

SEQUENCE LISTING

<110> GLAXOSMITHKLINE BIOLOGICALS S.A.

<120> USPA2 PROTEIN CONSTRUCTS AND USES THEREOF

<130> VR65032

<150> US 61/943,909

<151> 2014-02-24

<150> US 61/946,932

<151> 2014-03-03

<150> US 61/946,937

<151> 2014-03-03

<160> 88

<170> PatentIn version 3.5

<210> 1

<211> 630

<212> PRT

<213> *Moraxalla catarrhalis*

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Met Lys Thr Met Lys Leu Leu Pro Leu Lys Ile Ala Val Thr Ser Ala
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Met Ile Ile Gly Leu Gly Ala Ala Ser Thr Ala Asn Ala Gln Ala Lys
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Asn Asp Ile Thr Leu Glu Asp Leu Pro Tyr Leu Ile Lys Lys Ile Asp
35 40 45

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

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

Asn Lys Ala Leu Glu Glu Leu Asp Glu Asp Val Gly Trp Asn Gln Asn
85 90 95

Asp Ile Ala Asn Leu Glu Asp Asp Val Glu Thr Leu Thr Lys Asn Gln

100					105					110					
Asn	Ala	Leu	Ala	Glu	Gln	Gly	Glu	Ala	Ile	Lys	Glu	Asp	Leu	Gln	Gly
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Leu	Ala	Asp	Phe	Val	Glu	Gly	Gln	Glu	Gly	Lys	Ile	Leu	Gln	Asn	Glu
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Thr	Ser	Ile	Lys	Lys	Asn	Thr	Gln	Arg	Asn	Leu	Val	Asn	Gly	Phe	Glu
		145					150					155			160
Ile	Glu	Lys	Asn	Lys	Asp	Ala	Ile	Ala	Lys	Asn	Asn	Glu	Ser	Ile	Glu
				165					170					175	
Asp	Leu	Tyr	Asp	Phe	Gly	His	Glu	Val	Ala	Glu	Ser	Ile	Gly	Glu	Ile
			180					185					190		
His	Ala	His	Asn	Glu	Ala	Gln	Asn	Glu	Thr	Leu	Lys	Gly	Leu	Ile	Thr
		195					200					205			
Asn	Ser	Ile	Glu	Asn	Thr	Asn	Asn	Ile	Thr	Lys	Asn	Lys	Ala	Asp	Ile
		210					215					220			
Gln	Ala	Leu	Glu	Asn	Asn	Val	Val	Glu	Glu	Leu	Phe	Asn	Leu	Ser	Gly
		225					230					235			240
Arg	Leu	Ile	Asp	Gln	Lys	Ala	Asp	Ile	Asp	Asn	Asn	Ile	Asn	Asn	Ile
				245					250					255	
Tyr	Glu	Leu	Ala	Gln	Gln	Gln	Asp	Gln	His	Ser	Ser	Asp	Ile	Lys	Thr
			260					265						270	
Leu	Lys	Lys	Asn	Val	Glu	Glu	Gly	Leu	Leu	Glu	Leu	Ser	Gly	His	Leu
			275				280					285			
Ile	Asp	Gln	Lys	Thr	Asp	Ile	Ala	Gln	Asn	Gln	Ala	Asn	Ile	Gln	Asp
			290				295					300			
Leu	Ala	Thr	Tyr	Asn	Glu	Leu	Gln	Asp	Gln	Tyr	Ala	Gln	Lys	Gln	Thr
			305				310					315			320

Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn
325 330 335

Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr Ala Lys
340 345 350

Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn
355 360 365

Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala
370 375 380

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

Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala Asp Ile Ala Asn
405 410 415

Asn Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser
420 425 430

Ser Asp Ile Lys Thr Leu Ala Lys Ala Ser Ala Ala Asn Thr Asp Arg
435 440 445

Ile Ala Lys Asn Lys Ala Asp Ala Asp Ala Ser Phe Glu Thr Leu Thr
450 455 460

Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu His Asp Lys Leu
465 470 475 480

Ile Thr Ala Asn Lys Thr Ala Ile Asp Ala Asn Lys Ala Ser Ala Asp
485 490 495

Thr Lys Phe Ala Ala Thr Ala Asp Ala Ile Thr Lys Asn Gly Asn Ala
500 505 510

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

Gly Phe Asp Ser Arg Val Thr Ala Leu Asp Thr Lys Val Asn Ala Phe
530 535 540

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

Ala Gln Ala Ala Leu Ser Gly Leu Phe Gln Pro Tyr Ser Val Gly Lys
565 570 575

Phe Asn Ala Thr Ala Ala Leu Gly Gly Tyr Gly Ser Lys Ser Ala Val
580 585 590

Ala Ile Gly Ala Gly Tyr Arg Val Asn Pro Asn Leu Ala Phe Lys Ala
595 600 605

Gly Ala Ala Ile Asn Thr Ser Gly Asn Lys Lys Gly Ser Tyr Asn Ile
610 615 620

Gly Val Asn Tyr Glu Phe
625 630

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<213> Moraxella catarrhalis

<400> 2

Met Lys Thr Met Lys Leu Leu Pro Leu Lys Ile Ala Val Thr Ser Ala
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Met Ile Ile Gly Leu Gly Ala Ala Ser Thr Ala Asn Ala Gln Ser Arg
20 25 30

Asp Arg Ser Leu Glu Asp Ile Gln Asp Ser Ile Ser Lys Leu Val Gln
35 40 45

Asp Asp Ile Asn Thr Leu Lys Gln Asp Gln Gln Lys Met Asn Lys Tyr
50 55 60

Leu Leu Leu Asn Gln Leu Ala Asn Thr Leu Ile Thr Asp Glu Leu Asn

65		70		75		80
Asn Asn Val Ile Lys Asn Thr Asn Ser Ile Glu Ala Leu Gly Asp Glu	85		90		95	
Ile Gly Trp Leu Glu Asn Asp Ile Ala Asp Leu Glu Glu Gly Val Glu	100		105		110	
Glu Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp Glu Glu His	115		120		125	
Asp Arg Leu Ile Ala Gln Asn Gln Ala Asp Ile Gln Thr Leu Glu Asn	130		135		140	
Asn Val Val Glu Glu Leu Phe Asn Leu Ser Gly Arg Leu Ile Asp Gln	145		150		155	160
Glu Ala Asp Ile Ala Lys Asn Asn Ala Ser Ile Glu Glu Leu Tyr Asp	165		170		175	
Phe Asp Asn Glu Val Ala Glu Arg Ile Gly Glu Ile His Ala Tyr Thr	180		185		190	
Glu Glu Val Asn Lys Thr Leu Glu Asn Leu Ile Thr Asn Ser Val Lys	195		200		205	
Asn Thr Asp Asn Ile Asp Lys Asn Lys Ala Asp Ile Asp Asn Asn Ile	210		215		220	
Asn His Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser Asp	225		230		235	240
Ile Lys Thr Leu Lys Asn Asn Val Glu Glu Gly Leu Leu Glu Leu Ser	245		250		255	
Gly His Leu Ile Asp Gln Lys Ala Asp Leu Thr Lys Asp Ile Lys Ala	260		265		270	
Leu Glu Ser Asn Val Glu Glu Gly Leu Leu Asp Leu Ser Gly Arg Leu	275		280		285	

Leu Asp Gln Lys Ala Asp Leu Thr Lys Asp Ile Lys Ala Leu Glu Ser
290 295 300

Asn Val Glu Glu Gly Leu Leu Asp Leu Ser Gly Arg Leu Leu Asp Gln
305 310 315 320

Lys Ala Asp Ile Ala Gln Asn Gln Thr Asp Ile Gln Asp Leu Ala Ala
325 330 335

Tyr Asn Glu Leu Gln Asp Gln Tyr Ala Gln Lys Gln Thr Glu Ala Ile
340 345 350

Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Glu Asp
355 360 365

Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr
370 375 380

Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn
385 390 395 400

Ile Ala Lys Asn Gln Ala Asp Ile Ala Asn Asn Ile Asn Asn Ile Tyr
405 410 415

Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser Asp Ile Lys Thr Leu
420 425 430

Ala Lys Ala Ser Ala Ala Asn Thr Asn Arg Ile Ala Thr Ala Glu Leu
435 440 445

Gly Ile Ala Glu Asn Lys Lys Asp Ala Gln Ile Ala Lys Ala Gln Ala
450 455 460

Asn Ala Asn Lys Thr Ala Ile Asp Glu Asn Lys Ala Ser Ala Asp Thr
465 470 475 480

Lys Phe Ala Ala Thr Ala Asp Ala Ile Thr Lys Asn Gly Asn Ala Ile
485 490 495

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

Phe Asp Gly Arg Val Thr Ala Leu Asp Thr Lys Val Asn Ala Phe Asp
515 520 525

Gly Arg Ile Thr Ala Leu Asp Ser Lys Val Glu Asn Gly Met Ala Ala
530 535 540

Gln Ala Ala Leu Ser Gly Leu Phe Gln Pro Tyr Ser Val Gly Lys Phe
545 550 555 560

Asn Ala Thr Ala Ala Leu Gly Gly Tyr Gly Ser Lys Ser Ala Val Ala
565 570 575

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

Ala Ala Ile Asn Thr Ser Gly Asn Lys Lys Gly Ser Tyr Asn Ile Gly
595 600 605

Val Asn Tyr Glu Phe
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<400> 3

Met Lys Thr Met Lys Leu Leu Pro Leu Lys Ile Ala Val Thr Ser Ala
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Leu Ile Ile Gly Leu Gly Ala Ala Ser Thr Ala Asn Ala Gln Gln Gln
20 25 30

Leu Gln Thr Glu Thr Phe Leu Pro Asn Phe Leu Ser Asn Asp Asn Tyr
35 40 45

Asp Leu Thr Asp Pro Phe Tyr His Asn Met Ile Leu Gly Asp Thr Ala

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Leu 65	Leu 66	Asp 67	Lys 68	Gln 69	Asp 70	Gly 71	Ser 72	Gln 73	Pro 74	Gln 75	Leu 76	Lys 77	Phe 78	Tyr 79	Ser 80
Asn 85	Asp 86	Lys 87	Asp 88	Ser 89	Val 90	Pro 91	Asp 92	Ser 93	Leu 94	Leu 95	Phe 96	Ser 97	Lys 98	Leu 99	Leu 100
His 105	Glu 106	Gln 107	Gln 108	Leu 109	Asn 110	Gly 111	Phe 112	Lys 113	Lys 114	Gly 115	Asp 116	Thr 117	Ile 118	Ile 119	Pro 120
Leu 125	Asp 126	Lys 127	Asp 128	Gly 129	Lys 130	Pro 131	Val 132	Tyr 133	Gln 134	Val 135	Asp 136	Tyr 137	Lys 138	Leu 139	Asp 140
Gly 145	Lys 146	Gly 147	Lys 148	Lys 149	Gln 150	Lys 151	Arg 152	Arg 153	Gln 154	Val 155	Tyr 156	Ser 157	Val 158	Thr 159	Thr 160
Lys 165	Thr 166	Ala 167	Thr 168	Asp 169	Asp 170	Asp 171	Val 172	Asn 173	Ser 174	Ala 175	Tyr 176	Ser 177	Arg 178	Gly 179	Ile 180
Leu 185	Gly 186	Lys 187	Val 188	Asp 189	Asp 190	Leu 191	Asp 192	Asp 193	Glu 194	Met 195	Asn 196	Phe 197	Leu 198	Asn 199	His 200
Asp 205	Ile 206	Thr 207	Ser 208	Leu 209	Tyr 210	Asp 211	Val 212	Thr 213	Ala 214	Asn 215	Gln 216	Gln 217	Asp 218	Ala 219	Ile 220
Lys 225	Asp 226	Leu 227	Lys 228	Lys 229	Gly 230	Val 231	Lys 232	Gly 233	Leu 234	Asn 235	Lys 236	Glu 237	Leu 238	Lys 239	Glu 240
Leu 245	Asp 246	Lys 247	Glu 248	Val 249	Gly 250	Val 251	Leu 252	Ser 253	Arg 254	Asp 255	Ile 256	Gly 257	Ser 258	Leu 259	Asn 260
Asp 265	Asp 266	Val 267	Ala 268	Gln 269	Asn 270	Asn 271	Glu 272	Ser 273	Ile 274	Glu 275	Asp 276	Leu 277	Tyr 278	Asp 279	Phe 280
Ser 285	Gln 286	Glu 287	Val 288	Ala 289	Asp 290	Ser 291	Ile 292	Gly 293	Glu 294	Ile 295	His 296	Ala 297	His 298	Asn 299	Lys 300
Ala 305	Gln 306	Asn 307	Glu 308	Thr 309	Leu 310	Gln 311	Asp 312	Leu 313	Ile 314	Thr 315	Asn 316	Ser 317	Val 318	Glu 319	Asn 320

Thr Asn Asn Ile Thr Lys Asn Lys Ala Asp Ile Gln Ala Leu Glu Asn
275 280 285

Asn Val Val Glu Glu Leu Phe Asn Leu Ser Gly Arg Leu Ile Asp Gln
290 295 300

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

Glu Gly Leu Leu Glu Leu Ser Gly His Leu Ile Asp Gln Lys Ala Asp
325 330 335

Ile Ala Lys Asn Gln Ala Asp Ile Ala Gln Asn Gln Ala Asn Ile Gln
340 345 350

Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr Ala Lys Gln Gln
355 360 365

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

Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr Ala
385 390 395 400

Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu
405 410 415

Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala Asp Ile Ala Asn Asn Ile
420 425 430

Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser Asp
435 440 445

Ile Lys Thr Leu Ala Lys Ala Ser Ala Ala Asn Thr Asp Arg Ile Ala
450 455 460

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

Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu His Asp Lys Leu Ile Thr
485 490 495

Ala Asn Lys Thr Ala Ile Asp Glu Asn Lys Ala Ser Ala Asp Thr Lys
500 505 510

Phe Ala Ala Thr Ala Asp Ala Ile Thr Lys Asn Gly Asn Ala Ile Thr
515 520 525

Lys Asn Ala Lys Ser Ile Thr Asp Leu Gly Thr Lys Val Asp Gly Phe
530 535 540

Asp Ser Arg Val Thr Ala Leu Asp Thr Lys Val Asn Ala Phe Asp Gly
545 550 555 560

Arg Ile Thr Ala Leu Asp Ser Lys Val Glu Asn Gly Met Ala Ala Gln
565 570 575

Ala Ala Leu Ser Gly Leu Phe Gln Pro Tyr Ser Val Gly Lys Phe Asn
580 585 590

Ala Thr Ala Ala Leu Gly Gly Tyr Gly Ser Lys Ser Ala Val Ala Ile
595 600 605

Gly Ala Gly Tyr Arg Val Asn Pro Asn Leu Ala Phe Lys Ala Gly Ala
610 615 620

Ala Ile Asn Thr Ser Gly Asn Lys Lys Gly Ser Tyr Asn Ile Gly Val
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Asn Tyr Glu Phe

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Met Lys Thr Met Lys Leu Leu Pro Leu Lys Ile Ala Val Thr Ser Ala

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

Asn Val Glu Lys Gly Leu Leu Glu Leu Ser Gly His Leu Ile Asp Gln
 225 230 235 240

Lys Ala Asp Leu Thr Lys Asp Ile Lys Thr Leu Glu Ser Asn Val Glu
 245 250 255

Glu Gly Leu Leu Asp Leu Ser Gly Arg Leu Ile Asp Gln Lys Ala Asp
 260 265 270

Leu Thr Lys Asp Ile Lys Thr Leu Glu Ser Asn Val Glu Glu Gly Leu
 275 280 285

Leu Asp Leu Ser Gly Arg Leu Ile Asp Gln Lys Ala Asp Ile Ala Gln
 290 295 300

Asn Gln Ala Asn Ile Gln Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp
 305 310 315 320

Gln Tyr Ala Gln Lys Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala
 325 330 335

Ser Ser Glu Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu
 340 345 350

Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu
 355 360 365

Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala
 370 375 380

Asp Ile Ala Asn Asn Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln
 385 390 395 400

Asp Gln His Ser Ser Asp Ile Lys Thr Leu Ala Lys Ala Ser Ala Ala
 405 410 415

Asn Thr Asn Arg Ile Ala Thr Ala Glu Leu Gly Ile Ala Glu Asn Lys
 420 425 430

Lys Asp Ala Gln Ile Ala Lys Ala Gln Ala Asn Ala Asn Lys Thr Ala
435 440 445

Ile Asp Glu Asn Lys Ala Ser Ala Asp Thr Lys Phe Ala Ala Thr Ala
450 455 460

Asp Ala Ile Thr Lys Asn Gly Asn Ala Ile Thr Lys Asn Ala Lys Ser
465 470 475 480

Ile Thr Asp Leu Gly Thr Lys Val Asp Gly Phe Asp Ser Arg Val Thr
485 490 495

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

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

Leu Phe Gln Pro Tyr Ser Val Gly Lys Phe Asn Ala Thr Ala Ala Leu
530 535 540

Gly Gly Tyr Gly Ser Lys Ser Ala Val Ala Ile Gly Ala Gly Tyr Arg
545 550 555 560

Val Asn Pro Asn Leu Ala Phe Lys Ala Gly Ala Ala Ile Asn Thr Ser
565 570 575

Gly Asn Lys Lys Gly Ser Tyr Asn Ile Gly Val Asn Tyr Glu Phe
580 585 590

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<213> Moraxella catarrhalis

<400> 5

Met Lys Thr Met Lys Leu Leu Pro Leu Lys Ile Ala Val Thr Ser Ala
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Met Ile Ile Gly Leu Gly Ala Ala Ser Thr Ala Asn Ala Gln Gln Gln

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

Ser Ile Glu Asp Leu Tyr Asp Phe Ser Gln Glu Val Ala Asp Ser Ile
245 250 255

Gly Glu Ile His Ala His Asn Lys Ala Gln Asn Glu Thr Leu Gln Asp
260 265 270

Leu Ile Thr Asn Ser Val Glu Asn Thr Asn Asn Ile Thr Lys Asn Lys
275 280 285

Ala Asp Ile Gln Ala Leu Glu Asn Asn Val Val Glu Glu Leu Phe Asn
290 295 300

Leu Ser Gly Arg Leu Ile Asp Gln Lys Ala Asp Leu Thr Lys Asp Ile
305 310 315 320

Lys Thr Leu Glu Ser Asn Val Glu Glu Gly Leu Leu Glu Leu Ser Gly
325 330 335

His Leu Ile Asp Gln Lys Ala Asp Ile Ala Lys Asn Gln Ala Asp Ile
340 345 350

Ala Gln Asn Gln Ala Asn Ile Gln Asp Leu Ala Ala Tyr Asn Glu Leu
355 360 365

Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn
370 375 380

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

Asn Glu Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp
405 410 415

Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Glu Asp Leu
420 425 430

Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu
435 440 445

Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile
450 455 460

Ala Lys Asn Gln Ala Asp Ile Ala Asn Asn Ile Asn Asn Ile Tyr Glu
465 470 475 480

Leu Ala Gln Gln Gln Asp Gln His Ser Ser Asp Ile Lys Thr Leu Ala
485 490 495

Lys Ala Ser Ala Ala Asn Thr Asp Arg Ile Ala Lys Asn Lys Ala Asp
500 505 510

Ala Asp Ala Ser Phe Glu Thr Leu Thr Lys Asn Gln Asn Thr Leu Ile
515 520 525

Glu Lys Asp Lys Glu His Asp Lys Leu Ile Thr Ala Asn Lys Thr Ala
530 535 540

Ile Asp Glu Asn Lys Ala Ser Ala Asp Thr Lys Phe Ala Ala Thr Ala
545 550 555 560

Asp Ala Ile Thr Lys Asn Gly Asn Ala Ile Thr Lys Asn Ala Lys Ser
565 570 575

Ile Thr Asp Leu Gly Thr Lys Val Asp Ala Phe Asp Gly Arg Val Thr
580 585 590

Ala Leu Asp Thr Lys Val Asn Ala Phe Asp Gly Arg Ile Thr Ala Leu
595 600 605

Asp Ser Lys Val Glu Asn Gly Met Ala Ala Gln Ala Ala Leu Ser Gly
610 615 620

Leu Phe Gln Pro Tyr Ser Val Gly Lys Phe Asn Ala Thr Ala Ala Leu
625 630 635 640

Gly Gly Tyr Gly Ser Lys Ser Ala Val Ala Ile Gly Ala Gly Tyr Arg
645 650 655

Val Asn Pro Asn Leu Ala Phe Lys Ala Gly Ala Ala Ile Asn Thr Ser
660 665 670

Gly Asn Lys Lys Gly Ser Tyr Asn Ile Gly Val Asn Tyr Glu Phe
675 680 685

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Met Lys Thr Met Lys Leu Leu Pro Leu Lys Ile Ala Val Thr Ser Ala
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Met Ile Val Gly Leu Gly Met Ala Ser Thr Ala Asn Ala Gln Gln Gln
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Lys Ser Pro Lys Thr Glu Thr Phe Leu Pro Asn Ile Phe Phe Asn Glu
35 40 45

Tyr Ala Asp Asp Leu Asp Thr Leu Tyr His Asn Met Ile Leu Gly Asp
50 55 60

Thr Ala Ile Thr His Asp Asp Gln Tyr Lys Phe Tyr Ala Asp Asp Ala
65 70 75 80

Thr Glu Val Pro Asp Ser Leu Phe Phe Asn Lys Ile Leu His Asp Gln
85 90 95

Leu Leu Tyr Gly Phe Lys Glu Gly Asp Lys Ile Ile Pro Leu Asp Glu
100 105 110

Asn Gly Lys Pro Val Tyr Lys Leu Asp Lys Arg Leu Glu Asn Gly Val
115 120 125

Gln Lys Thr Val Tyr Ser Val Thr Thr Lys Thr Ala Thr Ala Asp Asp
130 135 140

Val Asn Ser Ala Tyr Ser Arg Gly Ile Gln Gly Asp Ile Asp Asp Leu
145 150 155 160

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

Lys Ile Phe Ala Asn Glu Glu Ser Val Gln Tyr Leu Asn Arg Glu Val
180 185 190

Gln Asn Asn Ile Glu Asn Ile His Glu Leu Ala Gln Gln Gln Asp Gln
195 200 205

His Ser Ser Asp Ile Lys Thr Leu Lys Lys Asn Val Glu Lys Asp Leu
210 215 220

Leu Asp Leu Ser Gly Arg Leu Ile Ala Gln Lys Glu Asp Ile Ala Gln
225 230 235 240

Asn Gln Thr Asp Ile Gln Asp Leu Ala Thr Tyr Asn Glu Leu Gln Asp
245 250 255

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

Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Ser Asn His Ile Lys
275 280 285

Thr Leu Glu Asn Asn Ile Glu Glu Gly Leu Leu Glu Leu Ser Gly His
290 295 300

Leu Ile Asp Gln Lys Ala Asp Leu Thr Lys Asp Ile Lys Ala Leu Glu
305 310 315 320

Ser Asn Val Glu Glu Gly Leu Leu Asp Leu Ser Gly Arg Leu Ile Asp
325 330 335

Gln Lys Ala Asp Ile Ala Gln Asn Gln Ala Asn Ile Gln Asp Leu Ala
340 345 350

Ala Tyr Asn Glu Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala
355 360 365

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

Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr Ala Lys Gln Gln
385 390 395 400

Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr Gln
405 410 415

Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr Ala
420 425 430

Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu
435 440 445

Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala Asp Ile Ala Asn Asn Ile
450 455 460

Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser Asp
465 470 475 480

Ile Lys Thr Leu Ala Lys Ala Ser Ala Ala Asn Thr Asp Arg Ile Ala
485 490 495

Lys Asn Lys Ala Asp Ala Asp Ala Ser Phe Glu Thr Leu Thr Lys Asn
500 505 510

Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu His Asp Lys Leu Ile Thr
515 520 525

Ala Asn Lys Thr Ala Ile Asp Ala Asn Lys Ala Ser Ala Asp Thr Lys
530 535 540

Phe Ala Ala Thr Ala Asp Ala Ile Thr Lys Asn Gly Asn Ala Ile Thr
545 550 555 560

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

Asp Gly Arg Val Thr Ala Leu Asp Thr Lys Val Asn Ala Leu Asp Thr
580 585 590

Lys Val Asn Ala Phe Asp Gly Arg Ile Thr Ala Leu Asp Ser Lys Val
595 600 605

Glu Asn Gly Met Ala Ala Gln Ala Ala Leu Ser Gly Leu Phe Gln Pro
610 615 620

Tyr Ser Val Gly Lys Phe Asn Ala Thr Ala Ala Leu Gly Gly Tyr Gly
625 630 635 640

Ser Lys Ser Ala Val Ala Ile Gly Ala Gly Tyr Arg Val Asn Pro Asn
645 650 655

Leu Ala Phe Lys Ala Gly Ala Ala Ile Asn Thr Ser Gly Asn Lys Lys
660 665 670

Gly Ser Tyr Asn Ile Gly Val Asn Tyr Glu Phe
675 680

<210> 7
<211> 684
<212> PRT
<213> Moraxella catarrhalis

<400> 7

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

Met Met Val Gly Leu Gly Met Ala Ser Thr Ala Asn Ala Gln Gln Gln
20 25 30

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

Asn Thr Glu Leu Thr Asp Pro Leu Tyr His Asn Met Ile Leu Gly Asn
50 55 60

Thr Ala Leu Leu Thr Gln Glu Asn Gln Tyr Lys Phe Tyr Ala Asp Asp
65 70 75 80

Gly Asn Gly Val Pro Asp Ser Leu Leu Phe Asn Lys Ile Leu His Asp
85 90 95

Gln Leu Leu His Gly Phe Lys Glu Gly Gly Thr Ile Ile Pro Leu Asp
100 105 110

Glu Asn Gly Lys Pro Val Tyr Lys Leu Asp Ser Ile Val Glu Gln Gly
115 120 125

Lys Thr Lys Thr Val Tyr Ser Val Thr Thr Lys Thr Ala Thr Ala Asp
130 135 140

Asp Val Asn Ser Ala Tyr Ser Arg Gly Ile Gln Gly Asp Ile Asp Asp
145 150 155 160

Leu Tyr Glu Ala Asn Lys Glu Asn Val Asn Arg Leu Ile Glu His Gly
165 170 175

Asp Lys Ile Phe Ala Asn Glu Glu Ser Val Gln Tyr Leu Asn Arg Glu
180 185 190

Val Gln Asn Asn Ile Glu Asn Ile His Glu Leu Ala Gln Gln Gln Asp
195 200 205

Gln His Ser Ser Asp Ile Lys Thr Leu Lys Lys Asn Val Glu Lys Asp
210 215 220

Leu Leu Asp Leu Ser Gly Arg Leu Ile Ala Gln Lys Glu Asp Ile Ala
225 230 235 240

Gln Asn Gln Thr Asp Ile Gln Asp Leu Ala Thr Tyr Asn Glu Leu Gln
245 250 255

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

Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Ser Asn His Ile
275 280 285

Lys Thr Leu Glu Asn Asn Ile Glu Glu Gly Leu Leu Glu Leu Ser Gly
290 295 300

His Leu Ile Asp Gln Lys Ala Asp Leu Thr Lys Asp Ile Lys Ala Leu
305 310 315 320

Glu Ser Asn Val Glu Glu Gly Leu Leu Asp Leu Ser Gly Arg Leu Ile
325 330 335

Asp Gln Lys Ala Asp Ile Ala Gln Asn Gln Ala Asn Ile Gln Asp Leu
340 345 350

Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu
355 360 365

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

Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr Ala Lys Gln
385 390 395 400

Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr
405 410 415

Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr
420 425 430

Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser
435 440 445

Glu Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala Asp Ile Ala Asn Asn
450 455 460

Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser
465 470 475 480

Asp Ile Lys Thr Leu Ala Lys Ala Ser Ala Ala Asn Thr Asp Arg Ile
485 490 495

Ala Lys Asn Lys Ala Asp Ala Asp Ala Ser Phe Glu Thr Leu Thr Lys
500 505 510

Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu His Asp Lys Leu Ile
515 520 525

Thr Ala Asn Lys Thr Ala Ile Asp Ala Asn Lys Ala Ser Ala Asp Thr
530 535 540

Lys Phe Ala Ala Thr Ala Asp Ala Ile Thr Lys Asn Gly Asn Ala Ile
545 550 555 560

Thr Lys Asn Ala Lys Ser Ile Thr Asp Leu Gly Thr Lys Val Asp Gly
565 570 575

Phe Asp Gly Arg Val Thr Ala Leu Asp Thr Lys Val Asn Ala Leu Asp
580 585 590

Thr Lys Val Asn Ala Phe Asp Gly Arg Ile Thr Ala Leu Asp Ser Lys
595 600 605

Val Glu Asn Gly Met Ala Ala Gln Ala Ala Leu Ser Gly Leu Phe Gln
610 615 620

Pro Tyr Ser Val Gly Lys Phe Asn Ala Thr Ala Ala Leu Gly Gly Tyr
625 630 635 640

Gly Ser Lys Ser Ala Val Ala Ile Gly Ala Gly Tyr Arg Val Asn Pro
645 650 655

Asn Leu Ala Phe Lys Ala Gly Ala Ala Ile Asn Thr Ser Gly Asn Lys
660 665 670

Lys Gly Ser Tyr Asn Ile Gly Val Asn Tyr Glu Phe
675 680

<210> 8
<211> 684
<212> PRT
<213> Moraxella catarrhalis

<400> 8

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

Met Ile Ile Gly Leu Gly Ala Ala Ser Thr Ala Asn Ala Gln Gln Gln
20 25 30

Gln Lys Thr Lys Thr Glu Val Phe Leu Pro Asn Leu Phe Asp Asn Asp
35 40 45

Tyr Tyr Asp Leu Thr Asp Pro Leu Tyr His Ser Met Ile Leu Gly Asp
50 55 60

Thr Ala Thr Leu Phe Asp Gln Gln Asp Asn Ser Lys Ser Gln Leu Lys
65 70 75 80

Phe Tyr Ser Asn Asp Lys Asp Ser Val Pro Asp Ser Leu Leu Phe Ser
85 90 95

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

Ile Ile Pro Leu Asp Lys Asp Gly Lys Pro Val Tyr Thr Gln Asp Thr
115 120 125

Arg Thr Lys Asp Gly Lys Val Glu Thr Val Tyr Ser Val Thr Thr Lys
130 135 140

Ile Ala Thr Gln Asp Asp Val Glu Gln Ser Ala Tyr Ser Arg Gly Ile
145 150 155 160

Gln Gly Asp Ile Asp Asp Leu Tyr Asp Ile Asn Arg Glu Val Asn Glu
165 170 175

Tyr Leu Lys Ala Thr His Asp Tyr Asn Glu Arg Gln Thr Glu Ala Ile
180 185 190

Asp Ala Leu Asn Lys Ala Ser Ser Ala Asn Thr Asp Arg Ile Asp Thr
195 200 205

Ala Glu Glu Arg Ile Asp Lys Asn Glu Tyr Asp Ile Lys Ala Leu Glu
210 215 220

Ser Asn Val Gly Lys Asp Leu Leu Asp Leu Ser Gly Arg Leu Ile Ala
225 230 235 240

Gln Lys Glu Asp Ile Asp Asn Asn Ile Asn His Ile Tyr Glu Leu Ala
245 250 255

Gln Gln Gln Asp Gln His Ser Ser Asp Ile Lys Thr Leu Lys Asn Asn
260 265 270

Val Glu Glu Gly Leu Leu Glu Leu Ser Gly His Leu Ile Asp Gln Lys
275 280 285

Ala Asp Leu Thr Lys Asp Ile Lys Thr Leu Glu Asn Asn Ile Glu Glu
290 295 300

Gly Leu Leu Glu Leu Ser Gly His Leu Ile Asp Gln Lys Ala Asp Leu
305 310 315 320

Thr Lys Asp Ile Lys Thr Leu Glu Asn Asn Ile Glu Glu Gly Leu Leu
325 330 335

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

Gln Ala Asn Ile Gln Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Gln
355 360 365

Tyr Ala Gln Lys Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser
370 375 380

Ser Glu Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu
385 390 395 400

Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn
405 410 415

Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr
420 425 430

Asn Glu Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp
435 440 445

Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn
450 455 460

Gln Ala Asp Ile Ala Asn Asn Ile Asn Asn Ile Tyr Glu Leu Ala Gln
465 470 475 480

Gln Gln Asp Gln His Ser Ser Asp Ile Lys Thr Leu Ala Lys Val Ser
485 490 495

Ala Ala Asn Thr Asp Arg Ile Ala Lys Asn Lys Ala Asp Ala Asp Ala
500 505 510

Ser Phe Glu Thr Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp
515 520 525

Lys Glu His Asp Lys Leu Ile Thr Ala Asn Lys Thr Ala Ile Asp Ala
530 535 540

Asn Lys Ala Ser Ala Asp Thr Lys Phe Ala Ala Thr Ala Asp Ala Ile
545 550 555 560

Thr Lys Asn Gly Asn Ala Ile Thr Lys Asn Ala Lys Ser Ile Thr Asp
565 570 575

Leu Gly Thr Lys Val Asp Gly Phe Asp Gly Arg Val Thr Ala Leu Asp
580 585 590

Thr Lys Val Asn Ala Phe Asp Gly Arg Ile Thr Ala Leu Asp Ser Lys
595 600 605

Val Glu Asn Gly Met Ala Ala Gln Ala Ala Leu Ser Gly Leu Phe Gln
610 615 620

Pro Tyr Ser Val Gly Lys Phe Asn Ala Thr Ala Ala Leu Gly Gly Tyr

Lys Thr Lys Thr Val Tyr Ser Val Thr Thr Lys Thr Ala Thr Ala Asp
130 135 140

Asp Val Asn Ser Ala Tyr Ser Arg Gly Ile Gln Gly Asp Ile Asp Asp
145 150 155 160

Leu Tyr Glu Ala Asn Lys Glu Asn Val Asn Arg Leu Ile Glu His Gly
165 170 175

Asp Lys Ile Phe Ala Asn Glu Glu Ser Val Gln Tyr Leu Asn Arg Glu
180 185 190

Val Gln Asn Asn Ile Glu Asn Ile Tyr Glu Leu Val Gln Gln Gln Asp
195 200 205

Gln His Ser Ser Asp Ile Lys Thr Leu Lys Lys Asn Val Glu Lys Asp
210 215 220

Leu Leu Asp Leu Ser Gly Arg Leu Ile Ala Gln Lys Glu Asp Ile Ala
225 230 235 240

Gln Asn Gln Thr Asp Ile Gln Asp Leu Ala Thr Tyr Asn Glu Leu Gln
245 250 255

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

Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Ser Asn His Ile
275 280 285

Lys Thr Leu Glu Asn Asn Ile Glu Glu Gly Leu Leu Glu Leu Ser Gly
290 295 300

His Leu Ile Asp Gln Lys Ala Asp Leu Thr Lys Asp Ile Lys Ala Leu
305 310 315 320

Glu Ser Asn Val Glu Glu Gly Leu Leu Asp Leu Ser Gly Arg Leu Ile
325 330 335

Asp Gln Lys Ala Asp Ile Ala Gln Asn Gln Ala Asn Ile Gln Asp Leu
340 345 350

Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu
355 360 365

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

Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr Ala Lys Gln
385 390 395 400

Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr
405 410 415

Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr
420 425 430

Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser
435 440 445

Glu Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala Asp Ile Ala Asn Asn
450 455 460

Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser
465 470 475 480

Asp Ile Lys Thr Leu Ala Lys Ala Ser Ala Ala Asn Thr Asp Arg Ile
485 490 495

Ala Lys Asn Lys Ala Asp Ala Asp Ala Ser Phe Glu Thr Leu Thr Lys
500 505 510

Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu His Asp Lys Leu Ile
515 520 525

Thr Ala Asn Lys Thr Ala Ile Asp Ala Asn Lys Ala Ser Ala Asp Thr
530 535 540

Lys Phe Ala Ala Thr Ala Asp Ala Ile Thr Lys Asn Gly Asn Ala Ile

545 550 555 560
 Thr Lys Asn Ala Lys Ser Ile Thr Asp Leu Gly Thr Lys Val Asp Gly
 565 570 575
 Phe Asp Gly Arg Val Thr Ala Leu Asp Thr Lys Val Asn Ala Leu Asp
 580 585 590
 Thr Lys Val Asn Ala Phe Asp Gly Arg Ile Thr Ala Leu Asp Ser Lys
 595 600 605
 Val Glu Asn Gly Met Ala Ala Gln Ala Ala Leu Ser Gly Leu Phe Gln
 610 615 620
 Pro Tyr Ser Val Gly Lys Phe Asn Ala Thr Ala Ala Leu Gly Gly Tyr
 625 630 635 640
 Gly Ser Lys Ser Ala Val Ala Ile Gly Ala Gly Tyr Arg Val Asn Pro
 645 650 655
 Asn Leu Ala Phe Lys Ala Gly Ala Ala Ile Asn Thr Ser Gly Asn Lys
 660 665 670
 Lys Gly Ser Tyr Asn Ile Gly Val Asn Tyr Glu Phe
 675 680

 <210> 10
 <211> 574
 <212> PRT
 <213> Moraxella catarrhalis

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

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

Gln Asp Ser Asp Asp Thr Gln Leu Lys Phe Tyr Ser Asn Asp Glu Tyr
65 70 75 80

Ser Val Pro Asp Ser Leu Leu Phe Asn Lys Met Leu His Glu Gln Gln
85 90 95

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

Gly Lys Pro Val Tyr Lys Val Asp Tyr Lys Leu Asp Gly Gln Glu Pro
115 120 125

Arg Arg Val Tyr Ser Val Thr Thr Lys Ile Ala Thr Gln Asp Asp Val
130 135 140

Asp Asn Ser Pro Tyr Ser Arg Gly Ile Gln Gly Asp Ile Asp Asp Leu
145 150 155 160

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

Lys Ile Phe Ala Asn Glu Glu Ser Val Gln Tyr Leu Asn Lys Glu Val
180 185 190

Gln Asn Asn Ile Glu Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln
195 200 205

His Ser Ser Asp Ile Lys Thr Leu Lys Lys Asn Val Glu Glu Gly Leu
210 215 220

Leu Glu Leu Ser Gly His Leu Ile Asp Gln Lys Ala Asp Leu Thr Lys
225 230 235 240

Asp Ile Lys Thr Leu Glu Ser Asn Val Glu Glu Gly Leu Leu Glu Leu
245 250 255

Ser Gly His Leu Ile Asp Gln Lys Ala Asp Ile Ala Lys Asn Gln Ala
260 265 270

Asp Ile Ala Gln Asn Gln Ala Asn Ile Gln Asp Leu Ala Ala Tyr Asn
275 280 285

Glu Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala
290 295 300

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

Ala Tyr Asn Glu Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala
325 330 335

Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala
340 345 350

Lys Asn Gln Ala Asp Ile Ala Asn Asn Ile Asn Asn Ile Tyr Glu Leu
355 360 365

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

Ala Ser Ala Ala Asn Thr Asp Arg Ile Ala Lys Asn Lys Ala Asp Ala
385 390 395 400

Asp Ala Ser Phe Glu Thr Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu
405 410 415

Lys Asp Lys Glu His Asp Lys Leu Ile Thr Ala Asn Lys Thr Ala Ile
420 425 430

Asp Ala Asn Lys Ala Ser Ala Asp Thr Lys Phe Ala Ala Thr Ala Asp
435 440 445

Ala Ile Thr Lys Asn Gly Asn Ala Ile Thr Lys Asn Ala Lys Ser Ile
450 455 460

Thr Asp Leu Gly Thr Lys Val Asp Ala Phe Asp Gly Arg Val Thr Ala

465 470 475 480
 Leu Asp Thr Lys Val Asn Ala Phe Asp Gly Arg Ile Thr Ala Leu Asp
 485 490 495
 Ser Lys Val Glu Asn Gly Met Ala Ala Gln Ala Ala Leu Ser Gly Leu
 500 505 510
 Phe Gln Pro Tyr Ser Val Gly Lys Phe Asn Ala Thr Ala Ala Leu Gly
 515 520 525
 Gly Tyr Gly Ser Lys Ser Ala Val Ala Ile Gly Ala Gly Tyr Arg Val
 530 535 540
 Asn Pro Asn Leu Ala Phe Lys Ala Gly Ala Ala Ile Asn Thr Ser Gly
 545 550 555 560
 Asn Lys Lys Gly Ser Tyr Asn Ile Gly Val Asn Tyr Glu Phe
 565 570

 <210> 11
 <211> 678
 <212> PRT
 <213> Moraxella catarrhalis

 <400> 11
 Met Lys Thr Met Lys Leu Leu Pro Leu Lys Ile Ala Val Thr Ser Ala
 1 5 10 15

 Leu Ile Val Gly Leu Gly Ala Ala Ser Thr Ala Asn Ala Gln Gln Gln
 20 25 30

 Pro Gln Thr Glu Thr Phe Phe Pro Asn Ile Phe Phe Asn Glu Asn His
 35 40 45

 Asp Ala Leu Asp Asp Val Tyr His Asn Met Ile Leu Gly Asp Thr Ala
 50 55 60

 Ile Thr Gln Asp Asn Gln Tyr Lys Phe Tyr Ala Asp Ala Ile Ser Glu
 65 70 75 80

Val Pro Asp Ser Leu Leu Phe Asn Lys Ile Leu His Asp Gln Gln Leu
85 90 95

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

Lys Pro Val Tyr Lys Leu Asp Glu Lys Val Glu Asn Gly Val Lys Lys
115 120 125

Ser Val Tyr Ser Val Thr Thr Lys Thr Ala Thr Arg Ala Asp Val Glu
130 135 140

Gln Ser Ala Tyr Ser Arg Gly Ile Gln Gly Asp Ile Asp Asp Leu Tyr
145 150 155 160

Glu Ala Asn Lys Glu Asn Val Asn Arg Leu Ile Glu His Gly Asp Lys
165 170 175

Ile Phe Ala Asn Glu Glu Ser Val Gln Tyr Leu Asn Lys Glu Val Gln
180 185 190

Asn Asn Ile Glu Asn Ile His Glu Leu Ala Gln Gln Gln Asp Gln His
195 200 205

Ser Ser Asp Ile Lys Thr Leu Lys Lys Asn Val Glu Glu Gly Leu Leu
210 215 220

Glu Leu Ser Gly His Leu Ile Asp Gln Lys Ala Asp Leu Thr Lys Asp
225 230 235 240

Ile Lys Thr Leu Glu Ser Asn Val Glu Glu Gly Leu Leu Asp Leu Ser
245 250 255

Gly Arg Leu Leu Asp Gln Lys Ala Asp Ile Ala Gln Asn Gln Ala Asn
260 265 270

Ile Gln Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr Ala Lys
275 280 285

Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn
290 295 300

Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala
305 310 315 320

Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser
325 330 335

Ser Glu Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu
340 345 350

Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn
355 360 365

Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr
370 375 380

Asn Glu Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp
385 390 395 400

Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Glu Asp Leu
405 410 415

Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu
420 425 430

Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile
435 440 445

Ala Lys Asn Gln Ala Asp Ile Ala Asn Asn Ile Asn Asn Ile Tyr Glu
450 455 460

Leu Ala Gln Gln Gln Asp Gln His Ser Ser Asp Ile Lys Thr Leu Ala
465 470 475 480

Lys Ala Ser Ala Ala Asn Thr Asp Arg Ile Ala Lys Asn Lys Ala Asp
485 490 495

Ala Asp Ala Ser Phe Glu Thr Leu Thr Lys Asn Gln Asn Thr Leu Ile

	500		505		510
Glu Lys Asp Lys Glu His Asp Lys Leu Ile Thr Ala Asn Lys Thr Ala	515		520		525
Ile Asp Ala Asn Lys Ala Ser Ala Asp Thr Lys Phe Ala Ala Thr Ala	530		535		540
Asp Ala Ile Thr Lys Asn Gly Asn Ala Ile Thr Lys Asn Ala Lys Ser	545		550		555
Ile Thr Asp Leu Gly Thr Lys Val Asp Ala Phe Asp Gly Arg Val Thr		565		570	575
Ala Leu Asp Thr Lys Val Asn Ala Leu Asp Thr Lys Val Asn Ala Phe		580		585	590
Asp Gly Arg Ile Thr Ala Leu Asp Ser Lys Val Glu Asn Gly Met Ala		595		600	605
Ala Gln Ala Ala Leu Ser Gly Leu Phe Gln Pro Tyr Ser Val Gly Lys		610		615	620
Phe Asn Ala Thr Ala Ala Leu Gly Gly Tyr Gly Ser Lys Ser Ala Val		625		630	635
Ala Ile Gly Ala Gly Tyr Arg Val Asn Pro Asn Leu Ala Phe Lys Ala		645		650	655
Gly Ala Ala Ile Asn Thr Ser Gly Asn Lys Lys Gly Ser Tyr Asn Ile		660		665	670
Gly Val Asn Tyr Glu Phe		675			

<210> 12
 <211> 678
 <212> PRT
 <213> Moraxella catarrhalis

 <400> 12

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

Met Ile Val Gly Leu Gly Ala Ala Ser Thr Ala Asn Ala Gln Gln Gln
 20 25 30

Gln Gln Pro Arg Thr Glu Thr Phe Phe Pro Asn Ile Phe Phe Asn Glu
 35 40 45

Asn His Asp Ala Leu Asp Asp Val Tyr His Asn Met Ile Leu Gly Asp
 50 55 60

Thr Ala Ile Thr Gln Asp Asn Gln Tyr Lys Phe Tyr Ala Asp Ala Ile
 65 70 75 80

Ser Glu Val Pro Asp Ser Leu Leu Phe Asn Lys Ile Leu His Asp Gln
 85 90 95

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

Asn Gly Lys Pro Val Tyr Lys Leu Asp Glu Lys Val Glu Asn Gly Val
 115 120 125

Lys Lys Ser Val Tyr Ser Val Thr Thr Lys Thr Ala Thr Arg Ala Asp
 130 135 140

Val Glu Gln Ser Ala Tyr Ser Arg Gly Ile Gln Gly Asp Ile Asp Asp
 145 150 155 160

Leu Tyr Glu Ala Asn Lys Glu Asn Val Asn Arg Leu Ile Glu His Gly
 165 170 175

Asp Lys Ile Phe Ala Asn Glu Glu Ser Val Gln Tyr Leu Asn Arg Glu
 180 185 190

Val Gln Asn Asn Ile Glu Asn Ile His Glu Leu Ala Gln Gln Gln Asp
 195 200 205

Gln His Ser Ser Asp Ile Lys Thr Leu Lys Lys Asn Val Glu Lys Asp
210 215 220

Leu Leu Asp Leu Ser Gly Arg Leu Ile Ala Gln Lys Glu Asp Ile Ala
225 230 235 240

Gln Asn Gln Thr Asp Ile Gln Asp Leu Ala Thr Tyr Asn Glu Leu Gln
245 250 255

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

Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Ser Asn His Ile
275 280 285

Lys Thr Leu Glu Asn Asn Ile Glu Glu Gly Leu Leu Glu Leu Ser Gly
290 295 300

His Leu Ile Asp Gln Lys Ala Asp Leu Thr Lys Asp Ile Lys Thr Leu
305 310 315 320

Glu Asn Asn Ile Glu Glu Gly Leu Leu Glu Leu Ser Gly His Leu Ile
325 330 335

Asp Gln Lys Ala Asp Leu Thr Lys Asp Ile Lys Ala Leu Glu Ser Asn
340 345 350

Val Glu Glu Gly Leu Leu Asp Leu Ser Gly Arg Leu Leu Asp Gln Lys
355 360 365

Ala Asp Ile Ala Gln Asn Gln Ala Asn Ile Gln Asp Leu Ala Ala Tyr
370 375 380

Asn Glu Leu Gln Asp Gln Tyr Ala Gln Lys Gln Thr Glu Ala Ile Asp
385 390 395 400

Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Glu Asp Leu
405 410 415

Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu

420	425	430
Ala Ile Asp Ala Leu Asn Lys	Ala Ser Ser Glu Asn Thr Gln Asn Ile	
435	440	445
Ala Lys Asn Gln Ala Asp Ile Ala Asn Asn Ile Asn Asn Ile Tyr Glu		
450	455	460
Leu Ala Gln Gln Gln Asp Gln His Ser Ser Asp Ile Lys Thr Leu Ala		
465	470	475
Lys Ala Ser Ala Ala Asn Thr Asp Arg Ile Ala Lys Asn Lys Ala Asp		
485	490	495
Ala Asp Ala Ser Phe Glu Thr Leu Thr Lys Asn Gln Asn Thr Leu Ile		
500	505	510
Glu Lys Asp Lys Glu His Asp Lys Leu Ile Thr Ala Asn Lys Thr Ala		
515	520	525
Ile Asp Thr Asn Lys Ala Ser Ala Asp Thr Lys Phe Ala Ala Thr Ala		
530	535	540
Asp Ala Ile Thr Lys Asn Gly Asn Ala Ile Thr Lys Asn Ala Lys Ser		
545	550	555
Ile Thr Asp Leu Gly Thr Lys Val Asp Gly Phe Asp Gly Arg Val Thr		
565	570	575
Ala Leu Asp Thr Lys Val Asn Ala Leu Asp Thr Lys Val Asn Ala Phe		
580	585	590
Asp Gly Arg Ile Thr Ala Leu Asp Ser Lys Val Glu Asn Gly Met Ala		
595	600	605
Ala Gln Ala Ala Leu Ser Gly Leu Phe Gln Pro Tyr Ser Val Gly Lys		
610	615	620
Phe Asn Ala Thr Ala Ala Leu Gly Gly Tyr Gly Ser Lys Ser Ala Val		
625	630	635
		640

Ala Ile Gly Ala Gly Tyr Arg Val Asn Pro Asn Leu Ala Phe Lys Ala
645 650 655

Gly Ala Ala Ile Asn Thr Ser Gly Asn Lys Lys Gly Ser Tyr Asn Ile
660 665 670

Gly Val Asn Tyr Glu Phe
675

<210> 13
<211> 587
<212> PRT
<213> Moraxella catarrhalis

<400> 13

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

Leu Ile Val Gly Leu Gly Ala Ala Ser Thr Ala Asn Ala Gln Leu Val
20 25 30

Glu Arg Phe Phe Pro Asn Ile Phe Leu Asp Lys Pro Leu Ala Lys Gln
35 40 45

His Tyr His Asn Val Val Val Gly Asp Thr Ser Ile Val Ser Asp Leu
50 55 60

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

Val Pro Asp Ser Leu Leu Phe Asn Lys Met Leu His Glu Gln Leu Leu
85 90 95

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

Lys Pro Val Tyr Lys Val Asp Tyr Lys Leu Asp Gly Lys Glu Pro Arg
115 120 125

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

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

Asp Phe Asp His Gln Val Thr Glu Arg Leu Thr Gln His Gly Lys Thr
165 170 175

Ile Tyr Arg Asn Gly Glu Arg Ile Leu Ala Asn Glu Glu Ser Val Gln
180 185 190

Tyr Leu Asn Lys Glu Val Gln Asn Asn Ile Glu His Ile Tyr Glu Leu
195 200 205

Ala Gln Gln Gln Asp Gln His Ser Ser Asp Ile Lys Thr Leu Glu Ser
210 215 220

Asn Val Glu Lys Gly Leu Leu Glu Leu Ser Gly His Leu Ile Asp Gln
225 230 235 240

Lys Ala Asp Leu Thr Lys Asp Ile Lys Thr Leu Glu Asn Asn Val Glu
245 250 255

Glu Gly Leu Leu Asp Leu Ser Gly Arg Leu Ile Asp Gln Lys Ala Asp
260 265 270

Ile Ala Gln Asn Gln Ala Asn Ile Gln Asp Leu Ala Ala Tyr Asn Glu
275 280 285

Leu Gln Asp Gln Tyr Ala Gln Lys Gln Thr Glu Ala Ile Asp Ala Leu
290 295 300

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

Tyr Asn Glu Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile
325 330 335

Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys

340	345	350
Asn Gln Ala Asp Ile Ala Asn Asn Ile Asn Asn Ile Tyr Glu Leu Ala		
355	360	365
Gln Gln Gln Asp Gln His Ser Ser Asp Ile Lys Thr Leu Ala Lys Ala		
370	375	380
Ser Ala Ala Asn Thr Asp Arg Ile Ala Lys Asn Lys Ala Asp Ala Asp		
385	390	395
Ala Ser Phe Glu Thr Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys		
405	410	415
Asp Lys Glu His Asp Lys Leu Ile Thr Ala Asn Lys Thr Ala Ile Asp		
420	425	430
Thr Asn Lys Ala Ser Ala Asp Thr Lys Phe Ala Ala Thr Ala Asp Ala		
435	440	445
Ile Thr Lys Asn Gly Asn Ala Ile Thr Lys Asn Ala Lys Ser Ile Thr		
450	455	460
Asp Leu Gly Thr Lys Val Asp Gly Phe Asp Ser Arg Val Thr Ala Leu		
465	470	475
Asp Thr Lys Val Asn Ala Leu Asp Thr Lys Val Asn Ala Leu Asp Thr		
485	490	495
Lys Val Asn Ala Phe Asp Gly Arg Ile Thr Ala Leu Asp Ser Lys Val		
500	505	510
Glu Asn Gly Met Ala Ala Gln Ala Ala Leu Ser Gly Leu Phe Gln Pro		
515	520	525
Tyr Ser Val Gly Lys Phe Asn Ala Thr Ala Ala Leu Gly Gly Tyr Gly		
530	535	540
Ser Lys Ser Ala Val Ala Ile Gly Ala Gly Tyr Arg Val Asn Pro Asn		
545	550	555
		560

Leu Ala Phe Lys Ala Gly Ala Ala Ile Asn Thr Ser Gly Asn Lys Lys
565 570 575

Gly Ser Tyr Asn Ile Gly Val Asn Tyr Glu Phe
580 585

<210> 14
<211> 678
<212> PRT
<213> Moraxella catarrhalis

<400> 14

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

Met Ile Val Gly Leu Gly Ala Ala Ser Thr Ala Asn Ala Gln Gln Gln
20 25 30

Gln Gln Pro Arg Thr Glu Thr Phe Phe Pro Asn Ile Phe Phe Asn Glu
35 40 45

Asn His Asp Ala Leu Asp Asp Val Tyr His Asn Met Ile Leu Gly Asp
50 55 60

Thr Ala Ile Thr Gln Asp Asn Gln Tyr Lys Phe Tyr Ala Asp Ala Ile
65 70 75 80

Ser Glu Val Pro Asp Ser Leu Leu Phe Asn Lys Ile Leu His Asp Gln
85 90 95

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

Asn Gly Lys Pro Val Tyr Lys Leu Asp Glu Lys Val Glu Asn Gly Val
115 120 125

Lys Lys Ser Val Tyr Ser Val Thr Thr Lys Thr Ala Thr Arg Ala Asp
130 135 140

Val Glu Gln Ser Ala Tyr Ser Arg Gly Ile Gln Gly Asp Ile Asp Asp
 145 150 155 160

Leu Tyr Glu Ala Asn Lys Glu Asn Val Asn Arg Leu Ile Glu His Gly
 165 170 175

Asp Lys Ile Phe Ala Asn Glu Glu Ser Val Gln Tyr Leu Asn Arg Glu
 180 185 190

Val Gln Asn Asn Ile Glu Asn Ile His Glu Leu Ala Gln Gln Gln Asp
 195 200 205

Gln His Ser Ser Asp Ile Lys Thr Leu Lys Lys Asn Val Glu Lys Asp
 210 215 220

Leu Leu Asp Leu Ser Gly Arg Leu Ile Ala Gln Lys Glu Asp Ile Ala
 225 230 235 240

Gln Asn Gln Thr Asp Ile Gln Asp Leu Ala Thr Tyr Asn Glu Leu Gln
 245 250 255

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

Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Ser Asn His Ile
 275 280 285

Lys Thr Leu Glu Asn Asn Ile Glu Glu Gly Leu Leu Glu Leu Ser Gly
 290 295 300

His Leu Ile Asp Gln Lys Ala Asp Leu Thr Lys Asp Ile Lys Thr Leu
 305 310 315 320

Glu Asn Asn Ile Glu Glu Gly Leu Leu Glu Leu Ser Gly His Leu Ile
 325 330 335

Asp Gln Lys Ala Asp Leu Thr Lys Asp Ile Lys Ala Leu Glu Ser Asn
 340 345 350

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

355								360										365
Ala	Asp	Ile	Ala	Gln	Asn	Gln	Ala	Asn	Ile	Gln	Asp	Leu	Ala	Ala	Tyr			
370						375					380							
Asn	Glu	Leu	Gln	Asp	Gln	Tyr	Ala	Gln	Lys	Gln	Thr	Glu	Ala	Ile	Asp			
385					390					395					400			
Ala	Leu	Asn	Lys	Ala	Ser	Ser	Glu	Asn	Thr	Gln	Asn	Ile	Glu	Asp	Leu			
				405					410					415				
Ala	Ala	Tyr	Asn	Glu	Leu	Gln	Asp	Ala	Tyr	Ala	Lys	Gln	Gln	Thr	Glu			
			420					425						430				
Ala	Ile	Asp	Ala	Leu	Asn	Lys	Ala	Ser	Ser	Glu	Asn	Thr	Gln	Asn	Ile			
		435					440					445						
Ala	Lys	Asn	Gln	Ala	Asp	Ile	Ala	Asn	Asn	Ile	Asn	Asn	Ile	Tyr	Glu			
	450					455					460							
Leu	Ala	Gln	Gln	Gln	Asp	Gln	His	Ser	Ser	Asp	Ile	Lys	Thr	Leu	Ala			
465					470					475					480			
Lys	Ala	Ser	Ala	Ala	Asn	Thr	Asp	Arg	Ile	Ala	Lys	Asn	Lys	Ala	Asp			
				485					490					495				
Ala	Asp	Ala	Ser	Phe	Glu	Thr	Leu	Thr	Lys	Asn	Gln	Asn	Thr	Leu	Ile			
		500						505						510				
Glu	Lys	Asp	Lys	Glu	His	Asp	Lys	Leu	Ile	Thr	Ala	Asn	Lys	Thr	Ala			
		515					520					525						
Ile	Asp	Thr	Asn	Lys	Ala	Ser	Ala	Asp	Thr	Lys	Phe	Ala	Ala	Thr	Ala			
	530					535					540							
Asp	Ala	Ile	Thr	Lys	Asn	Gly	Asn	Ala	Ile	Thr	Lys	Asn	Ala	Lys	Ser			
545					550					555					560			
Ile	Thr	Asp	Leu	Gly	Thr	Lys	Val	Asp	Gly	Phe	Asp	Gly	Arg	Val	Thr			
			565						570					575				

Ala Leu Asp Thr Lys Val Asn Ala Leu Asp Thr Lys Val Asn Ala Phe
580 585 590

Asp Gly Arg Ile Thr Ala Leu Asp Ser Lys Val Glu Asn Gly Met Ala
595 600 605

Ala Gln Ala Ala Leu Ser Gly Leu Phe Gln Pro Tyr Ser Val Gly Lys
610 615 620

Phe Asn Ala Thr Ala Ala Leu Gly Gly Tyr Gly Ser Lys Ser Ala Val
625 630 635 640

Ala Ile Gly Ala Gly Tyr Arg Val Asn Pro Asn Leu Ala Phe Lys Ala
645 650 655

Gly Ala Ala Ile Asn Thr Ser Gly Asn Lys Lys Gly Ser Tyr Asn Ile
660 665 670

Gly Val Asn Tyr Glu Phe
675

<210> 15
<211> 616
<212> PRT
<213> Moraxella catarrhalis

<400> 15

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

Leu Ile Val Gly Leu Gly Ala Ala Ser Thr Ala Asn Ala Gln Val Arg
20 25 30

Asp Lys Ser Leu Glu Asp Ile Glu Ala Leu Leu Gly Lys Ile Asp Ile
35 40 45

Ser Lys Leu Glu Lys Glu Lys Lys Gln Gln Thr Glu Leu Gln Lys Tyr
50 55 60

Leu Leu Leu Ser Gln Tyr Ala Asn Val Leu Thr Met Glu Glu Leu Asn
65 70 75 80

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

Ile Gly Trp Leu Glu Asn Asp Ile Ala Asp Leu Glu Glu Gly Val Glu
100 105 110

Glu Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp Glu Glu His
115 120 125

Asp Arg Leu Ile Ala Gln Asn Gln Ala Asp Ile Lys Thr Leu Glu Asn
130 135 140

Asn Val Val Glu Glu Leu Phe Asn Leu Ser Asp Arg Leu Ile Asp Gln
145 150 155 160

Glu Ala Asp Ile Ala Lys Asn Asn Ala Ser Ile Glu Glu Leu Tyr Asp
165 170 175

Phe Asp Asn Glu Val Ala Glu Arg Ile Gly Glu Ile His Ala Tyr Thr
180 185 190

Glu Glu Val Asn Lys Thr Leu Glu Lys Leu Ile Thr Asn Ser Val Lys
195 200 205

Asn Thr Asp Asn Ile Asp Lys Asn Lys Ala Asp Ile Gln Ala Leu Glu
210 215 220

Asn Asn Val Glu Glu Gly Leu Leu Glu Leu Ser Gly His Leu Ile Asp
225 230 235 240

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

Glu Glu Gly Leu Leu Asp Leu Ser Gly Arg Leu Leu Asp Gln Lys Ala
260 265 270

Asp Ile Ala Lys Asn Gln Ala Asp Ile Ala Gln Asn Gln Thr Asp Ile

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

Asn Ala Ile Thr Lys Asn Ala Lys Ser Ile Thr Asp Leu Gly Thr Lys
500 505 510

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

Ala Phe Asp Gly Arg Ile Thr Ala Leu Asp Ser Lys Val Glu Asn Gly
530 535 540

Met Ala Ala Gln Ala Ala Leu Ser Gly Leu Phe Gln Pro Tyr Ser Val
545 550 555 560

Gly Lys Phe Asn Ala Thr Ala Ala Leu Gly Gly Tyr Gly Ser Lys Ser
565 570 575

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

Lys Ala Gly Ala Ala Ile Asn Thr Ser Gly Asn Lys Lys Gly Ser Tyr
595 600 605

Asn Ile Gly Val Asn Tyr Glu Phe
610 615

<210> 16
<211> 676
<212> PRT
<213> Moraxella catarrhalis

<400> 16

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

Leu Ile Val Gly Leu Gly Ala Ala Ser Thr Ala Asn Ala Gln Ala Thr
20 25 30

Glu Thr Phe Leu Pro Asn Leu Phe Asp Asn Asp Tyr Thr Glu Thr Thr
35 40 45

Asp Pro Leu Tyr His Gly Met Ile Leu Gly Asn Thr Ala Ile Thr Gln
50 55 60

Asp Thr Gln Tyr Lys Phe Tyr Ala Glu Asn Gly Asn Glu Val Pro Asp
65 70 75 80

Ser Leu Phe Phe Asn Lys Ile Leu His Asp Gln Gln Leu Asn Gly Phe
85 90 95

Lys Glu Gly Asp Thr Ile Ile Pro Leu Asp Glu Asn Gly Lys Pro Val
100 105 110

Tyr Lys Leu Asp Glu Ile Thr Glu Asn Gly Val Lys Arg Lys Val Tyr
115 120 125

Ser Val Thr Thr Lys Thr Ala Thr Arg Glu Asp Val Glu Gln Ser Ala
130 135 140

Tyr Ser Arg Gly Ile Gln Gly Asp Ile Asp Asp Leu Tyr Glu Ala Asn
145 150 155 160

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

Asn Glu Glu Ser Val Gln Tyr Leu Asn Lys Glu Val Gln Asn Asn Ile
180 185 190

Glu Asn Ile His Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser Asp
195 200 205

Ile Lys Thr Leu Lys Lys Asn Val Glu Glu Gly Leu Leu Glu Leu Ser
210 215 220

Gly His Leu Ile Asp Gln Lys Ala Asp Leu Thr Lys Asp Ile Lys Ala
225 230 235 240

Leu Glu Ser Asn Val Glu Glu Gly Leu Leu Asp Leu Ser Gly His Leu
245 250 255

Ile Asp Gln Lys Ala Asp Leu Thr Lys Asp Ile Lys Ala Leu Glu Ser

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

Ser Ala Ala Asn Thr Asp Arg Ile Ala Lys Asn Lys Ala Asp Ala Asp
485 490 495

Ala Ser Phe Glu Thr Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys
500 505 510

Asp Lys Glu His Asp Lys Leu Ile Thr Ala Asn Lys Thr Ala Ile Asp
515 520 525

Ala Asn Lys Ala Ser Ala Asp Thr Lys Phe Ala Ala Thr Ala Asp Ala
530 535 540

Ile Thr Lys Asn Gly Asn Ala Ile Thr Lys Asn Ala Lys Ser Ile Thr
545 550 555 560

Asp Leu Gly Thr Lys Val Asp Gly Phe Asp Gly Arg Val Thr Ala Leu
565 570 575

Asp Thr Lys Val Asn Ala Leu Asp Thr Lys Val Asn Ala Phe Asp Gly
580 585 590

Arg Ile Thr Ala Leu Asp Ser Lys Val Glu Asn Gly Met Ala Ala Gln
595 600 605

Ala Ala Leu Ser Gly Leu Phe Gln Pro Tyr Ser Val Gly Lys Phe Asn
610 615 620

Ala Thr Ala Ala Leu Gly Gly Tyr Gly Ser Lys Ser Ala Val Ala Ile
625 630 635 640

Gly Ala Gly Tyr Arg Val Asn Pro Asn Leu Ala Phe Lys Ala Gly Ala
645 650 655

Ala Ile Asn Thr Ser Gly Asn Lys Lys Gly Ser Tyr Asn Ile Gly Val
660 665 670

Asn Tyr Glu Phe
675

<210> 17
 <211> 629
 <212> PRT
 <213> Moraxella catarrhalis

<400> 17

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

Leu Ile Val Gly Leu Gly Ala Ala Ser Thr Ala Asn Ala Gln Asn Gly
 20 25 30

Thr Ser Thr Lys Leu Lys Asn Leu Lys Glu Tyr Ala Gln Tyr Leu Asp
 35 40 45

Asn Tyr Ala Gln Tyr Leu Asp Asp Asp Ile Asp Asp Leu Asp Lys Glu
 50 55 60

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

Asp Leu Asn Lys Lys Leu Ser Arg Asp Ile Asp Ser Leu Arg Glu Asp
 85 90 95

Val Tyr Asp Asn Gln Tyr Glu Ile Val Asn Asn Gln Ala Asp Ile Glu
 100 105 110

Lys Asn Gln Asp Asp Ile Lys Glu Leu Glu Asn Asn Val Gly Lys Glu
 115 120 125

Leu Leu Asn Leu Ser Gly Arg Leu Leu Asp Gln Lys Ala Asp Ile Asp
 130 135 140

Asn Asn Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His
 145 150 155 160

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

Glu Leu Ser Gly His Leu Ile Asp Gln Lys Ser Asp Ile Ala Gln Asn

180					185					190					
Gln	Thr	Asp	Ile	Gln	Asp	Leu	Ala	Thr	Tyr	Asn	Glu	Leu	Gln	Asp	Gln
		195					200					205			
Tyr	Ala	Gln	Lys	Gln	Thr	Glu	Ala	Ile	Asp	Ala	Leu	Asn	Lys	Ala	Ser
	210					215					220				
Ser	Glu	Asn	Thr	Gln	Asn	Ile	Glu	Asp	Leu	Ala	Ala	Tyr	Asn	Glu	Leu
225					230					235					240
Gln	Asp	Ala	Tyr	Ala	Lys	Gln	Gln	Thr	Glu	Ala	Ile	Asp	Ala	Leu	Asn
				245					250					255	
Lys	Ala	Ser	Ser	Glu	Asn	Thr	Gln	Asn	Ile	Gln	Asp	Leu	Ala	Ala	Tyr
			260					265					270		
Asn	Glu	Leu	Gln	Asp	Ala	Tyr	Ala	Lys	Gln	Gln	Thr	Glu	Ala	Ile	Asp
		275					280					285			
Ala	Leu	Asn	Lys	Ala	Ser	Ser	Glu	Asn	Thr	Gln	Asn	Ile	Glu	Asp	Leu
	290					295					300				
Ala	Ala	Tyr	Asn	Glu	Leu	Gln	Asp	Ala	Tyr	Ala	Lys	Gln	Gln	Thr	Glu
305					310					315					320
Ala	Ile	Asp	Ala	Leu	Asn	Lys	Ala	Ser	Ser	Glu	Asn	Thr	Gln	Asn	Ile
				325					330					335	
Glu	Asp	Leu	Ala	Ala	Tyr	Asn	Glu	Leu	Gln	Asp	Ala	Tyr	Ala	Lys	Gln
			340					345					350		
Gln	Thr	Glu	Ala	Ile	Asp	Ala	Leu	Asn	Lys	Ala	Ser	Ser	Glu	Asn	Thr
		355					360					365			
Gln	Asn	Ile	Glu	Asp	Leu	Ala	Ala	Tyr	Asn	Glu	Leu	Gln	Asp	Ala	Tyr
	370					375					380				
Ala	Lys	Gln	Gln	Thr	Glu	Ala	Ile	Asp	Ala	Leu	Asn	Lys	Ala	Ser	Ser
385					390					395					400

Glu Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala Asp Ile Ala Asn Asn
405 410 415

Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser
420 425 430

Asp Ile Lys Thr Leu Ala Lys Ala Ser Ala Ala Asn Thr Asp Arg Ile
435 440 445

Ala Lys Asn Lys Ala Asp Ala Asp Ala Ser Phe Glu Thr Leu Thr Lys
450 455 460

Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu His Asp Lys Leu Ile
465 470 475 480

Thr Ala Asn Lys Thr Ala Ile Asp Ala Asn Lys Ala Ser Ala Asp Thr
485 490 495

Lys Phe Ala Ala Thr Ala Asp Ala Ile Thr Lys Asn Gly Asn Ala Ile
500 505 510

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

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

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

Gln Ala Ala Leu Ser Gly Leu Phe Gln Pro Tyr Ser Val Gly Lys Phe
565 570 575

Asn Ala Thr Ala Ala Leu Gly Gly Tyr Gly Ser Lys Ser Ala Val Ala
580 585 590

Ile Gly Ala Gly Tyr Arg Val Asn Pro Asn Leu Ala Phe Lys Ala Gly
595 600 605

Ala Ala Ile Asn Thr Ser Gly Asn Lys Lys Gly Ser Tyr Asn Ile Gly
610 615 620

Val Asn Tyr Glu Phe
625

<210> 18
<211> 683
<212> PRT
<213> Moraxella catarrhalis

<400> 18

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

Met Ile Val Gly Leu Gly Met Ala Ser Thr Ala Asn Ala Gln Gln Gln
20 25 30

Arg Ser Pro Lys Thr Glu Thr Phe Leu Pro Asn Ile Phe Phe Asn Glu
35 40 45

Tyr Ala Asp Asp Leu Asp Thr Leu Tyr His Asn Met Ile Leu Gly Asp
50 55 60

Thr Ala Ile Thr His Asp Asp Gln Tyr Lys Phe Tyr Ala Asp Asp Ala
65 70 75 80

Thr Glu Val Pro Asp Ser Leu Phe Phe Asn Lys Ile Leu His Asp Gln
85 90 95

Leu Leu Tyr Gly Phe Lys Glu Gly Asp Lys Ile Ile Pro Leu Asp Glu
100 105 110

Asn Gly Lys Pro Val Tyr Lys Leu Asp Lys Arg Leu Asp Asn Gly Val
115 120 125

Gln Lys Thr Val Tyr Ser Val Thr Thr Lys Thr Ala Thr Ala Asp Asp
130 135 140

Val Asn Ser Ala Tyr Ser Arg Gly Ile Gln Gly Asp Ile Asp Asp Leu

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

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

Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr Ala Lys Gln Gln
385 390 395 400

Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr Gln
405 410 415

Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr Ala
420 425 430

Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu
435 440 445

Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala Asp Ile Ala Asn Asn Ile
450 455 460

Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser Asp
465 470 475 480

Ile Lys Thr Leu Ala Lys Ala Ser Ala Ala Asn Thr Asp Arg Ile Ala
485 490 495

Lys Asn Lys Ala Asp Ala Asp Ala Ser Phe Glu Thr Leu Thr Lys Asn
500 505 510

Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu His Asp Lys Leu Ile Thr
515 520 525

Ala Asn Lys Thr Ala Ile Asp Ala Asn Lys Ala Ser Ala Asp Thr Lys
530 535 540

Phe Ala Ala Thr Ala Asp Ala Ile Thr Lys Asn Gly Asn Ala Ile Thr
545 550 555 560

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

Asp Gly Arg Val Thr Ala Leu Asp Thr Lys Val Asn Ala Leu Asp Thr
580 585 590

Lys Val Asn Ala Phe Asp Gly Arg Ile Thr Ala Leu Asp Ser Lys Val
595 600 605

Glu Asn Gly Met Ala Ala Gln Ala Ala Leu Ser Gly Leu Phe Gln Pro
610 615 620

Tyr Ser Val Gly Lys Phe Asn Ala Thr Ala Ala Leu Gly Gly Tyr Gly
625 630 635 640

Ser Lys Ser Ala Val Ala Ile Gly Ala Gly Tyr Arg Val Asn Pro Asn
645 650 655

Leu Ala Phe Lys Ala Gly Ala Ala Ile Asn Thr Ser Gly Asn Lys Lys
660 665 670

Gly Ser Tyr Asn Ile Gly Val Asn Tyr Glu Phe
675 680

<210> 19
<211> 700
<212> PRT
<213> Moraxella catarrhalis

<400> 19

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

Met Ile Val Gly Leu Gly Ala Ala Ser Thr Ala Asn Ala Gln Ala Gln
20 25 30

Ser Asn Arg Ser Leu Asp Gln Val Gln Ala Leu Leu Arg Gly Ile Asp
35 40 45

Glu Thr Lys Ile Lys Lys Glu Ile Gln Gln Ser Gln Gln Pro Glu Leu
50 55 60

Asn Lys Tyr Leu Thr Phe Asn Gln Leu Ala Asn Ala Leu Asn Ile Glu

65		70		75		80									
Glu	Leu	Asn	Asn	Asn	Val	Gln	Lys	Asn	Thr	Gln	Arg	Leu	Asp	Ser	Ala
			85					90					95		
Ala	Thr	Leu	Tyr	Gly	Asp	Leu	Ser	Lys	Thr	Val	Pro	Lys	Ser	Ile	Lys
		100						105					110		
Glu	Asn	Lys	Glu	Ser	Ile	Lys	Glu	Asn	Lys	Glu	Ser	Ile	Lys	Glu	Asn
		115					120					125			
Lys	Glu	Ser	Ile	Lys	Glu	Asn	Lys	Glu	Ser	Ile	Lys	Glu	Asn	Lys	Glu
	130					135					140				
Ser	Ile	Lys	Glu	Asn	Lys	Glu	Ser	Ile	Thr	Thr	Leu	Thr	Arg	Lys	Ser
145				150					155						160
Phe	Gln	Asn	Gln	Val	Asp	Ile	Val	Arg	Asn	Asn	Ala	Ser	Ile	Glu	Asp
			165					170						175	
Leu	Tyr	Ala	Tyr	Gly	Gln	Glu	Val	Ala	Lys	Ser	Ile	Gly	Glu	Ile	His
		180						185					190		
Ala	Tyr	Thr	Glu	Glu	Val	Asn	Lys	Thr	Leu	Glu	Asn	Leu	Ile	Thr	Asn
		195					200					205			
Ser	Val	Glu	Asn	Thr	Asn	Asn	Ile	Thr	Lys	Asn	Lys	Ala	Asp	Ile	Gln
	210					215					220				
Ala	Leu	Glu	Asn	Asn	Val	Val	Glu	Glu	Leu	Phe	Asn	Leu	Ser	Gly	Arg
225					230					235					240
Leu	Ile	Asp	Gln	Lys	Ala	Asp	Ile	Asp	Asn	Asn	Ile	Asn	Asn	Ile	Tyr
			245					250						255	
Glu	Leu	Ala	Gln	Gln	Gln	Asp	Gln	His	Ser	Ser	Asp	Ile	Lys	Thr	Leu
		260						265					270		
Lys	Lys	Asn	Val	Glu	Glu	Gly	Leu	Leu	Glu	Leu	Ser	Gly	His	Leu	Ile
		275					280					285			

Asp Gln Lys Ala Asp Leu Thr Lys Asp Ile Lys Thr Leu Glu Ser Asn
290 295 300

Val Glu Glu Gly Leu Leu Asp Leu Ser Gly Arg Leu Leu Asp Gln Lys
305 310 315 320

Ala Asp Ile Ala Gln Asn Gln Ala Asn Ile Gln Asp Leu Ala Ala Tyr
325 330 335

Asn Glu Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp
340 345 350

Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Glu Asp Leu
355 360 365

Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu
370 375 380

Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile
385 390 395 400

Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr Ala Lys Gln
405 410 415

Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr
420 425 430

Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr
435 440 445

Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser
450 455 460

Glu Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala Asp Ile Ala Asn Asn
465 470 475 480

Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser
485 490 495

Asp Ile Lys Thr Leu Ala Lys Ala Ser Ala Ala Asn Thr Asp Arg Ile
500 505 510

Ala Lys Asn Lys Ala Asp Ala Asp Ala Ser Phe Glu Thr Leu Thr Lys
515 520 525

Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu His Asp Lys Leu Ile
530 535 540

Thr Ala Asn Lys Thr Val Ile Asp Ala Asn Lys Ala Ser Ala Asp Thr
545 550 555 560

Lys Phe Ala Ala Thr Ala Asp Ala Ile Thr Lys Asn Gly Asn Ala Ile
565 570 575

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

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

Thr Lys Val Asn Ala Phe Asp Gly Arg Ile Thr Ala Leu Asp Ser Lys
610 615 620

Val Glu Asn Gly Met Ala Ala Gln Ala Ala Leu Ser Gly Leu Phe Gln
625 630 635 640

Pro Tyr Ser Val Gly Lys Phe Asn Ala Thr Ala Ala Leu Gly Gly Tyr
645 650 655

Gly Ser Lys Ser Ala Val Ala Ile Gly Ala Gly Tyr Arg Val Asn Pro
660 665 670

Asn Leu Ala Phe Lys Ala Gly Ala Ala Ile Asn Thr Ser Gly Asn Lys
675 680 685

Lys Gly Ser Tyr Asn Ile Gly Val Asn Tyr Glu Phe
690 695 700

<210> 20
 <211> 676
 <212> PRT
 <213> Moraxella catarrhalis

<400> 20

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

Leu Ile Val Gly Leu Gly Ala Ala Ser Thr Ala Asn Ala Gln Ala Thr
 20 25 30

Glu Thr Phe Leu Pro Asn Leu Phe Asp Asn Asp Tyr Ile Glu Thr Thr
 35 40 45

Asp Pro Leu Tyr His Gly Met Ile Leu Gly Asn Thr Ala Ile Thr Gln
 50 55 60

Asp Thr Gln Tyr Lys Phe Tyr Ala Glu Asn Gly Asn Glu Val Pro Asp
 65 70 75 80

Ser Leu Phe Phe Asn Lys Ile Leu His Asp Gln Gln Leu Asn Gly Phe
 85 90 95

Lys Glu Gly Asp Thr Ile Ile Pro Leu Asp Glu Asn Gly Lys Pro Val
 100 105 110

Tyr Lys Leu Asp Glu Ile Thr Glu Asn Gly Val Lys Arg Lys Val Tyr
 115 120 125

Ser Val Thr Thr Lys Thr Ala Thr Arg Glu Asp Val Glu Gln Ser Ala
 130 135 140

Tyr Ser Arg Gly Ile Gln Gly Asp Ile Asp Asp Leu Tyr Glu Ala Asn
 145 150 155 160

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

Asn Glu Glu Ser Val Gln Tyr Leu Asn Lys Glu Val Gln Asn Asn Ile
 180 185 190

Glu Asn Ile His Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser Asp
195 200 205

Ile Lys Thr Leu Lys Lys Asn Val Glu Glu Gly Leu Leu Glu Leu Ser
210 215 220

Gly His Leu Ile Asp Gln Lys Ala Asp Leu Thr Lys Asp Ile Lys Thr
225 230 235 240

Leu Glu Asn Asn Val Glu Glu Gly Leu Leu Glu Leu Ser Gly His Leu
245 250 255

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

Asn Val Glu Glu Gly Leu Leu Asp Leu Ser Gly Arg Leu Leu Asp Gln
275 280 285

Lys Ala Asp Ile Ala Lys Asn Gln Ala Asp Ile Ala Gln Asn Gln Thr
290 295 300

Asp Ile Gln Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Gln Tyr Ala
305 310 315 320

Gln Lys Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu
325 330 335

Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp
340 345 350

Gln Tyr Ala Gln Lys Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala
355 360 365

Ser Ser Glu Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu
370 375 380

Leu Gln Asp Gln Tyr Ala Gln Lys Gln Thr Glu Ala Ile Asp Ala Leu
385 390 395 400

Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala
405 410 415

Tyr Asn Glu Leu Gln Asp Gln Tyr Ala Gln Lys Gln Thr Glu Ala Ile
420 425 430

Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys
435 440 445

Asn Gln Ala Asp Ile Ala Asn Asn Ile Asn Asn Ile Tyr Glu Leu Ala
450 455 460

Gln Gln Gln Asp Gln His Ser Ser Asp Ile Lys Thr Leu Ala Lys Ala
465 470 475 480

Ser Ala Ala Asn Thr Asp Arg Ile Ala Lys Asn Lys Ala Asp Ala Asp
485 490 495

Ala Ser Phe Glu Thr Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys
500 505 510

Asp Lys Glu His Asp Lys Leu Ile Thr Ala Asn Lys Thr Ala Ile Asp
515 520 525

Ala Asn Lys Ala Ser Ala Asp Thr Lys Phe Ala Ala Thr Ala Asp Ala
530 535 540

Ile Thr Lys Asn Gly Asn Ala Ile Thr Lys Asn Ala Lys Ser Ile Thr
545 550 555 560

Asp Leu Gly Thr Lys Val Asp Gly Phe Asp Gly Arg Val Thr Ala Leu
565 570 575

Asp Thr Lys Val Asn Ala Leu Asp Thr Lys Val Asn Ala Phe Asp Gly
580 585 590

Arg Ile Thr Ala Leu Asp Ser Lys Val Glu Asn Gly Met Ala Ala Gln
595 600 605

Ala Ala Leu Ser Gly Leu Phe Gln Pro Tyr Ser Val Gly Lys Phe Asn
610 615 620

Ala Thr Ala Ala Leu Gly Gly Tyr Gly Ser Lys Ser Ala Val Ala Ile
625 630 635 640

Gly Ala Gly Tyr Arg Val Asn Pro Asn Leu Ala Phe Lys Ala Gly Ala
645 650 655

Ala Ile Asn Thr Ser Gly Asn Lys Lys Gly Ser Tyr Asn Ile Gly Val
660 665 670

Asn Tyr Glu Phe
675

<210> 21
<211> 678
<212> PRT
<213> Moraxella catarrhalis

<400> 21

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

Met Ile Ile Gly Leu Gly Ala Ala Ser Thr Ala Asn Ala Gln Leu Ala
20 25 30

Glu Gln Phe Phe Pro Asn Ile Phe Ser Asn His Ala Pro Val Lys Gln
35 40 45

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

Gln Asp Ser Asp Asp Thr Gln Leu Lys Phe Tyr Ser Asn Asp Glu Tyr
65 70 75 80

Ser Val Pro Asp Ser Leu Leu Phe Asn Lys Met Leu His Glu Gln Gln
85 90 95

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

Gly Lys Pro Val Tyr Lys Val Asp Tyr Lys Leu Asp Gly Gln Glu Pro
115 120 125

Arg Arg Val Tyr Ser Val Thr Thr Lys Ile Ala Thr Gln Asp Asp Val
130 135 140

Asp Asn Ser Pro Tyr Ser Arg Gly Ile Gln Gly Asp Ile Asp Asp Leu
145 150 155 160

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

Lys Ile Phe Ala Asn Glu Glu Ser Val Gln Tyr Leu Asn Lys Glu Val
180 185 190

Gln Asn Asn Ile Glu Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln
195 200 205

His Ser Ser Asp Ile Lys Thr Leu Lys Lys Asn Val Glu Glu Gly Leu
210 215 220

Leu Glu Leu Ser Gly Arg Leu Ile Asp Gln Lys Ala Asp Ile Ala Gln
225 230 235 240

Asn Gln Ala Asn Ile Gln Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp
245 250 255

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

Ser Ser Glu Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu
275 280 285

Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu
290 295 300

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

Tyr Asn Glu Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile
325 330 335

Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Glu Asp
340 345 350

Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr
355 360 365

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

Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr Ala Lys
385 390 395 400

Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn
405 410 415

Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala
420 425 430

Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser
435 440 445

Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala Asp Ile Ala Asn
450 455 460

Asn Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser
465 470 475 480

Ser Asp Ile Lys Thr Leu Ala Lys Val Ser Ala Ala Asn Thr Asp Arg
485 490 495

Ile Ala Lys Asn Lys Ala Asp Ala Asp Ala Ser Phe Glu Thr Leu Thr
500 505 510

Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu His Asp Lys Leu
515 520 525

Ile Thr Ala Asn Lys Thr Ala Ile Asp Ala Asn Lys Ala Ser Ala Asp
530 535 540

Thr Lys Phe Ala Ala Thr Ala Asp Ala Ile Thr Lys Asn Gly Asn Ala
545 550 555 560

Ile Thr Lys Asn Ala Lys Ser Ile Thr Asp Leu Gly Thr Lys Val Asp
565 570 575

Gly Phe Asp Gly Arg Val Thr Ala Leu Asp Thr Lys Val Asn Ala Phe
580 585 590

Asp Gly Arg Ile Thr Ala Leu Asp Ser Lys Val Glu Asn Gly Met Ala
595 600 605

Ala Gln Ala Ala Leu Ser Gly Leu Phe Gln Pro Tyr Ser Val Gly Lys
610 615 620

Phe Asn Ala Thr Ala Ala Leu Gly Gly Tyr Gly Ser Lys Ser Ala Val
625 630 635 640

Ala Ile Gly Ala Gly Tyr Arg Val Asn Pro Asn Leu Ala Phe Lys Ala
645 650 655

Gly Ala Ala Ile Asn Thr Ser Gly Asn Lys Lys Gly Ser Tyr Asn Ile
660 665 670

Gly Val Asn Tyr Glu Phe
675

<210> 22
<211> 613
<212> PRT
<213> Moraxella catarrhalis

<400> 22

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

Met Ile Ile Gly Leu Gly Ala Ala Ser Thr Ala Asn Ala Gln Ser Arg
20 25 30

Asp Arg Ser Leu Glu Asp Ile Gln Asp Ser Ile Ser Lys Leu Val Gln
35 40 45

Asp Asp Ile Asn Thr Leu Lys Gln Asp Gln Gln Lys Met Asn Lys Tyr
50 55 60

Leu Leu Leu Asn Gln Leu Ala Asn Thr Leu Ile Thr Asp Glu Leu Asn
65 70 75 80

Asn Asn Val Ile Lys Asn Thr Asn Ser Ile Glu Ala Leu Gly Asp Glu
85 90 95

Ile Gly Trp Leu Glu Asn Asp Ile Ala Asp Leu Glu Glu Gly Val Glu
100 105 110

Glu Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp Glu Glu His
115 120 125

Asp Arg Leu Ile Ala Gln Asn Gln Ala Asp Ile Gln Thr Leu Glu Asn
130 135 140

Asn Val Val Glu Glu Leu Phe Asn Leu Ser Gly Arg Leu Ile Asp Gln
145 150 155 160

Glu Ala Asp Ile Ala Lys Asn Asn Ala Ser Ile Glu Glu Leu Tyr Asp
165 170 175

Phe Asp Asn Glu Val Ala Glu Arg Ile Gly Glu Ile His Ala Tyr Thr
180 185 190

Glu Glu Val Asn Lys Thr Leu Glu Asn Leu Ile Thr Asn Ser Val Lys
195 200 205

Asn Thr Asp Asn Ile Asp Lys Asn Lys Ala Asp Ile Asp Asn Asn Ile
210 215 220

Asn His Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser Asp
225 230 235 240

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

Gly His Leu Ile Asp Gln Lys Ala Asp Leu Thr Lys Asp Ile Lys Ala
260 265 270

Leu Glu Ser Asn Val Glu Glu Gly Leu Leu Asp Leu Ser Gly Arg Leu
275 280 285

Leu Asp Gln Lys Ala Asp Leu Thr Lys Asp Ile Lys Ala Leu Glu Ser
290 295 300

Asn Val Glu Glu Gly Leu Leu Asp Leu Ser Gly Arg Leu Leu Asp Gln
305 310 315 320

Lys Ala Asp Ile Ala Gln Asn Gln Thr Asp Ile Gln Asp Leu Ala Ala
325 330 335

Tyr Asn Glu Leu Gln Asp Gln Tyr Ala Gln Lys Gln Thr Glu Ala Ile
340 345 350

Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Glu Asp
355 360 365

Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr
370 375 380

Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn
385 390 395 400

Ile Ala Lys Asn Gln Ala Asp Ile Ala Asn Asn Ile Asn Asn Ile Tyr
405 410 415

Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser Asp Ile Lys Thr Leu
420 425 430

Ala Lys Ala Ser Ala Ala Asn Thr Asn Arg Ile Ala Thr Ala Glu Leu
435 440 445

Gly Ile Ala Glu Asn Lys Lys Asp Ala Gln Ile Ala Lys Ala Gln Ala
450 455 460

Asn Ala Asn Lys Thr Ala Ile Asp Glu Asn Lys Ala Ser Ala Asp Thr
465 470 475 480

Lys Phe Ala Ala Thr Ala Asp Ala Ile Thr Lys Asn Gly Asn Ala Ile
485 490 495

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

Phe Asp Gly Arg Val Thr Ala Leu Asp Thr Lys Val Asn Ala Phe Asp
515 520 525

Gly Arg Ile Thr Ala Leu Asp Ser Lys Val Glu Asn Gly Met Ala Ala
530 535 540

Gln Ala Ala Leu Ser Gly Leu Phe Gln Pro Tyr Ser Val Gly Lys Phe
545 550 555 560

Asn Ala Thr Ala Ala Leu Gly Gly Tyr Gly Ser Lys Ser Ala Val Ala
565 570 575

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

Ala Ala Ile Asn Thr Ser Gly Asn Lys Lys Gly Ser Tyr Asn Ile Gly
595 600 605

Val Asn Tyr Glu Phe
610

<210> 23
<211> 589
<212> PRT
<213> Moraxella catarrhalis

<400> 23

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

Leu Ile Val Gly Leu Gly Ala Ala Ser Thr Ala Asn Ala Gln Ala Thr
20 25 30

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

Asp Pro Tyr Glu Leu Arg Asp Tyr Ile Glu Tyr Pro Thr Ala Ile Glu
50 55 60

Arg Phe Leu Leu Leu Ser Gln Tyr Gly Asn Thr Leu Thr Leu Glu Glu
65 70 75 80

Phe Asp Asn Asp Ile Glu Leu Leu Asp Gln Asp Val Glu Asp Leu Glu
85 90 95

Glu Ser Val Thr Glu Leu Ala Lys Asn Gln Asn Ser Leu Ile Glu Gln
100 105 110

Gly Glu Ala Ile Lys Glu Asp Leu Gln Gly Leu Ala Asp Phe Val Glu
115 120 125

Arg Gln Glu Asp Lys Ile Leu Gln Asn Glu Thr Ser Ile Lys Lys Asn
130 135 140

Thr Gln Arg Asn Leu Val Asn Gly Phe Glu Ile Glu Lys Asn Lys Asp
145 150 155 160

Ala Ile Ala Lys Asn Asn Glu Ser Ile Glu Asp Leu Tyr Asp Phe Gly
165 170 175

His Glu Val Ala Lys Ser Ile Gly Glu Ile His Ala His Asn Glu Ala
180 185 190

Gln Asn Glu Thr Leu Lys Asp Leu Ile Thr Asn Ser Val Lys Asn Thr
195 200 205

Asp Asn Ile Thr Lys Asn Lys Ala Asp Ile Gln Ala Leu Glu Ser Asn
210 215 220

Val Glu Lys Gly Leu Leu Glu Leu Ser Gly His Leu Ile Asp Gln Lys
225 230 235 240

Ala Asp Ile Asp Asn Asn Ile Asn Asn Ile His Glu Leu Ala Gln Gln
245 250 255

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

Glu Gly Leu Leu Glu Leu Ser Gly His Leu Ile Asp Gln Lys Ser Asp
275 280 285

Ile Ala Gln Asn Gln Ala Asn Ile Gln Asp Leu Ala Thr Tyr Asn Glu
290 295 300

Leu Gln Asp Gln Tyr Ala Gln Lys Gln Thr Glu Ala Ile Asp Ala Leu
305 310 315 320

Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala
325 330 335

Tyr Asn Glu Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile
340 345 350

Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys
355 360 365

Asn Gln Ala Asp Ile Ala Asn Asn Ile Asn Asn Ile Tyr Glu Leu Ala
370 375 380

Gln Gln Gln Asp Gln His Ser Ser Asp Ile Lys Thr Leu Ala Lys Ala
385 390 395 400

Ser Ala Ala Asn Thr Asp Arg Ile Ala Lys Asn Lys Ala Asp Ala Asp
405 410 415

Ala Ser Phe Glu Thr Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys
420 425 430

Asp Lys Glu His Asp Lys Leu Ile Thr Ala Asn Lys Thr Ala Ile Asp
435 440 445

Ala Asn Lys Ala Ser Ala Asp Thr Lys Phe Ala Ala Thr Ala Asp Ala
450 455 460

Ile Thr Lys Asn Gly Asn Ala Ile Thr Lys Asn Ala Lys Ser Ile Thr
465 470 475 480

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

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

Lys Val Glu Asn Gly Met Ala Ala Gln Ala Ala Leu Ser Gly Leu Phe
515 520 525

Gln Pro Tyr Ser Val Gly Lys Phe Asn Ala Thr Ala Ala Leu Gly Gly
530 535 540

Tyr Gly Ser Lys Ser Ala Val Ala Ile Gly Ala Gly Tyr Arg Val Asn
545 550 555 560

Pro Asn Leu Ala Phe Lys Ala Gly Ala Ala Ile Asn Thr Ser Gly Asn
565 570 575

Lys Lys Gly Ser Tyr Asn Ile Gly Val Asn Tyr Glu Phe
580 585

<210> 24

<211> 684

<212> PRT

<213> Moraxella catarrhalis

<400> 24

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

Met Met Val Gly Leu Gly Met Ala Ser Thr Ala Asn Ala Gln Gln Gln
20 25 30

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

Asn Thr Glu Leu Thr Asp Pro Leu Tyr His Asn Met Ile Leu Gly Asn
50 55 60

Thr Ala Leu Leu Thr Gln Glu Asn Gln Tyr Lys Phe Tyr Ala Asp Asp
65 70 75 80

Gly Asn Gly Val Pro Asp Ser Leu Leu Phe Asn Lys Ile Leu His Asp
85 90 95

Gln Leu Leu His Gly Phe Lys Glu Gly Asp Thr Ile Ile Pro Leu Asp
100 105 110

Glu Asn Gly Lys Pro Val Tyr Lys Leu Asp Ser Ile Val Glu Gln Gly
115 120 125

Lys Thr Lys Thr Val Tyr Ser Val Thr Thr Lys Thr Ala Thr Ala Asp
130 135 140

Asp Val Asn Ser Ala Tyr Ser Arg Gly Ile Gln Gly Asp Ile Asp Asp
145 150 155 160

Leu Tyr Glu Ala Asn Lys Glu Asn Val Asn Arg Leu Ile Glu His Gly
165 170 175

Asp Lys Ile Phe Ala Asn Glu Glu Ser Val Gln Tyr Leu Asn Arg Glu
180 185 190

Val Gln Asn Asn Ile Glu Asn Ile His Glu Leu Ala Gln Gln Gln Asp
195 200 205

Gln His Ser Ser Asp Ile Lys Thr Leu Lys Lys Asn Val Glu Lys Asp
210 215 220

Leu Leu Asp Leu Ser Gly Arg Leu Ile Ala Gln Lys Glu Asp Ile Ala
225 230 235 240

Gln Asn Gln Thr Asp Ile Gln Asp Leu Ala Thr Tyr Asn Glu Leu Gln
245 250 255

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

Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Ser Asn His Ile
275 280 285

Lys Thr Leu Glu Asn Asn Ile Glu Glu Gly Leu Leu Glu Leu Ser Gly
290 295 300

His Leu Ile Asp Gln Lys Ala Asp Leu Thr Lys Asp Ile Lys Ala Leu
305 310 315 320

Glu Ser Asn Val Glu Glu Gly Leu Leu Asp Leu Ser Gly Arg Leu Ile
325 330 335

Asp Gln Lys Ala Asp Ile Ala Gln Asn Gln Ala Asn Ile Gln Asp Leu
340 345 350

Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu
355 360 365

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

Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr Ala Lys Gln
385 390 395 400

Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr
405 410 415

Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr
420 425 430

Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser
435 440 445

Glu Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala Asp Ile Ala Asn Asn
450 455 460

Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser
465 470 475 480

Asp Ile Lys Thr Leu Ala Lys Ala Ser Ala Ala Asn Thr Asp Arg Ile
485 490 495

Ala Lys Asn Lys Ala Asp Ala Asp Ala Ser Phe Glu Thr Leu Thr Lys
500 505 510

Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu His Asp Lys Leu Ile
515 520 525

Thr Ala Asn Lys Thr Ala Ile Asp Ala Asn Lys Ala Ser Ala Asp Thr
530 535 540

Lys Phe Ala Ala Thr Ala Asp Ala Ile Thr Lys Asn Gly Asn Ala Ile
545 550 555 560

Thr Lys Asn Ala Lys Ser Ile Thr Asp Leu Gly Thr Lys Val Asp Gly
565 570 575

Phe Asp Gly Arg Val Thr Ala Leu Asp Thr Lys Val Asn Ala Leu Asp
580 585 590

Thr Lys Val Asn Ala Phe Asp Gly Arg Ile Thr Ala Leu Asp Ser Lys
595 600 605

Val Glu Asn Gly Met Ala Ala Gln Ala Ala Leu Ser Gly Leu Phe Gln
610 615 620

Pro Tyr Ser Val Gly Lys Phe Asn Ala Thr Ala Ala Leu Gly Gly Tyr
625 630 635 640

Gly Ser Lys Ser Ala Val Ala Ile Gly Ala Gly Tyr Arg Val Asn Pro
645 650 655

Asn Leu Ala Phe Lys Ala Gly Ala Ala Ile Asn Thr Ser Gly Asn Lys

660

665

670

Lys Gly Ser Tyr Asn Ile Gly Val Asn Tyr Glu Phe
 675 680

<210> 25

<211> 650

<212> PRT

<213> Moraxella catarrhalis

<400> 25

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

Leu Ile Val Gly Leu Gly Ala Ala Ser Thr Ala Asn Ala Gln Gln Gln
 20 25 30

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

Tyr Ile Glu Glu Thr Asp Leu Leu Tyr His Asn Met Ile Leu Gly Asp
 50 55 60

Thr Ala Ala Leu Val Asp Arg Gln Asn Tyr Ser Asn Ser Gln Leu Lys
 65 70 75 80

Phe Tyr Ser Asn Asp Glu Glu Ser Val Pro Asp Ser Leu Leu Phe Ser
 85 90 95

Lys Met Leu Asn Asn Gln Gln Leu Asn Gly Phe Lys Ala Gly Asp Ile
 100 105 110

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

Arg Val Glu Gly Gly Lys Thr Arg Thr Val Leu Ser Val Thr Thr Lys
 130 135 140

Ile Ala Thr Gln Gln Asp Val Asp Ser Ala Tyr Ser Arg Gly Ile Gln
 145 150 155 160

Gly Lys Val Asn Asp Leu Asp Asp Glu Met Asn Phe Leu Asn His Asp
165 170 175

Ile Thr Ser Leu Tyr Asp Val Thr Ala Asn Gln Gln Asp Asp Ile Lys
180 185 190

Gly Leu Lys Lys Gly Val Lys Asp Leu Lys Lys Gly Val Lys Gly Leu
195 200 205

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

Asp Ile Gly Ser Leu Asn Asp Asp Val Ala Gln Asn Asn Glu Ser Ile
225 230 235 240

Glu Asp Leu Tyr Asp Phe Ser Gln Glu Val Ala Asp Ser Ile Gly Glu
245 250 255

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

Thr Asn Ser Val Glu Asn Thr Asn Asn Ile Thr Lys Asn Lys Ala Asp
275 280 285

Ile Gln Ala Leu Glu Asn Asn Val Val Glu Glu Leu Phe Asn Leu Ser
290 295 300

Gly Arg Leu Ile Asp Gln Lys Ala Asp Leu Thr Lys Asp Ile Lys Thr
305 310 315 320

Leu Glu Ser Asn Val Glu Glu Gly Leu Leu Glu Leu Ser Gly His Leu
325 330 335

Ile Asp Gln Lys Ala Asp Ile Ala Lys Asn Gln Ala Asp Ile Ala Gln
340 345 350

Asn Gln Ala Asn Ile Gln Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp
355 360 365

Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala
370 375 380

Ser Ser Glu Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu
385 390 395 400

Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu
405 410 415

Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala
420 425 430

Asp Ile Ala Asn Asn Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln
435 440 445

Asp Gln His Ser Ser Asp Ile Lys Thr Leu Ala Lys Ala Ser Ala Ala
450 455 460

Asn Thr Asp Arg Ile Ala Lys Asn Lys Ala Asp Ala Asp Ala Ser Phe
465 470 475 480

Glu Thr Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu
485 490 495

His Asp Lys Leu Ile Thr Ala Asn Lys Thr Ala Ile Asp Glu Asn Lys
500 505 510

Ala Ser Ala Asp Thr Lys Phe Ala Ala Thr Ala Asp Ala Ile Thr Lys
515 520 525

Asn Gly Asn Ala Ile Thr Lys Asn Ala Lys Ser Ile Thr Asp Leu Gly
530 535 540

Thr Lys Val Asp Gly Phe Asp Gly Arg Val Thr Ala Leu Asp Thr Lys
545 550 555 560

Val Asn Ala Phe Asp Gly Arg Ile Thr Ala Leu Asp Ser Lys Val Glu
565 570 575

Asn Gly Met Ala Ala Gln Ala Ala Leu Ser Gly Leu Phe Gln Pro Tyr

580	585	590
Ser Val Gly Lys Phe Asn Ala Thr Ala Ala Leu Gly Gly Tyr Gly Ser		
595	600	605
Lys Ser Ala Val Ala Ile Gly Ala Gly Tyr Arg Val Asn Pro Asn Leu		
610	615	620
Ala Phe Lys Ala Gly Ala Ala Ile Asn Thr Ser Gly Asn Lys Lys Gly		
625	630	635
640		
Ser Tyr Asn Ile Gly Val Asn Tyr Glu Phe		
645	650	
<210> 26		
<211> 616		
<212> PRT		
<213> Moraxella catarrhalis		
<400> 26		
Met Lys Thr Met Lys Leu Leu Pro Leu Lys Ile Ala Val Thr Ser Ala		
1	5	10
15		
Leu Ile Val Gly Leu Gly Ala Val Ser Thr Thr Asn Ala Gln Ala Gln		
20	25	30
Ser Arg Ser Leu Asp Gln Ile Gln Thr Lys Leu Ala Asp Leu Ala Gly		
35	40	45
Lys Ile Ala Ala Gly Lys Asn Gly Gly Gly Gln Asn Asn Gln Asn Asn		
50	55	60
Gln Asn Asp Ile Asn Lys Tyr Leu Phe Leu Ser Gln Tyr Ala Asn Ile		
65	70	75
80		
Leu Thr Met Glu Glu Leu Asn Asn Asn Val Val Lys Asn Ser Ser Ser		
85	90	95
Ile Glu Thr Leu Glu Thr Asp Phe Gly Trp Leu Glu Asn Asp Val Ala		
100	105	110

Asp Leu Glu Asp Gly Val Glu Glu Leu Thr Lys Asn Gln Asn Thr Leu
115 120 125

Ile Glu Lys Asp Glu Glu His Asp Arg Leu Ile Ala Gln Asn Gln Ala
130 135 140

Asp Ile Gln Thr Leu Glu Asn Asn Val Val Glu Glu Leu Phe Asn Leu
145 150 155 160

Ser Asp Arg Leu Ile Asp Gln Lys Ala Asp Ile Ala Lys Asn Gln Ala
165 170 175

Asp Ile Ala Gln Asn Asn Glu Ser Ile Glu Glu Leu Tyr Asp Phe Asp
180 185 190

Asn Glu Val Ala Glu Lys Ile Gly Glu Ile His Ala Tyr Thr Glu Glu
195 200 205

Val Asn Lys Thr Leu Gln Asp Leu Ile Thr Asn Ser Val Lys Asn Thr
210 215 220

Asp Asn Ile Asp Lys Asn Lys Ala Asp Ile Asp Asn Asn Ile Asn His
225 230 235 240

Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser Asp Ile Lys
245 250 255

Thr Leu Lys Asn Asn Val Glu Glu Gly Leu Leu Glu Leu Ser Gly His
260 265 270

Leu Ile Asp Gln Lys Ala Asp Leu Thr Lys Asp Ile Lys Thr Leu Glu
275 280 285

Asn Asn Val Glu Glu Gly Leu Leu Asp Leu Ser Gly Arg Leu Ile Asp
290 295 300

Gln Lys Ala Asp Ile Ala Lys Asn Gln Ala Asp Ile Ala Gln Asn Gln
305 310 315 320

Thr Asp Ile Gln Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Gln Tyr
325 330 335

Ala Gln Lys Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser
340 345 350

Glu Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln
355 360 365

Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys
370 375 380

Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala Asp Ile
385 390 395 400

Ala Asn Asn Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln
405 410 415

His Ser Ser Asp Ile Lys Thr Leu Ala Lys Ala Ser Ala Ala Asn Thr
420 425 430

Asp Arg Ile Ala Lys Asn Lys Ala Asp Ala Asp Ala Ser Phe Glu Thr
435 440 445

Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu His Asp
450 455 460

Lys Leu Ile Thr Ala Asn Lys Thr Ala Ile Asp Glu Asn Lys Ala Ser
465 470 475 480

Ala Asp Thr Lys Phe Ala Ala Thr Ala Asp Ala Ile Thr Lys Asn Gly
485 490 495

Asn Ala Ile Thr Lys Asn Ala Lys Ser Ile Thr Asp Leu Gly Thr Lys
500 505 510

Val Asp Gly Phe Asp Gly Arg Val Thr Ala Leu Asp Thr Lys Val Asn
515 520 525

Ala Phe Asp Gly Arg Ile Thr Ala Leu Asp Ser Lys Val Glu Asn Gly

530 535 540
 Met Ala Ala Gln Ala Ala Leu Ser Gly Leu Phe Gln Pro Tyr Ser Val
 545 550 555 560
 Gly Lys Phe Asn Ala Thr Ala Ala Leu Gly Gly Tyr Gly Ser Lys Ser
 565 570 575
 Ala Val Ala Ile Gly Ala Gly Tyr Arg Val Asn Pro Asn Leu Ala Phe
 580 585 590
 Lys Ala Gly Ala Ala Ile Asn Thr Ser Gly Asn Lys Lys Gly Ser Tyr
 595 600 605
 Asn Ile Gly Val Asn Tyr Glu Phe
 610 615
 <210> 27
 <211> 668
 <212> PRT
 <213> Moraxella catarrhalis
 <400> 27
 Met Lys Thr Met Lys Leu Leu Pro Leu Lys Ile Ala Val Thr Ser Ala
 1 5 10 15
 Leu Ile Val Gly Leu Gly Thr Ala Ser Thr Ala Asn Ala Gln Val Ala
 20 25 30
 Ser Pro Ala Asn Gln Lys Ile Gln Gln Lys Ile Lys Lys Val Arg Lys
 35 40 45
 Glu Leu Arg Gln Asp Ile Lys Ser Leu Arg Asn Asp Ile Asp Ser Asn
 50 55 60
 Thr Ala Asp Ile Gly Ser Leu Asn Asp Asp Val Ala Asp Asn Gln Asp
 65 70 75 80
 Asp Ile Leu Asp Asn Gln Ala Asp Ile Ala Lys Asn Gln Asp Asp Ile
 85 90 95

Glu Lys Asn Gln Ala Asp Ile Lys Glu Leu Asp Lys Glu Val Gly Val
100 105 110

Leu Ser Arg Glu Ile Gly Ser Leu Asn Asp Asp Ile Ala Asp Asn Tyr
115 120 125

Thr Asp Ile Ile Asp Asn Tyr Thr Asp Ile Ile Asp Asn Gln Ala Asn
130 135 140

Ile Ala Lys Asn Gln Asp Asp Ile Glu Lys Asn Gln Ala Asp Ile Lys
145 150 155 160

Glu Leu Asp Lys Glu Val Gly Val Leu Ser Arg Glu Ile Gly Ser Leu
165 170 175

Asn Asp Asp Val Ala Asp Asn Gln Asp Asp Ile Ala Lys Asn Gln Ala
180 185 190

Asp Ile Gln Thr Leu Glu Asn Asn Val Glu Glu Gly Leu Leu Glu Leu
195 200 205

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

Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser Asp Ile
225 230 235 240

Lys Thr Leu Lys Lys Asn Val Glu Glu Gly Leu Leu Glu Leu Ser Gly
245 250 255

His Leu Ile Asp Gln Lys Thr Asp Ile Ala Gln Asn Gln Ala Asn Ile
260 265 270

Gln Asp Leu Ala Thr Tyr Asn Glu Leu Gln Asp Gln Tyr Ala Gln Glu
275 280 285

Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr
290 295 300

Gln Asn Ile Ala Lys Asn Ser Asn Arg Ile Lys Ala Leu Glu Ser Asn
305 310 315 320

Val Glu Glu Gly Leu Leu Glu Leu Ser Gly His Leu Ile Asp Gln Lys
325 330 335

Ala Asp Leu Thr Lys Asp Ile Lys Ala Leu Glu Ser Asn Val Glu Glu
340 345 350

Gly Leu Leu Glu Leu Ser Gly His Leu Ile Asp Gln Lys Ala Asp Ile
355 360 365

Ala Gln Asn Gln Ala Asn Ile Gln Asp Leu Ala Ala Tyr Asn Glu Leu
370 375 380

Gln Asp Gln Tyr Ala Gln Lys Gln Thr Glu Ala Ile Asp Ala Leu Asn
385 390 395 400

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

Asn Glu Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp
420 425 430

Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn
435 440 445

Gln Ala Asp Ile Ala Asn Asn Ile Asn Asn Ile Tyr Glu Leu Ala Gln
450 455 460

Gln Gln Asp Gln His Ser Ser Asp Ile Lys Thr Leu Ala Lys Ala Ser
465 470 475 480

Ala Ala Asn Thr Asp Arg Ile Ala Lys Asn Lys Ala Asp Ala Asp Ala
485 490 495

Ser Phe Glu Thr Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp
500 505 510

Lys Glu His Asp Lys Leu Ile Thr Ala Asn Lys Thr Ala Ile Asp Ala

515 520 525
 Asn Lys Val Ser Ala Asp Thr Lys Phe Ala Ala Thr Ala Asp Ala Ile
 530 535 540
 Thr Lys Asn Gly Asn Ala Ile Thr Lys Asn Ala Lys Ser Ile Thr Asp
 545 550 555 560
 Leu Gly Thr Lys Val Asp Ala Phe Asp Ser Arg Val Thr Ala Leu Asp
 565 570 575
 Thr Lys Val Asn Ala Phe Asp Gly Arg Ile Thr Ala Leu Asp Ser Lys
 580 585 590
 Val Glu Asn Gly Met Ala Ala Gln Ala Ala Leu Ser Gly Leu Phe Gln
 595 600 605
 Pro Tyr Ser Val Gly Lys Phe Asn Ala Thr Ala Ala Leu Gly Gly Tyr
 610 615 620
 Gly Ser Lys Ser Ala Val Ala Ile Gly Ala Gly Tyr Arg Val Asn Pro
 625 630 635 640
 Asn Leu Ala Phe Lys Ala Gly Ala Ala Ile Asn Thr Ser Gly Asn Lys
 645 650 655
 Lys Gly Ser Tyr Asn Ile Gly Val Asn Tyr Glu Phe
 660 665

<210> 28
 <211> 674
 <212> PRT
 <213> Moraxella catarrhalis

<400> 28

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

Met Ile Val Gly Leu Gly Ala Thr Ser Thr Val Asn Ala Gln Val Val
 20 25 30

Glu Gln Phe Phe Pro Asn Ile Phe Phe Asn Glu Asn His Asp Glu Leu
35 40 45

Asp Asp Ala Tyr His Asn Met Ile Leu Gly Asp Thr Ala Ile Val Ser
50 55 60

Asn Ser Gln Asp Asn Ser Thr Gln Leu Lys Phe Tyr Ser Asn Asp Glu
65 70 75 80

Asp Ser Val Pro Asp Ser Leu Leu Phe Ser Lys Leu Leu His Glu Gln
85 90 95

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

Asp Gly Lys Pro Val Tyr Thr Lys Asp Thr Arg Thr Lys Asp Gly Lys
115 120 125

Val Glu Thr Val Tyr Ser Val Thr Thr Lys Ile Ala Thr Gln Asp Asp
130 135 140

Val Glu Gln Ser Ala Tyr Ser Arg Gly Ile Gln Gly Asp Ile Asp Asp
145 150 155 160

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

Asp Tyr Asn Glu Arg Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala
180 185 190

Ser Ser Ala Asn Thr Asp Arg Ile Asp Thr Ala Glu Glu Arg Ile Asp
195 200 205

Lys Asn Glu Tyr Asp Ile Lys Ala Leu Glu Ser Asn Val Glu Glu Gly
210 215 220

Leu Leu Glu Leu Ser Gly His Leu Ile Asp Gln Lys Ala Asp Leu Thr
225 230 235 240

Lys Asp Ile Lys Ala Leu Glu Ser Asn Val Glu Glu Gly Leu Leu Glu
245 250 255

Leu Ser Gly His Leu Ile Asp Gln Lys Ala Asp Leu Thr Lys Asp Ile
260 265 270

Lys Ala Leu Glu Ser Asn Val Glu Glu Gly Leu Leu Asp Leu Ser Gly
275 280 285

Arg Leu Ile Asp Gln Lys Ala Asp Ile Ala Gln Asn Gln Ala Asn Ile
290 295 300

Gln Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr Ala Lys Gln
305 310 315 320

Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr
325 330 335

Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr
340 345 350

Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser
355 360 365

Glu Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln
370 375 380

Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys
385 390 395 400

Ala Ser Ser Glu Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn
405 410 415

Glu Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala
420 425 430

Leu Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Gln
435 440 445

Ala Asp Ile Ala Asn Asn Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln

450		455		460
Gln Asp Gln His Ser Ser Asp Ile Lys Thr Leu Ala Lys Ala Ser Ala				
465		470		480
Ala Asn Thr Asp Arg Ile Ala Lys Asn Lys Ala Asp Ala Asp Ala Ser				
		485	490	495
Phe Glu Thr Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys				
		500	505	510
Glu His Asp Lys Leu Ile Thr Ala Asn Lys Thr Ala Ile Asp Ala Asn				
		515	520	525
Lys Ala Ser Ala Asp Thr Lys Phe Ala Ala Thr Ala Asp Ala Ile Thr				
		530	535	540
Lys Asn Gly Asn Ala Ile Thr Lys Asn Ala Lys Ser Ile Thr Asp Leu				
545		550	555	560
Gly Thr Lys Val Asp Gly Phe Asp Gly Arg Val Thr Ala Leu Asp Thr				
		565	570	575
Lys Val Asn Ala Leu Asp Thr Lys Val Asn Ala Phe Asp Gly Arg Ile				
		580	585	590
Thr Ala Leu Asp Ser Lys Val Glu Asn Gly Met Ala Ala Gln Ala Ala				
		595	600	605
Leu Ser Gly Leu Phe Gln Pro Tyr Ser Val Gly Lys Phe Asn Ala Thr				
		610	615	620
Ala Ala Leu Gly Gly Tyr Gly Ser Lys Ser Ala Val Ala Ile Gly Ala				
625		630	635	640
Gly Tyr Arg Val Asn Pro Asn Leu Ala Phe Lys Ala Gly Ala Ala Ile				
		645	650	655
Asn Thr Ser Gly Asn Lys Lys Gly Ser Tyr Asn Ile Gly Val Asn Tyr				
		660	665	670

Glu Phe

<210> 29
<211> 613
<212> PRT
<213> *Moraxella catarrhalis*

<400> 29

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

Met Ile Ile Gly Leu Gly Ala Ala Ser Thr Ala Asn Ala Gln Ser Arg
20 25 30

Asp Arg Ser Leu Glu Asp Ile Gln Asp Ser Ile Ser Lys Leu Val Gln
35 40 45

Asp Asp Ile Asp Thr Leu Lys Gln Asp Gln Gln Lys Met Asn Lys Tyr
50 55 60

Leu Leu Leu Asn Gln Leu Ala Asn Thr Leu Ile Thr Asp Glu Leu Asn
65 70 75 80

Asn Asn Val Ile Lys Asn Thr Asn Ser Ile Glu Ala Leu Gly Asp Glu
85 90 95

Ile Gly Trp Leu Glu Asn Asp Ile Ala Asp Leu Glu Glu Gly Val Glu
100 105 110

Glu Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp Glu Glu His
115 120 125

Asp Arg Leu Ile Ala Gln Asn Gln Ala Asp Ile Gln Thr Leu Glu Asn
130 135 140

Asn Val Val Glu Glu Leu Phe Asn Leu Ser Gly Arg Leu Ile Asp Gln
145 150 155 160

Glu Ala Asp Ile Ala Lys Asn Asn Ala Ser Ile Glu Glu Leu Tyr Asp
165 170 175

Phe Asp Asn Glu Val Ala Glu Arg Ile Gly Glu Ile His Ala Tyr Thr
180 185 190

Glu Glu Val Asn Lys Thr Leu Glu Asn Leu Ile Thr Asn Ser Val Lys
195 200 205

Asn Thr Asp Asn Ile Asp Lys Asn Lys Ala Asp Ile Asp Asn Asn Ile
210 215 220

Asn His Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser Asp
225 230 235 240

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

Gly His Leu Ile Asp Gln Lys Ala Asp Leu Thr Lys Asp Ile Lys Ala
260 265 270

Leu Glu Ser Asn Val Glu Glu Gly Leu Leu Asp Leu Ser Gly Arg Leu
275 280 285

Leu Asp Gln Lys Ala Asp Leu Thr Lys Asp Ile Lys Ala Leu Glu Ser
290 295 300

Asn Val Glu Glu Gly Leu Leu Asp Leu Ser Gly Arg Leu Leu Asp Gln
305 310 315 320

Lys Ala Asp Ile Ala Gln Asn Gln Thr Asp Ile Gln Asp Leu Ala Ala
325 330 335

Tyr Asn Glu Leu Gln Asp Gln Tyr Ala Gln Lys Gln Thr Glu Ala Ile
340 345 350

Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Glu Asp
355 360 365

Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr

370																	
Glu	Ala	Ile	Asp	Ala	Leu	Asn	Lys	Ala	Ser	Ser	Glu	Asn	Thr	Gln	Asn		
385					390					395					400		
Ile	Ala	Lys	Asn	Gln	Ala	Asp	Ile	Ala	Asn	Asn	Ile	Asn	Asn	Ile	Tyr		
			405					410						415			
Glu	Leu	Ala	Gln	Gln	Gln	Asp	Gln	His	Ser	Ser	Asp	Ile	Lys	Thr	Leu		
			420					425					430				
Ala	Lys	Ala	Ser	Ala	Ala	Asn	Thr	Asn	Arg	Ile	Ala	Thr	Ala	Glu	Leu		
		435					440					445					
Gly	Ile	Ala	Glu	Asn	Lys	Lys	Asp	Ala	Gln	Ile	Ala	Lys	Ala	Gln	Ala		
	450					455					460						
Asn	Ala	Asn	Lys	Thr	Ala	Ile	Asp	Glu	Asn	Lys	Ala	Ser	Ala	Asp	Thr		
465					470					475					480		
Lys	Phe	Ala	Ala	Thr	Ala	Asp	Ala	Ile	Thr	Lys	Asn	Gly	Asn	Ala	Ile		
				485					490					495			
Thr	Lys	Asn	Ala	Lys	Ser	Ile	Thr	Asp	Leu	Gly	Thr	Lys	Val	Asp	Gly		
			500					505					510				
Phe	Asp	Gly	Arg	Val	Thr	Ala	Leu	Asp	Thr	Lys	Val	Asn	Ala	Phe	Asp		
		515					520					525					
Gly	Arg	Ile	Thr	Ala	Leu	Asp	Ser	Lys	Val	Glu	Asn	Gly	Met	Ala	Ala		
	530					535					540						
Gln	Ala	Ala	Leu	Ser	Gly	Leu	Phe	Gln	Pro	Tyr	Ser	Val	Gly	Lys	Phe		
545					550					555					560		
Asn	Ala	Thr	Ala	Ala	Leu	Gly	Gly	Tyr	Gly	Ser	Lys	Ser	Ala	Val	Ala		
				565					570					575			
Ile	Gly	Ala	Gly	Tyr	Arg	Val	Asn	Pro	Asn	Leu	Ala	Phe	Lys	Ala	Gly		
			580					585					590				

Ala Ala Ile Asn Thr Ser Gly Asn Lys Lys Gly Ser Tyr Asn Ile Gly
595 600 605

Val Asn Tyr Glu Phe
610

<210> 30
<211> 576
<212> PRT
<213> Moraxella catarrhalis

<400> 30

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

Met Ile Val Gly Leu Gly Ala Thr Ser Thr Val Asn Ala Gln Val Val
20 25 30

Glu Gln Phe Phe Pro Asn Ile Phe Phe Asn Glu Asn His Asp Glu Leu
35 40 45

Asp Asp Ala Tyr His Asn Met Ile Leu Gly Asp Thr Ala Ile Val Ser
50 55 60

Asn Ser Gln Asp Asn Ser Thr Gln Leu Lys Phe Tyr Ser Asn Asp Glu
65 70 75 80

Asp Ser Val Pro Asp Ser Leu Leu Phe Ser Lys Leu Leu His Glu Gln
85 90 95

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

Asp Gly Lys Pro Val Tyr Thr Lys Asp Thr Arg Thr Lys Asp Gly Lys
115 120 125

Val Glu Thr Val Tyr Ser Val Thr Thr Lys Ile Ala Thr Gln Asp Asp
130 135 140

Val Glu Gln Ser Ala Tyr Ser Arg Gly Ile Gln Gly Asp Ile Asp Asp
145 150 155 160

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

Asp Tyr Asn Glu Arg Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala
180 185 190

Ser Ser Ala Asn Thr Asp Arg Ile Asp Thr Ala Glu Glu Arg Ile Asp
195 200 205

Lys Asn Glu Tyr Asp Ile Lys Ala Leu Glu Ser Asn Val Glu Glu Gly
210 215 220

Leu Leu Glu Leu Ser Gly His Leu Ile Asp Gln Lys Ala Asp Leu Thr
225 230 235 240

Lys Asp Ile Lys Ala Leu Glu Ser Asn Val Glu Glu Gly Leu Leu Glu
245 250 255

Leu Ser Gly His Leu Ile Asp Gln Lys Ala Asp Leu Thr Lys Asp Ile
260 265 270

Lys Ala Leu Glu Ser Asn Val Glu Glu Gly Leu Leu Asp Leu Ser Gly
275 280 285

Arg Leu Leu Asp Gln Lys Ala Asp Ile Ala Lys Asn Gln Ala Asp Ile
290 295 300

Ala Gln Asn Gln Thr Asp Ile Gln Asp Leu Ala Ala Tyr Asn Glu Leu
305 310 315 320

Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn
325 330 335

Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala Asp
340 345 350

Ile Ala Asn Asn Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp

355								360									365
Gln	His	Ser	Ser	Asp	Ile	Lys	Thr	Leu	Ala	Lys	Ala	Ser	Ala	Ala	Asn		
370						375					380						
Thr	Asp	Arg	Ile	Ala	Lys	Asn	Lys	Ala	Asp	Ala	Asp	Ala	Ser	Phe	Glu		
385					390					395					400		
Thr	Leu	Thr	Lys	Asn	Gln	Asn	Thr	Leu	Ile	Glu	Lys	Asp	Lys	Glu	His		
				405					410					415			
Asp	Lys	Leu	Ile	Thr	Ala	Asn	Lys	Thr	Ala	Ile	Asp	Ala	Asn	Lys	Ala		
			420					425					430				
Ser	Ala	Asp	Thr	Lys	Phe	Ala	Ala	Thr	Ala	Asp	Ala	Ile	Thr	Lys	Asn		
		435					440					445					
Gly	Asn	Ala	Ile	Thr	Lys	Asn	Ala	Lys	Ser	Ile	Thr	Asp	Leu	Gly	Thr		
450						455					460						
Lys	Val	Asp	Gly	Phe	Asp	Gly	Arg	Val	Thr	Ala	Leu	Asp	Thr	Lys	Val		
465					470					475					480		
Asn	Ala	Leu	Asp	Thr	Lys	Val	Asn	Ala	Phe	Asp	Gly	Arg	Ile	Thr	Ala		
				485					490					495			
Leu	Asp	Ser	Lys	Val	Glu	Asn	Gly	Met	Ala	Ala	Gln	Ala	Ala	Leu	Ser		
			500					505						510			
Gly	Leu	Phe	Gln	Pro	Tyr	Ser	Val	Gly	Lys	Phe	Asn	Ala	Thr	Ala	Ala		
		515					520				525						
Leu	Gly	Gly	Tyr	Gly	Ser	Lys	Ser	Ala	Val	Ala	Ile	Gly	Ala	Gly	Tyr		
530						535					540						
Arg	Val	Asn	Pro	Asn	Leu	Ala	Phe	Lys	Ala	Gly	Ala	Ala	Ile	Asn	Thr		
545					550					555					560		
Ser	Gly	Asn	Lys	Lys	Gly	Ser	Tyr	Asn	Ile	Gly	Val	Asn	Tyr	Glu	Phe		
				565				570						575			

<210> 31
 <211> 684
 <212> PRT
 <213> Moraxella catarrhalis

<400> 31

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

Met Met Val Gly Leu Gly Met Ala Ser Thr Ala Asn Ala Gln Gln Gln
 20 25 30

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

Asn Thr Glu Leu Thr Asp Pro Leu Tyr His Asn Met Ile Leu Gly Asn
 50 55 60

Thr Ala Leu Leu Thr Gln Glu Asn Gln Tyr Lys Phe Tyr Ala Asp Asp
 65 70 75 80

Gly Asn Gly Val Pro Asp Ser Leu Leu Phe Asn Lys Ile Leu His Asp
 85 90 95

Gln Leu Leu His Gly Phe Lys Glu Gly Asp Thr Ile Ile Pro Leu Asp
 100 105 110

Glu Asn Gly Lys Pro Val Tyr Lys Leu Asp Ser Ile Val Glu Gln Gly
 115 120 125

Lys Thr Lys Thr Val Tyr Ser Val Thr Thr Lys Thr Ala Thr Ala Asp
 130 135 140

Asp Val Asn Ser Ala Tyr Ser Arg Gly Ile Gln Gly Asp Ile Asp Asp
 145 150 155 160

Leu Tyr Glu Ala Asn Lys Glu Asn Val Asn Arg Leu Ile Glu His Gly
 165 170 175

Asp Lys Ile Phe Ala Asn Glu Glu Ser Val Gln Tyr Leu Asn Arg Glu
180 185 190

Val Gln Asn Asn Ile Glu Asn Ile His Glu Leu Ala Gln Gln Gln Asp
195 200 205

Gln His Ser Ser Asp Ile Lys Thr Leu Lys Lys Asn Val Glu Lys Asp
210 215 220

Leu Leu Asp Leu Ser Gly Arg Leu Ile Ala Gln Lys Glu Asp Ile Ala
225 230 235 240

Gln Asn Gln Thr Asp Ile Gln Asp Leu Ala Thr Tyr Asn Glu Leu Gln
245 250 255

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

Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Ser Asn His Ile
275 280 285

Lys Thr Leu Glu Asn Asn Ile Glu Glu Gly Leu Leu Glu Leu Ser Gly
290 295 300

His Leu Ile Asp Gln Lys Ala Asp Leu Thr Lys Asp Ile Lys Ala Leu
305 310 315 320

Glu Ser Asn Val Glu Glu Gly Leu Leu Asp Leu Ser Gly Arg Leu Ile
325 330 335

Asp Gln Lys Ala Asp Ile Ala Gln Asn Gln Ala Asn Ile Gln Asp Leu
340 345 350

Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu
355 360 365

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

Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr Ala Lys Gln

385		390		395		400
Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr						
		405		410		415
Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr						
		420		425		430
Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser						
		435		440		445
Glu Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala Asp Ile Ala Asn Asn						
		450		455		460
Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser						
		465		470		475
Asp Ile Lys Thr Leu Ala Lys Ala Ser Ala Ala Asn Thr Asp Arg Ile						
		485		490		495
Ala Lys Asn Lys Ala Asp Ala Asp Ala Ser Phe Glu Thr Leu Thr Lys						
		500		505		510
Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu His Asp Lys Leu Ile						
		515		520		525
Thr Ala Asn Lys Thr Ala Ile Asp Ala Asn Lys Ala Ser Ala Asp Thr						
		530		535		540
Lys Phe Ala Ala Thr Ala Asp Ala Ile Thr Lys Asn Gly Asn Ala Ile						
		545		550		555
Thr Lys Asn Ala Lys Ser Ile Thr Asp Leu Gly Thr Lys Val Asp Gly						
		565		570		575
Phe Asp Gly Arg Val Thr Ala Leu Asp Thr Lys Val Asn Ala Leu Asp						
		580		585		590
Thr Lys Val Asn Ala Phe Asp Gly Arg Ile Thr Ala Leu Asp Ser Lys						
		595		600		605

Val Glu Asn Gly Met Ala Ala Gln Ala Ala Leu Ser Gly Leu Phe Gln
610 615 620

Pro Tyr Ser Val Gly Lys Phe Asn Ala Thr Ala Ala Leu Gly Gly Tyr
625 630 635 640

Gly Ser Lys Ser Ala Val Ala Ile Gly Ala Gly Tyr Arg Val Asn Pro
645 650 655

Asn Leu Ala Phe Lys Ala Gly Ala Ala Ile Asn Thr Ser Gly Asn Lys
660 665 670

Lys Gly Ser Tyr Asn Ile Gly Val Asn Tyr Glu Phe
675 680

<210> 32
<211> 686
<212> PRT
<213> Moraxella catarrhalis

<400> 32

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

Met Ile Ile Gly Leu Gly Ala Ala Ser Thr Ala Asn Ala Gln Ala Thr
20 25 30

Glu Thr Phe Leu Pro Asn Leu Phe Asp Asn Asp Tyr Thr Glu Thr Thr
35 40 45

Asp Pro Leu Tyr His Gly Met Ile Leu Gly Asn Thr Ala Ile Thr Gln
50 55 60

Asp Thr Gln Tyr Lys Phe Tyr Ala Glu Asn Gly Asn Glu Val Pro Asp
65 70 75 80

Ser Leu Phe Phe Asn Lys Ile Leu His Asp Gln Gln Leu Asn Gly Phe
85 90 95

Lys Glu Gly Asp Thr Ile Ile Pro Leu Asp Glu Asn Gly Lys Pro Val
100 105 110

Tyr Lys Leu Asp Glu Ile Thr Glu Asn Gly Val Lys Arg Lys Val Tyr
115 120 125

Ser Val Thr Thr Lys Thr Ala Thr Arg Glu Asp Val Glu Gln Ser Ala
130 135 140

Tyr Ser Arg Gly Ile Gln Gly Asp Ile Asp Asp Leu Tyr Glu Ala Asn
145 150 155 160

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

Asn Glu Glu Ser Val Gln Tyr Leu Asn Lys Glu Val Gln Asn Asn Ile
180 185 190

Glu Asn Ile His Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser Asp
195 200 205

Ile Lys Thr Leu Lys Lys Asn Val Glu Glu Gly Leu Leu Glu Leu Ser
210 215 220

Gly Arg Leu Ile Ala Gln Lys Glu Asp Ile Ala Gln Asn Gln Thr Asp
225 230 235 240

Ile Gln Asp Leu Ala Thr Tyr Asn Glu Leu Gln Asp Gln Tyr Ala Gln
245 250 255

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

Thr Gln Asn Ile Ala Lys Asn Ser Asn His Ile Lys Thr Leu Glu Asn
275 280 285

Asn Ile Glu Glu Gly Leu Leu Glu Leu Ser Gly His Leu Ile Asp Gln
290 295 300

Lys Ala Asp Leu Thr Lys Asp Ile Lys Ala Leu Glu Ser Asn Val Glu

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

Leu Ile Thr Ala Asn Lys Thr Ala Ile Asp Ala Asn Lys Ala Ser Ala
530 535 540

Asp Thr Lys Phe Ala Ala Thr Ala Asp Ala Ile Thr Lys Asn Gly Asn
545 550 555 560

Ala Ile Thr Lys Asn Ala Lys Ser Ile Thr Asp Leu Gly Thr Lys Val
565 570 575

Asp Gly Phe Asp Gly Arg Val Thr Ala Leu Asp Thr Lys Val Asn Ala
580 585 590

Leu Asp Thr Lys Val Asn Ala Phe Asp Gly Arg Ile Thr Ala Leu Asp
595 600 605

Ser Lys Val Glu Asn Gly Met Ala Ala Gln Ala Ala Leu Ser Gly Leu
610 615 620

Phe Gln Pro Tyr Ser Val Gly Lys Phe Asn Ala Thr Ala Ala Leu Gly
625 630 635 640

Gly Tyr Gly Ser Lys Ser Ala Val Ala Ile Gly Ala Gly Tyr Arg Val
645 650 655

Asn Pro Asn Leu Ala Phe Lys Ala Gly Ala Ala Ile Asn Thr Ser Gly
660 665 670

Asn Lys Lys Gly Ser Tyr Asn Ile Gly Val Asn Tyr Glu Phe
675 680 685

<210> 33
<211> 630
<212> PRT
<213> Moraxella catarrhalis

<400> 33

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

Met Ile Ile Gly Leu Gly Ala Ala Ser Thr Ala Asn Ala Gln Ala Lys
20 25 30

Asn Asp Ile Thr Leu Glu Asp Leu Pro Tyr Leu Ile Lys Lys Ile Asp
35 40 45

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

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

Asn Lys Ala Leu Glu Glu Leu Asp Glu Asp Val Gly Trp Asn Gln Asn
85 90 95

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

Asn Ala Leu Ala Glu Gln Gly Glu Ala Ile Lys Glu Asp Leu Gln Gly
115 120 125

Leu Ala Asp Phe Val Glu Gly Gln Glu Gly Lys Ile Leu Gln Asn Glu
130 135 140

Thr Ser Ile Lys Lys Asn Thr Gln Arg Asn Leu Val Asn Gly Phe Glu
145 150 155 160

Ile Glu Lys Asn Lys Asp Ala Ile Ala Lys Asn Asn Glu Ser Ile Glu
165 170 175

Asp Leu Tyr Asp Phe Gly His Glu Val Ala Glu Ser Ile Gly Glu Ile
180 185 190

His Ala His Asn Glu Ala Gln Asn Glu Thr Leu Lys Gly Leu Ile Thr
195 200 205

Asn Ser Ile Glu Asn Thr Asn Asn Ile Thr Lys Asn Lys Ala Asp Ile
210 215 220

Gln Ala Leu Glu Asn Asn Val Val Glu Glu Leu Phe Asn Leu Ser Gly

225		230		235		240									
Arg	Leu	Ile	Asp	Gln	Lys	Ala	Asp	Ile	Asp	Asn	Asn	Ile	Asn	Asn	Ile
			245						250					255	
Tyr	Glu	Leu	Ala	Gln	Gln	Gln	Asp	Gln	His	Ser	Ser	Asp	Ile	Lys	Thr
			260						265					270	
Leu	Lys	Lys	Asn	Val	Glu	Glu	Gly	Leu	Leu	Glu	Leu	Ser	Gly	His	Leu
			275											285	
Ile	Asp	Gln	Lys	Thr	Asp	Ile	Ala	Gln	Asn	Gln	Ala	Asn	Ile	Gln	Asp
			290						295					300	
Leu	Ala	Thr	Tyr	Asn	Glu	Leu	Gln	Asp	Gln	Tyr	Ala	Gln	Lys	Gln	Thr
305															320
Glu	Ala	Ile	Asp	Ala	Leu	Asn	Lys	Ala	Ser	Ser	Glu	Asn	Thr	Gln	Asn
															335
Ile	Glu	Asp	Leu	Ala	Ala	Tyr	Asn	Glu	Leu	Gln	Asp	Ala	Tyr	Ala	Lys
															350
Gln	Gln	Thr	Glu	Ala	Ile	Asp	Ala	Leu	Asn	Lys	Ala	Ser	Ser	Glu	Asn
															365
Thr	Gln	Asn	Ile	Glu	Asp	Leu	Ala	Ala	Tyr	Asn	Glu	Leu	Gln	Asp	Ala
															380
Tyr	Ala	Lys	Gln	Gln	Thr	Glu	Ala	Ile	Asp	Ala	Leu	Asn	Lys	Ala	Ser
385															400
Ser	Glu	Asn	Thr	Gln	Asn	Ile	Ala	Lys	Asn	Gln	Ala	Asp	Ile	Ala	Asn
															415
Asn	Ile	Asn	Asn	Ile	Tyr	Glu	Leu	Ala	Gln	Gln	Gln	Asp	Gln	His	Ser
															430
Ser	Asp	Ile	Lys	Thr	Leu	Ala	Lys	Ala	Ser	Ala	Ala	Asn	Thr	Asp	Arg
															445

Ile Ala Lys Asn Lys Ala Asp Ala Asp Ala Ser Phe Glu Thr Leu Thr
450 455 460

Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu His Asp Lys Leu
465 470 475 480

Ile Thr Ala Asn Lys Thr Ala Ile Asp Ala Asn Lys Ala Ser Ala Asp
485 490 495

Thr Lys Phe Ala Ala Thr Ala Asp Ala Ile Thr Lys Asn Gly Asn Ala
500 505 510

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

Gly Phe Asp Ser Arg Val Thr Ala Leu Asp Thr Lys Val Asn Ala Phe
530 535 540

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

Ala Gln Ala Ala Leu Ser Gly Leu Phe Gln Pro Tyr Ser Val Gly Lys
565 570 575

Phe Asn Ala Thr Ala Ala Leu Gly Gly Tyr Gly Ser Lys Ser Ala Val
580 585 590

Ala Ile Gly Ala Gly Tyr Arg Val Asn Pro Asn Leu Ala Phe Lys Ala
595 600 605

Gly Ala Ala Ile Asn Thr Ser Gly Asn Lys Lys Gly Ser Tyr Asn Ile
610 615 620

Gly Val Asn Tyr Glu Phe
625 630

<210> 34
<211> 616
<212> PRT

<213> Moraxella catarrhalis

<400> 34

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

Leu Ile Val Gly Leu Gly Ala Ala Ser Thr Ala Asn Ala Gln Ala Gln
20 25 30

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

Lys Ile Glu Gln Ala Lys Ser Gln Asn Gly Gln Ser Gln Lys Asp Ile
50 55 60

Asn Gln Tyr Leu Leu Leu Ser Gln Tyr Ala Asn Val Leu Thr Met Glu
65 70 75 80

Glu Leu Asn Asn Asn Val Val Lys Asn Ser Ser Ser Ile Glu Thr Leu
85 90 95

Asp Asn Asp Ile Ala Trp Leu Asn Asp Asp Leu Ile Asp Leu Asp Lys
100 105 110

Glu Val Gly Val Leu Ser Arg Asp Ile Gly Ser Leu His Asp Asp Val
115 120 125

Ala Gln Asn Gln Ala Asp Ile Lys Thr Leu Lys Asn Asn Val Val Glu
130 135 140

Glu Leu Phe Asn Leu Ser Asp Arg Leu Ile Asp Gln Glu Ala Asp Ile
145 150 155 160

Ala Gln Asn Asn Glu Ser Ile Glu Asp Leu Tyr Asp Phe Gly Arg Glu
165 170 175

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

Glu Thr Leu Lys Asp Leu Ile Thr Asn Ser Val Lys Asn Thr Asp Asn

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

His Ser Ser Asp Ile Lys Thr Leu Ala Lys Ala Ser Ala Ala Asn Thr
420 425 430

Asp Arg Ile Ala Lys Asn Lys Ala Asp Ala Asp Ala Ser Phe Glu Thr
435 440 445

Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu His Asp
450 455 460

Lys Leu Ile Thr Ala Asn Lys Thr Ala Ile Asp Ala Asn Lys Ala Ser
465 470 475 480

Ala Asp Thr Lys Phe Ala Ala Thr Ala Asp Ala Ile Thr Lys Asn Gly
485 490 495

Asn Ala Ile Thr Lys Asn Ala Lys Ser Ile Thr Asp Leu Gly Thr Lys
500 505 510

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

Ala Phe Asp Gly Arg Ile Thr Ala Leu Asp Ser Lys Val Glu Asn Gly
530 535 540

Met Ala Ala Gln Ala Ala Leu Ser Gly Leu Phe Gln Pro Tyr Ser Val
545 550 555 560

Gly Lys Phe Asn Ala Thr Ala Ala Leu Gly Gly Tyr Gly Ser Lys Ser
565 570 575

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

Lys Ala Gly Ala Ala Ile Asn Thr Ser Gly Asn Lys Lys Gly Ser Tyr
595 600 605

Asn Ile Gly Val Asn Tyr Glu Phe
610 615

<210> 35
 <211> 614
 <212> PRT
 <213> Moraxella catarrhalis

<400> 35

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

Met Ile Ile Gly Leu Gly Ala Thr Ser Thr Val Asn Ala Gln Val Val
 20 25 30

Glu Gln Phe Phe Pro Asn Ile Phe Phe Asn Glu Asn His Asp Glu Leu
 35 40 45

Asp Asp Ala Tyr His Asn Met Ile Leu Gly Asp Thr Ala Ile Val Ser
 50 55 60

Asn Ser Gln Asp Asn Ser Thr Gln Leu Lys Phe Tyr Ser Asn Asp Glu
 65 70 75 80

Asp Ser Val Pro Asp Ser Leu Leu Phe Ser Lys Leu Leu His Glu Gln
 85 90 95

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

Asp Gly Lys Pro Val Tyr Thr Lys Asp Thr Arg Thr Lys Asp Gly Lys
 115 120 125

Val Glu Thr Val Tyr Ser Val Thr Thr Lys Ile Ala Thr Gln Asp Asp
 130 135 140

Val Glu Gln Ser Ala Tyr Ser Arg Gly Ile Gln Gly Asp Ile Asp Asp
 145 150 155 160

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

Asp Tyr Asn Glu Arg Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala

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

Asn Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser
405 410 415

Ser Asp Ile Lys Thr Leu Ala Lys Val Ser Ala Ala Asn Thr Asp Arg
420 425 430

Ile Ala Lys Asn Lys Ala Asp Ala Asp Ala Ser Phe Glu Thr Leu Thr
435 440 445

Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu His Asp Lys Leu
450 455 460

Ile Thr Ala Asn Lys Thr Ala Ile Asp Ala Asn Lys Ala Ser Ala Asp
465 470 475 480

Thr Lys Phe Ala Ala Thr Ala Asp Ala Ile Thr Lys Asn Gly Asn Ala
485 490 495

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

Gly Phe Asp Gly Arg Val Thr Ala Leu Asp Thr Lys Val Asn Ala Phe
515 520 525

Asp Gly Arg Ile Thr Ala Leu Asp Ser Lys Val Glu Asn Gly Met Ala
530 535 540

Ala Gln Ala Ala Leu Ser Gly Leu Phe Gln Pro Tyr Ser Val Gly Lys
545 550 555 560

Phe Asn Ala Thr Ala Ala Leu Gly Gly Tyr Gly Ser Lys Ser Ala Val
565 570 575

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

Gly Ala Ala Ile Asn Thr Ser Gly Asn Lys Lys Gly Ser Tyr Asn Ile
595 600 605

Gly Val Asn Tyr Glu Phe
610

<210> 36
<211> 679
<212> PRT
<213> Moraxella catarrhalis

<400> 36

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

Met Ile Ile Gly Leu Gly Ala Ala Ser Thr Ala Asn Ala Gln Thr Thr
20 25 30

Glu Thr Phe Leu Pro Asn Leu Phe Asp Asn Asp Tyr Thr Glu Thr Thr
35 40 45

Asp Pro Leu Tyr His Gly Met Ile Leu Gly Asp Thr Ala Ile Thr Gln
50 55 60

Asp Thr Gln Tyr Lys Phe Tyr Ala Glu Asn Gly Asn Glu Val Pro Asp
65 70 75 80

Ser Leu Phe Phe Asn Lys Ile Leu His Asp Gln Leu Leu Asn Gly Phe
85 90 95

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

Tyr Lys Leu Asp Glu Arg Thr Glu Asn Gly Val Lys Arg Lys Val Tyr
115 120 125

Ser Val Thr Thr Lys Thr Ala Thr Gln Ala Asp Val Glu Gln Ser Ala
130 135 140

Tyr Ser Arg Gly Ile Gln Gly Asp Ile Asp Asp Leu Tyr Glu Ala Asn
145 150 155 160

Lys Glu Asn Val Asn Arg Leu Ile Glu His Gly Asp Lys Ile Phe Ala

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

Tyr Asn Glu Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile
 385 390 395 400

Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Glu Asp
 405 410 415

Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr
 420 425 430

Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn
 435 440 445

Ile Ala Lys Asn Gln Ala Asp Ile Ala Asn Asn Ile Asn Asn Ile Tyr
 450 455 460

Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser Asp Ile Lys Thr Leu
 465 470 475 480

Ala Lys Ala Ser Ala Ala Asn Thr Asp Arg Ile Ala Lys Asn Lys Ala
 485 490 495

Asp Ala Asp Ala Ser Phe Glu Thr Leu Thr Lys Asn Gln Asn Thr Leu
 500 505 510

Ile Glu Lys Asp Lys Glu His Asp Lys Leu Ile Thr Ala Asn Lys Thr
 515 520 525

Ala Ile Asp Ala Asn Lys Ala Ser Ala Asp Thr Lys Phe Ala Ala Thr
 530 535 540

Ala Asp Ala Ile Thr Lys Asn Gly Asn Ala Ile Thr Lys Asn Ala Lys
 545 550 555 560

Ser Ile Thr Asp Leu Gly Thr Lys Val Asp Gly Phe Asp Gly Arg Val
 565 570 575

Thr Ala Leu Asp Thr Lys Val Asn Ala Leu Asp Thr Lys Val Asn Ala
 580 585 590

Phe Asp Gly Arg Ile Thr Ala Leu Asp Ser Lys Val Glu Asn Gly Met
595 600 605

Ala Ala Gln Ala Ala Leu Ser Gly Leu Phe Gln Pro Tyr Ser Val Gly
610 615 620

Lys Phe Asn Ala Thr Ala Ala Leu Gly Gly Tyr Gly Ser Lys Ser Ala
625 630 635 640

Val Ala Ile Gly Ala Gly Tyr Arg Val Asn Pro Asn Leu Ala Phe Lys
645 650 655

Ala Gly Ala Ala Ile Asn Thr Ser Gly Asn Lys Lys Gly Ser Tyr Asn
660 665 670

Ile Gly Val Asn Tyr Glu Phe
675

<210> 37
<211> 724
<212> PRT
<213> Moraxella catarrhalis

<400> 37

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

Leu Ile Val Gly Leu Gly Ala Ala Ser Thr Ala Asn Ala Gln Glu Thr
20 25 30

Leu Glu Glu Val Leu Glu Ser Ile Lys Gln Ile Asn Glu Gln Asp Leu
35 40 45

Gln Asp Asp Ile Gly Tyr Asn Ser Ala Leu Asp Arg Tyr Leu Val Leu
50 55 60

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

Glu Lys Asn Ser Asn Ser Ile Ala Lys Asn Ser Asn Ser Ile Ala Asp

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

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

Glu Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln
325 330 335

Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys
340 345 350

Ala Ser Ser Glu Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn
355 360 365

Glu Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala
370 375 380

Leu Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Glu Asp Leu Ala
385 390 395 400

Ala Tyr Asn Glu Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala
405 410 415

Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Glu
420 425 430

Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr Ala Lys Gln Gln
435 440 445

Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr Gln
450 455 460

Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr Ala
465 470 475 480

Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu
485 490 495

Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala Asp Ile Ala Asn Asn Ile
500 505 510

Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser Asp
515 520 525

Ile Lys Thr Leu Ala Lys Ala Ser Ala Ala Asn Thr Asp Arg Ile Ala
530 535 540

Lys Asn Lys Ala Asp Ala Asp Ala Ser Phe Glu Thr Leu Thr Lys Asn
545 550 555 560

Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu His Asp Lys Leu Ile Thr
565 570 575

Ala Asn Lys Thr Ala Ile Asp Ala Asn Lys Ala Ser Ala Asp Thr Lys
580 585 590

Phe Ala Ala Thr Ala Asp Ala Ile Thr Lys Asn Gly Asn Ala Ile Thr
595 600 605

Lys Asn Ala Lys Ser Ile Thr Asp Leu Gly Thr Lys Val Asp Gly Phe
610 615 620

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

Arg Ile Thr Ala Leu Asp Ser Lys Val Glu Asn Gly Met Ala Ala Gln
645 650 655

Ala Ala Leu Ser Gly Leu Phe Gln Pro Tyr Ser Val Gly Lys Phe Asn
660 665 670

Ala Thr Ala Ala Leu Gly Gly Tyr Gly Ser Lys Ser Ala Val Ala Ile
675 680 685

Gly Ala Gly Tyr Arg Val Asn Pro Asn Leu Ala Phe Lys Ala Gly Ala
690 695 700

Ala Ile Asn Thr Ser Gly Asn Lys Lys Gly Ser Tyr Asn Ile Gly Val
705 710 715 720

Asn Tyr Glu Phe

<210> 38
<211> 611
<212> PRT
<213> Moraxella catarrhalis

<400> 38

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

Leu Ile Val Gly Leu Gly Ala Ala Ser Thr Ala Asn Ala Gln Ala Gln
20 25 30

Ala Arg Asp Arg Ser Leu Glu Asp Ile Gln Ala Leu Ile Gly Asn Ile
35 40 45

Asp Val Asp Lys Ile Arg Ser Gln Lys Gln Lys Asn Pro Glu Ile Phe
50 55 60

Gln Tyr Leu Leu Leu Asn Gln Leu Ser Asn Thr Leu Ile Thr Asp Glu
65 70 75 80

Leu Asn Asn Asn Val Ile Lys Asn Thr Asn Ser Ile Glu Thr Leu Asp
85 90 95

Asn Asp Ile Ala Trp Leu Asn Asp Asp Leu Ile Asp Leu Asp Lys Glu
100 105 110

Val Gly Val Leu Ser Arg Asp Ile Gly Ser Leu His Asp Asp Val Ala
115 120 125

Gln Asn Gln Ala Asp Ile Lys Thr Leu Glu Asn Asn Val Val Glu Glu
130 135 140

Leu Phe Asn Leu Ser Asp Arg Leu Ile Asp Gln Glu Ala Glu Ile Ala
145 150 155 160

Gln Asn Asn Glu Ser Ile Glu Asp Leu Tyr Asp Phe Gly Arg Glu Val
165 170 175

Ala Glu Ser Ile Gly Glu Ile His Ala His Asn Glu Ala Gln Asn Glu
180 185 190

Thr Leu Lys Asp Leu Ile Thr Asn Ser Val Lys Asn Thr Asp Asn Ile
195 200 205

Asp Lys Asn Lys Ala Asp Ile Gln Ala Leu Glu Asn Asn Val Glu Glu
210 215 220

Gly Leu Leu Glu Leu Ser Gly His Leu Ile Asp Gln Lys Ala Asp Leu
225 230 235 240

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

Asp Leu Ser Gly Arg Leu Leu Asp Gln Lys Ala Asp Ile Ala Lys Asn
260 265 270

Gln Ala Asp Ile Ala Gln Asn Gln Thr Asp Ile Gln Asp Leu Ala Ala
275 280 285

Tyr Asn Glu Leu Gln Asp Gln Tyr Ala Gln Lys Gln Thr Glu Ala Ile
290 295 300

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

Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr
325 330 335

Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn
340 345 350

Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr Ala Lys
355 360 365

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

Thr Gln Asn Ile Ala Lys Asn Gln Ala Asp Ile Ala Asn Asn Ile Asn
385 390 395 400

Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser Asp Ile
405 410 415

Lys Thr Leu Ala Lys Val Ser Ala Ala Asn Thr Asp Arg Ile Ala Lys
420 425 430

Asn Lys Ala Asp Ala Asp Ala Ser Phe Glu Thr Leu Thr Lys Asn Gln
435 440 445

Asn Thr Leu Ile Glu Lys Asp Lys Glu His Asp Lys Leu Ile Thr Ala
450 455 460

Asn Lys Thr Ala Ile Asp Ala Asn Lys Ala Ser Ala Asp Thr Lys Phe
465 470 475 480

Ala Ala Thr Ala Asp Ala Ile Thr Lys Asn Gly Asn Ala Ile Thr Lys
485 490 495

Asn Ala Lys Ser Ile Thr Asp Leu Gly Thr Lys Val Asp Gly Phe Asp
500 505 510

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

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

Ala Leu Ser Gly Leu Phe Gln Pro Tyr Ser Val Gly Lys Phe Asn Ala
545 550 555 560

Thr Ala Ala Leu Gly Gly Tyr Gly Ser Lys Ser Ala Val Ala Ile Gly
565 570 575

Ala Gly Tyr Arg Val Asn Pro Asn Leu Ala Phe Lys Ala Gly Ala Ala
580 585 590

Ile Asn Thr Ser Gly Asn Lys Lys Gly Ser Tyr Asn Ile Gly Val Asn
595 600 605

Tyr Glu Phe
610

<210> 39
<211> 511
<212> PRT
<213> Moraxella catarrhalis

<400> 39

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

Lys Ile Asp Gln Asn Glu Leu Glu Ala Asp Ile Gly Asp Ile Thr Ala
20 25 30

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

Glu Glu Leu Asn Lys Ala Leu Glu Glu Leu Asp Glu Asp Val Gly Trp
50 55 60

Asn Gln Asn Asp Ile Ala Asn Leu Glu Asp Asp Val Glu Thr Leu Thr
65 70 75 80

Lys Asn Gln Asn Ala Leu Ala Glu Gln Gly Glu Ala Ile Lys Glu Asp
85 90 95

Leu Gln Gly Leu Ala Asp Phe Val Glu Gly Gln Glu Gly Lys Ile Leu
100 105 110

Gln Asn Glu Thr Ser Ile Lys Lys Asn Thr Gln Arg Asn Leu Val Asn
115 120 125

Gly Phe Glu Ile Glu Lys Asn Lys Asp Ala Ile Ala Lys Asn Asn Glu
130 135 140

Ser Ile Glu Asp Leu Tyr Asp Phe Gly His Glu Val Ala Glu Ser Ile
145 150 155 160

Gly Glu Ile His Ala His Asn Glu Ala Gln Asn Glu Thr Leu Lys Gly
165 170 175

Leu Ile Thr Asn Ser Ile Glu Asn Thr Asn Asn Ile Thr Lys Asn Lys
180 185 190

Ala Asp Ile Gln Ala Leu Glu Asn Asn Val Val Glu Glu Leu Phe Asn
195 200 205

Leu Ser Gly Arg Leu Ile Asp Gln Lys Ala Asp Ile Asp Asn Asn Ile
210 215 220

Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser Asp
225 230 235 240

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

Gly His Leu Ile Asp Gln Lys Thr Asp Ile Ala Gln Asn Gln Ala Asn
260 265 270

Ile Gln Asp Leu Ala Thr Tyr Asn Glu Leu Gln Asp Gln Tyr Ala Gln
275 280 285

Lys Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn
290 295 300

Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala
305 310 315 320

Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser
325 330 335

Ser Glu Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu
340 345 350

Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn
355 360 365

Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala Asp
370 375 380

Ile Ala Asn Asn Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp
385 390 395 400

Gln His Ser Ser Asp Ile Lys Thr Leu Ala Lys Ala Ser Ala Ala Asn
405 410 415

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

Thr Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu His
435 440 445

Asp Lys Leu Ile Thr Ala Asn Lys Thr Ala Ile Asp Ala Asn Lys Ala
450 455 460

Ser Ala Asp Thr Lys Phe Ala Ala Thr Ala Asp Ala Ile Thr Lys Asn
465 470 475 480

Gly Asn Ala Ile Thr Lys Asn Ala Lys Ser Ile Thr Asp Leu Gly Thr
485 490 495

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

<210> 40
<211> 510
<212> PRT
<213> Moraxella catarrhalis

<400> 40

Ala Lys Asn Asp Ile Thr Leu Glu Asp Leu Pro Tyr Leu Ile Lys Lys
1 5 10 15

Ile Asp Gln Asn Glu Leu Glu Ala Asp Ile Gly Asp Ile Thr Ala Leu
20 25 30

Glu Lys Tyr Leu Ala Leu Ser Gln Tyr Gly Asn Ile Leu Ala Leu Glu

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

His Leu Ile Asp Gln Lys Thr Asp Ile Ala Gln Asn Gln Ala Asn Ile
260 265 270

Gln Asp Leu Ala Thr Tyr Asn Glu Leu Gln Asp Gln Tyr Ala Gln Lys
275 280 285

Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr
290 295 300

Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr
305 310 315 320

Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser
325 330 335

Glu Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln
340 345 350

Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys
355 360 365

Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala Asp Ile
370 375 380

Ala Asn Asn Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln
385 390 395 400

His Ser Ser Asp Ile Lys Thr Leu Ala Lys Ala Ser Ala Ala Asn Thr
405 410 415

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

Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu His Asp
435 440 445

Lys Leu Ile Thr Ala Asn Lys Thr Ala Ile Asp Ala Asn Lys Ala Ser
450 455 460

Ala Asp Thr Lys Phe Ala Ala Thr Ala Asp Ala Ile Thr Lys Asn Gly
465 470 475 480

Asn Ala Ile Thr Lys Asn Ala Lys Ser Ile Thr Asp Leu Gly Thr Lys
485 490 495

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

<210> 41
<211> 490
<212> PRT
<213> Moraxella catarrhalis

<400> 41

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

Lys Ile Asp Gln Asn Glu Leu Glu Ala Asp Ile Gly Asp Ile Thr Ala
20 25 30

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

Glu Glu Leu Asn Lys Ala Leu Glu Glu Leu Asp Glu Asp Val Gly Trp
50 55 60

Asn Gln Asn Asp Ile Ala Asn Leu Glu Asp Asp Val Glu Thr Leu Thr
65 70 75 80

Lys Asn Gln Asn Ala Leu Ala Glu Gln Gly Glu Ala Ile Lys Glu Asp
85 90 95

Leu Gln Gly Leu Ala Asp Phe Val Glu Gly Gln Glu Gly Lys Ile Leu
100 105 110

Gln Asn Glu Thr Ser Ile Lys Lys Asn Thr Gln Arg Asn Leu Val Asn
115 120 125

Gly Phe Glu Ile Glu Lys Asn Lys Asp Ala Ile Ala Lys Asn Asn Glu

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

Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn
355 360 365

Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala Asp
370 375 380

Ile Ala Asn Asn Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp
385 390 395 400

Gln His Ser Ser Asp Ile Lys Thr Leu Ala Lys Ala Ser Ala Ala Asn
405 410 415

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

Thr Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu His
435 440 445

Asp Lys Leu Ile Thr Ala Asn Lys Thr Ala Ile Asp Ala Asn Lys Ala
450 455 460

Ser Ala Asp Thr Lys Phe Ala Ala Thr Ala Asp Ala Ile Thr Lys Asn
465 470 475 480

Gly Asn Ala Ile Thr Lys Asn Ala Lys Ser
485 490

<210> 42
<211> 535
<212> PRT
<213> Moraxella catarrhalis

<400> 42

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

Lys Ile Asp Gln Asn Glu Leu Glu Ala Asp Ile Gly Asp Ile Thr Ala
20 25 30

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

Glu Glu Leu Asn Lys Ala Leu Glu Glu Leu Asp Glu Asp Val Gly Trp
50 55 60

Asn Gln Asn Asp Ile Ala Asn Leu Glu Asp Asp Val Glu Thr Leu Thr
65 70 75 80

Lys Asn Gln Asn Ala Leu Ala Glu Gln Gly Glu Ala Ile Lys Glu Asp
85 90 95

Leu Gln Gly Leu Ala Asp Phe Val Glu Gly Gln Glu Gly Lys Ile Leu
100 105 110

Gln Asn Glu Thr Ser Ile Lys Lys Asn Thr Gln Arg Asn Leu Val Asn
115 120 125

Gly Phe Glu Ile Glu Lys Asn Lys Asp Ala Ile Ala Lys Asn Asn Glu
130 135 140

Ser Ile Glu Asp Leu Tyr Asp Phe Gly His Glu Val Ala Glu Ser Ile
145 150 155 160

Gly Glu Ile His Ala His Asn Glu Ala Gln Asn Glu Thr Leu Lys Gly
165 170 175

Leu Ile Thr Asn Ser Ile Glu Asn Thr Asn Asn Ile Thr Lys Asn Lys
180 185 190

Ala Asp Ile Gln Ala Leu Glu Asn Asn Val Val Glu Glu Leu Phe Asn
195 200 205

Leu Ser Gly Arg Leu Ile Asp Gln Lys Ala Asp Ile Asp Asn Asn Ile
210 215 220

Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser Asp
225 230 235 240

Ile Lys Thr Leu Lys Lys Asn Val Glu Glu Gly Leu Leu Glu Leu Ser

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

Ser Ala Asp Thr Lys Phe Ala Ala Thr Ala Asp Ala Ile Thr Lys Asn
 465 470 475 480

Gly Asn Ala Ile Thr Lys Asn Ala Lys Ser Ile Thr Asp Leu Gly Thr
 485 490 495

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

Asn Ala Phe Asp Gly Arg Ile Thr Ala Leu Asp Ser Lys Val Glu Asn
 515 520 525

Gly Met Ala Ala Gln Ala Ala
 530 535

<210> 43
 <211> 534
 <212> PRT
 <213> Moraxella catarrhalis

<400> 43

Ala Lys Asn Asp Ile Thr Leu Glu Asp Leu Pro Tyr Leu Ile Lys Lys
 1 5 10 15

Ile Asp Gln Asn Glu Leu Glu Ala Asp Ile Gly Asp Ile Thr Ala Leu
 20 25 30

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

Glu Leu Asn Lys Ala Leu Glu Glu Leu Asp Glu Asp Val Gly Trp Asn
 50 55 60

Gln Asn Asp Ile Ala Asn Leu Glu Asp Asp Val Glu Thr Leu Thr Lys
 65 70 75 80

Asn Gln Asn Ala Leu Ala Glu Gln Gly Glu Ala Ile Lys Glu Asp Leu
 85 90 95

Gln Gly Leu Ala Asp Phe Val Glu Gly Gln Glu Gly Lys Ile Leu Gln
100 105 110

Asn Glu Thr Ser Ile Lys Lys Asn Thr Gln Arg Asn Leu Val Asn Gly
115 120 125

Phe Glu Ile Glu Lys Asn Lys Asp Ala Ile Ala Lys Asn Asn Glu Ser
130 135 140

Ile Glu Asp Leu Tyr Asp Phe Gly His Glu Val Ala Glu Ser Ile Gly
145 150 155 160

Glu Ile His Ala His Asn Glu Ala Gln Asn Glu Thr Leu Lys Gly Leu
165 170 175

Ile Thr Asn Ser Ile Glu Asn Thr Asn Asn Ile Thr Lys Asn Lys Ala
180 185 190

Asp Ile Gln Ala Leu Glu Asn Asn Val Val Glu Glu Leu Phe Asn Leu
195 200 205

Ser Gly Arg Leu Ile Asp Gln Lys Ala Asp Ile Asp Asn Asn Ile Asn
210 215 220

Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser Asp Ile
225 230 235 240

Lys Thr Leu Lys Lys Asn Val Glu Glu Gly Leu Leu Glu Leu Ser Gly
245 250 255

His Leu Ile Asp Gln Lys Thr Asp Ile Ala Gln Asn Gln Ala Asn Ile
260 265 270

Gln Asp Leu Ala Thr Tyr Asn Glu Leu Gln Asp Gln Tyr Ala Gln Lys
275 280 285

Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr
290 295 300

Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr

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

Met Ala Ala Gln Ala Ala
530

<210> 44
<211> 148
<212> PRT
<213> Moraxella catarrhalis

<400> 44

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

Lys Ile Asp Gln Asn Glu Leu Glu Ala Asp Ile Gly Asp Ile Thr Ala
20 25 30

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

Glu Glu Leu Asn Lys Ala Leu Glu Glu Leu Asp Glu Asp Val Gly Trp
50 55 60

Asn Gln Asn Asp Ile Ala Asn Leu Glu Asp Asp Val Glu Thr Leu Thr
65 70 75 80

Lys Asn Gln Asn Ala Leu Ala Glu Gln Gly Glu Ala Ile Lys Glu Asp
85 90 95

Leu Gln Gly Leu Ala Asp Phe Val Glu Gly Gln Glu Gly Lys Ile Leu
100 105 110

Gln Asn Glu Thr Ser Ile Lys Lys Asn Thr Gln Arg Asn Leu Val Asn
115 120 125

Gly Phe Glu Ile Glu Lys Asn Lys Asp Ala Ile Ala Lys Asn Asn Glu
130 135 140

Ser Ile Glu Asp
145

<210> 45
 <211> 154
 <212> PRT
 <213> Moraxella catarrhalis

<400> 45

Lys Asp Ala Ile Ala Lys Asn Asn Glu Ser Ile Glu Asp Leu Tyr Asp
 1 5 10 15

Phe Gly His Glu Val Ala Glu Ser Ile Gly Glu Ile His Ala His Asn
 20 25 30

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

Asn Thr Asn Asn Ile Thr Lys Asn Lys Ala Asp Ile Gln Ala Leu Glu
 50 55 60

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

Gln Lys Ala Asp Ile Asp Asn Asn Ile Asn Asn Ile Tyr Glu Leu Ala
 85 90 95

Gln Gln Gln Asp Gln His Ser Ser Asp Ile Lys Thr Leu Lys Lys Asn
 100 105 110

Val Glu Glu Gly Leu Leu Glu Leu Ser Gly His Leu Ile Asp Gln Lys
 115 120 125

Thr Asp Ile Ala Gln Asn Gln Ala Asn Ile Gln Asp Leu Ala Thr Tyr
 130 135 140

Asn Glu Leu Gln Asp Gln Tyr Ala Gln Lys
 145 150

<210> 46
 <211> 510
 <212> PRT
 <213> Moraxella catarrhalis

<400> 46

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

Lys Ile Asp Gln Asn Glu Leu Glu Ala Asp Ile Gly Asp Ile Thr Ala
20 25 30

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

Glu Glu Leu Asn Lys Ala Leu Glu Glu Leu Asp Glu Asp Val Gly Trp
50 55 60

Asn Gln Asn Asp Ile Ala Asn Leu Glu Asp Asp Val Glu Thr Leu Thr
65 70 75 80

Lys Asn Gln Asn Ala Leu Ala Glu Gln Gly Glu Ala Ile Lys Glu Asp
85 90 95

Leu Gln Gly Leu Ala Asp Phe Val Glu Gly Gln Glu Gly Lys Ile Leu
100 105 110

Gln Asn Glu Thr Ser Ile Lys Lys Asn Thr Gln Arg Asn Leu Val Asn
115 120 125

Gly Phe Glu Ile Glu Lys Asn Lys Asp Ala Ile Ala Lys Asn Asn Glu
130 135 140

Ser Ile Glu Asp Leu Tyr Asp Phe Gly His Glu Val Ala Glu Ser Ile
145 150 155 160

Gly Glu Ile His Ala His Asn Glu Ala Gln Asn Glu Thr Leu Lys Gly
165 170 175

Leu Ile Thr Asn Ser Ile Glu Asn Thr Asn Asn Ile Thr Lys Asn Lys
180 185 190

Ala Asp Ile Gln Ala Leu Glu Asn Asn Val Val Glu Glu Leu Phe Asn
195 200 205

Leu Ser Gly Arg Leu Ile Asp Gln Lys Ala Asp Ile Asp Asn Asn Ile
210 215 220

Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser Asp
225 230 235 240

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

Gly His Leu Ile Asp Gln Lys Thr Asp Ile Ala Gln Asn Gln Ala Asn
260 265 270

Ile Gln Asp Leu Ala Thr Tyr Asn Glu Leu Gln Asp Gln Tyr Ala Gln
275 280 285

Lys Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn
290 295 300

Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala
305 310 315 320

Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser
325 330 335

Ser Glu Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu
340 345 350

Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn
355 360 365

Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala Asp
370 375 380

Ile Ala Asn Asn Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp
385 390 395 400

Gln His Ser Ser Asp Ile Lys Thr Leu Ala Lys Ala Ser Ala Ala Asn
405 410 415

Thr Asp Arg Ile Ala Lys Asn Lys Ala Asp Ala Asp Ala Ser Phe Glu

420 425 430
 Thr Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu His
 435 440 445
 Asp Lys Leu Ile Thr Ala Asn Lys Thr Ala Ile Asp Ala Asn Lys Ala
 450 455 460
 Ser Ala Asp Thr Lys Phe Ala Ala Thr Ala Asp Ala Ile Thr Lys Asn
 465 470 475 480
 Gly Asn Ala Ile Thr Lys Asn Ala Lys Ser Ile Thr Asp Leu Gly Thr
 485 490 495
 Lys Val Asp Gly Phe Asp Ser Arg Val Thr Ala Leu Asp Thr
 500 505 510

 <210> 47
 <211> 511
 <212> PRT
 <213> Moraxella catarrhalis

 <400> 47
 Gln Ala Lys Asn Asp Ile Thr Leu Glu Asp Leu Pro Tyr Leu Ile Lys
 1 5 10 15
 Lys Ile Asp Gln Asn Glu Leu Glu Ala Asp Ile Gly Asp Ile Thr Ala
 20 25 30
 Leu Glu Lys Tyr Leu Ala Leu Ser Gln Tyr Gly Asn Ile Leu Ala Leu
 35 40 45
 Glu Glu Leu Asn Lys Ala Leu Glu Glu Leu Asp Glu Asp Val Gly Trp
 50 55 60
 Asn Gln Asn Asp Ile Ala Asn Leu Glu Asp Asp Val Glu Thr Leu Thr
 65 70 75 80
 Lys Asn Gln Asn Ala Leu Ala Glu Gln Gly Glu Ala Ile Lys Glu Asp
 85 90 95

Leu Gln Gly Leu Ala Asp Phe Val Glu Gly Gln Glu Gly Lys Ile Leu
100 105 110

Gln Asn Glu Thr Ser Ile Lys Lys Asn Thr Gln Arg Asn Leu Val Asn
115 120 125

Gly Phe Glu Ile Glu Lys Asn Lys Asp Ala Ile Ala Lys Asn Asn Glu
130 135 140

Ser Ile Glu Asp Leu Tyr Asp Phe Gly His Glu Val Ala Glu Ser Ile
145 150 155 160

Gly Glu Ile His Ala His Asn Glu Ala Gln Asn Glu Thr Leu Lys Gly
165 170 175

Leu Ile Thr Asn Ser Ile Glu Asn Thr Asn Asn Ile Thr Lys Asn Lys
180 185 190

Ala Asp Ile Gln Ala Leu Glu Asn Asn Val Val Glu Glu Leu Phe Asn
195 200 205

Leu Ser Gly Arg Leu Ile Asp Gln Lys Ala Asp Ile Asp Asn Asn Ile
210 215 220

Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser Asp
225 230 235 240

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

Gly His Leu Ile Asp Gln Lys Thr Asp Ile Ala Gln Asn Gln Ala Asn
260 265 270

Ile Gln Asp Leu Ala Thr Tyr Asn Glu Leu Gln Asp Gln Tyr Ala Gln
275 280 285

Lys Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn
290 295 300

Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala
305 310 315 320

Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser
325 330 335

Ser Glu Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu
340 345 350

Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn
355 360 365

Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala Asp
370 375 380

Ile Ala Asn Asn Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp
385 390 395 400

Gln His Ser Ser Asp Ile Lys Thr Leu Ala Lys Ala Ser Ala Ala Asn
405 410 415

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

Thr Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu His
435 440 445

Asp Lys Leu Ile Thr Ala Asn Lys Thr Ala Ile Asp Ala Asn Lys Ala
450 455 460

Ser Ala Asp Thr Lys Phe Ala Ala Thr Ala Asp Ala Ile Thr Lys Asn
465 470 475 480

Gly Asn Ala Ile Thr Lys Asn Ala Lys Ser Ile Thr Asp Leu Gly Thr
485 490 495

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

<210> 48

<211> 490
 <212> PRT
 <213> Moraxella catarrhalis

<400> 48

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

Lys Ile Asp Gln Asn Glu Leu Glu Ala Asp Ile Gly Asp Ile Thr Ala
 20 25 30

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

Glu Glu Leu Asn Lys Ala Leu Glu Glu Leu Asp Glu Asp Val Gly Trp
 50 55 60

Asn Gln Asn Asp Ile Ala Asn Leu Glu Asp Asp Val Glu Thr Leu Thr
 65 70 75 80

Lys Asn Gln Asn Ala Leu Ala Glu Gln Gly Glu Ala Ile Lys Glu Asp
 85 90 95

Leu Gln Gly Leu Ala Asp Phe Val Glu Gly Gln Glu Gly Lys Ile Leu
 100 105 110

Gln Asn Glu Thr Ser Ile Lys Lys Asn Thr Gln Arg Asn Leu Val Asn
 115 120 125

Gly Phe Glu Ile Glu Lys Asn Lys Asp Ala Ile Ala Lys Asn Asn Glu
 130 135 140

Ser Ile Glu Asp Leu Tyr Asp Phe Gly His Glu Val Ala Glu Ser Ile
 145 150 155 160

Gly Glu Ile His Ala His Asn Glu Ala Gln Asn Glu Thr Leu Lys Gly
 165 170 175

Leu Ile Thr Asn Ser Ile Glu Asn Thr Asn Asn Ile Thr Lys Asn Lys
 180 185 190

Ala Asp Ile Gln Ala Leu Glu Asn Asn Val Val Glu Glu Leu Phe Asn
195 200 205

Leu Ser Gly Arg Leu Ile Asp Gln Lys Ala Asp Ile Asp Asn Asn Ile
210 215 220

Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser Asp
225 230 235 240

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

Gly His Leu Ile Asp Gln Lys Thr Asp Ile Ala Gln Asn Gln Ala Asn
260 265 270

Ile Gln Asp Leu Ala Thr Tyr Asn Glu Leu Gln Asp Gln Tyr Ala Gln
275 280 285

Lys Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn
290 295 300

Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala
305 310 315 320

Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser
325 330 335

Ser Glu Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu
340 345 350

Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn
355 360 365

Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala Asp
370 375 380

Ile Ala Asn Asn Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp
385 390 395 400

Gln His Ser Ser Asp Ile Lys Thr Leu Ala Lys Ala Ser Ala Ala Asn
405 410 415

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

Thr Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu His
435 440 445

Asp Lys Leu Ile Thr Ala Asn Lys Thr Ala Ile Asp Ala Asn Lys Ala
450 455 460

Ser Ala Asp Thr Lys Phe Ala Ala Thr Ala Asp Ala Ile Thr Lys Asn
465 470 475 480

Gly Asn Ala Ile Thr Lys Asn Ala Lys Ser
485 490

<210> 49
<211> 535
<212> PRT
<213> Moraxella catarrhalis

<400> 49

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

Lys Ile Asp Gln Asn Glu Leu Glu Ala Asp Ile Gly Asp Ile Thr Ala
20 25 30

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

Glu Glu Leu Asn Lys Ala Leu Glu Glu Leu Asp Glu Asp Val Gly Trp
50 55 60

Asn Gln Asn Asp Ile Ala Asn Leu Glu Asp Asp Val Glu Thr Leu Thr
65 70 75 80

Lys Asn Gln Asn Ala Leu Ala Glu Gln Gly Glu Ala Ile Lys Glu Asp
85 90 95

Leu Gln Gly Leu Ala Asp Phe Val Glu Gly Gln Glu Gly Lys Ile Leu
100 105 110

Gln Asn Glu Thr Ser Ile Lys Lys Asn Thr Gln Arg Asn Leu Val Asn
115 120 125

Gly Phe Glu Ile Glu Lys Asn Lys Asp Ala Ile Ala Lys Asn Asn Glu
130 135 140

Ser Ile Glu Asp Leu Tyr Asp Phe Gly His Glu Val Ala Glu Ser Ile
145 150 155 160

Gly Glu Ile His Ala His Asn Glu Ala Gln Asn Glu Thr Leu Lys Gly
165 170 175

Leu Ile Thr Asn Ser Ile Glu Asn Thr Asn Asn Ile Thr Lys Asn Lys
180 185 190

Ala Asp Ile Gln Ala Leu Glu Asn Asn Val Val Glu Glu Leu Phe Asn
195 200 205

Leu Ser Gly Arg Leu Ile Asp Gln Lys Ala Asp Ile Asp Asn Asn Ile
210 215 220

Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser Asp
225 230 235 240

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

Gly His Leu Ile Asp Gln Lys Thr Asp Ile Ala Gln Asn Gln Ala Asn
260 265 270

Ile Gln Asp Leu Ala Thr Tyr Asn Glu Leu Gln Asp Gln Tyr Ala Gln
275 280 285

Lys Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn
290 295 300

Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala
305 310 315 320

Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser
325 330 335

Ser Glu Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu
340 345 350

Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn
355 360 365

Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala Asp
370 375 380

Ile Ala Asn Asn Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp
385 390 395 400

Gln His Ser Ser Asp Ile Lys Thr Leu Ala Lys Ala Ser Ala Ala Asn
405 410 415

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

Thr Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu His
435 440 445

Asp Lys Leu Ile Thr Ala Asn Lys Thr Ala Ile Asp Ala Asn Lys Ala
450 455 460

Ser Ala Asp Thr Lys Phe Ala Ala Thr Ala Asp Ala Ile Thr Lys Asn
465 470 475 480

Gly Asn Ala Ile Thr Lys Asn Ala Lys Ser Ile Thr Asp Leu Gly Thr
485 490 495

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

Asn Ala Phe Asp Gly Arg Ile Thr Ala Leu Asp Ser Lys Val Glu Asn
515 520 525

Gly Met Ala Ala Gln Ala Ala
530 535

<210> 50
<211> 534
<212> PRT
<213> Moraxella catarrhalis

<400> 50

Ala Lys Asn Asp Ile Thr Leu Glu Asp Leu Pro Tyr Leu Ile Lys Lys
1 5 10 15

Ile Asp Gln Asn Glu Leu Glu Ala Asp Ile Gly Asp Ile Thr Ala Leu
20 25 30

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

Glu Leu Asn Lys Ala Leu Glu Glu Leu Asp Glu Asp Val Gly Trp Asn
50 55 60

Gln Asn Asp Ile Ala Asn Leu Glu Asp Asp Val Glu Thr Leu Thr Lys
65 70 75 80

Asn Gln Asn Ala Leu Ala Glu Gln Gly Glu Ala Ile Lys Glu Asp Leu
85 90 95

Gln Gly Leu Ala Asp Phe Val Glu Gly Gln Glu Gly Lys Ile Leu Gln
100 105 110

Asn Glu Thr Ser Ile Lys Lys Asn Thr Gln Arg Asn Leu Val Asn Gly
115 120 125

Phe Glu Ile Glu Lys Asn Lys Asp Ala Ile Ala Lys Asn Asn Glu Ser
130 135 140

Ile Glu Asp Leu Tyr Asp Phe Gly His Glu Val Ala Glu Ser Ile Gly
145 150 155 160

Glu Ile His Ala His Asn Glu Ala Gln Asn Glu Thr Leu Lys Gly Leu
165 170 175

Ile Thr Asn Ser Ile Glu Asn Thr Asn Asn Ile Thr Lys Asn Lys Ala
180 185 190

Asp Ile Gln Ala Leu Glu Asn Asn Val Val Glu Glu Leu Phe Asn Leu
195 200 205

Ser Gly Arg Leu Ile Asp Gln Lys Ala Asp Ile Asp Asn Asn Ile Asn
210 215 220

Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser Asp Ile
225 230 235 240

Lys Thr Leu Lys Lys Asn Val Glu Glu Gly Leu Leu Glu Leu Ser Gly
245 250 255

His Leu Ile Asp Gln Lys Thr Asp Ile Ala Gln Asn Gln Ala Asn Ile
260 265 270

Gln Asp Leu Ala Thr Tyr Asn Glu Leu Gln Asp Gln Tyr Ala Gln Lys
275 280 285

Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr
290 295 300

Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr
305 310 315 320

Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser
325 330 335

Glu Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln
340 345 350

Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys
355 360 365

Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala Asp Ile
370 375 380

Ala Asn Asn Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln
385 390 395 400

His Ser Ser Asp Ile Lys Thr Leu Ala Lys Ala Ser Ala Ala Asn Thr
405 410 415

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

Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu His Asp
435 440 445

Lys Leu Ile Thr Ala Asn Lys Thr Ala Ile Asp Ala Asn Lys Ala Ser
450 455 460

Ala Asp Thr Lys Phe Ala Ala Thr Ala Asp Ala Ile Thr Lys Asn Gly
465 470 475 480

Asn Ala Ile Thr Lys Asn Ala Lys Ser Ile Thr Asp Leu Gly Thr Lys
485 490 495

Val Asp Gly Phe Asp Ser Arg Val Thr Ala Leu Asp Thr Lys Val Asn
500 505 510

Ala Phe Asp Gly Arg Ile Thr Ala Leu Asp Ser Lys Val Glu Asn Gly
515 520 525

Met Ala Ala Gln Ala Ala
530

<210> 51
<211> 510
<212> PRT
<213> Moraxella catarrhalis

<400> 51

Ala Lys Asn Asp Ile Thr Leu Glu Asp Leu Pro Tyr Leu Ile Lys Lys

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

Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser Asp Ile
225 230 235 240

Lys Thr Leu Lys Lys Asn Val Glu Glu Gly Leu Leu Glu Leu Ser Gly
245 250 255

His Leu Ile Asp Gln Lys Thr Asp Ile Ala Gln Asn Gln Ala Asn Ile
260 265 270

Gln Asp Leu Ala Thr Tyr Asn Glu Leu Gln Asp Gln Tyr Ala Gln Lys
275 280 285

Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr
290 295 300

Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr
305 310 315 320

Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser
325 330 335

Glu Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln
340 345 350

Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys
355 360 365

Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala Asp Ile
370 375 380

Ala Asn Asn Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln
385 390 395 400

His Ser Ser Asp Ile Lys Thr Leu Ala Lys Ala Ser Ala Ala Asn Thr
405 410 415

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

Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu His Asp
435 440 445

Lys Leu Ile Thr Ala Asn Lys Thr Ala Ile Asp Ala Asn Lys Ala Ser
450 455 460

Ala Asp Thr Lys Phe Ala Ala Thr Ala Asp Ala Ile Thr Lys Asn Gly
465 470 475 480

Asn Ala Ile Thr Lys Asn Ala Lys Ser Ile Thr Asp Leu Gly Thr Lys
485 490 495

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

<210> 52
<211> 1563
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA sequence for MC-001 construct

<400> 52
atgcaggcca aaaatgatat taccctggaa gatctgccgt atctgatcaa aaaaatcgat 60
cagaacgaac tggaagccga tattggtgat attaccgcac tggaaaaata tctggcactg 120
agccagtatg gaaatattct ggccctggaa gaactgaata aagctctgga agagctggat 180
gaagatgtgg gttggaatca gaatgatatc gccaatctgg aagatgatgt tgaaaccctg 240
acaaaaatc agaatgcact ggacgaacag ggtgaagcaa ttaaagaaga tctgcagggt 300
ctggcagatt ttgttgaagg tcaggaaggc aaaattctgc agaacgaaac cagcatcaaa 360
aaaaacaccc agcgtaattct ggtgaatggc tttgaaattg aaaaaaaca agatgccatt 420
gccaaaaaca acgaaagcat tgaagatctg tatgattttg gtcatagaagt tgccgaaagc 480
attggtgaaa ttcatagcaca taacgaagca cagaatgaaa ccctgaaagg tctgattacc 540
aacagcatcg aaaataccaa taacattacc aaaaacaaag cagatattca ggcgctggaa 600
aataatgttg tggaagaact gtttaattctg agcggctcgtc tgattgatca gaaagccgat 660
atcgataata acattaacaa catttatgaa ctggcacagc agcaggatca gcatagcagc 720

gatatacaaaa ccctgaaaaa aaacgttgaa gaaggtctgc tggaactgtc tggtcacctg	780
atcgatcaga aaactgatat tgcccagaat caggcaaata ttcaggatct ggccacctat	840
aatgaactgc aggatcagta tgcacagaaa cagaccgaag caattgatgc cctgaataaa	900
gcgagcagcg aaaacaccca gaatatcgaa gatctggcag catacaacga actgcaggat	960
gcctatgcaa aacagcagac tgaagccatc gacgcactga acaaggcaag ctctgaaaac	1020
acgcagaaca ttgaagatct ggctgcctat aatgaattac aggatgcgta tgccaaacag	1080
cagaccgaag cgattgatgc gctgaacaaa gcctcttctg aaaatacaca gaatatcgcc	1140
aaaaatcagg ccgatattgc caacaatatc aataatatct atgaactggc ccagcagcag	1200
gatcagcact cttctgatat caaaacactg gcaaaagcaa gcgcagcaaa taccgatcgt	1260
attgcgaaaa acaaagccga tgcagatgca agctttgaaa cactgacgaa aaaccagaac	1320
accctgattg aaaaagataa agaacatgat aaactgatca ccgccaataa aaccgcaatt	1380
gatgcaaata aagccagcgc agatacaaaa ttgacgcaa ccgcagatgc aattacaaaa	1440
aatggcaatg ccatcaccaa aaatgcaaaa agcattaccg atctgggcac caaagttgat	1500
ggttttgata gccgtgtgac cgactggat accaaagcaa gccatcatca tcaccaccac	1560
taa	1563

<210> 53
 <211> 520
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Protein sequence for MC-001 construct

<400> 53

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

Lys	Lys	Ile	Asp	Gln	Asn	Glu	Leu	Glu	Ala	Asp	Ile	Gly	Asp	Ile	Thr
			20					25					30		

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

Leu Glu Glu Leu Asn Lys Ala Leu Glu Glu Leu Asp Glu Asp Val Gly
50 55 60

Trp Asn Gln Asn Asp Ile Ala Asn Leu Glu Asp Asp Val Glu Thr Leu
65 70 75 80

Thr Lys Asn Gln Asn Ala Leu Ala Glu Gln Gly Glu Ala Ile Lys Glu
85 90 95

Asp Leu Gln Gly Leu Ala Asp Phe Val Glu Gly Gln Glu Gly Lys Ile
100 105 110

Leu Gln Asn Glu Thr Ser Ile Lys Lys Asn Thr Gln Arg Asn Leu Val
115 120 125

Asn Gly Phe Glu Ile Glu Lys Asn Lys Asp Ala Ile Ala Lys Asn Asn
130 135 140

Glu Ser Ile Glu Asp Leu Tyr Asp Phe Gly His Glu Val Ala Glu Ser
145 150 155 160

Ile Gly Glu Ile His Ala His Asn Glu Ala Gln Asn Glu Thr Leu Lys
165 170 175

Gly Leu Ile Thr Asn Ser Ile Glu Asn Thr Asn Asn Ile Thr Lys Asn
180 185 190

Lys Ala Asp Ile Gln Ala Leu Glu Asn Asn Val Val Glu Glu Leu Phe
195 200 205

Asn Leu Ser Gly Arg Leu Ile Asp Gln Lys Ala Asp Ile Asp Asn Asn
210 215 220

Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser
225 230 235 240

Asp Ile Lys Thr Leu Lys Lys Asn Val Glu Glu Gly Leu Leu Glu Leu
245 250 255

Ser Gly His Leu Ile Asp Gln Lys Thr Asp Ile Ala Gln Asn Gln Ala
260 265 270

Asn Ile Gln Asp Leu Ala Thr Tyr Asn Glu Leu Gln Asp Gln Tyr Ala
275 280 285

Gln Lys Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu
290 295 300

Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp
305 310 315 320

Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala
325 330 335

Ser Ser Glu Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu
340 345 350

Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu
355 360 365

Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala
370 375 380

Asp Ile Ala Asn Asn Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln
385 390 395 400

Asp Gln His Ser Ser Asp Ile Lys Thr Leu Ala Lys Ala Ser Ala Ala
405 410 415

Asn Thr Asp Arg Ile Ala Lys Asn Lys Ala Asp Ala Asp Ala Ser Phe
420 425 430

Glu Thr Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu
435 440 445

His Asp Lys Leu Ile Thr Ala Asn Lys Thr Ala Ile Asp Ala Asn Lys
450 455 460

Ala Ser Ala Asp Thr Lys Phe Ala Ala Thr Ala Asp Ala Ile Thr Lys

465		470		475		480
Asn Gly Asn Ala Ile Thr Lys Asn Ala Lys Ser Ile Thr Asp Leu Gly						
	485		490		495	
Thr Lys Val Asp Gly Phe Asp Ser Arg Val Thr Ala Leu Asp Thr Lys						
	500		505		510	
Ala Ser His His His His His						
	515		520			

<210> 54
 <211> 1539
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA sequence for MC-002 construct

<400> 54

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agccagtatg gaaatattct ggccctggaa gaactgaata aagctctgga agagctggat	180
gaagatgtgg gttggaatca gaatgatatc gccaatctgg aagatgatgt tgaaaccctg	240
acaaaaaatc agaatgcact ggcagaacag ggtgaagcaa ttaaagaaga tctgcagggt	300
ctggcagatt ttgttgaagg tcaggaaggc aaaattctgc agaacgaaac cagcatcaaa	360
aaaaacaccc agcgtaatct ggtgaatggc tttgaaattg aaaaaaaca agatgccatt	420
gccaaaaaca acgaaagcat tgaagatctg tatgattttg gtcatagaagt tgccgaaagc	480
attggtgaaa ttcatgcaca taacgaagca cagaatgaaa ccctgaaagg tctgattacc	540
aacagcatcg aaaataccaa taacattacc aaaaacaaag cagatattca ggcgctggaa	600
aataatgttg tggaagaact gtttaatctg agcggctcgtc tgattgatca gaaagccgat	660
atcgataata acattaacaa catttatgaa ctggcacagc agcaggatca gcatagcagc	720
gatatcaaaa ccctgaaaaa aaacgttgaa gaaggtctgc tggaactgtc tggtcacctg	780
atcgatcaga aaactgatat tgcccagaat caggcaaata ttcaggatct ggccacctat	840

aatgaactgc aggatcagta tgcacagaaa cagaccgaag caattgatgc cctgaataaa	900
gcgagcagcg aaaacaccca gaatatcgaa gatctggcag catacaacga actgcaggat	960
gcctatgcaa aacagcagac tgaagccatc gacgcactga acaaggcaag ctctgaaaac	1020
acgcagaaca ttgaagatct ggctgcctat aatgaattac aggatgcgta tgccaaacag	1080
cagaccgaag cgattgatgc gctgaacaaa gcctcttctg aaaatacaca gaatatcgcc	1140
aaaaatcagg ccgatattgc caacaatatc aataatatct atgaactggc ccagcagcag	1200
gatcagcact cttctgatat caaaacactg gcaaaagcaa gcgcagcaaa taccgatcgt	1260
attgcgaaaa acaaagccga tgcagatgca agctttgaaa cactgacgaa aaaccagaac	1320
accctgattg aaaaagataa agaacatgat aaactgatca ccgccaataa aaccgcaatt	1380
gatgcaaata aagccagcgc agataccaaa tttgcagcaa ccgcagatgc aattacaaaa	1440
aatggcaatg ccatcaccaa aaatgcaaaa agcattaccg atctgggcac caaagttgat	1500
ggttttgata gccgtgtgac cgactggat accaaataa	1539

<210> 55
 <211> 512
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Protein sequence for MC-002 construct

<400> 55

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

Lys	Lys	Ile	Asp	Gln	Asn	Glu	Leu	Glu	Ala	Asp	Ile	Gly	Asp	Ile	Thr
			20					25					30		

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

Leu	Glu	Glu	Leu	Asn	Lys	Ala	Leu	Glu	Glu	Leu	Asp	Glu	Asp	Val	Gly
	50					55					60				

Trp	Asn	Gln	Asn	Asp	Ile	Ala	Asn	Leu	Glu	Asp	Asp	Val	Glu	Thr	Leu
65					70					75				80	

Thr Lys Asn Gln Asn Ala Leu Ala Glu Gln Gly Glu Ala Ile Lys Glu
85 90 95

Asp Leu Gln Gly Leu Ala Asp Phe Val Glu Gly Gln Glu Gly Lys Ile
100 105 110

Leu Gln Asn Glu Thr Ser Ile Lys Lys Asn Thr Gln Arg Asn Leu Val
115 120 125

Asn Gly Phe Glu Ile Glu Lys Asn Lys Asp Ala Ile Ala Lys Asn Asn
130 135 140

Glu Ser Ile Glu Asp Leu Tyr Asp Phe Gly His Glu Val Ala Glu Ser
145 150 155 160

Ile Gly Glu Ile His Ala His Asn Glu Ala Gln Asn Glu Thr Leu Lys
165 170 175

Gly Leu Ile Thr Asn Ser Ile Glu Asn Thr Asn Asn Ile Thr Lys Asn
180 185 190

Lys Ala Asp Ile Gln Ala Leu Glu Asn Asn Val Val Glu Glu Leu Phe
195 200 205

Asn Leu Ser Gly Arg Leu Ile Asp Gln Lys Ala Asp Ile Asp Asn Asn
210 215 220

Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser
225 230 235 240

Asp Ile Lys Thr Leu Lys Lys Asn Val Glu Glu Gly Leu Leu Glu Leu
245 250 255

Ser Gly His Leu Ile Asp Gln Lys Thr Asp Ile Ala Gln Asn Gln Ala
260 265 270

Asn Ile Gln Asp Leu Ala Thr Tyr Asn Glu Leu Gln Asp Gln Tyr Ala
275 280 285

Gln Lys Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu
290 295 300

Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp
305 310 315 320

Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala
325 330 335

Ser Ser Glu Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu
340 345 350

Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu
355 360 365

Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala
370 375 380

Asp Ile Ala Asn Asn Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln
385 390 395 400

Asp Gln His Ser Ser Asp Ile Lys Thr Leu Ala Lys Ala Ser Ala Ala
405 410 415

Asn Thr Asp Arg Ile Ala Lys Asn Lys Ala Asp Ala Asp Ala Ser Phe
420 425 430

Glu Thr Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu
435 440 445

His Asp Lys Leu Ile Thr Ala Asn Lys Thr Ala Ile Asp Ala Asn Lys
450 455 460

Ala Ser Ala Asp Thr Lys Phe Ala Ala Thr Ala Asp Ala Ile Thr Lys
465 470 475 480

Asn Gly Asn Ala Ile Thr Lys Asn Ala Lys Ser Ile Thr Asp Leu Gly
485 490 495

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

<210> 56
<211> 1614
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA sequence for construct

<400> 56
atgcaggcca aaaatgatat taccctggaa gatctgccgt atctgatcaa aaaatcgat 60
cagaacgaac tggaagccga tattggtgat attaccgcac tggaataata tctggcactg 120
agccagtatg gaaatattct ggccctggaa gaactgaata aagctctgga agagctggat 180
gaagatgtgg gttggaatca gaatgatatc gccaatctgg aagatgatgt tgaaaccctg 240
acaaaaatc agaatgcact ggacgaacag ggtgaagcaa ttaaagaaga tctgcagggt 300
ctggcagatt ttgttgaagg tcaggaaggc aaaattctgc agaacgaaac cagcatcaaa 360
aaaaacaccc agcgtaattct ggtgaatggc ttgaaattg aaaaaaaca agatgccatt 420
gccaaaaaca acgaaagcat tgaagatctg tatgattttg gtcatagaagt tgccgaaagc 480
attggtgaaa ttcatagcaca taacgaagca cagaatgaaa ccctgaaagg tctgattacc 540
aacagcatcg aaaataccaa taacattacc aaaaacaaag cagatattca ggcgctggaa 600
aataatgttg tggaagaact gtttaattctg agcggctctg tgattgatca gaaagccgat 660
atcgataata acattaacaa catttatgaa ctggcacagc agcaggatca gcatagcagc 720
gatataaaaa ccctgaaaaa aaacgttgaa gaaggtctgc tggaactgtc tggtcacctg 780
atcgatcaga aaactgatat tgcccagaat caggcaaata ttcaggatct ggccacctat 840
aatgaactgc aggatcagta tgcacagaaa cagaccgaag caattgatgc cctgaataaa 900
gcgagcagcg aaaacaccca gaatatcgaa gatctggcag catacaacga actgcaggat 960
gcctatgcaa aacagcagac tgaagccatc gacgcactga acaaggcaag ctctgaaaac 1020
acgcagaaca ttgaagatct ggctgcctat aatgaattac aggatgcgta tgccaaacag 1080
cagaccgaag cgattgatgc gctgaacaaa gcctcttctg aaaatacaca gaatatcgcc 1140
aaaaatcagg ccgatattgc caacaatatc aataatatct atgaactggc ccagcagcag 1200

gatcagcact cttctgatat caaaacactg gcaaaagcaa gcgcagcaaa taccgatcgt	1260
attgcgaaaa acaaagccga tgcagatgca agctttgaaa cactgacgaa aaaccagaac	1320
accctgattg aaaaagataa agaacatgat aaactgatca ccgccaataa aaccgcaatt	1380
gatgcaaata aagccagcgc agatacaaaa ttgacagcaa ccgcagatgc aattacaaaa	1440
aatggcaatg ccatcaccaa aaatgccaaa agcattaccg atctgggcac caaagttgat	1500
ggttttgata gccgtgtgac cgactggat accaaagtta atgcatttga tggtcgtatt	1560
accgctctgg atagtaaagt tgaaaatgga atggcagcac aagcagcaca ctaa	1614

<210> 57
 <211> 537
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Protein sequence for construct

<400> 57

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

Lys	Lys	Ile	Asp	Gln	Asn	Glu	Leu	Glu	Ala	Asp	Ile	Gly	Asp	Ile	Thr
			20					25					30		

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

Leu	Glu	Glu	Leu	Asn	Lys	Ala	Leu	Glu	Glu	Leu	Asp	Glu	Asp	Val	Gly
	50					55					60				

Trp	Asn	Gln	Asn	Asp	Ile	Ala	Asn	Leu	Glu	Asp	Asp	Val	Glu	Thr	Leu
65					70					75					80

Thr	Lys	Asn	Gln	Asn	Ala	Leu	Ala	Glu	Gln	Gly	Glu	Ala	Ile	Lys	Glu
				85					90					95	

Asp	Leu	Gln	Gly	Leu	Ala	Asp	Phe	Val	Glu	Gly	Gln	Glu	Gly	Lys	Ile
			100					105					110		

Leu Gln Asn Glu Thr Ser Ile Lys Lys Asn Thr Gln Arg Asn Leu Val
115 120 125

Asn Gly Phe Glu Ile Glu Lys Asn Lys Asp Ala Ile Ala Lys Asn Asn
130 135 140

Glu Ser Ile Glu Asp Leu Tyr Asp Phe Gly His Glu Val Ala Glu Ser
145 150 155 160

Ile Gly Glu Ile His Ala His Asn Glu Ala Gln Asn Glu Thr Leu Lys
165 170 175

Gly Leu Ile Thr Asn Ser Ile Glu Asn Thr Asn Asn Ile Thr Lys Asn
180 185 190

Lys Ala Asp Ile Gln Ala Leu Glu Asn Asn Val Val Glu Glu Leu Phe
195 200 205

Asn Leu Ser Gly Arg Leu Ile Asp Gln Lys Ala Asp Ile Asp Asn Asn
210 215 220

Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser
225 230 235 240

Asp Ile Lys Thr Leu Lys Lys Asn Val Glu Glu Gly Leu Leu Glu Leu
245 250 255

Ser Gly His Leu Ile Asp Gln Lys Thr Asp Ile Ala Gln Asn Gln Ala
260 265 270

Asn Ile Gln Asp Leu Ala Thr Tyr Asn Glu Leu Gln Asp Gln Tyr Ala
275 280 285

Gln Lys Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu
290 295 300

Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp
305 310 315 320

Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala

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<210> 58
 <211> 1545
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA sequence for MC-004 construct

<400> 58
 atgcaggcca aaaatgatat taccctggaa gatctgccgt atctgatcaa aaaaatcgat 60
 cagaacgaac tggaagccga tattggtgat attaccgcac tggaaaaata tctggcactg 120
 agccagtatg gaaatattct ggccctggaa gaactgaata aagctctgga agagctggat 180
 gaagatgtgg gttggaatca gaatgatatc gccaatctgg aagatgatgt tgaaaccctg 240
 accaaaaatc agaatgcact ggacgaacag ggtgaagcaa ttaaagaaga tctgcagggt 300
 ctggcagatt ttgttgaagg tcaggaaggc aaaattctgc agaacgaaac cagcatcaaa 360
 aaaaacaccc agcgtaattct ggtgaatggc ttgaaattg aaaaaaaca agatgccatt 420
 gccaaaaaca acgaaagcat tgaagatctg tatgatattt gtcatgaagt tgccgaaagc 480
 attggtgaaa ttcatgcaca taacgaagca cagaatgaaa ccctgaaagg tctgattacc 540
 aacagcatcg aaaataccaa taacattacc aaaaacaaag cagatattca ggcgctggaa 600
 aataatgttg tggaagaact gtttaattctg agcggctctc tgattgatca gaaagccgat 660
 atcgataata acattaacaa catttatgaa ctggcacagc agcaggatca gcatagcagc 720
 gatatcaaaa ccctgaaaaa aaacgttgaa gaaggtctgc tggaactgtc tggtcacctg 780
 atcgatcaga aaactgatat tgcccagaat caggcaaata ttcaggatct ggccacctat 840
 aatgaactgc aggatcagta tgcacagaaa cagaccgaag caattgatgc cctgaataaa 900
 gcgagcagcg aaaacaccca gaatatcgaa gatctggcag catacaacga actgcaggat 960
 gcctatgcaa aacagcagac tgaagccatc gacgcactga acaaggcaag ctctgaaaac 1020
 acgcagaaca ttgaagatct ggctgcctat aatgaattac aggatgcgta tgccaaacag 1080
 cagaccgaag cgattgatgc gctgaacaaa gcctcttctg aaaatacaca gaatatcgcc 1140
 aaaaatcagg ccgatattgc caacaatatc aataatatct atgaactggc ccagcagcag 1200
 gatcagcact cttctgatat caaaacactg gcaaaagcaa ggcagcaaaa taccgatcgt 1260

attgcgaaaa acaaagccga tgcagatgca agctttgaaa cactgacgaa aaaccagaac 1320
accctgattg aaaaagataa agaacatgat aaactgatca ccgccaataa aaccgcaatt 1380
gatgcaaata aagccagcgc agataccaaa tttgcagcaa ccgcagatgc aattacaaaa 1440
aatggcaatg ccatcaccaa aaatgccaaa agcattaccg atctgggcac caaagttgat 1500
ggttttgata gccgtgtgac cgactggat accaaacatc attaa 1545

<210> 59
<211> 514
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein sequence for MC-004 construct

<400> 59

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

Lys Lys Ile Asp Gln Asn Glu Leu Glu Ala Asp Ile Gly Asp Ile Thr
20 25 30

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

Leu Glu Glu Leu Asn Lys Ala Leu Glu Glu Leu Asp Glu Asp Val Gly
50 55 60

Trp Asn Gln Asn Asp Ile Ala Asn Leu Glu Asp Asp Val Glu Thr Leu
65 70 75 80

Thr Lys Asn Gln Asn Ala Leu Ala Glu Gln Gly Glu Ala Ile Lys Glu
85 90 95

Asp Leu Gln Gly Leu Ala Asp Phe Val Glu Gly Gln Glu Gly Lys Ile
100 105 110

Leu Gln Asn Glu Thr Ser Ile Lys Lys Asn Thr Gln Arg Asn Leu Val
115 120 125

Asn Gly Phe Glu Ile Glu Lys Asn Lys Asp Ala Ile Ala Lys Asn Asn
130 135 140

Glu Ser Ile Glu Asp Leu Tyr Asp Phe Gly His Glu Val Ala Glu Ser
145 150 155 160

Ile Gly Glu Ile His Ala His Asn Glu Ala Gln Asn Glu Thr Leu Lys
165 170 175

Gly Leu Ile Thr Asn Ser Ile Glu Asn Thr Asn Asn Ile Thr Lys Asn
180 185 190

Lys Ala Asp Ile Gln Ala Leu Glu Asn Asn Val Val Glu Glu Leu Phe
195 200 205

Asn Leu Ser Gly Arg Leu Ile Asp Gln Lys Ala Asp Ile Asp Asn Asn
210 215 220

Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser
225 230 235 240

Asp Ile Lys Thr Leu Lys Lys Asn Val Glu Glu Gly Leu Leu Glu Leu
245 250 255

Ser Gly His Leu Ile Asp Gln Lys Thr Asp Ile Ala Gln Asn Gln Ala
260 265 270

Asn Ile Gln Asp Leu Ala Thr Tyr Asn Glu Leu Gln Asp Gln Tyr Ala
275 280 285

Gln Lys Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu
290 295 300

Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp
305 310 315 320

Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala
325 330 335

Ser Ser Glu Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu

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

His His

<210> 60
 <211> 1500
 <212> DNA
 <213> Artificial Sequence

<220>

<223> DNA sequence for MC-005 construct

<400> 60

atgcaggcca	aaaatgatat	taccctggaa	gatctgccgt	atctgatcaa	aaaaatcgat	60
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agccagtatg	gaaatattct	ggccctggaa	gaactgaata	aagctctgga	agagctggat	180
gaagatgtgg	gttggaatca	gaatgatatc	gccaatctgg	aagatgatgt	tgaaaccctg	240
acaaaaaatc	agaatgcact	ggcagaacag	ggtgaagcaa	ttaaagaaga	tctgcagggt	300
ctggcagatt	ttgttgaagg	tcaggaaggc	aaaattctgc	agaacgaaac	cagcatcaaa	360
aaaaacaccc	agcgtaatct	ggtgaatggc	tttgaaattg	aaaaaaacaa	agatgccatt	420
gccaaaaaca	acgaaagcat	tgaagatctg	tatgattttg	gtcatgaagt	tgccgaaagc	480
attggtgaaa	ttcatgcaca	taacgaagca	cagaatgaaa	ccctgaaagg	tctgattacc	540
aacagcatcg	aaaataccaa	taacattacc	aaaaacaaag	cagatattca	ggcgctggaa	600
aataatgttg	tggaagaact	gtttaatctg	agcggctcgtc	tgattgatca	gaaagccgat	660
atcgataata	acattaacaa	catttatgaa	ctggcacagc	agcaggatca	gcatagcagc	720
gatatcaaaa	ccctgaaaaa	aaacgttgaa	gaaggtctgc	tggaactgtc	tggtcacctg	780
atcgatcaga	aaactgatat	tgcccagaat	caggcaaata	ttcaggatct	ggccacctat	840
aatgaactgc	aggatcagta	tgcacagaaa	cagaccgaag	caattgatgc	cctgaataaa	900
gcgagcagcg	aaaacaccca	gaatatcgaa	gatctggcag	catacaacga	actgcaggat	960
gcctatgcaa	aacagcagac	tgaagccatc	gacgcactga	acaaggcaag	ctctgaaaac	1020
acgcagaaca	ttgaagatct	ggctgcctat	aatgaattac	aggatgcgta	tgccaaacag	1080
cagaccgaag	cgattgatgc	gctgaacaaa	gcctcttctg	aaaatacaca	gaatatcgcc	1140
aaaaatcagg	ccgatattgc	caacaatatc	aataatatct	atgaactggc	ccagcagcag	1200
gatcagcact	cttctgatat	caaaacactg	gcaaaagcaa	gcgagcaaaa	taccgatcgt	1260
attgcgaaaa	acaaagccga	tgcatgatgca	agctttgaaa	cactgacgaa	aaaccagaac	1320
accctgattg	aaaaagataa	agaacatgat	aaactgatca	ccgccaataa	aaccgcaatt	1380
gatgcaaata	aagccagcgc	agataccaaa	tttgagcaaa	ccgcagatgc	aattaccaaa	1440
aatggcaatg	ccatcaccaa	aaatgccaaa	agcgcaagcc	atcatcatca	ccaccactaa	1500

<210> 61
<211> 499
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein sequence for MC-005 construct

<400> 61

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

Lys Lys Ile Asp Gln Asn Glu Leu Glu Ala Asp Ile Gly Asp Ile Thr
20 25 30

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

Leu Glu Glu Leu Asn Lys Ala Leu Glu Glu Leu Asp Glu Asp Val Gly
50 55 60

Trp Asn Gln Asn Asp Ile Ala Asn Leu Glu Asp Asp Val Glu Thr Leu
65 70 75 80

Thr Lys Asn Gln Asn Ala Leu Ala Glu Gln Gly Glu Ala Ile Lys Glu
85 90 95

Asp Leu Gln Gly Leu Ala Asp Phe Val Glu Gly Gln Glu Gly Lys Ile
100 105 110

Leu Gln Asn Glu Thr Ser Ile Lys Lys Asn Thr Gln Arg Asn Leu Val
115 120 125

Asn Gly Phe Glu Ile Glu Lys Asn Lys Asp Ala Ile Ala Lys Asn Asn
130 135 140

Glu Ser Ile Glu Asp Leu Tyr Asp Phe Gly His Glu Val Ala Glu Ser
145 150 155 160

Ile Gly Glu Ile His Ala His Asn Glu Ala Gln Asn Glu Thr Leu Lys
165 170 175

Gly Leu Ile Thr Asn Ser Ile Glu Asn Thr Asn Asn Ile Thr Lys Asn
180 185 190

Lys Ala Asp Ile Gln Ala Leu Glu Asn Asn Val Val Glu Glu Leu Phe
195 200 205

Asn Leu Ser Gly Arg Leu Ile Asp Gln Lys Ala Asp Ile Asp Asn Asn
210 215 220

Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser
225 230 235 240

Asp Ile Lys Thr Leu Lys Lys Asn Val Glu Glu Gly Leu Leu Glu Leu
245 250 255

Ser Gly His Leu Ile Asp Gln Lys Thr Asp Ile Ala Gln Asn Gln Ala
260 265 270

Asn Ile Gln Asp Leu Ala Thr Tyr Asn Glu Leu Gln Asp Gln Tyr Ala
275 280 285

Gln Lys Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu
290 295 300

Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp
305 310 315 320

Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala
325 330 335

Ser Ser Glu Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu
340 345 350

Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu
355 360 365

Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala
370 375 380

Asp Ile Ala Asn Asn Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln
 385 390 395 400

Asp Gln His Ser Ser Asp Ile Lys Thr Leu Ala Lys Ala Ser Ala Ala
 405 410 415

Asn Thr Asp Arg Ile Ala Lys Asn Lys Ala Asp Ala Asp Ala Ser Phe
 420 425 430

Glu Thr Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu
 435 440 445

His Asp Lys Leu Ile Thr Ala Asn Lys Thr Ala Ile Asp Ala Asn Lys
 450 455 460

Ala Ser Ala Asp Thr Lys Phe Ala Ala Thr Ala Asp Ala Ile Thr Lys
 465 470 475 480

Asn Gly Asn Ala Ile Thr Lys Asn Ala Lys Ser Ala Ser His His His
 485 490 495

His His His

<210> 62
 <211> 1476
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA sequence for MC-006 construct

<400> 62
 atgcaggcca aaaatgatat taccctggaa gatctgccgt atctgatcaa aaaaatcgat 60
 cagaacgaac tggaagccga tattggtgat attaccgcac tggaaaaata tctggcactg 120
 agccagtatg gaaatattct ggccctggaa gaactgaata aagctctgga agagctggat 180
 gaagatgtgg gttggaatca gaatgatatc gccaatctgg aagatgatgt tgaaaccctg 240
 accaaaaatc agaatgcact ggcagaacag ggtgaagcaa ttaaagaaga tctgcagggt 300
 ctggcagatt ttgttgaagg tcaggaaggc aaaattctgc agaacgaaac cagcatcaaa 360

aaaaacaccc agcgtaatct ggtgaatggc tttgaaattg aaaaaaaca agatgccatt	420
gccccaaaaca acgaaagcat tgaagatctg tatgatcttg gtcataagtg tgccgaaagc	480
attggtgaaa ttcatgcaca taacgaagca cagaatgaaa ccctgaaagg tctgattacc	540
aacagcatcg aaaataccaa taacattacc aaaaacaaag cagatattca ggcgctggaa	600
aataatgttg tggaagaact gtttaatctg agcggctgctc tgattgatca gaaagccgat	660
atcgataata acattaacaa ctttatgaa ctggcacagc agcaggatca gcatagcagc	720
gatatcaaaa ccctgaaaaa aaacgttgaa gaaggtctgc tggaactgtc tggtcacctg	780
atcgatcaga aaactgatat tgcccagaat caggcaaata ttcaggatct ggccacctat	840
aatgaactgc aggatcagta tgcacagaaa cagaccgaag caattgatgc cctgaataaa	900
gcgagcagcg aaaacaccca gaatatcgaa gatctggcag catacaacga actgcaggat	960
gcctatgcaa aacagcagac tgaagccatc gacgcactga acaaggcaag ctctgaaaac	1020
acgcagaaca ttgaagatct ggctgcctat aatgaattac aggatgcgta tgccaaacag	1080
cagaccgaag cgattgatgc gctgaacaaa gcctcttctg aaaatacaca gaatatcgcc	1140
aaaaatcagg ccgatattgc caacaatatc aataatatct atgaactggc ccagcagcag	1200
gatcagcact cttctgatat caaaacactg gcaaaagcaa gcgcagcaaa taccgatcgt	1260
attgcgaaaa acaaagccga tgcagatgca agctttgaaa cactgacgaa aaaccagaac	1320
accctgattg aaaaagataa agaacatgat aaactgatca ccgccaataa aaccgcaatt	1380
gatgcaaata aagccagcgc agataccaaa tttgcagcaa ccgcagatgc aattacaaa	1440
aatggcaatg ccatcaccaa aaatgccaaa agctaa	1476

<210> 63

<211> 491

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein sequence for MC-006 construct

<400> 63

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

Lys Lys Ile Asp Gln Asn Glu Leu Glu Ala Asp Ile Gly Asp Ile Thr
20 25 30

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

Leu Glu Glu Leu Asn Lys Ala Leu Glu Glu Leu Asp Glu Asp Val Gly
50 55 60

Trp Asn Gln Asn Asp Ile Ala Asn Leu Glu Asp Asp Val Glu Thr Leu
65 70 75 80

Thr Lys Asn Gln Asn Ala Leu Ala Glu Gln Gly Glu Ala Ile Lys Glu
85 90 95

Asp Leu Gln Gly Leu Ala Asp Phe Val Glu Gly Gln Glu Gly Lys Ile
100 105 110

Leu Gln Asn Glu Thr Ser Ile Lys Lys Asn Thr Gln Arg Asn Leu Val
115 120 125

Asn Gly Phe Glu Ile Glu Lys Asn Lys Asp Ala Ile Ala Lys Asn Asn
130 135 140

Glu Ser Ile Glu Asp Leu Tyr Asp Phe Gly His Glu Val Ala Glu Ser
145 150 155 160

Ile Gly Glu Ile His Ala His Asn Glu Ala Gln Asn Glu Thr Leu Lys
165 170 175

Gly Leu Ile Thr Asn Ser Ile Glu Asn Thr Asn Asn Ile Thr Lys Asn
180 185 190

Lys Ala Asp Ile Gln Ala Leu Glu Asn Asn Val Val Glu Glu Leu Phe
195 200 205

Asn Leu Ser Gly Arg Leu Ile Asp Gln Lys Ala Asp Ile Asp Asn Asn
210 215 220

Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser
 225 230 235 240

Asp Ile Lys Thr Leu Lys Lys Asn Val Glu Glu Gly Leu Leu Glu Leu
 245 250 255

Ser Gly His Leu Ile Asp Gln Lys Thr Asp Ile Ala Gln Asn Gln Ala
 260 265 270

Asn Ile Gln Asp Leu Ala Thr Tyr Asn Glu Leu Gln Asp Gln Tyr Ala
 275 280 285

Gln Lys Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu
 290 295 300

Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp
 305 310 315 320

Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala
 325 330 335

Ser Ser Glu Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu
 340 345 350

Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu
 355 360 365

Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala
 370 375 380

Asp Ile Ala Asn Asn Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln
 385 390 395 400

Asp Gln His Ser Ser Asp Ile Lys Thr Leu Ala Lys Ala Ser Ala Ala
 405 410 415

Asn Thr Asp Arg Ile Ala Lys Asn Lys Ala Asp Ala Asp Ala Ser Phe
 420 425 430

Glu Thr Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu

435	440	445
His Asp Lys Leu Ile Thr Ala Asn Lys Thr Ala Ile Asp Ala Asn Lys		
450	455	460
Ala Ser Ala Asp Thr Lys Phe Ala Ala Thr Ala Asp Ala Ile Thr Lys		
465	470	475
		480
Asn Gly Asn Ala Ile Thr Lys Asn Ala Lys Ser		
485	490	

<210> 64
 <211> 1635
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA sequence for MC-007 construct

<400> 64	
atgcaggcca aaaatgatat taccctggaa gatctgccgt atctgatcaa aaaaatcgat	60
cagaacgaac tggaagccga tattggtgat attaccgcac tggaaaaata tctggcactg	120
agccagtatg gaaatattct ggccctggaa gaactgaata aagctctgga agagctggat	180
gaagatgtgg gttggaatca gaatgatatc gccaatctgg aagatgatgt tgaaaccctg	240
acaaaaatc agaatgcact ggcagaacag ggtgaagcaa ttaaagaaga tctgcagggt	300
ctggcagatt ttgttgaagg tcaggaaggc aaaattctgc agaacgaaac cagcatcaaa	360
aaaaacaccc agcgtaatct ggtgaatggc tttgaaattg aaaaaaaca agatgccatt	420
gccaaaaaca acgaaagcat tgaagatctg tatgatcttg gtcatagaagt tgccgaaagc	480
attggtgaaa ttcatgcaca taacgaagca cagaatgaaa ccctgaaagg tctgattacc	540
aacagcatcg aaaataccaa taacattacc aaaaacaaag cagatattca ggcgctggaa	600
aataatgttg tggaagaact gtttaatctg agcggctcgtc tgattgatca gaaagccgat	660
atcgataata acattaacaa catttatgaa ctggcacagc agcaggatca gcatagcagc	720
gatatcaaaa ccctgaaaaa aaacgttgaa gaaggtctgc tggaactgtc tggtcacctg	780
atcgatcaga aaactgatat tgcccagaat caggcaaata ttcaggatct ggccacctat	840
aatgaactgc aggatcagta tgcacagaaa cagaccgaag caattgatgc cctgaataaa	900

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gcgagcagcg aaaacaccca gaatatcgaa gatctggcag catacaacga actgcaggat      960
gcctatgcaa aacagcagac tgaagccatc gacgcactga acaaggcaag ctctgaaaac      1020
acgcagaaca ttgaagatct ggctgcctat aatgaattac aggatgcgta tgccaaacag      1080
cagaccgaag cgattgatgc gctgaacaaa gcctcttctg aaaatacaca gaatatcgcc      1140
aaaaatcagg ccgatattgc caacaatatc aataatatct atgaactggc ccagcagcag      1200
gatcagcact cttctgatat caaaacactg gcaaaagcaa gcgcagcaaa taccgatcgt      1260
attgcgaaaa acaaagccga tgcagatgca agctttgaaa cactgacgaa aaaccagaac      1320
accctgattg aaaaagataa agaacatgat aaactgatca ccgccaataa aaccgcaatt      1380
gatgcaaata aagccagcgc agataccaaa ttgacgcaa ccgcagatgc aattacaaaa      1440
aatggcaatg ccatcaccaa aaatgccaaa agcattaccg atctgggcac caaagttgat      1500
ggttttgata gccgtgtgac cgactggat accaaagtta atgcatttga tggtcgtatt      1560
accgctctgg atagtaaagt tgaaaatggg atggcagcac aggcagcagc aagccatcat      1620
catcaccacc actaa                                          1635

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<210> 65
<211> 544
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein sequence for MC-007 construct

<400> 65

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

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Lys Lys Ile Asp Gln Asn Glu Leu Glu Ala Asp Ile Gly Asp Ile Thr
20          25          30

```

```

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

```

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Leu Glu Glu Leu Asn Lys Ala Leu Glu Glu Leu Asp Glu Asp Val Gly
50          55          60

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Trp Asn Gln Asn Asp Ile Ala Asn Leu Glu Asp Asp Val Glu Thr Leu
65 70 75 80

Thr Lys Asn Gln Asn Ala Leu Ala Glu Gln Gly Glu Ala Ile Lys Glu
85 90 95

Asp Leu Gln Gly Leu Ala Asp Phe Val Glu Gly Gln Glu Gly Lys Ile
100 105 110

Leu Gln Asn Glu Thr Ser Ile Lys Lys Asn Thr Gln Arg Asn Leu Val
115 120 125

Asn Gly Phe Glu Ile Glu Lys Asn Lys Asp Ala Ile Ala Lys Asn Asn
130 135 140

Glu Ser Ile Glu Asp Leu Tyr Asp Phe Gly His Glu Val Ala Glu Ser
145 150 155 160

Ile Gly Glu Ile His Ala His Asn Glu Ala Gln Asn Glu Thr Leu Lys
165 170 175

Gly Leu Ile Thr Asn Ser Ile Glu Asn Thr Asn Asn Ile Thr Lys Asn
180 185 190

Lys Ala Asp Ile Gln Ala Leu Glu Asn Asn Val Val Glu Glu Leu Phe
195 200 205

Asn Leu Ser Gly Arg Leu Ile Asp Gln Lys Ala Asp Ile Asp Asn Asn
210 215 220

Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser
225 230 235 240

Asp Ile Lys Thr Leu Lys Lys Asn Val Glu Glu Gly Leu Leu Glu Leu
245 250 255

Ser Gly His Leu Ile Asp Gln Lys Thr Asp Ile Ala Gln Asn Gln Ala
260 265 270

Asn Ile Gln Asp Leu Ala Thr Tyr Asn Glu Leu Gln Asp Gln Tyr Ala
275 280 285

Gln Lys Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu
290 295 300

Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp
305 310 315 320

Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala
325 330 335

Ser Ser Glu Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu
340 345 350

Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu
355 360 365

Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala
370 375 380

Asp Ile Ala Asn Asn Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln
385 390 395 400

Asp Gln His Ser Ser Asp Ile Lys Thr Leu Ala Lys Ala Ser Ala Ala
405 410 415

Asn Thr Asp Arg Ile Ala Lys Asn Lys Ala Asp Ala Asp Ala Ser Phe
420 425 430

Glu Thr Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu
435 440 445

His Asp Lys Leu Ile Thr Ala Asn Lys Thr Ala Ile Asp Ala Asn Lys
450 455 460

Ala Ser Ala Asp Thr Lys Phe Ala Ala Thr Ala Asp Ala Ile Thr Lys
465 470 475 480

Asn Gly Asn Ala Ile Thr Lys Asn Ala Lys Ser Ile Thr Asp Leu Gly

	485		490		495
Thr Lys Val Asp Gly Phe Asp Ser Arg Val Thr Ala Leu Asp Thr Lys					
	500		505		510
Val Asn Ala Phe Asp Gly Arg Ile Thr Ala Leu Asp Ser Lys Val Glu					
	515		520		525
Asn Gly Met Ala Ala Gln Ala Ala Ala Ser His His His His His His					
	530		535		540

<210> 66
 <211> 1617
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA sequence for MC-008 construct

<400> 66	
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agccagtatg gaaatattct ggccctggaa gaactgaata aagctctgga agagctggat	180
gaagatgtgg gttggaatca gaatgatatc gccaatctgg aagatgatgt tgaaaccctg	240
acaaaaaatc agaatgcact ggacgaacag ggtgaagcaa tttaaagaaga tctgcagggt	300
ctggcagatt ttgttgaagg tcaggaaggc aaaattctgc agaacgaaac cagcatcaaa	360
aaaaacaccc agcgtaatct ggtgaatggc tttgaaattg aaaaaaaca agatgccatt	420
gccaaaaaca acgaaagcat tgaagatctg tatgattttg gtcatagaagt tgccgaaagc	480
attggtgaaa ttcatagcaca taacgaagca cagaatgaaa ccctgaaagg tctgattacc	540
aacagcatcg aaaataccaa taacattacc aaaaacaaag cagatattca ggcgctggaa	600
aataatgttg tggaagaact gtttaatctg agcggctcgtc tgattgatca gaaagccgat	660
atcgataata acattaacaa catttatgaa ctggcacagc agcaggatca gcatagcagc	720
gatatcaaaa ccctgaaaaa aaacgttgaa gaaggtctgc tggaactgtc tggtcacctg	780
atcgatcaga aaactgatat tgcccagaat caggcaaata ttcaggatct ggccacctat	840
aatgaactgc aggatcagta tgcacagaaa cagaccgaag caattgatgc cctgaataaa	900

gcgagcagcg aaaacaccca gaatatcgaa gatctggcag catacaacga actgcaggat 960
 gcctatgcaa aacagcagac tgaagccatc gacgcactga acaaggcaag ctctgaaaac 1020
 acgcagaaca ttgaagatct ggctgcctat aatgaattac aggatgcgta tgccaaacag 1080
 cagaccgaag cgattgatgc gctgaacaaa gcctcttctg aaaatacaca gaatatcgcc 1140
 aaaaatcagg ccgatattgc caacaatatc aataatatct atgaactggc ccagcagcag 1200
 gatcagcact cttctgatat caaaacactg gcaaaagcaa gcgcagcaaa taccgatcgt 1260
 attgcgaaaa acaaagccga tgcagatgca agctttgaaa cactgacgaa aaaccagaac 1320
 accctgattg aaaaagataa agaacatgat aaactgatca ccgccaataa aaccgcaatt 1380
 gatgcaaata aagccagcgc agataccaaa tttgcagcaa ccgcagatgc aattaccaaa 1440
 aatggcaatg ccatcaccaa aaatgccaaa agcattaccg atctgggcac caaagttgat 1500
 ggttttgata gccgtgtgac cgactggat accaaagtta atgcatttga tggtcgtatt 1560
 accgctctgg atagtaaagt tgaaaatggg atggcagcac aggcagcaca ccactaa 1617

<210> 67
 <211> 538
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Protein sequence for MC-008 construct

<400> 67

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

Lys Lys Ile Asp Gln Asn Glu Leu Glu Ala Asp Ile Gly Asp Ile Thr
 20 25 30

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

Leu Glu Glu Leu Asn Lys Ala Leu Glu Glu Leu Asp Glu Asp Val Gly
 50 55 60

Trp Asn Gln Asn Asp Ile Ala Asn Leu Glu Asp Asp Val Glu Thr Leu

65		70		75		80									
Thr	Lys	Asn	Gln	Asn	Ala	Leu	Ala	Glu	Gln	Gly	Glu	Ala	Ile	Lys	Glu
				85					90					95	
Asp	Leu	Gln	Gly	Leu	Ala	Asp	Phe	Val	Glu	Gly	Gln	Glu	Gly	Lys	Ile
			100					105					110		
Leu	Gln	Asn	Glu	Thr	Ser	Ile	Lys	Lys	Asn	Thr	Gln	Arg	Asn	Leu	Val
		115					120					125			
Asn	Gly	Phe	Glu	Ile	Glu	Lys	Asn	Lys	Asp	Ala	Ile	Ala	Lys	Asn	Asn
	130						135				140				
Glu	Ser	Ile	Glu	Asp	Leu	Tyr	Asp	Phe	Gly	His	Glu	Val	Ala	Glu	Ser
145					150					155					160
Ile	Gly	Glu	Ile	His	Ala	His	Asn	Glu	Ala	Gln	Asn	Glu	Thr	Leu	Lys
				165					170					175	
Gly	Leu	Ile	Thr	Asn	Ser	Ile	Glu	Asn	Thr	Asn	Asn	Ile	Thr	Lys	Asn
			180					185					190		
Lys	Ala	Asp	Ile	Gln	Ala	Leu	Glu	Asn	Asn	Val	Val	Glu	Glu	Leu	Phe
		195					200					205			
Asn	Leu	Ser	Gly	Arg	Leu	Ile	Asp	Gln	Lys	Ala	Asp	Ile	Asp	Asn	Asn
	210					215					220				
Ile	Asn	Asn	Ile	Tyr	Glu	Leu	Ala	Gln	Gln	Gln	Asp	Gln	His	Ser	Ser
225					230				235						240
Asp	Ile	Lys	Thr	Leu	Lys	Lys	Asn	Val	Glu	Glu	Gly	Leu	Leu	Glu	Leu
				245					250					255	
Ser	Gly	His	Leu	Ile	Asp	Gln	Lys	Thr	Asp	Ile	Ala	Gln	Asn	Gln	Ala
			260					265					270		
Asn	Ile	Gln	Asp	Leu	Ala	Thr	Tyr	Asn	Glu	Leu	Gln	Asp	Gln	Tyr	Ala
		275					280					285			

Gln Lys Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu
290 295 300

Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp
305 310 315 320

Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala
325 330 335

Ser Ser Glu Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu
340 345 350

Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu
355 360 365

Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala
370 375 380

Asp Ile Ala Asn Asn Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln
385 390 395 400

Asp Gln His Ser Ser Asp Ile Lys Thr Leu Ala Lys Ala Ser Ala Ala
405 410 415

Asn Thr Asp Arg Ile Ala Lys Asn Lys Ala Asp Ala Asp Ala Ser Phe
420 425 430

Glu Thr Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu
435 440 445

His Asp Lys Leu Ile Thr Ala Asn Lys Thr Ala Ile Asp Ala Asn Lys
450 455 460

Ala Ser Ala Asp Thr Lys Phe Ala Ala Thr Ala Asp Ala Ile Thr Lys
465 470 475 480

Asn Gly Asn Ala Ile Thr Lys Asn Ala Lys Ser Ile Thr Asp Leu Gly
485 490 495

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

Val Asn Ala Phe Asp Gly Arg Ile Thr Ala Leu Asp Ser Lys Val Glu
515 520 525

Asn Gly Met Ala Ala Gln Ala Ala His His
530 535

<210> 68
<211> 1614
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA sequence for MC-009 construct

<400> 68
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cagtatggaa atattctggc cctggaagaa ctgaataaag ctctggaaga gctggatgaa 180
gatgtgggtt ggaatcagaa tgatatcgcc aatctggaag atgatgttga aaccctgacc 240
aaaaatcaga atgcactggc agaacagggt gaagcaatta aagaagatct gcagggtctg 300
gcagattttg ttgaagggtca ggaaggcaaa attctgcaga acgaaaccag catcaaaaaa 360
aacacccagc gtaatctggt gaatggcttt gaaattgaaa aaaacaaaga tgccattgcc 420
aaaaacaacg aaagcattga agatctgtat gatcttgggtc atgaagttgc cgaaagcatt 480
ggtgaaattc atgcacataa cgaagcacag aatgaaaccc tgaaaggtct gattaccaac 540
agcatcgaaa ataccaataa cattacaaa aacaaagcag atattcaggc gctggaaaat 600
aatgttgtgg aagaactggt taatctgagc ggtcgtctga ttgatcagaa agccgatatc 660
gataataaca ttaacaacat ttatgaactg gcacagcagc aggatcagca tagcagcgat 720
atcaaaaccc tgaaaaaaaaa cggtgaagaa ggtctgctgg aactgtctgg tcacctgatc 780
gatcagaaaa ctgatattgc ccagaatcag gcaaattatc aggatctggc cacctataat 840
gaactgcagg atcagtatgc acagaaacag accgaagcaa ttgatgccct gaataaagcg 900
agcagcgaaa acacccagaa tatcgaagat ctggcagcat acaacgaact gcaggatgcc 960

tatgcaaac agcagactga agccatcgac gcactgaaca aggcaagctc tgaaaacacg	1020
cagaacattg aagatctggc tgcctataat gaattacagg atgcgtatgc caaacagcag	1080
accgaagcga ttgatgcgct gaacaaagcc tcttctgaaa atacacagaa tatcgccaaa	1140
aatcaggccg atattgccaa caatatcaat aatatctatg aactggccca gcagcaggat	1200
cagcactctt ctgatatcaa aacactggca aaagcaagcg cagcaaatac cgatcgtatt	1260
gcgaaaaaca aagccgatgc agatgcaagc tttgaaacac tgacgaaaaa ccagaacacc	1320
ctgattgaaa aagataaaga acatgataaa ctgatcaccg ccaataaaac cgcaattgat	1380
gcaaataaag ccagcgcaga taccaaattt gcagcaaccg cagatgcaat taccaaaaat	1440
ggcaatgcc a tcacaaaaa tgccaaaagc attaccgatc tgggcaccaa agttgatggt	1500
tttgatagcc gtgtgaccgc actggatacc aaagttaatg catttgatgg tcgtattacc	1560
gctctggata gtaaagttga aaatggtatg gcagcacagg cagcacacca ctaa	1614

<210> 69
 <211> 537
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Protein sequence for MC-009 construct

<400> 69

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

Lys	Ile	Asp	Gln	Asn	Glu	Leu	Glu	Ala	Asp	Ile	Gly	Asp	Ile	Thr	Ala
		20						25					30		

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

Glu	Glu	Leu	Asn	Lys	Ala	Leu	Glu	Glu	Leu	Asp	Glu	Asp	Val	Gly	Trp
	50					55					60				

Asn	Gln	Asn	Asp	Ile	Ala	Asn	Leu	Glu	Asp	Asp	Val	Glu	Thr	Leu	Thr
65					70				75					80	

Lys Asn Gln Asn Ala Leu Ala Glu Gln Gly Glu Ala Ile Lys Glu Asp
85 90 95

Leu Gln Gly Leu Ala Asp Phe Val Glu Gly Gln Glu Gly Lys Ile Leu
100 105 110

Gln Asn Glu Thr Ser Ile Lys Lys Asn Thr Gln Arg Asn Leu Val Asn
115 120 125

Gly Phe Glu Ile Glu Lys Asn Lys Asp Ala Ile Ala Lys Asn Asn Glu
130 135 140

Ser Ile Glu Asp Leu Tyr Asp Phe Gly His Glu Val Ala Glu Ser Ile
145 150 155 160

Gly Glu Ile His Ala His Asn Glu Ala Gln Asn Glu Thr Leu Lys Gly
165 170 175

Leu Ile Thr Asn Ser Ile Glu Asn Thr Asn Asn Ile Thr Lys Asn Lys
180 185 190

Ala Asp Ile Gln Ala Leu Glu Asn Asn Val Val Glu Glu Leu Phe Asn
195 200 205

Leu Ser Gly Arg Leu Ile Asp Gln Lys Ala Asp Ile Asp Asn Asn Ile
210 215 220

Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser Asp
225 230 235 240

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

Gly His Leu Ile Asp Gln Lys Thr Asp Ile Ala Gln Asn Gln Ala Asn
260 265 270

Ile Gln Asp Leu Ala Thr Tyr Asn Glu Leu Gln Asp Gln Tyr Ala Gln
275 280 285

Lys Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn
290 295 300

Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala
305 310 315 320

Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser
325 330 335

Ser Glu Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu
340 345 350

Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn
355 360 365

Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala Asp
370 375 380

Ile Ala Asn Asn Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp
385 390 395 400

Gln His Ser Ser Asp Ile Lys Thr Leu Ala Lys Ala Ser Ala Ala Asn
405 410 415

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

Thr Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu His
435 440 445

Asp Lys Leu Ile Thr Ala Asn Lys Thr Ala Ile Asp Ala Asn Lys Ala
450 455 460

Ser Ala Asp Thr Lys Phe Ala Ala Thr Ala Asp Ala Ile Thr Lys Asn
465 470 475 480

Gly Asn Ala Ile Thr Lys Asn Ala Lys Ser Ile Thr Asp Leu Gly Thr
485 490 495

Lys Val Asp Gly Phe Asp Ser Arg Val Thr Ala Leu Asp Thr Lys Val

500

505

510

Asn Ala Phe Asp Gly Arg Ile Thr Ala Leu Asp Ser Lys Val Glu Asn
 515 520 525

Gly Met Ala Ala Gln Ala Ala His His
 530 535

<210> 70
 <211> 1611
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA sequence for MC-010 construct

<400> 70
 atgcaggcca aaaatgatat taccctggaa gatctgccgt atctgatcaa aaaaatcgat 60
 cagaacgaac tggaagccga tattggtgat attaccgcac tggaataata tctggcactg 120
 agccagtatg gaaatattct ggccctggaa gaactgaata aagctctgga agagctggat 180
 gaagatgtgg gttggaatca gaatgatatc gccaatctgg aagatgatgt tgaaaccctg 240
 accaaaaatc agaatgcact ggacgaacag ggtgaagcaa ttaaagaaga tctgcagggt 300
 ctggcagatt ttgttgaagg tcaggaaggc aaaattctgc agaacgaaac cagcatcaaa 360
 aaaaacaccc agcgtaatct ggtgaatggc ttgaaattg aaaaaaaca agatgccatt 420
 gccaaaaaca acgaaagcat tgaagatctg tatgattttg gtcatagaagt tgccgaaagc 480
 attggtgaaa ttcatagcaca taacgaagca cagaatgaaa ccctgaaagg tctgattacc 540
 aacagcatcg aaaataccaa taacattacc aaaaacaaag cagatattca ggcgctggaa 600
 aataatgttg tggaagaact gtttaatctg agcggctctc tgattgatca gaaagccgat 660
 atcgataata acattaacaa catttatgaa ctggcacagc agcaggatca gcatagcagc 720
 gatatacaaa ccctgaaaaa aaacgttgaa gaaggtctgc tggaactgtc tggcacctg 780
 atcgatcaga aaactgatat tgcccagaat caggcaaata ttcaggatct ggccacctat 840
 aatgaactgc aggatcagta tgcacagaaa cagaccgaag caattgatgc cctgaataaa 900
 gcgagcagcg aaaacaccca gaatatcgaa gatctggcag catacaacga actgcaggat 960
 gcctatgcaa aacagcagac tgaagccatc gacgcactga acaaggcaag ctctgaaaac 1020

acgcagaaca ttgaagatct ggctgcctat aatgaattac aggatgcgta tgccaaacag 1080
 cagaccgaag cgattgatgc gctgaacaaa gcctcttctg aaaatacaca gaatatcgcc 1140
 aaaaatcagg ccgatattgc caacaatatc aataatatct atgaactggc ccagcagcag 1200
 gatcagcact cttctgatat caaaacactg gcaaaagcaa gcgcagcaaa taccgatcgt 1260
 attgcgaaaa acaaagccga tgcagatgca agctttgaaa cactgacgaa aaaccagaac 1320
 accctgattg aaaaagataa agaacatgat aaactgatca ccgccaataa aaccgcaatt 1380
 gatgcaaata aagccagcgc agatacaaaa tttgcagcaa ccgcagatgc aattacaaaa 1440
 aatggcaatg ccatcaccaa aaatgccaaa agcattaccg atctgggcac caaagttgat 1500
 ggttttgata gccgtgtgac cgactggat accaaagtta atgcatttga tggtcgtatt 1560
 accgctctgg atagtaaagt tgaaaatggg atggcagcac aggcagcata a 1611

<210> 71
 <211> 536
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Protein sequence for MC-010 construct

<400> 71

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

Lys Lys Ile Asp Gln Asn Glu Leu Glu Ala Asp Ile Gly Asp Ile Thr
 20 25 30

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

Leu Glu Glu Leu Asn Lys Ala Leu Glu Glu Leu Asp Glu Asp Val Gly
 50 55 60

Trp Asn Gln Asn Asp Ile Ala Asn Leu Glu Asp Asp Val Glu Thr Leu
 65 70 75 80

Thr Lys Asn Gln Asn Ala Leu Ala Glu Gln Gly Glu Ala Ile Lys Glu

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

Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp
305 310 315 320

Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala
325 330 335

Ser Ser Glu Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu
340 345 350

Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu
355 360 365

Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala
370 375 380

Asp Ile Ala Asn Asn Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln
385 390 395 400

Asp Gln His Ser Ser Asp Ile Lys Thr Leu Ala Lys Ala Ser Ala Ala
405 410 415

Asn Thr Asp Arg Ile Ala Lys Asn Lys Ala Asp Ala Asp Ala Ser Phe
420 425 430

Glu Thr Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu
435 440 445

His Asp Lys Leu Ile Thr Ala Asn Lys Thr Ala Ile Asp Ala Asn Lys
450 455 460

Ala Ser Ala Asp Thr Lys Phe Ala Ala Thr Ala Asp Ala Ile Thr Lys
465 470 475 480

Asn Gly Asn Ala Ile Thr Lys Asn Ala Lys Ser Ile Thr Asp Leu Gly
485 490 495

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

Val Asn Ala Phe Asp Gly Arg Ile Thr Ala Leu Asp Ser Lys Val Glu
515 520 525

Asn Gly Met Ala Ala Gln Ala Ala
530 535

<210> 72

<211> 1560

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA sequence for MC-011 construct

<400> 72

atggcgaaaa atgatattac cctggaagat ctgccgtatc tgatcaaaaa aatcgatcag	60
aacgaactgg aagccgatat tggatgatatt accgcactgg aaaaatatct ggcactgagc	120
cagtatggaa atattctggc cctggaagaa ctgaataaag ctctggaaga gctggatgaa	180
gatgtgggtt ggaatcagaa tgatatcgcc aatctggaag atgatgttga aaccctgacc	240
aaaaatcaga atgcactggc agaacagggt gaagcaatta aagaagatct gcagggtctg	300
gcagattttg ttgaagggtca ggaaggcaaa attctgcaga acgaaaccag catcaaaaaa	360
aacacccagc gtaatctggt gaatggcttt gaaattgaaa aaaacaaaga tgccattgcc	420
aaaaacaacg aaagcattga agatctgtat gatcttgggtc atgaagttgc cgaaagcatt	480
ggtgaaattc atgcacataa cgaagcacag aatgaaacct tgaaaggtct gattaccaac	540
agcatcgaaa ataccaataa cattacaaa aacaaagcag atattcaggc gctggaaaat	600
aatgttgtgg aagaactgtt taatctgagc ggtcgtctga ttgatcagaa agccgatatc	660
gataataaca ttaacaacat ttatgaactg gcacagcagc aggatcagca tagcagcgat	720
atcaaaacct tgaaaaaaaa cgttgaagaa ggtctgctgg aactgtctgg tcacctgatc	780
gatcagaaaa ctgatattgc ccagaatcag gcaaattatc aggatctggc cacctataat	840
gaactgcagg atcagtatgc acagaaacag accgaagcaa ttgatgccct gaataaagcg	900
agcagcgaaa acacccagaa tatcgaagat ctggcagcat acaacgaact gcaggatgcc	960
tatgcaaaac agcagactga agccatcgac gcactgaaca aggcaagctc tgaaaacacg	1020
cagaacattg aagatctggc tgcctataat gaattacagg atgcgtatgc caaacagcag	1080

accgaagcga ttgatgcgct gaacaaagcc ttttctgaaa atacacagaa tatcgccaaa 1140
aatcaggccg atattgccaa caatatcaat aatatctatg aactggccca gcagcaggat 1200
cagcactctt ctgatatcaa aacactggca aaagcaagcg cagcaaatac cgatcgtatt 1260
gcgaaaaaca aagccgatgc agatgcaagc tttgaaacac tgacgaaaaa ccagaacacc 1320
ctgattgaaa aagataaaga acatgataaa ctgatcaccg ccaataaaac cgcaattgat 1380
gcaaataaag ccagcgcaga taccaaattt gcagcaaccg cagatgcaat taccaaaaat 1440
ggcaatgcc a tcacaaaaa tgccaaaagc attacgcatc tgggcaccaa agttgatggt 1500
tttgatagcc gtgtgaccgc actggatacc aaagcaagcc atcatcatca ccaccactaa 1560

<210> 73
<211> 519
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein sequence for MC-011 construct

<400> 73

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

Lys Ile Asp Gln Asn Glu Leu Glu Ala Asp Ile Gly Asp Ile Thr Ala
20 25 30

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

Glu Glu Leu Asn Lys Ala Leu Glu Glu Leu Asp Glu Asp Val Gly Trp
50 55 60

Asn Gln Asn Asp Ile Ala Asn Leu Glu Asp Asp Val Glu Thr Leu Thr
65 70 75 80

Lys Asn Gln Asn Ala Leu Ala Glu Gln Gly Glu Ala Ile Lys Glu Asp
85 90 95

Leu Gln Gly Leu Ala Asp Phe Val Glu Gly Gln Glu Gly Lys Ile Leu

100							105							110						
Gln	Asn	Glu	Thr	Ser	Ile	Lys	Lys	Asn	Thr	Gln	Arg	Asn	Leu	Val	Asn					
		115							120					125						
Gly	Phe	Glu	Ile	Glu	Lys	Asn	Lys	Asp	Ala	Ile	Ala	Lys	Asn	Asn	Glu					
		130									140									
Ser	Ile	Glu	Asp	Leu	Tyr	Asp	Phe	Gly	His	Glu	Val	Ala	Glu	Ser	Ile					
		145									155				160					
Gly	Glu	Ile	His	Ala	His	Asn	Glu	Ala	Gln	Asn	Glu	Thr	Leu	Lys	Gly					
				165							170				175					
Leu	Ile	Thr	Asn	Ser	Ile	Glu	Asn	Thr	Asn	Asn	Ile	Thr	Lys	Asn	Lys					
				180							185				190					
Ala	Asp	Ile	Gln	Ala	Leu	Glu	Asn	Asn	Val	Val	Glu	Glu	Leu	Phe	Asn					
		195										205								
Leu	Ser	Gly	Arg	Leu	Ile	Asp	Gln	Lys	Ala	Asp	Ile	Asp	Asn	Asn	Ile					
		210										220								
Asn	Asn	Ile	Tyr	Glu	Leu	Ala	Gln	Gln	Gln	Asp	Gln	His	Ser	Ser	Asp					
		225									235				240					
Ile	Lys	Thr	Leu	Lys	Lys	Asn	Val	Glu	Glu	Gly	Leu	Leu	Glu	Leu	Ser					
					245					250					255					
Gly	His	Leu	Ile	Asp	Gln	Lys	Thr	Asp	Ile	Ala	Gln	Asn	Gln	Ala	Asn					
				260										270						
Ile	Gln	Asp	Leu	Ala	Thr	Tyr	Asn	Glu	Leu	Gln	Asp	Gln	Tyr	Ala	Gln					
		275												285						
Lys	Gln	Thr	Glu	Ala	Ile	Asp	Ala	Leu	Asn	Lys	Ala	Ser	Ser	Glu	Asn					
		290										300								
Thr	Gln	Asn	Ile	Glu	Asp	Leu	Ala	Ala	Tyr	Asn	Glu	Leu	Gln	Asp	Ala					
		305									315				320					

Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser
325 330 335

Ser Glu Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu
340 345 350

Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn
355 360 365

Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala Asp
370 375 380

Ile Ala Asn Asn Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp
385 390 395 400

Gln His Ser Ser Asp Ile Lys Thr Leu Ala Lys Ala Ser Ala Ala Asn
405 410 415

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

Thr Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu His
435 440 445

Asp Lys Leu Ile Thr Ala Asn Lys Thr Ala Ile Asp Ala Asn Lys Ala
450 455 460

Ser Ala Asp Thr Lys Phe Ala Ala Thr Ala Asp Ala Ile Thr Lys Asn
465 470 475 480

Gly Asn Ala Ile Thr Lys Asn Ala Lys Ser Ile Thr Asp Leu Gly Thr
485 490 495

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

Ser His His His His His His
515

<210> 74
 <211> 1893
 <212> DNA
 <213> Moraxella catarrhalis

<400> 74
 atgaaaacca tgaaacttct ccctctaaaa atcgctgtaa ccagtgccat gattattggc 60
 ttgggtgcgg catctactgc gaatgcgcag gctaaaaatg atataacttt agaggattta 120
 ccatatttaa taaaaaagat tgacaaaaat gaattggaag cagatatcgg agatattact 180
 gctcttgaaa agtatctagc acttagccag tatggcaata ttttagctct agaagagctc 240
 aacaaggctc tagaagagct cgacgaggat gttggatgga atcagaatga tattgcaaac 300
 ttggaagatg atgttgaaac gctcaccaaa aatcaaaatg ctttggctga acaaggtagag 360
 gcaattaaag aagatcttca agggcttgca gattttgtag aagggaaga gggtaaaatt 420
 ctacaaaatg aaacttcaat taaaaaaaaat actcagagaa accttggtcaa tgggtttgag 480
 attgagaaaa ataaagatgc tattgctaaa aacaatgagt ctatcgaaga tctttatgat 540
 tttggtcatg aggttgcaga aagtataggc gagatacatg ctcataatga agcgcaaaat 600
 gaaactctta aaggcttgat aacaaacagt attgagaata ctaataatat taccaaaaac 660
 aaagctgaca tccaagcact tgaaaacaat gtcgtagaag aactattcaa tctaagcggc 720
 cgcctaattg atcaaaaagc agatattgat aataacatca acaatatcta tgagctggca 780
 caacagcaag atcagcatag ctctgatatc aaacactta aaaaaaatgt cgaagaaggc 840
 ttgttgagc taagcggccta cctaattgat caaaaaacag atattgctca aaaccaagct 900
 aacatccaag atctggccac ttacaacgag ctacaagacc agtatgctca aaagcaaacc 960
 gaagcgattg acgctctaaa taaagcaagc tctgagaata cacaaaacat cgaagatctg 1020
 gccgcttaca acgagctaca agatgcctat gccaaacagc aaaccgaagc aattgacgct 1080
 ctaaataaag caagctctga gaatacaca aacatcgaag atctggccgc ttacaacgag 1140
 ctacaagatg cctatgccaa acagcaaacc gaagccattg acgctctaaa taaagcaagc 1200
 tctgagaata cacaaaacat tgctaaaaac caagcgata ttgctaataa catcaacaat 1260
 atctatgagc tggcacaaca gcaagatcag catagctctg atatcaaaac cttggcaaaa 1320
 gcaagtgctg ccaatactga tcgtattgct aaaaacaaag ccgatgctga tgcaagtttt 1380

gaaacgctca ccaaaaatca aaatactttg attgaaaaag ataaaagagca tgacaaatta	1440
attactgcaa acaaaactgc gattgatgcc aataaagcat ctgcggatac caagtttgca	1500
gcgacagcag acgccattac caaaaatgga aatgctatca ctaaaaacgc aaaatctatc	1560
actgatttgg gcactaaagt ggatggtttt gacagtcgtg taactgcatt agacaccaaa	1620
gtcaatgcct ttgatggtcg tatcacagct ttagacagta aagttgaaaa cggtatggct	1680
gccaagctg ccctaagtgg tctattccag ccttatagcg ttggtaagtt taatgcgacc	1740
gctgcacttg gtggctatgg ctcaaaatct gcggttgcta tcggtgctgg ctatcgtgtg	1800
aatccaaatc tggcgtttaa agctggcg gcgattaata ccagtggtaa taaaaaggc	1860
tcttataaca tcggtgtgaa ttacgagttc taa	1893

<210> 75
 <211> 44
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer sequence

<400> 75	
gaattcttaa ttaacatatg caggccaaaa atgatattac cctg	44

<210> 76
 <211> 43
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer sequence

<400> 76	
ggcgcgcctc gagttattat ttggtatcca gtgcggtcac acg	43

<210> 77
 <211> 43
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer sequence

<400> 77	
ggcgcgcctc gagttagtgt ttggtatcca gtgcggtcac acg	43

<210> 78
 <211> 46
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer sequence

 <400> 78
 ggcgcgccctc gagttagtgg tgtttggtat ccagtgcggt cacacg 46

 <210> 79
 <211> 66
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer sequence

 <400> 79
 ggcgcgccctc gagttagtgg tggatgatgat gatggcttgc gcttttggca tttttggtga 60
 tggcat 66

 <210> 80
 <211> 36
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer sequence

 <400> 80
 ccgctcgagc tagcttttgg catttttggg gatggc 36

 <210> 81
 <211> 43
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer sequence

 <400> 81
 ggaattccat atggcgaaaa atgatattac cctggaagat ctg 43

 <210> 82

<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer sequence

<400> 82
ggcgcgcctc gagttagtgg tgtgctgcct gtgctgccat accatt

46

<210> 83
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer sequence

<400> 83
ggcgcgcctc gagttatgct gcctgtgctg ccataccatt

40

<210> 84
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer sequence

<400> 84
cagttcatta taggtggcca gatcctg

27

<210> 85
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> N terminal amino acids of MC-001

<400> 85

Met Gln Ala Lys
1

<210> 86
<211> 11
<212> PRT
<213> Artificial Sequence

<220>

<223> N terminal amino acid sequence

<400> 86

Ala Lys Asn Asp Ile Thr Leu Glu Asp Leu Pro
1 5 10

<210> 87

<211> 1542

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA sequence for MC-003 Construct

<400> 87

atgcaggcca	aaaatgatat	taccctggaa	gatctgccgt	atctgatcaa	aaaaatcgat	60
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agccagtatg	gaaatattct	ggccctggaa	gaactgaata	aagctctgga	agagctggat	180
gaagatgtgg	gttggaatca	gaatgatatc	gccaatctgg	aagatgatgt	tgaaaccctg	240
acaaaaaatc	agaatgcact	ggcagaacag	ggtgaagcaa	ttaaagaaga	tctgcagggt	300
ctggcagatt	ttgttgaagg	tcaggaaggc	aaaattctgc	agaacgaaac	cagcatcaaa	360
aaaaacaccc	agcgtaatct	ggtgaatggc	tttgaaattg	aaaaaaacaa	agatgccatt	420
gccaaaaaca	acgaaagcat	tgaagatctg	tatgattttg	gtcatgaagt	tgccgaaagc	480
attggtgaaa	ttcatgcaca	taacgaagca	cagaatgaaa	ccctgaaagg	tctgattacc	540
aacagcatcg	aaaataccaa	taacattacc	aaaaacaaag	cagatattca	ggcgctggaa	600
aataatgttg	tggaagaact	gtttaatctg	agcggctcgtc	tgattgatca	gaaagccgat	660
atcgataata	acattaacaa	catttatgaa	ctggcacagc	agcaggatca	gcatagcagc	720
gatatcaaaa	ccctgaaaaa	aaacgttgaa	gaaggtctgc	tggaactgtc	tggtcacctg	780
atcgatcaga	aaactgatat	tgcccagaat	caggcaaata	ttcaggatct	ggccacctat	840
aatgaactgc	aggatcagta	tgcacagaaa	cagaccgaag	caattgatgc	cctgaataaa	900
gcgagcagcg	aaaacaccca	gaatatcgaa	gatctggcag	catacaacga	actgcaggat	960
gcctatgcaa	aacagcagac	tgaagccatc	gacgcactga	acaaggcaag	ctctgaaaac	1020

acgcagaaca ttgaagatct ggctgcctat aatgaattac aggatgcgta tgccaaacag 1080
 cagaccgaag cgattgatgc gctgaacaaa gcctcttctg aaaatacaca gaatatcgcc 1140
 aaaaatcagg ccgatattgc caacaatatc aataatatct atgaactggc ccagcagcag 1200
 gatcagcact cttctgatat caaaacactg gcaaaagcaa gcgcagcaaa taccgatcgt 1260
 attgcgaaaa acaaagccga tgcagatgca agctttgaaa cactgacgaa aaaccagaac 1320
 accctgattg aaaaagataa agaacatgat aaactgatca ccgccaataa aaccgcaatt 1380
 gatgcaaata aagccagcgc agatacaaaa tttgcagcaa ccgcagatgc aattacaaaa 1440
 aatggcaatg ccatcaccaa aaatgccaaa agcattaccg atctgggcac caaagttgat 1500
 ggttttgata gccgtgtgac cgactggat accaaacact aa 1542

<210> 88
 <211> 513
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Protein sequence for MC-003 Construct

<400> 88

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

Lys Lys Ile Asp Gln Asn Glu Leu Glu Ala Asp Ile Gly Asp Ile Thr
 20 25 30

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

Leu Glu Glu Leu Asn Lys Ala Leu Glu Glu Leu Asp Glu Asp Val Gly
 50 55 60

Trp Asn Gln Asn Asp Ile Ala Asn Leu Glu Asp Asp Val Glu Thr Leu
 65 70 75 80

Thr Lys Asn Gln Asn Ala Leu Ala Glu Gln Gly Glu Ala Ile Lys Glu
 85 90 95

Asp Leu Gln Gly Leu Ala Asp Phe Val Glu Gly Gln Glu Gly Lys Ile
100 105 110

Leu Gln Asn Glu Thr Ser Ile Lys Lys Asn Thr Gln Arg Asn Leu Val
115 120 125

Asn Gly Phe Glu Ile Glu Lys Asn Lys Asp Ala Ile Ala Lys Asn Asn
130 135 140

Glu Ser Ile Glu Asp Leu Tyr Asp Phe Gly His Glu Val Ala Glu Ser
145 150 155 160

Ile Gly Glu Ile His Ala His Asn Glu Ala Gln Asn Glu Thr Leu Lys
165 170 175

Gly Leu Ile Thr Asn Ser Ile Glu Asn Thr Asn Asn Ile Thr Lys Asn
180 185 190

Lys Ala Asp Ile Gln Ala Leu Glu Asn Asn Val Val Glu Glu Leu Phe
195 200 205

Asn Leu Ser Gly Arg Leu Ile Asp Gln Lys Ala Asp Ile Asp Asn Asn
210 215 220

Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser
225 230 235 240

Asp Ile Lys Thr Leu Lys Lys Asn Val Glu Glu Gly Leu Leu Glu Leu
245 250 255

Ser Gly His Leu Ile Asp Gln Lys Thr Asp Ile Ala Gln Asn Gln Ala
260 265 270

Asn Ile Gln Asp Leu Ala Thr Tyr Asn Glu Leu Gln Asp Gln Tyr Ala
275 280 285

Gln Lys Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu
290 295 300

Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp

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