

SEQUENCE LISTING

<110> GENOVIS AB

<120> Protease and binding polypeptide for O-glycoproteins

<130> N410795W0

<150> GB1708471.6

<151> 2017-05-26

<150> GB1708476.5

<151> 2017-05-26

<150> GB1806655.5

<151> 2018-04-24

<160> 50

<170> PatentIn version 3.5

<210> 1

<211> 361

<212> PRT

<213> Akkermansia muciniphila

<400> 1

Glu	Val	Thr	Val	Pro	Asp	Ala	Leu	Lys	Asp	Arg	Ile	Ala	Leu	Lys	Lys
1				5					10					15	

Thr	Ala	Arg	Gln	Leu	Asn	Ile	Val	Tyr	Phe	Leu	Gly	Ser	Asp	Thr	Glu
			20					25					30		

Pro	Val	Pro	Asp	Tyr	Glu	Arg	Arg	Leu	Ser	Glu	Leu	Leu	Leu	Tyr	Leu
			35				40					45			

Gln	Gln	Phe	Tyr	Gly	Lys	Glu	Met	Gln	Arg	His	Gly	Tyr	Gly	Ala	Arg
			50			55					60				

Ser	Phe	Gly	Leu	Asp	Ile	Lys	Ser	Pro	Gly	Arg	Val	Asn	Ile	Ile	Glu
65					70				75						80

Tyr	Lys	Ala	Lys	Asn	Pro	Ala	Ala	His	Tyr	Pro	Tyr	Glu	Asn	Gly	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

85

90

95

Gly Trp Lys Ala Ala Gln Glu Leu Asp Glu Phe Phe Lys Ala His Pro
 100 105 110

Asp Arg Lys Lys Ser Gln His Thr Leu Ile Ile Met Pro Thr Trp Asn
 115 120 125

Asp Glu Lys Asn Gly Pro Asp Asn Pro Gly Gly Val Pro Phe Tyr Gly
 130 135 140

Met Gly Arg Asn Cys Phe Ala Leu Asp Tyr Pro Ala Phe Asp Ile Lys
 145 150 155 160

His Leu Gly Gln Lys Thr Arg Glu Gly Arg Leu Leu Thr Lys Trp Tyr
 165 170 175

Gly Gly Met Ala His Glu Leu Gly His Gly Leu Asn Leu Pro His Asn
 180 185 190

His Gln Thr Ala Ser Asp Gly Lys Lys Tyr Gly Thr Ala Leu Met Gly
 195 200 205

Ser Gly Asn Tyr Thr Phe Gly Thr Ser Pro Thr Phe Leu Thr Pro Ala
 210 215 220

Ser Cys Ala Leu Leu Asp Ala Cys Glu Val Phe Ser Val Thr Pro Ser
 225 230 235 240

Gln Gln Phe Tyr Glu Gly Lys Pro Glu Val Glu Val Gly Asp Val Ala
 245 250 255

Ile Ser Phe Lys Gly Asp Gln Ile Leu Val Ser Gly Asn Tyr Lys Ser
 260 265 270

Pro Gln Thr Val Lys Ala Leu Asn Val Tyr Ile Gln Asp Pro Pro Tyr
 275 280 285

Ala Val Asn Gln Asp Tyr Asp Ala Val Ser Phe Ser Arg Arg Leu Gly
290 295 300

Lys Lys Ser Gly Lys Phe Ser Met Lys Ile Asp Lys Lys Glu Leu Glu
305 310 315 320

Gly Leu Asn Asn Asn Glu Phe Arg Ile Ser Leu Met Phe Ile Leu Ala
325 330 335

Asn Gly Leu His Met Gln Lys His Phe Thr Phe His Trp Asp Ala Leu
340 345 350

Gln Asp Tyr Arg Asp Gly Ser Lys Ser
355 360

<210> 2
<211> 371
<212> PRT
<213> Artificial Sequence

<220>
<223> LS (N terminal methionine and a C-terminal linker + His6 tag)

<400> 2

Met Glu Val Thr Val Pro Asp Ala Leu Lys Asp Arg Ile Ala Leu Lys
1 5 10 15

Lys Thr Ala Arg Gln Leu Asn Ile Val Tyr Phe Leu Gly Ser Asp Thr
20 25 30

Glu Pro Val Pro Asp Tyr Glu Arg Arg Leu Ser Glu Leu Leu Leu Tyr
35 40 45

Leu Gln Gln Phe Tyr Gly Lys Glu Met Gln Arg His Gly Tyr Gly Ala
50 55 60

Arg Ser Phe Gly Leu Asp Ile Lys Ser Pro Gly Arg Val Asn Ile Ile

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

Ser Pro Gln Thr Val Lys Ala Leu Asn Val Tyr Ile Gln Asp Pro Pro
 275 280 285

Tyr Ala Val Asn Gln Asp Tyr Asp Ala Val Ser Phe Ser Arg Arg Leu
 290 295 300

Gly Lys Lys Ser Gly Lys Phe Ser Met Lys Ile Asp Lys Lys Glu Leu
 305 310 315 320

Glu Gly Leu Asn Asn Asn Glu Phe Arg Ile Ser Leu Met Phe Ile Leu
 325 330 335

Ala Asn Gly Leu His Met Gln Lys His Phe Thr Phe His Trp Asp Ala
 340 345 350

Leu Gln Asp Tyr Arg Asp Gly Ser Lys Ser Gly Ser Gly His His His
 355 360 365

His His His
 370

<210> 3
 <211> 1116
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleotide sequence of LS

<400> 3
 atggaagtca ctgtgccgga cgccctgaaa gatcgcacgc cgctgaagaa aaccgctcgt 60
 cagctgaata tcgtctactt cctgggttct gataccgaac cggttccgga ctacgagcgc 120
 cgtctgagcg agctgctgtt gtatctgcag caattctatg gtaaagaaat gcagcgccat 180
 ggctatggcg cacgcagctt tggctcggac attaatgtcac cgggtcgtgt gaacattatc 240
 gagtacaaag cgaagaaccc ggcagcgcac taccggtatg agaatggtgg cggctggaaa 300

gctgcacaag aactggacga atttttcaag gcccattccag accgcaagaa aagccagcac 360
accctgatca tcatgcctac ctggaatgat gagaaaaatg gtcctgacaa tccgggtggc 420
gttccgttct atgggtatggg tcgtaattgt tttgcgttgg actacccggc gtttgatatc 480
aagcacctgg gtcagaaaac gcgtgagggt cgtctgctga cgaaatggta cgggtggcatg 540
gcgcacgaac tgggccacgg cctgaatctg ccgcacaatc accagaccgc gagcgatggc 600
aagaaatatg gcaccgccct gatgggtagc ggcaactaca cgttcggtagc cagcccgacg 660
ttcctgaccc cggcgagctg tgcgctgctg gatgcctgcg aagtgttcag cgttaccccg 720
agccaacagt tttatgaggg taagccagaa gtcgagggtg gtgatgttgc aatttccttc 780
aagggtgatc aaatcttggc cagcggtaac tacaagagcc cgcaaaccgt gaaagctctg 840
aacgtttaca ttcaggatcc gccgtacgcc gtgaaccaag actacgatgc agtgagcttt 900
agccgtcgtc tggggcaaaaa gtccggtaag tttagcatga agattgacaa aaaagaactg 960
gaaggcctga ataacaacga attccgtatt tccttgatgt tcattctggc aaacggctta 1020
cacatgcaga agcactttac gtttacttgg gatgcgctgc aagactaccg tgacggtagc 1080
aaatctgggtt cgggtcatca tcaccacat cactga 1116

<210> 4
<211> 385
<212> PRT
<213> Akkermansia muciniphila

<400> 4

Met Leu Lys Arg Leu Leu Ser Ala Phe Phe Ser Leu Phe Phe Leu Gly
1 5 10 15

Ala Ala Ser Gly Thr Ser Phe Ala Glu Val Thr Val Pro Asp Ala Leu
20 25 30

Lys Asp Arg Ile Ala Leu Lys Lys Thr Ala Arg Gln Leu Asn Ile Val
35 40 45

Tyr Phe Leu Gly Ser Asp Thr Glu Pro Val Pro Asp Tyr Glu Arg Arg

50

55

60

Leu Ser Glu Leu Leu Leu Tyr Leu Gln Gln Phe Tyr Gly Lys Glu Met
65 70 75 80

Gln Arg His Gly Tyr Gly Ala Arg Ser Phe Gly Leu Asp Ile Lys Ser
85 90 95

Pro Gly Arg Val Asn Ile Ile Glu Tyr Lys Ala Lys Asn Pro Ala Ala
100 105 110

His Tyr Pro Tyr Glu Asn Gly Gly Gly Trp Lys Ala Ala Gln Glu Leu
115 120 125

Asp Glu Phe Phe Lys Ala His Pro Asp Arg Lys Lys Ser Gln His Thr
130 135 140

Leu Ile Ile Met Pro Thr Trp Asn Asp Glu Lys Asn Gly Pro Asp Asn
145 150 155 160

Pro Gly Gly Val Pro Phe Tyr Gly Met Gly Arg Asn Cys Phe Ala Leu
165 170 175

Asp Tyr Pro Ala Phe Asp Ile Lys His Leu Gly Gln Lys Thr Arg Glu
180 185 190

Gly Arg Leu Leu Thr Lys Trp Tyr Gly Gly Met Ala His Glu Leu Gly
195 200 205

His Gly Leu Asn Leu Pro His Asn His Gln Thr Ala Ser Asp Gly Lys
210 215 220

Lys Tyr Gly Thr Ala Leu Met Gly Ser Gly Asn Tyr Thr Phe Gly Thr
225 230 235 240

Ser Pro Thr Phe Leu Thr Pro Ala Ser Cys Ala Leu Leu Asp Ala Cys
245 250 255

Glu Val Phe Ser Val Thr Pro Ser Gln Gln Phe Tyr Glu Gly Lys Pro
260 265 270

Glu Val Glu Val Gly Asp Val Ala Ile Ser Phe Lys Gly Asp Gln Ile
275 280 285

Leu Val Ser Gly Asn Tyr Lys Ser Pro Gln Thr Val Lys Ala Leu Asn
290 295 300

Val Tyr Ile Gln Asp Pro Pro Tyr Ala Val Asn Gln Asp Tyr Asp Ala
305 310 315 320

Val Ser Phe Ser Arg Arg Leu Gly Lys Lys Ser Gly Lys Phe Ser Met
325 330 335

Lys Ile Asp Lys Lys Glu Leu Glu Gly Leu Asn Asn Asn Glu Phe Arg
340 345 350

Ile Ser Leu Met Phe Ile Leu Ala Asn Gly Leu His Met Gln Lys His
355 360 365

Phe Thr Phe His Trp Asp Ala Leu Gln Asp Tyr Arg Asp Gly Ser Lys
370 375 380

Ser
385

<210> 5
<211> 361
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide capable of binding to O-glycans but lacks or has
reduced O-glycoprotein-specific endoprotease activity

<400> 5

Glu Val Thr Val Pro Asp Ala Leu Lys Asp Arg Ile Ala Leu Lys Lys
1 5 10 15

Thr Ala Arg Gln Leu Asn Ile Val Tyr Phe Leu Gly Ser Asp Thr Glu
20 25 30

Pro Val Pro Asp Tyr Glu Arg Arg Leu Ser Glu Leu Leu Tyr Leu
35 40 45

Gln Gln Phe Tyr Gly Lys Glu Met Gln Arg His Gly Tyr Gly Ala Arg
50 55 60

Ser Phe Gly Leu Asp Ile Lys Ser Pro Gly Arg Val Asn Ile Ile Glu
65 70 75 80

Tyr Lys Ala Lys Asn Pro Ala Ala His Tyr Pro Tyr Glu Asn Gly Gly
85 90 95

Gly Trp Lys Ala Ala Gln Glu Leu Asp Glu Phe Phe Lys Ala His Pro
100 105 110

Asp Arg Lys Lys Ser Gln His Thr Leu Ile Ile Met Pro Thr Trp Asn
115 120 125

Asp Glu Lys Asn Gly Pro Asp Asn Pro Gly Gly Val Pro Phe Tyr Gly
130 135 140

Met Gly Arg Asn Cys Phe Ala Leu Asp Tyr Pro Ala Phe Asp Ile Lys
145 150 155 160

His Leu Gly Gln Lys Thr Arg Glu Gly Arg Leu Leu Thr Lys Trp Tyr
165 170 175

Gly Gly Met Ala His Ala Leu Gly His Gly Leu Asn Leu Pro His Asn
180 185 190

His Gln Thr Ala Ser Asp Gly Lys Lys Tyr Gly Thr Ala Leu Met Gly

195

200

205

Ser Gly Asn Tyr Thr Phe Gly Thr Ser Pro Thr Phe Leu Thr Pro Ala
 210 215 220

Ser Cys Ala Leu Leu Asp Ala Cys Glu Val Phe Ser Val Thr Pro Ser
 225 230 235 240

Gln Gln Phe Tyr Glu Gly Lys Pro Glu Val Glu Val Gly Asp Val Ala
 245 250 255

Ile Ser Phe Lys Gly Asp Gln Ile Leu Val Ser Gly Asn Tyr Lys Ser
 260 265 270

Pro Gln Thr Val Lys Ala Leu Asn Val Tyr Ile Gln Asp Pro Pro Tyr
 275 280 285

Ala Val Asn Gln Asp Tyr Asp Ala Val Ser Phe Ser Arg Arg Leu Gly
 290 295 300

Lys Lys Ser Gly Lys Phe Ser Met Lys Ile Asp Lys Lys Glu Leu Glu
 305 310 315 320

Gly Leu Asn Asn Asn Glu Phe Arg Ile Ser Leu Met Phe Ile Leu Ala
 325 330 335

Asn Gly Leu His Met Gln Lys His Phe Thr Phe His Trp Asp Ala Leu
 340 345 350

Gln Asp Tyr Arg Asp Gly Ser Lys Ser
 355 360

<210> 6

<211> 371

<212> PRT

<213> Artificial Sequence

<220>

<223> LS E206A (N-terminal methionine and a C-terminal linker + His6 tag)

<400> 6

Met Glu Val Thr Val Pro Asp Ala Leu Lys Asp Arg Ile Ala Leu Lys
1 5 10 15

Lys Thr Ala Arg Gln Leu Asn Ile Val Tyr Phe Leu Gly Ser Asp Thr
20 25 30

Glu Pro Val Pro Asp Tyr Glu Arg Arg Leu Ser Glu Leu Leu Leu Tyr
35 40 45

Leu Gln Gln Phe Tyr Gly Lys Glu Met Gln Arg His Gly Tyr Gly Ala
50 55 60

Arg Ser Phe Gly Leu Asp Ile Lys Ser Pro Gly Arg Val Asn Ile Ile
65 70 75 80

Glu Tyr Lys Ala Lys Asn Pro Ala Ala His Tyr Pro Tyr Glu Asn Gly
85 90 95

Gly Gly Trp Lys Ala Ala Gln Glu Leu Asp Glu Phe Phe Lys Ala His
100 105 110

Pro Asp Arg Lys Lys Ser Gln His Thr Leu Ile Ile Met Pro Thr Trp
115 120 125

Asn Asp Glu Lys Asn Gly Pro Asp Asn Pro Gly Gly Val Pro Phe Tyr
130 135 140

Gly Met Gly Arg Asn Cys Phe Ala Leu Asp Tyr Pro Ala Phe Asp Ile
145 150 155 160

Lys His Leu Gly Gln Lys Thr Arg Glu Gly Arg Leu Leu Thr Lys Trp
165 170 175

Tyr Gly Gly Met Ala His Ala Leu Gly His Gly Leu Asn Leu Pro His
180 185 190

Asn His Gln Thr Ala Ser Asp Gly Lys Lys Tyr Gly Thr Ala Leu Met
195 200 205

Gly Ser Gly Asn Tyr Thr Phe Gly Thr Ser Pro Thr Phe Leu Thr Pro
210 215 220

Ala Ser Cys Ala Leu Leu Asp Ala Cys Glu Val Phe Ser Val Thr Pro
225 230 235 240

Ser Gln Gln Phe Tyr Glu Gly Lys Pro Glu Val Glu Val Gly Asp Val
245 250 255

Ala Ile Ser Phe Lys Gly Asp Gln Ile Leu Val Ser Gly Asn Tyr Lys
260 265 270

Ser Pro Gln Thr Val Lys Ala Leu Asn Val Tyr Ile Gln Asp Pro Pro
275 280 285

Tyr Ala Val Asn Gln Asp Tyr Asp Ala Val Ser Phe Ser Arg Arg Leu
290 295 300

Gly Lys Lys Ser Gly Lys Phe Ser Met Lys Ile Asp Lys Lys Glu Leu
305 310 315 320

Glu Gly Leu Asn Asn Asn Glu Phe Arg Ile Ser Leu Met Phe Ile Leu
325 330 335

Ala Asn Gly Leu His Met Gln Lys His Phe Thr Phe His Trp Asp Ala
340 345 350

Leu Gln Asp Tyr Arg Asp Gly Ser Lys Ser Gly Ser Gly His His His
355 360 365

His His His

<210> 7
 <211> 1116
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleotide sequence encoding LS E206A

<400> 7
 atggaagtca ctgtgccgga cgccctgaaa gatcgcacgc cgctgaagaa aaccgctcgt 60
 cagctgaata tcgtctactt cctgggttct gataccgaac cggttccgga ctacgagcgc 120
 cgtctgagcg agctgctgtt gtatctgcag caattctatg gtaaagaaat gcagcgccat 180
 ggctatggcg cacgcagctt tggctcggac attaatgcac cgggtcgtgt gaacattatc 240
 gagtacaaag cgaagaaccc ggcagcgcac taccgctatg agaatgggtg cggctggaaa 300
 gctgcacaag aactggacga atttttcaag gcccatccag accgcaagaa aagccagcac 360
 accctgatca tcatgcctac ctggaatgat gagaaaaatg gtcctgacaa tccgggtggc 420
 gttccgttct atggatatggg tcgtaattgt tttgcgttgg actacccggc gtttgatata 480
 aagcacctgg gtcagaaaac gcgtgagggt cgtctgctga cgaaatggta cgggtggcatg 540
 gcgcacgcgc tgggccacgg cctgaatctg ccgcacaatc accagaccgc gagcgtggc 600
 aagaaatatg gcaccgccct gatgggtagc ggcaactaca cgttcggtag cagcccgcgc 660
 ttcctgaccc cggcgagctg tgcgctgctg gatgcctgcg aagtgttcag cgttaccgcc 720
 agccaacagt tttatgaggg taagccagaa gtcgaggttg gtgatgttgc aatttccttc 780
 aagggtgatc aaatcttggc cagcggtaac tacaagagcc cgcaaaccgt gaaagctctg 840
 aacgtttaca ttcaggatcc gccgtacgcc gtgaaccaag actacgatgc agtgagcttt 900
 agccgtcgtc tgggcaaaaa gtccggtgaa tttagcatga agattgacaa aaaagaactg 960
 gaaggcctga ataacaacga attccgtatt tccttgatgt tcattctggc aaacggctta 1020
 cacatgcaga agcactttac gtttcactgg gatgcgctgc aagactaccg tgacggtagc 1080
 aaatctgggt cgggtcatca tcaccacat cactga 1116

<210> 8
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Metalloprotease domain motif

<400> 8

Gly Met Ala His Glu Leu Gly His Gly Leu
1 5 10

<210> 9
<211> 595
<212> PRT
<213> Akkermansia muciniphila

<400> 9

Met Lys Asn Leu Leu Phe Ala Leu Leu Thr Gly Ser Phe Cys Cys Cys
1 5 10 15

Tyr Ala Gln Gln Lys Ala Ala Pro Val Pro Glu Pro Glu Val Val Ala
20 25 30

Thr Pro Pro Ala Asp Ala Gly Arg Gly Leu Ile Arg Val Asp Ser Arg
35 40 45

Glu Ile Arg His Tyr Ser Gly Thr Arg Lys Glu Pro Asp Tyr Leu Val
50 55 60

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

Tyr Pro Pro Asn Tyr Gly Gly Ile Pro Lys Glu Ser Pro Ala Ile Val
85 90 95

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

Phe Val Phe Leu Ser Arg Gly Gly Leu Asp Gly Lys Trp Leu Ala Val
115 120 125

Thr Asn Asp Gly Lys Leu Glu Glu Asp Trp Lys Asp Pro Glu Lys Arg
130 135 140

Lys Asn Leu Lys Lys Leu Gly Gly Ile Met Arg Thr Pro Val Phe Val
145 150 155 160

Asn Lys Gly Arg Arg Val Ile Val Pro Phe His Asn Met Gly Gly Gly
165 170 175

Thr Lys Phe His Ile Ser Asp Asp Gly Gly Leu Thr Trp His Val Ser
180 185 190

Arg Asn Gly Val Thr Ser Pro Arg His Glu Ala Arg Pro Pro His Gln
195 200 205

Gly Val Arg Trp Phe Asn Asn Ala Val Glu Ala Thr Val Leu Glu Met
210 215 220

Lys Asp Gly Thr Leu Trp Ala Leu Ala Arg Thr Ser Gln Asp Gln Ala
225 230 235 240

Trp Gln Ala Phe Ser Lys Asp Tyr Gly Glu Thr Trp Ser Lys Pro Glu
245 250 255

Pro Ser Arg Phe Phe Gly Thr Leu Thr Met Asn Thr Leu Gly Arg Leu
260 265 270

Asp Asp Gly Thr Ile Val Ser Leu Trp Thr Asn Thr Met Ala Leu Pro
275 280 285

Glu Asn Ala Thr Ala Gly Asn Gly Thr Trp Glu Asp Val Phe Thr Asn
290 295 300

Arg Asp Ser His His Ile Ala Met Ser Gly Asp Glu Gly Lys Thr Trp
305 310 315 320

Tyr Gly Phe Arg Glu Ile Ile Leu Asp Glu His Arg Asn His Pro Gly
325 330 335

Tyr Ala Thr Leu Asp Gly Pro Glu Asp Arg Gly Lys His Gln Ser Glu
340 345 350

Met Val Gln Leu Asp Lys Asn Arg Ile Leu Ile Ser Leu Gly Gln His
355 360 365

Lys Asn His Arg Arg Leu Val Ile Val Asp Arg Arg Trp Val Gly Ala
370 375 380

Lys Thr Arg Ala Thr Gln Thr Gly Lys Asp Leu Asp Ser Gln Trp Thr
385 390 395 400

Ile His Thr Tyr Ile Pro Gln Lys Lys Gly His Cys Ser Tyr Asn Arg
405 410 415

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

Val Leu Gln Ile Lys Arg Leu Asp Asp Pro Glu Leu Val Asn Glu Lys
435 440 445

Ser Asn Val Asp Tyr Arg Asn Gly Gly Ala Thr Trp Asn Phe Pro Asn
450 455 460

Gly Thr Thr Gly Leu Val Lys Phe Arg Phe Arg Val Val Asp Gly Glu
465 470 475 480

Gln Ala Asp Asp Ser Gly Leu Gln Val Ser Leu Thr Asp Arg Leu Phe
485 490 495

Asn Ala Cys Asp Ser Thr Thr Lys Asp Tyr Ala Leu Phe Thr Phe Pro
500 505 510

Ile Arg Leu Lys Pro Ala Pro His Leu Leu Leu Gly Met Lys Lys Val
515 520 525

Pro Phe Thr Pro Gly Ala Trp His Glu Ile Ser Leu Leu Trp Gln Gly
530 535 540

Gly Gln Ala Val Val Ser Leu Asp Gly Lys Lys Ala Gly Thr Leu Lys
545 550 555 560

Met Ala Asn Lys Ser Pro Asn Gly Ala Ser Tyr Ile His Phe Ile Ser
565 570 575

Thr Gly Ser Gln Pro Asp Ala Gly Ile Leu Leu Asp Thr Val Asn Ala
580 585 590

Arg Val Lys
595

<210> 10
<211> 577
<212> PRT
<213> Akkermansia muciniphila

<400> 10

Gln Gln Lys Ala Ala Pro Val Pro Glu Pro Glu Val Val Ala Thr Pro
1 5 10 15

Pro Ala Asp Ala Gly Arg Gly Leu Ile Arg Val Asp Ser Arg Glu Ile
20 25 30

Arg His Tyr Ser Gly Thr Arg Lys Glu Pro Asp Tyr Leu Val Ser Arg
35 40 45

Asp Asn Gly Lys Thr Trp Glu Met Lys Ala Ala Pro Ala Gly Tyr Pro
50 55 60

Pro Asn Tyr Gly Gly Ile Pro Lys Glu Ser Pro Ala Ile Val Arg Asn
65 70 75 80

Pro Leu Thr Arg Glu Phe Ile Arg Val Gln Pro Ile Gly Gly Phe Val
85 90 95

Phe Leu Ser Arg Gly Gly Leu Asp Gly Lys Trp Leu Ala Val Thr Asn
100 105 110

Asp Gly Lys Leu Glu Glu Asp Trp Lys Asp Pro Glu Lys Arg Lys Asn
115 120 125

Leu Lys Lys Leu Gly Gly Ile Met Arg Thr Pro Val Phe Val Asn Lys
130 135 140

Gly Arg Arg Val Ile Val Pro Phe His Asn Met Gly Gly Gly Thr Lys
145 150 155 160

Phe His Ile Ser Asp Asp Gly Gly Leu Thr Trp His Val Ser Arg Asn
165 170 175

Gly Val Thr Ser Pro Arg His Glu Ala Arg Pro Pro His Gln Gly Val
180 185 190

Arg Trp Phe Asn Asn Ala Val Glu Ala Thr Val Leu Glu Met Lys Asp
195 200 205

Gly Thr Leu Trp Ala Leu Ala Arg Thr Ser Gln Asp Gln Ala Trp Gln
210 215 220

Ala Phe Ser Lys Asp Tyr Gly Glu Thr Trp Ser Lys Pro Glu Pro Ser
225 230 235 240

Arg Phe Phe Gly Thr Leu Thr Met Asn Thr Leu Gly Arg Leu Asp Asp
245 250 255

Gly Thr Ile Val Ser Leu Trp Thr Asn Thr Met Ala Leu Pro Glu Asn
260 265 270

Ala Thr Ala Gly Asn Gly Thr Trp Glu Asp Val Phe Thr Asn Arg Asp
275 280 285

Ser His His Ile Ala Met Ser Gly Asp Glu Gly Lys Thr Trp Tyr Gly
290 295 300

Phe Arg Glu Ile Ile Leu Asp Glu His Arg Asn His Pro Gly Tyr Ala
305 310 315 320

Thr Leu Asp Gly Pro Glu Asp Arg Gly Lys His Gln Ser Glu Met Val
325 330 335

Gln Leu Asp Lys Asn Arg Ile Leu Ile Ser Leu Gly Gln His Lys Asn
340 345 350

His Arg Arg Leu Val Ile Val Asp Arg Arg Trp Val Gly Ala Lys Thr
355 360 365

Arg Ala Thr Gln Thr Gly Lys Asp Leu Asp Ser Gln Trp Thr Ile His
370 375 380

Thr Tyr Ile Pro Gln Lys Lys Gly His Cys Ser Tyr Asn Arg Lys Pro
385 390 395 400

Ser Ala Glu Leu Val Gln Asp Pro Ser Gly Gly Thr Lys Lys Val Leu
405 410 415

Gln Ile Lys Arg Leu Asp Asp Pro Glu Leu Val Asn Glu Lys Ser Asn
420 425 430

Val Asp Tyr Arg Asn Gly Gly Ala Thr Trp Asn Phe Pro Asn Gly Thr
435 440 445

Thr Gly Leu Val Lys Phe Arg Phe Arg Val Val Asp Gly Glu Gln Ala
450 455 460

Asp Asp Ser Gly Leu Gln Val Ser Leu Thr Asp Arg Leu Phe Asn Ala
465 470 475 480

Cys Asp Ser Thr Thr Lys Asp Tyr Ala Leu Phe Thr Phe Pro Ile Arg
485 490 495

Leu Lys Pro Ala Pro His Leu Leu Leu Gly Met Lys Lys Val Pro Phe
500 505 510

Thr Pro Gly Ala Trp His Glu Ile Ser Leu Leu Trp Gln Gly Gly Gln
515 520 525

Ala Val Val Ser Leu Asp Gly Lys Lys Ala Gly Thr Leu Lys Met Ala
530 535 540

Asn Lys Ser Pro Asn Gly Ala Ser Tyr Ile His Phe Ile Ser Thr Gly
545 550 555 560

Ser Gln Pro Asp Ala Gly Ile Leu Leu Asp Thr Val Asn Ala Arg Val
565 570 575

Lys

<210> 11

<211> 589

<212> PRT

<213> Artificial Sequence

<220>

<223> Am1757 (N-terminal methionine and a C-terminal linker + His6 tag)

<400> 11

Met Gln Gln Lys Ala Ala Pro Val Pro Glu Pro Glu Val Val Ala Thr
1 5 10 15

Pro Pro Ala Asp Ala Gly Arg Gly Leu Ile Arg Val Asp Ser Arg Glu
20 25 30

Ile Arg His Tyr Ser Gly Thr Arg Lys Glu Pro Asp Tyr Leu Val Ser
35 40 45

Arg Asp Asn Gly Lys Thr Trp Glu Met Lys Ala Ala Pro Ala Gly Tyr
50 55 60

Pro Pro Asn Tyr Gly Gly Ile Pro Lys Glu Ser Pro Ala Ile Val Arg
65 70 75 80

Asn Pro Leu Thr Arg Glu Phe Ile Arg Val Gln Pro Ile Gly Gly Phe
85 90 95

Val Phe Leu Ser Arg Gly Gly Leu Asp Gly Lys Trp Leu Ala Val Thr
100 105 110

Asn Asp Gly Lys Leu Glu Glu Asp Trp Lys Asp Pro Glu Lys Arg Lys
115 120 125

Asn Leu Lys Lys Leu Gly Gly Ile Met Arg Thr Pro Val Phe Val Asn
130 135 140

Lys Gly Arg Arg Val Ile Val Pro Phe His Asn Met Gly Gly Gly Thr
145 150 155 160

Lys Phe His Ile Ser Asp Asp Gly Gly Leu Thr Trp His Val Ser Arg
165 170 175

Asn Gly Val Thr Ser Pro Arg His Glu Ala Arg Pro Pro His Gln Gly
180 185 190

Val Arg Trp Phe Asn Asn Ala Val Glu Ala Thr Val Leu Glu Met Lys
195 200 205

Asp Gly Thr Leu Trp Ala Leu Ala Arg Thr Ser Gln Asp Gln Ala Trp
210 215 220

Gln Ala Phe Ser Lys Asp Tyr Gly Glu Thr Trp Ser Lys Pro Glu Pro
225 230 235 240

Ser Arg Phe Phe Gly Thr Leu Thr Met Asn Thr Leu Gly Arg Leu Asp
245 250 255

Asp Gly Thr Ile Val Ser Leu Trp Thr Asn Thr Met Ala Leu Pro Glu
260 265 270

Asn Ala Thr Ala Gly Asn Gly Thr Trp Glu Asp Val Phe Thr Asn Arg
275 280 285

Asp Ser His His Ile Ala Met Ser Gly Asp Glu Gly Lys Thr Trp Tyr
290 295 300

Gly Phe Arg Glu Ile Ile Leu Asp Glu His Arg Asn His Pro Gly Tyr
305 310 315 320

Ala Thr Leu Asp Gly Pro Glu Asp Arg Gly Lys His Gln Ser Glu Met
325 330 335

Val Gln Leu Asp Lys Asn Arg Ile Leu Ile Ser Leu Gly Gln His Lys
340 345 350

Asn His Arg Arg Leu Val Ile Val Asp Arg Arg Trp Val Gly Ala Lys
355 360 365

Thr Arg Ala Thr Gln Thr Gly Lys Asp Leu Asp Ser Gln Trp Thr Ile
370 375 380

His Thr Tyr Ile Pro Gln Lys Lys Gly His Cys Ser Tyr Asn Arg Lys
385 390 395 400

Pro Ser Ala Glu Leu Val Gln Asp Pro Ser Gly Gly Thr Lys Lys Val

405

410

415

Leu Gln Ile Lys Arg Leu Asp Asp Pro Glu Leu Val Asn Glu Lys Ser
 420 425 430

Asn Val Asp Tyr Arg Asn Gly Gly Ala Thr Trp Asn Phe Pro Asn Gly
 435 440 445

Thr Thr Gly Leu Val Lys Phe Arg Phe Arg Val Val Asp Gly Glu Gln
 450 455 460

Ala Asp Asp Ser Gly Leu Gln Val Ser Leu Thr Asp Arg Leu Phe Asn
 465 470 475 480

Ala Cys Asp Ser Thr Thr Lys Asp Tyr Ala Leu Phe Thr Phe Pro Ile
 485 490 495

Arg Leu Lys Pro Ala Pro His Leu Leu Leu Gly Met Lys Lys Val Pro
 500 505 510

Phe Thr Pro Gly Ala Trp His Glu Ile Ser Leu Leu Trp Gln Gly Gly
 515 520 525

Gln Ala Val Val Ser Leu Asp Gly Lys Lys Ala Gly Thr Leu Lys Met
 530 535 540

Ala Asn Lys Ser Pro Asn Gly Ala Ser Tyr Ile His Phe Ile Ser Thr
 545 550 555 560

Gly Ser Gln Pro Asp Ala Gly Ile Leu Leu Asp Thr Val Asn Ala Arg
 565 570 575

Val Lys Gly Ser Gly Leu Glu His His His His His His
 580 585

<210> 12

<211> 419

<212> PRT

<213> Akkermansia muciniphila

<400> 12

Met Thr Trp Leu Leu Cys Gly Arg Gly Lys Trp Asn Lys Val Lys Arg
1 5 10 15

Met Met Asn Ser Val Phe Lys Cys Leu Met Ser Ala Val Cys Ala Val
20 25 30

Ala Leu Pro Ala Phe Gly Gln Glu Glu Lys Thr Gly Phe Pro Thr Asp
35 40 45

Arg Ala Val Thr Val Phe Ser Ala Gly Glu Gly Asn Pro Tyr Ala Ser
50 55 60

Ile Arg Ile Pro Ala Leu Leu Ser Ile Gly Lys Gly Gln Leu Leu Ala
65 70 75 80

Phe Ala Glu Gly Arg Tyr Lys Asn Thr Asp Gln Gly Glu Asn Asp Ile
85 90 95

Ile Met Ser Val Ser Lys Asn Gly Gly Lys Thr Trp Ser Arg Pro Arg
100 105 110

Ala Ile Ala Lys Ala His Gly Ala Thr Phe Asn Asn Pro Cys Pro Val
115 120 125

Tyr Asp Ala Lys Thr Arg Thr Val Thr Val Val Phe Gln Arg Tyr Pro
130 135 140

Ala Gly Val Lys Glu Arg Gln Pro Asn Ile Pro Asp Gly Trp Asp Asp
145 150 155 160

Glu Lys Cys Ile Arg Asn Phe Met Ile Gln Ser Arg Asn Gly Gly Ser
165 170 175

Ser Trp Thr Lys Pro Gln Glu Ile Thr Lys Thr Thr Lys Arg Pro Ser
180 185 190

Gly Val Asp Ile Met Ala Ser Gly Pro Asn Ala Gly Thr Gln Leu Lys
195 200 205

Ser Gly Ala His Lys Gly Arg Leu Val Ile Pro Met Asn Glu Gly Pro
210 215 220

Phe Gly Lys Trp Val Ile Ser Cys Ile Tyr Ser Asp Asp Gly Gly Lys
225 230 235 240

Ser Trp Lys Leu Gly Gln Pro Thr Ala Asn Met Lys Gly Met Val Asn
245 250 255

Glu Thr Ser Ile Ala Glu Thr Asp Asn Gly Gly Val Val Met Val Ala
260 265 270

Arg His Trp Gly Ala Gly Asn Cys Arg Arg Ile Ala Trp Ser Gln Asp
275 280 285

Gly Gly Glu Thr Trp Gly Gln Val Glu Asp Ala Pro Glu Leu Phe Cys
290 295 300

Asp Ser Thr Gln Asn Ser Leu Met Thr Tyr Ser Leu Ser Asp Gln Pro
305 310 315 320

Ala Tyr Gly Gly Lys Ser Arg Ile Leu Phe Ser Gly Pro Ser Ala Gly
325 330 335

Arg Arg Ile Lys Gly Gln Val Ala Met Ser Tyr Asp Asn Gly Lys Thr
340 345 350

Trp Pro Val Lys Lys Leu Leu Gly Glu Gly Gly Phe Ala Tyr Ser Ser
355 360 365

Leu Ala Met Val Glu Pro Gly Ile Val Gly Val Leu Tyr Glu Glu Asn

370

375

380

Gln Glu His Ile Lys Lys Leu Lys Phe Val Pro Ile Thr Met Glu Trp
 385 390 395 400

Leu Thr Asp Gly Glu Asp Thr Gly Leu Ala Pro Gly Lys Lys Ala Pro
 405 410 415

Val Leu Lys

<210> 13
 <211> 381
 <212> PRT
 <213> Akkermansia muciniphila

<400> 13

Gln Glu Glu Lys Thr Gly Phe Pro Thr Asp Arg Ala Val Thr Val Phe
 1 5 10 15

Ser Ala Gly Glu Gly Asn Pro Tyr Ala Ser Ile Arg Ile Pro Ala Leu
 20 25 30

Leu Ser Ile Gly Lys Gly Gln Leu Leu Ala Phe Ala Glu Gly Arg Tyr
 35 40 45

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

Asn Gly Gly Lys Thr Trp Ser Arg Pro Arg Ala Ile Ala Lys Ala His
 65 70 75 80

Gly Ala Thr Phe Asn Asn Pro Cys Pro Val Tyr Asp Ala Lys Thr Arg
 85 90 95

Thr Val Thr Val Val Phe Gln Arg Tyr Pro Ala Gly Val Lys Glu Arg
 100 105 110

Gln Pro Asn Ile Pro Asp Gly Trp Asp Asp Glu Lys Cys Ile Arg Asn
115 120 125

Phe Met Ile Gln Ser Arg Asn Gly Gly Ser Ser Trp Thr Lys Pro Gln
130 135 140

Glu Ile Thr Lys Thr Thr Lys Arg Pro Ser Gly Val Asp Ile Met Ala
145 150 155 160

Ser Gly Pro Asn Ala Gly Thr Gln Leu Lys Ser Gly Ala His Lys Gly
165 170 175

Arg Leu Val Ile Pro Met Asn Glu Gly Pro Phe Gly Lys Trp Val Ile
180 185 190

Ser Cys Ile Tyr Ser Asp Asp Gly Gly Lys Ser Trp Lys Leu Gly Gln
195 200 205

Pro Thr Ala Asn Met Lys Gly Met Val Asn Glu Thr Ser Ile Ala Glu
210 215 220

Thr Asp Asn Gly Gly Val Val Met Val Ala Arg His Trp Gly Ala Gly
225 230 235 240

Asn Cys Arg Arg Ile Ala Trp Ser Gln Asp Gly Gly Glu Thr Trp Gly
245 250 255

Gln Val Glu Asp Ala Pro Glu Leu Phe Cys Asp Ser Thr Gln Asn Ser
260 265 270

Leu Met Thr Tyr Ser Leu Ser Asp Gln Pro Ala Tyr Gly Gly Lys Ser
275 280 285

Arg Ile Leu Phe Ser Gly Pro Ser Ala Gly Arg Arg Ile Lys Gly Gln
290 295 300

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

Leu Gly Glu Gly Gly Phe Ala Tyr Ser Ser Leu Ala Met Val Glu Pro
 325 330 335

Gly Ile Val Gly Val Leu Tyr Glu Glu Asn Gln Glu His Ile Lys Lys
 340 345 350

Leu Lys Phe Val Pro Ile Thr Met Glu Trp Leu Thr Asp Gly Glu Asp
 355 360 365

Thr Gly Leu Ala Pro Gly Lys Lys Ala Pro Val Leu Lys
 370 375 380

<210> 14
 <211> 393
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Am0707 (including N-terminal methionine and a C-terminal linker + His6 tag)

<400> 14

Met Gln Glu Glu Lys Thr Gly Phe Pro Thr Asp Arg Ala Val Thr Val
 1 5 10 15

Phe Ser Ala Gly Glu Gly Asn Pro Tyr Ala Ser Ile Arg Ile Pro Ala
 20 25 30

Leu Leu Ser Ile Gly Lys Gly Gln Leu Leu Ala Phe Ala Glu Gly Arg
 35 40 45

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

Lys Asn Gly Gly Lys Thr Trp Ser Arg Pro Arg Ala Ile Ala Lys Ala
 65 70 75 80

His Gly Ala Thr Phe Asn Asn Pro Cys Pro Val Tyr Asp Ala Lys Thr
85 90 95

Arg Thr Val Thr Val Val Phe Gln Arg Tyr Pro Ala Gly Val Lys Glu
100 105 110

Arg Gln Pro Asn Ile Pro Asp Gly Trp Asp Asp Glu Lys Cys Ile Arg
115 120 125

Asn Phe Met Ile Gln Ser Arg Asn Gly Gly Ser Ser Trp Thr Lys Pro
130 135 140

Gln Glu Ile Thr Lys Thr Thr Lys Arg Pro Ser Gly Val Asp Ile Met
145 150 155 160

Ala Ser Gly Pro Asn Ala Gly Thr Gln Leu Lys Ser Gly Ala His Lys
165 170 175

Gly Arg Leu Val Ile Pro Met Asn Glu Gly Pro Phe Gly Lys Trp Val
180 185 190

Ile Ser Cys Ile Tyr Ser Asp Asp Gly Gly Lys Ser Trp Lys Leu Gly
195 200 205

Gln Pro Thr Ala Asn Met Lys Gly Met Val Asn Glu Thr Ser Ile Ala
210 215 220

Glu Thr Asp Asn Gly Gly Val Val Met Val Ala Arg His Trp Gly Ala
225 230 235 240

Gly Asn Cys Arg Arg Ile Ala Trp Ser Gln Asp Gly Gly Glu Thr Trp
245 250 255

Gly Gln Val Glu Asp Ala Pro Glu Leu Phe Cys Asp Ser Thr Gln Asn
260 265 270

Ser Leu Met Thr Tyr Ser Leu Ser Asp Gln Pro Ala Tyr Gly Gly Lys
275 280 285

Ser Arg Ile Leu Phe Ser Gly Pro Ser Ala Gly Arg Arg Ile Lys Gly
290 295 300

Gln Val Ala Met Ser Tyr Asp Asn Gly Lys Thr Trp Pro Val Lys Lys
305 310 315 320

Leu Leu Gly Glu Gly Gly Phe Ala Tyr Ser Ser Leu Ala Met Val Glu
325 330 335

Pro Gly Ile Val Gly Val Leu Tyr Glu Glu Asn Gln Glu His Ile Lys
340 345 350

Lys Leu Lys Phe Val Pro Ile Thr Met Glu Trp Leu Thr Asp Gly Glu
355 360 365

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

Gly Leu Glu His His His His His His
385 390

<210> 15
<211> 2133
<212> PRT
<213> Streptococcus oralis

<400> 15

Met Asp Lys Arg Phe Phe Glu Lys Arg Cys Lys Phe Ser Ile Arg Lys
1 5 10 15

Phe Thr Leu Gly Val Ala Ser Val Met Ile Gly Ala Thr Phe Phe Ala
20 25 30

Ala Ser Pro Val Leu Ala Asp Gln Ala Arg Val Gly Ser Thr Asp Asn

35

40

45

Leu Pro Ser Glu Leu Ala Asp Leu Asp Lys Lys Ala Ser Asp Glu Gly
 50 55 60

His Asp Phe Asp Lys Glu Ala Ala Ala Gln Asn Pro Gly Ser Ala Glu
 65 70 75 80

Thr Thr Glu Gly Pro Gln Thr Glu Glu Glu Leu Leu Ala Gln Glu Lys
 85 90 95

Glu Lys Ser Glu Lys Pro Ser Asn Leu Pro Lys Glu Leu Glu Asp Lys
 100 105 110

Leu Glu Lys Ala Glu Asp Asn Gly Arg Glu Val Asp Lys Asp Gln Leu
 115 120 125

Ala Gln Asp Thr Gly Lys Leu Val Pro Glu Asp Val Ala Lys Thr Thr
 130 135 140

Asn Gly Glu Leu Asn Tyr Gly Ala Thr Val Lys Ile Lys Thr Pro Ser
 145 150 155 160

Gly Glu Gly Ser Gly Ile Val Val Ala Lys Asp Leu Val Leu Thr Val
 165 170 175

Ser His Asn Phe Ile Lys Asp Ser Gln Glu Gly Asn Ile Arg Lys Val
 180 185 190

Val Asp Asn Asp Gln Gly Asp Gly Asp Ile Tyr Ser Ile Ser Tyr Pro
 195 200 205

Gly Leu Pro Asp Val Lys Phe Ser Lys Lys Asp Ile Ile His Trp Asp
 210 215 220

Arg Glu Gly Tyr Leu Lys Gly Phe Lys Asn Asp Leu Ala Leu Val Arg
 225 230 235 240

Leu Arg Thr Val Leu Glu Asn Thr Pro Val Glu Val Thr Lys Lys Pro
245 250 255

Val Val Lys Lys Ile Gly Asp Lys Leu His Val Phe Gly Tyr Pro Glu
260 265 270

Gly Lys Leu Asn Pro Ile Val Asn Thr Thr Val Asp Phe Ala Glu Pro
275 280 285

Tyr Gly Glu Gly Val Gln Gly Ile Gly Tyr Gln Gly Gly Lys Pro Gly
290 295 300

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

His Gln Asn Gly Val Val Gly Lys Arg Ser Gly Gly Ile Leu Phe Ser
325 330 335

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

Val Lys Pro Ala Asp Leu Glu Glu Lys Glu Lys Pro Ala Glu Glu Lys
355 360 365

Pro Lys Glu Asp Lys Pro Ala Ala Ala Lys Pro Glu Thr Pro Lys Ala
370 375 380

Val Thr Pro Glu Trp Gln Thr Val Ala Asn Lys Glu Gln Gln Gly Thr
385 390 395 400

Val Thr Ile Arg Glu Glu Lys Gly Val Arg Tyr Asn Gln Leu Ser Ser
405 410 415

Thr Ala Gln Asn Asp Asn Asp Gly Lys Pro Ala Leu Phe Glu Lys Gln
420 425 430

Gly Leu Thr Val Asp Ala Asn Gly Asn Ala Thr Val Asp Leu Thr Phe
435 440 445

Lys Asp Asp Ser Glu Lys Gly Lys Ser Arg Phe Gly Val Phe Leu Lys
450 455 460

Phe Lys Asp Thr Lys Asn Asn Val Phe Val Gly Tyr Asp Gln Gly Gly
465 470 475 480

Trp Phe Trp Glu Tyr Lys Thr Pro Gly Asn Ser Thr Trp Tyr Lys Gly
485 490 495

Asn Arg Val Ala Ala Pro Glu Pro Gly Ser Val Asn Arg Leu Ser Ile
500 505 510

Thr Leu Lys Ser Asp Gly Gln Leu Asn Ala Ser Asn Asn Asp Val Asn
515 520 525

Leu Phe Asp Thr Val Thr Leu Pro Gly Ala Val Asn Glu Asn Leu Lys
530 535 540

Asn Glu Lys Lys Ile Leu Leu Lys Ala Gly Thr Tyr Ser Asn Asp Arg
545 550 555 560

Thr Val Val Ser Val Lys Thr Asp Asn Gln Glu Gly Val Lys Ala Asp
565 570 575

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

Val Thr Tyr Asp Thr Ile Gln Ser Lys Val Leu Lys Ala Val Ile Asp
595 600 605

Gln Ala Phe Pro Arg Val Lys Glu Tyr Thr Leu Asn Gly His Thr Leu
610 615 620

Pro Gly Gln Val Gln Gln Phe Asn Gln Val Phe Ile Asn Asn His Arg
625 630 635 640

Ile Thr Pro Glu Val Thr Tyr Lys Lys Ile Asn Glu Thr Thr Ala Glu
645 650 655

Tyr Leu Met Lys Leu Arg Asp Asp Ala His Leu Ile Asn Ala Glu Met
660 665 670

Thr Val Arg Leu Gln Val Val Asp Asn Gln Leu His Phe Asp Val Thr
675 680 685

Lys Ile Val Asn His Asn Gln Val Thr Pro Gly Gln Lys Ile Asp Asp
690 695 700

Glu Arg Lys Leu Leu Ser Thr Ile Ser Phe Leu Gly Asn Ala Leu Val
705 710 715 720

Ser Val Ser Ser Asp Gln Ala Gly Ala Lys Phe Asp Gly Ala Thr Met
725 730 735

Ser Asn Asn Thr His Val Ser Gly Asp Asp His Ile Asp Val Thr Asn
740 745 750

Pro Met Lys Asp Leu Ala Lys Gly Tyr Met Tyr Gly Phe Val Ser Thr
755 760 765

Asp Lys Leu Ala Ala Gly Val Trp Ser Asn Ser Gln Asn Ser Tyr Gly
770 775 780

Gly Gly Ser Asn Asp Trp Thr Arg Leu Thr Ala Tyr Lys Glu Thr Val
785 790 795 800

Gly Asn Ala Asn Tyr Val Gly Ile His Ser Ser Glu Trp Gln Trp Glu
805 810 815

Lys Ala Tyr Lys Gly Ile Val Phe Pro Glu Tyr Thr Lys Glu Leu Pro

820

825

830

Ser Ala Lys Val Val Ile Thr Glu Asp Ala Asn Ala Asp Asn Lys Val
 835 840 845

Asp Trp Gln Asp Gly Ala Ile Ala Tyr Arg Ser Ile Met Asn Asn Pro
 850 855 860

Gln Gly Trp Glu Lys Val Lys Asp Ile Thr Ala Tyr Arg Ile Ala Met
 865 870 875 880

Asn Phe Gly Ser Gln Ala Gln Asn Pro Phe Leu Met Thr Leu Asp Gly
 885 890 895

Ile Lys Lys Ile Asn Leu His Thr Asp Gly Leu Gly Gln Gly Val Leu
 900 905 910

Leu Lys Gly Tyr Gly Ser Glu Gly His Asp Ser Gly His Leu Asn Tyr
 915 920 925

Ala Asp Ile Gly Lys Arg Ile Gly Gly Val Glu Asp Phe Lys Thr Leu
 930 935 940

Ile Glu Lys Ala Lys Lys Tyr Gly Ala His Leu Gly Ile His Val Asn
 945 950 955 960

Ala Ser Glu Thr Tyr Pro Glu Ser Lys Tyr Phe Asn Glu Asn Ile Leu
 965 970 975

Arg Lys Asn Pro Asp Gly Ser Tyr Ser Tyr Gly Trp Asn Trp Leu Asp
 980 985 990

Gln Gly Ile Asn Ile Asp Ala Ala Tyr Asp Leu Ala His Gly Arg Leu
 995 1000 1005

Ala Arg Trp Glu Asp Leu Lys Lys Lys Leu Gly Glu Gly Leu Asp
 1010 1015 1020

Phe	Ile	Tyr	Val	Asp	Val	Trp	Gly	Asn	Gly	Gln	Ser	Gly	Asp	Asn
1025						1030					1035			
Gly	Ala	Trp	Ala	Thr	His	Val	Leu	Ala	Lys	Glu	Ile	Asn	Lys	Gln
1040						1045					1050			
Gly	Trp	Arg	Phe	Ala	Ile	Glu	Trp	Gly	His	Gly	Gly	Glu	Tyr	Asp
1055						1060					1065			
Ser	Thr	Phe	Gln	His	Trp	Ala	Ala	Asp	Leu	Thr	Tyr	Gly	Gly	Tyr
1070						1075					1080			
Thr	Asn	Lys	Gly	Ile	Asn	Ser	Ala	Ile	Thr	Arg	Phe	Ile	Arg	Asn
1085						1090					1095			
His	Gln	Lys	Asp	Ser	Trp	Val	Gly	Asp	Tyr	Arg	Ser	Tyr	Gly	Gly
1100						1105					1110			
Ala	Ala	Asn	Tyr	Pro	Leu	Leu	Gly	Gly	Tyr	Ser	Met	Lys	Asp	Phe
1115						1120					1125			
Glu	Gly	Trp	Gln	Gly	Arg	Ser	Asp	Tyr	Asn	Gly	Tyr	Val	Thr	Asn
1130						1135					1140			
Leu	Phe	Ala	His	Asp	Val	Met	Thr	Lys	Tyr	Phe	Gln	His	Phe	Thr
1145						1150					1155			
Val	Ser	Lys	Trp	Glu	Asn	Gly	Thr	Pro	Val	Thr	Met	Thr	Asp	Asn
1160						1165					1170			
Gly	Ser	Thr	Tyr	Lys	Trp	Thr	Pro	Glu	Met	Lys	Val	Glu	Leu	Val
1175						1180					1185			
Asp	Ala	Ala	Gly	Asn	Lys	Val	Val	Val	Thr	Arg	Lys	Ser	Asn	Asp
1190						1195					1200			

Val	Asn	Ser	Pro	Gln	Tyr	Arg	Glu	Arg	Thr	Val	Thr	Leu	Asn	Gly
1205						1210					1215			
Arg	Val	Ile	Gln	Asp	Gly	Ser	Ala	Tyr	Leu	Thr	Pro	Trp	Asn	Trp
1220						1225					1230			
Asp	Ala	Asn	Gly	Lys	Lys	Leu	Pro	Thr	Glu	Lys	Glu	Lys	Met	Tyr
1235						1240					1245			
Tyr	Phe	Asn	Thr	Gln	Ala	Gly	Ala	Thr	Thr	Trp	Thr	Leu	Pro	Ser
1250						1255					1260			
Asp	Trp	Ala	Asn	Ser	Lys	Val	Tyr	Leu	Tyr	Lys	Leu	Thr	Asp	Gln
1265						1270					1275			
Gly	Lys	Thr	Glu	Glu	Gln	Glu	Leu	Thr	Val	Thr	Asp	Gly	Lys	Ile
1280						1285					1290			
Thr	Leu	Asp	Leu	Leu	Ala	Asn	Gln	Pro	Tyr	Val	Leu	Tyr	Arg	Ser
1295						1300					1305			
Lys	Gln	Thr	Asn	Pro	Glu	Met	Ser	Trp	Ser	Glu	Gly	Met	His	Ile
1310						1315					1320			
Tyr	Asp	Gln	Gly	Phe	Asn	Ser	Gly	Thr	Leu	Lys	His	Trp	Thr	Ile
1325						1330					1335			
Ser	Gly	Asp	Ala	Ser	Lys	Ala	Glu	Ile	Val	Lys	Ser	Gln	Gly	Ala
1340						1345					1350			
Asn	Glu	Met	Leu	Arg	Ile	Gln	Gly	Asn	Lys	Ser	Lys	Val	Ser	Leu
1355						1360					1365			
Thr	Gln	Lys	Leu	Thr	Gly	Leu	Lys	Pro	Asn	Thr	Lys	Tyr	Ala	Val
1370						1375					1380			

Tyr Val Gly Val Asp Asn Arg Ser Asn Ala Lys Ala Ser Ile Thr
1385 1390 1395

Val Asn Thr Gly Glu Lys Glu Val Thr Thr Tyr Thr Asn Lys Ser
1400 1405 1410

Leu Ala Leu Asn Tyr Ile Lys Ala Tyr Ala His Asn Asn Arg Arg
1415 1420 1425

Glu Asn Ala Thr Val Asp Asp Thr Ser Tyr Phe Gln Asn Met Tyr
1430 1435 1440

Ala Phe Phe Thr Thr Gly Ser Asp Val Ser Asn Val Thr Leu Thr
1445 1450 1455

Leu Ser Arg Glu Ala Gly Asp Glu Ala Thr Tyr Phe Asp Glu Ile
1460 1465 1470

Arg Thr Phe Glu Asn Asn Ser Ser Met Tyr Gly Asp Lys His Asp
1475 1480 1485

Thr Gly Gln Gly Thr Phe Lys Gln Asp Phe Glu Asn Val Ala Gln
1490 1495 1500

Gly Ile Phe Pro Phe Val Val Gly Gly Val Glu Gly Val Glu Asp
1505 1510 1515

Asn Arg Thr His Leu Ser Glu Lys His Asp Pro Tyr Thr Gln Arg
1520 1525 1530

Gly Trp Asn Gly Lys Lys Val Asp Asp Val Ile Glu Gly Asn Trp
1535 1540 1545

Ser Leu Lys Thr Asn Gly Leu Val Ser Arg Arg Asn Leu Val Tyr
1550 1555 1560

Gln Thr Ile Pro Gln Asn Phe Arg Phe Glu Ala Gly Lys Thr Tyr

1565

1570

1575

Arg Val Thr Phe Glu Tyr Glu Ala Gly Ser Asp Asn Thr Tyr Ala
1580 1585 1590

Phe Val Val Gly Lys Gly Glu Phe Gln Ser Gly Arg Arg Gly Thr
1595 1600 1605

Gln Ala Ser Asn Leu Glu Met His Glu Leu Pro Asn Thr Trp Thr
1610 1615 1620

Asp Ser Lys Lys Ala Lys Lys Val Thr Phe Leu Val Thr Gly Ala
1625 1630 1635

Glu Thr Gly Asp Thr Trp Val Gly Ile Tyr Ser Thr Gly Asn Ala
1640 1645 1650

Ser Asn Thr Arg Gly Asp Ala Gly Gly Asn Ala Asn Phe Arg Gly
1655 1660 1665

Tyr Asn Asp Phe Met Met Asp Asn Leu Gln Ile Glu Glu Ile Thr
1670 1675 1680

Leu Thr Gly Lys Met Leu Thr Glu Asn Ala Leu Lys Asn Tyr Leu
1685 1690 1695

Pro Thr Val Ala Met Thr Asn Tyr Thr Lys Glu Ser Met Asp Ala
1700 1705 1710

Leu Lys Glu Ala Val Phe Asn Leu Ser Gln Ala Asp Asp Asp Ile
1715 1720 1725

Ser Val Glu Glu Ala Arg Ala Glu Ile Ala Lys Ile Glu Ala Leu
1730 1735 1740

Lys Asn Ala Leu Val Gln Lys Lys Thr Ala Leu Val Ala Glu Asp
1745 1750 1755

Phe	Glu	Ser	Leu	Asp	Ala	Pro	Ala	Gln	Pro	Gly	Glu	Gly	Leu	Glu
1760						1765					1770			
Asn	Ala	Phe	Asp	Gly	Asn	Val	Ser	Ser	Leu	Trp	His	Thr	Ser	Trp
1775						1780					1785			
Asn	Gly	Gly	Asp	Val	Gly	Lys	Pro	Ala	Thr	Met	Val	Leu	Lys	Glu
1790						1795					1800			
Pro	Thr	Glu	Ile	Thr	Gly	Leu	Arg	Tyr	Val	Pro	Arg	Ala	Ser	Asp
1805						1810					1815			
Ser	Asn	Gly	Asn	Leu	Arg	Asp	Val	Lys	Leu	Val	Val	Thr	Asp	Glu
1820						1825					1830			
Ser	Gly	Lys	Glu	His	Thr	Phe	Asn	Val	Thr	Asp	Trp	Pro	Asn	Asn
1835						1840					1845			
Asn	Lys	Pro	Lys	Asp	Ile	Asp	Phe	Gly	Lys	Thr	Ile	Lys	Ala	Lys
1850						1855					1860			
Lys	Ile	Val	Leu	Thr	Gly	Thr	Lys	Thr	Tyr	Gly	Asp	Gly	Gly	Asp
1865						1870					1875			
Lys	Tyr	Gln	Ser	Ala	Ala	Glu	Leu	Ile	Phe	Thr	Arg	Pro	Gln	Val
1880						1885					1890			
Ala	Glu	Thr	Pro	Leu	Asp	Leu	Ser	Gly	Tyr	Glu	Ala	Ala	Leu	Ala
1895						1900					1905			
Lys	Ala	Gln	Lys	Leu	Thr	Asp	Lys	Asp	Asn	Gln	Glu	Glu	Val	Ala
1910						1915					1920			
Ser	Val	Gln	Ala	Ser	Met	Lys	Tyr	Ala	Thr	Asp	Asn	His	Leu	Leu
1925						1930					1935			

Thr	Glu	Arg	Met	Val	Ala	Tyr	Phe	Ala	Asp	Tyr	Leu	Asn	Gln	Leu
1940						1945					1950			
Lys	Asp	Ser	Ala	Thr	Lys	Pro	Asp	Ala	Pro	Thr	Ser	Ser	Lys	Gly
1955						1960					1965			
Glu	Glu	Gln	Pro	Pro	Val	Leu	Asp	Val	Pro	Glu	Phe	Lys	Gly	Gly
1970						1975					1980			
Val	Asn	Ala	Thr	Glu	Ala	Ala	Val	His	Glu	Val	Pro	Glu	Phe	Lys
1985						1990					1995			
Gly	Gly	Val	Asn	Ala	Val	Gln	Ala	Leu	Val	His	Glu	Leu	Pro	Glu
2000						2005					2010			
Tyr	Lys	Gly	Gly	Ala	Asn	Ala	Val	Leu	Ala	Ala	Ala	Asn	Glu	Val
2015						2020					2025			
Pro	Glu	Tyr	Lys	Gly	Gly	Ala	Asn	Ala	Val	Glu	Ala	Leu	Val	Asn
2030						2035					2040			
Glu	Lys	Pro	Ala	Tyr	Thr	Gly	Val	Leu	Ala	Thr	Ala	Gly	Asp	Gln
2045						2050					2055			
Ala	Ala	Pro	Thr	Val	Glu	Lys	Pro	Glu	Tyr	Pro	Leu	Thr	Pro	Ser
2060						2065					2070			
Pro	Val	Ala	Asp	Thr	Lys	Thr	Pro	Gly	Ala	Lys	Asp	Glu	Glu	Lys
2075						2080					2085			
Leu	Pro	Ala	Thr	Gly	Glu	His	Ser	Ser	Glu	Val	Ala	Leu	Phe	Leu
2090						2095					2100			
Ala	Ser	Val	Ser	Ile	Ala	Leu	Ser	Ala	Ala	Val	Leu	Ala	Thr	Lys
2105						2110					2115			

Arg Lys Glu Glu Gly Ser Gly Leu Glu His His His His His His
 2120 2125 2130

<210> 16
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> E206A forward primer

<400> 16
 atggcgcacg cgctgggcca cg 22

<210> 17
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> E206A reverse primer

<400> 17
 gccaccgtac catttcgtc 19

<210> 18
 <211> 166
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> EPO

<400> 18

Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu
 1 5 10 15

Leu Glu Ala Lys Glu Ala Glu Asp Ile Thr Thr Gly Cys Ala Glu His
 20 25 30

Cys Ser Leu Asp Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asp Phe
 35 40 45

Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp
50 55 60

Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu
65 70 75 80

Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp
85 90 95

Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu
100 105 110

Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala
115 120 125

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

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

Cys Arg Thr Gly Asp Arg
165

<210> 19

<400> 19
000

<210> 20

<211> 361

<212> PRT

<213> Artificial Sequence

<220>

<223> Polypeptide capable of binding to O-glycans but lacks or has
reduced O-glycoprotein-specific endoprotease activity

<400> 20

Glu Val Thr Val Pro Asp Ala Leu Lys Asp Arg Ile Ala Leu Lys Lys
1 5 10 15

Thr Ala Arg Gln Leu Asn Ile Val Tyr Phe Leu Gly Ser Asp Thr Glu
20 25 30

Pro Val Pro Asp Tyr Glu Arg Arg Leu Ser Glu Leu Leu Tyr Leu
35 40 45

Gln Gln Phe Tyr Gly Lys Glu Met Gln Arg His Gly Tyr Gly Ala Arg
50 55 60

Ser Phe Gly Leu Asp Ile Lys Ser Pro Gly Arg Val Asn Ile Ile Glu
65 70 75 80

Tyr Lys Ala Lys Asn Pro Ala Ala His Tyr Pro Tyr Glu Asn Gly Gly
85 90 95

Gly Trp Lys Ala Ala Gln Glu Leu Asp Glu Phe Phe Lys Ala His Pro
100 105 110

Asp Arg Lys Lys Ser Gln His Thr Leu Ile Ile Met Pro Thr Trp Asn
115 120 125

Asp Glu Lys Asn Gly Pro Asp Asn Pro Gly Gly Val Pro Phe Tyr Gly
130 135 140

Met Gly Arg Asn Cys Phe Ala Leu Asp Tyr Pro Ala Phe Asp Ile Lys
145 150 155 160

His Leu Gly Gln Lys Thr Arg Glu Gly Arg Leu Leu Thr Lys Trp Tyr
165 170 175

Gly Gly Met Ala Ala Ala Leu Gly His Gly Leu Asn Leu Pro His Asn
180 185 190

His Gln Thr Ala Ser Asp Gly Lys Lys Tyr Gly Thr Ala Leu Met Gly

195

200

205

Ser Gly Asn Tyr Thr Phe Gly Thr Ser Pro Thr Phe Leu Thr Pro Ala
 210 215 220

Ser Cys Ala Leu Leu Asp Ala Cys Glu Val Phe Ser Val Thr Pro Ser
 225 230 235 240

Gln Gln Phe Tyr Glu Gly Lys Pro Glu Val Glu Val Gly Asp Val Ala
 245 250 255

Ile Ser Phe Lys Gly Asp Gln Ile Leu Val Ser Gly Asn Tyr Lys Ser
 260 265 270

Pro Gln Thr Val Lys Ala Leu Asn Val Tyr Ile Gln Asp Pro Pro Tyr
 275 280 285

Ala Val Asn Gln Asp Tyr Asp Ala Val Ser Phe Ser Arg Arg Leu Gly
 290 295 300

Lys Lys Ser Gly Lys Phe Ser Met Lys Ile Asp Lys Lys Glu Leu Glu
 305 310 315 320

Gly Leu Asn Asn Asn Glu Phe Arg Ile Ser Leu Met Phe Ile Leu Ala
 325 330 335

Asn Gly Leu His Met Gln Lys His Phe Thr Phe His Trp Asp Ala Leu
 340 345 350

Gln Asp Tyr Arg Asp Gly Ser Lys Ser
 355 360

<210> 21

<211> 371

<212> PRT

<213> Artificial Sequence

<220>

<223> LS HE206AA or LS H205A/E206A (including N-terminal methionine
and C-terminal linker)

<400> 21

Met Glu Val Thr Val Pro Asp Ala Leu Lys Asp Arg Ile Ala Leu Lys
1 5 10 15

Lys Thr Ala Arg Gln Leu Asn Ile Val Tyr Phe Leu Gly Ser Asp Thr
20 25 30

Glu Pro Val Pro Asp Tyr Glu Arg Arg Leu Ser Glu Leu Leu Leu Tyr
35 40 45

Leu Gln Gln Phe Tyr Gly Lys Glu Met Gln Arg His Gly Tyr Gly Ala
50 55 60

Arg Ser Phe Gly Leu Asp Ile Lys Ser Pro Gly Arg Val Asn Ile Ile
65 70 75 80

Glu Tyr Lys Ala Lys Asn Pro Ala Ala His Tyr Pro Tyr Glu Asn Gly
85 90 95

Gly Gly Trp Lys Ala Ala Gln Glu Leu Asp Glu Phe Phe Lys Ala His
100 105 110

Pro Asp Arg Lys Lys Ser Gln His Thr Leu Ile Ile Met Pro Thr Trp
115 120 125

Asn Asp Glu Lys Asn Gly Pro Asp Asn Pro Gly Gly Val Pro Phe Tyr
130 135 140

Gly Met Gly Arg Asn Cys Phe Ala Leu Asp Tyr Pro Ala Phe Asp Ile
145 150 155 160

Lys His Leu Gly Gln Lys Thr Arg Glu Gly Arg Leu Leu Thr Lys Trp
165 170 175

Tyr Gly Gly Met Ala Ala Ala Leu Gly His Gly Leu Asn Leu Pro His
180 185 190

Asn His Gln Thr Ala Ser Asp Gly Lys Lys Tyr Gly Thr Ala Leu Met
195 200 205

Gly Ser Gly Asn Tyr Thr Phe Gly Thr Ser Pro Thr Phe Leu Thr Pro
210 215 220

Ala Ser Cys Ala Leu Leu Asp Ala Cys Glu Val Phe Ser Val Thr Pro
225 230 235 240

Ser Gln Gln Phe Tyr Glu Gly Lys Pro Glu Val Glu Val Gly Asp Val
245 250 255

Ala Ile Ser Phe Lys Gly Asp Gln Ile Leu Val Ser Gly Asn Tyr Lys
260 265 270

Ser Pro Gln Thr Val Lys Ala Leu Asn Val Tyr Ile Gln Asp Pro Pro
275 280 285

Tyr Ala Val Asn Gln Asp Tyr Asp Ala Val Ser Phe Ser Arg Arg Leu
290 295 300

Gly Lys Lys Ser Gly Lys Phe Ser Met Lys Ile Asp Lys Lys Glu Leu
305 310 315 320

Glu Gly Leu Asn Asn Asn Glu Phe Arg Ile Ser Leu Met Phe Ile Leu
325 330 335

Ala Asn Gly Leu His Met Gln Lys His Phe Thr Phe His Trp Asp Ala
340 345 350

Leu Gln Asp Tyr Arg Asp Gly Ser Lys Ser Gly Ser Gly His His His
355 360 365

His His His

<210> 22
 <211> 1116
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleotide sequence encoding LS HE206AA or LS H205A/E206A

<400> 22
 atggaagtca ctgtgccgga cgccctgaaa gatcgcatcg cgctgaagaa aaccgctcgt 60
 cagctgaata tcgtctactt cctgggttct gataccgaac cggttccgga ctacgagcgc 120
 cgtctgagcg agctgctgtt gtatctgcag caattctatg gtaaagaaat gcagcgccat 180
 ggctatggcg cacgcagctt tggctcggac attaagtcac cgggtcgtgt gaacattatc 240
 gagtacaaag cgaagaaccc ggcagcgcat taccgctatg agaatgggtgg cggctggaaa 300
 gctgcacaag aactggacga atttttcaag gcccatccag accgcaagaa aagccagcac 360
 accctgatca tcatgcctac ctggaatgat gagaaaaatg gtcctgacaa tccgggtggc 420
 gttccgttct atggatatggg tcgtaattgt tttgcgttgg actacccggc gtttgatatac 480
 aagcacctgg gtcagaaaac gcgtgagggt cgtctgctga cgaaatggta cgggtggcatg 540
 gcggccgcgc tgggccacgg cctgaatctg ccgcacaatc accagaccgc gagcgaatggc 600
 aagaaatatg gcaccgccct gatgggtagc ggcaactaca cgttcggtagc cagccccgacg 660
 ttcctgaccc cggcgagctg tgcgctgctg gatgcctgcg aagtgttcag cgttacccccg 720
 agccaacagt tttatgaggg taagccagaa gtcgaggttg gtgatgttgc aatttccttc 780
 aagggtgatc aaatcttggg cagcggtaac tacaagagcc cgcaaaccgt gaaagctctg 840
 aacgtttaca ttcaggatcc gccgtacgcc gtgaaccaag actacgatgc agtgagcttt 900
 agccgtcgtc tgggcaaaaa gtccggtaag tttagcatga agattgacaa aaaagaactg 960
 gaaggcctga ataacaacga attccgtatt tccttgatgt tcattctggc aaacggctta 1020
 cacatgcaga agcactttac gtttcactgg gatgcgctgc aagactaccg tgacggtagc 1080
 aaatctgggtt cgggtcatca tcaccacat cactga 1116

<210> 23
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> disrupted metalloprotease motif

<400> 23

Gly Met Ala His Ala Leu Gly His Gly Leu
1 5 10

<210> 24
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> disrupted metalloprotease motif

<400> 24

Gly Met Ala Ala Glu Leu Gly His Gly Leu
1 5 10

<210> 25
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> disrupted metalloprotease motif

<400> 25

Gly Met Ala Ala Ala Leu Gly His Gly Leu
1 5 10

<210> 26
<211> 882
<212> PRT
<213> Pseudomonas aeruginosa

<400> 26

Ala Thr Gln Glu Glu Ile Leu Asp Ala Ala Leu Val Ser Gly Asp Ser
1 5 10 15

Ser Gln Leu Thr Asp Ser His Leu Val Ala Leu Arg Leu Gln Gln Gln
20 25 30

Val Glu Arg Ile Arg Gln Thr Arg Thr Gln Leu Leu Asp Gly Leu Tyr
35 40 45

Gln Asn Leu Ser Gln Ala Tyr Asp Pro Gly Ala Ala Ser Met Trp Val
50 55 60

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

Gly Arg Val Leu Ala Ser Leu Ser Leu Glu Ala Gly Gly Arg Gly Leu
85 90 95

Ala Tyr Gly Thr Asn Val Leu Thr Gln Leu Ser Gly Thr Asn Ala Ala
100 105 110

His Ala Pro Leu Leu Lys Arg Ala Val Gln Trp Leu Val Asn Gly Asp
115 120 125

Pro Gly Ala Ala Thr Ala Lys Asp Phe Lys Val Ser Val Val Gly Val
130 135 140

Asp Lys Thr Ala Ala Leu Asn Gly Leu Lys Ser Ala Gly Leu Gln Pro
145 150 155 160

Ala Asp Ala Ala Cys Asn Ala Leu Thr Asp Ala Ser Cys Ala Ser Thr
165 170 175

Ser Lys Leu Leu Val Leu Gly Asn Gly Ala Ser Ala Ala Ser Leu Ser
180 185 190

Ala Thr Val Arg Ala Arg Leu Gln Ala Gly Leu Pro Ile Leu Phe Val
195 200 205

His Thr Asn Gly Trp Asn Gln Ser Ser Thr Gly Gln Gln Ile Leu Ala
210 215 220

Gly Leu Gly Leu Gln Glu Gly Pro Tyr Gly Gly Asn Tyr Trp Asp Lys
225 230 235 240

Asp Arg Val Pro Ser Ser Arg Thr Arg Thr Arg Ser Val Glu Leu Gly
245 250 255

Gly Ala Tyr Gly Gln Asp Pro Ala Leu Val Gln Gln Ile Val Asp Gly
260 265 270

Ser Trp Arg Thr Asp Tyr Asp Trp Ser Lys Cys Thr Ser Tyr Val Gly
275 280 285

Arg Thr Thr Cys Asp Asp Val Pro Gly Leu Ser Asp Phe Ser Lys Arg
290 295 300

Val Asp Val Leu Lys Gly Ala Leu Asp Ala Tyr Asn Gln Lys Ala Gln
305 310 315 320

Asn Leu Phe Ala Leu Pro Gly Thr Thr Ser Leu Arg Leu Trp Leu Leu
325 330 335

Trp Ala Asp Ala Val Arg Gln Asn Ile Arg Tyr Pro Met Asp Lys Ala
340 345 350

Ala Asp Thr Ala Arg Phe Gln Glu Thr Phe Val Ala Asp Ala Ile Val
355 360 365

Gly Tyr Val Arg Glu Ala Gly Ala Ala Gln Lys Glu Leu Gly Ser Tyr
370 375 380

Ala Gly Gln Arg Gln Gln Ser Met Pro Val Ser Gly Ser Glu Glu Thr
 385 390 395 400

Leu Thr Leu Thr Leu Pro Ser Ala Gln Gly Phe Thr Ala Ile Gly Arg
 405 410 415

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

Gln Ala Ser Leu Ala Val Gly Leu Asn Thr Gln Arg Ile Gly Ser Thr
 435 440 445

Arg Leu Trp Asn Thr Arg Gln Tyr Asp Arg Pro Arg Phe Leu Lys Ser
 450 455 460

Pro Asp Ile Lys Leu Gln Ala Asn Gln Ser Val Ala Leu Val Ser Pro
 465 470 475 480

Tyr Gly Gly Leu Leu Gln Leu Val Tyr Ser Gly Ala Thr Pro Gly Gln
 485 490 495

Thr Val Thr Val Lys Val Thr Gly Ala Ala Ser Gln Pro Phe Leu Asp
 500 505 510

Ile Gln Pro Gly Glu Asp Ser Ser Gln Ala Ile Ala Asp Phe Ile Gln
 515 520 525

Ala Leu Asp Ala Asp Lys Ala Asp Trp Leu Glu Ile Arg Ser Gly Ser
 530 535 540

Val Glu Val His Ala Lys Val Glu Lys Val Arg Gly Ser Ile Asp Lys
 545 550 555 560

Asp Tyr Gly Gly Asp Val Gln Arg Phe Ile Arg Glu Leu Asn Glu Val
 565 570 575

Phe Ile Asp Asp Ala Tyr Thr Leu Ala Gly Phe Ala Ile Pro Asn Gln

580

585

590

Ala Lys Thr Pro Ala Ile Gln Gln Glu Cys Ala Ala Arg Gly Trp Asp
 595 600 605

Cys Asp Ser Glu Thr Leu His Lys Leu Pro Gly Thr Gln His Ile Asn
 610 615 620

Val Asp Gln Tyr Ala Gln Cys Gly Gly Gly Cys Ser Gly Asn Pro Tyr
 625 630 635 640

Asp Gln Thr Trp Gly Leu Asn Pro Arg Gly Trp Gly Glu Ser His Glu
 645 650 655

Leu Gly His Asn Leu Gln Val Asn Arg Leu Lys Val Tyr Gly Gly Arg
 660 665 670

Ser Gly Glu Ile Ser Asn Gln Ile Phe Pro Leu His Lys Asp Trp Arg
 675 680 685

Val Leu Arg Glu Phe Gly Gln Asn Leu Asp Asp Thr Arg Val Asn Tyr
 690 695 700

Arg Asn Ala Tyr Asn Leu Ile Val Ala Gly Arg Ala Glu Ala Asp Pro
 705 710 715 720

Leu Ala Gly Val Tyr Lys Arg Leu Trp Glu Asp Pro Gly Thr Tyr Ala
 725 730 735

Leu Asn Gly Glu Arg Met Ala Phe Tyr Thr Gln Trp Val His Tyr Trp
 740 745 750

Ala Asp Leu Lys Asn Asp Pro Leu Gln Gly Trp Asp Ile Trp Thr Leu
 755 760 765

Leu Tyr Leu His Gln Arg Gln Val Asp Lys Ser Asp Trp Asp Ala Asn
 770 775 780

Lys Ala Ala Leu Gly Tyr Gly Thr Tyr Ala Gln Arg Pro Gly Asn Ser
785 790 795 800

Gly Asp Ala Ser Ser Thr Asp Gly Asn Asp Asn Leu Leu Leu Gly Leu
805 810 815

Ser Trp Leu Thr Gln Arg Asp Gln Arg Pro Thr Phe Ala Leu Trp Gly
820 825 830

Ile Arg Thr Ser Ala Ala Ala Gln Ala Gln Val Ala Ala Tyr Gly Phe
835 840 845

Ala Glu Gln Pro Ala Phe Phe Tyr Ala Asn Asn Arg Thr Asn Glu Tyr
850 855 860

Ser Thr Val Lys Leu Leu Asp Met Ser Gln Gly Ser Pro Ala Trp Pro
865 870 875 880

Phe Pro

<210> 27
<211> 536
<212> PRT
<213> Bacteroides thetaiotaomicron

<400> 27

Asp Lys Trp Glu Lys Glu Phe Arg Ile Arg Ser Tyr Glu Pro Tyr Ser
1 5 10 15

Asn Ile Ala Glu Trp Ala Asp Lys Leu Met Thr Lys Lys Tyr Ser Asp
20 25 30

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

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

Trp Glu Thr Gly Thr Glu Tyr Lys Gln Thr Ala Ser Ser Gly Asp Val
65 70 75 80

Tyr Met Leu Asn Pro Gly Val Asn Lys Leu Thr Met Lys Gly Glu Gly
85 90 95

Gln Leu Phe Val Met Tyr Asn Thr Glu Leu Thr Ser Asn Thr Ala Lys
100 105 110

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

Phe Asp Leu Lys Glu His Lys Thr Asp Glu Lys Tyr Ala Glu Leu Leu
130 135 140

Lys Lys Ser Thr His Lys Tyr Phe Cys Ile Arg Gly Glu Lys Ile Met
145 150 155 160

Phe Tyr Phe His Arg Asn Lys Leu Leu Glu Tyr Val Pro Asn Asn Ile
165 170 175

Leu Ser Ala Ile His Leu Trp Asp Asn Ile Val Gly Trp Gln Gln Glu
180 185 190

Leu Met Gly Ile Asp Asp Val Arg Pro Ser Gln Val Asn Asn His Leu
195 200 205

Phe Ala Ile Ser Pro Glu Gly Ser Tyr Met Trp Ala Ser Asp Tyr Gln
210 215 220

Ile Gly Phe Val Tyr Thr Tyr Leu Gly Asn Ile Leu Leu Glu Asp Asn
225 230 235 240

Val Met Ala Ala Glu Asp Asn Ala Trp Gly Pro Ala His Glu Ile Gly

245

250

255

His Val His Gln Ala Ala Ile Asn Trp Ala Ser Ser Thr Glu Ser Ser
260 265 270

Asn Asn Leu Phe Ser Asn Phe Ile Ile Tyr Lys Leu Gly Lys Tyr Lys
275 280 285

Ser Arg Gly Asn Gly Leu Gly Ser Val Ala Thr Ala Arg Tyr Ala Asn
290 295 300

Gly Gln Ala Trp Tyr Asn Met Gly Asp Ala Thr His Gln Asn Glu Asp
305 310 315 320

Thr Glu Thr His Met Arg Met Asn Trp Gln Leu Trp Ile Tyr Tyr His
325 330 335

Arg Cys Glu Tyr Lys Thr Asp Phe Trp Gln Thr Leu Phe Lys Leu Met
340 345 350

Arg Glu Val Asn Met Thr Glu Gly Glu Asp Pro Gly Lys Lys Gln Leu
355 360 365

Glu Phe Ala Lys Met Ala Ser Lys Ala Ala Asn Gln Asn Leu Thr Asp
370 375 380

Phe Phe Glu Met Trp Gly Phe Phe Glu Pro Val Asn Thr Thr Ile Glu
385 390 395 400

Gln Tyr Gly Thr Tyr Lys Tyr Tyr Val Ser Asp Ala Met Ile Arg Glu
405 410 415

Ala Lys Glu Tyr Met Ala Gln Phe Pro Ala Pro Lys His Ala Phe Gln
420 425 430

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

Tyr Ser Ala Val Gly Asp Val Gly Tyr Tyr Thr Gln Phe Lys Glu Asn
 450 455 460

Gln Lys Ile Thr Lys Ala Ile Thr Ala Glu Leu Ala Gly Arg Lys Val
 465 470 475 480

Ser Ile Gln Asn Gly Asp Glu Ala Val Ala Phe Glu Leu Arg Glu Asn
 485 490 495

Asp Glu Asn Gly Lys Leu Leu Tyr Phe Ser Thr Phe Thr Thr Phe Glu
 500 505 510

Ile Pro Ser Ser Ile Leu Met Val Asn Ala Lys Leu Tyr Ala Val Gln
 515 520 525

Ala Asp Gly Lys Arg Ile Leu Leu
 530 535

<210> 28
 <211> 507
 <212> PRT
 <213> Clostridium perfringens

<400> 28

Val Leu Glu Leu Glu Met Arg Gly Asp Ser Ile Ser Glu Ala Lys Lys
 1 5 10 15

Arg Lys Val Trp Asn Phe Gln Asp Trp Gln Ile Thr Gly Leu Ser Ala
 20 25 30

Arg Ala Gly Asp Lys Ile Thr Val Tyr Val Asp Val Ala Glu Gly Asp
 35 40 45

Pro Thr Pro Thr Leu Leu Tyr Lys Gln Ser Leu Thr Gln His Gly Gly
 50 55 60

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

Glu Ile Asn Tyr Glu Ser Asn Gly Ile Pro Lys Asp Val Ile Gln Gly
85 90 95

Gly Asp Leu Phe Phe Thr Asn Tyr Lys Ser Asp Ser Gln Lys Arg Ala
100 105 110

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

Gly Lys Ser Asp Glu Asn Glu Val Met Lys Glu Leu Glu Ala Tyr Val
130 135 140

Glu Lys Ile Lys Ala Glu Pro Lys Thr Thr Pro Asn Ile Phe Ala Val
145 150 155 160

Ser Ser Asn Lys Ser Leu Glu Phe Val Gln Ala Thr Tyr Ala Leu Asp
165 170 175

Trp Tyr Lys Lys Asn Asn Lys Thr Pro Lys Tyr Thr Ala Glu Gln Trp
180 185 190

Asp Gln Tyr Ile Ala Asp Ala Met Gly Phe Trp Gly Phe Asp Asn Ser
195 200 205

Lys Asp Val Asn Ser Asp Phe Asn Phe Arg Ile Met Pro Met Val Lys
210 215 220

Asn Leu Ser Gly Gly Ala Phe Met Asn Ala Gly Asn Gly Val Ile Gly
225 230 235 240

Ile Arg Pro Gly Asn Gln Asp Ala Ile Leu Ala Ala Asn Lys Gly Trp
245 250 255

Gly Val Ala His Glu Leu Gly His Asn Phe Asp Thr Gly Gly Arg Thr

260

265

270

Ile Val Glu Val Thr Asn Asn Met Met Pro Leu Phe Phe Glu Ser Lys
 275 280 285

Tyr Lys Thr Lys Thr Arg Ile Thr Asp Gln Asn Ile Trp Glu Asn Asn
 290 295 300

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

Asn Lys Ala Asp Ser Thr His Leu Ala Gln Leu Ala Pro Leu Trp Gln
 325 330 335

Leu Tyr Leu Tyr Asp Asn Thr Phe Tyr Gly Lys Phe Glu Arg Gln Phe
 340 345 350

Arg Glu Arg Asp Phe Gly Asn Lys Asn Arg Glu Asp Ile Tyr Lys Ser
 355 360 365

Trp Val Val Ala Ala Ser Asp Ala Met Glu Leu Asp Leu Thr Glu Phe
 370 375 380

Phe Ala Arg His Gly Ile Arg Val Asp Asp Lys Val Lys Glu Asp Leu
 385 390 395 400

Ala Lys Tyr Pro Lys Pro Asp Lys Lys Ile Tyr Tyr Leu Asn Asp Leu
 405 410 415

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

Val Ser Thr Ser Gly Ser Asn Gly Asn Ile Lys Leu Ser Phe Ser Val
 435 440 445

Asp Asp Glu Asn Lys Asp Asn Ile Leu Gly Tyr Glu Ile Arg Arg Asp
 450 455 460

Gly Lys Tyr Val Gly Phe Thr Ser Asn Asp Ser Phe Val Asp Thr Lys
 465 470 475 480

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

Lys Leu Asn Thr Leu Asn Pro Ile Glu Val Asn
 500 505

<210> 29

<211> 892

<212> PRT

<213> Artificial Sequence

<220>

<223> polypeptide having O-glycoprotein-specific endoprotease activity
 (including N-terminal methionine and a C-terminal linker + His6
 tag)

<400> 29

Met Ala Thr Gln Glu Glu Ile Leu Asp Ala Ala Leu Val Ser Gly Asp
 1 5 10 15

Ser Ser Gln Leu Thr Asp Ser His Leu Val Ala Leu Arg Leu Gln Gln
 20 25 30

Gln Val Glu Arg Ile Arg Gln Thr Arg Thr Gln Leu Leu Asp Gly Leu
 35 40 45

Tyr Gln Asn Leu Ser Gln Ala Tyr Asp Pro Gly Ala Ala Ser Met Trp
 50 55 60

Val Leu Pro Ala Asn Pro Asp Asn Thr Leu Pro Phe Leu Ile Gly Asp
 65 70 75 80

Lys Gly Arg Val Leu Ala Ser Leu Ser Leu Glu Ala Gly Gly Arg Gly
 85 90 95

Leu Ala Tyr Gly Thr Asn Val Leu Thr Gln Leu Ser Gly Thr Asn Ala
100 105 110

Ala His Ala Pro Leu Leu Lys Arg Ala Val Gln Trp Leu Val Asn Gly
115 120 125

Asp Pro Gly Ala Ala Thr Ala Lys Asp Phe Lys Val Ser Val Val Gly
130 135 140

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

Pro Ala Asp Ala Ala Cys Asn Ala Leu Thr Asp Ala Ser Cys Ala Ser
165 170 175

Thr Ser Lys Leu Leu Val Leu Gly Asn Gly Ala Ser Ala Ala Ser Leu
180 185 190

Ser Ala Thr Val Arg Ala Arg Leu Gln Ala Gly Leu Pro Ile Leu Phe
195 200 205

Val His Thr Asn Gly Trp Asn Gln Ser Ser Thr Gly Gln Gln Ile Leu
210 215 220

Ala Gly Leu Gly Leu Gln Glu Gly Pro Tyr Gly Gly Asn Tyr Trp Asp
225 230 235 240

Lys Asp Arg Val Pro Ser Ser Arg Thr Arg Thr Arg Ser Val Glu Leu
245 250 255

Gly Gly Ala Tyr Gly Gln Asp Pro Ala Leu Val Gln Gln Ile Val Asp
260 265 270

Gly Ser Trp Arg Thr Asp Tyr Asp Trp Ser Lys Cys Thr Ser Tyr Val
275 280 285

Gly Arg Thr Thr Cys Asp Asp Val Pro Gly Leu Ser Asp Phe Ser Lys
290 295 300

Arg Val Asp Val Leu Lys Gly Ala Leu Asp Ala Tyr Asn Gln Lys Ala
305 310 315 320

Gln Asn Leu Phe Ala Leu Pro Gly Thr Thr Ser Leu Arg Leu Trp Leu
325 330 335

Leu Trp Ala Asp Ala Val Arg Gln Asn Ile Arg Tyr Pro Met Asp Lys
340 345 350

Ala Ala Asp Thr Ala Arg Phe Gln Glu Thr Phe Val Ala Asp Ala Ile
355 360 365

Val Gly Tyr Val Arg Glu Ala Gly Ala Ala Gln Lys Glu Leu Gly Ser
370 375 380

Tyr Ala Gly Gln Arg Gln Gln Ser Met Pro Val Ser Gly Ser Glu Glu
385 390 395 400

Thr Leu Thr Leu Thr Leu Pro Ser Ala Gln Gly Phe Thr Ala Ile Gly
405 410 415

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

Gly Gln Ala Ser Leu Ala Val Gly Leu Asn Thr Gln Arg Ile Gly Ser
435 440 445

Thr Arg Leu Trp Asn Thr Arg Gln Tyr Asp Arg Pro Arg Phe Leu Lys
450 455 460

Ser Pro Asp Ile Lys Leu Gln Ala Asn Gln Ser Val Ala Leu Val Ser
465 470 475 480

Pro Tyr Gly Gly Leu Leu Gln Leu Val Tyr Ser Gly Ala Thr Pro Gly

485

490

495

Gln Thr Val Thr Val Lys Val Thr Gly Ala Ala Ser Gln Pro Phe Leu
 500 505 510

Asp Ile Gln Pro Gly Glu Asp Ser Ser Gln Ala Ile Ala Asp Phe Ile
 515 520 525

Gln Ala Leu Asp Ala Asp Lys Ala Asp Trp Leu Glu Ile Arg Ser Gly
 530 535 540

Ser Val Glu Val His Ala Lys Val Glu Lys Val Arg Gly Ser Ile Asp
 545 550 555 560

Lys Asp Tyr Gly Gly Asp Val Gln Arg Phe Ile Arg Glu Leu Asn Glu
 565 570 575

Val Phe Ile Asp Asp Ala Tyr Thr Leu Ala Gly Phe Ala Ile Pro Asn
 580 585 590

Gln Ala Lys Thr Pro Ala Ile Gln Gln Glu Cys Ala Ala Arg Gly Trp
 595 600 605

Asp Cys Asp Ser Glu Thr Leu His Lys Leu Pro Gly Thr Gln His Ile
 610 615 620

Asn Val Asp Gln Tyr Ala Gln Cys Gly Gly Gly Cys Ser Gly Asn Pro
 625 630 635 640

Tyr Asp Gln Thr Trp Gly Leu Asn Pro Arg Gly Trp Gly Glu Ser His
 645 650 655

Glu Leu Gly His Asn Leu Gln Val Asn Arg Leu Lys Val Tyr Gly Gly
 660 665 670

Arg Ser Gly Glu Ile Ser Asn Gln Ile Phe Pro Leu His Lys Asp Trp
 675 680 685

Arg Val Leu Arg Glu Phe Gly Gln Asn Leu Asp Asp Thr Arg Val Asn
690 695 700

Tyr Arg Asn Ala Tyr Asn Leu Ile Val Ala Gly Arg Ala Glu Ala Asp
705 710 715 720

Pro Leu Ala Gly Val Tyr Lys Arg Leu Trp Glu Asp Pro Gly Thr Tyr
725 730 735

Ala Leu Asn Gly Glu Arg Met Ala Phe Tyr Thr Gln Trp Val His Tyr
740 745 750

Trp Ala Asp Leu Lys Asn Asp Pro Leu Gln Gly Trp Asp Ile Trp Thr
755 760 765

Leu Leu Tyr Leu His Gln Arg Gln Val Asp Lys Ser Asp Trp Asp Ala
770 775 780

Asn Lys Ala Ala Leu Gly Tyr Gly Thr Tyr Ala Gln Arg Pro Gly Asn
785 790 795 800

Ser Gly Asp Ala Ser Ser Thr Asp Gly Asn Asp Asn Leu Leu Leu Gly
805 810 815

Leu Ser Trp Leu Thr Gln Arg Asp Gln Arg Pro Thr Phe Ala Leu Trp
820 825 830

Gly Ile Arg Thr Ser Ala Ala Ala Gln Ala Gln Val Ala Ala Tyr Gly
835 840 845

Phe Ala Glu Gln Pro Ala Phe Phe Tyr Ala Asn Asn Arg Thr Asn Glu
850 855 860

Tyr Ser Thr Val Lys Leu Leu Asp Met Ser Gln Gly Ser Pro Ala Trp
865 870 875 880

Pro Phe Pro Gly Ser Gly His His His His His His
885 890

<210> 30
<211> 546
<212> PRT
<213> Artificial Sequence

<220>
<223> polypeptide having O-glycoprotein-specific endoprotease activity
(including N-terminal methionine and a C-terminal linker + His6
tag)

<400> 30

Met Asp Lys Trp Glu Lys Glu Phe Arg Ile Arg Ser Tyr Glu Pro Tyr
1 5 10 15

Ser Asn Ile Ala Glu Trp Ala Asp Lys Leu Met Thr Lys Lys Tyr Ser
20 25 30

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

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

Ile Trp Glu Thr Gly Thr Glu Tyr Lys Gln Thr Ala Ser Ser Gly Asp
65 70 75 80

Val Tyr Met Leu Asn Pro Gly Val Asn Lys Leu Thr Met Lys Gly Glu
85 90 95

Gly Gln Leu Phe Val Met Tyr Asn Thr Glu Leu Thr Ser Asn Thr Ala
100 105 110

Lys Pro Ile Lys Ile His Ile Pro Leu Gly Ser Gly Thr Val Asn Gly
115 120 125

Phe Phe Asp Leu Lys Glu His Lys Thr Asp Glu Lys Tyr Ala Glu Leu
130 135 140

Leu Lys Lys Ser Thr His Lys Tyr Phe Cys Ile Arg Gly Glu Lys Ile
145 150 155 160

Met Phe Tyr Phe His Arg Asn Lys Leu Leu Glu Tyr Val Pro Asn Asn
165 170 175

Ile Leu Ser Ala Ile His Leu Trp Asp Asn Ile Val Gly Trp Gln Gln
180 185 190

Glu Leu Met Gly Ile Asp Asp Val Arg Pro Ser Gln Val Asn Asn His
195 200 205

Leu Phe Ala Ile Ser Pro Glu Gly Ser Tyr Met Trp Ala Ser Asp Tyr
210 215 220

Gln Ile Gly Phe Val Tyr Thr Tyr Leu Gly Asn Ile Leu Leu Glu Asp
225 230 235 240

Asn Val Met Ala Ala Glu Asp Asn Ala Trp Gly Pro Ala His Glu Ile
245 250 255

Gly His Val His Gln Ala Ala Ile Asn Trp Ala Ser Ser Thr Glu Ser
260 265 270

Ser Asn Asn Leu Phe Ser Asn Phe Ile Ile Tyr Lys Leu Gly Lys Tyr
275 280 285

Lys Ser Arg Gly Asn Gly Leu Gly Ser Val Ala Thr Ala Arg Tyr Ala
290 295 300

Asn Gly Gln Ala Trp Tyr Asn Met Gly Asp Ala Thr His Gln Asn Glu
305 310 315 320

Asp Thr Glu Thr His Met Arg Met Asn Trp Gln Leu Trp Ile Tyr Tyr

325

330

335

His Arg Cys Glu Tyr Lys Thr Asp Phe Trp Gln Thr Leu Phe Lys Leu
 340 345 350

Met Arg Glu Val Asn Met Thr Glu Gly Glu Asp Pro Gly Lys Lys Gln
 355 360 365

Leu Glu Phe Ala Lys Met Ala Ser Lys Ala Ala Asn Gln Asn Leu Thr
 370 375 380

Asp Phe Phe Glu Met Trp Gly Phe Phe Glu Pro Val Asn Thr Thr Ile
 385 390 395 400

Glu Gln Tyr Gly Thr Tyr Lys Tyr Tyr Val Ser Asp Ala Met Ile Arg
 405 410 415

Glu Ala Lys Glu Tyr Met Ala Gln Phe Pro Ala Pro Lys His Ala Phe
 420 425 430

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

Arg Tyr Ser Ala Val Gly Asp Val Gly Tyr Tyr Thr Gln Phe Lys Glu
 450 455 460

Asn Gln Lys Ile Thr Lys Ala Ile Thr Ala Glu Leu Ala Gly Arg Lys
 465 470 475 480

Val Ser Ile Gln Asn Gly Asp Glu Ala Val Ala Phe Glu Leu Arg Glu
 485 490 495

Asn Asp Glu Asn Gly Lys Leu Leu Tyr Phe Ser Thr Phe Thr Thr Phe
 500 505 510

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

Gln Ala Asp Gly Lys Arg Ile Leu Leu Gly Ser Gly His His His His
530 535 540

His His
545

<210> 31
<211> 517
<212> PRT
<213> Artificial Sequence

<220>
<223> polypeptide having O-glycoprotein-specific endoprotease activity
(including N-terminal methionine and a C-terminal linker + His6
tag)

<400> 31

Met Val Leu Glu Leu Glu Met Arg Gly Asp Ser Ile Ser Glu Ala Lys
1 5 10 15

Lys Arg Lys Val Trp Asn Phe Gln Asp Trp Gln Ile Thr Gly Leu Ser
20 25 30

Ala Arg Ala Gly Asp Lys Ile Thr Val Tyr Val Asp Val Ala Glu Gly
35 40 45

Asp Pro Thr Pro Thr Leu Leu Tyr Lys Gln Ser Leu Thr Gln His Gly
50 55 60

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

Pro Glu Ile Asn Tyr Glu Ser Asn Gly Ile Pro Lys Asp Val Ile Gln
85 90 95

Gly Gly Asp Leu Phe Phe Thr Asn Tyr Lys Ser Asp Ser Gln Lys Arg
100 105 110

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

Leu Gly Lys Ser Asp Glu Asn Glu Val Met Lys Glu Leu Glu Ala Tyr
130 135 140

Val Glu Lys Ile Lys Ala Glu Pro Lys Thr Thr Pro Asn Ile Phe Ala
145 150 155 160

Val Ser Ser Asn Lys Ser Leu Glu Phe Val Gln Ala Thr Tyr Ala Leu
165 170 175

Asp Trp Tyr Lys Lys Asn Asn Lys Thr Pro Lys Tyr Thr Ala Glu Gln
180 185 190

Trp Asp Gln Tyr Ile Ala Asp Ala Met Gly Phe Trp Gly Phe Asp Asn
195 200 205

Ser Lys Asp Val Asn Ser Asp Phe Asn Phe Arg Ile Met Pro Met Val
210 215 220

Lys Asn Leu Ser Gly Gly Ala Phe Met Asn Ala Gly Asn Gly Val Ile
225 230 235 240

Gly Ile Arg Pro Gly Asn Gln Asp Ala Ile Leu Ala Ala Asn Lys Gly
245 250 255

Trp Gly Val Ala His Glu Leu Gly His Asn Phe Asp Thr Gly Gly Arg
260 265 270

Thr Ile Val Glu Val Thr Asn Asn Met Met Pro Leu Phe Phe Glu Ser
275 280 285

Lys Tyr Lys Thr Lys Thr Arg Ile Thr Asp Gln Asn Ile Trp Glu Asn
290 295 300

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

Tyr Asn Lys Ala Asp Ser Thr His Leu Ala Gln Leu Ala Pro Leu Trp
325 330 335

Gln Leu Tyr Leu Tyr Asp Asn Thr Phe Tyr Gly Lys Phe Glu Arg Gln
340 345 350

Phe Arg Glu Arg Asp Phe Gly Asn Lys Asn Arg Glu Asp Ile Tyr Lys
355 360 365

Ser Trp Val Val Ala Ala Ser Asp Ala Met Glu Leu Asp Leu Thr Glu
370 375 380

Phe Phe Ala Arg His Gly Ile Arg Val Asp Asp Lys Val Lys Glu Asp
385 390 395 400

Leu Ala Lys Tyr Pro Lys Pro Asp Lys Lys Ile Tyr Tyr Leu Asn Asp
405 410 415

Leu Ala Met Asn Tyr Lys Gly Asp Gly Phe Thr Glu Asn Ala Lys Val
420 425 430

Ser Val Ser Thr Ser Gly Ser Asn Gly Asn Ile Lys Leu Ser Phe Ser
435 440 445

Val Asp Asp Glu Asn Lys Asp Asn Ile Leu Gly Tyr Glu Ile Arg Arg
450 455 460

Asp Gly Lys Tyr Val Gly Phe Thr Ser Asn Asp Ser Phe Val Asp Thr
465 470 475 480

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

Arg Lys Leu Asn Thr Leu Asn Pro Ile Glu Val Asn Gly Ser Gly His

500

505

510

His His His His His
515

<210> 32
<211> 923
<212> PRT
<213> *Pseudomonas aeruginosa*

<400> 32

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

Ser Arg Ser Pro Ile Pro Arg His Arg Ala Leu Leu Ala Gly Phe Cys
20 25 30

Leu Ala Gly Ala Leu Ser Ala Gln Ala Ala Thr Gln Glu Glu Ile Leu
35 40 45

Asp Ala Ala Leu Val Ser Gly Asp Ser Ser Gln Leu Thr Asp Ser His
50 55 60

Leu Val Ala Leu Arg Leu Gln Gln Gln Val Glu Arg Ile Arg Gln Thr
65 70 75 80

Arg Thr Gln Leu Leu Asp Gly Leu Tyr Gln Asn Leu Ser Gln Ala Tyr
85 90 95

Asp Pro Gly Ala Ala Ser Met Trp Val Leu Pro Ala Asn Pro Asp Asn
100 105 110

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

Ser Leu Glu Ala Gly Gly Arg Gly Leu Ala Tyr Gly Thr Asn Val Leu
130 135 140

Thr Gln Leu Ser Gly Thr Asn Ala Ala His Ala Pro Leu Leu Lys Arg
 145 150 155 160

Ala Val Gln Trp Leu Val Asn Gly Asp Pro Gly Ala Ala Thr Ala Lys
 165 170 175

Asp Phe Lys Val Ser Val Val Gly Val Asp Lys Thr Ala Ala Leu Asn
 180 185 190

Gly Leu Lys Ser Ala Gly Leu Gln Pro Ala Asp Ala Ala Cys Asn Ala
 195 200 205

Leu Thr Asp Ala Ser Cys Ala Ser Thr Ser Lys Leu Leu Val Leu Gly
 210 215 220

Asn Gly Ala Ser Ala Ala Ser Leu Ser Ala Thr Val Arg Ala Arg Leu
 225 230 235 240

Gln Ala Gly Leu Pro Ile Leu Phe Val His Thr Asn Gly Trp Asn Gln
 245 250 255

Ser Ser Thr Gly Gln Gln Ile Leu Ala Gly Leu Gly Leu Gln Glu Gly
 260 265 270

Pro Tyr Gly Gly Asn Tyr Trp Asp Lys Asp Arg Val Pro Ser Ser Arg
 275 280 285

Thr Arg Thr Arg Ser Val Glu Leu Gly Gly Ala Tyr Gly Gln Asp Pro
 290 295 300

Ala Leu Val Gln Gln Ile Val Asp Gly Ser Trp Arg Thr Asp Tyr Asp
 305 310 315 320

Trp Ser Lys Cys Thr Ser Tyr Val Gly Arg Thr Thr Cys Asp Asp Val
 325 330 335

Pro Gly Leu Ser Asp Phe Ser Lys Arg Val Asp Val Leu Lys Gly Ala
340 345 350

Leu Asp Ala Tyr Asn Gln Lys Ala Gln Asn Leu Phe Ala Leu Pro Gly
355 360 365

Thr Thr Ser Leu Arg Leu Trp Leu Leu Trp Ala Asp Ala Val Arg Gln
370 375 380

Asn Ile Arg Tyr Pro Met Asp Lys Ala Ala Asp Thr Ala Arg Phe Gln
385 390 395 400

Glu Thr Phe Val Ala Asp Ala Ile Val Gly Tyr Val Arg Glu Ala Gly
405 410 415

Ala Ala Gln Lys Glu Leu Gly Ser Tyr Ala Gly Gln Arg Gln Gln Ser
420 425 430

Met Pro Val Ser Gly Ser Glu Glu Thr Leu Thr Leu Thr Leu Pro Ser
435 440 445

Ala Gln Gly Phe Thr Ala Ile Gly Arg Met Ala Ala Pro Gly Lys Arg
450 455 460

Leu Ser Ile Arg Ile Glu Asp Ala Gly Gln Ala Ser Leu Ala Val Gly
465 470 475 480

Leu Asn Thr Gln Arg Ile Gly Ser Thr Arg Leu Trp Asn Thr Arg Gln
485 490 495

Tyr Asp Arg Pro Arg Phe Leu Lys Ser Pro Asp Ile Lys Leu Gln Ala
500 505 510

Asn Gln Ser Val Ala Leu Val Ser Pro Tyr Gly Gly Leu Leu Gln Leu
515 520 525

Val Tyr Ser Gly Ala Thr Pro Gly Gln Thr Val Thr Val Lys Val Thr

530

535

540

Gly Ala Ala Ser Gln Pro Phe Leu Asp Ile Gln Pro Gly Glu Asp Ser
 545 550 555 560

Ser Gln Ala Ile Ala Asp Phe Ile Gln Ala Leu Asp Ala Asp Lys Ala
 565 570 575

Asp Trp Leu Glu Ile Arg Ser Gly Ser Val Glu Val His Ala Lys Val
 580 585 590

Glu Lys Val Arg Gly Ser Ile Asp Lys Asp Tyr Gly Gly Asp Val Gln
 595 600 605

Arg Phe Ile Arg Glu Leu Asn Glu Val Phe Ile Asp Asp Ala Tyr Thr
 610 615 620

Leu Ala Gly Phe Ala Ile Pro Asn Gln Ala Lys Thr Pro Ala Ile Gln
 625 630 635 640

Gln Glu Cys Ala Ala Arg Gly Trp Asp Cys Asp Ser Glu Thr Leu His
 645 650 655

Lys Leu Pro Gly Thr Gln His Ile Asn Val Asp Gln Tyr Ala Gln Cys
 660 665 670

Gly Gly Gly Cys Ser Gly Asn Pro Tyr Asp Gln Thr Trp Gly Leu Asn
 675 680 685

Pro Arg Gly Trp Gly Glu Ser His Glu Leu Gly His Asn Leu Gln Val
 690 695 700

Asn Arg Leu Lys Val Tyr Gly Gly Arg Ser Gly Glu Ile Ser Asn Gln
 705 710 715 720

Ile Phe Pro Leu His Lys Asp Trp Arg Val Leu Arg Glu Phe Gly Gln
 725 730 735

Asn Leu Asp Asp Thr Arg Val Asn Tyr Arg Asn Ala Tyr Asn Leu Ile
740 745 750

Val Ala Gly Arg Ala Glu Ala Asp Pro Leu Ala Gly Val Tyr Lys Arg
755 760 765

Leu Trp Glu Asp Pro Gly Thr Tyr Ala Leu Asn Gly Glu Arg Met Ala
770 775 780

Phe Tyr Thr Gln Trp Val His Tyr Trp Ala Asp Leu Lys Asn Asp Pro
785 790 795 800

Leu Gln Gly Trp Asp Ile Trp Thr Leu Leu Tyr Leu His Gln Arg Gln
805 810 815

Val Asp Lys Ser Asp Trp Asp Ala Asn Lys Ala Ala Leu Gly Tyr Gly
820 825 830

Thr Tyr Ala Gln Arg Pro Gly Asn Ser Gly Asp Ala Ser Ser Thr Asp
835 840 845

Gly Asn Asp Asn Leu Leu Leu Gly Leu Ser Trp Leu Thr Gln Arg Asp
850 855 860

Gln Arg Pro Thr Phe Ala Leu Trp Gly Ile Arg Thr Ser Ala Ala Ala
865 870 875 880

Gln Ala Gln Val Ala Ala Tyr Gly Phe Ala Glu Gln Pro Ala Phe Phe
885 890 895

Tyr Ala Asn Asn Arg Thr Asn Glu Tyr Ser Thr Val Lys Leu Leu Asp
900 905 910

Met Ser Gln Gly Ser Pro Ala Trp Pro Phe Pro
915 920

<210> 33
<211> 857
<212> PRT
<213> Bacteroides thetaiotaomicron

<400> 33

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

Phe Thr Val Ser Leu Ala Cys Lys Asp Thr Glu Lys Ser Ile Ile Asn
20 25 30

Ser Ser Phe Ser Ile Ser Glu Glu Tyr Leu Ile Gln Asn Leu Asp Lys
35 40 45

Ser Ser Thr Ser Val Gln Ile Pro Ile Asn Thr Ser Met Glu Leu Ala
50 55 60

Gln Trp Ser Val Ser Tyr Glu Ala Asn Trp Leu Gln Cys Ser Lys Gln
65 70 75 80

Lys Thr Ala Ala Glu Gly Thr Phe Leu Arg Ile Thr Val Asn Glu Asn
85 90 95

Thr Gly Glu Thr Lys Arg Thr Ala Asn Ile Lys Val Thr Ser Thr Thr
100 105 110

Ala Thr Tyr Thr Ile Thr Val Asn Gln Tyr Ala Lys Gly Glu Val Ile
115 120 125

Val Glu Gly Asp Ile Lys Val Thr Pro Thr Gly Gly Lys Ala Ser Glu
130 135 140

His Gln Glu Gly Gln Asp Ile Glu Asn Thr Tyr Asp Gly Lys Phe Ser
145 150 155 160

Thr Asp Gly Ala Ala Pro Phe His Thr Pro Trp Gly Gln Ser Ala Lys

165

170

175

Phe Pro Val Thr Leu Glu Tyr Tyr Phe Lys Gly Asp Thr Glu Ile Asp
 180 185 190

Tyr Leu Ile Tyr Tyr Thr Arg Ser Gly Asn Gly Asn Phe Gly Lys Val
 195 200 205

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

Gly Glu Tyr Asp Phe Lys Glu Gln Asn Ala Pro Ser Lys Val Ser Phe
 225 230 235 240

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

Leu Gly Asp Phe Val Ser Cys Asp Glu Met Glu Phe Tyr Lys Thr Asn
 260 265 270

Thr Asp Lys Thr Leu Asp Lys Gln Leu Leu Thr Val Phe Thr Asp Ile
 275 280 285

Thr Cys Thr Glu Ile Lys Asn Asn Val Thr Asn Glu Gln Ile Gln Ala
 290 295 300

Leu Pro Asp Tyr Phe Val Arg Ile Ala Glu Ala Val Arg Asp Asn Thr
 305 310 315 320

Tyr Asp Lys Trp Glu Lys Glu Phe Arg Ile Arg Ser Tyr Glu Pro Tyr
 325 330 335

Ser Asn Ile Ala Glu Trp Ala Asp Lys Leu Met Thr Lys Lys Tyr Ser
 340 345 350

Asp Leu Asp Asn Pro Thr Gly Ile Ser Val Lys Ala Gly Asp Asp Ile
 355 360 365

Ile Val Leu Val Gly Asp Thr Tyr Gly Gln Asn Ile Ser Met Gln Cys
370 375 380

Ile Trp Glu Thr Gly Thr Glu Tyr Lys Gln Thr Ala Ser Ser Gly Asp
385 390 395 400

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

Gly Gln Leu Phe Val Met Tyr Asn Thr Glu Leu Thr Ser Asn Thr Ala
420 425 430

Lys Pro Ile Lys Ile His Ile Pro Leu Gly Ser Gly Thr Val Asn Gly
435 440 445

Phe Phe Asp Leu Lys Glu His Lys Thr Asp Glu Lys Tyr Ala Glu Leu
450 455 460

Leu Lys Lys Ser Thr His Lys Tyr Phe Cys Ile Arg Gly Glu Lys Ile
465 470 475 480

Met Phe Tyr Phe His Arg Asn Lys Leu Leu Glu Tyr Val Pro Asn Asn
485 490 495

Ile Leu Ser Ala Ile His Leu Trp Asp Asn Ile Val Gly Trp Gln Gln
500 505 510

Glu Leu Met Gly Ile Asp Asp Val Arg Pro Ser Gln Val Asn Asn His
515 520 525

Leu Phe Ala Ile Ser Pro Glu Gly Ser Tyr Met Trp Ala Ser Asp Tyr
530 535 540

Gln Ile Gly Phe Val Tyr Thr Tyr Leu Gly Asn Ile Leu Leu Glu Asp
545 550 555 560

Asn Val Met Ala Ala Glu Asp Asn Ala Trp Gly Pro Ala His Glu Ile
565 570 575

Gly His Val His Gln Ala Ala Ile Asn Trp Ala Ser Ser Thr Glu Ser
580 585 590

Ser Asn Asn Leu Phe Ser Asn Phe Ile Ile Tyr Lys Leu Gly Lys Tyr
595 600 605

Lys Ser Arg Gly Asn Gly Leu Gly Ser Val Ala Thr Ala Arg Tyr Ala
610 615 620

Asn Gly Gln Ala Trp Tyr Asn Met Gly Asp Ala Thr His Gln Asn Glu
625 630 635 640

Asp Thr Glu Thr His Met Arg Met Asn Trp Gln Leu Trp Ile Tyr Tyr
645 650 655

His Arg Cys Glu Tyr Lys Thr Asp Phe Trp Gln Thr Leu Phe Lys Leu
660 665 670

Met Arg Glu Val Asn Met Thr Glu Gly Glu Asp Pro Gly Lys Lys Gln
675 680 685

Leu Glu Phe Ala Lys Met Ala Ser Lys Ala Ala Asn Gln Asn Leu Thr
690 695 700

Asp Phe Phe Glu Met Trp Gly Phe Phe Glu Pro Val Asn Thr Thr Ile
705 710 715 720

Glu Gln Tyr Gly Thr Tyr Lys Tyr Tyr Val Ser Asp Ala Met Ile Arg
725 730 735

Glu Ala Lys Glu Tyr Met Ala Gln Phe Pro Ala Pro Lys His Ala Phe
740 745 750

Gln Tyr Ile Glu Asp Arg Lys Lys Ser Glu Phe Pro Ser Asn Asp Tyr
755 760 765

Arg Tyr Ser Ala Val Gly Asp Val Gly Tyr Tyr Thr Gln Phe Lys Glu
770 775 780

Asn Gln Lys Ile Thr Lys Ala Ile Thr Ala Glu Leu Ala Gly Arg Lys
785 790 795 800

Val Ser Ile Gln Asn Gly Asp Glu Ala Val Ala Phe Glu Leu Arg Glu
805 810 815

Asn Asp Glu Asn Gly Lys Leu Leu Tyr Phe Ser Thr Phe Thr Thr Phe
820 825 830

Glu Ile Pro Ser Ser Ile Leu Met Val Asn Ala Lys Leu Tyr Ala Val
835 840 845

Gln Ala Asp Gly Lys Arg Ile Leu Leu
850 855

<210> 34
<211> 1687
<212> PRT
<213> Clostridium perfringens

<400> 34

Met Asn Lys Arg Lys Ile Ala Ala Ile Ile Leu Ala Thr Met Ile Thr
1 5 10 15

Asn Leu Ser Ala Thr Thr Ile Asp Val Leu Ala Gln Glu Leu Asn Thr
20 25 30

Lys Asn Asn Ser Lys Val Glu Val Ser His Asp Asp Glu Ser His Gln
35 40 45

Ala Arg Val Ser Lys Phe Asp Leu Tyr Asn Ser Asp Lys Leu Asp Ala
50 55 60

Tyr Asn Gln Glu Phe Gln Val Ser Arg Ser Asn Ile Lys Ser Ile Asn
65 70 75 80

Asn Asn Gly Gly Lys Tyr Asn Ser Ser Thr Ile Asp Lys Ala Ile Asp
85 90 95

Gly Asn Leu Glu Thr His Trp Glu Thr Gly Lys Pro Asn Asp Ala Asn
100 105 110

Phe Thr Asn Glu Val Val Val Thr Phe Asn Glu Ile Thr Asn Ile Asp
115 120 125

Arg Ile Val Tyr Ser Ala Arg Arg Asp Ser Ala Arg Gly Lys Gly Phe
130 135 140

Ala Lys Glu Phe Glu Ile Tyr Ala Ser Leu Lys Asp Glu Gly Asp Asp
145 150 155 160

Phe Asn Leu Val Ser Ser Gly Glu Tyr Thr Glu Ser Thr Arg Asp Leu
165 170 175

Val Glu Ile Lys Phe Asn Pro Thr Asp Phe Lys Arg Leu Lys Phe Lys
180 185 190

Phe Lys Lys Ala Asp Gln Asn Trp Ala Ser Ala Ala Glu Phe Met Phe
195 200 205

Tyr Lys Glu Asp Lys Leu Asn Glu Lys Phe Asn Gly Leu Phe Thr Asp
210 215 220

Ser Ser Met Asn Lys Val Ser Glu Glu Phe Asn Thr Leu Glu Lys Leu
225 230 235 240

Asn Ala Phe Glu Asn Glu Leu Lys Asp His Pro Ile Tyr Asp Leu Tyr
245 250 255

Lys Glu Gly Leu Asn Asn Ala Arg Ala Ile Leu Thr Glu Thr Ser Glu
260 265 270

Asn Pro Thr Lys Ala Thr Leu Gly Gln Ile Thr Tyr Asn Leu Asn Asp
275 280 285

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

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

Asp Asn Asp Val Asn Thr Tyr Trp Glu Thr Gly Thr Leu Asn Ser Ser
325 330 335

Ser Phe Asn Asn Glu Val Glu Val Glu Phe Asn Asp Leu Val Thr Leu
340 345 350

Asp Arg Ile Val Tyr Gly Ser Arg Gln Ser Asp Leu Lys Gly Phe Ala
355 360 365

Glu Glu Val Tyr Ile Tyr Ala Ser Arg Thr Ser Lys Gly Asp Thr Tyr
370 375 380

Lys Leu Val Ala Thr Gly Ala His Glu Ala Thr Lys Gly Leu Val Glu
385 390 395 400

Ala Lys Phe Glu Pro Thr Glu Phe Lys Arg Val Lys Phe Lys Phe Lys
405 410 415

Lys Ser Lys Gln Asn Ser Ala Thr Leu Asn Glu Leu Met Phe Tyr Lys
420 425 430

Pro Asp Glu Val Tyr Ser Ser Ile Pro Lys Leu Phe Thr Asp Gly Thr
435 440 445

Met Ser Glu Leu Ser Glu Glu Phe Asn Ser Leu Glu Lys Ile Asn Ala
450 455 460

Phe Lys Glu Lys Ala Lys Asn His Pro Leu Tyr Asn Asp Phe Asn Glu
465 470 475 480

Thr Ile Glu Leu Ala Glu Ser Leu Ile Ser Asn Pro Arg Lys Glu Asp
485 490 495

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

Arg Lys Val Trp Asn Phe Gln Asp Trp Gln Ile Thr Gly Leu Ser Ala
515 520 525

Arg Ala Gly Asp Lys Ile Thr Val Tyr Val Asp Val Ala Glu Gly Asp
530 535 540

Pro Thr Pro Thr Leu Leu Tyr Lys Gln Ser Leu Thr Gln His Gly Gly
545 550 555 560

Ala Thr Ser Phe Gln Leu Lys Pro Gly Lys Asn Glu Ile Thr Ile Pro
565 570 575

Glu Ile Asn Tyr Glu Ser Asn Gly Ile Pro Lys Asp Val Ile Gln Gly
580 585 590

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

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

Gly Lys Ser Asp Glu Asn Glu Val Met Lys Glu Leu Glu Ala Tyr Val
625 630 635 640

Glu Lys Ile Lys Ala Glu Pro Lys Thr Thr Pro Asn Ile Phe Ala Val

645

650

655

Ser Ser Asn Lys Ser Leu Glu Phe Val Gln Ala Thr Tyr Ala Leu Asp
 660 665 670

Trp Tyr Lys Lys Asn Asn Lys Thr Pro Lys Tyr Thr Ala Glu Gln Trp
 675 680 685

Asp Gln Tyr Ile Ala Asp Ala Met Gly Phe Trp Gly Phe Asp Asn Ser
 690 695 700

Lys Asp Val Asn Ser Asp Phe Asn Phe Arg Ile Met Pro Met Val Lys
 705 710 715 720

Asn Leu Ser Gly Gly Ala Phe Met Asn Ala Gly Asn Gly Val Ile Gly
 725 730 735

Ile Arg Pro Gly Asn Gln Asp Ala Ile Leu Ala Ala Asn Lys Gly Trp
 740 745 750

Gly Val Ala His Glu Leu Gly His Asn Phe Asp Thr Gly Gly Arg Thr
 755 760 765

Ile Val Glu Val Thr Asn Asn Met Met Pro Leu Phe Phe Glu Ser Lys
 770 775 780

Tyr Lys Thr Lys Thr Arg Ile Thr Asp Gln Asn Ile Trp Glu Asn Asn
 785 790 795 800

Thr Tyr Pro Lys Val Gly Leu Asp Asp Tyr Ser Asn Asn Glu Leu Tyr
 805 810 815

Asn Lys Ala Asp Ser Thr His Leu Ala Gln Leu Ala Pro Leu Trp Gln
 820 825 830

Leu Tyr Leu Tyr Asp Asn Thr Phe Tyr Gly Lys Phe Glu Arg Gln Phe
 835 840 845

Arg Glu Arg Asp Phe Gly Asn Lys Asn Arg Glu Asp Ile Tyr Lys Ser
850 855 860

Trp Val Val Ala Ala Ser Asp Ala Met Glu Leu Asp Leu Thr Glu Phe
865 870 875 880

Phe Ala Arg His Gly Ile Arg Val Asp Asp Lys Val Lys Glu Asp Leu
885 890 895

Ala Lys Tyr Pro Lys Pro Asp Lys Lys Ile Tyr Tyr Leu Asn Asp Leu
900 905 910

Ala Met Asn Tyr Lys Gly Asp Gly Phe Thr Glu Asn Ala Lys Val Ser
915 920 925

Val Ser Thr Ser Gly Ser Asn Gly Asn Ile Lys Leu Ser Phe Ser Val
930 935 940

Asp Asp Glu Asn Lys Asp Asn Ile Leu Gly Tyr Glu Ile Arg Arg Asp
945 950 955 960

Gly Lys Tyr Val Gly Phe Thr Ser Asn Asp Ser Phe Val Asp Thr Lys
965 970 975

Ser Asn Leu Asp Glu Asp Gly Val Tyr Val Val Thr Pro Tyr Asp Arg
980 985 990

Lys Leu Asn Thr Leu Asn Pro Ile Glu Val Asn Ala Leu Gln Pro Thr
995 1000 1005

Leu Ser Val Asn Pro Val Ile Thr Leu Ala Leu Gly Glu Glu Phe
1010 1015 1020

Asn Glu Glu Glu Tyr Ile Val Ala Lys Asp Ile Lys Gly Asn Ser
1025 1030 1035

Leu	Ser	Glu	Ser	Val	Lys	Val	Lys	Ser	Ser	Asn	Val	Asn	Thr	Ser
1040						1045					1050			
Lys	Val	Gly	Glu	Tyr	Glu	Val	Leu	Tyr	Ser	Leu	Glu	Asp	Ser	Lys
1055						1060					1065			
Gly	Asn	Glu	Tyr	Thr	Lys	Thr	Ser	Lys	Val	Asn	Val	Val	Ser	Arg
1070						1075					1080			
Lys	Glu	Tyr	Met	Ser	Asp	Leu	Thr	Pro	Lys	Gln	Ser	Ser	Asn	Gly
1085						1090					1095			
Trp	Gly	Thr	Val	Arg	Lys	Asp	Lys	Ser	Ile	Ser	Gly	Gly	Val	Ile
1100						1105					1110			
Gly	Leu	Thr	Arg	Asp	Gly	Asp	Phe	Val	Asp	Tyr	Asn	Lys	Gly	Leu
1115						1120					1125			
Gly	Leu	His	Ser	Asn	Ala	Glu	Tyr	Val	Tyr	Asp	Leu	Glu	Gly	Lys
1130						1135					1140			
Asp	Tyr	Asp	Tyr	Phe	Glu	Ser	Tyr	Val	Gly	Val	Asp	Lys	Ala	Met
1145						1150					1155			
Ser	Ser	Arg	Pro	Ala	Ser	Ser	Val	Ile	Phe	Lys	Val	Leu	Val	Asp
1160						1165					1170			
Gly	Glu	Glu	Lys	Phe	Asn	Ser	Gly	Val	Met	Arg	Ser	Thr	Thr	Pro
1175						1180					1185			
Gln	Lys	Tyr	Val	Lys	Val	Asp	Val	Lys	Asn	Ala	Lys	Glu	Leu	Lys
1190						1195					1200			
Leu	Ile	Val	Asn	Asp	Ala	Gly	Asp	Gly	Asp	Ser	Ser	Asp	His	Ala
1205						1210					1215			

Ser Phe Gly Asp Ala Lys Leu Ala Thr Leu Ser Ser Lys Pro Ile
 1220 1225 1230
 Ile Lys Gly Glu Asn Leu Ala Tyr Ser Met Asp Glu Lys Val Asp
 1235 1240 1245
 Leu Met Lys Gly Ile Thr Ala Thr Asp Ile Glu Asp Gly Asn Ile
 1250 1255 1260
 Thr Ser Lys Val Gln Ile Lys Ser Ser Asp Phe Val Glu Gly Lys
 1265 1270 1275
 Ser Gly Ile Phe Thr Val Val Tyr Ser Val Thr Asp Ser Asp Gly
 1280 1285 1290
 Leu Thr Ser Glu Cys Ser Arg Thr Ile Ala Val Thr Asp Lys Glu
 1295 1300 1305
 Thr Gln Leu Ser Asp Leu Asn Trp Lys Ser Ala Thr Ile Gly Ser
 1310 1315 1320
 Gly Ser Val Arg Lys Asp Arg Ala Val Ser Gly Asn Gln Ile Arg
 1325 1330 1335
 Leu Leu Asn Glu Asp Asn Ser Val Glu Thr Phe Ala Lys Gly Ile
 1340 1345 1350
 Gly Thr His Ser Tyr Ser Glu Ile Val Tyr Asn Ser Glu Gly Tyr
 1355 1360 1365
 Asp Ile Phe Asp Thr Trp Val Gly Ile Asp Arg His Val Ala Asp
 1370 1375 1380
 Lys Lys Val Ser Ser Val Lys Phe Lys Val Tyr Val Asp Gly Glu
 1385 1390 1395
 Leu Lys Ala Glu Thr Asp Val Met Arg Ile Asp Thr Pro Lys Lys

1400		1405		1410
Arg Leu Val Val Asp Val	Arg Asn Ser Lys Glu Ile	Lys Leu Val		
1415	1420	1425		
Val Asp Val Ala Asp Asn	Gly Asn Asn Trp Asp His	Ala Asp Trp		
1430	1435	1440		
Ala Asp Ala Lys Phe Arg	Asn Leu Ala Glu Tyr Asp	Ala Ser Glu		
1445	1450	1455		
Leu Asn Lys Ala Ile Glu	Glu Ala Lys Lys Leu Asp	Leu Asn Asn		
1460	1465	1470		
Tyr Thr Glu Glu Ser Ser	Glu Ala Leu Lys Asn Ala	Ile Ser Lys		
1475	1480	1485		
Gly Glu Glu Ala Leu Leu	Ser Lys Asp Lys Glu Thr	Ile Asn Ser		
1490	1495	1500		
Ala Leu Glu Glu Leu Asn	Lys Glu Met Asn Ser Leu	Val Lys Val		
1505	1510	1515		
Asp Leu Asn Ala Val Ile	Asn Ile Pro Asp Lys Tyr	Leu Leu Lys		
1520	1525	1530		
Ser Ile Gln Asn Gln Leu	Asn Lys Thr Gly Asp Ile	Thr Leu Gly		
1535	1540	1545		
Asp Met Tyr Ser Leu Thr	Thr Leu Thr Leu Ser Gly	Val Glu Asp		
1550	1555	1560		
Leu Thr Gly Leu Glu Asn	Ala Lys Asn Leu Glu Thr	Leu Asn Met		
1565	1570	1575		
Asp Tyr Asn Glu Val Lys	Asp Leu Arg Pro Leu Ser	Lys Leu Lys		
1580	1585	1590		

Lys Leu Asn Thr Leu Asn Ala Gln Glu Gln Phe Ile Ala Ala Gly
 1595 1600 1605

Glu Leu Lys Pro Ser Asn Gly Lys Val Ile Gly Asp Ser Lys Val
 1610 1615 1620

Tyr Asn Arg Glu Gly Lys Asn Val Ala Lys Thr Ile Arg Val Val
 1625 1630 1635

Asp Lys Asn Gly Asn Thr Ile Leu Glu Gln Asp Ala Lys Asp Glu
 1640 1645 1650

Phe Thr Ile Asn Thr Lys Asp Leu Ser Ser Gly Leu Tyr Gly Val
 1655 1660 1665

His Val Leu Phe Glu Asp Glu Gly Phe Ser Gly Val Met Phe Tyr
 1670 1675 1680

Leu Phe Asn Val
 1685

<210> 35
 <211> 882
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Polypeptide capable of binding to O-glycans but lack or has
 reduced O-glycoprotein-specific endoprotease activity -
 Pseudomonas aeruginosa PA01 (double mutant with removed signal
 sequence)

<400> 35

Ala Thr Gln Glu Glu Ile Leu Asp Ala Ala Leu Val Ser Gly Asp Ser
 1 5 10 15

Ser Gln Leu Thr Asp Ser His Leu Val Ala Leu Arg Leu Gln Gln Gln
 20 25 30

Val Glu Arg Ile Arg Gln Thr Arg Thr Gln Leu Leu Asp Gly Leu Tyr
35 40 45

Gln Asn Leu Ser Gln Ala Tyr Asp Pro Gly Ala Ala Ser Met Trp Val
50 55 60

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

Gly Arg Val Leu Ala Ser Leu Ser Leu Glu Ala Gly Gly Arg Gly Leu
85 90 95

Ala Tyr Gly Thr Asn Val Leu Thr Gln Leu Ser Gly Thr Asn Ala Ala
100 105 110

His Ala Pro Leu Leu Lys Arg Ala Val Gln Trp Leu Val Asn Gly Asp
115 120 125

Pro Gly Ala Ala Thr Ala Lys Asp Phe Lys Val Ser Val Val Gly Val
130 135 140

Asp Lys Thr Ala Ala Leu Asn Gly Leu Lys Ser Ala Gly Leu Gln Pro
145 150 155 160

Ala Asp Ala Ala Cys Asn Ala Leu Thr Asp Ala Ser Cys Ala Ser Thr
165 170 175

Ser Lys Leu Leu Val Leu Gly Asn Gly Ala Ser Ala Ala Ser Leu Ser
180 185 190

Ala Thr Val Arg Ala Arg Leu Gln Ala Gly Leu Pro Ile Leu Phe Val
195 200 205

His Thr Asn Gly Trp Asn Gln Ser Ser Thr Gly Gln Gln Ile Leu Ala
210 215 220

Gly Leu Gly Leu Gln Glu Gly Pro Tyr Gly Gly Asn Tyr Trp Asp Lys
225 230 235 240

Asp Arg Val Pro Ser Ser Arg Thr Arg Thr Arg Ser Val Glu Leu Gly
245 250 255

Gly Ala Tyr Gly Gln Asp Pro Ala Leu Val Gln Gln Ile Val Asp Gly
260 265 270

Ser Trp Arg Thr Asp Tyr Asp Trp Ser Lys Cys Thr Ser Tyr Val Gly
275 280 285

Arg Thr Thr Cys Asp Asp Val Pro Gly Leu Ser Asp Phe Ser Lys Arg
290 295 300

Val Asp Val Leu Lys Gly Ala Leu Asp Ala Tyr Asn Gln Lys Ala Gln
305 310 315 320

Asn Leu Phe Ala Leu Pro Gly Thr Thr Ser Leu Arg Leu Trp Leu Leu
325 330 335

Trp Ala Asp Ala Val Arg Gln Asn Ile Arg Tyr Pro Met Asp Lys Ala
340 345 350

Ala Asp Thr Ala Arg Phe Gln Glu Thr Phe Val Ala Asp Ala Ile Val
355 360 365

Gly Tyr Val Arg Glu Ala Gly Ala Ala Gln Lys Glu Leu Gly Ser Tyr
370 375 380

Ala Gly Gln Arg Gln Gln Ser Met Pro Val Ser Gly Ser Glu Glu Thr
385 390 395 400

Leu Thr Leu Thr Leu Pro Ser Ala Gln Gly Phe Thr Ala Ile Gly Arg
405 410 415

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

Gln Ala Ser Leu Ala Val Gly Leu Asn Thr Gln Arg Ile Gly Ser Thr
435 440 445

Arg Leu Trp Asn Thr Arg Gln Tyr Asp Arg Pro Arg Phe Leu Lys Ser
450 455 460

Pro Asp Ile Lys Leu Gln Ala Asn Gln Ser Val Ala Leu Val Ser Pro
465 470 475 480

Tyr Gly Gly Leu Leu Gln Leu Val Tyr Ser Gly Ala Thr Pro Gly Gln
485 490 495

Thr Val Thr Val Lys Val Thr Gly Ala Ala Ser Gln Pro Phe Leu Asp
500 505 510

Ile Gln Pro Gly Glu Asp Ser Ser Gln Ala Ile Ala Asp Phe Ile Gln
515 520 525

Ala Leu Asp Ala Asp Lys Ala Asp Trp Leu Glu Ile Arg Ser Gly Ser
530 535 540

Val Glu Val His Ala Lys Val Glu Lys Val Arg Gly Ser Ile Asp Lys
545 550 555 560

Asp Tyr Gly Gly Asp Val Gln Arg Phe Ile Arg Glu Leu Asn Glu Val
565 570 575

Phe Ile Asp Asp Ala Tyr Thr Leu Ala Gly Phe Ala Ile Pro Asn Gln
580 585 590

Ala Lys Thr Pro Ala Ile Gln Gln Glu Cys Ala Ala Arg Gly Trp Asp
595 600 605

Cys Asp Ser Glu Thr Leu His Lys Leu Pro Gly Thr Gln His Ile Asn

610

615

620

Val Asp Gln Tyr Ala Gln Cys Gly Gly Gly Cys Ser Gly Asn Pro Tyr
 625 630 635 640

Asp Gln Thr Trp Gly Leu Asn Pro Arg Gly Trp Gly Glu Ser Ala Ala
 645 650 655

Leu Gly His Asn Leu Gln Val Asn Arg Leu Lys Val Tyr Gly Gly Arg
 660 665 670

Ser Gly Glu Ile Ser Asn Gln Ile Phe Pro Leu His Lys Asp Trp Arg
 675 680 685

Val Leu Arg Glu Phe Gly Gln Asn Leu Asp Asp Thr Arg Val Asn Tyr
 690 695 700

Arg Asn Ala Tyr Asn Leu Ile Val Ala Gly Arg Ala Glu Ala Asp Pro
 705 710 715 720

Leu Ala Gly Val Tyr Lys Arg Leu Trp Glu Asp Pro Gly Thr Tyr Ala
 725 730 735

Leu Asn Gly Glu Arg Met Ala Phe Tyr Thr Gln Trp Val His Tyr Trp
 740 745 750

Ala Asp Leu Lys Asn Asp Pro Leu Gln Gly Trp Asp Ile Trp Thr Leu
 755 760 765

Leu Tyr Leu His Gln Arg Gln Val Asp Lys Ser Asp Trp Asp Ala Asn
 770 775 780

Lys Ala Ala Leu Gly Tyr Gly Thr Tyr Ala Gln Arg Pro Gly Asn Ser
 785 790 795 800

Gly Asp Ala Ser Ser Thr Asp Gly Asn Asp Asn Leu Leu Leu Gly Leu
 805 810 815

Ser Trp Leu Thr Gln Arg Asp Gln Arg Pro Thr Phe Ala Leu Trp Gly
820 825 830

Ile Arg Thr Ser Ala Ala Ala Gln Ala Gln Val Ala Ala Tyr Gly Phe
835 840 845

Ala Glu Gln Pro Ala Phe Phe Tyr Ala Asn Asn Arg Thr Asn Glu Tyr
850 855 860

Ser Thr Val Lys Leu Leu Asp Met Ser Gln Gly Ser Pro Ala Trp Pro
865 870 875 880

Phe Pro

<210> 36

<211> 536

<212> PRT

<213> Artificial Sequence

<220>

<223> Polypeptide capable of binding to O-glycans but lack or has
reduced O-glycoprotein-specific endoprotease activity -
Bacteroides thetaiotaomicron VPI-5482 (double mutant with removed
signal and other immature sequences)

<400> 36

Asp Lys Trp Glu Lys Glu Phe Arg Ile Arg Ser Tyr Glu Pro Tyr Ser
1 5 10 15

Asn Ile Ala Glu Trp Ala Asp Lys Leu Met Thr Lys Lys Tyr Ser Asp
20 25 30

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

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

Trp Glu Thr Gly Thr Glu Tyr Lys Gln Thr Ala Ser Ser Gly Asp Val
65 70 75 80

Tyr Met Leu Asn Pro Gly Val Asn Lys Leu Thr Met Lys Gly Glu Gly
85 90 95

Gln Leu Phe Val Met Tyr Asn Thr Glu Leu Thr Ser Asn Thr Ala Lys
100 105 110

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

Phe Asp Leu Lys Glu His Lys Thr Asp Glu Lys Tyr Ala Glu Leu Leu
130 135 140

Lys Lys Ser Thr His Lys Tyr Phe Cys Ile Arg Gly Glu Lys Ile Met
145 150 155 160

Phe Tyr Phe His Arg Asn Lys Leu Leu Glu Tyr Val Pro Asn Asn Ile
165 170 175

Leu Ser Ala Ile His Leu Trp Asp Asn Ile Val Gly Trp Gln Gln Glu
180 185 190

Leu Met Gly Ile Asp Asp Val Arg Pro Ser Gln Val Asn Asn His Leu
195 200 205

Phe Ala Ile Ser Pro Glu Gly Ser Tyr Met Trp Ala Ser Asp Tyr Gln
210 215 220

Ile Gly Phe Val Tyr Thr Tyr Leu Gly Asn Ile Leu Leu Glu Asp Asn
225 230 235 240

Val Met Ala Ala Glu Asp Asn Ala Trp Gly Pro Ala Ala Ala Ile Gly
245 250 255

His Val His Gln Ala Ala Ile Asn Trp Ala Ser Ser Thr Glu Ser Ser
260 265 270

Asn Asn Leu Phe Ser Asn Phe Ile Ile Tyr Lys Leu Gly Lys Tyr Lys
275 280 285

Ser Arg Gly Asn Gly Leu Gly Ser Val Ala Thr Ala Arg Tyr Ala Asn
290 295 300

Gly Gln Ala Trp Tyr Asn Met Gly Asp Ala Thr His Gln Asn Glu Asp
305 310 315 320

Thr Glu Thr His Met Arg Met Asn Trp Gln Leu Trp Ile Tyr Tyr His
325 330 335

Arg Cys Glu Tyr Lys Thr Asp Phe Trp Gln Thr Leu Phe Lys Leu Met
340 345 350

Arg Glu Val Asn Met Thr Glu Gly Glu Asp Pro Gly Lys Lys Gln Leu
355 360 365

Glu Phe Ala Lys Met Ala Ser Lys Ala Ala Asn Gln Asn Leu Thr Asp
370 375 380

Phe Phe Glu Met Trp Gly Phe Phe Glu Pro Val Asn Thr Thr Ile Glu
385 390 395 400

Gln Tyr Gly Thr Tyr Lys Tyr Tyr Val Ser Asp Ala Met Ile Arg Glu
405 410 415

Ala Lys Glu Tyr Met Ala Gln Phe Pro Ala Pro Lys His Ala Phe Gln
420 425 430

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

Tyr Ser Ala Val Gly Asp Val Gly Tyr Tyr Thr Gln Phe Lys Glu Asn
450 455 460

Gln Lys Ile Thr Lys Ala Ile Thr Ala Glu Leu Ala Gly Arg Lys Val
465 470 475 480

Ser Ile Gln Asn Gly Asp Glu Ala Val Ala Phe Glu Leu Arg Glu Asn
485 490 495

Asp Glu Asn Gly Lys Leu Leu Tyr Phe Ser Thr Phe Thr Thr Phe Glu
500 505 510

Ile Pro Ser Ser Ile Leu Met Val Asn Ala Lys Leu Tyr Ala Val Gln
515 520 525

Ala Asp Gly Lys Arg Ile Leu Leu
530 535

<210> 37

<211> 507

<212> PRT

<213> Artificial Sequence

<220>

<223> Polypeptide capable of binding to O-glycans but lack or has
reduced O-glycoprotein-specific endoprotease activity -
Clostridium perfringens (double mutant with removed signal and
other immature sequences)

<400> 37

Val Leu Glu Leu Glu Met Arg Gly Asp Ser Ile Ser Glu Ala Lys Lys
1 5 10 15

Arg Lys Val Trp Asn Phe Gln Asp Trp Gln Ile Thr Gly Leu Ser Ala
20 25 30

Arg Ala Gly Asp Lys Ile Thr Val Tyr Val Asp Val Ala Glu Gly Asp
35 40 45

Pro Thr Pro Thr Leu Leu Tyr Lys Gln Ser Leu Thr Gln His Gly Gly
50 55 60

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

Glu Ile Asn Tyr Glu Ser Asn Gly Ile Pro Lys Asp Val Ile Gln Gly
85 90 95

Gly Asp Leu Phe Phe Thr Asn Tyr Lys Ser Asp Ser Gln Lys Arg Ala
100 105 110

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

Gly Lys Ser Asp Glu Asn Glu Val Met Lys Glu Leu Glu Ala Tyr Val
130 135 140

Glu Lys Ile Lys Ala Glu Pro Lys Thr Thr Pro Asn Ile Phe Ala Val
145 150 155 160

Ser Ser Asn Lys Ser Leu Glu Phe Val Gln Ala Thr Tyr Ala Leu Asp
165 170 175

Trp Tyr Lys Lys Asn Asn Lys Thr Pro Lys Tyr Thr Ala Glu Gln Trp
180 185 190

Asp Gln Tyr Ile Ala Asp Ala Met Gly Phe Trp Gly Phe Asp Asn Ser
195 200 205

Lys Asp Val Asn Ser Asp Phe Asn Phe Arg Ile Met Pro Met Val Lys
210 215 220

Asn Leu Ser Gly Gly Ala Phe Met Asn Ala Gly Asn Gly Val Ile Gly
225 230 235 240

Ile Arg Pro Gly Asn Gln Asp Ala Ile Leu Ala Ala Asn Lys Gly Trp

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

Asp Asp Glu Asn Lys Asp Asn Ile Leu Gly Tyr Glu Ile Arg Arg Asp
450 455 460

Gly Lys Tyr Val Gly Phe Thr Ser Asn Asp Ser Phe Val Asp Thr Lys
465 470 475 480

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

Lys Leu Asn Thr Leu Asn Pro Ile Glu Val Asn
500 505

<210> 38
<211> 892
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide capable of binding to O-glycans but lack or has
reduced O-glycoprotein-specific endoprotease activity -
Pseudomonas aeruginosa PA01 (double mutant with removed signal
sequence, with N-term Met, C-term linker/tag)

<400> 38

Met Ala Thr Gln Glu Glu Ile Leu Asp Ala Ala Leu Val Ser Gly Asp
1 5 10 15

Ser Ser Gln Leu Thr Asp Ser His Leu Val Ala Leu Arg Leu Gln Gln
20 25 30

Gln Val Glu Arg Ile Arg Gln Thr Arg Thr Gln Leu Leu Asp Gly Leu
35 40 45

Tyr Gln Asn Leu Ser Gln Ala Tyr Asp Pro Gly Ala Ala Ser Met Trp
50 55 60

Val Leu Pro Ala Asn Pro Asp Asn Thr Leu Pro Phe Leu Ile Gly Asp
65 70 75 80

Lys Gly Arg Val Leu Ala Ser Leu Ser Leu Glu Ala Gly Gly Arg Gly
85 90 95

Leu Ala Tyr Gly Thr Asn Val Leu Thr Gln Leu Ser Gly Thr Asn Ala
100 105 110

Ala His Ala Pro Leu Leu Lys Arg Ala Val Gln Trp Leu Val Asn Gly
115 120 125

Asp Pro Gly Ala Ala Thr Ala Lys Asp Phe Lys Val Ser Val Val Gly
130 135 140

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

Pro Ala Asp Ala Ala Cys Asn Ala Leu Thr Asp Ala Ser Cys Ala Ser
165 170 175

Thr Ser Lys Leu Leu Val Leu Gly Asn Gly Ala Ser Ala Ala Ser Leu
180 185 190

Ser Ala Thr Val Arg Ala Arg Leu Gln Ala Gly Leu Pro Ile Leu Phe
195 200 205

Val His Thr Asn Gly Trp Asn Gln Ser Ser Thr Gly Gln Gln Ile Leu
210 215 220

Ala Gly Leu Gly Leu Gln Glu Gly Pro Tyr Gly Gly Asn Tyr Trp Asp
225 230 235 240

Lys Asp Arg Val Pro Ser Ser Arg Thr Arg Thr Arg Ser Val Glu Leu
245 250 255

Gly Gly Ala Tyr Gly Gln Asp Pro Ala Leu Val Gln Gln Ile Val Asp
260 265 270

Gly Ser Trp Arg Thr Asp Tyr Asp Trp Ser Lys Cys Thr Ser Tyr Val
275 280 285

Gly Arg Thr Thr Cys Asp Asp Val Pro Gly Leu Ser Asp Phe Ser Lys
290 295 300

Arg Val Asp Val Leu Lys Gly Ala Leu Asp Ala Tyr Asn Gln Lys Ala
305 310 315 320

Gln Asn Leu Phe Ala Leu Pro Gly Thr Thr Ser Leu Arg Leu Trp Leu
325 330 335

Leu Trp Ala Asp Ala Val Arg Gln Asn Ile Arg Tyr Pro Met Asp Lys
340 345 350

Ala Ala Asp Thr Ala Arg Phe Gln Glu Thr Phe Val Ala Asp Ala Ile
355 360 365

Val Gly Tyr Val Arg Glu Ala Gly Ala Ala Gln Lys Glu Leu Gly Ser
370 375 380

Tyr Ala Gly Gln Arg Gln Gln Ser Met Pro Val Ser Gly Ser Glu Glu
385 390 395 400

Thr Leu Thr Leu Thr Leu Pro Ser Ala Gln Gly Phe Thr Ala Ile Gly
405 410 415

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

Gly Gln Ala Ser Leu Ala Val Gly Leu Asn Thr Gln Arg Ile Gly Ser
435 440 445

Thr Arg Leu Trp Asn Thr Arg Gln Tyr Asp Arg Pro Arg Phe Leu Lys
450 455 460

Ser Pro Asp Ile Lys Leu Gln Ala Asn Gln Ser Val Ala Leu Val Ser
465 470 475 480

Pro Tyr Gly Gly Leu Leu Gln Leu Val Tyr Ser Gly Ala Thr Pro Gly
485 490 495

Gln Thr Val Thr Val Lys Val Thr Gly Ala Ala Ser Gln Pro Phe Leu
500 505 510

Asp Ile Gln Pro Gly Glu Asp Ser Ser Gln Ala Ile Ala Asp Phe Ile
515 520 525

Gln Ala Leu Asp Ala Asp Lys Ala Asp Trp Leu Glu Ile Arg Ser Gly
530 535 540

Ser Val Glu Val His Ala Lys Val Glu Lys Val Arg Gly Ser Ile Asp
545 550 555 560

Lys Asp Tyr Gly Gly Asp Val Gln Arg Phe Ile Arg Glu Leu Asn Glu
565 570 575

Val Phe Ile Asp Asp Ala Tyr Thr Leu Ala Gly Phe Ala Ile Pro Asn
580 585 590

Gln Ala Lys Thr Pro Ala Ile Gln Gln Glu Cys Ala Ala Arg Gly Trp
595 600 605

Asp Cys Asp Ser Glu Thr Leu His Lys Leu Pro Gly Thr Gln His Ile
610 615 620

Asn Val Asp Gln Tyr Ala Gln Cys Gly Gly Gly Cys Ser Gly Asn Pro
625 630 635 640

Tyr Asp Gln Thr Trp Gly Leu Asn Pro Arg Gly Trp Gly Glu Ser Ala
645 650 655

Ala Leu Gly His Asn Leu Gln Val Asn Arg Leu Lys Val Tyr Gly Gly

660

665

670

Arg Ser Gly Glu Ile Ser Asn Gln Ile Phe Pro Leu His Lys Asp Trp
 675 680 685

Arg Val Leu Arg Glu Phe Gly Gln Asn Leu Asp Asp Thr Arg Val Asn
 690 695 700

Tyr Arg Asn Ala Tyr Asn Leu Ile Val Ala Gly Arg Ala Glu Ala Asp
 705 710 715 720

Pro Leu Ala Gly Val Tyr Lys Arg Leu Trp Glu Asp Pro Gly Thr Tyr
 725 730 735

Ala Leu Asn Gly Glu Arg Met Ala Phe Tyr Thr Gln Trp Val His Tyr
 740 745 750

Trp Ala Asp Leu Lys Asn Asp Pro Leu Gln Gly Trp Asp Ile Trp Thr
 755 760 765

Leu Leu Tyr Leu His Gln Arg Gln Val Asp Lys Ser Asp Trp Asp Ala
 770 775 780

Asn Lys Ala Ala Leu Gly Tyr Gly Thr Tyr Ala Gln Arg Pro Gly Asn
 785 790 795 800

Ser Gly Asp Ala Ser Ser Thr Asp Gly Asn Asp Asn Leu Leu Leu Gly
 805 810 815

Leu Ser Trp Leu Thr Gln Arg Asp Gln Arg Pro Thr Phe Ala Leu Trp
 820 825 830

Gly Ile Arg Thr Ser Ala Ala Ala Gln Ala Gln Val Ala Ala Tyr Gly
 835 840 845

Phe Ala Glu Gln Pro Ala Phe Phe Tyr Ala Asn Asn Arg Thr Asn Glu
 850 855 860

Tyr Ser Thr Val Lys Leu Leu Asp Met Ser Gln Gly Ser Pro Ala Trp
865 870 875 880

Pro Phe Pro Gly Ser Gly His His His His His His
885 890

<210> 39
<211> 546
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide capable of binding to O-glycans but lack or has
reduced O-glycoprotein-specific endoprotease activity -
Bacteroides thetaiotaomicron VPI-5482 (double mutant with removed
signal and other sequences from immature protein, with N-term

<400> 39

Met Asp Lys Trp Glu Lys Glu Phe Arg Ile Arg Ser Tyr Glu Pro Tyr
1 5 10 15

Ser Asn Ile Ala Glu Trp Ala Asp Lys Leu Met Thr Lys Lys Tyr Ser
20 25 30

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

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

Ile Trp Glu Thr Gly Thr Glu Tyr Lys Gln Thr Ala Ser Ser Gly Asp
65 70 75 80

Val Tyr Met Leu Asn Pro Gly Val Asn Lys Leu Thr Met Lys Gly Glu
85 90 95

Gly Gln Leu Phe Val Met Tyr Asn Thr Glu Leu Thr Ser Asn Thr Ala

100

105

110

Lys Pro Ile Lys Ile His Ile Pro Leu Gly Ser Gly Thr Val Asn Gly
 115 120 125

Phe Phe Asp Leu Lys Glu His Lys Thr Asp Glu Lys Tyr Ala Glu Leu
 130 135 140

Leu Lys Lys Ser Thr His Lys Tyr Phe Cys Ile Arg Gly Glu Lys Ile
 145 150 155 160

Met Phe Tyr Phe His Arg Asn Lys Leu Leu Glu Tyr Val Pro Asn Asn
 165 170 175

Ile Leu Ser Ala Ile His Leu Trp Asp Asn Ile Val Gly Trp Gln Gln
 180 185 190

Glu Leu Met Gly Ile Asp Asp Val Arg Pro Ser Gln Val Asn Asn His
 195 200 205

Leu Phe Ala Ile Ser Pro Glu Gly Ser Tyr Met Trp Ala Ser Asp Tyr
 210 215 220

Gln Ile Gly Phe Val Tyr Thr Tyr Leu Gly Asn Ile Leu Leu Glu Asp
 225 230 235 240

Asn Val Met Ala Ala Glu Asp Asn Ala Trp Gly Pro Ala Ala Ala Ile
 245 250 255

Gly His Val His Gln Ala Ala Ile Asn Trp Ala Ser Ser Thr Glu Ser
 260 265 270

Ser Asn Asn Leu Phe Ser Asn Phe Ile Ile Tyr Lys Leu Gly Lys Tyr
 275 280 285

Lys Ser Arg Gly Asn Gly Leu Gly Ser Val Ala Thr Ala Arg Tyr Ala
 290 295 300

Asn Gly Gln Ala Trp Tyr Asn Met Gly Asp Ala Thr His Gln Asn Glu
305 310 315 320

Asp Thr Glu Thr His Met Arg Met Asn Trp Gln Leu Trp Ile Tyr Tyr
325 330 335

His Arg Cys Glu Tyr Lys Thr Asp Phe Trp Gln Thr Leu Phe Lys Leu
340 345 350

Met Arg Glu Val Asn Met Thr Glu Gly Glu Asp Pro Gly Lys Lys Gln
355 360 365

Leu Glu Phe Ala Lys Met Ala Ser Lys Ala Ala Asn Gln Asn Leu Thr
370 375 380

Asp Phe Phe Glu Met Trp Gly Phe Phe Glu Pro Val Asn Thr Thr Ile
385 390 395 400

Glu Gln Tyr Gly Thr Tyr Lys Tyr Tyr Val Ser Asp Ala Met Ile Arg
405 410 415

Glu Ala Lys Glu Tyr Met Ala Gln Phe Pro Ala Pro Lys His Ala Phe
420 425 430

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

Arg Tyr Ser Ala Val Gly Asp Val Gly Tyr Tyr Thr Gln Phe Lys Glu
450 455 460

Asn Gln Lys Ile Thr Lys Ala Ile Thr Ala Glu Leu Ala Gly Arg Lys
465 470 475 480

Val Ser Ile Gln Asn Gly Asp Glu Ala Val Ala Phe Glu Leu Arg Glu
485 490 495

Asn Asp Glu Asn Gly Lys Leu Leu Tyr Phe Ser Thr Phe Thr Thr Phe
500 505 510

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

Gln Ala Asp Gly Lys Arg Ile Leu Leu Gly Ser Gly His His His His
530 535 540

His His
545

<210> 40
<211> 517
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide capable of binding to O-glycans but lack or has
reduced O-glycoprotein-specific endoprotease activity -
Clostridium perfringens (double mutant with removed signal and
other sequences from immature protein, with N-term Met, C-term

<400> 40

Met Val Leu Glu Leu Glu Met Arg Gly Asp Ser Ile Ser Glu Ala Lys
1 5 10 15

Lys Arg Lys Val Trp Asn Phe Gln Asp Trp Gln Ile Thr Gly Leu Ser
20 25 30

Ala Arg Ala Gly Asp Lys Ile Thr Val Tyr Val Asp Val Ala Glu Gly
35 40 45

Asp Pro Thr Pro Thr Leu Leu Tyr Lys Gln Ser Leu Thr Gln His Gly
50 55 60

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

Pro Glu Ile Asn Tyr Glu Ser Asn Gly Ile Pro Lys Asp Val Ile Gln
85 90 95

Gly Gly Asp Leu Phe Phe Thr Asn Tyr Lys Ser Asp Ser Gln Lys Arg
100 105 110

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

Leu Gly Lys Ser Asp Glu Asn Glu Val Met Lys Glu Leu Glu Ala Tyr
130 135 140

Val Glu Lys Ile Lys Ala Glu Pro Lys Thr Thr Pro Asn Ile Phe Ala
145 150 155 160

Val Ser Ser Asn Lys Ser Leu Glu Phe Val Gln Ala Thr Tyr Ala Leu
165 170 175

Asp Trp Tyr Lys Lys Asn Asn Lys Thr Pro Lys Tyr Thr Ala Glu Gln
180 185 190

Trp Asp Gln Tyr Ile Ala Asp Ala Met Gly Phe Trp Gly Phe Asp Asn
195 200 205

Ser Lys Asp Val Asn Ser Asp Phe Asn Phe Arg Ile Met Pro Met Val
210 215 220

Lys Asn Leu Ser Gly Gly Ala Phe Met Asn Ala Gly Asn Gly Val Ile
225 230 235 240

Gly Ile Arg Pro Gly Asn Gln Asp Ala Ile Leu Ala Ala Asn Lys Gly
245 250 255

Trp Gly Val Ala Ala Ala Leu Gly His Asn Phe Asp Thr Gly Gly Arg
260 265 270

Thr Ile Val Glu Val Thr Asn Asn Met Met Pro Leu Phe Phe Glu Ser
275 280 285

Lys Tyr Lys Thr Lys Thr Arg Ile Thr Asp Gln Asn Ile Trp Glu Asn
290 295 300

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

Tyr Asn Lys Ala Asp Ser Thr His Leu Ala Gln Leu Ala Pro Leu Trp
325 330 335

Gln Leu Tyr Leu Tyr Asp Asn Thr Phe Tyr Gly Lys Phe Glu Arg Gln
340 345 350

Phe Arg Glu Arg Asp Phe Gly Asn Lys Asn Arg Glu Asp Ile Tyr Lys
355 360 365

Ser Trp Val Val Ala Ala Ser Asp Ala Met Glu Leu Asp Leu Thr Glu
370 375 380

Phe Phe Ala Arg His Gly Ile Arg Val Asp Asp Lys Val Lys Glu Asp
385 390 395 400

Leu Ala Lys Tyr Pro Lys Pro Asp Lys Lys Ile Tyr Tyr Leu Asn Asp
405 410 415

Leu Ala Met Asn Tyr Lys Gly Asp Gly Phe Thr Glu Asn Ala Lys Val
420 425 430

Ser Val Ser Thr Ser Gly Ser Asn Gly Asn Ile Lys Leu Ser Phe Ser
435 440 445

Val Asp Asp Glu Asn Lys Asp Asn Ile Leu Gly Tyr Glu Ile Arg Arg
450 455 460

Asp Gly Lys Tyr Val Gly Phe Thr Ser Asn Asp Ser Phe Val Asp Thr
465 470 475 480

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

Arg Lys Leu Asn Thr Leu Asn Pro Ile Glu Val Asn Gly Ser Gly His
500 505 510

His His His His His
515

<210> 41
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Metalloprotease motif

<400> 41

His Glu Leu Gly His
1 5

<210> 42
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Metalloprotease motif

<400> 42

His Glu Ile Gly His
1 5

<210> 43
<211> 10
<212> PRT
<213> Artificial Sequence

<220>

<223> Metalloprotease motif

<400> 43

Gly Val Ala His Glu Leu Gly His Asn Phe
1 5 10

<210> 44

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> disrupted metalloprotease motif

<400> 44

His Ala Leu Gly His
1 5

<210> 45

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> disrupted metalloprotease motif

<400> 45

Ala Glu Leu Gly His
1 5

<210> 46

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> disrupted metalloprotease motif

<400> 46

Ala Ala Leu Gly His
1 5

<210> 47
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> glycodrosocin peptide with O-gly site on the T

<400> 47

Gly Lys Pro Arg Pro Tyr Ser Pro Arg Pro Thr Ser His Pro Arg Pro
1 5 10 15

Ile Arg Val

<210> 48
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Non-O-glycosylated peptide

<400> 48

Tyr Ile Tyr Gly Ser Phe Lys
1 5

<210> 49
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Non-O-glycosylated peptide

<400> 49

Lys Lys Leu Val Phe Phe Ala
1 5

<210> 50

<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Non-O-glycosylated peptide

<400> 50

Phe	Leu	Pro	Leu	Ile	Leu	Gly	Lys	Leu	Val	Lys	Gly	Leu	Leu
1				5					10				