcactg ctaacaactg 1740
 ccatgtactc ctgagaaaac cctgtggaag ttacaaaccca gttgactatc cttcagccag 1800
 ccatgtactc ctgagaaaac cctgtggaag ttacaaaccca gttgactatc cttcagccag 1860
 ccatgtactc ctgagaaaac cctgtggaag ttacaaaccca gttgactatc cttcagccag 1920
 ccatgtactc ctgagaaaac cctgtggaag ttacaaaccca gttgactatc cttcagccag 1980
 ccatgtactc ctgagaaaac cctgtggaag ttacaaaccca gttgactatc cttcagccag 2040
 ccatgtactc ctgagaaaac cctgtggaag ttacaaaccca gttgactatc cttcagccag 2100
 ccatgtactc ctgagaaaac cctgtggaag ttacaaaccca gttgactatc cttcagccag 2105

<400> 191

ftgtgtgcgc	cttaagygaa	agaaacttgc	tgatgcctgc	acagggccct	g
tgccctgggt	caggaaattg	gaccttcagc	gaccttcagc	ccctaacctt	60
catgaccaca	ggctccagg	gctgtgttgc	cccttcagta	cccttcagta	120
tgccaacac	gagtgtgtta	tgaaagaaac	cgctgttgaa	cccttcagta	180
tgtgtgtgac	aaccggggc	agaccttcgc	cggtccctaa	atgacccatt	240
ccagcttgg	acctaccct	actatatac	tgtctgggag	ccctgtgttg	300
tggtgtgac	gaccttcgc	cggtccctaa	cggtccctaa	atgacccatt	360
ccagcttgg	acctaccct	actatatac	tgtctgggag	ccctgtgttg	420
acgaattgac	agaccttcag	cccttcagta	cggttcagta	tgctgtccat	480
ggcttcagct	ggtgttcag	catgttcag	gaggttcag	ggcttcagct	540
ggcttcagac	tggtaccaca	aggaactata	ccgttcagct	tggtaccaga	600
ggcttcagac	gaccttcag	ctcttcagg	ggaggtcga	ggttcagagg	660
ggcttcagag	gagtgtgtg	caggcacct	caagcttgga	ggcttcaggg	720
cccttggtgc	ttctataatt	accttcagt	ctacaactat	gaccttaaaa	780
tacaggcccg	tgcttcagaa	acacttcgt	ccagaaatga	cagcttcgggt	840
gaccttcagt	gaccttcag	cccttcagta	gaccttcagga	ggcaggaaga	900
ggacacagat	ttctgtcagc	tggtgttcag	cggttcagga	cggttcaggg	960
ggacacacaa	ctgcccgtgc	tgccccctac	gtagcttcct	ctaacacatt	1020
ttctgcccgc	ggagtgagct	ggagtgagct	ggagtgagct	ggagtgagct	1080
agggtgtgct	tggtgtgagc	ggcttcagaa	ggcttcagaa	ggcttcagaa	1140
ggagtgatgt	ggacacagcg	tggtaccct	catcttcgaa	ggtgctcgtc	1200
ggtgagtcag	ggttcagct	cccttcagta	cccttcagta	ggttcagta	1260
ggccctgcgc	acctaccct	cccttcagta	cccttcagta	ggcttcagta	1320
cccttcagac	cccttcagta	cccttcagta	cccttcagta	ggcttcagta	1380
atgtgtgcct	tggttcagta	cccttcagta	cccttcagta	ggcttcagta	1440
ggcatgtggc	ggcatgtggc	ggcatgtggc	ggcatgtggc	ggcatgtggc	1500
aggcttcagca	ggcatgtggc	ggcatgtggc	ggcatgtggc	ggcatgtggc	1560
ggcatgtggc	ggcatgtggc	ggcatgtggc	ggcatgtggc	ggcatgtggc	1620
aggatgtggg	catatgtgga	ggcatgtggc	ggcatgtggc	ggcatgtggc	1680
ctgcttcagg	ctgcttcagg	ctgcttcagg	ctgcttcagg	ctgcttcagg	1740
aggatgtgca	ggcatgtggc	ggcatgtggc	ggcatgtggc	ggcatgtggc	1800
ttcatgttca	ggcatgtggc	ggcatgtggc	ggcatgtggc	ggcatgtggc	1860
ttgtttaagac	ggcatgtggc	ggcatgtggc	ggcatgtggc	ggcatgtggc	1920
taagcgtgtgc	ggcatgtggc	ggcatgtggc	ggcatgtggc	ggcatgtggc	1971

<400> 192
 caagtctgcgc gctggctgc caaaggcgag gagctgcgcg gaatagcttg gctagagact 60
 taacctggga agggagggag agtgcgact actggcgga cggatccca cacagtctct 120
 gactctgtgc ctggcaggtg acactgact cctgcagccc ccagcatgtg gacagcgctg 180
 ggcccccgcc tcacacttgc cctgtgtgtg gttgttgcat gggccacggg gctgaagccc 240
 acagcacccc ccactctcac gggccggccc ttgtgtgtcg catgtgatat gcccacacag 300
 gactgttgcc cgcgccacaa gatgccattg gacccaagg acatgaagc cttgtatgt 360
 cagttctcac ctacacaggg ttttgttaat cagaaacata ccactctcta ccgttgacgg 420
 aatgacagcc tctgggtaca cctgagatg cctgaaggag acgtggaaca ctacattcgt 480
 acacaggagc ctgcagggtg ggcagtctac gactgggag actgctggcc agtgttggtg 540
 cgcacactgc aggacaaagg ttgtacccg cgattatac gccatttgt agccattcgc 600
 caccctgat ggcacaaagg ggcgttagcc aaggagcgcc agtatgagtt tgagttcgtc 720
 gcatggcagt tcatgtctga gcatgtcgga ttgttcaagg cgtttcggcc tgcgacacac 780
 ttgggtctct acccttccc tgaatttac aaccatgat atgtgcagaa ctggagagcc 840
 tatacagucc gctgccctga ttgttaggtc tccgaaatg accagctggc ctggctcttg 900

gccgagagca cggccctctt cccctctgtc tacttggaag agacactggtc ttccctccact 960
caggccacc cacttgccag ctttcgttgc tagtcgttgc ctcgctgtgc tagactgtccac 1020
cagccaccac atttgatgac caggaggtcc tacttggtccac gacacacccac 1080
acagggtcta gcgagatgga tctcatctcc accattgtgt agatgtgtgc cctgtgtgca 1140
gtctggttca tccctctgtgtg tgaacgaggg tttaaccaca gcaacgagac ctgcccagac 1200
ctcaaggatt atctgacctg gtcatgtgta cccatgtctg tcaatgtgtc ctgtggtctgc 1260
cagtaaccac gctgggccca gtgcccattgc cagtgtccagc gtgtgctgcg ggaaccccaac 1320
gtctacacct tccgtccacc cagtgtccagc agcttccgtc tagtgcctag ccaacgcaac 1380
gatgagccgc gctgtgccgc agatgtggaa ctcagttggc cgaacgcgaac ccactacag 1440
atgcaatttc gctgccagtgt ctaattaggg ttgggtcgtgt agcaatgtcca gtgtgacccg 1500
aggcggggcag ctgtgggtgtc cagtgtggcc ttgggtcgtgt cccaacctac ttgtcctgtc 1560
gcagttgccag tccgtgccct cactagact ttgttaagggt cttctaccca gctgtccagc 1620
cagcttgccct ctgtcccaag gggtctgtca ggcatgttag agccctgtcaag gggtgtgaca 1680
accaggtctt ggaagggtgc agccctgtgt gatgtccgtt agcatgtctt taccagctcc 1740
caccctctgt tctaagggtg aggggcagtc cctgtgaag taccgttctt cccgtgcaga 1800
gaggaagagg ggcacagctg ggccggggag gacctgaacc tactcccttg ccccttgata 1860
gtttattat attattltgg ggtctcttlt gtaaatlaaa tataaaacaa ct 1912

<210> 193
<211> 1537
<212> DNA
<213> Ovis aries

<220>
<223> Hya12 DNA

gcaaatgaca ctgacttctt gcagcccca gcatgtggac aggccttggc cccgcgtca 60
cactggccct gttgttgttg gttgcattgg ccaagagct gaagccaca gacaccca 120
ttctcacagg gtcgccctt gttgttgtgc cacaacacac ttgtgtccac 180
gccacaaggt gccattgac ccaagaca tacttgacct tgaatgtcag gcttaccata 240
accagggttt tgaataacaa tcttctaccc tgaacccgtg ggcattgtat 300
cacacttcaa ctggttgtgg aggtcagtcc atgtgtgtgt gccaagaa tt ggcagcctt 360
gggtacacct ggaatgtctg aaggacaag ttgaacacta catctgtaca caggagcctg 420
cagggtctgc agtcatcgac ttgggaaggc ggccggccagt gtgtgtgtgc aaactgtcag 480
acaaggatgt gtatcccgcc gtatcccgcc agttgtgtgc cagtccacac cccgattggc 540
caccagcag catagtccaag gaggcgcagt atgagtgtga gttcgtctga cgcagattca 600
tgcctggagc actgcgattt gtcaaggcgt ttccggcctcg gcaacctatgt ggcttctac 660
tcttccctga ctgttacaac catgtatatg ttgcaaaact ggagacacct atcaggtccgt 720
gacctgatgt tgaagtctcc cgaatatgac agctgttctg gctctgtggc gagagcag 780
cccttctccc ctgtgtctac ctggaagaa cgtgtgtctc cgttccacac gccaacatg 840
cactcccaat ctacttctac acgagctctc cctacagccg ttgacttaca ggccttagcg 960
agatggatct catcttccac atgtgtgaga gtgtctggcc gtgtgtcagc ggcgttcatc 1020
tctgtgggtga cgcaggtgtt accacacaga acgagacct cgaacgctc aaggaattac 1080
tgactctgtc actgttacc tatgttctca atgttctctg ggtctgccag tactgtcagct 1140
gggcccagtg ccaatggctg gggtcgtgtg ttgcgcggga cccaacgtt cacaccttcc 1200
tgcaacctca ttccgtctag ttgccttagc cgtacccat ggcacctgtat ggcctgcggc 1260
tgcgaaccaga agttgtggcc accgcacaac cctacagag cactttcgtc 1320
gccagtctca ttgggtcttg gctgtgtccc accctacgtg cctgtctgca gttgtcagct 1380
gggtgtccag ttgggtcttg gctgtgtccc accctacgtg cctgtctgca gttgtcagct 1440
tggccttcac ctggaactctg taagggtctc acccagctgc caggccagct ggcctctgccc 1500
acaagggttc tgcagggcat tgccttagc ttccgtctag ttgccttagc cctgtctgccc 1537

<210> 194
<211> 1967
<212> DNA
<213> Ovis aries
<220>
<223> Hya1uronidase DNA

<400> 194
actccctgtt atctctgttc ttgtgtgaga gacagacaga attgactgtc gtgtctatcc 60
accaggttac agatgagaca acttgcaaaa catctcctaa tacgaagaa gaagagtatt 120
taaacgtaaa tcatcatatt tcatttttat ccatcaagt agcttcatc ttgttttcta 180

tcttgcatac aatatagatg tgcataagcg aacccaatg tgcataagtc aaaaagtct tttcatagtc 240
atcgctctt gtgaaggaac tgcataagcg aacccaatg tgcataagtc aaaaagtct tttcatagtc 300
ggccagtga acaacccagg cggcgctcgc cttcctctcg cttccatgtt ggttggctct 360
ggacttcaga gcaacccctc ttattccaac cacttctctc cttccatgtt ggttggctct 420
agctgaacgt tgttgttaaa tctttaaac accctccagt cttgaactc tctctgttaa 480
aaggaagcccc caaaaaagt ctaagggaac atttatatac ttattttatg ctgatatg 540
tggctacatc cctacaataa atggaataac aggccaaac gtaatatg gaattcccc 600
ttgttgaaac ttatatac atggaataac aggccaaac gtaatatg gaattcccc 660
aatgtgaac atttggaac cgttggaac atgttggaac atgttggaac atgttggaac 720
aaacttgaaa cctaagatg tttaacagg tttaacagg tttaacagg tttaacagg 780
tccacaactc agttccag agttccaa gattgcaaa gttgatttg agacagcag 840
aaagatttc atgcaagga ctttaaac tttaaac tttaaac tttaaac tttaaac 900
gggtattat cttttcccg attgttaac tcaataatat aacccagctta cttacaatg 960
aaattgctt gatitgaac aatgtatctc ttatgtatctc gactgttgtt ggaaggaag 1020
caatgcctt tttcccttg ttattttga ttatattga ttatattga ttatattga 1080
ctttatgtt cgtaaccttg tccaaggagc catctcgttg tctaataatg cgaagtgttg 1140
aagtccaat cggttttg tatatacccg ttcagtttt actgtatgtt cttacaata 1200
ccttctcag gttgaccttg tgaattcgtt tgttgtagatc gttgctctag gttgctctg 1260
gatataatg ttgggtcagt tgaatcctta ccaatcctag tcaatcttga tgaacctag 1320
caatatatg aacatacac tgaatcctta ccaatcctag tcaatcttga tgaacctag 1380
gtgcagccaa gtgctttg accgatgaag agttgtgaac aggaatacaat ggaattccaag 1440
cgaatactt caccctgaac caatgaaatt tgcataata acttggaag gttggaata 1500
cacagtacct ggaagaatc caattgaagc cttgcaaac ttcttgata aattttattg 1560
cagtgttat gccacaatc actgttaaga gagagtgtgat ataaaaaatg ttcatagtgt 1620
taattctctt agccagatg accattgtat gttgaagtctc gttgaagtctc agccagtatc 1680
tcaatcctct agccagatg aggcatactc taccacccgtc agccagtatc aacccctcac 1740
tacagccacc acagtatctc catgtatctc ttgaagaaacg tccctctgagt gccccaagt 1800
caggtgtttg gaagccatcg ccaacgtcac tattaacaaat tatataaaat caaacacatc attaaaaat 1860
gaacacttc agtcagtcc atgtatcaaa gtattcaaaa aaaaaaaa aaaaaaaa 1920
aaattcagt cttataga aaaaaaaa aaaaaaaa aaaaaaaa aaaaaaaa 1967

<210> 195
<211> 2116
<212> DNA
<213> Homo sapiens

<220>
<223> HAS1

<400> 195

cyyagaaag agagagcccg gccagaccac ctcgcatgag acagcagagc gcgcaccaag 60
ccactctgc atgcctcgcc tgcctccggc tgcctccggc tgcctccggc tgcctccggc 120
atcgctacg cttcctcgcc ttccggcctt accgggcctt cctttcagcg cacttgttgg 180
cgagagacc cttcgcgtac cttgcgttgc cttgcgttgc cttgcgttgc cttgcgttgc 240
cgagagacc cttcgcgtac cttgcgttgc cttgcgttgc cttgcgttgc cttgcgttgc 300
tgatgtcagc caccgcgcgc agtgtgtgcg tgaacctctc cgtccatacc gaaagacccc 360
cgtacctcgc ccagttgcct gcttcccgcc gctccctgtc gttaccccgcg gctgcgctcg 420
gcttccctat ggtgaacccg cgtacagatc ctaacatgtt gaacatgttcc gaacatgttcc 480
ggagagctt cgttcagatg gaaccccgca cgtacagtgt gtcacagtgtg gtcacagtgtg 540
ccttggaacc cgtgcgcgcg ggcgcgcgtg gtcacagtgtg gtcacagtgtg gtcacagtgtg 600
aggaatcctg gtcgcgtcag gtcgcgtcag gtcgcgtcag gtcgcgtcag gtcgcgtcag 660
cgcagcgcgt ggcagagcca tgtacagatc tttaacaggc cttcaaggcg cttcaaggcg 720
cgyttgaact cgtcaggttc tgtacatctcg acaacaagtt ggaacaagtt ggaacaagtt 780
agcttccccc gttacatcccc ggtttagggg tgtttagggg tgtttagggg tgtttagggg 840
tcttaacccc tcttgatccc tttgtcagat tcttaagcag cttgcgatac ttgtgtagct 900
tcaatgttga gctggcttgt cagagtctat ttccactgtt atctctgcac agcgttcttc 960
taggctcata taggaataac cttcttgagc agttcttga ggccttctga aacccaagat 1020
tcttggttac taccaaagtac accctccaag tccgctgtca ctcagagagc cctctgttct 1140
tggtgttatg taccgaagtac accctccaag tccgctgtca ctcagagagc cctctgttct 1200
tccctgcgtg gctgagcccc gctgagcccc gctgagcccc gctgagcccc gctgagcccc 1260
accaacgcgt cttgttgcac cgttgatgac cgttgatgac cgttgatgac cgttgatgac 1320
gacctgtccc gttctacgcg gttctacgcg gttctacgcg gttctacgcg gttctacgcg 1380
gggctctgct gttggtctgc acttggtctg acttggtctg acttggtctg acttggtctg 1440
tgtgtgctgc cgttgatgac ggttccaaag ggttccaaag ggttccaaag ggttccaaag 1500
gcaacccggg gctgcttggg agttcctggg agttcctggg agttcctggg agttcctggg 1560
ggacccctgt gctgcttggg actaagttac actaagttac actaagttac actaagttac 1620
ggagcctgct gctgcttggg actaagttac actaagttac actaagttac actaagttac 1680
ggagcctgct gctgcttggg actaagttac actaagttac actaagttac actaagttac 1740
ggagcctgct gctgcttggg actaagttac actaagttac actaagttac actaagttac 1800
ggagcctgct gctgcttggg actaagttac actaagttac actaagttac actaagttac 1860
ggagcctgct gctgcttggg actaagttac actaagttac actaagttac actaagttac 1920
ggagcctgct gctgcttggg actaagttac actaagttac actaagttac actaagttac 1967

ttgggtactg ttggccatg ttgacgtgt actgggtggg cgtgcggagg cgtgcggagg cttgcccggc 1740
gagccaggg gagccagag gagccagag gagccagag gagccagag gagccagag gagccagag gagccagag 1800
gtcttcagg gtcttcagg gtcttcagg gtcttcagg gtcttcagg gtcttcagg gtcttcagg gtcttcagg 1860
tctctgggg tctctgggg tctctgggg tctctgggg tctctgggg tctctgggg tctctgggg tctctgggg 1920
ctgactata ttggactgg gactctggg gactctggg gactctggg gactctggg gactctggg gactctggg 2040
atttctact ttggtcagg ttggtcagg ttggtcagg ttggtcagg ttggtcagg ttggtcagg ttggtcagg 2100
aaaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaaaa 2116

<210> 196

<211> 3275

<212> DNA

<213> Homo sapiens

<220>

<223> HAS2

<400> 196

gaagtcaaga gctctggaa gaattacca gttccttggt ctagcagcct ctagcagcct ctagcagcct ctagcagcct 60
attgaaaccg attgaaaccg attgaaaccg attgaaaccg attgaaaccg attgaaaccg attgaaaccg attgaaaccg 120
aagagatttt taagaaacga taagaaacga taagaaacga taagaaacga taagaaacga taagaaacga taagaaacga 180
ctgttatccc cgttatccc cgttatccc cgttatccc cgttatccc cgttatccc cgttatccc cgttatccc 240
aagaaaaaag aagaattaat ttatttttaa agcataattt agcataattt agcataattt agcataattt agcataattt 300
ttgaacggaa acataaagag aatatatagg aatatatagg aatatatagg aatatatagg aatatatagg aatatatagg 360
acatttaaga cttccctatc ctttttaaat gtgtttttta aatttcttat tttttttggc tttttttggc tttttttggc 420
cgttcgtctc aatttcatct gatctcttat taccctcaatt ttggaacatg cccggccacg cccggccacg cccggccacg 480
acctcccggg accacacaga caggctcggag acgacattat gagccagagg ttgaacagat ttggagttct 540
gcatctcttg aggtttctat gttatccttgag aataattgga accacactct ttggagttct ttggagttct 600
tcttctctct ggaattcacag ttgtttggac ttgtttggac ttgtttggac ttgtttggac ttgtttggac ttgtttggac 660
ttactatttc cttgtttggc ttgtttggc ttgtttggc ttgtttggc ttgtttggc ttgtttggc ttgtttggc ttgtttggc 720
cctgtttggc ttgtttggc ttgtttggc ttgtttggc ttgtttggc ttgtttggc ttgtttggc ttgtttggc 780
gaacaaaaaa gtgtcccttt gcatcgtctgc ctatacagaa gatccagact acttaaggaa 840
atgttttgca ttgtttgaaa ggtctaaacc tttaacccta cctctgggat aagaattgta aagaattgta aagaattgta 900
caaatcagcc acttatatct ggaagaacaa cttccacgaa aaggttcccg gttagagcaga 1020
tgagttcacat aagaacagct cgcacacagt aacgcgaattg gtccttgcca acaaaagtat 1080
ctgcatcatg caaaaattgg gtgaaaag gtgaaaag gtgaaaag gtgaaaag gtgaaaag gtgaaaag gtgaaaag 1140
ggtgcctttt aatatagaaa gggccttgca gttcttatc ttgtttggac ttgtttggac ttgtttggac ttgtttggac 1200
atcttcagat tttaacagat acgatctctg gatctcatc ttgtttggag ttgtttggag ttgtttggag ttgtttggag 1260
gtgagcgaat gtgattatg ttacagtttg ttatttcagac actatgcttg acccagcttc 1320
gattgccttt aatatagaaa gggccttgca gttcttatc ttgtttggac ttgtttggac ttgtttggac ttgtttggac 1380
ttggaccctc ttgaaattgca gaaactccc ttgtttggag ttgtttggag ttgtttggag ttgtttggag ttgtttggag 1440
tcaagaaatt atggccaacc aatgttagct ttgtttggag ttgtttggag ttgtttggag ttgtttggag ttgtttggag 1500
gctgagcctg gcttatgcaa caaaaatacac agctcgtatct aagtgcctta ctgaaaacac 1560
tatagaatat ctacgaatggc ttacacagca gaaacgggtgg agcaagttcct acttccgaga 1620
atgtcgttac aatgcgaatg gttttcacaa acatcacatg ttgattgacct acgaagcgat 1680
tatcacttga tcttttctct tctttctcat ttgccacagt ttgccacagt ttgccacagt ttgccacagt ttgccacagt 1740
taaaatttgg aacattctcc tcttcttggt aacgttccag ctagttaggt tcatataatc 1800
atcttttggc agctgcttta gaggaaatat cgttcatgttc ttcatgtctc ttcatgtctc ttcatgtctc 1860
gttatcacatg tccggtttac ttcccggcaa gattgtttgca atgtccaacaa ttatgccaac 1920
ttgggtgggg accatcgaat ttgtattttc ttcatatagg ttcatatagg ttcatatagg ttcatatagg ttcatatagg 1980
aaggtccatt ttcaaatcc tcttggttgg ttcaattgtt ttcaattgtt ttcaattgtt ttcaattgtt ttcaattgtt 2040
aaggtccatt ttcaaatcc ttcaattgtt ttcaattgtt ttcaattgtt ttcaattgtt ttcaattgtt ttcaattgtt 2100
ctatttgggt atgtctttga cgtcttcatc aataaagtgt ttcaattgtt ttcaattgtt ttcaattgtt ttcaattgtt 2160
gaaaggacaa caatatgaca ttgttcttga ttgttctcatc aataaagtgt ttcaattgtt ttcaattgtt ttcaattgtt 2220
gtcacaacaa acacacttgg tcccttaggg gctgttagag attgttggcat attgttggcat attgttggcat attgttggcat 2280
caccaaaagg gacatatcac ttgtcgttgg attgttagaa agacatttat atgggttat atgggttat atgggttat 2340
tttcatcttg ccaagttaaa acatacacat aactcagat taacctgtta ttcaattgtt ttcaattgtt ttcaattgtt 2400
tttcatatga aatgggata attctttgtt ttcttcatc ttcttcatc ttcttcatc ttcttcatc ttcttcatc 2460
ttgaaagtgt ttgcccata taccctcata gacctgtct ttcttcatc ttcttcatc ttcttcatc ttcttcatc 2520
aaaggtattt ggaacaccaa ttcaaacctta ttcaaacctta ttcaaacctta ttcaaacctta ttcaaacctta ttcaaacctta 2580
gttttgatag atgataattt ttgtttttta ttgtttttta ttgtttttta ttgtttttta ttgtttttta ttgtttttta 2640
gaaatggccaa aggaatttt tttaaggttt tttaaggttt tttaaggttt tttaaggttt tttaaggttt tttaaggttt 2700
gtgtttttta attttgtatg ccaattctaa agcaaattt ttgcatattt ttgcatattt ttgcatattt ttgcatattt 2760
tttcttgccaa aataaacctg ttcttccctt ttcttccctt ttcttccctt ttcttccctt ttcttccctt ttcttccctt 2820
atacttaaaa aatccttgccc aaaaatgtga gcttggttga ctgttggttga gcttggttga gcttggttga gcttggttga 2880
ataaaaatgt ttcttctctc ttaacccttt ttaacccttt ttaacccttt ttaacccttt ttaacccttt ttaacccttt 2940
tatttaaacct tttaaacct tttaaacct tttaaacct tttaaacct tttaaacct tttaaacct tttaaacct 3000

3108SEQP1
cctatcacac ttggaagta aatatataca ctttcgtgtg taacctaaata aaaaatcgtt 3060
gaaatcaag gtcaattt ttcataga tttaaaaaa aggaatat 3120
agtcttgaa agaaaagat aacatggtat tcaaaagtat 3180
ataatcttg gagatcttg cagtgtttc ccagaacag tcaagtggaa agtggagaaa 3240
ttatctgtat aattttggac acatacaatg cagt

<210> 197
<211> 4220
<212> DNA
<213> Homo sapiens

<220>
<223> HAS3 transcript variant 1

<400> 197

gagttgcctc ggcctctgct tgaacctgtg ggcctctgct ttggtctgct cttccctac ccgaagcgca 120
ggcagggcagg ggggtcccg cgcgcctctt cagcatatgc cgttgcagct gacgacagcc 180
ctgcgtgttg ttggcaccag cctgtttgcc ctggcagtc cctgtcagcc 240
tatgtgacgg gtaccagtt catccacag gaaaagcat acctgtcctt cggcctgtac 300
ggcgccatcc ttgcccctga cgtctcatc cagagccttt ttgccttctt ggagcacagg 360
cgcatgacac gtgcccggca ggcctctgac ctgcacccctt cgcggcgggg ctggtgtgca 420
cagcgcatct ccttccctga cctcaagttg gtcatgtgtg ttgatgtgcaa ccgccaaggag 540
gacgcccata ttgtgttgcc gacgacaatt ccatgagga ggcaggggtg agacggaggg cagcctgag 600
gagggcattg accgtgtgcy ggaatgtgtg ggaatgtgtg cgggccagca ccttctgcy catcatgag 720
aagtgtgggg gaaagtgtga gttcatgtac acggccctca agggccctcg cagcctgac catcgagatg 840
gactacatcc agttgtgcga ccttgacatc ggtctgacac ctgtgacac aggtctgac cagcctgac catcgagatg 900
cttcgagttc ttgagagga tccccaagt ggggagtcy ggggagatg ccagatctc 960
aacaaagtac actcatgtat ttccctctg agcagcgtgc ggtactgtat ggccttcaac 1020
atgtaccgca acagcctct ctagagttc ctgaggaat ggtacggac agccggagca gaaagtctta 1080
ggcagacagt gcaagtctcg ggaatgacgg caacctcaac accgagttc gaggcccttgc 1140
tacgaaata agtatccg cgcctccaag ttccctcag agacccccac taagtacctc 1200
cogtvgctca accagcaaac cgcctggagc aagcttact ttccggagtt gctctacaac 1260
ttctgttgtt tccatagca ccaacctctg atgacactag agtccagtgt caccgggttc 1320
ttccctctc ttctcatg caggttata cagctttct accgggccc catctggaa 1380
attctctct tctgctgac ggtgcagctg gttggcatta tcaagcccac ctacgccc 1440
agcctctgc cggccaagt cttggccat gtaacatg acctccctc ctatagttc 1500
tttggccgaa aaaaactgt gttgaactt cattggctc catctgtgtc 1620
gcagtctcc ttggaggtt ggtctacac gcttatgtc aggtacctg cagtggaca 1680
gagctagcct tcttgtctc ttgggtata ctgtatgtc gtaactgtt ggcctctc 1740
atgtctatc ttggccctat cgcgcggcga ttgtggagaa agccggagca gtaacgctg 1800
agggaagggt gttggaggtg taaagtgtcaa ttggtgtaag 1860
aggggaagggt aatggaaggt aaaaagcag gttggaggtg ggaagtgac 1920
gtctctaat gttccaaagg acaaatctaa aatgcaaaag acggtgatgt agtatgtc 1980
gacagctctg tttagaggtg gcaacactga tccccagat gcaaggctgc aggggatct 2040
gtgtttcag actgcctgc ttgctgcatc ttgacatag cagttagctc cttctggtc 2100
ccaggggca cttgaagtt gttctaagc caatccagtc gcaacctgtg 2160
atagagttc gagttgagc aacctgcgg gagagttct ccaggtctt gttacacac 2220
ccagagttg caggaagat ttacttgac ggttagtga ttgtaccccc 2280
acccccccc taagtatca tcaatgtccaat aagtatgcca ttggtctg 2340
gacctatct ttggcatcag aaaaacaggt ccaggaatgt ttgctttatgt gagataccc 2400
actccaatc acaattccag ggaatgagcca aaccagcag gagttagcac ttgaactgt 2460
ttaaaagtgc acattaaaaa ggaaggttt ccaggaagga caaagagatc gttgtgtg 2520
ttaagaggtc cataagttac acagagttc ttgtgttcc accgtgaaac ttgtcagag 2580
tttagaggt ttcttagctt gttctgtatc gttgtgtggt agataaaag attaaagccc 2640
aaatgttca gaaaagaagt gaagttcttg gatatctttggt ctgtatactc ttgaaatccc 2700
ctcaaatca gctctgatc ggtctgatc gaggtctaa cactcaactc ctcaagcc 2760
acatttttg acatttttg tcttatagaa gcttccagcag gcttccagcag gaggcaagc 2820
ttcttctgac aatgtgggcg aatatggga gctctgatc caatcttgga 2880
gtctcttgga gctgcttgga ttgacatgtg gtaacttgga 2940
caagtgtga aatgttgga ttctttccag ttctttccag aaaaaccaact agggagatgaa 3180

acatggtccat acatccctaa gttcttgctt tctctctcat gccctctgag gctgtttttg
 3240
 gctgttttcc cctctgctgt ttgtgggaat gagggaagc cattttccaa tgaacttgca
 3300
 tccaggtctgt tctcagcggt ttgagttaa aacctgggat cctgactaag cctttgactt
 3360
 aagggttgct tgccttgccct ccaaatgtcc ttctcagag gggccagcta acccgtgtag
 3420
 aaccagctat aaggttgaca gcagacaaga gggccaagcct ctagtgtacc aagtgcctcc
 3480
 tacaagaagc caaggtgtgc tctgagccac agatgggcaa accctgtgtc ttctcttcat
 3540
 cttccagaa cttcaaggtt ttccaaggtt agtcaagct tgcacacatc cacaagctc
 3600
 gactttctgg taagacttgt gtttgacatc agaccacac catgaaggtc ggaagagcagc
 3660
 aggcatttgc taaggcagct gatccagca atcgttctgc tggccaagaa gttaaactat
 3720
 tttaggcatt agaattgagag aaatccggtc agccaagtgc agagtccaag cttcgcctag
 3780
 ggttgttttt tcttcagcat ttacttgag attaatgtag gatgacaggt tctccttgct
 3840
 gtctacatc cagctctgcc ttgcacttg gtcgtcaact ttctccaat caaaaaaag
 3900
 cagttacag tagttgggtc acaacgggtt accctgcactg gtttttctaa gttattttgt
 3960
 acatlttcca gcagcaaaac caactgggt cttagctt atccccgtt cttgcaagg
 4020
 aagagccttt atacaatttg acgcatlttg gtttttctc attgagatt caaatctctt
 4080
 ttgttatgt tttaataa atttgtaaac atatttat ttaccgtctt ttttttttt
 4140
 tttaatttt caggtcaagt tttttatct gcaattatt gtcaaaaata agattctcac
 4200
 atatgccgtt tatctcgaaa

<210> 198

<211> 1229

<212> DNA

<213> Homo sapiens

<220>

<223> HAS3 transcript variant 2

<400> 198

ggaaggagcat ggaagccggc cgggcttgct gactccgga gcgcggcagc cggcgagcag
 60
 atgcccgtgc agtctacgac agcccctgct gttgttgagc ccaagcctgtt tgccttgca
 120
 gttccttggt gactctatgc agctctatgc agggctatcc agtctcatcc cagggaaa
 180
 cactacctgt ccttcggcct gtacggcgc atccctggcc tgcacctgct cattcagagc
 240
 ccttttgctt tcttgagca ccggcgcat cgaagtgcgg gccagggcctt gaagctgccc
 300
 tccccgcggc ggggctctggt ggcacttgtc attgccgcat accaaggagc cccctgactc
 360
 ttgcgcaagt gcttcgctc ggcacagtc atctcctcc ctgacctcaa ggtgtgctatg
 420
 gttgttgatg gcaacggcca ggaaggacggc tacatgtctgg acatcttcca cgaagtgtctg
 480
 ggcgggcccag agcaggcccgg cttcttcttg ttggcgcagca acttccatga ggcagggcga
 540
 ggttagagccgt aggcagctt gcagaaagtc gtcgggattt ggtgcgggcc ccttgcgggc
 600
 agcaacctct cgtgcattcat gcagaaagtc ggaagccaagc gcgaaggtcat gttacaagccg
 660
 ttcaaggccc tccggcatct ggttggaact atccagggtt gcgactcttg cactgtgtctg
 720
 gatccagctt gccacctga gatgcttcca gttccttgag aggtatcccc agtaggggga
 780
 gtcgggggag atgttccagc cccaaggaaa ggtatggcag gttatggcag tagagggatga
 840
 gctgcgggag atgttccagc cccaaggaaa ggtatggcag aacggccacg ttcttagagag
 900
 cagttagctg atttccaat ggttagcagg ggaactatg tgaacttgga cctgcagggc
 960
 aatgtatccc tgaaggaaaag tccaagaaga caattcaaga ggaacttgag aacaatggtg
 1020
 cagaaagctg tgggacgaaa gcacagcagg cttctgggag gcttgagatc tttctctca
 1080
 aggcagagat tatccccac tgcacagtt cacatgccac aataaacatc tcaaccttcag
 1140
 tcaagaaaaa cgaaggaa aaaaaaaa aaaaaaaa aaaaaaaa aaaaaaaa
 1200
 aaaaaaaa

<210> 199

<211> 509

<212> PRT

<213> Pan troglodyte

<220>

<223> Precursor chimpanzee PH20 XP_527873

<400> 199

Met Gly Val Leu Lys Phe Lys His Ile Phe Arg Ser Phe Val Lys
 1
 Ser Ser Gly Val Ser Gln Ile Val Phe Thr Phe Leu Leu Ile Pro Cys
 20
 Cys Leu Thr Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro
 35
 Phe Leu Trp Ala Trp Asn Ala Pro Ser Gln Phe Cys Leu Gly Lys Phe
 50
 Asp Gln Pro Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg
 60
 Page 219

3108SEQPC1

65 Ile Asn Val Thr Gly 70 Gln Asp Val Thr Ile Phe Tyr Val Asp Arg Leu
 85 Gly Tyr Tyr Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly
 100 Gly Ile Pro Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys
 115 Lys Asp Ile Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val
 130 Ile Asp Trp Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro
 145 150 Lys Asp Val Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn
 165 Val Gln Leu Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe
 180 Glu Lys Ala Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys
 195 200 Leu Leu Arg Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys
 210 215 Tyr Asn His His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn
 225 230 Val Glu Ile Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser
 245 250 Thr Ala Leu Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val
 260 265 Ala Ala Thr Leu Tyr Val Arg Asn Arg Val Gln Glu Ala Ile Arg Val
 275 280 Ser Lys Ile Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Val Tyr Thr
 290 295 Arg Ile Val Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu
 305 310 Leu Val Tyr Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile
 325 330 Val Ile Trp Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu
 340 345 Leu Leu Asp Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn
 355 360 Val Thr Leu Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln
 370 375 Gly Val Cys Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu
 385 390 Asn Pro Asp Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr
 405 410 Val Arg Gly Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys
 420 425 Phe Tyr Cys Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp
 435 440 Val Lys Asp Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys
 450 455 Ile Asp Ala Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Ser Gln Ile
 465 470 Phe Tyr Asn Ala Ser Pro Ser Thr Leu Ser Ala Thr Met Phe Ile Val
 485 490 Ser Ile Leu Phe Leu Ile Ile Ser Ser Val Ala Ser Leu
 500 505

<210> 200

<211> 474

<212> PRT

<213> Pan troglodyte

<220>

<223> mature chimpanzee PH20 XP_527873

<400> 200

Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1 5 10 15

3108SEQPC1

Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
 20 25 30
 Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Val
 35 40 45
 Thr Gly Gln Asp Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
 50 55 60
 Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
 65 70 75 80
 Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
 85 90 95
 Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
 100 105 110
 Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
 115 120 125
 Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
 130 135 140
 Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
 145 150 155 160
 Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
 165 170 175
 Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
 180 185 190
 His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
 195 200 205
 Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
 210 215 220
 Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
 225 230 235 240
 Leu Tyr Val Arg Asn Arg Val Gln Glu Ala Ile Arg Val Ser Lys Ile
 245 250 255
 Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Val Tyr Thr Arg Ile Val
 260 265 270
 Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
 275 280 285
 Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
 290 295 300
 Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
 305 310 315 320
 Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
 325 330 335
 Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
 340 345 350
 Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
 355 360 365
 Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
 370 375 380
 Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
 385 390 395 400
 Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
 405 410 415
 Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala
 420 425 430
 Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Ser Gln Ile Phe Tyr Asn
 435 440 445
 Ala Ser Pro Ser Thr Leu Ser Ala Thr Met Phe Ile Val Ser Ile Leu
 450 455 460
 Phe Leu Ile Ile Ser Ser Val Ala Ser Leu
 465 470

<210> 201

<211> 477

<212> PRT

<213> Macaca mulatta

<220>

<223> mature Rhesus monkey PH20 EHH17639

<400> 201

3108SEQPC1

Leu Asn Phe Arg Ala Pro Pro Ile Ile Pro Asn Val Pro Phe Leu Trp
 1 5 10 15
 Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asn Glu Pro
 20 25 30
 Leu Asp Met Ser Leu Phe Thr Leu Met Gly Ser Pro Arg Ile Asn Ile
 35 40 45
 Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
 50 55 60
 Pro Tyr Ile Asp Leu Thr Thr Gly Val Thr Val His Gly Gly Ile Pro
 65 70 75 80
 Gln Lys Val Ser Leu Gln Asp His Leu Asp Lys Ser Lys Gln Asp Ile
 85 90 95
 Leu Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
 100 105 110
 Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
 115 120 125
 Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
 130 135 140
 Ser Leu Pro Gln Ala Thr Asp Lys Ala Lys Gln Glu Phe Glu Lys Ala
 145 150 155 160
 Gly Lys Asp Phe Met Leu Glu Thr Ile Lys Leu Gly Arg Ser Leu Arg
 165 170 175
 Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
 180 185 190
 His Tyr Arg Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asp Val Glu Ile
 195 200 205
 Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
 210 215 220
 Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Val Val Val Ala Thr
 225 230 235 240
 Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
 245 250 255
 Pro Asp Ala Lys Asn Pro Leu Pro Val Phe Val Tyr Ala Arg Leu Val
 260 265 270
 Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Arg Glu Glu Leu Val Ser
 275 280 285
 Thr Leu Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
 290 295 300
 Gly Ser Leu Ser Ile Thr Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
 305 310 315 320
 Thr Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
 325 330 335
 Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
 340 345 350
 Ile Arg Lys Asp Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
 355 360 365
 Asn Phe Asp Ile Arg Leu Glu Lys Gly Gly Lys Phe Thr Val His Gly
 370 375 380
 Lys Pro Thr Val Glu Asp Leu Glu Glu Phe Ser Glu Lys Phe Tyr Cys
 385 390 395 400
 Ser Cys Tyr Thr Asn Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
 405 410 415
 Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala
 420 425 430
 Ser Leu Lys Pro Pro Val Glu Thr Glu Gly Ser Pro Pro Ile Phe Tyr
 435 440 445
 Asn Thr Ser Ser Ser Thr Val Ser Thr Thr Met Phe Ile Trp Arg Leu
 450 455 460
 Glu Val Trp Asp Gln Gly Ile Ser Arg Ile Gly Phe Phe
 465 470 475

<210> 202

<211> 475

<212> PRT

<213> Macaca fascicularis

<220>

<223> mature Cynomolgus monkey PH20 P38568.1

3108SEQPC1

<400> 202

Leu Asn Phe Arg Ala Pro Pro Ile Ile Pro Asn Val Pro Phe Leu Trp
 1 5 10 15
 Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asn Glu Pro
 20 25 30
 Leu Asp Met Ser Leu Phe Thr Leu Met Gly Ser Pro Arg Ile Asn Val
 35 40 45
 Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
 50 55 60
 Pro Tyr Ile Asp Leu Thr Thr Gly Val Thr Val His Gly Gly Ile Pro
 65 70 75 80
 Gln Lys Val Ser Leu Gln Asp His Leu Asp Lys Ser Lys Gln Asp Ile
 85 90 95
 Leu Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
 100 105 110
 Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
 115 120 125
 Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
 130 135 140
 Ser Leu Pro Gln Ala Thr Asp Lys Ala Lys Gln Glu Phe Glu Lys Ala
 145 150 155 160
 Gly Lys Asp Phe Met Leu Glu Thr Ile Lys Leu Gly Arg Ser Leu Arg
 165 170 175
 Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
 180 185 190
 His Tyr Arg Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asp Val Glu Ile
 195 200 205
 Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
 210 215 220
 Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Val Val Val Ala Thr
 225 230 235 240
 Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
 245 250 255
 Pro Asp Ala Lys Asn Pro Leu Pro Val Phe Val Tyr Ala Arg Leu Val
 260 265 270
 Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Arg Glu Glu Leu Val Ser
 275 280 285
 Thr Leu Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
 290 295 300
 Gly Ser Leu Ser Ile Thr Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
 305 310 315 320
 Thr Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
 325 330 335
 Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
 340 345 350
 Ile Arg Lys Asp Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
 355 360 365
 Asn Phe Asp Ile Arg Leu Glu Lys Gly Gly Lys Phe Thr Val His Gly
 370 375 380
 Lys Pro Thr Val Glu Asp Leu Glu Glu Phe Ser Glu Lys Phe Tyr Cys
 385 390 395 400
 Ser Cys Tyr Thr Asn Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
 405 410 415
 Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala
 420 425 430
 Ser Leu Lys Pro Pro Val Glu Thr Glu Gly Ser Pro Pro Ile Phe Tyr
 435 440 445
 Asn Thr Ser Ser Ser Thr Val Ser Thr Thr Met Phe Ile Val Asn Ile
 450 455 460
 Leu Phe Leu Ile Ile Ser Ser Val Ala Ser Leu
 465 470 475

<210> 203

<211> 518

<212> PRT

<213> Bos taurus

3108SEQPC1

<220>

<223> Mature cow PH20

<400> 203

```

Leu Asp Phe Arg Ala Pro Pro Leu Ile Ser Asn Thr Ser Phe Leu Trp
 1      5      10      15
Ala Trp Asn Ala Pro Val Glu Arg Cys Val Asn Arg Arg Phe Gln Leu
 20      25      30
Pro Pro Asp Leu Arg Leu Phe Ser Val Lys Gly Ser Pro Gln Lys Ser
 35      40      45
Ala Thr Gly Gln Phe Ile Thr Leu Phe Tyr Ala Asp Arg Leu Gly Tyr
 50      55      60
Tyr Pro His Ile Asp Glu Lys Thr Gly Lys Thr Val Phe Gly Gly Ile
 65      70      75      80
Pro Gln Leu Gly Asn Leu Lys Ser His Met Glu Lys Ala Lys Asn Asp
 85      90      95
Ile Ala Tyr Tyr Ile Pro Asn Asp Ser Val Gly Leu Ala Val Ile Asp
100      105      110
Trp Glu Asn Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp
115      120      125
Val Tyr Arg Asp Glu Ser Val Glu Leu Val Leu Gln Lys Asn Pro Gln
130      135      140
Leu Ser Phe Pro Glu Ala Ser Lys Ile Ala Lys Val Asp Phe Glu Thr
145      150      155      160
Ala Gly Lys Ser Phe Met Gln Glu Thr Leu Lys Leu Gly Lys Leu Leu
165      170      175
Arg Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn
180      185      190
His Asn His Asn Gln Pro Thr Tyr Asn Gly Asn Cys Pro Asp Val Glu
195      200      205
Lys Arg Arg Asn Asp Asp Leu Glu Trp Leu Trp Lys Glu Ser Thr Ala
210      215      220
Leu Phe Pro Ser Val Tyr Leu Asn Ile Arg Leu Lys Ser Thr Gln Asn
225      230      235      240
Ala Ala Leu Tyr Val Arg Asn Arg Val Gln Glu Ala Ile Arg Leu Ser
245      250      255
Lys Ile Ala Ser Val Glu Ser Pro Leu Pro Val Phe Val Tyr Ala Arg
260      265      270
Pro Val Phe Thr Asp Gly Ser Ser Thr Tyr Leu Ser Gln Gly Asp Leu
275      280      285
Val Asn Ser Val Gly Glu Ile Val Ser Leu Gly Ala Ser Gly Ile Ile
290      295      300
Met Trp Gly Ser Leu Asn Leu Ser Leu Ser Met Gln Ser Cys Met Asn
305      310      315      320
Leu Gly Thr Tyr Leu Asn Thr Thr Leu Asn Pro Tyr Ile Ile Asn Val
325      330      335
Thr Leu Ala Ala Lys Met Cys Ser Gln Val Leu Cys His Asn Glu Gly
340      345      350
Val Cys Thr Arg Lys His Trp Asn Ser Ser Asp Tyr Leu His Leu Asn
355      360      365
Pro Met Asn Phe Ala Ile Gln Thr Gly Glu Gly Gly Lys Tyr Thr Val
370      375      380
Pro Gly Thr Val Thr Leu Glu Asp Leu Gln Lys Phe Ser Asp Thr Phe
385      390      395      400
Tyr Cys Ser Cys Tyr Ala Asn Ile His Cys Lys Lys Arg Val Asp Ile
405      410      415
Lys Asn Val His Ser Val Asn Val Cys Met Ala Glu Asp Ile Cys Ile
420      425      430
Asp Ser Pro Val Lys Leu Gln Pro Ser Asp His Ser Ser Ser Gln Glu
435      440      445
Ala Ser Thr Thr Thr Phe Ser Ile Ser Pro Ser Thr Thr Thr Ala
450      455      460
Thr Val Ser Pro Cys Thr Pro Glu Lys His Ser Pro Glu Cys Leu Lys
465      470      475      480
Val Arg Cys Ser Glu Val Ile Pro Asn Val Thr Gln Lys Ala Cys Gln
485      490      495
Ser Val Lys Leu Lys Asn Ile Ser Tyr Gln Ser Pro Ile Gln Asn Ile
500      505      510

```

3108SEQPC1

Lys Asn Gln Thr Thr Tyr
515

<210> 204
<211> 439
<212> PRT
<213> Bos taurus

<220>
<223> mature cow PH20 AAP55713

<400> 204
Leu Asp Phe Arg Ala Pro Pro Leu Ile Ser Asn Thr Ser Phe Leu Trp
1 5 10 15
Ala Trp Asn Ala Pro Val Glu Arg Cys Val Asn Arg Arg Phe Gln Leu
20 25 30
Pro Pro Asp Leu Arg Leu Phe Ser Val Lys Gly Ser Pro Gln Lys Ser
35 40 45
Ala Thr Gly Gln Phe Ile Thr Leu Phe Tyr Ala Asp Arg Leu Gly Tyr
50 55 60
Tyr Pro His Ile Asp Glu Lys Thr Gly Lys Thr Val Phe Gly Gly Ile
65 70 75 80
Pro Gln Leu Gly Asn Leu Lys Ser His Leu Glu Lys Ala Lys Asn Asp
85 90 95
Ile Ala Tyr Tyr Ile Pro Asn Asp Ser Val Gly Leu Ala Val Ile Asp
100 105 110
Trp Glu Asn Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp
115 120 125
Val Tyr Arg Asp Glu Ser Val Glu Leu Val Leu Gln Lys Asn Pro Gln
130 135 140
Leu Ser Phe Pro Glu Ala Ser Lys Ile Ala Lys Val Asp Phe Glu Thr
145 150 155 160
Ala Gly Lys Ser Phe Met Gln Glu Thr Leu Lys Leu Gly Lys Leu Leu
165 170 175
Arg Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn
180 185 190
His Asn His Asn Gln Pro Thr Tyr Asn Gly Asn Cys Pro Asp Val Glu
195 200 205
Lys Arg Arg Asn Asp Asp Leu Glu Trp Leu Trp Lys Glu Ser Thr Ala
210 215 220
Leu Phe Pro Ser Val Tyr Leu Asn Ile Arg Leu Lys Ser Thr Gln Asn
225 230 235 240
Ala Ala Leu Tyr Val Arg Asn Arg Val Gln Glu Ala Ile Arg Leu Ser
245 250 255
Lys Ile Ala Ser Val Glu Ser Pro Leu Pro Val Phe Val Tyr Ala Arg
260 265 270
Pro Val Phe Thr Asp Gly Ser Ser Thr Tyr Leu Ser Gln Gly Asp Leu
275 280 285
Val Asn Ser Val Gly Glu Ile Val Ser Leu Gly Ala Ser Gly Ile Ile
290 295 300
Met Trp Gly Ser Leu Asn Leu Ser Leu Ser Val Gln Ser Cys Met Asn
305 310 315 320
Leu Gly Thr Tyr Leu Asn Thr Thr Leu Asn Pro Tyr Ile Ile Asn Val
325 330 335
Thr Leu Ala Ala Lys Met Cys Ser Gln Val Leu Cys His Asp Gly Gly
340 345 350
Val Cys Thr Arg Lys His Trp Asn Ser Ser Asp Tyr Leu His Leu Asn
355 360 365
Pro Met Asn Phe Ala Ile Gln Thr Gly Glu Gly Gly Lys Tyr Thr Val
370 375 380
Pro Gly Thr Leu Thr Leu Glu Asp Leu Gln Lys Phe Ser Asp Thr Phe
385 390 395 400
Tyr Cys Ser Cys Tyr Ser Asn Leu Ser Cys Lys Lys Arg Val Asp Ile
405 410 415
Lys Asn Val His Ser Val Asp Val Cys Met Ala Glu Asp Val Cys Ile
420 425 430
Asp Ala Phe Leu Lys Pro Pro
435

3108SEQPC1

<210> 205
 <211> 477
 <212> PRT
 <213> Mus musculus

<220>
 <223> Mature mouse PH20 NP_001073344.1

<400> 205

Val	Asp	Tyr	Arg	Ala	Ala	Pro	Ile	Leu	Ser	Asn	Thr	Thr	Phe	Leu	Trp
1				5					10					15	
Ile	Trp	Asn	Val	Pro	Thr	Glu	Arg	Cys	Val	Gly	Asn	Val	Asn	Asp	Pro
		20						25					30		
Ile	Asp	Leu	Ser	Phe	Phe	Ser	Leu	Ile	Gly	Ser	Pro	Arg	Lys	Thr	Ala
		35					40					45			
Thr	Gly	Gln	Pro	Val	Thr	Leu	Phe	Tyr	Val	Asp	Arg	Leu	Gly	Leu	Tyr
	50					55				60					
Pro	His	Ile	Asp	Ala	Asn	Gln	Ala	Glu	His	Tyr	Gly	Gly	Ile	Pro	Gln
65					70					75				80	
Arg	Gly	Asp	Tyr	Gln	Ala	His	Leu	Arg	Lys	Ala	Lys	Thr	Asp	Ile	Glu
			85						90				95		
His	Tyr	Ile	Pro	Asp	Asp	Lys	Leu	Gly	Leu	Ala	Ile	Ile	Asp	Trp	Glu
			100					105					110		
Glu	Trp	Arg	Pro	Thr	Trp	Leu	Arg	Asn	Trp	Lys	Pro	Lys	Asp	Asn	Tyr
		115					120					125			
Arg	Asn	Lys	Ser	Ile	Glu	Leu	Val	Gln	Ser	Thr	Asn	Pro	Gly	Leu	Ser
	130					135					140				
Ile	Thr	Glu	Ala	Thr	Gln	Lys	Ala	Ile	Gln	Gln	Phe	Glu	Glu	Ala	Gly
145					150					155				160	
Arg	Lys	Phe	Met	Glu	Gly	Thr	Leu	His	Leu	Gly	Lys	Phe	Leu	Arg	Pro
			165						170					175	
Asn	Gln	Leu	Trp	Gly	Tyr	Tyr	Leu	Phe	Pro	Asp	Cys	Tyr	Asn	Asn	Lys
		180						185					190		
Phe	Gln	Asp	Pro	Lys	Tyr	Asp	Gly	Gln	Cys	Pro	Ala	Val	Glu	Lys	Lys
		195					200					205			
Arg	Asn	Asp	Asn	Leu	Lys	Trp	Leu	Trp	Lys	Ala	Ser	Thr	Gly	Leu	Tyr
	210					215						220			
Pro	Ser	Val	Tyr	Leu	Lys	Lys	Asp	Leu	Lys	Ser	Asn	Arg	Gln	Ala	Thr
225					230					235				240	
Leu	Tyr	Val	Arg	Tyr	Arg	Val	Val	Glu	Ala	Ile	Arg	Val	Ser	Lys	Val
			245						250					255	
Gly	Asn	Ala	Ser	Asp	Pro	Val	Pro	Ile	Phe	Val	Tyr	Ile	Arg	Leu	Val
		260						265					270		
Phe	Thr	Asp	Arg	Thr	Ser	Glu	Tyr	Leu	Leu	Glu	Asp	Asp	Leu	Val	Asn
		275					280					285			
Thr	Ile	Gly	Glu	Ile	Val	Ala	Leu	Gly	Thr	Ser	Gly	Ile	Ile	Ile	Trp
	290					295					300				
Asp	Ala	Met	Ser	Leu	Ala	Gln	Arg	Ala	Ala	Gly	Cys	Pro	Ile	Leu	His
305					310					315				320	
Lys	Tyr	Met	Gln	Thr	Thr	Leu	Asn	Pro	Tyr	Ile	Val	Asn	Val	Thr	Leu
			325						330					335	
Ala	Ala	Lys	Met	Cys	Ser	Gln	Thr	Leu	Cys	Asn	Glu	Lys	Gly	Met	Cys
		340						345					350		
Ser	Arg	Arg	Lys	Glu	Ser	Ser	Asp	Val	Tyr	Leu	His	Leu	Asn	Pro	Ser
		355					360					365			
His	Phe	Asp	Ile	Met	Leu	Thr	Glu	Thr	Gly	Lys	Tyr	Glu	Val	Leu	Gly
	370					375					380				
Asn	Pro	Arg	Val	Gly	Asp	Leu	Glu	Tyr	Phe	Ser	Glu	His	Phe	Lys	Cys
385					390					395				400	
Ser	Cys	Phe	Ser	Arg	Met	Thr	Cys	Lys	Glu	Thr	Ser	Asp	Val	Lys	Asn
			405						410					415	
Val	Gln	Asp	Val	Asn	Val	Cys	Val	Gly	Asp	Asn	Val	Cys	Ile	Lys	Ala
		420						425					430		
Lys	Val	Glu	Pro	Asn	Pro	Ala	Phe	Tyr	Leu	Leu	Pro	Gly	Lys	Ser	Leu
		435					440					445			
Leu	Phe	Met	Thr	Thr	Leu	Gly	His	Val	Leu	Tyr	His	Leu	Pro	Gln	Asp
	450					455					460				

3108SEQPC1

Ile Phe Val Phe Pro Arg Lys Thr Leu Val Ser Thr Pro
 465 470 475

<210> 206

<211> 477

<212> PRT

<213> Rattus norvegicus

<220>

<223> Mature rat PH20 NP_446419.1

<400> 206

Val Asp Tyr Arg Ala Thr Pro Val Leu Ser Asp Thr Thr Phe Val Trp
 1 5 10 15
 Val Trp Asn Val Pro Thr Glu Ala Cys Val Glu Asn Val Thr Glu Pro
 20 25 30
 Ile Asp Leu Ser Phe Phe Ser Leu Ile Gly Ser Pro Arg Lys Thr Ala
 35 40 45
 Ile Gly Gln Pro Val Thr Leu Phe Tyr Val Asp Arg Leu Gly Asn Tyr
 50 55 60
 Pro His Ile Asp Ala Gln Gln Thr Glu His His Gly Gly Ile Pro Gln
 65 70 75 80
 Lys Gly Asp Leu Thr Thr His Leu Val Lys Ala Lys Glu Asp Val Glu
 85 90 95
 Arg Tyr Ile Pro Thr Asp Lys Leu Gly Leu Ala Ile Ile Asp Trp Glu
 100 105 110
 Glu Trp Arg Pro Thr Trp Met Arg Asn Trp Thr Pro Lys Asp Ile Tyr
 115 120 125
 Arg Asn Lys Ser Ile Glu Leu Val Gln Ala Ala Asp Pro Ala Ile Asn
 130 135 140
 Ile Thr Glu Ala Thr Val Arg Ala Lys Ala Gln Phe Glu Gly Ala Ala
 145 150 155 160
 Lys Glu Phe Met Glu Gly Thr Leu Lys Leu Gly Lys His Ile Arg Pro
 165 170 175
 Lys His Leu Trp Gly Phe Tyr Leu Phe Pro Asp Cys Tyr Asn Asn Lys
 180 185 190
 Phe Gln Val Asp Asn Tyr Asp Gly Gln Cys Pro Asp Val Glu Lys Lys
 195 200 205
 Arg Asn Asp Asp Leu Asp Trp Leu Trp Lys Glu Ser Thr Gly Leu Tyr
 210 215 220
 Pro Ser Val Tyr Leu Lys Lys Asp Leu Lys Ser Ser Arg Lys Ala Thr
 225 230 235 240
 Leu Tyr Val Arg Tyr Arg Val Leu Glu Ser Ile Arg Val Ser Lys Val
 245 250 255
 Ser Asp Glu Ser Asn Pro Val Pro Ile Phe Val Tyr Ile Arg Leu Val
 260 265 270
 Phe Thr Asp His Val Ser Glu Tyr Leu Leu Glu Asp Asp Leu Val Asn
 275 280 285
 Thr Ile Gly Glu Ile Val Ala Gln Gly Thr Ser Gly Ile Ile Ile Trp
 290 295 300
 Asp Ala Met Ser Leu Ala Gln Arg Ser Ala Gly Cys Pro Ile Leu Arg
 305 310 315 320
 Gln Tyr Met Lys Thr Thr Leu Asn Pro Tyr Ile Val Asn Val Thr Leu
 325 330 335
 Ala Ala Lys Met Cys Ser Gln Thr Leu Cys Lys Glu Lys Gly Met Cys
 340 345 350
 Ser Arg Lys Thr Glu Ser Ser Asp Ala Tyr Leu His Leu Asp Pro Ser
 355 360 365
 Ser Phe Ser Ile Asn Val Thr Glu Ala Gly Lys Tyr Glu Val Leu Gly
 370 375 380
 Lys Pro Glu Val Lys Asp Leu Glu Tyr Phe Ser Glu His Phe Lys Cys
 385 390 395 400
 Ser Cys Phe Ser Lys Met Thr Cys Glu Glu Thr Ser Asp Met Arg Ser
 405 410 415
 Ile Gln Asp Val Asn Val Cys Met Gly Asp Asn Val Cys Ile Lys Ala
 420 425 430
 Thr Leu Gly Pro Asn Ser Ala Phe His Leu Leu Pro Gly Lys Gly Leu
 435 440 445

3108SEQPC1

Leu Leu Met Thr Thr Leu Ala His Ile Leu His His Leu Pro His Asp
 450 455 460
 Ile Phe Val Phe Pro Trp Lys Met Leu Val Ser Thr Pro
 465 470 475

<210> 207

<211> 510

<212> PRT

<213> *Oryctolagus cuniculus*

<220>

<223> Mature rabbit PH20 NP_001076141.1

<400> 207

Ala Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1 5 10 15
 Ala Trp Asn Ala Pro Thr Glu Phe Cys Leu Gly Lys Ser Gly Glu Pro
 20 25 30
 Leu Asp Met Ser Leu Phe Ser Leu Phe Gly Ser Pro Arg Lys Asn Lys
 35 40 45
 Thr Gly Gln Gly Ile Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
 50 55 60
 Pro Tyr Ile Asp Pro His Thr Gly Ala Ile Val His Gly Arg Ile Pro
 65 70 75 80
 Gln Leu Gly Pro Leu Gln Gln His Leu Thr Lys Leu Arg Gln Glu Ile
 85 90 95
 Leu Tyr Tyr Met Pro Lys Asp Asn Val Gly Leu Ala Val Ile Asp Trp
 100 105 110
 Glu Glu Trp Leu Pro Thr Trp Leu Arg Asn Trp Lys Pro Lys Asp Ile
 115 120 125
 Tyr Arg Ile Lys Ser Ile Glu Leu Val Lys Ser Gln His Pro Gln Tyr
 130 135 140
 Asn His Ser Tyr Ala Thr Glu Lys Ala Lys Arg Asp Phe Glu Lys Ala
 145 150 155 160
 Gly Lys Asp Phe Met Glu Glu Thr Leu Lys Leu Gly Arg Leu Leu Arg
 165 170 175
 Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
 180 185 190
 His Tyr Asp Lys Pro Asn Leu Tyr Lys Gly Ser Cys Phe Asp Ile Glu
 195 200 205
 Lys Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Lys Glu Ser Thr Ala
 210 215 220
 Leu Phe Pro Ser Val Tyr Leu Thr Ser Arg Ala Arg Ser Ala Thr Ala
 225 230 235 240
 Leu Ser Lys Leu Tyr Val Val Arg Asn Arg Val His Glu Ala Ile Arg
 245 250 255
 Val Ser Lys Ile Pro Asp Asp Lys Ser Pro Leu Pro Asn Phe Val Tyr
 260 265 270
 Thr Arg Leu Val Phe Thr Asp Gln Ile Phe Gln Phe Leu Ser His His
 275 280 285
 Asp Leu Val Tyr Thr Ile Gly Glu Ile Val Ala Leu Gly Ala Ser Gly
 290 295 300
 Ile Val Val Trp Gly Ser Gln Ser Leu Ala Arg Ser Met Lys Ser Cys
 305 310 315 320
 Leu His Leu Asp Asn Tyr Met Lys Thr Ile Leu Asn Pro Tyr Leu Ile
 325 330 335
 Asn Val Thr Leu Ala Ala Lys Met Cys Asn Gln Val Leu Cys Gln Glu
 340 345 350
 Gln Gly Val Cys Thr Arg Lys Asn Trp Asn Pro Asn Asp Tyr Leu His
 355 360 365
 Leu Asn Pro Gly Asn Phe Ala Ile Gln Leu Gly Ser Asn Gly Thr Tyr
 370 375 380
 Lys Val Asp Gly Lys Pro Thr Leu Thr Asp Leu Glu Gln Phe Ser Lys
 385 390 395 400
 Asn Phe Gln Cys Ser Cys Tyr Thr Asn Leu Asn Cys Lys Glu Arg Thr
 405 410 415
 Asp Met Asn Asn Val Arg Thr Val Asn Val Cys Ala Val Glu Asn Val
 420 425 430

3108SEQPC1

Cys Ile Asp Thr Asn Val Gly Pro Gln Ala Val Thr Tyr Ala Pro Lys
 435 440 445
 Glu Lys Lys Asp Val Ala His Ile Leu Ser Asn Thr Thr Ser Ile Asn
 450 455 460
 Ser Ser Thr Thr Met Ser Leu Pro Phe Pro Arg Lys His Val Ser Gly
 465 470 475 480
 Cys Leu Leu Val Leu Cys Met Tyr Ser Gln Tyr Leu Asn Ile Cys Tyr
 485 490 495
 Arg Leu Val Ala Ile Gly Ile Gln His Gly Tyr Tyr Leu Lys
 500 505 510

<210> 208

<211> 494

<212> PRT

<213> *Cavia porcellus*

<220>

<223> mature guinea pig PH20 NP_001166492.1

<400> 208

Asp Lys Arg Ala Pro Pro Leu Ile Pro Asn Val Pro Leu Leu Trp Val
 1 5 10 15
 Trp Asn Ala Pro Thr Glu Phe Cys Ile Gly Gly Thr Asn Gln Pro Leu
 20 25 30
 Asp Met Ser Phe Phe Ser Ile Val Gly Thr Pro Arg Lys Asn Ile Thr
 35 40 45
 Gly Gln Ser Ile Thr Leu Tyr Tyr Val Asp Arg Leu Gly Tyr Tyr Pro
 50 55 60
 Tyr Ile Asp Pro His Thr Gly Ala Ile Val His Gly Gly Leu Pro Gln
 65 70 75 80
 Leu Met Asn Leu Gln Gln His Leu Arg Lys Ser Arg Gln Asp Ile Leu
 85 90 95
 Phe Tyr Met Pro Thr Asp Ser Val Gly Leu Ala Val Ile Asp Trp Glu
 100 105 110
 Glu Trp Arg Pro Thr Trp Thr Arg Asn Trp Arg Pro Lys Asp Ile Tyr
 115 120 125
 Arg Asn Lys Ser Ile Glu Leu Val Lys Ser Gln His Pro Gln Tyr Asn
 130 135 140
 His Ser Tyr Ala Val Ala Val Ala Lys Arg Asp Phe Glu Arg Thr Gly
 145 150 155 160
 Lys Ala Phe Met Leu Glu Thr Leu Lys Leu Gly Lys Ser Leu Arg Pro
 165 170 175
 Ser Ser Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn Thr His
 180 185 190
 Phe Thr Lys Pro Asn Tyr Asp Gly His Cys Pro Pro Ile Glu Leu Gln
 195 200 205
 Arg Asn Asn Asp Leu Gln Trp Leu Trp Asn Asp Ser Thr Ala Leu Tyr
 210 215 220
 Pro Ser Val Tyr Leu Thr Ser Arg Val Arg Ser Ser Gln Asn Gly Ala
 225 230 235 240
 Leu Tyr Val Arg Asn Arg Val His Glu Ser Ile Arg Val Ser Lys Leu
 245 250 255
 Met Asp Asp Lys Asn Pro Leu Pro Ile Tyr Val Tyr Ile Arg Leu Val
 260 265 270
 Phe Thr Asp Gln Thr Thr Thr Phe Leu Glu Leu Asp Asp Leu Val His
 275 280 285
 Ser Val Gly Glu Ile Val Pro Leu Gly Val Ser Gly Ile Ile Ile Trp
 290 295 300
 Gly Ser Leu Ser Leu Thr Arg Ser Leu Val Ser Cys Ile Gly Leu Glu
 305 310 315 320
 Asn Tyr Met Lys Gly Thr Leu Leu Pro Tyr Leu Ile Asn Val Thr Leu
 325 330 335
 Ala Ala Lys Met Cys Gly Gln Val Leu Cys Lys Asn Gln Gly Ile Cys
 340 345 350
 Thr Arg Lys Asp Trp Asn Thr Asn Thr Tyr Leu His Leu Asn Ala Thr
 355 360 365
 Asn Phe Asp Ile Glu Leu Gln Gln Asn Gly Lys Phe Val Val His Gly
 370 375 380

3108SEQPC1

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

<210> 209
 <211> 540
 <212> PRT
 <213> vulpes vulpes

<220>
 <223> Precursor Red Fox PH20

<400> 209
 Met Gly Val Leu Arg Phe Gln Asn Ile Phe Phe Arg Ser Phe Leu Gly
 1 5 10 15
 Ser Ser Gly Thr Gln Ala Val Phe Ile Phe Leu Leu Ile Pro Arg
 20 25 30
 Cys Leu Thr Gln Glu Phe Arg Ala Pro Pro Phe Ile Pro Asn Val Ser
 35 40 45
 Phe Leu Trp Gly Trp Asn Ala Pro Thr Glu Leu Cys Ala Lys Arg Phe
 50 55 60
 Asn Val Gln Leu Asp Leu Asn Leu Phe Ser Leu Ile Gly Ser Pro Leu
 65 70 75 80
 Lys Thr Val Val Gly Gln Gly Ile Ala Ile Phe Tyr Ala Asp Arg Leu
 85 90 95
 Gly Tyr Tyr Pro His Ile Asn Lys Thr Thr Gly Lys His Val Asn Gly
 100 105 110
 Gly Ile Pro Gln Leu Gly Ser Leu Lys Lys His Leu Asp Lys Ala Lys
 115 120 125
 Lys Asp Ile Ser His Tyr Ile Glu Thr Asp Ser Met Gly Leu Ala Val
 130 135 140
 Ile Asp Trp Asp Ser Trp Arg Pro Asn Trp Ala Arg Asn Trp Arg Pro
 145 150 155 160
 Lys His Ile Tyr Lys Glu Gln Ser Ile Asp Leu Ala Gln Gln Gln His
 165 170 175
 Ile His Leu Asn Leu Thr Glu Val Thr Gln Ile Ala Gln Ala Asp Phe
 180 185 190
 Glu Lys Ala Ala Arg Cys Phe Met Gln Glu Thr Leu Lys Leu Gly Lys
 195 200 205
 Phe Leu Arg Pro Asn Tyr Leu Trp Gly Phe Tyr Leu Tyr Pro Asp Cys
 210 215 220
 Tyr Asn Tyr Asn Tyr Lys Asn Pro Asn Tyr Asn Gly Ser Cys Tyr Asp
 225 230 235 240
 Ile Glu Glu Arg Arg Asn Asp Glu Ile Asp Trp Leu Trp Lys Glu Ser
 245 250 255
 Thr Ala Leu Phe Pro Ser Ile Tyr Leu Lys Ser Lys Leu Lys Ser Ser
 260 265 270
 Pro Phe Thr Ala Leu Tyr Val Arg Asn Arg Val Leu Glu Ala Ile Arg
 275 280 285
 Val Ser Lys Val Lys Asp Ile Lys His Pro Leu Pro Ile Phe Val Tyr
 290 295 300
 Ala Arg Pro Val Phe Thr Asp Val Leu Leu Thr Tyr Leu Thr Glu Asp
 305 310 315 320
 Asp Leu Val Asn Thr Ile Gly Glu Ser Val Ser Leu Gly Val Ser Gly
 325 330 335
 Ile Val Met Trp Gly Ser Leu Asn Leu Thr Glu Asn Val Gln Ile Cys
 340 345 350

3108SEQPC1

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

<210> 210
 <211> 505
 <212> PRT
 <213> vulpes vulpes

<220>
 <223> Mature Red Fox PH20 Q29152

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

3108SEQPC1

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

<210> 211

<211> 585

<212> PRT

<213> Artificial Sequence

<220>

<223> Human Serum Albumin (aa 25-609)

<400> 211

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

3108SEQPC1

210 215 220
 Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys
 225 230 235 240
 Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
 245 250 255
 Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
 260 265 270
 Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
 275 280 285
 Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
 290 295 300
 Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
 305 310 315 320
 Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
 325 330 335
 Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
 340 345 350
 Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
 355 360 365
 Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
 370 375 380
 Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
 385 390 395 400
 Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
 405 410 415
 Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
 420 425 430
 Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
 435 440 445
 Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
 450 455 460
 Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
 465 470 475 480
 Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
 485 490 495
 Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
 500 505 510
 Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
 515 520 525
 Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
 530 535 540
 Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
 545 550 555 560
 Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
 565 570 575
 Ala Ala Ser Gln Ala Ala Leu Gly Leu
 580 585

<210> 212
 <211> 1662
 <212> DNA
 <213> Homo sapiens

<220>
 <223> HAS3 variant 1 cDNA

<400> 212
 atgccggtgc agctgacgac agccctgcgt gtgggtgggca ccagcctggt tgccctggca 60
 gtgctgggtg gcatcctggc agcctatgtg acgggctacc agttcatcca cacggaaaag 120
 cactacctgt ccttcggcct gtacggcgcc atcctgggcc tgcacctgct cattcagagc 180
 ctgtttgcct tcctggagca ccggcgcatg cgacgtgccg gccaggccct gaagctgccc 240
 tccccgcggc ggggctcggg ggccactgtg attgccgcat accaggagga ccctgactac 300
 ttgcgcaagt gcctgcgctc ggcccagcgc atctccttcc ctgacctcaa ggtggtcatg 360
 gtgggtggatg gcaaccgcca ggaggacgcc tacatgctgg acatcttcca cgagggtgctg 420
 ggcggcaccg agcaggccgg cttctttgtg tggcgagca acttccatga ggcaggcgag 480
 ggtgagacgg aggccagcct gcaggagggc atggaccgtg tgcgggatgt ggtgcgggcc 540
 agcaccttct cgtgcatcat gcagaagtgg ggaggcaagc gcgaggtcat gtacacggcc 600

[illegible]

```
<210> 213
<211> 10836
<212> DNA
<213> Artificial Sequence
```

2400	ggtttgtccgc	cagaaaccacag	gtaagtgcgcg	tgltgtgttc	ccgcggtccct	ggtcctctta	2400
2340	aggtgtgggg	agaaaccgtat	ataagtgcag	tagtgcgcgt	gaaactgtct	ttttcgcaacg	2340
2280	gaagtgtgcg	cgggtttaaac	tgggaaagt	atgtcgtgtg	ctgtctccgc	ctttttccgc	2280
2220	cactccgccac	agttcccgcac	aggttgggtg	cgatgtaccc	ggtgtccctga	ggtgtccctga	2220
2160	atccatcgag	tggagaaagag	catgttgtag	gtcccgtgtc	ccgtgttggtg	gacagagcgca	2160
2100	ccaactaacgt	agaaaccagga	gattcgtcgc	ttccgcgcgc	ctcaaccgcg	cgtctctgtc	2100
2040	taattctatc	aaaaagbact	gtcccgtcct	tggggaatcc	caggggaccgt	cgttaaacctc	2040
1980	aaatttatcg	atgtccctccc	gttcaaccccc	ccccccaaacc	gtcccctgag	gagcttgagag	1980
1920	agacataata	gtcaacagaca	tacaaactaa	agaaattaca	aaaacaatatg	caaaattcga	1920
1860	tcgttttaact	tttaaaagaa	aagggtgagt	tgggtggtat	gtgtgacggg	aaagaaatagt	1860
1800	atcgatttga	ggagagagaca	gagacagatc	catgttgatga	gttgacaaggat	ctcgacggtga	1800
1740	atcgtttcag	accacccctc	caaccctcgg	gggaccctgac	aggccctggag	gaaatagaaag	1740
1680	aaagaattgt	tttctgttac	tttctatagt	gaaatagagt	aggcaggggat	attcacctatt	1680
1620	aaacaaattgg	ctgttgttata	taaaatttat	cataatgtata	gtagggagct	tgttaggtttt	1620
1560	gaatgaacca	gaaattatgg	aatatagtaa	atgtgcgaagt	tgtgtgaaatt	tggtttaacat	1560
1500	taacataatc	acacagcttaa	tacactctct	aatgtgaaga	tcgcaaaaacc	agcaagaaat	1500
1440	taataaatctc	ctggaaacaga	ttttgaaatca	cacgaaacgg	tgtgagtggtg	acagaaat	1440
1380	ttgggtttgc	tcgaaaaaac	tcatttgcac	cactgtctgt	ccctggaaatg	ctagtgtgag	1380
1320	gtctccaggca	agatctcttg	ctgttgaaag	atacctaag	gatcaacagc	tcctgtgggat	1320
1260	gtctgaaggct	attgaggtcc	aacagcatct	gttgcacaatc	acagtcttgg	gcatccaagca	1260
1200	gagcctctgac	gtacaggtcca	gcaaatattt	gtctgtgata	gtctcagcag	agacaacattt	1200
1140	atgagccttgg	ttctctgtgtg	tcctgtggagc	agcagtagagc	actatgtcgc	cagcgttcaat	1140
1080	agtgagctccc	accaaaggccaa	agbaagagt	gttgcagaga	gaaaaaagag	cagtgtggat	1080
1020	gagggacaact	tggagaagt	aatatatata	atataaagt	gtaaaaaatg	aaacttatgg	1020
960	aaaagttaaga	ccaccgcaca	gcaagcggcc	gctgatcttc	agaccttgag	gtaggagatat	960
900	caaaagtatag	agataaaaaga	caccaagaa	gctttagaca	agatatagaga	agagcaaaaac	900
840	tcagtatcag	aagaaacttag	atcatatat	atacagtag	caaccctcta	tgtgtgtcac	840
780	ctgtttagaa	catcagaag	ctgttagacaa	atacttgtag	agctacaacc	atcccctcag	780
720	aaataaaaac	ataatagtat	ggcaagcgag	gagctagaa	gatctgcaggt	taatcccctgc	720
660	ggaggaatta	gattcgcgat	ggaaaaaaat	cgtttaagc	cagggtggaaa	gaaaaaatat	660
600	attttgacta	gctgaggtcta	gaaagttaga	gattgtgtgc	agagctgtcag	tattaaagcgg	600
540	cgtcttctgc	aagcgtcgac	ggcaagggc	gagggtgtgc	gactgttgag	tacgccaasa	540
480	cgtccgaaca	ggagaaagtga	agccaagaag	aaaccagagg	agctctctcgc	acgcagagat	480
420	ctctgttaac	ttagatctcc	ctgagaccct	ttagtctcagt	tgtgaaaatat	ctagcagctga	420
360	taagcctcca	taagcctctgc	cttgagtgtc	tcaagttagtg	tgtgtcccctc	tgtgtgttga	360
300	ttctgttata	gaccagatct	gagccttgga	gtctcttgc	taactagga	accacactgt	300
240	tgaattgcgc	cattgcagag	atatgttat	taagtgtcta	gtctgatata	taaaacgtgtc	240
180	gtacagtctg	gacttatag	gaaagcaaca	gacgtgtctg	acatgtatgtg	gacgaaccac	180
120	gtacagctcc	tcaagaagca	agaaaaagca	cgtgtgcatc	cgatgtgtgtg	aaatataagtg	120

[illegible]

3108SEQPC1

```
gccaatacgc caaacccgcct ctccccgcgc gttggccgat tcattaatgc agctggcacg 10620
acagggtttcc cgactggaaa gcgggcagtg agcgcaacgc aattaatgtg agttagctca 10680
ctcattaggc accccaggct ttacacttta tgcttccggc tcgtatgttg tgtggaattg 10740
tgagcggata acaatttcac acaggaaaaca gctatgacca tgattacgcc aagcgcgcaa 10800
ttaaccctca ctaaagggaa caaaagctgg agctgc 10836
```