

SEQUENCE LISTING

<110> Encodia, Inc
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<120> MODIFIED CLEAVASES, USES THEREOF AND RELATED KITS

<130> 4614-2001340

<150> US 62/823,927
 <151> 2019-03-26

<150> US 62/824,157
 <151> 2019-03-26

<150> US 62/931,737
 <151> 2019-11-06

<160> 41

<170> PatentIn version 3.5

<210> 1
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> DPP3 motif

<220>
 <221> misc_feature
 <222> (3)..(4)
 <223> Xaa can be any naturally occurring amino acid

<400> 1

His Glu Xaa Xaa Gly His
 1 5

<210> 2
 <211> 6
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 <213> Artificial Sequence

<220>
<223> DPP3 motif

<220>
<221> misc_feature
<222> (3)..(3)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (6)..(6)
<223> Xaa can be naturally occurring glutamic acid (Glu) or aspartic acid (Asp)

<400> 2

Glu Glu Xaa Arg Ala Xaa
1 5

<210> 3
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> P5 primer

<400> 3
aatgatacgg cgaccaccga 20

<210> 4
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> P7 primer

<400> 4
caagcagaag acggcatacg agat 24

<210> 5
<211> 737
<212> PRT
<213> Homo sapiens

<220>

<221> Dipeptidyl peptidase 3 (DPP3)

<222> (1)..(737)

<223> UniProt Accession No. Q9NY33

<400> 5

Met Ala Asp Thr Gln Tyr Ile Leu Pro Asn Asp Ile Gly Val Ser Ser
1 5 10 15

Leu Asp Cys Arg Glu Ala Phe Arg Leu Leu Ser Pro Thr Glu Arg Leu
20 25 30

Tyr Ala Tyr His Leu Ser Arg Ala Ala Trp Tyr Gly Gly Leu Ala Val
35 40 45

Leu Leu Gln Thr Ser Pro Glu Ala Pro Tyr Ile Tyr Ala Leu Leu Ser
50 55 60

Arg Leu Phe Arg Ala Gln Asp Pro Asp Gln Leu Arg Gln His Ala Leu
65 70 75 80

Ala Glu Gly Leu Thr Glu Glu Glu Tyr Gln Ala Phe Leu Val Tyr Ala
85 90 95

Ala Gly Val Tyr Ser Asn Met Gly Asn Tyr Lys Ser Phe Gly Asp Thr
100 105 110

Lys Phe Val Pro Asn Leu Pro Lys Glu Lys Leu Glu Arg Val Ile Leu
115 120 125

Gly Ser Glu Ala Ala Gln Gln His Pro Glu Glu Val Arg Gly Leu Trp
130 135 140

Gln Thr Cys Gly Glu Leu Met Phe Ser Leu Glu Pro Arg Leu Arg His
145 150 155 160

Leu Gly Leu Gly Lys Glu Gly Ile Thr Thr Tyr Phe Ser Gly Asn Cys

165	170	175
Thr Met Glu Asp Ala Lys Leu Ala Gln Asp Phe Leu Asp Ser Gln Asn		
180	185	190
Leu Ser Ala Tyr Asn Thr Arg Leu Phe Lys Glu Val Asp Gly Glu Gly		
195	200	205
Lys Pro Tyr Tyr Glu Val Arg Leu Ala Ser Val Leu Gly Ser Glu Pro		
210	215	220
Ser Leu Asp Ser Glu Val Thr Ser Lys Leu Lys Ser Tyr Glu Phe Arg		
225	230	235
Gly Ser Pro Phe Gln Val Thr Arg Gly Asp Tyr Ala Pro Ile Leu Gln		
245	250	255
Lys Val Val Glu Gln Leu Glu Lys Ala Lys Ala Tyr Ala Ala Asn Ser		
260	265	270
His Gln Gly Gln Met Leu Ala Gln Tyr Ile Glu Ser Phe Thr Gln Gly		
275	280	285
Ser Ile Glu Ala His Lys Arg Gly Ser Arg Phe Trp Ile Gln Asp Lys		
290	295	300
Gly Pro Ile Val Glu Ser Tyr Ile Gly Phe Ile Glu Ser Tyr Arg Asp		
305	310	315
Pro Phe Gly Ser Arg Gly Glu Phe Glu Gly Phe Val Ala Val Val Asn		
325	330	335
Lys Ala Met Ser Ala Lys Phe Glu Arg Leu Val Ala Ser Ala Glu Gln		
340	345	350
Leu Leu Lys Glu Leu Pro Trp Pro Pro Thr Phe Glu Lys Asp Lys Phe		
355	360	365

Leu Thr Pro Asp Phe Thr Ser Leu Asp Val Leu Thr Phe Ala Gly Ser
 370 375 380

Gly Ile Pro Ala Gly Ile Asn Ile Pro Asn Tyr Asp Asp Leu Arg Gln
 385 390 395 400

Thr Glu Gly Phe Lys Asn Val Ser Leu Gly Asn Val Leu Ala Val Ala
 405 410 415

Tyr Ala Thr Gln Arg Glu Lys Leu Thr Phe Leu Glu Glu Asp Asp Lys
 420 425 430

Asp Leu Tyr Ile Leu Trp Lys Gly Pro Ser Phe Asp Val Gln Val Gly
 435 440 445

Leu His Glu Leu Leu Gly His Gly Ser Gly Lys Leu Phe Val Gln Asp
 450 455 460

Glu Lys Gly Ala Phe Asn Phe Asp Gln Glu Thr Val Ile Asn Pro Glu
 465 470 475 480

Thr Gly Glu Gln Ile Gln Ser Trp Tyr Arg Ser Gly Glu Thr Trp Asp
 485 490 495

Ser Lys Phe Ser Thr Ile Ala Ser Ser Tyr Glu Glu Cys Arg Ala Glu
 500 505 510

Ser Val Gly Leu Tyr Leu Cys Leu His Pro Gln Val Leu Glu Ile Phe
 515 520 525

Gly Phe Glu Gly Ala Asp Ala Glu Asp Val Ile Tyr Val Asn Trp Leu
 530 535 540

Asn Met Val Arg Ala Gly Leu Leu Ala Leu Glu Phe Tyr Thr Pro Glu
 545 550 555 560

Ala Phe Asn Trp Arg Gln Ala His Met Gln Ala Arg Phe Val Ile Leu

565

570

575

Arg Val Leu Leu Glu Ala Gly Glu Gly Leu Val Thr Ile Thr Pro Thr
 580 585 590

Thr Gly Ser Asp Gly Arg Pro Asp Ala Arg Val Arg Leu Asp Arg Ser
 595 600 605

Lys Ile Arg Ser Val Gly Lys Pro Ala Leu Glu Arg Phe Leu Arg Arg
 610 615 620

Leu Gln Val Leu Lys Ser Thr Gly Asp Val Ala Gly Gly Arg Ala Leu
 625 630 635 640

Tyr Glu Gly Tyr Ala Thr Val Thr Asp Ala Pro Pro Glu Cys Phe Leu
 645 650 655

Thr Leu Arg Asp Thr Val Leu Leu Arg Lys Glu Ser Arg Lys Leu Ile
 660 665 670

Val Gln Pro Asn Thr Arg Leu Glu Gly Ser Asp Val Gln Leu Leu Glu
 675 680 685

Tyr Glu Ala Ser Ala Ala Gly Leu Ile Arg Ser Phe Ser Glu Arg Phe
 690 695 700

Pro Glu Asp Gly Pro Glu Leu Glu Glu Ile Leu Thr Gln Leu Ala Thr
 705 710 715 720

Ala Asp Ala Arg Phe Trp Lys Gly Pro Ser Glu Ala Pro Ser Gly Gln
 725 730 735

Ala

<210> 6

<211> 710

<212> PRT

<213> *Saccharomyces cerevisiae*

<220>

<221> Dipeptidyl peptidase 3 (DPP3)

<222> (1)..(710)

<223> UniProt Accession No. Q08225

<400> 6

Met Ser His Phe Phe Ala Asp His Asp Ala Pro Leu Ser Met Leu Ser
1 5 10 15

Val Lys Thr Glu Tyr Phe Pro Gln Leu Thr Asp Lys Glu Gln Lys Tyr
20 25 30

Ala His Phe Met Ser Lys Ala Ser His Ala Gly Ser Arg Val Val Met
35 40 45

Arg Gln Val Ser His Glu Ser Glu Pro Ile Phe Asp Leu Ile Leu Ala
50 55 60

Ile His Ser Lys Leu Asn Gly Lys Tyr Pro Glu Asp Asp Ile Thr Gln
65 70 75 80

Lys Gln Gln Thr Gly Leu Tyr Leu Glu Tyr Val Ser Gln Phe Leu Ser
85 90 95

Asn Leu Gly Asn Phe Lys Ser Phe Gly Asp Thr Lys Phe Ile Pro Arg
100 105 110

Cys Glu Val Lys Phe Phe Lys Gln Leu Leu Glu Leu Ala Lys Ile Asn
115 120 125

Pro Cys Ser Ser Pro Leu Thr Leu Ser Pro Val Asp Val Asn His Glu
130 135 140

Phe Thr Ser His His Leu Phe Ser Thr Ile Asn Glu Leu Ile Asp Ile
145 150 155 160

Gly Ile Tyr His Val Glu Glu Lys Ala Ala Leu Leu Gly Phe Pro Ser
165 170 175

Gln Gly Tyr Thr Ser Ala Tyr Tyr Leu Gly Leu Pro Val Thr Pro Glu
180 185 190

Asp Met Ala Leu Leu Lys Glu Gln Leu Phe Ala Glu Leu Ala Ile Leu
195 200 205

Pro Glu Asn Thr Arg Ile Asn Lys Val Gly Glu Asn Ser Phe Gln Ile
210 215 220

Trp Val Ala Ser Glu Asn Val Lys Asn Gln Ile Thr Glu Thr Tyr Pro
225 230 235 240

Ser Gly Gln Ile Thr Leu Ser Asn Ala Val Thr Lys Val Glu Phe Ile
245 250 255

Phe Gly Asp His Ser Arg Glu Met Arg Leu Val Ala Ser Tyr Leu Lys
260 265 270

Glu Ala Gln Lys Phe Ala Ala Asn Asp Thr Gln Lys Ala Met Leu Gln
275 280 285

Glu Tyr Ile Asn His Phe Val Thr Gly Ser Ser Gln Ala His Lys Glu
290 295 300

Ala Gln Lys Leu Trp Val Lys Asp Ile Ser Pro Val Ile Glu Thr Asn
305 310 315 320

Ile Gly Phe Ile Glu Thr Tyr Arg Glu Pro Ser Gly Ile Ile Gly Glu
325 330 335

Phe Glu Ser Leu Val Ala Ile Gln Asn Lys Glu Arg Thr Ala Lys Phe
340 345 350

Ser Ser Val Asn Asn Ala Glu Glu Phe Ile Ser Leu Leu Pro Trp Ser
355 360 365

Lys Asp Tyr Glu Lys Pro Ile Phe Asn Pro Pro Asp Phe Thr Ser Leu
 370 375 380

Glu Val Leu Thr Phe Thr Gly Ser Gly Ile Pro Ala Gly Ile Asn Ile
 385 390 395 400

Pro Asn Tyr Asp Asp Val Arg Leu Lys Ile Gly Phe Lys Asn Val Ser
 405 410 415

Leu Gly Asn Ile Leu Ser Ala Ala Ala Lys Ser Ser Ser Lys His Pro
 420 425 430

Pro Ser Phe Ile Ser Gln Glu Asp Arg Pro Ile Phe Glu Lys Tyr Gln
 435 440 445

Ser Asp Ser Phe Glu Val Gln Val Gly Ile His Glu Leu Leu Gly His
 450 455 460

Gly Ser Gly Lys Leu Leu Thr Glu Phe Thr Asp Gly Phe Asn Phe Asp
 465 470 475 480

Lys Glu Asn Pro Pro Leu Gly Leu Asp Gly Lys Pro Val Ser Thr Tyr
 485 490 495

Tyr Lys Val Gly Glu Thr Trp Gly Ser Lys Phe Gly Gln Leu Ala Gly
 500 505 510

Pro Phe Glu Glu Cys Arg Ala Glu Val Ile Ala Met Phe Leu Leu Thr
 515 520 525

Asn Lys Lys Ile Leu Asp Ile Phe Gly Phe His Asp Val Glu Ser Gln
 530 535 540

Asp Lys Val Ile Tyr Ala Gly Tyr Leu Gln Met Ala Arg Ala Gly Leu
 545 550 555 560

Leu Ala Leu Glu Tyr Trp Asn Pro Lys Thr Gly Lys Trp Gly Gln Pro
565 570 575

His Met Gln Ala Arg Phe Ser Ile Met Lys Thr Phe Met Lys His Ser
580 585 590

Thr Asp Lys Asn Phe Leu Lys Leu Glu Met Asn Ser Thr Asn Asp Asp
595 600 605

Phe Ala Ile Lys Leu Asp Lys Ser Leu Ile Lys Thr Ala Gly His Glu
610 615 620

Cys Val Lys Asp Tyr Leu Lys His Leu His Val Tyr Lys Cys Ser Gly
625 630 635 640

Asp Val Glu Gln Gly Ser Lys Tyr Phe Ile Asp Arg Ser Thr Val Thr
645 650 655

Pro Asp Leu Ala Ser Leu Arg Asp Ile Val Leu Ser Lys Arg Leu Pro
660 665 670

Arg Arg Gln Phe Ile Gln Ser Asn Ser Tyr Ile Asp Asp Asn Asn Lys
675 680 685

Val Thr Leu Lys Glu Tyr Asp Glu Thr Pro Gln Gly Met Leu Gln Ser
690 695 700

Phe Leu Asp Arg Glu Leu
705 710

<210> 7
<211> 674
<212> PRT
<213> Bacteroides thetaiotaomicron

<220>
<221> Dipeptidyl peptidase 3 (DPP3)
<222> (1)..(674)
<223> UniProt Accession No. Q8A6N1

<400> 7

Met Ala Val Thr Ala Thr Ile Leu Ala Ser Cys Gly Gly Ala Lys Thr
1 5 10 15

Thr Thr Ala Glu Ala Asp Lys Phe Asp Tyr Thr Val Glu Gln Phe Ala
20 25 30

Asp Leu Gln Ile Leu Arg Tyr Lys Val Pro Glu Phe Glu Thr Leu Thr
35 40 45

Leu Lys Gln Lys Glu Leu Val Tyr Tyr Leu Thr Gln Ala Ala Leu Glu
50 55 60

Gly Arg Asp Ile Leu Phe Asp Gln Asn Gly Lys Tyr Asn Leu Arg Ile
65 70 75 80

Arg Arg Met Leu Glu Ala Val Tyr Thr Asn Tyr Lys Gly Asp Lys Ser
85 90 95

Ala Pro Asp Phe Lys Asn Met Glu Val Tyr Leu Lys Arg Val Trp Phe
100 105 110

Ser Asn Gly Ile His His His Tyr Gly Met Glu Lys Phe Val Pro Gly
115 120 125

Phe Ser Gln Asp Phe Leu Lys Gln Ala Val Leu Gly Thr Asp Ala Gln
130 135 140

Leu Leu Pro Leu Ser Glu Gly Gln Thr Ala Glu Gln Leu Cys Asp Glu
145 150 155 160

Leu Phe Pro Val Met Phe Asp Pro Ala Ile Leu Ala Lys Arg Val Asn
165 170 175

Gln Ala Asp Gly Glu Asp Leu Val Leu Thr Ser Ala Cys Asn Tyr Tyr
180 185 190

Asp Gly Val Thr Gln Gln Glu Ala Glu Ser Phe Tyr Gly Ala Met Lys
195 200 205

Asp Pro Lys Asp Glu Thr Pro Val Ser Tyr Gly Leu Asn Ser Arg Leu
210 215 220

Val Lys Glu Asp Gly Lys Gln Glu Lys Val Trp Lys Val Gly Gly Leu
225 230 235 240

Tyr Thr Gln Ala Ile Glu Lys Ile Val Tyr Trp Leu Lys Lys Ala Glu
245 250 255

Thr Val Ala Glu Asn Asp Ala Gln Lys Ala Val Ile Ser Lys Leu Ile
260 265 270

Gln Phe Tyr Glu Thr Gly Ser Leu Lys Asp Phe Asp Glu Tyr Ala Ile
275 280 285

Leu Trp Val Lys Asp Leu Asp Ser Arg Ile Asp Phe Val Asn Gly Phe
290 295 300

Thr Glu Ser Tyr Gly Asp Pro Leu Gly Val Lys Ala Ser Trp Glu Ser
305 310 315 320

Leu Val Asn Phe Lys Asp Leu Asp Ala Thr His Arg Thr Glu Ile Ile
325 330 335

Ser Ser Asn Ala Gln Trp Phe Glu Asp His Ser Pro Val Asp Lys Ser
340 345 350

Phe Lys Lys Glu Lys Val Lys Gly Val Ser Ala Lys Val Ile Thr Ala
355 360 365

Ala Ile Leu Ala Gly Asp Leu Tyr Pro Ala Thr Ala Ile Gly Ile Asn
370 375 380

Leu Pro Asn Ala Asn Trp Ile Arg Ala His His Gly Ser Lys Ser Val

385		390		395		400									
Thr	Ile	Gly	Asn	Ile	Thr	Asp	Ala	Tyr	Asn	Lys	Ala	Ala	His	Gly	Asn
			405						410					415	
Gly	Phe	Asn	Glu	Glu	Phe	Val	Cys	Asn	Asp	Glu	Glu	Arg	Gln	Arg	Ile
			420					425					430		
Asp	Gln	Tyr	Gly	Asp	Leu	Thr	Gly	Glu	Leu	His	Thr	Asp	Leu	His	Glu
		435					440					445			
Cys	Leu	Gly	His	Gly	Ser	Gly	Lys	Leu	Leu	Pro	Gly	Val	Asp	Pro	Asp
	450					455					460				
Ala	Leu	Lys	Ala	Tyr	Gly	Ser	Thr	Ile	Glu	Glu	Ala	Arg	Ala	Asp	Leu
465					470					475					480
Phe	Gly	Leu	Tyr	Tyr	Val	Ala	Asp	Pro	Lys	Leu	Val	Glu	Leu	Lys	Leu
			485						490					495	
Val	Pro	Asp	Ala	Glu	Ala	Tyr	Lys	Ala	Glu	Tyr	Tyr	Thr	Phe	Leu	Met
			500					505					510		
Asn	Gly	Leu	Met	Thr	Gln	Leu	Val	Arg	Ile	Glu	Pro	Gly	Asn	Asn	Ile
		515					520					525			
Glu	Glu	Ala	His	Met	Arg	Asn	Arg	Gln	Leu	Ile	Ala	Arg	Trp	Val	Phe
	530					535					540				
Glu	Lys	Gly	Ala	Pro	Asp	Lys	Val	Val	Glu	Met	Val	Lys	Lys	Asp	Gly
545					550					555					560
Lys	Thr	Tyr	Val	Val	Val	Asn	Asp	Tyr	Glu	Lys	Val	Arg	Gln	Leu	Phe
			565						570					575	
Gly	Glu	Leu	Leu	Ala	Glu	Ile	Gln	Arg	Ile	Lys	Ser	Thr	Gly	Asp	Phe
			580					585					590		

Glu Gly Ala Arg Thr Leu Val Glu Asn Tyr Ala Val Lys Val Asp Pro
 595 600 605

Ala Leu His Ala Glu Val Leu Ala Arg Tyr Lys Lys Leu Asn Leu Ala
 610 615 620

Pro Tyr Lys Gly Phe Ile Asn Pro Val Tyr Glu Leu Val Thr Asp Lys
 625 630 635 640

Asp Gly Asn Ile Thr Asp Val Thr Val Ser Tyr Asn Glu Asp Tyr Val
 645 650 655

Glu Gln Met Leu Arg Tyr Ser Lys Asp Tyr Ser Pro Leu Pro Ser Val
 660 665 670

Asn Asn

<210> 8
 <211> 558
 <212> PRT
 <213> Caldithrix abyssi

<220>
 <221> Dipeptidyl peptidase 3 (DPP3)
 <222> (1)..(558)
 <223> UniProt Accession No. H1XW48

<400> 8

Met Lys Arg Ile Leu Leu Val Leu Leu Thr Leu Val Phe Leu Gly Ala
 1 5 10 15

Ile Ala Cys Gln Lys Lys Glu Glu Asn Lys Thr Glu Met Val Lys Leu
 20 25 30

Lys Arg Met Ile Ala Gln Phe Ala Pro Thr Glu Ile Lys Tyr Asp His
 35 40 45

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

Ala Ala Lys Ile Met Asp Glu Ile Phe Leu Asp Gln Val Tyr Ser Lys
65 70 75 80

Asn Phe Glu Ile Arg Glu Gln Leu Arg Ala Ser Ser Asp Pro Leu Asp
85 90 95

Gln Leu Arg Leu Glu Tyr Phe Thr Ile Met Phe Gly Pro Phe Asp Arg
100 105 110

Leu Asn His Asp Lys Pro Phe Ile Gly Asn Thr Pro Lys Pro Lys Gly
115 120 125

Ala Asn Phe Tyr Pro Pro Asp Met Thr Arg Glu Glu Phe Glu Asn Trp
130 135 140

Leu Lys Ala His Pro Glu Asp Glu Ala Ala Phe Thr Ser Glu Phe Thr
145 150 155 160

Val Ile Arg Arg Gln Asp Gly Lys Leu Val Ala Ile Pro Tyr Ser Glu
165 170 175

Tyr Tyr Lys Glu Tyr Leu Thr Arg Ala Ala Asp Tyr Leu Lys Lys Ala
180 185 190

Ala Glu Phe Ala Asp Asn Pro Ser Leu Lys Lys Tyr Leu Gln Leu Arg
195 200 205

Ala Glu Ala Phe Leu Asn Asn Asp Tyr Tyr Glu Ser Asp Leu Ala Trp
210 215 220

Met Asp Leu Asn Asp His Thr Ile Glu Val Val Ile Gly Pro Tyr Glu
225 230 235 240

Val Tyr Glu Asp Lys Leu Phe Asn Tyr Lys Ala Ala Phe Glu Ala Phe
245 250 255

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

Gly Tyr Leu Asp Glu Met Glu Lys Asn Leu Pro Ile Pro Asp Ala Tyr
275 280 285

Lys Asn Phe Asn Arg Gly Ser Glu Ser Pro Met Val Val Val Gln Glu
290 295 300

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

Asn Leu Pro Asn Asp Glu Arg Val Arg Glu Ala Lys Gly Ser Lys Lys
325 330 335

Val Met Leu Lys Asn Ile His Glu Ala Lys Phe Asp Lys Leu Leu Lys
340 345 350

Pro Ile Ala Glu Lys Val Leu Phe Ala Glu Gln Leu Pro Leu Val Thr
355 360 365

Phe Glu Gly Phe Phe Asn His Thr Leu Met His Glu Ile Ser His Gly
370 375 380

Leu Gly Pro Gly Lys Ile Val Leu Asn Gly Arg Gln Thr Glu Val Lys
385 390 395 400

Lys Glu Leu Lys Glu Thr Tyr Ser Ser Ile Glu Glu Cys Lys Ala Asp
405 410 415

Val Leu Gly Met Tyr Asn Asn Leu Phe Met Ile Glu Lys Gly Val Tyr
420 425 430

Pro Pro Glu Phe Glu Lys Gln Ile Tyr Val Thr Phe Leu Ala Gly Ile
435 440 445

Phe Arg Thr Ile Arg Phe Gly Ile Asn Glu Ala His Gly Ala Gly Asn
450 455 460

Ala Val Ile Phe Asn Tyr Leu Leu Glu Lys Gly Ala Tyr Gln Phe Asp
465 470 475 480

Pro Ala Ala His Arg Val Lys Val Asn Phe Glu Lys Ile Lys Asp Gly
485 490 495

Val Arg Asp Leu Ala Asn Lys Val Leu Thr Ile Gln Ala Gln Gly Asp
500 505 510

Tyr Met Ala Ala Lys Asn Leu Leu Glu Thr Tyr Ala Val Glu Ser Glu
515 520 525

Pro Ile Met Ile Met Arg Ala Arg Leu Gln Glu Leu Pro Val Asp Ile
530 535 540

Lys Pro Ile Phe Gln Ile Glu Lys Glu Leu Gly Asn Ser Asn
545 550 555

<210> 9
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Substrate Sequence

<400> 9

Asp Arg Val Tyr Ile His Pro Phe
1 5

<210> 10
<211> 703
<212> PRT
<213> *Aspergillus fumigatus*

<220>
<221> Dipeptidyl peptidase 5 (DPP5)

<222> (1)..(703)

<223> Uniprot accession P0C959

<400> 10

Leu Thr Pro Glu Gln Leu Ile Thr Ala Pro Arg Arg Ser Glu Ala Ile
1 5 10 15

Pro Asp Pro Ser Gly Lys Val Ala Val Phe Ser Thr Ser Gln Tyr Ser
20 25 30

Phe Glu Thr His Lys Arg Thr Ser Trp Trp Ser Leu Leu Asp Leu Lys
35 40 45

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

Val Trp Leu Ser Asp Asp Ser Ile Leu Tyr Val Asn Ser Thr Asn Ala
65 70 75 80

Asp Ile Pro Gly Gly Val Glu Leu Trp Val Thr Gln Ala Ser Ser Phe
85 90 95

Ala Lys Gly Tyr Lys Ala Ala Ser Leu Pro Ala Ser Phe Ser Gly Leu
100 105 110

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

Gln Ser Tyr Pro Asn Gly Thr Ala Tyr Asn Glu Glu Leu Ala Thr Ala
130 135 140

Pro Leu Ser Ser Ala Arg Ile Tyr Asp Ser Ile Tyr Val Arg His Trp
145 150 155 160

Asp Tyr Trp Leu Ser Thr Thr Phe Asn Ala Val Phe Ser Gly Thr Leu
165 170 175

Lys Lys Gly His Gly Lys Asn Gly Tyr Ser Leu Asp Gly Glu Leu Lys

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

Ser Ala Leu Trp Thr Asn Trp Asn Val Tyr Thr Ala Lys Pro Glu Lys
 385 390 395 400

Gly Val Ile Lys Lys Ile Ala Ser Ala Asn Glu Ile Asp Pro Glu Leu
 405 410 415

Lys Gly Leu Gly Pro Ser Asp Ile Ser Glu Phe Tyr Phe Gln Gly Asn
 420 425 430

Phe Thr Asp Ile His Ala Trp Val Ile Tyr Pro Glu Asn Phe Asp Lys
 435 440 445

Ser Lys Lys Tyr Pro Leu Ile Phe Phe Ile His Gly Gly Pro Gln Gly
 450 455 460

Asn Trp Ala Asp Gly Trp Ser Thr Arg Trp Asn Pro Lys Ala Trp Ala
 465 470 475 480

Asp Gln Gly Tyr Val Val Val Ala Pro Asn Pro Thr Gly Ser Thr Gly
 485 490 495

Phe Gly Gln Ala Leu Thr Asp Ala Ile Gln Asn Asn Trp Gly Gly Ala
 500 505 510

Pro Tyr Asp Asp Leu Val Lys Cys Trp Glu Tyr Val His Glu Asn Leu
 515 520 525

Asp Tyr Val Asp Thr Asp His Gly Val Ala Ala Gly Ala Ser Tyr Gly
 530 535 540

Gly Phe Met Ile Asn Trp Ile Gln Gly Ser Pro Leu Gly Arg Lys Phe
 545 550 555 560

Lys Ala Leu Val Ser His Asp Gly Thr Phe Val Ala Asp Ala Lys Val
 565 570 575

Ser Thr Glu Glu Leu Trp Phe Met Gln Arg Glu Phe Asn Gly Thr Phe

580

585

590

Trp Asp Ala Arg Asp Asn Tyr Arg Arg Trp Asp Pro Ser Ala Pro Glu
 595 600 605

Arg Ile Leu Gln Phe Ala Thr Pro Met Leu Val Ile His Ser Asp Lys
 610 615 620

Asp Tyr Arg Leu Pro Val Ala Glu Gly Leu Ser Leu Phe Asn Val Leu
 625 630 635 640

Gln Glu Arg Gly Val Pro Ser Arg Phe Leu Asn Phe Pro Asp Glu Asn
 645 650 655

His Trp Val Val Asn Pro Glu Asn Ser Leu Val Trp His Gln Gln Ala
 660 665 670

Leu Gly Trp Ile Asn Lys Tyr Ser Gly Val Glu Lys Ser Asn Pro Asn
 675 680 685

Ala Val Ser Leu Glu Asp Thr Val Val Pro Val Val Asn Tyr Asn
 690 695 700

<210> 11

<211> 689

<212> PRT

<213> Porphyromonas gingivalis

<220>

<221> Dipeptidyl peptidase 7 (DPP7)

<222> (1)..(689)

<223> UniProt Accession No. B2RKV3

<400> 11

Ala Asp Lys Gly Met Trp Leu Leu Asn Glu Leu Asn Gln Glu Asn Leu
 1 5 10 15

Asp Arg Met Arg Glu Leu Gly Phe Thr Leu Pro Leu Asp Ser Leu Tyr
 20 25 30

Ser Phe Asp Lys Pro Ser Ile Ala Asn Ala Val Val Ile Phe Gly Gly
35 40 45

Gly Cys Thr Gly Ile Thr Val Ser Asp Gln Gly Leu Ile Phe Thr Asn
50 55 60

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

Asp Tyr Leu Arg Asp Gly Phe Val Ser Arg Thr Met Gly Glu Glu Leu
85 90 95

Pro Ile Pro Gly Leu Ser Val Lys Tyr Leu Arg Lys Ile Val Lys Val
100 105 110

Thr Asp Lys Val Glu Gly Gln Leu Lys Gly Ile Thr Asp Glu Met Glu
115 120 125

Arg Leu Arg Lys Ala Gln Glu Val Cys Gln Glu Leu Ala Lys Lys Glu
130 135 140

Asn Ala Asp Glu Asn Gln Leu Cys Ile Val Glu Pro Phe Tyr Ser Asn
145 150 155 160

Asn Glu Tyr Phe Leu Ile Val Tyr Asp Val Phe Lys Asp Val Arg Met
165 170 175

Val Phe Ala Pro Pro Ser Ser Val Gly Lys Phe Gly Gly Asp Thr Asp
180 185 190

Asn Trp Met Trp Pro Arg His Thr Gly Asp Phe Ser Val Phe Arg Val
195 200 205

Tyr Ala Gly Ala Asp Asn Arg Pro Ala Glu Tyr Ser Lys Asp Asn Lys
210 215 220

Pro Tyr Lys Pro Val Tyr Phe Ala Ala Val Ser Met Gln Gly Tyr Lys
 225 230 235 240

Ala Asp Asp Tyr Ala Met Thr Ile Gly Phe Pro Gly Ser Thr Asp Arg
 245 250 255

Tyr Leu Thr Ser Trp Gly Val Glu Asp Arg Ile Glu Asn Glu Asn Asn
 260 265 270

Pro Arg Ile Glu Val Arg Gly Ile Lys Gln Gly Ile Trp Lys Glu Ala
 275 280 285

Met Ser Ala Asp Gln Ala Thr Arg Ile Lys Tyr Ala Ser Lys Tyr Ala
 290 295 300

Gln Ser Ala Asn Tyr Trp Lys Asn Ser Ile Gly Met Asn Arg Gly Leu
 305 310 315 320

Ala Arg Leu Asp Val Ile Gly Arg Lys Arg Ala Glu Glu Arg Ala Phe
 325 330 335

Ala Asp Trp Ile Arg Lys Asn Gly Lys Ser Ala Val Tyr Gly Asp Val
 340 345 350

Leu Ser Ser Leu Glu Lys Ala Tyr Lys Glu Gly Ala Lys Ala Asn Arg
 355 360 365

Glu Met Thr Tyr Leu Ser Glu Thr Leu Phe Gly Gly Thr Glu Val Val
 370 375 380

Arg Phe Ala Gln Phe Ala Asn Ala Leu Ala Thr Asn Pro Asp Ala His
 385 390 395 400

Ala Gly Ile Leu Lys Ser Leu Asp Asp Lys Tyr Lys Asp Tyr Leu Pro
 405 410 415

Ser Leu Asp Arg Lys Val Leu Pro Ala Met Leu Asp Ile Val Arg Arg
 420 425 430

Arg Ile Pro Ala Asp Lys Leu Pro Asp Ile Phe Lys Asn Val Ile Asp
435 440 445

Lys Lys Phe Lys Gly Asp Thr Lys Lys Tyr Ala Asp Phe Val Phe Asp
450 455 460

Lys Ser Val Val Pro Tyr Ser Asp Lys Phe His Ala Met Leu Lys Ser
465 470 475 480

Met Asp Lys Glu Lys Phe Ala Lys Ala Ile Glu Lys Asp Pro Ala Val
485 490 495

Glu Leu Ser Lys Ser Val Ile Ala Ala Ala Arg Ala Ile Gln Ala Asp
500 505 510

Ala Met Ala Asn Ala Tyr Ala Ile Glu Lys Gly Lys Arg Leu Phe Phe
515 520 525

Ala Gly Leu Arg Glu Met Tyr Pro Gly Arg Ala Leu Pro Ser Asp Ala
530 535 540

Asn Phe Thr Met Arg Met Ser Tyr Gly Ser Ile Lys Gly Tyr Glu Pro
545 550 555 560

Gln Asp Gly Ala Trp Tyr Asn Tyr His Thr Thr Gly Lys Gly Val Leu
565 570 575

Glu Lys Gln Asp Pro Lys Ser Asp Glu Phe Ala Val Gln Glu Asn Ile
580 585 590

Leu Asp Leu Phe Arg Thr Lys Asn Tyr Gly Arg Tyr Ala Glu Asn Gly
595 600 605

Gln Leu His Ile Ala Phe Leu Ser Asn Asn Asp Ile Thr Gly Gly Asn
610 615 620

Ser Gly Ser Pro Val Phe Asp Lys Asn Gly Arg Leu Ile Gly Leu Ala
 625 630 635 640

Phe Asp Gly Asn Trp Glu Ala Met Ser Gly Asp Ile Glu Phe Glu Pro
 645 650 655

Asp Leu Gln Arg Thr Ile Ser Val Asp Ile Arg Tyr Val Leu Phe Met
 660 665 670

Ile Asp Lys Trp Gly Gln Cys Pro Arg Leu Ile Gln Glu Leu Lys Leu
 675 680 685

Ile

<210> 12
 <211> 699
 <212> PRT
 <213> Porphyromonas gingivalis

<220>
 <221> Dipeptidyl peptidase 11 (DPP11)
 <222> (1)..(699)
 <223> UniProt Accession No. B2RID1

<400> 12

Asp Glu Gly Met Trp Leu Met Gln Gln Leu Gly Arg Lys Tyr Ala Gln
 1 5 10 15

Met Lys Glu Arg Gly Leu Lys Met Lys Glu Tyr Asp Leu Tyr Asn Pro
 20 25 30

Asn Gly Thr Ser Leu Lys Asp Ala Val Val Leu Phe Asp Gly Gly Cys
 35 40 45

Thr Gly Glu Val Val Ser Asp Arg Gly Leu Val Leu Thr Asn His His
 50 55 60

Cys Gly Tyr Asp Met Ile Gln Ala His Ser Thr Leu Glu His Asn Tyr

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

Ile Asp Asn Asp Ile Arg Ile Arg Met Arg Asp Ile Arg Gln Gly Val
275 280 285

Met Leu Arg Glu Met Leu Ala Asp Pro Gln Ile Lys Ile Met Tyr Ser
290 295 300

Ala Lys Tyr Ala Ala Ser Gln Asn Ala Tyr Lys Arg Ala Ile Gly Ala
305 310 315 320

Asn Trp Ala Ile Lys Thr Arg Gly Leu Arg Gln Asn Lys Gln Ala Met
325 330 335

Gln Asp Arg Leu Ile Ala Trp Gly Ala Lys Gln Gly Thr Pro Arg Tyr
340 345 350

Glu Glu Ala Val His Glu Ile Asp Ala Thr Val Ala Lys Arg Ala Asp
355 360 365

Leu Arg Arg Arg Tyr Trp Met Ile Glu Glu Gly Ile Ile Arg Gly Ile
370 375 380

Glu Phe Ala Arg Ser Pro Ile Pro Thr Glu Asp Glu Thr Lys Ala Leu
385 390 395 400

Gln Gly Asn Asp Ala Ser Ala Arg Lys Glu Ala Ile Asp Lys Ile Arg
405 410 415

Thr Arg Tyr Ser Lys Phe Ala Asn Lys Asp Tyr Ser Ala Glu Val Asp
420 425 430

Lys Lys Val Ala Val Ala Met Leu Thr Glu Tyr Leu Lys Glu Ile Pro
435 440 445

Tyr Glu Asn Leu Pro Leu His Leu Arg Leu Val Lys Asp Arg Phe Ala
450 455 460

Gly Asp Val Gln Ala Tyr Val Asp Asp Ile Phe Ala Arg Ser Val Phe

465		470		475		480									
Gly	Ser	Glu	Ala	Gln	Phe	Asp	Ala	Phe	Ala	Ala	Val	Pro	Ser	Val	Glu
				485					490					495	
Lys	Leu	Ala	Glu	Asp	Pro	Met	Val	Leu	Phe	Ala	Ser	Ser	Val	Phe	Asp
			500					505					510		
Glu	Tyr	Arg	Lys	Leu	Tyr	Asn	Glu	Leu	Arg	Pro	Tyr	Asp	Asp	Pro	Ile
		515					520					525			
Leu	Arg	Ala	Gln	Arg	Thr	Tyr	Ile	Ala	Gly	Leu	Leu	Glu	Met	Asp	Gly
	530					535					540				
Asp	Gln	Asp	Gln	Phe	Pro	Asp	Ala	Asn	Leu	Thr	Leu	Arg	Phe	Thr	Tyr
545					550					555					560
Gly	Gln	Val	Lys	Gly	Tyr	Ser	Pro	Arg	Asp	Asn	Val	Tyr	Tyr	Gly	His
				565					570					575	
Gln	Thr	Thr	Leu	Asp	Gly	Val	Met	Glu	Lys	Glu	Asp	Pro	Asp	Asn	Trp
			580					585					590		
Glu	Phe	Val	Val	Asp	Pro	Lys	Leu	Lys	Ala	Val	Tyr	Glu	Arg	Lys	Asp
		595					600					605			
Phe	Gly	Arg	Tyr	Ala	Asp	Arg	Ser	Gly	Arg	Met	Pro	Val	Ala	Phe	Cys
	610					615					620				
Ala	Thr	Thr	His	Thr	Thr	Gly	Gly	Asn	Ser	Gly	Ser	Pro	Val	Met	Asn
625					630					635					640
Ala	Asn	Gly	Glu	Leu	Ile	Gly	Leu	Asn	Phe	Asp	Arg	Asn	Trp	Glu	Gly
				645					650					655	
Val	Gly	Gly	Asp	Ile	Gln	Tyr	Leu	Ala	Asp	Tyr	Gln	Arg	Ser	Ile	Ile
			660					665					670		

Val Asp Ile Arg Tyr Val Leu Leu Val Ile Asp Lys Val Gly Gly Cys
675 680 685

Gln Arg Leu Leu Asp Glu Met Asn Ile Val Pro
690 695

<210> 13
<211> 698
<212> PRT
<213> Pseudoxanthomonas mexicana

<220>
<221> Dipeptidyl Aminopeptidase BII (DAP BII)
<222> (1)..(698)
<223> UniProt Accession No. V5YM14

<400> 13

Gly Glu Gly Met Trp Val Pro Gln Gln Leu Pro Glu Ile Ala Gly Pro
1 5 10 15

Leu Lys Lys Ala Gly Leu Lys Leu Ser Pro Gln Gln Ile Ser Asp Leu
20 25 30

Thr Gly Asp Pro Met Gly Ala Val Val Ala Leu Gly Gly Cys Thr Ala
35 40 45

Ser Phe Val Ser Pro Asn Gly Leu Val Val Thr Asn His His Cys Ala
50 55 60

Tyr Gly Ala Ile Gln Leu Asn Ser Thr Ala Glu Asn Asn Leu Ile Lys
65 70 75 80

Asn Gly Phe Asn Ala Pro Thr Thr Ala Asp Glu Val Ser Ala Gly Pro
85 90 95

Asn Ala Arg Val Phe Val Leu Asp Glu Ile Thr Asp Val Thr Lys Asp
100 105 110

Ala Lys Ala Ala Ile Ala Ala Ala Gly Asp Asp Ala Leu Ala Arg Thr
115 120 125

Lys Ala Leu Glu Ala Phe Glu Lys Lys Leu Ile Ala Asp Cys Glu Ala
130 135 140

Glu Ala Gly Phe Arg Cys Arg Leu Tyr Ser Phe Ser Gly Gly Asn Thr
145 150 155 160

Tyr Arg Leu Phe Lys Asn Leu Glu Ile Lys Asp Val Arg Leu Ala Tyr
165 170 175

Ala Pro Pro Gly Ser Val Gly Lys Phe Gly Gly Asp Ile Asp Asn Trp
180 185 190

Met Trp Pro Arg His Thr Gly Asp Phe Ala Phe Tyr Arg Ala Tyr Val
195 200 205

Gly Lys Asp Gly Lys Pro Ala Ala Phe Ser Lys Asp Asn Val Pro Tyr
210 215 220

Gln Pro Lys His Trp Leu Lys Phe Ala Asp Gln Pro Leu Gly Ala Gly
225 230 235 240

Asp Phe Val Met Val Ala Gly Tyr Pro Gly Ser Thr Asn Arg Tyr Ala
245 250 255

Leu Ala Ala Glu Phe Asp Asn Thr Ala Gln Trp Thr Tyr Pro Thr Ile
260 265 270

Ala Arg His Tyr Lys Asn Gln Ile Ala Met Val Glu Ala Ala Gly Lys
275 280 285

Gln Asn Ala Asp Ile Gln Val Lys Tyr Ala Ala Thr Met Ala Gly Trp
290 295 300

Asn Asn Thr Ser Lys Asn Tyr Asp Gly Gln Leu Glu Gly Phe Lys Arg
305 310 315 320

Ile Asp Ala Ala Gly Gln Lys Leu Arg Glu Glu Ala Ala Val Leu Gly
325 330 335

Trp Leu Lys Gly Gln Gly Ala Lys Gly Gln Pro Ala Leu Asp Ala His
340 345 350

Ala Lys Leu Leu Asp Leu Leu Glu Gln Ser Lys Ala Thr Arg Asp Arg
355 360 365

Asp Leu Thr Leu Ala Leu Phe Asn Asn Thr Ala Met Leu Gly Ser Ala
370 375 380

Thr Gln Leu Tyr Arg Leu Ser Ile Glu Arg Glu Lys Pro Asn Ala Glu
385 390 395 400

Arg Glu Ser Gly Tyr Gln Glu Arg Asp Leu Pro Ala Ile Glu Gly Gly
405 410 415

Leu Lys Gln Leu Glu Arg Arg Tyr Val Ala Ala Met Asp Arg Gln Leu
420 425 430

Gln Glu Tyr Trp Leu Asn Glu Tyr Ile Lys Leu Pro Ala Asp Gln Arg
435 440 445

Val Ala Ala Val Asp Ala Trp Leu Gly Gly Asn Asp Ala Ala Ala Val
450 455 460

Lys Arg Ala Leu Asp Arg Leu Ala Gly Thr Lys Leu Gly Ser Thr Glu
465 470 475 480

Glu Arg Leu Lys Trp Phe Ala Ala Asp Arg Lys Ala Phe Glu Ala Ser
485 490 495

Asn Asp Pro Ala Ile Gln Tyr Ala Val Ala Val Met Pro Thr Leu Leu
500 505 510

Lys Leu Glu Gln Glu Arg Lys Thr Arg Ala Gly Glu Asn Leu Ala Ala
515 520 525

Arg Pro Val Tyr Leu Gln Ala Leu Ala Asp Tyr Lys Lys Ser Gln Gly
530 535 540

Glu Phe Val Tyr Pro Asp Ala Asn Leu Ser Leu Arg Ile Thr Phe Gly
545 550 555 560

Asn Val Met Gly Tyr Ala Pro Lys Asp Gly Met Glu Tyr Thr Pro Phe
565 570 575

Thr Thr Leu Glu Gly Val Val Ala Lys Glu Thr Gly Gln Asp Pro Phe
580 585 590

Asp Ser Pro Lys Ala Leu Leu Asp Ala Val Ala Ala Lys Arg Tyr Gly
595 600 605

Gly Leu Glu Asp Lys Arg Ile Gly Ser Val Pro Val Asn Tyr Leu Ser
610 615 620

Asp Leu Asp Ile Thr Gly Gly Asn Ser Gly Ser Pro Val Leu Asp Ala
625 630 635 640

His Gly Lys Leu Val Gly Leu Ala Phe Asp Gly Asn Trp Glu Ser Val
645 650 655

Ser Ser Asn Trp Val Phe Asp Pro Lys Met Thr Arg Met Ile Ala Val
660 665 670

Asp Gly Arg Tyr Leu Arg Trp Ile Met Gln Glu Val Tyr Pro Ala Pro
675 680 685

Gln Leu Leu Lys Glu Met Asn Val Gly Lys
690 695

<210> 14
<211> 696

<212> PRT
 <213> Porphyromonas endodontalis

<220>
 <221> Dipeptidyl peptidase 11 (DPP11)
 <222> (1)..(696)
 <223> UniProt Accession No. F8WQK8

<400> 14

Asp Gly Gly Met Trp Leu Met Gln Gln Ile Asn Gly Gln Val Ala Arg
 1 5 10 15

Met Lys Ser Leu Gly Met Gln Leu Glu Ala Ala Asp Ile Tyr Asn Pro
 20 25 30

Asn Gly Ser Ser Leu Lys Asp Ala Val Val Met Phe Asp Gly Gly Cys
 35 40 45

Thr Gly Val Leu Val Ser Asn Gln Gly Leu Leu Leu Thr Asn His His
 50 55 60

Cys Gly Tyr Asp Gln Ile Gln Lys His Ser Ser Val Gln His Asn Tyr
 65 70 75 80

Leu Lys Asp Gly Phe Trp Ser Tyr Ser Leu Ala Glu Glu Leu Val Asn
 85 90 95

Pro Gly Leu Glu Val Glu Ile Val Asp Glu Ile Thr Asp Val Thr Ala
 100 105 110

Ala Val Lys Lys Glu Leu Glu Arg Ile Lys Lys Pro Ser Gly Leu Glu
 115 120 125

Phe Leu Ser Pro Arg Tyr Leu Ser Ser Leu Ala Pro Glu Ile Val Gly
 130 135 140

Lys Lys Ala Ala Ser Arg Pro Gly Tyr Arg Tyr Glu Ile Lys Ala Phe
 145 150 155 160

Tyr Gly Gly Asn Arg Tyr Tyr Met Phe Thr Lys Lys Val Phe Arg Asp
165 170 175

Val Arg Leu Val Ala Ala Pro Pro Ser Ser Ile Gly Lys Phe Gly Ser
180 185 190

Asp Thr Asp Asn Trp Ala Trp Pro Arg His Thr Gly Asp Phe Ser Ile
195 200 205

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

Asp Asn Val Pro Tyr Arg Pro Lys Arg Trp Val Lys Val Asn Ala Gln
225 230 235 240

Gly Val Lys Glu Gly Asp Phe Ala Leu Ile Met Gly Tyr Pro Gly Thr
245 250 255

Thr Tyr Lys Phe Phe Thr Ala Asp Glu Val Thr Glu Trp Ser Glu Ile
260 265 270

Asp Asn Asn Ile Arg Ile Glu Met Arg Gly Ile Leu Gln Asp Val Met
275 280 285

Leu Arg Glu Met Leu Ala Asp Pro Lys Ile Asn Ile Met Tyr Ala Ala
290 295 300

Lys Tyr Ala Ser Ser Gln Asn Gly Tyr Lys Arg Ala Gln Gly Ala Asn
305 310 315 320

Trp Ala Ile Arg Arg Arg Ser Leu Arg Glu Ile Lys Leu Ala Gln Gln
325 330 335

Gln Glu Val Leu Ala Trp Ala Lys Gln Lys Gly Ile Ala Thr Thr Glu
340 345 350

Glu Ala Val Arg Ala Ile Ser Lys Ala Ile Glu Gly Arg Gln Asp Leu

355

360

365

Arg Met Arg Gln Arg Tyr Leu Leu Glu Gly Ile Leu Met Gly Ile Glu
 370 375 380

Met Ser Asn Ala Pro Ala Ala Asp Ser Asp Ile Ala Asp His Trp Asp
 385 390 395 400

Asp Pro Ala Arg Arg Glu Ala Gly Leu Gln Ser Ile Arg Lys Gln Phe
 405 410 415

Glu Ala Phe Phe Asn Lys Asp Tyr Ser Pro Glu Val Glu Lys Asp Gln
 420 425 430

Leu Ala Ile Ala Leu Leu Thr Arg Tyr Ala Glu Arg Ile Pro Ala Glu
 435 440 445

Lys Gln Pro Ile Ser Ile Arg Glu Gly Ile Ala Glu Tyr Gly Ser Ala
 450 455 460

Lys Ala Tyr Val Glu Met Ile Phe Asp Lys Ser Ile Tyr Ala Ser Arg
 465 470 475 480

Glu Arg Phe Glu Glu Phe Met Lys Asn Pro Asp Arg Asp Arg Leu Leu
 485 490 495

Arg Asp Pro Met Ser Arg Phe Ala Ala Ser Val Ala Tyr Glu His Gln
 500 505 510

Lys Leu Ala Lys Glu Val Ala Ala Phe Asp Ala Pro Leu Ala Ala Ala
 515 520 525

Gln Arg Ser Tyr Val Ala Ser Val Leu Asp Met Lys Gly Gln Pro Asn
 530 535 540

Leu Ala Pro Asp Ala Asn Leu Thr Leu Arg Phe Thr Tyr Gly Glu Ile
 545 550 555 560

Lys Gly Tyr Gln Pro Arg Asp Val Val Thr Tyr Gly Ala Lys Ser Thr
565 570 575

Leu Glu Gly Val Met Glu Lys Glu Asp Pro Asn Asn Trp Glu Tyr Val
580 585 590

Val Asp Pro Lys Leu Lys Ala Leu Tyr Glu Ala Lys Asn Tyr Gly Arg
595 600 605

Tyr Ala Asn Ser Asp Gly Ser Met Pro Val Asn Phe Cys Ala Thr Thr
610 615 620

His Thr Thr Gly Gly Asn Ser Gly Ser Pro Val Met Asn Ala Arg Gly
625 630 635 640

Glu Leu Ile Gly Leu Asn Phe Asp Arg Asn Trp Glu Gly Val Gly Gly
645 650 655

Asp Ile Glu Tyr Leu Pro Asn Tyr Gln Arg Ser Ile Ile Leu Asp Ile
660 665 670

Arg Tyr Leu Leu Phe Ile Ile Asp Lys Phe Ala Gly Cys Gln Arg Leu
675 680 685

Ile Asp Glu Ile Gln Pro Gln Phe
690 695

<210> 15
<211> 738
<212> PRT
<213> Rattus norvegicus

<220>
<221> Dipeptidyl peptidase 3 (DPP3)
<222> (1)..(738)
<223> UniProt Accession No. 055096

<400> 15

Met Ala Asp Thr Gln Tyr Ile Leu Pro Asn Asp Ile Gly Val Ser Ser
 1 5 10 15

Leu Asp Cys Arg Glu Ala Phe Arg Leu Leu Ser Pro Thr Glu Arg Leu
 20 25 30

Tyr Ala His His Leu Ser Arg Ala Ala Trp Tyr Gly Gly Leu Ala Val
 35 40 45

Leu Leu Gln Thr Ser Pro Glu Ala Pro Tyr Ile Tyr Ala Leu Leu Ser
 50 55 60

Arg Leu Phe Arg Ala Gln Asp Pro Asp Gln Leu Arg Gln His Ala Leu
 65 70 75 80

Ala Glu Gly Leu Thr Glu Glu Glu Tyr Gln Ala Phe Leu Val Tyr Ala
 85 90 95

Ala Gly Val Tyr Ser Asn Met Gly Asn Tyr Lys Ser Phe Gly Asp Thr
 100 105 110

Lys Phe Val Pro Asn Leu Pro Lys Glu Lys Leu Glu Arg Val Ile Leu
 115 120 125

Gly Ser Lys Ala Ala Gln Gln His Pro Glu Glu Val Arg Ser Leu Trp
 130 135 140

Gln Thr Cys Gly Glu Leu Met Phe Ser Leu Glu Pro Arg Leu Arg His
 145 150 155 160

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

Ala Met Glu Asp Ala Lys Leu Ala Gln Asp Phe Leu Asp Ser Gln Asn
 180 185 190

Leu Ser Ala Tyr Asn Thr Arg Leu Phe Lys Val Val Gly Gln Glu Gly
 195 200 205

Lys Tyr His Tyr Glu Val Arg Leu Ala Ser Val Leu Asn Thr Glu Pro
 210 215 220

Ala Leu Asp Ser Glu Leu Thr Ser Lys Leu Lys Ser Tyr Glu Phe Gln
 225 230 235 240

Gly Asn His Phe Gln Val Thr Arg Gly Asp Tyr Ala Pro Ile Leu Gln
 245 250 255

Lys Val Val Glu His Leu Glu Lys Ala Lys Ala Tyr Ala Ala Asn Ser
 260 265 270

His Gln Glu Gln Met Leu Ala Gln Tyr Val Glu Ser Phe Thr Gln Gly
 275 280 285

Ser Ile Glu Ala His Lys Arg Gly Ser Arg Phe Trp Ile Gln Asp Lys
 290 295 300

Gly Pro Ile Val Glu Ser Tyr Ile Gly Phe Ile Glu Ser Tyr Arg Asp
 305 310 315 320

Pro Phe Gly Ser Arg Gly Glu Phe Glu Gly Phe Val Ala Met Val Asn
 325 330 335

Lys Asp Met Ser Ala Lys Phe Glu Arg Leu Val Ala Ser Ala Glu Gln
 340 345 350

Leu Leu Lys Glu Leu Pro Trp Pro Pro Ala Phe Glu Lys Asp Lys Phe
 355 360 365

Leu Thr Pro Asp Phe Thr Ser Leu Asp Val Leu Thr Phe Ala Gly Ser
 370 375 380

Gly Ile Pro Ala Gly Ile Asn Ile Pro Asn Tyr Asp Asp Leu Arg Gln
 385 390 395 400

Thr Glu Gly Phe Lys Asn Val Ser Leu Gly Asn Val Leu Ala Val Ala
405 410 415

Tyr Ala Thr Lys Arg Glu Lys Leu Thr Phe Met Glu Glu Glu Asp Lys
420 425 430

Asp Leu Tyr Ile Arg Trp Lys Gly Pro Ser Phe Asp Val Gln Val Gly
435 440 445

Leu His Glu Leu Leu Gly His Gly Ser Gly Lys Leu Phe Val Gln Asp
450 455 460

Glu Lys Gly Ala Phe Asn Phe Asp Gln Glu Thr Val Ile Asn Pro Glu
465 470 475 480

Thr Gly Glu Gln Ile Gln Ser Trp Tyr Arg Ser Gly Glu Thr Trp Asp
485 490 495

Ser Lys Phe Ser Thr Ile Ala Ser Ser Tyr Glu Glu Cys Arg Ala Glu
500 505 510

Ser Val Gly Leu Tyr Leu Cys Leu Asn Pro Gln Val Leu Gln Ile Phe
515 520 525

Gly Phe Glu Gly Thr Asp Ala Glu Asp Val Ile Tyr Val Asn Trp Leu
530 535 540

Asn Met Val Arg Ala Gly Leu Leu Ala Leu Glu Phe Tyr Thr Pro Glu
545 550 555 560

Thr Ala Asn Trp Arg Gln Ala His Met Gln Ala Arg Phe Val Ile Leu
565 570 575

Arg Val Leu Leu Glu Ala Gly Glu Gly Leu Val Thr Val Thr Pro Thr
580 585 590

Thr Gly Ser Asp Gly Arg Pro Asp Ala Arg Val His Leu Asp Arg Ser
595 600 605

Lys Ile Arg Ser Val Gly Lys Pro Ala Leu Glu Arg Phe Leu Arg Arg
610 615 620

Leu Gln Val Leu Lys Ser Thr Gly Asp Val Val Ala Gly Arg Ala Leu
625 630 635 640

Tyr Glu Gly Tyr Ala Ala Val Thr Asp Ala Pro Pro Glu Cys Phe Leu
645 650 655

Thr Leu Arg Asp Thr Val Leu Leu Arg Lys Glu Ser Arg Lys Leu Ile
660 665 670

Val Gln Pro Asn Thr Arg Leu Glu Gly Ser Glu Val Gln Leu Val Glu
675 680 685

Tyr Glu Ala Ser Ala Ala Gly Leu Ile Arg Ser Phe Cys Glu Arg Phe
690 695 700

Pro Glu Asp Gly Pro Glu Leu Glu Glu Val Leu Thr Gln Leu Ala Thr
705 710 715 720

Ala Asp Ala Gln Phe Trp Arg Asp Gln Val Gln Glu Ala Pro Ser Gly
725 730 735

Gln Ala

<210> 16
<211> 660
<212> PRT
<213> Porphyromonas gingivalis

<220>
<221> Dipeptidyl peptidase 5 (DPP5)
<222> (1)..(660)
<223> Uniprot accession B2RIT0

<400> 16

Thr Asn Thr Gly Glu His Leu Thr Pro Glu Leu Phe Met Thr Leu Ser
 1 5 10 15

Arg Val Ser Glu Met Ala Leu Ser Pro Asp Gly Lys Thr Ala Val Tyr
 20 25 30

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

Phe Thr Val Asn Leu Asp Gly Ser Gly Arg Lys Gln Ile Thr Asp Thr
 50 55 60

Glu Ser Asn Glu Tyr Ala Pro Ala Trp Met Ala Asp Gly Lys Arg Ile
 65 70 75 80

Ala Phe Met Ser Asn Glu Gly Gly Ser Met Gln Leu Trp Val Met Asn
 85 90 95

Ala Asp Gly Thr Glu Arg Arg Gln Leu Ser Asn Ile Glu Gly Gly Ile
 100 105 110

Thr Gly Phe Leu Phe Ser Pro Asp Glu Lys Gln Val Leu Phe Thr Lys
 115 120 125

Asp Ile Lys Phe Gly Lys Arg Thr Lys Asp Ile Tyr Pro Asp Leu Asp
 130 135 140

Lys Ala Thr Gly Arg Ile Ile Thr Asp Leu Met Tyr Lys His Trp Asp
 145 150 155 160

Glu Trp Val Glu Thr Ile Pro His Pro Phe Ile Ala Asn Ala Thr Asp
 165 170 175

Gly Met Ile Thr Thr Gly Lys Asp Ile Met Glu Gly Glu Pro Tyr Glu
 180 185 190

Ala Pro Met Lys Pro Trp Ser Gly Ile Glu Asp Phe Ser Trp Ser Pro

205

Thr Ala Glu Asn Lys Ala Ile Leu Asp Arg Leu Thr Pro Ile Ala Cys
385 390 395 400

Glu Lys Arg Trp Met Lys Thr Thr Asp Gly Gly Asn Met Leu Thr Trp
405 410 415

Val Val Leu Pro Pro Asp Phe Asp Lys Asn Lys Lys Tyr Pro Ala Ile
420 425 430

Leu Tyr Cys Gln Gly Gly Pro Gln Asn Thr Val Ser Gln Phe Trp Ser
435 440 445

Phe Arg Trp Asn Leu Arg Leu Met Ala Glu Gln Gly Tyr Ile Val Ile
450 455 460

Ala Pro Asn Arg His Gly Val Pro Gly Phe Gly Gln Lys Trp Asn Glu
465 470 475 480

Gln Ile Ser Gly Asp Tyr Gly Gly Gln Asn Met Arg Asp Tyr Leu Thr
485 490 495

Ala Val Asp Glu Met Lys Lys Glu Pro Tyr Val Asp Gly Asp Arg Ile
500 505 510

Gly Ala Val Gly Ala Ser Tyr Gly Gly Phe Ser Val Tyr Trp Leu Ala
515 520 525

Gly His His Asp Lys Arg Phe Ala Ala Phe Ile Ala His Ala Gly Ile
530 535 540

Phe Asn Leu Glu Met Gln Tyr Ala Thr Thr Glu Glu Met Trp Phe Ala
545 550 555 560

Asn Trp Asp Ile Gly Gly Pro Phe Trp Glu Lys Asp Asn Val Val Ala
565 570 575

Gln Arg Thr Tyr Ala Thr Ser Pro His Lys Tyr Val Gln Asn Trp Asp
580 585 590

Thr Pro Ile Leu Met Ile His Gly Glu Leu Asp Phe Arg Ile Leu Ala

595

600

605

Ser Gln Ala Met Ala Ala Phe Asp Ala Ala Gln Leu Arg Gly Val Pro
 610 615 620

Ser Glu Met Leu Ile Tyr Pro Asp Glu Asn His Trp Val Leu Gln Pro
 625 630 635 640

Gln Asn Ala Leu Leu Phe His Arg Thr Phe Phe Gly Trp Leu Asp Arg
 645 650 655

Trp Leu Lys Lys
 660

<210> 17
 <211> 698
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Modified Dipeptidyl Aminopeptidase BII (DAP BII)

<400> 17

Gly Glu Gly Met Trp Val Pro Gln Gln Leu Pro Glu Ile Ala Gly Pro
 1 5 10 15

Leu Lys Lys Ala Gly Leu Lys Leu Ser Pro Gln Gln Ile Ser Asp Leu
 20 25 30

Thr Gly Asp Pro Met Gly Ala Val Val Ala Leu Gly Gly Cys Thr Ala
 35 40 45

Ser Phe Val Ser Pro Asn Gly Leu Val Val Thr Asn His His Cys Ala
 50 55 60

Tyr Gly Ala Ile Gln Leu Asn Ser Thr Ala Glu Asn Asn Leu Ile Lys
 65 70 75 80

Asn Gly Phe Asn Ala Pro Thr Thr Ala Asp Glu Val Ser Ala Gly Pro

85

90

95

Asn Ala Arg Val Phe Val Leu Asp Glu Ile Thr Asp Val Thr Lys Asp
 100 105 110

Ala Lys Ala Ala Ile Ala Ala Ala Gly Asp Asp Ala Leu Ala Arg Thr
 115 120 125

Lys Ala Leu Glu Ala Phe Glu Lys Lys Leu Ile Ala Asp Cys Glu Ala
 130 135 140

Glu Ala Gly Phe Arg Cys Arg Leu Tyr Ser Phe Ser Gly Gly Asn Thr
 145 150 155 160

Tyr Arg Leu Phe Lys Asn Leu Glu Ile Lys Asp Val Arg Leu Ala Tyr
 165 170 175

Ala Pro Pro Gly Ser Val Gly Lys Phe Gly Gly Val Ala Ser Leu Gly
 180 185 190

Met Trp Pro Ser His Thr Gly Asp Phe Ala Phe Tyr Arg Ala Tyr Val
 195 200 205

Gly Lys Asp Gly Lys Pro Ala Ala Phe Ser Lys Asp Asn Val Pro Tyr
 210 215 220

Gln Pro Lys His Trp Leu Lys Phe Ala Asp Gln Pro Leu Gly Ala Gly
 225 230 235 240

Asp Phe Val Met Val Ala Gly Tyr Pro Gly Ser Thr Asn Arg Tyr Ala
 245 250 255

Leu Ala Ala Glu Phe Asp Asn Thr Ala Gln Trp Thr Tyr Pro Thr Ile
 260 265 270

Ala Arg His Tyr Lys Asn Gln Ile Ala Met Val Glu Ala Ala Gly Lys
 275 280 285

Gln Asn Ala Asp Ile Gln Val Lys Tyr Ala Ala Thr Met Trp Gly Trp
 290 295 300

Asn Asn Thr Ser Lys Lys Tyr Asp Gly Gln Leu Glu Gly Phe Lys Arg
 305 310 315 320

Ile Asp Ala Ala Gly Gln Lys Leu Arg Glu Glu Ala Ala Val Leu Gly
 325 330 335

Trp Leu Lys Gly Gln Gly Ala Lys Gly Gln Pro Ala Leu Asp Ala His
 340 345 350

Ala Lys Leu Leu Asp Leu Leu Glu Gln Ser Lys Ala Thr Arg Asp Arg
 355 360 365

Asp Leu Thr Leu Ala Leu Phe Asn Asn Thr Ala Met Leu Gly Ser Ala
 370 375 380

Thr Gln Leu Tyr Arg Leu Ser Ile Glu Arg Glu Lys Pro Asn Ala Glu
 385 390 395 400

Arg Glu Ser Gly Tyr Gln Glu Arg Asp Leu Pro Ala Ile Glu Gly Gly
 405 410 415

Leu Lys Gln Leu Glu Arg Arg Tyr Val Ala Ala Met Asp Arg Gln Leu
 420 425 430

Gln Glu Tyr Trp Leu Asn Glu Tyr Ile Lys Leu Pro Ala Asp Gln Arg
 435 440 445

Val Ala Ala Val Asp Ala Trp Leu Gly Gly Asn Asp Ala Ala Ala Val
 450 455 460

Lys Arg Ala Leu Asp Arg Leu Ala Gly Thr Lys Leu Gly Ser Thr Glu
 465 470 475 480

Glu Arg Leu Lys Trp Phe Ala Ala Asp Arg Lys Ala Phe Glu Ala Ser

485

490

495

Asn Asp Pro Ala Ile Gln Tyr Ala Val Ala Val Met Pro Thr Leu Leu
 500 505 510

Lys Leu Glu Gln Glu Arg Lys Thr Arg Ala Gly Glu Asn Leu Ala Ala
 515 520 525

Arg Pro Val Tyr Leu Gln Ala Leu Ala Asp Tyr Lys Lys Ser Gln Gly
 530 535 540

Glu Phe Val Tyr Pro Asp Ala Asn Leu Ser Leu Arg Ile Thr Phe Gly
 545 550 555 560

Asn Val Met Gly Tyr Ala Pro Lys Asp Gly Met Glu Tyr Thr Pro Phe
 565 570 575

Thr Thr Leu Glu Gly Val Val Ala Lys Glu Thr Gly Gln Asp Pro Phe
 580 585 590

Asp Ser Pro Lys Ala Leu Leu Asp Ala Val Ala Ala Lys Arg Tyr Gly
 595 600 605

Gly Leu Glu Asp Lys Arg Ile Gly Ser Val Pro Val Asn Tyr Leu Ser
 610 615 620

Asp Leu Asp Ile Thr Gly Gly Asn Ser Gly Ser Pro Val Leu Asp Ala
 625 630 635 640

His Gly Lys Leu Val Gly Leu Ala Phe Ala Gly Asn Trp Glu Ser Val
 645 650 655

Ser Ser Asn Trp Val Phe Asp Pro Lys Met Thr Arg Met Ile Ala Val
 660 665 670

Asp Gly Arg Tyr Leu Arg Trp Ile Met Gln Glu Val Tyr Pro Ala Pro
 675 680 685

Gln Leu Leu Lys Glu Met Asn Val Gly Lys
690 695

<210> 18
<211> 698
<212> PRT
<213> Artificial Sequence

<220>
<223> Modified Dipeptidyl Aminopeptidase BII (DAP BII)

<400> 18

Gly Glu Gly Met Trp Val Pro Gln Gln Leu Pro Glu Ile Ala Gly Pro
1 5 10 15

Leu Lys Lys Ala Gly Leu Lys Leu Ser Pro Gln Gln Ile Ser Asp Leu
20 25 30

Thr Gly Asp Pro Met Gly Ala Val Val Ala Leu Gly Gly Cys Thr Ala
35 40 45

Ser Phe Val Ser Pro Asn Gly Leu Val Val Thr Asn His His Cys Ala
50 55 60

Tyr Gly Ala Ile Gln Leu Asn Ser Thr Ala Glu Asn Asn Leu Ile Lys
65 70 75 80

Asn Gly Phe Asn Ala Pro Thr Thr Ala Asp Glu Val Ser Ala Gly Pro
85 90 95

Asn Ala Arg Val Phe Val Leu Asp Glu Ile Thr Asp Val Thr Lys Asp
100 105 110

Ala Lys Ala Ala Ile Ala Ala Ala Gly Asp Asp Ala Leu Ala Arg Thr
115 120 125

Lys Ala Leu Glu Ala Phe Glu Lys Lys Leu Ile Ala Asp Cys Glu Ala
130 135 140

Glu Ala Gly Phe Arg Cys Arg Leu Tyr Ser Phe Ser Gly Gly Asn Thr
 145 150 155 160

Tyr Arg Leu Phe Lys Asn Leu Glu Ile Lys Asp Val Arg Leu Ala Tyr
 165 170 175

Ala Pro Pro Gly Ser Val Gly Lys Phe Gly Gly Asp Ile Asp Met Gly
 180 185 190

Met Trp Pro Thr His Thr Gly Asp Phe Ala Phe Tyr Arg Ala Tyr Val
 195 200 205

Gly Lys Asp Gly Lys Pro Ala Ala Phe Ser Lys Asp Asn Val Pro Tyr
 210 215 220

Gln Pro Lys His Trp Leu Lys Phe Ala Asp Gln Pro Leu Gly Ala Gly
 225 230 235 240

Asp Phe Val Met Val Ala Gly Tyr Pro Gly Ser Thr Asn Arg Tyr Ala
 245 250 255

Leu Ala Ala Glu Phe Asp Asn Thr Ala Gln Trp Thr Tyr Pro Thr Ile
 260 265 270

Ala Arg His Tyr Lys Asn Gln Ile Ala Met Val Glu Ala Ala Gly Lys
 275 280 285

Gln Asn Ala Asp Ile Gln Val Lys Tyr Ala Ala Thr Met Ala Gly Trp
 290 295 300

Asn Arg Thr Ser Lys Asn Tyr Asp Gly Gln Leu Glu Gly Phe Lys Arg
 305 310 315 320

Ile Asp Ala Ala Gly Gln Lys Leu Arg Glu Glu Ala Ala Val Leu Gly
 325 330 335

Trp Leu Lys Gly Gln Gly Ala Lys Gly Gln Pro Ala Leu Asp Ala His

340	345	350
Ala Lys Leu Leu Asp Leu Leu Glu Gln Ser Lys Ala Thr Arg Asp Arg		
355	360	365
Asp Leu Thr Leu Ala Leu Phe Asn Asn Thr Ala Met Leu Gly Ser Ala		
370	375	380
Thr Gln Leu Tyr Arg Leu Ser Ile Glu Arg Glu Lys Pro Asn Ala Glu		
385	390	395
Arg Glu Ser Gly Tyr Gln Glu Arg Asp Leu Pro Ala Ile Glu Gly Gly		
405	410	415
Leu Lys Gln Leu Glu Arg Arg Tyr Val Ala Ala Met Asp Arg Gln Leu		
420	425	430
Gln Glu Tyr Trp Leu Asn Glu Tyr Ile Lys Leu Pro Ala Asp Gln Arg		
435	440	445
Val Ala Ala Val Asp Ala Trp Leu Gly Gly Asn Asp Ala Ala Ala Val		
450	455	460
Lys Arg Ala Leu Asp Arg Leu Ala Gly Thr Lys Leu Gly Ser Thr Glu		
465	470	475
Glu Arg Leu Lys Trp Phe Ala Ala Asp Arg Lys Ala Phe Glu Ala Ser		
485	490	495
Asn Asp Pro Ala Ile Gln Tyr Ala Val Ala Val Met Pro Thr Leu Leu		
500	505	510
Lys Leu Glu Gln Glu Arg Lys Thr Arg Ala Gly Glu Asn Leu Ala Ala		
515	520	525
Arg Pro Val Tyr Leu Gln Ala Leu Ala Asp Tyr Lys Lys Ser Gln Gly		
530	535	540

Glu Phe Val Tyr Pro Asp Ala Asn Leu Ser Leu Arg Ile Thr Phe Gly
 545 550 555 560

Asn Val Met Gly Tyr Ala Pro Lys Asp Gly Met Glu Tyr Thr Pro Phe
 565 570 575

Thr Thr Leu Glu Gly Val Val Ala Lys Glu Thr Gly Gln Asp Pro Phe
 580 585 590

Asp Ser Pro Lys Ala Leu Leu Asp Ala Val Ala Ala Lys Arg Tyr Gly
 595 600 605

Gly Leu Glu Asp Lys Arg Ile Gly Ser Val Pro Val Asn Tyr Leu Ser
 610 615 620

Asp Leu Asp Ile Thr Gly Gly Asn Ser Gly Ser Pro Val Leu Asp Ala
 625 630 635 640

His Gly Lys Leu Val Gly Leu Ala Phe Ala Gly Asn Trp Glu Ser Val
 645 650 655

Ser Ser Asn Trp Val Phe Asp Pro Lys Met Thr Arg Met Ile Ala Val
 660 665 670

Asp Gly Arg Tyr Leu Arg Trp Ile Met Gln Glu Val Tyr Pro Ala Pro
 675 680 685

Gln Leu Leu Lys Glu Met Asn Val Gly Lys
 690 695

<210> 19

<211> 698

<212> PRT

<213> Artificial Sequence

<220>

<223> Modified Dipeptidyl Aminopeptidase BII (DAP BII)

<400> 19

Gly Glu Gly Met Trp Val Pro Gln Gln Leu Pro Glu Ile Ala Gly Pro
 1 5 10 15

Leu Lys Lys Ala Gly Leu Lys Leu Ser Pro Gln Gln Ile Ser Asp Leu
 20 25 30

Thr Gly Asp Pro Met Gly Ala Val Val Ala Leu Gly Gly Cys Thr Ala
 35 40 45

Ser Phe Val Ser Pro Asn Gly Leu Val Val Thr Asn His His Cys Ala
 50 55 60

Tyr Gly Ala Ile Gln Leu Asn Ser Thr Ala Glu Asn Asn Leu Ile Lys
 65 70 75 80

Asn Gly Phe Asn Ala Pro Thr Thr Ala Asp Glu Val Ser Ala Gly Pro
 85 90 95

Asn Ala Arg Val Phe Val Leu Asp Glu Ile Thr Asp Val Thr Lys Asp
 100 105 110

Ala Lys Ala Ala Ile Ala Ala Ala Gly Asp Asp Ala Leu Ala Arg Thr
 115 120 125

Lys Ala Leu Glu Ala Phe Glu Lys Lys Leu Ile Ala Asp Cys Glu Ala
 130 135 140

Glu Ala Gly Phe Arg Cys Arg Leu Tyr Ser Phe Ser Gly Gly Asn Thr
 145 150 155 160

Tyr Arg Leu Phe Lys Asn Leu Glu Ile Lys Asp Val Arg Leu Ala Tyr
 165 170 175

Ala Pro Pro Gly Ser Val Gly Lys Phe Gly Gly Asp Ile Asp Met Gly
 180 185 190

Met Trp Pro Val His Thr Gly Asp Phe Ala Phe Tyr Arg Ala Tyr Val

Arg Glu Ser Gly Tyr Gln Glu Arg Asp Leu Pro Ala Ile Glu Gly Gly
405 410 415

Leu Lys Gln Leu Glu Arg Arg Tyr Val Ala Ala Met Asp Arg Gln Leu
420 425 430

Gln Glu Tyr Trp Leu Asn Glu Tyr Ile Lys Leu Pro Ala Asp Gln Arg
435 440 445

Val Ala Ala Val Asp Ala Trp Leu Gly Gly Asn Asp Ala Ala Ala Val
450 455 460

Lys Arg Ala Leu Asp Arg Leu Ala Gly Thr Lys Leu Gly Ser Thr Glu
465 470 475 480

Glu Arg Leu Lys Trp Phe Ala Ala Asp Arg Lys Ala Phe Glu Ala Ser
485 490 495

Asn Asp Pro Ala Ile Gln Tyr Ala Val Ala Val Met Pro Thr Leu Leu
500 505 510

Lys Leu Glu Gln Glu Arg Lys Thr Arg Ala Gly Glu Asn Leu Ala Ala
515 520 525

Arg Pro Val Tyr Leu Gln Ala Leu Ala Asp Tyr Lys Lys Ser Gln Gly
530 535 540

Glu Phe Val Tyr Pro Asp Ala Asn Leu Ser Leu Arg Ile Thr Phe Gly
545 550 555 560

Asn Val Met Gly Tyr Ala Pro Lys Asp Gly Met Glu Tyr Thr Pro Phe
565 570 575

Thr Thr Leu Glu Gly Val Val Ala Lys Glu Thr Gly Gln Asp Pro Phe
580 585 590

Asp Ser Pro Lys Ala Leu Leu Asp Ala Val Ala Ala Lys Arg Tyr Gly

595

600

605

Gly Leu Glu Asp Lys Arg Ile Gly Ser Val Pro Val Asn Tyr Leu Ser
 610 615 620

Asp Leu Asp Ile Thr Gly Gly Asn Ser Gly Ser Pro Val Leu Asp Ala
 625 630 635 640

His Gly Lys Leu Val Gly Leu Ala Phe Ala Gly Asn Trp Glu Ser Val
 645 650 655

Ser Ser Asn Trp Val Phe Asp Pro Lys Met Thr Arg Met Ile Ala Val
 660 665 670

Asp Gly Arg Tyr Leu Arg Trp Ile Met Gln Glu Val Tyr Pro Ala Pro
 675 680 685

Gln Leu Leu Lys Glu Met Asn Val Gly Lys
 690 695

<210> 20
 <211> 722
 <212> PRT
 <213> Pseudoxanthomonas mexicana

<220>
 <221> Dipeptidyl Aminopeptidase BII (DAP BII) with Signal Sequence
 <222> (1)..(722)
 <223> UniProt Accession No. V5YM14

<400> 20

Met Arg Pro Asn Leu Leu Ala Ala Ala Ile Ala Val Pro Leu Ser Leu
 1 5 10 15

Leu Ala Ala Gln Ile Ala Gln Ala Gly Glu Gly Met Trp Val Pro Gln
 20 25 30

Gln Leu Pro Glu Ile Ala Gly Pro Leu Lys Lys Ala Gly Leu Lys Leu
 35 40 45

Ser Pro Gln Gln Ile Ser Asp Leu Thr Gly Asp Pro Met Gly Ala Val
50 55 60

Val Ala Leu Gly Gly Cys Thr Ala Ser Phe Val Ser Pro Asn Gly Leu
65 70 75 80

Val Val Thr Asn His His Cys Ala Tyr Gly Ala Ile Gln Leu Asn Ser
85 90 95

Thr Ala Glu Asn Asn Leu Ile Lys Asn Gly Phe Asn Ala Pro Thr Thr
100 105 110

Ala Asp Glu Val Ser Ala Gly Pro Asn Ala Arg Val Phe Val Leu Asp
115 120 125

Glu Ile Thr Asp Val Thr Lys Asp Ala Lys Ala Ala Ile Ala Ala Ala
130 135 140

Gly Asp Asp Ala Leu Ala Arg Thr Lys Ala Leu Glu Ala Phe Glu Lys
145 150 155 160

Lys Leu Ile Ala Asp Cys Glu Ala Glu Ala Gly Phe Arg Cys Arg Leu
165 170 175

Tyr Ser Phe Ser Gly Gly Asn Thr Tyr Arg Leu Phe Lys Asn Leu Glu
180 185 190

Ile Lys Asp Val Arg Leu Ala Tyr Ala Pro Pro Gly Ser Val Gly Lys
195 200 205

Phe Gly Gly Asp Ile Asp Asn Trp Met Trp Pro Arg His Thr Gly Asp
210 215 220

Phe Ala Phe Tyr Arg Ala Tyr Val Gly Lys Asp Gly Lys Pro Ala Ala
225 230 235 240

Phe Ser Lys Asp Asn Val Pro Tyr Gln Pro Lys His Trp Leu Lys Phe
245 250 255

Ala Asp Gln Pro Leu Gly Ala Gly Asp Phe Val Met Val Ala Gly Tyr
260 265 270

Pro Gly Ser Thr Asn Arg Tyr Ala Leu Ala Ala Glu Phe Asp Asn Thr
275 280 285

Ala Gln Trp Thr Tyr Pro Thr Ile Ala Arg His Tyr Lys Asn Gln Ile
290 295 300

Ala Met Val Glu Ala Ala Gly Lys Gln Asn Ala Asp Ile Gln Val Lys
305 310 315 320

Tyr Ala Ala Thr Met Ala Gly Trp Asn Asn Thr Ser Lys Asn Tyr Asp
325 330 335

Gly Gln Leu Glu Gly Phe Lys Arg Ile Asp Ala Ala Gly Gln Lys Leu
340 345 350

Arg Glu Glu Ala Ala Val Leu Gly Trp Leu Lys Gly Gln Gly Ala Lys
355 360 365

Gly Gln Pro Ala Leu Asp Ala His Ala Lys Leu Leu Asp Leu Leu Glu
370 375 380

Gln Ser Lys Ala Thr Arg Asp Arg Asp Leu Thr Leu Ala Leu Phe Asn
385 390 395 400

Asn Thr Ala Met Leu Gly Ser Ala Thr Gln Leu Tyr Arg Leu Ser Ile
405 410 415

Glu Arg Glu Lys Pro Asn Ala Glu Arg Glu Ser Gly Tyr Gln Glu Arg
420 425 430

Asp Leu Pro Ala Ile Glu Gly Gly Leu Lys Gln Leu Glu Arg Arg Tyr
435 440 445

Val Ala Ala Met Asp Arg Gln Leu Gln Glu Tyr Trp Leu Asn Glu Tyr
450 455 460

Ile Lys Leu Pro Ala Asp Gln Arg Val Ala Ala Val Asp Ala Trp Leu
465 470 475 480

Gly Gly Asn Asp Ala Ala Ala Val Lys Arg Ala Leu Asp Arg Leu Ala
485 490 495

Gly Thr Lys Leu Gly Ser Thr Glu Glu Arg Leu Lys Trp Phe Ala Ala
500 505 510

Asp Arg Lys Ala Phe Glu Ala Ser Asn Asp Pro Ala Ile Gln Tyr Ala
515 520 525

Val Ala Val Met Pro Thr Leu Leu Lys Leu Glu Gln Glu Arg Lys Thr
530 535 540

Arg Ala Gly Glu Asn Leu Ala Ala Arg Pro Val Tyr Leu Gln Ala Leu
545 550 555 560

Ala Asp Tyr Lys Lys Ser Gln Gly Glu Phe Val Tyr Pro Asp Ala Asn
565 570 575

Leu Ser Leu Arg Ile Thr Phe Gly Asn Val Met Gly Tyr Ala Pro Lys
580 585 590

Asp Gly Met Glu Tyr Thr Pro Phe Thr Thr Leu Glu Gly Val Val Ala
595 600 605

Lys Glu Thr Gly Gln Asp Pro Phe Asp Ser Pro Lys Ala Leu Leu Asp
610 615 620

Ala Val Ala Ala Lys Arg Tyr Gly Gly Leu Glu Asp Lys Arg Ile Gly
625 630 635 640

Ser Val Pro Val Asn Tyr Leu Ser Asp Leu Asp Ile Thr Gly Gly Asn
645 650 655

Ser Gly Ser Pro Val Leu Asp Ala His Gly Lys Leu Val Gly Leu Ala
660 665 670

Phe Asp Gly Asn Trp Glu Ser Val Ser Ser Asn Trp Val Phe Asp Pro
675 680 685

Lys Met Thr Arg Met Ile Ala Val Asp Gly Arg Tyr Leu Arg Trp Ile
690 695 700

Met Gln Glu Val Tyr Pro Ala Pro Gln Leu Leu Lys Glu Met Asn Val
705 710 715 720

Gly Lys

<210> 21
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Test peptide

<400> 21

Ala Ala Ala Arg
1

<210> 22
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Test peptide

<220>
<221> MISC_FEATURE
<222> (19)..(19)

<223> 3' - azide

<400> 22

Ala Ala Gly Val Ala Met Pro Gly Ala Glu Asp Asp Val Val Gly Ser
1 5 10 15

Gly Ser Lys

<210> 23

<211> 698

<212> PRT

<213> Artificial Sequence

<220>

<223> Modified Dipeptidyl Aminopeptidase BII (DAP BII)

<400> 23

Gly Glu Gly Met Trp Val Pro Gln Gln Leu Pro Glu Ile Ala Gly Pro
1 5 10 15

Leu Lys Lys Ala Gly Leu Lys Leu Ser Pro Gln Gln Ile Ser Asp Leu
20 25 30

Thr Gly Asp Pro Met Gly Ala Val Val Ala Leu Gly Gly Cys Thr Ala
35 40 45

Ser Phe Val Ser Pro Asn Gly Leu Val Val Thr Asn His His Cys Ala
50 55 60

Tyr Gly Ala Ile Gln Leu Asn Ser Thr Ala Glu Asn Asn Leu Ile Lys
65 70 75 80

Asn Gly Phe Asn Ala Pro Thr Thr Ala Asp Glu Val Ser Ala Gly Pro
85 90 95

Asn Ala Arg Val Phe Val Leu Asp Glu Ile Thr Asp Val Thr Lys Asp
100 105 110

Ala Lys Ala Ala Ile Ala Ala Ala Gly Asp Asp Ala Leu Ala Arg Thr
115 120 125

Lys Ala Leu Glu Ala Phe Glu Lys Lys Leu Ile Ala Asp Cys Glu Ala
130 135 140

Glu Ala Gly Phe Arg Cys Arg Leu Tyr Ser Phe Ser Gly Gly Asn Thr
145 150 155 160

Tyr Arg Leu Phe Lys Asn Leu Glu Ile Lys Asp Val Arg Leu Ala Tyr
165 170 175

Ala Pro Pro Gly Ser Val Gly Lys Phe Gly Gly Asp Ile Asp Met Gly
180 185 190

Met Trp Pro Thr His Thr Gly Asp Phe Ala Phe Tyr Arg Ala Tyr Val
195 200 205

Gly Lys Asp Gly Lys Pro Ala Ala Phe Ser Lys Asp Asn Val Pro Tyr
210 215 220

Gln Pro Lys His Trp Leu Lys Phe Ala Asp Gln Pro Leu Gly Ala Gly
225 230 235 240

Asp Phe Val Met Val Ala Gly Tyr Pro Gly Ser Thr Asn Arg Tyr Ala
245 250 255

Leu Ala Ala Glu Phe Asp Asn Thr Ala Gln Trp Thr Tyr Pro Thr Ile
260 265 270

Ala Arg His Tyr Lys Asn Gln Ile Ala Met Val Glu Ala Ala Gly Lys
275 280 285

Gln Asn Ala Asp Ile Gln Val Lys Tyr Ala Ala Thr Met Ala Gly Trp
290 295 300

Asn Arg Lys Ser Lys Asn Tyr Asp Gly Gln Leu Glu Gly Phe Lys Arg
305 310 315 320

Ile Asp Ala Ala Gly Gln Lys Leu Arg Glu Glu Ala Ala Val Leu Gly
325 330 335

Trp Leu Lys Gly Gln Gly Ala Lys Gly Gln Pro Ala Leu Asp Ala His
340 345 350

Ala Lys Leu Leu Asp Leu Leu Glu Gln Ser Lys Ala Thr Arg Asp Arg
355 360 365

Asp Leu Thr Leu Ala Leu Phe Asn Asn Thr Ala Met Leu Gly Ser Ala
370 375 380

Thr Gln Leu Tyr Arg Leu Ser Ile Glu Arg Glu Lys Pro Asn Ala Glu
385 390 395 400

Arg Glu Ser Gly Tyr Gln Glu Arg Asp Leu Pro Ala Ile Glu Gly Gly
405 410 415

Leu Lys Gln Leu Glu Arg Arg Tyr Val Ala Ala Met Asp Arg Gln Leu
420 425 430

Gln Glu Tyr Trp Leu Asn Glu Tyr Ile Lys Leu Pro Ala Asp Gln Arg
435 440 445

Val Ala Ala Val Asp Ala Trp Leu Gly Gly Asn Asp Ala Ala Ala Val
450 455 460

Lys Arg Ala Leu Asp Arg Leu Ala Gly Thr Lys Leu Gly Ser Thr Glu
465 470 475 480

Glu Arg Leu Lys Trp Phe Ala Ala Asp Arg Lys Ala Phe Glu Ala Ser
485 490 495

Asn Asp Pro Ala Ile Gln Tyr Ala Val Ala Val Met Pro Thr Leu Leu
500 505 510

Lys Leu Glu Gln Glu Arg Lys Thr Arg Ala Gly Glu Asn Leu Ala Ala
515 520 525

Arg Pro Val Tyr Leu Gln Ala Leu Ala Asp Tyr Lys Lys Ser Gln Gly
530 535 540

Glu Phe Val Tyr Pro Asp Ala Asn Leu Ser Leu Arg Ile Thr Phe Gly
545 550 555 560

Asn Val Met Gly Tyr Ala Pro Lys Asp Gly Met Glu Tyr Thr Pro Phe
565 570 575

Thr Thr Leu Glu Gly Val Val Ala Lys Glu Thr Gly Gln Asp Pro Phe
580 585 590

Asp Ser Pro Lys Ala Leu Leu Asp Ala Val Ala Ala Lys Arg Tyr Gly
595 600 605

Gly Leu Glu Asp Lys Arg Ile Gly Ser Val Pro Val Asn Tyr Leu Ser
610 615 620

Asp Leu Asp Ile Thr Gly Gly Asn Ser Gly Ser Pro Val Leu Asp Ala
625 630 635 640

His Gly Lys Leu Val Gly Leu Ala Phe Ala Gly Asn Trp Glu Ser Val
645 650 655

Ser Ser Asn Trp Val Phe Asp Pro Lys Met Thr Arg Met Ile Ala Val
660 665 670

Asp Gly Arg Tyr Leu Arg Trp Ile Met Gln Glu Val Tyr Pro Ala Pro
675 680 685

Gln Leu Leu Lys Glu Met Asn Val Gly Lys
690 695

<210> 24
<211> 698

<212> PRT
<213> Artificial Sequence

<220>
<223> Modified Dipeptidyl Aminopeptidase BII (DAP BII)

<400> 24

Gly Glu Gly Met Trp Val Pro Gln Gln Leu Pro Glu Ile Ala Gly Pro
1 5 10 15

Leu Lys Lys Ala Gly Leu Lys Leu Ser Pro Gln Gln Ile Ser Asp Leu
20 25 30

Thr Gly Asp Pro Met Gly Ala Val Val Ala Leu Gly Gly Cys Thr Ala
35 40 45

Ser Phe Val Ser Pro Asn Gly Leu Val Val Thr Asn His His Cys Ala
50 55 60

Tyr Gly Ala Ile Gln Leu Asn Ser Thr Ala Glu Asn Asn Leu Ile Lys
65 70 75 80

Asn Gly Phe Asn Ala Pro Thr Thr Ala Asp Glu Val Ser Ala Gly Pro
85 90 95

Asn Ala Arg Val Phe Val Leu Asp Glu Ile Thr Asp Val Thr Lys Asp
100 105 110

Ala Lys Ala Ala Ile Ala Ala Ala Gly Asp Asp Ala Leu Ala Arg Thr
115 120 125

Lys Ala Leu Glu Ala Phe Glu Lys Lys Leu Ile Ala Asp Cys Glu Ala
130 135 140

Glu Ala Gly Phe Arg Cys Arg Leu Tyr Ser Phe Ser Gly Gly Asn Thr
145 150 155 160

Tyr Arg Leu Phe Lys Asn Leu Glu Ile Lys Asp Val Arg Leu Ala Tyr
165 170 175

Ala Pro Pro Gly Ser Val Gly Lys Phe Gly Gly Asp Ile Asp Met Gly
180 185 190

Met Trp Pro Thr His Thr Gly Asp Phe Ala Phe Tyr Arg Ala Tyr Val
195 200 205

Gly Lys Asp Gly Lys Pro Ala Ala Phe Ser Lys Asp Asn Val Pro Tyr
210 215 220

Gln Pro Lys His Trp Leu Lys Phe Ala Asp Gln Pro Leu Gly Ala Gly
225 230 235 240

Asp Phe Val Met Val Ala Gly Tyr Pro Gly Ser Thr Asn Arg Tyr Ala
245 250 255

Leu Ala Ala Glu Phe Asp Asn Thr Ala Gln Trp Thr Tyr Pro Thr Ile
260 265 270

Ala Arg His Tyr Lys Asn Gln Ile Ala Met Val Glu Ala Ala Gly Lys
275 280 285

Gln Asn Ala Asp Ile Gln Val Lys Tyr Ala Ala Thr Met Ala Gly Trp
290 295 300

Asn Arg Thr Ser Lys Asn Tyr Asp Gly Gln Leu Glu Gly Phe Lys Arg
305 310 315 320

Ile Asp Ala Ala Gly Gln Lys Leu Arg Glu Glu Ala Ala Val Leu Gly
325 330 335

Trp Leu Lys Gly Gln Gly Ala Lys Gly Gln Pro Ala Leu Asp Ala His
340 345 350

Ala Lys Leu Leu Asp Leu Leu Glu Gln Ser Lys Ala Thr Arg Asp Arg
355 360 365

Asp Leu Thr Leu Ala Leu Phe Asn Asn Thr Ala Met Leu Gly Ser Ala
 370 375 380

Thr Gln Leu Tyr Arg Leu Ser Ile Glu Arg Glu Lys Pro Asn Ala Glu
 385 390 395 400

Arg Glu Ser Gly Tyr Gln Glu Arg Asp Leu Pro Ala Ile Glu Gly Gly
 405 410 415

Leu Lys Gln Leu Glu Arg Arg Tyr Val Ala Ala Met Asp Arg Gln Leu
 420 425 430

Gln Glu Tyr Trp Leu Asn Glu Tyr Ile Lys Leu Pro Ala Asp Gln Arg
 435 440 445

Val Ala Ala Val Asp Ala Trp Leu Gly Gly Asn Asp Ala Ala Ala Val
 450 455 460

Lys Arg Ala Leu Asp Arg Leu Ala Gly Thr Lys Leu Gly Ser Thr Glu
 465 470 475 480

Glu Arg Leu Lys Trp Phe Ala Ala Asp Arg Lys Ala Phe Glu Ala Ser
 485 490 495

Asn Asp Pro Ala Ile Gln Tyr Ala Val Ala Val Met Pro Thr Leu Leu
 500 505 510

Lys Leu Glu Gln Glu Arg Lys Thr Arg Ala Gly Glu Lys Leu Ala Val
 515 520 525

Arg Pro Val Tyr Leu Gln Ala Leu Ala Asp Tyr Lys Lys Ser Gln Gly
 530 535 540

Glu Phe Val Tyr Pro Asp Ala Asn Leu Ser Leu Arg Ile Thr Phe Gly
 545 550 555 560

Asn Val Met Gly Tyr Ala Pro Lys Asp Gly Met Glu Tyr Thr Pro Phe
 565 570 575

Thr Thr Leu Glu Gly Val Val Ala Lys Glu Thr Gly Gln Asp Pro Phe
580 585 590

Asp Ser Pro Lys Ala Leu Leu Asp Ala Val Ala Val Lys Arg Tyr Gly
595 600 605

Gly Leu Glu Asp Lys Arg Ile Gly Ser Val Pro Val Asn Tyr Leu Ser
610 615 620

Asp Leu Asp Ile Thr Gly Gly Asn Ser Gly Ser Pro Val Leu Asp Ala
625 630 635 640

His Gly Lys Leu Val Gly Leu Ala Phe Ala Gly Asn Trp Glu Ser Val
645 650 655

Ser Ser Asn Trp Val Phe Asp Pro Lys Met Thr Arg Met Ile Ala Val
660 665 670

Asp Gly Arg Tyr Leu Arg Trp Ile Met Gln Glu Val Tyr Pro Ala Pro
675 680 685

Gln Leu Leu Asn Glu Met Asn Val Gly Lys
690 695

<210> 25
<211> 698
<212> PRT
<213> Artificial Sequence

<220>
<223> Modified Dipeptidyl Aminopeptidase BII (DAP BII)

<400> 25

Gly Glu Gly Met Trp Val Pro Gln Gln Leu Pro Glu Ile Ala Gly Pro
1 5 10 15

Leu Lys Lys Ala Gly Leu Lys Leu Ser Pro Gln Gln Ile Ser Asp Leu
20 25 30

Thr Gly Asp Pro Met Gly Ala Val Val Ala Leu Gly Gly Cys Thr Ala
35 40 45

Ser Phe Val Ser Pro Asn Gly Leu Val Val Thr Asn His His Cys Ala
50 55 60

Tyr Gly Ala Ile Gln Leu Asn Ser Thr Ala Glu Asn Asn Leu Ile Lys
65 70 75 80

Asn Gly Phe Asn Ala Pro Thr Thr Ala Asp Glu Val Ser Ala Gly Pro
85 90 95

Asn Ala Arg Val Phe Val Leu Asp Glu Ile Thr Asp Val Thr Lys Asp
100 105 110

Ala Lys Ala Ala Ile Ala Ala Ala Gly Asp Asp Ala Leu Thr Arg Thr
115 120 125

Lys Ala Leu Glu Ala Phe Glu Lys Lys Leu Ile Ala Asp Cys Glu Ala
130 135 140

Glu Ala Gly Phe Arg Cys Arg Leu Tyr Ser Phe Ser Gly Gly Asn Thr
145 150 155 160

Tyr Arg Leu Phe Lys Asn Leu Glu Ile Lys Asp Val Arg Leu Ala Tyr
165 170 175

Ala Pro Pro Gly Ser Val Gly Lys Phe Gly Gly Asp Ile Asp Met Gly
180 185 190

Met Trp Pro Thr His Thr Gly Asp Phe Ala Phe Tyr Arg Ala Tyr Val
195 200 205

Gly Lys Asp Gly Lys Pro Ala Ala Phe Ser Lys Asp Asn Val Pro Tyr
210 215 220

Gln Pro Lys His Trp Leu Lys Phe Ala Asp Gln Pro Leu Val Ala Gly
 225 230 235 240

Asp Phe Val Met Val Ala Gly Tyr Pro Gly Ser Thr Asn Arg Tyr Ala
 245 250 255

Leu Ala Ala Glu Phe Asp Asn Thr Ala Gln Trp Thr Tyr Pro Thr Ile
 260 265 270

Ala Arg His Tyr Lys Asn Gln Ile Ala Met Val Glu Ala Ala Gly Lys
 275 280 285

Gln Asn Ala Asp Ile Gln Val Lys Tyr Ala Ala Thr Met Ala Gly Trp
 290 295 300

Asn Arg Thr Ser Lys Asn Tyr Asp Gly Gln Leu Glu Gly Phe Lys Arg
 305 310 315 320

Ile Asp Ala Ala Gly Gln Lys Leu Arg Glu Glu Ala Ala Val Leu Gly
 325 330 335

Trp Leu Lys Gly Gln Gly Ala Lys Gly Gln Pro Ala Leu Asp Ala His
 340 345 350

Ala Lys Leu Leu Asp Leu Leu Glu Gln Ser Lys Ala Thr Arg Asp Arg
 355 360 365

Asp Leu Thr Leu Ala Leu Phe Asn Asn Thr Ala Met Leu Gly Ser Ala
 370 375 380

Thr Gln Leu Tyr Arg Leu Ser Ile Glu Arg Glu Lys Pro Asn Ala Glu
 385 390 395 400

Arg Glu Ser Gly Tyr Gln Glu Arg Asp Leu Pro Ala Ile Glu Gly Gly
 405 410 415

Leu Lys Gln Leu Glu Arg Arg Tyr Val Ala Ala Met Asp Arg Gln Leu
 420 425 430

Gln Glu Tyr Trp Leu Asn Glu Tyr Ile Lys Leu Pro Ala Asp Gln Arg
435 440 445

Val Ala Ala Val Asp Ala Trp Leu Gly Gly Asn Asp Ala Ala Ala Val
450 455 460

Lys Arg Ala Leu Asp Arg Leu Ala Gly Thr Lys Leu Gly Ser Thr Glu
465 470 475 480

Glu Arg Leu Lys Trp Phe Ala Ala Asp Arg Lys Ala Phe Glu Ala Ser
485 490 495

Asn Asp Pro Ala Ile Gln Tyr Ala Val Ala Val Met Pro Thr Leu Leu
500 505 510

Lys Leu Glu Gln Glu Arg Lys Thr Arg Ala Gly Glu Asn Leu Ala Ala
515 520 525

Arg Pro Val Tyr Leu Gln Ala Leu Ala Asp Tyr Lys Lys Ser Gln Gly
530 535 540

Glu Phe Val Tyr Pro Asp Ala Asn Leu Ser Leu Arg Ile Thr Phe Gly
545 550 555 560

Asn Val Met Gly Tyr Ala Pro Lys Asp Gly Met Glu Tyr Thr Pro Phe
565 570 575

Thr Thr Leu Glu Gly Val Val Ala Lys Glu Thr Gly Gln Asp Pro Phe
580 585 590

Asp Ser Pro Lys Ala Leu Leu Asp Ala Val Ala Ala Lys Arg Tyr Gly
595 600 605

Gly Leu Glu Asp Lys Arg Ile Gly Ser Val Pro Val Asn Tyr Leu Ser
610 615 620

Asp Leu Asp Ile Thr Gly Gly Asn Ser Gly Ser Pro Val Leu Asp Ala
625 630 635 640

His Gly Lys Leu Val Gly Leu Ala Phe Ala Gly Asn Trp Glu Ser Val
645 650 655

Ser Ser Asn Trp Val Phe Asp Pro Lys Met Thr Arg Met Ile Ala Val
660 665 670

Asp Gly Arg Tyr Leu Arg Trp Ile Met Gln Glu Val Tyr Pro Ala Pro
675 680 685

Gln Leu Leu Lys Glu Met Asn Val Gly Lys
690 695

<210> 26
<211> 698
<212> PRT
<213> Artificial Sequence

<220>
<223> Modified Dipeptidyl Aminopeptidase BII (DAP BII)

<400> 26

Gly Glu Gly Met Trp Val Pro Gln Gln Leu Pro Glu Ile Ala Gly Pro
1 5 10 15

Leu Lys Lys Ala Gly Leu Lys Leu Ser Pro Gln Gln Ile Ser Asp Leu
20 25 30

Thr Gly Asp Pro Met Gly Ala Val Val Ala Leu Gly Gly Cys Thr Ala
35 40 45

Ser Phe Val Ser Pro Asn Gly Leu Val Val Thr Asn His His Cys Ala
50 55 60

Tyr Gly Ala Ile Gln Leu Asn Ser Thr Ala Glu Asn Asn Leu Ile Lys
65 70 75 80

Asn Gly Phe Asn Ala Pro Thr Thr Ala Asp Glu Val Ser Ala Gly Pro
85 90 95

Asn Ala Arg Val Phe Val Leu Asp Glu Ile Thr Asp Val Thr Lys Asp
100 105 110

Ala Lys Ala Ala Ile Ala Ala Ala Gly Asp Asp Ala Leu Ala Arg Thr
115 120 125

Lys Ala Leu Glu Ala Phe Glu Lys Lys Leu Ile Ala Asp Cys Glu Ala
130 135 140

Glu Ala Gly Phe Arg Cys Arg Leu Tyr Ser Phe Ser Gly Gly Asn Thr
145 150 155 160

Tyr Arg Leu Phe Lys Asn Leu Glu Ile Lys Asp Val Arg Leu Ala Tyr
165 170 175

Ala Pro Pro Gly Ser Val Gly Lys Phe Gly Gly Asp Ile Asp Met Gly
180 185 190

Met Trp Pro Thr His Thr Gly Asp Phe Ala Phe Tyr Arg Ala Tyr Val
195 200 205

Gly Lys Asp Gly Lys Pro Ala Ala Phe Ser Lys Asp Asn Val Pro Tyr
210 215 220

Gln Pro Lys His Trp Leu Lys Phe Ala Asp Gln Pro Leu Gly Ala Gly
225 230 235 240

Asp Phe Val Met Val Ala Gly Tyr Pro Gly Ser Thr Asn Arg Tyr Ala
245 250 255

Leu Ala Ala Glu Phe Asp Asn Thr Ala Gln Trp Thr Tyr Pro Thr Ile
260 265 270

Ala Arg His Tyr Lys Asn Gln Ile Ala Met Val Glu Ala Ala Gly Lys
275 280 285

Gln Asn Ala Asp Ile Gln Val Lys Tyr Ala Ala Thr Met Ala Gly Trp
 290 295 300

Asn Arg Thr Ser Lys Asn Tyr Asp Gly Gln Leu Glu Gly Phe Lys Arg
 305 310 315 320

Ile Asp Ala Ala Gly Gln Lys Leu Arg Glu Glu Ala Ala Val Leu Gly
 325 330 335

Trp Leu Lys Gly Gln Gly Ala Lys Gly Gln Pro Ala Leu Asp Ala His
 340 345 350

Ala Lys Leu Leu Asp Leu Leu Glu Gln Ser Lys Ala Thr Arg Asp Arg
 355 360 365

Asp Leu Thr Leu Ala Leu Phe Asn Asn Thr Ala Met Leu Gly Ser Ala
 370 375 380

Thr Gln Leu Tyr Arg Leu Ser Ile Glu Arg Glu Lys Pro Asn Ala Glu
 385 390 395 400

Arg Glu Ser Gly Tyr Gln Glu Arg Asp Leu Pro Ala Ile Glu Gly Gly
 405 410 415

Leu Lys Gln Leu Glu Arg Arg Tyr Val Ala Ala Met Asp Arg Gln Leu
 420 425 430

Gln Glu Tyr Trp Leu Asn Glu Tyr Ile Lys Leu Pro Ala Asp Gln Arg
 435 440 445

Val Ala Ala Val Asp Ala Trp Leu Gly Gly Asn Asp Ala Ala Ala Val
 450 455 460

Lys Arg Ala Leu Asp Arg Leu Ala Gly Thr Lys Leu Gly Ser Thr Glu
 465 470 475 480

Glu Arg Leu Lys Trp Phe Ala Ala Asp Arg Lys Ala Phe Glu Ala Ser
485 490 495

Asn Asp Pro Ala Ile Gln Tyr Ala Val Ala Val Met Pro Thr Leu Leu
500 505 510

Lys Leu Glu Gln Glu Arg Lys Thr Arg Ala Gly Glu Asn Leu Ala Ala
515 520 525

Arg Pro Val Tyr Leu Gln Ala Leu Ala Asp Tyr Lys Lys Ser Gln Gly
530 535 540

Glu Leu Val Tyr Pro Asp Ala Asn Leu Ser Leu Arg Ile Thr Phe Gly
545 550 555 560

Asn Val Met Gly Tyr Ala Pro Lys Asp Gly Met Glu Tyr Thr Pro Phe
565 570 575

Thr Thr Leu Glu Gly Val Val Ala Lys Glu Thr Gly Gln Asp Pro Phe
580 585 590

Asp Ser Pro Lys Ala Leu Leu Asp Ala Val Ala Ala Lys Arg Tyr Gly
595 600 605

Gly Leu Glu Asp Lys Arg Ile Gly Ser Val Pro Val Asn Tyr Leu Ser
610 615 620

Asp Leu Asp Ile Thr Gly Gly Asn Ser Gly Ser Pro Val Leu Asp Ala
625 630 635 640

His Gly Lys Leu Val Gly Leu Ala Phe Ala Gly Asn Trp Glu Ser Val
645 650 655

Ser Ser Asn Trp Val Phe Asp Pro Lys Met Thr Arg Met Ile Ala Val
660 665 670

Asp Gly Arg Tyr Leu Arg Trp Ile Met Gln Glu Val Tyr Pro Ala Pro
675 680 685

Gln Leu Leu Lys Glu Met Asn Val Gly Lys
690 695

<210> 27
<211> 698
<212> PRT
<213> Artificial Sequence

<220>
<223> Modified Dipeptidyl Aminopeptidase BII (DAP BII)

<400> 27

Gly Glu Gly Met Trp Val Pro Gln Gln Leu Pro Glu Ile Ala Gly Pro
1 5 10 15

Leu Lys Lys Ala Gly Leu Lys Leu Ser Pro Gln Gln Ile Ser Asp Leu
20 25 30

Thr Gly Asp Pro Met Gly Ala Val Val Ala Leu Gly Gly Cys Thr Ala
35 40 45

Ser Phe Val Ser Pro Asn Gly Leu Val Val Thr Asn His His Cys Ala
50 55 60

Tyr Gly Ala Ile Gln Leu Asn Ser Thr Ala Glu Asn Asn Leu Ile Lys
65 70 75 80

Asn Gly Phe Asn Ala Pro Thr Thr Ala Asp Glu Val Ser Ala Gly Pro
85 90 95

Asn Ala Arg Val Phe Val Leu Asp Glu Ile Thr Asp Val Thr Lys Asp
100 105 110

Ala Lys Ala Ala Ile Ala Ala Ala Gly Asp Asp Ala Leu Ala Arg Thr
115 120 125

Lys Ala Leu Glu Ala Phe Glu Lys Lys Leu Ile Ala Asp Cys Glu Ala
130 135 140

Glu Ala Gly Phe Arg Cys Arg Leu Tyr Ser Phe Ser Gly Gly Asn Thr
 145 150 155 160

Tyr Arg Leu Phe Lys Asn Leu Glu Ile Lys Asp Val Arg Leu Ala Tyr
 165 170 175

Ala Pro Pro Gly Ser Val Gly Lys Phe Gly Gly Asp Ile Asp Met Gly
 180 185 190

Met Trp Pro Thr His Thr Gly Asp Phe Ala Phe Tyr Arg Ala Tyr Val
 195 200 205

Gly Lys Asp Gly Lys Pro Ala Ala Phe Ser Lys Asp Asn Val Pro Tyr
 210 215 220

Gln Pro Lys His Trp Leu Lys Phe Ala Asp Gln Pro Leu Gly Ala Gly
 225 230 235 240

Asp Phe Val Met Val Ala Gly Tyr Pro Gly Ser Thr Asn Arg Tyr Ala
 245 250 255

Leu Ala Ala Glu Phe Asp Asn Thr Ala Gln Trp Thr Tyr Pro Thr Ile
 260 265 270

Ala Arg His Tyr Lys Asn Gln Ile Ala Met Val Glu Ala Ala Gly Lys
 275 280 285

Gln Asn Ala Asp Ile Gln Val Lys Tyr Ala Ala Thr Met Ala Gly Trp
 290 295 300

Asn Arg Thr Ser Lys Asn Tyr Asp Gly Gln Leu Glu Gly Phe Lys Arg
 305 310 315 320

Ile Asp Ala Ala Gly Gln Lys Leu Arg Glu Glu Ala Ala Val Leu Gly
 325 330 335

Trp Leu Lys Gly Gln Gly Ala Lys Gly Gln Pro Ala Leu Asp Ala His
340 345 350

Ala Lys Leu Leu Asp Leu Leu Glu Gln Ser Lys Ala Thr Arg Asp Arg
355 360 365

Asp Leu Thr Leu Ala Leu Phe Asn Asn Thr Ala Met Leu Gly Ser Ala
370 375 380

Thr Gln Leu Tyr Arg Leu Ser Ile Glu Arg Glu Lys Pro Asn Ala Glu
385 390 395 400

Arg Glu Ser Gly Tyr Gln Glu Arg Asp Leu Pro Ala Ile Glu Gly Gly
405 410 415

Leu Lys Gln Leu Glu Arg Arg Tyr Val Ala Ala Met Asp Arg Gln Leu
420 425 430

Gln Glu Tyr Trp Leu Asn Glu Tyr Ile Lys Leu Pro Ala Asp Gln Arg
435 440 445

Val Ala Ala Val Asp Ala Trp Leu Gly Gly Asn Asp Ala Ala Ala Val
450 455 460

Lys Arg Ala Leu Asp Arg Leu Ala Gly Thr Lys Leu Gly Ser Thr Glu
465 470 475 480

Glu Arg Leu Lys Trp Phe Ala Ala Asp Arg Lys Ala Phe Glu Ala Ser
485 490 495

Asn Asp Pro Ala Ile Gln Tyr Ala Val Ala Val Met Pro Thr Leu Leu
500 505 510

Lys Leu Glu Gln Glu Arg Lys Thr Arg Ala Gly Glu Asn Leu Ala Ala
515 520 525

Arg Pro Val Tyr Leu Gln Ala Leu Ala Asp Tyr Lys Lys Ser Gln Gly
530 535 540

Glu Phe Val Tyr Pro Asp Ala Asn Leu Ser Leu Arg Ile Thr Phe Gly
 545 550 555 560

Asn Val Met Gly Tyr Ala Pro Lys Asp Gly Met Glu Tyr Thr Pro Phe
 565 570 575

Thr Thr Leu Glu Gly Val Val Ala Lys Glu Thr Gly Gln Asp Pro Phe
 580 585 590

Asp Ser Pro Lys Ala Leu Leu Asp Ala Val Ala Ala Lys Arg Tyr Gly
 595 600 605

Gly Leu Glu Asp Lys Arg Ile Gly Ser Val Pro Val Asn Tyr Leu Ser
 610 615 620

Asp Leu Asp Ile Thr Gly Gly Asn Ser Gly Ser Pro Val Leu Asp Ala
 625 630 635 640

His Gly Lys Leu Val Gly Leu Ala Phe Ala Val Asn Trp Glu Ser Val
 645 650 655

Ser Ser Asn Trp Val Phe Asp Pro Ile Met Thr Arg Met Ile Ala Val
 660 665 670

Asp Gly Arg Tyr Leu Arg Trp Ile Met Gln Glu Val Tyr Pro Ala Pro
 675 680 685

Gln Leu Leu Lys Glu Met Asn Val Gly Lys
 690 695

<210> 28

<211> 698

<212> PRT

<213> Artificial Sequence

<220>

<223> Modified Dipeptidyl Aminopeptidase BII (DAP BII)

<400> 28

Gly Glu Gly Met Trp Val Pro Gln Gln Leu Pro Glu Ile Ala Gly Pro
1 5 10 15

Leu Lys Lys Ala Gly Leu Lys Leu Ser Pro Gln Gln Ile Ser Asp Leu
20 25 30

Thr Gly Asp Pro Met Gly Ala Val Val Ala Leu Gly Gly Cys Thr Ala
35 40 45

Ser Phe Val Ser Pro Asn Gly Leu Val Val Thr Asn His His Cys Ala
50 55 60

Tyr Gly Ala Ile Gln Leu Asn Ser Thr Ala Glu Asn Asn Leu Ile Lys
65 70 75 80

Asn Gly Phe Asn Ala Pro Thr Thr Ala Asp Glu Val Ser Ala Gly Pro
85 90 95

Asn Ala Arg Val Phe Val Leu Asp Glu Ile Thr Asp Val Thr Lys Asp
100 105 110

Ala Lys Ala Ala Ile Ala Ala Ala Gly Asp Asp Ala Leu Ala Arg Thr
115 120 125

Lys Ala Leu Glu Ala Phe Glu Lys Lys Leu Ile Ala Asp Cys Glu Ala
130 135 140

Glu Ala Gly Phe Arg Cys Arg Leu Tyr Ser Phe Ser Gly Gly Asn Thr
145 150 155 160

Tyr Arg Leu Phe Lys Asn Leu Glu Ile Lys Asp Val Arg Leu Ala Tyr
165 170 175

Ala Pro Pro Gly Ser Val Gly Lys Phe Gly Gly Asp Ile Asp Met Gly
180 185 190

Met Trp Pro Thr His Thr Gly Asp Phe Ala Phe Tyr Arg Ala Tyr Val
195 200 205

Gly Lys Asp Gly Lys Pro Ala Ala Phe Ser Lys Asp Asn Val Pro Tyr
210 215 220

Gln Pro Lys His Trp Leu Lys Phe Ala Asp Gln Pro Leu Gly Ala Gly
225 230 235 240

Asp Phe Val Met Val Ala Gly Tyr Pro Gly Ser Thr Asn Arg Tyr Ala
245 250 255

Leu Ala Ala Glu Phe Asp Asn Thr Ala Gln Trp Thr Tyr Pro Thr Ile
260 265 270

Ala Arg His Tyr Lys Asn Gln Ile Ala Met Val Glu Ala Ala Gly Lys
275 280 285

Gln Asn Ala Asp Ile Gln Val Lys Tyr Ala Ala Thr Met Ala Gly Trp
290 295 300

Asn Arg Thr Ser Lys Asn Tyr Asp Gly Gln Leu Glu Gly Phe Lys Arg
305 310 315 320

Ile Asp Ala Ala Gly Gln Lys Leu Arg Glu Glu Ala Ala Val Leu Gly
325 330 335

Trp Leu Lys Gly Gln Gly Ala Lys Gly Gln Pro Ala Leu Asp Ala His
340 345 350

Ala Lys Leu Leu Asp Leu Leu Glu Gln Ser Lys Ala Thr Arg Asp Arg
355 360 365

Asp Leu Thr Leu Ala Leu Phe Asn Asn Thr Ala Met Leu Gly Ser Ala
370 375 380

Thr Gln Leu Tyr Arg Leu Ser Ile Glu Arg Glu Lys Pro Asn Ala Glu
385 390 395 400

Arg Glu Ser Gly Tyr Gln Glu Arg Asp Leu Pro Ala Ile Glu Gly Gly
405 410 415

Leu Lys Gln Leu Glu Arg Arg Tyr Val Ala Ala Met Asp Arg Gln Leu
420 425 430

Gln Glu Tyr Trp Leu Asn Glu Tyr Ile Lys Leu Pro Ala Asp Gln Arg
435 440 445

Val Ala Ala Val Asp Ala Trp Leu Gly Gly Asn Asp Ala Ala Ala Val
450 455 460

Lys Arg Ala Leu Asp Arg Leu Ala Gly Thr Lys Leu Gly Ser Thr Glu
465 470 475 480

Glu Arg Leu Lys Trp Phe Ala Ala Asp Arg Lys Ala Phe Glu Ala Ser
485 490 495

Asn Asp Pro Ala Ile Gln Tyr Ala Val Ala Val Met Pro Thr Leu Leu
500 505 510

Lys Leu Glu Gln Glu Arg Lys Thr Arg Ala Gly Glu Asn Leu Ala Ala
515 520 525

Arg Pro Val Tyr Leu Gln Ala Leu Ala Asp Tyr Lys Lys Ser Gln Gly
530 535 540

Glu Phe Val Tyr Pro Asp Ala Asn Leu Ser Leu Arg Ile Thr Phe Gly
545 550 555 560

Asn Val Met Gly Tyr Ala Pro Lys Asp Gly Met Glu Tyr Thr Pro Phe
565 570 575

Thr Thr Leu Glu Gly Val Val Ala Lys Glu Thr Gly Gln Asp Pro Phe
580 585 590

Asp Ser Pro Lys Ala Leu Leu Asp Ala Val Ala Ala Lys Arg Tyr Gly
595 600 605

Gly Leu Glu Asp Lys Arg Ile Gly Ser Val Pro Val Asn Tyr Leu Ser
610 615 620

Asp Leu Asp Ile Thr Gly Gly Asn Ser Gly Ser Pro Val Leu Asp Ala
625 630 635 640

His Gly Lys Leu Val Gly Leu Ala Phe Ala Val Asn Trp Glu Ser Val
645 650 655

Ser Ser Asn Trp Val Phe Asp Pro Lys Met Thr Arg Met Ile Ala Val
660 665 670

Asp Gly Arg Tyr Leu Arg Trp Ile Met Gln Glu Val Tyr Pro Ala Pro
675 680 685

Gln Leu Leu Lys Glu Met Asn Val Gly Lys
690 695

<210> 29
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Test Peptide

<400> 29

Ala Arg Ala Ala
1

<210> 30
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Test Peptide

<400> 30

Ile His Ala Gly Tyr Ala Trp
1 5

<210> 31

<211> 698

<212> PRT

<213> Artificial Sequence

<220>

<223> Modified Dipeptidyl Aminopeptidase BII (DAP BII)

<400> 31

Gly Glu Gly Met Trp Val Pro Gln Gln Leu Pro Glu Ile Ala Gly Pro
1 5 10 15

Leu Lys Lys Ala Gly Leu Lys Leu Ser Pro Gln Gln Ile Ser Asp Leu
20 25 30

Thr Gly Asp Pro Met Gly Ala Val Val Ala Leu Gly Gly Cys Thr Ala
35 40 45

Ser Phe Val Ser Pro Asn Gly Leu Val Val Thr Asn His His Cys Ala
50 55 60

Tyr Gly Ala Ile Gln Leu Asn Ser Thr Ala Glu Asn Asn Leu Ile Lys
65 70 75 80

Asn Gly Phe Asn Ala Pro Thr Thr Ala Asp Glu Val Ser Ala Gly Pro
85 90 95

Asn Ala Arg Val Phe Val Leu Asp Glu Ile Thr Asp Val Thr Lys Asp
100 105 110

Ala Lys Ala Ala Ile Ala Ala Ala Gly Asp Asp Ala Leu Ala Arg Thr
115 120 125

Lys Ala Leu Glu Ala Phe Glu Lys Lys Leu Ile Ala Asp Cys Glu Ala
130 135 140

Glu Ala Gly Phe Arg Cys Arg Leu Tyr Ser Phe Ser Gly Gly Asn Thr
 145 150 155 160

Tyr Arg Leu Phe Lys Asn Leu Glu Ile Lys Asp Val Arg Leu Ala Tyr
 165 170 175

Ala Pro Pro Gly Ser Val Gly Lys Phe Gly Gly Asp Ile Asp Cys Leu
 180 185 190

Met Trp Pro Lys His Thr Gly Asp Phe Ala Phe Tyr Arg Ala Tyr Val
 195 200 205

Gly Lys Asp Gly Lys Pro Ala Ala Phe Ser Lys Asp Asn Val Pro Tyr
 210 215 220

Gln Pro Lys His Trp Leu Lys Phe Ala Asp Gln Pro Leu Gly Ala Gly
 225 230 235 240

Asp Phe Val Met Val Ala Gly Tyr Pro Gly Ser Thr Asn Arg Tyr Ala
 245 250 255

Leu Ala Ala Glu Phe Asp Asn Thr Ala Gln Trp Thr Tyr Pro Thr Ile
 260 265 270

Ala Arg His Tyr Lys Asn Gln Ile Ala Met Val Glu Ala Ala Gly Lys
 275 280 285

Gln Asn Ala Asp Ile Gln Val Lys Tyr Ala Ala Thr Met Ala Gly Trp
 290 295 300

Asn Arg Thr Ser Lys Asp Tyr Asp Gly Gln Leu Glu Gly Phe Lys Arg
 305 310 315 320

Ile Asp Ala Ala Gly Gln Lys Leu Arg Glu Glu Ala Ala Val Leu Gly
 325 330 335

Trp Leu Lys Gly Gln Gly Ala Lys Gly Gln Pro Ala Leu Asp Ala His
 340 345 350

Ala Lys Leu Leu Asp Leu Leu Glu Gln Ser Lys Ala Thr Arg Asp Arg
 355 360 365

Asp Leu Thr Leu Ala Leu Phe Asn Asn Thr Ala Met Leu Gly Ser Ala
 370 375 380

Thr Gln Leu Tyr Arg Leu Ser Ile Glu Arg Glu Lys Pro Asn Ala Glu
 385 390 395 400

Arg Glu Ser Gly Tyr Gln Glu Arg Asp Leu Pro Ala Ile Glu Gly Gly
 405 410 415

Leu Lys Gln Leu Glu Arg Arg Tyr Val Ala Ala Met Asp Arg Gln Leu
 420 425 430

Gln Glu Tyr Trp Leu Asn Glu Tyr Ile Lys Leu Pro Ala Asp Gln Arg
 435 440 445

Val Ala Ala Val Asp Ala Trp Leu Gly Gly Asn Asp Ala Ala Ala Val
 450 455 460

Lys Arg Ala Leu Asp Arg Leu Ala Gly Thr Lys Leu Gly Ser Thr Glu
 465 470 475 480

Glu Arg Leu Lys Trp Phe Ala Ala Asp Arg Lys Ala Phe Glu Ala Ser
 485 490 495

Asn Asp Pro Ala Ile Gln Tyr Ala Val Ala Val Met Pro Thr Leu Leu
 500 505 510

Lys Leu Glu Gln Glu Arg Lys Thr Arg Ala Gly Glu Asn Leu Ala Ala
 515 520 525

Arg Pro Val Tyr Leu Gln Ala Leu Ala Asp Tyr Lys Lys Ser Gln Gly
 530 535 540

Glu Phe Val Tyr Pro Asp Ala Asn Leu Ser Leu Arg Ile Thr Phe Gly
 545 550 555 560

Asn Val Met Gly Tyr Ala Pro Lys Asp Gly Met Glu Tyr Thr Pro Phe
 565 570 575

Thr Thr Leu Glu Gly Val Val Ala Lys Glu Thr Gly Gln Asp Pro Phe
 580 585 590

Asp Ser Pro Lys Ala Leu Leu Asp Ala Val Ala Ala Lys Arg Tyr Gly
 595 600 605

Gly Leu Glu Asp Lys Arg Ile Gly Ser Val Pro Val Asn Tyr Leu Ser
 610 615 620

Asp Leu Asp Ile Thr Gly Gly Asn Ser Gly Ser Pro Val Leu Asp Ala
 625 630 635 640

His Gly Lys Leu Val Gly Leu Ala Phe Asp Tyr Asn Trp Glu Gly Gly
 645 650 655

Ser Ser Asn Trp Val Phe Asp Pro Lys Met Thr Arg Met Ile Ala Val
 660 665 670

Asp Gly Arg Tyr Leu Arg Trp Ile Met Gln Glu Val Tyr Pro Ala Pro
 675 680 685

Gln Leu Leu Lys Glu Met Asn Val Gly Lys
 690 695

<210> 32

<211> 698

<212> PRT

<213> Artificial Sequence

<220>

<223> Modified Dipeptidyl Aminopeptidase BII (DAP BII)

<400> 32

Gly Glu Gly Met Trp Val Pro Gln Gln Leu Pro Glu Ile Ala Gly Pro
1 5 10 15

Leu Lys Lys Ala Gly Leu Lys Leu Ser Pro Gln Gln Ile Ser Asp Leu
20 25 30

Thr Gly Asp Pro Met Gly Ala Val Val Ala Leu Gly Gly Cys Thr Ala
35 40 45

Ser Phe Val Ser Pro Asn Gly Leu Val Val Thr Asn His His Cys Ala
50 55 60

Tyr Gly Ala Ile Gln Leu Asn Ser Thr Ala Glu Asn Asn Leu Ile Lys
65 70 75 80

Asn Gly Phe Asn Ala Pro Thr Thr Ala Asp Glu Val Ser Ala Gly Pro
85 90 95

Asn Ala Arg Val Phe Val Leu Asp Glu Ile Thr Asp Val Thr Lys Asp
100 105 110

Ala Lys Ala Ala Ile Ala Ala Ala Gly Asp Asp Ala Leu Ala Arg Thr
115 120 125

Lys Ala Leu Glu Ala Phe Glu Lys Lys Leu Ile Ala Asp Cys Glu Ala
130 135 140

Glu Ala Gly Phe Arg Cys Arg Leu Tyr Ser Phe Ser Gly Gly Asn Thr
145 150 155 160

Tyr Arg Leu Phe Lys Asn Leu Glu Ile Lys Asp Val Arg Leu Ala Tyr
165 170 175

Ala Pro Pro Gly Ser Val Gly Lys Phe Gly Gly Asp Ile Asp Cys Leu
180 185 190

Met Trp Pro Arg His Thr Gly Asp Phe Ala Phe Tyr Arg Ala Tyr Val
195 200 205

Gly Lys Asp Gly Lys Pro Ala Ala Phe Ser Lys Asp Asn Val Pro Tyr
210 215 220

Gln Pro Lys His Trp Leu Lys Phe Ala Asp Gln Pro Leu Gly Ala Gly
225 230 235 240

Asp Phe Val Met Val Ala Gly Tyr Pro Gly Ser Thr Asn Arg Tyr Ala
245 250 255

Leu Ala Ala Glu Phe Asp Asn Thr Ala Gln Trp Thr Tyr Pro Thr Ile
260 265 270

Ala Arg His Tyr Lys Asn Gln Ile Ala Met Val Glu Ala Ala Gly Lys
275 280 285

Gln Asn Ala Asp Ile Gln Val Lys Tyr Ala Ala Thr Met Ala Gly Trp
290 295 300

Asn Arg Thr Ser Lys Asp Tyr Asp Gly Gln Leu Glu Gly Phe Lys Arg
305 310 315 320

Ile Asp Ala Ala Gly Gln Lys Leu Arg Glu Glu Ala Ala Val Leu Gly
325 330 335

Trp Leu Lys Gly Gln Gly Ala Lys Gly Gln Pro Ala Leu Asp Ala His
340 345 350

Ala Lys Leu Leu Asp Leu Leu Glu Gln Ser Lys Ala Thr Arg Asp Arg
355 360 365

Asp Leu Thr Leu Ala Leu Phe Asn Asn Thr Ala Met Leu Gly Ser Ala
370 375 380

Thr Gln Leu Tyr Arg Leu Ser Ile Glu Arg Glu Lys Pro Asn Ala Glu
385 390 395 400

Arg Glu Ser Gly Tyr Gln Glu Arg Asp Leu Pro Ala Ile Glu Gly Gly
405 410 415

Leu Lys Gln Leu Glu Arg Arg Tyr Val Ala Ala Met Asp Arg Gln Leu
420 425 430

Gln Glu Tyr Trp Leu Asn Glu Tyr Ile Lys Leu Pro Ala Asp Gln Arg
435 440 445

Val Ala Ala Val Asp Ala Trp Leu Gly Gly Asn Asp Ala Ala Ala Val
450 455 460

Lys Arg Ala Leu Asp Arg Leu Ala Gly Thr Lys Leu Gly Ser Thr Glu
465 470 475 480

Glu Arg Leu Lys Trp Phe Ala Ala Asp Arg Lys Ala Phe Glu Ala Ser
485 490 495

Asn Asp Pro Ala Ile Gln Tyr Ala Val Ala Val Met Pro Thr Leu Leu
500 505 510

Lys Leu Glu Gln Glu Arg Lys Thr Arg Ala Gly Glu Asn Leu Ala Ala
515 520 525

Arg Pro Val Tyr Leu Gln Ala Leu Ala Asp Tyr Lys Lys Ser Gln Gly
530 535 540

Glu Phe Val Tyr Pro Asp Ala Asn Leu Ser Leu Arg Ile Thr Phe Gly
545 550 555 560

Asn Val Met Gly Tyr Ala Pro Lys Asp Gly Met Glu Tyr Thr Pro Phe
565 570 575

Thr Thr Leu Glu Gly Val Val Ala Lys Glu Thr Gly Gln Asp Pro Phe
580 585 590

Asp Ser Pro Lys Ala Leu Leu Asp Ala Val Ala Ala Lys Arg Tyr Gly
595 600 605

Gly Leu Glu Asp Lys Arg Ile Gly Ser Val Pro Val Asn Tyr Leu Ser
610 615 620

Asp Leu Asp Ile Thr Gly Gly Asn Ser Gly Ser Pro Val Leu Asp Ala
625 630 635 640

His Gly Lys Leu Val Gly Leu Ala Phe Asp Tyr Asn Trp Glu Gly Gly
645 650 655

Ser Ser Asn Trp Val Phe Asp Pro Lys Met Thr Arg Met Ile Ala Val
660 665 670

Asp Gly Arg Tyr Leu Arg Trp Ile Met Gln Glu Val Tyr Pro Ala Pro
675 680 685

Gln Leu Leu Lys Glu Met Asn Val Gly Lys
690 695

<210> 33
<211> 698
<212> PRT
<213> Artificial Sequence

<220>
<223> Modified Dipeptidyl Aminopeptidase BII (DAP BII)

<400> 33

Gly Glu Gly Met Trp Val Pro Gln Gln Leu Pro Glu Ile Ala Gly Pro
1 5 10 15

Leu Lys Lys Ala Gly Leu Lys Leu Ser Pro Gln Gln Ile Ser Asp Leu
20 25 30

Thr Gly Asp Pro Met Gly Ala Val Val Ala Leu Gly Gly Cys Thr Ala
35 40 45

Ser Phe Val Ser Pro Asn Gly Leu Val Val Thr Asn His His Cys Ala
50 55 60

Tyr Gly Ala Ile Gln Leu Asn Ser Thr Ala Glu Asn Asn Leu Ile Lys
65 70 75 80

Asn Gly Phe Asn Ala Pro Thr Thr Ala Asp Glu Val Ser Ala Gly Pro
85 90 95

Asn Ala Arg Val Phe Val Leu Asp Glu Ile Thr Asp Val Thr Lys Asp
100 105 110

Ala Lys Ala Ala Ile Ala Ala Ala Gly Asp Asp Ala Leu Ala Arg Thr
115 120 125

Lys Ala Leu Glu Ala Phe Glu Lys Lys Leu Ile Ala Asp Cys Glu Ala
130 135 140

Glu Ala Gly Phe Arg Cys Arg Leu Tyr Ser Phe Ser Gly Gly Asn Thr
145 150 155 160

Tyr Arg Leu Phe Lys Asn Leu Glu Ile Lys Asp Val Arg Leu Ala Tyr
165 170 175

Ala Pro Pro Gly Ser Val Gly Lys Phe Gly Gly Asp Ile Asp Phe Phe
180 185 190

Met Trp Pro Arg His Thr Gly Asp Phe Ala Phe Tyr Arg Ala Tyr Val
195 200 205

Gly Lys Asp Gly Lys Pro Ala Ala Phe Ser Lys Asp Asn Val Pro Tyr
210 215 220

Gln Pro Lys His Trp Leu Lys Phe Ala Asp Gln Pro Leu Gly Ala Gly
225 230 235 240

Asp Phe Val Met Val Ala Gly Tyr Pro Gly Ser Thr Asn Arg Tyr Ala
245 250 255

Leu Ala Ala Glu Phe Asp Asn Thr Ala Gln Trp Thr Tyr Pro Thr Ile
260 265 270

Ala Arg His Tyr Lys Asn Gln Ile Ala Met Val Glu Ala Ala Gly Lys
275 280 285

Gln Asn Ala Asp Ile Gln Val Lys Tyr Ala Ala Thr Met Ala Gly Trp
290 295 300

Asn Arg Thr Ser Lys Gly Tyr Asp Gly Gln Leu Glu Gly Phe Lys Arg
305 310 315 320

Ile Asp Ala Ala Gly Gln Lys Leu Arg Glu Glu Ala Ala Val Leu Gly
325 330 335

Trp Leu Lys Gly Gln Gly Ala Lys Gly Gln Pro Ala Leu Asp Ala His
340 345 350

Ala Lys Leu Leu Asp Leu Leu Glu Gln Ser Lys Ala Thr Arg Asp Arg
355 360 365

Asp Leu Thr Leu Ala Leu Phe Asn Asn Thr Ala Met Leu Gly Ser Ala
370 375 380

Thr Gln Leu Tyr Arg Leu Ser Ile Glu Arg Glu Lys Pro Asn Ala Glu
385 390 395 400

Arg Glu Ser Gly Tyr Gln Glu Arg Asp Leu Pro Ala Ile Glu Gly Gly
405 410 415

Leu Lys Gln Leu Glu Arg Arg Tyr Val Ala Ala Met Asp Arg Gln Leu
420 425 430

Gln Glu Tyr Trp Leu Asn Glu Tyr Ile Lys Leu Pro Ala Asp Gln Arg
435 440 445

Val Ala Ala Val Asp Ala Trp Leu Gly Gly Asn Asp Ala Ala Ala Val
 450 455 460

Lys Arg Ala Leu Asp Arg Leu Ala Gly Thr Lys Leu Gly Ser Thr Glu
 465 470 475 480

Glu Arg Leu Lys Trp Phe Ala Ala Asp Arg Lys Ala Phe Glu Ala Ser
 485 490 495

Asn Asp Pro Ala Ile Gln Tyr Ala Val Ala Val Met Pro Thr Leu Leu
 500 505 510

Lys Leu Glu Gln Glu Arg Lys Thr Arg Ala Gly Glu Asn Leu Ala Ala
 515 520 525

Arg Pro Val Tyr Leu Gln Ala Leu Ala Asp Tyr Lys Lys Ser Gln Gly
 530 535 540

Glu Phe Val Tyr Pro Asp Ala Asn Leu Ser Leu Arg Ile Thr Phe Gly
 545 550 555 560

Asn Val Met Gly Tyr Ala Pro Lys Asp Gly Met Glu Tyr Thr Pro Phe
 565 570 575

Thr Thr Leu Glu Gly Val Val Ala Lys Glu Thr Gly Gln Asp Pro Phe
 580 585 590

Asp Ser Pro Lys Ala Leu Leu Asp Ala Val Ala Ala Lys Arg Tyr Gly
 595 600 605

Gly Leu Glu Asp Lys Arg Ile Gly Ser Val Pro Val Asn Tyr Leu Ser
 610 615 620

Asp Leu Asp Ile Thr Gly Gly Asn Ser Gly Ser Pro Val Leu Asp Ala
 625 630 635 640

His Gly Lys Leu Val Gly Leu Ala Phe Asp His Asn Trp Glu Ser Glu
 645 650 655

Ser Ser Asn Trp Val Phe Asp Pro Lys Met Thr Arg Met Ile Ala Val
660 665 670

Asp Gly Arg Tyr Leu Arg Trp Ile Met Gln Glu Val Tyr Pro Ala Pro
675 680 685

Gln Leu Leu Lys Glu Met Asn Val Gly Lys
690 695

<210> 34
<211> 698
<212> PRT
<213> Artificial Sequence

<220>
<223> Modified Dipeptidyl Aminopeptidase BII (DAP BII)

<400> 34

Gly Glu Gly Met Trp Val Pro Gln Gln Leu Pro Glu Ile Ala Gly Pro
1 5 10 15

Leu Lys Lys Ala Gly Leu Lys Leu Ser Pro Gln Gln Ile Ser Asp Leu
20 25 30

Thr Gly Asp Pro Met Gly Ala Val Val Ala Leu Gly Gly Cys Thr Ala
35 40 45

Ser Phe Val Ser Pro Asn Gly Leu Val Val Thr Asn His His Cys Ala
50 55 60

Tyr Gly Ala Ile Gln Leu Asn Ser Thr Ala Glu Asn Asn Leu Ile Lys
65 70 75 80

Asn Gly Phe Asn Ala Pro Thr Thr Ala Asp Glu Val Ser Ala Gly Pro
85 90 95

Asn Ala Arg Val Phe Val Leu Asp Glu Ile Thr Asp Val Thr Lys Asp
100 105 110

Ala Lys Ala Ala Ile Ala Ala Ala Gly Asp Asp Ala Leu Ala Arg Thr
115 120 125

Lys Ala Leu Glu Ala Phe Glu Lys Lys Leu Ile Ala Asp Cys Glu Ala
130 135 140

Glu Ala Gly Phe Arg Cys Arg Leu Tyr Ser Phe Ser Gly Gly Asn Thr
145 150 155 160

Tyr Arg Leu Phe Lys Asn Leu Glu Ile Lys Asp Val Arg Leu Ala Tyr
165 170 175

Ala Pro Pro Gly Ser Val Gly Lys Phe Gly Gly Asp Ile Asp Arg Leu
180 185 190

Met Trp Pro Arg His Thr Gly Asp Phe Ala Phe Tyr Arg Ala Tyr Val
195 200 205

Gly Lys Asp Gly Lys Pro Ala Ala Phe Ser Lys Asp Asn Val Pro Tyr
210 215 220

Gln Pro Lys His Trp Leu Lys Phe Ala Asp Gln Pro Leu Gly Ala Gly
225 230 235 240

Asp Phe Val Met Val Ala Gly Tyr Pro Gly Ser Thr Asn Arg Tyr Ala
245 250 255

Leu Ala Ala Glu Phe Asp Asn Thr Ala Gln Trp Thr Tyr Pro Thr Ile
260 265 270

Ala Arg His Tyr Lys Asn Gln Ile Ala Met Val Glu Ala Ala Gly Lys
275 280 285

Gln Asn Ala Asp Ile Gln Val Lys Tyr Ala Ala Thr Met Ala Gly Trp
290 295 300

Asn Ser Thr Ser Lys Leu Tyr Asp Gly Gln Leu Glu Gly Phe Lys Arg
 305 310 315 320

Ile Asp Ala Ala Gly Gln Lys Leu Arg Glu Glu Ala Ala Val Leu Gly
 325 330 335

Trp Leu Lys Gly Gln Gly Ala Lys Gly Gln Pro Ala Leu Asp Ala His
 340 345 350

Ala Lys Leu Leu Asp Leu Leu Glu Gln Ser Lys Ala Thr Arg Asp Arg
 355 360 365

Asp Leu Thr Leu Ala Leu Phe Asn Asn Thr Ala Met Leu Gly Ser Ala
 370 375 380

Thr Gln Leu Tyr Arg Leu Ser Ile Glu Arg Glu Lys Pro Asn Ala Glu
 385 390 395 400

Arg Glu Ser Gly Tyr Gln Glu Arg Asp Leu Pro Ala Ile Glu Gly Gly
 405 410 415

Leu Lys Gln Leu Glu Arg Arg Tyr Val Ala Ala Met Asp Arg Gln Leu
 420 425 430

Gln Glu Tyr Trp Leu Asn Glu Tyr Ile Lys Leu Pro Ala Asp Gln Arg
 435 440 445

Val Ala Ala Val Asp Ala Trp Leu Gly Gly Asn Asp Ala Ala Ala Val
 450 455 460

Lys Arg Ala Leu Asp Arg Leu Ala Gly Thr Lys Leu Gly Ser Thr Glu
 465 470 475 480

Glu Arg Leu Lys Trp Phe Ala Ala Asp Arg Lys Ala Phe Glu Ala Ser
 485 490 495

Asn Asp Pro Ala Ile Gln Tyr Ala Val Ala Val Met Pro Thr Leu Leu
 500 505 510

Lys Leu Glu Gln Glu Arg Lys Thr Arg Ala Gly Glu Asn Leu Ala Ala
515 520 525

Arg Pro Val Tyr Leu Gln Ala Leu Ala Asp Tyr Lys Lys Ser Gln Gly
530 535 540

Glu Phe Val Tyr Pro Asp Ala Asn Leu Ser Leu Arg Ile Thr Phe Gly
545 550 555 560

Asn Val Met Gly Tyr Ala Pro Lys Asp Gly Met Glu Tyr Thr Pro Phe
565 570 575

Thr Thr Leu Glu Gly Val Val Ala Lys Glu Thr Gly Gln Asp Pro Phe
580 585 590

Asp Ser Pro Lys Ala Leu Leu Asp Ala Val Ala Ala Lys Arg Tyr Gly
595 600 605

Gly Leu Glu Asp Lys Arg Ile Gly Ser Val Pro Val Asn Tyr Leu Ser
610 615 620

Asp Leu Asp Ile Thr Gly Gly Asn Ser Gly Ser Pro Val Leu Asp Ala
625 630 635 640

His Gly Lys Leu Val Gly Leu Ala Phe Asp Thr Asn Trp Glu Thr Ser
645 650 655

Ser Ser Asn Trp Val Phe Asp Pro Lys Met Thr Arg Met Ile Ala Val
660 665 670

Asp Gly Arg Tyr Leu Arg Trp Ile Met Gln Glu Val Tyr Pro Ala Pro
675 680 685

Gln Leu Leu Lys Glu Met Asn Val Gly Lys
690 695

<210> 35
 <211> 698
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Modified Dipeptidyl Aminopeptidase BII (DAP BII)

<400> 35

Gly Glu Gly Met Trp Val Pro Gln Gln Leu Pro Glu Ile Ala Gly Pro
 1 5 10 15

Leu Lys Lys Ala Gly Leu Lys Leu Ser Pro Gln Gln Ile Ser Asp Leu
 20 25 30

Thr Gly Asp Pro Met Gly Ala Val Val Ala Leu Gly Gly Cys Thr Ala
 35 40 45

Ser Phe Val Ser Pro Asn Gly Leu Val Val Thr Asn His His Cys Ala
 50 55 60

Tyr Gly Ala Ile Gln Leu Asn Ser Thr Ala Glu Asn Asn Leu Ile Lys
 65 70 75 80

Asn Gly Phe Asn Ala Pro Thr Thr Ala Asp Glu Val Ser Ala Gly Pro
 85 90 95

Asn Ala Arg Val Phe Val Leu Asp Glu Ile Thr Asp Val Thr Lys Asp
 100 105 110

Ala Lys Ala Ala Ile Ala Ala Ala Gly Asp Asp Ala Leu Ala Arg Thr
 115 120 125

Lys Ala Leu Glu Ala Phe Glu Lys Lys Leu Ile Ala Asp Cys Glu Ala
 130 135 140

Glu Ala Gly Phe Arg Cys Arg Leu Tyr Ser Phe Ser Gly Gly Asn Thr
 145 150 155 160

Tyr Arg Leu Phe Lys Asn Leu Glu Ile Lys Asp Val Arg Leu Ala Tyr
165 170 175

Ala Pro Pro Gly Ser Val Gly Lys Phe Gly Gly Asp Ile Asp Ser Trp
180 185 190

Met Trp Pro His His Thr Gly Asp Phe Ala Phe Tyr Arg Ala Tyr Val
195 200 205

Gly Lys Asp Gly Lys Pro Ala Ala Phe Ser Lys Asp Asn Val Pro Tyr
210 215 220

Gln Pro Lys His Trp Leu Lys Phe Ala Asp Gln Pro Leu Gly Ala Gly
225 230 235 240

Asp Phe Val Met Val Ala Gly Tyr Pro Gly Ser Thr Asn Arg Tyr Ala
245 250 255

Leu Ala Ala Glu Phe Asp Asn Thr Ala Gln Trp Thr Tyr Pro Thr Ile
260 265 270

Ala Arg His Tyr Lys Asn Gln Ile Ala Met Val Glu Ala Ala Gly Lys
275 280 285

Gln Asn Ala Asp Ile Gln Val Lys Tyr Ala Ala Thr Met Ala Gly Trp
290 295 300

Asn Ala Thr Ser Lys Asn Tyr Asp Gly Gln Leu Glu Gly Phe Lys Arg
305 310 315 320

Ile Asp Ala Ala Gly Gln Lys Leu Arg Glu Glu Ala Ala Val Leu Gly
325 330 335

Trp Leu Lys Gly Gln Gly Ala Lys Gly Gln Pro Ala Leu Asp Ala His
340 345 350

Ala Lys Leu Leu Asp Leu Leu Glu Gln Ser Lys Ala Thr Arg Asp Arg
355 360 365

Asp Leu Thr Leu Ala Leu Phe Asn Asn Thr Ala Met Leu Gly Ser Ala
370 375 380

Thr Gln Leu Tyr Arg Leu Ser Ile Glu Arg Glu Lys Pro Asn Ala Glu
385 390 395 400

Arg Glu Ser Gly Tyr Gln Glu Arg Asp Leu Pro Ala Ile Glu Gly Gly
405 410 415

Leu Lys Gln Leu Glu Arg Arg Tyr Val Ala Ala Met Asp Arg Gln Leu
420 425 430

Gln Glu Tyr Trp Leu Asn Glu Tyr Ile Lys Leu Pro Ala Asp Gln Arg
435 440 445

Val Ala Ala Val Asp Ala Trp Leu Gly Gly Asn Asp Ala Ala Ala Val
450 455 460

Lys Arg Ala Leu Asp Arg Leu Ala Gly Thr Lys Leu Gly Ser Thr Glu
465 470 475 480

Glu Arg Leu Lys Trp Phe Ala Ala Asp Arg Lys Ala Phe Glu Ala Ser
485 490 495

Asn Asp Pro Ala Ile Gln Tyr Ala Val Ala Val Met Pro Thr Leu Leu
500 505 510

Lys Leu Glu Gln Glu Arg Lys Thr Arg Ala Gly Glu Asn Leu Ala Ala
515 520 525

Arg Pro Val Tyr Leu Gln Ala Leu Ala Asp Tyr Lys Lys Ser Gln Gly
530 535 540

Glu Phe Val Tyr Pro Asp Ala Asn Leu Ser Leu Arg Ile Thr Phe Gly
545 550 555 560

Asn Val Met Gly Tyr Ala Pro Lys Asp Gly Met Glu Tyr Thr Pro Phe
565 570 575

Thr Thr Leu Glu Gly Val Val Ala Lys Glu Thr Gly Gln Asp Pro Phe
580 585 590

Asp Ser Pro Lys Ala Leu Leu Asp Ala Val Ala Ala Lys Arg Tyr Gly
595 600 605

Gly Leu Glu Asp Lys Arg Ile Gly Ser Val Pro Val Asn Tyr Leu Ser
610 615 620

Asp Leu Asp Ile Thr Gly Gly Asn Ser Gly Ser Pro Val Leu Asp Ala
625 630 635 640

His Gly Lys Leu Val Gly Leu Ala Phe Gly Gly Asn Trp Glu Ser Val
645 650 655

Ser Ser Asn Trp Val Phe Asp Pro Lys Met Thr Arg Met Ile Ala Val
660 665 670

Asp Gly Arg Tyr Leu Arg Trp Ile Met Gln Glu Val Tyr Pro Ala Pro
675 680 685

Gln Leu Leu Lys Glu Met Asn Val Gly Lys
690 695

<210> 36
<211> 698
<212> PRT
<213> Artificial Sequence

<220>
<223> Modified Dipeptidyl Aminopeptidase BII (DAP BII)

<400> 36

Gly Glu Gly Met Trp Val Pro Gln Gln Leu Pro Glu Ile Ala Gly Pro
1 5 10 15

Leu Lys Lys Ala Gly Leu Lys Leu Ser Pro Gln Gln Ile Ser Asp Leu
20 25 30

Thr Gly Asp Pro Met Gly Ala Val Val Ala Leu Gly Gly Cys Thr Ala
35 40 45

Ser Phe Val Ser Pro Asn Gly Leu Val Val Thr Asn His His Cys Ala
50 55 60

Tyr Gly Ala Ile Gln Leu Asn Ser Thr Ala Glu Asn Asn Leu Ile Lys
65 70 75 80

Asn Gly Phe Asn Ala Pro Thr Thr Ala Asp Glu Val Ser Ala Gly Pro
85 90 95

Asn Ala Arg Val Phe Val Leu Asp Glu Ile Thr Asp Val Thr Lys Asp
100 105 110

Ala Lys Ala Ala Ile Ala Ala Ala Gly Asp Asp Ala Leu Ala Arg Thr
115 120 125

Lys Ala Leu Glu Ala Phe Glu Lys Lys Leu Ile Ala Asp Cys Glu Ala
130 135 140

Glu Ala Gly Phe Arg Cys Arg Leu Tyr Ser Phe Ser Gly Gly Asn Thr
145 150 155 160

Tyr Arg Leu Phe Lys Asn Leu Glu Ile Lys Asp Val Arg Leu Ala Tyr
165 170 175

Ala Pro Pro Gly Ser Val Gly Lys Phe Gly Gly Asp Ile Asp Thr Trp
180 185 190

Met Trp Pro His His Thr Gly Asp Phe Ala Phe Tyr Arg Ala Tyr Val
195 200 205

Gly Lys Asp Gly Lys Pro Ala Ala Phe Ser Lys Asp Asn Val Pro Tyr
210 215 220

Gln Pro Lys His Trp Leu Lys Phe Ala Asp Gln Pro Leu Gly Ala Gly
 225 230 235 240

Asp Phe Val Met Val Ala Gly Tyr Pro Gly Ser Thr Asn Arg Tyr Ala
 245 250 255

Leu Ala Ala Glu Phe Asp Asn Thr Ala Gln Trp Thr Tyr Pro Thr Ile
 260 265 270

Ala Arg His Tyr Lys Asn Gln Ile Ala Met Val Glu Ala Ala Gly Lys
 275 280 285

Gln Asn Ala Asp Ile Gln Val Lys Tyr Ala Ala Thr Met Ala Gly Trp
 290 295 300

Asn Ala Thr Ser Lys Asn Tyr Asp Gly Gln Leu Glu Gly Phe Lys Arg
 305 310 315 320

Ile Asp Ala Ala Gly Gln Lys Leu Arg Glu Glu Ala Ala Val Leu Gly
 325 330 335

Trp Leu Lys Gly Gln Gly Ala Lys Gly Gln Pro Ala Leu Asp Ala His
 340 345 350

Ala Lys Leu Leu Asp Leu Leu Glu Gln Ser Lys Ala Thr Arg Asp Arg
 355 360 365

Asp Leu Thr Leu Ala Leu Phe Asn Asn Thr Ala Met Leu Gly Ser Ala
 370 375 380

Thr Gln Leu Tyr Arg Leu Ser Ile Glu Arg Glu Lys Pro Asn Ala Glu
 385 390 395 400

Arg Glu Ser Gly Tyr Gln Glu Arg Asp Leu Pro Ala Ile Glu Gly Gly
 405 410 415

Leu Lys Gln Leu Glu Arg Arg Tyr Val Ala Ala Met Asp Arg Gln Leu
420 425 430

Gln Glu Tyr Trp Leu Asn Glu Tyr Ile Lys Leu Pro Ala Asp Gln Arg
435 440 445

Val Ala Ala Val Asp Ala Trp Leu Gly Gly Asn Asp Ala Ala Ala Val
450 455 460

Lys Arg Ala Leu Asp Arg Leu Ala Gly Thr Lys Leu Gly Ser Thr Glu
465 470 475 480

Glu Arg Leu Lys Trp Phe Ala Ala Asp Arg Lys Ala Phe Glu Ala Ser
485 490 495

Asn Asp Pro Ala Ile Gln Tyr Ala Val Ala Val Met Pro Thr Leu Leu
500 505 510

Lys Leu Glu Gln Glu Arg Lys Thr Arg Ala Gly Glu Asn Leu Ala Ala
515 520 525

Arg Pro Val Tyr Leu Gln Ala Leu Ala Asp Tyr Lys Lys Ser Gln Gly
530 535 540

Glu Phe Val Tyr Pro Asp Ala Asn Leu Ser Leu Arg Ile Thr Phe Gly
545 550 555 560

Asn Val Met Gly Tyr Ala Pro Lys Asp Gly Met Glu Tyr Thr Pro Phe
565 570 575

Thr Thr Leu Glu Gly Val Val Ala Lys Glu Thr Gly Gln Asp Pro Phe
580 585 590

Asp Ser Pro Lys Ala Leu Leu Asp Ala Val Ala Ala Lys Arg Tyr Gly
595 600 605

Gly Leu Glu Asp Lys Arg Ile Gly Ser Val Pro Val Asn Tyr Leu Ser
610 615 620

Asp Leu Asp Ile Thr Gly Gly Asn Ser Gly Ser Pro Val Leu Asp Ala
625 630 635 640

His Gly Lys Leu Val Gly Leu Ala Phe Gly Gly Asn Trp Glu Ser Val
645 650 655

Ser Ser Asn Trp Val Phe Asp Pro Lys Met Thr Arg Met Ile Ala Val
660 665 670

Asp Gly Arg Tyr Leu Arg Trp Ile Met Gln Glu Val Tyr Pro Ala Pro
675 680 685

Gln Leu Leu Lys Glu Met Asn Val Gly Lys
690 695

<210> 37
<211> 698
<212> PRT
<213> Artificial Sequence

<220>
<223> Modified Dipeptidyl Aminopeptidase BII (DAP BII)

<400> 37

Gly Glu Gly Met Trp Val Pro Gln Gln Leu Pro Glu Ile Ala Gly Pro
1 5 10 15

Leu Lys Lys Ala Gly Leu Lys Leu Ser Pro Gln Gln Ile Ser Asp Leu
20 25 30

Thr Gly Asp Pro Met Gly Ala Val Val Ala Leu Gly Gly Cys Thr Ala
35 40 45

Ser Phe Val Ser Pro Asn Gly Leu Val Val Thr Asn His His Cys Ala
50 55 60

Tyr Gly Ala Ile Gln Leu Asn Ser Thr Ala Glu Asn Asn Leu Ile Lys
65 70 75 80

Asn Gly Phe Asn Ala Pro Thr Thr Ala Asp Glu Val Ser Ala Gly Pro
85 90 95

Asn Ala Arg Val Phe Val Leu Asp Glu Ile Thr Asp Val Thr Lys Asp
100 105 110

Ala Lys Ala Ala Ile Ala Ala Ala Gly Asp Asp Ala Leu Ala Arg Thr
115 120 125

Lys Ala Leu Glu Ala Phe Glu Lys Lys Leu Ile Ala Asp Cys Glu Ala
130 135 140

Glu Ala Gly Phe Arg Cys Arg Leu Tyr Ser Phe Ser Gly Gly Asn Thr
145 150 155 160

Tyr Arg Leu Phe Lys Asn Leu Glu Ile Lys Asp Val Arg Leu Ala Tyr
165 170 175

Ala Pro Pro Gly Ser Val Gly Lys Phe Gly Gly Asp Ile Asp Met Trp
180 185 190

Met Trp Pro His His Thr Gly Asp Phe Ala Phe Tyr Arg Ala Tyr Val
195 200 205

Gly Lys Asp Gly Lys Pro Ala Ala Phe Ser Lys Asp Asn Val Pro Tyr
210 215 220

Gln Pro Lys His Trp Leu Lys Phe Ala Asp Gln Pro Leu Gly Ala Gly
225 230 235 240

Asp Phe Val Met Val Ala Gly Tyr Pro Gly Ser Thr Asn Arg Tyr Ala
245 250 255

Leu Ala Ala Glu Phe Asp Asn Thr Ala Gln Trp Thr Tyr Pro Thr Ile
260 265 270

Ala Arg His Tyr Lys Asn Gln Ile Ala Met Val Glu Ala Ala Gly Lys
275 280 285

Gln Asn Ala Asp Ile Gln Val Lys Tyr Ala Ala Thr Met Ala Gly Trp
290 295 300

Asn Ala Thr Ser Lys Asn Tyr Asp Gly Gln Leu Glu Gly Phe Lys Arg
305 310 315 320

Ile Asp Ala Ala Gly Gln Lys Leu Arg Glu Glu Ala Ala Val Leu Gly
325 330 335

Trp Leu Lys Gly Gln Gly Ala Lys Gly Gln Pro Ala Leu Asp Ala His
340 345 350

Ala Lys Leu Leu Asp Leu Leu Glu Gln Ser Lys Ala Thr Arg Asp Arg
355 360 365

Asp Leu Thr Leu Ala Leu Phe Asn Asn Thr Ala Met Leu Gly Ser Ala
370 375 380

Thr Gln Leu Tyr Arg Leu Ser Ile Glu Arg Glu Lys Pro Asn Ala Glu
385 390 395 400

Arg Glu Ser Gly Tyr Gln Glu Arg Asp Leu Pro Ala Ile Glu Gly Gly
405 410 415

Leu Lys Gln Leu Glu Arg Arg Tyr Val Ala Ala Met Asp Arg Gln Leu
420 425 430

Gln Glu Tyr Trp Leu Asn Glu Tyr Ile Lys Leu Pro Ala Asp Gln Arg
435 440 445

Val Ala Ala Val Asp Ala Trp Leu Gly Gly Asn Asp Ala Ala Ala Val
450 455 460

Lys Arg Ala Leu Asp Arg Leu Ala Gly Thr Lys Leu Gly Ser Thr Glu
465 470 475 480

Glu Arg Leu Lys Trp Phe Ala Ala Asp Arg Lys Ala Phe Glu Ala Ser
485 490 495

Asn Asp Pro Ala Ile Gln Tyr Ala Val Ala Val Met Pro Thr Leu Leu
500 505 510

Lys Leu Glu Gln Glu Arg Lys Thr Arg Ala Gly Glu Asn Leu Ala Ala
515 520 525

Arg Pro Val Tyr Leu Gln Ala Leu Ala Asp Tyr Lys Lys Ser Gln Gly
530 535 540

Glu Phe Val Tyr Pro Asp Ala Asn Leu Ser Leu Arg Ile Thr Phe Gly
545 550 555 560

Asn Val Met Gly Tyr Ala Pro Lys Asp Gly Met Glu Tyr Thr Pro Phe
565 570 575

Thr Thr Leu Glu Gly Val Val Ala Lys Glu Thr Gly Gln Asp Pro Phe
580 585 590

Asp Ser Pro Lys Ala Leu Leu Asp Ala Val Ala Ala Lys Arg Tyr Gly
595 600 605

Gly Leu Glu Asp Lys Arg Ile Gly Ser Val Pro Val Asn Tyr Leu Ser
610 615 620

Asp Leu Asp Ile Thr Gly Gly Asn Ser Gly Ser Pro Val Leu Asp Ala
625 630 635 640

His Gly Lys Leu Val Gly Leu Ala Phe Gly Gly Asn Trp Glu Ser Val
645 650 655

Ser Ser Asn Trp Val Phe Asp Pro Lys Met Thr Arg Met Ile Ala Val
660 665 670

Asp Gly Arg Tyr Leu Arg Trp Ile Met Gln Glu Val Tyr Pro Ala Pro
675 680 685

Gln Leu Leu Lys Glu Met Asn Val Gly Lys
690 695

<210> 38
<211> 698
<212> PRT
<213> Artificial Sequence

<220>
<223> Modified Dipeptidyl Aminopeptidase BII (DAP BII)

<400> 38

Gly Glu Gly Met Trp Val Pro Gln Gln Leu Pro Glu Ile Ala Gly Pro
1 5 10 15

Leu Lys Lys Ala Gly Leu Lys Leu Ser Pro Gln Gln Ile Ser Asp Leu
20 25 30

Thr Gly Asp Pro Met Gly Ala Val Val Ala Leu Gly Gly Cys Thr Ala
35 40 45

Ser Phe Val Ser Pro Asn Gly Leu Val Val Thr Asn His His Cys Ala
50 55 60

Tyr Gly Ala Ile Gln Leu Asn Ser Thr Ala Glu Asn Asn Leu Ile Lys
65 70 75 80

Asn Gly Phe Asn Ala Pro Thr Thr Ala Asp Glu Val Ser Ala Gly Pro
85 90 95

Asn Ala Arg Val Phe Val Leu Asp Glu Ile Thr Asp Val Thr Lys Asp
100 105 110

Ala Lys Ala Ala Ile Ala Ala Ala Gly Asp Asp Ala Leu Ala Arg Thr
115 120 125

Lys Ala Leu Glu Ala Phe Glu Lys Lys Leu Ile Ala Asp Cys Glu Ala
130 135 140

Glu Ala Gly Phe Arg Cys Arg Leu Tyr Ser Phe Ser Gly Gly Asn Thr
145 150 155 160

Tyr Arg Leu Phe Lys Asn Leu Glu Ile Lys Asp Val Arg Leu Ala Tyr
165 170 175

Ala Pro Pro Gly Ser Val Gly Lys Phe Gly Gly Asp Ile Asp Val Trp
180 185 190

Met Trp Pro Arg His Thr Gly Asp Phe Ala Phe Tyr Arg Ala Tyr Val
195 200 205

Gly Lys Asp Gly Lys Pro Ala Ala Phe Ser Lys Asp Asn Val Pro Tyr
210 215 220

Gln Pro Lys His Trp Leu Lys Phe Ala Asp Gln Pro Leu Gly Ala Gly
225 230 235 240

Asp Phe Val Met Val Ala Gly Tyr Pro Gly Ser Thr Asn Arg Tyr Ala
245 250 255

Leu Ala Ala Glu Phe Asp Asn Thr Ala Gln Trp Thr Tyr Pro Thr Ile
260 265 270

Ala Arg His Tyr Lys Asn Gln Ile Ala Met Val Glu Ala Ala Gly Lys
275 280 285

Gln Asn Ala Asp Ile Gln Val Lys Tyr Ala Ala Thr Met Ala Gly Trp
290 295 300

Asn Ala Thr Ser Lys Asn Tyr Asp Gly Gln Leu Glu Gly Phe Lys Arg
305 310 315 320

Ile Asp Ala Ala Gly Gln Lys Leu Arg Glu Glu Ala Ala Val Leu Gly
325 330 335

Trp Leu Lys Gly Gln Gly Ala Lys Gly Gln Pro Ala Leu Asp Ala His
340 345 350

Ala Lys Leu Leu Asp Leu Leu Glu Gln Ser Lys Ala Thr Arg Asp Arg
355 360 365

Asp Leu Thr Leu Ala Leu Phe Asn Asn Thr Ala Met Leu Gly Ser Ala
370 375 380

Thr Gln Leu Tyr Arg Leu Ser Ile Glu Arg Glu Lys Pro Asn Ala Glu
385 390 395 400

Arg Glu Ser Gly Tyr Gln Glu Arg Asp Leu Pro Ala Ile Glu Gly Gly
405 410 415

Leu Lys Gln Leu Glu Arg Arg Tyr Val Ala Ala Met Asp Arg Gln Leu
420 425 430

Gln Glu Tyr Trp Leu Asn Glu Tyr Ile Lys Leu Pro Ala Asp Gln Arg
435 440 445

Val Ala Ala Val Asp Ala Trp Leu Gly Gly Asn Asp Ala Ala Ala Val
450 455 460

Lys Arg Ala Leu Asp Arg Leu Ala Gly Thr Lys Leu Gly Ser Thr Glu
465 470 475 480

Glu Arg Leu Lys Trp Phe Ala Ala Asp Arg Lys Ala Phe Glu Ala Ser
485 490 495

Asn Asp Pro Ala Ile Gln Tyr Ala Val Ala Val Met Pro Thr Leu Leu
500 505 510

Lys Leu Glu Gln Glu Arg Lys Thr Arg Ala Gly Glu Asn Leu Ala Ala
515 520 525

Arg Pro Val Tyr Leu Gln Ala Leu Ala Asp Tyr Lys Lys Ser Gln Gly
530 535 540

Glu Phe Val Tyr Pro Asp Ala Asn Leu Ser Leu Arg Ile Thr Phe Gly
545 550 555 560

Asn Val Met Gly Tyr Ala Pro Lys Asp Gly Met Glu Tyr Thr Pro Phe
565 570 575

Thr Thr Leu Glu Gly Val Val Ala Lys Glu Thr Gly Gln Asp Pro Phe
580 585 590

Asp Ser Pro Lys Ala Leu Leu Asp Ala Val Ala Ala Lys Arg Tyr Gly
595 600 605

Gly Leu Glu Asp Lys Arg Ile Gly Ser Val Pro Val Asn Tyr Leu Ser
610 615 620

Asp Leu Asp Ile Thr Gly Gly Asn Ser Gly Ser Pro Val Leu Asp Ala
625 630 635 640

His Gly Lys Leu Val Gly Leu Ala Phe Ser Gly Asn Trp Glu Ser Val
645 650 655

Ser Ser Asn Trp Val Phe Asp Pro Lys Met Thr Arg Met Ile Ala Val
660 665 670

Asp Gly Arg Tyr Leu Arg Trp Ile Met Gln Glu Val Tyr Pro Ala Pro
675 680 685

Gln Leu Leu Lys Glu Met Asn Val Gly Lys
690 695

<210> 39

<211> 698

<212> PRT

<213> Artificial Sequence

<220>

<223> Modified Dipeptidyl Aminopeptidase BII (DAP BII)

<400> 39

Gly Glu Gly Met Trp Val Pro Gln Gln Leu Pro Glu Ile Ala Gly Pro
1 5 10 15

Leu Lys Lys Ala Gly Leu Lys Leu Ser Pro Gln Gln Ile Ser Asp Leu
20 25 30

Thr Gly Asp Pro Met Gly Ala Val Val Ala Leu Gly Gly Cys Thr Ala
35 40 45

Ser Phe Val Ser Pro Asn Gly Leu Val Val Thr Asn His His Cys Ala
50 55 60

Tyr Gly Ala Ile Gln Leu Asn Ser Thr Ala Glu Asn Asn Leu Ile Lys
65 70 75 80

Asn Gly Phe Asn Ala Pro Thr Thr Ala Asp Glu Val Ser Ala Gly Pro
85 90 95

Asn Ala Arg Val Phe Val Leu Asp Glu Ile Thr Asp Val Thr Lys Asp
100 105 110

Ala Lys Ala Ala Ile Ala Ala Ala Gly Asp Asp Ala Leu Ala Arg Thr
115 120 125

Lys Ala Leu Glu Ala Phe Glu Lys Lys Leu Ile Ala Asp Cys Glu Ala
130 135 140

Glu Ala Gly Phe Arg Cys Arg Leu Tyr Ser Phe Ser Gly Gly Asn Thr
145 150 155 160

Tyr Arg Leu Phe Lys Asn Leu Glu Ile Lys Asp Val Arg Leu Ala Tyr
165 170 175

Ala Pro Pro Gly Ser Val Gly Lys Phe Gly Gly Asp Ile Asp Ser Trp
180 185 190

Met Trp Pro Arg His Thr Gly Asp Phe Ala Phe Tyr Arg Ala Tyr Val
195 200 205

Gly Lys Asp Gly Lys Pro Ala Ala Phe Ser Lys Asp Asn Val Pro Tyr
210 215 220

Gln Pro Lys His Trp Leu Lys Phe Ala Asp Gln Pro Leu Gly Ala Gly
225 230 235 240

Asp Phe Val Met Val Ala Gly Tyr Pro Gly Ser Thr Asn Arg Tyr Ala
245 250 255

Leu Ala Ala Glu Phe Asp Asn Thr Ala Gln Trp Thr Tyr Pro Thr Ile
260 265 270

Ala Arg His Tyr Lys Asn Gln Ile Ala Met Val Glu Ala Ala Gly Lys
275 280 285

Gln Asn Ala Asp Ile Gln Val Lys Tyr Ala Ala Thr Met Ala Gly Trp
290 295 300

Asn Gly Thr Ser Lys Asn Tyr Asp Gly Gln Leu Glu Gly Phe Lys Arg
305 310 315 320

Ile Asp Ala Ala Gly Gln Lys Leu Arg Glu Glu Ala Ala Val Leu Gly
325 330 335

Trp Leu Lys Gly Gln Gly Ala Lys Gly Gln Pro Ala Leu Asp Ala His
340 345 350

Ala Lys Leu Leu Asp Leu Leu Glu Gln Ser Lys Ala Thr Arg Asp Arg
355 360 365

Asp Leu Thr Leu Ala Leu Phe Asn Asn Thr Ala Met Leu Gly Ser Ala
370 375 380

Thr Gln Leu Tyr Arg Leu Ser Ile Glu Arg Glu Lys Pro Asn Ala Glu
 385 390 395 400

Arg Glu Ser Gly Tyr Gln Glu Arg Asp Leu Pro Ala Ile Glu Gly Gly
 405 410 415

Leu Lys Gln Leu Glu Arg Arg Tyr Val Ala Ala Met Asp Arg Gln Leu
 420 425 430

Gln Glu Tyr Trp Leu Asn Glu Tyr Ile Lys Leu Pro Ala Asp Gln Arg
 435 440 445

Val Ala Ala Val Asp Ala Trp Leu Gly Gly Asn Asp Ala Ala Ala Val
 450 455 460

Lys Arg Ala Leu Asp Arg Leu Ala Gly Thr Lys Leu Gly Ser Thr Glu
 465 470 475 480

Glu Arg Leu Lys Trp Phe Ala Ala Asp Arg Lys Ala Phe Glu Ala Ser
 485 490 495

Asn Asp Pro Ala Ile Gln Tyr Ala Val Ala Val Met Pro Thr Leu Leu
 500 505 510

Lys Leu Glu Gln Glu Arg Lys Thr Arg Ala Gly Glu Asn Leu Ala Ala
 515 520 525

Arg Pro Val Tyr Leu Gln Ala Leu Ala Asp Tyr Lys Lys Ser Gln Gly
 530 535 540

Glu Phe Val Tyr Pro Asp Ala Asn Leu Ser Leu Arg Ile Thr Phe Gly
 545 550 555 560

Asn Val Met Gly Tyr Ala Pro Lys Asp Gly Met Glu Tyr Thr Pro Phe
 565 570 575

Thr Thr Leu Glu Gly Val Val Ala Lys Glu Thr Gly Gln Asp Pro Phe
 580 585 590

Asp Ser Pro Lys Ala Leu Leu Asp Ala Val Ala Ala Lys Arg Tyr Gly
595 600 605

Gly Leu Glu Asp Lys Arg Ile Gly Ser Val Pro Val Asn Tyr Leu Ser
610 615 620

Asp Leu Asp Ile Thr Gly Gly Asn Ser Gly Ser Pro Val Leu Asp Ala
625 630 635 640

His Gly Lys Leu Val Gly Leu Ala Phe Ser Gly Asn Trp Glu Ser Val
645 650 655

Ser Ser Asn Trp Val Phe Asp Pro Lys Met Thr Arg Met Ile Ala Val
660 665 670

Asp Gly Arg Tyr Leu Arg Trp Ile Met Gln Glu Val Tyr Pro Ala Pro
675 680 685

Gln Leu Leu Lys Glu Met Asn Val Gly Lys
690 695

<210> 40
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Test Peptide

<400> 40

Gly Arg Phe Ser Gly Ile Tyr
1 5

<210> 41
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

<223> Test Peptide

<400> 41

Trp	Thr	Gln	Ile	Phe	Gly	Ala
1				5		