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AP ARIPO특허 : 케냐, 레소토, 말라위, 수단, 스와질랜드, 우간다, 가나, 감비아, 짐바브웨,

EA 유라시아특허 : 아르메니아, 아제르바이잔, 벨라루스, 키르기스스탄, 카자흐스탄, 몰도바, 러시아, 타지키스탄, 투르크멘,

EP 유럽특허 : 오스트리아, 벨기에, 스위스, 독일, 덴마크, 스페인, 프랑스, 영국, 그리스, 아일랜드, 이탈리아, 룩셈부르크, 모나코, 네덜란드, 포르투갈, 스웨덴, 핀란드, 사이프러스,

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요약

본 발명은 분리된 항원성 *Porphyromonas gingivalis* 폴리펩티드 또는 뉴클레오티드에 관한 것이다. 상기 폴리펩티드는 SEQ. ID. NO. 265 내지 SEQ. ID. NO. 528, SEQ. ID. NO. 531 및 SEQ. ID. NO. 532로 이루어진 군으로부터 선택되는 아미노산 서열; 또는 SEQ. ID. NO. 265 내지 SEQ. ID. NO. 528, SEQ. ID. NO. 531 및 SEQ. ID. NO. 532로 이루어진 군으로부터 선택되는 아미노산 서열과 적어도 85%, 바람직하게는 적어도 95%의 상동성을 가지는 아미노산 서열; 또는 SEQ. ID. NO. 265 내지 SEQ. ID. NO. 528, SEQ. ID. NO. 531 및 SEQ. ID. NO. 532로 이루어진 군으로부터 선택되는 인접한(contiguous) 아미노산 서열에 상동성을 가지는 40개 이상의 아미노산의 인접 서열을 가지는 40개 이상의 아미노산을 포함한다.

대표도

도 1

색인어

Porphyromonas gingivalis, 치주염, 폴리펩티드, 뉴클레오티드

명세서

기술분야

본 발명은 *P. gingivalis* 뉴클레오티드 서열, *P. gingivalis* 폴리펩티드 및 *P. gingivalis*를 검출하기 위한 프로브에 관한 것이다. *P. gingivalis* 폴리펩티드 및 뉴클레오티드는 *P. gingivalis*에 대하여 개체에서 면역반응을 일으켜 치주염(periodontitis)으로 알려진 질병을 치료하거나 예방하거나 경감시키는 데 사용되는 조성물에 이용될 수 있다.

배경기술

치주 질환은 치아의 지지조직의 박테리아-관련 염증성 질환으로, 잇몸 조직의 비특이적이고 가역적인 염증으로 상대적으로 병세가 가벼운 형태의 치은염(gingivitis)으로부터 치아 지지 조직의 파괴를 가져오는 더욱 공격적인 형태의 치주염(periodontitis)까지 그 범주에 속한다. 치주염은 특이적인 그람-음성 박테리아 집합체의 하부 잇몸 감염과 관련이 있으며, 이것은 치주조직을 파괴하여 주요한 공중 건강 문제로 대두된다. 성인 치주염의 병변에서의 *P. gingivalis* 미생물은 혐기성 조건하에서 살아가는 하부 잇몸의 플로라(flora)의 50%까지 회수될 수 있어서 상당한 관심의 대상이 되고 있으나, *P. gingivalis*는 건강한 부위에서는 거의 회수되지 않아서 낮은 비율로 존재한다. 하부 잇몸 치태(plaque)에서 *P. gingivalis* 수준이 비례적으로 증가하는 것은 치주염 통증의 증가와 관련이 있으며, 배양가능한 하부 잇몸의 미생물 집단에서 이 미생물이 박멸되면 이들 질환이 완치된다. 인간이 아닌 영장류 동물에서의 치주염 병변의 진행은 *P. gingivalis*의 하부 잇몸의 이식에 의하여 밝혀졌다. 동물 및 인간 모두에서의 이러한 발견은 성인 치주염의 발생에 있어서 *P. gingivalis*의 주요한 역할을 시사한다.

*P. gingivalis*는 흑색으로 착색되어 있으며, 혐기성, 비당분해성(asaccharolytic), 단백분해성(preteolytic)의 그람-음성 간균(rod)으로, 특이한 아미노산의 신진대사로부터 에너지를 얻는다. 이 미생물은 철이라는 절대적인 성장요인을 가지며, 바람직하게는 헴(haeme) 또는 그 Fe(III) 산화생성물인 헤민(haemin)의 형태이며, 과도한 헤민의 조건하에서 성장할 때는 실험동물 내에서 강한 독성을 띤다. 많은 독성 요인은 캡슐, 부착인자(adhesin), 세포독소(cytotoxin) 및 세포의 가수분해 효소를 비롯한 *P. gingivalis*의 병원성과 관련 있다.

P. gingivalis 군락형성을 예방, 제거 또는 경감하기 위한 효과적이고 안전한 백신을 개발하기 위하여, 특이적 항체의 생성을 통하여 면역원으로서 유용성을 가지는 독성과 관련된 항원을 동정하고 생산할 필요가 있다. *P. gingivalis* 배양액에서 직접 항원을 분리하려는 시도가 있어 왔으나 이는 종종 어려운 문제가 따랐다. 예를 들어 상기 설명된 바와 같이, *P. gingivalis*는 엄격한(strict) 혐기세균으로 분리하여 생육하기 어려울 수 있다. 다수의 유기체를 시험관내에서(in vitro) 배양할 경우 많은 독성 유전자가 하향 조절되어 그에 의해 코드된 단백질이 더 이상 발현되지 않는다고 알려져 있다. 순수한 백신 후보인자를 정제하기 위하여 종래의 화학적 방법이 적용되었으나, 잠재적으로 중요한 (방어적인) 분자를 동정할 수는 없었다. 유기체가 시험관내에서 생육된다 하더라도 유전자가 존재하기 때문에 (전사되지는 않음) DNA 시퀀싱을 이용하여 동정되고 클론되어 재조합 DNA 단백질로서 생산된다. 유사한 방법으로 방어적인 항원 또는 치료적인 표적물이 시험관내에서 유기체에 의하여 일시적으로 발현되거나 낮은 수준으로 생성되어 종래의 방법으로는 지극히 어려웠던 이들 분자들의 동정을 가능하게 하고 있다.

치료학적 표적물의 혈청학적 동정으로는 웨스턴 블로팅(Western Blotting) 또는 ELISA와 같은 표준 방법을 이용하여 검출되는 반응(response)에 한정된다. 여기서의 제한은 동물 또는 인간에 의하여 생성되는 반응의 레벨 및 이러한 반응이 보호적인지, 유해한지 또는 아무런 관련이 없는지를 결정하는 것 양자에 해당된다. 이러한 제한은 잠재적인 치료적 또는 예방적인 표적물에 대한 시퀀싱 접근방법에는 존재하지 않는다.

또한 *P. gingivalis*는 광범위하게 활성을 가지는 프로테아제를 생성시킨다고 잘 알려져 있으며(University of Melbourne 국제특허출원 No. PCT/AU96/00673, 미국특허 제5,475,097호 및 5,523,390), 이들 프로테아제에 의한 분해로 인하여 온전한 단백질의 동정이 어려워진다.

발명의 상세한 설명

본 발명자들은 *P. gingivalis* 폴리펩티드를 재조합 생산하는 데 유용한 *P. gingivalis* 뉴클레오티드를 분리하고 *P. gingivalis*에 특이적인 뉴클레오티드 프로브를 개발하기 위한 노력을 하였다. 하기에 기재된 DNA 서열은 백신 후보인자로 유용한 잠재성을 가지는 다수의 *P. gingivalis* 서열에서 선택된다. 이것은 *P. gingivalis* DNA 서열로부터 유도된 단백질 서열을 공지된 단백질 서열 데이터베이스에 비교하는 단계가 포함된다. 유용한 백신 후보인자를 선택하는 데 사용되는 몇가지 특징은 다음과 같다: 외부 막 단백질 또는 분비 단백질과 같은 예상되는 세포에서 위치, 효소 또는 단백질 분해활성

과 같은 유사한 단백질의 특정 기능적 활성, 비활성화되거나 차단될 경우 유기체에 유해하거나 치명적인 필수 대사 경로에 관여하는 단백질, 유기체의 병원성, 예를 들어 적세포(red cell) 용해, 세포 응집 또는 세포 수용체에 관여하는 것으로 기대되는 단백질, 및 백신 효과를 가지는 것으로 밝혀진 단백질에 유사한 단백질.

본 발명의 제1 특징에 따르면 분리된 항원성 *Porphyromonas gingivalis* 폴리펩티드가 제공되며, 상기 폴리펩티드는 하기의 아미노산을 포함한다:

SEQ. ID. NO. 265 내지 SEQ. ID. NO. 528, SEQ. ID. NO. 531 및 SEQ. ID. NO. 532로 이루어진 군으로부터 선택되는 아미노산 서열; 또는

SEQ. ID. NO. 265 내지 SEQ. ID. NO. 528, SEQ. ID. NO. 531 및 SEQ. ID. NO. 532로 이루어진 군으로부터 선택되는 아미노산 서열과 적어도 85%, 바람직하게는 적어도 95%의 상동성을 가지는 아미노산 서열; 또는

SEQ. ID. NO. 265 내지 SEQ. ID. NO. 528, SEQ. ID. NO. 531 및 SEQ. ID. NO. 532로 이루어진 군으로부터 선택되는 인접한(contiguous) 서열에 상동성을 가지는 40개 이상의 아미노산의 인접 서열을 가지는 40개 이상의 아미노산.

본 발명의 바람직한 구체예에서 폴리펩티드는 하기의 아미노산 서열을 포함한다:

SEQ. ID. NO. 386 내지 SEQ. ID. NO. 528 및 SEQ. ID. NO. 532로 이루어진 군으로부터 선택되는 아미노산 서열; 또는

SEQ. ID. NO. 386 내지 SEQ. ID. NO. 528 및 SEQ. ID. NO. 532로 이루어진 군으로부터 선택되는 아미노산 서열과 적어도 85%, 바람직하게는 95%의 상동성을 가지는 아미노산 서열; 또는

SEQ. ID. NO. 386 내지 SEQ. ID. NO. 528 및 SEQ. ID. NO. 532로 이루어진 군으로부터 선택되는 인접한 서열에 상동성을 가지는 40개 이상의 아미노산의 인접 서열을 가지는 40개 이상의 아미노산.

상기 폴리펩티드에 대한 상동성(%)은 표준 단백질 스코어링 매트릭스(Blosum 50)를 이용하는 Needleman and Munsch (9)의 정렬 알고리즘(alignment algorithm)으로 계산하였다.

본 발명의 바람직한 구체예에서 폴리펩티드는 하기의 군으로부터 선택되는 아미노산 서열을 포함한다:

SEQ. ID. NO. 386, SEQ. ID. NO. 424, SEQ. ID. NO. 425, SEQ. ID. NO. 434, SEQ. ID. NO. 447, SEQ. ID. NO. 458, SEQ. ID. NO. 475, SEQ. ID. NO. 498, SEQ. ID. NO. 499, SEQ. ID. NO. 500, SEQ. ID. NO. 501, SEQ. ID. NO. 387, SEQ. ID. NO. 400, SEQ. ID. NO. 411, SEQ. ID. NO. 419, SEQ. ID. NO. 420, SEQ. ID. NO. 427, SEQ. ID. NO. 429, SEQ. ID. NO. 433, SEQ. ID. NO. 437, SEQ. ID. NO. 438, SEQ. ID. NO. 443, SEQ. ID. NO. 444, SEQ. ID. NO. 448, SEQ. ID. NO. 449, SEQ. ID. NO. 452, SEQ. ID. NO. 455, SEQ. ID. NO. 457, SEQ. ID. NO. 459, SEQ. ID. NO. 461, SEQ. ID. NO. 462, SEQ. ID. NO. 463, SEQ. ID. NO. 467, SEQ. ID. NO. 468, SEQ. ID. NO. 469, SEQ. ID. NO. 482, SEQ. ID. NO. 484, SEQ. ID. NO. 485, SEQ. ID. NO. 494, SEQ. ID. NO. 508, SEQ. ID. NO. 509, SEQ. ID. NO. 510, SEQ. ID. NO. 520, SEQ. ID. NO. 521, SEQ. ID. NO. 522, SEQ. ID. NO. 525, SEQ. ID. NO. 526, SEQ. ID. NO. 528, SEQ. ID. NO. 389, SEQ. ID. NO. 390 및 SEQ. ID. NO. 391.

본 발명의 다른 구체예에서 상기 폴리펩티드는 SEQ. ID. NO. 303의 잔기 422 내지 531, SEQ. ID. NO. 303의 잔기 534 내지 582, SEQ. ID. NO. 301의 잔기 127 내지 232, SEQ. ID. NO. 301의 잔기 240 내지 259, SEQ. ID. NO. 295의 잔기 139 내지 156, SEQ. ID. NO. 295의 잔기 160 내지 178, SEQ. ID. NO. 295의 잔기 180 내지 207, SEQ. ID. NO. 295의 잔기 221 내지 257, SEQ. ID. NO. 295의 잔기 259 내지 323, SEQ. ID. NO. 299의 잔기 885 내지 985, SEQ. ID. NO. 363의 잔기 147 내지 259, SEQ. ID. NO. 344의 잔기 140 내지 252, SEQ. ID. NO. 353의 잔기 247 내지 356, SEQ. ID. NO. 353의 잔기 359 내지 391, SEQ. ID. NO. 300의 잔기 120 내지 254, SEQ. ID. NO. 286의 잔기 287 내지 311, SEQ. ID. NO. 286의 잔기 313 내지 352, SEQ. ID. NO. 286의 잔기 354 내지 401, SEQ. ID. NO. 287의 잔기 208 내지 252, SEQ. ID. NO. 287의 잔기 259 내지 373, SEQ. ID. NO. 293의 잔기 5 내지 120, SEQ. ID. NO. 293의 잔기 123 내지 139, SEQ. ID. NO. 265의 잔기 233 내지 339, SEQ. ID. NO. 278의 잔기 67 내지 228, SEQ. ID. NO. 274의 잔기 130 내지 172, SEQ. ID. NO. 274의 잔기 174 내지 238, SEQ. ID. NO. 274의 잔기 99 내지 112, SEQ. ID. NO. 274의 잔기 114 내지 128, SEQ. ID. NO. 285의 잔기 26 내지 69, SEQ. ID. NO. 285의 잔기 71 내지 128, SEQ. ID. NO. 285의 잔기 130 내지 146, SEQ. ID. NO. 327의 잔기 620 내지 636, SEQ. ID. NO. 327의 잔기 638 내지 775, SEQ. ID. NO. 301의 잔기 397 내지 505, SEQ. ID. NO. 301의 잔기 528 내지 545, SEQ. ID. NO. 301의 잔기 556 내지 612, 631 of SEQ. ID. NO. 301의 잔기 614 내지 631, SEQ. ID.

NO. 301의 잔기 633 내지 650, SEQ. ID. NO. 299의 잔기 553 내지 687, SEQ. ID. NO. 289의 잔기 305 내지 447, SEQ. ID. NO. 364의 잔기 1 내지 52, SEQ. ID. NO. 364의 잔기 65 내지 74, SEQ. ID. NO. 275의 잔기 486 내지 604, SEQ. ID. NO. 272의 잔기 158 내지 267, SEQ. ID. NO. 272의 잔기 270 내지 282, SEQ. ID. NO. 273의 잔기 163 내지 237, SEQ. ID. NO. 273의 잔기 240 내지 251, SEQ. ID. NO. 282의 잔기 213 내지 344, SEQ. ID. NO. 292의 잔기 183 내지 324, SEQ. ID. NO. 292의 잔기 327 내지 341, SEQ. ID. NO. 292의 잔기 352 내지 372, SEQ. ID. NO. 271의 잔기 141 내지 166, SEQ. ID. NO. 271의 잔기 168 내지 232, SEQ. ID. NO. 302의 잔기 1 내지 13, SEQ. ID. NO. 302의 잔기 15 내지 28, SEQ. ID. NO. 302의 잔기 30 내지 72, SEQ. ID. NO. 277의 잔기 476 내지 529, SEQ. ID. NO. 299의 잔기 41 내지 146, SEQ. ID. NO. 299의 잔기 149 내지 162, SEQ. ID. NO. 299의 잔기 166 내지 177, SEQ. ID. NO. 299의 잔기 192 내지 203, SEQ. ID. NO. 290의 잔기 71 내지 343, SEQ. ID. NO. 290의 잔기 346 내지 363, SEQ. ID. NO. 331의 잔기 36 내지 240, SEQ. ID. NO. 331의 잔기 242 내지 270, SEQ. ID. NO. 375의 잔기 1 내지 192, SEQ. ID. NO. 375의 잔기 266 내지 290, SEQ. ID. NO. 279의 잔기 23 내지 216, SEQ. ID. NO. 279의 잔기 220 내지 270, SEQ. ID. NO. 279의 잔기 285 내지 386, SEQ. ID. NO. 297의 잔기 84 내지 234, SEQ. ID. NO. 297의 잔기 248 내지 259, SEQ. ID. NO. 297의 잔기 261 내지 269, SEQ. ID. NO. 294의 잔기 275 내지 402, SEQ. ID. NO. 298의 잔기 1 내지 171, SEQ. ID. NO. 307의 잔기 403 내지 417, SEQ. ID. NO. 307의 잔기 420 내지 453, SEQ. ID. NO. 307의 잔기 456 내지 464, SEQ. ID. NO. 307의 잔기 468 내지 690, SEQ. ID. NO. 304의 잔기 1 내지 285, SEQ. ID. NO. 304의 잔기 287 내지 315, SEQ. ID. NO. 304의 잔기 318 내지 336, SEQ. ID. NO. 342의 잔기 255 내지 269, SEQ. ID. NO. 342의 잔기 271 내지 337, SEQ. ID. NO. 281의 잔기 347 내지 467, SEQ. ID. NO. 375의 잔기 116 내지 136, SEQ. ID. NO. 375의 잔기 138 내지 357, SEQ. ID. NO. 364의 잔기 133 내지 423, SEQ. ID. NO. 305의 잔기 141 내지 299, SEQ. ID. NO. 296의 잔기 202 내지 365, SEQ. ID. NO. 288의 잔기 134 내지 426, SEQ. ID. NO. 276의 잔기 1 내지 218, SEQ. ID. NO. 280의 잔기 1 내지 246, SEQ. ID. NO. 364의 잔기 444 내지 608, SEQ. ID. NO. 283의 잔기 10 내지 686, SEQ. ID. NO. 296의 잔기 1 내지 148, SEQ. ID. NO. 287의 잔기 1 내지 191, SEQ. ID. NO. 287의 잔기 193 내지 204, SEQ. ID. NO. 287의 잔기 209 내지 373, SEQ. ID. NO. 284의 잔기 211 내지 470, SEQ. ID. NO. 284의 잔기 472 내지 482, SEQ. ID. NO. 281의 잔기 133 내지 144, SEQ. ID. NO. 281의 잔기 146 내지 336, SEQ. ID. NO. 303의 잔기 1 내지 264, SEQ. ID. NO. 303의 잔기 265 내지 295, SEQ. ID. NO. 303의 잔기 297 내지 326, SEQ. ID. NO. 303의 잔기 328 내지 338, SEQ. ID. NO. 353의 잔기 247 내지 356, SEQ. ID. NO. 353의 잔기 358 내지 391, SEQ. ID. NO. 298의 잔기 257 내지 288, SEQ. ID. NO. 298의 잔기 290 내지 385, SEQ. ID. NO. 298의 잔기 245 내지 256, SEQ. ID. NO. 303의 잔기 422 내지 802, SEQ. ID. NO. 303의 잔기 803 내지 814, SEQ. ID. NO. 295의 잔기 139 내지 156, SEQ. ID. NO. 295의 잔기 160 내지 340, SEQ. ID. NO. 282의 잔기 145 내지 361, SEQ. ID. NO. 282의 잔기 363 내지 387, SEQ. ID. NO. 282의 잔기 398 내지 471, SEQ. ID. NO. 320의 잔기 573 내지 679, SEQ. ID. NO. 291의 잔기 27 내지 168, SEQ. ID. NO. 291의 잔기 170 내지 183, SEQ. ID. NO. 291의 잔기 185 내지 415, SEQ. ID. NO. 364의 잔기 1 내지 301, SEQ. ID. NO. 337의 잔기 114 내지 702, SEQ. ID. NO. 321의 잔기 377 내지 412, SEQ. ID. NO. 321의 잔기 413 내지 772, SEQ. ID. NO. 265의 잔기 14 내지 454, SEQ. ID. NO. 268의 잔기 129 내지 614, SEQ. ID. NO. 300의 잔기 1 내지 930, SEQ. ID. NO. 300의 잔기 932 내지 1046, SEQ. ID. NO. 364의 잔기 1 내지 301, SEQ. ID. NO. 381의 잔기 1 내지 42, SEQ. ID. NO. 381의 잔기 44 내지 973, SEQ. ID. NO. 358의 잔기 1 내지 93, SEQ. ID. NO. 358의 잔기 95 내지 179, SEQ. ID. NO. 358의 잔기 181 내지 227, SEQ. ID. NO. 337의 잔기 114 내지 702, SEQ. ID. NO. 355의 잔기 1 내지 659, SEQ. ID. NO. 355의 잔기 661 내지 907, SEQ. ID. NO. 370의 잔기 1 내지 131, SEQ. ID. NO. 370의 잔기 133 내지 601, SEQ. ID. NO. 344의 잔기 1 내지 813, SEQ. ID. NO. 321의 잔기 377 내지 412, SEQ. ID. NO. 321의 잔기 413 내지 772, 및 SEQ. ID. NO. 364의 잔기 189 내지 614.

본 발명의 제2 특징에 따르면, SEQ. ID. NO. 386 내지 SEQ. ID. NO. 528 및 SEQ. ID. NO. 532 중 표 3에 기재된 리더 서열을 제외한 서열로 이루어지는 균으로부터 선택되는 아미노산 서열을 포함하는 분리된 항원성 *Porphyromonas gingivalis* 폴리펩티드가 제공된다.

본 발명의 제3 특징에 따르면, 상기 제1 특징에 따르는 폴리펩티드를 코드하는 뉴클레오티드 서열 및 엄격한 조건하에서 이들에 혼성화되는 서열을 포함하는 분리된 DNA 분자가 제공된다.

상기 분리된 DNA 분자는 SEQ. ID. NO. 1 내지 SEQ. ID. NO. 264, SEQ. ID. NO. 529 및 SEQ. ID. NO. 530으로 이루어진 균으로부터 선택되는 뉴클레오티드 서열을 포함한다.

본 발명의 제4 특징에 따르면 전사 조절 인자에 연결된 본 발명의 제2 특징에 따르는 DNA 분자를 포함하는 재조합 발현 벡터가 제공된다.

본 발명은 또한 이러한 재조합 발현 벡터를 포함하는 세포를 제공한다.

본 발명의 다른 특징에 따르면, 폴리펩티드가 발현되도록 하는 조건하에서 세포를 배양하는 것을 포함하는 *P. gingivalis* 폴리펩티드의 생성방법을 제공한다.

본 발명의 또 다른 특징에 따르면, 상기 제1 특징에 따르는 유효량의 폴리펩티드를 하나 이상 또는 상기 제2 특징에 따르는 폴리펩티드를 하나 이상 또는 이들 양자 및 약제학적으로 허용가능한 담체를 포함하는 *P. gingivalis*에 대하여 면역 반응을 유발하는 데 사용되기 위한 조성물을 제공한다. 여기서 약제학적으로 허용가능한 담체로는 애쥬번트가 바람직하다. 본 발명의 또 다른 특징에 따르면, 상기 조성물을 피검체에 투여하여 *P. gingivalis* 감염을 치료하는 방법이 제공된다. 이러한 처리는 예방적인 측면 또는 치료적인 측면일 수 있다.

본 발명의 또 다른 특징에 따르면, 상기 제1 특징에 따르는 폴리펩티드에 대하여 생성되는 항체가 제공된다. 상기 항체는 폴리클론 또는 모노클론 항체일 수 있다. 본 발명은 또는 이들 항체를 포함하는 조성물을 제공한다. 이들 조성물은 치마제(dentrifice), 양치질약(mouthwash) 등과 같은 경구용 제제에 적합하게 될 수 있다.

본 발명의 또 다른 특징에 따르면, 18개 이상의 뉴클레오티드를 포함하고, SEQ. ID. NO. 1 내지 SEQ. ID. NO. 121, SEQ. ID. NO. 529 및 이들에 상보적인 서열로 이루어진 군으로부터 선택되는 인접하는 뉴클레오티드 서열과 상동성을 가지는 18개 이상의 뉴클레오티드의 인접 서열을 포함하는 뉴클레오티드 프로브를 제공한다. 상기 프로브는 검출가능한 표지를 추가로 포함하는 것이 바람직하다.

본 발명은 또한 하기 단계로 이루어지는 *P. gingivalis* 핵산을 샘플내에서 검출하는 방법을 제공한다:

(a) 샘플내에서 프로브와 *P. gingivalis* 핵산의 혼성체를 형성할 수 있는 조건하에서 뉴클레오티드 프로브와 샘플을 접촉시키는 단계; 및

(b) 상기 (a) 단계에서 형성된 혼성체를 검출하는 단계

—여기에서 혼성체가 검출된다는 것은 샘플내에 *P. gingivalis* 핵산이 존재하는 것을 의미한다—.

용어의 정의

정제되거나 분리된 폴리펩티드 또는 실제로 순수한 폴리펩티드의 제조물은 본 명세서에서 같은 의미로 사용되며, 다른 단백질, 지질 및 (폴리펩티드의 생성에 관여하는) 핵산과 분리된 폴리펩티드를 의미한다. 상기 폴리펩티드는 그것을 정제하는 데 사용되는 물질(e.g. 항체) 또는 겔 매트릭스(e.g. 폴리아크릴아미드)도 분리되는 것이 바람직하다. 폴리펩티드는 정제된 제조물중 적어도 10, 20, 50 70, 80 또는 95% 건조 중량을 구성하는 것이 바람직하다. 또한 상기 제조물은 단백질 시퀀싱을 가능하게 하는 충분한 폴리펩티드; 적어도 1, 10, 또는 100 mg의 폴리펩티드를 포함하는 것이 바람직하다.

식물이나 동물의 경우 세포의 정제된 제조물은 세포의 시험관내 제조물을 의미하는 것이며, 그 자체의 식물 또는 동물을 의미하는 것은 아니다. 배양된 세포 또는 미생물 세포의 경우, 적어도 10%, 바람직하게는 50%의 세포 제조물로 이루어진다.

정제되거나 분리되거나 또는 실질적으로 순수한 핵산(e.g. 실질적으로 순수한 DNA; 본 명세서에서는 혼용하여 사용됨)은 하기에 기재된 것중 하나 또는 양자의 핵산을 의미한다: 핵산이 유도되는 유기체의 자연적으로 생성된 게놈에서 밀접하게 인접된 코딩 서열의 양말단(즉 5' 말단 및 3' 말단)과 밀접하게 인접되지 않은 것; 핵산이 유도되는 유기체에서 생성되는 핵산이 실질적으로 존재하지 않는 것. 예를 들어 이 용어는 자가복제할 수 있는 플라스미드나 바이러스 또는 원핵생물이나 진핵생물의 게놈 DNA 내에 통합된 재조합 DNA, 또는 다른 DNA 서열에 관계없이 분리된 분자(e.g. PCR 또는 제한 효소 처리에 의하여 생성된 cDNA 또는 게놈 DNA 단편)로 존재하는 재조합 DNA를 포함한다. 실질적으로 순수한 DNA는 또한 부가적인 *P. gingivalis* DNA 서열을 코드하는 하이브리드 유전자의 일부인 재조합 DNA를 포함한다.

"contig"란 용어는 유기체의 게놈 서열의 연속적인 스트레치(stretch)를 나타내는 핵산을 의미한다.

"오픈 리딩 프레임(open reading frame)"은 ORF로 표시되기도 하며, 폴리펩티드를 코드하는 핵산영역이다. 이 영역은 코딩 서열의 일부 또는 전체 서열을 의미할 수 있으며, 종결 코돈에서 종결 코돈 또는 개시 코돈에서 개시 코돈으로 결정될 수 있다.

"코딩 서열(coding sequence)"은 적당한 조절 서열의 제어하에서 메신저 RNA로 전사되거나 폴리펩티드로 번역되는 핵산을 의미한다. 코딩 서열의 경계는 5' 말단의 번역 개시 코돈 및 3' 말단의 번역 종결 코돈에 의하여 결정된다. 코딩 서열은 메신저 RNA 합성 DNA, 및 재조합 핵산 서열을 포함할 수 있으나 이에 한정되는 것은 아니다.

본 명세서에서 핵산의 "상보인자(complement)"는 원래의 서열과 왓슨-크릭 염기쌍의 형성에 참여하는 역평행 또는 안티센스 서열을 의미한다.

"유전자 생성물(gene product)"은 유전자에 의하여 특이적으로 코드되는 단백질 또는 구조 RNA를 의미한다.

"프로브(probe)"는 관심의 대상이 되는 분자와 특이적으로 결합하는 핵산, 펩타이드 또는 다른 화합물질을 의미한다. 프로브는 종종 표지와 결합되어 있거나 결합될 수 있다. 표지는 검출가능한 화학적 모이어티이다. 일반적인 표지로는 염료, 방사성동위원소, 발광 및 화학발광 모이어티, 형광물질, 효소, 침전제, 증폭서열 등이 있다. 관심이 대상이 되는 분자에 특이적으로 결합하여 그 분자를 이동하지 못하게 하는 핵산, 펩타이드, 또는 다른 화합물질을 여기에서는 "포획 리간드(capture ligand)"라 한다. 포획 리간드는 나이트로-셀룰로스, 유리, 나일론 막, 비드, 입자 등과 같은 지지체와 결합되거나 결합될 수 있는 것이 일반적이다. 혼성화의 특이성은 뉴클레오티드의 염기쌍 조성, 및 반응의 온도 그리고 염농도와 같은 조건에 의존한다. 이 분야의 당업자라면 실험을 통하여 이러한 조건들을 용이하게 결정할 수 있다.

"상동성(Homologous)"은 두 개의 폴리펩티드 또는 두 개의 핵산 분자 사이에서의 서열 유사성 또는 서열 일치성을 의미한다. 두 개의 비교되는 서열내의 위치가 동일한 염기 또는 아미노산 모노머 서브유닛에 의하여 채워지는 경우, 즉 각각 두 개의 DNA 분자의 위치가 아데닌에 의하여 채워진다면 그 분자는 그 위치에서 상동성을 가진다고 한다. 두 개의 서열의 상동성(%)은 두 개의 서열에 의하여 공유되는 일치하거나 동일성을 가지는 위치의 수를 비교되는 전체 위치의 수로 나눈 다음 100을 곱하여 얻어진다.

펩티드, 단백질 및 폴리펩티드는 여기에서 서로 혼용하여 사용된다.

"면역원성 성분(immunogenic component)"이란 숙주 동물에서 체액성 및/또는 세포성 면역 반응을 유발할 수 있는 *P. gingivalis* 폴리펩티드, 이들의 유사체 또는 단편과 같은 모이어티이다.

"항원성 성분(antigenic component)"이란 충분한 친화도로 특이적 항원에 결합하여 검지가 가능한 항원-항체 복합체를 형성할 수 있는 *P. gingivalis* 폴리펩티드, 이들의 유사체 또는 단편과 같은 모이어티이다.

본 명세서에서 "세포 특이성 프로모터(cell-specific promoter)"란 프로모터로서 제공되는, 즉 프로모터에 작동적으로 연결된 선택된 DNA 서열의 발현을 조절하고 조직의 특이적 세포에서 선택된 DNA 서열의 발현에 영향을 미치는 DNA 서열을 의미한다. 이 용어는 또한 하나의 조직에서 주로 선택된 DNA의 발현을 조절하나 다른 조직에서도 발현을 유발할 수 있는 이른바 "누설(leaky)" 프로모터를 포함한다.

본 명세서에서 "조절 서열(control sequence)"은 숙주 유기체에 의하여 인식되어 연결되어 있는 코드된 서열의 발현에 영향을 미치는 염기서열을 가지는 핵산을 의미한다. 이러한 조절 서열의 특성은 숙주 유기체에 따라 다르다: 원핵생물에서 이러한 조절 서열들은 일반적으로 프로모터, 리보솜 결합 자리, 종결인자 및 몇몇 경우에 작동자(operator)를 포함한다; 진핵생물에서는 상기 조절 서열들로 프로모터, 종결인자 및 몇몇 경우 인핸서가 포함된다. 조절 서열이란 용어는 최소한 발현에 필수적인 모든 성분을 포괄하고, 유용한 부가의 성분들, 예를 들면 리더 서열을 포함할 수 있다.

본 명세서에서 "작동가능하게 결합된(operably linked)"은 의도된 방법으로 기능을 하도록 결합되거나 연결된 서열을 의미한다. 예를 들어, 조절 서열과 숙주 세포와 양립하는 조건하에서 코딩 서열의 발현이 이루어질 수 있도록 접합에 의하여 조절 서열이 코딩 서열에 작동적으로 연결된다.

본 명세서에서 "샘플(sample)"은 자연환경에서의 샘플뿐만 아니라 시험관내 세포 구성물에서 분리되거나 개체로부터 분리된 조직 또는 체액(혈장, 혈청, 중추신경계 유체, 림프, 눈물, 타액 및 조직편을 포함하나 이에 한정되는 것은 아님)과 같은 생물학적 샘플을 의미한다.

별도의 기재가 없다면 본 발명은 이 분야의 당업자에게 널리 알려진 종래의 화학적, 분자생물학적, 미생물학적, 재조합 DNA, 및 면역학적 방법을 이용하여 실시될 수 있다. 이러한 기술을 기재한 문헌으로는 J. Perbal, A Practical Guide to Molecular Cloning, John Wiley and Sons (1984), J. Sambrook et al., Molecular Cloning: A Laboratory Manual, Cold

Spring Harbour Laboratory Press (1989), T.A. Brown (editor), Essential Molecular Biology: A Practical Approach, Volumes 1 and 2, IRL Press (1991), D.M. Glover and B.D. Hames (editors), DNA Cloning: A Practical Approach, Volumes 1-4, IRL Press (1995 and 1996), and F.M. Ausubel et al. (Editors), Current Protocols in Molecular Biology, Greene Pub. Associates and Wiley-Interscience (1988, including all updates until present) 등이 있으며 이들은 본 명세서에 참고로 인용된다.

약제학적으로 수용가능한 담체

본 발명의 항체, 폴리펩티드 및 DNA는 담체 또는 희석제를 포함하는 조성물에 함유될 수 있다. 이들 조성물은 담체 또는 희석제가 약제학적으로 수용가능한 약제학적 조성물을 포함한다. 약제학적으로 수용가능한 담체 또는 희석제는 경구, 직장, 비강, 국소(협측(buccal) 및 설하(sublingual) 포함), 질(vaginal), 비경구(피부, 근육, 정맥, 피내(皮内), 포막내(intrathecal) 및 경막 포함) 투여에 적합한 조성물에 사용될 수 있는 것을 포함한다. 이들은 사용되는 투여량과 농도에서 수용체에 비독성이다. 약제학적으로 수용가능한 담체 또는 희석제의 대표적인 예로는 물, (인산염 완충 염수 또는 트리스-완충 염수와 같은) 생리적 pH에서 바람직할 정도로 완충된 등장 용액을 포함하나 이에 한정되는 것은 아니며, 하나 이상의 만니톨, 락토스, 트레할로스(trehalose), 텍스트로스, 글리세롤, 에탄올 또는 (인간 혈청 알부민과 같은) 폴리펩티드를 포함할 수 있다. 상기 조성물은 단위 투여량 형태로 존재할 수 있으며 의학 분야에서 잘 알려진 방법에 의하여 제조될 수 있다.

서열 목록(Sequence Listings)에 기재된 아미노산에 대한 변형은 이 분야의 당업자라면 충분히 이해될 수 있다. 이러한 변형은 아미노산 잔기의 결실, 삽입, 또는 치환일 수 있다. 변형된 폴리펩티드는 천연생성물(즉, 자연물에서 정제되거나 분리된 것) 또는 합성생성물(예를 들어 코딩 DNA상의 부위 특이성 돌연변이(site-directed mutagenesis))중 하나일 수 있다. 서열 목록에 기재된 서열과 적어도 85% 이상, 바람직하게는 95% 이상의 동일성을 가지는 그러한 변형된 폴리펩티드도 본 발명의 범위에 포함된다. 이들 변형된 폴리펩티드에 대한 항체는 또한 서열 목록에 기재된 서열중 하나를 가지는 폴리펩티드에 결합한다. 동일성(%)의 수준은 상기 기재된 바와 같이 계산되었다.

공통된 기원(common ancestor)에 분기되어 관련되어 있다면 단백질 서열이 상동성을 가진다. 그러므로, 단백질의 종(species) 동족체는 다른 종에서 자연적으로 생성된 등가의 단백질이 될 것이다. 하나의 종에서 동족체는 다수의 대립형질 변종으로 존재할 수 있고, 이들은 단백질의 동족체로 간주될 수 있다. 대립형질 변종과 종 동족체는 이 분야에서 잘 알려진 하기의 표준 방법에 의하여 얻어질 수 있다.

대립형질 변종은 개개 유기체에서 자연적으로 생성되는 변종이다.

돌연변이체, 변종 및 동족체-핵산

돌연변이 폴리뉴클레오티드는 뉴클레오티드 잔기가 소실, 삽입 또는 치환된 하나 이상의 돌연변이를 포함한다. 돌연변이는 천연생성물(즉, 자연물에서 분리된 것) 또는 합성생성물(예를 들어 DNA 상에 부위 특이성 돌연변이에 의해 생성된 것)중 하나일 수 있다. 자연적으로 생성된 것 또는 재조합(즉 재조합 DNA 기술에 의하여 제조됨)중 어느 것도 본 발명의 폴리뉴클레오티드가 될 수 있음은 명백하다.

대립형질 변종은 개개 유기체에서 자연적으로 생성되는 변종이다.

공통된 기원에 분기되어 관련되어 있다면 뉴클레오티드 서열이 상동성을 가진다. 그러므로, 폴리뉴클레오티드의 종(species) 동족체는 다른 종에서 자연적으로 생성된 등가의 폴리뉴클레오티드가 될 것이다. 하나의 종에서 동족체는 다수의 대립형질 변종으로 존재할 수 있고, 이들은 폴리뉴클레오티드의 동족체로 간주될 수 있다. 대립형질 변종과 종 동족체는 이 분야에서 잘 알려진 하기의 표준 방법에 의하여 얻어질 수 있다.

항체 생성

본 발명의 폴리펩티드에 대하여 특이적인 항체는 모노클론이든 폴리클론이든 하기에 기재된 표준 방법을 사용하여 이 분야의 통상의 지식을 가진 자에 의하여 제조될 수 있으나 이들 방법에 한정되는 것은 아니다: Harlow *et al.* Antibodies: A Laboratory Manual, Cold Springs Harbor Laboratory Press (1988), 및 D. Catty (editor), Antibodies: A Practical Approach, IRL Press (1988).

단백질의 항원결정기에 대한 폴리클론 항체를 제조하는 방법에 사용되는 다양한 방법이 이 분야에 잘 알려져 있다. 폴리클론 항체를 제조하기 위한 다수의 숙주 동물이 폴리펩티드 제조물을 하나 이상 주입하여 면역화하여 항체를 생성하기 위해 사용될 수 있으며, 상기 동물로는 토끼, 마우스, 쥐 등이 있으며 이에 한정되는 것은 아니다. 숙주의 종류에 따라 숙주 동물에서의 면역 반응을 증가하기 위하여 다양한 애주번트가 사용될 수 있으며, (완전 및 불완전) Freund's, 알루미늄 하이드록사이드와 같은 미네랄 겔, 리조레시틴과 같은 표면 활성 물질, 플루로닉 폴리올, 다가음이온(polyanion), 오일 에멀전, 키홀 림페트(keyhole limpet) 헤모시아닌, 디니트로페놀 및 BCG(Bacille Calmette-Guerin)와 코리네박테리아 파뮴(Corynebacterium parvum)과 같은 잠재적으로 유용한 인간 애주번트를 포함하나 이에 한정되는 것은 아니다.

단백질의 항원결정기에 대한 모노클론 항체는 배양액에서 연속 세포주에 의한 항체 분자를 생산하기 위한 기술을 이용하여 제조될 수 있다. 이러한 기술로는 기초적인 기술로 하이브리도마법(Kohler and Milstein (1975, Nature 256, 493-497)) 및 최근에 알려진 인간 B-세포 하이브리도마법(Kesber et al. 1983, Immunology today 4:72)과 EBV-하이브리도마법(Cole et al. 1985, Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, Inc. pp. 77-96)이 있으나 이에 한정되는 것은 아니다. 또한 적당한 항원 특이성을 가지는 항체 분자의 유전자를 적당한 생물학적 활성을 가지는 인간 항체 분자의 유전자와 결합시켜 "키메라 항체(chimeric antibodies)"를 생성하는 기술도 이용되고 있다(Morrison et al. 1984, Proc. Natl. Acad. Sci., 81:6851-6855; Neuberger et al. 1984 Nature 312:604-608; Takeda et al. 1985 Nature 31:452-454). 대안적인 방법으로 단일 사슬(single chain) 항체를 생성하기 위한 방법(미국특허 제4,946,778호)이 4-특이성 단일 사슬 항체에도 적용될 수 있다.

모노클론 항체의 재조합 인간 또는 인간화(humanized) 항체가 인간의 질병 치료에 바람직하게 사용될 수 있다. 인간화 항체는 하기 문헌에 기재된 절차에 따라 제조될 수 있다(e.g. Jones et al. 1986, Nature 321:522-25; Reichman et al. 1988 Nature 332:323-27; Verhoeyen et al. 1988, Science 239:1534-36). 인간화 모노클론 항체를 생성하기 위한 최근에 기술된 "유전자 전환 돌연변이(gene conversion metagenesis)" 법도 인간화 항체의 생성에 이용될 수 있다(Carter et al. 1992 Proc. Natl. Acad. Sci. U.S.A. 89:4285-89). 대안적인 방법으로 중(heavy) 영역과 경(light) 영역의 불규칙한 조합의 재조합 라이브러리를 제조하는 기술도 재조합 항체를 생산하는 데 이용될 수 있다(e.g. Huse et al. 1989 Science 246:1275-81).

Fu F(ab1) and F(ab2)과 같은 분자의 유전자형(idiotype)을 포함하는 항체 단편들도 공지의 방법으로 생산될 수 있다. 예를 들어 그러한 단편들로는 하기의 것들이 있으나 이에 한정되는 것은 아니다: 완전한 항체 분자의 펩신 분해에 의하여 생성된 F(ab) E2 단편; F(ab')2 단편의 이황화 결합을 환원함으로써 생성되는 Fab' 단편; 및 파파인과 환원제로 항체 분자를 처리하여 생성되는 두 개의 Fab 단편. 대안적인 방법으로, 단백질에 대한 바람직한 특이성으로 모노클론 Fab 단편을 빠르고 쉽게 동정하기 위하여 Fab 발현 라이브러리도 제조될 수 있다(Huse et al. 1989, Science 246:1275-1281).

애주번트

"애주번트(adjuvant)"는 백신 조성물의 면역원성과 효능을 증가시키는 하나 이상의 물질을 포함하는 조성물을 포함한다. 적당한 애주번트의 비제한적인 예로는 하기의 것들을 들 수 있다: 스쿠알란 및 스쿠알린(또는 다른 동물성 오일); 블록 코폴리머; TweenTM-80과 같은 세정제; QuilTM A, Drakeol 또는 Marcol과 같은 미네랄 오일, 땅콩유와 같은 식물성 오일; 코리네박테리아 파뮴과 같은 코리네박테리아 유래의 애주번트; 프로피오니박테리아 좌창(Propionibacterium acne)과 같은 프로피오니박테리아 유래의 애주번트; 미코박테리아 보비스(Mycobacterium bovis) (Bacillus Calmetic and Guerinn 또는 BCG); 인터루킨 2 및 인터루킨-12와 같은 인터루킨; 인터루킨 1과 같은 모노카인; 종양 괴사 인자(tumour necrosis factor); 감마 인터페론과 같은 인터페론; 사포닌-알루미늄 하이드록사이드 또는 Quil-A 알루미늄 하이드록사이드와 같은 조합물; 리포솜; ISCOM 애주번트; 미코박테리아 세포벽 추출물; 뮤라밀 디펩타이드 또는 다른 유도체와 같은 합성 글리코펩타이드; 에브리딘(Avridine); 지질(Lipid) A; 텍스트란 설페이트; 알루미늄 포스페이트를 가지는 DEAE-텍스트란 또는 DHAE-텍스트란; Carbopol' EMA와 같은 카르복시폴리메틸렌; Neocryl A640과 같은 아크릴 코폴리머 에멀전(e.g. 미국특허 제5,047,238호); 우두(vaccinia) 또는 동물성 포스바이러스(posvirus) 단백질; 콜레라 독소(toxin)과 같은 바이러스 아류(sub-viral) 입자 애주번트 또는 이들의 혼합물.

본 명세서에서 엄격한(stringent) 조건이란 (1) 세정(washing)액으로 낮은 이온 강도와 높은 온도, 예를 들어 50℃의 0.015 M NaCl/0.0015 M 시트르산 나트륨/0.1% NaDodSO₄를 사용하거나; (2) 포름아미드, 예를 들어 0.1% 소 태아 혈청 알부민, 0.1% 피콜(Ficoll), 0.1% 폴리비닐피롤리돈, 750 mM의 NaCl, 75 mM의 시트르산 나트륨을 함유하는 42℃에서 pH 6.5인 50 mM 인산나트륨 버퍼를 포함하는 50% (vol/vol)의 포름아미드와 같은 변성제를 이용하여 혼성화를 실시

하거나; (3) 50% 포름아미드, 5 x SSC (0.75 M NaCl, 0.075 M 소듐 시트레이트), 50 mM 소듐 포스페이트(pH 6.8), 0.1% 소듐 피로포스페이트, 5 x Denhardt's 용액, 초음파처리된 연어 정충(sperm) DNA (50 mg/ml), 0.1% SDS 및 0.2 x SSC와 0.1% SDS 내의 42℃의 10% 텍스트란 설페이트를 사용하는 것을 의미한다.

본 발명에는 DNA 백신화도 포함될 수 있다. DNA 백신화에 대해서는 Donnelly et al, Journal of Immunological Methods 176(1994) 145-152에 기재되어 있으며 본 명세서에 참고로 인용된다.

본 명세서에서 "포함한다(comprise 또는 comprising)"라는 의미는 명시된 구성요소 또는 구성요소의 그룹을 포함하는 것으로 이해되며, 다른 구성요소 또는 이들의 그룹을 배제하는 것은 아니다.

도면의 간단한 설명

도 1은 투여후 4일째(손상은 이 시점에서 최대 크기였음)의 실험 결과를 보인 것이다.

도 2는 재조합 단백질을 조합하여 이용한 개별적인 실험 결과를 보인 것이다.

실시예

시퀀싱하기 위한 *P. gingivalis* 라이브러리 제조

P. gingivalis 게놈 DNA의 DNA 서열을 결정하기 위하여 Mamur J. (J. Mol. Biol. **3**, 208-218, 1961)에 기재된 방법으로 *P. gingivalis* 균주 W50 (ATCC 53978)에서 분리하였다. DNA 단편의 클로닝은 Fleischmann *et al.*, (Science; **269**, 496-512, 1995)(2)에 기재된 방법으로 실시하였다. 간단히 설명하면, *P. gingivalis*의 정제된 게놈 DNA를 단편으로 만들고 Bal31 뉴클레아제로 처리하여 블런트(blunt) 말단을 만든 다음 1% 아가로스 겔에 두 번 걸었다. 1.6-2.0 kb의 DNA 단편은 겔에서 절제되어 회수되었다. 그런 다음 이 DNA를 벡터 pUC18 (*Sma*I로 절단되고 포스포릴화되지 않음 (dephosphorylated); Pharmacia)에 결합시키고 1% 아가로스 겔에서 전기영동하였다. 선형 벡터와 하나의 삽입물을 포함하는 상기 단편을 절제하고 정제하는 과정을 반복하여 삽입물이 없는 벡터가 감소되도록 하였다. 회수된 벡터와 삽입된 DNA를 T4 DNA 폴리머라제를 이용하여 블런트 말단이 되도록 하고, 환형 DNA가 형성되도록 최종 결합을 실시하였다. 에피쿠리안 콜리(Epicurian Coli)의 전기영동에 적합한(Electroporation-Competent) 세포(Stratagene)를 상기 결합된 DNA로 형질전환하고 X-gal을 포함하는 SOB 한천 항생제 분산 평판 상에 플레이트하고 37℃에서 하룻밤 동안 배양하였다. 삽입물을 포함하는 콜로니는 흰색으로 나타났으며, 삽입물이 없는 콜로니(벡터만)는 청색을 띠었다. 흰색 콜로니가 선정되어 시퀀싱하기 위한 플라스미드 DNA의 적출에 적합하도록 확장될 때까지 평판들을 4℃에서 저장하였다.

DNA 시퀀싱

96개의 깊은(deep) 웰 플레이트내에 50-100ug/ml의 앰피실린이 공급된 1.5ml의 LB, TB 또는 SOB 육즙내로 박테리아 콜로니를 선택함으로써 플라스미드 DNA를 제조하였다. 플라스미드 DNA를 QIAprep Spin 또는 QIAprep 96 Turbo 소형 키트(miniprep kits) (QIAGEN GmbH, Germany)를 사용하여 분리하였다. 96 웰의 그리드화된 배열내로 DNA를 용리하여 -20℃에 저장하였다.

M13 Universal 전방향 및 역방향 시퀀싱 프라이머를 이용하여 AmpliTaq DNA polymerase FS (PE Applied Biosystems, Foster City, CA)를 포함하는 ABI PRISM Dye Terminator 및 ABI PRISM BIGDye Terminator Cycle Sequencing Ready Reaction 키트를 사용하여 시퀀싱 반응을 실시하였다. Perkin-Elmer GeneAmp 9700 (PE Applied Biosystems) 또는 Hybaid PCR Express (Hybaid, UK) 열 순환기(thermal cycler)중 하나를 사용하여 시퀀싱 반응을 수행하였다. 시퀀싱 반응물을 ABI PRISM 377 DNA 서열분석기(sequencer; PE Applied Biosystems)를 이용하여 분석하였다.

얻어진 서열들은 하기에 기재되어 있다. 이들 서열들의 관계는 표 1에 기재되어 있다. 서열 상동성 배열법(FASTA), 신호 서열 예정법(signal sequence prediction; PSORT, SignalP) 또는 ORF 예정법(GeneMark)을 조합하여 개시 코돈을 산출하였다.

표 1: 선택된 단백질에 대한 각각의 서열 ID의 관계

단백질 이름	ORF의 DNA 서열	ORF의 아미노산 서열	단백질의 DNA 서열	단백질의 아미노산 서열
PG1	1	265	122	386
PG10	2	266	123	387
PG100	3	267	124	388
PG101	4	268		
PG102	5	269	125, 126	389, 390
PG104	6	270	127	391
PG105	7	271	128	392
PG106	8	272	129	393
PG107	9	273	130, 131, 132	394, 395, 396
PG108	10	274	133	397
PG109	11	275	134, 135	398, 399
PG11	12	276	136	400
PG110	13	277	137	401
PG111	14	278		
PG112	15	279	138, 139	402, 403
PG113	16	280	140	404
PG114	17	281	141	405
PG115	18	282	142	406
PG116	19	283	143	407
PG117	20	284	144	408
PG118	21	285	145	409
PG119	22	286	146	410
PG12	23	287	147	411
PG120	24	288	148	412

단백질 이름	ORF의 DNA 서열	ORF의 아미노산 서열	단백질의 DNA 서열	단백질의 아미노산 서열
PG121	25	289	149	413
PG122	26	290	150	414
PG123	27	291	151	415
PG124	28	292	152	416
PG125	29	293	153	417
PG126	30	294	154	418
PG13	31	295	155	419
PG14	32	296	156	420
PG15	33	297	157	421
PG16	34	298	158	422
PG18	35	299	159	423
PG2	36	300	160, 161	424, 425
PG21	37	301	162	426
PG22	38	302	163	427
PG23	39	303	164	428
PG24	40	304	165	429
PG25	41	305	166	430
PG27	42	306	167	431
PG28	43	307	168	432
PG29	44	308	169	433
PG3	45	309	170	434
PG30	46	310	171	435
PG31	47	311	172	436
PG32	48	312	173	437
PG33	49	313	174	438
PG34	50	314	175, 176	439, 440
PG35	51	315	177	441
PG36	52	316	178	442
PG37	53	317	179, 180	443, 444
PG38	54	318	181	445

단백질 이름	ORF의 DNA 서열	ORF의 아미노산 서열	단백질의 DNA 서열	단백질의 아미노산 서열
PG39	55	319	182	446
PG4	56	320	183	447
PG40	57	321	184	448
PG41	58	322	185	449
PG42	59	323	186	450
PG43	60	324	187	451
PG44	61	325	188	452
PG45	62	326	189	453
PG46	63	327	190	454
PG47	64	328	191	455
PG48	65	329	192	456
PG49	66	330	193	457
PG5	67	331	194	458
PG50	68	332	195	459
PG51	69	333	196	460
PG52	70	334	197	461
PG53	71	335	198	462
PG54	72	336	199	463
PG55	73	337	200	464
PG56	74	338	201, 202	465, 466
PG57	75	339	203, 204, 205	467, 468, 469
PG58	76	340	206, 207	470, 471
PG59	77	341	208, 209, 210	472, 473, 474
PG6	78	342	211	475
PG60	79	343	212	476
PG61	80	344	213	477
PG62	81	345	214	478
PG63	82	346	215	479
PG64	83	347	216	480
PG65	84	348	217	481

단백질 이름	ORF의 DNA 서열	ORF의 아미노산 서열	단백질의 DNA 서열	단백질의 아미노산 서열
PG66	85	349	218	482
PG67	86	350	219	483
PG68	87	351	220, 221	484, 485
PG69	88	352	222	486
PG7	89	353	223	487
PG70	90	354	224	488
PG71	91	355	225	489
PG72	92	356	226	490
PG73	93	357	227	491
PG74	94	358	228	492
PG75	95	359	229	493
PG76	96	360	230	494
PG77	97	361	231	495
PG78	98	362	232	496
PG79	99	363	233	497
PG8	100	364	234, 235, 236, 237	498, 499, 500, 501
PG80	101	365	238	502
PG81	102	366	102	366
PG82	103	367	239	503
PG83	104	368	240	504
PG84	105	369	241, 242	505, 506
PG85	106	370	243	507
PG86	107	371	244, 245	508, 509
PG87	108	372	246	510
PG88	109	373	247, 248, 249	511, 512, 513
PG89	110	374	250	514
PG9	111	375	251, 252, 253	515, 516, 517
PG90	112	376	254, 255	518, 519
PG91	113	377	256	520

단백질 이름	ORF의 DNA 서열	ORF의 아미노산 서열	단백질의 DNA 서열	단백질의 아미노산 서열
PG92	114	378	257	521
PG93	115	379	258	522
PG94	116	380	259	523
PG95	117	381	260	524
PG96	118	382	261	525
PG97	119	383	262	526
PG98	120	384	263	527
PG99	121	385	264	528
PG127	529	531	530	532

DNA 서열 분석

FASTA 포맷(format)의 DNA 파일을 GCG 포맷으로 변환하고 데이터베이스에 넣었다. DNA 파일을 ANGIS(Australian Genomic Information Service, University of Sydney, Australia)로부터 구입한 프로그램 Flip을 이용하여 아미노산 파일로 번역하였다. 단백질에 대하여 일련의 생명정보과학적 분석을 행하여 가능한 백신 후보인자를 선택하였다. 사용된 프로그램은 FASTA 동족체 검색(searching) (1), PSORT (2,3), SignalP (4), TopPred (5), 및 GeneMark (6)이다. 상기 단백질 및 그것들의 생명정보과학적 결과들을 원하는 특성을 가지는 단백질을 검색하고 회수하기 위한 관례적인 서면(written) 데이터베이스에 저장하였다.

이들 단백질에 대한 FASTA 상동성 결과를 표면 위치 또는 백신 효과를 제시하는 단백질과 함께 나열하여 검사하였다. FASTA 알고리즘을 이용한 ANGIS에 의하여 수집된 비중첩성 박테리아 단백질 데이터베이스에 대한 상동성을 알아보기 위하여 모든 단백질을 조사하였다. FASTA 검색에 사용되는 고정값들(settings)은 Ktup = 2, 갭 형성 페널티(penalty) =

-12, 갭 신장 패널티 = -2, 선택 유도배열(deriving alignment in opt)에서의 너비 = 16 및 Blosum 50 스코어링(scoring) 매트릭스이었다. 통계학적 확률과 아미노산 배열에 의하여 상당한 상동성을 알아보기 위하여 개개의 FASTA 검색 결과를 조사하였다. 결과는 표 2에 기재되어 있다.

그런 다음 단백질 트리밍(trimming) 프로그램(ANGIS)을 사용하여 첫째, 둘째, 셋째, 넷째, 및 다섯째 메치오닌 잔기로 단백질 파일들을 정리하였다. 그런 다음 정리된 단백질을 PSORT 분석하여 신호 서열을 검출하고, 세포 위치를 예측하였다. >0.8의 외부막의 PSORT 확률을 보이는 단백질은 표면에 위치하는 것으로 간주되었다. 2차 신호 서열 검출 프로그램인 SignalP도 수행되어 PSORT로 인식되지 않았던 신호를 검출하였다. 다른 방법들에 의하여 인식된 모든 단백질도 PSORT 및 SignalP에 의하여 분석되었다. 이전에는, 박테리아 외막의 C-말단 아미노산이 외막에서의 단백질의 어셈블리에 중요한 것으로 알려져 있었다(7). 외막 단백질의 일반적인 구조의 정의는 N-말단에서의 신호 서열 및 C-말단의 티로신 또는 페닐알라닌의 존재로서 결정되었다. 많은 선택된 단백질은 이러한 특징적인 구조를 나타내었다. 막에 걸려있는 도메인(MSD)의 위치와 수를 결정하기 위하여 TopPred 프로그램이 사용되었고 그러한 서열의 존재는 외막과 같은 막에 우선적으로 부착된다는 것을 나타낸다. 선택된 단백질의 C-말단 아미노산으로 PSORT, SignalP 및 TopPred 분석 결과는 표 3에 기재되어 있다.

많은 *P. gingivalis* 외막 단백질의 C-말단으로부터 70개의 아미노산이 50-100%의 단백질 서열 동일성을 공유하였다. 이들 단백질은 RGP1, RGP2, KGP, HagA, HagC, HagD, prtH 및 prtT를 포함한다. 이들 공통적인 모티브는 외막에 대한 단백질의 부착 또는 이동(sorting)에 관여할 수 있다. 기재된 단백질 데이터는 상기 기재된 바와 같이 FASTA 상동성을 이용하여 조사되었고 C-말단에서 유사한 모티브를 나타내는 다수의 신규의 단백질이 동정되었다. 이 결과는 표 4에 기재되어 있다.

TonBIII 박스는 광범위한 박테리아에서 TonB 외막 수용체내에 존재하는 30개 아미노산 모티브이다. *P. gingivalis*의 TonBIII(8)는 상기 기재된 FASTA에 의한 상동성에 대한 단백질 데이터 세트를 검색하는 데 사용되었다. 상당한 상동성을 보이는 이들 단백질은 표 5에 나열되어 있다.

표2 : 비만복성(non-redundant)단백질 데이터베이스에 대한 ORF의 FASTA단백질 상동성 결과

단백질 이름	상동성	진뱅크 수탁번호	상동체의 길이	단백질 P. gingivalis 의 길이	상동성 결과		
					동일성(%)	중첩	E 수치
PG1	48kD outer membrane protein, <i>Actinobacillus pleuropneumoniae</i>	U24492	449aa	451aa	32	454aa	1.40E-42
PG2	Outer membrane protein (usc), <i>Bacteroides thetaiotaomicron</i>	L49338	1038aa	1017aa, 1014aa	28	1089aa	4.60E-32
PG3	Outer membrane porin F adhesin, <i>Pseudomonas fluorescens</i>	U19743	317aa	223aa	35	167aa	1.10E-10
PG4	Outer membrane protein A, <i>Escherichia fergusonii</i>	M69352	243aa	672aa	48	88aa	4.10E-10
PG5	Adhesin protein (AdcA), <i>Streptococcus pneumoniae</i>	Z71552	423aa	315aa	25	279aa	8.40E-15
PG6	Hemolysin A (phxA), <i>Prevotella melanogenica</i>	U27587	332aa	324aa	60	308aa	3.00E-74
PG7	Hemolysin (IVC), <i>Serpulina lyodysenteriae</i>	X73141	208aa	404aa	33	268aa	1.40E-24
PG8	Heme uptake protein A, <i>Bacteriodes fragilis</i>	X97122	431aa	588aa, 550aa, 458aa	79	417aa	6.70E-121
PG9	Internalin A (inlA), <i>Lysisteria monocytogenes</i>	M67471	744aa	1266aa, 1232aa, 1174aa	38	340aa	7.30E-23

단백질 이름	상동성	진행크 수탁번호	상동체의 길이	단백질 P. gingivalis 의 길이	상동성 결과		
					동일성(%)	중첩	E 수치
PG10	Macrophage infectivity potentiator (MIP), Legionella oakridgensis.	U92214	234aa	185aa	50	201aa	4.70E-31
PG11	Haemagglutinin (pga), Prevotella intermedia.	AF017417	309aa	313aa	44	309aa	3.60E-44
PG12	Outer membrane lipoprotein, Haemophilus influenzae	M68502	274aa	271aa	36	254aa	9.80E-27
PG13	FerriC receptor (cfrA), Campylobacter coli	U80812	666aa	757aa	24	625aa	1.20E-18
PG14	36kD antigen, Helicobacter pylori	U86610	329aa	331aa	37	326aa	1.10E-35
PG15	Outer membrane protein, Erwinia amylovora	X77921	377aa	267aa	30	253aa	5.40E-08
PG16	C terminal protease, Bartonella bacilliformis	L37094	434aa	569aa	36	357aa	3.00E-35
PG18	Protein-export membrane protein (secD), Helicobacter pylori	AB000652	503aa	961aa	32	611aa	1.10E-36
PG21	Surface antigen gene, Methanosaarchae mazet	X84710	783aa	621aa	37	331aa	6.20E-33
PG22	Alpha-hemolysin gene, Aeromonas hydrophila	L36462	65aa	106aa	57	67aa	2.60E-14
PG23	cfpA/cpB protease, Bacillus subtilis	D26185	810aa	859aa	45	655aa	7.10E-122
PG24	Putative hemolysin, Streptococcus mutans	AF051356	445aa	417aa	29	432aa	1.80E-29

단백질 이름	상동성	진뱅크 수탁번호	상동체의 길이	단백질 P. gingivialis 의 길이	상동성 결과		
					동일성(%)	중첩	E 수치
PG25	Cysteine protease, <i>Porphyromonas gingivialis</i>	U54891	1723aa	293aa	42	142aa	1.10E-12
PG27	TonB linked adhesin, <i>Porphyromonas gingivialis</i>	Y07818	1092aa	312aa	45	360aa	3.20E-41
PG28	Cysteine protease / hemagglutinin, <i>Porphyromonas gingivialis</i>	S75942	886aa	643aa	35	838aa	7.00E-90
PG30	Putative NIPD lipoprotein, <i>Aquifex aeolicus</i>	AB000754	187aa	337aa	42	142aa	1.80E-12
PG31	Hemolysin (llyc), <i>Serpulina lyodysenteriae</i>	X73141	141aa	151aa	31	123aa	1.80E-07
PG32	Major outer membrane protein (oprF), <i>Pseudomonas aeruginosa</i>	M94078	350aa	391aa	26	382aa	3.40E-07
PG33	Major outer membrane protein (oprF), <i>Pseudomonas fluorescens</i>	L21200	317aa	385aa	32	163aa	2.30E-06
PG34	Putative membrane protein, <i>Rhodobacter capsulatus</i>	Q07396	193aa	190aa	46	190aa	2.20E-36
PG35	Colicin 1 receptor, <i>Escherichia coli</i>	U04229	663aa	833aa	25	590aa	2.40E-10
PG36	Outer membrane antigen (omaB7), <i>Pasteurella multocida</i>	U80439	789aa	891aa	21	694aa	3.70E-10
PG37	Cationic outer membrane protein (ompH), <i>Yersinia enterocolitica</i>	M34854	104aa	174aa, 170aa	27	168aa	4.30E-07

단백질 이름	상동성	진행크 수탁번호	상동체의 길이	단백질 P. gingivalis 의 길이	상동성 결과		
					동일성(%)	중첩	E 수치
PG38	Cationic outer membrane protein (ompH), <i>Yersinia enterocolitica</i>	M34854	164aa	163aa	23	160aa	5.90E-05
PG39	Outer membrane protein (ompC) <i>Bacteroides thetaiotaomicron</i>	LA8338	1038aa	827aa	24	347aa	1.50E-08
PG40	Heme receptor (Hut A), <i>Vibrio cholera</i>	Q56644	683aa	772aa	23	722aa	4.90E-09
PG41	Outer membrane protein (olp), <i>Escherichia coli</i>	X54049	485aa	482aa	22	438aa	4.60E-09
PG42	Neuraminidase, <i>Micromonospora viridifaciens</i>	D01045	847aa	492aa	32	375aa	2.10E-22
PG43	Immunoreactive outer membrane protein (omp28), <i>Brucella melitensis</i>	U30815	250aa	245aa	24	178aa	0.0015
PG44	Macrophage infectivity potentiator, <i>Legionella israelensis</i>	U92208	242aa	276aa	35	219aa	9.10E-18
PG45	Outer membrane protein, <i>Neisseria meningitidis</i>	AF021245	797aa	775aa	21	699aa	0.0034
PG46	Outer membrane protein 85, <i>Neisseria gonorrhoeae</i>	UB1989	732aa	774aa	31	117aa	0.00098
PG47	Outer membrane protein (ompC) <i>Bacteroides thetaiotaomicron</i>	LA8338	1038aa	867aa	20	962aa	1.00E-03

단백질 이름	상동성	진뱅크 수탁번호	상동체의 길이	단백질 P. gingivitis 의 길이	상동성 결과		
					동일성(%)	중첩	E 수치
PG46	Immunoglobulin binding surface protein (sir22), Streptococcus pyogenes	X75750	365aa	431aa	25	269aa	5.20E-05
PG49	Fimbriin (orf2), Porphyromonas gingivalis	D42067	453aa	333aa	23	296aa	0.062
PG50	Outer membrane protein (usc) Bacteroides theletaeomicron	L49338	1038aa	848aa	26	579aa	1.60E-11
PG51	PGA antigen, Porphyromonas gingivalis	X65038	202aa	202aa	54	126aa	1.20E-25
PG52	Alkaline protease secretion apparatus (aprt) Pseudomonas aeruginosa	X64558	481aa	455aa	21	427aa	3.50E-06
PG53	Protein export protein (tolC), Salmonella enteritidis Pseudomonas aeruginosa	U25178	491aa	444aa	23	438aa	6.20E-11
PG54	Protease I, Acinetobacter ltyicus	I5128	653aa	940aa	24	695aa	1.50E-22
PG55	Fimbriin (orf3), Porphyromonas gingivalis	D42067	670aa	670aa	43	688aa	4.90E-106
PG56	Cysteine protease Porphyromonas gingivalis	U68468	364aa	1282aa, 1274aa	25	212aa	0.00012
PG57	Cysteine protease, Porphyromonas gingivalis	U68468	1358aa	924aa, 922aa, 921aa	31	742aa	1.40E-23
PG60	Outer membrane protein 11, Helicobacter pylori	AB000562	186aa	547aa	25	183aa	2.20E+00
PG61	Ferric pseudobactin M114 receptor protein (pbuA), Pseudomonas sp.	X73412	826aa	749aa	22	565aa	1.00E-05

단백질 이름	상동성	진뱅크 수탁번호	상동체의 길이	단백질 P. gingivalis 의 길이	상동성 결과		
					동일성(%)	중첩	E 수치
PG66	Attachment and invasion protein (ail), <i>Salmonella typhimurium</i>	AF007380	165aa	206aa	21	140aa	1.90E+00
PG68	Serum opacity factor, <i>Streptococcus pyogenes</i>	U02290	1025aa	1225aa, 1224aa	24	176aa	2.10E-01
PG69	Vacuolating cytotoxin (vacA), <i>Helicobacter pylori</i>	U83261	160aa	425aa	32	111aa	1.20E+00
PG70	Outer membrane protein, <i>Neisseria gonorrhoea</i>	U52069	174aa	268aa	22	153aa	6.90E+00
PG71	Gliding motility protein (gldA), <i>Flavobacterium johnsoniae</i>	AF007381	578aa	834aa	23	572aa	3.90E-25
PG75	Class 3 outer membrane porin (porB), <i>Neisseria meningitidis</i>	U07191	332aa	391aa	23	239aa	4.60E-01
PG81	Outer membrane protein (ompA), <i>Shigella dysenteriae</i>	V01344	351aa	>235aa	26	166aa	3.10E-01
PG82	Outer membrane protein (alkL), <i>Pseudomonas oleovorans</i>	X65836	230aa	434aa	26	136aa	2.80E+00
PG83	Gliding motility protein (gldA), <i>Flavobacterium johnsoniae</i>	AF007381	578aa	926aa	21	639aa	8.50E-09
PG87	Hypothetical protein, <i>Mycobacterium tuberculosis</i>	AI021942	877aa	781aa	29	794aa	2.20E-34

단백질 이름	상동성	진뱅크 수탁번호	상동체의 길이	단백질 P. gingivalis 의 길이	상동성 결과		
					동일성(%)	중첩	E 수치
PG69	NADH-ubiquinone oxidoreductase, Helicobacter pylori	AE000631	512aa	259aa	24	166aa	3.90E-01
PG91	Neuraminidase (nanH), Bacteroides fragilis	D28483	544aa	540aa	24	251aa	1.60E+00
PG92	Hypothetical protein, Mycobacterium tuberculosis	AL021942	877aa	771aa	29	770aa	8.00E-30
PG93	Cytochrome protein P1, Mycoplasma pneumoniae	X07191	219aa	778aa	41	63aa	6.90E-01
PG94	Arginyl endopeptidase, Porphyromonas gingivalis	D28470	991aa	1157aa	24	328aa	7.60E-08
PG95	Sensor protein (EVGS), Escherichia coli	D14008	1197aa	961aa	28	511aa	2.60E-17
PG105	Plasma cell membrane glycoprotein, Human	P22413	873aa	448aa	34	404aa	5.60E-33
PG106	Hypothetical secreted protein, Helicobacter pylori	OZ4951	242aa	248aa	30	252aa	7.60E-22
PG107	Cell division ATP binding protein, Mycobacterium leprae	OS2883	228aa	246aa, 241aa, 232aa	46	193aa	1.20E-26
PG108	ABC transporter, Archaeoglobus fulgidis	OZ9244	228aa	218aa	51	219aa	3.80E-41
PG109	Proteinase IV, Escherichia coli	F84936	618aa	585aa, 589aa	38	597aa	1.10E-57
PG110	Peptidase translocase, Staphylococcus aureus	O06446	843aa	523aa	43	521aa	8.00E-71
PG111	ABC transporter, Streptococcus sp.	P73758	574aa	>720aa	40	579aa	1.70E-73
PG112	Glycoseyl transferase, Erwina amylovora	Q46834	351aa	375aa, 362aa	31	363aa	1.60E-32

단백질 이름	상동성	진뱅크 수탁번호	상동체의 길이	단백질 P. gingivialis 의 길이	상동성 결과		
					동일성(%)	중첩	E 수치
PG113	Heat shock protein (dnaK), <i>Tetrahymena pallidum</i>	ABE01203	635aa	640aa	62	644aa	9.10E-138
PG114	Dihydropyranide dehydrogenase, <i>Clostridium magnum</i>	Q59289	578aa	449aa	37	450aa	3.80E-54
PG115	Zinc protease, <i>Escherichia coli</i>	P31828	931aa	941aa	27	980aa	6.60E-57
PG116	Heat shock protein (HSPG), <i>Escherichia coli</i>	P10413	824aa	684aa	32	827aa	4.60E-48
PG117	Transcriptional regulator, <i>Aerifex aerifex</i>	O68591	506aa	464aa	39	389aa	2.40E-49
PG118	ABC transporter, <i>Bacillus subtilis</i>	H70019	281aa	250aa	59	251aa	1.50E-60
PG119	ATP-dependent protease, <i>Aerifex aerifex</i>	O68827	444aa	461aa	46	458aa	1.60E-77
PG120	Nitrogen assimilation regulatory protein, <i>Bradyrhizobium sp.</i>	P10576	480aa	457aa	49	242aa	3.80E-45
PG121	Cobalamin synthesis protein, <i>Bacillus megaterium</i>	E1331323	367aa	602aa	36	324aa	8.20E-37
PG122	Outer membrane integrity (ola), <i>Haemophilus influenzae</i>	P71397	819aa	443aa	37	441aa	1.90E-54
PG123	Fimbriin, <i>Porphyromonas gingivialis</i>	D1034032	480aa	478aa	32	480aa	7.30E-48
PG124	Heat shock protein (dnaJ), <i>Leptospira interrogans</i>	AF007813	369aa	383aa	46	356aa	2.30E-57

단백질 이름	상동성	진뱅크 수탁번호	상동체의 길이	단백질 P. gingivalis 의 길이	상동성 결과		
					동일성 (%)	중첩	E 수치
PG125	Cobalamin biosynthesis protein(CBIK), <i>Salmonella typhimurium</i>	Q08592	264aa	293aa	37	259aa	3.70E-26
PG126	ABC-type permease, <i>Pseudomonas aeruginosa</i>	O08878	326aa	356aa	33	333aa	1.30E-30
PG127	Endonuclease excision repair protein (uvrB), <i>Pseudomonas aeruginosa</i>	X93486	670aa	676aa	50	675aa	1.10E-134

표3 : 단백질의 PSORT, Signalp 및 TopPred 분석결과

신호(signal) 존재 결과는 PSORT 또는 Signalp 중 하나에 의해 검출된 신호 서열이 존재함을 의미한다. 괄호안의 용어는 SPORT에 의해 결정된 신호서열의 형태를 나타낸다. 세포위치와 확률 수치는 PSORT로 얻은 것이며 외막(OM), 내막(IM), 주변공간(periplasmic space:PS) 또는 세포질(C) 세포구획에 단백질이 존재할 가능성을 나타낸다. 막통과 도메인(TMD)의 수는 TopPred에 의해 결정되었으며 분해되지 않는 신호서열을 포함하지 않는다.

단백질 이름	단백질 seq ID 번호	단백질 길이	신호서열 존재여부	ORF 내의 메치오닌	SignalP 분해 자리	PSORT 분해 자리	세포위치 및 확률수치				C-말단 아미노산	TMD의 수
							OM	IM	PS	C		
PG1	386	451aa	Y	1	24	34	0	0	0	0.22	N	0
PG2	424	1017aa	Y	1	20	20	0.94	0	0.33	0	F	3
PG2	425	1014aa	Y	2	17	17	0.94	0	0.29	0	F	3
PG3	434	1239aa	Y (인포프로테인)	1	-	18	0.79	0.76	0	0	K	3
PG4	447	972aa	Y (인포프로테인)	1	22	22	0.79	0.7	0	0	R	0
PG5	458	315aa	Y	1	40	35	0	0.25	0	0	R	0
PG6	475	324aa	N	1	-	-	0	0	0	0.2	S	1
PG7	487	404aa	N	1	7	-	0	0.42	0	0	E	3
PG8	498	598aa	N	1	-	-	0	0	0	0.22	N	0
PG8	499	550aa	N	2	-	-	0	0	0	0.25	N	0

단백질 이름	단백질 seq ID 번호	단백질 길이	신호서열 존재여부	ORF 내의 메치오닌	SignalP 문해 자리	PSORT 문해 자리	세포위치 및 확률수치				C-말단 아마노산	TMD의 수
							OM	IM	PS	C		
PC8	500	458aa	N	3	-	-	0	0	0	0.34	N	0
PC8	501	426aa	N	4	-	-	0	0	0	0.24	N	0
PC9	515	1266aa	N	1	7	-	0	0	0	0.22	E	1
PC9	516	1232aa	N	2	-	-	0	0	0	0.39	E	1
PC9	517	1174aa	N	3	-	-	0	0	0	0.47	E	1
PC10	387	105aa	N	1	-	-	0	0	0	0.11	K	0
PC11	400	313aa	Y	1	22	28	0.24	0	0.93	0	R	1
PC12	411	271aa	Y (리포프로틴인)	3	27	29	0.79	0.7	0	0	R	0
PC13	419	752aa	Y	1	23	25	0.94	0	0.29	0	N	0
PC14	420	331aa	Y (분해불가)	1	35	28	0	0.58	0	0	K	1
PC15	421	287aa	Y	2	24	18	0	0.11	0	0	K	1
PC16	422	569aa	Y (리포프로틴인)	1	24	18	0.79	0.7	0	0	G	0
PC18	423	981aa	Y	1	30	-	0	0.56	0	0	K	11
PC21	426	821aa	Y	2	24	27	0.34	0	0.37	0	G	1
PC22	427	106aa	Y	1	41	41	0	0.29	0	0	P	0
PC23	428	859aa	N (분해불가)	1	-	-	0	0.12	0	0	A	1

단백질 이름	단백질 seq ID 번호	단백질 길이	신호서열 존재여부	ORF 내의 메치오닌	SignalF 분해 지리	PSORT 분해 지리	세포위치 및 핵률수치				C-말단 아미노산	TMD의 수
							OM	IM	PS	C		
PG24	429	417aa	Y	1	19	19	0	0.44	0	0	N	3
PG25	430	293aa	Y	1	27	28	0.2	0	0.02	0	R	0
PG27	431	312aa	N	1	-	-	0	0	0	0.28	Q	1
PG28	432	843aa	Y	1	21	21	0.03	0	0.24	0	H	1
PG29	433	290aa	Y	1	18	16	0.28	0	0.94	0	K	1
PG30	435	327aa	Y	1	21	21	0.24	0	0.4	0	K	0
PG31	436	151aa	N	1	-	-	0	0	0	0.3	T	0
PG32	437	391aa	Y	1	20	20	0.02	0	0.13	0	K	0
PG33	438	385aa	Y	1	26	26	0.01	0	0.31	0	E	1
PG34	439	190aa	Y	1	-	13	0	0.5	0	0	A	5
PG34	440	188aa	Y (분해불가)	2	-	47	0	0.5	0	0	A	4
PG35	441	823aa	Y	1	22	22	0.94	0	0.37	0	F	1
PG36	442	891aa	Y (분해불가)	1	-	40	0	0.31	0	0	F	2
PG37	443	174aa	Y (분해불가)	1	28	24	0	0.35	0	0	K	0

단백질 이름	단백질 seq ID 번호	단백질 길이	신호서열 존재여부	ORF 내의 메치오닌	SignalP 분해 치리	PSORT 분해 치리	세포위치 및 핵률수치				C-말단 아미노산	TMD의 수
							OM	IM	PS	C		
PG37	444	170aa	Y (분해불가)	2	24	20	0	0.35	0	0	K	0
PG38	445	163aa	Y	1	18	18	0.21	0	0.93	0	K	1
PG39	446	827aa	Y	1	36	36	0.93	0	0.25	0	P	3
PG40	448	772aa	Y	2	19	19	0.94	0	0.32	0	F	4
PG41	449	462aa	Y	2	27	27	0.25	0	0.54	0	Q	2
PG42	450	492aa	Y	5	30	-	0	0	0.00	0.13	Q	2
PG43	451	245aa	Y (분해불가)	2	28	22	0	0.38	0	0	K	1
PG44	452	276aa	Y	1	19	24	0.15	0	0.89	0	K	0
PG45	453	775aa	Y (리포포문타인)	1	19	23	0.79	0.7	0	0	P	4
PG46	454	774aa	Y	1	27	27	0.73	0	0.22	0	P	2
PG47	455	867aa	Y	1	24	24	0.94	0	0.38	0	P	2
PG48	456	431aa	Y	1	24	24	0	0.1	0	0	R	1
PG49	457	333aa	Y (분해불가)	1	24	18	0	0.12	0	0	I	0
PG50	459	848aa	Y	1	21	21	0.94	0	0.34	0	F	3
PG51	460	202aa	Y	1	26	25	0.2	0	0.61	0	S	0
PG52	461	455aa	Y (분해불가)	1	23	21	0	0.18	0	0	P	1

단백질 이름	단백질 seq ID 번호	단백질 길이	신호서열 존재 여부	ORF 내의 메치오닌	SignalP 분해 자리	PSORT 분해 자리	OM				세포위치 및 확률수치	C-말단 아미노산	TM/D의 수
							OM	M	PS	C			
PG53	462	444aa	Y	1	14	17	0.36	0	0.22	0	D		2
PG54	463	940aa	Y	1	27	20	0.86	0	0.25	0	Q		5
PG55	464	670aa	Y (인포프로테인)	1	23	23	0.79	0.7	0	0	K		2
PG56	465	1282aa	Y (분해불가)	1	-	21	0	0.04	0	0	K		4
PG56	466	1274aa	N	2	-	-	0	0	0	0.27	K		5
PG57	467	925aa	Y	1	28	24	0.53	0	0.2	0	P		3
PG57	468	922aa	Y	2	25	21	0.53	0	0.2	0	P		3
PG57	469	921aa	Y	3	24	20	0.53	0	0.2	0	P		3
PG58	470	593aa	Y	1	24	24	0.82	0	0.19	0	F		1
PG58	471	589aa	Y	2	20	20	0.82	0	0.19	0	F		1
PG59	472	348aa	Y	1	37	-	0	0.18	0	0	P		1
PG59	473	345aa	Y	2	36	56	0.92	0	0.15	0	F		1
PG59	474	330aa	Y	3	21	41	0.93	0	0.25	0	P		1
PG60	476	547aa	Y	1	28	28	0.93	0	0.25	0	F		0
PG61	477	749aa	Y	2	21	21	0.94	0	0.29	0	F		3
PG62	478	494aa	Y	1	21	21	0.93	0	0.24	0	P		2

단백질 이름	단백질 seq ID 번호	단백질 길이	신호서열 존재여부	ORF 내의 메치오닌	SignalP 분해 자리	PSORT				세포위치 및 핵률수치	C-말단 아미노산	TMD의 수
						OM	IM	PS	C			
PG3	479	294aa	Y	1	20	20	0.93	0	0.24	0	F	1
PG4	480	204aa	Y	1	20	20	0.93	0	0.19	0	F	1
PG5	481	243aa	Y	1	18	18	0.93	0	0.25	0	F	1
PG6	482	208aa	Y	1	21	21	0.94	0	0.3	0	F	1
PG7	483	950aa	Y	1	28	36	0.93	0	0.27	0	Y	4
PG8	484	1228aa	Y	1	25	25	0.91	0	0.31	0	Y	0
PG8	485	1225aa	Y	2	24	24	0.91	0	0.31	0	Y	0
PG9	486	425aa	Y	1	29	29	0.93	0	0.21	0	F	1
PG10	488	260aa	Y	1	18	24	0.93	0	0.24	0	F	0
PG11	489	834aa	Y	2	20	20	0.94	0	0.31	0	N	2
PG12	490	989aa	Y	1	27	27	0.94	0	0.32	0	H	2
PG13	491	382aa	Y	2	20	20	0.94	0	0.3	0	L	1
PG14	492	222aa	Y	1	24	24	0.94	0	0.32	0	L	0
PG15	493	391aa	Y	1	26	26	0.94	0	0.3	0	H	1
PG16	494	446aa	Y	1	21	22	0.94	0	0.32	0	V	3
PG17	495	308aa	Y	2	28	28	0.94	0	0.38	0	K	0

단백질 이름	단백질 seq ID 번호	단백질 길이	신호서열 존재여부	ORF 내의 메치오닌	SignalP 분해 자리	PSORT 분해 자리	세로위치 및 핵률수치				C-말단 아미노산	TMD의 수
							OM	IM	PS	C		
PC78	496	314aa	Y	1	23	23	0.94	0	0.29	0	D	0
PC79	497	285aa	Y	1	-	32	0.93	0	0.26	0	G	2
PC80	502	240aa	Y	1	19	19	0.93	0	0.22	0	N	2
PC81	366	>235aa	Y	1	28	20	0.93	0	0.21	0	Q	1
PC82	503	434aa	Y	1	30	24	0.93	0	0.2	0	N	3
PC83	504	928aa	Y	1	23	57	0.93	0	0.21	0	S	1
PC84	505	400aa	Y	1	25	25	0.93	0	0.25	0	N	1
PC84	506	386aa	Y	2	23	23	0.93	0	0.25	0	N	1
PC85	507	581aa	Y	1	20	20	0.93	0	0.46	0	L	2
PC86	508	238aa	Y	1	44	-	0	0	0	0.12	H	0
PC86	509	211aa	Y	2	16	46	0.91	0	0.03	0	H	0
PC87	510	281aa	Y	1	28	47	0.89	0	0.21	0	N	2
PC88	511	271aa	Y	2	28	19	0.89	0	0.25	0	P	0
PC88	512	270aa	Y	3	27	18	0.89	0	0.25	0	P	0
PC88	513	287aa	Y	4	24	18	0.89	0	0.23	0	P	0
PC89	514	259aa	Y	2	23	25	0.88	0	0.25	0	N	1

단백질 이름	단백질 seq ID 번호	단백질 길이	신호서열 존재여부	ORF 내의 메치오닌	SignalF 분해 자리	PSORT 분해 자리	세포위치 및 핵물수치				C-말단 아미노산	TMD의 수	
							OM	IM	PS	C			
PC90	518	228aa	Y	1	22	21	0.85	0	0.44	0	K	0	
PC90	519	228aa	Y	2	21	20	0.85	0	0.44	0	K	0	
PC91	520	540aa	Y	1	25	25	0.85	0	0.20	0	E	0	
PC92	521	771aa	Y	2	19	19	0.85	0	0.3	0	R	3	
PC93	522	770aa	Y	1	25	25	0.85	0	0.37	0	R	4	
PC94	523	1157aa	Y	1	23	28	0.8	0	0.25	0	Q	5	
PC95	524	951aa	Y (리포프로틴인)	1		19	0.79	0.87	0	0	V	1	
PC96	525	569aa	Y	1	23	23	0.40	0	0.83	0	K	0	
PC97	526	437aa	Y	1	22	23	0.92	0	0.65	0	Q	0	
PC98	527	318aa	Y (리포프로틴인)	1	19	19	0.79	0.7	0	0	L	1	
PC99	528	461aa	Y (분해불가)	1	22	20	0	0	0.3	0	R	0	
PC100	388	279aa	Y	1	20	18	0.26	0	0.54	0	I	0	
PC101	288	>157aa	N (불인전환 ORF)		-	-					R	1	
PC102	388	562aa	Y	1	29	29	0.19	0	0.4	0	S	3	
PC102	390	558aa	Y	2	25	25	0.26	0	0.46	0	S	3	
PC104	391	381aa	Y	1	17	17	0.62	0	0.22		R	0	

단백질 이름	단백질 seq ID 번호	단백질 길이	신호서열 존재여부	ORF 내의 메치오닌	SignalP 분석 자리	PSORT 분석 자리	세포위치 및 확률수치					C-말단 아미노산	TMD의 수
							OM	IM	PS	C			
PG106	392	449aa	Y	1	22	19	0.31	0	0.91	0	P	3	
PG106	393	246aa	Y	2	41	49	0	0	0	0.02	L	0	
PG107	394	246aa	N	1	-	-	0	0	0	0.32	D	1	
PG107	395	241aa	N	2	-	-	0	0	0	0.3	D	1	
PG107	396	232aa	N	3	-	-	0	0	0	0.21	D	1	
PG108	397	219aa	N	1	-	-	0	0	0	0.19	R	1	
PG108	398	505aa	Y	1	35	37	0.26	0	0.93	0	Y	3	
PG109	399	589aa	Y	2	29	31	0.27	0	0.93	0	Y	3	
PG110	401	>523aa	N	1	-	-	0	0	0	0.38	incomplete	0	
PG111	278	>720aa	N (불완전한 ORF)		-	-	-	-	-	-	G	1	
PG112	402	375aa	Y	1	-	43	0	0.12	0	0	N	1	
PG112	403	362aa	Y	2	-	30	0	0	0.12	0	N	1	
PG113	404	640aa	N	1	-	-	0	0	0	0.25	K	1	
PG114	405	449aa	N	1	-	-	0	0.12	0	0	G	4	
PG115	406	941aa	Y	1	23	22	0.13	0	0.92	0	Q	2	
PG116	407	884aa	N	1	-	-	0	0.12	0	0	L	2	

단백질 이름	단백질 seq ID 번호	단백질 길이	신호서열 존재여부	ORF 내의 메치오닌	SignalP 분해 자리	PSORT 분해 자리	세포위치 및 확률수치				C-말단 아미노산	TMD의 수
							OM	IM	PS	C		
PG17	408	464aa	N	1	-	-	0	0.19	0	0	L	1
PG18	409	250aa	N	1	-	-	0	0	0	0.27	E	1
PG19	410	461aa	N	1	-	-	0	0.28	0	0	E	2
PG20	412	457aa	N	1	-	-	0	0	0	0.21	E	0
PG21	413	902aa	N	1	-	-	0	0	0	0.31	E	3
PG22	414	443aa	N	1	-	-	0	0	0	0.14	Q	4
PG23	415	479aa	Y	2	22	22	0.26	0	0.84	0	K	0
PG24	416	383aa	N	1	-	-	0	0	0	0.29	D	2
PG25	417	283aa	Y	1	23	15	0.18	0	0.83	0	R	1
PG26	418	356aa	N	1	-	-	0	0.52	0	0	D	9
PG27	592	978aa	N	1	-	-	0	0	0	0.28	A	2

표 4: *P. gingivalis* 아지닌 프로테아제 1 (RGP1), 아지닌 프로테아제 2 (RGP2), 및 시스테인 프로테아제/헤마글루티닌 (prtT)의 C-말단으로부터 70개의 아미노산을 가지는 다양한 단백질의 동일성(%) 및 유사성(%)

단백질 이름	동일성(%)			유사성(%)		
	RGP1	RGP2	prtT	RGP1	RGP2	prtT
PG21	17	29	21	40	57	49
PG25	43	41	9	64	73	14
PG27	41	33	7	73	74	11
PG28	21	26	34	49	57	74
PG54	19	13	16	40	43	33
PG57	11	14	19	20	24	34
PG91	31	21	39	57	53	74
PG96	0	13	20	0	24	43
PG97	10	26	33	14	47	61
PG98	16	20	0	47	54	0
PG99	19	0	26	41	0	54
PG100	20	21	24	39	57	41
PG101	11	16	27	17	39	60
PG102	27	20	31	50	61	61
PG104	16	23	26	46	44	49

표 5: *P. gingivalis*의 TonBIII 박스를 가지는 다양한 단백질의

동일성(%) 및 유사성(%)

단백질 이름	동일성(%)	유사성(%)
PG2	46	71
PG13	57	93
PG35	50	96
PG47	39	71
PG50	54	93

제조합 *P. gingivalis* 유전자의 클로닝, 발현 및 정제

PG1

유래된 단백질의 5' 및 3' 영역에 대한 올리고뉴클레오타이드를 사용하여 TaqPlus Precision PCR 시스템(Stratagene) 및 PTC-100(MJ Research) 열순환기 또는 유사한 장치로 *P. gingivalis* W50 의 게놈 DNA의 제조물로부터 관심이 있는 유전자를 증폭하였다. 5' 올리고뉴클레오타이드 프라이머 서열은 GCGCCATATGCTGGCCGAACCGGCC이었고, 3' 올리고뉴클레오타이드 프라이머 서열은 GCGCCTCGAGTCAATTCATTTCTTATAGAG이었다. PCR 단편을 정제하고 Nde I, Xho I 제한효소(Promega)로 분해한 다음 플라스미드 pProEx-1 (Gibco-BRL)의 대응 자리에 결합시킨 후 *E. coli* ER1793 세포로 형질전환시켰다(Elizabeth Raleigh, New England Biolabs 제공). 올바른 삽입물을 발현시키는 클론을 선별하여 제조합 단백질을 발현시키기 위하여 0.1mM IPTG (Promega)의 존재 또는 부존재하에 유도하였다. *P. gingivalis* 제조합 단백질에 융합된 헥사히스타민 태그(tag)를 검출하기 위한 상기 기재된 토끼의 항혈청 및 안티-헥사히스타민 항체(Clontech) 중 하나를 사용하여 SDS-PAGE 분석법 및 웨스턴 블롯으로 제조합 단백질의 발현여부를 결정하였다. 바인딩 버퍼(Novagen)에서 초음파 처리하여 *E. coli* 세포를 파괴하고 사코실(N-라우릴 사코실)을 최종 농도가 1%가 되도록 첨가하여 용해시킴으로써 PG1를 정제하였다. 그런 다음, 바인딩 버퍼내에서 사코실의 농도가 0.1%가 되도록 희석하고, 니켈-니트릴로트리아세탄 칼럼(Ni-NTA; Qiagen)에 결합시키고, 세정한 후에 결합된 단백질을 Qiagen 권고사항에 따라 용리 버퍼(Novagen)내의 1M 이미다졸로 용리시켜 모든 버퍼에 0.1% 사코실이 첨가되도록 하였다. 정제에 이어 샘플을 500mM NaCl, 20mM 트리스, 0.1% 사코실에 대하여 pH 7.4에서 투석하여 이미다졸을 제거하고 필요한 만큼 농축하고 사용전까지 4℃에서 저장하였다. 순도와 항원성은 선택된 항혈청(상기 기재된 것)을 이용하여 SDS-PAGE 및 웨스턴 블롯으로 분석하였고 단백질 농도는 BCA 분석법(Pierce)으로 결정하였다.

PG2

하기 사항을 제외하고 PG1과 본질적으로 동일한 방법을 PG2에도 사용하였다. 5' 올리고뉴클레오타이드 프라이머 서열은 CGCGGTATACATGAAAAGAATGACGC이고, 3' 올리고뉴클레오타이드 프라이머 서열은 CGCGAGATCTGAAAGACAACCTGAATACC이고 PCR 생성물은 BstZ 171 및 Bgl II 제한효소 자리를 이용하여 pGex-stop RBS(IV) (Patent application WO9619496, JC Cox, SE Edwards, I Frazer and EA Webb. 인간 파필로마 바이러스 항원의 변종)에 클론하였다. PG2을 용해하기 위하여 2% 사코실을 사용하였고 용해물 버퍼와 모든 다른 된 버퍼에 8M의 유레아를 첨가하였다. 연속적인 투석에 의하여 정제된 단백질에서 유레아(차레로 4M, 2M, 1M, 0.5M, 및 0M (50mM 트리스, 500mM NaCl, 0.1% 사코실, pH 7.4 내에 함유))를 제거하였다. 정제된 단백질을 필요시까지 4℃에 저장하였다.

PG3

하기 사항을 제외하고 PG1과 본질적으로 동일한 방법을 PG3에도 사용하였다. 5' 올리고뉴클레오타이드 프라이머 서열은 GCGCGTATACATGAAGAAATCAAGTGTAG이고, 3' 올리고뉴클레오타이드 프라이머 서열은 GCGCAGATCTCTTCAGCGTACCTTGCTGTG이고, Pfu DNA 폴리머라제(Stratagene)를 이용하여 DNA를 증폭시켰다. PCR 생성물을 pCR-Blunt에 직접 클론한 다음, Bst Z171 및 Bgl II 제한효소 자리를 이용하여 발현 플라스미드 pGex-stop RBS(IV)내로 서브클로닝하기 전에 *E. coli* Top10F'(Invitrogen) 내로 형질전환하고 *E. coli* BL21DE3 (Pharmacia Biotech) 내로 형질전환하였다. 하기 변형은 PG1 방법에서 PG3을 정제하기 위해 수행된 것이다. 제조합 단백질을 발현하는 세포를 바인딩 버퍼에서 초음파 처리하여 파괴하고 불용성 함유물(inclusion bodies)은 원심분리에 의하여 농축시켰다. 그런 다음 불용물을 바인딩 버퍼내의 6M 유레아 (Sigma)에 용해시키고, 용리 버퍼에 첨가된 6M의 유레아로 용리하였다. 몇몇 예에서 이 단계에서 유레아 대신 6M의 구아니딘 하이드로클로라이드(Sigma)를 사용하였다. 유레아

(또는 그 대신 구아니딘 하이드로클로라이드)는 (차례로 3M, 1.5M, 0.5M, 및 0M의 유레아(50mM 트리스, 500mM NaCl, 8% 글리세롤, pH 7.4 내에 함유)에 대한 연속적인 투석에 의하여 정제된 단백질에서 제거되었다. 정제된 단백질을 필요시까지 -80℃에서 동결저장하였다. 단백질을 쿨마시 플러스 단백질 분석법(Pierce)으로 결정하였다.

PG4

하기 사항을 제외하고 PG3과 본질적으로 동일한 방법을 PG4에도 사용하였다. 5' 올리고뉴클레오타이드 프라이머 서열은 CTTCTGTATACTTACAGCGGACATCATAAAATC이고, 3' 올리고뉴클레오타이드 프라이머 서열은 TTCCAGGAGGGTACCACGCAACTCTTCTTCGAT이고, Tth XL PCR 키트(Perkin Elmer)로 DNA를 증폭하였다. Bst Z171 및 Kpn I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pGex-stop RBS(IV)에 클론하여 *E. coli* ER1793 내로 형질전환하였다.

PG5

하기 사항을 제외하고 PG3과 본질적으로 동일한 방법을 PG5에도 사용하였다. 5' 올리고뉴클레오타이드 프라이머 서열은 TTGCAACATATGATCAGAACGATACTTTCA이고, 3' 올리고뉴클레오타이드 프라이머 서열은 AGCAATCTCGAGCGGTTCATGAGCCAAAGC이고 Tth XL PCR 키트로 DNA를 증폭하였다. Nde I 및 Xho I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24(Novagen)로 클론하여 *E. coli* BL21(Pharmacia Biotech) 내로 형질전환하였다. 상기 단백질은 낮은 농도의 유레아에서 불용성이기 때문에 유레아의 농도가 1M을 넘어가면 더 이상 유레아를 제거하지 않았다. 정제된 단백질은 필요시까지 4℃에 저장하였다.

PG6

하기 사항을 제외하고 PG3과 본질적으로 동일한 방법을 PG6에도 사용하였다. 5' 올리고뉴클레오타이드 프라이머 서열은 TTAAACATATGTGCCTCGAACCCATAATTGCTCCG이고, 3' 올리고뉴클레오타이드 프라이머 서열은 CGTCCGCGGAAGCTTTGATCGGCCATTGCTACT이고 Tth XL PCR 키트로 DNA를 증폭하였다. Nde I 및 Hind III 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21 내로 형질전환하였다.

PG8

하기 사항을 제외하고 PG3과 본질적으로 동일한 방법을 PG8에도 사용하였다. 5' 올리고뉴클레오타이드 프라이머 서열은 CGCGGTATACATGGAGTTCAAGATTGTG이고, 3' 올리고뉴클레오타이드 프라이머 서열은 CGCGAGATCTGTTTTCTGAAAGCTTTTC이고 TaqPlus Precision PCR 시스템을 이용하여 DNA를 증폭하였다. Nde I 및 Xho I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pProEx-1에 클론하여 *E. coli* ER1793에 형질전환하였다.

PG8A

PG8A는 PG8의 짧은 형태로서 처음 173 아미노산이 제거된 것이다. 하기 사항을 제외하고 PG3에 사용된 방법과 본질적으로 동일한 방법을 PG8A에도 사용하였다. 5' 올리고뉴클레오타이드 프라이머 서열은 CGCGGTATACATGGAAACTTAAAGAAC이고, 3' 올리고뉴클레오타이드 프라이머 서열은 CGCGAGATCTGTTTTCTGAAAGCTTTTC이고, TaqPlus Precision PCR 시스템으로 DNA를 증폭하였다. Bst Z171 및 Bgl II 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pGex-stop RBS(IV) 내로 클론하여 *E. coli* ER1793 내로 형질전환하였다. 정제된 단백질을 투석하기 전에 EDTA (Sigma)를 최종 농도가 10mM이 되도록 첨가하였다.

PG10

하기 사항을 제외하고 PG3과 본질적으로 동일한 방법을 PG10에도 사용하였다. 5' 올리고뉴클레오타이드 프라이머 서열은 CGCGGATATCATGGATAAAGTGAGCTATGC이고, 3' 올리고뉴클레오타이드 프라이머 서열은 CGCGAGATCTTTTGTGATACTCAATAATTC이고, TaqPlus Precision PCR 시스템을 이용하여 DNA를 증폭하였다. PCR 생성물을 Eco RV 및 Bgl II 으로 절단한 다음 Bst Z171 및 Bgl II 제한효소 자리를 이용하여 발현 플라스미드 pGex-stop RBS(IV)에 결합시키고 *E. coli* ER1793 내로 형질전환하였다.

PG11

하기 사항을 제외하고 PG1과 본질적으로 동일한 방법을 PG11에도 사용하였다. 5' 올리고뉴클레오타이드 프라이머 서열은 GCGCGTATACATGAGAGCAAACATTTGGCAGATACTTTCCG 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 GCGCAGATCTGCGCAAGCGCAGTATATCGCC이고 Tli DNA 폴리머라제(Promega)를 이용하여 DNA를 증폭하였다. PCR 생성물을 pCR-Blunt 내로 클론하고 Bst Z171 및 Bgl II 제한효소 자리를 이용하여 발현 플라스미드 pGex-stop RBS(IV)에 서브클로닝하기 전에 *E. coli* top10F' 내로 형질전환하고 *E. coli* ER1793 내로 형질전환하였다. 바인딩 버퍼 (Qiagen) 내의 2% 사코실로 *E. coli* 세포를 용해시켜 PG11을 정제하고 바인딩 버퍼내에서 사코실의 농도가 0.1%가 되도록 희석하고, 니켈-니트릴로트리아세트산 칼럼(Ni-NTA; Qiagen)에 결합시키고, 세정한 후에 Qiagen 권고사항에 따라 1M 이미다졸 (용리 버퍼내의 0.7% CHAPS (Sigma); Qiagen)로 결합된 단백질을 용리시켰다. 정제에 이어 샘플을 500mM NaCl, 20mM 트리스, 0.7% CHAPS, 20% 클리세올(Sigma) 대하여 pH 7.4에서 투석하여 이미다졸을 제거하고 필요한 만큼 농축하고 사용전까지 4℃에서 저장하였다.

PG12

하기 사항을 제외하고 PG1과 본질적으로 동일한 방법을 PG12에도 사용하였다. 5' 올리고뉴클레오타이드 프라이머 서열은 GCGCGTATACATGAATAGCAGACATCTGACAATCACAATCATTGCCGG이고, 3' 올리고뉴클레오타이드 프라이머 서열은 GCGCAGATCTGCTGTTCTGTGAGTGCAGTTGTTTAAGTG 이고, Tli DNA 폴리머라제를 이용하여 DNA를 증폭시켰다. PCR 생성물을 pCR-Blunt내로 클론하고 여 Bst Z171 및 Bgl II 제한효소 자리를 이용하여 발현 플라스미드 pGex-stop RBS(IV)내로 서브클로닝하기 전에 *E. coli* top10F' 세포내로 형질전환하고 *E. coli* BL21 내로 형질전환하였다. 50mM 트리스, 50mM NaCl, pH 8.0 내의 0.5% DHPC(1,2-디헵타노일-*sn*-글리세로-3-포스포콜린; Avanti)가 사코실 대신에 함유물을 용해시키기 위하여 사용되고 Ni-NTA에 첨가되기 전에 DHPC가 0.1%로 희석되고 모든 버퍼에 0.1% DHPC를 첨가한 것을 제외하고 PG11과 본질적으로 동일한 방법으로 재조합 단백질을 정제하였다.

PG13

하기 사항을 제외하고 PG3과 본질적으로 동일한 방법을 PG13에도 사용하였다. 5' 올리고뉴클레오타이드 프라이머 서열은 GCGCCATATGCGGACAAAACTATCTTTTTTTGCG이고, 3' 올리고뉴클레오타이드 프라이머 서열은 GCGCCTCGAGTTGTTGAATCGAATCGCTATTTGAGC이고, Tli DNA 폴리머라제를 이용하여 DNA를 증폭하였다. PCR 생성물을 Nde I 및 Xho I 제한효소 자리를 이용하여 발현 플라스미드 pET24b 에 클론하고 *E. coli* BL21내로 형질전환하였다. 6M 유레아를 사용한 PG3과 본질적으로 동일한 방법으로 재조합 단백질을 정제하였고 1% NOG (n-옥틸 글루코사이드; Sigma)를 투석용 버퍼에 첨가하였다. 상기 단백질은 낮은 농도의 유레아에서는 불용성이기 때문에 유레아의 농도가 2M을 넘어가면 더 이상 유레아를 제거하지 않았다. 정제된 단백질은 필요할 때까지 4℃에서 저장하였다.

PG14

하기 사항을 제외하고 PG1과 본질적으로 동일한 방법을 PG14에도 사용하였다. 5' 올리고뉴클레오타이드 프라이머 서열은 GCGCGGCGCCATGACGGACAACAAACAACGTAATATCG 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 GCGCCTCGAGTTACTTTCGTATGATCACGGACATACCC이고, Tli DNA 폴리머라제를 이용하여 DNA를 증폭하였다. PCR 생성물을 Ehe I 및 Xho I 제한효소 자리를 이용하여 발현 플라스미드 pProEx-1 에 클론하고 *E. coli* BL21내로 형질전환하였다. PG12와 본질적으로 동일한 방법으로 재조합 단백질을 정제하였다.

PG15

하기 사항을 제외하고 PG3과 본질적으로 동일한 방법을 PG15에도 사용하였다. 5' 올리고뉴클레오타이드 프라이머 서열은 CAAAAGTATACTAATAAATATCATTTCTCAA 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 GCTTATGGTACCTTTGGTCTTATCTATTAT 이고, Tth XL PCR 키트로 DNA를 증폭하였다. PCR 생성물을 Bst Z171 및 Kpn I 제한효소 자리를 이용하여 발현 플라스미드 pGex-stop RBS(IV) 에 클론하고 *E. coli* ER1793 내로 형질전환하였다.

PG22

하기 사항을 제외하고 PG1과 본질적으로 동일한 방법을 PG22에도 사용하였다. 5' 올리고뉴클레오타이드 프라이머 서열은 CCCCCGATCCGATGCGACTGATCAAGGC 이고, 3' 올리고뉴클레오타이드 프라이머 서열은

CCCCCTCGAGCGGAACGGGGTCATAGCC이고, TaqPlus Precision PCR 시스템으로 DNA를 증폭하였다. PCR 생성물을 Bam HI 및 Xho I 제한효소 자리를 이용하여 발현 플라스미드 pET24b 에 클론하고 *E. coli* BL21DE3 내로 형질전환하였다. PG22가 일단 정제되면 1M의 이미다졸이 존재하는 것을 제외하고 PG1과 동일한 방법으로 투석을 실시하였다.

PG24

하기 사항을 제외하고 PG3과 본질적으로 동일한 방법을 PG24에도 사용하였다. 5' 올리고뉴클레오타이드 프라이머 서열은 CGCGGTATACATGAATTACCTGTACATAC 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 CGCGGGATCCGTTTCGATTGGTCGTCGATGG이고, TaqPlus Precision PCR 시스템으로 DNA를 증폭하였다. PCR 생성물을 Bst Z171 및 Bam HI 제한효소로 분해하고 Bst Z171 및 Bgl II 제한효소 자리를 이용하여 발현 플라스미드 pGex-stop RBS(IV) 에 결합하고 *E. coli* ER1793 내로 형질전환하였다. PG24의 발현 수준이 낮았기 때문에 작은 규모인 것을 제외시켜 정제하지 않았다.

PG24A

PG24의 변형체도 클론되어 발현되도록 하였다. PG24A는 예상되는 N-말단 서열이 제거된 것을 제외하고 PG24와 동일하다. PG3과 본질적으로 동일한 방법을 PG24에도 사용하였다. 5' 올리고뉴클레오타이드 프라이머 서열은 CGCGCATATGGAGATTGCTTTCCTTCTTCG 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 CGCGCTCGAGTTAGTTCGATTGGTCGTCG 이고, TaqPlus Precision PCR 시스템으로 DNA를 증폭하였다. PCR 생성물을 Nde I 및 Xho I 제한효소 자리를 이용하여 발현 플라스미드 pProEx-1에 클론하여 *E. coli* ER1793 내로 형질전환하였다. 함유물을 용해시키기 위하여 8M의 유레아를 사용하고 버퍼내에 Ni-NTA 칼럼 정제용으로 사용된 것을 제외하고 PG3와 본질적으로 동일한 방법으로 재조합 단백질을 정제하였다. 유레아는 연속적인 투석에 의하여 제거하였다(50mM 트리스, 500mM NaCl, 8% 글리세롤, pH 7.4에서 유레아의 농도가 차례로 4M, 2M, 1M, 0.5M, 0M임). 정제된 단백질을 필요시까지 -80℃에서 동결저장하였다.

PG29

하기 사항을 제외하고 PG3과 본질적으로 동일한 방법을 PG29에도 사용하였다. 5' 올리고뉴클레오타이드 프라이머 서열은 GCGCGATATCGCTAGCATGAAAAAGCTATTTCTC 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 GCGCAGATCTCTCGAGTTTGCCATCGGATTGCGGATTG 이고, Pfu DNA 폴리머라제를 이용하여 DNA를 증폭시켰다. PCR 생성물을 pCR-Blunt(InVitrogen)에 클론한 다음, EcoR V 및 Bgl II 제한효소 자리를 이용하여 발현 플라스미드 pGex-stop RBS(IV)내로 서브클론하기 전에 *E. coli* Top10F'(InVitrogen) 내로 형질전환하고 *E. coli* BL21 내로 형질전환하였다. 정제과정중에는 6M 유레아를 사용하였다.

PG30

하기 사항을 제외하고 PG3과 본질적으로 동일한 방법을 PG30에도 사용하였다. 예상되는 N-말단 신호 서열은 재조합 단백질에서 제거되었다. 5' 올리고뉴클레오타이드 프라이머 서열은 TACGGAATTCGTGACCCCCGTCAGAAATGTGCGC 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 CTATGCGGCCGCTTTGATCCTCAAGGCTTTGCCCGG 이고, Tth XL PCR 키트로 DNA를 증폭하였다. Eco RI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. PG30의 *E. coli* 전체 용해물(lysate)에 대하여 발현 및 면역반응성 실험을 실시하였다. 재조합 *E. coli*의 10ml 배양액을 고급 육즙(terrific broth)에서 OD가 2.0(A_{600nm})이 될 때까지 생장시키고 세포를 0.5mM IPTG로 유도한 다음 4시간 뒤에 샘플 분석을 실시하였다. 이 실험에서 정제는 하지 않았다.

PG31

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG31에도 사용하였다. 5' 올리고뉴클레오타이드 프라이머 서열은 CGGGGAATTCGCAAAAATCAATTTCTATGCTGAA 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 CTATGCGGCCGCTGTATGCAATAGGGAAAGCTCCGA 이고, Tth XL PCR 키트로 DNA를 증폭하였다. Eco RI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG32

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG32에도 사용하였다. 예상되는 N-말단 신호 서열은 재조합 단백질에서 제거되었다. 5' 올리고뉴클레오타이드 프라이머 서열은 CGCAGAATTCCAGGAGAATACTGTACCGGCAACG 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 CTATGCGGCCGCCTTGGAGCGAACGATTACAACAC 이고, Tth XL PCR 키트로 DNA를 증폭하였다. Eco RI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG33

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG33에도 사용하였다. 예상되는 N-말단 신호 서열은 재조합 단백질에서 제거되었다. 5' 올리고뉴클레오타이드 프라이머 서열은 TGCAGAATTCCAAGAAGCTACTACACAGAACAAA 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 CTATGCGGCCGCTTCCGCTGCAGTCATTACTACAA 이고, Tth XL PCR 키트로 DNA를 증폭하였다. Eco RI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG35

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG35에도 사용하였다. 5' 올리고뉴클레오타이드 프라이머 서열은 GCGCGAATTCATGAAACAATAACATTATCAGC 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 GCGTGCGGCCGCGAAATTGATCTTTGTACCGACGA 이고, Tth XL PCR 키트로 DNA를 증폭하였다. Eco RI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG36

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG36에도 사용하였다. 5' 올리고뉴클레오타이드 프라이머 서열은 AAAGGAATTCTACAAAAAGATTATTGCCGTAGCA 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 CTATGCGGCCGCGAACTCCTGTCCGAGCACAAAGT 이고, Tth XL PCR 키트로 DNA를 증폭하였다. Eco RI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG37

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG37에도 사용하였다. 5' 올리고뉴클레오타이드 프라이머 서열은 TGGCGAATTCAAACGGTTTTTTGATTTTGATCGGC 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 CTATGCGGCCGCCTTGCTAAAGCCCATCTTGCTCAG 이고, Tth XL PCR 키트로 DNA를 증폭하였다. Eco RI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG38

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG38에도 사용하였다. 예상되는 N-말단 신호 서열은 재조합 단백질에서 제거되었다. 5' 올리고뉴클레오타이드 프라이머 서열은 CCTCGAATTCCAAAAGGTGGCAGTGGTAAACACT 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 CTATGCGGCCGCCTTGATTCCGAGTTTCGCTTTTAC 이고, Tth XL PCR 키트로 DNA를 증폭하였다. Eco RI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG39

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG39에도 사용하였다. 예상되는 N-말단 신호 서열은 재조합 단백질에서 제거되었다. 5' 올리고뉴클레오타이드 프라이머 서열은 AGCTGGATCCCAAGGCGTCAGGGTATCGGGCTAT

이고, 3' 올리고뉴클레오타이드 프라이머 서열은 CTATGCGGCCGCGAATTCGACGAGGAGACGCAGGT 이고, Tth XL PCR 키트로 DNA를 증폭하였다. Bam HI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG40

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG40에도 사용하였다. 예상되는 N-말단 신호 서열은 재조합 단백질에서 제거되었다. 5' 올리고뉴클레오타이드 프라이머 서열은 GGCTGAATTCAAGACGGACAACGTCCCCGACAGAT 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 CTATGCGGCCGCGAAGTTGACCATAACCTTACCCA 이고, Tth XL PCR 키트로 DNA를 증폭하였다. Eco RI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG41

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG41에도 사용하였다. 예상되는 N-말단 신호 서열은 재조합 단백질에서 제거되었다. 5' 올리고뉴클레오타이드 프라이머 서열은 GACTGAATTCCAAAACGCCTCCGAAACGACGGTA 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 CTATGCGGCCGCTTGTTCGGGAATCCCCATGCCGTT 이고, Tth XL PCR 키트로 DNA를 증폭하였다. Eco RI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG42

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG42에도 사용하였다. 5' 올리고뉴클레오타이드 프라이머 서열은 GTTTGAATTCGCAAATAATACTCTTTTGCGAAG 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 GAGTGC GGCCGCTTTGCCGGACATCGAAGAGATCGTC 이고, Tth XL PCR 키트로 DNA를 증폭하였다. Eco RI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG43

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG43에도 사용하였다. 5' 올리고뉴클레오타이드 프라이머 서열은 GCGCGAATTCAAAAAAGAAAAACTTTGGATTGCG 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 CTATGCGGCCGCTTCAAAGCGAAGAAAGCCTTAAC 이고, Tth XL PCR 키트로 DNA를 증폭하였다. Eco RI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG44

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG44에도 사용하였다. 예상되는 N-말단 신호 서열은 재조합 단백질에서 제거되었다. 5' 올리고뉴클레오타이드 프라이머 서열은 AGCCGAATTCTGTAAAGAAAAATGCTGACACTACC 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 CTATGCGGCCGCTTTTCCCGGGCTTGATCCCGAT 이고, Tth XL PCR 키트로 DNA를 증폭하였다. Eco RI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG45

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG45에도 사용하였다. 예상되는 N-말단 신호 서열은 재조합 단백질에서 제거되었다. 5' 올리고뉴클레오타이드 프라이머 서열은 GACAGGATCCTGCTCCACCACAAAGAATCTGCCG 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 CTATGCGGCCGCGAAGGGATAGCCGACAGCCAAAT 이고, Tth XL PCR

키트로 DNA를 증폭하였다. Bam HI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG46

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG46에도 사용하였다. 예상되는 N-말단 신호 서열은 재조합 단백질에서 제거되었다. 5' 올리고뉴클레오타이드 프라이머 서열은 CTCGGAATTCCGTTATGTGCCGGACGGTAGCAGA 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 CTATGCGGCCGCGAACGGATAGCCTACTGCAATGT 이고, Tth XL PCR 키트로 DNA를 증폭하였다. Eco RI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG47

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG47에도 사용하였다. 예상되는 N-말단 신호 서열은 재조합 단백질에서 제거되었다. 5' 올리고뉴클레오타이드 프라이머 서열은 CGCCGAATTCCAAACAGTGGTGACCGGTAAGGTGATCGATTTCAGAA 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 CTATGCGGCCGCGAAGTTTACACGAATACCGGTAGACCAAGTGC GGCC 이고, Tth XL PCR 키트로 DNA를 증폭하였다. Eco RI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG48

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG48에도 사용하였다. 예상되는 N-말단 신호 서열은 재조합 단백질에서 제거되었다. 5' 올리고뉴클레오타이드 프라이머 서열은 TGCTGAATTCCAAAAATCCAAGCAGGTACAGCGA 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 CTATGCGGCCGCTCGTAACCATAGTCTTGGGTTTTTG 이고, Tth XL PCR 키트로 DNA를 증폭하였다. Eco RI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG49

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG49에도 사용하였다. 예상되는 N-말단 신호 서열은 재조합 단백질에서 제거되었다. 5' 올리고뉴클레오타이드 프라이머 서열은 GAACGGATCCAACGAGCCGGTGGGAAGACAGATCC 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 GAGTGCGGCCGCTAATCTCGACTTCATACTTGTACCA 이고, Tth XL PCR 키트로 DNA를 증폭하였다. Bam HI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG50

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG50에도 사용하였다. 예상되는 N-말단 신호 서열은 재조합 단백질에서 제거되었다. 5' 올리고뉴클레오타이드 프라이머 서열은 GCTGGGATCCGCGACAGACACTGAGTTCAAGTAC 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 CTATGCGGCCGCGAACTTCACTACCAAGCCCATGT 이고, Tth XL PCR 키트로 DNA를 증폭하였다. Bam HI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG51

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG51에도 사용하였다. 예상되는 N-말단 신호 서열은 재조합 단백질에서 제거되었다. 5' 올리고뉴클레오타이드 프라이머 서열은 TCTTGAATTCGCGCAAAGTCTTTTCAGCACCGAA

이고, 3' 올리고뉴클레오타이드 프라이머 서열은 CTATGCGGCCGCACTTTTTTCGTGGGATCACTCTCTT 이고, Tth XL PCR 키트로 DNA를 증폭하였다. Eco RI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG52A

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG52에도 사용하였다. 5' 올리고뉴클레오타이드 프라이머 서열은 AGAAGAATTCAAACGGACAATCCTCCTGACGGCA 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 CTATGCGGCCGCGAAGTCTTTGCCCTGATAGAAATC 이고, Tth XL PCR 키트로 DNA를 증폭하였다. Eco RI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG53

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG53에도 사용하였다. 예상되는 N-말단 신호 서열은 재조합 단백질에서 제거되었다. 5' 올리고뉴클레오타이드 프라이머 서열은 GGCTGAATTCGCGAATCCCCTTACGGGCCAATCG 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 CTATGCGGCCGCGTCCGAAAGGCAGCCGTAATAGG 이고, Tth XL PCR 키트로 DNA를 증폭하였다. Eco RI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG54

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG54에도 사용하였다. 예상되는 N-말단 신호 서열은 재조합 단백질에서 제거되었다. 5' 올리고뉴클레오타이드 프라이머 서열은 CGCTGAATTCAGATTTTCGTTCGGAGGGGAACCC 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 CTATGCGGCCGCTGCTTACGATCTTTTGGCTCA 이고, Tth XL PCR 키트로 DNA를 증폭하였다. Eco RI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG55

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG55에도 사용하였다. 예상되는 N-말단 신호 서열은 재조합 단백질에서 제거되었다. 5' 올리고뉴클레오타이드 프라이머 서열은 CGAGGGATCCGAGCTCTCTATTTGCGATGGCGAG 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 GAGTGC GGCCGCTCTTACCTGACTTCTTGTCACGAAT 이고, Tth XL PCR 키트로 DNA를 증폭하였다. Eco RI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG56

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG56에도 사용하였다. 5' 올리고뉴클레오타이드 프라이머 서열은 AAATGGATCCCGAAAAATTTTGAGCTTTTTTGATG 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 CTATGCGGCCGCTTTGATTCGTAATTTTCCGTATC 이고, Tth XL PCR 키트로 DNA를 증폭하였다. Bam HI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG57

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG57에도 사용하였다. 예상되는 N-말단 신호 서열은 재조합 단백질에서 제거되었다. 5' 올리고뉴클레오타이드 프라이머 서열은 TGCTGGATCCCAAGAGATCTCAGGCATGAATGCA 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 GAGTGC GGCCGCTCGGCCTCTTTATCTCTACCTTTTC 이고, Tth XL

PCR 키트로 DNA를 증폭하였다. Bam HI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG58

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG58에도 사용하였다. 예상되는 N-말단 신호 서열은 재조합 단 백질에서 제거되었다. 5' 올리고뉴클레오타이드 프라이머 서열은 CGGTGAATTCCAAACCCACGAAATACAGAAACC 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 GAGTGC GGCCGCTGAAAGTCCAGCTAAAACCGGCGAA 이고, Tth XL PCR 키트로 DNA를 증폭하였다. Eco RI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG59

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG59에도 사용하였다. 예상되는 N-말단 신호 서열은 재조합 단 백질에서 제거되었다. 5' 올리고뉴클레오타이드 프라이머 서열은 TGCTGAATTCCAACAAGAGAAGCAGGTGTTTCAT 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 GAGTGC GGCCGCTGAAGATGCTCTTATCGTCCAAACG 이고, Tth XL PCR 키트로 DNA를 증폭하였다. Eco RI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG60

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG60에도 사용하였다. 예상되는 N-말단 신호 서열은 재조합 단 백질에서 제거되었다. 5' 올리고뉴클레오타이드 프라이머 서열은 GGCGGAATTCCAGATGCTCAATACTCCTTTCGAG 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 GAGTGC GGCCGCTGAAGAGGTAGGAGATATTGCAGAT 이고, Tth XL PCR 키트로 DNA를 증폭하였다. Eco RI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG61

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG61에도 사용하였다. 예상되는 N-말단 신호 서열은 재조합 단 백질에서 제거되었다. 5' 올리고뉴클레오타이드 프라이머 서열은 AGCAGAATTCCCCGTCTCCAACAGCGAGATAGAT 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 GAGTGC GGCCGCTGAAATCGATTGTCAGACTACCCAG 이고, Tth XL PCR 키트로 DNA를 증폭하였다. Eco RI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG62

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG62에도 사용하였다. 예상되는 N-말단 신호 서열은 재조합 단 백질에서 제거되었다. 5' 올리고뉴클레오타이드 프라이머 서열은 TGCTGAATTCCAGCGGTTTCCGATGGTGCAGGGA 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 GAGTGC GGCCGCTGAAGTGAAATCCGACACGCAGCTG 이고, Tth XL PCR 키트로 DNA를 증폭하였다. Eco RI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG63

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG63에도 사용하였다. 예상되는 N-말단 신호 서열은 재조합 단 백질에서 제거되었다. 5' 올리고뉴클레오타이드 프라이머 서열은 GGCAGAATTCCAAGAAGCAAACACTGCATCTGAC 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 GAGTGC GGCCGCTGAAAGTGTACGCAACACCCACGCC 이고, Tth XL

PCR 키트로 DNA를 증폭하였다. Eco RI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG64

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG64에도 사용하였다. 예상되는 N-말단 신호 서열은 재조합 단 백질에서 제거되었다. 5' 올리고뉴클레오타이드 프라이머 서열은 TGCTGAATTCCAGAGTCGTCCTGCTCTTAGACTG 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 GAGTGCGGCCGCTGAAGCGAACACCGAGACCCACAAA 이고, Tth XL PCR 키트로 DNA를 증폭하였다. Eco RI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG65

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG65에도 사용하였다. 예상되는 N-말단 신호 서열은 재조합 단 백질에서 제거되었다. 5' 올리고뉴클레오타이드 프라이머 서열은 GGCCGGATCCATCGGACAAAGCCGCCCGGCACTT 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 GAGTGCGGCCGCTAAAGCGGTAACCTATGCCACGAA 이고, Tth XL PCR 키트로 DNA를 증폭하였다. Bam HI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG66

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG66에도 사용하였다. 예상되는 N-말단 신호 서열은 재조합 단 백질에서 제거되었다. 5' 올리고뉴클레오타이드 프라이머 서열은 GTTTGAATTCCAAGACGTTATCAGACCATGGTCA 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 GAGTGCGGCCGCTAAAATGAGTGGAGAGCGTGGCCAT 이고, Tth XL PCR 키트로 DNA를 증폭하였다. Eco RI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG67

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG67에도 사용하였다. 예상되는 N-말단 신호 서열은 재조합 단 백질에서 제거되었다. 5' 올리고뉴클레오타이드 프라이머 서열은 GAACGAGCTCGCGGAACGTCCTATGGCCGGAGCA 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 GAGTGCGGCCGCTATACCAAGTATTCGTGATGGGACG 이고, Tth XL PCR 키트로 DNA를 증폭하였다. Sac I 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG68

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG68에도 사용하였다. 예상되는 N-말단 신호 서열은 재조합 단 백질에서 제거되었다. 5' 올리고뉴클레오타이드 프라이머 서열은 GCTTGCGGCCGCCCTTATGAAAGATTTGCAGAT 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 GGTGCTCGAGTATACTCAACAAGCACCTTATGCAC 이고, Tth XL PCR 키트로 DNA를 증폭하였다. Not I 및 Xho I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG69

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG69에도 사용하였다. 예상되는 N-말단 신호 서열은 재조합 단 백질에서 제거되었다. 5' 올리고뉴클레오타이드 프라이머 서열은 TGCTGAATTCCAGGAAGGGGAGGGGAGTGCCCGA 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 GAGTGCGGCCGCTGAAGCTGTAGCGGGCTTTGAACCA 이고, Tth XL

PCR 키트로 DNA를 증폭하였다. Eco RI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG70

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG70에도 사용하였다. 예상되는 N-말단 신호 서열은 재조합 단백질에서 제거되었다. 5' 올리고뉴클레오타이드 프라이머 서열은 CGGTGGATCCTCGCAAATGCTCTTCTCAGAGAAT 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 GAGTGCGGCCGCTAAACGAAATATCGATACCAACATC 이고, Tth XL PCR 키트로 DNA를 증폭하였다. Bam HI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG71

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG71에도 사용하였다. 예상되는 N-말단 신호 서열은 재조합 단백질에서 제거되었다. 5' 올리고뉴클레오타이드 프라이머 서열은 TGCTGAATTCCAGAACAATACCTCGATGTACAC 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 GAGTGCGGCCGCTATTGCCGGTAGGATTTCTTGTCC 이고, Tth XL PCR 키트로 DNA를 증폭하였다. Eco RI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG72

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG72에도 사용하였다. 예상되는 N-말단 신호 서열은 재조합 단백질에서 제거되었다. 5' 올리고뉴클레오타이드 프라이머 서열은 TGCTGAATTCGGAGAGCGACTGGAGACGGACAGC 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 GAGTGCGGCCGCTATGATTGCCTTTCAGAAAAGCTAT 이고, Tth XL PCR 키트로 DNA를 증폭하였다. Eco RI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG73

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG73에도 사용하였다. 예상되는 N-말단 신호 서열은 재조합 단백질에서 제거되었다. 5' 올리고뉴클레오타이드 프라이머 서열은 CGGTGAATTCCAACAGACAGGACCGCCGAACGC 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 GAGTGCGGCCGCTTAAGAAAGGTATCTGATAGATCAG 이고, Tth XL PCR 키트로 DNA를 증폭하였다. Eco RI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG74

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG74에도 사용하였다. 예상되는 N-말단 신호 서열은 재조합 단백질에서 제거되었다. 5' 올리고뉴클레오타이드 프라이머 서열은 TGCTGAATTCCAAGAAAATAATACAGAAAAGTCA 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 GAGTGCGGCCGCTGAGGTTTAATCCTATGCCAATACT 이고, Tth XL PCR 키트로 DNA를 증폭하였다. Eco RI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG75

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG75에도 사용하였다. 예상되는 N-말단 신호 서열은 재조합 단백질에서 제거되었다. 5' 올리고뉴클레오타이드 프라이머 서열은 GGCGGGATCCGCTCAGGAGCAACTGAATGTGGTA 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 GAGTGCGGCCGCTGTGGAACAAATTGCGCAATCCATC 이고, Tth XL

PCR 키트로 DNA를 증폭하였다. Bam HI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG76

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG76에도 사용하였다. 예상되는 N-말단 신호 서열은 재조합 단 백질에서 제거되었다. 5' 올리고뉴클레오타이드 프라이머 서열은 AGCAGAATTTCGGAACGCACAGAGCTTTTGGGAA 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 GAGTGCGGCCGCTTACCTGCACCTTATGACTGAATAC 이고, Tth XL PCR 키트로 DNA를 증폭하였다. Eco RI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG77

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG77에도 사용하였다. 예상되는 N-말단 신호 서열은 재조합 단 백질에서 제거되었다. 5' 올리고뉴클레오타이드 프라이머 서열은 TGCTGAATTCCAAGAGAAAAAGGATAGTCTCTCT 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 GAGTGCGGCCGCTCTTCTTATCGCCATAGAATACAGG 이고, Tth XL PCR 키트로 DNA를 증폭하였다. Eco RI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG78

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG78에도 사용하였다. 예상되는 N-말단 신호 서열은 재조합 단 백질에서 제거되었다. 5' 올리고뉴클레오타이드 프라이머 서열은 GGCAGAATTCCAGGATTCTTCCACGGTAGCAAT 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 GAGTGCGGCCGCTATCATGATAGTAAAGACTGGTTCT 이고, Tth XL PCR 키트로 DNA를 증폭하였다. Eco RI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG79

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG79에도 사용하였다. 5' 올리고뉴클레오타이드 프라이머 서열은 TGCTGAATTTCGTAGTGACGCTGCTCGTAATTGTC 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 GAGTGCGGCCGCTGCCGTCCTGCCTTTCTGCCTGACG 이고, Tth XL PCR 키트로 DNA를 증폭하였다. Eco RI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG80

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG80에도 사용하였다. 예상되는 N-말단 신호 서열은 재조합 단 백질에서 제거되었다. 5' 올리고뉴클레오타이드 프라이머 서열은 GGCCGAATTCCAAAACGTGCAGTTGCACTACGAT 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 GAGTGCGGCCGCTGTTGAAAGTCCATTTGACCGCAAG 이고, Tth XL PCR 키트로 DNA를 증폭하였다. Eco RI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG81

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG81에도 사용하였다. 예상되는 N-말단 신호 서열은 재조합 단 백질에서 제거되었다. 5' 올리고뉴클레오타이드 프라이머 서열은 GTTTGAATTCCAGGATTTTCTCTATGAAATAGGA 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 GAGTGCGGCCGCTTTGTTTATTACAAAAAGTCTTACG 이고, Tth

XL PCR 키트로 DNA를 증폭하였다. Eco RI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG82

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG82에도 사용하였다. 예상되는 N-말단 신호 서열은 재조합 단백질에서 제거되었다. 5' 올리고뉴클레오타이드 프라이머 서열은 GAACGAATTCCAGAACAACAACCTTTACCGAGTCG 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 GAGTGCGGCCGCTGTTTCAGTTTCAGCTTTTTTAAACCA 이고, Tth XL PCR 키트로 DNA를 증폭하였다. Eco RI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG84

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG84에도 사용하였다. 예상되는 N-말단 신호 서열은 재조합 단백질에서 제거되었다. 5' 올리고뉴클레오타이드 프라이머 서열은 TGCTGGATCCCAAGATGATGACATCTTCGAAGAT 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 GAGTGCGGCCGCTATTGCGTCCCCGCCACTACGTCC 이고, Tth XL PCR 키트로 DNA를 증폭하였다. Bam HI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG85

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG85에도 사용하였다. 예상되는 N-말단 신호 서열은 재조합 단백질에서 제거되었다. 5' 올리고뉴클레오타이드 프라이머 서열은 CGGTGAATTCGTACCAACGGACAGCACGGAATCG 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 GAGTGCGGCCGCTCAGATTGGTGCTATAAGAAAGGTA 이고, Tth XL PCR 키트로 DNA를 증폭하였다. Eco RI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG86

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG86에도 사용하였다. 예상되는 N-말단 신호 서열은 재조합 단백질에서 제거되었다. 5' 올리고뉴클레오타이드 프라이머 서열은 TGCTGGATCCCAACGCATGATCATCTCATCGAA 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 GAGTGCGGCCGCTGTGGTTCAGGCCGTGGGCAAATCT 이고, Tth XL PCR 키트로 DNA를 증폭하였다. Bam HI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG87

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG87에도 사용하였다. 예상되는 N-말단 신호 서열은 재조합 단백질에서 제거되었다. 5' 올리고뉴클레오타이드 프라이머 서열은 GGCGGAATTCCAGAGCTATGTGGACTACGTCGAT 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 GAGTGCGGCCGCTATTACTGTGATTAGCGCGACGCTG 이고, Tth XL PCR 키트로 DNA를 증폭하였다. Eco RI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG88

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG88에도 사용하였다. 예상되는 N-말단 신호 서열은 재조합 단백질에서 제거되었다. 5' 올리고뉴클레오타이드 프라이머 서열은 AGCAGAATTCGCCGAATCGAAGTCTGTCTCTTTC 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 GAGTGCGGCCGCTCGGCAAGTAACGCTTTAGTGGGGA 이고, Tth XL

PCR 키트로 DNA를 증폭하였다. Eco RI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG89

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG89에도 사용하였다. 예상되는 N-말단 신호 서열은 재조합 단 백질에서 제거되었다. 5' 올리고뉴클레오타이드 프라이머 서열은 TGCTGAATTCCAATCGAAGTTAAAGATCAAGAGC 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 GAGTGC GGCCGCTATTAGTCCAAAGACCCACGGTAAA 이고, Tth XL PCR 키트로 DNA를 증폭하였다. Eco RI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG90

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG90에도 사용하였다. 예상되는 N-말단 신호 서열은 재조합 단 백질에서 제거되었다. 5' 올리고뉴클레오타이드 프라이머 서열은 GGCAGAATTCCAAACAACGACGAACAGTAGCCGG 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 GAGTGC GGCCGCTTTTTTGTGTGATACTGTTTGGGC 이고, Tth XL PCR 키트로 DNA를 증폭하였다. Eco RI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG91

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG91에도 사용하였다. 예상되는 N-말단 신호 서열은 재조합 단 백질에서 제거되었다. 5' 올리고뉴클레오타이드 프라이머 서열은 TGCTGAATTCCAGACGATGGGAGGAGATGATGTC 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 GAGTGC GGCCGCTTTCCACGATGAGCTTCTCTACGAA 이고, Tth XL PCR 키트로 DNA를 증폭하였다. Eco RI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG92

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG92에도 사용하였다. 예상되는 N-말단 신호 서열은 재조합 단 백질에서 제거되었다. 5' 올리고뉴클레오타이드 프라이머 서열은 GGCCGAGCTCCGCGATGCACAAAGCTCTGTCTCT 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 GAGTGC GGCCGCTTCGAGGACGATTGCTTAGTTTCGTA 이고, Tth XL PCR 키트로 DNA를 증폭하였다. Eco RI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG93

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG93에도 사용하였다. 예상되는 N-말단 신호 서열은 재조합 단 백질에서 제거되었다. 5' 올리고뉴클레오타이드 프라이머 서열은 GGCCGAGCTCCAAGAGGAAGGTATTTGGAATACC 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 GAGTGC GGCCGCTGCGAATCACTGCGAAGCGAATTAG 이고, Tth XL PCR 키트로 DNA를 증폭하였다. Eco RI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG94

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG94에도 사용하였다. 예상되는 N-말단 신호 서열은 재조합 단 백질에서 제거되었다. 5' 올리고뉴클레오타이드 프라이머 서열은 GGCCGAGCTCCAAGAGGAAGGTATTTGGAATACC 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 GAGTGC GGCCGCTTTGTCCTACCACGATCATTTTCTT 이고, Tth XL

PCR 키트로 DNA를 증폭하였다. Eco RI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG95

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG95에도 사용하였다. 예상되는 N-말단 신호 서열은 재조합 단백질에서 제거되었다. 5' 올리고뉴클레오타이드 프라이머 서열은 GGCCGAGCTCTGTGGAAAAAAGAAAAACACTCT 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 GAGTGC GGCCGCTAACTGTCTCCTTGTCGCTCCCCGG 이고, Tth XL PCR 키트로 DNA를 증폭하였다. Sac I 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG96

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG96에도 사용하였다. 예상되는 N-말단 신호 서열은 재조합 단백질에서 제거되었다. 5' 올리고뉴클레오타이드 프라이머 서열은 TGCTGAGCTCCAAACGCAAATGCAAGCAGACCGA 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 GAGTGC GGCCGCTTTTGAGAATTTTCATTGTCTCACG 이고, Tth XL PCR 키트로 DNA를 증폭하였다. Sac I 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG97

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG97에도 사용하였다. 예상되는 N-말단 신호 서열은 재조합 단백질에서 제거되었다. 5' 올리고뉴클레오타이드 프라이머 서열은 GGCGGGATCCCAGTTTGTTCGGCTCCCACCACA 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 GAGTGC GGCCGCTCTGTTTGATGAGCTTAGTGGTATA 이고, Tth XL PCR 키트로 DNA를 증폭하였다. Bam HI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG98

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG98에도 사용하였다. 예상되는 N-말단 신호 서열은 재조합 단백질에서 제거되었다. 5' 올리고뉴클레오타이드 프라이머 서열은 AGCAGAATTCCAAGAAAGAGTCGATGAAAAAGTA 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 GAGTGC GGCCGCTTAGCTGTGTAACATTAAGTTTTTTATTGAT 이고, Tth XL PCR 키트로 DNA를 증폭하였다. Eco RI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG99

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG99에도 사용하였다. 예상되는 N-말단 신호 서열은 재조합 단백질에서 제거되었다. 5' 올리고뉴클레오타이드 프라이머 서열은 TGCTGAATTCAAGACAATTCTTCTTACAAACCT 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 GAGTGC GGCCGCTTCGAATCACGACTTTTCTCACAAA 이고, Tth XL PCR 키트로 DNA를 증폭하였다. Eco RI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG100

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG100에도 사용하였다. 예상되는 N-말단 신호 서열은 재조합 단백질에서 제거되었다. 5' 올리고뉴클레오타이드 프라이머 서열은 GGCAGAATTCCAGTCTTTGAGCACAAATCAAAGTA 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 GAGTGC GGCCGCTGATAGCCAGCTTGATGCTCTTAGC 이고, Tth XL

PCR 키트로 DNA를 증폭하였다. Eco RI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG101

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG101에도 사용하였다. 5' 올리고뉴클레오타이드 프라이머 서열은 TGCTGAATTCAAAGGCAAGGGCGATCTGGTCGGG 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 GAGTGC GGCCGCTTCTCTTCTCGA ACTTG GCCGAGTA 이고, Tth XL PCR 키트로 DNA를 증폭하였다. Eco RI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다..

PG102

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG102에도 사용하였다. 예상되는 N-말단 신호 서열은 재조합 단백질에서 제거되었다. 5' 올리고뉴클레오타이드 프라이머 서열은 GGCCGAATTCCAGATGGATATTGGTGGAGACGAT 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 GAGTGC GGCCGCTTCTCTACAATGATTTTTTCCACGAA 이고, Tth XL PCR 키트로 DNA를 증폭하였다. Eco RI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

PG104

하기 사항을 제외하고 PG30과 본질적으로 동일한 방법을 PG104에도 사용하였다. 예상되는 N-말단 신호 서열은 재조합 단백질에서 제거되었다. 5' 올리고뉴클레오타이드 프라이머 서열은 GAACGGATCCAACGTGTCTGCTCAGTCACCCGA 이고, 3' 올리고뉴클레오타이드 프라이머 서열은 GAGTGC GGCCGCTTCTGAGCGATACTTTTGCACGTAT 이고, Tth XL PCR 키트로 DNA를 증폭하였다. Bam HI 및 Not I 제한효소 자리를 이용하여 PCR 생성물을 발현 플라스미드 pET24a에 클론하여 *E. coli* BL21DE3 내로 형질전환하였다. *E. coli* 전체 용해물에 대하여 발현 및 면역반응성 실험을 실시하였다. 이 실험에서 정제는 행하지 않았다.

동물의 항혈청 및 인간(환자)의 혈청

재조합 *P. gingivalis* 단백질의 발현과 리폴딩(refolding)을 검출하기 위한 다양한 항혈청이 제시되었다. 전체 세포의 항혈청은 뉴질랜드 흰 토끼에 대략 2mg의 단백질을 포함하는 초음파처리된 *P. gingivalis* (균주 W50)를 3번 주입하여 얻어졌다. 첫 번째 투여는 프로인드 완전 애주번트(Freunds complete adjuvant; FCA)로 공급되고 두 번째와 세 번째 투여는 3주 간격으로 프로인드 불완전 애주번트(Freunds incomplete adjuvant; IFA)로 공급되었다. 뒷다리의 근육내로 투여하고 (1ml), 마지막 투여 후 7일째에 토끼에서 채혈하여, 응고시키고 혈청을 제거한 다음 -20℃에서 필요시까지 저장하였다. 제2의 토끼 항혈청은 Doidg and Trust T. *et al* 1994에 기재된 방법에 따라 *P. gingivalis* W50으로부터 유도한 사코실 불용성 분획(각각의 단백질의 투여량은 1mg)을 면역원으로 사용된 것을 제외하고 유사한 방법으로 생산하였다. 제3의 토끼 항혈청은 Doidg P. and Trust TJ. (1994 Infect Immun 62:4526-33)에 기재된 방법에 따라 *P. gingivalis* W50으로부터 유도한 사코실 불용성 분획(각각의 단백질의 투여량은 0.69mg)을 면역원으로 사용된 것을 제외하고 제1의 토끼 항혈청과 유사한 방법으로 생산하였다.

"보호된 쥐의 혈청(protected rat serum)" 푸울도 이들 실험에 사용되었고 포르말린으로 사멸된 FIA의 *P. gingivalis* 세포 (strain ATCC 33277; 2 doses of 2×10^9 cells, 3 weeks apart)으로 면역화된 쥐로부터 얻었다. 그런 다음 마지막 투여 후 2주째에 살아있는 *P. gingivalis* 세포(strain 33277)를 앞서 설명된 방법 (Klaussen B. *et al*. 1991, Oral Microbiol Immunol 6:193-201)으로 쥐에 투여하여 마지막 투여 접종 후 6주째(희생 시점)에 이들 쥐에서 혈청을 얻었다.

인간의 혈청은 외래 환자 진료소의 치주염 치료 또는 진단을 받은 성인 환자에서 얻었다. 이들 환자들은 6mm의 부착손실 (attachment loss)을 가진 적어도 6개 이상의 이를 가졌으며 *P. gingivalis* 특이성 DNA 프로브를 사용하여 검출되는 아래 잇몸 플라크에 존재하는 *P. gingivalis*를 가졌다. 이들 환자에서 혈청을 모아 치주가 건강한 환자에서 얻은 혈청과 비교하였다.

면역화 및 무린 손상 모델 프로토콜(Murine Lesion Model Protocols)

피하의 종기 형성으로부터 마우스를 보호함에 있어서 재조합 *P. gingivalis* 단백질로 마우스를 면역화하는 효과를 평가하기 위하여 마우스의 종기 모델을 사용하였다. 이 모델은 치주염에 대한 백신의 가능성을 예견하는 것으로 사용되었다 (Bird PS, et al. 1995 J. Periodontol. 66:351-362). 10 또는 20mg의 재조합 *P. gingivalis* 단백질, 20mg의 *E. coli* 용해 단백질, 불완전한 프로인드 애주번트(IFA; Sigma)내에 에멀전화된 *P. gingivalis* 균주 33277의 2×10^9 포르말린 사멸된 세포를 포함하는 0.1ml를 0일에 피하내로 주입하여 BALB/c 생후 6-8 주된 마우스를 면역화하였다. 21일에 마우스에 동일한 투여량으로 재주입한 다음 1주 후에 채혈하여 항체 수준을 평가하였다. 35일째에 모든 마우스에 살아있는 *P. gingivalis* (ATCC 33277)의 대략 2×10^9 세포를 복부의 피하내로 주입하였다. 투여후 마우스의 체중 감소를 매일 관찰하고 그 후 10일 동안 손상부위(lesion)의 크기를 매일 측정하였다. 손상부위의 크기는 길이와 폭을 측정하여 mm^2 로 나타내었다. 시험군을 Kruskal-Wallis oneway ANOVA를 이용하여 통계학적으로 분석하였고, Instat 통계학적 패키지를 사용하는 Mann-Whitney rank sum test 또는 unpaired t test를 이용하여 개별적으로 고찰하였다.

도 1은 투여후 4일째(손상은 이 시점에서 최대 크기였음)의 실험 결과를 보인 것이다. *E. coli* 용해물로 면역화된 대조부 마우스는 큰 손상을 보임에 반하여 *P. gingivalis* 균주 33277의 사멸된 세포로 면역화된 마우스는 완전히 보호되었다. 이것은 전체 세포가 *P. gingivalis*에 대하여 보호할 수 있는 반면 *E. coli* 단백질로 면역화된 마우스는 보호되지 않는다는 것을 나타내는 것이다. 다양한 PG 재조합 단백질이 공급된 마우스는 PG2, PG22, PG24 및 PG29의 경우 상당한 수준의 보호를 보여주었으나($p < 0.05$ unpaired t test), PG8A는 *E. coli* 대조군에 비하여 상당히 다른 수준은 아니었다($p = 0.07$).

도 2는 재조합 단백질을 조합하여 이용한 개별적인 실험 결과를 보인 것이다. PG1 + PG2를 공급받은 마우스는 *E. coli* 용해물이 공급된 대조군 마우스에 비하여 상당한 수준으로 보호됨을 보여준다($p < 0.026$ unpaired t test).

면역스크리닝(Immunoscreening)

클론된 후보자들을 15ml의 고급(Terrific) 육즙에서 배양하고, IPTG로 유도하여 유도 후 4시간 뒤에 샘플을 취하였다. 1 ml의 배양액을 제거하여 펠릿화하고 배양액의 OD $A_{600\text{nm}}$ 을 8로 나눔으로써 결정된 PBS의 부피에서 세포를 재현탁하였다. 용해물($100\mu\text{l}$)의 분취량(aliquot)을 $100\mu\text{l}$ 의 2x 샘플 환원(reducing) 버퍼(125mM 트리스, pH 6.8, 20% 글리세롤, 4% SDS, 80mM DTT, 0.03% 브로모페놀 블루)에 첨가하고 10분간 가열하였다. 4-20% 1.0mm 트리스-글리세린 겔(Novex)을 사용하여 제조사의 권고사항에 따라 Laemmli UK. 1970 (Nature 227:680-685)의 방법으로 SDS-PAGE를 수행하였다. 트랜스블로팅(transblotting)에 의하여 Hybond-C 엑스트라 나이트로셀룰로스 막(Amersham)에 단백질을 옮긴 다음 20mM 트리스, 0.5M NaCl, 0.05% 트윈-20, pH 7.5 (TTBS) 내의 5% 스킴(skim) 밀크 내의 상온(RT)에서, 2 시간동안 차단하였다.

토끼의 anti-*P. gingivalis* 전체 세포의 혈청, 쥐의 보호성 혈청, 인간 치주염 환자의 혈청 풀, 및 많은 경우에 anti-T7-Tag 항체 HRP 컨쥬게이트(Novagen)로 개별적으로 면역스크리닝을 실시하였다. 사용 전에, 토끼, 쥐 및 인간 혈청은 각각 TTBS내의 5% 스킴 밀크내에서 각각 1/5000, 1/1000 및 1/500으로 희석시키고 (토끼 혈청에 대하여) $100\mu\text{l}$ 또는 (쥐와 인간 혈청에 대하여) $250\mu\text{l}$ 의 *E. coli* 추출물(20mg/ml; Promega)로 상온에서 6 시간동안 흡수시켰다(absorb).

상기 흡수된 항혈청으로 상온에서 하룻밤동안 막을 배양하거나 1/5000으로 희석된 anti-T7-Tag 컨쥬게이트로 상온에서 한시간동안 막을 배양하였다. 3x10min TTBS로 세정한 후에, TTBS 내의 5% 스킴 밀크에서 1/5000 으로 희석된 HRP-컨쥬게이트된 항-토끼(Silenus), 항-마우스(Silenus) 또는 항-인간(KPL) 항체를 상온에서 1시간 동안 첨가하였다. 면역보호성 단백질을 검출하기 위하여 TMB 막 퍼옥시다제 기질(KPL)dfm 첨가하기 전에 막을 세척하였다. 재조합 *P. gingivalis* 단백질의 반응성 결과는 표 7에 기재되어 있다.

또한 *P. gingivalis* 재조합 단백질(투여하기 전)로 면역화된 쥐에서 얻어진 혈청(1/1000으로 희석된 혈청 풀)에 대하여 상기 기재된 방법과 유사한 기술을 이용하여 천연의 전체 W50 *P. gingivalis* 단백질의 웨스턴 블롯에 대한 반응성을 분석하였다. PG2, PG8A, PG29 및 PG3은 모두 천연의 W50 블롯의 재조합 PG 단백질의 분자량과 유사한 분자량에서 밴드를 보였다. 이것은 PG 단백질이 W50 균주에서 발현되고 재조합 단백질이 천연 단백질에 대하여 적어도 하나의 동일한 면역 원성을 가진다는 것을 나타내는 것이다.

m-RNA 분석

핫 페놀(Hot Phenol) RNA 추출법

P. gingivalis W50 세포 (150ml 배양액)를 50% 글리세롤과 혼합하여 중간(mid) 대수기(OD A₆₀₀=0.18)까지 혐기적으로 성장시켜 RNA 추출시까지 -70℃에 저장하였다. 6000g에서 원심분리에서 세포를 펠릿화하고 8ml의 ASE (20mM NaOAc, 0.5% SDS, 1mM EDTA)에 재현탁하였다. 동일한 부피의 20mM NaOAc(pH 4.5)-포화 페놀을 첨가하고 30초간 진탕하여 혼합한 다음 5분간 65℃에서 배양한 후, 5초간 더 진탕하고 배양을 반복하였다. 냉각한 후에 2ml의 클로로포름을 첨가하고 5초간 진탕하여 혼합한 다음 혼합물을 4℃에서 10분간 10000g에서 원심회전(spin)시켰다. 최상단의 수상(aqueous phase)을 옮겨 페놀과 클로로포름 단계를 반복하여 다시 추출하였다. 상기 수상을 다시 옮겨 100U RNase 저해제(RNasin; Promega)을 첨가하였다. RNA를 3배 부피의 100% 에탄올로 -20℃에서 하룻밤동안 침전시켰다. RNA 침전물을 4℃에서 15분간 10000g에서 원심분리하여 회수하고 100% 에탄올로 세정하여 건조하고 1μl의 새로운 RNase 저해제를 함유하는 600μl의 살균, 탈이온 dH₂O에서 재현탁하였다. RNA를 분취하여 -70℃에서 저장하였다. RNA 농도는 분광광도계를 이용하여 결정하였다. 포름알데히드 RNA 겔은 RNA가 보존되어 있음을 확인시켜준다(Sambrook J. et al. 1989, Molecular Cloning. A laboratory manual. Cold Spring Laboratory Press, New York. 2nd Edition).

RT-PCR

분리된 RNA를 역전사(RT)의 주형으로 이용하여 cDNA를 제조하였다. 각각의 RNA 전사체는 서로 다른 수준으로 존재할 가능성이 크므로 다양한 RNA 농축물을 사용하였다. 폴리머라제 체인 반응법(PCR)을 이용하여 cDNA를 연속적으로 증폭하였다. PCR에 관한 하기 사항을 제외하고 제조사의 프로토콜에 따라 GeneAmpTM RNA PCR 키트(Perkin Elmer)를 이용하여 RT-PCR를 수행하였다; 35 사이클을 하기와 같이 수행하였다: 30초간 95℃에서 용융단계, 30초간 50-60℃에서 열처리(Anneal) 단계, 1분동안 72℃에서 신장(Extension) 단계. PTC-100 Programable Thermal Controller (MJ Research Inc.)를 이용하여 증폭하였다. 증폭된 생성물이 오염된 DNA로부터 생성된 것이 아님을 나타내기 위한 대조부로서 평행 튜브로부터 역전사효소(RTase)를 제외시켰다. 에티뮴 브로마이드를 함유하는 1% 아가로스상의 DNA 마커(GIBCO 1kB 래더)에 대하여 PCR 생성물을 검사하였다.

하기 사항을 제외하고 상기 기재된 "제조합 *P. gingivalis* 유전자의 클로닝, 발현 및 정제"의 항목에서 사용된 올리고뉴클레오타이드를 이용하여 RT-PCR 결과를 표 6에 기재하였다. PG1에 대하여 사용된 3' 역방향(reverse) 프라이머는 GCGCCTCGAGATTCATTTTCTTATAGAG이고, PG4에 대한 5' 전방향 프라이머는 CTTCTTGTCGACTACAGCGGACATCATAAAATC이고 3' 역방향 프라이머는 TTCCACCTCGAGTTAACGCAACTCTTCTTCGAT이고, PG6에 대한 5' 전방향 프라이머는 TAAAGAATTCTGCCTCGAACCCATAATTGCTCCG이고, PG10에 대한 5' 전방향 프라이머는 CGCGCATATGGATAAAGTGAGCTATGC이고 3' 역방향 프라이머는 CGCGCTCGAGTTTGTGTAATCAATAATTC이고, PG13에 대한 5' 전방향 프라이머는 GCCCGCGCCATGCGGACAAAACTATCTTTTGTGCG이고 3' 역방향 프라이머는 GCCCGCGCCTTAGTTGTTGAATCGAATCGCTATTTGAGC이었다. *P. gingivalis* 전사체의 증폭은 특정 후보인자에 대한 RNA가 존재하고 그 단백질이 생성된다는 사실을 나타내는 것이다. 그러나 증폭이 이루어지지 않았다고 하더라도 이것은 그 유전자가 절대로 전사되지 않는다는 것을 나타내는 것은 아니며, 배양 조건의 결과 또는 회수될 경우 세포 상태의 결과일 수 있다.

표 6. 시험관내에서 성장된 *P. gingivalis* W50의 PG m-RNA의 발현.

+ 기호는 아가로스 겔에서 가시적인 밴드이고, -는 아가로스 겔에서 밴드가

존재하지 않음을 의미하고, ND(not detected)는 검출되지 않음을 의미한다.

PG #	RNA (mg)	열처리 (Annealing) 온도(℃)	RT-PCR	PCR (-RT)	단편의 대략적 크기(bp)	단편의 예상 크기(bp)
1	0.15	55	+	-	1300	1362
2	1.0	50	+	-	3200	3051
3	0.15	60	+	-	720	690
4	2.9	55	-	-	N.D.	2000
5	0.02	50	+	-	1000	947
6	1.0	55	+	-	1000	972
8A	0.15	50	+	-	1200	1278
10	0.15	55	+	-	590	585
11	0.10	60	+	-	960	942
12	0.02	60	+	-	880	831
13	1.0	50	+	-	2150	2274
14	0.15	60	+	-	1050	996
22	1.0	60	-	-	N.D.	228
24	1.0	55	+	+	1150	1194
29	0.15	60	+	-	880	885

표 7: 토끼, 쥐 및 인간의 항혈청에 대하여 *E.coli*에서의 발현된 단백질의 면역블롯의 결과. 추론된(Deduced) MW는 *P. gingivalis* 단백질의 아미노산 서열로부터 계산된 것이고, 이들중 몇몇은 N-말단 신호 서열이 제거된 것이다. 겔보기(Apparent) MW는 SDS-PAGE 겔에서 결정된 것이다. N- 및 C-말단 태그를 재조합 단백질의 추론된 MW에 대략 2.5 KDa 으로 첨가하였다. + : positive, - : negative, +/- : weak positive, ND : not done.

단백질 번호	추론된 MW (KDa)	겔보기 MW (KDa)	항혈청 반응성			
			T7	토끼	쥐	인간
PG1	47.5	63	ND	-	-	-
PG2	112.4	125.7	ND	+	-	-
PG3	22.6	18.3	ND	_a	-	-
PG4	75	90.6	ND	-	-	-
PG5	34.9	43.8	ND	-	-	-
PG6	36.7	47.1	ND	-	-	-
PG8	67.5	63.1	ND	_b	-	-
PG8A	47.7	90.6	ND	-	-	-
PG10	21.3	25.5	ND	+	-	+
PG11	36.2	42.4	ND	-	-	-
PG12	30.7	30.6	ND	-	-	-
PG13	84.5	101	ND	-	-	-
PG14	36	42.4	ND	-	+	+
PG22	8.6	11.1	ND	-	-	-
PG24A	47	63.1	ND	-	-	-
PG29	31.1	40.9	ND	-	+	+

단백질 번호	추론된 MW (KDa)	겔보기 MW (KDa)	항혈청 반응성			
			T7	토끼	쥐	인간
PG30	35.1	46.9	+	-	-	-
PG31	16.7	-	-	-	-	-
PG32	41.2	59.5	+	+	+	-
PG33	39.9	52.7	+	+	+	-
PG35	92.6	116.6	+	-	-	-
PG36	98.9	120.2	-	-	-	-
PG37	18.8	23.1	+	+	-	-
PG38	16.1	22.9	+	-	-	-
PG39	87.9	116.6	+	-	-	-
PG40	76.6	103.1	+	-	-	-
PG41	48.3	81.1	+	-	+	+
PG42	59.3	73.9	+	-	-	-
PG43	27.1	50.3	+	-	-	-
PG44	28.6	32.3	+	-	+	-
PG45	84	100.6	+	-	-	-
PG46	83	97.7	+	-	-	-
PG47	93.7	42.5	+	+	-	+
PG48	45.2	37.9	+	-	-	-
PG49	33.3	64.1	+	-	+	-
PG50	91.9	113.2	+	+	-	-
PG51	19.6	27.2	+	-	-	-
PG52	50.4	64.4	+	+	-	+
PG53	47.4	45.4	+	-	-	+
PG54	101.4	46.7	+	+	-	-
PG55	70.4	68.4	+	-	-	-
PG56	142.3	-	-	-	-	-
PG57	100	134.5	+	+	+	+
PG58	63	82.9	+	-	-	-
PG59	33.3	43.6	+	-	-	-
PG60	55.6	77.8	+	-	-	-
PG61	81.5	107.3	+	-	-	-

단백질 번호	추론된 MW (KDa)	겔보기 MW (KDa)	항혈청 반응성			
			T7	토끼	쥐	인간
PG62	51.9	58.4	+	-	-	-
PG63	29.6	43.6	+	-	-	-
PG64	18.5	26.9	+	-	-	-
PG65	25.9	28.8	+	-	-	-
PG66	22.2	25.1	+	+	-	-
PG67	103.7	105	+	-	-	-
PG68	133.3	30.7	+	-	+	+
PG69	44.4	50.8	+	-	-	-
PG70	25.9	30.8	+	-	-	-
PG71	88.9	105.5	+	-	-	-
PG72	40.7	49.8	+	-	-	-
PG73	40.7	29	+/-	-	-	-
PG74	22.2	32.5	+	-	-	-
PG75	40.7	46.7	+	-	-	-
PG76	48.1	55.6	+	-	-	+
PG77	29.6	36.9	+	-	-	-
PG78	33.3	35.4	+	-	-	-
PG79	33.3	-	-	-	-	-
PG80	25.9	20.5	+	-	-	-
PG81	23	25.8	+	-	-	-
PG82	44.8	48.5	+	-	-	-
PG84	41.7	52.4	+	-	-	+/-
PG85	62.7	72.4	+	-	-	-
PG86	21.7	27.4	+	-	-	+/-
PG87	83	91.3	+	-	-	+
PG88	27	40.1	+	-	-	-
PG89	26.2	29.4	+	-	-	-
PG90	23	28.4	+	-	-	-
PG91	57.2	85.7	+	+	+	+
PG92	83.6	110.4	+	-	-	+
PG93	83.4	110.4	+	-	-	+

단백질 번호	추론된 MW (KDa)	겔보기 MW (KDa)	항혈청 반응성			
			T7	토끼	쥐	인간
PG96	59.3	70.3	+	+	+	+
PG97	44.4	57.5	+	-	+	+
PG98	33.3	36	+	-	-	-
PG99	40.7	55.6	+	-	+	+
PG100	29.6	10.8	+	-	-	-
PG101	14.8	19.7, 14.1	+	-	-	-
PG102	59.3	70.3	+	-	-	+
PG104	40.7	57.5	+	-	-	+

a. 사코실 불용성 *P. gingivalis* 항원에 대한 토끼 항혈청으로 검출한 양성 반응.

b. 전체 *P. gingivalis*에 대한 토끼 항혈청과 약한 양성 반응을 나타내는 정제된 단백질.

이 분야의 통상의 지식을 가진 자라면 본 발명의 사상과 범위를 벗어나지 않고 상기 기재된 특정 실시예로부터 많은 변형 및/또는 변경이 이루어질 수 있음을 이해할 수 있다. 그러므로 본 발명의 실시에는 예시적으로 이해되어야 하며 이에 한정되는 것으로 이해해서는 안된다.

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(57) 청구의 범위

청구항 1.

하기 아미노산 서열로 이루어지는 분리된 항원성 *Porphyromonas gingivalis* 폴리펩티드:

SEQ. ID. NO. 265 내지 SEQ. ID. NO. 528, SEQ. ID. NO. 531 및 SEQ. ID. NO. 532로 이루어진 군으로부터 선택되는 아미노산 서열; 또는

서열번호 SEQ. ID. NO. 265 내지 SEQ. ID. NO. 528, SEQ. ID. NO. 531 및 SEQ. ID. NO. 532으로 이루어진 군으로부터 선택되는 연속 아미노산 서열과 동일한, 길이 40개 이상의 연속 아미노산 서열.

청구항 2.

제1항에 있어서,

SEQ. ID. NO. 265 내지 SEQ. ID. NO. 528, SEQ. ID. NO. 531 및 SEQ. ID. NO. 532으로 이루어진 군으로부터 선택되는 아미노산 서열로 이루어지는 폴리펩티드.

청구항 3.

삭제

청구항 4.

제1항에 있어서,

서열번호 SEQ. ID. NO. 265 내지 SEQ. ID. NO. 528, SEQ. ID. NO. 531 및 SEQ. ID. NO. 532으로 이루어진 군으로부터 선택되는 연속 아미노산 서열과 동일한, 길이 40개 이상의 연속 아미노산 서열로 이루어지는 폴리펩티드.

청구항 5.

제1항에 있어서,

SEQ. ID. NO. 386 내지 SEQ. ID. NO. 528 및 SEQ. ID. NO. 532로 이루어진 군으로부터 선택되는 아미노산 서열; 또는

SEQ. ID. NO. 386 내지 SEQ. ID. NO. 528 및 SEQ. ID. NO. 532로 이루어진 군으로부터 선택되는 연속 아미노산 서열과 동일한, 길이 40개 이상의 연속 아미노산 서열.

청구항 6.

제1항에 있어서,

SEQ. ID. NO. 386 내지 SEQ. ID. NO. 528 및 SEQ. ID. NO. 532로 이루어진 군으로부터 선택되는 아미노산 서열로 이루어지는 폴리펩티드.

청구항 7.

삭제

청구항 8.

제1항에 있어서,

SEQ. ID. NO. 386 내지 SEQ. ID. NO. 528 및 SEQ. ID. NO. 532로 이루어진 군으로부터 선택되는 연속 아미노산 서열과 동일한, 길이 40개 이상의 연속 아미노산 서열로 이루어지는 폴리펩티드.

청구항 9.

제6항에 있어서,

하기로 이루어지는 군으로부터 선택되는 아미노산 서열로 이루어지는 폴리펩티드:

SEQ. ID. NO. 386, SEQ. ID. NO. 424, SEQ. ID. NO. 425, SEQ. ID. NO. 434, SEQ. ID. NO. 447, SEQ. ID. NO. 458, SEQ. ID. NO. 475, SEQ. ID. NO. 498, SEQ. ID. NO. 499, SEQ. ID. NO. 500, SEQ. ID. NO. 501, SEQ. ID. NO. 387, SEQ. ID. NO. 400, SEQ. ID. NO. 411, SEQ. ID. NO. 419, SEQ. ID. NO. 420, SEQ. ID. NO. 427, SEQ. ID. NO. 429, SEQ. ID. NO. 433, SEQ. ID. NO. 437, SEQ. ID. NO. 438, SEQ. ID. NO. 443, SEQ. ID. NO. 444, SEQ. ID. NO. 448, SEQ. ID. NO. 449, SEQ. ID. NO. 452, SEQ. ID. NO. 455, SEQ. ID. NO. 457, SEQ. ID. NO. 459, SEQ. ID. NO. 461, SEQ. ID. NO. 462, SEQ. ID. NO. 463, SEQ. ID. NO. 467, SEQ. ID. NO. 468, SEQ. ID. NO. 469, SEQ. ID. NO. 482, SEQ. ID. NO. 484, SEQ. ID. NO. 485, SEQ. ID. NO. 494, SEQ. ID. NO. 508, SEQ. ID. NO. 509, SEQ. ID. NO. 510, SEQ. ID. NO. 520, SEQ. ID. NO. 521, SEQ. ID. NO. 522, SEQ. ID. NO. 525, SEQ. ID. NO. 526, SEQ. ID. NO. 528, SEQ. ID. NO. 389, SEQ. ID. NO. 390 및 SEQ. ID. NO. 391.

청구항 10.

SEQ. ID. NO. 386 내지 SEQ. ID. NO. 528 및 SEQ. ID. NO. 532 중 표 3에 기재된 리더 서열을 제외한 서열로 이루어지는 군으로부터 선택되는 아미노산 서열로 이루어지는 분리된 항원성 *Porphyromonas gingivalis* 폴리펩티드.

청구항 11.

제1항 내지 제10항 중 어느 한 항의 폴리펩티드를 코딩하는 뉴클레오티드 서열로 이루어지는 분리된 DNA 분자.

청구항 12.

제11항에 있어서,

SEQ. ID. NO. 1 내지 SEQ. ID. NO. 264, SEQ. ID. NO. 529 및 SEQ. ID. NO. 530으로 이루어진 군으로부터 선택되는 뉴클레오티드 서열로 이루어지는 분리된 DNA 분자.

청구항 13.

전사 조절 인자에 연결된 제11항의 DNA 분자를 포함하는 재조합 발현 벡터.

청구항 14.

제13항의 재조합 발현 벡터를 포함하는 세포.

청구항 15.

제14항의 세포를 배양하는 것을 포함하는 *P. gingivalis* 폴리펩티드의 생산 방법.

청구항 16.

제1항 내지 제10항 중 어느 한 항의 적어도 하나의 유효량의 폴리펩티드 및 약제학적으로 허용가능한 담체를 포함하는, *P. gingivalis*에 대하여 면역 반응을 유발하여, 치주질환의 치료에 사용하기 위한 조성물.

청구항 17.

제16항에 있어서, 제11항의 적어도 하나의 DNA 분자를 추가로 포함하는 조성물.

청구항 18.

제16항에 있어서,

상기 약제학적으로 허용가능한 담체가 애주번트(adjuvant)인 조성물.

청구항 19.

제16항의 조성물을 피검체에 투여하여 *P. gingivalis* 감염을 처치하는 약물의 제조에 사용하는 방법.

청구항 20.

제19항에 있어서, 상기 감염의 처치는 예방적인 것을 특징으로 하는 방법.

청구항 21.

제19항에 있어서, 상기 감염의 처치는 치료적인 것을 특징을 하는 방법.

청구항 22.

제11항의 적어도 하나의 유효량의 DNA 분자 및 약제학적으로 허용가능한 담체를 포함하는, *P. gingivalis*에 대하여 면역 반응을 유발하여, 치주질환의 치료에 사용하기 위한 조성물.

청구항 23.

제22항에 있어서, 상기 약제학적으로 허용가능한 담체가 애쥬번트인 조성물.

청구항 24.

제22항의 조성물을 피검체에 투여하여 *P. gingivalis* 감염을 처치하는 약물의 제조에 사용하는 방법.

청구항 25.

제24항에 있어서, 상기 감염의 처치는 예방적인 것을 특징으로 하는 방법.

청구항 26.

제24항에 있어서, 상기 감염의 처치는 치료적인 것을 특징을 하는 방법.

청구항 27.

제1항 내지 제10항 중 어느 한 항의 폴리펩티드에 대항하여 생성되는 항체.

청구항 28.

제27항에 있어서,

상기 항체가 폴리클론인 항체.

청구항 29.

제27항에 있어서,

상기 항체가 모노클론인 항체.

청구항 30.

제27항의 항체 중 적어도 하나를 포함하는 치주질환 치료용 조성물.

청구항 31.

제30항에 있어서,

상기 조성물이 경구용에 적합한 조성물.

청구항 32.

SEQ. ID. NO. 1 내지 SEQ. ID. NO. 121, SEQ. ID. NO. 529 및 이에 상보적 서열로 이루어진 군으로부터 선택되는 연속 뉴클레오티드 서열과 동일한, 길이 18개 이상의 연속 뉴클레오티드 서열로 이루어지는 뉴클레오티드 프로브.

청구항 33.

제32항에 있어서,

검출가능한 표지를 추가로 포함하는 뉴클레오티드 프로브.

청구항 34.

샘플내에서 *P. gingivalis* 핵산의 존재를 검출하는 방법에 있어서,

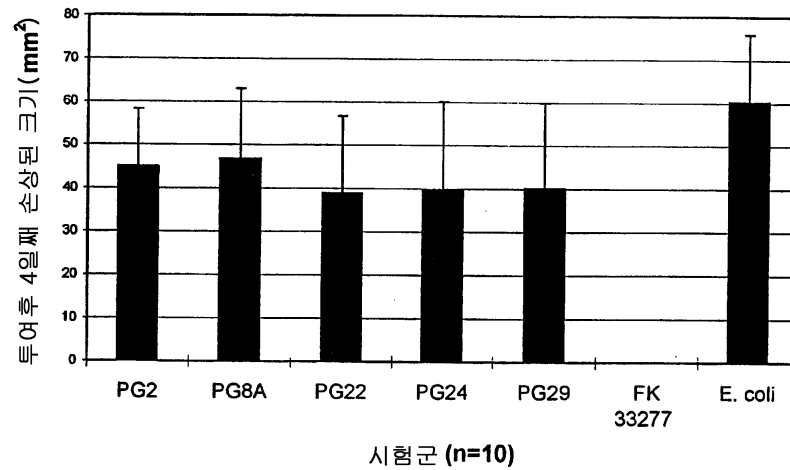
(a) 샘플을 제32항 또는 제33항의 뉴클레오티드 프로브와 접촉시켜, 샘플내에서 프로브와 *P. gingivalis* 핵산 사이에 혼성체가 형성되도록 하는 단계; 및

(b) 상기 (a) 단계에서 형성된 혼성체를 검출하는 단계

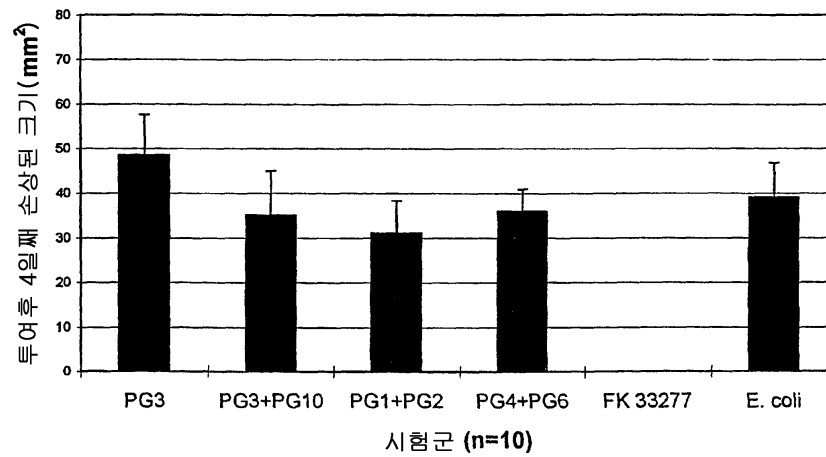
를 포함하고, 여기서 혼성체가 검출된다는 것은 샘플내에 *P. gingivalis* 핵산이 존재하는 것을 의미하는 방법.

도면

도면1



도면2



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<213> Porphyromonas gingivalis

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<212> DNA

<213> Porphyromonas gingivalis

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<213> Porphyromonas gingivalis

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<211> 735

<212> DNA

<213> Porphyromonas gingivalis

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<213> Porphyromonas gingivalis

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gccgagtact tcgtcgtcca gcaaggaaag gcatggcaag tactcaaaag agaggaatac      720
acctatgagg acaatatctg catacaatat ttggctatta acggtaccga cacaaggtg      780
tacaagcgag acatcgagag cgataagtcc atctccgcaa atgtcattga cattccgtca      840
atgccggaac agacctggcc taatatgtac ggattcaacg caaagcgact gaaagagact      900
tattcctcct acgaaggaga tgtggctact cctatatctg actatatcta tacgtacaag      960
gctcttacct caatggcaac accttcgaca gaagctcagg tagcagtcta tctcaatccg      1020
tcaacggacc ggttagtgat tctggccaac ggcatacacac atctgagcat gtacgacttg      1080
cagggtaagc ttatccgtga ttgtgccttg agcggcgata aggtggaaat ggggtgtcga      1140
tctttgacca aaggacata cctgcttaaa gtgaatacgg atcagggagc ctttgtgaga      1200
aaagtcgtga ttcga      1215
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<211>      454
<212>      PRT
<213>      Porphyromonas gingivalis
<400>      265
Phe Cys Val Met Ala Lys Val Ile Lys Thr Lys Lys Gly Leu Ala Leu
  1             5             10             15
Asn Leu Lys Gly Lys Pro Leu Pro Glu Met Leu Ala Glu Pro Ala Gln
      20             25             30
Ser Pro Thr Tyr Ala Val Val Pro Asp Asp Phe Glu Gly Val Ile Pro
      35             40             45
Lys Val Thr Ala Arg Pro Gly Asp Lys Val Arg Ala Gly Ser Ala Leu
      50             55             60
Met His His Lys Ala Tyr Pro Glu Met Lys Phe Thr Ser Pro Val Ser
      65             70             75             80
Gly Glu Val Ile Ala Val Asn Arg Gly Ala Lys Arg Lys Val Leu Ser
      85             90             95
Ile Glu Val Lys Pro Asp Gly Leu Asn Glu Tyr Glu Ser Phe Pro Val
      100            105            110
Gly Asp Pro Ser Ala Leu Ser Ala Glu Gln Ile Lys Glu Leu Leu Leu

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115          120          125
Ser Ser Gly Met Trp Gly Phe Ile Lys Gln Arg Pro Tyr Asp Ile Val
130          135          140
Ala Thr Pro Asp Ile Ala Pro Arg Asp Ile Tyr Ile Thr Ala Asn Phe
145          150          155          160
Thr Ala Pro Leu Ala Pro Asp Phe Asp Phe Ile Val Arg Gly Glu Glu
165          170          175
Arg Ala Leu Gln Thr Ala Ile Asp Ala Leu Ala Lys Leu Thr Thr Gly
180          185          190
Lys Val Tyr Val Gly Leu Lys Pro Gly Ser Ser Leu Gly Leu His Asn
195          200          205
Ala Glu Ile Val Glu Val His Gly Pro His Pro Ala Gly Asn Val Gly
210          215          220
Val Leu Ile Asn His Thr Lys Pro Ile Asn Arg Gly Glu Thr Val Trp
225          230          235          240
Thr Leu Lys Ala Thr Asp Leu Ile Val Ile Gly Arg Phe Leu Leu Thr
245          250          255
Gly Lys Ala Asp Phe Thr Arg Met Ile Ala Met Thr Gly Ser Asp Ala
260          265          270
Ala Ala His Gly Tyr Val Arg Ile Met Pro Gly Cys Asn Val Phe Ala
275          280          285
Ser Phe Pro Gly Arg Leu Thr Ile Lys Glu Ser His Glu Arg Val Ile
290          295          300
Asp Gly Asn Val Leu Thr Gly Lys Lys Leu Cys Glu Lys Glu Pro Phe
305          310          315          320
Leu Ser Ala Arg Cys Asp Gln Ile Thr Val Ile Pro Glu Gly Asp Asp
325          330          335
Val Asp Glu Leu Phe Gly Trp Ala Ala Pro Arg Leu Asp Gln Tyr Ser
340          345          350
Met Ser Arg Ala Tyr Phe Ser Trp Leu Gln Gly Lys Asn Lys Glu Tyr
355          360          365
Val Leu Asp Ala Arg Ile Lys Gly Gly Glu Arg Ala Met Ile Met Ser
370          375          380
Asn Glu Tyr Asp Arg Val Phe Pro Met Asp Ile Tyr Pro Glu Tyr Leu
385          390          395          400
Leu Lys Ala Ile Ile Ala Phe Asp Ile Asp Lys Met Glu Asp Leu Gly
405          410          415
Ile Tyr Glu Val Ala Pro Glu Asp Phe Ala Thr Cys Glu Phe Val Asp
420          425          430
Thr Ser Lys Ile Glu Leu Gln Arg Ile Val Arg Glu Gly Leu Asp Met
435          440          445
Leu Tyr Lys Glu Met Asn
450
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<211> 201
<212> PRT
<213> Porphyromonas gingivalis
<400> 266
Glu Leu Ser Lys Cys Tyr Met Asp Lys Val Ser Tyr Ala Leu Gly Leu
1 5 10 15
Ser Ile Gly Asn Asn Phe Lys Ser Ser Gly Ile Asp Ser Val Val Met
20 25 30

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Asp Asp Phe Met Gln Gly Leu Ser Asp Val Leu Glu Glu Lys Ala Pro
   35                               40                               45
Gln Leu Ser Tyr Asp Glu Ala Lys Arg Glu Ile Glu Ala Tyr Phe Met
   50                               55                               60
Asp Leu Gln Gln Lys Ala Val Lys Leu Asn Lys Glu Ala Gly Glu Glu
   65                               70                               75                               80
Phe Leu Lys Ile Asn Ala His Lys Glu Gly Val Thr Thr Leu Pro Ser
   85                               90                               95
Gly Leu Gln Tyr Glu Val Ile Lys Met Gly Glu Gly Pro Lys Pro Thr
  100                               105                               110
Leu Ser Asp Thr Val Thr Cys His Tyr His Gly Thr Leu Ile Asn Gly
  115                               120                               125
Ile Val Phe Asp Ser Ser Met Asp Arg Gly Glu Pro Ala Ser Phe Pro
  130                               135                               140
Leu Arg Gly Val Ile Ala Gly Trp Thr Glu Ile Leu Gln Leu Met Pro
  145                               150                               155                               160
Val Gly Ser Lys Trp Lys Val Thr Ile Pro Ser Asp Leu Ala Tyr Gly
  165                               170                               175
Asp Arg Gly Ala Gly Glu His Ile Lys Pro Gly Ser Thr Leu Ile Phe
  180                               185                               190
Ile Ile Glu Leu Leu Ser Ile Asn Lys
  195                               200
<210>      267
<211>      279
<212>      PRT
<213>      Porphyromonas gingivalis
<400>      267
Gln Lys Asn Lys Arg Lys Met Lys Lys Ala Leu Leu Ile Gly Ala Ala
   1                               5                               10                               15
Leu Leu Gly Ala Val Ser Phe Ala Ser Ala Gln Ser Leu Ser Thr Ile
  20                               25                               30
Lys Val Gln Asn Asn Ser Val Gln Gln Pro Arg Glu Glu Ala Thr Ile
  35                               40                               45
Gln Val Cys Gly Glu Leu Ala Ala Glu Gln Val Asp Cys Ile Gly Thr Gly
  50                               55                               60
Asn Ser Ala Ile Ile Ala Ala Ala Ala Lys Phe Glu Ser Asp Asp Leu
  65                               70                               75                               80
Glu Ser Tyr Val Gly Trp Glu Ile Met Ser Val Asp Phe Phe Pro Gly
  85                               90                               95
Tyr Lys Ala Cys Lys Tyr Thr Ser Ala Val Trp Ala Asp Asp Met Thr
  100                               105                               110
Ile Leu Gly Gln Ser Glu Asp Ser Asp Pro Glu Met Gln Thr Ile Asn
  115                               120                               125
Asn Leu Ala Leu Lys Thr Ser Val Lys Ile Glu Ala Gly Lys Asn Tyr
  130                               135                               140
Ile Val Gly Tyr Ile Ala Asn Thr Ala Gly Gly His Pro Ile Gly Cys
  145                               150                               155                               160
Asp Gln Gly Pro Ala Val Asp Gly Tyr Gly Asp Leu Val Ser Ile Ser
  165                               170                               175
Glu Asp Gly Gly Ala Thr Phe Pro Pro Phe Glu Ser Leu His Gln Ala
  180                               185                               190
Val Pro Thr Leu Asn Tyr Asn Ile Tyr Val Val Val His Leu Lys Lys

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195          200          205
Gly Glu Gly Val Glu Ala Val Leu Thr Asn Asp Lys Ala Asn Ala Tyr
210          215          220
Val Gln Asn Gly Val Ile Tyr Val Ala Gly Ala Asn Gly Arg Gln Val
225          230          235          240
Ser Leu Phe Asp Met Asn Gly Lys Val Val Tyr Thr Gly Val Ser Glu
245          250          255
Thr Ile Ala Ala Pro Gln Lys Gly Met Tyr Ile Leu Arg Val Gly Ala
260          265          270
Lys Ser Ile Lys Leu Ala Ile
275
<210> 268
<211> 157
<212> PRT
<213> Porphyromonas gingivalis
<400> 268
Arg Xaa Phe Leu Pro Glu Lys Ala Leu Tyr Ile Gly Cys Arg Val Glu
1 5 10 15
Thr Gln Glu Gly His Ala Val Gly Phe Gly Leu Asp Asp Gly Pro Ala
20 25 30
Met Lys Gly Lys Gly Asp Leu Val Gly Ser Tyr Leu Pro Gly Ala Ala
35 40 45
Pro Met Pro Phe Val Pro Leu Ser Asp Ile Pro Ala Arg Ser Met Asp
50 55 60
Ala Asn Phe Tyr Ile Tyr Ser Arg Ile Ser Leu Gly Ser Gly Thr Gln
65 70 75 80
Asp Val Leu Gln His Arg Met Lys Val Tyr Pro Asn Pro Ala Thr Thr
85 90 95
Glu Leu His Val Glu Ala Leu Ser Ala Trp Val Gly Glu Gln Ala Ala
100 105 110
Val Tyr Asp Met Arg Gly Arg Arg Val Ser Ala Arg Thr Val Asp Ser
115 120 125
Glu Lys Leu Cys Ile Asp Ile Ala Ser Leu Pro Val Gly Val Tyr Met
130 135 140
Leu Arg Ile Gly Ser Tyr Ser Ala Lys Phe Glu Lys Arg
145 150 155
<210> 269
<211> 562
<212> PRT
<213> Porphyromonas gingivalis
<400> 269
Thr Arg Asn Val Ser Leu Ile Lys Met Pro Arg Ile Met Lys Leu Lys
1 5 10 15
Ile Ala Leu Arg Leu Leu Leu Ala Thr Phe Ala Ile Val Leu Phe Ser
20 25 30
Pro Leu Ala Lys Ala Gln Met Asp Ile Gly Gly Asp Asp Val Leu Ile
35 40 45
Glu Thr Met Ser Thr Leu Ser Gly Tyr Ser Glu Asp Phe Tyr Tyr Lys
50 55 60
Met Ala Val Ala Asp Asn Gly Trp Ile Tyr Val Met Leu Asp Phe Ser
65 70 75 80
Arg Ile Tyr Phe Asp Asp Val Arg Leu Tyr Arg Ser Lys Asp Gly Gly

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

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                    500                      505                      510
Val Val Tyr Asp Met Gln Gly Arg Ile Val Glu Lys Val Ser Phe Ser
    515                      520                      525
Gly Lys Glu Tyr Lys Leu Asn Val Gln Tyr Leu Ser Lys Gly Thr Tyr
    530                      535                      540
Met Leu Lys Val Val Ala Asp Thr Glu Tyr Phe Val Glu Lys Ile Ile
545                      550                      555                      560
Val Glu
<210>      270
<211>      391
<212>      PRT
<213>      Porphyromonas gingivalis
<400>      270
Gln Met Lys Arg Leu Leu Pro Phe Leu Leu Leu Ala Gly Leu Val Ala
  1                      5                      10                      15
Val Gly Asn Val Ser Ala Gln Ser Pro Arg Ile Pro Gln Val Asp Val
    20                      25                      30
His Thr Arg Ile Ala Arg Asn Ala Arg Tyr Arg Leu Asp Lys Ile Ser
    35                      40                      45
Val Pro Asp Ser Arg Gln Ile Phe Asp Tyr Phe Tyr Lys Glu Glu Thr
    50                      55                      60
Ile Pro Thr Lys Ile Gln Thr Thr Thr Gly Gly Ala Ile Thr Ser Ile
  65                      70                      75                      80
Asp Ser Leu Phe Tyr Glu Asp Asp Arg Leu Val Gln Val Arg Tyr Phe
    85                      90                      95
Asp Asn Asn Leu Glu Leu Lys Gln Ala Glu Lys Tyr Val Tyr Asp Gly
    100                      105                      110
Ser Lys Leu Val Leu Arg Glu Ile Arg Lys Ser Pro Thr Asp Glu Thr
    115                      120                      125
Pro Ile Lys Lys Val Ser Tyr His Tyr Leu Cys Gly Ser Asp Met Pro
    130                      135                      140
Phe Glu Ile Thr Thr Glu Met Ser Asp Gly Tyr Phe Glu Ser His Thr
145                      150                      155                      160
Leu Asn Tyr Leu Asn Gly Lys Ile Ala Arg Ile Asp Ile Met Thr Gln
    165                      170                      175
Gln Asn Pro Ser Ala Glu Leu Ile Glu Thr Gly Arg Met Val Tyr Glu
    180                      185                      190
Phe Asp Ala Asn Asn Asp Ala Val Leu Leu Arg Asp Ser Val Phe Leu
    195                      200                      205
Pro Leu Gln Asn Lys Trp Val Glu Met Phe Thr His Arg Tyr Thr Tyr
    210                      215                      220
Asp Asn Lys His Asn Cys Ile Arg Trp Glu Gln Asp Glu Phe Gly Thr
225                      230                      235                      240
Leu Thr Leu Ala Asn Asn Phe Glu Tyr Asp Thr Thr Ile Pro Leu Ser
    245                      250                      255
Ser Val Leu Phe Pro Thr His Glu Glu Phe Phe Arg Pro Leu Leu Pro
    260                      265                      270
Asn Phe Met Lys His Met Arg Thr Lys Gln Thr Tyr Phe Asn Asn Ser
    275                      280                      285
Gly Glu Gly Leu Ser Glu Val Cys Asp Tyr Asn Tyr Phe Tyr Thr Asp
    290                      295                      300
Met Gln Gly Asn Ala Leu Thr Asp Val Ala Val Asn Glu Ser Ile Lys

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305              310              315              320
Ile Tyr Pro Arg Pro Ala Thr Asp Phe Leu Arg Ile Glu Gly Ser Gln
              325              330              335
Leu Leu Arg Leu Ser Leu Phe Asp Met Asn Gly Lys Leu Ile Arg Ala
              340              345              350
Thr Glu Leu Thr Gly Asp Leu Ala Ile Ile Gly Val Ala Ser Leu Pro
              355              360              365
Arg Gly Thr Tyr Ile Ala Glu Ile Thr Ala Ala Asn Ser Lys Thr Ile
              370              375              380
Arg Ala Lys Val Ser Leu Arg
385              390
<210>      271
<211>      428
<212>      PRT
<213>      Porphyromonas gingivalis
<400>      271
Lys Arg Asn Pro Leu Pro Leu Thr Ala Ser Asn Arg Lys Ile Phe Ile
  1              5              10              15
Lys Met Arg Gln His Leu Ser Leu Phe Pro Phe Ile Leu Phe Leu Leu
              20              25              30
Leu Ala Phe Ser Tyr Val Gly Cys Arg Thr Val Arg Gln Thr Pro Lys
              35              40              45
Gln Ser Glu Arg Tyr Val Val Val Leu Ser Leu Asp Gly Phe Arg Pro
              50              55              60
Asp Tyr Thr Asp Arg Ala Arg Thr Pro Ala Leu Asp Arg Met Ala Gln
              65              70              75              80
Glu Gly Leu Ser Gly Ser Leu Gln Pro Cys Phe Pro Ser Leu Thr Phe
              85              90              95
Pro Asn His Tyr Ser Met Ala Thr Gly Leu Tyr Pro Asp His His Gly
              100              105              110
Ile Val Ala Asn Glu Phe Val Asp Ser Leu Leu Gly Ile Phe Arg Ile
              115              120              125
Ser Asp Arg Lys Ala Val Glu Thr Pro Gly Phe Trp Gly Gly Glu Pro
              130              135              140
Val Trp Asn Thr Ala Ala Arg Gln Gly Ile Arg Thr Gly Val Tyr Phe
              145              150              155              160
Trp Val Gly Ser Glu Thr Ala Val Asn Gly Asn Arg Pro Trp Arg Trp
              165              170              175
Lys Lys Phe Ser Ser Thr Val Pro Phe Arg Asp Arg Ala Asp Ser Val
              180              185              190
Ile Ala Trp Leu Gly Leu Pro Glu Lys Glu Arg Pro Arg Leu Leu Met
              195              200              205
Trp Tyr Ile Glu Glu Pro Asp Met Ile Gly His Ser Gln Thr Pro Glu
              210              215              220
Ser Pro Leu Thr Leu Ala Met Val Glu Arg Leu Asp Ser Val Val Gly
              225              230              235              240
Tyr Phe Arg Lys Arg Leu Asp Ser Leu Pro Ile Ala Ala Gln Thr Asp
              245              250              255
Phe Ile Ile Val Ser Asp His Gly Met Ala Thr Tyr Glu Asn Glu Lys
              260              265              270
Cys Val Asn Leu Ser His Tyr Leu Pro Ala Asp Ser Phe Leu Tyr Met
              275              280              285

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Ala Thr Gly Ala Phe Thr His Leu Tyr Pro Lys Pro Ser Tyr Thr Glu
290 295 300
Arg Ala Tyr Glu Ile Leu Arg Ala Ile Pro His Ile Ser Val Tyr Arg
305 310 315 320
Lys Gly Glu Val Pro Lys Arg Leu Arg Cys Gly Thr Asn Pro Arg Leu
325 330 335
Gly Glu Leu Val Val Ile Pro Asp Ile Gly Ser Thr Val Phe Phe Ala
340 345 350
Ile Asn Glu Asp Val Arg Pro Gly Ala Ala His Gly Tyr Asp Asn Gln
355 360 365
Ala Pro Glu Met Arg Ala Leu Leu Arg Ala Val Gly Pro Asp Phe Arg
370 375 380
Pro Gly Ser Arg Val Glu Asn Leu Pro Asn Ile Thr Ile Tyr Pro Leu
385 390 395 400
Ile Cys Arg Leu Leu Gly Ile Glu Pro Ala Pro Asn Asp Ala Asp Glu
405 410 415
Thr Leu Leu Asn Gly Leu Ile Arg Asp Lys Arg Pro
420 425
<210> 272
<211> 282
<212> PRT
<213> Porphyromonas gingivalis
<400> 272
Leu Ser Arg Gly Val Phe Pro Leu Met Tyr Gly Arg Arg Gly Ser Ile
1 5 10 15
Arg Ala Ser Ser Gly His Arg Asp Lys Ile Phe Lys Asn Thr Ile Ile
20 25 30
Arg Phe Ile Thr Met Lys Val Gly Leu Phe Ile Pro Cys Tyr Val Asn
35 40 45
Ala Val Tyr Pro Glu Val Gly Ile Ala Thr Tyr Lys Leu Leu Lys Ser
50 55 60
Leu Asp Ile Asp Val Asp Tyr Pro Met Asp Gln Thr Cys Cys Gly Gln
65 70 75 80
Pro Met Ala Asn Ala Gly Phe Glu Gln Lys Ala Gln Lys Leu Ala Leu
85 90 95
Arg Phe Glu Glu Leu Phe Glu Ser Tyr Asp Val Val Val Gly Pro Ser
100 105 110
Ala Ser Cys Val Ala Phe Val Lys Glu Asn Tyr Asp His Ile Leu Arg
115 120 125
Pro Thr Gly His Val Cys Lys Ser Ala Ala Lys Val Arg Asp Ile Cys
130 135 140
Glu Phe Leu His Asp Asp Leu Lys Ile Thr Ser Leu Pro Ser Arg Phe
145 150 155 160
Ala His Lys Val Ser Leu His Asn Ser Cys His Gly Val Arg Glu Leu
165 170 175
His Leu Ser Thr Pro Ser Glu Val His Arg Pro Tyr His Asn Lys Val
180 185 190
Arg Arg Leu Leu Glu Met Val Gln Gly Ile Glu Val Phe Glu Pro Lys
195 200 205
Arg Ile Asp Glu Cys Cys Gly Phe Gly Gly Met Tyr Ser Val Glu Glu
210 215 220
Pro Glu Val Ser Thr Cys Met Gly His Asp Lys Val Leu Asp His Ile

225	230								235					240			
Ser	Thr	Gly	Ala	Glu	Tyr	Ile	Thr	Gly	Pro	Asp	Ser	Ser	Cys	Leu	Met		
				245				250				255					
His	Met	Gln	Gly	Val	Ile	Asp	Arg	Glu	Lys	Leu	Pro	Ile	Lys	Thr	Ile		
				260				265				270					
His	Ala	Val	Glu	Ile	Leu	Ala	Ala	Asn	Leu								
				275				280									
<210>		273															
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Pro	Leu	Lys	Lys	Arg	Met	Asp	Ile	Val	Ser	Met	Ala	Asp	Lys	Ala	Leu		
1					5					10					15		
Val	Val	Glu	Met	Arg	Asp	Val	Thr	Leu	Cys	Gln	Glu	Glu	Asn	Val	Ile		
				20				25				30					
Phe	Gln	Asn	Leu	Asn	Leu	Thr	Leu	Ser	Ala	Gly	Asp	Phe	Val	Tyr	Leu		
				35				40				45					
Ile	Gly	Ser	Val	Gly	Ser	Gly	Lys	Ser	Thr	Leu	Leu	Lys	Ala	Leu	Tyr		
				50				55				60					
Ala	Glu	Val	Pro	Ile	Ser	Ala	Gly	Tyr	Ala	Arg	Val	Ile	Asp	Tyr	Asp		
65					70				75				80				
Leu	Ala	Lys	Leu	Lys	Arg	Lys	Gln	Leu	Pro	Tyr	Leu	Arg	Arg	Asn	Leu		
				85				90				95					
Gly	Ile	Val	Phe	Gln	Asp	Phe	Gln	Leu	Leu	Asn	Gly	Arg	Thr	Val	Ala		
				100				105				110					
Glu	Asn	Leu	Asp	Phe	Val	Leu	Arg	Ala	Thr	Asp	Trp	Lys	Asn	Arg	Ala		
				115				120				125					
Asp	Arg	Glu	Gln	Arg	Ile	Glu	Glu	Val	Leu	Thr	Arg	Val	Gly	Met	Ser		
				130				135				140					
Arg	Lys	Ala	Tyr	Lys	Arg	Pro	His	Glu	Leu	Ser	Gly	Gly	Glu	Gln	Gln		
145					150				155				160				
Arg	Val	Gly	Ile	Ala	Arg	Ala	Leu	Leu	Ala	Lys	Pro	Ala	Leu	Ile	Leu		
				165				170				175					
Ala	Asp	Glu	Pro	Thr	Gly	Asn	Leu	Asp	Ser	Val	Thr	Gly	Leu	Gln	Ile		
				180				185				190					
Ala	Ser	Leu	Leu	Tyr	Glu	Ile	Ser	Lys	Gln	Gly	Thr	Ala	Val	Leu	Met		
				195				200				205					
Ser	Thr	His	Asn	Ser	Ser	Leu	Leu	Ser	His	Leu	Pro	Ala	Arg	Thr	Leu		
				210				215				220					
Ala	Val	Arg	Lys	Asn	Gly	Asp	Ala	Ser	Ser	Leu	Val	Glu	Leu	Ser	Ala		
225					230				235				240				
Asp	Ala	Val	Ser	Arg	Lys	Asn	Thr	Glu	Ile	Asp							
				245				250									
<210>		274															
<211>		238															
<212>		PRT															
<213>		Porphyromonas gingivalis															
<400>		274															
Thr	Arg	His	Cys	Pro	Ala	Cys	Arg	Ser	Ser	Phe	His	Leu	Ile	Lys	Thr		
1					5					10					15		
Ser	Lys	Thr	Met	Ile	Glu	Ile	Ser	Asn	Leu	Thr	Lys	Val	Phe	Arg	Thr		

	20		25		30										
Glu	Glu	Ile	Glu	Thr	Val	Ala	Leu	Asp	Gly	Val	Ser	Leu	Lys	Val	Asp
	35						40					45			
Lys	Gly	Glu	Phe	Ile	Ala	Ile	Met	Gly	Pro	Ser	Gly	Cys	Gly	Lys	Ser
	50					55					60				
Thr	Leu	Leu	Asn	Ile	Leu	Gly	Leu	Leu	Asp	Asn	Pro	Thr	Ser	Gly	Ile
65					70					75					80
Tyr	Lys	Leu	Asp	Gly	Ala	Glu	Val	Gly	Asn	Leu	Arg	Glu	Lys	Asp	Arg
			85					90					95		
Thr	Ala	Val	Arg	Lys	Gly	Asn	Ile	Gly	Phe	Val	Phe	Gln	Ser	Phe	Asn
			100					105					110		
Leu	Ile	Glu	Glu	Met	Thr	Val	Ser	Glu	Asn	Val	Glu	Leu	Pro	Leu	Val
	115						120					125			
Tyr	Leu	Gly	Val	Lys	Ala	Ser	Glu	Arg	Lys	Glu	Arg	Val	Glu	Glu	Ala
130						135					140				
Leu	Arg	Lys	Met	Ser	Ile	Ser	His	Arg	Ala	Gly	His	Phe	Pro	Asn	Gln
145					150					155					160
Leu	Ser	Gly	Gly	Gln	Gln	Gln	Arg	Val	Ala	Ile	Ala	Arg	Ala	Val	Val
			165						170					175	
Ala	Asn	Pro	Lys	Leu	Ile	Leu	Ala	Asp	Glu	Pro	Thr	Gly	Asn	Leu	Asp
			180					185					190		
Ser	Lys	Asn	Gly	Ala	Asp	Val	Met	Glu	Leu	Leu	Arg	Gly	Leu	Asn	Arg
	195						200					205			
Glu	Gly	Ala	Thr	Ile	Val	Met	Val	Thr	His	Ser	Glu	His	Asp	Ala	Arg
210						215					220				
Ser	Ala	Gly	Arg	Ile	Ile	Asn	Leu	Phe	Asp	Gly	Lys	Ile	Arg		
225					230					235					
<210>	275														
<211>	604														
<212>	PRT														
<213>	Porphyromonas gingivalis														
<400>	275														
Ser	Thr	Glu	Thr	Asn	Ser	Lys	Ser	Glu	Met	Lys	Glu	Phe	Phe	Lys	Met
1				5				10						15	
Phe	Phe	Ala	Ser	Ile	Leu	Gly	Val	Ile	Thr	Ala	Gly	Ile	Ile	Leu	Phe
		20						25					30		
Cys	Ile	Phe	Leu	Phe	Ile	Phe	Phe	Gly	Ile	Val	Ala	Gly	Ile	Ala	Ser
	35						40					45			
Lys	Ala	Thr	Gly	Gly	Thr	Ile	Pro	Lys	Ile	Glu	Ala	Asn	Ser	Ile	Leu
	50					55					60				
His	Ile	Xaa	Asn	Ser	Ser	Phe	Pro	Glu	Ile	Val	Ser	Ala	Asn	Pro	Trp
65					70					75					80
Ser	Met	Leu	Thr	Gly	Lys	Asp	Glu	Ser	Val	Ser	Leu	Ser	Gln	Ala	Val
			85					90					95		
Glu	Ala	Ile	Gly	Gln	Ala	Lys	Asn	Asn	Pro	Asn	Ile	Thr	Gly	Ile	Phe
			100					105					110		
Leu	Asp	Leu	Asp	Asn	Leu	Ser	Val	Gly	Met	Ala	Ser	Ala	Glu	Glu	Leu
	115						120					125			
Arg	Arg	Ala	Leu	Gln	Asp	Phe	Lys	Met	Ser	Gly	Lys	Phe	Val	Val	Ser
	130					135					140				
Tyr	Ala	Asp	Arg	Tyr	Thr	Gln	Lys	Gly	Tyr	Tyr	Leu	Ser	Ser	Ile	Ala
145					150					155					160

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

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Ile Glu Val Leu Arg Glu Leu Arg Ser Met Pro Pro Arg Pro Ser Gly
580 585 590
Ile Gln Ala Arg Leu Pro Tyr Tyr Phe Met Pro Tyr
595 600
<210> 276
<211> 324
<212> PRT
<213> Porphyromonas gingivalis
<400> 276
Leu Thr Leu Phe Cys Cys Asn Tyr Phe Lys Gln Met Arg Ala Asn Ile
1 5 10 15
Trp Gln Ile Leu Ser Val Ser Val Leu Phe Phe Phe Gly Thr Ala Ile
20 25 30
Gly Gln Ala Gln Ser Arg Asn Arg Thr Tyr Glu Ala Tyr Val Lys Gln
35 40 45
Tyr Ala Asp Glu Ala Ile Arg Gln Met Ser Arg Tyr Asn Ile Pro Ala
50 55 60
Ser Ile Thr Ile Ala Gln Ala Leu Val Glu Thr Gly Ala Gly Ala Ser
65 70 75 80
Thr Leu Ala Ser Val His Asn Asn His Phe Gly Ile Lys Cys His Lys
85 90 95
Ser Trp Thr Gly Lys Arg Thr Tyr Arg Thr Asp Asp Ala Pro Asn Glu
100 105 110
Cys Phe Arg Ser Tyr Ser Ala Ala Arg Glu Ser Tyr Glu Asp His Ser
115 120 125
Arg Phe Leu Leu Gln Pro Arg Tyr Arg Pro Leu Phe Lys Leu Asp Arg
130 135 140
Glu Asp Tyr Arg Gly Trp Ala Thr Gly Leu Gln Arg Cys Gly Tyr Ala
145 150 155 160
Thr Asn Arg Gly Tyr Ala Asn Leu Leu Ile Lys Met Val Glu Leu Tyr
165 170 175
Glu Leu Tyr Ala Leu Asp Arg Glu Lys Tyr Pro Ser Trp Phe His Lys
180 185 190
Ser Tyr Pro Gly Ser Asn Lys Lys Ser His Gln Thr Thr Lys Gln Lys
195 200 205
Gln Ser Gly Leu Lys His Glu Ala Tyr Phe Ser Tyr Gly Leu Leu Tyr
210 215 220
Ile Ile Ala Lys Gln Gly Asp Thr Phe Asp Ser Leu Ala Glu Glu Phe
225 230 235 240
Asp Met Arg Ala Ser Lys Leu Ala Lys Tyr Asn Asp Ala Pro Val Asp
245 250 255
Phe Pro Ile Glu Lys Gly Asp Val Ile Tyr Leu Glu Lys Lys His Ala
260 265 270
Cys Ser Ile Ser Lys His Thr Gln His Val Val Arg Val Gly Asp Ser
275 280 285
Met His Ser Ile Ser Gln Arg Tyr Gly Ile Arg Met Lys Asn Leu Tyr
290 295 300
Lys Leu Asn Asp Lys Asp Gly Glu Tyr Ile Pro Gln Glu Gly Asp Ile
305 310 315 320
Leu Arg Leu Arg
<210> 277
<211> 533


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<212>      PRT
<213>      Porphyromonas gingivalis
<400>      277
Arg Ile Pro Asp Glu Gln Thr Gly Arg Ile Met Asp Gly Arg Arg Tyr
 1              5              10              15
Ser Asp Gly Leu His Gln Ala Ile Glu Ala Lys Glu His Val Lys Val
      20              25              30
Glu Ala Ala Thr Gln Thr Phe Ala Thr Ile Thr Leu Gln Asn Tyr Phe
      35              40              45
Arg Met Tyr His Lys Leu Ala Gly Met Thr Gly Thr Ala Glu Thr Glu
      50              55              60
Ala Gly Glu Leu Trp Asp Ile Tyr Lys Leu Asp Val Val Val Ile Pro
      65              70              75              80
Thr Asn Lys Pro Ile Ala Arg Lys Asp Met Asn Asp Arg Ile Tyr Lys
      85              90              95
Thr Ala Arg Glu Lys Tyr Ala Ala Val Ile Glu Glu Ile Val Arg Leu
      100             105             110
Val Glu Glu Gly Arg Pro Val Leu Val Gly Thr Thr Ser Val Glu Ile
      115             120             125
Ser Glu Leu Leu Ser Arg Met Leu Arg Leu Arg Gly Ile Gln His Asn
      130             135             140
Val Leu Asn Ala Lys Leu His Gln Lys Glu Ala Glu Ile Val Ala Gln
      145             150             155             160
Ala Gly Gln Lys Gly Thr Val Thr Ile Ala Thr Asn Met Ala Gly Arg
      165             170             175
Gly Thr Asp Ile Lys Leu Ser Ala Glu Val Lys Lys Ala Gly Gly Leu
      180             185             190
Ala Ile Ile Gly Thr Glu Arg His Glu Ser Arg Arg Val Asp Arg Gln
      195             200             205
Leu Arg Gly Arg Ser Gly Arg Gln Gly Asp Pro Gly Ser Ser Ile Phe
      210             215             220
Tyr Val Ser Leu Glu Asp His Leu Met Arg Leu Phe Ala Thr Glu Lys
      225             230             235             240
Ile Ala Ser Leu Met Asp Arg Leu Gly Phe Lys Glu Gly Glu Val Leu
      245             250             255
Glu Asn Asn Met Leu Ser Lys Ser Val Glu Arg Ala Gln Lys Lys Val
      260             265             270
Glu Glu Asn Asn Phe Gly Ile Arg Lys His Leu Leu Glu Tyr Asp Asp
      275             280             285
Val Met Asn Ser Gln Arg Glu Val Ile Tyr Thr Arg Arg Arg His Ala
      290             295             300
Leu Met Gly Glu Arg Ile Gly Met Asp Val Leu Asn Thr Ile Tyr Asp
      305             310             315             320
Val Cys Lys Ala Leu Ile Asp Asn Tyr Ala Glu Ala Asn Asp Phe Glu
      325             330             335
Gly Phe Lys Glu Asp Leu Met Arg Ala Leu Ala Ile Glu Ser Pro Ile
      340             345             350
Thr Gln Glu Ile Phe Arg Gly Lys Lys Ala Glu Glu Leu Thr Asp Met
      355             360             365
Leu Phe Asp Glu Ala Tyr Lys Ser Phe Gln Arg Lys Met Asp Leu Ile
      370             375             380
Ala Glu Val Ala His Pro Val Val His Gln Val Phe Glu Thr Gln Ala

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385                390                395                400
Ala Val Tyr Glu Arg Ile Leu Ile Pro Ile Thr Asp Gly Lys Arg Val
                405                410                415
Tyr Asn Ile Gly Cys Asn Leu Arg Glu Ala Asp Glu Thr Gln Gly Lys
                420                425                430
Ser Ile Ile Lys Glu Phe Glu Lys Ala Ile Val Leu His Thr Ile Asp
                435                440                445
Glu Ser Trp Lys Glu His Leu Arg Glu Met Asp Glu Leu Arg Asn Ser
                450                455                460
Val Gln Asn Ala Ser Tyr Glu Asn Lys Asp Pro Leu Leu Ile Tyr Lys
465                470                475                480
Leu Glu Ser Tyr Glu Leu Phe Arg Lys Met Val Glu Ala Met Asn Arg
                485                490                495
Lys Thr Val Ala Ile Leu Met Arg Ala Arg Ile Pro Val Pro Glu Ala
                500                505                510
Pro Ser Gln Glu Glu Leu Glu His Arg Arg Gln Ile Glu Ile Arg His
                515                520                525
Ala Thr Gln Gln Arg
                530
<210>      278
<211>      720
<212>      PRT
<213>      Porphyromonas gingivalis
<400>      278
Lys Ser Cys Arg Val Ile Gly Gln Thr Arg Arg Tyr Gly Cys Cys Pro
  1                5                10                15
Val Gly Leu Arg Pro Cys His Gln Ser Leu Ser Gly Val Cys Arg Cys
                20                25                30
Leu Phe Gln Ser Arg Pro Ala Val Ala Phe Ala Arg Lys Gly Gln Arg
                35                40                45
Arg His Arg Arg Ser Glu Ser Gly Arg Arg Ile Arg Ala Leu Gln Gly
                50                55                60
Val Gln His His Gln Thr Asn Glu His Glu Val Met Ile Ser Val Asn
                65                70                75                80
Asn Leu Thr Val Asp Phe Gly Thr Arg Leu Leu Phe Asp Gln Val Ser
                85                90                95
Phe Val Ile Asn Arg Arg Asp Arg Ile Ala Leu Val Gly Lys Asn Gly
                100                105                110
Ala Gly Lys Ser Thr Leu Leu Lys Leu Ile Ala Gly Met Glu Glu Pro
                115                120                125
Thr Ser Gly His Ile Ala Arg Pro Lys Gly Ile Arg Ile Gly Tyr Leu
                130                135                140
Pro Gln Val Met Arg Leu Gln Asp Gly His Thr Val Tyr Glu Glu Val
145                150                155                160
Glu Gln Ala Phe Asn Asp Ile Arg Gln Ile Glu Glu Glu Ile Arg Arg
                165                170                175
Leu Ser Asp Glu Met Ala Gly Arg Thr Asp Tyr Glu Ser Asp Asp Tyr
                180                185                190
Ile Arg Leu Ile Glu His Tyr Thr Asn Met Ser Glu Thr Leu Ser Leu
                195                200                205
Met Gln Gln Gly Asn Tyr His Ala Ala Ile Glu Gln Thr Leu Ile Gly
                210                215                220

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

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Tyr Arg Arg Gln Lys Glu Val Ala Lys Gln Leu Arg Thr Leu Glu Arg
 645 650 655
 Thr Val Ala Thr Cys Glu Glu Arg Ile Gly Lys Leu Glu Ser Glu Leu
 660 665 670
 Gln Ala Ile Glu Met Leu Leu Gln Asp Pro Lys His Ala Thr Asp Ala
 675 680 685
 Asn Leu Phe Glu Arg Tyr Ala Gly Met Lys Gln Glu Leu Glu Lys Ala
 690 695 700
 Met Glu Asp Trp Glu Gln Ala Ser Glu Ala Leu Ser Glu Ala Gln Gly
 705 710 715 720
 <210> 279
 <211> 386
 <212> PRT
 <213> Porphyromonas gingivalis
 <400> 279
 Tyr Leu Lys Leu Leu Ile Leu Gln Ile Ala Leu Met Asn Phe Leu Lys
 1 5 10 15
 Lys Glu Pro Phe Lys Ile Phe Ser Met Ile Tyr Leu Leu Leu Asp Thr
 20 25 30
 Ile Thr Asn Arg Ala Gly Thr Glu Arg Ala Val Ile Asn Leu Ala Asn
 35 40 45
 Asn Leu His Ala Asn Gly His Arg Val Ser Leu Val Ser Val Cys Thr
 50 55 60
 Lys Glu Gly Glu Pro Ser Phe Gln Val Glu Lys Gly Ile Glu Val His
 65 70 75 80
 His Leu Gly Ile Arg Leu Tyr Gly Asn Ala Leu Ala Arg Lys Thr Val
 85 90 95
 Tyr Phe Lys Ala Tyr Arg Arg Ile Lys Ala Leu Tyr Lys Lys Arg Glu
 100 105 110
 Pro Val Leu Leu Ile Gly Thr Asn Ile Phe Ile Asn Thr Ile Leu Ser
 115 120 125
 Gln Ile Ser Asn Arg Gly Arg Ile Phe Thr Ile Gly Cys Glu His Ile
 130 135 140
 Ser Tyr Asp Ile Ala Arg Pro Ile Thr Lys Arg Ile Arg Gly Phe Leu
 145 150 155 160
 Tyr Ser Gly Leu Asp Ala Val Val Ala Leu Thr Lys Arg Asp Gln Gln
 165 170 175
 Ser Phe Glu Ala Ile Leu Arg Gly Arg Ser Lys Ala Tyr Val Ile Pro
 180 185 190
 Asn Gln Val Ser Phe Thr Thr Val Gln Arg Asp Ala Thr Thr His Lys
 195 200 205
 Gln Met Leu Ala Ile Gly Arg Leu Thr Tyr Gln Lys Gly Phe Glu Phe
 210 215 220
 Met Ile Glu Asp Ala Ser Arg Val Leu Arg Glu Arg Pro Asp Trp Lys
 225 230 235 240
 Leu Ile Ile Val Gly Asp Gly Glu Asn Glu Ser Met Leu Arg Lys Glu
 245 250 255
 Ile Ala Ser Arg Asn Met Glu Ser Gln Ile Glu Ile His Pro Ser Thr
 260 265 270
 Pro Glu Ile Arg Lys Tyr Tyr Glu Ser Ser Ala Ile Tyr Leu Met Thr
 275 280 285
 Ser Arg Phe Glu Gly Leu Pro Met Val Leu Leu Glu Ala Glu Ala Tyr

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290                295                300
Ala Leu Pro Ile Ile Ser Tyr Asp Cys Pro Thr Gly Pro Arg Glu Leu
305                310                315                320
Ile Glu Asn Gly Arg Asn Gly Phe Leu Val Pro Met Glu Ala His Glu
                325                330                335
Asp Phe Ala Asp Lys Leu Arg Leu Leu Met Asp Asp Glu Thr Leu Arg
                340                345                350
Lys Lys Met Gly Gln Glu Ser Glu Leu Met Val Lys Ser Tyr Ser Pro
                355                360                365
Ala Asn Ile Tyr Glu Cys Trp Lys Lys Leu Phe Val Glu Ile Gly Tyr
                370                375                380
Met Asn
385
<210>      280
<211>      655
<212>      PRT
<213>      Porphyromonas gingivalis
<400>      280
Thr Thr Lys Glu Asn Glu Thr Thr Thr Lys Asn Glu Tyr Arg Ile Met
  1              5              10              15
Gly Lys Ile Ile Gly Ile Asp Leu Gly Thr Thr Asn Ser Cys Val Ser
              20              25              30
Val Leu Glu Gly Asn Glu Pro Ile Val Ile Thr Asn Ser Glu Gly Lys
              35              40              45
Arg Thr Thr Pro Ser Val Val Ala Phe Val Asp Gly Gly Glu Arg Lys
              50              55              60
Val Gly Asp Pro Ala Lys Arg Gln Ala Ile Thr Asn Pro Thr Lys Thr
              65              70              75              80
Ile Tyr Ser Ile Lys Arg Phe Met Gly Glu Thr Tyr Asp Gln Val Ser
              85              90              95
Arg Glu Val Glu Arg Val Pro Phe Lys Val Val Arg Gly Asp Asn Asn
              100             105             110
Thr Pro Arg Val Asp Ile Asp Gly Arg Leu Tyr Thr Pro Gln Glu Ile
              115             120             125
Ser Ala Met Ile Leu Gln Lys Met Lys Lys Thr Ala Glu Asp Tyr Leu
              130             135             140
Gly Gln Glu Val Thr Glu Ala Val Ile Thr Val Pro Ala Tyr Phe Asn
              145             150             155             160
Asp Ala Gln Arg Gln Ala Thr Lys Glu Ala Gly Glu Ile Ala Gly Leu
              165             170             175
Lys Val Arg Arg Ile Val Asn Glu Pro Thr Ala Ala Ser Leu Ala Tyr
              180             185             190
Gly Leu Asp Lys Ser Asn Lys Asp Met Lys Ile Ala Val Phe Asp Leu
              195             200             205
Gly Gly Gly Thr Phe Asp Ile Ser Ile Leu Glu Leu Gly Asp Gly Val
              210             215             220
Phe Glu Val Lys Ser Thr Asn Gly Asp Thr His Leu Gly Gly Asp Asp
              225             230             235             240
Phe Asp His Val Ile Ile Asp Trp Leu Ala Glu Glu Phe Lys Ser Gln
              245             250             255
Glu Gly Val Asp Leu Arg Gln Asp Pro Met Ala Met Gln Arg Leu Lys
              260             265             270

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Glu Ala Ala Glu Lys Ala Lys Ile Glu Leu Ser Ser Thr Ser Ser Thr
 275 280 285
 Glu Ile Asn Leu Pro Tyr Ile Met Pro Val Asn Gly Ile Pro Lys His
 290 295 300
 Leu Val Met Thr Leu Thr Arg Ala Lys Phe Glu Gln Leu Ala Asp Arg
 305 310 315 320
 Leu Ile Gln Ala Cys Val Ala Pro Cys Glu Thr Ala Leu Lys Asp Ala
 325 330 335
 Gly Met Ser Arg Gly Asp Ile Asp Glu Val Ile Leu Val Gly Gly Ser
 340 345 350
 Thr Arg Ile Pro Ala Ile Gln Glu Ile Val Glu Lys Ile Phe Gly Lys
 355 360 365
 Ala Pro Ser Lys Gly Val Asn Pro Asp Glu Val Val Ala Val Gly Ala
 370 375 380
 Ala Ile Gln Gly Gly Val Leu Thr Gly Glu Val Lys Asp Val Leu Leu
 385 390 395 400
 Leu Asp Val Thr Pro Leu Ser Leu Gly Ile Glu Thr Met Gly Gly Val
 405 410 415
 Met Thr Arg Leu Ile Asp Ala Asn Thr Thr Ile Pro Thr Lys Lys Ser
 420 425 430
 Glu Ile Phe Thr Thr Ala Val Asp Asn Gln Pro Ser Val Glu Ile His
 435 440 445
 Val Leu Gln Gly Glu Arg Ser Leu Ala Lys Asp Asn Lys Ser Ile Gly
 450 455 460
 Arg Phe Asn Leu Asp Gly Ile Ala Pro Ala Pro Arg Gln Thr Pro Gln
 465 470 475 480
 Ile Glu Val Thr Phe Asp Ile Asp Ala Asn Gly Ile Leu Asn Val Thr
 485 490 495
 Ala His Asp Lys Ala Thr Gly Lys Lys Gln Asn Ile Arg Ile Glu Ala
 500 505 510
 Ser Ser Gly Leu Ser Asp Asp Glu Ile Lys Arg Met Lys Glu Glu Ala
 515 520 525
 Gln Ala Asn Ala Glu Ala Asp Lys Lys Glu Lys Glu Arg Ile Asp Lys
 530 535 540
 Ile Asn Gln Ala Asp Ser Met Ile Phe Gln Thr Glu Lys Gln Leu Lys
 545 550 555 560
 Glu Leu Gly Asp Lys Phe Pro Ala Asp Lys Lys Ala Pro Ile Asp Thr
 565 570 575
 Ala Leu Asp Lys Leu Lys Glu Ala His Lys Ala Gln Asp Val Ala Ala
 580 585 590
 Ile Asp Thr Ala Met Ala Glu Leu Gln Thr Ala Leu Ser Ala Ala Gly
 595 600 605
 Glu Glu Leu Tyr Lys Asn Ala Gly Ala Ala Gln Gly Gly Ala Gln Pro
 610 615 620
 Gly Pro Asp Phe Gly Gly Ala Gln Gly Pro Ser Ala Gly Asp Gln Pro
 625 630 635 640
 Ser Asp Asp Lys Asn Val Thr Asp Val Asp Phe Glu Glu Val Lys
 645 650 655
 <210> 281
 <211> 467
 <212> PRT
 <213> Porphyromonas gingivalis

<400> 281
 Lys Trp Ala Arg Thr Thr Thr Leu Arg Ile Ser Asn Ala Thr Ile Tyr
 1 5 10 15
 Lys Thr Met Arg Tyr Asp Leu Ala Ile Ile Gly Gly Gly Pro Ala Gly
 20 25 30
 Tyr Thr Ala Ala Glu Arg Ala Ala Lys Gly Gly Leu Lys Thr Leu Leu
 35 40 45
 Ile Glu Lys Asn Ala Leu Gly Gly Val Cys Leu Asn Glu Gly Cys Ile
 50 55 60
 Pro Thr Lys Thr Leu Leu Tyr Ser Ala Lys Val Leu His Gln Ile Ala
 65 70 75 80
 Thr Ala Ser Lys Tyr Ala Val Ser Gly Thr Ala Asp Gly Leu Asp Leu
 85 90 95
 Gly Lys Val Ile Ala Arg Lys Gly Lys Ile Ile Arg Lys Leu Thr Ala
 100 105 110
 Gly Ile Arg Ser Arg Leu Thr Glu Ala Gly Val Glu Met Val Thr Ala
 115 120 125
 Glu Ala Thr Val Thr Gly Cys Asp Ala Asp Gly Ile Ile Gly Ile Thr
 130 135 140
 Ala Gly Glu Ala Gln Tyr Lys Ala Ala Asn Leu Leu Leu Cys Thr Gly
 145 150 155 160
 Ser Glu Thr Phe Ile Pro Pro Ile Pro Gly Val Glu Gln Thr Glu Tyr
 165 170 175
 Trp Thr Asn Arg Glu Ala Leu Gln Asn Lys Glu Ile Pro Thr Ser Leu
 180 185 190
 Val Ile Ile Gly Gly Gly Val Ile Gly Met Glu Phe Ala Ser Phe Phe
 195 200 205
 Asn Gly Ile Gly Thr Gln Val His Val Val Glu Met Leu Pro Glu Ile
 210 215 220
 Leu Asn Gly Ile Asp Pro Glu His Ala Ala Met Leu Arg Ala His Tyr
 225 230 235 240
 Glu Lys Glu Gly Ile Lys Phe Tyr Leu Gly His Lys Val Thr Ser Val
 245 250 255
 Arg Asn Gly Ala Val Thr Val Glu Tyr Glu Gly Glu Ser Lys Glu Ile
 260 265 270
 Glu Gly Glu Arg Ile Leu Met Ser Val Gly Arg Arg Pro Val Leu Gln
 275 280 285
 Gly Phe Glu Ser Leu Gly Leu Val Leu Ala Gly Lys Gly Val Lys Thr
 290 295 300
 Asn Glu Arg Met Gln Thr Ser Leu Pro Asn Val Tyr Ala Ala Gly Asp
 305 310 315 320
 Ile Thr Gly Phe Ser Leu Leu Ala His Thr Ala Val Arg Glu Ala Glu
 325 330 335
 Val Ala Val Asp Gln Ile Leu Gly Lys Thr Asp Glu Thr Met Ser Tyr
 340 345 350
 Arg Ala Val Pro Gly Val Val Tyr Thr Asn Pro Glu Val Ala Gly Val
 355 360 365
 Gly Glu Thr Glu Glu Ser Leu Arg Lys Ala Gly Arg Ala Tyr Thr Val
 370 375 380
 Arg Arg Leu Pro Met Ala Phe Ser Gly Arg Phe Val Ala Glu Asn Glu
 385 390 395 400
 Gln Gly Asn Gly Glu Cys Lys Leu Leu Leu Asp Glu Glu Asn Arg Leu

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                405                410                415
Ile Gly Ala His Leu Ile Gly Asn Pro Ala Gly Glu Leu Ile Val Thr
                420                425                430
Ala Ala Met Ala Ile Glu Thr Gly Met Thr Asp Arg Gln Ile Glu Arg
                435                440                445
Ile Ile Phe Pro His Pro Thr Val Gly Glu Ile Leu Lys Glu Thr Leu
                450                455                460
Ala Gly Gly
465
<210>      282
<211>      945
<212>      PRT
<213>      Porphyromonas gingivalis
<400>      282
Pro Lys Ile Leu Met Glu Leu Lys Arg Phe Leu Ser Leu Gly Leu Leu
  1          5          10          15
Leu Val Gly Phe Ile Pro Met Lys Leu Ser Ala Gln Gln Ala Gln Pro
          20          25          30
Leu Pro Thr Asp Pro Ala Val Arg Val Gly Lys Leu Asp Asn Gly Leu
          35          40          45
Thr Tyr Phe Ile Arg His Asn Glu Asn Pro Lys Asp Arg Ala Asp Phe
          50          55          60
Phe Ile Ala Gln Lys Val Gly Ser Ile Leu Glu Glu Asp Ser Gln Ser
          65          70          75          80
Gly Leu Ala His Phe Leu Glu His Met Ala Phe Asn Gly Thr Lys Asn
          85          90          95
Phe Pro Gly Lys Asn Leu Ile Asn Tyr Leu Glu Thr Ile Gly Val Arg
          100         105         110
Phe Gly Gln Asn Leu Asn Ala Ser Thr Gly Phe Asp Lys Thr Glu Tyr
          115         120         125
Thr Ile Met Asp Val Pro Thr Thr Arg Gln Gly Ile Ile Asp Ser Cys
          130         135         140
Leu Leu Ile Leu His Asp Trp Ser Asn Asn Ile Thr Leu Asp Gly His
          145         150         155         160
Glu Ile Asp Glu Glu Arg Gly Val Ile Gln Glu Glu Trp Arg Ala Arg
          165         170         175
Arg Asp Ala Asn Leu Arg Met Phe Glu Ala Ile Leu Ala Lys Ala Met
          180         185         190
Pro Gly Asn Lys Tyr Ala Glu Arg Met Pro Ile Gly Leu Met Asp Val
          195         200         205
Val Leu Asn Phe Lys His Asp Glu Leu Arg Asn Tyr Tyr Lys Lys Trp
          210         215         220
Tyr Arg Pro Asp Leu Gln Gly Leu Val Ile Val Gly Asp Ile Asp Val
          225         230         235         240
Asp Tyr Val Glu Asn Lys Ile Lys Glu Leu Phe Lys Asp Val Pro Ala
          245         250         255
Pro Val Asn Pro Ala Glu Arg Ile Tyr Thr Pro Val Glu Asp Asn Asp
          260         265         270
Glu Pro Ile Val Ala Ile Ala Thr Asp Ala Glu Ala Thr Thr Thr Gln
          275         280         285
Leu Ser Ile Ser Phe Lys Ser Asp Pro Thr Pro Gln Glu Val Arg Gly
          290         295         300

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Ser Ile Phe Gly Leu Val Glu Asp Tyr Met Lys Gln Val Ile Thr Thr
305 310 315 320
Ala Val Asn Glu Arg Leu Ser Glu Ile Thr His Lys Pro Asn Ala Pro
325 330 335
Phe Leu Ser Ala Gly Ala Phe Phe Ser Asn Phe Met Tyr Ile Thr Gln
340 345 350
Thr Lys Asp Ala Phe Asn Phe Val Ala Thr Val Arg Glu Gly Glu Ala
355 360 365
Glu Lys Ala Met Asn Ala Leu Val Ala Glu Ile Glu Ser Leu Arg Gln
370 375 380
Phe Gly Ile Thr Lys Gly Glu Tyr Asp Arg Ala Arg Thr Asn Val Leu
385 390 395 400
Lys Arg Tyr Glu Asn Gln Tyr Asn Glu Arg Asp Lys Arg Lys Asn Asn
405 410 415
Ala Tyr Ala Asn Glu Tyr Ser Thr Tyr Phe Thr Asp Gly Gly Tyr Ile
420 425 430
Pro Gly Ile Glu Val Glu Tyr Gln Thr Val Asn Ala Phe Ala Pro Gln
435 440 445
Val Pro Leu Glu Ala Phe Asn Gln Ala Ile Ala Gln Met Ile Asp Pro
450 455 460
Val Lys Asn Ala Val Val Thr Leu Thr Gly Pro Ser Lys Ala Glu Ala
465 470 475 480
Lys Ile Pro Ser Glu Ala Asp Phe Leu Ala Ala Phe Lys Ala Ala Arg
485 490 495
Gln Gln Lys Val Glu Ala Lys Lys Asp Glu Val Ser Asp Gln Lys Leu
500 505 510
Met Glu Lys Ala Pro Lys Ala Gly Lys Ile Val Ser Glu Lys Lys Asp
515 520 525
Gln Lys Phe Gly Thr Thr Glu Leu Thr Leu Ser Asn Gly Ile Lys Val
530 535 540
Tyr Leu Lys Lys Thr Asp Phe Lys Ser Asn Glu Ile Leu Met Ser Ala
545 550 555 560
Leu Ser Pro Gly Gly Ile Leu Ser Gly Lys His Ala Pro Asn Gln Ser
565 570 575
Val Met Asn Ser Phe Met Asn Val Gly Gly Leu Gly Asn Phe Asp Ala
580 585 590
Ile Gln Leu Asp Lys Val Leu Thr Gly Arg Ser Ala Ser Val Ser Pro
595 600 605
Ser Leu Ser Leu Leu Ser Glu Gly Leu Ser Gly Lys Thr Thr Val Glu
610 615 620
Asp Met Glu Thr Phe Phe Gln Leu Ile Tyr Leu Gln Met Thr Ala Asn
625 630 635 640
Arg Lys Asp Pro Glu Ala Phe Lys Ala Thr Gln Glu Lys Leu Tyr Asn
645 650 655
Asn Leu Lys Asn Gln Glu Ala Asn Pro Met Ala Ala Leu Met Asp Ser
660 665 670
Ile Arg His Thr Met Tyr Gly Asp Asn Pro Met Met Lys Pro Met Lys
675 680 685
Ala Ala Asp Val Glu Lys Val Asn Tyr Asp Gln Val Met Ala Phe Tyr
690 695 700
Asn Glu Arg Phe Ala Asp Ala Gly Asp Phe Met Phe Phe Phe Ile Gly
705 710 715 720

Asn Leu Asp Glu Ala Lys Met Lys Pro Leu Ile Glu Thr Tyr Leu Ala
 725 730 735
 Ser Leu Pro Asn Leu Lys Arg Gly Asp Lys Met Asn Lys Ala Gln Val
 740 745 750
 Pro Ala Ala Arg Ser Gly Lys Ile Asp Cys Lys Phe Glu Lys Glu Met
 755 760 765
 Asp Thr Pro Ser Thr Thr Ile Phe Asp Val Val Ser Gly Asn Val Glu
 770 775 780
 Tyr Thr Leu Lys Asn Ser Leu Leu Leu Glu Val Phe Ser Ala Val Met
 785 790 795 800
 Asp Gln Val Tyr Thr Ala Thr Val Arg Glu Lys Glu Gly Gly Ala Tyr
 805 810 815
 Ser Val Ala Ala Phe Gly Gly Leu Glu Gln Tyr Pro Gln Pro Lys Ala
 820 825 830
 Leu Met Gln Ile Tyr Phe Pro Thr Asp Pro Ala Arg Ala Glu Glu Met
 835 840 845
 Asn Ala Ile Val Phe Ala Glu Leu Glu Lys Leu Ala Lys Glu Gly Pro
 850 855 860
 Asn Val Glu Tyr Phe Lys Lys Thr Ile Glu Asn Leu Asn Lys Gln His
 865 870 875 880
 Lys Glu Ser Leu Arg Glu Asn Arg Phe Trp Leu Glu Ala Met Lys Ala
 885 890 895
 Ser Phe Phe Glu Gly Asn Asp Phe Ile Thr Asp Tyr Glu Ser Val Leu
 900 905 910
 Asn Gly Leu Thr Pro Ala Glu Leu Gln Lys Phe Ala Ala Asp Leu Leu
 915 920 925
 Lys Gln Gln Asn Arg Val Val Val Met Met Ala Pro Val Ala Lys Ala
 930 935 940
 Gln
 945
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 Phe Pro Val Ile Lys Lys Phe Leu Tyr Ser Asp His Glu Ile Phe Leu
 20 25 30
 Arg Glu Ile Val Ser Asn Ala Val Asp Ala Thr Gln Lys Leu Lys Thr
 35 40 45
 Leu Thr Ser Val Gly Glu Phe Lys Gly Glu Thr Gly Asp Leu Arg Val
 50 55 60
 Thr Val Ser Val Asp Glu Val Ala Arg Thr Ile Thr Val Ser Asp Arg
 65 70 75 80
 Gly Val Gly Met Thr Glu Glu Glu Val Glu Lys Tyr Ile Asn Gln Ile
 85 90 95
 Ala Phe Ser Ser Ala Glu Glu Phe Leu Glu Lys Tyr Lys Asp Asp Lys
 100 105 110
 Ala Ala Ile Ile Gly His Phe Gly Leu Gly Phe Tyr Ser Ala Phe Met
 115 120 125
 Val Ser Glu Arg Val Asp Val Ile Thr Arg Ser Phe Arg Glu Asp Ala

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

545	550										555					560				
Leu	Pro	Asp	Ser	Tyr	Asn	Leu	Val	Leu	Asn	Thr	Asp	His	Pro	Leu	Ile					
				565					570					575						
Asp	Arg	Val	Leu	Ser	Gly	Glu	Lys	Glu	Ser	Val	Glu	Pro	Ser	Leu	Thr					
				580					585					590						
Glu	Leu	Arg	Ala	Lys	Ile	Ala	Glu	Leu	Lys	Ala	Glu	Glu	Ala	Lys	Leu					
				595					600					605						
Leu	Asp	Glu	Glu	Lys	Gly	Lys	Lys	Pro	Glu	Glu	Ile	Pro	Val	Ala	Thr					
				610					615					620						
Lys	Glu	Ala	Lys	Glu	Asn	Asn	Ala	Val	Glu	Gln	Ala	Lys	Thr	Glu	Gly					
				625					630					635						
Ser	Ile	Asn	Asp	Gln	Leu	Thr	Lys	Tyr	Ala	Gln	Asp	Asn	Glu	Leu	Ile					
				645					650					655						
Gly	Gln	Leu	Ile	Asp	Leu	Ala	Leu	Leu	Gly	Ser	Gly	Leu	Leu	Thr	Gly					
				660					665					670						
Glu	Ala	Leu	Ala	Glu	Phe	Ile	Arg	Arg	Ser	Gln	Arg	Leu	Leu							
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Arg	Ala	Met	Glu	Lys	Leu	Ile	Asp	Ile	Leu	Val	Val	Asp	Asp	Asp	Val					
			20			25			30											
Ala	Val	Cys	Ala	Ala	Leu	Arg	Leu	Val	Leu	Lys	Arg	Ala	Gly	Tyr	Asn					
			35			40			45											
Pro	Val	Ile	Ala	Asn	Ser	Pro	Asp	Glu	Ala	Leu	Ser	Ile	Met	Arg	Asn					
			50			55			60											
Pro	Asp	Gly	Gly	Cys	Lys	Pro	Ala	Val	Ile	Leu	Met	Asp	Met	Asn	Phe					
			65			70			75				80							
Ser	Leu	Ser	Thr	Ser	Gly	Arg	Glu	Gly	Leu	Glu	Leu	Leu	Glu	Lys	Met					
				85			90			95										
Gln	Ile	Phe	Thr	Ser	Cys	Pro	Val	Ile	Leu	Met	Thr	Ala	Trp	Ala	Ser					
			100			105			110											
Ile	Pro	Leu	Ala	Val	Glu	Gly	Met	Arg	Leu	Gly	Ala	Phe	Asp	Phe	Ile					
			115			120			125											
Gly	Lys	Pro	Trp	Asp	Asn	Asp	Arg	Leu	Leu	Arg	Thr	Ile	Asp	Thr	Ala					
			130			135			140											
Leu	His	Leu	Ala	Ala	Pro	Ser	Ala	Val	Ala	Asn	Pro	Ser	Glu	Gln	Ser					
			145			150			155				160							
Asp	Arg	Asp	Thr	Ala	Arg	Gln	Pro	Lys	Ala	Thr	Val	Gln	Glu	Asn	Asp					
				165			170			175										
Pro	Cys	Ala	His	Ile	Ile	Gly	Arg	Ser	Asp	Ala	Ile	Cys	Lys	Ile	Lys					
			180			185			190											
Glu	Arg	Ile	Arg	Arg	Ile	Ala	Pro	Thr	His	Ala	Ser	Val	Leu	Ile	Thr					
			195			200			205											
Gly	Glu	Ser	Gly	Thr	Gly	Lys	Glu	Leu	Ile	Ala	Glu	Ala	Leu	His	Arg					
			210			215			220											
Gly	Ser	Lys	Arg	Ala	Ser	Ala	Pro	Phe	Val	Lys	Val	Asn	Leu	Gly	Gly					
			225			230			235				240							

Ile Pro Glu Ser Leu Phe Glu Ser Glu Leu Phe Gly His Lys Lys Gly
245 250 255
Ala Phe Thr Asn Ala Phe Ser Asp Arg Lys Gly Arg Phe Glu Leu Ala
260 265 270
Asp Gly Gly Thr Ile Phe Leu Asp Glu Ile Gly Glu Leu Pro Val Gly
275 280 285
Asn Gln Val Lys Leu Leu Arg Val Leu Gln Glu Gln Thr Phe Glu Pro
290 295 300
Leu Gly Glu Ser Val Ser His Arg Val Asp Ile Arg Val Val Ser Ala
305 310 315 320
Thr Asn Ala Ser Leu Glu Arg Met Val Ala Glu Gly Arg Phe Arg Glu
325 330 335
Asp Leu Tyr Tyr Arg Ile Asn Leu Ile His Leu His Leu Pro Pro Leu
340 345 350
Arg Glu Arg Gln Glu Asp Ile Gln Leu Leu Val Glu Ala Phe Ser Glu
355 360 365
Ala Phe Ala Gln Ser Asn Gly Leu Pro His Ala Val Trp Ser Ala Glu
370 375 380
Ala Met Arg Arg Ile Cys Ala Met Pro Leu Pro Gly Asn Val Arg Glu
385 390 395 400
Leu Lys Asn Val Val Glu Arg Thr Leu Leu Leu Ser Gly Ser Arg Glu
405 410 415
Ile Ser Ala Arg Asp Val Ala Asp Phe Gly Ser Gln Val Thr Ala Ala
420 425 430
Asp His Ser Asp Glu Arg Ala Leu Thr Asp Met Glu Glu Ala Ala Ile
435 440 445
Arg Glu Thr Leu Thr Lys Tyr Asn Gly Asn Val Ser Arg Ala Ala Arg
450 455 460
Ala Leu Gly Leu Ser Arg Ala Ala Leu Tyr Arg Arg Met Glu Lys Tyr
465 470 475 480
Gly Leu
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Arg Ser Leu Gln Ser Phe Gln Asn Lys Lys His Ser Ser Met Leu Lys
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Ile Lys Asn Leu His Ala Thr Val Gln Gly Lys Glu Ile Leu Lys Gly
20 25 30
Ile Asn Leu Glu Ile Asn Ala Gly Glu Ile His Ala Ile Met Gly Pro
35 40 45
Asn Gly Ser Gly Lys Ser Thr Leu Ser Ser Val Leu Val Gly His Pro
50 55 60
Ser Phe Glu Val Thr Glu Gly Glu Val Thr Phe Asn Gly Ile Asp Leu
65 70 75 80
Leu Glu Leu Glu Pro Glu Glu Arg Ala His Leu Gly Leu Phe Leu Ser
85 90 95
Phe Gln Tyr Pro Val Glu Ile Pro Gly Val Ser Met Val Asn Phe Met
100 105 110
Arg Ala Ala Val Asn Glu His Arg Lys Ala Ile Gly Ala Glu Pro Val
115 120 125

Ser Ala Ser Asp Phe Leu Lys Met Met Arg Glu Lys Arg Ala Ile Val
130 135 140
Glu Leu Asp Asn Lys Leu Ala Ser Arg Ser Val Asn Glu Gly Phe Ser
145 150 155 160
Gly Gly Glu Lys Lys Arg Asn Glu Ile Phe Gln Met Ala Met Leu Glu
165 170 175
Pro Lys Leu Ala Ile Leu Asp Glu Thr Asp Ser Gly Leu Asp Ile Asp
180 185 190
Ala Leu Arg Ile Val Ala Gly Gly Val Asn Arg Leu Arg Ser Pro Glu
195 200 205
Asn Ala Ala Ile Val Ile Thr His Tyr Gln Arg Leu Leu Glu Tyr Ile
210 215 220
Lys Pro Asp Phe Val His Val Leu Tyr Lys Gly Arg Ile Val Lys Ser
225 230 235 240
Gly Gly Ala Glu Leu Ala Leu Thr Leu Glu Glu Lys Gly Tyr Asp Trp
245 250 255
Ile Lys Glu Glu Ile Gly Glu
260
<210> 286
<211> 462
<212> PRT
<213> Porphyromonas gingivalis
<400> 286
Ser Met Ala Lys Glu Lys Thr Ile Tyr Val Cys Arg Ser Cys Gly Thr
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Lys Tyr Ala Lys Trp Gln Gly Asn Cys Asn Ala Cys Gly Glu Trp Asn
20 25 30
Cys Ile Asp Glu Glu Lys Val Pro Ala Pro Ala Ser Gly Lys His Ala
35 40 45
Ala Lys Ser Phe Met Pro Arg Glu Gln Asp Asn Arg Pro Arg Leu Leu
50 55 60
Gln Asp Val Glu Ser Gly Asp Glu Glu Arg Ile Arg Leu Gly Asp Glu
65 70 75 80
Glu Phe Asp Arg Val Leu Gly Gly Gly Ile Val Lys Gly Ala Phe Val
85 90 95
Leu Leu Gly Gly Glu Pro Gly Ile Gly Lys Ser Thr Leu Ile Leu Gln
100 105 110
Thr Val Leu Arg Leu Pro Gln Leu Arg Thr Leu Tyr Val Ser Gly Glu
115 120 125
Glu Ser Ala Arg Gln Leu Lys Met Arg Ala Glu Arg Leu Gly Gln Ala
130 135 140
Met Asn Gly Cys Tyr Val Tyr Cys Glu Thr Asn Ile Glu Arg Ile Leu
145 150 155 160
Ser Arg Ala Glu Glu Leu Thr Pro Asp Leu Leu Val Ile Asp Ser Ile
165 170 175
Gln Thr Val Tyr Thr Glu Glu Met Glu Ser Ser Ala Gly Ser Val Gly
180 185 190
Gln Ile Arg Glu Cys Ala Ala Leu Leu Lys Tyr Cys Lys Thr Thr
195 200 205
Gly Ile Pro Val Ile Val Ile Gly His Ile Thr Lys Glu Gly Ser Ile
210 215 220
Ala Gly Pro Lys Val Leu Glu His Ile Val Asp Thr Val Leu Leu Phe

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

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


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

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

His Ile Val Leu Asn Ser Gly Ala Lys Ser Glu Arg Tyr Val Lys Gly
 500 505 510
 Ala Tyr Pro Ala Leu Ile Pro Gln Ala Phe Val Gln Tyr Gly Asn Phe
 515 520 525
 Val Gly Glu Ser Leu Ser Cys Val Ala Ser Phe Pro Ser Val Arg Ser
 530 535 540
 Val Thr Val Gly Ile Met Leu Gly Lys Ala Val Lys Leu Ala Glu Gly
 545 550 555 560
 Tyr Leu Asp Thr His Ser Lys Lys Val Val Met Asn Arg Asp Phe Leu
 565 570 575
 His Glu Leu Ala Arg Gln Ala Gly Cys Ser Glu Asp Ile His Ala Ile
 580 585 590
 Ile Asp Ser Leu Asn Leu Ala Arg Glu Leu Trp Thr Met Pro Ser Ala
 595 600 605
 Glu Asp Ser Asp Arg Leu Leu Arg Lys Ile Ala Glu Arg Ser Trp Glu
 610 615 620
 Thr Cys Arg Pro Ser Val Pro Ser Ala Glu Leu Glu Leu Leu Leu Ile
 625 630 635 640
 Asp Glu Ser Gly Ala Ile Arg Phe Arg Ile Gly Gly Glu
 645 650
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 <211> 451
 <212> PRT
 <213> Porphyromonas gingivalis
 <400> 290
 Gln Gln Arg Pro His Arg Ile Ile Met Leu Arg Thr Phe Arg Ile Gly
 1 5 10 15
 Gly Ile His Pro Pro Glu Asn Lys Leu Ser Ala Gly Lys Pro Val Glu
 20 25 30
 Val Leu Pro Ile Pro Ser Gln Val Val Ile Pro Leu Gly Gln His Ile
 35 40 45
 Gly Ala Pro Ala Thr Ala Thr Val Lys Lys Gly Asp Glu Val Lys Val
 50 55 60
 Gly Thr Ile Ile Ala Gln Ala Gly Gly Phe Val Ser Ala Asn Ile His
 65 70 75 80
 Ser Ser Val Ser Gly Lys Val Leu Lys Ile Asp Asn Val Tyr Asp Ser
 85 90 95
 Ser Gly Tyr Pro Lys Pro Ala Val Phe Ile Ser Val Glu Gly Asp Glu
 100 105 110
 Trp Glu Glu Gly Ile Asp Arg Ser Pro Ala Ile Val Lys Glu Cys Asn
 115 120 125
 Leu Asp Ala Lys Glu Ile Val Ala Lys Ile Ser Ala Ala Gly Ile Val
 130 135 140
 Gly Leu Gly Gly Ala Thr Phe Pro Thr His Val Lys Leu Ser Pro Pro
 145 150 155 160
 Pro Gly Asn Lys Ala Glu Ile Leu Ile Ile Asn Ala Val Glu Cys Glu
 165 170 175
 Pro Tyr Leu Thr Ser Asp His Val Leu Met Leu Glu His Gly Glu Glu
 180 185 190
 Ile Met Ile Gly Val Ser Ile Leu Met Lys Ala Ile Gln Val Asn Lys
 195 200 205
 Ala Val Ile Gly Val Glu Asn Asn Lys Lys Asp Ala Ile Ala His Leu

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210                215                220
Thr Lys Leu Ala Thr Ala Tyr Pro Gly Ile Glu Val Met Pro Leu Lys
225                230                235                240
Val Gln Tyr Pro Gln Gly Gly Glu Lys Gln Leu Ile Asp Ala Val Ile
245                250                255
Arg Lys Gln Val Lys Ser Gly Ala Leu Pro Ile Ser Thr Gly Ala Val
260                265                270
Val Gln Asn Val Gly Thr Val Phe Ala Val Tyr Glu Ala Val Gln Lys
275                280                285
Asn Lys Pro Leu Val Glu Arg Ile Val Thr Val Thr Gly Lys Lys Leu
290                295                300
Ser Arg Pro Ser Asn Leu Leu Val Arg Ile Gly Thr Pro Ile Ala Ala
305                310                315                320
Leu Ile Glu Ala Ala Gly Gly Leu Pro Glu Asn Thr Gly Lys Ile Ile
325                330                335
Gly Gly Gly Pro Met Met Gly Arg Ala Leu Leu Ser Pro Asp Val Pro
340                345                350
Val Thr Lys Gly Ser Ser Gly Val Leu Ile Leu Asp Arg Glu Glu Ala
355                360                365
Val Arg Lys Pro Met Arg Asp Cys Ile Arg Cys Ala Lys Cys Val Gly
370                375                380
Val Cys Pro Met Gly Leu Asn Pro Ala Phe Leu Met Arg Asp Thr Leu
385                390                395                400
Tyr Lys Ser Trp Glu Thr Ala Glu Lys Gly Asn Val Val Asp Cys Ile
405                410                415
Glu Cys Gly Ser Cys Ser Phe Thr Cys Pro Ala Asn Arg Pro Leu Leu
420                425                430
Asp Tyr Ile Arg Gln Ala Lys Lys Thr Val Met Gly Ile Gln Arg Ala
435                440                445
Arg Lys Gln
450
<210>    291
<211>    489
<212>    PRT
<213>    Porphyromonas gingivalis
<400>    291
Met Asn Ser Gln Lys Lys Glu Ala Phe Asn Met Lys Arg Ile Gln Leu
1                5                10                15
Thr Leu Ile Ala Leu Phe Ala Ala Val Ala Gly Leu Val Ala Gln Asn
20                25                30
Ala Tyr Glu Gly Val Ile Ser Tyr Lys Ile Ser Leu Asp Lys Thr Gly
35                40                45
Asn Lys Val Val Leu Asn Gly Ala Ala Asp Met Ser Asn Leu Lys Leu
50                55                60
Lys Ser Thr Gln Met Ile Ile Val Thr Pro Ile Leu Arg Ser Glu Asp
65                70                75                80
Gly Thr Ser Arg Val Glu Phe Pro Ser Val Val Ile Thr Gly Arg Asn
85                90                95
Arg Thr Lys Ala Leu Lys Arg Glu Ile Ala Phe Ser Ser Ala Leu Pro
100               105               110
Gln Ala Lys His Ala Ala Gln Tyr Ile Arg Arg His Asn Gly Lys Ser
115               120               125

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Glu Gln Phe Ala Phe Thr Gly Glu His Ala Tyr Ala Ser Trp Met Met
 130 135 140
 Asp Ala Lys Phe Val Val Arg Glu Glu Val Arg Gly Cys Ala Lys Cys
 145 150 155 160
 Pro Val Gly Leu Ser Ser Asn Ile Val Pro Phe Asp Pro Leu Phe Asn
 165 170 175
 Pro Ala Glu Ala Pro Tyr Leu Leu Ala His Ile Thr Pro Ala Glu Glu
 180 185 190
 Val Glu Lys Gln Arg Glu Ser Ser Phe Asp Ala Tyr Ile Asn Phe Lys
 195 200 205
 Val Asn Lys Ala Asp Val Leu Pro Glu Tyr Arg Asn Asn Lys Ala Glu
 210 215 220
 Leu Glu Lys Ile Lys Glu Phe Val Ser Thr Val Lys Ala Asn Pro Asn
 225 230 235 240
 Tyr Ser Val Asn Lys Met Ile Ile Glu Gly Phe Ala Ser Pro Glu Ala
 245 250 255
 Ser Ile Ala His Asn Lys Ala Leu Ser Glu Arg Arg Ala Lys Arg Leu
 260 265 270
 Ala Glu Glu Leu Val Arg Lys Tyr Gly Lys Thr Leu Pro Asn Ile Thr
 275 280 285
 Thr Glu Phe Gly Gly Glu Asp Trp Lys Gly Leu Lys Leu Ala Ile Glu
 290 295 300
 Lys Ser Asp Ile Ala Asp Arg Asp Arg Val Leu Glu Ile Ile Asn Ser
 305 310 315 320
 Asp Lys Tyr Ala Asp Asp Asp Ala Arg Glu Gln Ala Leu Lys Gln Leu
 325 330 335
 Ser Ser Tyr Arg Tyr Ile Leu Asp Gln Ile Tyr Pro Asn Leu Arg Arg
 340 345 350
 Asn Thr Ile Thr Met Gly Tyr Ile Val Arg Asp Tyr Thr Leu Glu Glu
 355 360 365
 Ala Arg Glu Ile Ile Lys Thr Ala Pro Lys Glu Leu Ser Glu Ala Glu
 370 375 380
 Met Tyr Arg Val Ala Met Ser Tyr Pro Glu Gly His Gln Glu Arg Leu
 385 390 395 400
 Phe Ala Leu Asn Thr Thr Leu Lys Tyr Phe Pro Glu Ser Val Thr Gly
 405 410 415
 Arg Ile Asn Leu Ala Val Ala Ala Phe Asn Gly Gly Asp Val Gln Gln
 420 425 430
 Ala Ile Ala Leu Leu Ser Pro Ile Gln Thr Glu Lys Gly Val Ser Asn
 435 440 445
 Ile Leu Gly Ala Ala Tyr Ala Arg Thr Gly Asp Phe Ala Arg Ala Glu
 450 455 460
 Thr Phe Phe Arg Lys Ala Val Ala Glu Gly Asp Ala Asn Ala Gln Arg
 465 470 475 480
 Asn Leu Asp Met Leu Leu Gly Lys Lys
 485
 <210> 292
 <211> 384
 <212> PRT
 <213> Porphyromonas gingivalis
 <400> 292
 Asp Met Ala Glu Lys Arg Asp Tyr Tyr Glu Val Leu Gly Val Ser Lys

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1           5           10           15
Asn Ala Thr Asp Asp Glu Leu Lys Lys Ala Tyr Arg Lys Lys Ala Ile
           20           25           30
Gln Tyr His Pro Asp Lys Asn Pro Gly Asp Lys Glu Ala Glu Glu His
           35           40           45
Phe Lys Glu Val Ala Glu Ala Tyr Asp Val Leu Ser Asp Pro Gln Lys
           50           55           60
Arg Ser Gln Tyr Asp Gln Phe Gly His Ala Gly Leu Gly Gly Ala Ala
           65           70           75           80
Gly Gly Gly Phe Ser Gly Gly Gly Met Ser Met Glu Asp Ile Phe Ser
           85           90           95
Arg Phe Gly Asp Leu Phe Gly Gly Phe Gly Gly Phe Gly Gly Phe Ser
           100           105           110
Asp Met Gly Gly Gly Ser Arg Arg Arg Val Arg Arg Gly Ser Asp Leu
           115           120           125
Arg Val Arg Val Lys Leu Ser Leu Ala Asp Ile Ser Lys Gly Val Glu
           130           135           140
Lys Lys Val Lys Val Lys Lys Gln Val Val Cys Ser Lys Cys Arg Gly
           145           150           155           160
Asp Gly Thr Glu Glu Ala Asn Gly Lys Thr Thr Cys Gln Thr Cys His
           165           170           175
Gly Thr Gly Val Val Thr Arg Val Ser Asn Thr Phe Leu Gly Ala Met
           180           185           190
Gln Thr Gln Ser Thr Cys Pro Thr Cys His Gly Glu Gly Glu Ile Ile
           195           200           205
Thr Lys Pro Cys Ser Lys Cys Lys Gly Glu Gly Val Glu Ile Gly Glu
           210           215           220
Glu Val Ile Ser Phe His Ile Pro Ala Gly Val Ala Glu Gly Met Gln
           225           230           235           240
Met Ser Val Asn Gly Lys Gly Asn Ala Ala Pro Arg Gly Gly Val Asn
           245           250           255
Gly Asp Leu Ile Val Val Ile Ala Glu Glu Pro Asp Pro Asn Leu Ile
           260           265           270
Arg Asn Gly Asn Asp Leu Ile Tyr Asn Leu Leu Ile Ser Val Pro Leu
           275           280           285
Ala Ile Lys Gly Gly Ser Val Glu Val Pro Thr Ile Asp Gly Arg Ala
           290           295           300
Lys Ile Arg Ile Glu Ala Gly Thr Gln Pro Gly Lys Met Leu Arg Leu
           305           310           315           320
Arg Asn Lys Gly Leu Pro Ser Val Asn Gly Tyr Gly Met Gly Asp Gln
           325           330           335
Leu Val Asn Val Asn Val Tyr Ile Pro Glu Ser Ile Asp Ala Lys Asp
           340           345           350
Glu Gln Ala Ile Ala Ala Met Glu Asn Ser Asp Ser Phe Lys Pro Thr
           355           360           365
Asp Ala Ala Arg Lys Asp Ile Asp Lys Lys Tyr Arg Glu Met Leu Asp
           370           375           380
<210>      293
<211>      309
<212>      PRT
<213>      Porphyromonas gingivalis
<400>      293

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

Ala Thr Ser Ala Arg

305

<210> 294

<211> 491

<212> PRT

<213> Porphyromonas gingivalis

<400> 294

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

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

465						470						475						480
Phe	Arg	Arg	Arg	Arg	Phe	Lys	Glu	Glu	Thr	Asp								
					485						490							
<210>	295																	
<211>	763																	
<212>	PRT																	
<213>	Porphyromonas gingivalis																	
<400>	295																	
His	Phe	Leu	Val	Thr	Ile	Met	Arg	Thr	Lys	Thr	Ile	Phe	Phe	Ala	Ile			
1				5					10					15				
Ile	Ser	Phe	Ile	Ala	Leu	Leu	Ser	Ser	Ser	Leu	Ser	Ala	Gln	Ser	Lys			
				20					25					30				
Ala	Val	Leu	Thr	Gly	Ser	Val	Ser	Asp	Ala	Glu	Thr	Gly	Glu	Pro	Leu			
		35					40					45						
Ala	Gly	Ala	Arg	Ile	Glu	Val	Lys	His	Thr	Asn	Ile	Val	Ala	Gly	Ala			
50						55					60							
Asp	Ala	Gly	Gly	His	Phe	Glu	Ile	Lys	Asn	Leu	Pro	Ala	Gly	Gln	His			
65					70					75					80			
Thr	Ile	Ile	Cys	Ser	Leu	Gly	Gly	Tyr	Gly	Gln	Lys	Glu	Glu	Val	Val			
				85					90					95				
Ala	Ile	Glu	Ala	Gly	Gln	Thr	Lys	Thr	Ile	Ser	Phe	Ala	Leu	Arg	Leu			
			100					105					110					
Arg	Thr	Asn	Asn	Leu	Glu	Glu	Val	Val	Val	Thr	Gly	Thr	Gly	Thr	Arg			
		115					120					125						
Tyr	Arg	Leu	Val	Asp	Ala	Pro	Val	Ala	Thr	Glu	Val	Leu	Thr	Ala	Lys			
130						135					140							
Asp	Ile	Ala	Ser	Phe	Ser	Ala	Pro	Thr	Ser	Glu	Ala	Leu	Leu	Gln	Gly			
145					150					155					160			
Leu	Ser	Pro	Ser	Phe	Asp	Phe	Gly	Pro	Asn	Leu	Met	Gly	Ser	Phe	Met			
				165					170					175				
Gln	Leu	Asn	Gly	Leu	Ser	Ser	Lys	Tyr	Ile	Leu	Ile	Leu	Ile	Asp	Gly			
			180					185					190					
Lys	Arg	Val	Tyr	Gly	Asp	Val	Gly	Gly	Gln	Ala	Asp	Leu	Ser	Arg	Ile			
		195					200					205						
Ser	Pro	Asp	Gln	Ile	Glu	Arg	Ile	Glu	Leu	Val	Lys	Gly	Ala	Ser	Ser			
210						215					220							
Ser	Leu	Tyr	Gly	Ser	Asp	Ala	Ile	Ala	Gly	Val	Ile	Asn	Val	Ile	Thr			
225					230					235					240			
Lys	Lys	Asn	Thr	Asn	Arg	Leu	Ser	Ala	Tyr	Thr	Ser	His	Arg	Ile	Ser			
				245					250					255				
Lys	Tyr	Asn	Asp	Arg	Gln	Thr	Asn	Thr	Ser	Leu	Asp	Ile	Asn	Ile	Gly			
			260					265					270					
Lys	Phe	Ser	Ser	Asn	Thr	Asn	Tyr	Phe	Phe	Tyr	His	Thr	Asp	Gly	Trp			
		275					280					285						
Gln	Asn	Ser	Pro	Phe	Glu	Ile	Lys	Lys	Lys	Lys	Gly	Ser	Gly	Glu	Pro			
290						295					300							
Val	Leu	Glu	Glu	Thr	Tyr	Lys	Lys	Thr	Phe	Arg	Ala	Gln	Glu	Asn	Gln			
305					310					315					320			
Gly	Val	Ser	Gln	Ser	Leu	Ser	Tyr	Tyr	Ala	Thr	Asn	Asn	Leu	Ser	Phe			
				325					330					335				
Ser	Gly	Asn	Val	Gln	Tyr	Asn	Lys	Arg	Gln	Ile	Phe	Thr	Pro	Thr	Phe			
			340					345					350					

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

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<210>      296
<211>      365
<212>      PRT
<213>      Porphyromonas gingivalis
<400>      296
Cys Cys Ala Arg Leu Arg Asp Thr Ser Pro Arg Lys Lys Ser Phe Arg
 1           5           10           15
Asn Asp Thr Val Phe Pro Tyr Phe Val Ile His Leu Ile Lys His Ile
      20           25           30
Ile Ile Met Thr Asp Asn Lys Gln Arg Asn Ile Val Phe Pro Ala Phe
      35           40           45
Leu Leu Leu Leu Gly Val Ile Ala Val Val Thr Ile Val Gly Phe Phe
      50           55           60
Met Leu Arg Pro Ala Glu Glu Ile Ile Gln Gly Gln Ile Glu Val Thr
      65           70           75           80
Glu Tyr Arg Val Ser Ser Lys Val Pro Gly Arg Ile Lys Glu Leu Arg
      85           90           95
Val Ser Glu Gly Gln Gln Val Gln Ala Gly Asp Thr Leu Ala Val Ile
      100           105           110
Glu Ala Pro Asp Val Ala Ala Lys Met Glu Gln Ala Lys Ala Ala Glu
      115           120           125
Ala Ala Ala Gln Ala Gln Asn Ala Lys Ala Leu Lys Gly Ala Arg Ser
      130           135           140
Glu Gln Ile Gln Ala Ala Tyr Glu Met Trp Gln Lys Ala Gln Ala Gly
      145           150           155           160
Val Ala Ile Ala Thr Lys Thr His Gln Arg Val Gln Asn Leu Tyr Asp
      165           170           175
Gln Gly Val Val Pro Ala Gln Lys Leu Asp Glu Ala Thr Ala Gln Arg
      180           185           190
Asp Ala Ala Ile Ala Thr Gln Lys Ala Ala Glu Ala Gln Tyr Asn Met
      195           200           205
Ala Arg Asn Gly Ala Glu Arg Glu Asp Lys Leu Ala Ala Ser Ala Leu
      210           215           220
Val Asp Arg Ala Arg Gly Ala Val Ala Glu Val Glu Ser Tyr Ile Asn
      225           230           235           240
Glu Thr Tyr Leu Ile Ala Pro Arg Ala Gly Glu Val Ser Glu Ile Phe
      245           250           255
Pro Lys Ala Gly Glu Leu Val Gly Thr Gly Ala Pro Ile Met Asn Ile
      260           265           270
Ala Glu Met Gly Asp Met Trp Ala Ser Phe Ala Val Arg Glu Asp Phe
      275           280           285
Leu Ser Ser Met Thr Met Gly Ala Val Leu Glu Thr Val Val Pro Ala
      290           295           300
Leu Asn Glu Glu Lys Val Arg Phe Lys Ile Thr Phe Ile Lys Asn Met
      305           310           315           320
Gly Thr Tyr Ala Ala Trp Lys Ala Thr Lys Thr Thr Gly Gln Tyr Asp
      325           330           335
Leu Lys Thr Phe Glu Val Lys Ala Thr Leu Ala Asp Lys Asp Lys Ala
      340           345           350
Gln Lys Leu Arg Pro Gly Met Ser Val Ile Ile Arg Lys
      355           360           365
<210>      297

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<211>      320
<212>      PRT
<213>      Porphyromonas gingivalis
<400>      297
Pro Gln Ser Ser Pro Asp Arg Arg Ser Phe Gln Asn Val Met Asn Lys
  1              5              10              15
Tyr His Ser Gln Ser Val Leu Glu Val Gly Lys Ile Gly Ile Val Ile
      20              25              30
Ile Phe Ala Pro Ile Val Arg Asn Val His Gln Gln Pro Pro Phe Leu
      35              40              45
Ser His Lys Ser Ile Met Arg Ile Val Ser Asn Phe Leu Phe Val Ser
      50              55              60
Phe Ser Val Leu Leu Phe Ala Ser Cys Arg Ser Gln Arg Glu Lys Val
      65              70              75              80
Val Tyr Leu Gln Asp Ile Gln Thr Phe Asn Arg Glu Ile Ile Ala Lys
      85              90              95
Pro Tyr Asp Val Lys Ile Glu Lys Asp Asp Val Leu Asn Ile Leu Val
      100             105             110
Ser Ser Arg Asp Pro Glu Leu Ser Thr Pro Tyr Asn Gln Val Leu Thr
      115             120             125
Thr Arg Ala Leu Ala Arg Asn Gly Tyr Gly Thr Asn Ser Asn Glu Gly
      130             135             140
Phe Leu Val Asp Ser Lys Gly Tyr Ile Asn Tyr Pro Ile Leu Gly Gln
      145             150             155             160
Ile Tyr Val Glu Gly Leu Thr Arg Thr Glu Leu Glu Lys Glu Ile Gln
      165             170             175
Lys Arg Ile Ile Ser Ser Gly Phe Ile Lys Asp Pro Thr Val Thr Val
      180             185             190
Gln Leu Gln Asn Phe Lys Val Ser Val Leu Gly Glu Val Asn His Pro
      195             200             205
Gly Ser Met Ser Val Lys Gly Glu Arg Ile Thr Leu Leu Glu Ala Ile
      210             215             220
Gly Met Ala Gly Asp Leu Thr Ile Tyr Gly Arg Arg Asp Arg Val Phe
      225             230             235             240
Val Ile Arg Glu Thr Asp Gly His Arg Glu Val Phe Gln Thr Asp Leu
      245             250             255
Arg Lys Ala Asp Leu Leu Ala Ser Pro Val Tyr Tyr Leu His Gln Asn
      260             265             270
Asp Val Ile Tyr Val Glu Pro Asn Asp Lys Lys Thr Gln Met Ser Glu
      275             280             285
Ile Asn Gln Asn Asn Asn Val Asn Val Trp Leu Ser Val Thr Ser Thr
      290             295             300
Leu Val Ser Ile Ser Thr Leu Thr Ile Thr Ile Ile Asp Lys Thr Lys
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  1              5              10              15
Thr Asn Leu Phe Leu Ser Leu Leu Val Ile Phe Ile Thr Gly Ser Phe

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

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            435                440                445
Ile Ala Lys Pro Glu Asp Phe Ser Ile Thr Asn Glu Asp Tyr Ala Ala
  450                455                460
Phe Cys Lys Met Met Glu Glu Lys Lys Phe Asp Tyr Asp Arg Gln Ser
465                470                475                480
Gly Lys Met Leu Asp Lys Leu Glu Glu Leu Ala Lys Ile Glu Gly Tyr
            485                490                495
Leu Pro Glu Ala Asn Ser Glu Leu Lys Ala Leu Arg Glu Lys Leu Lys
            500                505                510
Pro Asn Leu Ser Arg Asp Leu Leu Arg Phe Lys Lys Glu Ile Thr Asn
            515                520                525
Tyr Leu Asn Asn Glu Ile Val Thr Arg Tyr Tyr Tyr Glu Arg Gly Ser
            530                535                540
Ile Arg Gln Ser Leu Pro Glu Asp Lys Val Val Lys Glu Ala Ile Lys
545                550                555                560
Leu Leu Lys Asp His Pro Glu Gln Ile Arg Gln Ile Leu Ala Ala Pro
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Lys Ala Glu Asn Lys Gly
            580
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Ala Leu Ala Ile Ile Cys Ala Phe Tyr Leu Ser Phe Ser Phe Val Thr
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Asn Arg Tyr Glu Lys Lys Ala Lys Ala Met Gly Asp Val Ala Gly Met
            35                40                45
Ala Tyr Leu Asp Ser Met Ser Asn Glu Lys Val Trp Phe Gly Tyr Thr
            50                55                60
Leu Lys Glu Ala Gln Ala Gln Gln Ile Gly Leu Gly Leu Asp Leu Lys
  65                70                75                80
Gly Gly Met Asn Val Ile Leu Lys Leu Asn Ala Ser Asp Leu Leu Arg
            85                90                95
Asn Leu Ser Asn Lys Ser Leu Asp Pro Asn Phe Asn Lys Ala Leu Glu
            100                105                110
Asn Ala Ala Lys Ser Thr Glu Gln Ser Asp Phe Ile Asp Ile Phe Val
            115                120                125
Lys Glu Tyr Arg Lys Leu Asp Pro Asn Gly Arg Leu Ala Val Ile Phe
            130                135                140
Gly Ser Gly Asp Leu Arg Asp Gln Ile Thr Ala Lys Ser Thr Asp Ala
145                150                155                160
Asp Val Val Arg Leu Leu Lys Glu Lys Tyr Asn Ser Ala Val Glu Ala
            165                170                175
Ser Phe Asn Val Leu Arg Ala Arg Ile Asp Ala Phe Gly Val Val Ala
            180                185                190
Pro Asn Leu Gln Arg Leu Glu Gly Gln Gly Arg Ile Leu Val Glu Leu
            195                200                205
Pro Gly Val Lys Asp Pro Glu Arg Val Arg Thr Leu Leu Gln Arg Ser
            210                215                220

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

Leu Thr Arg Ile Val Phe Glu Lys Leu Ala Lys Lys Gly Arg Leu Asp
 645 650 655
 Lys Ile Thr Phe Thr Thr Ser Ile Thr Arg Asn Leu Leu Val Asn Pro
 660 665 670
 Ser Tyr Asn Ile Leu Gly Lys Arg Lys Thr Gly Phe Ile Ile Pro Val
 675 680 685
 Ile Ile Ile Val Leu Gly Leu Ile Ala Ser Phe Thr Ile Gly Leu Asn
 690 695 700
 Arg Gly Ile Glu Phe Ser Gly Gly Arg Asn Tyr Val Val Lys Phe Asp
 705 710 715 720
 Gln Pro Val Ser Ser Glu Ala Val Arg Ser Ala Leu Ser Ser Pro Leu
 725 730 735
 Gln Glu Lys Val Leu Val Thr Ser Ile Gly Thr Glu Gly Thr Glu Val
 740 745 750
 Arg Ile Ser Thr Asn Tyr Lys Ile Gln Glu Glu Ser Glu Glu Thr Glu
 755 760 765
 Ala Glu Ile Thr Asp Lys Leu Tyr Gln Ser Leu Lys Gly Phe Tyr Thr
 770 775 780
 Gln Gln Pro Thr Ala Asp Gln Phe Leu Asp Asn Ile Ile Ser Ser Gln
 785 790 795 800
 Lys Val Ser Pro Ser Met Ser Ser Asp Ile Thr Arg Gly Ala Ile Trp
 805 810 815
 Ala Val Leu Leu Ser Met Ile Phe Met Ala Ile Tyr Ile Leu Ile Arg
 820 825 830
 Phe Arg Asp Ile Ser Phe Ser Ala Gly Val Phe Val Ser Val Ala Ala
 835 840 845
 Thr Thr Phe Cys Ile Ile Ala Leu Tyr Ala Leu Leu Trp Lys Ile Leu
 850 855 860
 Pro Phe Thr Met Glu Ile Asp Gln Asn Phe Ile Ala Ala Ile Leu Ala
 865 870 875 880
 Ile Ile Gly Tyr Ser Leu Asn Asp Thr Val Val Val Phe Asp Arg Ile
 885 890 895
 Arg Glu Thr Met Lys Leu Tyr Pro Asn Arg Asp Arg Tyr Gln Val Ile
 900 905 910
 Asn Asp Ala Leu Asn Ser Thr Leu Gly Arg Thr Leu Asn Thr Ser Leu
 915 920 925
 Thr Thr Phe Ile Val Met Leu Val Ile Phe Ile Phe Gly Gly Ala Thr
 930 935 940
 Met Arg Ser Phe Thr Phe Ser Ile Leu Leu Gly Ile Val Ile Gly Thr
 945 950 955 960
 Tyr Ser Thr Leu Phe Val Ala Thr Pro Leu Ala Tyr Glu Ile Gln Lys
 965 970 975
 Arg Lys Leu Asn Lys Ala Ala Lys Lys
 980 985
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 <213> Porphyromonas gingivalis
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 1 5 10 15
 Asn Ser Asn Asn Phe Lys Phe Asn Ala Lys Glu Lys Ser Met Lys Arg

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

435	440	445
Tyr Tyr Asn Pro Phe Asp Val Asn Gly Asp Leu Ala Asp Val Tyr Tyr		
450	455	460
Met Tyr Gly Ala Thr Arg Pro Ser Met Thr Glu Pro Tyr Phe Ala Lys		
465	470	475
Met Arg Pro Phe Ser Ser Glu Ser His Gln Ala Asn Val Asn Gly Phe		
485	490	495
Ala Gln Ile Thr Pro Ile Lys Gly Leu Thr Leu Lys Ala Gln Ala Gly		
500	505	510
Val Asp Ile Thr Asn Thr Arg Thr Ser Ser Lys Arg Met Pro Asn Asn		
515	520	525
Pro Tyr Asp Ser Thr Pro Leu Gly Glu Arg Arg Glu Arg Ala Tyr Arg		
530	535	540
Asp Val Ser Lys Ser Phe Thr Asn Thr Ala Glu Tyr Lys Phe Ser Ile		
545	550	555
Asp Glu Lys His Asp Leu Thr Ala Leu Met Gly His Glu Tyr Ile Glu		
565	570	575
Tyr Glu Gly Asp Val Ile Gly Ala Ser Ser Lys Gly Phe Glu Ser Asp		
580	585	590
Lys Leu Met Leu Leu Ser Gln Gly Lys Thr Gly Asn Ser Leu Ser Leu		
595	600	605
Pro Glu His Arg Val Ala Glu Tyr Ala Tyr Leu Ser Phe Phe Ser Arg		
610	615	620
Phe Asn Tyr Gly Phe Asp Lys Trp Met Tyr Ile Asp Phe Ser Val Arg		
625	630	635
Asn Asp Gln Ser Ser Arg Phe Gly Ser Asn Asn Arg Ser Ala Trp Phe		
645	650	655
Tyr Ser Val Gly Gly Met Phe Asp Ile Tyr Asn Lys Phe Ile Gln Glu		
660	665	670
Ser Asn Trp Leu Ser Asp Leu Arg Leu Lys Met Ser Tyr Gly Thr Thr		
675	680	685
Gly Asn Ser Glu Ile Gly Asn Tyr Asn His Gln Ala Leu Val Thr Val		
690	695	700
Asn Asn Tyr Thr Glu Asp Ala Met Gly Leu Ser Ile Ser Thr Ala Gly		
705	710	715
Asn Pro Asp Leu Ser Trp Glu Lys Gln Ser Gln Phe Asn Phe Gly Leu		
725	730	735
Ala Ala Gly Ala Phe Asn Asn Arg Leu Ser Ala Glu Val Asp Phe Tyr		
740	745	750
Val Arg Thr Thr Asn Asp Met Leu Ile Asp Val Pro Met Pro Tyr Ile		
755	760	765
Ser Gly Phe Phe Ser Gln Tyr Gln Asn Val Gly Ser Met Lys Asn Thr		
770	775	780
Gly Val Asp Leu Ser Leu Lys Gly Thr Ile Tyr Gln Asn Lys Asp Trp		
785	790	795
Asn Val Tyr Ala Ser Ala Asn Phe Asn Tyr Asn Arg Gln Glu Ile Thr		
805	810	815
Lys Leu Phe Phe Gly Leu Asn Lys Tyr Met Leu Pro Asn Thr Gly Thr		
820	825	830
Ile Trp Glu Ile Gly Tyr Pro Asn Ser Phe Tyr Met Ala Glu Tyr Ala		
835	840	845
Gly Ile Asp Lys Lys Thr Gly Lys Gln Leu Trp Tyr Val Pro Gly Gln		

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      850              855              860
Val Asp Ala Asp Gly Asn Lys Val Thr Thr Ser Gln Tyr Ser Ala Asp
865              870              875              880
Leu Glu Thr Arg Ile Asp Lys Ser Val Thr Pro Pro Ile Thr Gly Gly
      885              890              895
Phe Ser Leu Gly Ala Ser Trp Lys Gly Leu Ser Leu Asp Ala Asp Phe
      900              905              910
Ala Tyr Ile Val Gly Lys Trp Met Ile Asn Asn Asp Arg Tyr Phe Thr
      915              920              925
Glu Asn Ala Gly Gly Leu Met Gln Leu Asn Lys Asp Lys Met Leu Leu
      930              935              940
Asn Ala Trp Thr Glu Asp Asn Lys Glu Thr Asp Val Pro Lys Leu Gly
945              950              955              960
Gln Ser Pro Gln Phe Asp Thr His Leu Leu Glu Asn Ala Ser Phe Leu
      965              970              975
Arg Leu Lys Asn Leu Lys Leu Thr Tyr Val Leu Pro Asn Ser Leu Phe
      980              985              990
Ala Gly Gln Asn Val Ile Gly Gly Ala Arg Val Tyr Leu Met Ala Arg
      995              1000              1005
Asn Leu Leu Thr Val Thr Lys Tyr Lys Gly Phe Asp Pro Glu Ala Gly
      1010              1015              1020
Gly Asn Val Gly Lys Asn Gln Tyr Pro Asn Ser Lys Gln Tyr Val Ala
1025              1030              1035              1040
Gly Ile Gln Leu Ser Phe
      1045

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

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

Val Trp Asn Ala Ser Gly Ser Asn Thr Ile Thr Lys Glu Lys Phe Ile
595 600 605
Thr Val Asn Ala Val Met Pro Val Ala Glu Phe Val Gly Thr Pro Thr
610 615 620
Glu Ile Glu Glu Gly Gln Thr Val Ser Phe Gln Asn Gln Ser Thr Asn
625 630 635 640
Ala Thr Asn Tyr Val Trp Ile Phe Asp Gly Gly Thr Pro Ala Thr Ser
645 650 655
Glu Asp Glu Asn Pro Thr Val Leu Tyr Ser Lys Ala Gly Gln Tyr Asp
660 665 670
Val Thr Leu Lys Ala Ile Ser Ala Ser Gly Glu Thr Val Lys Thr Lys
675 680 685
Glu Lys Tyr Ile Thr Val Lys Lys Ala Pro Val Pro Ala Pro Val Ala
690 695 700
Asp Phe Glu Gly Thr Pro Arg Lys Val Lys Lys Gly Glu Thr Val Thr
705 710 715 720
Phe Lys Asp Leu Ser Thr Asn Asn Pro Thr Ser Trp Leu Trp Val Phe
725 730 735
Glu Gly Gly Ser Pro Ala Thr Ser Thr Glu Gln Asn Pro Val Val Thr
740 745 750
Tyr Asn Glu Thr Gly Lys Tyr Asp Val Gln Leu Thr Ala Thr Asn Glu
755 760 765
Gly Gly Ser Asn Val Lys Lys Ala Glu Asp Tyr Ile Glu Val Ile Leu
770 775 780
Asp Asp Ser Val Glu Asp Ile Val Ala Gln Thr Gly Ile Val Ile Arg
785 790 795 800
Pro Gln Asn Gly Thr Lys Gln Ile Leu Ile Glu Ala Asn Ala Ala Ile
805 810 815
Lys Ala Ile Val Leu Tyr Asp Ile Asn Gly Arg Val Val Leu Lys Thr
820 825 830
Thr Pro Asn Gln Leu Arg Ser Thr Val Asp Leu Ser Ile Leu Pro Glu
835 840 845
Gly Ile Tyr Thr Ile Asn Ile Lys Thr Glu Lys Ser Ala Arg Thr Glu
850 855 860
Lys Ile His Ile Gly
865
<210> 302
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<212> PRT
<213> Porphyromonas gingivalis
<400> 302
Leu Ser Tyr Ser Gly Glu Ser Asp Ala Lys Glu Ser Asp Gln Asn Cys
1 5 10 15
Arg Lys Cys Thr Phe Ile Gly Phe Glu Lys Arg Val Asn Thr Met Arg
20 25 30
Leu Ile Lys Ala Phe Leu Val Gln Leu Leu Leu Pro Ile Phe Phe
35 40 45
Tyr Lys Arg Phe Ile Ser Pro Leu Thr Pro Pro Ser Cys Arg Phe Thr
50 55 60
Pro Ser Cys Ser Ser Tyr Ala Ile Glu Ala Leu Arg Lys Tyr Gly Pro
65 70 75 80
Gly Lys Gly Leu Leu Leu Ser Ile Lys Arg Ile Leu Arg Cys His Pro

85 90 95
 Trp Gly Gly Ser Gly Tyr Asp Pro Val Pro
 100 105
 <210> 303
 <211> 861
 <212> PRT
 <213> Porphyromonas gingivalis
 <400> 303
 Leu Glu Met Ala Tyr Asp Phe Thr Gln Thr Phe Arg Asn Ser Leu Glu
 1 5 10 15
 Tyr Ser Tyr Gln Glu Ala Thr Arg Leu Gly Val Val Ala Val Thr Gln
 20 25 30
 Asp Met Leu Val Leu Gly Ile Ile Arg Asp Gly Asp Asn Gly Ala Ile
 35 40 45
 Asp Ile Met Arg His Tyr Gly Ile Asn Leu Tyr Glu Leu Lys Arg Leu
 50 55 60
 Ile Glu Leu Glu Ala Ile Ala Glu Ser Leu Pro Ala Ser Pro Glu Gly
 65 70 75 80
 Ser Pro Ile Phe Thr Pro Ser Ala Arg Glu Ala Ile Asp Asp Ala Thr
 85 90 95
 Asp Ile Cys Ala Asp Met Glu Asp Glu Ala Val Ser Pro Val His Leu
 100 105 110
 Leu Leu Ser Ile Leu Asn Ser Thr Gln Glu Ser Leu Val Gln Lys Ile
 115 120 125
 Phe Met Lys Gln Gly Ile Lys Tyr Asp Thr Ile Leu Ser Asp Tyr Phe
 130 135 140
 Gly Gln Arg Asn Pro Ser Glu Gly Lys Ser Pro Ser Glu Met Glu Ile
 145 150 155 160
 Leu Asp Gly Tyr Gln Asp Asn Asp Phe Asp Asp Glu Glu Asp Glu Ser
 165 170 175
 Ser Pro Pro Ser Gly Asn Ser Gly Thr Gly Gly Gly Ser Gly Asp Ala
 180 185 190
 Pro Glu Gln Asn Thr Gly Gly Gly Asp Thr Thr Thr Thr Thr Arg Ser
 195 200 205
 Gly Gly Asp Thr Pro Ala Leu Asp Thr Phe Gly Thr Asp Ile Thr Ala
 210 215 220
 Met Ala Ala Ala Gly Lys Leu Asp Pro Val Val Gly Arg Glu Gln Glu
 225 230 235 240
 Ile Glu Arg Val Ile Gln Ile Leu Ser Arg Arg Lys Lys Asn Asn Pro
 245 250 255
 Val Leu Ile Gly Glu Pro Gly Val Gly Lys Ser Ala Ile Val Glu Gly
 260 265 270
 Leu Ala Glu Arg Ile Val Asn Arg Lys Val Ser Arg Ile Leu Phe Asp
 275 280 285
 Lys Arg Ile Ile Ser Leu Asp Leu Ala Gln Met Val Ala Gly Thr Lys
 290 295 300
 Tyr Arg Gly Gln Phe Glu Glu Arg Leu Lys Ala Val Leu Asp Glu Leu
 305 310 315 320
 Lys Lys Asn Pro Gln Ile Ile Leu Phe Ile Asp Glu Ile His Thr Ile
 325 330 335
 Val Gly Ala Gly Ser Ala Ala Gly Ser Met Asp Thr Ala Asn Met Leu
 340 345 350

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

Gly Lys Thr Glu Ile Arg Arg Met Val Asp Ile Glu Leu Lys Ala Val
770 775 780
Leu Ala Arg Ile His Arg Ala Gly Tyr Asp Leu Val Leu Thr Asp Glu
785 790 795 800
Ala Lys Asp Val Ile Ala Thr Lys Gly Tyr Asp Leu Gln Tyr Gly Ala
805 810 815
Arg Pro Leu Lys Arg Thr Leu Gln Asn Glu Val Glu Asp Arg Leu Thr
820 825 830
Asp Leu Ile Leu Ser Gly Gln Ile Glu Lys Gly Gln Thr Leu Thr Leu
835 840 845
Ser Ala Arg Asp Gly Glu Ile Ile Val Gln Glu Gln Ala
850 855 860
<210> 304
<211> 456
<212> PRT
<213> Porphyromonas gingivalis
<400> 304
Arg Gly Gly Gln Ile Arg Arg His His Thr Asp Ser Ser Arg Gly Ser
1 5 10 15
Asp Ser Lys Ala Cys Arg Phe Ser Phe His Ala Glu Thr Ile Gly Phe
20 25 30
Ser Asn His Gln Arg Ala Lys Met Asn Tyr Leu Tyr Ile Leu Ile Thr
35 40 45
Leu Leu Leu Ser Gly Phe Phe Ser Gly Ala Glu Ile Ala Phe Leu Ser
50 55 60
Ser Asp Lys Leu Arg Leu Glu Leu Asp Arg Asn Arg Gly Asp Leu Thr
65 70 75 80
Gly Arg Ala Leu Asn Leu Leu Tyr Arg His Pro Asp Gln Leu Val Thr
85 90 95
Thr Leu Leu Val Gly Asn Asn Ile Val Leu Val Val Tyr Gly Leu Leu
100 105 110
Met Ala Gly Leu Leu Ala Ala Pro Leu Ala Gln Trp Ile Asp Asn Asp
115 120 125
Ala Met Ile Val Val Leu Gln Ser Val Leu Ser Thr Ile Ile Ile Leu
130 135 140
Phe Thr Gly Glu Phe Leu Pro Lys Ala Ile Phe Lys Thr Asn Ala Asn
145 150 155 160
Met Met Met Arg Val Phe Ala Leu Pro Ile Val Ala Ile Tyr Tyr Leu
165 170 175
Leu Tyr Pro Leu Ser Lys Leu Phe Thr Gly Leu Ser Arg Ser Phe Ile
180 185 190
Arg Leu Val Asp Lys Asn Tyr Val Pro Thr Thr Val Gly Leu Gly Arg
195 200 205
Val Asp Leu Asp His Tyr Leu Ala Glu Asn Met Ser Gly Glu Asn Glu
210 215 220
Gln Asn Asp Leu Thr Thr Glu Val Lys Ile Ile Gln Asn Ala Leu Asp
225 230 235 240
Phe Ser Gly Ile Gln Val Arg Asp Cys Met Ile Pro Arg Asn Glu Met
245 250 255
Ile Ala Cys Glu Leu Gln Thr Asp Ile Glu Val Leu Lys Thr Thr Phe
260 265 270
Ile Asp Thr Gly Leu Ser Lys Ile Ile Ile Tyr Arg Gln Asn Ile Asp

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

<210> 305

<211> 299

<212> PRT

<213> Porphyromonas gingivalis

<400> 305

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

Val Glu Thr Gly Val Ala Asn Gly Thr Tyr Ile Tyr Glu Val Glu Val
195 200 205
Lys Tyr Pro Asp Gly Val Ser Pro Lys Val Ala Val Thr Val Thr Val
210 215 220
Thr Asn Ser Ser Leu Ser Asn Val Asp Gly Gln Ala Pro Tyr Thr Leu
225 230 235 240
Arg Val Glu Gly Lys Lys Ile Ile Ala Glu Ala His Gly Met Ile Thr
245 250 255
Leu Tyr Asp Ile Asn Gly Arg Thr Val Ala Val Ala Pro Asn Arg Leu
260 265 270
Glu Tyr Met Ala Gln Thr Gly Phe Tyr Ala Val Arg Phe Asp Val Gly
275 280 285
Asn Lys His His Val Ser Lys Ile Gln Val Arg
290 295
<210> 306
<211> 377
<212> PRT
<213> Porphyromonas gingivalis
<400> 306
Leu Phe Asn His Lys Lys Ser Trp Tyr Glu Thr Phe Gln Phe Tyr Leu
1 5 10 15
Val Val Phe Arg Ser Gly Phe Ile Leu Leu Cys Glu Asn Thr Leu Ala
20 25 30
Gln Gln Lys Thr Glu Glu Phe Ala Pro Val Ser Asp Leu Arg Ala Glu
35 40 45
Ala Tyr Gly Ser Thr Val Phe Leu His Trp Thr Pro Pro Tyr Asp Asn
50 55 60
Pro Met Ile Pro Leu Ser Glu Ser Phe Glu Ser Gly Ile Pro Ala Ile
65 70 75 80
Trp Lys Thr Ile Asp Ala Asp Gly Asp Gly Tyr Asn Trp Met His Leu
85 90 95
Thr Asn Phe Thr Gly Gln Ser Gly Leu Cys Val Ser Ser Ala Ser Tyr
100 105 110
Ile Gly Gly Val Gly Ala Leu Thr Pro Asp Asn Tyr Leu Ile Thr Pro
115 120 125
Glu Leu Lys Leu Pro Thr Asp Ala Leu Val Glu Ile Ile Tyr Trp Val
130 135 140
Cys Thr Gln Asp Leu Thr Ala Pro Ser Glu His Tyr Ala Val Tyr Ser
145 150 155 160
Ser Ser Thr Gly Asn Asn Ala Ala Asp Phe Val Asn Leu Leu Tyr Glu
165 170 175
Glu Thr Leu Thr Ala Lys Arg Ile Gln Ser Pro Glu Leu Ile Arg Gly
180 185 190
Asn Arg Thr Gln Gly Val Trp Tyr Gln Arg Lys Val Val Leu Pro Asn
195 200 205
Asp Thr Lys Tyr Val Ala Phe Arg His Phe Asn Ser Thr Asp Asn Phe
210 215 220
Trp Leu Asn Leu Asp Glu Val Ser Ile Leu Tyr Thr Pro Leu Pro Arg
225 230 235 240
Arg Ala Pro Cys Pro His Pro Gly Gly Tyr Thr Tyr Ser Val Phe Arg
245 250 255
Asp Gly Gln Lys Ile Ala Ser Gly Leu Ser Ala Leu Ala Tyr Ile Asp

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                260                265                270
Thr Asp Val Pro Tyr Gly Thr Gln Asp Tyr Cys Val Gln Val Asn Tyr
    275                280                285
Leu Gln Gly Asp Ser Tyr Lys Val Cys Lys Asn Ile Val Val Ala Asn
    290                295                300
Ser Ala Asn Ile Tyr Gly Ala Asp Lys Pro Phe Ala Leu Thr Val Val
    305                310                315                320
Gly Lys Thr Ile Val Ala Ser Ala Phe Lys Gly Glu Ile Thr Leu Tyr
    325                330                335
Asp Ile Arg Gly Arg Leu Ile Ala Ser Gly Cys Asp Thr Leu Arg Tyr
    340                345                350
Lys Ala Glu Asn Gly Phe Tyr Leu Ile Lys Ile Gln Val Asn Gly Thr
    355                360                365
Val Tyr Thr Glu Lys Ile Gln Ile Gln
    370                375
<210>    307
<211>    849
<212>    PRT
<213>    Porphyromonas gingivalis
<400>    307
Phe Gly Ile Ser Pro Ser Met Lys Lys Ser Phe Leu Leu Ala Ile Val
  1                5                10                15
Met Leu Phe Gly Ile Ala Met Gln Gly His Ser Ala Pro Val Thr Lys
    20                25                30
Glu Arg Ala Leu Ser Leu Ala Arg Leu Ala Leu Arg Gln Val Ser Leu
    35                40                45
Arg Met Gly Gln Thr Ala Val Ser Asp Lys Ile Ser Ile Asp Tyr Val
    50                55                60
Tyr Arg Gln Gly Asp Ala Glu Arg Gly Ile Thr Ser Gln Glu Glu Gly
    65                70                75                80
Ser Pro Ala Tyr Phe Tyr Val Ala Asn Arg Gly Asn Asn Glu Gly Tyr
    85                90                95
Ala Leu Val Ala Ala Asp Asp Arg Ile Pro Thr Ile Leu Ala Tyr Ser
    100                105                110
Pro Ile Gly Arg Phe Asp Met Asp Ser Met Pro Asp Asn Leu Arg Met
    115                120                125
Trp Leu Gln Ile Tyr Asp Gln Glu Ile Gly Leu Ile Leu Ser Gly Lys
    130                135                140
Ala Gln Leu Asn Glu Glu Ile Leu Arg Thr Glu Gly Val Pro Ala Glu
    145                150                155                160
Val His Ala Leu Met Asp Asn Gly His Phe Ala Asn Asp Pro Met Arg
    165                170                175
Trp Asn Gln Gly Tyr Pro Trp Asn Asn Lys Glu Pro Leu Leu Pro Asn
    180                185                190
Gly Asn His Ala Tyr Thr Gly Cys Val Ala Thr Ala Ala Ala Gln Ile
    195                200                205
Met Arg Tyr His Ser Trp Pro Leu Gln Gly Glu Gly Ser Phe Asp Tyr
    210                215                220
His Ala Gly Ser Leu Val Gly Asn Trp Ser Gly Thr Phe Gly Glu Met
    225                230                235                240
Tyr Asp Trp Ile Asn Met Pro Gly Asn Pro Asp Leu Asp Asn Leu Thr
    245                250                255

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

His Asn Arg Val Leu Pro Asp Phe Thr Leu Lys Asn Leu Gly Leu Pro
 675 680 685
 Phe Asn Gly Glu Leu Val Val Val Phe Arg Gln Thr Gln Ser Ser Ser
 690 695 700
 Gly Ser Leu Trp Ala Ala Gln Glu Thr Val His Ile Lys Gln Gly Glu
 705 710 715 720
 Thr Phe Val Tyr Lys Pro Val Val Glu Gly Pro Ile Pro Asp Gly Ser
 725 730 735
 Tyr Arg Ala Thr Leu His Ala Phe Val Asn Gly Gln Gln Gln Leu Tyr
 740 745 750
 Leu Lys Gly Lys Arg Asn Tyr Thr Val Lys Ile Val Asn Gly Thr Ala
 755 760 765
 Val Glu Ala Ile Glu Ser Ser Glu Glu Ile Arg Val Phe Pro Asn Pro
 770 775 780
 Ala Arg Asp Tyr Val Glu Ile Ser Ala Pro Cys Ile Pro Gln Glu Thr
 785 790 795 800
 Ser Ile Ile Leu Phe Asp Leu Ser Gly Lys Ile Val Met Lys Asn Ser
 805 810 815
 Leu Ser Ala Gly His Gly Arg Met Asp Val Ser Arg Leu Pro Asn Gly
 820 825 830
 Ala Tyr Ile Leu Lys Val Asp Gly Tyr Thr Thr Lys Ile Asn Ile Val
 835 840 845
 His
 <210> 308
 <211> 295
 <212> PRT
 <213> Porphyromonas gingivalis
 <400> 308
 Thr Lys Lys Thr Leu Met Lys Lys Leu Phe Leu Ser Leu Thr Ser Leu
 1 5 10 15
 Val Met Val Phe Ala Val Ala Ser Cys Asp Ile Ile Asp Lys Asp Gln
 20 25 30
 Thr Leu Leu Pro Ala Pro Thr Asn Val Thr Pro Asp Asn Pro Asp Asp
 35 40 45
 Asn Pro Ser Glu Ile Asp Ile Thr Gln Thr His Thr Glu Lys Tyr Val
 50 55 60
 Leu Ala Glu Glu Phe Thr Gly Gln Lys Cys Leu Asn Cys Pro Lys Gly
 65 70 75 80
 His Arg Lys Leu Ala Ala Leu Lys Glu Gln Tyr Gly Lys Arg Leu Thr
 85 90 95
 Val Val Gly Ile His Ala Gly Pro Gly Ser Leu Val Pro Pro Leu Phe
 100 105 110
 Arg Thr Glu Ala Gly Asp Ala Tyr Tyr Ser Lys Phe Ala Asn Asn Thr
 115 120 125
 Pro Leu Pro Ala Leu Met Val Ser Arg Lys Lys Phe Gly Ser Ser Tyr
 130 135 140
 Val Tyr Asp Lys Ser Tyr Lys Thr Trp Asp Val Pro Ile Ala Glu Gln
 145 150 155 160
 Met Glu Gln Lys Ala Lys Ile Asn Ile Phe Ala Val Ala Glu Tyr Thr
 165 170 175
 Asp Thr Gln Lys Ile Lys Val Thr Val Lys Gly Lys Ile Leu Glu Gly
 180 185 190

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Asn Thr Leu Pro Lys Ser Met Val Gln Val Tyr Leu Leu Glu Asp Lys
    195                200                205
Leu Ile Ala Pro Gln Val Asp Gly Asn Thr Thr Val Glu Asn Tyr Glu
    210                215                220
His Asn His Val Leu Arg Gly Ala Val Asn Gly Ile Trp Gly Glu Glu
    225                230                235                240
Phe Val Asn Leu Lys Asp Tyr Leu Tyr Thr Tyr Ala Val Glu Pro Leu
    245                250                255
Ser Gly Met Ser Phe Val Ala Glu Asn Tyr Ser Ile Val Ala Phe Val
    260                265                270
Tyr Asp Val Gln Thr Phe Glu Val Tyr Asp Val Val His Val Lys Ile
    275                280                285
Asn Pro Gln Ser Asp Gly Lys
    290                295
<210>      309
<211>      230
<212>      PRT
<213>      Porphyromonas gingivalis
<400>      309
Thr Asn Lys Lys Glu Glu Thr Met Lys Lys Ser Ser Val Val Ala Ser
  1                5                10                15
Val Leu Ala Val Ala Leu Val Phe Ala Gly Cys Gly Leu Asn Asn Met
    20                25                30
Ala Lys Gly Gly Leu Ile Gly Ala Gly Val Gly Gly Ala Ile Gly Ala
    35                40                45
Gly Val Gly Asn Val Ala Gly Asn Thr Ala Val Gly Ala Ile Val Gly
    50                55                60
Thr Ala Val Gly Gly Ala Ala Gly Ala Leu Ile Gly Lys Lys Met Asp
    65                70                75                80
Lys Gln Lys Lys Glu Leu Glu Ala Ala Val Pro Asp Ala Thr Ile Gln
    85                90                95
Thr Val Asn Asp Gly Glu Ala Ile Leu Val Thr Phe Asp Ser Gly Ile
    100                105                110
Leu Phe Ala Thr Asn Ser Ser Thr Leu Ser Pro Asn Ser Arg Thr Ala
    115                120                125
Leu Thr Lys Phe Ala Ala Asn Met Asn Lys Asn Pro Asp Thr Asp Ile
    130                135                140
Arg Ile Val Gly His Thr Asp Asn Thr Gly Ser Asp Lys Ile Asn Asp
    145                150                155                160
Pro Leu Ser Glu Arg Arg Ala Ala Ser Val Tyr Ser Phe Leu Asn Ser
    165                170                175
Gln Gly Val Ser Met Ser Arg Met Ala Ala Glu Gly Arg Gly Ser His
    180                185                190
Glu Pro Val Ala Asp Asn Ser Thr Val Ala Gly Arg Ser Ala Asn Arg
    195                200                205
Arg Val Glu Val Tyr Ile Leu Pro Asn Ala Lys Met Ile Glu Gln Ala
    210                215                220
Gln Gln Gly Thr Leu Lys
    225                230
<210>      310
<211>      342
<212>      PRT

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<213>    Porphyromonas gingivalis
<400>    310
Asn Arg Asn Arg Asn Met Ser Lys Lys Ser Ile Leu Leu Leu Cys Cys
 1             5             10             15
Ser Leu Cys Phe Ile Ser Ala Thr Lys Ala Val Thr Pro Val Arg Asn
          20             25             30
Val Arg Asn Ser Gln Val Asn Ser Lys Ala Lys Thr Glu Arg Thr Lys
      35             40             45
Pro Ser Asp Ser Val Arg Tyr Ile Ser Asn Met Ile Ala Asp Arg Leu
      50             55             60
Glu Phe Arg Asn Lys Ile Ser Ser Glu Lys Glu Val Arg Lys Ala Glu
      65             70             75             80
Tyr Glu Asn Arg Leu Ala Met Glu Ala Leu Asn Tyr Pro Ala Ile Asp
          85             90             95
Leu Tyr Gly Glu Asp Ser Trp Ser Glu Tyr Val Asn Pro Phe Val Gly
      100             105             110
Ala Gly Thr Asp Val Glu Ile Pro Asn Ser Tyr Asp Ile Asp Cys Ser
      115             120             125
Ser Phe Val Met Pro Val Glu Asp Lys Gln Val Thr Ser Gln Phe Gly
      130             135             140
Tyr Arg Arg Arg Phe Gly Arg Met His Tyr Gly Ile Asp Leu Ser Val
      145             150             155             160
Asn Arg Gly Asp Thr Ile Arg Ala Ala Phe Asp Gly Lys Val Arg Val
          165             170             175
Arg Ser Tyr Glu Ala Arg Gly Tyr Gly Tyr Tyr Ile Val Leu Arg His
          180             185             190
Pro Asn Gly Leu Glu Thr Val Tyr Gly His Met Ser Arg Gln Leu Val
          195             200             205
Asp Glu Asn Gln Ile Val Arg Ala Gly Gln Pro Ile Gly Leu Gly Gly
      210             215             220
Ser Thr Gly Arg Ser Thr Gly Pro His Leu His Phe Glu Thr Arg Phe
      225             230             235             240
Met Gly Ile Pro Ile Asn Pro Ser Thr Ile Ile Asp Phe Asp Asn Gly
          245             250             255
Val Pro Leu Arg Asp Ile Tyr Thr Phe Lys Arg Gly Ser Asn Ser Arg
          260             265             270
Tyr Ala Lys Ala Ser Lys Thr Ser Ser Arg Tyr Ala Lys Lys Gly Lys
          275             280             285
Lys Gly Arg Gln Ala Ser Ser Pro Met Thr Tyr Arg Ile Lys Lys Gly
          290             295             300
Asp Thr Leu Glu Thr Ile Ala Lys Arg His Gly Thr Ser Val Gln Lys
      305             310             315             320
Leu Cys Ala Thr Asn Gly Ile Gly Lys Ser Lys Ile Leu Thr Pro Gly
          325             330             335
Lys Ala Leu Arg Ile Lys
          340
<210>    311
<211>    159
<212>    PRT
<213>    Porphyromonas gingivalis
<400>    311
Pro Ser Lys Thr Ile Ile Lys Thr Met Ala Lys Ile Asn Phe Tyr Ala

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1           5           10           15
Glu Gly Val Ser Leu Pro Arg Ile Arg Arg Arg Ile Val Gly Lys Trp
           20           25           30
Ile Ala Glu Val Cys Ser Arg Tyr Gly Lys Ala Val Gly Glu Ile Ser
           35           40           45
Tyr Leu Phe Cys Asp Asp Glu Tyr Ile Leu Lys Ala Asn Gln Glu Phe
           50           55           60
Leu Asp His Asp Tyr Tyr Thr Asp Ile Ile Thr Phe Asp Ser Cys Glu
           65           70           75           80
Ala Asp Thr Val Asn Gly Asp Leu Leu Ile Ser Leu Asp Thr Val Arg
           85           90           95
Ser Asn Ala Arg Ala Leu Asp Leu Arg Tyr Glu Asp Glu Leu His Arg
           100          105          110
Val Ile Ile His Gly Ile Leu His Leu Cys Gly Leu Lys Asp Lys Ser
           115          120          125
Lys Lys Asp Glu Ala Gln Met Arg Ala Ala Glu Glu Lys Ala Leu Val
           130          135          140
Met Leu Arg Glu Thr Ile Gly Ser Glu Leu Ser Leu Leu His Thr
           145          150          155
<210>      312
<211>      395
<212>      PRT
<213>      Porphyromonas gingivalis
<400>      312
Lys Ser Lys Thr Met Lys Val Lys Tyr Leu Met Leu Thr Leu Val Gly
1           5           10           15
Ala Ile Ala Leu Asn Ala Ser Ala Gln Glu Asn Thr Val Pro Ala Thr
           20           25           30
Gly Gln Leu Pro Ala Lys Asn Val Ala Phe Ala Arg Asn Lys Ala Gly
           35           40           45
Ser Asn Trp Phe Val Thr Leu Gln Gly Gly Val Ala Ala Gln Phe Leu
           50           55           60
Asn Asp Asn Asn Asn Lys Asp Leu Met Asp Arg Leu Gly Ala Ile Gly
           65           70           75           80
Ser Leu Ser Val Gly Lys Tyr His Ser Pro Phe Phe Ala Thr Arg Leu
           85           90           95
Gln Ile Asn Gly Gly Gln Ala His Thr Phe Leu Gly Lys Asn Gly Glu
           100          105          110
Gln Glu Ile Asn Thr Asn Phe Gly Ala Ala His Phe Asp Phe Met Phe
           115          120          125
Asp Val Val Asn Tyr Phe Ala Pro Tyr Arg Glu Asn Arg Phe Phe His
           130          135          140
Leu Ile Pro Trp Val Gly Val Gly Tyr Gln His Lys Phe Ile Gly Ser
           145          150          155          160
Glu Trp Ser Lys Asp Asn Val Glu Ser Leu Thr Ala Asn Val Gly Val
           165          170          175
Met Met Ala Phe Arg Leu Gly Lys Arg Val Asp Phe Val Ile Glu Ala
           180          185          190
Gln Ala Ala His Ser Asn Leu Asn Leu Ser Arg Ala Tyr Asn Ala Lys
           195          200          205
Lys Thr Pro Val Phe Glu Asp Pro Ala Gly Arg Tyr Tyr Asn Gly Phe
           210          215          220

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Gln Gly Met Ala Thr Ala Gly Leu Asn Phe Arg Leu Gly Ala Val Gly
 225 230 235 240
 Phe Asn Ala Ile Xaa Pro Met Asp Tyr Ala Leu Ile Asn Asp Leu Asn
 245 250 255
 Gly Gln Ile Asn Arg Leu Arg Ser Glu Val Glu Glu Leu Ser Lys Arg
 260 265 270
 Pro Val Ser Cys Pro Glu Cys Pro Glu Val Thr Pro Val Thr Lys Thr
 275 280 285
 Glu Asn Ile Leu Thr Glu Lys Ala Val Leu Phe Arg Phe Asp Ser His
 290 295 300
 Val Val Asp Lys Asp Gln Leu Ile Asn Leu Tyr Asp Val Ala Gln Phe
 305 310 315 320
 Val Lys Glu Thr Asn Glu Pro Ile Thr Val Val Gly Tyr Ala Asp Pro
 325 330 335
 Thr Gly Asn Thr Gln Tyr Asn Glu Lys Leu Ser Glu Arg Arg Ala Lys
 340 345 350
 Ala Val Val Asp Val Leu Thr Gly Lys Tyr Gly Val Pro Ser Glu Leu
 355 360 365
 Ile Ser Val Glu Trp Lys Gly Asp Ser Thr Gln Pro Phe Ser Lys Lys
 370 375 380
 Ala Trp Asn Arg Val Val Ile Val Arg Ser Lys
 385 390 395
 <210> 313
 <211> 387
 <212> PRT
 <213> Porphyromonas gingivalis
 <400> 313
 Tyr Lys Met Thr Tyr Arg Ile Met Lys Ala Lys Ser Leu Leu Leu Ala
 1 5 10 15
 Leu Ala Gly Leu Ala Cys Thr Phe Ser Ala Thr Ala Gln Glu Ala Thr
 20 25 30
 Thr Gln Asn Lys Ala Gly Met His Thr Ala Phe Gln Arg Asp Lys Ala
 35 40 45
 Ser Asp His Trp Phe Ile Asp Ile Ala Gly Gly Ala Gly Met Ala Leu
 50 55 60
 Ser Gly Trp Asn Asn Asp Val Asp Phe Val Asp Arg Leu Ser Ile Val
 65 70 75 80
 Pro Thr Phe Gly Ile Gly Lys Trp His Glu Pro Tyr Phe Gly Thr Arg
 85 90 95
 Leu Gln Phe Thr Gly Phe Asp Ile Tyr Gly Phe Pro Gln Gly Ser Lys
 100 105 110
 Glu Arg Asn His Asn Tyr Phe Gly Asn Ala His Leu Asp Phe Met Phe
 115 120 125
 Asp Leu Thr Asn Tyr Phe Gly Val Tyr Arg Pro Asn Arg Val Phe His
 130 135 140
 Ile Ile Pro Trp Ala Gly Ile Gly Phe Gly Tyr Lys Phe His Ser Glu
 145 150 155 160
 Asn Ala Asn Gly Glu Lys Val Gly Ser Lys Asp Asp Met Thr Gly Thr
 165 170 175
 Val Asn Val Gly Leu Met Leu Lys Phe Arg Leu Ser Arg Val Val Asp
 180 185 190

Phe Asn Ile Glu Gly Gln Ala Phe Ala Gly Lys Met Asn Phe Ile Gly
 195 200 205
 Thr Lys Arg Gly Lys Ala Asp Phe Pro Val Met Ala Thr Ala Gly Leu
 210 215 220
 Thr Phe Asn Leu Gly Lys Thr Glu Trp Thr Glu Ile Val Pro Met Asp
 225 230 235 240
 Tyr Ala Leu Val Asn Asp Leu Asn Asn Gln Ile Asn Ser Leu Arg Gly
 245 250 255
 Gln Val Glu Glu Leu Ser Arg Arg Pro Val Ser Cys Pro Glu Cys Pro
 260 265 270
 Glu Pro Thr Gln Pro Thr Val Thr Arg Val Val Val Asp Asn Val Val
 275 280 285
 Tyr Phe Arg Ile Asn Ser Ala Lys Ile Asp Arg Asn Gln Glu Ile Asn
 290 295 300
 Val Tyr Asn Thr Ala Glu Tyr Ala Lys Thr Asn Asn Ala Pro Ile Lys
 305 310 315 320
 Val Val Gly Tyr Ala Asp Glu Lys Thr Gly Thr Ala Ala Tyr Asn Met
 325 330 335
 Lys Leu Ser Glu Arg Arg Ala Lys Ala Val Ala Lys Met Leu Glu Lys
 340 345 350
 Tyr Gly Val Ser Ala Asp Arg Ile Thr Ile Glu Trp Lys Gly Ser Ser
 355 360 365
 Glu Gln Ile Tyr Glu Glu Asn Ala Trp Asn Arg Ile Val Val Met Thr
 370 375 380
 Ala Ala Glu
 385
 <210> 314
 <211> 195
 <212> PRT
 <213> Porphyromonas gingivalis
 <400> 314
 Val Ile Gly Ile Ile Met Glu Phe Phe Met Leu Phe Ile Ala Ala Val
 1 5 10 15
 Phe Val Asn Asn Val Val Leu Ser Gln Phe Leu Gly Ile Cys Pro Phe
 20 25 30
 Leu Gly Val Ser Lys Lys Val Asp Thr Ser Ile Gly Met Gly Ala Ala
 35 40 45
 Val Thr Phe Val Leu Ala Leu Ala Thr Leu Val Thr Phe Leu Ile Gln
 50 55 60
 Lys Phe Val Leu Asp Arg Phe Gly Leu Gly Phe Met Gln Thr Ile Ala
 65 70 75 80
 Phe Ile Leu Val Ile Ala Ala Leu Val Gln Met Val Glu Ile Ile Leu
 85 90 95
 Lys Lys Val Ser Pro Pro Leu Tyr Gln Ala Leu Gly Val Phe Leu Pro
 100 105 110
 Leu Ile Thr Thr Asn Cys Cys Val Leu Gly Val Ala Ile Leu Val Ile
 115 120 125
 Gln Lys Asp Tyr Thr Leu Leu Gln Ser Phe Val Tyr Ala Ile Ser Thr
 130 135 140
 Ala Ile Gly Phe Thr Leu Ala Met Val Thr Phe Ala Gly Ile Arg Glu
 145 150 155 160
 Gln Leu Asp Met Thr Asn Leu Pro Lys Ala Met Lys Gly Ile Pro Ser

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                165                170                175
Ala Leu Leu Ala Ala Gly Ile Leu Ala Met Ala Phe Met Gly Phe Ser
                180                185                190
Gly Ile Ala
                195
<210>      315
<211>      876
<212>      PRT
<213>      Porphyromonas gingivalis
<400>      315
Tyr Arg Ser Tyr Arg Gly Ile Gly Ser Gly Thr His Ser Pro Asn Leu
  1          5          10          15
Lys Asn Arg Leu Lys Arg Ile Gly Ile Arg Ile Pro Asn Arg His Tyr
          20          25          30
Ile His Ile Lys Pro Ile Lys Pro Lys Asn Lys Met Lys Gln Leu Asn
          35          40          45
Ile Ile Ser Phe Ile Ile Ala Phe Leu Phe Leu Gly Thr Ser Ala Ser
          50          55          60
Ala Gln Gln Ser Gly Gly Ser Val Thr Gly Thr Val Val Asp Lys Ser
          65          70          75          80
Ser Lys Glu Pro Ile Ala Tyr Val Gln Val Phe Val Lys Gly Thr Thr
          85          90          95
Leu Gly Thr Ser Thr Asp Ala Asn Gly Asn Tyr Ser Ile Lys Gly Ile
          100          105          110
Pro Ser Gly Asn Gln Thr Ile Val Ala Arg Leu Met Gly Tyr Ser Thr
          115          120          125
Cys Glu Glu Lys Val His Ile Glu Lys Gly Gly Ser Arg His Val Asp
          130          135          140
Leu Tyr Leu Thr Glu Glu Ile Leu Ser Leu Asp Gly Val Val Val Ser
          145          150          155          160
Ala Asn Arg Asn Glu Thr Phe Arg Arg Gln Ala Pro Ser Leu Val Thr
          165          170          175
Val Leu Ser Pro Glu Leu Phe Leu Lys Thr Asn Ser Thr Asn Leu Ser
          180          185          190
Gln Gly Leu Lys Phe Gln Pro Gly Leu Arg Val Glu Asp Asn Cys Gln
          195          200          205
Asn Cys Gly Phe Asn Gln Val Arg Ile Asn Gly Leu Glu Gly Ala Tyr
          210          215          220
Ser Gln Ile Leu Ile Asp Ser His Pro Ile Phe Ser Ser Leu Ala Gly
          225          230          235          240
Val Tyr Gly Leu Glu Gln Met Pro Ala Asn Met Ile Glu Arg Val Glu
          245          250          255
Val Ile Arg Gly Gly Gly Ser Ala Leu Phe Gly Ser Asn Ala Val Gly
          260          265          270
Gly Val Ile Asn Val Ile Thr Lys Glu Pro Leu Arg Asn Ser Ala Glu
          275          280          285
Ile Ser His Ser Thr Met Thr Phe Asp His Ala Lys Gly Trp Gly Ser
          290          295          300
Phe Gln Asn Thr Thr Gln Phe Asn Gly Ser Met Leu Thr Glu Asp Arg
          305          310          315          320
Lys Ala Gly Val Met Val Phe Gly Gln His Asn Tyr Arg Pro Gly Gln
          325          330          335

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

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Phe Ala Ile Asn Leu Ser Gly Thr Phe Thr Gly Lys Met Asp Val Val
    755                      760                      765
His Glu Ala Tyr Glu Gly Asp Ile Pro Ala Glu His Ile Ala Pro Asp
    770                      775                      780
Gly Ser Phe Asp Phe Glu Met Asn Gly Gln Gln Phe Lys Gly Leu Ala
    785                      790                      795                      800
Glu Gly His Ala Lys Leu Val Lys Thr Pro Ala Phe Ala Asp Ile Asp
    805                      810                      815
Leu Lys Leu Ser His Asp Phe His Leu Ala Ser Thr Met Thr Leu Glu
    820                      825                      830
Leu Asn Ala Gly Ile Gln Asn Ile Phe Asn Ser Tyr Gln Lys Asp Thr
    835                      840                      845
Asp Lys Gly Pro Gly Arg Ala Ser Thr Tyr Val Tyr Gly Pro Met Gln
    850                      855                      860
Pro Arg Arg Ile Phe Val Gly Thr Lys Ile Asn Phe
    865                      870                      875
<210>      316
<211>      899
<212>      PRT
<213>      Porphyromonas gingivalis
<400>      316
Ile Leu Asn His Leu Arg Lys Thr Met Tyr Lys Lys Ile Ile Ala Val
  1                      5                      10                      15
Ala Ala Leu Phe Cys Ala Ser Ile Gly Ile Leu Lys Gly Gln Ser Ser
    20                      25                      30
Asp Leu Thr Pro Gln Asp Thr Ile Tyr Ser Pro Glu Ile Ser Tyr Ala
    35                      40                      45
Lys Pro Ile His Lys Thr Ile Ala Ser Ile Glu Ile Glu Gly Met Arg
    50                      55                      60
Ser Phe Asp Asp Phe Val Leu Arg Asn Leu Ser Gly Leu Ala Val Gly
    65                      70                      75                      80
Asp Glu Val Leu Ile Pro Gly Asp Ala Met Ser Ala Ala Val Asn Arg
    85                      90                      95
Ile Met Arg Gln Gly Tyr Phe Ser Asn Val Arg Ile Ile Ala Asp Lys
    100                     105                     110
Tyr Val Gly Asn Lys Val Tyr Leu Lys Ile Ile Val Thr Glu Arg Pro
    115                     120                     125
Arg Ile Ser Lys Val Thr Phe Ser Gly Val Lys Lys Ser Glu Arg Glu
    130                     135                     140
Asp Leu Glu Met Lys Ile Gly Leu Arg Glu Gly Ile Gln Met Thr Arg
    145                     150                     155                     160
Asn Asn Glu Asp Lys Val Arg Gln Ile Val Gln Lys Tyr Phe Ser Glu
    165                     170                     175
Lys Gly Tyr Arg Asp Ala Ser Ile Arg Ile Thr Gln Glu Pro Asp Leu
    180                     185                     190
Ser Lys Asp Gly Phe Val Asn Val Leu Ile Ser Ile Glu Lys Lys Ser
    195                     200                     205
Lys Thr Lys Val Asn Glu Ile Tyr Phe Ser Gly Asn Lys Ala Leu Ser
    210                     215                     220
Asn His Lys Leu Arg Met Ala Met Lys Asn Thr Asn Ala Lys Phe Ser
    225                     230                     235                     240
Leu Arg Lys His Ile Arg Ser Ser Phe Leu Lys Leu Phe Ser Thr His

```

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

				660					665					670		
Thr	Ser	Ile	Asp	Asn	Pro	Ile	Tyr	Thr	Arg	Ser	Gly	Ser	Asp	Phe	Met	
		675					680					685				
Val	Ser	Val	Ala	Ala	Thr	Leu	Pro	Tyr	Ser	Leu	Trp	Asp	Asn	His	Asp	
	690					695					700					
Tyr	Ala	Ser	Gln	Asn	Leu	Ser	Val	Ser	Asp	Arg	Tyr	Arg	Phe	Ile	Glu	
705					710					715					720	
Tyr	His	Lys	Trp	Lys	Phe	Arg	Gly	Arg	Val	Phe	Thr	Pro	Leu	Leu	Asn	
				725					730						735	
Pro	Ala	Thr	His	Lys	Tyr	Thr	Pro	Val	Leu	Met	Ser	Arg	Val	Glu	Gly	
			740					745					750			
Ala	Val	Leu	Gly	Ser	Tyr	Asn	Ser	Asn	Lys	Lys	Ser	Pro	Phe	Gly	Thr	
		755					760					765				
Phe	Tyr	Met	Gly	Gly	Asp	Gly	Met	Ser	Ser	Tyr	Tyr	Gly	Gly	Tyr	Met	
	770					775					780					
Asn	Glu	Thr	Ile	Gly	Leu	Arg	Gly	Tyr	Lys	Asn	Gly	Ser	Ile	Ala	Gly	
785					790						795				800	
Asn	Asn	Tyr	Asp	Tyr	Ala	Tyr	Ala	Tyr	Met	Arg	Leu	Thr	Met	Glu	Leu	
				805					810						815	
Arg	Phe	Pro	Ile	Leu	Phe	Glu	Asn	Ser	Phe	Asn	Ala	Trp	Leu	Leu	Ala	
			820					825					830			
Phe	Ala	Glu	Ala	Gly	Asn	Ala	Trp	Arg	Ser	Ile	Asp	Asn	Tyr	Asn	Pro	
		835					840					845				
Phe	Asn	Leu	Lys	Arg	Ser	Ala	Gly	Val	Gly	Leu	Arg	Val	Thr	Leu	Pro	
	850					855					860					
Met	Val	Gly	Met	Leu	Gly	Ile	Asp	Trp	Gly	Tyr	Gly	Phe	Asp	Arg	Pro	
865					870						875				880	
Asp	Asn	Ser	Leu	Gln	Arg	Gly	Gly	Ser	Asn	Val	His	Phe	Val	Leu	Gly	
				885					890						895	
Gln	Glu	Phe														
<210>		317														
<211>		177														
<212>		PRT														
<213>		Porphyromonas gingivalis														
<400>		317														
Gln	Ile	Asn	Met	Asn	Gly	Asp	Met	Lys	Arg	Phe	Leu	Ile	Leu	Ile	Gly	
1				5					10					15		
Phe	Ala	Leu	Ala	Val	Ala	Phe	Ser	Gly	Phe	Ser	Gln	Lys	Phe	Ala	Leu	
			20					25					30			
Val	Asp	Met	Glu	Tyr	Ile	Leu	Arg	Asn	Ile	Pro	Asp	Tyr	Glu	Met	Met	
		35					40					45				
Asn	Glu	Gln	Leu	Glu	Gln	Val	Ser	Lys	Lys	Trp	Gln	Asn	Glu	Ile	Glu	
	50					55					60					
Ala	Leu	Glu	Asn	Glu	Ala	G										

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130          135          140
Tyr Gln Met Val Leu Asp Arg Gly Thr Ser Gly Ile Ile Phe Ala Ser
145          150          155          160
Pro Ser Ile Asp Ile Ser Asp Leu Val Leu Ser Lys Met Gly Phe Ser
          165          170          175
Lys
<210>      318
<211>      170
<212>      PRT
<213>      Porphyromonas gingivalis
<400>      318
Arg Ile Asn Lys Gln His Glu Met Lys Lys Phe Phe Leu Met Leu Leu
  1          5          10          15
Met Ala Leu Pro Leu Ser Leu Leu Ala Gln Lys Val Ala Val Val Asn
          20          25          30
Thr Glu Glu Ile Ile Ser Lys Met Pro Glu Gln Val Ala Ala Thr Lys
          35          40          45
Gln Leu Asn Glu Leu Ala Glu Lys Tyr Arg Leu Asp Leu Lys Ser Met
          50          55          60
Asp Asp Glu Phe Ala Lys Lys Thr Glu Glu Phe Val Lys Glu Lys Asp
          65          70          75          80
Ser Leu Leu Glu Asn Ile Arg Asn Arg Arg Gln Gln Glu Leu Gln Asp
          85          90          95
Ile Gln Thr Arg Tyr Gln Gln Ser Tyr Gln Thr Met Gln Glu Asp Leu
          100          105          110
Gln Lys Arg Gln Gln Gln Leu Phe Ala Pro Ile Gln Gln Lys Val Ala
          115          120          125
Asp Ala Ile Lys Lys Val Gly Asp Glu Glu Asn Cys Ala Tyr Ile Met
          130          135          140
Glu Ala Gly Met Met Leu Tyr Thr Gly Ala Thr Ala Ile Asp Leu Thr
145          150          155          160
Ala Lys Val Lys Ala Lys Leu Gly Ile Lys
          165          170
<210>      319
<211>      828
<212>      PRT
<213>      Porphyromonas gingivalis
<400>      319
Ile Met Lys Glu Ala Ile Pro Arg Lys Asn Lys Tyr Ile Lys Leu Asn
  1          5          10          15
Gly Ile Tyr Arg Leu Ser Phe Ile Leu Leu Cys Cys Leu Leu Cys Ser
          20          25          30
Gln Ala Ala Met Ala Gln Gly Val Arg Val Ser Gly Tyr Val Leu Asp
          35          40          45
Arg Gly Glu Lys Pro Ile Pro Phe Ala Gly Val Lys Val Arg Gly Thr
          50          55          60
Gly Thr Gly Ala Thr Thr Asn Leu Lys Gly Tyr Tyr Glu Phe Arg Met
          65          70          75          80
Lys Ala Thr Thr Asp Ser Ile Thr Ile Glu Phe Ser Ser Met Gly Tyr
          85          90          95
Gln Gly Val Ser Arg Ser Phe Pro Ser Leu Thr Lys Asp Thr Arg Leu
          100          105          110

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

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Leu Ile Pro Gly Ile Arg Ala Ser Trp Trp Ser Phe Asn Lys Glu Leu
 530 535 540
 Leu Val Ser Pro Arg Ile Ser Val Gly Tyr Ser Pro Glu Ser Asn Pro
 545 550 555 560
 Ala Leu Val Leu Arg Ala Ala Ala Gly Leu Tyr Tyr Gln Ala Pro Phe
 565 570 575
 Tyr Lys Glu Leu Arg Gln Thr His Lys Asp Ala Glu Gly Asn Asn Val
 580 585 590
 Val Val Leu Asn Glu Lys Ile Arg Ser Gln Gly Ala Phe His Ile Leu
 595 600 605
 Ala Gly Ala Asp Tyr Thr Phe Glu Met Gly Gly Arg Lys Tyr Lys Phe
 610 615 620
 Thr Ala Glu Ala Tyr Tyr Lys Ser Leu Phe Asn Ile Asn Pro Tyr Ile
 625 630 635 640
 Ile Glu Asn Val Lys Ile Arg Tyr Leu Gly Glu Asn Ile Gly Ser Gly
 645 650 655
 Tyr Ala Ala Gly Ile Asp Leu Lys Leu Phe Gly Glu Leu Val Pro Gly
 660 665 670
 Val Asp Ser Trp Leu Thr Ala Ser Ile Ile Lys Ala Arg Gln Lys Leu
 675 680 685
 Asp Gly Tyr Gly Ser Leu Pro Leu Met Asn Ala Pro Thr Tyr Asn Phe
 690 695 700
 Ser Phe Phe Leu Gln Glu Tyr Val Pro Gly Asn Lys Arg Ile Thr Ala
 705 710 715 720
 Thr Leu Arg Ala Ala Leu Ser Gly Gly Leu Pro Gln Leu Asn Pro Ser
 725 730 735
 Lys Gly Leu Ser Ser Pro Ala Phe Thr Ala Pro Ala Tyr Lys Arg Val
 740 745 750
 Asp Leu Gly Val Met Tyr Lys Trp Leu Asp Pro Asp Asp Ser Phe Ala
 755 760 765
 Gly Arg Ser Lys Trp Leu Met Gly Val Lys Gly Ala Tyr Ile Gly Ala
 770 775 780
 Asp Leu Phe Asn Leu Phe Asp Met Thr Asn Val Asn Ser Tyr Tyr Trp
 785 790 795 800
 Val Ser Asp Ala Tyr Gln Gln Gln Tyr Ala Val Pro Asn Tyr Leu Thr
 805 810 815
 Arg Arg Gln Phe Asn Leu Arg Leu Leu Val Glu Phe
 820 825
 <210> 320
 <211> 679
 <212> PRT
 <213> Porphyromonas gingivalis
 <400> 320
 Pro Ile Pro Phe Leu Leu Asn Met Tyr Ser Gly His His Lys Ile His
 1 5 10 15
 Tyr Pro Phe Leu Ile Leu Leu Val Cys Leu Ala Phe Ala Ala Cys Lys
 20 25 30
 Ser Val Lys Leu Lys Asp Ala Glu Lys Ala His Asp Arg Gln Glu Tyr
 35 40 45
 Thr Lys Ala Ala Asp Met Tyr Asn Thr Leu Tyr Arg Arg Thr Arg Arg
 50 55 60
 Lys Gln Val Glu Met Lys Ala Tyr Thr Ala Phe Arg Ser Gly Glu Asn

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

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                485                490                495
Thr Arg Tyr Val Met Leu Ala Gly Ala Ser Gly Tyr Leu Asn Gln Tyr
      500                505                510
Val Glu Leu Lys Thr Asp Thr Ala Lys Gln Ser Glu Thr Tyr Tyr Val
      515                520                525
Asp Phe Phe Leu Ala Ser Arg Glu Lys Ala Glu Gly Leu Gln Asn Ile
      530                535                540
Phe Tyr Asp Phe Asp Lys Ala Thr Leu Arg Pro Glu Ser Met Lys Ser
545                550                555                560
Leu Asp Glu Leu Ile Arg Ile Leu Thr Asp Asn Pro Asp Ile Arg Ile
      565                570                575
Glu Leu Gly Ser His Ala Asp Arg Lys Gly Pro Asp Ala Tyr Asn Leu
      580                585                590
Gly Leu Ser Asp Arg Arg Ala Lys Ser Val Val Asp Tyr Leu Thr Ser
      595                600                605
Arg Gly Ile Ala Ala Asp Arg Leu Thr Trp Lys Gly Tyr Gly Lys Ser
      610                615                620
Val Pro Lys Thr Val Thr Ala Lys Ile Ala Glu Arg His Asp Phe Leu
625                630                635                640
Lys Glu Gly Asp Val Leu Thr Glu Glu Phe Val Ala Pro Leu Thr Glu
      645                650                655
Glu Gln Gln Ser Val Cys Asp Gln Leu Asn Arg Arg Thr Glu Phe Arg
      660                665                670
Val Ile Glu Glu Glu Leu Arg
      675
<210>      321
<211>      772
<212>      PRT
<213>      Porphyromonas gingivalis
<400>      321
Pro Ala Gln Pro Lys Thr Tyr Cys Ile Arg Tyr Phe Arg Arg Glu Val
  1                5                10                15
Ser Pro Arg Arg Gln Thr Glu Arg Thr Leu Tyr Ala Asp Lys Met Arg
      20                25                30
Arg His Ile Val Lys Cys Cys Pro Ser Ala Ser Ile Leu Leu Gln Glu
      35                40                45
Tyr Ser Thr Thr Glu Leu Phe Ile His His Phe Asn Ile Ser Ile Ile
      50                55                60
Met Lys Lys Phe Phe Phe Ala Leu Leu Ser Ile Gly Ile Ser Ala Gln
      65                70                75                80
Ala Phe Ala Lys Thr Asp Asn Val Pro Thr Asp Ser Leu Arg Val His
      85                90                95
Asn Leu Gln Thr Val Thr Val Tyr Ser Thr Arg Thr Ala Val Pro Leu
      100                105                110
Lys Lys Ile Pro Ala Lys Met Glu Leu Ile Ser Ser Arg Asn Ile Lys
      115                120                125
Gln Ser Gly Phe Asn Asn Met Thr Asp Ile Leu Lys Thr Gln Ser Ser
      130                135                140
Leu Asp Val Ile Gln Tyr Pro Gly Phe Ser Ser Asn Ile Gly Ile Arg
145                150                155                160
Gly Phe Lys Pro Ser Gly Lys Tyr Val Thr Val Leu Val Asn Gly Ile
      165                170                175

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

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Asn Ile Thr Thr Tyr Ile Asn Ala Asp Lys Ala Arg Met Ser Gly Ile
    595                      600                      605
Glu Ala Leu Leu Ser Tyr Asp Phe Gly Ser Leu Phe Ala Asn Lys Phe
    610                      615                      620
Ser Leu Arg Ala Phe Ala Asn Ala Thr Ile Met Leu Asn Ser Glu Met
    625                      630                      635                      640
Lys Lys Ser Gln Thr Asp Ala Pro Trp Ser Glu Met Tyr Tyr Val Arg
    645                      650                      655
Lys Gln Asn Ile Thr Phe Gly Ile Glu Tyr Arg Gly Lys Glu Gly Leu
    660                      665                      670
Glu Val Met Leu Asn Gly Arg Phe Met Gly Arg Arg Ile Glu Gln Asn
    675                      680                      685
Trp Tyr Ala Tyr Tyr Pro Glu Val Arg Pro Glu Leu Gln Gln Leu Leu
    690                      695                      700
Ala Ala Glu Glu Pro Glu Leu Ala Ala Gln Gly Leu Leu Arg His Pro
    705                      710                      715                      720
Gln Ala Met Val Phe Asn Ala Ser Ala Tyr Tyr His Met Asn Lys Tyr
    725                      730                      735
Leu Thr Phe Gly Val Asn Leu Asn Asn Ile Leu Asp Glu Leu Tyr Thr
    740                      745                      750
Glu Lys Asp Gly Tyr His Met Pro Gly Arg Asn Ile Met Gly Lys Val
    755                      760                      765
Met Val Asn Phe
    770
<210>    322
<211>    484
<212>    PRT
<213>    Porphyromonas gingivalis
<400>    322
Gly Arg Ala Ser Ser Pro Tyr Arg Gln Met Asp Gly Ile Leu Asn Asp
    1                      5                      10                      15
Glu Tyr Arg Gln Ala Ser Met Asn Arg Phe Ser Asn His Trp Pro Cys
    20                      25                      30
Ile Leu Val Gly Phe Val Leu Trp Phe Val Ser Ala Ser Arg Thr Val
    35                      40                      45
Ala Gln Asn Ala Ser Glu Thr Thr Val Ser Tyr Asp Thr Asp Thr Ala
    50                      55                      60
Val Leu Ser Glu Ala Asp Val Leu Arg Ile Ala Leu Ser Glu Asn Ala
    65                      70                      75                      80
Thr Val Lys Val Ala Asp Met Asp Val Arg Lys Gln Glu Tyr Ala Arg
    85                      90                      95
Arg Ala Ala Arg Ala Asp Leu Phe Pro Lys Val Asp Leu Asn Gly Val
    100                      105                      110
Tyr Ser His Thr Leu Lys Lys Gln Val Leu Tyr Ile Asp Met Pro Gly
    115                      120                      125
Phe Ser Ser Ser Glu Gly Ile Glu Met Gly Arg Thr His Asn Thr Gln
    130                      135                      140
Gly Gly Val Asn Val Ser Met Pro Leu Val Ser Ala Gln Leu Trp Lys
    145                      150                      155                      160
Ser Ile Ala Met Thr Gly Glu Gln Leu Asp Leu Ala Leu Glu Lys Ala
    165                      170                      175
Arg Ser Ser Arg Ile Asp Leu Val Ala Glu Val Lys Lys Ala Tyr Leu

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180          185          190
Ser Val Leu Leu Ala Glu Asp Ser Tyr Gly Val Phe Lys Arg Ser Tyr
195          200          205
Asp Asn Ala Leu Ala Asn Tyr Lys Asn Ile Ser Asp Lys Phe Asp Arg
210          215          220
Gly Leu Val Ala Glu Tyr Asp Lys Ile Arg Ala Asn Val Gln Val Arg
225          230          235          240
Asn Ile Glu Pro Asn Leu Leu Gln Ala Gln Asn Ser Val Ala Leu Ala
245          250          255
Leu Trp Gln Leu Lys Val Leu Met Ser Met Glu Val Glu Thr Pro Ile
260          265          270
Arg Leu Ser Gly Ser Leu Ser Asp Tyr Lys Glu Gln Val Tyr Thr Gly
275          280          285
Tyr Phe Ala Ala Asp Thr Leu Ile Ser Asn Asn Ser Ser Leu Arg Gln
290          295          300
Leu Asp Ile Gln Arg Arg Leu Ala Val Ser Ala Asp Lys Leu Asn Lys
305          310          315          320
Tyr Ser Phe Leu Pro Thr Leu Asn Leu Gly Gly Gln Tyr Thr Tyr Ser
325          330          335
Leu Asn Ser Asn Asp Ile Lys Phe Trp Gly Glu Gly Gln Arg Trp Thr
340          345          350
Pro Phe Ser Thr Ile Ser Leu Ser Leu Tyr Ile Pro Ile Phe Asn Gly
355          360          365
Gly Lys Arg Leu Tyr Asn Val Lys Gln Ser Ala Leu Ser Ile Arg Gln
370          375          380
Ile Asp Leu Gln Arg Arg His Ile Glu Gln Ser Ile Arg Met Gly Ile
385          390          395          400
Lys Asn Gln Asn Asp Arg Leu Arg Thr Cys Met Gln Arg Phe Val Ala
405          410          415
Ser Glu Glu Ala Val Arg Ser Ala Glu Lys Gly Tyr Gln Ile Ala Glu
420          425          430
Lys Arg Tyr Gln Thr Gly Glu Gly Thr Leu Val Glu Leu Asn Asp Ala
435          440          445
Asp Val Ala Leu Leu Gln Ala Arg Leu Asn Tyr Asn Gln Ala Ile Phe
450          455          460
Asp Phe Met Thr Ala Lys Ala Glu Leu Asp Lys Met Asn Gly Met Gly
465          470          475          480
Ile Pro Glu Gln
<210> 323
<211> 540
<212> PRT
<213> Porphyromonas gingivalis
<400> 323
Phe His Asn Phe Asp Phe Leu Asn Gly Ile Lys Leu Phe Ser Met Ala
1 5 10 15
Asn Asn Thr Leu Leu Ala Lys Thr Arg Arg Tyr Val Cys Leu Val Gly
20 25 30
Phe Cys Trp Leu Met Ala Met Met His Leu Ser Gly Gln Glu Val Thr
35 40 45
Met Trp Gly Asp Ser His Gly Val Ala Pro Asn Gln Val Arg Arg Thr
50 55 60
Leu Val Lys Val Ala Leu Ser Glu Ser Leu Pro Pro Gly Ala Lys Gln

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


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                485                490                495
Ser Gly Ser Ser Ala Tyr Ser Asp Met Thr Leu Leu Ala Asp Gly Thr
      500                505                510
Ile Gly Tyr Phe Val Glu Glu Gly Asp Glu Ile Ser Leu Val Phe Ile
      515                520                525
Arg Phe Val Leu Asp Asp Leu Phe Asp Val Arg Gln
      530                535                540
<210>      324
<211>      293
<212>      PRT
<213>      Porphyromonas gingivalis
<400>      324
Lys Ser Pro Ser Asp Ser Ala Leu Pro Ser Val Trp Ser Ala Asn Thr
  1                5                10                15
Ile Ser Gly Leu Val Gly Gly Lys Arg Ile Thr Leu Leu Ile Leu Tyr
      20                25                30
Ser Met Ala Ile Arg Ser Ser Asn Ile Glu Ser Ile Gln Cys Phe Val
      35                40                45
Met Lys Lys Glu Lys Leu Trp Ile Ala Ile Val Ala Gly Leu Ala Phe
      50                55                60
Val Leu Gly Leu Tyr Ala Leu Gly Arg Ser Val Ala Gln Leu Arg Arg
      65                70                75                80
Ser Gln Pro Ser Val Thr Val Thr Gly Met Ala Glu Arg Asn Phe Lys
      85                90                95
Ser Asp Leu Ile Val Trp Thr Ala Ser Tyr Gln Leu Gln Met Met Asp
      100                105                110
Leu Glu Ser Ala Tyr Lys Ala Leu Lys Glu Lys Gln Ile Leu Val Ala
      115                120                125
Asp Tyr Leu Lys Asn Lys Gln Leu Pro Asp Ser Ser Tyr Ile Phe Ser
      130                135                140
Ser Val Ala Ile Ser Lys Glu Tyr Asn Tyr Tyr Tyr Asp Pro Arg Gln
      145                150                155                160
Glu Gln Asn Val Arg Thr Phe Ala Gly Tyr Leu Leu Ser Gln Thr Val
      165                170                175
Thr Val Thr Ser Gln Asp Ile Glu His Val Glu Lys Ile Ser Arg Asp
      180                185                190
Ile Thr Glu Leu Ile Asn Gln Gly Val Glu Ile Thr Ser Asp Arg Pro
      195                200                205
Ala Tyr Tyr Tyr Thr Lys Leu Asn Asp Leu Lys Val Glu Met Leu Arg
      210                215                220
Asn Ala Ser Glu Asp Ala Phe Asn Arg Ala Ser Val Ile Ala Glu Gly
      225                230                235                240
Ser Gly Ser Ser Val Gly Lys Met Leu Ser Ser Ser Met Gly Val Phe
      245                250                255
Gln Ile Val Gly Leu Asn Ser Asn Glu Asp Tyr Ser Trp Gly Gly Ser
      260                265                270
Phe Asn Thr Ser Ser Lys Met Lys Thr Ala Ser Ile Thr Val Lys Ala
      275                280                285
Ser Phe Ala Leu Lys
      290
<210>      325
<211>      280

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<212>      PRT
<213>      Porphyromonas gingivalis
<400>      325
Gly Lys Leu Gln Met Lys Lys Thr Ile Ala Ile Ile Ala Ser Ala Leu
 1             5             10             15
Leu Ala Leu Gly Ala Val Gly Cys Lys Lys Asn Ala Asp Thr Thr Ala
 20             25             30
Val Ser Glu Lys Asp Ser Ile Ala Leu Ser Met Gly Ile Leu Tyr Gly
 35             40             45
Gln Asp Phe Ala Asn Gln Phe Glu Met Ser Arg Leu Gln Gly Gln Pro
 50             55             60
Ile Asp Ser Val Ala Phe Leu Asp Gly Phe Lys Tyr Gly Ile Asp Thr
 65             70             75             80
Thr Arg Phe Ser Tyr Asn Leu Gly Ala Ile Tyr Ala Ser Asn Ile Ala
 85             90             95
Arg Gln Leu Ala His Asp Ser Ile Asp Ile Asp Lys Phe Tyr Ala Ala
100            105            110
Met Arg Ala Ala Leu Leu Lys Asp Thr Val Ser Ile Ala Met Lys Pro
115            120            125
Ala Asp Ala Gln Ala Phe Met Gln Arg Ile Gln Ala Lys Lys Gln Arg
130            135            140
Glu Asn Asn Met Lys Gln Phe Gly Gln Asn Ile Glu Lys Gly Asn Glu
145            150            155            160
Tyr Ile Asp Thr Phe Lys Lys Glu Asp Gly Val Thr Val Thr Thr Thr
165            170            175
Gly Leu Ala Tyr Lys Thr Leu Gln Glu Gly Thr Gly Ala Thr Pro Ser
180            185            190
Leu Ala Asp Thr Val Arg Val Lys Tyr Val Gly Thr Leu Val Asp Gly
195            200            205
Lys Glu Phe Asp Lys Asn Glu Glu Gly Ile Glu Phe Ala Val Thr Gly
210            215            220
Val Ile Lys Gly Trp Thr Glu Met Leu Gln Leu Met Lys Val Gly Gln
225            230            235            240
Lys Val Arg Val Val Ile Pro Gln Glu Leu Ala Tyr Gly Glu Thr Gly
245            250            255
Asn Tyr Thr Ile Glu Pro Phe Ser Thr Leu Thr Phe Glu Met Glu Leu
260            265            270
Ile Gly Ile Lys Pro Gly Lys Lys
275            280

<210>      326
<211>      803
<212>      PRT
<213>      Porphyromonas gingivalis
<400>      326
Cys Arg Lys Gln Lys Leu Ser Asn Pro Lys Arg Ser Arg Tyr Pro Cys
 1             5             10             15
Arg Arg Ile Ser Phe Arg Gln Ser Asp Lys Asn Pro Met Lys Val Leu
 20             25             30
Arg Gln Val Phe Leu Pro Ile Leu Phe Val Leu Leu Thr Gly Ala Cys
 35             40             45
Ser Thr Thr Lys Asn Leu Pro Glu Gly Glu Gln Leu Tyr Ile Gly Met
 50             55             60

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

Phe Gln Ala Ser Ala Thr Ala Leu Asn Arg Ala His Tyr Phe Ser Met
 485 490 495
 Tyr Ser Phe Gly Phe Ser Thr Thr Tyr Glu Phe Gln Pro Ser Lys Glu
 500 505 510
 His Arg His Ala Ile Phe Pro Leu Lys Leu Asn Tyr Asn Leu Leu Gly
 515 520 525
 His Gln Thr Glu Thr Phe Gln Ala Ile Thr Ala Asn Asn Pro Pro Leu
 530 535 540
 Leu Leu Ser Leu Gln Ser Gln Phe Leu Ala Gln Met Gly Tyr Ile Tyr
 545 550 555 560
 Thr Phe Asn Lys Ser Val Ser Glu Lys Ser Pro His His Leu Trp Met
 565 570 575
 Gln Phe Gly Leu Ser Glu Ala Gly Asn Leu Leu Asn Leu Ile Tyr Leu
 580 585 590
 Ala Ala Gly Lys Lys Tyr Ser Asp Thr Lys Asn Phe Val Gly Val Pro
 595 600 605
 Phe Ser Gln Phe Ile Lys Ala Thr Gly Glu Leu Arg Tyr Ser Tyr Thr
 610 615 620
 Ile Asp Arg Asn Gln Ser Leu Ala Thr Arg Phe Gly Thr Gly Val Ile
 625 630 635 640
 Tyr Ser Tyr Gly Asn Met Arg Val Ala Pro Tyr Ser Glu Gln Phe Tyr
 645 650 655
 Val Gly Gly Ala Asn Ser Ile Arg Ala Phe Thr Val Arg Ser Ile Gly
 660 665 670
 Pro Gly Arg Phe Asn Pro Asp Ser Asp Asn Gln Tyr Ser Tyr Leu Asp
 675 680 685
 Gln Val Gly Glu Phe Lys Leu Glu Ala Asn Val Glu Tyr Arg Gly Lys
 690 695 700
 Leu Phe Gly Asp Leu His Ala Ala Val Phe Leu Asp Ala Gly Asn Val
 705 710 715 720
 Trp Leu Leu Arg Glu Asp Ser Ser Arg Pro Gly Gly Ala Leu Ser Glu
 725 730 735
 Val Gly Ser Val Ser Asn Phe Leu Asn Ser Ile Ala Leu Gly Thr Gly
 740 745 750
 Val Gly Leu Arg Tyr Asp Leu Ala Phe Leu Val Val Arg Val Asp Val
 755 760 765
 Gly Phe Gly Leu His Leu Pro Tyr Asn Thr Gly Lys Lys Gly Tyr Tyr
 770 775 780
 Asn Ile Pro Arg Phe Lys Asp Ala Ile Gly Phe His Leu Ala Val Gly
 785 790 795 800
 Tyr Pro Phe
 <210> 327
 <211> 783
 <212> PRT
 <213> Porphyromonas gingivalis
 <400> 327
 Ser Leu Ser Pro Tyr Ile Arg Phe Pro Met Ser Ser His Ser Val Arg
 1 5 10 15
 Tyr Leu Ile Gly Ile Ala Gly Cys Leu Leu Leu Met Leu Ala Ser Ser
 20 25 30
 Cys Ser Val Thr Arg Tyr Val Pro Asp Gly Ser Arg Leu Leu Asp Arg
 35 40 45

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

Gly Tyr Asn Tyr Gln Thr Arg Pro Glu Phe Asp Arg Val Ile Leu Ser
 465 470 475 480
 Ala Gln Leu Asn Tyr Ser Trp Gln Thr Tyr Leu His Asn Arg Leu Arg
 485 490 495
 His Thr Ile Arg Leu Leu Asp Val Asp Tyr Leu His Leu Pro Tyr Ile
 500 505 510
 Asp Pro Asp Phe Ala Gln Ser Leu Pro Pro Thr Thr Ala Leu Tyr Asn
 515 520 525
 Tyr Thr Glu Gln Phe Ile Leu Gly Ser Ala Tyr Ile Leu Asn Tyr Thr
 530 535 540
 Thr Ala Ser Ser Met Glu Arg Thr Val Ser Asn Pro Phe Thr Ala Arg
 545 550 555 560
 Phe Ser Ile Gln Thr Ala Gly Asn Leu Leu Gln Ala Ile Ser Tyr Leu
 565 570 575
 Thr Asp Ser Pro Lys Asp Glu His Gly Leu Tyr Lys Met Phe Gly Leu
 580 585 590
 His Tyr Ala Gln Phe Val Lys Leu Asp Leu Asp Leu Ala Lys Thr Val
 595 600 605
 Leu Leu Glu Lys Asp Asn Thr Leu Ala Leu His Leu Gly Phe Gly Leu
 610 615 620
 Ala Phe Pro Tyr Gly Asn Ala Arg His Ile Pro Phe Glu Leu Arg Tyr
 625 630 635 640
 Phe Ala Gly Gly Ser Asn Ser Val Arg Gly Trp Ser Val Arg Thr Leu
 645 650 655
 Gly Pro Gly Ser Met Lys Met Thr Pro Asp Lys Thr Phe Phe Asp Gln
 660 665 670
 Met Gly Asp Ile Arg Leu Asp Leu Asn Val Glu Tyr Arg Thr Lys Leu
 675 680 685
 Phe Trp Lys Phe Arg Ala Ala Ala Phe Val Asp Ala Gly Asn Val Trp
 690 695 700
 Thr Ile Lys Glu Tyr Glu Asn Gln Glu Asp Gly Leu Phe Arg Phe Asp
 705 710 715 720
 Arg Phe Tyr Lys Glu Ile Ala Leu Ala Tyr Gly Leu Gly Leu Arg Leu
 725 730 735
 Asp Phe Asp Tyr Phe Leu Val Arg Leu Asp Ala Gly Leu Lys Ala Tyr
 740 745 750
 Asp Pro Gln Gln Thr Gly Arg Tyr Lys Trp Ala Ile Thr Arg Pro Asn
 755 760 765
 Leu Ser Ser Asn Phe Ala Trp His Ile Ala Val Gly Tyr Pro Phe
 770 775 780
 <210> 328
 <211> 875
 <212> PRT
 <213> Porphyromonas gingivalis
 <400> 328
 Val Glu Ser Lys Leu Leu Cys Leu Met Arg Lys Arg Ile Leu Gln Leu
 1 5 10 15
 Phe Leu Thr Ala Leu Leu Leu Ala Leu Gly Ser Ser Leu Ala Ile Ala
 20 25 30
 Gln Thr Val Val Thr Gly Lys Val Ile Asp Ser Glu Thr Ser Glu Pro
 35 40 45
 Leu Ile Gly Val Ser Val Ser Thr Gly Gln Gly Ala Ser Leu Arg Gly

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

465	470								475							480	
Ala	Gly	Tyr	Asp	Gly	Arg	Tyr	Tyr	Arg	Gly	Asp	His	Tyr	Asp	Lys	Ile		
				485					490					495			
Thr	Asp	Leu	Leu	Gly	Gly	Ser	Tyr	Tyr	Ile	Glu	Asp	Pro	Lys	Thr	Lys		
				500					505					510			
Leu	Ala	Tyr	His	Ala	Glu	Gly	Gln	Gln	Leu	Lys	Val	Gly	Asp	Ile	Val		
				515					520					525			
Asn	Arg	Asp	Tyr	Thr	Gly	Glu	Ile	Met	Trp	His	Gly	Leu	Phe	Ala	Gln		
				530					535					540			
Met	Glu	His	Ser	Ser	Glu	Trp	Ile	Asp	Ala	Phe	Val	Ser	Gly	Ser	Ile		
545					550					555					560		
Asn	Tyr	Glu	Leu	Tyr	Arg	Asn	His	Asn	Tyr	Gly	Gly	Ser	Lys	Ser	Thr		
				565					570					575			
Gly	Tyr	Leu	Pro	Gly	Val	Ser	Pro	Trp	Lys	Ser	Phe	Leu	Pro	Trp	Ser		
				580					585					590			
Gly	Lys	Ala	Gly	Leu	Ser	Tyr	Lys	Phe	Ala	Gln	Gly	His	Asn	Val	Phe		
				595					600					605			
Ala	Asn	Gly	Gly	Phe	Phe	Thr	Arg	Ala	Pro	Leu	Phe	Gly	Asn	Ile	Tyr		
				610					615					620			
Ala	Ala	Gly	Ala	Ile	Ile	Pro	Asn	Asp	Lys	Ala	Asn	Met	Glu	Lys	Val		
625					630					635					640		
Leu	Thr	Gly	Glu	Val	Gly	Tyr	Gly	Phe	Thr	Asn	His	Lys	Asn	Phe	Glu		
				645					650					655			
Phe	Asn	Ile	Asn	Gly	Tyr	Tyr	Thr	Lys	Trp	Met	Asp	Arg	Val	Thr	Ser		
				660					665					670			
Lys	Arg	Ile	Gly	Asn	Glu	Tyr	Val	Tyr	Leu	Asn	Gly	Val	Asp	Ala	Val		
				675					680					685			
His	Cys	Gly	Val	Glu	Ala	Glu	Val	Ser	Tyr	Arg	Pro	Ile	Arg	Gln	Ile		
				690					695					700			
Asp	Leu	Arg	Gly	Met	Phe	Ser	Leu	Gly	Asp	Trp	Thr	Trp	Gln	Asn	Asn		
705					710					715					720		
Val	Ser	Tyr	Thr	Ser	Tyr	Asp	Glu	Ala	Gly	Asn	Glu	Thr	Gly	Gln	Asp		
				725					730					735			
Ile	Thr	Tyr	Ile	Lys	Gly	Leu	His	Val	Gly	Asp	Ala	Ala	Gln	Met	Thr		
				740					745					750			
Ala	Ala	Val	Ser	Ala	Asp	Ile	Glu	Leu	Phe	Lys	Gly	Phe	His	Val	Ile		
				755					760					765			
Gly	Lys	Tyr	Asn	Phe	Leu	Gly	Lys	Asn	Tyr	Ala	Gly	Phe	Asn	Pro	Ala		
				770					775					780			
Thr	Arg	Asn	Ala	Gln	Gln	Tyr	Glu	Ala	Asp	Gly	Lys	Glu	Ile	Val	Glu		
785					790					795					800		
Ser	Trp	Lys	Leu	Pro	Asp	Val	Gly	Leu	Phe	Asp	Leu	Ser	Ala	Ser	Tyr		
				805					810					815			
Asn	Phe	Lys	Leu	Gly	Ser	Leu	Ser	Thr	Thr	Phe	Tyr	Phe	Asn	Met	Asp		
				820					825					830			
Asn	Val	Ala	Asp	Lys	Arg	Tyr	Val	Ser	Asp	Ala	Asp	Asp	Asn	Ile	Ile		
				835					840					845			
Gly	Lys	Lys	His	Asp	Glu	Ala	Ser	Ala	Leu	Val	Trp	Tyr	Gly	Phe	Gly		
				850					855					860			
Arg	Thr	Trp	Ser	Thr	Gly	Ile	Arg	Val	Asn	Phe							
865					870					875							
<210>		329															


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<211>      460
<212>      PRT
<213>      Porphyromonas gingivalis
<400>      329
Asn Arg Cys Asn Pro Ser Arg Gln Tyr Phe His Leu Ser Gln Asn Asp
 1              5              10              15
Val Gly Arg Ser Leu Arg Ala Phe Leu Ile His Leu Ser Met Lys Phe
      20              25              30
Ser Ile Arg Leu Phe Leu Cys Ile Ile Phe Leu Leu Ser Ala Phe Ile
      35              40              45
Leu Pro Ala Leu Gly Gln Lys Ser Lys Gln Val Gln Arg Leu Glu Lys
      50              55              60
Gln Arg Lys Glu Ala Leu Lys Ala Ile Glu Lys Thr Asp Arg Glu Leu
      65              70              75              80
Arg Asn Thr Lys Lys Asp Lys Gln Asp Lys Gln Lys His Leu Asn Leu
      85              90              95
Leu Asn Lys Gln Val Ala Gln Arg Lys Gln Met Val Gln Leu Leu Asp
      100              105              110
Asn Glu Val Lys Glu Leu Gln Ser Asp Ile Asp Ser Met Thr Gly Val
      115              120              125
Cys His Gln Leu Ser Val Glu Glu Lys Ala Arg Ser Asp Glu Tyr Ala
      130              135              140
Gln Ala Leu Gln Ser Met Gln Lys Arg Lys Arg Ser Leu Asp Arg Ile
      145              150              155              160
Leu Phe Ile Ser Ser Ala Lys Ser Phe Asp Glu Gly Met Arg Arg Met
      165              170              175
Arg Phe Leu Glu Gln Tyr Ala Ser Ala Tyr Lys Leu Ala Ser Val Arg
      180              185              190
Leu Arg Asp Thr Arg Ser Lys Leu Glu Thr Glu Arg Ala Thr Val Glu
      195              200              205
Asp Ala Lys Lys Glu Lys Gly His Leu Leu Val Ile Arg Glu Glu Glu
      210              215              220
Lys Lys Lys Leu Glu Gly Gln Gln Ala Glu Gln Arg Arg Gln Val Gln
      225              230              235              240
Ala Leu Gly Ala Lys Gln Lys Asp Leu Glu Ala Gln Leu Arg Lys Gln
      245              250              255
Lys Lys Gln Ala Glu Ala Leu Asn Arg Lys Ile Glu Lys Gln Ile Ala
      260              265              270
Lys Glu Ile Glu Ala Ala Glu Arg Arg Ala Arg Glu Glu Arg Glu Arg
      275              280              285
Leu Ala Arg Glu Ala Lys Ala Lys Gly Lys Pro Val Pro Ala Glu Pro
      290              295              300
Glu Arg Lys Ala Glu Thr Lys Gly Gly Tyr Ala Met Asp Ala Ser Glu
      305              310              315              320
Arg Ala Leu Ser Gly Ser Phe Ala Gln Asn Lys Gly Arg Leu Pro Gly
      325              330              335
Pro Val Arg Gly Arg Tyr Arg Ile Val Ser Asp Phe Gly Val His Gln
      340              345              350
His Ser Glu Leu Lys Lys Val Gln Val Asn Asn Gly Gly Ile Asp Ile
      355              360              365
Ala Val Ala Thr Gly Ser Asp Ala Thr Ser Val Phe Asp Gly Val Val
      370              375              380

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Ser Ser Val Phe Val Ile Pro Gly Tyr Asn Ser Ala Val Met Val Arg
 385 390 395 400
 His Gly Asn Tyr Ile Thr Val Tyr Ala Asn Leu Ser Lys Val Tyr Val
 405 410 415
 Asn Ser Gly Thr Arg Val Lys Thr Gly Gln Ala Leu Gly Arg Ala Tyr
 420 425 430
 Thr Asp Pro Ser Asn Asn Gln Thr Ile Ile His Phe Glu Ile Trp Lys
 435 440 445
 Glu Arg Ser Lys Gln Asn Pro Arg Leu Trp Leu Arg
 450 455 460
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 <211> 342
 <212> PRT
 <213> Porphyromonas gingivalis
 <400> 330
 Ser Phe Tyr Gln Glu Ile Asp Arg Leu Met Lys Lys Tyr Leu Leu Tyr
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 Ala Ser Leu Leu Thr Ser Val Leu Leu Phe Ser Cys Ser Lys Asn Asn
 20 25 30
 Pro Asn Glu Pro Val Glu Asp Arg Ser Ile Glu Ile Ser Ile Arg Val
 35 40 45
 Asp Asp Phe Thr Lys Thr Gly Glu Ala Val Arg Tyr Glu Arg Asn Gln
 50 55 60
 Gly Ser Ala Ala Glu Arg Leu Ile Thr Asn Leu Tyr Leu Leu Leu Phe
 65 70 75 80
 Asp Gln Ser Gly Ala Asn Pro Ala Lys Tyr Tyr Ile Thr Gly Asn Thr
 85 90 95
 Phe Thr Gly Gly Thr Trp Leu Pro Asp Asp Met Lys Val Lys Leu Asp
 100 105 110
 Met Thr Gln Ser Glu Ala Gly Glu Arg Lys Val Tyr Val Val Ala Asn
 115 120 125
 Val Asp Asn Ala Val Lys Thr Ala Leu Asp Ala Val Ala Asn Glu Ser
 130 135 140
 Asp Leu Gln Thr Val Lys Arg Thr Thr Ala Met Pro Trp Ser Thr Asp
 145 150 155 160
 Ile Ala Ser Pro Phe Leu Met Ser Gly Asn Lys Thr His Asp Phe Leu
 165 170 175
 Ala Asn Arg Leu Leu Asp Asn Val Pro Leu Val Arg Ala Ile Ala Lys
 180 185 190
 Val Glu Leu Asn Ile Ser Leu Ser Glu Lys Phe Gln Ile Val Pro Ile
 195 200 205
 Ile Val Asn Gly Ser Leu Ser Glu Phe Lys Phe Arg Tyr Val Asn Phe
 210 215 220
 Asp Lys Glu Thr Tyr Val Val Lys Pro Thr Thr Lys Pro Asp Asn Leu
 225 230 235 240
 Ile Ser Ser Ala Asn Gly Val Trp Pro Gln Ile Thr Asp Trp Thr Val
 245 250 255
 Trp Gly Ala Ser Leu Asn Thr Ser Pro Ala Pro Asp Ala Gly Thr Gly
 260 265 270
 Tyr Thr Leu Asp Ala Asn Gly Lys Val Thr Ala Leu Arg Ile Val Thr
 275 280 285
 Tyr Leu Asn Glu Arg Asp Ser Lys Gly Ala Thr Val Glu Val Ala Leu

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

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Ile Ala Arg Ala Leu Ala His Glu Arg
325

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<213> Porphyromonas gingivalis
<400> 332

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

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

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770              775              780
Glu Leu Asp Ile Met Gln Asn Asn Pro Glu Ile Thr Asp Glu Thr Gly
785              790              795              800
Lys Ala Pro Arg Ile Asp Glu Leu Lys Lys Thr Pro Ala Phe Phe Asp
              805              810              815
Leu Gly Leu Lys Val Gly Tyr Asp Phe His Val Phe Gln Ala Thr Glu
              820              825              830
Val Gln Leu Tyr Val Gly Met Asn Asn Ile Phe Asn Ser Phe Gln Lys
              835              840              845
Asp Phe Asp Arg Gly Ala Ala Arg Asp Ser Gly Tyr Ile Tyr Gly Pro
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Thr Gln Pro Arg Thr Gly Tyr Met Gly Leu Val Val Lys Phe
865              870              875
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<213>      Porphyromonas gingivalis
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Thr Leu Ile Gly Ile Leu Phe Ser Ser Pro Ser Leu Val Arg Ala Gln
              20              25              30
Ser Leu Phe Ser Thr Glu His Val Leu Gln Leu Tyr Asn Lys Ile Leu
              35              40              45
Tyr Gly Glu Ser Ala Ala Asp Thr Val Ala Glu Lys Thr Ala Gly Glu
              50              55              60
Ser Ala Phe Pro Phe Ile Asp Lys Leu Ile Asn Leu Gly Arg Thr Phe
              65              70              75              80
Leu Gly Lys Pro Tyr Arg Tyr Arg Gly Pro Ser Pro Trp Pro Met Asp
              85              90              95
Cys Ser Gly Tyr Val Ser Tyr Leu Tyr Ser Lys Phe Asp Ile Lys Leu
              100              105              110
Pro Arg Gly Ala Ala Ala Gln Ser Gln Tyr Thr Asn Pro Ile Glu Arg
              115              120              125
Glu Asp Val Arg Pro Gly Asp Leu Leu Phe Phe Lys Gly Arg Asn Ala
              130              135              140
Arg Ser Asn Arg Ile Gly His Val Ala Leu Val Val Ser Val Asp Glu
              145              150              155              160
Asp Asp Ile Thr Met Met His Ser Arg Asn Ser Arg Gly Ile Val Ile
              165              170              175
Glu Lys Leu Asn Arg Ser Ala Tyr Phe Ser Arg Arg Leu Val Ser Tyr
              180              185              190
Gly Arg Val Pro Gly Ala Lys Arg Val Ile Pro Arg Lys Ser
              195              200              205
<210>      334
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<212>      PRT
<213>      Porphyromonas gingivalis
<400>      334
Lys Gly Thr Trp Asn Arg Lys Asn Arg Arg Glu Glu Met Lys Arg Thr
  1              5              10              15
Ile Leu Leu Thr Ala Leu Thr Val Leu Ser Ser Leu Ser Leu Leu Arg

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

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 450 455 460
 Lys Asp Phe
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 <213> Porphyromonas gingivalis
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 Asn Met Thr Leu Glu Glu Cys Ile Asp Tyr Ala Arg Arg His Ser Ser
 35 40 45
 Ala Val Ala Leu Ser Ala Ala Glu Leu Glu Gln Ser Lys Ala Asp Tyr
 50 55 60
 Leu Gln Ala Val Gly Asn Phe Leu Pro Arg Val Ser Ala Gly Thr Gly
 65 70 75 80
 Ala Ser Trp Asn Phe Gly Arg Gly Leu Asp Ala Glu Thr Asn Thr Tyr
 85 90 95
 Thr Asp Ile Asn Ser Phe Asn Asn Ser Tyr Ser Ile His Ala Thr Met
 100 105 110
 Thr Leu Phe Asp Gly Leu Gln Ser Val Tyr Arg Leu Arg Met Ala His
 115 120 125
 Ala Arg Arg Glu Ala Ser Arg Leu Ser Val Arg Glu Gln Gln Glu Leu
 130 135 140
 Ala Ala Leu Gly Thr Thr Glu Ala Tyr Tyr Asp Leu Val Tyr Ala Arg
 145 150 155 160
 Gln Met Gln Glu Leu Ala Met Gln Lys Tyr Glu Glu Ser Ser Arg Leu
 165 170 175
 His Arg Gln Thr Ala Arg Met Glu Glu Leu Gly Met Lys Ser Arg Pro
 180 185 190
 Asp Val Leu Glu Met Gln Ser Arg Met Ala Gly Asp Arg Leu Ala Leu
 195 200 205
 Thr Gln Ala Asp Asn Gln Cys Ile Ile Ala Leu Ile Arg Leu Lys Glu
 210 215 220
 Lys Met Asn Phe Pro Ile Asp Asp Glu Leu Val Val Asp Asp Met Pro
 225 230 235 240
 Ala Asp Ser Leu Ser Ala Asp Met Ala Glu Ser Asp Ser Ser Ala Gly
 245 250 255
 Val Phe Ala Arg Ala Ala His His His Pro Val Leu Leu Arg Ala Lys
 260 265 270
 Leu Asp Glu Gln Ala Ala Thr Asp Arg Leu Arg Ala Ala Arg Gly Ala
 275 280 285
 Phe Leu Pro Ser Val Ser Val Ser Gly Gly Trp Asn Thr Gly Phe Ser
 290 295 300
 Arg Phe Leu Asn Gly Ser Asp Tyr Thr Pro Phe Ser Glu Gln Phe Arg
 305 310 315 320
 Asn Arg Arg Gly Glu Tyr Val Ser Leu Asn Leu Ser Ile Pro Ile Phe
 325 330 335

Ser Gly Phe Ser Leu Val Ser His Leu Arg Gln Ala Arg Ala Glu Arg
340 345 350
Arg Ala Ala Ile Val Arg Arg Gly Glu Ala Glu Arg Arg Leu Tyr Ser
355 360 365
Glu Ile Ala Gln Ala Met Ala Asp Arg Asp Ala Ala Leu Ala Ser Tyr
370 375 380
Arg Gln Ala Lys Glu His Thr Asp Ala Met Gln Thr Ala Tyr Glu Ala
385 390 395 400
Val Leu Gln Arg Tyr Glu Glu Gly Leu Asn Thr Ala Ile Asp Leu Thr
405 410 415
Thr Gln Ala Asn Arg Leu Leu Asp Ala Arg Val Gln Arg Leu Arg Ala
420 425 430
Ala Met Thr Tyr Arg Leu Lys Cys Lys Leu Ile Ala Tyr Tyr Gly Cys
435 440 445
Leu Ser Asp
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<213> Porphyromonas gingivalis
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Tyr Asn Ser Asp Lys Ser Met Asn Lys Phe Tyr Lys Ser Leu Leu Gln
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Ser Gly Leu Ala Ala Phe Val Ser Met Ala Thr Ala Leu Thr Ala Ser
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Ala Gln Ile Ser Phe Gly Gly Glu Pro Leu Ser Phe Ser Ser Arg Ser
50 55 60
Ala Gly Thr His Ser Phe Asp Asp Ala Met Thr Ile Arg Leu Thr Pro
65 70 75 80
Asp Phe Asn Pro Glu Asp Leu Ile Ala Gln Ser Arg Trp Gln Ser Gln
85 90 95
Arg Asp Gly Arg Pro Val Arg Ile Gly Gln Val Ile Pro Val Asp Val
100 105 110
Asp Phe Ala Ser Lys Ala Ser His Ile Ser Ser Ile Gly Asp Val Asp
115 120 125
Val Tyr Arg Leu Gln Phe Lys Leu Glu Gly Ala Lys Ala Ile Thr Leu
130 135 140
Tyr Tyr Asp Ala Phe Asn Ile Pro Glu Gly Gly Arg Leu Tyr Ile Tyr
145 150 155 160
Thr Pro Asp His Glu Ile Val Leu Gly Ala Tyr Thr Asn Ala Thr His
165 170 175
Arg Arg Asn Gly Ala Phe Ala Thr Glu Pro Val Pro Gly Ser Glu Leu
180 185 190
Ile Met Asp Tyr Glu Val Ser Arg Gly Gly Thr Leu Pro Asp Ile Lys
195 200 205
Ile Ser Gly Ala Gly Tyr Ile Phe Asp Lys Val Gly Gly Arg Pro Val
210 215 220
Thr Asp Asn His Tyr Gly Ile Gly Glu Asp Asp Ser Asp Ser Asp Cys
225 230 235 240
Glu Ile Asn Ile Asn Cys Pro Glu Gly Ala Asp Trp Gln Ala Glu Lys

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Cys	Ser	Gly	Asn	Leu	Leu	Asn	Asn	Thr	Lys	Gly	Asp	Phe	Thr	Pro	Leu												
275																280								285			
Ile	Ile	Ser	Ala	Gly	His	Cys	Ala	Ser	Ile	Thr	Thr	Asn	Phe	Gly	Val												
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Thr	Gln	Ser	Glu	Leu	Asp	Lys	Trp	Ile	Phe	Thr	Phe	His	Tyr	Glu	Lys												
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Arg	Gly	Cys	Ser	Asn	Gly	Thr	Leu	Ala	Ile	Phe	Arg	Gly	Asn	Ser	Ile												
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Ile	Gly	Ala	Ser	Met	Lys	Ala	Phe	Leu	Pro	Ile	Lys	Gly	Lys	Ser	Asp												
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Gly	Leu	Leu	Leu	Gln	Leu	Asn	Asp	Glu	Val	Pro	Leu	Arg	Tyr	Arg	Val												
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Tyr	Tyr	Asn	Gly	Trp	Asp	Ser	Thr	Pro	Asp	Ile	Pro	Ser	Ser	Gly	Ala												
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Gly	Ile	His	His	Pro	Ala	Gly	Asp	Ala	Met	Lys	Ile	Ser	Ile	Leu	Lys												
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Lys	Thr	Pro	Ala	Leu	Asn	Thr	Trp	Ile	Ser	Ser	Ser	Gly	Ser	Gly	Gly												
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Thr	Asp	Asp	His	Phe	Tyr	Phe	Lys	Tyr	Asp	Gln	Gly	Gly	Thr	Glu	Gly												
420																425								430			
Gly	Ser	Ser	Gly	Ser	Ser	Leu	Phe	Asn	Gln	Asn	Lys	His	Val	Val	Gly												
435																440								445			
Thr	Leu	Thr	Gly	Gly	Ala	Gly	Asn	Cys	Gly	Gly	Thr	Glu	Phe	Tyr	Gly												
450																455								460			
Arg	Leu	Asn	Ser	His	Trp	Asn	Glu	Tyr	Ala	Ser	Asp	Gly	Asn	Thr	Ser												
465																470								475			
Arg	Met	Asp	Ile	Tyr	Leu	Asp	Pro	Gln	Asn	Asn	Gly	Gln	Thr	Thr	Ile												
485																490								495			
Leu	Asn	Gly	Thr	Tyr	Arg	Asp	Gly	Tyr	Lys	Pro	Leu	Pro	Ser	Val	Pro												
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Arg	Leu	Leu	Leu	Gln	Ser	Thr	Gly	Asp	Gln	Val	Glu	Leu	Asn	Trp	Thr												
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Ala	Val	Pro	Ala	Asp	Gln	Tyr	Pro	Ser	Ser	Tyr	Gln	Val	Glu	Tyr	His												
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Ile	Phe	Arg	Asn	Gly	Lys	Glu	Ile	Ala	Thr	Thr	Lys	Glu	Leu	Ser	Tyr												
545																550								555			
Ser	Asp	Ala	Ile	Asp	Glu	Ser	Ile	Ile	Gly	Ser	Gly	Ile	Ile	Arg	Tyr												
565																570								575			
Glu	Val	Ser	Ala	Arg	Phe	Ile	Tyr	Pro	Ser	Pro	Leu	Asp	Gly	Val	Glu												
580																585								590			
Ser	Tyr	Lys	Asp	Thr	Asp	Lys	Thr	Ser	Ala	Asp	Leu	Ala	Ile	Gly	Asp												
595																600								605			
Ile	Gln	Thr	Lys	Leu	Lys	Pro	Asp	Val	Thr	Pro	Leu	Pro	Gly	Gly	Gly												
610																615								620			
Val	Ser	Leu	Ser	Trp	Lys	Val	Pro	Phe	Leu	Ser	Gln	Leu	Val	Ser	Arg												
625																630								635			
Phe	Gly	Glu	Ser	Pro	Asn	Pro	Val	Phe	Lys	Thr	Phe	Glu	Val	Pro	Tyr												
645																650								655			
Val	Ser	Ala	Ala	Ala	Ala	Gln	Thr	Pro	Asn	Pro	Pro	Val	Gly	Val	Val												

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        660                665                670
Ile Ala Asp Lys Phe Met Ala Gly Thr Tyr Pro Glu Lys Ala Ala Ile
    675                680                685
Ala Ala Val Tyr Val Met Pro Ser Ala Pro Asp Ser Thr Phe His Leu
    690                695                700
Phe Leu Lys Ser Asn Thr Asn Arg Arg Leu Gln Lys Val Thr Thr Pro
705                710                715                720
Ser Asp Trp Gln Ala Gly Thr Trp Leu Arg Ile Asn Leu Asp Lys Pro
    725                730                735
Phe Pro Val Asn Asn Asp His Met Leu Phe Ala Gly Ile Arg Met Pro
    740                745                750
Asn Lys Tyr Lys Leu Asn Arg Ala Ile Arg Tyr Val Arg Asn Pro Asp
    755                760                765
Asn Leu Phe Ser Ile Thr Gly Lys Lys Ile Ser Tyr Asn Asn Gly Val
    770                775                780
Ser Phe Glu Gly Tyr Gly Ile Pro Ser Leu Leu Gly Tyr Met Ala Ile
785                790                795                800
Lys Tyr Leu Val Val Asn Thr Asp Ala Pro Lys Ile Asp Met Ser Leu
    805                810                815
Val Gln Glu Pro Tyr Ala Lys Gly Thr Asn Val Ala Pro Phe Pro Glu
    820                825                830
Leu Val Gly Ile Tyr Val Tyr Lys Asn Gly Thr Phe Ile Gly Thr Gln
    835                840                845
Asp Pro Ser Val Thr Thr Tyr Ser Val Ser Asp Gly Thr Glu Ser Asp
    850                855                860
Glu Tyr Glu Ile Lys Leu Val Tyr Lys Gly Ser Gly Ile Ser Asn Gly
865                870                875                880
Val Ala Gln Ile Glu Asn Asn Asn Ala Val Val Ala Tyr Pro Ser Val
    885                890                895
Val Thr Asp Arg Phe Ser Ile Lys Asn Ala His Met Val His Ala Ala
    900                905                910
Ala Leu Tyr Ser Leu Asp Gly Lys Gln Val Arg Ser Trp Asn Asn Leu
    915                920                925
Arg Asn Gly Val Thr Phe Ser Val Gln Gly Leu Thr Ala Gly Thr Tyr
    930                935                940
Met Leu Val Met Gln Thr Ala Asn Gly Pro Val Ser Gln Lys Ile Val
945                950                955                960
Lys Gln
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<212>    PRT
<213>    Porphyromonas gingivalis
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Asp His Tyr Asn Thr Glu Ser Tyr Leu Ser Leu Arg Arg Asn Gln Thr
    20                25                30
Met Lys Tyr Leu Ile Arg Leu Phe Leu Ser Leu Met Leu Leu Ser Leu
    35                40                45
Trp Thr Gly Cys Thr His Glu Glu Leu Ser Ile Cys Asp Gly Glu Asn
    50                55                60
Thr Leu Val Leu Arg Val Glu Thr Gly Lys Ala Pro Asn Ala Arg Ala

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65		70		75		80									
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				85					90					95	
Ser	Val	Leu	Phe	Tyr	Leu	Glu	Gly	Gln	Leu	Arg	Trp	Gln	Val	Lys	Ser
			100					105					110		
Thr	Asp	Tyr	Gln	Ile	His	Glu	Gly	Ala	Tyr	Ile	Ile	Pro	Val	Lys	Glu
		115					120					125			
Gln	Met	Arg	Pro	Leu	Phe	Asn	Gly	Asn	Asn	Asn	Phe	Ser	Ile	Tyr	Val
	130					135					140				
Val	Ala	Asn	Leu	Asp	Phe	Asn	Ala	Pro	Ala	Thr	Glu	Ala	Ala	Leu	Ser
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Gln	Phe	Val	Val	Glu	Lys	Ser	Ile	Glu	Val	Ser	Ser	Thr	Thr	Ala	Pro
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			245					250						255	
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		260					265					270			
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Ser	Gln	Asn	Val	Ser	Leu	Pro	Ser	Thr	His	Tyr	Val	Tyr	Ser	Gln	Asp	180	185	190
Gly	Tyr	Phe	Arg	Ser	Gln	Arg	Phe	Ile	Glu	Val	Thr	Leu	Tyr	Pro	Phe	195	200	205
Arg	Tyr	Asn	Pro	Val	Arg	Gln	Glu	Ile	Leu	Phe	Ala	Lys	Lys	Ile	Glu	210	215	220
Val	Thr	Ile	Thr	Phe	Asp	Asn	Pro	Gln	Pro	Pro	Leu	Gln	Lys	Asn	Thr	225	230	235
Gly	Ile	Phe	Asn	Lys	Val	Ala	Ser	Ser	Ala	Phe	Ile	Asn	Tyr	Glu	Ala	245	250	255
Asp	Gly	Lys	Ser	Ala	Ile	Glu	Asn	Asp	Met	Val	Phe	Ser	Arg	Gly	Thr	260	265	270
Thr	Thr	Tyr	Ile	Ser	Gly	Asn	Val	Ala	Ser	Asn	Leu	Pro	Gln	Asn	Cys	275	280	285
Asp	Tyr	Leu	Val	Ile	Tyr	Asp	Asp	Met	Phe	Asn	Val	Asn	Gln	Gln	Pro	290	295	300
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Phe	Asp	Val	Ala	Ala	Val	Ser	Ile	Lys	Asp	Val	Leu	Asn	Ser	Phe	Pro	325	330	335
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Arg	Ser	Val	Tyr	Asn	Gln	Ser	Asn	Ala	Lys	Arg	Thr	Leu	Asp	Gly	Lys	355	360	365
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Asp	Thr	Asp	Asn	Thr	Lys	Val	Pro	Thr	Ser	Phe	Ile	His	Asn	Val	Ser	385	390	395
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Gly	Arg	Phe	Ser	Val	Thr	Asn	Ala	His	Glu	Leu	His	Asn	Leu	Ile	Glu	435	440	445
Lys	Thr	Ile	Asn	Lys	Glu	Ile	Ser	Tyr	Asn	Pro	Ile	Ala	His	Lys	Asn	450	455	460
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Asn	Thr	Ser	Ser	Gln	Gly	Leu	Cys	Thr	Ser	Leu	Ser	Cys	Ser	Ser	Ala	545	550	555
Val	Ala	Asp	Ser	Thr	Ile	Arg	Ser	Leu	Gly	Glu	Val	Leu	Thr	Thr	Tyr	565	570	575

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Glu	Tyr	Leu	Pro	Tyr	Ser	Leu	Tyr	His	Asn	Leu	Ser	Thr	Val	Val	Gly	610	615	620
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Ser	Lys	Phe	Asn	Phe	Asn	Leu	Leu	Gly	Asp	Pro	Ala	Leu	Asn	Ile	Met	645	650	655
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Pro	Glu	Lys	Gly	Val	Leu	His	Phe	Thr	Asn	Asn	Gly	Ser	Ile	Gln	Val	690	695	700
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Ala	Pro	Val	Ile	Asn	Glu	Glu	Asp	Lys	Gln	Thr	Phe	Ile	Ser	Asn	Arg	945	950	955
Thr	Trp	Gln	Leu	Tyr	Ser	Ser	Asn	Gly	Thr	Phe	Pro	Leu	Asn	Phe	His	965	970	975
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 Ala Asp Phe Leu Ser Ala Arg Cys Asp Ile Val Cys Glu Asn Tyr Gln
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Pro Tyr Gly His Asn Gly Leu Cys Thr Tyr Ser His Ile Arg Ser Gly					
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His Tyr Ala Val Met Val Ser Thr Thr Gly Thr Ala Ile Glu Asp Phe					
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	260	265	270		
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Ile Met Lys Tyr Gln Leu Tyr Thr Ala Val Ile Met Ala Leu Ser Val
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Ser Ser Val Cys Gly Gln Thr Pro Arg Asn Thr Glu Thr Lys Arg Pro
            35                40                45
Asp Thr Leu Arg Arg Glu Leu Thr Ile Val Asn Asp Gln Thr Val Glu
            50                55                60
Met Glu His Ala Asp Pro Leu Pro Ala Ala Tyr Lys Ala Ile Glu Pro
  65                70                75                80
Arg Leu Lys Pro Phe Arg Pro Glu Tyr Asn Lys Arg Thr Phe Gly Phe
            85                90                95
Val Pro Glu Val Ser Ser Ser Gly Arg Asn Asn Leu Pro Asn Ile Leu
            100                105                110
Pro Thr Glu Gly His Met Lys His Arg Gly Tyr Leu Asn Ile Gly Ile
            115                120                125
Gly His Thr Leu Asn Gln Arg Met Asp Ala Gly Tyr Arg Leu Ile Asp
            130                135                140
Ala Glu Gln Glu Arg Leu Asn Leu Phe Leu Ser Tyr Arg Gly Met Lys
  145                150                155                160
Ser Ala Phe Asn Thr Gly Asp Phe Asp Gly Asp Arg Lys Asp Arg Arg
            165                170                175
Met Met Ala Gly Val Asp Tyr Glu Gln Arg Arg Pro Ser Phe Val Leu
            180                185                190
Ala Thr Gly Leu Tyr Tyr Ser Asn His Tyr Phe Asn Asn Tyr Gly Arg
            195                200                205
Gly Ala Thr Thr Asn Val Gly Ser Ile Pro Gln Leu Ser Thr Pro Val
            210                215                220
Thr Pro Gln Met Asp Asn Gly Thr His Asn Val Arg Val Tyr Leu Gly
  225                230                235                240
Ala Lys Asn Asp Val Ile Asp Ala Arg Ile Asp Tyr Arg Phe Phe Arg
            245                250                255
Ser Ile Pro Tyr Leu Gly Thr Asp Pro Met Lys Ala Leu Thr Glu His
            260                265                270
Thr Pro Glu Leu Asn Val Thr Met Ser Asn Glu Leu Ser Asp Asp Ile
            275                280                285
Lys Leu Gly Val Glu Val Arg Thr Gly Gly Leu Phe Phe Ala Lys Asn
            290                295                300
Ser Glu Met Ile Gln Thr Gly Val Leu Ser Glu Thr Asp Arg Asn Leu
  305                310                315                320

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Tyr Tyr Val Glu Gly Ala Pro Thr Ile Gly Phe Val Gly Asp Ser Asp
 325 330 335
 Asn Met Gln Trp Asn Ile Gln Ala Gly Val Gly Ile Ser Ser His Phe
 340 345 350
 Gly Ala Lys Gly Arg Leu Phe Phe Trp Pro Lys Leu Asp Ala Ser Leu
 355 360 365
 Ser Ile Phe Pro Ser Trp Arg Val Tyr Ala Lys Ala Phe Gly Gly Val
 370 375 380
 Ile Arg Asn Gly Leu Ala Asp Val Met Gln Glu Glu Met Pro Tyr Leu
 385 390 395 400
 Met Pro Asn Thr Ile Val Leu Pro Ser Arg Asn Ala Leu Thr Ala Gln
 405 410 415
 Leu Gly Val Lys Gly Asn Ile Ala Asp Val Val Arg Met Glu Val Tyr
 420 425 430
 Gly Asp Phe Ser Lys Leu Thr Gly Val Pro Phe Tyr Thr Pro Thr Leu
 435 440 445
 Pro Leu Tyr Asn Pro Ser Asp Leu Tyr Gln Tyr Asn Val Ser Phe Leu
 450 455 460
 Pro Ile Tyr Ala Asp Gly Ser Arg Trp Arg Ala Gly Gly Lys Leu Glu
 465 470 475 480
 Tyr Ser Tyr Arg Asp Met Leu Arg Phe Leu Val Asp Ala Ser Tyr Gly
 485 490 495
 Lys Trp Asn Leu Asp Gly Gly Leu Val Ala Ser Met Gln Pro Asp Leu
 500 505 510
 Ile Leu Lys Ala Glu Val Gly Val His Pro Ile Ala Pro Leu Asp Val
 515 520 525
 Arg Leu Arg Tyr Thr Gln Leu Asn Gly Arg Tyr Arg Tyr Ser Phe Gly
 530 535 540
 Ser Ala Gly Ser Glu Ala Leu Gly Ile Gly Asn Val His Leu Leu Ser
 545 550 555 560
 Ala Asp Val Ser Tyr Lys Leu Lys Lys Asn Leu Ser Leu Tyr Leu Lys
 565 570 575
 Ile Asp Asn Met Leu Ala Glu Thr Thr Glu Leu Ile Gly Tyr Tyr Pro
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 Met Gln Pro Phe His Cys Phe Ala Gly Phe Ser Trp Thr Phe
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 Ile Phe Ala His Tyr Pro His Asn Leu Val Phe Met Ile Arg Lys His
 20 25 30
 Phe Gly Ile Ile Leu Gly Phe Leu Ser Leu Val Phe Ser Ala Gly Ala
 35 40 45
 Gln Gln Glu Lys Gln Val Phe His Phe Leu Asn Leu Pro Ala Thr Ala
 50 55 60
 Gln Ala Leu Ala Ala Gly Gly Lys Ala Ile Thr Ile Val Asp Asp Asn
 65 70 75 80
 Pro Gly Leu Ala Phe Glu Asn Pro Ala Leu Leu Gly Tyr Glu Ser Gly

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

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

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

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

340																345				350							
His	Asn	Thr	Asp	Asn	Tyr	Glu	Gln	Arg	His	Tyr	His	Ala	Ile	Met	Thr												
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His	Ser	Phe	Ser	Pro	Ser	Val	Ile	Leu	Asn	Leu	Thr	Ala	His	Tyr	Thr												
370																375				380							
Ala	Gly	Tyr	Gly	Tyr	Thr	Asp	Glu	Tyr	Arg	Thr	Gly	Arg	Lys	Leu	Lys												
385																390				395				400			
Glu	Tyr	Ala	Leu	Gln	Pro	Tyr	Val	Glu	Asn	Ser	Val	Thr	Val	Lys	Lys												
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Thr	Asp	Leu	Ile	Arg	Gln	Lys	Tyr	Leu	Asp	Asn	Asp	Phe	Gly	Gly	Leu												
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Ile	Gly	Ser	Leu	Asn	Trp	His	Thr	Gly	Ala	Trp	Asp	Leu	Gln	Phe	Gly												
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Ala	Ser	Gly	Asn	Ile	Tyr	Lys	Gly	Asp	His	Phe	Gly	Arg	Ile	Thr	Tyr												
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Ile	Lys	Lys	Tyr	Asn	Gln	Pro	Leu	Ala	Pro	Asp	Phe	Glu	Tyr	Tyr	Arg												
465																470				475				480			
Asn	Arg	Ala	Asp	Lys	Arg	Glu	Gly	Ala	Ala	Phe	Ala	Lys	Ala	Asn	Trp												
485																490				495							
Gln	Ile	Thr	Pro	Glu	Leu	Asn	Met	Tyr	Ala	Asp	Leu	Gln	Tyr	Arg	Thr												
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Gly	Ser	Met	Gln	His	Ile	Asp	Leu	Asp	Lys	Thr	Phe	Arg	Phe	Leu	Asn												
530																535				540							
Pro	Lys	Ala	Gly	Leu	Thr	Tyr	Ser	Phe	Asp	Asp	Ala	His	Thr	Ala	Tyr												
545																550				555				560			
Ala	Ser	Val	Ala	Val	Ala	His	Arg	Glu	Pro	Asn	Arg	Thr	Asn	Tyr	Thr												
565																570				575							
Glu	Ala	Gly	Ile	Gly	Gln	Tyr	Pro	Thr	Pro	Glu	Arg	Leu	Ile	Asp	Tyr												
580																585				590							
Glu	Leu	Gly	Tyr	Arg	Tyr	Ala	Ser	Pro	Leu	Leu	Ser	Ala	Gly	Val	Gly												
595																600				605							
Leu	Tyr	Tyr	Met	Gln	Tyr	Lys	Asp	Gln	Leu	Val	Leu	Asp	Gly	Arg	Leu												
610																615				620							
Ser	Asp	Val	Gly	Gln	Met	Leu	Thr	Ser	Asn	Val	Pro	Asp	Ser	Tyr	Arg												
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Met	Gly	Leu	Glu	Leu	Thr	Leu	Gly	Trp	Gln	Ile	Leu	Pro	Arg	Leu	Leu												
645																650				655							
Arg	Trp	Asp	Ala	Ser	Phe	Thr	Met	Ser	Arg	Asn	Lys	Ile	Asp	Arg	Tyr												
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Val	Gln	Tyr	Thr	Ser	Val	Tyr	Asp	Ala	Asp	Tyr	Asn	Trp	Leu	Glu	Leu												
675																680				685							
Lys	Glu	Glu	Thr	Leu	Glu	Ser	Thr	Asp	Ile	Ala	Tyr	Ser	Pro	Asn	Val												
690																695				700							
Ile	Ala	Gly	Ser	Met	Leu	Thr	Leu	Ser	His	Ala	Gly	Phe	Glu	Met	Ala												
705																710				715				720			
Trp	Thr	Ser	Arg	Phe	Val	Ser	Lys	Gln	Tyr	Leu	Asp	Asn	Thr	Gln	Arg												
725																730				735							
Ser	Asp	Arg	Met	Leu	Ser	Ser	Tyr	Trp	Val	Asn	Asp	Leu	Arg	Leu	Gly												
740																745				750							
Tyr	Val	Leu	Pro	Val	His	Phe	Val	Lys	Arg	Val	Ala	Leu	Gly	Val	Gln												

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          755              760              765
Leu Asn Asn Leu Phe Asn Leu Met Tyr Ala Ser Asn Ala Tyr Ile Tyr
   770              775              780
Asp Ala Gly Tyr Val Gln Ala Ser Gly Glu Leu Ser Ala Tyr Ala Asp
   785              790              795              800
Leu Arg Tyr Tyr Pro Gln Ala Gly Phe Asn Ala Leu Gly Ser Leu Thr
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Ile Asp Phe
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<213>    Porphyromonas gingivalis
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Ser Tyr Ala Asp Thr Arg Leu Gln Pro Arg Arg Ala Val Arg Leu Arg
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Ala Gly Thr Arg Thr Lys Met Lys Arg Arg Phe Leu Ser Leu Leu Leu
          35              40              45
Leu Tyr Ile Leu Ser Ser Ile Ser Leu Ser Ala Gln Arg Phe Pro Met
          50              55              60
Val Gln Gly Ile Glu Leu Asp Thr Asp Ser Leu Phe Ser Leu Pro Lys
          65              70              75              80
Arg Pro Trp Arg Ala Ile Gly Lys Thr Ile Gly Val Asn Leu Ala Val
          85              90              95
Trp Gly Phe Asp His Phe Ile Met Asn Glu Asp Phe Ala Asp Ile Ser
          100              105              110
Trp Gln Thr Ile Lys Ser Asn Phe Gln Thr Gly Phe Gly Trp Asp Asn
          115              120              125
Asp Lys Phe Val Thr Asn Leu Phe Ala His Pro Tyr His Gly Ser Leu
          130              135              140
Tyr Phe Asn Ala Ala Arg Ser Asn Gly Leu Ser Phe Arg His Ser Ala
          145              150              155              160
Pro Phe Ala Phe Phe Gly Ser Leu Met Trp Glu Leu Leu Met Glu Asn
          165              170              175
Glu Pro Pro Ser Ile Asn Asp Leu Cys Ala Thr Thr Ile Gly Gly Ile
          180              185              190
Ala Leu Gly Glu Met Gly His Arg Leu Ser Asp Leu Leu Ile Asp Asn
          195              200              205
Arg Thr Thr Gly Trp Glu Arg Met Gly Arg Glu Val Ala Ile Ala Leu
          210              215              220
Ile Asn Pro Met Arg Phe Leu Asn Arg Leu Thr Ala Gly Glu Val Thr
          225              230              235              240
Ser Val Gly Ser Arg Ser Gly Gln Ile Phe Gln Ser Val Pro Ile Asn
          245              250              255
Ile Val Val Asp Ala Gly Phe Arg Phe Leu Ala Asp Lys Arg His Ala
          260              265              270
Arg Thr Gly Ala Thr Ala Leu Thr Leu Asn Leu Arg Phe Asp Tyr Gly
          275              280              285
Asp Pro Phe Arg Ser Glu Thr Phe Ser Pro Tyr Asp Phe Phe Gln Phe
          290              295              300
Lys Ala Gly Leu Ser Phe Ser Glu Ser Gln Pro Leu Leu Ser Gln Ile

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305					310				315				320			
Asn	Leu	Ile	Gly	Ile	Leu	Ser	Gly	Cys	Gln	Leu	Leu	Ala	His	Glu	Arg	
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Thr	Val	Leu	Val	Gly	Gly	Leu	Phe	Gln	His	Phe	Asp	Tyr	Tyr	Asn	Ser	
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Glu	Lys	Arg	Ile	Ser	Lys	Asn	Ser	Glu	Glu	Val	Leu	Val	Thr	Pro	Tyr	
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Arg	Ile	Ser	Gln	Val	Ala	Ala	Leu	Gly	Gly	Gly	Leu	Ile	Phe	Gln	His	
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His	Gly	Lys	Phe	Arg	Arg	Arg	Pro	Leu	Glu	Leu	Tyr	Ala	Glu	Thr	Tyr	
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Leu	Asn	Val	Val	Pro	Met	Gly	Ala	Ser	Leu	Ser	Asp	His	Tyr	Asn	Val	
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Asp	Asn	Arg	Asp	Tyr	Asn	Leu	Gly	Ser	Gly	Leu	Ser	Gly	Lys	Leu	Tyr	
				420				425				430				
Leu	Gly	Ala	Thr	Tyr	Asn	Asp	Leu	Trp	Ser	Trp	Leu	Leu	Gly	Val	Glu	
				435				440				445				
Ser	Tyr	Arg	Leu	Tyr	Thr	Trp	Ile	Gly	Tyr	Glu	Glu	Pro	His	Gln	Lys	
				450				455				460				
Asn	Thr	Asp	Val	Ser	Ser	Phe	Met	Val	Gln	Gly	Asp	Glu	Ser	Lys	Ala	
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Arg	Leu	Leu	Val	Thr	Ser	Ser	Glu	Phe	Ala	Phe	His	Pro	Gly	Pro	Trp	
				485				490				495				
His	Val	Ala	Ile	Val	Ala	Arg	Arg	Phe	Ile	Arg	Lys	Thr	Ala	Tyr	Gln	
				500				505				510				
Phe	Tyr	Pro	Asn	Val	Ser	Phe	Asp	Thr	Gly	Asp	Ile	Gln	Leu	Arg	Val	
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Gly	Phe	His	Phe													
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Lys	Arg	Arg	Lys	Lys	Gln	Met	Lys	Arg	Leu	Ile	Val	Phe	Leu	Ala	Met	
1				5				10				15				
Gly	Gly	Leu	Leu	Phe	Thr	Leu	Ala	Asn	Ala	Gln	Glu	Ala	Asn	Thr	Ala	
				20				25				30				
Ser	Asp	Thr	Pro	Lys	Lys	Asp	Trp	Thr	Ile	Lys	Gly	Val	Thr	Gly	Leu	
				35				40				45				
Asn	Ala	Ser	Gln	Thr	Ser	Leu	Thr	Asn	Trp	Ala	Ala	Gly	Gly	Glu	Asn	
				50				55				60				
Thr	Val	Ala	Gly	Asn	Leu	Tyr	Leu	Asn	Ile	Asp	Ala	Asn	Tyr	Leu	Lys	
65				70				75				80				
Asp	Lys	Trp	Ser	Trp	Asp	Asn	Gly	Leu	Arg	Thr	Asp	Phe	Gly	Leu	Thr	
				85				90				95				
Tyr	Thr	Thr	Ala	Asn	Lys	Trp	Asn	Lys	Ser	Val	Asp	Lys	Ile	Glu	Leu	
				100				105				110				
Phe	Thr	Lys	Ala	Gly	Tyr	Glu	Ile	Gly	Lys	His	Trp	Tyr	Gly	Ser	Ala	
				115				120				125				
Leu	Phe	Thr	Phe	Leu	Ser	Gln	Tyr	Ala	Lys	Gly	Tyr	Glu	Lys	Pro	Ser	
130				135				140								

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Asp His Leu Thr Gly Val Lys His Ile Ser Asn Phe Phe Ala Pro Ala
145          150          155          160
Tyr Leu Thr Leu Gly Ile Gly Ala Asp Tyr Lys Pro Asn Glu Lys Phe
          165          170          175
Ser Leu Tyr Leu Ser Pro Thr Thr Gly Lys Leu Thr Val Val Ala Asp
          180          185          190
Asp Tyr Leu Ser Ser Leu Gly Ala Phe Gly Val Lys Val Gly Glu Lys
          195          200          205
Thr Met Phe Glu Leu Gly Ala Leu Val Val Gly Ser Ala Asn Ile Asn
          210          215          220
Leu Met Glu Asn Val Asn Leu Ile Thr Lys Ala Ser Phe Phe Ser Ala
225          230          235          240
Tyr Thr His Asp Phe Gly Asn Ile Asp Ile Asn Trp Glu Ala Met Leu
          245          250          255
Ala Met Lys Ile Asn Lys Phe Leu Thr Ala Thr Ile Ala Thr Asn Leu
          260          265          270
Ile Tyr Asp Asp Asp Val Lys Ile Asn Asp Gly Pro Lys Ile Gln Phe
          275          280          285
Lys Glu Val Val Gly Val Gly Val Ala Tyr Thr Phe
          290          295          300
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<213>      Porphyromonas gingivalis
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  1          5          10          15
Lys Met Lys Lys Met Ile Leu Ala Ala Thr Met Leu Leu Ala Thr Ile
          20          25          30
Gly Phe Ala Asn Ala Gln Ser Arg Pro Ala Leu Arg Leu Asp Ala Asn
          35          40          45
Phe Val Gly Ser Asn Leu Met Gln Lys Val Ala Asn Thr Ser Val Asn
          50          55          60
Asn Lys Met Ile Val Gly Leu Arg Val Gly Ala Ala Ala Glu Phe Ala
          65          70          75          80
Leu Ser Asn Asp Gly Phe Tyr Leu Ala Pro Gly Leu Ala Tyr Thr Met
          85          90          95
Arg Gly Ala Lys Met Glu Ser Leu Ser Glu Thr Thr Thr Arg Leu His
          100          105          110
Tyr Leu Gln Ile Pro Val Asn Ala Gly Met Arg Phe Ser Phe Ala Asp
          115          120          125
Asn Met Ala Ile Ser Leu Glu Ala Gly Pro Tyr Phe Ala Tyr Gly Val
          130          135          140
Ala Gly Thr Ile Lys Thr Lys Val Ala Gly Val Thr Ala Ser Val Asp
145          150          155          160
Ala Phe Gly Asp Asn Gly Tyr Asn Arg Phe Asp Leu Gly Leu Gly Leu
          165          170          175
Ser Ala Ala Leu Ser Tyr Asp Arg Tyr Tyr Val Gln Ile Gly Tyr Glu
          180          185          190
His Gly Leu Leu Asn Met Leu Lys Asp Ala Pro Asp Lys Thr Ser Leu
          195          200          205
Arg Asn His Asp Phe Phe Val Gly Leu Gly Val Arg Phe

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

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 <213> Porphyromonas gingivalis
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 Lys Arg Lys Ser Met Lys Arg Met Leu Leu Leu Leu Val Val Leu Leu
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 Tyr Gly Ile Ala Gly Arg Leu Ala Ala Gln Asp Val Ile Arg Pro Trp
 20 25 30
 Ser Leu Gln Val Gly Ala Gly Tyr Ser Asp Thr Glu Asn Ile Pro Gly
 35 40 45
 Gly Phe Thr Tyr Gly Phe Tyr Leu Gly Lys Arg Met Gly Ser Phe Leu
 50 55 60
 Glu Val Gly Leu Ser Met Tyr Asn Ser Thr Arg Gln Thr Ala Asn Asn

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

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

Ala Pro Ser Met Gly Asn Ala Gly Ser Val Asn Phe Ser Phe Asp Asn
645 650 655
Asn Leu Glu Ala Lys Ile Lys Ser Lys Ser Asp Ser Thr Gly Ile Lys
660 665 670
Lys Ile Ser Leu Ile Asp Gln Phe Thr Trp Ser Thr Ser Tyr Asn Met
675 680 685
Phe Ala Asp Ser Ile Arg Trp Ser Asn Ile Ser Ala Ser Leu Ala Leu
690 695 700
Arg Leu Ser Lys Ser Phe Thr Leu Arg Leu Ser Gly Leu Phe Asp Pro
705 710 715 720
Tyr Leu Thr Lys Tyr Tyr Glu Gly Glu Asp Gly Lys Ile Ile Pro Tyr
725 730 735
Lys Ser Asn Asp Leu Arg Ile Phe Asn Gly Lys Gly Leu Ala Arg Leu
740 745 750
Ile Ser Thr Gly Thr Ser Phe Ser Tyr Thr Leu Asn Lys Glu Ser Leu
755 760 765
Ser Gly Leu Ile Ala Leu Phe Ser Gly Lys Lys Glu Arg Arg Asp Glu
770 775 780
Lys Lys Asn Thr Gly Ala Thr Pro His Glu Gly Asp Asp Ala Ala Asp
785 790 795 800
Ile Leu Glu Gly Gly Arg Pro Gln Asn Glu Ser Gly Gly Ser Leu Leu
805 810 815
Glu Arg Asn Arg Gln Gly Gly Ala Val Asp Gln Asp Gly Tyr Phe Ala
820 825 830
Tyr Ser Ile Pro Trp Ser Leu Ser Phe Asp Tyr Ser Trp Asn Ile Ala
835 840 845
Thr Asp Tyr Asn Arg Tyr Asn Val Asn Lys Met Glu His Tyr Tyr Arg
850 855 860
Val Thr Gln Asn Leu Ser Phe Arg Gly Asn Ile Gln Pro Thr Pro Asn
865 870 875 880
Trp Ser Phe Gly Phe Asn Ala Asn Tyr Asn Phe Asp Leu Lys Lys Ile
885 890 895
Thr Ser Leu Thr Cys Asn Val Thr Arg Asp Met His Cys Trp Ala Ile
900 905 910
Ser Ala Ser Phe Ile Pro Ile Gly Ala Tyr Lys Ser Tyr Asn Phe Val
915 920 925
Ile Ser Val Lys Ser Ser Leu Leu Gln Asp Leu Lys Tyr Gln Gln Ser
930 935 940
Asn Arg Pro Ile Thr Asn Thr Trp Tyr
945 950
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20 25 30
Ile Leu Ala Val Phe Leu Leu Phe Cys Thr Val Phe Thr Phe Gln Ile
35 40 45
Lys Ala Arg Pro Tyr Glu Arg Phe Ala Asp Val Glu Lys Pro Trp Ile

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

465					470								475								480
Ser	Asn	Gly	Thr	Val	His	Tyr	Asp	Val	Ser	Thr	Lys	Lys	Leu	Thr	Trp						
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Thr	Thr	Gly	Thr	Ile	Leu	Ser	Ser	Ser	Glu	Ala	Thr	Ile	Thr	Tyr	Arg						
				500								505								510	
Ile	Tyr	Ala	Asp	Leu	Asp	Tyr	Ile	Gln	Asn	Asn	Asp	Ile	Pro	Val	Asn						
				515								520								525	
Thr	Thr	Ser	Ala	Ile	Gly	Pro	Asp	Leu	Gly	Gly	Phe	Asp	Thr	Asn	Thr						
				530								535								540	
Glu	Ala	Lys	Leu	Thr	Tyr	Thr	Asn	Ser	Asn	Gly	Glu	Pro	Asn	Gln	Gln						
545					550								555								560
Leu	Ile	Phe	Pro	Arg	Pro	Thr	Val	Lys	Leu	Gly	Tyr	Gly	Val	Ile	Lys						
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Arg	His	Tyr	Val	Leu	Val	Asn	Lys	Asp	Gly	Gln	Pro	Ile	Gln	Ala	Asn						
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Gly	Thr	Val	Val	Ser	Ser	Leu	Ser	Glu	Ala	His	Val	Leu	Gln	Ser	Gln						
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Asp	Phe	Phe	Leu	Pro	Ser	Gly	Gly	Gly	His	Ile	Val	Pro	Lys	Trp	Ile						
				610								615								620	
Lys	Leu	Asp	Lys	Thr	Thr	Glu	Ala	Leu	Gln	Tyr	Tyr	Ser	Val	Pro	Pro						
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Thr	Asn	Thr	Val	Ile	Thr	Thr	Ala	Asp	Gly	Lys	Arg	Tyr	Arg	Phe	Val						
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Glu	Val	Pro	Gly	Ser	Thr	Pro	Asn	Pro	Gly	Gln	Ile	Gly	Ile	Ser	Trp						
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Lys	Lys	Pro	Ala	Gly	Asn	Ala	Tyr	Phe	Ala	Tyr	Lys	Leu	Leu	Asn	Tyr						
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Trp	Met	Gly	Gly	Thr	Thr	Asp	Gln	Gln	Ser	Glu	Trp	Asp	Val	Thr	Ser						
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Asn	Trp	Thr	Gly	Ala	Gln	Val	Pro	Leu	Thr	Gly	Glu	Asp	Val	Glu	Phe						
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Ala	Thr	Thr	Glu	Asn	Phe	Gly	Ser	Pro	Ala	Val	Ala	Asp	Leu	His	Val						
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Pro	Thr	Thr	Asn	Pro	Lys	Ile	Ile	Gly	Asn	Leu	Ile	Asn	Asn	Ser	Asp						
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Lys	Asp	Leu	Val	Val	Thr	Thr	Ser	Ser	Gln	Leu	Thr	Ile	Asn	Gly	Val						
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Val	Glu	Asp	Asn	Asn	Pro	Asn	Val	Gly	Thr	Ile	Val	Val	Lys	Ser	Ser						
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Lys	Asp	Asn	Pro	Thr	Gly	Thr	Leu	Leu	Phe	Ala	Asn	Pro	Gly	Tyr	Asn						
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Gln	Asn	Val	Gly	Gly	Thr	Val	Glu	Phe	Tyr	Asn	Gln	Gly	Tyr	Asp	Cys						
				805								810								815	
Ala	Asp	Cys	Gly	Met	Tyr	Arg	Arg	Ser	Trp	Gln	Tyr	Phe	Gly	Ile	Pro						
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Val	Asn	Glu	Ser	Gly	Phe	Pro	Ile	Asn	Asp	Val	Gly	Gly	Asn	Glu	Thr						
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Val	Asn	Gln	Trp	Val	Glu	Pro	Phe	Asn	Gly	Asp	Lys	Trp	Arg	Pro	Ala						
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Pro</																					

885															890					895				
Met	Ile	Cys	Val	Cys	Asp	Ala	Phe	Leu	Asn	Leu	Thr	Arg	Thr	Ser	Gly									
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Ile	Asp	Ile	Lys	Gln	Gly	Ile	Val	Phe	Pro	Pro	Glu	Val	Glu	Gln	Thr									
930					935					940														
Val	Tyr	Leu	Phe	Asn	Thr	Gly	Thr	Arg	Asp	Gln	Trp	Arg	Lys	Leu	Asn									
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Lys	Asn	Thr	Ala	Gly	Gln	Asp	Asn	Leu	Pro	Asp	Arg	Ile	Pro	Ser	Met									
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His	Ser	Phe	Leu	Val	Lys	Met	Gln	Asn	Gly	Ala	Ser	Cys	Thr	Leu	Xaa									
995					1000					1005														
Ile	Leu	Tyr	Asp	Lys	Leu	Leu	Lys	Asn	Thr	Thr	Val	Asn	Asn	Gly	Asn									
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Pro	Ser	Leu	Val	Met	Asp	Val	Leu	Gly	Asn	Glu	Ser	Ala	Asp	Arg	Leu									
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Ser	Asp	Ile	Gly	Asn	Asp	Lys	Phe	Gln	Val	Ala	Gly	Val	Pro	Glu	Leu									
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1105					1110					1115					1120									
Leu	Glu	Phe	Ala	Leu	Ser	Asp	His	Phe	Ala	Lys	Gly	Ala	Val	Tyr	Leu									
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His	Asp	Leu	Gln	Ser	Gly	Ala	Lys	His	Arg	Ile	Thr	Asn	Ser	Thr	Ser									
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Tyr	Ser	Phe	Asp	Ala	Lys	Arg	Gly	Asp	Ser	Gly	Ala	Arg	Phe	Arg	Leu									
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Ser	Tyr	Gly	Cys	Asp	Glu	Asn	Val	Asp	Asp	Ser	His	Val	Val	Ser	Thr									
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Asn	Gly	Arg	Glu	Ile	Ile	Ile	Leu	Asn	Gln	Asp	Ala	Leu	Asp	Cys	Thr									
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Val	Thr	Leu	Phe	Thr	Ile	Glu	Gly	Lys	Leu	Leu	Arg	Arg	Leu	Lys	Val									
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Leu	Ala	Gly	His	Arg	Glu	Val	Met	Lys	Val	Gln	Thr	Gly	Gly	Ala	Tyr									
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Ile	Val	His	Leu	Gln	Asn	Ala	Phe	Thr	Asn	Asp	Val	His	Lys	Val	Leu									
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Val	Glu	Tyr																						
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Thr Met Glu Val Lys Lys Asn Thr Val Val Leu Arg Leu Leu Ile Trp
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 Phe Val Ala Ile Leu Leu Phe His Ser Ser Arg Leu Trp Gly Gln Glu
 20 25 30
 Gly Glu Gly Ser Ala Arg Tyr Arg Phe Lys Gly Phe Val Asp Thr Tyr
 35 40 45
 His Ala Val Arg Ser Ser Ser Pro Phe Asp Phe Met Ser Ser Arg Thr
 50 55 60
 Arg Val Arg Gly Glu Leu Glu Arg Ser Phe Gly Asn Ser Lys Val Ala
 65 70 75 80
 Val Ser Val Asn Ala Thr Tyr Asn Ala Leu Leu Lys Asp Glu Thr Gly
 85 90 95
 Leu Arg Leu Arg Glu Ala Phe Phe Glu His Gln Glu Glu His Trp Gly
 100 105 110
 Leu Arg Leu Gly Arg Gln Ile Val Ile Trp Gly Ala Ala Asp Gly Val
 115 120 125
 Arg Ile Thr Asp Leu Ile Ser Pro Met Asp Met Thr Glu Phe Leu Ala
 130 135 140
 Gln Asp Tyr Asp Asp Ile Arg Met Pro Val Asn Ala Leu Arg Phe Ser
 145 150 155 160
 Val Phe Asn Glu Ser Met Lys Val Glu Val Val Val Leu Pro Val Phe
 165 170 175
 Glu Gly Tyr Arg Leu Pro Val Asp Pro Arg Asn Pro Trp Asn Ile Phe
 180 185 190
 Ser Leu Ser Pro Ile Ala Gln Gly Met Asn Ile Val Trp Lys Glu Glu
 195 200 205
 Ala Gly Lys Pro Ala Phe Lys Val Ala Asn Ile Glu Tyr Gly Ala Arg
 210 215 220
 Trp Ser Thr Thr Leu Ser Gly Ile Asp Phe Ala Leu Ala Ala Leu His
 225 230 235 240
 Thr Trp Asn Lys Met Pro Val Ile Glu Val Gln Gly Ile Val Pro Thr
 245 250 255
 Glu Ile Ile Val Ser Pro Arg Tyr Tyr Arg Met Gly Phe Val Gly Gly
 260 265 270
 Asp Leu Ser Val Pro Val Gly Gln Phe Val Phe Arg Gly Glu Ala Ala
 275 280 285
 Phe Asn Ile Asp Lys His Phe Thr Tyr Lys Ser His Ala Glu Gln Glu
 290 295 300
 Gly Phe Gln Thr Ile Asn Trp Leu Ala Gly Ala Asp Trp Tyr Ala Pro
 305 310 315 320
 Gly Glu Trp Met Ile Ser Gly Gln Phe Ser Met Glu Ser Ile Phe Arg
 325 330 335
 Tyr Arg Asp Phe Ile Ser Gln Arg Gln His Ser Thr Leu Ile Thr Leu
 340 345 350
 Asn Val Ser Lys Lys Phe Phe Gly Ser Thr Leu Gln Leu Ser Asp Phe
 355 360 365
 Thr Tyr Tyr Asp Leu Thr Gly Lys Gly Trp Phe Ser Arg Phe Ala Ala
 370 375 380
 Asp Tyr Ala Leu Asn Asp Gln Ile His Leu Met Ala Gly Tyr Asp Trp
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 Phe Ser Ser Lys Gly Ser Gly Ile Phe Asp Arg Tyr Lys Asp Asn Ser
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Glu Leu Trp Phe Lys Ala Arg Tyr Ser Phe
420 425
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Glu Gly Leu Arg Val Asn Pro Ile Gly Ala Ala Ala Ile Val Ala Phe
35 40 45
Ile Ile Asp Leu Leu Leu Leu Cys Cys Ser Ala Phe Met Ser Ser Cys
50 55 60
Glu Val Ala Tyr Phe Ser Leu Lys Pro Ile Asp Leu Gln Asn Ile Arg
65 70 75 80
Glu Arg Asn His Ser Ser Asp Ile Ala Leu Ser Asn Leu Leu Asp Asn
85 90 95
Ser Asn Gln Leu Leu Ala Thr Ile Leu Ile Gly Asn Asn Val Ile Asn
100 105 110
Val Ala Ile Val Ile Leu Ser Asn Tyr Ala Ile Glu Gln Thr Phe Val
115 120 125
Phe Ser Ser Pro Ile Ile Gly Phe Leu Ile Gln Thr Ile Leu Leu Thr
130 135 140
Thr Val Leu Leu Leu Phe Gly Glu Ile Leu Pro Lys Val Tyr Ala Arg
145 150 155 160
Lys Asn Pro Leu Gln Tyr Ser Arg Phe Ser Ala Ala Ala Met Ser Val
165 170 175
Ile Tyr Lys Ile Leu Ser Pro Phe Ser Lys Leu Leu Val Lys Ser Thr
180 185 190
Gly Ile Val Thr Arg Gly Ile Ser Lys Lys Lys Tyr Asp Met Ser Val
195 200 205
Asp Glu Leu Ser Lys Ala Val Ala Leu Thr Thr Thr Glu Gly Glu Pro
210 215 220
Glu Glu Lys Glu Met Ile Asn Glu Ile Ile Lys Phe Tyr Asn Lys Thr
225 230 235 240
Ala Cys Glu Ile Met Val Pro Arg Ile Asp Ile Val Asp Val Asp Leu
245 250 255
Ser Trp Pro Phe Arg Lys Met Leu Asp Phe Val Val Ser Ser Gly Tyr
260 265 270
Ser Arg Leu Pro Val Ser Glu Gly Ser Glu Asp Asn Ile Lys Gly Val
275 280 285
Ile Tyr Ile Lys Asp Leu Ile Pro His Met Asp Lys Gly Asp Glu Phe
290 295 300
Asp Trp His Pro Leu Ile Arg Lys Ala Tyr Phe Val Pro Glu Asn Lys
305 310 315 320
Arg Ile Asp Asp Leu Leu Glu Glu Phe Arg Ala Asn Lys Val His Val
325 330 335
Ser Ile Val Val Asp Glu Phe Gly Gly Thr Cys Gly Leu Ile Thr Met
340 345 350
Glu Asp Ile Leu Glu Glu Ile Val Gly Glu Ile Thr Asp Glu Tyr Asp

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

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


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785                790                795                800
Gln Thr Lys Tyr Asp Gly Asn Val Phe Asn Asn Ile Gly Ile Ala Lys
      805                810                815
Gln Leu Phe Asp Lys Lys Leu Arg Val Ser Leu Ser Ala Asn Asn Ile
      820                825                830
His Ala Lys Tyr Ser Thr Trp Lys Ser Arg Thr Ile Gly Asn Gly Phe
      835                840                845
Thr Ile Tyr Ser Glu Asn Ala Gly Ile Gln Arg Ser Val Ser Leu Ser
      850                855                860
Leu Thr Tyr Ser Phe Gly Lys Met Asn Thr Gln Val Arg Lys Val Glu
865                870                875                880
Arg Thr Ile Val Asn Asp Asp Leu Lys Gln Thr Ser Ser Gln Gly Gln
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Gln Gly Gly Gly Gln Gly Asn Pro Thr Gly Asn
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Ala Gln Gly His Gln Gln Gly Arg Ser Asp Gln Asp Arg Leu Pro Pro
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Val Arg Gly Tyr Arg Tyr Ala Arg Cys Leu Gly Arg Tyr Glu Gly Phe
      35                40                45
Gly Glu Arg Met Arg Leu Ser Ala Ile Leu Ile Ala Leu Ile Val Met
      50                55                60
Leu Pro Ala Val Leu Ser Gly Gln His Tyr Tyr Ser Met Ala Gly Glu
      65                70                75                80
Arg Leu Glu Thr Asp Ser Ile Arg Pro Asn Glu Leu Ser Ala Ser Ile
      85                90                95
Arg Ser Ala Leu Phe Phe Arg Asn Asn Glu Tyr Asn Ala Arg Ser Val
      100                105                110
Lys Gly Tyr Thr Leu Pro Gly Ala Arg Val Ser Ala Phe Ala Ser Tyr
      115                120                125
Ser Leu Pro Ala Ala His Gly Val Lys Leu Ser Leu Gly Val Ser Thr
      130                135                140
Leu Asn Tyr Trp Gly Ala Ser Arg Tyr Pro Ala Gly Ile Ala Tyr Ser
      145                150                155                160
Asp Leu Pro Tyr Trp Thr Asp Tyr Asn Asp Tyr Val Arg Leu Arg Ile
      165                170                175
Leu Pro Tyr Val Gln Ala Met Leu Lys Pro Thr Ala Thr Thr Ala Leu
      180                185                190
Met Leu Gly Asn Ile Ala Gly Gly Thr Ala His Gly Leu Ile Glu Pro
      195                200                205
Ile Tyr Asn Pro Glu Leu Asp Leu Thr Ala Asp Pro Glu Ala Gly Val
      210                215                220
Gln Phe Arg Gly Asp Trp Thr Arg Phe Arg Met Asp Val Trp Val Asn
      225                230                235                240
Trp Met Ser Met Ile Phe Lys Asn Asp Asn His Gln Glu Ser Phe Val
      245                250                255

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Phe Gly Leu Ser Thr Thr Ser Lys Leu Leu Ser Gly Glu Gly Lys Trp
 260 265 270
 Arg Leu Glu Leu Pro Leu Gln Ala Ile Ala Thr His Arg Gly Gly Glu
 275 280 285
 Tyr Asn Trp Ala Gln Gln Asp Thr Val His Thr Trp Val Asn Gly Ala
 290 295 300
 Val Gly Leu Lys Leu Ser Tyr Arg Pro Arg Thr Asp Lys Pro Met Gln
 305 310 315 320
 Ile Trp Gly Ser Ala Tyr Gly Val Ala Ala Leu Ser Ser Gly Gly Tyr
 325 330 335
 Phe Pro Tyr Glu Arg Gly Trp Gly Gly Tyr Leu Ser Leu Gly Met Asp
 340 345 350
 Leu Glu His Phe Ala Phe Arg Thr Asp Tyr Trp Tyr Gly Arg His Tyr
 355 360 365
 Val Ser Pro Phe Ala Ala Pro Phe Ala Asn Ser Leu Thr Tyr Asp Lys
 370 375 380
 Gln Pro Leu Thr Asn Gly Trp Gly Asp Tyr Ile Arg Leu Tyr Ala Asp
 385 390 395 400
 Tyr Ser Trp Arg Met Ala Arg Ser Val Ser Leu Ala Ala Val Ala Arg
 405 410 415
 Val Trp Phe Gln Pro Ser Asp Arg Phe Ala Met Ser His Ala Leu Glu
 420 425 430
 Leu Thr Met Arg Ile Asp Pro Lys Phe Pro Ile Ala Phe Leu Lys Gly
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 Asn His
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 Arg Ser Glu His Met Arg Ser Ala Asp Ser Ser Pro Ala Tyr Ser Pro
 35 40 45
 Ile Gly Ser Leu Ser Ser Ser His Ser Phe Asp Ser Ile Pro Asp Gln
 50 55 60
 Arg Met Asn Lys Ser Leu Ser Leu Ala Cys Leu Ile Leu Cys Gly
 65 70 75 80
 Met Pro Ala Ile Ala Gln Gln Thr Gly Pro Ala Glu Arg Ser Gly Glu
 85 90 95
 Pro Ser Leu Ala Glu Arg Val Phe Gly Leu Glu Gln Lys Gln Lys Lys
 100 105 110
 Leu Lys Val Tyr Leu Gly Ile Gln Ser Phe Tyr Asp Gln Pro Leu Val
 115 120 125
 Asp Asp Glu Ser His Ile Gly His Phe Lys Val Gln Glu Leu Arg Met
 130 135 140
 Ser Ala His Gly Glu Leu Asn Arg His Leu Ser Phe Asp Trp Arg Gln
 145 150 155 160
 Arg Leu Asn Arg Ala Ala Asp Gly Thr Ser Phe Ala Asp Asn Leu Ser

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

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

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Gly	Val	Thr	Ser	Phe	Phe	Ile	Pro	Thr	Ser	Leu	Asn	Leu	Gly	Thr	Gly					
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Leu	Leu	Tyr	Pro	Ile	Asp	Asp	Tyr	Asn	Ser	Ile	Asn	Phe	Asn	Leu	Glu					
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Leu	Ser	Lys	Leu	Leu	Val	Pro	Thr	Pro	Pro	Ile	Met	Asp	Gln	Asn	Asp					
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Gln	Ala	Gly	Tyr	Glu	Ala	Ala	Leu	Lys	Lys	Tyr	Gln	Glu	Thr	Ser	Ser					
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Ile	Ser	Gly	Ile	Phe	Ser	Ser	Phe	Gly	Asp	Ala	Pro	Gly	Gly	Leu	Lys					
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Glu	Glu	Phe	Arg	Glu	Ile	Thr	Trp	Gly	Leu	Gly	Ala	Glu	Tyr	Ser	Tyr					
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Asp	Asp	Lys	Phe	Phe	Val	Arg	Ala	Gly	Tyr	Ser	Tyr	Leu	His	Pro	Thr					
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Lys	Gly	Asn	Leu	Gln	Tyr	Phe	Thr	Ala	Gly	Ala	Gly	Phe	Lys	Met	Asn					
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Ile	Phe	Arg	Ile	Asp	Ala	Ser	Tyr	Leu	Leu	Ser	Thr	Ile	Gln	Ser	Asn					
				370					375					380						
Pro	Leu	Asp	Gln	Thr	Leu	Arg	Phe	Thr	Leu	Ala	Phe	Asp	Met	Asp	Gly					
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Leu	Arg	Asn	Leu	Phe	His															
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Cys	Leu	Ala	Leu	Met	Met	Ser	Gly	Val	Leu	Gly	Gly	Asn	Ala	Gln	Ser					
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Phe	Trp	Glu	Glu	Ile	Ala	Pro	Pro	Phe	Ile	Ser	Asn	Glu	Pro	Asn	Val					
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Lys	Tyr	Ile	Ile	Pro	Asn	Met	Gly	Ile	Asp	Ser	Lys	Gly	Thr	Ile	Tyr					
				50					55					60						
Val	Thr	Val	Thr	Lys	Arg	Ile	Gln	Gln	Gly	Ala	Asn	Tyr	Thr	Ser	Glu					
65					70					75					80					
Gln	Leu	Gly	Met	Tyr	Tyr	Arg	Pro	Leu	Gly	Asp	Asn	Glu	Gln	Trp	Trp					
				85					90					95						
Lys	His	Asp	Pro	Tyr	Phe	Asp	Asp	Lys	Ile	Val	Ala	Asp	Ile	Gln	Thr					
				100					105					110						
Asp	Ala	Tyr	Gly	Arg	Val	Tyr	Val	Cys	Thr	Thr	Ser	Ser	Arg	Asp	Gln					
				115					120					125						
Glu	Tyr	Gln	Leu	Tyr	Ile	Asn	Glu	Gln	Asn	Glu	Trp	Arg	Cys	Ile	Phe					
				130					135					140						
Lys	Thr	Ser	Val	Ser	Thr	Tyr	Glu	His	Gly	Met	Ala	Val	Phe	Arg	Ser					
145					150					155					160					
Ser	Thr	Gly	Val	Thr	Tyr	Ile	Gly	Thr	Arg	His	His	Ile	Phe	Ala	Ser					
				165					170					175						
Gly	Val	Asn	Asp	Phe	Glu	Phe	Asn	Thr	Ile	Tyr	Glu	Asp	Ser	Thr	Pro					
				180					185					190						

Met Ser Cys Arg Phe Ala Glu Ala Thr Asn Ser Gly Thr Ile Tyr Leu
195 200 205
Ala Leu Met His Glu Thr Thr Met Ser Thr Thr Ile Leu Thr Tyr Gln
210 215 220
Asn Gly Glu Phe Val Asp Ile Ser Glu Ser Glu Leu Ser Asn Ser Ile
225 230 235 240
Ile Ala Ser Met Cys Ser Asn Lys Glu Gly Asp Ile Ile Ala Leu Val
245 250 255
Thr Ser Tyr Thr Gly Phe Met Ser Gly Thr Leu Ala Ile Arg Lys Ala
260 265 270
Asp Glu Gly Lys Trp Gln Leu Val Gly Gly Asp Ile Gln Asn Ala Ile
275 280 285
Val Gln Asn Ile Cys Met Met Asp Asp Asn Lys Ile Ala Cys Glu Val
290 295 300
Phe Gly Thr Pro Asn Gly Val Asp Gly Arg Thr Arg Val Cys Val Ser
305 310 315 320
Asp Ala Ser Val Phe Asp Phe Glu Trp Tyr Glu Asp Glu Ile Tyr Gly
325 330 335
Gly Leu Ile Phe Asp Thr Phe Phe Tyr Ser Pro Trp Asp Lys Leu Leu
340 345 350
Tyr Ala Lys Phe Gly Gly Ile Met Leu Arg Ser Lys Glu Ser Phe Ile
355 360 365
Thr Ser Phe Ile Ser Pro Thr Val Val Gln Gly Val Asp Val Tyr Thr
370 375 380
Leu Ala Gly Lys Ile Arg Ile Glu Ser Glu Thr Pro Val Ser Glu Val
385 390 395 400
Leu Leu Phe Asp Leu Ala Gly Arg Met Val Leu Arg Gln Thr Ile Asp
405 410 415
Asn Lys Ile Tyr Ser Asp Ile Asp Thr Asn Gly Leu Lys Arg Ser Gly
420 425 430
Ile Tyr Val Val Ser Val Arg Leu Ser Ser Gly Gln Val Phe Ser His
435 440 445
Lys Val Gln Val
450
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<211> 331
<212> PRT
<213> Porphyromonas gingivalis
<400> 361
Gly Leu Tyr Gly Met Ser Val Val Pro Ile Ile Ile Tyr Leu Cys Gly
1 5 10 15
Ile Ser Asn Tyr Ala Arg Leu Met Ile Ile Arg Cys Leu Ile Arg Arg
20 25 30
Pro Arg Thr Val Leu Phe Gly Leu Ile Phe Val Val Gly Leu Phe Ser
35 40 45
Ala Met Ala Gln Glu Lys Lys Asp Ser Leu Ser Thr Val Gln Pro Val
50 55 60
Pro Asn Ser Ser Met Val Glu Gln Thr Pro Leu Leu Ser Ile Asp His
65 70 75 80
Pro Val Leu Pro Ala Ser Phe Gln Asn Thr Arg Thr Leu Lys Arg Phe
85 90 95
Arg Asp Lys His Leu Ser Asp Ala Leu Leu Asn Gly Leu Lys Pro His

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100      105      110
Arg Ser Ser Leu Gln Leu Asn Glu Glu Leu Asn Phe Ala Ala Glu Arg
115      120      125
Arg Asp Phe Val Ser Pro Leu Leu Gln Thr Arg His Ala Ala Gly Val
130      135      140
Leu Ser Trp Arg Pro Thr Asp Arg Met His Phe Tyr Thr Ser Gly Asn
145      150      155      160
Ile Gly Leu Gly His Asp Leu Leu Thr Gly Val Arg Lys Asp Phe Gly
165      170      175
Trp Asn Ala Gly Ala Asp Phe Leu Leu Ser Gln Asn Leu Thr Ala His
180      185      190
Val Gln Gly Gly Trp Gln Gln Asn Phe Gly Phe Ile Pro Met Thr Ala
195      200      205
Val Asn Gly Gln Leu Arg Trp Gln Ala Thr Glu Arg Leu Ser Phe Thr
210      215      220
Thr Gly Ile Asp Tyr Arg Gln Val Gln Trp Asn Ala Phe Asp Asn Arg
225      230      235      240
Thr Phe Ser Leu Lys Gly Ser Ala Arg Tyr Glu Val Met Asp Asn Val
245      250      255
Phe Val Asn Gly Phe Gly Ser Tyr Pro Leu Tyr Ser Ser Thr Arg Ser
260      265      270
Gly Leu Asn Met Ala Val Pro Met His Gly Phe Gly Pro Gln Tyr Gly
275      280      285
Gly Ser Leu Glu Leu Lys Val Ser Glu Arg Phe Gly Phe Ala Val Gly
290      295      300
Met Glu Arg Glu Tyr Asn Ile Trp Thr Arg Arg Trp Glu Thr His Tyr
305      310      315      320
Phe Ala Tyr Pro Val Phe Tyr Gly Asp Lys Lys
325      330
<210>      362
<211>      329
<212>      PRT
<213>      Porphyromonas gingivalis
<400>      362
Glu Thr Asn Ser Trp Val Ser Ser Asp Cys Asn Ser Thr Thr Met Lys
1      5      10      15
Thr Asn Arg Arg Tyr Ala Phe Val Leu Pro Leu Leu Leu Leu Thr Gly
20      25      30
Leu Leu Ala Trp Gly Gln Asp Ser Ser His Gly Ser Asn Thr Ala Phe
35      40      45
Ala Thr Asp Ser Ser Ser Arg Glu Leu Pro Thr Glu Gln Ser Ala Tyr
50      55      60
Arg Ile His Ser Ala Tyr Met Val Gly Gly Gly Gly Ser Ile Thr Arg
65      70      75      80
Asp Thr Tyr Leu Ser Pro Leu Arg Tyr Gly Gly Trp Thr Leu Asn Leu
85      90      95
Leu Gly Glu Lys Thr Phe Pro Leu Lys Ala Ser Asp Ser Arg Trp Met
100      105      110
Ile Arg Thr Gly His Glu Leu Asp Phe Ala Leu Met Asp Asn Pro Ala
115      120      125
Asn Asn Ala His Phe Tyr Ser Leu Leu Tyr Asn Gly Ser Ala Ala Ala
130      135      140

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Leu Tyr Arg Leu Gly Ala Lys His Leu Arg Ala Ala Trp Met Asp Asn
 145 150 155 160
 Leu Arg Leu Ala Phe Gly Pro Gly Leu Glu Ile Gly Leu Gly Gly Ile
 165 170 175
 Tyr Ser Thr Arg Asn Gly Asn Asn Pro Ala Thr Leu Lys Leu Tyr Thr
 180 185 190
 Asn Ala Ile Ala Gln Ala Ser Ile Gly Tyr Tyr Val Pro Ser Glu Thr
 195 200 205
 Phe Pro Leu Tyr Phe Arg Leu Leu Ser Gln Ile Asn Leu Phe Gly Ile
 210 215 220
 Ala Tyr Gly Asn Gly Phe Gly Glu Ser Tyr Tyr Glu Asn Phe Leu Leu
 225 230 235 240
 Asn Asn Gly Ile Ala Gly Ser Leu His Phe Thr Tyr Pro Gly Lys Phe
 245 250 255
 Thr Arg Phe Thr Thr Leu Ile Thr Ala Asp Ile Pro Ile Arg Asn Phe
 260 265 270
 Cys Thr Leu Arg Val Gly Tyr Arg Tyr Ser His Leu Gly Ser Ser Leu
 275 280 285
 Asn Ala Leu Asp Thr Arg Ile His Ser His Thr Ala Phe Ile Gly Phe
 290 295 300
 Val Thr Glu Phe Tyr Arg Phe Arg Gly Arg Lys Ala Met Asn Thr Gly
 305 310 315 320
 Arg Arg Thr Ser Leu Tyr Tyr His Asp
 325
 <210> 363
 <211> 319
 <212> PRT
 <213> Porphyromonas gingivalis
 <400> 363
 Phe Thr Ser Gly Thr Ile Phe Val Arg Ile Ala Ile Ser Gly Arg Val
 1 5 10 15
 Val Cys Arg Glu Val Glu Asp Asn Gly Arg Arg Glu Ala Val Arg His
 20 25 30
 Asp Gly Met Val Val Thr Leu Leu Val Ile Val Gly Ile Val Val Val
 35 40 45
 Val Arg Tyr Ser Leu Arg Val His Val His Lys Thr Gly Thr Val Val
 50 55 60
 Ser Ala Ala Ile Phe Gly Phe Ile Leu Leu Gly Lys Thr Val Pro Cys
 65 70 75 80
 Asp Thr Arg Asn Phe Ser Ser Glu Ser Asp Glu Pro Glu Ser Arg
 85 90 95
 Val Ala Thr Glu Ile Ala His Leu Cys Glu Ile Gly Phe Gln Ile His
 100 105 110
 Ala Ser Ser Ile His Val Ala Val Arg Thr Asp Phe Gly Gln Ala Gly
 115 120 125
 Ile His Cys Pro Met Ala Thr Asp Ala Ser Ala Thr Glu Phe Asp Arg
 130 135 140
 Ser Ala Glu Cys Ala Glu Arg Thr Ser Ala Gln Ile Asp Thr Ala Ile
 145 150 155 160
 Arg Ser Gln Ser Gln Ile Ile Arg Thr His Ile Asp Thr Cys Pro Lys
 165 170 175
 Ser Ser Gly Thr Ile Gly Gly Ser Thr His Thr Ser Leu His Leu Lys


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180          185          190
Val Phe Asp Gly Arg Gly Glu Val Gly His Ile His Pro Lys Asp Gly
195          200          205
Leu Arg Phe Gly Val Val Glu Gly Tyr Ser Ile Gly Ser Tyr Val Asp
210          215          220
Ala Ile Gly Ile Gly Ala Thr His Ala Lys Ala Gly Ile Ser Asp Thr
225          230          235          240
Arg Thr Gly Ile Ala Gly Gly Tyr His Gly Gly Ser Gln His Gln Gln
245          250          255
Ile Gly Asp Val Thr Thr Ile Ile Gly Leu Gly Lys Phe Gly Leu Ala
260          265          270
Asn Val Gly Val Ser Asp Arg Gly Phe Arg Arg Gly Ala Ser Ser Tyr
275          280          285
Asp Leu Tyr Gly Leu Glu Leu His Ile Ala Lys Thr Ile Tyr Leu Ala
290          295          300
Val Gly Asp Gly Cys Leu Cys Arg Gln Ala Glu Arg Gln Asp Gly
305          310          315
<210>      364
<211>      614
<212>      PRT
<213>      Porphyromonas gingivalis
<400>      364
Pro Tyr Asn Val Gln Ser Ile Ser Asn Lys Thr Ile Lys Lys Gln Met
1      5      10      15
Glu Asn Leu Lys Asn Ile Gln Pro Arg Glu Asp Phe Asn Trp Glu Glu
20      25      30
Phe Glu Ala Gly Gly Val His Ala Ala Val Ser Arg Gln Glu Gln Glu
35      40      45
Ala Ala Tyr Asp Lys Thr Leu Asn Thr Ile Lys Glu Lys Glu Val Val
50      55      60
Met Gly Arg Val Thr Ala Ile Asn Lys Arg Glu Val Val Ile Asn Val
65      70      75      80
Gly Tyr Lys Ser Glu Gly Val Val Pro Ala Thr Glu Phe Arg Tyr Asn
85      90      95
Pro Glu Leu Lys Val Gly Asp Glu Val Glu Val Tyr Ile Glu Asn Gln
100     105     110
Glu Asp Lys Lys Gly Gln Leu Val Leu Ser His Arg Lys Gly Arg Ala
115     120     125
Ala Arg Ser Trp Glu Arg Val Asn Glu Ala Leu Glu Lys Asp Glu Ile
130     135     140
Val Lys Gly Tyr Val Lys Cys Arg Thr Lys Gly Gly Met Ile Val Asp
145     150     155     160
Val Phe Gly Ile Glu Ala Phe Leu Pro Gly Ser Gln Ile Asp Val Arg
165     170     175
Pro Ile Arg Asp Tyr Asp Ala Phe Val Glu Lys Thr Met Glu Phe Lys
180     185     190
Ile Val Lys Ile Asn Gln Glu Tyr Lys Asn Val Val Val Ser His Lys
195     200     205
Val Leu Ile Glu Ala Glu Leu Glu Gln Gln Lys Lys Glu Ile Ile Gly
210     215     220
Lys Leu Glu Lys Gly Gln Val Leu Glu Gly Ile Val Lys Asn Ile Thr
225     230     235     240

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Ser Tyr Gly Val Phe Ile Asp Leu Gly Gly Val Asp Gly Leu Ile His
 245 250 255
 Ile Thr Asp Leu Ser Trp Gly Arg Val Ala His Pro Glu Glu Ile Val
 260 265 270
 Gln Leu Asp Gln Lys Ile Asn Val Val Ile Leu Asp Phe Asp Glu Asp
 275 280 285
 Arg Lys Arg Ile Ala Leu Gly Leu Lys Gln Leu Met Pro His Pro Trp
 290 295 300
 Asp Ala Leu Asp Ser Glu Leu Lys Val Gly Asp Lys Val Lys Gly Lys
 305 310 315 320
 Val Val Val Met Ala Asp Tyr Gly Ala Phe Val Glu Ile Ala Gln Gly
 325 330 335
 Val Glu Gly Leu Ile His Val Ser Glu Met Ser Trp Thr Gln His Leu
 340 345 350
 Arg Ser Ala Gln Asp Phe Leu His Val Gly Asp Glu Val Glu Ala Val
 355 360 365
 Ile Leu Thr Leu Asp Arg Glu Glu Arg Lys Met Ser Leu Gly Leu Lys
 370 375 380
 Gln Leu Lys Pro Asp Pro Trp Ala Asp Ile Glu Thr Arg Phe Pro Val
 385 390 395 400
 Gly Ser Arg His His Ala Arg Val Arg Asn Phe Thr Asn Phe Gly Val
 405 410 415
 Phe Val Glu Ile Glu Glu Gly Val Asp Gly Leu Ile His Ile Ser Asp
 420 425 430
 Leu Ser Trp Thr Lys Lys Ile Lys His Pro Ser Glu Phe Thr Glu Val
 435 440 445
 Gly Ala Asp Ile Glu Val Gln Val Ile Glu Ile Asp Lys Glu Asn Arg
 450 455 460
 Arg Leu Ser Leu Gly His Lys Gln Leu Glu Glu Asn Pro Trp Asp Val
 465 470 475 480
 Phe Glu Thr Val Phe Thr Val Gly Ser Ile His Glu Gly Thr Val Ile
 485 490 495
 Glu Val Met Asp Lys Gly Ala Val Val Ser Leu Pro Tyr Gly Val Glu
 500 505 510
 Gly Phe Ala Thr Pro Lys His Met Val Lys Glu Asp Gly Ser Gln Ala
 515 520 525
 Val Leu Glu Glu Lys Leu Pro Phe Lys Val Ile Glu Phe Asn Lys Asp
 530 535 540
 Ala Lys Arg Ile Ile Val Ser His Ser Arg Val Phe Glu Asp Glu Gln
 545 550 555 560
 Lys Met Ala Gln Arg Glu Ala Asn Ala Glu Arg Lys Ala Glu Ala Lys
 565 570 575
 Ala Ala Gln Lys Glu Ala Ala Ala Glu Ala Ala Asn Pro Ala Gln Ala
 580 585 590
 Val Glu Lys Ala Thr Leu Gly Asp Leu Gly Glu Leu Ala Ala Leu Lys
 595 600 605
 Glu Lys Leu Ser Glu Asn
 610
 <210> 365
 <211> 243
 <212> PRT
 <213> Porphyromonas gingivalis

<400> 365
 Ser Thr Ile Met Lys Lys Ala Ile Leu Ser Gly Ala Ala Leu Leu Leu
 1 5 10 15
 Gly Leu Cys Ala Asn Ala Gln Asn Val Gln Leu His Tyr Asp Phe Gly
 20 25 30
 His Ser Ile Tyr Asp Glu Leu Asp Gly Arg Pro Lys Leu Thr Thr Thr
 35 40 45
 Val Glu Asn Phe Thr Pro Asp Lys Trp Gly Ser Thr Phe Phe Phe Ile
 50 55 60
 Asp Met Asp Tyr Thr Gly Lys Gly Ile Gln Ser Ala Tyr Trp Glu Ile
 65 70 75 80
 Ser Arg Glu Leu Lys Phe Trp Gln Ala Pro Val Ser Ile His Leu Glu
 85 90 95
 Tyr Asn Gly Gly Leu Ser Thr Ser Phe Thr Phe Gly His Asp Ala Leu
 100 105 110
 Ile Gly Ala Thr Tyr Thr Tyr Asn Asn Pro Ser Phe Thr Arg Gly Phe
 115 120 125
 Thr Ile Thr Pro Met Tyr Lys His Leu Gly Ala His Asp Phe His Thr
 130 135 140
 Tyr Gln Ile Thr Gly Thr Trp Tyr Met His Phe Leu Asp Gly Leu Leu
 145 150 155 160
 Thr Phe Asn Gly Phe Leu Asp Leu Trp Gly Phe Pro Gln Glu Asn Pro
 165 170 175
 Ile Gly Gly Pro Val Leu Lys Glu Gly Asp Lys Phe Val Phe Leu Ser
 180 185 190
 Glu Pro Gln Phe Trp Ile Asn Leu Asn Arg Ile Lys Gly Ile Asp Lys
 195 200 205
 Asp Phe Asn Leu Ser Ile Gly Thr Glu Met Glu Ile Ser Arg Asn Phe
 210 215 220
 Ala Arg Met Asp Lys Phe Ser Cys Ile Pro Thr Leu Ala Val Lys Trp
 225 230 235 240

Thr Phe Asn

<210> 366

<211> 235

<212> PRT

<213> Porphyromonas gingivalis

<400> 366

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

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115          120          125
Thr Ala Arg Leu Ser Pro Tyr Val Ala Ala Gly Leu Ser Leu Gly Phe
130          135          140
Ala Ser Gly Ala Lys Gly Ser Ala Phe Ala Pro Gly Ile Thr Ala Gly
145          150          155          160
Met Gly Val Lys Tyr Lys Leu Lys Pro Arg Ile Asn Val Gly Ile Glu
165          170          175
Tyr Ser Phe Thr Gly Leu Leu Thr Asp Ala Leu Asp Ala Leu Thr Asp
180          185          190
Lys Ser Val Trp Leu Glu Asp Pro Tyr Lys Ile Asn Asp Ser Trp Val
195          200          205
Lys Asn Lys Asp Ala Thr Gly Ala Leu Val Leu Arg Ile Thr Tyr Asp
210          215          220
Phe Gly Leu Arg Lys Thr Phe Cys Asn Lys Gln
225          230          235
<210>      367
<211>      436
<212>      PRT
<213>      Porphyromonas gingivalis
<400>      367
Asn Ile Met Tyr Lys Asp Tyr Lys Gly Leu Tyr Ala Ser Leu Arg Trp
1          5          10          15
Tyr Ala Leu Ile Ile Gly Leu Leu Phe Ala Ala Asp Gly Ile Gln Ala
20          25          30
Gln Asn Asn Asn Phe Thr Glu Ser Pro Tyr Thr Arg Phe Gly Leu Gly
35          40          45
Arg Leu Gly Glu Arg Thr Thr Ile Ser Gly His Ser Met Gly Gly Leu
50          55          60
Gly Val Gly Leu Arg Gln Gly Thr Tyr Val Asn Ala Val Asn Pro Ala
65          70          75          80
Ser Tyr Ser Ala Val Asp Ser Met Thr Phe Ile Phe Asp Phe Gly Ala
85          90          95
Ser Thr Gly Ile Thr Trp Tyr Ala Glu Asn Gly Lys Lys Asp Asn Arg
100          105          110
Lys Met Gly Asn Ile Glu Tyr Phe Ala Met Leu Phe Pro Ile Ser Lys
115          120          125
Ser Ile Ala Met Ser Ala Gly Val Leu Pro Tyr Ser Ala Ser Gly Tyr
130          135          140
Gln Phe Gly Ser Val Asp Gln Val Glu Gly Gly Ser Val Gln Tyr Thr
145          150          155          160
Arg Lys Tyr Leu Gly Thr Gly Asn Leu Asn Asp Leu Tyr Val Gly Ile
165          170          175
Gly Ala Thr Pro Phe Lys Asn Phe Ser Ile Gly Ala Asn Ala Ser Ser
180          185          190
Leu Phe Gly Arg Phe Thr His Ser Arg Gln Val Ile Phe Ser Thr Glu
195          200          205
Ala Pro Tyr Asn Pro Val His Leu Ser Thr Leu Tyr Leu Lys Ala Ala
210          215          220
Lys Phe Asp Phe Gly Met Gln Tyr His Leu Leu Leu Lys Ser Asp Arg
225          230          235          240
Ser Leu Val Ile Gly Ala Val Tyr Ser Pro Arg Val Lys Met His Ser
245          250          255

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Glu Leu Thr Gln Ile Lys Asn Gln Val Gln Asn Gly Val Val Val Glu
 260 265 270
 Ser Glu Thr Gln Glu Tyr Ile Lys Gly Met Asp Tyr Tyr Thr Leu Pro
 275 280 285
 His Thr Leu Gly Ile Gly Phe Ser Tyr Glu Lys Lys Asp Lys Leu Leu
 290 295 300
 Leu Gly Ala Asp Val Gln Tyr Ser Lys Trp Lys Gly Glu Lys Phe Tyr
 305 310 315 320
 Lys Ser Asp Cys Lys Phe Gln Asp Arg Ile Arg Val Ser Leu Gly Gly
 325 330 335
 Glu Ile Ile Pro Asp Ile Asn Ala Val Gly Met Trp Pro Lys Val Arg
 340 345 350
 Tyr Arg Phe Gly Leu His Gly Glu Asn Ser Tyr Leu Lys Val Pro Thr
 355 360 365
 Lys Gly Gly Val Tyr Gln Gly Tyr His Ile Val Gly Ala Val Phe Gly
 370 375 380
 Ile Gly Ile Pro Leu Asn Asp Arg Arg Ser Phe Val Asn Val Ser Leu
 385 390 395 400
 Glu Tyr Asp Arg Leu Ile Pro Lys Glu Gly Met Ile Lys Glu Asn Ala
 405 410 415
 Leu Lys Leu Thr Phe Gly Leu Thr Phe Asn Glu Ser Trp Phe Lys Lys
 420 425 430
 Leu Lys Leu Asn
 435
 <210> 368
 <211> 945
 <212> PRT
 <213> Porphyromonas gingivalis
 <400> 368
 Asn Thr Ile Ser Glu Asn Gly Asn Asp Ser Thr Tyr Phe Ser Phe Gln
 1 5 10 15
 Thr Phe Leu Met Arg Ser Ile Tyr Gln Leu Leu Leu Ser Ile Leu Leu
 20 25 30
 Ala Ser Leu Gly Phe Val Gly Leu Glu Ala Gln Gln Ala Gly Val Ala
 35 40 45
 Gly Arg Val Leu Asp Glu Glu Gly Asn Pro Met Ile Gln Ala Asn Val
 50 55 60
 Gln Leu Val Gln Ser Thr Gly Gln Val Ala Val Ala Ala Gly Ala Thr
 65 70 75 80
 Asn Glu Lys Gly Leu Phe Ser Leu Lys Thr Ser Gln Glu Gly Asp Tyr
 85 90 95
 Ile Leu Arg Val Ser Tyr Val Gly Tyr Thr Thr His Asp Glu Lys Ile
 100 105 110
 Ser Leu Arg Asn Gly Gln Thr Ile Thr Leu Lys Asp Ile Ser Met Asn
 115 120 125
 Glu Asp Ala Arg Leu Leu Gln Ser Val Thr Val Gln Ala Lys Ala Ala
 130 135 140
 Glu Val Val Val Arg Asn Asp Thr Leu Glu Phe Asn Ala Gly Ser Tyr
 145 150 155 160
 Thr Val Ala Gln Gly Ala Ser Ile Glu Glu Leu Ile Lys Lys Leu Pro
 165 170 175
 Gly Ala Glu Ile Gly Ser Asp Gly Lys Ile Thr Ile Asn Gly Lys Asp

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

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        595                600                605
Asp Lys Leu Ala Phe Asn Arg Val Asn Leu Ser Pro Met Leu Arg Ile
 610                615                620
Asn Tyr Lys Pro Ser Arg Thr Thr Asn Leu Arg Val Asp Tyr Arg Gly
 625                630                635                640
Arg Thr Thr Gln Pro Ser Ile Asn Gln Ile Ala Pro Val Gln Asp Ile
        645                650                655
Thr Asn Pro Leu Phe Val Thr Glu Gly Asn Pro Gly Leu Lys Pro Ser
        660                665                670
Tyr Ser Asn Asn Val Met Ala Met Phe Ser Asp Phe Asp Ala Lys Ser
        675                680                685
Gln Arg Ala Phe Asn Ile Val Phe Phe Gly Asn Tyr Thr Phe Asp Asp
 690                695                700
Ile Val Pro Asn Thr His Tyr Asp Pro Ser Thr Gly Ile Arg Thr Thr
 705                710                715                720
Arg Tyr Glu Asn Ala Ser Gly Thr Trp Gln Ala Asn Leu His Gly Thr
        725                730                735
Leu Ser Leu Pro Leu Lys Asn Arg Ala Phe Ser Phe Arg Met Ser Leu
        740                745                750
Phe Asn Arg Leu Ala Glu Gly Gln Ser Phe Ile Asn Asp Asp Lys Asn
        755                760                765
Lys Ala Leu Ser Phe Arg Thr Arg Glu Arg Leu Thr Leu Thr Tyr Arg
 770                775                780
Asn Asn Trp Ile Asp Thr Ser Ile Gly Gly Asn Ile Gly Phe Tyr Met
 785                790                795                800
Ala Asn Asn Ser Leu Ser Gly Gln Lys Asp Ser Arg Thr Tyr Asp Phe
        805                810                815
Gly Gly Asn Tyr Gln Val Ala Leu Thr Leu Pro Tyr Gly Phe Arg Ile
        820                825                830
Asp Ser Asp Val Glu Tyr Asn Thr Asn Ser Gly Tyr Ser Gly Gly Phe
        835                840                845
Ser Leu Asp Glu Trp Leu Trp Asn Ala Ser Leu Ser Tyr Ser Phe Leu
 850                855                860
Arg Asp Lys Ala Gly Thr Leu Arg Val Asn Gly Tyr Asp Ile Leu Gly
 865                870                875                880
Gln Arg Ser Ser Ile Ser Arg Ser Ala Ser Ala Ile Asn Ile Glu Glu
        885                890                895
Ser Met Ser Asn Thr Ile Gly Arg Tyr Val Met Val Asp Phe Ile Tyr
        900                905                910
Arg Phe Asn Ala Phe Ser Gly Gly Ser Arg Ser Asp His Gln Arg
 915                920                925
Gly Asn Met Asn Arg Pro Gly Pro Pro Phe Gly Gly Gly Arg Arg Pro
 930                935                940
Ser
945
<210>    369
<211>    412
<212>    PRT
<213>    Porphyromonas gingivalis
<400>    369
Gly Glu Tyr Pro Ala Asn Ser Asn Asp Lys Lys Glu Met Val Met Lys
 1                5                10                15

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Leu Ile Lys Arg Ser Leu Leu Leu Leu Gly Ala Val Leu Leu Ile Thr
 20 25 30
 Leu Pro Ala Tyr Ser Gln Asn Asp Asp Ile Phe Glu Asp Asp Ile Tyr
 35 40 45
 Thr Ser Arg Lys Glu Ile Arg Lys Gln Asn Gln Val Lys Asp Trp Gln
 50 55 60
 Asn Gln Glu Asp Gly Tyr Gly Asp Asp Thr Glu Tyr Thr Val Ala Ser
 65 70 75 80
 Asp Arg Asp Ile Asp Ala Tyr Asn Arg Arg Asp Gly Gln Ser Tyr Asp
 85 90 95
 Gly Lys Lys Leu Ser Lys Asp Lys Lys Arg Asp Ser Thr Arg Ser Ser
 100 105 110
 Val Pro Gly Arg Tyr Ser Arg Arg Leu Ala Arg Phe Tyr Lys Pro Asn
 115 120 125
 Thr Ile Val Ile Ser Gly Ala Asp Asn Val Tyr Val Thr Asp Asp Gly
 130 135 140
 Glu Tyr Phe Val Tyr Gly Asp Glu Tyr Tyr Asp Asp Ala Ser Ser Val
 145 150 155 160
 Asn Ile Tyr Ile Asn Ser Pro Trp Cys Asp Pro Phe Pro Tyr Thr Ser
 165 170 175
 Trp Tyr Pro Ser Phe Ser Gly Trp Tyr Asn Tyr Thr Trp Asn Tyr Pro
 180 185 190
 Trp Phe Tyr Tyr Gly Ser His Ile Gly Trp Gly Gly Tyr Tyr Pro Gly
 195 200 205
 Tyr Asn Trp Tyr Trp Ser Tyr Tyr Tyr Asp Pro Phe Tyr Asn Pro Tyr
 210 215 220
 Gly Ile Gly Met Gly Trp Gly Tyr Pro Tyr Gly Trp Gly Ser Tyr Tyr
 225 230 235 240
 Gly Trp Gly Gly Tyr Pro Gly Val Ile His His Tyr His His Tyr Pro
 245 250 255
 Lys Lys Thr Tyr Ser Asn Gly Gln His Ser Gly Ala Tyr Tyr Ser Tyr
 260 265 270
 Gly Arg Pro Asn Arg Ile Lys Gly Gly Thr Ser Gly Ala Lys Leu Gly
 275 280 285
 Thr Gly Arg Tyr Asp Arg Ile Gln Asn Ser Ser Ser Gln Lys Asn Lys
 290 295 300
 Phe Gly Leu Gln Ser Asn Lys Pro Asn Asn Asn Leu Gln Asn Val Lys
 305 310 315 320
 Ser Gly Arg Thr Gly Arg Ala Asn Arg Asp Arg Asn Ile Glu Thr Val
 325 330 335
 Thr Pro Asn Asn Gly Gln Lys Gln Asn Arg Pro Val Phe Gln Gln Asn
 340 345 350
 Gln Ser Gly Asn Asp Arg Pro Thr Gly Arg Asn Ile Arg Ser Glu Arg
 355 360 365
 Gln Gly Glu Asn Asn Asp Arg Thr Phe Ser Thr Pro Ser Arg Ser Asn
 370 375 380
 Ser Asn Gly Gly Phe Ser Thr Pro Ser Arg Ser Ser Ser Gly Ser Met
 385 390 395 400
 Ser Gly Gly Gly Gly Arg Ser Gly Arg Gly Arg Asn
 405 410
 <210> 370
 <211> 601


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

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385                390                395                400
Tyr Gly Thr Gly Leu Arg Ile Asn Val Ser His Val Arg Gly Leu Asp
                405                410                415
Lys Lys Met Leu Lys Glu Asn Pro Asp Glu Leu Ile Gly Thr Asp Gly
                420                425                430
Tyr Thr Val Ser Phe Phe Gly Met Gly Asp Leu Tyr Tyr Ser Asp Ile
                435                440                445
Asp Val Glu Ile Thr Lys Lys Val Ser Pro Gly Phe Asn Phe Thr Leu
                450                455                460
Thr Tyr Leu Asn Gln Ile Tyr Asn Asn Lys Val Leu His Gly Ala Ala
465                470                475                480
Gly Glu Lys Pro Glu Lys Ile Tyr Ala Asn Ile Phe Val Tyr Asp Gly
                485                490                495
Lys Tyr Lys Leu Ser Asn Lys Val Ala Leu Arg Thr Glu Leu Gln Tyr
                500                505                510
Leu His Thr Lys Gln Asp Gln Gly Asp Trp Ile Tyr Gly Met Ala Glu
                515                520                525
Leu Ser Ile Leu Pro Ser Leu Met Leu Ser Leu Ser Glu Gln Tyr Asn
                530                535                540
Ile Gly Glu Thr Lys Lys His Tyr Val Met Gly Ser Val Thr Tyr Thr
545                550                555                560
His Gly Ala His Arg Val Ala Phe Ser Ala Gly Lys Thr Arg Ala Gly
                565                570                575
Met Asn Cys Ser Gly Gly Val Cys Arg Val Val Pro Glu Thr Gln Gly
                580                585                590
Phe Tyr Leu Ser Tyr Ser Thr Asn Leu
                595                600
<210>    371
<211>    252
<212>    PRT
<213>    Porphyromonas gingivalis
<400>    371
Arg Gly Ser Ser Ser Gly Ile Ser Ala Arg Gly Arg Asp Met Arg Ser
  1                5                10                15
Leu Phe Leu Ser Ala Leu Arg Ser Ser Ser Leu His Gly Ser Glu Arg
                20                25                30
Arg Ser Arg Ile Ser Ser Ser Val Val Met Ser Ile Arg Gln Lys Ile
                35                40                45
Arg Leu Phe His Leu Ser Val Cys Ala Gln Thr His Asp His Leu Ile
                50                55                60
Glu Ile His Leu Val Cys Ile Glu Phe Gly Ala Ile Asp Thr Asp Glu
  65                70                75                80
Phe Arg Leu Ser Ser His Ala Tyr Thr Thr Ser Pro Thr His Thr Gly
                85                90                95
Ala Ile His His Asn Cys Ile Glu Arg Ser Tyr Gly Arg Tyr Leu Val
                100                105                110
Thr Phe Gly Gln Glu Arg Asn Glu Leu His His His Ser Arg Pro Asp
                115                120                125
Arg Asn Ala Glu Val Tyr Arg Phe Pro Phe Asp Asn Ala Phe His Ser
                130                135                140
Ile Arg Tyr Glu Ala Phe Arg Pro Ile Arg Pro Ile Val Cys His Asp
145                150                155                160

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Asp His Phe Ile Ala Ile Gly Ser His Leu Phe Phe Lys Asp Asn Gln
      165                      170                      175
Ile Phe Ser Ser Gly Ser Gln Tyr Asp Asn Tyr Thr Val Ala Cys Phe
      180                      185                      190
Val Glu Ser Leu His Asp Arg Glu Gln Arg Ser His Thr His Thr Ala
      195                      200                      205
Ser Gly Thr Asn His Cys Ala Asp Leu Phe Asp Met Arg Thr Leu Ser
      210                      215                      220
Gln Arg Thr Tyr His Ile Arg Asp Ile Val Ala Asp Phe Glu Phe Gly
      225                      230                      235                      240
Gln Phe Leu Gly Arg Phe Ala His Gly Leu Asn His
      245                      250

<210>      372
<211>      790
<212>      PRT
<213>      Porphyromonas gingivalis
<400>      372
Leu Leu Phe Ser Ser Pro Leu Pro Arg Met Asp Arg Pro Lys Pro Ser
  1              5              10              15
Tyr Ile Val Arg Ile Ala Ala Ile Leu Cys Leu Phe Val Gly Arg Pro
      20              25              30
Leu Phe Ala Gln Ser Tyr Val Asp Tyr Val Asp Pro Leu Ile Gly Thr
      35              40              45
Leu Ser Ser Phe Glu Leu Ser Ala Gly Asn Thr Tyr Pro Val Ile Gly
      50              55              60
Leu Pro Trp Gly Met Asn Ser Trp Thr Pro Met Thr Gly Val Pro Gly
      65              70              75              80
Asp Gly Trp Gln Tyr Thr Tyr Ser Ala His Lys Ile Arg Gly Phe Lys
      85              90              95
Gln Thr His Gln Pro Ser Pro Trp Ile Asn Asp Tyr Gly Gln Phe Ser
      100             105             110
Leu Leu Pro Leu Thr Ala Pro Gln Lys Pro Ser Ser Asn Asp Ser Ile
      115             120             125
Ala Leu Thr Lys Trp Cys Lys Gln Leu Phe Ser Asp Glu Gln Thr Ser
      130             135             140
Trp Phe Ser His Lys Ala Glu Thr Ala Thr Pro Tyr Tyr Tyr Ser Val
      145             150             155             160
Tyr Leu Ala Asp Tyr Asp Thr Arg Val Glu Met Ala Pro Thr Glu Arg
      165             170             175
Ala Ala Ile Phe Arg Ile Arg Tyr Ser Gly Asn Thr Glu Ser Gly Ser
      180             185             190
Gly Arg Trp Leu Arg Leu Asp Ala Phe Thr Gly Gly Ser Glu Ile Ser
      195             200             205
Ile Val Asp Pro His Thr Val Val Gly Ile Ser Arg Lys Asn Ser Gly
      210             215             220
Gly Val Pro Ala Asn Phe Ala Cys Tyr Phe Ile Leu Gln Ser Asp Thr
      225             230             235             240
Pro Met Ala Asp Val Leu Leu Glu Thr Asp Thr Gly Lys Ser Asp Glu
      245             250             255
Gly Thr Arg Ala Trp Ala Ala Cys Arg Phe Asp Ser Gln Glu Val Thr
      260             265             270
Val Arg Val Ala Ser Ser Phe Ile Ser Val Glu Gln Ala Glu Arg Asn

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275	280	285
Leu Ala Glu Val Lys Gly Gln Ser Phe Asp Arg Ile Arg Leu Ala Gly		
290	295	300
Arg Glu Ala Trp Asn Lys Val Leu Gly Arg Ile His Val Glu Gly Gly		
305	310	315
Thr Lys Asp Glu Arg Thr Thr Phe Tyr Ser Ala Leu Tyr Arg Cys Leu		
325	330	335
Leu Phe Pro Arg Arg Phe Tyr Glu Glu Asp Ala Ser Gly Asn Phe Val		
340	345	350
His Tyr Ser Pro Tyr Asn Gly Glu Val Leu Pro Gly Tyr Leu Tyr Thr		
355	360	365
Asp Thr Gly Phe Trp Asp Thr Phe Arg Ala Leu Phe Pro Leu Leu Asn		
370	375	380
Leu Leu Tyr Pro Asp Glu Asn Ile Lys Ile Gln Glu Gly Leu Leu Asn		
385	390	395
Val Tyr Arg Glu Ser Gly Phe Phe Pro Glu Trp Ala Ser Pro Gly His		
405	410	415
Arg Asp Cys Met Ile Gly Asn Asn Ser Ala Ser Val Leu Ala Asp Ala		
420	425	430
Tyr Leu Lys Gly Val Arg Val Glu Asp Thr Arg Thr Leu Met Asn Gly		
435	440	445
Leu Leu His Ala Thr Lys Ala Val His Pro Lys Ile Ser Ser Thr Gly		
450	455	460
Arg Lys Gly Trp Glu Trp Tyr Asn Ser Leu Gly Tyr Val Pro Ala Asp		
465	470	475
Ala Gly Ile Asp Glu Ser Ala Ala Arg Thr Leu Glu Tyr Ala Tyr Asn		
485	490	495
Asp Trp Cys Ile Leu Arg Leu Gly Arg Thr Leu Gly Trp Asp Arg Ala		
500	505	510
Ala Leu Asp Thr Leu Ala His Arg Ser Met Asn Tyr Arg His Leu Phe		
515	520	525
Asp Pro Glu Thr Lys Leu Met Arg Gly Arg Asn Gln Asp Gly Ser Phe		
530	535	540
Arg Thr Pro Phe Ser Pro Phe Lys Trp Gly Asp Val Phe Thr Glu Gly		
545	550	555
Asn Ala Trp His Tyr Thr Trp Ser Val Phe His Asp Val Gln Gly Leu		
565	570	575
Ile Asp Leu Met Gly Gly Asp Arg Pro Phe Val Ser Met Leu Asp Ser		
580	585	590
Val Phe Asn Thr Pro Pro Met Phe Asp Glu Ser Tyr Tyr Gly Phe Val		
595	600	605
Ile His Glu Ile Arg Glu Met Gln Ile Ala Asp Met Gly Asn Tyr Ala		
610	615	620
His Gly Asn Gln Pro Ile Gln His Met Ile Tyr Leu Tyr Asn His Ala		
625	630	635
Gly His Pro Trp Lys Ala Gln Glu Arg Leu Arg Glu Val Met Gly Arg		
645	650	655
Leu Tyr Arg Pro Thr Pro Asp Gly Tyr Cys Gly Asp Glu Asp Asn Gly		
660	665	670
Gln Thr Ser Ala Trp Tyr Val Phe Ser Ala Leu Gly Phe Tyr Pro Val		
675	680	685
Thr Pro Ala Thr Asp Gln Tyr Val Leu Gly Ser Pro Ile Phe Ser Lys		

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        690                695                700
Val Ile Leu Ser Phe Pro Asp Gly His Lys Thr Val Leu His Ala Pro
705                710                715                720
Ala Asn Ser Ala Asp Thr Pro Tyr Ile Arg Ser Ile Ser Val Glu Gly
        725                730                735
Lys Glu Trp Ser Cys Asn Tyr Leu Thr His Glu Gln Leu Arg Ser Ser
        740                745                750
Ala Ser Ile Gln Trp Met Met Asp Thr Lys Pro Asn Tyr Asn Arg Gly
        755                760                765
Met Lys Glu Ser Asp Arg Pro Tyr Ser Phe Ser Thr Glu Gln Gln Arg
        770                775                780
Arg Ala Asn His Ser Asn
785                790
<210>      373
<211>      286
<212>      PRT
<213>      Porphyromonas gingivalis
<400>      373
Ile Cys Gly Ser Lys Met Asn Leu Ser Gly Leu Gln Ser Phe Thr Met
  1                5                10                15
Met Lys Ser Met Arg Ser Val Leu Leu Leu Leu Phe Pro Leu Ser Leu
        20                25                30
Ile Thr Ala Leu Gly Cys Ser Asn Lys Ala Ala Glu Ser Lys Ser
        35                40                45
Val Ser Phe Asp Ser Ala Tyr Leu Glu Arg Tyr Ile Pro Leu Arg Ala
        50                55                60
Asp Ile Asp Thr Pro Ser Leu His Val Met Ile Ser Tyr Val Tyr Pro
        65                70                75                80
Ser Gly Asp Asp Met Leu Thr Glu Ile Phe Asn Gly Leu Leu Phe Gly
        85                90                95
Asp Ser Leu Met Asp Ser Ser Ser Pro Glu Asn Ala Met Glu Gly Tyr
        100               105               110
Ala Gln Met Leu Gly Glu Asp Tyr Arg Ser Asn Asn Ala Glu Ala Asn
        115               120               125
Leu Gln Gly Leu Pro Ser Asp Leu Leu Asp Tyr Ile Tyr Lys Gln Glu
        130               135               140
Asn Thr Ile Ala Tyr Cys Asp Thr Gly Leu Ile Ser Thr Arg Ile Asn
        145               150               155               160
Thr Tyr Thr Tyr Glu Gly Gly Ala His Thr Glu Asn Thr Val Arg Phe
        165               170               175
Ala Asn Ile Leu Arg Thr Thr Gly Lys Val Leu Glu Glu Arg Asp Ile
        180               185               190
Phe Lys Ile Asp Tyr Ala Glu Arg Leu Ser Ala Leu Ile Ile Gly Gln
        195               200               205
Leu Val His Asp Phe Gly Lys Thr Thr Pro Ala Glu Leu Asp Ala Ile
        210               215               220
Gly Phe Phe Asn Ala Glu Glu Ile Gln Pro Asn Gly Asn Phe Met Ile
        225               230               235               240
Asp Asp Lys Gly Leu Thr Tyr Cys Phe Asn Glu Tyr Gln Ile Ala Ala
        245               250               255
Tyr Ala Arg Gly Ala Val Tyr Val Arg Leu Gly Tyr Asp Val Leu Ala
        260               265               270

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Pro Leu Leu Arg Asp Asp Ser Pro Leu Lys Arg Tyr Leu Pro
 275 280 285
 <210> 374
 <211> 378
 <212> PRT
 <213> Porphyromonas gingivalis
 <400> 374
 Gly Ile Ile Ser Val Leu Ser His Val Val Asp Arg Pro Gln Trp Gly
 1 5 10 15
 Ala Ser Pro Glu Ala Ala Gly Thr His Ser Val Tyr Ser Ile Leu His
 20 25 30
 Pro Ser Ala Gly Ile Ile Arg Ile Arg Ser Met Gly Ile Ile Ser Ala
 35 40 45
 Cys Arg Ile Ala Ile Leu Ala Gly Lys His Pro Arg Ser Gly Leu Ser
 50 55 60
 Arg Ala Asn Val Gly Ile Leu Ser Tyr Asn Pro Glu Asn Thr Pro Glu
 65 70 75 80
 Lys Lys Arg Lys Leu Gln Glu Lys Asn Val Phe Leu Gln Ile Arg Leu
 85 90 95
 Arg Gln Ser Phe Asn Asn Leu Ile Pro Ser Leu Pro Phe Arg Ile Asp
 100 105 110
 Asn Thr Lys Lys Ile Thr Glu Met Lys Lys Thr Thr Leu Thr Gly Ser
 115 120 125
 Ile Cys Ala Leu Leu Leu Phe Leu Gly Leu Ser Ala Asn Ala Gln Ser
 130 135 140
 Lys Leu Lys Ile Lys Ser Ile Glu Ala Ala Thr Thr Phe Ser Ser Ala
 145 150 155 160
 Thr Ala Gly Asn Gly Phe Gly Gly Asn Ile Phe Gly Met Asp Met Ser
 165 170 175
 Ile Arg Met Arg Val His His Ser Ile Leu Pro Glu Gly Leu Asp Phe
 180 185 190
 Ser Val Gly Ile His Glu Arg Arg Ala His Trp Glu Glu Ala Gly Ser
 195 200 205
 Pro Lys Leu Met Tyr Thr Asn Val Pro Ser Ile Ile Gly Ile Val Glu
 210 215 220
 Lys Val Ile Val Phe Glu Asp Ala Glu Asp Phe Phe Asp Lys Lys Ala
 225 230 235 240
 Leu Gly Arg Phe Leu Ile Ser Leu Gly Ile Ser Tyr Thr Lys His Leu
 245 250 255
 Gly Ala Tyr Trp Gly Trp Thr Asn Asp Ala His Ile Leu Phe Ser Pro
 260 265 270
 Ile Pro Lys Ser Lys Val His Tyr Asp Thr Tyr Thr Arg Ala Gly Ser
 275 280 285
 Asp Leu Val Leu Gln Ser Glu Asp Val Ala Thr Val Ser Asn Gly Phe
 290 295 300
 Ser Pro Gly Ile Gly Leu Lys Ser Ser Ile Trp Trp Lys Met Pro Ile
 305 310 315 320
 Lys Ser Lys Tyr Asp Phe Arg Leu Gly Phe Ser Leu Gly Tyr Glu Tyr
 325 330 335
 Leu Asn Leu Leu Tyr Pro Tyr Arg Asn Phe Lys Leu Asp Gly Asn Lys
 340 345 350
 Pro Leu Ser Ala Leu Ser Pro Arg Met Asn His Ile Gly His Val Gly

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          355              360              365
Phe Asn Phe Thr Val Gly Leu Trp Thr Asn
    370              375
<210>    375
<211>    1269
<212>    PRT
<213>    Porphyromonas gingivalis
<400>    375
Val Lys Cys Met Gly Lys Tyr Lys Arg Ala Lys Tyr Arg Tyr Trp Leu
  1          5          10          15
Phe Pro Phe Cys Ser Asp Tyr Tyr Thr Phe Glu Gly Val Thr Phe Leu
    20          25          30
Cys Ala Ser Asp Asp Met Thr Thr Lys Lys Pro Gln Ala Ile Leu Asp
    35          40          45
Leu Glu Lys Ala Tyr Asn Ile Glu Ile Pro Asp Leu Ser Ser Gln Glu
    50          55          60
Gly Ile Ser Trp Ser Val Asn Arg Tyr Phe Lys Gln Asp Ser Ser Gly
    65          70          75          80
Ala Val Val Glu Leu Cys Leu Arg Glu Cys Gln Ile Glu Ser Met Thr
    85          90          95
Trp Leu Ile Asp Phe Pro Ala Leu Lys Lys Leu Asp Leu Ser Tyr Asn
    100          105          110
Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Thr Lys
    115          120          125
Leu Arg Leu Arg Ser Asn Gln Ile Arg Lys Leu Glu Gly Leu Asp Ser
    130          135          140
Leu Thr Ser Leu Thr Lys Leu Ser Leu Ser Asp Asn Gln Ile Ser Lys
    145          150          155          160
Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Ala Glu Leu Tyr Leu Leu
    165          170          175
Asp Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu
    180          185          190
Ala Thr Leu Glu Leu Ser Gly Asn Gln Ile Arg Lys Leu Glu Gly Leu
    195          200          205
Glu Arg Leu Thr Ser Leu Ala Thr Leu Glu Leu Ser Gly Asn Gln Ile
    210          215          220
Arg Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Thr Lys Leu Arg
    225          230          235          240
Leu Arg Ser Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr
    245          250          255
Ser Leu Ala Thr Leu Glu Leu Ser Gly Asn Gln Ile Arg Lys Leu Glu
    260          265          270
Gly Leu Glu Arg Leu Thr Ser Leu Ala Thr Leu Glu Leu Ser Gly Asn
    275          280          285
Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Ser Ser Leu Thr Lys
    290          295          300
Leu Arg Leu Arg Ser Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg
    305          310          315          320
Leu Thr Ser Leu Thr Lys Leu Ser Leu Ser Asp Asn Gln Ile Ser Lys
    325          330          335
Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Ala Glu Leu Tyr Leu Leu
    340          345          350

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

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Glu Tyr Leu Gln Thr Glu Leu Asn Gln Leu Ser Leu Arg Gly Glu Val		
770	775	780
Leu Tyr Tyr Arg Glu Asn Glu Lys Leu Asn Asn Tyr Val Trp Leu Asp		
785	790	795 800
Pro Ala Ala Phe Val Gln Met Ile His Gly Glu Ile Leu Gln Lys Asp		
	805	810 815
Asn Ile Asn Arg Gly Thr Val Pro Lys Asp Ile Phe Glu Cys Lys Leu		
	820	825 830
His Asn Leu Ser Ser Gly Ser Ile Phe Glu Glu Asp Gly Gln Asn Gly		
	835	840 845
Asn Met Ile Leu Gln Leu Leu Leu Glu Glu Leu Ile Val Tyr Glu Asp		
	850	855 860
Lys Asp Cys Tyr Val Ile Pro Gly Tyr Leu Pro Leu His Ser Asp Asp		
865	870	875 880
Glu Ala Tyr Lys Trp Leu Thr Leu Gly Phe Glu Arg Pro Asn Phe Val		
	885	890 895
Leu Lys Phe Glu Arg Phe Ile Pro Phe Gly Leu Ile Asn Gln Ile Ile		
	900	905 910
Ala Tyr Tyr Gly Arg Glu Glu Gly Ala Leu Lys Arg Tyr Trp Arg Asp		
	915	920 925
Gln Val Ile Phe Thr Ala Gly Arg Glu Met Asp Arg Gln Thr Leu Glu		
	930	935 940
Gln Glu Glu Glu Lys Glu Gly Leu Pro Lys Thr Asn Ala Glu Asp Tyr		
945	950	955 960
Gln Ile Trp Ile Lys Leu Asp Phe Thr Asp Leu Ala Ile Ser Val Phe		
	965	970 975
Ile Lys Glu Gln Arg Lys Thr Ser Ala Lys Asp Met Gln Arg Lys Glu		
	980	985 990
Ala Thr Ile Leu Ser Asp Met Leu Asp Met Tyr Trp Asn Asn Ile Pro		
	995	1000 1005
Pro Arg Glu Gln Ile Gly Asp Lys Asp Thr Glu Gln Thr Arg Ser Thr		
1010	1015	1020
Ile Arg Glu Thr Asn Arg Lys Lys Arg Pro Ile Gln Asp Leu Tyr Leu		
1025	1030	1035 1040
Ser Cys Ala Gln Ala Asp Lys Asp Leu Thr Glu Ser His Tyr Ile His		
	1045	1050 1055
Leu Gly Thr Leu Asp Asp Glu Ser Lys Thr Thr Ala Arg Ile Ala Ala		
	1060	1065 1070
Tyr Pro Leu Lys Asn Gly Val Ile Asp Lys Glu Arg Val Arg Glu Val		
	1075	1080 1085
Ser Thr Arg Pro Tyr Lys His Leu Ser Val Asn Lys Asn Leu Ala Thr		
1090	1095	1100
Ala Lys Gln Ile Phe Ile Ser Tyr Ser Lys Glu Asp Gln Thr Glu Leu		
1105	1110	1115 1120
Glu Thr Cys Leu Gln Phe Phe Lys Pro Leu Glu Lys Asn Gly Gln Ile		
	1125	1130 1135
Glu Ile Tyr Tyr Asp Lys Leu Thr Lys Phe Glu Thr Pro Ile His Pro		
	1140	1145 1150
Glu Ile Arg Lys Arg Ile Val Glu Ala Asp Cys Ile Ile Ala Leu Ile		
	1155	1160 1165
Ser Gln Arg Tyr Leu Ala Thr Asp Tyr Ile Leu Asp His Glu Leu Pro		
1170	1175	1180

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Val Phe Arg Glu Tyr Asn Lys Thr Ile Val Pro Ile Leu Ile Lys Pro
1185          1190          1195          1200
Cys Thr Phe Glu Asp Asp Glu Phe Leu Arg Glu Lys Tyr Phe Ala Gln
          1205          1210          1215
Lys Ala Gln Ile Ile Asn Leu Gly Lys Glu Gly Lys Thr Ile Lys Ala
          1220          1225          1230
Tyr Asp Ser Ile Thr Ala Ser Ala His Arg Asp Glu Asn Trp Val Ala
          1235          1240          1245
Val Val Arg Glu Phe Lys Glu Lys Ile Leu Arg Ile Thr Lys Gln Glu
          1250          1255          1260
Val Asn Thr Asp Glu
1265
<210>      376
<211>      231
<212>      PRT
<213>      Porphyromonas gingivalis
<400>      376
Lys Phe Met Met Lys Lys Ala Phe Val Phe Val Leu Leu Val Cys Leu
  1           5           10           15
Phe Ser Ser Phe Ser Ser Ser Ala Gln Thr Thr Thr Asn Ser Ser Arg
          20           25           30
Ser Tyr Phe Thr Gly Arg Ile Glu Lys Val Ser Leu Asn Leu Gly Val
          35           40           45
Pro Pro Val Ser Thr Glu Val Trp Gly Met Thr His Asp Ala Asn Gly
          50           55           60
Leu Pro Phe Glu Ile Pro Ile Ser Phe Ser Arg Phe Asn Ser Gln Gly
          65           70           75           80
Asp Ile Ala Thr Thr Tyr Tyr Ile Ala Asn Ser Glu Ala Thr Leu Asn
          85           90           95
Glu Trp Cys Asp Tyr Ala His Pro Gly Gly Ile Val Arg Val Glu Gly
          100          105          110
Arg Phe Trp Lys Met Thr Tyr Asn Ile Pro Thr Tyr Asn Ala Val Cys
          115          120          125
Thr Arg Ile Thr Phe Glu Asn Gln Glu Ile Glu Gly Thr Ile Val Leu
          130          135          140
Ile Pro Lys Pro Lys Val Ser Leu Pro His Val Ser Glu Ser Val Pro
          145          150          155          160
Cys Ile Arg Thr Glu Ala Gly Arg Glu Phe Ile Leu Cys Glu Glu Asp
          165          170          175
Asp Thr Phe Val Ser His Asp Gly Asn Glu Val Thr Ile Gly Gly Lys
          180          185          190
Pro Phe Leu Leu Asn Thr Asn Val Lys Ile Val Gly Asp Val Ser Gln
          195          200          205
Lys Tyr Ala Val Gly Val Gly Glu Ile Arg Phe Leu Gln Ile Cys Ala
          210          215          220
Gln Thr Val Ser Gln Gln Lys
225          230
<210>      377
<211>      563
<212>      PRT
<213>      Porphyromonas gingivalis
<400>      377

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

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Asn Tyr Asp Lys Ile His Asn Lys Asp Leu Trp Ser Asp Thr Phe Thr
    420                      425                      430
Tyr Thr Ser Ser Ala Asn Ala Leu Tyr Thr Pro Gln Val Asp Ile Asn
    435                      440                      445
Pro Thr Lys Gly Leu Val Cys Trp Ser Trp Val Glu Tyr Leu Pro Gly
    450                      455                      460
Lys Arg Ile Val Trp Ser Asp Thr Gln Trp Thr His Ala Asn Gly Val
    465                      470                      475                      480
Glu Asp Ile Val Met Gln Glu Gly Ser Met Lys Leu Tyr Pro Asn Pro
    485                      490                      495
Ala Gln Glu Tyr Ala Val Ile Ser Leu Pro Thr Ala Ala Asn Cys Lys
    500                      505                      510
Ala Val Val Tyr Asp Met Gln Gly Arg Val Val Ala Glu Ala Ser Phe
    515                      520                      525
Ser Gly Asn Glu Tyr Arg Leu Asn Val Gln His Leu Ala Lys Gly Thr
    530                      535                      540
Tyr Ile Leu Lys Val Val Ser Asp Thr Glu Arg Phe Val Glu Lys Leu
    545                      550                      555                      560
Ile Val Glu
<210>      378
<211>      786
<212>      PRT
<213>      Porphyromonas gingivalis
<400>      378
Ile Val Tyr Leu Cys His Cys Met Asn His Arg Arg Ser Lys Thr Met
  1                      5                      10                      15
Leu Thr Ile Arg Asn Phe Leu Leu Phe Cys Cys Leu Ser Leu Ile Ala
    20                      25                      30
Phe Ala Ala Asp Ala Gln Ser Ser Val Ser Ser Gly Arg Arg Leu Thr
    35                      40                      45
Glu Tyr Val Asn Pro Phe Ile Gly Thr Ala Asn Tyr Gly Thr Thr Asn
    50                      55                      60
Pro Gly Ala Val Leu Pro Asn Gly Leu Met Ser Val Thr Pro Phe Asn
    65                      70                      75                      80
Val Ser Gly Ser Thr Glu Asn Arg Phe Asp Lys Asp Ser Arg Trp Trp
    85                      90                      95
Ser Ala Pro Tyr Ser Ala Asp Asn Ser Tyr Cys Ile Gly Phe Ser His
    100                      105                      110
Val Asn Leu Ser Gly Val Gly Cys Pro Glu Leu Ser Gly Ile Leu Leu
    115                      120                      125
Met Ala Thr Ser Gly Thr Phe Asp Pro Asp Tyr Cys Cys Tyr Gly Ser
    130                      135                      140
Ser Leu Ser Arg Glu Tyr Ala Arg Pro Gly Glu Tyr Lys Ala Val Leu
    145                      150                      155                      160
Asp Lys Tyr Gly Ile Asp Ala Ala Val Thr Val Thr Glu Arg Thr Ala
    165                      170                      175
Leu Thr Glu Phe Ala Phe Pro Glu Gly Glu Gly His Ile Leu Leu Asn
    180                      185                      190
Leu Gly Gln Ala Leu Ser Asn Glu Ser Gly Ala Ser Val Arg Phe Leu
    195                      200                      205
Asn Asp Ser Thr Val Val Gly Ser Arg Leu Met Gly Thr Phe Cys Tyr
    210                      215                      220

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

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Glu Pro Asp Ile Ala Tyr Pro Tyr Leu Phe Ser Tyr Phe Pro Lys Glu
 645 650 655
 Ala Trp Arg Thr Gln Lys Leu Thr Arg Glu Leu Ile Asp Lys His Phe
 660 665 670
 Cys Asn Ala Pro Asn Gly Leu Pro Gly Asn Asp Asp Ala Gly Thr Met
 675 680 685
 Ser Ala Trp Leu Val Tyr Ser Met Leu Gly Phe Tyr Pro Asp Cys Pro
 690 695 700
 Gly Ser Pro Thr Tyr Thr Leu Thr Ser Pro Val Phe Pro Arg Val Arg
 705 710 715 720
 Ile Arg Leu Asn Pro Gln Tyr Tyr Pro Gln Gly Glu Leu Ile Ile Thr
 725 730 735
 Thr Asn Thr Glu Asn Gln Pro Thr Asp Ser Ile Tyr Ile His Thr Val
 740 745 750
 Ser Leu Gly Asn Lys Thr Leu Pro His Gly Thr Arg His Ile Ser His
 755 760 765
 Ala Asp Leu Val Arg Cys Gly His Leu Arg Tyr Glu Leu Ser Asn Arg
 770 775 780
 Pro Arg
 785
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 <211> 814
 <212> PRT
 <213> Porphyromonas gingivalis
 <400> 379
 Pro Arg Phe His Pro Gly Gly Thr His Ala Gln Leu Cys Arg Asn Gly
 1 5 10 15
 Arg Arg Asn Gln Lys Ser Asn Gln Ser Ser Cys Phe Gly Gly Gly Thr
 20 25 30
 Ala Pro Arg Phe Phe Ile Met Cys Lys Ile Arg Phe Ser Leu Leu Gln
 35 40 45
 Ala Leu Val Val Cys Leu Leu Phe Thr Ser Phe Ser Leu Gln Ala Gln
 50 55 60
 Glu Glu Gly Ile Trp Asn Thr Leu Leu Ala Ile His Lys Thr Glu Lys
 65 70 75 80
 Ala Val Glu Thr Pro Lys Lys Val Phe Ala Val Ala Asn Gly Val Leu
 85 90 95
 Tyr Ser Val Gly Lys Glu Ala Pro His Glu Ala Lys Ile Phe Asp Arg
 100 105 110
 Ile Ser Gly Leu Ser Asp Thr Ser Val Ser Ser Ile Ala Tyr Ser Glu
 115 120 125
 Gln Leu Lys Ser Leu Val Ile Tyr Tyr Ala Ser Gly Asn Ile Asp Ile
 130 135 140
 Leu Asp Glu Ala Gly Arg Val Thr Asn Val Pro Ala Leu Lys Asp Asn
 145 150 155 160
 Ile Asp Leu Ile Asp Lys Thr Leu Asn Arg Leu Leu Ile Val Gly Asn
 165 170 175
 Arg Ala Tyr Leu Ala Gly Gly Phe Gly Leu Ser Val Leu Asp Val Ala
 180 185 190
 Glu Ala Arg Ile Pro Ala Thr Tyr Ala Lys Gly Thr Lys Val Thr Asp
 195 200 205
 Val Ala Lys Leu Asp Asn Asp Arg Leu Leu Met Leu Lys Glu Gly Gln

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

625						630						635						640
Leu	Asp	Lys	Val	Thr	Val	Thr	Asp	Ile	Val	Val	Asp	Lys	Leu	Asn	His			
				645				650				655						
Lys	Trp	Val	Ala	Thr	Gln	Gly	Thr	Gly	Leu	Tyr	Leu	Leu	Ser	Glu	Asp			
				660				665				670						
Cys	Ser	Lys	Ile	Leu	Ala	Gln	Phe	Thr	Val	Glu	Asn	Ser	Pro	Leu	Leu			
				675				680				685						
Ser	Asn	Asn	Ile	Leu	Ser	Leu	Ala	Leu	Asn	Asp	Asp	Asn	Gly	Leu	Leu			
				690				695				700						
Tyr	Ile	Gly	Thr	Ala	Asp	Gly	Leu	Met	Thr	Phe	Gln	Thr	Gly	Thr	Gly			
705				710				715				720						
Ser	Gly	Ser	Ala	Ser	Glu	Leu	Asp	Gly	Val	Tyr	Val	Tyr	Pro	Asn	Pro			
				725				730				735						
Leu	Arg	Pro	Glu	Tyr	Pro	Asp	Gly	Val	Thr	Ile	Ala	Gly	Leu	Gln	Ala			
				740				745				750						
Gly	Cys	Ser	Val	Lys	Ile	Thr	Asp	Thr	Thr	Gly	Arg	Leu	Leu	Tyr	Gln			
				755				760				765						
Thr	Glu	Ser	Val	Thr	Thr	Glu	Val	Lys	Trp	Asn	Ala	Arg	Gly	Ala	Asp			
				770				775				780						
Gly	Asn	Arg	Val	Ala	Ser	Gly	Val	Tyr	Ala	Val	Ala	Val	Tyr	Asp	Pro			
785				790				795				800						
Val	Ser	Lys	Lys	Ser	Lys	Leu	Ile	Arg	Phe	Ala	Val	Ile	Arg					
				805				810										
<210>		380																
<211>		1162																
<212>		PRT																
<213>		Porphyromonas gingivalis																
<400>		380																
Ala	Ile	Ser	Gln	Met	Lys	Arg	Ile	Leu	Pro	Ile	Val	Ala	Phe	Leu	Ser			
1					5					10					15			
Leu	Phe	Leu	Ala	Leu	Ala	Leu	Pro	Ala	Lys	Ala	Gln	Arg	Ala	Met	Gly			
				20				25				30						
Lys	Thr	Ala	Asp	Arg	Ser	Leu	Met	Ala	Ser	Gly	His	Trp	Val	Lys	Ile			
				35				40				45						
Arg	Val	Asp	Ala	Ser	Gly	Val	Tyr	Arg	Leu	Thr	Asp	Glu	Gln	Leu	Arg			
				50				55				60						
Ala	Asn	Gly	Phe	Ser	Asp	Pro	Ser	Lys	Val	Gly	Val	Phe	Gly	Tyr	Gly			
65				70				75				80						
Gly	Gly	Val	Leu	Pro	Glu	Asp	Leu	Ser	Arg	Ile	Thr	Thr	Asp	Asp	Leu			
				85				90				95						
Pro	Pro	Val	Pro	Val	Leu	Arg	Gln	Gly	Asn	Ala	Leu	Tyr	Phe	Tyr	Ala			
				100				105				110						
Val	Gly	Pro	Val	Thr	Trp	Phe	Tyr	Asn	Pro	Ala	Lys	Thr	Thr	Met	Glu			
				115				120				125						
His	Thr	Val	Asn	Thr	Tyr	Ser	Thr	His	Gly	Tyr	Tyr	Phe	Leu	Ser	Asp			
130				135				140										
Ala	Ala	Gly	Ala	Pro	Leu	Gln	Met	Ser	Gln	Tyr	Thr	Gly	Gly	Gly	Ala			
145				150				155				160						
Ser	Ala	Glu	Ala	Leu	Ile	Asp	Tyr	Tyr	Asp	Glu	Leu	Met	Leu	His	Glu			
				165				170				175						
Gln	Glu	Leu	Tyr	Ser	Pro	Lys	Glu	Ser	Gly	Arg	Asp	Leu	Tyr	Gly	Glu			
				180				185				190						

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

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

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Ala Leu Ala Glu Gly Asp His Thr Ala Arg Leu Thr Val Trp Asp Ile
1025 1030 1035 1040
Phe Asn Asn Ala Val His His Asp Phe Ser Phe Arg Val Val Asp Gly
1045 1050 1055
Ile Ala Pro Asp Val Ala Asp Val Ile Leu Phe Pro Asn Pro Val Arg
1060 1065 1070
Glu Ser Ala Thr Phe Arg Ile Phe His Asn Arg Pro Gly Ser Asp Leu
1075 1080 1085
Asn Val Ala Val Glu Ile Tyr Asp Phe Thr Gly Arg Leu Val Asn Ser
1090 1095 1100
Leu Pro Val Lys Thr Tyr Ser Ser Ser Tyr Gly Glu Pro Ile Glu Ile
1105 1110 1115 1120
Lys Trp Asp Leu Thr Ser Lys Tyr Gly Val Lys Ile Gly Asn Gly Phe
1125 1130 1135
Tyr Leu Tyr Arg Cys Val Val Asn Ser Pro Gly Gly Gln Thr Ala Ser
1140 1145 1150
Met Ala Lys Lys Met Ile Val Val Gly Gln
1155 1160
<210> 381
<211> 973
<212> PRT
<213> Porphyromonas gingivalis
<400> 381
Phe Tyr Thr Gly Ile Asp Leu His Ile Glu Ser Gln Met Lys Lys Leu
1 5 10 15
Phe Pro Leu Leu Leu Leu Ile Leu Ser Ile Leu Val Gly Cys Gly Lys
20 25 30
Lys Glu Lys His Ser Val Thr Glu Ile Ala Arg Glu Lys Lys Arg Ile
35 40 45
Thr Ala Leu Leu Tyr Glu Lys Glu Leu Pro Thr Asp Ser Val Lys Gln
50 55 60
Leu Tyr Glu Asn Ser Val Gln Asn Lys Asn Leu Val Gly Gln Met Leu
65 70 75 80
Phe Ala Ile Glu Val Gly Lys Arg Met Arg Asn Met Ser Gln Tyr Thr
85 90 95
Asp Ala Met Leu Tyr His Gln Lys Gly Leu Asn Ala Ala Leu Asn Leu
100 105 110
Arg Asp Thr Ile Val Ala Ala Gln Ala Trp Asn His Leu Gly Thr Asp
115 120 125
Ser Arg Arg Ile Gly Ala Leu Ala Glu Ala Ser Asp Tyr His Tyr Lys
130 135 140
Ala Leu Ser Leu Ile Glu Ser Phe Ser Gly Asn Gln Asn Arg Pro Ala
145 150 155 160
Ile Lys Ala Arg Ser Ala Ala Leu Asn Gly Ile Gly Asn Ile Asn Leu
165 170 175
Glu Leu Gly Tyr His Asp Glu Ala Glu Lys Asn Phe Leu Lys Ala Leu
180 185 190
Gln Gly Glu Lys Glu Leu Asp Ser Pro Leu Gly Gln Ala Ile Asn Tyr
195 200 205
Ala Asn Leu Gly Arg Ile Tyr Arg Gln Arg Lys Glu Tyr Asp Lys Ala
210 215 220
Arg Thr Tyr Phe Leu Leu Ser Leu Glu Gln Asn Asn Met Ala Glu Asn

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

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        645                650                655
Ile Ser Ile Pro Thr Gln Asn Gln Ser Ser Ser Ala Glu Ile Leu Pro
        660                665                670
Trp Leu Pro Ser Ser Asp Asp Ile Val Met Pro Val His Ile Ala Pro
        675                680                685
Asp Asp Ser Pro Thr Ser Pro Met Val Ala Ala Leu Asn His Arg Phe
        690                695                700
Glu Asp Glu Arg Pro Thr Ile Leu Leu Val Glu Asp Asn Lys Asp Ile
705                710                715                720
Asn Leu Leu Val Lys Leu Leu Leu Cys Asp Arg Tyr Asn Val Leu Ser
        725                730                735
Ala Ala Asn Gly Lys Glu Gly Ile Ala Leu Ala Thr Glu His Ile Pro
        740                745                750
Asp Ile Ile Ile Thr Asp Ile Met Met Pro Ile Met Asp Gly Ile Glu
        755                760                765
Met Thr Ile Arg Met Lys Gln Ser Pro Leu Leu Cys His Ile Pro Ile
        770                775                780
Val Ala Leu Thr Ala Lys Ser Thr Glu Gln Asp Arg Leu Glu Gly Ile
785                790                795                800
Lys Ser Gly Val Val Ser Tyr Leu Cys Lys Pro Phe Ser Pro Glu Glu
        805                810                815
Leu Leu Met Arg Ile Glu Gln Leu Leu Lys Asp Arg Glu Leu Leu Lys
        820                825                830
Lys Phe Tyr Met Gln Lys Leu Met Leu Asp Arg Lys Pro Glu Glu Glu
        835                840                845
Pro Gln Pro Ile Asp Asp Ser Ser Met Gln Phe Leu Leu Ala Ala Lys
        850                855                860
Asp Ala Val Ser Gly Gly Ile Lys Gln Asn Pro Asp Phe Ser Ala Gln
865                870                875                880
Asp Leu Ala Glu Lys Met Cys Met Ser Pro Ser Gln Leu Asn Arg Lys
        885                890                895
Leu Thr Ser Val Val Gly Cys Ser Thr Ile Gly Tyr Ile Gln Gln Ile
        900                905                910
Lys Ile Lys Leu Ala Cys Lys Leu Leu Ala Asp Glu Ser Lys Asn Ile
        915                920                925
Ser Asp Ile Ser Ile Glu Ala Gly Phe Ser Asp Pro Ala Tyr Phe Ser
        930                935                940
Arg Thr Phe Lys Arg Tyr Met Asn Cys Ser Pro Ser Gln Tyr Arg Gln
945                950                955                960
Lys Leu Leu Ala Met Pro Gly Ser Asp Lys Glu Thr Val
        965                970

<210>      382
<211>      563
<212>      PRT
<213>      Porphyromonas gingivalis
<400>      382
His His Lys Thr Tyr Gln Thr Met Lys Lys Leu Leu Gln Ala Lys Ala
  1                5                10                15
Leu Ile Leu Ala Leu Gly Leu Phe Gln Leu Pro Ala Ile Ala Gln Thr
        20                25                30
Gln Met Gln Ala Asp Arg Thr Asn Gly Gln Phe Ala Thr Glu Glu Met
        35                40                45

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

Phe Lys Phe Thr Cys Met Asn Glu Thr Asn Thr Cys Thr Val Thr Gly
 465 470 475 480
 Ala Ala Lys Ala Leu Arg Ala Trp Phe Asn Ala Gly Arg Ser Glu Leu
 485 490 495
 Ala Val Ser Val Ser Leu Asn Ile Ala Gly Thr Tyr Arg Ile Lys Leu
 500 505 510
 Tyr Asn Thr Ala Gly Glu Glu Val Ala Ala Met Thr Lys Glu Leu Val
 515 520 525
 Ala Gly Thr Ser Val Phe Ser Met Asp Val Tyr Ser Gln Ala Pro Gly
 530 535 540
 Thr Tyr Val Leu Val Val Glu Gly Asn Gly Ile Arg Glu Thr Met Lys
 545 550 555 560
 Ile Leu Lys
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 <211> 437
 <212> PRT
 <213> Porphyromonas gingivalis
 <400> 383
 Thr Thr Asn Arg Lys Pro Asn Thr Asn Met Lys Leu Ser Ser Lys Lys
 1 5 10 15
 Ile Leu Ala Ile Ile Ala Leu Leu Thr Met Gly His Ala Val Gln Ala
 20 25 30
 Gln Phe Val Pro Ala Pro Thr Thr Gly Ile Arg Met Ser Val Thr Thr
 35 40 45
 Thr Lys Ala Val Gly Glu Lys Ile Glu Leu Leu Val His Ser Ile Glu
 50 55 60
 Lys Lys Gly Ile Trp Ile Asp Leu Asn Gly Asp Ala Thr Tyr Gln Gln
 65 70 75 80
 Gly Glu Glu Ile Thr Val Phe Asp Glu Ala Tyr His Glu Tyr Thr Ile
 85 90 95
 Gly Thr Gln Thr Leu Thr Ile Tyr Gly Asn Thr Thr Arg Leu Gly Cys
 100 105 110
 Arg Ser Thr Gly Ala Thr Ala Val Asp Val Thr Lys Asn Pro Asn Leu
 115 120 125
 Thr Tyr Leu Ala Cys Pro Lys Asn Asn Leu Lys Ser Leu Asp Leu Thr
 130 135 140
 Gln Asn Pro Lys Leu Leu Arg Val Trp Cys Asp Ser Asn Glu Ile Glu
 145 150 155 160
 Ser Leu Asp Leu Ser Gly Asn Pro Ala Leu Ile Ile Leu Gly Cys Asp
 165 170 175
 Arg Asn Lys Leu Thr Glu Leu Lys Thr Asp Asn Asn Pro Lys Leu Ala
 180 185 190
 Ser Leu Trp Cys Ser Asp Asn Asn Leu Thr Glu Leu Glu Leu Ser Ala
 195 200 205
 Asn Pro Arg Leu Asn Asp Leu Trp Cys Phe Gly Asn Arg Ile Thr Lys
 210 215 220
 Leu Asp Leu Ser Ala Asn Pro Leu Leu Val Thr Leu Trp Cys Ser Asp
 225 230 235 240
 Asn Glu Leu Ser Thr Leu Asp Leu Ser Lys Asn Ser Asp Val Ala Tyr
 245 250 255
 Leu Trp Cys Ser Ser Asn Lys Leu Thr Ser Leu Asn Leu Ser Gly Val
 260 265 270

Lys Gly Leu Ser Val Leu Val Cys His Ser Asn Gln Ile Ala Gly Glu
 275 280 285
 Glu Met Thr Lys Val Val Asn Ala Leu Pro Thr Leu Ser Pro Gly Ala
 290 295 300
 Gly Ala Gln Ser Lys Phe Val Val Val Asp Leu Lys Asp Thr Asp Glu
 305 310 315 320
 Lys Asn Ile Cys Thr Val Lys Asp Val Glu Lys Ala Lys Ser Lys Asn
 325 330 335
 Trp Arg Val Phe Asp Phe Asn Gly Asp Ser Asp Asn Met Leu Pro Tyr
 340 345 350
 Glu Gly Ser Pro Thr Ser Asn Leu Ala Val Asp Ala Pro Thr Val Arg
 355 360 365
 Ile Tyr Pro Asn Pro Val Gly Arg Tyr Ala Leu Val Glu Ile Pro Glu
 370 375 380
 Ser Leu Leu Gly Gln Glu Ala Ala Leu Tyr Asp Met Asn Gly Val Lys
 385 390 395 400
 Val Tyr Ser Phe Ala Val Glu Ser Leu Arg Gln Asn Ile Asp Leu Thr
 405 410 415
 His Leu Pro Asp Gly Thr Tyr Phe Phe Arg Leu Asp Asn Tyr Thr Thr
 420 425 430
 Lys Leu Ile Lys Gln
 435
 <210> 384
 <211> 318
 <212> PRT
 <213> Porphyromonas gingivalis
 <400> 384
 Asn His Leu Lys Thr Asn Ile Lys Met Arg Lys Thr Ile Ile Phe Cys
 1 5 10 15
 Leu Leu Leu Ala Leu Phe Gly Cys Ser Trp Ala Gln Glu Arg Val Asp
 20 25 30
 Glu Lys Val Phe Ser Ala Gly Thr Ser Ile Phe Arg Gly Ile Leu Glu
 35 40 45
 Lys Val Lys Ala Pro Leu Met Tyr Gly Asp Arg Glu Val Trp Gly Met
 50 55 60
 Ala Arg Ala Ser Glu Asp Phe Phe Phe Ile Leu Pro Val Thr Asp Asp
 65 70 75 80
 Leu Thr Pro Val Leu Phe Tyr Asn Arg Leu Thr Asn Glu Pro Cys Phe
 85 90 95
 Val Ser Asp Gln Gly Ile Thr Glu Tyr Phe Lys Phe Ala Gln Glu Gly
 100 105 110
 Asp Tyr Ile Glu Val Glu Gly Ser Ser Val Phe Met Ala Asn Leu Leu
 115 120 125
 Tyr Tyr Arg Phe Phe Pro Thr Arg Ile Thr Ser Tyr Asn Ala Pro Ile
 130 135 140
 Glu Gly Val Val Ser Lys Thr Gly Asn Pro Ala Phe Thr Ile Pro Met
 145 150 155 160
 Leu Pro Gly Val Ser Asp Cys Ile Glu Ile Ser Asn Asn Arg Lys Val
 165 170 175
 Phe Leu Thr Asn Gln Leu Gly Val Val Asn Ile Thr Asp Gly Met Glu
 180 185 190
 Pro Pro Ile Ile Ala Gly Val Ser Ala Ser Tyr Gly Ser Ser Val Arg


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195                200                205
Val Tyr Gly His Val Ser Gln Arg Trp Asp Ile Ile Gly His Cys Tyr
210                215                220
Leu Asp Ile Tyr Pro Thr Asn Cys Tyr Pro Leu Ser Thr Lys Pro Val
225                230                235                240
Ala Gly Asp Asp Glu Val Phe Val Lys Gln Gln Gly Arg Gln Ile Glu
245                250                255
Ile Asp Ser Asn Ser Pro Ile Val Gln Val Val Val Tyr Asp Leu Glu
260                265                270
Gly Lys Ser Val Phe Arg Lys Arg Met Thr Glu Asn Ala Tyr Thr Leu
275                280                285
Ser Phe Arg Ala Pro Met Leu Gly Phe Met Thr Ile Met Ile Glu Thr
290                295                300
Gln Asn Ser Ile Ile Asn Lys Lys Leu Asn Val Thr Gln Leu
305                310                315
<210>    385
<211>    461
<212>    PRT
<213>    Porphyromonas gingivalis
<400>    385
Arg Arg Ala Val Lys Ile Arg Ser Pro Pro His Ile His Ser Leu Phe
1          5          10          15
Val Arg Lys Cys Leu Phe Ser Asp Phe Lys Tyr Leu Tyr Leu Ser Arg
20          25          30
Lys Ile Thr Gln Glu Arg Leu Gly Arg Leu Ser Ile Arg Leu Lys Ser
35          40          45
Tyr Asn Pro Ile Ile Ile Ile Glu Met Lys Lys Thr Thr Ile Ile Ser
50          55          60
Leu Ile Val Phe Gly Ala Phe Phe Ala Ala Val Gly Gln Thr Lys Asp
65          70          75          80
Asn Ser Ser Tyr Lys Pro Phe Ser Lys Glu Asp Ile Ala Gly Gly Val
85          90          95
Tyr Ser Leu Pro Thr Gln Asn Arg Ala Gln Lys Asp Asn Ala Glu Trp
100         105         110
Leu Leu Thr Ala Thr Val Ser Thr Asn Gln Ser Ala Asp Thr His Phe
115         120         125
Ile Phe Asp Glu Asn Asn Arg Tyr Ile Ala Arg Asp Ile Lys Ala Asn
130         135         140
Gly Val Arg Lys Ser Thr Asp Ser Ile Tyr Tyr Asp Ala Asn Gly Arg
145         150         155         160
Ile Ser His Val Asp Leu Tyr Ile Ser Phe Ser Gly Gly Glu Pro Ala
165         170         175
Leu Asp Thr Arg Phe Lys Tyr Thr Tyr Asp Asp Glu Gly Lys Met Thr
180         185         190
Val Arg Glu Val Phe Met Leu Val Met Asp Pro Asn Thr Pro Ile Ser
195         200         205
Arg Leu Glu Tyr His Tyr Asp Ala Gln Gly Arg Leu Thr His Trp Ile
210         215         220
Ser Phe Ala Phe Gly Ala Glu Ser Gln Lys Asn Thr Tyr His Tyr Asn
225         230         235         240
Glu Lys Gly Leu Leu Val Ser Glu Val Leu Ser Asn Ala Met Gly Thr
245         250         255

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Thr Tyr Ser Asp Thr Gly Lys Thr Glu Tyr Ser Tyr Asp Asp Ala Asp
 260 265 270
 Asn Met Val Lys Ala Glu Tyr Phe Val Val Gln Gln Gly Lys Ala Trp
 275 280 285
 Gln Val Leu Lys Arg Glu Glu Tyr Thr Tyr Glu Asp Asn Ile Cys Ile
 290 295 300
 Gln Tyr Leu Ala Ile Asn Gly Thr Asp Thr Lys Val Tyr Lys Arg Asp
 305 310 315 320
 Ile Glu Ser Asp Lys Ser Ile Ser Ala Asn Val Ile Asp Ile Pro Ser
 325 330 335
 Met Pro Glu Gln Thr Trp Pro Asn Met Tyr Gly Phe Asn Ala Lys Arg
 340 345 350
 Leu Lys Glu Thr Tyr Ser Ser Tyr Glu Gly Asp Val Ala Thr Pro Ile
 355 360 365
 Phe Asp Tyr Ile Tyr Thr Tyr Lys Ala Leu Thr Ser Met Ala Thr Pro
 370 375 380
 Ser Thr Glu Ala Gln Val Ala Val Tyr Leu Asn Pro Ser Thr Asp Arg
 385 390 395 400
 Leu Val Ile Leu Ala Asn Gly Ile Thr His Leu Ser Met Tyr Asp Leu
 405 410 415
 Gln Gly Lys Leu Ile Arg Asp Cys Ala Leu Ser Gly Asp Lys Val Glu
 420 425 430
 Met Gly Val Gly Ser Leu Thr Lys Gly Thr Tyr Leu Leu Lys Val Asn
 435 440 445
 Thr Asp Gln Gly Ala Phe Val Arg Lys Val Val Ile Arg
 450 455 460
 <210> 386
 <211> 451
 <212> PRT
 <213> Porphyromonas gingivalis
 <400> 386
 Met Ala Lys Val Ile Lys Thr Lys Lys Gly Leu Ala Leu Asn Leu Lys
 1 5 10 15
 Gly Lys Pro Leu Pro Glu Met Leu Ala Glu Pro Ala Gln Ser Pro Thr
 20 25 30
 Tyr Ala Val Val Pro Asp Asp Phe Glu Gly Val Ile Pro Lys Val Thr
 35 40 45
 Ala Arg Pro Gly Asp Lys Val Arg Ala Gly Ser Ala Leu Met His His
 50 55 60
 Lys Ala Tyr Pro Glu Met Lys Phe Thr Ser Pro Val Ser Gly Glu Val
 65 70 75 80
 Ile Ala Val Asn Arg Gly Ala Lys Arg Lys Val Leu Ser Ile Glu Val
 85 90 95
 Lys Pro Asp Gly Leu Asn Glu Tyr Glu Ser Phe Pro Val Gly Asp Pro
 100 105 110
 Ser Ala Leu Ser Ala Glu Gln Ile Lys Glu Leu Leu Leu Ser Ser Gly
 115 120 125
 Met Trp Gly Phe Ile Lys Gln Arg Pro Tyr Asp Ile Val Ala Thr Pro
 130 135 140
 Asp Ile Ala Pro Arg Asp Ile Tyr Ile Thr Ala Asn Phe Thr Ala Pro
 145 150 155 160
 Leu Ala Pro Asp Phe Asp Phe Ile Val Arg Gly Glu Glu Arg Ala Leu

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                165                170                175
Gln Thr Ala Ile Asp Ala Leu Ala Lys Leu Thr Thr Gly Lys Val Tyr
                180                185                190
Val Gly Leu Lys Pro Gly Ser Ser Leu Gly Leu His Asn Ala Glu Ile
                195                200                205
Val Glu Val His Gly Pro His Pro Ala Gly Asn Val Gly Val Leu Ile
                210                215                220
Asn His Thr Lys Pro Ile Asn Arg Gly Glu Thr Val Trp Thr Leu Lys
225                230                235                240
Ala Thr Asp Leu Ile Val Ile Gly Arg Phe Leu Leu Thr Gly Lys Ala
                245                250                255
Asp Phe Thr Arg Met Ile Ala Met Thr Gly Ser Asp Ala Ala Ala His
                260                265                270
Gly Tyr Val Arg Ile Met Pro Gly Cys Asn Val Phe Ala Ser Phe Pro
                275                280                285
Gly Arg Leu Thr Ile Lys Glu Ser His Glu Arg Val Ile Asp Gly Asn
                290                295                300
Val Leu Thr Gly Lys Lys Leu Cys Glu Lys Glu Pro Phe Leu Ser Ala
305                310                315                320
Arg Cys Asp Gln Ile Thr Val Ile Pro Glu Gly Asp Asp Val Asp Glu
                325                330                335
Leu Phe Gly Trp Ala Ala Pro Arg Leu Asp Gln Tyr Ser Met Ser Arg
                340                345                350
Ala Tyr Phe Ser Trp Leu Gln Gly Lys Asn Lys Glu Tyr Val Leu Asp
                355                360                365
Ala Arg Ile Lys Gly Gly Glu Arg Ala Met Ile Met Ser Asn Glu Tyr
                370                375                380
Asp Arg Val Phe Pro Met Asp Ile Tyr Pro Glu Tyr Leu Leu Lys Ala
385                390                395                400
Ile Ile Ala Phe Asp Ile Asp Lys Met Glu Asp Leu Gly Ile Tyr Glu
                405                410                415
Val Ala Pro Glu Asp Phe Ala Thr Cys Glu Phe Val Asp Thr Ser Lys
                420                425                430
Ile Glu Leu Gln Arg Ile Val Arg Glu Gly Leu Asp Met Leu Tyr Lys
                435                440                445
Glu Met Asn
                450
<210>      387
<211>      195
<212>      PRT
<213>      Porphyromonas gingivalis
<400>      387
Met Asp Lys Val Ser Tyr Ala Leu Gly Leu Ser Ile Gly Asn Asn Phe
  1          5          10          15
Lys Ser Ser Gly Ile Asp Ser Val Val Met Asp Asp Phe Met Gln Gly
          20          25          30
Leu Ser Asp Val Leu Glu Glu Lys Ala Pro Gln Leu Ser Tyr Asp Glu
          35          40          45
Ala Lys Arg Glu Ile Glu Ala Tyr Phe Met Asp Leu Gln Gln Lys Ala
          50          55          60
Val Lys Leu Asn Lys Glu Ala Gly Glu Glu Phe Leu Lys Ile Asn Ala
          65          70          75          80

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His Lys Glu Gly Val Thr Thr Leu Pro Ser Gly Leu Gln Tyr Glu Val
85 90 95
Ile Lys Met Gly Glu Gly Pro Lys Pro Thr Leu Ser Asp Thr Val Thr
100 105 110
Cys His Tyr His Gly Thr Leu Ile Asn Gly Ile Val Phe Asp Ser Ser
115 120 125
Met Asp Arg Gly Glu Pro Ala Ser Phe Pro Leu Arg Gly Val Ile Ala
130 135 140
Gly Trp Thr Glu Ile Leu Gln Leu Met Pro Val Gly Ser Lys Trp Lys
145 150 155 160
Val Thr Ile Pro Ser Asp Leu Ala Tyr Gly Asp Arg Gly Ala Gly Glu
165 170 175
His Ile Lys Pro Gly Ser Thr Leu Ile Phe Ile Ile Glu Leu Leu Ser
180 185 190
Ile Asn Lys
195
<210> 388
<211> 273
<212> PRT
<213> Porphyromonas gingivalis
<400> 388
Met Lys Lys Ala Leu Leu Ile Gly Ala Ala Leu Leu Gly Ala Val Ser
1 5 10 15
Phe Ala Ser Ala Gln Ser Leu Ser Thr Ile Lys Val Gln Asn Asn Ser
20 25 30
Val Gln Gln Pro Arg Glu Glu Ala Thr Ile Gln Val Cys Gly Glu Leu
35 40 45
Ala Glu Gln Val Asp Cys Ile Gly Thr Gly Asn Ser Ala Ile Ile Ala
50 55 60
Ala Ala Ala Lys Phe Glu Ser Asp Asp Leu Glu Ser Tyr Val Gly Trp
65 70 75 80
Glu Ile Met Ser Val Asp Phe Phe Pro Gly Tyr Lys Ala Cys Lys Tyr
85 90 95
Thr Ser Ala Val Trp Ala Asp Asp Met Thr Ile Leu Gly Gln Ser Glu
100 105 110
Asp Ser Asp Pro Glu Met Gln Thr Ile Asn Asn Leu Ala Leu Lys Thr
115 120 125
Ser Val Lys Ile Glu Ala Gly Lys Asn Tyr Ile Val Gly Tyr Ile Ala
130 135 140
Asn Thr Ala Gly Gly His Pro Ile Gly Cys Asp Gln Gly Pro Ala Val
145 150 155 160
Asp Gly Tyr Gly Asp Leu Val Ser Ile Ser Glu Asp Gly Gly Ala Thr
165 170 175
Phe Pro Pro Phe Glu Ser Leu His Gln Ala Val Pro Thr Leu Asn Tyr
180 185 190
Asn Ile Tyr Val Val Val His Leu Lys Lys Gly Glu Gly Val Glu Ala
195 200 205
Val Leu Thr Asn Asp Lys Ala Asn Ala Tyr Val Gln Asn Gly Val Ile
210 215 220
Tyr Val Ala Gly Ala Asn Gly Arg Gln Val Ser Leu Phe Asp Met Asn
225 230 235 240
Gly Lys Val Val Tyr Thr Gly Val Ser Glu Thr Ile Ala Ala Pro Gln

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                245                250                255
Lys Gly Met Tyr Ile Leu Arg Val Gly Ala Lys Ser Ile Lys Leu Ala
                260                265                270
Ile
<210>      389
<211>      554
<212>      PRT
<213>      Porphyromonas gingivalis
<400>      389
Met Pro Arg Ile Met Lys Leu Lys Ile Ala Leu Arg Leu Leu Leu Ala
  1          5          10          15
Thr Phe Ala Ile Val Leu Phe Ser Pro Leu Ala Lys Ala Gln Met Asp
          20          25          30
Ile Gly Gly Asp Asp Val Leu Ile Glu Thr Met Ser Thr Leu Ser Gly
          35          40          45
Tyr Ser Glu Asp Phe Tyr Tyr Lys Met Ala Val Ala Asp Asn Gly Trp
          50          55          60
Ile Tyr Val Met Leu Asp Phe Ser Arg Ile Tyr Phe Asp Asp Val Arg
          65          70          75          80
Leu Tyr Arg Ser Lys Asp Gly Gly Ala Thr Tyr Gln Lys Leu Gly Ser
          85          90          95
Leu Gly Ser Leu Val Pro Tyr Asp Phe Asp Val Ser His Cys Asp Phe
          100          105          110
Ile Val Thr Gly Lys Asp Glu Asp Asp Ile Asn Val Trp Thr Val Met
          115          120          125
Thr Ala Phe Glu Tyr Val Gly Gly Thr Ile Gly Asn Gly Val Leu Leu
          130          135          140
Met His Arg His Asp Ala Asp Ile Asn Asn Thr Glu Cys Val Tyr Lys
          145          150          155          160
Lys Asp Phe Pro Asn Asn Arg Leu Met Gly Val Ala Ile Ala Ser Asn
          165          170          175
Tyr Arg Ala Pro Ser Pro Tyr Gly Leu Gly Gly Asp Pro Phe Ala Leu
          180          185          190
Ala Val Ala Val Ser Gly Ser Gly Ser Asp His Ser Phe Leu Asp Tyr
          195          200          205
Ile Phe Ser Leu Asp Gly Gly Val His Phe Glu Gln Lys Arg Ile Tyr
          210          215          220
Thr Arg Pro Gln Lys Leu Thr Ile Asn Arg Val Asp Leu Ser Leu Gly
          225          230          235          240
Ser Thr Ser Pro Ser Leu Gly Phe Asn Thr Trp Pro Leu Met Gly Val
          245          250          255
Val Phe Glu Met Asn Lys Asn Leu Asp Gly Phe Asp Ile Gly Phe Ile
          260          265          270
Ser Asn Phe Val Asp Tyr Asp Pro Arg Tyr Ala Trp Ser Glu Pro Ile
          275          280          285
Ile Ile Glu Glu Asp Cys Gly Trp Thr Asp Phe Asn Pro Leu Gly Ala
          290          295          300
Leu Ser Ile Glu Ile Gln Met Met Leu Asp Asp Asn Ser Asp Asn Thr
          305          310          315          320
Val Gly Gly Glu Arg Ser His Asn Phe Leu Ile Thr Tyr Pro Gly His
          325          330          335
Tyr Val Tyr Pro Lys Gln Ser Phe Asn Tyr Ser Pro Gly His Thr Pro

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        340                345                350
Thr  Lys  Lys  Asp  Leu  Val  Phe  Lys  His  Cys  Ile  Gly  Ile  Pro  Ala  Leu
        355                360                365
Ala  Tyr  Asp  Lys  Glu  Gly  Asp  Arg  Tyr  Leu  Thr  Thr  Phe  Gln  Asp  His
        370                375                380
Asn  Leu  Met  Arg  Tyr  Arg  Trp  Ile  Lys  Tyr  Asp  Asp  Ile  Asn  Ser  Phe
385                390                395                400
Tyr  Gly  Trp  Ser  Trp  Pro  Tyr  Val  Tyr  Ala  Lys  Glu  Ala  Lys  Asp  Lys
        405                410                415
Lys  Arg  Arg  Arg  Pro  Gln  Val  Ala  Leu  Asn  Pro  Thr  Asn  Gly  Lys  Ala
        420                425                430
Cys  Trp  Val  Trp  His  Thr  Arg  Lys  Ser  Pro  Tyr  Asp  Glu  Thr  Lys  Pro
        435                440                445
His  Pro  Thr  Pro  Val  Ile  Ile  Lys  His  Phe  Leu  Trp  Ser  Asp  Thr  Glu
        450                455                460
Trp  Val  His  Ala  Leu  Asp  Val  Gly  Asp  Val  Leu  Gln  Lys  Glu  Gly  Ser
465                470                475                480
Met  Lys  Leu  Tyr  Pro  Asn  Pro  Ala  Lys  Glu  Tyr  Val  Leu  Ile  Asn  Leu
        485                490                495
Pro  Lys  Glu  Gly  Gly  His  Glu  Ala  Val  Val  Tyr  Asp  Met  Gln  Gly  Arg
        500                505                510
Ile  Val  Glu  Lys  Val  Ser  Phe  Ser  Gly  Lys  Glu  Tyr  Lys  Leu  Asn  Val
        515                520                525
Gln  Tyr  Leu  Ser  Lys  Gly  Thr  Tyr  Met  Leu  Lys  Val  Val  Ala  Asp  Thr
530                535                540
Glu  Tyr  Phe  Val  Glu  Lys  Ile  Ile  Val  Glu
545                550
<210>      390
<211>      550
<212>      PRT
<213>      Porphyromonas gingivalis
<400>      390
Met  Lys  Leu  Lys  Ile  Ala  Leu  Arg  Leu  Leu  Leu  Ala  Thr  Phe  Ala  Ile
  1                5                10                15
Val  Leu  Phe  Ser  Pro  Leu  Ala  Lys  Ala  Gln  Met  Asp  Ile  Gly  Gly  Asp
        20                25                30
Asp  Val  Leu  Ile  Glu  Thr  Met  Ser  Thr  Leu  Ser  Gly  Tyr  Ser  Glu  Asp
        35                40                45
Phe  Tyr  Tyr  Lys  Met  Ala  Val  Ala  Asp  Asn  Gly  Trp  Ile  Tyr  Val  Met
        50                55                60
Leu  Asp  Phe  Ser  Arg  Ile  Tyr  Phe  Asp  Asp  Val  Arg  Leu  Tyr  Arg  Ser
        65                70                75                80
Lys  Asp  Gly  Gly  Ala  Thr  Tyr  Gln  Lys  Leu  Gly  Ser  Leu  Gly  Ser  Leu
        85                90                95
Val  Pro  Tyr  Asp  Phe  Asp  Val  Ser  His  Cys  Asp  Phe  Ile  Val  Thr  Gly
        100                105                110
Lys  Asp  Glu  Asp  Asp  Ile  Asn  Val  Trp  Thr  Val  Met  Thr  Ala  Phe  Glu
        115                120                125
Tyr  Val  Gly  Gly  Thr  Ile  Gly  Asn  Gly  Val  Leu  Leu  Met  His  Arg  His
        130                135                140
Asp  Ala  Asp  Ile  Asn  Asn  Thr  Glu  Cys  Val  Tyr  Lys  Lys  Asp  Phe  Pro
145                150                155                160

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Asn Asn Arg Leu Met Gly Val Ala Ile Ala Ser Asn Tyr Arg Ala Pro
    165                      170                      175
Ser Pro Tyr Gly Leu Gly Gly Asp Pro Phe Ala Leu Ala Val Ala Val
    180                      185                      190
Ser Gly Ser Gly Ser Asp His Ser Phe Leu Asp Tyr Ile Phe Ser Leu
    195                      200                      205
Asp Gly Gly Val His Phe Glu Gln Lys Arg Ile Tyr Thr Arg Pro Gln
    210                      215                      220
Lys Leu Thr Ile Asn Arg Val Asp Leu Ser Leu Gly Ser Thr Ser Pro
    225                      230                      235                      240
Ser Leu Gly Phe Asn Thr Trp Pro Leu Met Gly Val Val Phe Glu Met
    245                      250                      255
Asn Lys Asn Leu Asp Gly Phe Asp Ile Gly Phe Ile Ser Asn Phe Val
    260                      265                      270
Asp Tyr Asp Pro Arg Tyr Ala Trp Ser Glu Pro Ile Ile Ile Glu Glu
    275                      280                      285
Asp Cys Gly Trp Thr Asp Phe Asn Pro Leu Gly Ala Leu Ser Ile Glu
    290                      295                      300
Ile Gln Met Met Leu Asp Asp Asn Ser Asp Asn Thr Val Gly Gly Glu
    305                      310                      315                      320
Arg Ser His Asn Phe Leu Ile Thr Tyr Pro Gly His Tyr Val Tyr Pro
    325                      330                      335
Lys Gln Ser Phe Asn Tyr Ser Pro Gly His Thr Pro Thr Lys Lys Asp
    340                      345                      350
Leu Val Phe Lys His Cys Ile Gly Ile Pro Ala Leu Ala Tyr Asp Lys
    355                      360                      365
Glu Gly Asp Arg Tyr Leu Thr Thr Phe Gln Asp His Asn Leu Met Arg
    370                      375                      380
Tyr Arg Trp Ile Lys Tyr Asp Asp Ile Asn Ser Phe Tyr Gly Trp Ser
    385                      390                      395                      400
Trp Pro Tyr Val Tyr Ala Lys Glu Ala Lys Asp Lys Lys Arg Arg Arg
    405                      410                      415
Pro Gln Val Ala Leu Asn Pro Thr Asn Gly Lys Ala Cys Trp Val Trp
    420                      425                      430
His Thr Arg Lys Ser Pro Tyr Asp Glu Thr Lys Pro His Pro Thr Pro
    435                      440                      445
Val Ile Ile Lys His Phe Leu Trp Ser Asp Thr Glu Trp Val His Ala
    450                      455                      460
Leu Asp Val Gly Asp Val Leu Gln Lys Glu Gly Ser Met Lys Leu Tyr
    465                      470                      475                      480
Pro Asn Pro Ala Lys Glu Tyr Val Leu Ile Asn Leu Pro Lys Glu Gly
    485                      490                      495
Gly His Glu Ala Val Val Tyr Asp Met Gln Gly Arg Ile Val Glu Lys
    500                      505                      510
Val Ser Phe Ser Gly Lys Glu Tyr Lys Leu Asn Val Gln Tyr Leu Ser
    515                      520                      525
Lys Gly Thr Tyr Met Leu Lys Val Val Ala Asp Thr Glu Tyr Phe Val
    530                      535                      540
Glu Lys Ile Ile Val Glu
    545                      550
<210>    391
<211>    390

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<212>      PRT
<213>      Porphyromonas gingivalis
<400>      391
Met Lys Arg Leu Leu Pro Phe Leu Leu Leu Ala Gly Leu Val Ala Val
  1              5              10              15
Gly Asn Val Ser Ala Gln Ser Pro Arg Ile Pro Gln Val Asp Val His
      20              25              30
Thr Arg Ile Ala Arg Asn Ala Arg Tyr Arg Leu Asp Lys Ile Ser Val
      35              40              45
Pro Asp Ser Arg Gln Ile Phe Asp Tyr Phe Tyr Lys Glu Glu Thr Ile
      50              55              60
Pro Thr Lys Ile Gln Thr Thr Thr Gly Gly Ala Ile Thr Ser Ile Asp
      65              70              75              80
Ser Leu Phe Tyr Glu Asp Asp Arg Leu Val Gln Val Arg Tyr Phe Asp
      85              90              95
Asn Asn Leu Glu Leu Lys Gln Ala Glu Lys Tyr Val Tyr Asp Gly Ser
      100              105              110
Lys Leu Val Leu Arg Glu Ile Arg Lys Ser Pro Thr Asp Glu Thr Pro
      115              120              125
Ile Lys Lys Val Ser Tyr His Tyr Leu Cys Gly Ser Asp Met Pro Phe
      130              135              140
Glu Ile Thr Thr Glu Met Ser Asp Gly Tyr Phe Glu Ser His Thr Leu
      145              150              155              160
Asn Tyr Leu Asn Gly Lys Ile Ala Arg Ile Asp Ile Met Thr Gln Gln
      165              170              175
Asn Pro Ser Ala Glu Leu Ile Glu Thr Gly Arg Met Val Tyr Glu Phe
      180              185              190
Asp Ala Asn Asn Asp Ala Val Leu Leu Arg Asp Ser Val Phe Leu Pro
      195              200              205
Leu Gln Asn Lys Trp Val Glu Met Phe Thr His Arg Tyr Thr Tyr Asp
      210              215              220
Asn Lys His Asn Cys Ile Arg Trp Glu Gln Asp Glu Phe Gly Thr Leu
      225              230              235              240
Thr Leu Ala Asn Asn Phe Glu Tyr Asp Thr Thr Ile Pro Leu Ser Ser
      245              250              255
Val Leu Phe Pro Thr His Glu Glu Phe Phe Arg Pro Leu Leu Pro Asn
      260              265              270
Phe Met Lys His Met Arg Thr Lys Gln Thr Tyr Phe Asn Asn Ser Gly
      275              280              285
Glu Gly Leu Ser Glu Val Cys Asp Tyr Asn Tyr Phe Tyr Thr Asp Met
      290              295              300
Gln Gly Asn Ala Leu Thr Asp Val Ala Val Asn Glu Ser Ile Lys Ile
      305              310              315              320
Tyr Pro Arg Pro Ala Thr Asp Phe Leu Arg Ile Glu Gly Ser Gln Leu
      325              330              335
Leu Arg Leu Ser Leu Phe Asp Met Asn Gly Lys Leu Ile Arg Ala Thr
      340              345              350
Glu Leu Thr Gly Asp Leu Ala Ile Ile Gly Val Ala Ser Leu Pro Arg
      355              360              365
Gly Thr Tyr Ile Ala Glu Ile Thr Ala Ala Asn Ser Lys Thr Ile Arg
      370              375              380
Ala Lys Val Ser Leu Arg

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385	390															
<210>	392															
<211>	411															
<212>	PRT															
<213>	Porphyromonas gingivalis															
<400>	392															
Met	Arg	Gln	His	Leu	Ser	Leu	Phe	Pro	Phe	Ile	Leu	Phe	Leu	Leu	Leu	
1				5					10					15		
Ala	Phe	Ser	Tyr	Val	Gly	Cys	Arg	Thr	Val	Arg	Gln	Thr	Pro	Lys	Gln	
			20					25					30			
Ser	Glu	Arg	Tyr	Val	Val	Val	Leu	Ser	Leu	Asp	Gly	Phe	Arg	Pro	Asp	
		35					40					45				
Tyr	Thr	Asp	Arg	Ala	Arg	Thr	Pro	Ala	Leu	Asp	Arg	Met	Ala	Gln	Glu	
	50					55					60					
Gly	Leu	Ser	Gly	Ser	Leu	Gln	Pro	Cys	Phe	Pro	Ser	Leu	Thr	Phe	Pro	
65					70					75					80	
Asn	His	Tyr	Ser	Met	Ala	Thr	Gly	Leu	Tyr	Pro	Asp	His	His	Gly	Ile	
				85					90					95		
Val	Ala	Asn	Glu	Phe	Val	Asp	Ser	Leu	Leu	Gly	Ile	Phe	Arg	Ile	Ser	
			100					105					110			
Asp	Arg	Lys	Ala	Val	Glu	Thr	Pro	Gly	Phe	Trp	Gly	Gly	Glu	Pro	Val	
		115					120					125				
Trp	Asn	Thr	Ala	Ala	Arg	Gln	Gly	Ile	Arg	Thr	Gly	Val	Tyr	Phe	Trp	
	130					135					140					
Val	Gly	Ser	Glu	Thr	Ala	Val	Asn	Gly	Asn	Arg	Pro	Trp	Arg	Trp	Lys	
145					150				155						160	
Lys	Phe	Ser	Ser	Thr	Val	Pro	Phe	Arg	Asp	Arg	Ala	Asp	Ser	Val	Ile	
				165					170					175		
Ala	Trp	Leu	Gly	Leu	Pro	Glu	Lys	Glu	Arg	Pro	Arg	Leu	Leu	Met	Trp	
			180					185					190			
Tyr	Ile	Glu	Glu	Pro	Asp	Met	Ile	Gly	His	Ser	Gln	Thr	Pro	Glu	Ser	
		195					200					205				
Pro	Leu	Thr	Leu	Ala	Met	Val	Glu	Arg	Leu	Asp	Ser	Val	Val	Gly	Tyr	
		210				215					220					
Phe	Arg	Lys	Arg	Leu	Asp	Ser	Leu	Pro	Ile	Ala	Ala	Gln	Thr	Asp	Phe	
225					230					235					240	
Ile	Ile	Val	Ser	Asp	His	Gly	Met	Ala	Thr	Tyr	Glu	Asn	Glu	Lys	Cys	
				245					250					255		
Val	Asn	Leu	Ser	His	Tyr	Leu	Pro	Ala	Asp	Ser	Phe	Leu	Tyr	Met	Ala	
			260					265					270			
Thr	Gly	Ala	Phe	Thr	His	Leu	Tyr	Pro	Lys	Pro	Ser	Tyr	Thr	Glu	Arg	
		275					280					285				
Ala	Tyr	Glu	Ile	Leu	Arg	Ala	Ile	Pro	His	Ile	Ser	Val	Tyr	Arg	Lys	
		290				295					300					
Gly	Glu	Val	Pro	Lys	Arg	Leu	Arg	Cys	Gly	Thr	Asn	Pro	Arg	Leu	Gly	
305					310					315					320	
Glu	Leu	Val	Val	Ile	Pro	Asp	Ile	Gly	Ser	Thr	Val	Phe	Phe	Ala		

Gly Ser Arg Val Glu Asn Leu Pro Asn Ile Thr Ile Tyr Pro Leu Ile
370 375 380
Cys Arg Leu Leu Gly Ile Glu Pro Ala Pro Asn Asp Ala Asp Glu Thr
385 390 395 400
Leu Leu Asn Gly Leu Ile Arg Asp Lys Arg Pro
405 410
<210> 393
<211> 246
<212> PRT
<213> Porphyromonas gingivalis
<400> 393
Met Lys Val Gly Leu Phe Ile Pro Cys Tyr Val Asn Ala Val Tyr Pro
1 5 10 15
Glu Val Gly Ile Ala Thr Tyr Lys Leu Leu Lys Ser Leu Asp Ile Asp
20 25 30
Val Asp Tyr Pro Met Asp Gln Thr Cys Cys Gly Gln Pro Met Ala Asn
35 40 45
Ala Gly Phe Glu Gln Lys Ala Gln Lys Leu Ala Leu Arg Phe Glu Glu
50 55 60
Leu Phe Glu Ser Tyr Asp Val Val Val Gly Pro Ser Ala Ser Cys Val
65 70 75 80
Ala Phe Val Lys Glu Asn Tyr Asp His Ile Leu Arg Pro Thr Gly His
85 90 95
Val Cys Lys Ser Ala Ala Lys Val Arg Asp Ile Cys Glu Phe Leu His
100 105 110
Asp Asp Leu Lys Ile Thr Ser Leu Pro Ser Arg Phe Ala His Lys Val
115 120 125
Ser Leu His Asn Ser Cys His Gly Val Arg Glu Leu His Leu Ser Thr
130 135 140
Pro Ser Glu Val His Arg Pro Tyr His Asn Lys Val Arg Arg Leu Leu
145 150 155 160
Glu Met Val Gln Gly Ile Glu Val Phe Glu Pro Lys Arg Ile Asp Glu
165 170 175
Cys Cys Gly Phe Gly Gly Met Tyr Ser Val Glu Glu Pro Glu Val Ser
180 185 190
Thr Cys Met Gly His Asp Lys Val Leu Asp His Ile Ser Thr Gly Ala
195 200 205
Glu Tyr Ile Thr Gly Pro Asp Ser Ser Cys Leu Met His Met Gln Gly
210 215 220
Val Ile Asp Arg Glu Lys Leu Pro Ile Lys Thr Ile His Ala Val Glu
225 230 235 240
Ile Leu Ala Ala Asn Leu
245
<210> 394
<211> 246
<212> PRT
<213> Porphyromonas gingivalis
<400> 394
Met Asp Ile Val Ser Met Ala Asp Lys Ala Leu Val Val Glu Met Arg
1 5 10 15
Asp Val Thr Leu Cys Gln Glu Glu Asn Val Ile Phe Gln Asn Leu Asn
20 25 30

Leu Thr Leu Ser Ala Gly Asp Phe Val Tyr Leu Ile Gly Ser Val Gly
 35 40 45
 Ser Gly Lys Ser Thr Leu Leu Lys Ala Leu Tyr Ala Glu Val Pro Ile
 50 55 60
 Ser Ala Gly Tyr Ala Arg Val Ile Asp Tyr Asp Leu Ala Lys Leu Lys
 65 70 75 80
 Arg Lys Gln Leu Pro Tyr Leu Arg Arg Asn Leu Gly Ile Val Phe Gln
 85 90 95
 Asp Phe Gln Leu Leu Asn Gly Arg Thr Val Ala Glu Asn Leu Asp Phe
 100 105 110
 Val Leu Arg Ala Thr Asp Trp Lys Asn Arg Ala Asp Arg Glu Gln Arg
 115 120 125
 Ile Glu Glu Val Leu Thr Arg Val Gly Met Ser Arg Lys Ala Tyr Lys
 130 135 140
 Arg Pro His Glu Leu Ser Gly Gly Glu Gln Gln Arg Val Gly Ile Ala
 145 150 155 160
 Arg Ala Leu Leu Ala Lys Pro Ala Leu Ile Leu Ala Asp Glu Pro Thr
 165 170 175
 Gly Asn Leu Asp Ser Val Thr Gly Leu Gln Ile Ala Ser Leu Leu Tyr
 180 185 190
 Glu Ile Ser Lys Gln Gly Thr Ala Val Leu Met Ser Thr His Asn Ser
 195 200 205
 Ser Leu Leu Ser His Leu Pro Ala Arg Thr Leu Ala Val Arg Lys Asn
 210 215 220
 Gly Asp Ala Ser Ser Leu Val Glu Leu Ser Ala Asp Ala Val Ser Arg
 225 230 235 240
 Lys Asn Thr Glu Ile Asp
 245
 <210> 395
 <211> 241
 <212> PRT
 <213> Porphyromonas gingivalis
 <400> 395
 Met Ala Asp Lys Ala Leu Val Val Glu Met Arg Asp Val Thr Leu Cys
 1 5 10 15
 Gln Glu Glu Asn Val Ile Phe Gln Asn Leu Asn Leu Thr Leu Ser Ala
 20 25 30
 Gly Asp Phe Val Tyr Leu Ile Gly Ser Val Gly Ser Gly Lys Ser Thr
 35 40 45
 Leu Leu Lys Ala Leu Tyr Ala Glu Val Pro Ile Ser Ala Gly Tyr Ala
 50 55 60
 Arg Val Ile Asp Tyr Asp Leu Ala Lys Leu Lys Arg Lys Gln Leu Pro
 65 70 75 80
 Tyr Leu Arg Arg Asn Leu Gly Ile Val Phe Gln Asp Phe Gln Leu Leu
 85 90 95
 Asn Gly Arg Thr Val Ala Glu Asn Leu Asp Phe Val Leu Arg Ala Thr
 100 105 110
 Asp Trp Lys Asn Arg Ala Asp Arg Glu Gln Arg Ile Glu Glu Val Leu
 115 120 125
 Thr Arg Val Gly Met Ser Arg Lys Ala Tyr Lys Arg Pro His Glu Leu
 130 135 140
 Ser Gly Gly Glu Gln Gln Arg Val Gly Ile Ala Arg Ala Leu Leu Ala

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145                150                155                160
Lys Pro Ala Leu Ile Leu Ala Asp Glu Pro Thr Gly Asn Leu Asp Ser
                165                170                175
Val Thr Gly Leu Gln Ile Ala Ser Leu Leu Tyr Glu Ile Ser Lys Gln
                180                185                190
Gly Thr Ala Val Leu Met Ser Thr His Asn Ser Ser Leu Leu Ser His
                195                200                205
Leu Pro Ala Arg Thr Leu Ala Val Arg Lys Asn Gly Asp Ala Ser Ser
                210                215                220
Leu Val Glu Leu Ser Ala Asp Ala Val Ser Arg Lys Asn Thr Glu Ile
225                230                235                240
Asp
<210>      396
<211>      232
<212>      PRT
<213>      Porphyromonas gingivalis
<400>      396
Met Arg Asp Val Thr Leu Cys Gln Glu Glu Asn Val Ile Phe Gln Asn
  1                5                10                15
Leu Asn Leu Thr Leu Ser Ala Gly Asp Phe Val Tyr Leu Ile Gly Ser
                20                25                30
Val Gly Ser Gly Lys Ser Thr Leu Leu Lys Ala Leu Tyr Ala Glu Val
                35                40                45
Pro Ile Ser Ala Gly Tyr Ala Arg Val Ile Asp Tyr Asp Leu Ala Lys
  50                55                60
Leu Lys Arg Lys Gln Leu Pro Tyr Leu Arg Arg Asn Leu Gly Ile Val
  65                70                75                80
Phe Gln Asp Phe Gln Leu Leu Asn Gly Arg Thr Val Ala Glu Asn Leu
                85                90                95
Asp Phe Val Leu Arg Ala Thr Asp Trp Lys Asn Arg Ala Asp Arg Glu
                100                105                110
Gln Arg Ile Glu Glu Val Leu Thr Arg Val Gly Met Ser Arg Lys Ala
                115                120                125
Tyr Lys Arg Pro His Glu Leu Ser Gly Gly Glu Gln Gln Arg Val Gly
                130                135                140
Ile Ala Arg Ala Leu Leu Ala Lys Pro Ala Leu Ile Leu Ala Asp Glu
145                150                155                160
Pro Thr Gly Asn Leu Asp Ser Val Thr Gly Leu Gln Ile Ala Ser Leu
                165                170                175
Leu Tyr Glu Ile Ser Lys Gln Gly Thr Ala Val Leu Met Ser Thr His
                180                185                190
Asn Ser Ser Leu Leu Ser His Leu Pro Ala Arg Thr Leu Ala Val Arg
                195                200                205
Lys Asn Gly Asp Ala Ser Ser Leu Val Glu Leu Ser Ala Asp Ala Val
                210                215                220
Ser Arg Lys Asn Thr Glu Ile Asp
225                230
<210>      397
<211>      219
<212>      PRT
<213>      Porphyromonas gingivalis
<400>      397

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

<210> 398
 <211> 595
 <212> PRT
 <213> Porphyromonas gingivalis
 <400> 398

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

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

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                    565                      570                      575
Met Pro Pro Arg Pro Ser Gly Ile Gln Ala Arg Leu Pro Tyr Tyr Phe
                    580                      585                      590
Met Pro Tyr
                    595
<210>      399
<211>      589
<212>      PRT
<213>      Porphyromonas gingivalis
<400>      399
Met Phe Phe Ala Ser Ile Leu Gly Val Ile Thr Ala Gly Ile Ile Leu
  1          5          10          15
Phe Cys Ile Phe Leu Phe Ile Phe Phe Gly Ile Val Ala Gly Ile Ala
          20          25          30
Ser Lys Ala Thr Gly Gly Thr Ile Pro Lys Ile Glu Ala Asn Ser Ile
          35          40          45
Leu His Ile Xaa Asn Ser Ser Phe Pro Glu Ile Val Ser Ala Asn Pro
          50          55          60
Trp Ser Met Leu Thr Gly Lys Asp Glu Ser Val Ser Leu Ser Gln Ala
          65          70          75          80
Val Glu Ala Ile Gly Gln Ala Lys Asn Asn Pro Asn Ile Thr Gly Ile
          85          90          95
Phe Leu Asp Leu Asp Asn Leu Ser Val Gly Met Ala Ser Ala Glu Glu
          100          105          110
Leu Arg Arg Ala Leu Gln Asp Phe Lys Met Ser Gly Lys Phe Val Val
          115          120          125
Ser Tyr Ala Asp Arg Tyr Thr Gln Lys Gly Tyr Tyr Leu Ser Ser Ile
          130          135          140
Ala Asp Lys Leu Tyr Leu Asn Pro Lys Gly Met Leu Gly Leu Ile Gly
          145          150          155          160
Ile Ala Thr Gln Thr Met Phe Tyr Lys Asp Ala Leu Asp Lys Phe Gly
          165          170          175
Val Lys Met Glu Ile Phe Lys Val Gly Thr Tyr Lys Ala Ala Val Glu
          180          185          190
Pro Phe Met Leu Asn Arg Met Ser Asp Ala Asn Arg Glu Gln Ile Thr
          195          200          205
Thr Tyr Ile Asn Gly Leu Trp Asp Lys Ile Thr Ser Asp Ile Ala Glu
          210          215          220
Ser Arg Lys Thr Ala Met Asp Ser Val Lys Met Phe Ala Asp Lys Gly
          225          230          235          240
Glu Met Phe Gly Leu Ala Glu Lys Ala Val Glu Met Lys Leu Val Asp
          245          250          255
Glu Leu Ala Tyr Arg Thr Asp Val Glu Lys Glu Leu Lys Lys Met Ser
          260          265          270
Gln Arg Gly Glu Lys Asp Glu Leu Arg Phe Val Ser Leu Ser Gln Val
          275          280          285
Leu Ala Asn Gly Pro Met Asn Lys Thr Lys Gly Ser Arg Ile Ala Val
          290          295          300
Leu Phe Ala Glu Gly Glu Ile Thr Glu Glu Ile Ile Lys Lys Pro Phe
          305          310          315          320
Asp Thr Asp Gly Ser Ser Ile Thr Gln Glu Leu Ala Lys Glu Ile Lys
          325          330          335

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Ala Ala Ala Asp Asp Asp Asp Ile Lys Ala Val Val Leu Arg Val Asn
340 345 350
Ser Pro Gly Gly Ser Ala Phe Thr Ser Glu Gln Ile Trp Lys Gln Val
355 360 365
Ala Asp Leu Lys Ala Lys Lys Pro Ile Val Val Ser Met Gly Asp Val
370 375 380
Ala Ala Ser Gly Gly Tyr Tyr Ile Ala Cys Ala Ala Asn Ser Ile Val
385 390 395 400
Ala Glu His Thr Thr Leu Thr Gly Ser Ile Gly Ile Phe Gly Met Phe
405 410 415
Pro Asn Phe Ala Gly Val Ala Lys Lys Ile Gly Val Asn Met Asp Val
420 425 430
Val Gln Thr Ser Lys Tyr Ala Asp Leu Gly Asn Thr Phe Ala Pro Met
435 440 445
Thr Val Glu Asp Arg Ala Leu Ile Gln Arg Tyr Ile Glu Gln Gly Tyr
450 455 460
Asp Leu Phe Leu Thr Arg Val Ser Glu Gly Arg Asn Arg Thr Lys Ala
465 470 475 480
Gln Ile Asp Ser Ile Ala Gln Gly Arg Val Trp Leu Gly Asp Lys Ala
485 490 495
Leu Ala Leu Gly Leu Val Asp Glu Leu Gly Gly Leu Asp Thr Ala Ile
500 505 510
Lys Arg Ala Ala Lys Leu Ala Gln Leu Gly Gly Asn Tyr Ser Ile Glu
515 520 525
Tyr Gly Lys Thr Lys Arg Asn Phe Phe Glu Glu Leu Leu Ser Ser Ser
530 535 540
Ala Ala Asp Met Lys Ser Ala Ile Leu Ser Thr Ile Leu Ser Asp Pro
545 550 555 560
Glu Ile Glu Val Leu Arg Glu Leu Arg Ser Met Pro Pro Arg Pro Ser
565 570 575
Gly Ile Gln Ala Arg Leu Pro Tyr Tyr Phe Met Pro Tyr
580 585
<210> 400
<211> 313
<212> PRT
<213> Porphyromonas gingivalis
<400> 400
Met Arg Ala Asn Ile Trp Gln Ile Leu Ser Val Ser Val Leu Phe Phe
1 5 10 15
Phe Gly Thr Ala Ile Gly Gln Ala Gln Ser Arg Asn Arg Thr Tyr Glu
20 25 30
Ala Tyr Val Lys Gln Tyr Ala Asp Glu Ala Ile Arg Gln Met Ser Arg
35 40 45
Tyr Asn Ile Pro Ala Ser Ile Thr Ile Ala Gln Ala Leu Val Glu Thr
50 55 60
Gly Ala Gly Ala Ser Thr Leu Ala Ser Val His Asn Asn His Phe Gly
65 70 75 80
Ile Lys Cys His Lys Ser Trp Thr Gly Lys Arg Thr Tyr Arg Thr Asp
85 90 95
Asp Ala Pro Asn Glu Cys Phe Arg Ser Tyr Ser Ala Ala Arg Glu Ser
100 105 110
Tyr Glu Asp His Ser Arg Phe Leu Leu Gln Pro Arg Tyr Arg Pro Leu


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115          120          125
Phe Lys Leu Asp Arg Glu Asp Tyr Arg Gly Trp Ala Thr Gly Leu Gln
130          135          140
Arg Cys Gly Tyr Ala Thr Asn Arg Gly Tyr Ala Asn Leu Leu Ile Lys
145          150          155          160
Met Val Glu Leu Tyr Glu Leu Tyr Ala Leu Asp Arg Glu Lys Tyr Pro
165          170          175
Ser Trp Phe His Lys Ser Tyr Pro Gly Ser Asn Lys Lys Ser His Gln
180          185          190
Thr Thr Lys Gln Lys Gln Ser Gly Leu Lys His Glu Ala Tyr Phe Ser
195          200          205
Tyr Gly Leu Leu Tyr Ile Ile Ala Lys Gln Gly Asp Thr Phe Asp Ser
210          215          220
Leu Ala Glu Glu Phe Asp Met Arg Ala Ser Lys Leu Ala Lys Tyr Asn
225          230          235          240
Asp Ala Pro Val Asp Phe Pro Ile Glu Lys Gly Asp Val Ile Tyr Leu
245          250          255
Glu Lys Lys His Ala Cys Ser Ile Ser Lys His Thr Gln His Val Val
260          265          270
Arg Val Gly Asp Ser Met His Ser Ile Ser Gln Arg Tyr Gly Ile Arg
275          280          285
Met Lys Asn Leu Tyr Lys Leu Asn Asp Lys Asp Gly Glu Tyr Ile Pro
290          295          300
Gln Glu Gly Asp Ile Leu Arg Leu Arg
305          310
<210>      401
<211>      523
<212>      PRT
<213>      Porphyromonas gingivalis
<400>      401
Met Asp Gly Arg Arg Tyr Ser Asp Gly Leu His Gln Ala Ile Glu Ala
1          5          10          15
Lys Glu His Val Lys Val Glu Ala Ala Thr Gln Thr Phe Ala Thr Ile
20          25          30
Thr Leu Gln Asn Tyr Phe Arg Met Tyr His Lys Leu Ala Gly Met Thr
35          40          45
Gly Thr Ala Glu Thr Glu Ala Gly Glu Leu Trp Asp Ile Tyr Lys Leu
50          55          60
Asp Val Val Val Ile Pro Thr Asn Lys Pro Ile Ala Arg Lys Asp Met
65          70          75          80
Asn Asp Arg Ile Tyr Lys Thr Ala Arg Glu Lys Tyr Ala Ala Val Ile
85          90          95
Glu Glu Ile Val Arg Leu Val Glu Glu Gly Arg Pro Val Leu Val Gly
100          105          110
Thr Thr Ser Val Glu Ile Ser Glu Leu Leu Ser Arg Met Leu Arg Leu
115          120          125
Arg Gly Ile Gln His Asn Val Leu Asn Ala Lys Leu His Gln Lys Glu
130          135          140
Ala Glu Ile Val Ala Gln Ala Gly Gln Lys Gly Thr Val Thr Ile Ala
145          150          155          160
Thr Asn Met Ala Gly Arg Gly Thr Asp Ile Lys Leu Ser Ala Glu Val
165          170          175

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Lys Lys Ala Gly Gly Leu Ala Ile Ile Gly Thr Glu Arg His Glu Ser
 180 185 190
 Arg Arg Val Asp Arg Gln Leu Arg Gly Arg Ser Gly Arg Gln Gly Asp
 195 200 205
 Pro Gly Ser Ser Ile Phe Tyr Val Ser Leu Glu Asp His Leu Met Arg
 210 215 220
 Leu Phe Ala Thr Glu Lys Ile Ala Ser Leu Met Asp Arg Leu Gly Phe
 225 230 235 240
 Lys Glu Gly Glu Val Leu Glu Asn Asn Met Leu Ser Lys Ser Val Glu
 245 250 255
 Arg Ala Gln Lys Lys Val Glu Glu Asn Asn Phe Gly Ile Arg Lys His
 260 265 270
 Leu Leu Glu Tyr Asp Asp Val Met Asn Ser Gln Arg Glu Val Ile Tyr
 275 280 285
 Thr Arg Arg Arg His Ala Leu Met Gly Glu Arg Ile Gly Met Asp Val
 290 295 300
 Leu Asn Thr Ile Tyr Asp Val Cys Lys Ala Leu Ile Asp Asn Tyr Ala
 305 310 315 320
 Glu Ala Asn Asp Phe Glu Gly Phe Lys Glu Asp Leu Met Arg Ala Leu
 325 330 335
 Ala Ile Glu Ser Pro Ile Thr Gln Glu Ile Phe Arg Gly Lys Lys Ala
 340 345 350
 Glu Glu Leu Thr Asp Met Leu Phe Asp Glu Ala Tyr Lys Ser Phe Gln
 355 360 365
 Arg Lys Met Asp Leu Ile Ala Glu Val Ala His Pro Val Val His Gln
 370 375 380
 Val Phe Glu Thr Gln Ala Ala Val Tyr Glu Arg Ile Leu Ile Pro Ile
 385 390 395 400
 Thr Asp Gly Lys Arg Val Tyr Asn Ile Gly Cys Asn Leu Arg Glu Ala
 405 410 415
 Asp Glu Thr Gln Gly Lys Ser Ile Ile Lys Glu Phe Glu Lys Ala Ile
 420 425 430
 Val Leu His Thr Ile Asp Glu Ser Trp Lys Glu His Leu Arg Glu Met
 435 440 445
 Asp Glu Leu Arg Asn Ser Val Gln Asn Ala Ser Tyr Glu Asn Lys Asp
 450 455 460
 Pro Leu Leu Ile Tyr Lys Leu Glu Ser Tyr Glu Leu Phe Arg Lys Met
 465 470 475 480
 Val Glu Ala Met Asn Arg Lys Thr Val Ala Ile Leu Met Arg Ala Arg
 485 490 495
 Ile Pro Val Pro Glu Ala Pro Ser Gln Glu Glu Leu Glu His Arg Arg
 500 505 510
 Gln Ile Glu Ile Arg His Ala Thr Gln Gln Arg
 515 520
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 <211> 375
 <212> PRT
 <213> Porphyromonas gingivalis
 <400> 402
 Met Asn Phe Leu Lys Lys Glu Pro Phe Lys Ile Phe Ser Met Ile Tyr
 1 5 10 15
 Leu Leu Leu Asp Thr Ile Thr Asn Arg Ala Gly Thr Glu Arg Ala Val

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                20                25                30
Ile Asn Leu Ala Asn Asn Leu His Ala Asn Gly His Arg Val Ser Leu
      35                40                45
Val Ser Val Cys Thr Lys Glu Gly Glu Pro Ser Phe Gln Val Glu Lys
      50                55                60
Gly Ile Glu Val His His Leu Gly Ile Arg Leu Tyr Gly Asn Ala Leu
      65                70                75                80
Ala Arg Lys Thr Val Tyr Phe Lys Ala Tyr Arg Arg Ile Lys Ala Leu
      85                90                95
Tyr Lys Lys Arg Glu Pro Val Leu Leu Ile Gly Thr Asn Ile Phe Ile
      100                105                110
Asn Thr Ile Leu Ser Gln Ile Ser Asn Arg Gly Arg Ile Phe Thr Ile
      115                120                125
Gly Cys Glu His Ile Ser Tyr Asp Ile Ala Arg Pro Ile Thr Lys Arg
      130                135                140
Ile Arg Gly Phe Leu Tyr Ser Gly Leu Asp Ala Val Val Ala Leu Thr
      145                150                155                160
Lys Arg Asp Gln Gln Ser Phe Glu Ala Ile Leu Arg Gly Arg Ser Lys
      165                170                175
Ala Tyr Val Ile Pro Asn Gln Val Ser Phe Thr Thr Val Gln Arg Asp
      180                185                190
Ala Thr Thr His Lys Gln Met Leu Ala Ile Gly Arg Leu Thr Tyr Gln
      195                200                205
Lys Gly Phe Glu Phe Met Ile Glu Asp Ala Ser Arg Val Leu Arg Glu
      210                215                220
Arg Pro Asp Trp Lys Leu Ile Ile Val Gly Asp Gly Glu Asn Glu Ser
      225                230                235                240
Met Leu Arg Lys Glu Ile Ala Ser Arg Asn Met Glu Ser Gln Ile Glu
      245                250                255
Ile His Pro Ser Thr Pro Glu Ile Arg Lys Tyr Tyr Glu Ser Ser Ala
      260                265                270
Ile Tyr Leu Met Thr Ser Arg Phe Glu Gly Leu Pro Met Val Leu Leu
      275                280                285
Glu Ala Glu Ala Tyr Ala Leu Pro Ile Ile Ser Tyr Asp Cys Pro Thr
      290                295                300
Gly Pro Arg Glu Leu Ile Glu Asn Gly Arg Asn Gly Phe Leu Val Pro
      305                310                315                320
Met Glu Ala His Glu Asp Phe Ala Asp Lys Leu Arg Leu Leu Met Asp
      325                330                335
Asp Glu Thr Leu Arg Lys Lys Met Gly Gln Glu Ser Glu Leu Met Val
      340                345                350
Lys Ser Tyr Ser Pro Ala Asn Ile Tyr Glu Cys Trp Lys Lys Leu Phe
      355                360                365
Val Glu Ile Gly Tyr Met Asn
      370                375
<210>      403
<211>      362
<212>      PRT
<213>      Porphyromonas gingivalis
<400>      403
Met Ile Tyr Leu Leu Leu Asp Thr Ile Thr Asn Arg Ala Gly Thr Glu
      1                5                10                15

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Arg Ala Val Ile Asn Leu Ala Asn Asn Leu His Ala Asn Gly His Arg
 20 25 30
 Val Ser Leu Val Ser Val Cys Thr Lys Glu Gly Glu Pro Ser Phe Gln
 35 40 45
 Val Glu Lys Gly Ile Glu Val His His Leu Gly Ile Arg Leu Tyr Gly
 50 55 60
 Asn Ala Leu Ala Arg Lys Thr Val Tyr Phe Lys Ala Tyr Arg Arg Ile
 65 70 75 80
 Lys Ala Leu Tyr Lys Lys Arg Glu Pro Val Leu Leu Ile Gly Thr Asn
 85 90 95
 Ile Phe Ile Asn Thr Ile Leu Ser Gln Ile Ser Asn Arg Gly Arg Ile
 100 105 110
 Phe Thr Ile Gly Cys Glu His Ile Ser Tyr Asp Ile Ala Arg Pro Ile
 115 120 125
 Thr Lys Arg Ile Arg Gly Phe Leu Tyr Ser Gly Leu Asp Ala Val Val
 130 135 140
 Ala Leu Thr Lys Arg Asp Gln Gln Ser Phe Glu Ala Ile Leu Arg Gly
 145 150 155 160
 Arg Ser Lys Ala Tyr Val Ile Pro Asn Gln Val Ser Phe Thr Thr Val
 165 170 175
 Gln Arg Asp Ala Thr Thr His Lys Gln Met Leu Ala Ile Gly Arg Leu
 180 185 190
 Thr Tyr Gln Lys Gly Phe Glu Phe Met Ile Glu Asp Ala Ser Arg Val
 195 200 205
 Leu Arg Glu Arg Pro Asp Trp Lys Leu Ile Ile Val Gly Asp Gly Glu
 210 215 220
 Asn Glu Ser Met Leu Arg Lys Glu Ile Ala Ser Arg Asn Met Glu Ser
 225 230 235 240
 Gln Ile Glu Ile His Pro Ser Thr Pro Glu Ile Arg Lys Tyr Tyr Glu
 245 250 255
 Ser Ser Ala Ile Tyr Leu Met Thr Ser Arg Phe Glu Gly Leu Pro Met
 260 265 270
 Val Leu Leu Glu Ala Glu Ala Tyr Ala Leu Pro Ile Ile Ser Tyr Asp
 275 280 285
 Cys Pro Thr Gly Pro Arg Glu Leu Ile Glu Asn Gly Arg Asn Gly Phe
 290 295 300
 Leu Val Pro Met Glu Ala His Glu Asp Phe Ala Asp Lys Leu Arg Leu
 305 310 315 320
 Leu Met Asp Asp Glu Thr Leu Arg Lys Lys Met Gly Gln Glu Ser Glu
 325 330 335
 Leu Met Val Lys Ser Tyr Ser Pro Ala Asn Ile Tyr Glu Cys Trp Lys
 340 345 350
 Lys Leu Phe Val Glu Ile Gly Tyr Met Asn
 355 360
 <210> 404
 <211> 640
 <212> PRT
 <213> Porphyromonas gingivalis
 <400> 404
 Met Gly Lys Ile Ile Gly Ile Asp Leu Gly Thr Thr Asn Ser Cys Val
 1 5 10 15
 Ser Val Leu Glu Gly Asn Glu Pro Ile Val Ile Thr Asn Ser Glu Gly

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

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            435                440                445
Gly Arg Phe Asn Leu Asp Gly Ile Ala Pro Ala Pro Arg Gln Thr Pro
 450                455                460
Gln Ile Glu Val Thr Phe Asp Ile Asp Ala Asn Gly Ile Leu Asn Val
 465                470                475                480
Thr Ala His Asp Lys Ala Thr Gly Lys Lys Gln Asn Ile Arg Ile Glu
            485                490                495
Ala Ser Ser Gly Leu Ser Asp Asp Glu Ile Lys Arg Met Lys Glu Glu
            500                505                510
Ala Gln Ala Asn Ala Glu Ala Asp Lys Lys Glu Lys Glu Arg Ile Asp
            515                520                525
Lys Ile Asn Gln Ala Asp Ser Met Ile Phe Gln Thr Glu Lys Gln Leu
            530                535                540
Lys Glu Leu Gly Asp Lys Phe Pro Ala Asp Lys Lys Ala Pro Ile Asp
 545                550                555                560
Thr Ala Leu Asp Lys Leu Lys Glu Ala His Lys Ala Gln Asp Val Ala
            565                570                575
Ala Ile Asp Thr Ala Met Ala Glu Leu Gln Thr Ala Leu Ser Ala Ala
            580                585                590
Gly Glu Glu Leu Tyr Lys Asn Ala Gly Ala Ala Gln Gly Gly Ala Gln
            595                600                605
Pro Gly Pro Asp Phe Gly Gly Ala Gln Gly Pro Ser Ala Gly Asp Gln
            610                615                620
Pro Ser Asp Asp Lys Asn Val Thr Asp Val Asp Phe Glu Glu Val Lys
 625                630                635                640
<210>      405
<211>      449
<212>      PRT
<213>      Porphyromonas gingivalis
<400>      405
Met Arg Tyr Asp Leu Ala Ile Ile Gly Gly Gly Pro Ala Gly Tyr Thr
  1                5                10                15
Ala Ala Glu Arg Ala Ala Lys Gly Gly Leu Lys Thr Leu Leu Ile Glu
            20                25                30
Lys Asn Ala Leu Gly Gly Val Cys Leu Asn Glu Gly Cys Ile Pro Thr
            35                40                45
Lys Thr Leu Leu Tyr Ser Ala Lys Val Leu His Gln Ile Ala Thr Ala
            50                55                60
Ser Lys Tyr Ala Val Ser Gly Thr Ala Asp Gly Leu Asp Leu Gly Lys
  65                70                75                80
Val Ile Ala Arg Lys Gly Lys Ile Ile Arg Lys Leu Thr Ala Gly Ile
            85                90                95
Arg Ser Arg Leu Thr Glu Ala Gly Val Glu Met Val Thr Ala Glu Ala
            100                105                110
Thr Val Thr Gly Cys Asp Ala Asp Gly Ile Ile Gly Ile Thr Ala Gly
            115                120                125
Glu Ala Gln Tyr Lys Ala Ala Asn Leu Leu Leu Cys Thr Gly Ser Glu
            130                135                140
Thr Phe Ile Pro Pro Ile Pro Gly Val Glu Gln Thr Glu Tyr Trp Thr
 145                150                155                160
Asn Arg Glu Ala Leu Gln Asn Lys Glu Ile Pro Thr Ser Leu Val Ile
            165                170                175

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Ile Gly Gly Gly Val Ile Gly Met Glu Phe Ala Ser Phe Phe Asn Gly
180 185 190
Ile Gly Thr Gln Val His Val Val Glu Met Leu Pro Glu Ile Leu Asn
195 200 205
Gly Ile Asp Pro Glu His Ala Ala Met Leu Arg Ala His Tyr Glu Lys
210 215 220
Glu Gly Ile Lys Phe Tyr Leu Gly His Lys Val Thr Ser Val Arg Asn
225 230 235 240
Gly Ala Val Thr Val Glu Tyr Glu Gly Glu Ser Lys Glu Ile Glu Gly
245 250 255
Glu Arg Ile Leu Met Ser Val Gly Arg Arg Pro Val Leu Gln Gly Phe
260 265 270
Glu Ser Leu Gly Leu Val Leu Ala Gly Lys Gly Val Lys Thr Asn Glu
275 280 285
Arg Met Gln Thr Ser Leu Pro Asn Val Tyr Ala Ala Gly Asp Ile Thr
290 295 300
Gly Phe Ser Leu Leu Ala His Thr Ala Val Arg Glu Ala Glu Val Ala
305 310 315 320
Val Asp Gln Ile Leu Gly Lys Thr Asp Glu Thr Met Ser Tyr Arg Ala
325 330 335
Val Pro Gly Val Val Tyr Thr Asn Pro Glu Val Ala Gly Val Gly Glu
340 345 350
Thr Glu Glu Ser Leu Arg Lys Ala Gly Arg Ala Tyr Thr Val Arg Arg
355 360 365
Leu Pro Met Ala Phe Ser Gly Arg Phe Val Ala Glu Asn Glu Gln Gly
370 375 380
Asn Gly Glu Cys Lys Leu Leu Leu Asp Glu Glu Asn Arg Leu Ile Gly
385 390 395 400
Ala His Leu Ile Gly Asn Pro Ala Gly Glu Leu Ile Val Thr Ala Ala
405 410 415
Met Ala Ile Glu Thr Gly Met Thr Asp Arg Gln Ile Glu Arg Ile Ile
420 425 430
Phe Pro His Pro Thr Val Gly Glu Ile Leu Lys Glu Thr Leu Ala Gly
435 440 445
Gly
<210> 406
<211> 941
<212> PRT
<213> Porphyromonas gingivalis
<400> 406
Met Glu Leu Lys Arg Phe Leu Ser Leu Gly Leu Leu Leu Val Gly Phe
1 5 10 15
Ile Pro Met Lys Leu Ser Ala Gln Gln Ala Gln Pro Leu Pro Thr Asp
20 25 30
Pro Ala Val Arg Val Gly Lys Leu Asp Asn Gly Leu Thr Tyr Phe Ile
35 40 45
Arg His Asn Glu Asn Pro Lys Asp Arg Ala Asp Phe Phe Ile Ala Gln
50 55 60
Lys Val Gly Ser Ile Leu Glu Glu Asp Ser Gln Ser Gly Leu Ala His
65 70 75 80
Phe Leu Glu His Met Ala Phe Asn Gly Thr Lys Asn Phe Pro Gly Lys
85 90 95

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

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

Thr Thr Glu Leu Thr Leu Ser Asn Gly Ile Lys Val Tyr Leu Lys Lys
530 535 540

Thr Asp Phe Lys Ser Asn Glu Ile Leu Met Ser Ala Leu Ser Pro Gly
545 550 555 560

Gly Ile Leu Ser Gly Lys His Ala Pro Asn Gln Ser Val Met Asn Ser
565 570 575

Phe Met Asn Val Gly Gly Leu Gly Asn Phe Asp Ala Ile Gln Leu Asp
580 585 590

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

Leu Ser Glu Gly Leu Ser Gly Lys Thr Thr Val Glu Asp Met Glu Thr
610 615 620

Phe Phe Gln Leu Ile Tyr Leu Gln Met Thr Ala Asn Arg Lys Asp Pro
625 630 635 640

Glu Ala Phe Lys Ala Thr Gln Glu Lys Leu Tyr Asn Asn Leu Lys Asn
645 650 655

Gln Glu Ala Asn Pro Met Ala Ala Leu Met Asp Ser Ile Arg His Thr
660 665 670

Met Tyr Gly Asp Asn Pro Met Met Lys Pro Met Lys Ala Ala Asp Val
675 680 685

Glu Lys Val Asn Tyr Asp Gln Val Met Ala Phe Tyr Asn Glu Arg Phe
690 695 700

Ala Asp Ala Gly Asp Phe Met Phe Phe Phe Ile Gly Asn Leu Asp Glu
705 710 715 720

Ala Lys Met Lys Pro Leu Ile Glu Thr Tyr Leu Ala Ser Leu Pro Asn
725 730 735

Leu Lys Arg Gly Asp Lys Met Asn Lys Ala Gln Val Pro Ala Ala Arg
740 745 750

Ser Gly Lys Ile Asp Cys Lys Phe Glu Lys Glu Met Asp Thr Pro Ser
755 760 765

Thr Thr Ile Phe Asp Val Val Ser Gly Asn Val Glu Tyr Thr Leu Lys
770 775 780

Asn Ser Leu Leu Leu Glu Val Phe Ser Ala Val Met Asp Gln Val Tyr
785 790 795 800

Thr Ala Thr Val Arg Glu Lys Glu Gly Gly Ala Tyr Ser Val Ala Ala
805 810 815

Phe Gly Gly Leu Glu Gln Tyr Pro Gln Pro Lys Ala Leu Met Gln Ile
820 825 830

Tyr Phe Pro Thr Asp Pro Ala Arg Ala Glu Glu Met Asn Ala Ile Val
835 840 845

Phe Ala Glu Leu Glu Lys Leu Ala Lys Glu Gly Pro Asn Val Glu Tyr
850 855 860

Phe Lys Lys Thr Ile Glu Asn Leu Asn Lys Gln His Lys Glu Ser Leu
865 870 875 880

Arg Glu Asn Arg Phe Trp Leu Glu Ala Met Lys Ala Ser Phe Phe Glu
885 890 895

Gly Asn Asp Phe Ile Thr Asp Tyr Glu Ser Val Leu Asn Gly Leu Thr
900 905 910

Pro Ala Glu Leu Gln Lys Phe Ala Ala Asp Leu Leu Lys Gln Gln Asn
915 920 925

Arg Val Val Val Met Met Ala Pro Val Ala Lys Ala Gln
 930 935 940
 <210> 407
 <211> 684
 <212> PRT
 <213> Porphyromonas gingivalis
 <400> 407
 Met Ser Lys Lys Gly Thr Ile Gly Val Thr Ser Asp Asn Ile Phe Pro
 1 5 10 15
 Val Ile Lys Lys Phe Leu Tyr Ser Asp His Glu Ile Phe Leu Arg Glu
 20 25 30
 Ile Val Ser Asn Ala Val Asp Ala Thr Gln Lys Leu Lys Thr Leu Thr
 35 40 45
 Ser Val Gly Glu Phe Lys Gly Glu Thr Gly Asp Leu Arg Val Thr Val
 50 55 60
 Ser Val Asp Glu Val Ala Arg Thr Ile Thr Val Ser Asp Arg Gly Val
 65 70 75 80
 Gly Met Thr Glu Glu Glu Val Glu Lys Tyr Ile Asn Gln Ile Ala Phe
 85 90 95
 Ser Ser Ala Glu Glu Phe Leu Glu Lys Tyr Lys Asp Asp Lys Ala Ala
 100 105 110
 Ile Ile Gly His Phe Gly Leu Gly Phe Tyr Ser Ala Phe Met Val Ser
 115 120 125
 Glu Arg Val Asp Val Ile Thr Arg Ser Phe Arg Glu Asp Ala Thr Ala
 130 135 140
 Val Lys Trp Ser Cys Asp Gly Ser Pro Glu Tyr Thr Leu Glu Pro Ala
 145 150 155 160
 Asp Lys Ala Asp Arg Gly Thr Asp Ile Val Met His Ile Asp Glu Glu
 165 170 175
 Asn Ser Glu Phe Leu Lys Lys Glu Lys Ile Glu Gly Leu Leu Gly Lys
 180 185 190
 Tyr Cys Lys Phe Leu Thr Val Pro Ile Ile Phe Gly Lys Lys Gln Glu
 195 200 205
 Trp Lys Asp Gly Lys Met Gln Asp Thr Asp Glu Asp Asn Gln Ile Asn
 210 215 220
 Asp Thr His Pro Ala Trp Thr Lys Lys Pro Ala Asp Leu Lys Asp Glu
 225 230 235 240
 Asp Tyr Lys Glu Phe Tyr Arg Ser Leu Tyr Pro Met Ser Glu Glu Pro
 245 250 255
 Leu Phe Trp Ile His Leu Asn Val Asp Tyr Pro Phe Asn Leu Thr Gly
 260 265 270
 Ile Leu Tyr Phe Pro Lys Ile Lys Asn Asn Leu Asp Leu Gln Arg Asn
 275 280 285
 Lys Ile Gln Leu Tyr Cys Asn Gln Val Tyr Val Thr Asp Glu Val Gln
 290 295 300
 Gly Ile Val Pro Asp Phe Leu Thr Leu Leu His Gly Val Ile Asp Ser
 305 310 315 320
 Pro Asp Ile Pro Leu Asn Val Ser Arg Ser Tyr Leu Gln Ser Asp Ala
 325 330 335
 Asn Val Lys Lys Ile Ser Ser His Ile Thr Lys Lys Val Ala Asp Arg
 340 345 350
 Leu Glu Glu Ile Phe Lys Asn Asp Arg Pro Thr Phe Glu Glu Lys Trp

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        355                360                365
Asp Ser Leu Lys Leu Phe Val Glu Tyr Gly Met Leu Thr Asp Glu Lys
 370                375                380
Phe Tyr Glu Arg Ala Ala Lys Phe Phe Leu Phe Thr Asp Met Asp Gly
385                390                395                400
His Lys Tyr Thr Phe Asp Glu Tyr Arg Thr Leu Val Glu Gly Val Gln
        405                410                415
Thr Asp Lys Asp Gly Gln Val Val Tyr Leu Tyr Ala Thr Asp Lys His
        420                425                430
Gly Gln Tyr Ser His Val Lys Arg Ala Ser Asp Lys Gly Tyr Ser Val
        435                440                445
Met Leu Leu Asp Gly Gln Leu Asp Pro His Ile Val Ser Leu Leu Glu
        450                455                460
Gln Lys Leu Glu Lys Thr His Phe Val Arg Val Asp Ser Asp Thr Ile
465                470                475                480
Asn Asn Leu Ile Arg Lys Glu Glu Arg Ala Glu Val Lys Leu Ser Asp
        485                490                495
Thr Glu Arg Ala Thr Leu Val Lys Leu Phe Glu Ala Arg Leu Pro Arg
        500                505                510
Asp Glu Lys Lys His Phe Asn Val Ala Phe Glu Ser Leu Gly Ala Glu
        515                520                525
Gly Glu Ala Ile Leu Ile Thr Gln Ala Glu Phe Met Arg Arg Met Arg
        530                535                540
Asp Met Ala Gln Leu Gln Pro Gly Met Ser Phe Tyr Gly Glu Leu Pro
545                550                555                560
Asp Ser Tyr Asn Leu Val Leu Asn Thr Asp His Pro Leu Ile Asp Arg
        565                570                575
Val Leu Ser Gly Glu Lys Glu Ser Val Glu Pro Ser Leu Thr Glu Leu
        580                585                590
Arg Ala Lys Ile Ala Glu Leu Lys Ala Glu Glu Ala Lys Leu Leu Asp
        595                600                605
Glu Glu Lys Gly Lys Lys Pro Glu Glu Ile Pro Val Ala Thr Lys Glu
        610                615                620
Ala Lys Glu Asn Asn Ala Val Glu Gln Ala Lys Thr Glu Gly Ser Ile
625                630                635                640
Asn Asp Gln Leu Thr Lys Tyr Ala Gln Asp Asn Glu Leu Ile Gly Gln
        645                650                655
Leu Ile Asp Leu Ala Leu Leu Gly Ser Gly Leu Leu Thr Gly Glu Ala
        660                665                670
Leu Ala Glu Phe Ile Arg Arg Ser Gln Arg Leu Leu
        675                680
<210>    408
<211>    464
<212>    PRT
<213>    Porphyromonas gingivalis
<400>    408
Met Glu Lys Leu Ile Asp Ile Leu Val Val Asp Asp Asp Val Ala Val
  1                5                10                15
Cys Ala Ala Leu Arg Leu Val Leu Lys Arg Ala Gly Tyr Asn Pro Val
        20                25                30
Ile Ala Asn Ser Pro Asp Glu Ala Leu Ser Ile Met Arg Asn Pro Asp
        35                40                45

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

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<210>      409
<211>      250
<212>      PRT
<213>      Porphyromonas gingivalis
<400>      409
Met Leu Lys Ile Lys Asn Leu His Ala Thr Val Gln Gly Lys Glu Ile
 1          5          10          15
Leu Lys Gly Ile Asn Leu Glu Ile Asn Ala Gly Glu Ile His Ala Ile
          20          25          30
Met Gly Pro Asn Gly Ser Gly Lys Ser Thr Leu Ser Ser Val Leu Val
          35          40          45
Gly His Pro Ser Phe Glu Val Thr Glu Gly Glu Val Thr Phe Asn Gly
          50          55          60
Ile Asp Leu Leu Glu Leu Glu Pro Glu Glu Arg Ala His Leu Gly Leu
          65          70          75          80
Phe Leu Ser Phe Gln Tyr Pro Val Glu Ile Pro Gly Val Ser Met Val
          85          90          95
Asn Phe Met Arg Ala Ala Val Asn Glu His Arg Lys Ala Ile Gly Ala
          100          105          110
Glu Pro Val Ser Ala Ser Asp Phe Leu Lys Met Met Arg Glu Lys Arg
          115          120          125
Ala Ile Val Glu Leu Asp Asn Lys Leu Ala Ser Arg Ser Val Asn Glu
          130          135          140
Gly Phe Ser Gly Gly Glu Lys Lys Arg Asn Glu Ile Phe Gln Met Ala
          145          150          155          160
Met Leu Glu Pro Lys Leu Ala Ile Leu Asp Glu Thr Asp Ser Gly Leu
          165          170          175
Asp Ile Asp Ala Leu Arg Ile Val Ala Gly Gly Val Asn Arg Leu Arg
          180          185          190
Ser Pro Glu Asn Ala Ala Ile Val Ile Thr His Tyr Gln Arg Leu Leu
          195          200          205
Glu Tyr Ile Lys Pro Asp Phe Val His Val Leu Tyr Lys Gly Arg Ile
          210          215          220
Val Lys Ser Gly Gly Ala Glu Leu Ala Leu Thr Leu Glu Glu Lys Gly
          225          230          235          240
Tyr Asp Trp Ile Lys Glu Glu Ile Gly Glu
          245          250

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<210>      410
<211>      461
<212>      PRT
<213>      Porphyromonas gingivalis
<400>      410
Met Ala Lys Glu Lys Thr Ile Tyr Val Cys Arg Ser Cys Gly Thr Lys
 1          5          10          15
Tyr Ala Lys Trp Gln Gly Asn Cys Asn Ala Cys Gly Glu Trp Asn Cys
          20          25          30
Ile Asp Glu Glu Lys Val Pro Ala Pro Ala Ser Gly Lys His Ala Ala
          35          40          45
Lys Ser Phe Met Pro Arg Glu Gln Asp Asn Arg Pro Arg Leu Leu Gln
          50          55          60
Asp Val Glu Ser Gly Asp Glu Glu Arg Ile Arg Leu Gly Asp Glu Glu
          65          70          75          80

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Phe Asp Arg Val Leu Gly Gly Gly Ile Val Lys Gly Ala Phe Val Leu
 85 90 95
 Leu Gly Gly Glu Pro Gly Ile Gly Lys Ser Thr Leu Ile Leu Gln Thr
 100 105 110
 Val Leu Arg Leu Pro Gln Leu Arg Thr Leu Tyr Val Ser Gly Glu Glu
 115 120 125
 Ser Ala Arg Gln Leu Lys Met Arg Ala Glu Arg Leu Gly Gln Ala Met
 130 135 140
 Asn Gly Cys Tyr Val Tyr Cys Glu Thr Asn Ile Glu Arg Ile Leu Ser
 145 150 155 160
 Arg Ala Glu Glu Leu Thr Pro Asp Leu Leu Val Ile Asp Ser Ile Gln
 165 170 175
 Thr Val Tyr Thr Glu Glu Met Glu Ser Ser Ala Gly Ser Val Gly Gln
 180 185 190
 Ile Arg Glu Cys Ala Ala Leu Leu Lys Tyr Cys Lys Thr Thr Gly
 195 200 205
 Ile Pro Val Ile Val Ile Gly His Ile Thr Lys Glu Gly Ser Ile Ala
 210 215 220
 Gly Pro Lys Val Leu Glu His Ile Val Asp Thr Val Leu Leu Phe Asp
 225 230 235 240
 Gly Asp Lys His His Leu Tyr Arg Ile Leu Arg Gly Gln Lys Asn Arg
 245 250 255
 Tyr Gly Ser Thr Ser Glu Leu Gly Ile Tyr Glu Met Arg Gln Asp Gly
 260 265 270
 Leu Arg Gly Val Glu Asn Pro Ser Glu His Leu Ile Thr Arg Asn Arg
 275 280 285
 Glu Asp Leu Ser Gly Ile Ala Ile Ala Val Ala Met Glu Gly Ile Arg
 290 295 300
 Pro Ile Leu Ile Glu Ala Gln Ala Leu Val Ser Ser Ala Ile Tyr Ala
 305 310 315 320
 Asn Pro Gln Arg Ser Ala Thr Gly Phe Asp Ile Arg Arg Met Asn Met
 325 330 335
 Leu Leu Ala Val Leu Glu Lys Arg Ala Gly Phe Lys Leu Ile Gln Lys
 340 345 350
 Asp Val Phe Leu Asn Ile Ala Gly Gly Ile Lys Ile Ala Asp Pro Ala
 355 360 365
 Thr Asp Leu Ala Val Ile Ser Ala Val Leu Ala Ser Ser Leu Asp Ile
 370 375 380
 Val Ile Pro Pro Ala Val Cys Met Thr Gly Glu Val Gly Leu Ser Gly
 385 390 395 400
 Glu Ile Arg Pro Val Ser Arg Ile Glu Gln Arg Ile Thr Glu Ala Arg
 405 410 415
 Arg Ile Gly Phe Lys Glu Ile Leu Val Pro Ala Asp Asn Phe Arg Gln
 420 425 430
 Glu Asp Ala Gly Arg Phe Gly Ile Arg Leu Val Pro Val Arg Lys Val
 435 440 445
 Glu Glu Ala Phe Arg His Leu Phe Ser Lys Gly Arg Glu
 450 455 460
 <210> 411
 <211> 271
 <212> PRT
 <213> Porphyromonas gingivalis

<400> 411
Met Asn Ser Arg His Leu Thr Ile Thr Ile Ile Ala Gly Leu Ser Leu
1 5 10 15
Phe Val Leu Thr Leu Gly Gly Cys Ser Val Ala Gln Gln Asp Thr Gln
20 25 30
Trp Thr Leu Gly Gly Lys Leu Phe Thr Ser Ala Trp Ile Gln Arg Ser
35 40 45
Ala Glu Tyr Gln Ala Leu Cys Ile Gln Ala Tyr Asn Ile Ala Thr Glu
50 55 60
Arg Val Asp Ala Leu Pro Ala Glu Arg Lys Gln Gly Asp Arg Pro Tyr
65 70 75 80
Ala Ile Val Thr Asp Ile Asp Glu Thr Ile Leu Asp Asn Thr Pro Asn
85 90 95
Ser Val Tyr Gln Ala Leu Arg Gly Lys Asp Tyr Asp Glu Glu Thr Trp
100 105 110
Gly Lys Trp Cys Ala Gln Ala Asp Ala Asp Thr Leu Ala Gly Ala Leu
115 120 125
Ser Phe Phe Leu His Ala Ala Asn Lys Gly Ile Glu Val Phe Tyr Val
130 135 140
Thr Asn Arg Arg Asp Asn Leu Arg Glu Ala Thr Leu Gln Asn Leu Gln
145 150 155 160
Arg Tyr Gly Phe Pro Phe Ala Asp Glu Glu His Leu Leu Thr Thr His
165 170 175
Gly Pro Ser Asp Lys Glu Pro Arg Arg Leu Lys Ile Gln Glu Gln Tyr
180 185 190
Glu Ile Val Leu Leu Ile Gly Asp Asn Leu Gly Asp Phe His His Phe
195 200 205
Phe Asn Thr Lys Glu Glu Ser Gly Arg Lys Gln Ala Leu Gly Leu Thr
210 215 220
Ala Gly Glu Phe Gly Arg His Phe Ile Met Leu Pro Asn Pro Asn Tyr
225 230 235 240
Gly Ser Trp Glu Pro Ala Trp Tyr Gly Gly Lys Tyr Pro Pro Leu Pro
245 250 255
Glu Arg Asp Lys Ala Leu Lys Gln Leu His Ser Gln Asn Ser Arg
260 265 270

<210> 412
<211> 417
<212> PRT
<213> Porphyromonas gingivalis
<400> 412

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

Val Ser Asp Arg Lys Gly Tyr Phe Glu Glu Ala Ser Gly Gly Thr Ile
100 105 110
Phe Leu Asp Glu Val Gly Glu Leu Pro Leu Pro Thr Gln Ala Arg Leu
115 120 125
Leu Arg Val Leu Glu Thr Gly Glu Phe Ile Pro Val Gly Ala Ser Gln
130 135 140
Ser Gln Lys Thr Asp Val Arg Ile Val Ala Ala Thr Asn Val Asn Leu
145 150 155 160
Lys Glu Ala Val Ala Asn Gly Lys Phe Arg Glu Asp Leu Phe Phe Arg
165 170 175
Leu Asn Thr Val Pro Ile Glu Val Pro Ala Leu Arg Met Arg Pro Asp
180 185 190
Asp Val Pro Leu Leu Phe Arg Arg Phe Ala Ala Asp Ser Ala Glu Lys
195 200 205
Tyr Arg Met Pro Pro Leu Arg Leu Ser Asp Glu Ala Arg Thr Ile Leu
210 215 220
Met Arg Tyr Arg Trp Pro Gly Asn Val Arg Glu Leu Arg Asn Ile Thr
225 230 235 240
Asp Arg Leu Ser Ile Leu Glu Glu Glu Arg Thr Val Ser Ala Glu Thr
245 250 255
Ile Thr Arg Tyr Leu Asp Ala Glu Gly Met Gln Asp Leu His Pro Val
260 265 270
Val Ile Arg Arg Asn Glu Thr Thr Glu Ala Asp Lys Gln Ile Pro His
275 280 285
Tyr Glu Arg Glu Ile Ile Tyr Gln Val Leu Tyr Asp Met Lys Lys Glu
290 295 300
Ile Ala Asp Leu Lys Gly Met Met Asn Arg Leu Ala His His Glu Gln
305 310 315 320
Pro Ser Trp Pro Val Gly Ser Asp Val Trp Gly Asn Asp Asp Lys Arg
325 330 335
Thr Ala Asp Pro Lys Trp Gly Val Ser Thr His Lys Ala Pro Ile Ala
340 345 350
Asn Ala Ala Glu Pro Val Glu Pro Ile Gln Glu Ala Ser Glu Tyr Thr
355 360 365
Glu Asp Pro Val Ser Leu Glu Glu Val Glu Lys Lys Met Ile Ser Leu
370 375 380
Ala Leu Glu Arg His Gly Gly Arg Arg Lys Gln Thr Ala Glu Glu Leu
385 390 395 400
Lys Ile Ser Glu Arg Thr Leu Tyr Arg Lys Ile Lys Glu Tyr Gly Leu
405 410 415
Glu
<210> 413
<211> 602
<212> PRT
<213> Porphyromonas gingivalis
<400> 413
Met Ile Leu Leu Phe Gly Gly Thr Thr Glu Gly Arg Ala Ala Ala Arg
1 5 10 15
Val Leu Asp Glu Ala Gly Ser Pro Phe Phe Tyr Ser Thr Lys Gly Asn
20 25 30
Leu Gln Glu Ile Gln Ser Ser His Gly His Arg Leu Thr Gly Ala Met
35 40 45

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

Ala Leu Ile Pro Gln Ala Phe Val Gln Tyr Gly Asn Phe Val Gly Glu
 465 470 475 480
 Ser Leu Ser Cys Val Ala Ser Phe Pro Ser Val Arg Ser Val Thr Val
 485 490 495
 Gly Ile Met Leu Gly Lys Ala Val Lys Leu Ala Glu Gly Tyr Leu Asp
 500 505 510
 Thr His Ser Lys Lys Val Val Met Asn Arg Asp Phe Leu His Glu Leu
 515 520 525
 Ala Arg Gln Ala Gly Cys Ser Glu Asp Ile His Ala Ile Ile Asp Ser
 530 535 540
 Leu Asn Leu Ala Arg Glu Leu Trp Thr Met Pro Ser Ala Glu Asp Ser
 545 550 555 560
 Asp Arg Leu Leu Arg Lys Ile Ala Glu Arg Ser Trp Glu Thr Cys Arg
 565 570 575
 Pro Ser Val Pro Ser Ala Glu Leu Glu Leu Leu Ile Asp Glu Ser
 580 585 590
 Gly Ala Ile Arg Phe Arg Ile Gly Gly Glu
 595 600
 <210> 414
 <211> 443
 <212> PRT
 <213> Porphyromonas gingivalis
 <400> 414
 Met Leu Arg Thr Phe Arg Ile Gly Gly Ile His Pro Pro Glu Asn Lys
 1 5 10 15
 Leu Ser Ala Gly Lys Pro Val Glu Val Leu Pro Ile Pro Ser Gln Val
 20 25 30
 Val Ile Pro Leu Gly Gln His Ile Gly Ala Pro Ala Thr Ala Thr Val
 35 40 45
 Lys Lys Gly Asp Glu Val Lys Val Gly Thr Ile Ile Ala Gln Ala Gly
 50 55 60
 Gly Phe Val Ser Ala Asn Ile His Ser Ser Val Ser Gly Lys Val Leu
 65 70 75 80
 Lys Ile Asp Asn Val Tyr Asp Ser Ser Gly Tyr Pro Lys Pro Ala Val
 85 90 95
 Phe Ile Ser Val Glu Gly Asp Glu Trp Glu Glu Gly Ile Asp Arg Ser
 100 105 110
 Pro Ala Ile Val Lys Glu Cys Asn Leu Asp Ala Lys Glu Ile Val Ala
 115 120 125
 Lys Ile Ser Ala Ala Gly Ile Val Gly Leu Gly Gly Ala Thr Phe Pro
 130 135 140
 Thr His Val Lys Leu Ser Pro Pro Pro Gly Asn Lys Ala Glu Ile Leu
 145 150 155 160
 Ile Ile Asn Ala Val Glu Cys Glu Pro Tyr Leu Thr Ser Asp His Val
 165 170 175
 Leu Met Leu Glu His Gly Glu Glu Ile Met Ile Gly Val Ser Ile Leu
 180 185 190
 Met Lys Ala Ile Gln Val Asn Lys Ala Val Ile Gly Val Glu Asn Asn
 195 200 205
 Lys Lys Asp Ala Ile Ala His Leu Thr Lys Leu Ala Thr Ala Tyr Pro
 210 215 220
 Gly Ile Glu Val Met Pro Leu Lys Val Gln Tyr Pro Gln Gly Gly Glu

225					230					235					240	
Lys	Gln	Leu	Ile	Asp	Ala	Val	Ile	Arg	Lys	Gln	Val	Lys	Ser	Gly	Ala	
				245					250					255		
Leu	Pro	Ile	Ser	Thr	Gly	Ala	Val	Val	Gln	Asn	Val	Gly	Thr	Val	Phe	
				260					265					270		
Ala	Val	Tyr	Glu	Ala	Val	Gln	Lys	Asn	Lys	Pro	Leu	Val	Glu	Arg	Ile	
				275					280					285		
Val	Thr	Val	Thr	Gly	Lys	Lys	Leu	Ser	Arg	Pro	Ser	Asn	Leu	Leu	Val	
				290					295					300		
Arg	Ile	Gly	Thr	Pro	Ile	Ala	Ala	Leu	Ile	Glu	Ala	Ala	Gly	Gly	Leu	
305					310					315					320	
Pro	Glu	Asn	Thr	Gly	Lys	Ile	Ile	Gly	Gly	Gly	Pro	Met	Met	Gly	Arg	
				325					330					335		
Ala	Leu	Leu	Ser	Pro	Asp	Val	Pro	Val	Thr	Lys	Gly	Ser	Ser	Gly	Val	
				340					345					350		
Leu	Ile	Leu	Asp	Arg	Glu	Glu	Ala	Val	Arg	Lys	Pro	Met	Arg	Asp	Cys	
				355					360					365		
Ile	Arg	Cys	Ala	Lys	Cys	Val	Gly	Val	Cys	Pro	Met	Gly	Leu	Asn	Pro	
				370					375					380		
Ala	Phe	Leu	Met	Arg	Asp	Thr	Leu	Tyr	Lys	Ser	Trp	Glu	Thr	Ala	Glu	
385					390					395					400	
Lys	Gly	Asn	Val	Val	Asp	Cys	Ile	Glu	Cys	Gly	Ser	Cys	Ser	Phe	Thr	
				405					410					415		
Cys	Pro	Ala	Asn	Arg	Pro	Leu	Leu	Asp	Tyr	Ile	Arg	Gln	Ala	Lys	Lys	
				420					425					430		
Thr	Val	Met	Gly	Ile	Gln	Arg	Ala	Arg	Lys	Gln						
				435					440							
<210>			415													
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<213>			Porphyromonas gingivalis													
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Met	Lys	Arg	Ile	Gln	Leu	Thr	Leu	Ile	Ala	Leu	Phe	Ala	Ala	Val	Ala	
1					5					10					15	
Gly	Leu	Val	Ala	Gln	Asn	Ala	Tyr	Glu	Gly	Val	Ile	Ser	Tyr	Lys	Ile	
				20					25					30		
Ser	Leu	Asp	Lys	Thr	Gly	Asn	Lys	Val	Val	Leu	Asn	Gly	Ala	Ala	Asp	
				35					40					45		
Met	Ser	Asn	Leu	Lys	Leu	Lys	Ser	Thr	Gln	Met	Ile	Ile	Val	Thr	Pro	
				50					55					60		
Ile	Leu	Arg	Ser	Glu	Asp	Gly	Thr	Ser	Arg	Val	Glu	Phe	Pro	Ser	Val	
				65					70					75		
Val	Ile	Thr	Gly	Arg	Asn	Arg	Thr	Lys	Ala	Leu	Lys	Arg	Glu	Ile	Ala	
				85					90					95		
Phe	Ser	Ser	Ala	Leu	Pro	Gln	Ala	Lys	His	Ala	Ala	Gln	Tyr	Ile	Arg	
				100					105					110		
Arg	His	Asn	Gly	Lys	Ser	Glu	Gln	Phe	Ala	Phe	Thr	Gly	Glu	His	Ala	
				115					120					125		
Tyr	Ala	Ser	Trp	Met	Met	Asp	Ala	Lys	Phe	Val	Val	Arg	Glu	Glu	Val	
				130					135					140		
Arg	Gly	Cys	Ala	Lys	Cys	Pro	Val	Gly	Leu	Ser	Ser	Asn	Ile	Val	Pro	
145					150					155					160	

Phe Asp Pro Leu Phe Asn Pro Ala Glu Ala Pro Tyr Leu Leu Ala His
 165 170 175
 Ile Thr Pro Ala Glu Glu Val Glu Lys Gln Arg Glu Ser Ser Phe Asp
 180 185 190
 Ala Tyr Ile Asn Phe Lys Val Asn Lys Ala Asp Val Leu Pro Glu Tyr
 195 200 205
 Arg Asn Asn Lys Ala Glu Leu Glu Lys Ile Lys Glu Phe Val Ser Thr
 210 215 220
 Val Lys Ala Asn Pro Asn Tyr Ser Val Asn Lys Met Ile Ile Glu Gly
 225 230 235 240
 Phe Ala Ser Pro Glu Ala Ser Ile Ala His Asn Lys Ala Leu Ser Glu
 245 250 255
 Arg Arg Ala Lys Arg Leu Ala Glu Glu Leu Val Arg Lys Tyr Gly Lys
 260 265 270
 Thr Leu Pro Asn Ile Thr Thr Glu Phe Gly Gly Glu Asp Trp Lys Gly
 275 280 285
 Leu Lys Leu Ala Ile Glu Lys Ser Asp Ile Ala Asp Arg Asp Arg Val
 290 295 300
 Leu Glu Ile Ile Asn Ser Asp Lys Tyr Ala Asp Asp Ala Arg Glu
 305 310 315 320
 Gln Ala Leu Lys Gln Leu Ser Ser Tyr Arg Tyr Ile Leu Asp Gln Ile
 325 330 335
 Tyr Pro Asn Leu Arg Arg Asn Thr Ile Thr Met Gly Tyr Ile Val Arg
 340 345 350
 Asp Tyr Thr Leu Glu Glu Ala Arg Glu Ile Ile Lys Thr Ala Pro Lys
 355 360 365
 Glu Leu Ser Glu Ala Glu Met Tyr Arg Val Ala Met Ser Tyr Pro Glu
 370 375 380
 Gly His Gln Glu Arg Leu Phe Ala Leu Asn Thr Thr Leu Lys Tyr Phe
 385 390 395 400
 Pro Glu Ser Val Thr Gly Arg Ile Asn Leu Ala Val Ala Ala Phe Asn
 405 410 415
 Gly Gly Asp Val Gln Gln Ala Ile Ala Leu Leu Ser Pro Ile Gln Thr
 420 425 430
 Glu Lys Gly Val Ser Asn Ile Leu Gly Ala Ala Tyr Ala Arg Thr Gly
 435 440 445
 Asp Phe Ala Arg Ala Glu Thr Phe Phe Arg Lys Ala Val Ala Glu Gly
 450 455 460
 Asp Ala Asn Ala Gln Arg Asn Leu Asp Met Leu Leu Gly Lys Lys
 465 470 475
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 <212> PRT
 <213> Porphyromonas gingivalis
 <400> 416
 Met Ala Glu Lys Arg Asp Tyr Tyr Glu Val Leu Gly Val Ser Lys Asn
 1 5 10 15
 Ala Thr Asp Asp Glu Leu Lys Lys Ala Tyr Arg Lys Lys Ala Ile Gln
 20 25 30
 Tyr His Pro Asp Lys Asn Pro Gly Asp Lys Glu Ala Glu Glu His Phe
 35 40 45
 Lys Glu Val Ala Glu Ala Tyr Asp Val Leu Ser Asp Pro Gln Lys Arg

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50          55          60
Ser Gln Tyr Asp Gln Phe Gly His Ala Gly Leu Gly Gly Ala Ala Gly
65          70          75          80
Gly Gly Phe Ser Gly Gly Gly Met Ser Met Glu Asp Ile Phe Ser Arg
85          90          95
Phe Gly Asp Leu Phe Gly Gly Phe Gly Gly Phe Gly Gly Phe Ser Asp
100        105        110
Met Gly Gly Gly Ser Arg Arg Arg Val Arg Arg Gly Ser Asp Leu Arg
115        120        125
Val Arg Val Lys Leu Ser Leu Ala Asp Ile Ser Lys Gly Val Glu Lys
130        135        140
Lys Val Lys Val Lys Lys Gln Val Val Cys Ser Lys Cys Arg Gly Asp
145        150        155        160
Gly Thr Glu Glu Ala Asn Gly Lys Thr Thr Cys Gln Thr Cys His Gly
165        170        175
Thr Gly Val Val Thr Arg Val Ser Asn Thr Phe Leu Gly Ala Met Gln
180        185        190
Thr Gln Ser Thr Cys Pro Thr Cys His Gly Glu Gly Glu Ile Ile Thr
195        200        205
Lys Pro Cys Ser Lys Cys Lys Gly Glu Gly Val Glu Ile Gly Glu Glu
210        215        220
Val Ile Ser Phe His Ile Pro Ala Gly Val Ala Glu Gly Met Gln Met
225        230        235        240
Ser Val Asn Gly Lys Gly Asn Ala Ala Pro Arg Gly Gly Val Asn Gly
245        250        255
Asp Leu Ile Val Val Ile Ala Glu Glu Pro Asp Pro Asn Leu Ile Arg
260        265        270
Asn Gly Asn Asp Leu Ile Tyr Asn Leu Leu Ile Ser Val Pro Leu Ala
275        280        285
Ile Lys Gly Gly Ser Val Glu Val Pro Thr Ile Asp Gly Arg Ala Lys
290        295        300
Ile Arg Ile Glu Ala Gly Thr Gln Pro Gly Lys Met Leu Arg Leu Arg
305        310        315        320
Asn Lys Gly Leu Pro Ser Val Asn Gly Tyr Gly Met Gly Asp Gln Leu
325        330        335
Val Asn Val Asn Val Tyr Ile Pro Glu Ser Ile Asp Ala Lys Asp Glu
340        345        350
Gln Ala Ile Ala Ala Met Glu Asn Ser Asp Ser Phe Lys Pro Thr Asp
355        360        365
Ala Ala Arg Lys Asp Ile Asp Lys Lys Tyr Arg Glu Met Leu Asp
370        375        380
<210>    417
<211>    293
<212>    PRT
<213>    Porphyromonas gingivalis
<400>    417
Met Lys Lys Leu Ile Leu Ala Thr Leu Gly Leu Met Ala Ile Ala Met
1          5          10          15
Leu Ser Cys Ser Ser Asn Asn Lys Asp Leu Glu Asn Lys Gly Glu Ala
20        25        30
Thr Leu Leu Val Thr Phe Gly Ser Ser Tyr Lys Ala Pro Arg Glu Thr
35        40        45

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Tyr Ala Lys Ile Glu Lys Thr Phe Ala Ala Ala Tyr Pro Asp Gln Arg
 50 55 60
 Ile Ser Trp Thr Tyr Thr Ser Ser Ile Ile Arg Lys Lys Leu Ala Gln
 65 70 75 80
 Gln Gly Ile Tyr Ile Asp Ala Pro Asp Glu Ala Leu Glu Lys Leu Ala
 85 90 95
 Arg Leu Gly Tyr Lys Lys Ile Asn Val Gln Ser Leu His Val Ile Pro
 100 105 110
 Gly Arg Glu Tyr Asp Glu Met Ile Asp Phe Val Asn Lys Phe Lys Ala
 115 120 125
 Ala His Ser Asp Ile Thr Val Lys Val Gly Ala Pro Leu Phe Asp Thr
 130 135 140
 Asp Glu Asp Met Arg Glu Val Ala Glu Ile Leu His Lys Arg Phe Gln
 145 150 155 160
 Gln Thr Ile Glu Lys Gly Glu Ala Ile Val Phe Met Gly His Gly Thr
 165 170 175
 Glu His Ala Ala Asn Asp Arg Tyr Ala Arg Ile Asn Lys Ile Met Lys
 180 185 190
 Asn Tyr Ser Lys Phe Met Ile Val Gly Thr Val Glu Ser Asp Pro Ser
 195 200 205
 Ile Asn Asp Val Ile Ala Glu Leu Lys Glu Thr Gly Ala Thr Ala Val
 210 215 220
 Thr Met Met Pro Leu Met Ser Val Ala Gly Asp His Ala Thr Asn Asp
 225 230 235 240
 Met Ala Gly Asp Glu Asp Asp Ser Trp Lys Thr Leu Leu Thr Asn Ala
 245 250 255
 Gly Tyr Thr Val Ser Ile Asp Lys Leu Asp Asn Gly Asn Phe Ser Ala
 260 265 270
 Leu Gly Asp Ile Glu Glu Ile Arg Asn Ile Trp Leu Lys His Met Lys
 275 280 285
 Ala Thr Ser Ala Arg
 290
 <210> 418
 <211> 356
 <212> PRT
 <213> Porphyromonas gingivalis
 <400> 418
 Met Thr Ser Val Ser His Leu Arg Thr Ile Ser Val Ala Gly Ile Leu
 1 5 10 15
 Ala Ala Leu Gly Gly Ala Val Leu Ile Leu Phe Gly Val Asn Leu Phe
 20 25 30
 Leu Gly Ser Val Ala Ile Pro Met Ser Glu Ile Phe Arg His Leu Phe
 35 40 45
 Ser Asp Arg Pro Glu Gly Gly Glu Ala Leu Val His Tyr Asn Ile Leu
 50 55 60
 Trp Lys Ser Arg Leu Pro Glu Ala Leu Thr Ala Ala Phe Ala Gly Ala
 65 70 75 80
 Gly Leu Ser Val Ser Gly Leu Gln Met Gln Thr Val Phe Arg Asn Pro
 85 90 95
 Leu Ala Gly Pro Ser Val Leu Gly Ile Ser Ser Gly Ala Ser Leu Gly
 100 105 110
 Val Ala Leu Val Val Leu Leu Ser Gly Ser Leu Gly Gly Val Ala Leu

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115          120          125
Ser Ser Leu Gly Tyr Met Gly Glu Val Ala Met Asn Ile Ala Ala Ala
130          135          140
Val Gly Ser Leu Ala Val Met Gly Leu Ile Val Phe Val Ser Thr Lys
145          150          155          160
Val Arg Ser His Val Thr Leu Leu Ile Ile Gly Val Met Ile Gly Tyr
165          170          175
Val Ala Thr Ala Val Ile Gly Val Phe Lys Phe Phe Ser Ile Glu Glu
180          185          190
Asp Ile Arg Ala Tyr Val Ile Trp Gly Leu Gly Ser Phe Ser Arg Ala
195          200          205
Thr Asp Ser Gln Leu Ser Phe Phe Ala Ile Leu Met Leu Ile Phe Ile
210          215          220
Pro Ala Gly Met Leu Leu Val Lys Gln Leu Asn Leu Leu Leu Leu Gly
225          230          235          240
Glu Ser Tyr Ala Arg Asn Leu Gly Leu Asn Thr Arg Arg Ala Arg Leu
245          250          255
Leu Val Ile Ser Ser Ala Gly Leu Leu Ile Ala Thr Val Thr Ala Tyr
260          265          270
Cys Gly Pro Ile Gly Phe Leu Gly Met Ala Val Pro His Leu Ala Arg
275          280          285
Val Ile Phe His Thr Ser Asp His Arg Ile Leu Met Pro Ala Thr Cys
290          295          300
Leu Ile Gly Ser Ala Leu Ala Leu Phe Cys Asn Ile Ile Ala Arg Met
305          310          315          320
Pro Gly Phe Glu Gly Ala Leu Pro Val Asn Ser Val Thr Ala Leu Val
325          330          335
Gly Ala Pro Ile Ile Val Thr Val Leu Phe Arg Arg Arg Arg Phe Lys
340          345          350
Glu Glu Thr Asp
355
<210> 419
<211> 757
<212> PRT
<213> Porphyromonas gingivalis
<400> 419
Met Arg Thr Lys Thr Ile Phe Phe Ala Ile Ile Ser Phe Ile Ala Leu
1 5 10 15
Leu Ser Ser Ser Leu Ser Ala Gln Ser Lys Ala Val Leu Thr Gly Ser
20 25 30
Val Ser Asp Ala Glu Thr Gly Glu Pro Leu Ala Gly Ala Arg Ile Glu
35 40 45
Val Lys His Thr Asn Ile Val Ala Gly Ala Asp Ala Gly Gly His Phe
50 55 60
Glu Ile Lys Asn Leu Pro Ala Gly Gln His Thr Ile Ile Cys Ser Leu
65 70 75 80
Gly Gly Tyr Gly Gln Lys Glu Glu Val Val Ala Ile Glu Ala Gly Gln
85 90 95
Thr Lys Thr Ile Ser Phe Ala Leu Arg Leu Arg Thr Asn Asn Leu Glu
100 105 110
Glu Val Val Val Thr Gly Thr Gly Thr Arg Tyr Arg Leu Val Asp Ala
115 120 125

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

Asn Leu Tyr Leu Gly Asn Ala Asp Leu Lys Pro Gln Met Ser Asp Tyr
 545 550 555 560
 Tyr Ala Leu Gly Leu Glu Tyr Asn Gln Gly Pro Ile Ser Phe Ser Ala
 565 570 575
 Thr Val Tyr Asp Asn Glu Leu Arg Asn Leu Ile Ser Phe Met Asp Ile
 580 585 590
 Pro Thr Ser Pro Glu His Glu Ala Gln Gly Ile Lys Lys Thr Lys Gln
 595 600 605
 Tyr Ala Asn Ile Gly Lys Ala Arg Ser Arg Gly Leu Asp Val Leu Cys
 610 615 620
 Asp Ala Ser Ile Gly Trp Gly Ile Lys Leu Gly Ala Gly Tyr Ser Leu
 625 630 635 640
 Val Glu Ala Lys Asn Leu Gln Thr Asp Glu Trp Leu Glu Gly Ala Ala
 645 650 655
 Arg His Arg Ala Asn Val His Ala Asp Trp Val His Tyr Trp Gly Gln
 660 665 670
 Tyr Arg Leu Gly Val Ser Leu Phe Gly Arg Ile Gln Ser Glu Arg Tyr
 675 680 685
 Tyr Lys Asp Gly Asn Ala Pro Asp Tyr Thr Leu Trp Arg Leu Ala Thr
 690 695 700
 Ser His Arg Phe Ala His Phe Arg His Ile Ile Leu Asp Gly Thr Leu
 705 710 715 720
 Gly Ile Asp Asn Leu Phe Asp Tyr Val Asp Asp Arg Pro Met Gly Val
 725 730 735
 Asn Tyr Ala Thr Val Thr Pro Gly Arg Thr Phe Phe Ala Gln Ile Ala
 740 745 750
 Ile Arg Phe Asn Asn
 755
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 <211> 331
 <212> PRT
 <213> Porphyromonas gingivalis
 <400> 420
 Met Thr Asp Asn Lys Gln Arg Asn Ile Val Phe Pro Ala Phe Leu Leu
 1 5 10 15
 Leu Leu Gly Val Ile Ala Val Val Thr Ile Val Gly Phe Phe Met Leu
 20 25 30
 Arg Pro Ala Glu Glu Ile Ile Gln Gly Gln Ile Glu Val Thr Glu Tyr
 35 40 45
 Arg Val Ser Ser Lys Val Pro Gly Arg Ile Lys Glu Leu Arg Val Ser
 50 55 60
 Glu Gly Gln Gln Val Gln Ala Gly Asp Thr Leu Ala Val Ile Glu Ala
 65 70 75 80
 Pro Asp Val Ala Ala Lys Met Glu Gln Ala Lys Ala Ala Glu Ala Ala
 85 90 95
 Ala Gln Ala Gln Asn Ala Lys Ala Leu Lys Gly Ala Arg Ser Glu Gln
 100 105 110
 Ile Gln Ala Ala Tyr Glu Met Trp Gln Lys Ala Gln Ala Gly Val Ala
 115 120 125
 Ile Ala Thr Lys Thr His Gln Arg Val Gln Asn Leu Tyr Asp Gln Gly
 130 135 140
 Val Val Pro Ala Gln Lys Leu Asp Glu Ala Thr Ala Gln Arg Asp Ala

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

 <210> 421
 <211> 267
 <212> PRT
 <213> Porphyromonas gingivalis
 <400> 421
 Met Arg Ile Val Ser Asn Phe Leu Phe Val Ser Phe Ser Val Leu Leu
 1 5 10 15
 Phe Ala Ser Cys Arg Ser Gln Arg Glu Lys Val Val Tyr Leu Gln Asp
 20 25 30
 Ile Gln Thr Phe Asn Arg Glu Ile Ile Ala Lys Pro Tyr Asp Val Lys
 35 40 45
 Ile Glu Lys Asp Asp Val Leu Asn Ile Leu Val Ser Ser Arg Asp Pro
 50 55 60
 Glu Leu Ser Thr Pro Tyr Asn Gln Val Leu Thr Thr Arg Ala Leu Ala
 65 70 75 80
 Arg Asn Gly Tyr Gly Thr Asn Ser Asn Glu Gly Phe Leu Val Asp Ser
 85 90 95
 Lys Gly Tyr Ile Asn Tyr Pro Ile Leu Gly Gln Ile Tyr Val Glu Gly
 100 105 110
 Leu Thr Arg Thr Glu Leu Glu Lys Glu Ile Gln Lys Arg Ile Ile Ser
 115 120 125
 Ser Gly Phe Ile Lys Asp Pro Thr Val Thr Val Gln Leu Gln Asn Phe
 130 135 140
 Lys Val Ser Val Leu Gly Glu Val Asn His Pro Gly Ser Met Ser Val
 145 150 155 160
 Lys Gly Glu Arg Ile Thr Leu Leu Glu Ala Ile Gly Met Ala Gly Asp
 165 170 175
 Leu Thr Ile Tyr Gly Arg Arg Asp Arg Val Phe Val Ile Arg Glu Thr
 180 185 190

Asp Gly His Arg Glu Val Phe Gln Thr Asp Leu Arg Lys Ala Asp Leu
 195 200 205
 Leu Ala Ser Pro Val Tyr Tyr Leu His Gln Asn Asp Val Ile Tyr Val
 210 215 220
 Glu Pro Asn Asp Lys Lys Thr Gln Met Ser Glu Ile Asn Gln Asn Asn
 225 230 235 240
 Asn Val Asn Val Trp Leu Ser Val Thr Ser Thr Leu Val Ser Ile Ser
 245 250 255
 Thr Leu Thr Ile Thr Ile Ile Asp Lys Thr Lys
 260 265
 <210> 422
 <211> 569
 <212> PRT
 <213> Porphyromonas gingivalis
 <400> 422
 Met Lys Lys Thr Asn Leu Phe Leu Ser Leu Leu Val Ile Phe Ile Thr
 1 5 10 15
 Gly Ser Phe Met Thr Ala Cys Ala Gln Lys Ser Lys Thr Asn Lys Leu
 20 25 30
 Thr Glu Glu Asp Arg Ser Arg Asn Glu Tyr Val Gln Ser Met Asp Val
 35 40 45
 Leu Ser Asn Ile Ile Gly Asn Val Arg Leu Tyr Phe Val Asp Thr Ile
 50 55 60
 Ser Ile Lys His Met Thr Arg Arg Gly Ile Asp Ala Met Leu Gly Gly
 65 70 75 80
 Leu Asp Pro Tyr Thr Glu Tyr Ile Pro Tyr Glu Glu Met Asp Glu Leu
 85 90 95
 Lys Leu Met Thr Thr Gly Glu Tyr Ala Gly Val Gly Ala Ile Ile Ser
 100 105 110
 Gln Arg Pro Asp Ser Ala Val Ile Ile Gln Arg Pro Met Glu Gly Met
 115 120 125
 Pro Ala Asp Glu Ala Gly Leu Ile Ala Gly Asp Arg Ile Leu Thr Ile
 130 135 140
 Asp Gly Lys Asp Phe Arg Lys Ser Thr Thr Pro Lys Val Ser Gln Ala
 145 150 155 160
 Leu Lys Gly Ile Ala Gly Thr Val Ala Lys Val Thr Val Met Arg Tyr
 165 170 175
 Gly Glu Thr Lys Pro Arg Thr Phe Ser Val Lys Arg Gln Lys Val Ile
 180 185 190
 Met Asn Ser Val Thr Tyr Ser Gly Met Leu Asp Gly Ser Ile Gly Tyr
 195 200 205
 Ile Arg Leu Asn Asn Phe Thr Asp Lys Ser Ala Glu Glu Val Arg Thr
 210 215 220
 Ala Leu Leu Asp Leu Arg Asp Lys Gln Gly Ala Lys Gly Leu Ile Leu
 225 230 235 240
 Asp Leu Arg Gly Asn Gly Gly Gly Leu Met Gln Ala Ala Ile Glu Ile
 245 250 255
 Val Asn Leu Phe Val Pro Lys Gly Lys Glu Val Val Thr Thr Lys Gly
 260 265 270
 Arg Ile Ala Glu Ser Ala Ser Val Phe Arg Thr Leu Thr Glu Pro Ile
 275 280 285
 Asp Thr Lys Leu Pro Ile Val Val Leu Ile Asp Gly Gln Ser Ala Ser

290 295 300
 Ser Ser Glu Ile Val Ala Gly Ala Leu Gln Asp Met Asp Arg Ala Val
 305 310 315 320
 Leu Met Gly Gln Lys Ser Tyr Gly Lys Gly Leu Val Gln Thr Thr Arg
 325 330 335
 Gln Leu Pro Tyr Asn Gly Val Ile Lys Leu Thr Thr Ala Lys Tyr Tyr
 340 345 350
 Ile Pro Ser Gly Arg Cys Ile Gln Arg Leu Asp Tyr Ser Arg Thr Asn
 355 360 365
 Arg Thr Gly Met Ala Thr Ala Ile Pro Asp Ser Leu His Lys Ile Phe
 370 375 380
 Tyr Thr Ala Ala Gly Arg Arg Val Glu Asp Ala Gly Gly Ile Leu Pro
 385 390 395 400
 Asp Ile Glu Val Lys Gln Asp Thr Ala Ala Thr Leu Leu Tyr Tyr Met
 405 410 415
 Ala Ile Asn Asn Asp Val Phe Asp Phe Val Thr Gly Tyr Val Leu Lys
 420 425 430
 His Lys Thr Ile Ala Lys Pro Glu Asp Phe Ser Ile Thr Asn Glu Asp
 435 440 445
 Tyr Ala Ala Phe Cys Lys Met Met Glu Glu Lys Lys Phe Asp Tyr Asp
 450 455 460
 Arg Gln Ser Gly Lys Met Leu Asp Lys Leu Glu Glu Leu Ala Lys Ile
 465 470 475 480
 Glu Gly Tyr Leu Pro Glu Ala Asn Ser Glu Leu Lys Ala Leu Arg Glu
 485 490 495
 Lys Leu Lys Pro Asn Leu Ser Arg Asp Leu Leu Arg Phe Lys Lys Glu
 500 505 510
 Ile Thr Asn Tyr Leu Asn Asn Glu Ile Val Thr Arg Tyr Tyr Tyr Glu
 515 520 525
 Arg Gly Ser Ile Arg Gln Ser Leu Pro Glu Asp Lys Val Val Lys Glu
 530 535 540
 Ala Ile Lys Leu Leu Lys Asp His Pro Glu Gln Ile Arg Gln Ile Leu
 545 550 555 560
 Ala Ala Pro Lys Ala Glu Asn Lys Gly
 565
 <210> 423
 <211> 981
 <212> PRT
 <213> Porphyromonas gingivalis
 <400> 423
 Met Gln Asn Lys Gly Phe Val Ile Val Ile Thr Ser Ala Leu Ala Ile
 1 5 10 15
 Ile Cys Ala Phe Tyr Leu Ser Phe Ser Phe Val Thr Asn Arg Tyr Glu
 20 25 30
 Lys Lys Ala Lys Ala Met Gly Asp Val Ala Gly Met Ala Tyr Leu Asp
 35 40 45
 Ser Met Ser Asn Glu Lys Val Trp Phe Gly Tyr Thr Leu Lys Glu Ala
 50 55 60
 Gln Ala Gln Gln Ile Gly Leu Gly Leu Asp Leu Lys Gly Gly Met Asn
 65 70 75 80
 Val Ile Leu Lys Leu Asn Ala Ser Asp Leu Leu Arg Asn Leu Ser Asn
 85 90 95

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

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

Val Met Leu Val Ile Phe Ile Phe Gly Gly Ala Thr Met Arg Ser Phe
930 935 940
Thr Phe Ser Ile Leu Leu Gly Ile Val Ile Gly Thr Tyr Ser Thr Leu
945 950 955 960
Phe Val Ala Thr Pro Leu Ala Tyr Glu Ile Gln Lys Arg Lys Leu Asn
965 970 975
Lys Ala Ala Lys Lys
980
<210> 424
<211> 1017
<212> PRT
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        675                680                685
Glu Gly Gly Ser Pro Ala Thr Ser Thr Glu Gln Asn Pro Val Val Thr
 690                695                700
Tyr Asn Glu Thr Gly Lys Tyr Asp Val Gln Leu Thr Ala Thr Asn Glu
 705                710                715                720
Gly Gly Ser Asn Val Lys Lys Ala Glu Asp Tyr Ile Glu Val Ile Leu
        725                730                735
Asp Asp Ser Val Glu Asp Ile Val Ala Gln Thr Gly Ile Val Ile Arg
        740                745                750
Pro Gln Asn Gly Thr Lys Gln Ile Leu Ile Glu Ala Asn Ala Ala Ile
        755                760                765
Lys Ala Ile Val Leu Tyr Asp Ile Asn Gly Arg Val Val Leu Lys Thr
        770                775                780
Thr Pro Asn Gln Leu Arg Ser Thr Val Asp Leu Ser Ile Leu Pro Glu
 785                790                795                800
Gly Ile Tyr Thr Ile Asn Ile Lys Thr Glu Lys Ser Ala Arg Thr Glu
        805                810                815
Lys Ile His Ile Gly
        820
<210>      427
<211>      76
<212>      PRT
<213>      Porphyromonas gingivalis
<400>      427
Met Arg Leu Ile Lys Ala Phe Leu Val Gln Leu Leu Leu Leu Pro Ile
  1                5                10                15
Phe Phe Tyr Lys Arg Phe Ile Ser Pro Leu Thr Pro Pro Ser Cys Arg
        20                25                30
Phe Thr Pro Ser Cys Ser Ser Tyr Ala Ile Glu Ala Leu Arg Lys Tyr
        35                40                45
Gly Pro Gly Lys Gly Leu Leu Leu Ser Ile Lys Arg Ile Leu Arg Cys
        50                55                60
His Pro Trp Gly Gly Ser Gly Tyr Asp Pro Val Pro
  65                70                75
<210>      428
<211>      859
<212>      PRT
<213>      Porphyromonas gingivalis
<400>      428
Met Ala Tyr Asp Phe Thr Gln Thr Phe Arg Asn Ser Leu Glu Tyr Ser
  1                5                10                15
Tyr Gln Glu Ala Thr Arg Leu Gly Val Val Ala Val Thr Gln Asp Met
        20                25                30
Leu Val Leu Gly Ile Ile Arg Asp Gly Asp Asn Gly Ala Ile Asp Ile
        35                40                45
Met Arg His Tyr Gly Ile Asn Leu Tyr Glu Leu Lys Arg Leu Ile Glu
        50                55                60
Leu Glu Ala Ile Ala Glu Ser Leu Pro Ala Ser Pro Glu Gly Ser Pro
  65                70                75                80
Ile Phe Thr Pro Ser Ala Arg Glu Ala Ile Asp Asp Ala Thr Asp Ile
        85                90                95
Cys Ala Asp Met Glu Asp Glu Ala Val Ser Pro Val His Leu Leu Leu

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

515	520	525
Val Val Ala Leu Met Thr Gly	Val Pro Ala Glu Arg Leu Ser Thr Gly	
530	535	540
Glu Gly Glu Arg Leu Arg Thr Met Ala Asp Asp Leu Lys Thr Lys Val		
545	550	555
Val Gly Gln Asp Thr Ala Ile Glu Lys Met Val His Ala Ile Gln Arg		
565	570	575
Asn Arg Leu Gly Leu Arg Asn Glu Lys Lys Pro Ile Gly Ser Phe Leu		
580	585	590
Phe Leu Gly Pro Thr Gly Val Gly Lys Thr Tyr Leu Ala Lys Lys Leu		
595	600	605
Ala Glu Tyr Leu Phe Glu Asp Glu Asn Ala Met Ile Arg Val Asp Met		
610	615	620
Ser Glu Tyr Met Glu Lys Phe Ser Val Ser Arg Leu Val Gly Ala Pro		
625	630	635
Pro Gly Tyr Val Gly Tyr Glu Glu Gly Gly Gln Leu Thr Glu Arg Val		
645	650	655
Arg Arg Lys Pro Tyr Ser Val Val Leu Leu Asp Glu Ile Glu Lys Ala		
660	665	670
His Ala Asp Val Phe Asn Leu Leu Leu Gln Val Met Asp Glu Gly Gln		
675	680	685
Leu Thr Asp Ser Leu Gly Arg Arg Val Asn Phe Lys Asn Thr Val Ile		
690	695	700
Ile Ile Thr Ser Asn Val Gly Thr Arg Gln Leu Lys Asp Phe Gly Gln		
705	710	715
Gly Ile Gly Phe Arg Ser Glu Lys Asp Glu Glu Ala Asn Lys Glu His		
725	730	735
Ser Arg Ser Val Ile Gln Lys Ala Leu Asn Lys Thr Phe Ser Pro Glu		
740	745	750
Phe Leu Asn Arg Leu Asp Asp Ile Ile Leu Phe Asp Gln Leu Gly Lys		
755	760	765
Thr Glu Ile Arg Arg Met Val Asp Ile Glu Leu Lys Ala Val Leu Ala		
770	775	780
Arg Ile His Arg Ala Gly Tyr Asp Leu Val Leu Thr Asp Glu Ala Lys		
785	790	795
Asp Val Ile Ala Thr Lys Gly Tyr Asp Leu Gln Tyr Gly Ala Arg Pro		
805	810	815
Leu Lys Arg Thr Leu Gln Asn Glu Val Glu Asp Arg Leu Thr Asp Leu		
820	825	830
Ile Leu Ser Gly Gln Ile Glu Lys Gly Gln Thr Leu Thr Leu Ser Ala		
835	840	845
Arg Asp Gly Glu Ile Ile Val Gln Glu Gln Ala		
850	855	
<210>	429	
<211>	417	
<212>	PRT	
<213>	Porphyromonas gingivalis	
<400>	429	
Met Asn Tyr Leu Tyr Ile Leu Ile Thr Leu Leu Leu Ser Gly Phe Phe		
1	5	10
Ser Gly Ala Glu Ile Ala Phe Leu Ser Ser Asp Lys Leu Arg Leu Glu		
20	25	30


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Leu Asp Arg Asn Arg Gly Asp Leu Thr Gly Arg Ala Leu Asn Leu Leu
    35                      40                      45
Tyr Arg His Pro Asp Gln Leu Val Thr Thr Leu Leu Val Gly Asn Asn
    50                      55                      60
Ile Val Leu Val Val Tyr Gly Leu Leu Met Ala Gly Leu Leu Ala Ala
    65                      70                      75                      80
Pro Leu Ala Gln Trp Ile Asp Asn Asp Ala Met Ile Val Val Leu Gln
    85                      90                      95
Ser Val Leu Ser Thr Ile Ile Ile Leu Phe Thr Gly Glu Phe Leu Pro
    100                     105                     110
Lys Ala Ile Phe Lys Thr Asn Ala Asn Met Met Met Arg Val Phe Ala
    115                     120                     125
Leu Pro Ile Val Ala Ile Tyr Tyr Leu Leu Tyr Pro Leu Ser Lys Leu
    130                     135                     140
Phe Thr Gly Leu Ser Arg Ser Phe Ile Arg Leu Val Asp Lys Asn Tyr
    145                     150                     155                     160
Val Pro Thr Thr Val Gly Leu Gly Arg Val Asp Leu Asp His Tyr Leu
    165                     170                     175
Ala Glu Asn Met Ser Gly Glu Asn Glu Gln Asn Asp Leu Thr Thr Glu
    180                     185                     190
Val Lys Ile Ile Gln Asn Ala Leu Asp Phe Ser Gly Ile Gln Val Arg
    195                     200                     205
Asp Cys Met Ile Pro Arg Asn Glu Met Ile Ala Cys Glu Leu Gln Thr
    210                     215                     220
Asp Ile Glu Val Leu Lys Thr Thr Phe Ile Asp Thr Gly Leu Ser Lys
    225                     230                     235                     240
Ile Ile Ile Tyr Arg Gln Asn Ile Asp Asp Val Val Gly Tyr Ile His
    245                     250                     255
Ser Ser Glu Met Phe Arg Gly Gln Asp Trp Gln Lys Arg Ile Asn Thr
    260                     265                     270
Thr Val Phe Val Pro Glu Ser Met Tyr Ala Asn Lys Leu Met Arg Leu
    275                     280                     285
Leu Met Gln Arg Lys Lys Ser Ile Ala Ile Val Ile Asp Glu Leu Gly
    290                     295                     300
Gly Thr Ala Gly Met Val Thr Leu Glu Asp Leu Val Glu Glu Ile Phe
    305                     310                     315                     320
Gly Asp Ile Glu Asp Glu His Asp Thr Arg Lys Ile Ile Ala Lys Gln
    325                     330                     335
Leu Gly Pro His Thr Tyr Leu Val Ser Gly Arg Met Glu Ile Asp Asp
    340                     345                     350
Val Asn Glu Arg Phe Gly Leu Ser Leu Pro Glu Ser Asp Asp Tyr Leu
    355                     360                     365
Thr Val Ala Gly Phe Ile Leu Asn Ser His Gln Asn Ile Pro Gln Ala
    370                     375                     380
Asn Glu Val Val Glu Ile Ala Pro Tyr Thr Phe Thr Ile Leu Arg Ser
    385                     390                     395                     400
Ser Ser Thr Lys Ile Glu Leu Val Lys Met Ser Ile Asp Asp Gln Ser
    405                     410                     415
Asn
<210>    430
<211>    293
<212>    PRT

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<213>    Porphyromonas gingivalis
<400>    430
Met Lys Gln Asn Tyr Phe Lys Arg Val Cys Ser Leu Leu Trp Leu Val
 1             5             10             15
Leu Pro Met Leu Ile Met Pro Leu Glu Val Ala Ala Gln Glu Ile Ile
      20             25             30
Pro Asn Glu Glu Val Leu Glu Ser Leu Thr Phe Val Ala Pro Val Glu
      35             40             45
Glu Thr Asp Ala Ile Glu Ala Glu Val Glu Ala Leu Gln Glu Ile Val
      50             55             60
Ala Thr Glu Glu Ile Ala Glu Gln Ala Val Arg Ser Tyr Thr Tyr Thr
      65             70             75             80
Val Tyr Arg Asp Gly Val Lys Ile Ala Ser Gly Leu Thr Glu Pro Thr
      85             90             95
Phe Leu Asp Glu Asp Val Pro Ala Gly Glu His Thr Tyr Cys Val Glu
      100            105            110
Val Gln Tyr Gln Gly Gly Val Ser Asp Lys Val Cys Val Asp Val Glu
      115            120            125
Val Lys Asp Phe Lys Pro Val Thr Asn Leu Thr Gly Thr Ala Ser Asn
      130            135            140
Asp Glu Val Ser Leu Asp Trp Asp Gly Val Glu Glu Lys Ala Glu Glu
      145            150            155            160
Pro Ala Ser Asp Lys Ala Val Ser Tyr Asn Val Tyr Lys Asn Gly Thr
      165            170            175
Leu Ile Gly Asn Thr Ala Glu Thr His Tyr Val Glu Thr Gly Val Ala
      180            185            190
Asn Gly Thr Tyr Ile Tyr Glu Val Glu Val Lys Tyr Pro Asp Gly Val
      195            200            205
Ser Pro Lys Val Ala Val Thr Val Thr Val Thr Asn Ser Ser Leu Ser
      210            215            220
Asn Val Asp Gly Gln Ala Pro Tyr Thr Leu Arg Val Glu Gly Lys Lys
      225            230            235            240
Ile Ile Ala Glu Ala His Gly Met Ile Thr Leu Tyr Asp Ile Asn Gly
      245            250            255
Arg Thr Val Ala Val Ala Pro Asn Arg Leu Glu Tyr Met Ala Gln Thr
      260            265            270
Gly Phe Tyr Ala Val Arg Phe Asp Val Gly Asn Lys His His Val Ser
      275            280            285
Lys Ile Gln Val Arg
      290
<210>    431
<211>    312
<212>    PRT
<213>    Porphyromonas gingivalis
<400>    431
Met Ile Pro Leu Ser Glu Ser Phe Glu Ser Gly Ile Pro Ala Ile Trp
 1             5             10             15
Lys Thr Ile Asp Ala Asp Gly Asp Gly Tyr Asn Trp Met His Leu Thr
      20             25             30
Asn Phe Thr Gly Gln Ser Gly Leu Cys Val Ser Ser Ala Ser Tyr Ile
      35             40             45
Gly Gly Val Gly Ala Leu Thr Pro Asp Asn Tyr Leu Ile Thr Pro Glu

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50          55          60
Leu Lys Leu Pro Thr Asp Ala Leu Val Glu Ile Ile Tyr Trp Val Cys
65          70          75          80
Thr Gln Asp Leu Thr Ala Pro Ser Glu His Tyr Ala Val Tyr Ser Ser
85          90          95
Ser Thr Gly Asn Asn Ala Ala Asp Phe Val Asn Leu Leu Tyr Glu Glu
100        105        110
Thr Leu Thr Ala Lys Arg Ile Gln Ser Pro Glu Leu Ile Arg Gly Asn
115        120        125
Arg Thr Gln Gly Val Trp Tyr Gln Arg Lys Val Val Leu Pro Asn Asp
130        135        140
Thr Lys Tyr Val Ala Phe Arg His Phe Asn Ser Thr Asp Asn Phe Trp
145        150        155        160
Leu Asn Leu Asp Glu Val Ser Ile Leu Tyr Thr Pro Leu Pro Arg Arg
165        170        175
Ala Pro Cys Pro His Pro Gly Gly Tyr Thr Tyr Ser Val Phe Arg Asp
180        185        190
Gly Gln Lys Ile Ala Ser Gly Leu Ser Ala Leu Ala Tyr Ile Asp Thr
195        200        205
Asp Val Pro Tyr Gly Thr Gln Asp Tyr Cys Val Gln Val Asn Tyr Leu
210        215        220
Gln Gly Asp Ser Tyr Lys Val Cys Lys Asn Ile Val Val Ala Asn Ser
225        230        235        240
Ala Asn Ile Tyr Gly Ala Asp Lys Pro Phe Ala Leu Thr Val Val Gly
245        250        255
Lys Thr Ile Val Ala Ser Ala Phe Lys Gly Glu Ile Thr Leu Tyr Asp
260        265        270
Ile Arg Gly Arg Leu Ile Ala Ser Gly Cys Asp Thr Leu Arg Tyr Lys
275        280        285
Ala Glu Asn Gly Phe Tyr Leu Ile Lys Ile Gln Val Asn Gly Thr Val
290        295        300
Tyr Thr Glu Lys Ile Gln Ile Gln
305          310
<210>      432
<211>      843
<212>      PRT
<213>      Porphyromonas gingivalis
<400>      432
Met Lys Lys Ser Phe Leu Leu Ala Ile Val Met Leu Phe Gly Ile Ala
1          5          10          15
Met Gln Gly His Ser Ala Pro Val Thr Lys Glu Arg Ala Leu Ser Leu
20        25        30
Ala Arg Leu Ala Leu Arg Gln Val Ser Leu Arg Met Gly Gln Thr Ala
35        40        45
Val Ser Asp Lys Ile Ser Ile Asp Tyr Val Tyr Arg Gln Gly Asp Ala
50        55        60
Glu Arg Gly Ile Thr Ser Gln Glu Glu Gly Ser Pro Ala Tyr Phe Tyr
65        70        75        80
Val Ala Asn Arg Gly Asn Asn Glu Gly Tyr Ala Leu Val Ala Ala Asp
85        90        95
Asp Arg Ile Pro Thr Ile Leu Ala Tyr Ser Pro Ile Gly Arg Phe Asp
100       105       110

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

Val Asp Asn Asn Glu Gly Lys Leu Ser Ile Val Pro Asn Ser Phe Val
530 535 540
Ala Asp Leu Asn Ser Tyr Glu His Ser Thr Ile Thr Val Gln Phe Asn
545 550 555 560
Ser Asp Ser Pro Asp Glu Ile Arg Thr Pro Val Ala Phe Ala Leu Ser
565 570 575
Thr Gly Ala Thr Ala Asp Asp Val Ile Ser Leu Gly Trp Val Met Ala
580 585 590
Glu Val Pro Gly Gly Ser Ser Asn Tyr Pro Val Val Trp Ser Lys Asp
595 600 605
Val Leu Thr Leu Ser Glu Gly Asp Tyr Thr Leu Trp Tyr Arg Phe Ser
610 615 620
Ile Asn Asn Gln Lys Asp Glu Trp Lys Lys Ile Gly Ser Val Ser Val
625 630 635 640
Lys Thr Pro Thr Glu Tyr Thr His Pro Leu Phe Glu Val Gly His Asn
645 650 655
Gln Thr Ser Thr Tyr Thr Leu Asp Met Ala His Asn Arg Val Leu Pro
660 665 670
Asp Phe Thr Leu Lys Asn Leu Gly Leu Pro Phe Asn Gly Glu Leu Val
675 680 685
Val Val Phe Arg Gln Thr Gln Ser Ser Ser Gly Ser Leu Trp Ala Ala
690 695 700
Gln Glu Thr Val His Ile Lys Gln Gly Glu Thr Phe Val Tyr Lys Pro
705 710 715 720
Val Val Glu Gly Pro Ile Pro Asp Gly Ser Tyr Arg Ala Thr Leu His
725 730 735
Ala Phe Val Asn Gly Gln Gln Gln Leu Tyr Leu Lys Gly Lys Arg Asn
740 745 750
Tyr Thr Val Lys Ile Val Asn Gly Thr Ala Val Glu Ala Ile Glu Ser
755 760 765
Ser Glu Glu Ile Arg Val Phe Pro Asn Pro Ala Arg Asp Tyr Val Glu
770 775 780
Ile Ser Ala Pro Cys Ile Pro Gln Glu Thr Ser Ile Ile Leu Phe Asp
785 790 795 800
Leu Ser Gly Lys Ile Val Met Lys Asn Ser Leu Ser Ala Gly His Gly
805 810 815
Arg Met Asp Val Ser Arg Leu Pro Asn Gly Ala Tyr Ile Leu Lys Val
820 825 830
Asp Gly Tyr Thr Thr Lys Ile Asn Ile Val His
835 840
<210> 433
<211> 290
<212> PRT
<213> Porphyromonas gingivalis
<400> 433
Met Lys Lys Leu Phe Leu Ser Leu Thr Ser Leu Val Met Val Phe Ala
1 5 10 15
Val Ala Ser Cys Asp Ile Ile Asp Lys Asp Gln Thr Leu Leu Pro Ala
20 25 30
Pro Thr Asn Val Thr Pro Asp Asn Pro Asp Asp Asn Pro Ser Glu Ile
35 40 45
Asp Ile Thr Gln Thr His Thr Glu Lys Tyr Val Leu Ala Glu Glu Phe

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50          55          60
Thr Gly Gln Lys Cys Leu Asn Cys Pro Lys Gly His Arg Lys Leu Ala
65          70          75          80
Ala Leu Lys Glu Gln Tyr Gly Lys Arg Leu Thr Val Val Gly Ile His
85          90          95
Ala Gly Pro Gly Ser Leu Val Pro Pro Leu Phe Arg Thr Glu Ala Gly
100        105        110
Asp Ala Tyr Tyr Ser Lys Phe Ala Asn Asn Thr Pro Leu Pro Ala Leu
115        120        125
Met Val Ser Arg Lys Lys Phe Gly Ser Ser Tyr Val Tyr Asp Lys Ser
130        135        140
Tyr Lys Thr Trp Asp Val Pro Ile Ala Glu Gln Met Glu Gln Lys Ala
145        150        155        160
Lys Ile Asn Ile Phe Ala Val Ala Glu Tyr Thr Asp Thr Gln Lys Ile
165        170        175
Lys Val Thr Val Lys Gly Lys Ile Leu Glu Gly Asn Thr Leu Pro Lys
180        185        190
Ser Met Val Gln Val Tyr Leu Leu Glu Asp Lys Leu Ile Ala Pro Gln
195        200        205
Val Asp Gly Asn Thr Thr Val Glu Asn Tyr Glu His Asn His Val Leu
210        215        220
Arg Gly Ala Val Asn Gly Ile Trp Gly Glu Glu Phe Val Asn Leu Lys
225        230        235        240
Asp Tyr Leu Tyr Thr Tyr Ala Val Glu Pro Leu Ser Gly Met Ser Phe
245        250        255
Val Ala Glu Asn Tyr Ser Ile Val Ala Phe Val Tyr Asp Val Gln Thr
260        265        270
Phe Glu Val Tyr Asp Val Val His Val Lys Ile Asn Pro Gln Ser Asp
275        280        285
Gly Lys
290
<210>      434
<211>      223
<212>      PRT
<213>      Porphyromonas gingivalis
<400>      434
Met Lys Lys Ser Ser Val Val Ala Ser Val Leu Ala Val Ala Leu Val
1          5          10          15
Phe Ala Gly Cys Gly Leu Asn Asn Met Ala Lys Gly Gly Leu Ile Gly
20        25        30
Ala Gly Val Gly Gly Ala Ile Gly Ala Gly Val Gly Asn Val Ala Gly
35        40        45
Asn Thr Ala Val Gly Ala Ile Val Gly Thr Ala Val Gly Gly Ala Ala
50        55        60
Gly Ala Leu Ile Gly Lys Lys Met Asp Lys Gln Lys Lys Glu Leu Glu
65        70        75        80
Ala Ala Val Pro Asp Ala Thr Ile Gln Thr Val Asn Asp Gly Glu Ala
85        90        95
Ile Leu Val Thr Phe Asp Ser Gly Ile Leu Phe Ala Thr Asn Ser Ser
100       105       110
Thr Leu Ser Pro Asn Ser Arg Thr Ala Leu Thr Lys Phe Ala Ala Asn
115       120       125

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Met Asn Lys Asn Pro Asp Thr Asp Ile Arg Ile Val Gly His Thr Asp
  130                      135                      140
Asn Thr Gly Ser Asp Lys Ile Asn Asp Pro Leu Ser Glu Arg Arg Ala
 145                      150                      155                      160
Ala Ser Val Tyr Ser Phe Leu Asn Ser Gln Gly Val Ser Met Ser Arg
                      165                      170                      175
Met Ala Ala Glu Gly Arg Gly Ser His Glu Pro Val Ala Asp Asn Ser
                      180                      185                      190
Thr Val Ala Gly Arg Ser Ala Asn Arg Arg Val Glu Val Tyr Ile Leu
                      195                      200                      205
Pro Asn Ala Lys Met Ile Glu Gln Ala Gln Gln Gly Thr Leu Lys
  210                      215                      220
<210>      435
<211>      337
<212>      PRT
<213>      Porphyromonas gingivalis
<400>      435
Met Ser Lys Lys Ser Ile Leu Leu Leu Cys Cys Ser Leu Cys Phe Ile
  1                      5                      10                      15
Ser Ala Thr Lys Ala Val Thr Pro Val Arg Asn Val Arg Asn Ser Gln
                      20                      25                      30
Val Asn Ser Lys Ala Lys Thr Glu Arg Thr Lys Pro Ser Asp Ser Val
                      35                      40                      45
Arg Tyr Ile Ser Asn Met Ile Ala Asp Arg Leu Glu Phe Arg Asn Lys
  50                      55                      60
Ile Ser Ser Glu Lys Glu Val Arg Lys Ala Glu Tyr Glu Asn Arg Leu
  65                      70                      75                      80
Ala Met Glu Ala Leu Asn Tyr Pro Ala Ile Asp Leu Tyr Gly Glu Asp
                      85                      90                      95
Ser Trp Ser Glu Tyr Val Asn Pro Phe Val Gly Ala Gly Thr Asp Val
                      100                      105                      110
Glu Ile Pro Asn Ser Tyr Asp Ile Asp Cys Ser Ser Phe Val Met Pro
                      115                      120                      125
Val Glu Asp Lys Gln Val Thr Ser Gln Phe Gly Tyr Arg Arg Arg Phe
  130                      135                      140
Gly Arg Met His Tyr Gly Ile Asp Leu Ser Val Asn Arg Gly Asp Thr
  145                      150                      155                      160
Ile Arg Ala Ala Phe Asp Gly Lys Val Arg Val Arg Ser Tyr Glu Ala
                      165                      170                      175
Arg Gly Tyr Gly Tyr Tyr Ile Val Leu Arg His Pro Asn Gly Leu Glu
                      180                      185                      190
Thr Val Tyr Gly His Met Ser Arg Gln Leu Val Asp Glu Asn Gln Ile
                      195                      200                      205
Val Arg Ala Gly Gln Pro Ile Gly Leu Gly Gly Ser Thr Gly Arg Ser
  210                      215                      220
Thr Gly Pro His Leu His Phe Glu Thr Arg Phe Met Gly Ile Pro Ile
  225                      230                      235                      240
Asn Pro Ser Thr Ile Ile Asp Phe Asp Asn Gly Val Pro Leu Arg Asp
                      245                      250                      255
Ile Tyr Thr Phe Lys Arg Gly Ser Asn Ser Arg Tyr Ala Lys Ala Ser
                      260                      265                      270
Lys Thr Ser Ser Arg Tyr Ala Lys Lys Gly Lys Lys Gly Arg Gln Ala

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275 280 285
 Ser Ser Pro Met Thr Tyr Arg Ile Lys Lys Gly Asp Thr Leu Glu Thr
 290 295 300
 Ile Ala Lys Arg His Gly Thr Ser Val Gln Lys Leu Cys Ala Thr Asn
 305 310 315 320
 Gly Ile Gly Lys Ser Lys Ile Leu Thr Pro Gly Lys Ala Leu Arg Ile
 325 330 335
 Lys
 <210> 436
 <211> 151
 <212> PRT
 <213> Porphyromonas gingivalis
 <400> 436
 Met Ala Lys Ile Asn Phe Tyr Ala Glu Gly Val Ser Leu Pro Arg Ile
 1 5 10 15
 Arg Arg Arg Ile Val Gly Lys Trp Ile Ala Glu Val Cys Ser Arg Tyr
 20 25 30
 Gly Lys Ala Val Gly Glu Ile Ser Tyr Leu Phe Cys Asp Asp Glu Tyr
 35 40 45
 Ile Leu Lys Ala Asn Gln Glu Phe Leu Asp His Asp Tyr Tyr Thr Asp
 50 55 60
 Ile Ile Thr Phe Asp Ser Cys Glu Ala Asp Thr Val Asn Gly Asp Leu
 65 70 75 80
 Leu Ile Ser Leu Asp Thr Val Arg Ser Asn Ala Arg Ala Leu Asp Leu
 85 90 95
 Arg Tyr Glu Asp Glu Leu His Arg Val Ile Ile His Gly Ile Leu His
 100 105 110
 Leu Cys Gly Leu Lys Asp Lys Ser Lys Lys Asp Glu Ala Gln Met Arg
 115 120 125
 Ala Ala Glu Glu Lys Ala Leu Val Met Leu Arg Glu Thr Ile Gly Ser
 130 135 140
 Glu Leu Ser Leu Leu His Thr
 145 150
 <210> 437
 <211> 391
 <212> PRT
 <213> Porphyromonas gingivalis
 <400> 437
 Met Lys Val Lys Tyr Leu Met Leu Thr Leu Val Gly Ala Ile Ala Leu
 1 5 10 15
 Asn Ala Ser Ala Gln Glu Asn Thr Val Pro Ala Thr Gly Gln Leu Pro
 20 25 30
 Ala Lys Asn Val Ala Phe Ala Arg Asn Lys Ala Gly Ser Asn Trp Phe
 35 40 45
 Val Thr Leu Gln Gly Gly Val Ala Ala Gln Phe Leu Asn Asp Asn Asn
 50 55 60
 Asn Lys Asp Leu Met Asp Arg Leu Gly Ala Ile Gly Ser Leu Ser Val
 65 70 75 80
 Gly Lys Tyr His Ser Pro Phe Phe Ala Thr Arg Leu Gln Ile Asn Gly
 85 90 95
 Gly Gln Ala His Thr Phe Leu Gly Lys Asn Gly Glu Gln Glu Ile Asn
 100 105 110

Thr Asn Phe Gly Ala Ala His Phe Asp Phe Met Phe Asp Val Val Asn
 115 120 125
 Tyr Phe Ala Pro Tyr Arg Glu Asn Arg Phe Phe His Leu Ile Pro Trp
 130 135 140
 Val Gly Val Gly Tyr Gln His Lys Phe Ile Gly Ser Glu Trp Ser Lys
 145 150 155 160
 Asp Asn Val Glu Ser Leu Thr Ala Asn Val Gly Val Met Met Ala Phe
 165 170 175
 Arg Leu Gly Lys Arg Val Asp Phe Val Ile Glu Ala Gln Ala Ala His
 180 185 190
 Ser Asn Leu Asn Leu Ser Arg Ala Tyr Asn Ala Lys Lys Thr Pro Val
 195 200 205
 Phe Glu Asp Pro Ala Gly Arg Tyr Tyr Asn Gly Phe Gln Gly Met Ala
 210 215 220
 Thr Ala Gly Leu Asn Phe Arg Leu Gly Ala Val Gly Phe Asn Ala Ile
 225 230 235 240
 Xaa Pro Met Asp Tyr Ala Leu Ile Asn Asp Leu Asn Gly Gln Ile Asn
 245 250 255
 Arg Leu Arg Ser Glu Val Glu Glu Leu Ser Lys Arg Pro Val Ser Cys
 260 265 270
 Pro Glu Cys Pro Glu Val Thr Pro Val Thr Lys Thr Glu Asn Ile Leu
 275 280 285
 Thr Glu Lys Ala Val Leu Phe Arg Phe Asp Ser His Val Val Asp Lys
 290 295 300
 Asp Gln Leu Ile Asn Leu Tyr Asp Val Ala Gln Phe Val Lys Glu Thr
 305 310 315 320
 Asn Glu Pro Ile Thr Val Val Gly Tyr Ala Asp Pro Thr Gly Asn Thr
 325 330 335
 Gln Tyr Asn Glu Lys Leu Ser Glu Arg Arg Ala Lys Ala Val Val Asp
 340 345 350
 Val Leu Thr Gly Lys Tyr Gly Val Pro Ser Glu Leu Ile Ser Val Glu
 355 360 365
 Trp Lys Gly Asp Ser Thr Gln Pro Phe Ser Lys Lys Ala Trp Asn Arg
 370 375 380
 Val Val Ile Val Arg Ser Lys
 385 390
 <210> 438
 <211> 385
 <212> PRT
 <213> Porphyromonas gingivalis
 <400> 438
 Met Thr Tyr Arg Ile Met Lys Ala Lys Ser Leu Leu Leu Ala Leu Ala
 1 5 10 15
 Gly Leu Ala Cys Thr Phe Ser Ala Thr Ala Gln Glu Ala Thr Thr Gln
 20 25 30
 Asn Lys Ala Gly Met His Thr Ala Phe Gln Arg Asp Lys Ala Ser Asp
 35 40 45
 His Trp Phe Ile Asp Ile Ala Gly Gly Ala Gly Met Ala Leu Ser Gly
 50 55 60
 Trp Asn Asn Asp Val Asp Phe Val Asp Arg Leu Ser Ile Val Pro Thr
 65 70 75 80
 Phe Gly Ile Gly Lys Trp His Glu Pro Tyr Phe Gly Thr Arg Leu Gln

										85					90					95									
Phe	Thr	Gly	Phe	Asp	Ile	Tyr	Gly	Phe	Pro	Gln	Gly	Ser	Lys	Glu	Arg														
										100					105					110									
Asn	His	Asn	Tyr	Phe	Gly	Asn	Ala	His	Leu	Asp	Phe	Met	Phe	Asp	Leu														
										115					120					125									
Thr	Asn	Tyr	Phe	Gly	Val	Tyr	Arg	Pro	Asn	Arg	Val	Phe	His	Ile	Ile														
										130					135					140									
Pro	Trp	Ala	Gly	Ile	Gly	Phe	Gly	Tyr	Lys	Phe	His	Ser	Glu	Asn	Ala														
										145					150					155					160				
Asn	Gly	Glu	Lys	Val	Gly	Ser	Lys	Asp	Asp	Met	Thr	Gly	Thr	Val	Asn														
										165					170					175									
Val	Gly	Leu	Met	Leu	Lys	Phe	Arg	Leu	Ser	Arg	Val	Val	Asp	Phe	Asn														
										180					185					190									
Ile	Glu	Gly	Gln	Ala	Phe	Ala	Gly	Lys	Met	Asn	Phe	Ile	Gly	Thr	Lys														
										195					200					205									
Arg	Gly	Lys	Ala	Asp	Phe	Pro	Val	Met	Ala	Thr	Ala	Gly	Leu	Thr	Phe														
										210					215					220									
Asn	Leu	Gly	Lys	Thr	Glu	Trp	Thr	Glu	Ile	Val	Pro	Met	Asp	Tyr	Ala														
										225					230					235					240				
Leu	Val	Asn	Asp	Leu	Asn	Asn	Gln	Ile	Asn	Ser	Leu	Arg	Gly	Gln	Val														
										245					250					255									
Glu	Glu	Leu	Ser	Arg	Arg	Pro	Val	Ser	Cys	Pro	Glu	Cys	Pro	Glu	Pro														
										260					265					270									
Thr	Gln	Pro	Thr	Val	Thr	Arg	Val	Val	Val	Asp	Asn	Val	Val	Tyr	Phe														
										275					280					285									
Arg	Ile	Asn	Ser	Ala	Lys	Ile	Asp	Arg	Asn	Gln	Glu	Ile	Asn	Val	Tyr														
										290					295					300									
Asn	Thr	Ala	Glu	Tyr	Ala	Lys	Thr	Asn	Asn	Ala	Pro	Ile	Lys	Val	Val														
										305					310					315					320				
Gly	Tyr	Ala	Asp	Glu	Lys	Thr	Gly	Thr	Ala	Ala	Tyr	Asn	Met	Lys	Leu														
										325					330					335									
Ser	Glu	Arg	Arg	Ala	Lys	Ala	Val	Ala	Lys	Met	Leu	Glu	Lys	Tyr	Gly														
										340					345					350									
Val	Ser	Ala	Asp	Arg	Ile	Thr	Ile	Glu	Trp	Lys	Gly	Ser	Ser	Glu	Gln														
										355					360					365									
Ile	Tyr	Glu	Glu	Asn	Ala	Trp	Asn	Arg	Ile	Val	Val	Met	Thr	Ala	Ala														
										370					375					380									
Glu																													
385																													
<210>																439													
<211>																190													
<212>																PRT													
<213>																Porphyromonas gingivalis													
<400>																439													
Met	Glu	Phe	Phe	Met	Leu	Phe	Ile	Ala	Ala	Val	Phe	Val	Asn	Asn	Val														
										1					5					10					15				
Val	Leu	Ser	Gln	Phe	Leu	Gly	Ile	Cys	Pro	Phe	Leu	Gly	Val	Ser	Lys														
										20					25					30									
Lys	Val	Asp	Thr	Ser	Ile	Gly	Met	Gly	Ala	Ala	Val	Thr	Phe	Val	Leu														
										35					40					45									
Ala	Leu	Ala	Thr	Leu	Val	Thr	Phe	Leu	Ile	Gln	Lys	Phe	Val	Leu	Asp														
										50					55					60									

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Arg Phe Gly Leu Gly Phe Met Gln Thr Ile Ala Phe Ile Leu Val Ile
 65              70              75              80
Ala Ala Leu Val Gln Met Val Glu Ile Ile Leu Lys Lys Val Ser Pro
              85              90              95
Pro Leu Tyr Gln Ala Leu Gly Val Phe Leu Pro Leu Ile Thr Thr Asn
      100              105              110
Cys Cys Val Leu Gly Val Ala Ile Leu Val Ile Gln Lys Asp Tyr Thr
      115              120              125
Leu Leu Gln Ser Phe Val Tyr Ala Ile Ser Thr Ala Ile Gly Phe Thr
      130              135              140
Leu Ala Met Val Thr Phe Ala Gly Ile Arg Glu Gln Leu Asp Met Thr
 145              150              155              160
Asn Leu Pro Lys Ala Met Lys Gly Ile Pro Ser Ala Leu Leu Ala Ala
      165              170              175
Gly Ile Leu Ala Met Ala Phe Met Gly Phe Ser Gly Ile Ala
      180              185              190

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<210>      440
<211>      186
<212>      PRT
<213>      Porphyromonas gingivalis
<400>      440

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

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<210>      441
<211>      833
<212>      PRT
<213>      Porphyromonas gingivalis
<400>      441

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Met Lys Gln Leu Asn Ile Ile Ser Phe Ile Ile Ala Phe Leu Phe Leu
  1              5              10              15

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

Asp Leu Gln Gly Gly Gly Met Tyr Arg His Thr Phe Gly Glu Asn Trp
 435 440 445
 Asp Phe Thr Gly Gly Leu Glu Tyr Ile Tyr Gly Gln Leu Asp Asp Arg
 450 455 460
 Ser Gly Tyr Arg Pro Ser Lys Ile Asp Gln Asn Thr Ser Thr Phe Ser
 465 470 475 480
 Gln Tyr Asp Gln Leu Glu Tyr Lys Thr Glu Lys Leu Ser Ala Leu Ile
 485 490 495
 Gly Ala Arg Ile Asp Tyr Val Leu Leu Asn Gln Asp Gly Lys Arg Tyr
 500 505 510
 Ile Asp Pro Leu Phe Ile Phe Ser Pro Arg Ala Asn Val Arg Tyr Asn
 515 520 525
 Pro Asn Lys Asn Leu Ser Phe Arg Leu Ser Tyr Ser Glu Gly Phe Arg
 530 535 540
 Ala Pro Gln Tyr Phe Asp Glu Asp Leu His Val Glu Leu Ala Gly Gly
 545 550 555 560
 Thr Pro Ile Ser Arg Val Leu Ser Pro Asn Leu Lys Glu Glu Arg Ser
 565 570 575
 Arg Ser Ile Ser Ala Ser Phe Asp Tyr Tyr His Arg Ala Asp Glu Trp
 580 585 590
 Gln Phe Asn Ile Met Gly Glu Ala Phe Ser Thr Phe Ile Ser Asn Gln
 595 600 605
 Phe Lys Pro Ser Asp Lys Val Glu Thr Thr Ser Asp Gly Lys Glu Trp
 610 615 620
 Ile Ile Arg Thr Ile Tyr Asn Asp Lys Asp Gly Val Ser Lys Val Tyr
 625 630 635 640
 Gly Val Asn Leu Glu Gly Arg Ile Ala Tyr Asn Lys Ser Phe Asp Leu
 645 650 655
 Gln Leu Gly Gly Thr Trp Gln Arg Ser Arg Tyr Gly Ser Ile Tyr Thr
 660 665 670
 Ala Val Glu Ala Asp Lys Thr Thr Gly Gln Ala Glu Ile Ser Val Lys
 675 680 685
 Asp Tyr Val Arg Thr Pro Asn Leu Tyr Gly Tyr Phe Val Ala Thr Val
 690 695 700
 Arg Pro Thr Glu His Phe Ala Ile Asn Leu Ser Gly Thr Phe Thr Gly
 705 710 715 720
 Lys Met Asp Val Val His Glu Ala Tyr Glu Gly Asp Ile Pro Ala Glu
 725 730 735
 His Ile Ala Pro Asp Gly Ser Phe Asp Phe Glu Met Asn Gly Gln Gln
 740 745 750
 Phe Lys Gly Leu Ala Glu Gly His Ala Lys Leu Val Lys Thr Pro Ala
 755 760 765
 Phe Ala Asp Ile Asp Leu Lys Leu Ser His Asp Phe His Leu Ala Ser
 770 775 780
 Thr Met Thr Leu Glu Leu Asn Ala Gly Ile Gln Asn Ile Phe Asn Ser
 785 790 795 800
 Tyr Gln Lys Asp Thr Asp Lys Gly Pro Gly Arg Ala Ser Thr Tyr Val
 805 810 815
 Tyr Gly Pro Met Gln Pro Arg Arg Ile Phe Val Gly Thr Lys Ile Asn
 820 825 830
 Phe
 <210> 442

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<211>      891
<212>      PRT
<213>      Porphyromonas gingivalis
<400>      442
Met Tyr Lys Lys Ile Ile Ala Val Ala Ala Leu Phe Cys Ala Ser Ile
  1           5           10           15
Gly Ile Leu Lys Gly Gln Ser Ser Asp Leu Thr Pro Gln Asp Thr Ile
      20           25           30
Tyr Ser Pro Glu Ile Ser Tyr Ala Lys Pro Ile His Lys Thr Ile Ala
      35           40           45
Ser Ile Glu Ile Glu Gly Met Arg Ser Phe Asp Asp Phe Val Leu Arg
      50           55           60
Asn Leu Ser Gly Leu Ala Val Gly Asp Glu Val Leu Ile Pro Gly Asp
      65           70           75           80
Ala Met Ser Ala Ala Val Asn Arg Ile Met Arg Gln Gly Tyr Phe Ser
      85           90           95
Asn Val Arg Ile Ile Ala Asp Lys Tyr Val Gly Asn Lys Val Tyr Leu
      100          105          110
Lys Ile Ile Val Thr Glu Arg Pro Arg Ile Ser Lys Val Thr Phe Ser
      115          120          125
Gly Val Lys Lys Ser Glu Arg Glu Asp Leu Glu Met Lys Ile Gly Leu
      130          135          140
Arg Glu Gly Ile Gln Met Thr Arg Asn Asn Glu Asp Lys Val Arg Gln
      145          150          155          160
Ile Val Gln Lys Tyr Phe Ser Glu Lys Gly Tyr Arg Asp Ala Ser Ile
      165          170          175
Arg Ile Thr Gln Glu Pro Asp Leu Ser Lys Asp Gly Phe Val Asn Val
      180          185          190
Leu Ile Ser Ile Glu Lys Lys Ser Lys Thr Lys Val Asn Glu Ile Tyr
      195          200          205
Phe Ser Gly Asn Lys Ala Leu Ser Asn His Lys Leu Arg Met Ala Met
      210          215          220
Lys Asn Thr Asn Ala Lys Phe Ser Leu Arg Lys His Ile Arg Ser Ser
      225          230          235          240
Phe Leu Lys Leu Phe Ser Thr His Lys Phe Val Glu Glu Ser Tyr Arg
      245          250          255
Glu Asp Leu Val Arg Leu Ile Glu Lys Tyr Gln Glu Tyr Gly Tyr Arg
      260          265          270
Asp Ala Glu Ile Leu Thr Asp Ser Val Val Lys Ala Pro Asp Gly Lys
      275          280          285
Arg Val Asp Ile Tyr Leu Asn Ile Glu Glu Gly Gln Lys Tyr Tyr Ile
      290          295          300
Lys Asp Val Asn Phe Val Gly Asn Ser Gln Tyr Pro Ser Glu Tyr Leu
      305          310          315          320
Glu Arg Val Leu Gly Ile Lys Ser Gly Asp Val Tyr Asn Gln Arg Arg
      325          330          335
Leu Ala Lys Arg Leu Asn Glu Asp Glu Asp Ala Val Gly Asn Leu Tyr
      340          345          350
Tyr Asn Asn Gly Tyr Ile Phe Ala Trp Val Asp Pro Val Glu Thr Asn
      355          360          365
Val Val Gly Asp Ser Val Ser Leu Asp Ile Arg Ile Ala Glu Gly Lys
      370          375          380

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

Tyr Met Arg Leu Thr Met Glu Leu Arg Phe Pro Ile Leu Phe Glu Asn
805 810 815
Ser Phe Asn Ala Trp Leu Leu Ala Phe Ala Glu Ala Gly Asn Ala Trp
820 825 830
Arg Ser Ile Asp Asn Tyr Asn Pro Phe Asn Leu Lys Arg Ser Ala Gly
835 840 845
Val Gly Leu Arg Val Thr Leu Pro Met Val Gly Met Leu Gly Ile Asp
850 855 860
Trp Gly Tyr Gly Phe Asp Arg Pro Asp Asn Ser Leu Gln Arg Gly Gly
865 870 875 880
Ser Asn Val His Phe Val Leu Gly Gln Glu Phe
885 890

<210> 443
<211> 174
<212> PRT
<213> Porphyromonas gingivalis
<400> 443

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

<210> 444
<211> 170
<212> PRT
<213> Porphyromonas gingivalis
<400> 444

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

Ser Met Tyr Lys Lys Tyr Gln Ser Asp Leu Val Phe Leu Ser Ala Ala
65 70 75 80
Gln Lys Lys Thr Gln Glu Glu Ala Ile Val Lys Lys Glu Gln Gln Ala
85 90 95
Ser Glu Leu Lys Arg Lys Tyr Phe Gly Pro Glu Gly Glu Leu Tyr Lys
100 105 110
Lys Arg Ser Asp Leu Met Lys Pro Ile Gln Asp Glu Ile Trp Asn Ala
115 120 125
Ile Lys Glu Ile Ala Lys Arg Asn Asn Tyr Gln Met Val Leu Asp Arg
130 135 140
Gly Thr Ser Gly Ile Ile Phe Ala Ser Pro Ser Ile Asp Ile Ser Asp
145 150 155 160
Leu Val Leu Ser Lys Met Gly Phe Ser Lys
165 170

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

Gly Ile Lys
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Ile Tyr Arg Leu Ser Phe Ile Leu Leu Cys Cys Leu Leu Cys Ser Gln
20 25 30
Ala Ala Met Ala Gln Gly Val Arg Val Ser Gly Tyr Val Leu Asp Arg
35 40 45
Gly Glu Lys Pro Ile Pro Phe Ala Gly Val Lys Val Arg Gly Thr Gly

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

465	470										475					480				
Val	Gly	Tyr	Asn	Leu	Pro	His	Ser	Glu	Thr	Val	Leu	Leu	Met	Tyr	Asn					
				485					490					495						
Asn	Leu	Tyr	Ala	Asp	Thr	Gln	Met	Arg	Gly	Thr	Arg	Leu	Ser	Ala	Phe					
				500					505					510						
Val	Gln	Asp	Arg	Phe	Asn	Phe	Ser	Met	Gly	Gly	Gly	Thr	Phe	Ser	Leu					
				515					520					525						
Ile	Pro	Gly	Ile	Arg	Ala	Ser	Trp	Trp	Ser	Phe	Asn	Lys	Glu	Leu	Leu					
				530					535					540						
Val	Ser	Pro	Arg	Ile	Ser	Val	Gly	Tyr	Ser	Pro	Glu	Ser	Asn	Pro	Ala					
545					550					555					560					
Leu	Val	Leu	Arg	Ala	Ala	Ala	Gly	Leu	Tyr	Tyr	Gln	Ala	Pro	Phe	Tyr					
				565					570					575						
Lys	Glu	Leu	Arg	Gln	Thr	His	Lys	Asp	Ala	Glu	Gly	Asn	Asn	Val	Val					
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Val	Leu	Asn	Glu	Lys	Ile	Arg	Ser	Gln	Gly	Ala	Phe	His	Ile	Leu	Ala					
				595					600					605						
Gly	Ala	Asp	Tyr	Thr	Phe	Glu	Met	Gly	Gly	Arg	Lys	Tyr	Lys	Phe	Thr					
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Ala	Glu	Ala	Tyr	Tyr	Lys	Ser	Leu	Phe	Asn	Ile	Asn	Pro	Tyr	Ile	Ile					
625					630					635					640					
Glu	Asn	Val	Lys	Ile	Arg	Tyr	Leu	Gly	Glu	Asn	Ile	Gly	Ser	Gly	Tyr					
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Ala	Ala	Gly	Ile	Asp	Leu	Lys	Leu	Phe	Gly	Glu	Leu	Val	Pro	Gly	Val					
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Asp	Ser	Trp	Leu	Thr	Ala	Ser	Ile	Ile	Lys	Ala	Arg	Gln	Lys	Leu	Asp					
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Gly	Tyr	Gly	Ser	Leu	Pro	Leu	Met	Asn	Ala	Pro	Thr	Tyr	Asn	Phe	Ser					
				690					695					700						
Phe	Phe	Leu	Gln	Glu	Tyr	Val	Pro	Gly	Asn	Lys	Arg	Ile	Thr	Ala	Thr					
705					710					715					720					
Leu	Arg	Ala	Ala	Leu	Ser	Gly	Gly	Leu	Pro	Gln	Leu	Asn	Pro	Ser	Lys					
				725					730					735						
Gly	Leu	Ser	Ser	Pro	Ala	Phe	Thr	Ala	Pro	Ala	Tyr	Lys	Arg	Val	Asp					
				740					745					750						
Leu	Gly	Val	Met	Tyr	Lys	Trp	Leu	Asp	Pro	Asp	Asp	Ser	Phe	Ala	Gly					
				755					760					765						
Arg	Ser	Lys	Trp	Leu	Met	Gly	Val	Lys	Gly	Ala	Tyr	Ile	Gly	Ala	Asp					
				770					775					780						
Leu	Phe	Asn	Leu	Phe	Asp	Met	Thr	Asn	Val	Asn	Ser	Tyr	Tyr	Trp	Val					
785					790					795					800					
Ser	Asp	Ala	Tyr	Gln	Gln	Gln	Tyr	Ala	Val	Pro	Asn	Tyr	Leu	Thr	Arg					
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Arg	Gln	Phe	Asn	Leu	Arg	Leu	Leu	Val	Glu	Phe										
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Met	Tyr	Ser	Gly	His	His	Lys	Ile	His	Tyr	Pro	Phe	Leu	Ile	Leu	Leu					
1				5				10				15								

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

His Phe Glu Leu Pro Ala Ile Tyr Thr Glu Ile Gln Gly Tyr Val Met
 435 440 445
 Asp Arg Glu Glu Asn Pro Ile Ala Gly Ala Thr Val Arg Ile Val Gly
 450 455 460
 Glu Arg Gly Pro Val Gly Gln Gly Phe Val Thr Thr Arg Asp Asp Gly
 465 470 475 480
 Ser Tyr Lys Met Ser Val Gln Gly Asp Thr Arg Tyr Val Met Leu Ala
 485 490 495
 Gly Ala Ser Gly Tyr Leu Asn Gln Tyr Val Glu Leu Lys Thr Asp Thr
 500 505 510
 Ala Lys Gln Ser Glu Thr Tyr Tyr Val Asp Phe Phe Leu Ala Ser Arg
 515 520 525
 Glu Lys Ala Glu Gly Leu Gln Asn Ile Phe Tyr Asp Phe Asp Lys Ala
 530 535 540
 Thr Leu Arg Pro Glu Ser Met Lys Ser Leu Asp Glu Leu Ile Arg Ile
 545 550 555 560
 Leu Thr Asp Asn Pro Asp Ile Arg Ile Glu Leu Gly Ser His Ala Asp
 565 570 575
 Arg Lys Gly Pro Asp Ala Tyr Asn Leu Gly Leu Ser Asp Arg Arg Ala
 580 585 590
 Lys Ser Val Val Asp Tyr Leu Thr Ser Arg Gly Ile Ala Ala Asp Arg
 595 600 605
 Leu Thr Trp Lys Gly Tyr Gly Lys Ser Val Pro Lys Thr Val Thr Ala
 610 615 620
 Lys Ile Ala Glu Arg His Asp Phe Leu Lys Glu Gly Asp Val Leu Thr
 625 630 635 640
 Glu Glu Phe Val Ala Pro Leu Thr Glu Glu Gln Gln Ser Val Cys Asp
 645 650 655
 Gln Leu Asn Arg Arg Thr Glu Phe Arg Val Ile Glu Glu Glu Leu Arg
 660 665 670
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 Asn Leu Gln Thr Val Thr Val Tyr Ser Thr Arg Thr Ala Val Pro Leu
 35 40 45
 Lys Lys Ile Pro Ala Lys Met Glu Leu Ile Ser Ser Arg Asn Ile Lys
 50 55 60
 Gln Ser Gly Phe Asn Asn Met Thr Asp Ile Leu Lys Thr Gln Ser Ser
 65 70 75 80
 Leu Asp Val Ile Gln Tyr Pro Gly Phe Ser Ser Asn Ile Gly Ile Arg
 85 90 95
 Gly Phe Lys Pro Ser Gly Lys Tyr Val Thr Val Leu Val Asn Gly Ile
 100 105 110
 Pro Ala Gly Thr Asp Asn Ile Ser Thr Leu Asn Thr Ser Asn Ile Glu
 115 120 125
 Gln Ile Glu Ile Leu Lys Gly Pro Phe Ser Ser Ile Tyr Gly Thr Asn

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

545					550								555								560
Ser	Leu	Arg	Ala	Phe	Ala	Asn	Ala	Thr	Ile	Met	Leu	Asn	Ser	Glu	Met						
				565								570								575	
Lys	Lys	Ser	Gln	Thr	Asp	Ala	Pro	Trp	Ser	Glu	Met	Tyr	Tyr	Val	Arg						
				580								585								590	
Lys	Gln	Asn	Ile	Thr	Phe	Gly	Ile	Glu	Tyr	Arg	Gly	Lys	Glu	Gly	Leu						
				595								600								605	
Glu	Val	Met	Leu	Asn	Gly	Arg	Phe	Met	Gly	Arg	Arg	Ile	Glu	Gln	Asn						
				610								615								620	
Trp	Tyr	Ala	Tyr	Tyr	Pro	Glu	Val	Arg	Pro	Glu	Leu	Gln	Gln	Leu	Leu						
				625								630								635	
Ala	Ala	Glu	Glu	Pro	Glu	Leu	Ala	Ala	Gln	Gly	Leu	Leu	Arg	His	Pro						
				645								650								655	
Gln	Ala	Met	Val	Phe	Asn	Ala	Ser	Ala	Tyr	Tyr	His	Met	Asn	Lys	Tyr						
				660								665								670	
Leu	Thr	Phe	Gly	Val	Asn	Leu	Asn	Asn	Ile	Leu	Asp	Glu	Leu	Tyr	Thr						
				675								680								685	
Glu	Lys	Asp	Gly	Tyr	His	Met	Pro	Gly	Arg	Asn	Ile	Met	Gly	Lys	Val						
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Met	Val	Asn	Phe																		
				705																	
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Leu	Trp	Phe	Val	Ser	Ala	Ser	Arg	Thr	Val	Ala	Gln	Asn	Ala	Ser	Glu						
				20								25								30	
Thr	Thr	Val	Ser	Tyr	Asp	Thr	Asp	Thr	Ala	Val	Leu	Ser	Glu	Ala	Asp						
				35								40								45	
Val	Leu	Arg	Ile	Ala	Leu	Ser	Glu	Asn	Ala	Thr	Val	Lys	Val	Ala	Asp						
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Met	Asp	Val	Arg	Lys	Gln	Glu	Tyr	Ala	Arg	Arg	Ala	Ala	Arg	Ala	Asp						
				65								70								75	
Leu	Phe	Pro	Lys	Val	Asp	Leu	Asn	Gly	Val	Tyr	Ser	His	Thr	Leu	Lys						
				85								90								95	
Lys	Gln	Val	Leu	Tyr	Ile	Asp	Met	Pro	Gly	Phe	Ser	Ser	Ser	Glu	Gly						
				100								105								110	
Ile	Glu	Met	Gly	Arg	Thr	His	Asn	Thr	Gln	Gly	Gly	Val	Asn	Val	Ser						
				115								120								125	
Met	Pro	Leu	Val	Ser	Ala	Gln	Leu	Trp	Lys	Ser	Ile	Ala	Met	Thr	Gly						
				130								135								140	
Glu	Gln	Leu	Asp	Leu	Ala	Leu	Glu	Lys	Ala	Arg	Ser	Ser	Arg	Ile	Asp						
				145								150								155	
Leu	Val	Ala	Glu	Val	Lys	Lys	Ala	Tyr	Leu	Ser	Val	Leu	Leu	Ala	Glu						
				165								170								175	
Asp	Ser	Tyr	Gly	Val	Phe	Lys	Arg	Ser	Tyr	Asp	Asn	Ala	Leu	Ala	Asn						
				180								185								190	
Tyr	Lys	Asn	Ile	Ser	Asp	Lys	Phe	Asp	Arg	Gly	Leu	Val	Ala	Glu	Tyr						
				195								200								205	

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

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115          120          125
Leu Pro Leu Lys Glu Leu Ser Pro Ala Ser Arg Arg Leu Tyr Arg Gly
130          135          140
Tyr Glu Ala Leu Phe Val Pro Gly Asp Gly Gly Ser Arg Asn Tyr Arg
145          150          155          160
Ile Pro Ala Ile Leu Lys Thr Ala Asn Gly Thr Leu Ile Ala Met Ala
165          170          175
Asp Arg Arg Lys Tyr Asn Gln Thr Asp Leu Pro Glu Asp Ile Asp Ile
180          185          190
Val Met Arg Arg Ser Thr Asp Gly Gly Lys Ser Trp Ser Asp Pro Arg
195          200          205
Ile Ile Val Gln Gly Glu Gly Arg Asn His Gly Phe Gly Asp Val Ala
210          215          220
Leu Val Gln Thr Gln Ala Gly Lys Leu Leu Met Ile Phe Val Gly Gly
225          230          235          240
Val Gly Leu Trp Gln Ser Thr Pro Asp Arg Pro Gln Arg Thr Tyr Ile
245          250          255
Ser Glu Ser Arg Asp Glu Gly Leu Thr Trp Ser Pro Pro Arg Asp Ile
260          265          270
Thr His Phe Ile Phe Gly Lys Asp Cys Ala Asp Pro Gly Arg Ser Arg
275          280          285
Trp Leu Ala Ser Phe Cys Ala Ser Gly Gln Gly Leu Val Leu Pro Ser
290          295          300
Gly Arg Ile Thr Phe Val Ala Ala Ile Arg Glu Ser Gly Gln Glu Tyr
305          310          315          320
Val Leu Asn Asn Tyr Val Leu Tyr Ser Asp Asp Glu Gly Asp Thr Trp
325          330          335
Gln Leu Ser Asp Cys Ala Tyr Arg Arg Gly Asp Glu Ala Lys Leu Ser
340          345          350
Leu Met Pro Asp Gly Arg Val Leu Met Ser Ile Arg Asn Gln Gly Arg
355          360          365
Gln Glu Ser Arg Gln Arg Phe Phe Ala Leu Ser Ser Asp Asp Gly Leu
370          375          380
Thr Trp Glu Arg Ala Lys Gln Phe Glu Gly Ile His Asp Pro Gly Cys
385          390          395          400
Asn Gly Ala Met Leu Gln Val Lys Arg Asn Gly Arg Asp Gln Val Leu
405          410          415
His Ser Leu Pro Leu Gly Pro Asp Gly Arg Arg Asp Gly Ala Val Tyr
420          425          430
Leu Phe Asp His Val Ser Gly Arg Trp Ser Ala Pro Val Val Val Asn
435          440          445
Ser Gly Ser Ser Ala Tyr Ser Asp Met Thr Leu Leu Ala Asp Gly Thr
450          455          460
Ile Gly Tyr Phe Val Glu Glu Gly Asp Glu Ile Ser Leu Val Phe Ile
465          470          475          480
Arg Phe Val Leu Asp Asp Leu Phe Asp Val Arg Gln
485          490
<210> 451
<211> 245
<212> PRT
<213> Porphyromonas gingivalis
<400> 451

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

<210> 452
<211> 276
<212> PRT
<213> Porphyromonas gingivalis
<400> 452

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

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115          120          125
Ala Phe Met Gln Arg Ile Gln Ala Lys Lys Gln Arg Glu Asn Asn Met
130          135          140
Lys Gln Phe Gly Gln Asn Ile Glu Lys Gly Asn Glu Tyr Ile Asp Thr
145          150          155          160
Phe Lys Lys Glu Asp Gly Val Thr Val Thr Thr Thr Gly Leu Ala Tyr
165          170          175
Lys Thr Leu Gln Glu Gly Thr Gly Ala Thr Pro Ser Leu Ala Asp Thr
180          185          190
Val Arg Val Lys Tyr Val Gly Thr Leu Val Asp Gly Lys Glu Phe Asp
195          200          205
Lys Asn Glu Glu Gly Ile Glu Phe Ala Val Thr Gly Val Ile Lys Gly
210          215          220
Trp Thr Glu Met Leu Gln Leu Met Lys Val Gly Gln Lys Val Arg Val
225          230          235          240
Val Ile Pro Gln Glu Leu Ala Tyr Gly Glu Thr Gly Asn Tyr Thr Ile
245          250          255
Glu Pro Phe Ser Thr Leu Thr Phe Glu Met Glu Leu Ile Gly Ile Lys
260          265          270
Pro Gly Lys Lys
275
<210> 453
<211> 775
<212> PRT
<213> Porphyromonas gingivalis
<400> 453
Met Lys Val Leu Arg Gln Val Phe Leu Pro Ile Leu Phe Val Leu Leu
1 5 10 15
Thr Gly Ala Cys Ser Thr Thr Lys Asn Leu Pro Glu Gly Glu Gln Leu
20 25 30
Tyr Ile Gly Met Gly Lys Thr Gln Ile Leu Arg Gln Asp Lys Ser His
35 40 45
Ala Gly Gln Gln Ala Leu Thr Glu Val Glu Ser Thr Leu Lys Val Thr
50 55 60
Pro Asn Gly Ala Ile Phe Gly Ser Ala Ser Ala Ser Leu Pro Lys Ile
65 70 75 80
Pro Phe Gly Leu Trp Leu Tyr Asn Ser Phe Val Gly Asp Ser Thr Val
85 90 95
Ile Ser Lys Trp Ile Phe Asp Lys Phe Ala Ala Lys Pro Val Phe Ile
100 105 110
Ser Gln Val Lys Ser Asp Ser Arg Ala Lys Val Ala Thr Asn Ile Leu
115 120 125
Arg Glu His Gly Tyr Phe Asp Ala Lys Val Lys Ser Ser Val Thr Thr
130 135 140
Leu Lys Lys Asp Ser Leu Lys Ala Lys Ile Ser Tyr Thr Val Asp Met
145 150 155 160
Ala Ser Pro Tyr His Tyr Asp Ser Ile Ile Pro Leu Pro Ile Ser Thr
165 170 175
Phe Pro Asp Ser Ile Leu Ala Tyr Arg Gln Thr Pro Ser Leu Ile Arg
180 185 190
Lys Gly Asp Gln Phe Asn Leu Ala Lys Leu His Glu Glu Arg Gln Thr
195 200 205

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Ile	Ser	Ala	Leu	Leu	Arg	Asp	Asn	Gly	Tyr	Tyr	Tyr	Phe	Arg	Pro	Gln	210	215	220
Asp	Ile	Ile	Tyr	Glu	Ala	Asp	Thr	Leu	Leu	Val	Arg	Gly	Ala	Val	Cys	225	230	235
Leu	Arg	Ala	Lys	Leu	Ser	Glu	Asp	Thr	Pro	Pro	Gln	Ala	Met	Arg	Pro	245	250	255
Trp	Arg	Ile	Gly	Lys	Arg	Thr	Ala	Val	Leu	Leu	Gly	Met	Asn	Gly	Glu	260	265	270
Ser	Pro	Thr	Asp	Ser	Leu	Glu	Val	Glu	Asp	Met	Lys	Val	Leu	Tyr	Tyr	275	280	285
Arg	Lys	Met	Pro	Val	Arg	Pro	Lys	Ile	Leu	Ala	Lys	Arg	Phe	Arg	Phe	290	295	300
Phe	Ser	Gly	Asn	Leu	Tyr	Arg	Gln	Lys	Asp	Asp	Glu	Thr	Thr	Arg	Lys	305	310	315
Ser	Leu	Ala	Arg	Leu	Gly	Ala	Phe	Ser	Val	Ile	Asp	Leu	Asn	Phe	Leu	325	330	335
Gln	Arg	Asp	Ser	Ile	Ser	Gly	Leu	Leu	Asp	Val	Arg	Leu	Leu	Thr	Thr	340	345	350
Leu	Asp	Lys	Pro	Trp	Asp	Ala	Ser	Leu	Glu	Thr	Leu	Phe	Thr	Ser	Lys	355	360	365
Ser	Asn	Asp	Phe	Ile	Gly	Pro	Gly	Leu	Asn	Phe	Ala	Leu	Ala	Arg	Arg	370	375	380
Asn	Val	Phe	Gly	Gly	Gly	Glu	Asn	Leu	Ser	Trp	Asn	Ile	Gly	Gly	Ser	385	390	395
Tyr	Glu	Trp	Glu	Thr	Gly	Asn	Arg	Pro	Glu	Asn	Ser	Ser	Asn	Arg	Leu	405	410	415
Ile	Asp	Ile	Asn	Ser	Tyr	Asn	Met	Asn	Thr	Ala	Val	Asn	Leu	Ser	Phe	420	425	430
Pro	Ser	Ile	Val	Phe	Pro	Gly	Leu	Leu	Asp	Lys	Tyr	Tyr	Tyr	Tyr	Pro	435	440	445
Thr	Thr	Thr	Thr	Phe	Gln	Ala	Ser	Ala	Thr	Ala	Leu	Asn	Arg	Ala	His	450	455	460
Tyr	Phe	Ser	Met	Tyr	Ser	Phe	Gly	Phe	Ser	Thr	Thr	Tyr	Glu	Phe	Gln	465	470	475
Pro	Ser	Lys	Glu	His	Arg	His	Ala	Ile	Phe	Pro	Leu	Lys	Leu	Asn	Tyr	485	490	495
Asn	Leu	Leu	Gly	His	Gln	Thr	Glu	Thr	Phe	Gln	Ala	Ile	Thr	Ala	Asn	500	505	510
Asn	Pro	Pro	Leu	Leu	Leu	Ser	Leu	Gln	Ser	Gln	Phe	Leu	Ala	Gln	Met	515	520	525
Gly	Tyr	Ile	Tyr	Thr	Phe	Asn	Lys	Ser	Val	Ser	Glu	Lys	Ser	Pro	His	530	535	540
His	Leu	Trp	Met	Gln	Phe	Gly	Leu	Ser	Glu	Ala	Gly	Asn	Leu	Leu	Asn	545	550	555
Leu	Ile	Tyr	Leu	Ala	Ala	Gly	Lys	Lys	Tyr	Ser	Asp	Thr	Lys	Asn	Phe	565	570	575
Val	Gly	Val	Pro	Phe	Ser	Gln	Phe	Ile	Lys	Ala	Thr	Gly	Glu	Leu	Arg	580	585	590
Tyr	Ser	Tyr	Thr	Ile	Asp	Arg	Asn	Gln	Ser	Leu	Ala	Thr	Arg	Phe	Gly	595	600	605
Thr	Gly	Val	Ile	Tyr	Ser	Tyr	Gly	Asn	Met	Arg	Val	Ala	Pro	Tyr	Ser	610	615	620

Glu Gln Phe Tyr Val Gly Gly Ala Asn Ser Ile Arg Ala Phe Thr Val
 625 630 635 640
 Arg Ser Ile Gly Pro Gly Arg Phe Asn Pro Asp Ser Asp Asn Gln Tyr
 645 650 655
 Ser Tyr Leu Asp Gln Val Gly Glu Phe Lys Leu Glu Ala Asn Val Glu
 660 665 670
 Tyr Arg Gly Lys Leu Phe Gly Asp Leu His Ala Ala Val Phe Leu Asp
 675 680 685
 Ala Gly Asn Val Trp Leu Leu Arg Glu Asp Ser Ser Arg Pro Gly Gly
 690 695 700
 Ala Leu Ser Glu Val Gly Ser Val Ser Asn Phe Leu Asn Ser Ile Ala
 705 710 715 720
 Leu Gly Thr Gly Val Gly Leu Arg Tyr Asp Leu Ala Phe Leu Val Val
 725 730 735
 Arg Val Asp Val Gly Phe Gly Leu His Leu Pro Tyr Asn Thr Gly Lys
 740 745 750
 Lys Gly Tyr Tyr Asn Ile Pro Arg Phe Lys Asp Ala Ile Gly Phe His
 755 760 765
 Leu Ala Val Gly Tyr Pro Phe
 770 775
 <210> 454
 <211> 774
 <212> PRT
 <213> Porphyromonas gingivalis
 <400> 454
 Met Ser Ser His Ser Val Arg Tyr Leu Ile Gly Ile Ala Gly Cys Leu
 1 5 10 15
 Leu Leu Met Leu Ala Ser Ser Cys Ser Val Thr Arg Tyr Val Pro Asp
 20 25 30
 Gly Ser Arg Leu Leu Asp Arg Val Thr Ile Ala Ser Glu Thr Gly Ser
 35 40 45
 Ile Ala Leu Pro Glu Asp Ile Arg Asp Tyr Thr Leu Gln Gln Pro Asn
 50 55 60
 Tyr Arg Leu Phe Gly Met Thr Arg Trp Leu Leu Arg Val Tyr Ser Ser
 65 70 75 80
 Ser Asn Pro Asn Ser Asn Ser Trp Trp Asn Arg Ser Leu Arg Lys Met
 85 90 95
 Gly Glu Pro Pro Val Leu Ile Asp Ser Val Leu Thr Asp Arg Thr Ala
 100 105 110
 Asn Arg Leu Ala Lys Ala Met Ala Gly Asp Gly Phe Leu Asp Ala Thr
 115 120 125
 Ala Arg Ala Val Val Asp Thr Gly Leu Tyr Lys Lys Ala Arg Ile Thr
 130 135 140
 Tyr Leu Ile Gln Pro Gly Ser Arg Tyr Tyr Ile Arg Asn Met Ala Leu
 145 150 155 160
 Asp Val Lys Asn Pro Leu Leu Pro Pro Val Ala Leu Gly Asn Ser Leu
 165 170 175
 Pro Ser Ala Tyr Lys Val Gly Ile Ser Glu Gly Ser Pro Leu Ser Pro
 180 185 190
 Ile Val Leu Asp Glu Glu Arg Lys Ala Ile Ala Arg His Met Arg Asn
 195 200 205
 Asn Gly Phe Trp Lys Phe Ser Ala Glu Asp Val Tyr Tyr Glu Ala Asp

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

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625                630                635                640
Gly Trp Ser Val Arg Thr Leu Gly Pro Gly Ser Met Lys Met Thr Pro
        645                650                655
Asp Lys Thr Phe Phe Asp Gln Met Gly Asp Ile Arg Leu Asp Leu Asn
        660                665                670
Val Glu Tyr Arg Thr Lys Leu Phe Trp Lys Phe Arg Ala Ala Ala Phe
        675                680                685
Val Asp Ala Gly Asn Val Trp Thr Ile Lys Glu Tyr Glu Asn Gln Glu
        690                695                700
Asp Gly Leu Phe Arg Phe Asp Arg Phe Tyr Lys Glu Ile Ala Leu Ala
705                710                715                720
Tyr Gly Leu Gly Leu Arg Leu Asp Phe Asp Tyr Phe Leu Val Arg Leu
        725                730                735
Asp Ala Gly Leu Lys Ala Tyr Asp Pro Gln Gln Thr Gly Arg Tyr Lys
        740                745                750
Trp Ala Ile Thr Arg Pro Asn Leu Ser Ser Asn Phe Ala Trp His Ile
        755                760                765
Ala Val Gly Tyr Pro Phe
        770
<210>      455
<211>      867
<212>      PRT
<213>      Porphyromonas gingivalis
<400>      455
Met Arg Lys Arg Ile Leu Gln Leu Phe Leu Thr Ala Leu Leu Leu Ala
  1                5                10                15
Leu Gly Ser Ser Leu Ala Ile Ala Gln Thr Val Val Thr Gly Lys Val
        20                25                30
Ile Asp Ser Glu Thr Ser Glu Pro Leu Ile Gly Val Ser Val Ser Thr
        35                40                45
Gly Gln Gly Ala Ser Leu Arg Gly Val Thr Thr Asp Met Asp Gly Gly
        50                55                60
Phe Arg Phe Glu Val Pro Ala Lys Ser Val Leu Thr Phe Arg Cys Val
        65                70                75                80
Gly Tyr Ala Thr Val Thr Arg Ser Ile Gly Arg Gly Ser Gln Glu Asp
        85                90                95
Leu Gly Thr Ile Leu Leu Asp Pro Gln Ala Ile Gly Leu Asp Glu Ile
        100                105                110
Gln Val Ile Ala Ser Val Val Pro Lys Asp Arg Met Thr Pro Val Pro
        115                120                125
Val Ser Asn Ile Arg Val Ala Asp Ile Gln Ala Ala Ser Leu Asn Val
        130                135                140
Glu Phe Pro Glu Leu Val Lys Ser Thr Pro Ser Thr Tyr Thr Thr Lys
145                150                155                160
Gly Ser Gly Gly Phe Gly Asp Gly Arg Thr Asn Val Arg Gly Phe Asp
        165                170                175
Thr Tyr Asn Phe Gly Val Leu Ile Asn Gly Val Pro Val Asn Gly Met
        180                185                190
Glu Asp Gly Lys Val Tyr Trp Ser Asn Trp Ser Gly Leu Met Asn Gln
        195                200                205
Ala Ser Thr Ile Gln Ile Gln Arg Gly Leu Gly Ala Ser Lys Leu Gly
        210                215                220

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

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Phe Thr Asn His Lys Asn Phe Glu Phe Asn Ile Asn Gly Tyr Tyr Thr
 645 650 655
 Lys Trp Met Asp Arg Val Thr Ser Lys Arg Ile Gly Asn Glu Tyr Val
 660 665 670
 Tyr Leu Asn Gly Val Asp Ala Val His Cys Gly Val Glu Ala Glu Val
 675 680 685
 Ser Tyr Arg Pro Ile Arg Gln Asn Asn Val Ser Tyr Thr Ser Tyr Asp Glu
 690 695 700
 Gly Asp Trp Thr Trp Gln Asn Asn Val Ser Tyr Thr Ser Tyr Asp Glu
 705 710 715 720
 Ala Gly Asn Glu Thr Gly Gln Asp Ile Thr Tyr Ile Lys Gly Leu His
 725 730 735
 Val Gly Asp Ala Ala Gln Met Thr Ala Ala Val Ser Ala Asp Ile Glu
 740 745 750
 Leu Phe Lys Gly Phe His Val Ile Gly Lys Tyr Asn Phe Leu Gly Lys
 755 760 765
 Asn Tyr Ala Gly Phe Asn Pro Ala Thr Arg Asn Ala Gln Gln Tyr Glu
 770 775 780
 Ala Asp Gly Lys Glu Ile Val Glu Ser Trp Lys Leu Pro Asp Val Gly
 785 790 795 800
 Leu Phe Asp Leu Ser Ala Ser Tyr Asn Phe Lys Leu Gly Ser Leu Ser
 805 810 815
 Thr Thr Phe Tyr Phe Asn Met Asp Asn Val Ala Asp Lys Arg Tyr Val
 820 825 830
 Ser Asp Ala Asp Asp Asn Ile Ile Gly Lys Lys His Asp Glu Ala Ser
 835 840 845
 Ala Leu Val Trp Tyr Gly Phe Gly Arg Thr Trp Ser Thr Gly Ile Arg
 850 855 860
 Val Asn Phe
 865
 <210> 456
 <211> 431
 <212> PRT
 <213> Porphyromonas gingivalis
 <400> 456
 Met Lys Phe Ser Ile Arg Leu Phe Leu Cys Ile Ile Phe Leu Leu Ser
 1 5 10 15
 Ala Phe Ile Leu Pro Ala Leu Gly Gln Lys Ser Lys Gln Val Gln Arg
 20 25 30
 Leu Glu Lys Gln Arg Lys Glu Ala Leu Lys Ala Ile Glu Lys Thr Asp
 35 40 45
 Arg Glu Leu Arg Asn Thr Lys Lys Asp Lys Gln Asp Lys Gln Lys His
 50 55 60
 Leu Asn Leu Leu Asn Lys Gln Val Ala Gln Arg Lys Gln Met Val Gln
 65 70 75 80
 Leu Leu Asp Asn Glu Val Lys Glu Leu Gln Ser Asp Ile Asp Ser Met
 85 90 95
 Thr Gly Val Cys His Gln Leu Ser Val Glu Glu Lys Ala Arg Ser Asp
 100 105 110
 Glu Tyr Ala Gln Ala Leu Gln Ser Met Gln Lys Arg Lys Arg Ser Leu
 115 120 125
 Asp Arg Ile Leu Phe Ile Ser Ser Ala Lys Ser Phe Asp Glu Gly Met

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130          135          140
Arg Arg Met Arg Phe Leu Glu Gln Tyr Ala Ser Ala Tyr Lys Leu Ala
145          150          155          160
Ser Val Arg Leu Arg Asp Thr Arg Ser Lys Leu Glu Thr Glu Arg Ala
165          170          175
Thr Val Glu Asp Ala Lys Lys Glu Lys Gly His Leu Leu Val Ile Arg
180          185          190
Glu Glu Glu Lys Lys Lys Leu Glu Gly Gln Gln Ala Glu Gln Arg Arg
195          200          205
Gln Val Gln Ala Leu Gly Ala Lys Gln Lys Asp Leu Glu Ala Gln Leu
210          215          220
Arg Lys Gln Lys Lys Gln Ala Glu Ala Leu Asn Arg Lys Ile Glu Lys
225          230          235          240
Gln Ile Ala Lys Glu Ile Glu Ala Ala Glu Arg Arg Ala Arg Glu Glu
245          250          255
Arg Glu Arg Leu Ala Arg Glu Ala Lys Ala Lys Gly Lys Pro Val Pro
260          265          270
Ala Glu Pro Glu Arg Lys Ala Glu Thr Lys Gly Gly Tyr Ala Met Asp
275          280          285
Ala Ser Glu Arg Ala Leu Ser Gly Ser Phe Ala Gln Asn Lys Gly Arg
290          295          300
Leu Pro Gly Pro Val Arg Gly Arg Tyr Arg Ile Val Ser Asp Phe Gly
305          310          315          320
Val His Gln His Ser Glu Leu Lys Lys Val Gln Val Asn Asn Gly Gly
325          330          335
Ile Asp Ile Ala Val Ala Thr Gly Ser Asp Ala Thr Ser Val Phe Asp
340          345          350
Gly Val Val Ser Ser Val Phe Val Ile Pro Gly Tyr Asn Ser Ala Val
355          360          365
Met Val Arg His Gly Asn Tyr Ile Thr Val Tyr Ala Asn Leu Ser Lys
370          375          380
Val Tyr Val Asn Ser Gly Thr Arg Val Lys Thr Gly Gln Ala Leu Gly
385          390          395          400
Arg Ala Tyr Thr Asp Pro Ser Asn Asn Gln Thr Ile Ile His Phe Glu
405          410          415
Ile Trp Lys Glu Arg Ser Lys Gln Asn Pro Arg Leu Trp Leu Arg
420          425          430
<210> 457
<211> 333
<212> PRT
<213> Porphyromonas gingivalis
<400> 457
Met Lys Lys Tyr Leu Leu Tyr Ala Ser Leu Leu Thr Ser Val Leu Leu
1 5 10 15
Phe Ser Cys Ser Lys Asn Asn Pro Asn Glu Pro Val Glu Asp Arg Ser
20 25 30
Ile Glu Ile Ser Ile Arg Val Asp Asp Phe Thr Lys Thr Gly Glu Ala
35 40 45
Val Arg Tyr Glu Arg Asn Gln Gly Ser Ala Ala Glu Arg Leu Ile Thr
50 55 60
Asn Leu Tyr Leu Leu Leu Phe Asp Gln Ser Gly Ala Asn Pro Ala Lys
65 70 75 80

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Tyr Tyr Ile Thr Gly Asn Thr Phe Thr Gly Gly Thr Trp Leu Pro Asp
 85 90 95
 Asp Met Lys Val Lys Leu Asp Met Thr Gln Ser Glu Ala Gly Glu Arg
 100 105 110
 Lys Val Tyr Val Val Ala Asn Val Asp Asn Ala Val Lys Thr Ala Leu
 115 120 125
 Asp Ala Val Ala Asn Glu Ser Asp Leu Gln Thr Val Lys Arg Thr Thr
 130 135 140
 Ala Met Pro Trp Ser Thr Asp Ile Ala Ser Pro Phe Leu Met Ser Gly
 145 150 155 160
 Asn Lys Thr His Asp Phe Leu Ala Asn Arg Leu Leu Asp Asn Val Pro
 165 170 175
 Leu Val Arg Ala Ile Ala Lys Val Glu Leu Asn Ile Ser Leu Ser Glu
 180 185 190
 Lys Phe Gln Ile Val Pro Ile Ile Val Asn Gly Ser Leu Ser Glu Phe
 195 200 205
 Lys Phe Arg Tyr Val Asn Phe Asp Lys Glu Thr Tyr Val Val Lys Pro
 210 215 220
 Thr Thr Lys Pro Asp Asn Leu Ile Ser Ser Ala Asn Gly Val Trp Pro
 225 230 235 240
 Gln Ile Thr Asp Trp Thr Val Trp Gly Ala Ser Leu Asn Thr Ser Pro
 245 250 255
 Ala Pro Asp Ala Gly Thr Gly Tyr Thr Leu Asp Ala Asn Gly Lys Val
 260 265 270
 Thr Ala Leu Arg Ile Val Thr Tyr Leu Asn Glu Arg Asp Ser Lys Gly
 275 280 285
 Ala Thr Val Glu Val Ala Leu Pro Arg Val Asp Asp Gly Thr Leu Pro
 290 295 300
 Pro Pro Glu Phe Gly Pro Glu Leu Tyr Arg Leu Pro Leu Pro Asp Lys
 305 310 315 320
 Ile Leu Arg Asn His Trp Tyr Lys Tyr Glu Val Glu Ile
 325 330
 <210> 458
 <211> 315
 <212> PRT
 <213> Porphyromonas gingivalis
 <400> 458
 Met Ile Arg Thr Ile Leu Ser Arg Tyr Val Ser Ser Asn Phe Trp Ser
 1 5 10 15
 Arg Gly Ala Thr Phe Phe Phe Thr Ile Phe Pro Ala Phe Ile Leu Ala
 20 25 30
 Ala Thr Ala Leu Pro Ala Cys Gly Gly Gly Thr Ala Ser Gly Ser Asp
 35 40 45
 Arg Thr Leu Ala Val Thr Ile Glu Pro Gln Lys Tyr Phe Ile Glu Ser
 50 55 60
 Ile Ala Asp Lys Ser Val Gln Val Val Ala Leu Val Pro Ala Gly Ser
 65 70 75 80
 Asn Pro Glu Glu Tyr Asp Pro Ser Pro Thr Val Met Lys Arg Leu Ser
 85 90 95
 Glu Ala Asp Ala Tyr Phe Tyr Ile Gly Gly Leu Gly Phe Glu Gln Arg
 100 105 110
 Asn Leu Ala Ala Ile Arg Asp Asn Asn Pro Lys Leu Pro Leu Phe Glu

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115          120          125
Met Gly Lys Ala Leu Ala Asp Ala Gly Ser Ala Asp Leu His Gly Ser
130          135          140
Cys Thr Asp His Ser His Thr Asp Leu His Ala His Asp Pro His Tyr
145          150          155          160
Trp Ser Ser Val Val Gly Ala Lys Ala Leu Ser Arg Ala Ala Tyr Asp
165          170          175
Ala Leu Val Glu Leu Tyr Pro Asn Glu Lys Asp Lys Trp Asp Lys Gly
180          185          190
His Asp Arg Leu Asn Gly Arg Ile Asp Ser Val Lys Arg Leu Val Asp
195          200          205
Thr Met Phe Ala Asn Gly Lys Ala Asp Lys Ala Phe Val Ile Tyr His
210          215          220
Pro Ser Leu Ser Phe Phe Ala Gln Glu Phe Gly Leu Arg Gln Ile Val
225          230          235          240
Ile Glu Glu Asp Gly Lys Glu Pro Thr Ala Ala His Leu Arg Arg Val
245          250          255
Ile Asp Gln Ala Arg Ala Asp Gly Val Arg Ile Val Phe Ile Gln Pro
260          265          270
Glu Phe Glu Thr Arg Gln Ala Glu Asp Ile Ala Arg Glu Ile Gly Ala
275          280          285
Arg Pro Val Arg Ile Asn Pro Leu Arg Ser Ser Trp Glu Glu Glu Ile
290          295          300
Leu His Ile Ala Arg Ala Leu Ala His Glu Arg
305          310          315
<210>      459
<211>      848
<212>      PRT
<213>      Porphyromonas gingivalis
<400>      459
Met Ile Gly Lys Lys Ile Phe Phe Ile Leu Leu Ala Leu Ile Ala Phe
1      5      10      15
Ser Gly Leu Asn Ala Ala Thr Asp Thr Glu Phe Lys Tyr Pro Thr Asp
20      25      30
Ala Asn Ile Ile Gly His Val Lys Asp Ser Lys Thr Gly Glu His Leu
35      40      45
Val Gly Ile Thr Ile Ala Ile Lys Gly Thr Thr Phe Gly Thr Ser Thr
50      55      60
Asp Ala Thr Gly His Tyr Tyr Leu Arg Asn Leu Arg Pro Gly Glu Ile
65      70      75      80
Thr Leu Ile Met Arg Gly Met Gly Tyr Lys Ser Gln Glu Arg Val Val
85      90      95
Arg Val Glu Lys Asp Lys Thr Ile Glu Val Asn Phe Glu Ala Glu Glu
100     105     110
Asp Ala Ile Asn Leu Asp Glu Val Val Ile Ser Ala Asn Arg Glu Leu
115     120     125
Thr Leu Arg Arg Leu Ala Pro Thr Leu Val Asn Val Leu Asn Glu Lys
130     135     140
Val Phe Ser Gln Val Asn Ala Ser Asn Leu Ala Gln Gly Leu Ser Phe
145     150     155     160
Gln Pro Gly Val Arg Val Glu Asn Asn Cys Gln Asn Cys Gly Phe Asn
165     170     175

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

Met Tyr His Arg Phe Gly Asn Val Gln Thr Asn Phe Leu Val Glu Gly
595 600 605
Phe Tyr Thr Arg Leu Leu Asp Val Phe Thr Asn Glu Glu Gln Pro Asp
610 615 620
Gln His Asp Gly Ile Lys Arg Tyr Thr Arg Ile Asn Gly Ser Gly Ala
625 630 635 640
Lys Val Phe Gly Leu Asn Leu Glu Gly Lys Val Ala Tyr Lys Ser Phe
645 650 655
Gln Leu Gln Ala Gly Leu Thr Leu Ala Ser Asn Lys Tyr Asp Glu Ala
660 665 670
Gln Glu Trp Gly Leu Asn Thr Val Lys Asp Thr Asn Gly Ala Phe Val
675 680 685
Thr Glu Ala Asn Ala Asn Gly Gln Gln Glu Tyr Lys Asn Glu Ser Met
690 695 700
Thr Asp Thr Gln Ile Thr Arg Thr Pro Ser Val Tyr Gly Tyr Phe Thr
705 710 715 720
Leu Ala Tyr Asn Pro Ala His Ser Trp Asn Ile Ala Leu Thr Gly Ala
725 730 735
Tyr Thr Gly Gln Met Tyr Val Pro His Ala Ile Glu Tyr Gly Val Lys
740 745 750
Ser Ala Glu Leu Asp Ile Met Gln Asn Asn Pro Glu Ile Thr Asp Glu
755 760 765
Thr Gly Lys Ala Pro Arg Ile Asp Glu Leu Lys Lys Thr Pro Ala Phe
770 775 780
Phe Asp Leu Gly Leu Lys Val Gly Tyr Asp Phe His Val Phe Gln Ala
785 790 795 800
Thr Glu Val Gln Leu Tyr Val Gly Met Asn Asn Ile Phe Asn Ser Phe
805 810 815
Gln Lys Asp Phe Asp Arg Gly Ala Ala Arg Asp Ser Gly Tyr Ile Tyr
820 825 830
Gly Pro Thr Gln Pro Arg Thr Gly Tyr Met Gly Leu Val Val Lys Phe
835 840 845
<210> 460
<211> 202
<212> PRT
<213> Porphyromonas gingivalis
<400> 460
Met Thr Val Lys Arg Ala Val Arg Ile Ala Leu Leu Thr Leu Ile Gly
1 5 10 15
Ile Leu Phe Ser Ser Pro Ser Leu Val Arg Ala Gln Ser Leu Phe Ser
20 25 30
Thr Glu His Val Leu Gln Leu Tyr Asn Lys Ile Leu Tyr Gly Glu Ser
35 40 45
Ala Ala Asp Thr Val Ala Glu Lys Thr Ala Gly Glu Ser Ala Phe Pro
50 55 60
Phe Ile Asp Lys Leu Ile Asn Leu Gly Arg Thr Phe Leu Gly Lys Pro
65 70 75 80
Tyr Arg Tyr Arg Gly Pro Ser Pro Trp Pro Met Asp Cys Ser Gly Tyr
85 90 95
Val Ser Tyr Leu Tyr Ser Lys Phe Asp Ile Lys Leu Pro Arg Gly Ala
100 105 110
Ala Ala Gln Ser Gln Tyr Thr Asn Pro Ile Glu Arg Glu Asp Val Arg

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115          120          125
Pro Gly Asp Leu Leu Phe Phe Lys Gly Arg Asn Ala Arg Ser Asn Arg
130          135          140
Ile Gly His Val Ala Leu Val Val Ser Val Asp Glu Asp Asp Ile Thr
145          150          155          160
Met Met His Ser Arg Asn Ser Arg Gly Ile Val Ile Glu Lys Leu Asn
165          170          175
Arg Ser Ala Tyr Phe Ser Arg Arg Leu Val Ser Tyr Gly Arg Val Pro
180          185          190
Gly Ala Lys Arg Val Ile Pro Arg Lys Ser
195          200
<210> 461
<211> 455
<212> PRT
<213> Porphyromonas gingivalis
<400> 461
Met Lys Arg Thr Ile Leu Leu Thr Ala Leu Thr Val Leu Ser Ser Leu
1 5 10 15
Ser Leu Leu Arg Ala Gln Asn Glu Ser Glu Ala Ser Thr Asn Pro Met
20 25 30
Ser Gly Leu Ser Leu Glu Asp Cys Ile Arg Ile Ala Lys Glu Arg Asn
35 40 45
Leu Asn Leu Arg Arg Gln Glu Ile Glu Gln Glu Asn Arg Ile Ile Ser
50 55 60
Leu Asp Ala Ala Arg His Ser Phe Leu Pro Ser Val Asn Ala Gly Ile
65 70 75 80
Gly His Asn Tyr Ser Phe Gly Arg Ser Lys Asp Lys Thr Gly Val Thr
85 90 95
Val Asp Arg Ser Ser Met Asn Thr Asn Leu Ser Ile Gly Ala Ser Val
100 105 110
Glu Val Phe Ser Gly Thr Arg Arg Leu His Asp Leu Lys Gln Gln Lys
115 120 125
Tyr Asn Val Glu Asp Gly Ile Ala Arg Leu Gln Lys Ala Arg Glu Asp
130 135 140
Leu Ser Leu Gln Ile Ala Ala Leu Tyr Ile Asn Leu Leu Phe Arg Gln
145 150 155 160
Glu Met Thr Arg Thr Ala Glu Thr Gln Leu Ala Leu Ile Arg Glu Gln
165 170 175
Arg Asn Arg Thr Ala Glu Met Val Arg Val Gly Lys Trp Ala Glu Gly
180 185 190
Lys Leu Leu Asp Ile Asn Ala Gln Met Ala Lys Asp Glu Gln Leu Leu
195 200 205
Val Gln Tyr Arg Ser Glu Glu Glu Leu Ala Arg Leu Asp Leu Gly Gln
210 215 220
Ala Leu Glu Leu Glu His Pro Glu Ser Ile Ala Val Lys Ala Pro Asp
225 230 235 240
Thr Asp Val Leu Val Ala Glu Arg Leu Gly Ser Leu Leu Ala Pro Glu
245 250 255
Glu Ile Tyr Arg Thr Ala Leu Gly Leu Lys Pro Ala Leu His Ser Ser
260 265 270
Glu Leu Gln Ile Ala Ser Ala Arg Glu Gly Leu Ala Ser Ala Arg Ala
275 280 285

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Ala Tyr Phe Pro Thr Leu Ser Leu Ser Ala Gly Tyr Ser Asn Gly Tyr
 290 295 300
 Phe Arg Asp Leu Gly Lys Glu Tyr Ala Ala Ile Asn Pro Ser Phe Ser
 305 310 315 320
 Glu Gln Trp Lys Asn Asn Gly Ser Tyr Ser Ile Gly Leu Ser Leu Asn
 325 330 335
 Ile Pro Ile Phe Ser Ala Met Gln Thr Gln Asp Arg Val Arg Ser Ser
 340 345 350
 Arg Leu Gln Ile Arg Ser Ser Glu Leu Arg Leu Val Glu Glu Lys Lys
 355 360 365
 Ala Leu Tyr Lys Glu Ile Arg Gln Ala Tyr Ser Asn Ala Val Ala Ala
 370 375 380
 Asp Lys Ala Ile Ala Ala Ala Glu Asn Ser Lys Ala Ala Thr Leu Lys
 385 390 395 400
 Ala Tyr Glu Tyr Ala Arg Asp Ser Phe Glu Ala Gly Arg Leu Ser Ala
 405 410 415
 Tyr Glu Tyr Ala Glu Ala Lys Thr Lys Tyr Ala Leu Ser Gln Val Glu
 420 425 430
 Glu Leu Arg Ala Lys Tyr Asp Phe Ile Tyr Lys Ala Lys Val Leu Asp
 435 440 445
 Phe Tyr Gln Gly Lys Asp Phe
 450 455
 <210> 462
 <211> 444
 <212> PRT
 <213> Porphyromonas gingivalis
 <400> 462
 Met Arg Phe Gln His Tyr Leu Ile Cys Thr Ala Ala Val Ala Ala Leu
 1 5 10 15
 Ala Ala Asn Pro Leu Thr Gly Gln Ser Asn Met Thr Leu Glu Glu Cys
 20 25 30
 Ile Asp Tyr Ala Arg Arg His Ser Ala Val Ala Leu Ser Ala Ala
 35 40 45
 Glu Leu Glu Gln Ser Lys Ala Asp Tyr Leu Gln Ala Val Gly Asn Phe
 50 55 60
 Leu Pro Arg Val Ser Ala Gly Thr Gly Ala Ser Trp Asn Phe Gly Arg
 65 70 75 80
 Gly Leu Asp Ala Glu Thr Asn Thr Tyr Thr Asp Ile Asn Ser Phe Asn
 85 90 95
 Asn Ser Tyr Ser Ile His Ala Thr Met Thr Leu Phe Asp Gly Leu Gln
 100 105 110
 Ser Val Tyr Arg Leu Arg Met Ala His Ala Arg Arg Glu Ala Ser Arg
 115 120 125
 Leu Ser Val Arg Glu Gln Gln Glu Leu Ala Ala Leu Gly Thr Thr Glu
 130 135 140
 Ala Tyr Tyr Asp Leu Val Tyr Ala Arg Gln Met Gln Glu Leu Ala Met
 145 150 155 160
 Gln Lys Tyr Glu Glu Ser Ser Arg Leu His Arg Gln Thr Ala Arg Met
 165 170 175
 Glu Glu Leu Gly Met Lys Ser Arg Pro Asp Val Leu Glu Met Gln Ser
 180 185 190
 Arg Met Ala Gly Asp Arg Leu Ala Leu Thr Gln Ala Asp Asn Gln Cys


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195                200                205
Ile Ile Ala Leu Ile Arg Leu Lys Glu Lys Met Asn Phe Pro Ile Asp
210                215                220
Asp Glu Leu Val Val Asp Asp Met Pro Ala Asp Ser Leu Ser Ala Asp
225                230                235                240
Met Ala Glu Ser Asp Ser Ser Ala Gly Val Phe Ala Arg Ala Ala His
245                250                255
His His Pro Val Leu Leu Arg Ala Lys Leu Asp Glu Gln Ala Ala Thr
260                265                270
Asp Arg Leu Arg Ala Ala Arg Gly Ala Phe Leu Pro Ser Val Ser Val
275                280                285
Ser Gly Gly Trp Asn Thr Gly Phe Ser Arg Phe Leu Asn Gly Ser Asp
290                295                300
Tyr Thr Pro Phe Ser Glu Gln Phe Arg Asn Arg Arg Gly Glu Tyr Val
305                310                315                320
Ser Leu Asn Leu Ser Ile Pro Ile Phe Ser Gly Phe Ser Leu Val Ser
325                330                335
His Leu Arg Gln Ala Arg Ala Glu Arg Arg Ala Ala Ile Val Arg Arg
340                345                350
Gly Glu Ala Glu Arg Arg Leu Tyr Ser Glu Ile Ala Gln Ala Met Ala
355                360                365
Asp Arg Asp Ala Ala Leu Ala Ser Tyr Arg Gln Ala Lys Glu His Thr
370                375                380
Asp Ala Met Gln Thr Ala Tyr Glu Ala Val Leu Gln Arg Tyr Glu Glu
385                390                395                400
Gly Leu Asn Thr Ala Ile Asp Leu Thr Thr Gln Ala Asn Arg Leu Leu
405                410                415
Asp Ala Arg Val Gln Arg Leu Arg Ala Ala Met Thr Tyr Arg Leu Lys
420                425                430
Cys Lys Leu Ile Ala Tyr Tyr Gly Cys Leu Ser Asp
435                440
<210> 463
<211> 940
<212> PRT
<213> Porphyromonas gingivalis
<400> 463
Met Asn Lys Phe Tyr Lys Ser Leu Leu Gln Ser Gly Leu Ala Ala Phe
1 5 10 15
Val Ser Met Ala Thr Ala Leu Thr Ala Ser Ala Gln Ile Ser Phe Gly
20 25 30
Gly Glu Pro Leu Ser Phe Ser Ser Arg Ser Ala Gly Thr His Ser Phe
35 40 45
Asp Asp Ala Met Thr Ile Arg Leu Thr Pro Asp Phe Asn Pro Glu Asp
50 55 60
Leu Ile Ala Gln Ser Arg Trp Gln Ser Gln Arg Asp Gly Arg Pro Val
65 70 75 80
Arg Ile Gly Gln Val Ile Pro Val Asp Val Asp Phe Ala Ser Lys Ala
85 90 95
Ser His Ile Ser Ser Ile Gly Asp Val Asp Val Tyr Arg Leu Gln Phe
100 105 110
Lys Leu Glu Gly Ala Lys Ala Ile Thr Leu Tyr Tyr Asp Ala Phe Asn
115 120 125

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

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Ser Ile Ile Gly Ser Gly Ile Ile Arg Tyr Glu Val Ser Ala Arg Phe
545                550                555                560
Ile Tyr Pro Ser Pro Leu Asp Gly Val Glu Ser Tyr Lys Asp Thr Asp
                565                570                575
Lys Thr Ser Ala Asp Leu Ala Ile Gly Asp Ile Gln Thr Lys Leu Lys
                580                585                590
Pro Asp Val Thr Pro Leu Pro Gly Gly Val Ser Leu Ser Trp Lys
                595                600                605
Val Pro Phe Leu Ser Gln Leu Val Ser Arg Phe Gly Glu Ser Pro Asn
                610                615                620
Pro Val Phe Lys Thr Phe Glu Val Pro Tyr Val Ser Ala Ala Ala Ala
625                630                635                640
Gln Thr Pro Asn Pro Pro Val Gly Val Val Ile Ala Asp Lys Phe Met
                645                650                655
Ala Gly Thr Tyr Pro Glu Lys Ala Ala Ile Ala Ala Val Tyr Val Met
                660                665                670
Pro Ser Ala Pro Asp Ser Thr Phe His Leu Phe Leu Lys Ser Asn Thr
                675                680                685
Asn Arg Arg Leu Gln Lys Val Thr Thr Pro Ser Asp Trp Gln Ala Gly
                690                695                700
Thr Trp Leu Arg Ile Asn Leu Asp Lys Pro Phe Pro Val Asn Asn Asp
705                710                715                720
His Met Leu Phe Ala Gly Ile Arg Met Pro Asn Lys Tyr Lys Leu Asn
                725                730                735
Arg Ala Ile Arg Tyr Val Arg Asn Pro Asp Asn Leu Phe Ser Ile Thr
                740                745                750
Gly Lys Lys Ile Ser Tyr Asn Asn Gly Val Ser Phe Glu Gly Tyr Gly
                755                760                765
Ile Pro Ser Leu Leu Gly Tyr Met Ala Ile Lys Tyr Leu Val Val Asn
                770                775                780
Thr Asp Ala Pro Lys Ile Asp Met Ser Leu Val Gln Glu Pro Tyr Ala
785                790                795                800
Lys Gly Thr Asn Val Ala Pro Phe Pro Glu Leu Val Gly Ile Tyr Val
                805                810                815
Tyr Lys Asn Gly Thr Phe Ile Gly Thr Gln Asp Pro Ser Val Thr Thr
                820                825                830
Tyr Ser Val Ser Asp Gly Thr Glu Ser Asp Glu Tyr Glu Ile Lys Leu
                835                840                845
Val Tyr Lys Gly Ser Gly Ile Ser Asn Gly Val Ala Gln Ile Glu Asn
                850                855                860
Asn Asn Ala Val Val Ala Tyr Pro Ser Val Val Thr Asp Arg Phe Ser
865                870                875                880
Ile Lys Asn Ala His Met Val His Ala Ala Ala Leu Tyr Ser Leu Asp
                885                890                895
Gly Lys Gln Val Arg Ser Trp Asn Asn Leu Arg Asn Gly Val Thr Phe
                900                905                910
Ser Val Gln Gly Leu Thr Ala Gly Thr Tyr Met Leu Val Met Gln Thr
                915                920                925
Ala Asn Gly Pro Val Ser Gln Lys Ile Val Lys Gln
                930                935                940
<210>      464
<211>      670

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<212>      PRT
<213>      Porphyromonas gingivalis
<400>      464
Met Lys Tyr Leu Ile Arg Leu Phe Leu Ser Leu Met Leu Leu Ser Leu
  1              5              10              15
Trp Thr Gly Cys Thr His Glu Glu Leu Ser Ile Cys Asp Gly Glu Asn
  20              25              30
Thr Leu Val Leu Arg Val Glu Thr Gly Lys Ala Pro Asn Ala Arg Ala
  35              40              45
Thr Glu Pro Gly Gln Gly Ile Tyr Asn Glu Asn Lys Val Gly Ser Ile
  50              55              60
Ser Val Leu Phe Tyr Leu Glu Gly Gln Leu Arg Trp Gln Val Lys Ser
  65              70              75              80
Thr Asp Tyr Gln Ile His Glu Gly Ala Tyr Ile Ile Pro Val Lys Glu
  85              90              95
Gln Met Arg Pro Leu Phe Asn Gly Asn Asn Asn Phe Ser Ile Tyr Val
  100             105             110
Val Ala Asn Leu Asp Phe Asn Ala Pro Ala Thr Glu Ala Ala Leu Ser
  115             120             125
Gln Phe Val Val Glu Lys Ser Ile Glu Val Ser Ser Thr Thr Ala Pro
  130             135             140
Ala Asp Phe Val Met Leu Ala His Gly Asn Lys Gln Ile Asn Met Ala
  145             150             155             160
Thr Thr Glu Gly Lys Leu Leu Gly Asp Tyr Lys Leu Lys Arg Val Ala
  165             170             175
Ala Lys Ile Arg Met Ile Lys Pro Thr Ile Asn Val Gln Gly Tyr Glu
  180             185             190
Val Val Gly Asn Ile Gln Ala Lys Phe Arg Asn Ser Val Thr Lys Gly
  195             200             205
Phe Leu Thr Thr Glu Ala Gln Glu Ile Pro Ala Ala Ala Ser Tyr Lys
  210             215             220
Thr Ser Glu Tyr Leu Asp Ile Ala Glu Ser Ala Pro Ala Asn Ser Ile
  225             230             235             240
His Phe Tyr Ser Tyr Tyr Asn Lys Trp Thr Leu Ser Thr Pro Glu Lys
  245             250             255
Arg Pro Glu Phe Phe Ile Met Val Lys Phe Lys Lys Thr Gly Gln Pro
  260             265             270
Asp Asn Thr Ala Lys Pro Tyr Tyr Tyr Arg Val Pro Leu Glu Ser Gln
  275             280             285
Asp Asn Gln Val Lys Ser Asn Val Leu Tyr Asn Leu Asn Val Lys Ile
  290             295             300
Glu Ile Leu Gly Ser Leu Gln Glu Pro Glu Ala Val Ser Val Asn Gly
  305             310             315             320
Thr Leu Ala Ile Glu Glu Trp Ile Leu His Gln Asp Ala Phe Asn Leu
  325             330             335
Pro Ala Thr Asn Tyr Leu Ile Val Glu Gln His Glu Ile Phe Met Asn
  340             345             350
Asn Val Asn Thr Tyr Ser Val Lys Tyr Gln Thr Ser Gln Lys Pro Ile
  355             360             365
Ser Ile Ser Ile Gln Ser Val Thr Phe Ser Tyr Val Ser Ser Asp Gly
  370             375             380
Thr Gln His Asn Asp Leu Val Ala Ser Ser Ser Asp Gln Tyr Pro Thr

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385						390						395						400
Ile	Thr	Ser	Asp	Asn	Thr	Ser	Ile	Ile	Ile	Thr	Ser	Lys	Ile	Pro	Val			
				405					410					415				
Asn	Asn	Val	Pro	Lys	Lys	Ile	Val	Phe	Glu	Val	Thr	Asn	Gly	Val	Ala			
				420					425					430				
Gly	Leu	Lys	Glu	Thr	Val	Thr	Val	Leu	Gln	Tyr	Pro	Ala	Gln	Phe	Ile			
				435					440					445				
Val	Asn	Thr	Leu	Gly	Thr	Ala	Ser	Ala	Trp	Arg	Pro	Asp	Gly	Ser	Leu			
				450					455					460				
Ala	Pro	Gly	Leu	Asn	Asn	Lys	Ala	Ile	Tyr	His	Val	Val	Val	Leu	Val			
465					470					475					480			
Pro	Pro	Glu	Asn	Leu	Phe	Glu	Asp	Gly	Thr	Gln	Thr	Ile	Ile	Gly	Tyr			
				485					490					495				
Pro	Pro	Thr	Glu	Thr	Ile	Ser	Phe	His	Lys	Lys	Glu	Asn	Asn	Thr	Tyr			
				500					505					510				
Pro	Ile	Val	Trp	Ser	Asp	Thr	Asn	Thr	Thr	Lys	Gln	Asp	Leu	Glu	Thr			
				515					520					525				
Ser	Arg	Met	Ile	Ser	Pro	Ser	Phe	Glu	Leu	Ala	Ser	Gln	Leu	Gly	Ala			
				530					535					540				
Thr	Leu	Pro	Met	Pro	Tyr	Leu	Glu	Tyr	Trp	Pro	Gly	Thr	Ser	Tyr	Leu			
545					550					555					560			
Leu	Asp	Tyr	Ser	Gly	Asn	Tyr	Asn	Asn	Lys	Arg	Tyr	Ala	Leu	Phe	Asn			
				565					570					575				
Cys	Ala	Phe	Tyr	Trp	Glu	Lys	Arg	Lys	Val	Asn	Asn	Glu	Glu	Ile	Lys			
				580					585					590				
Phe	Asp	Asp	Trp	Arg	Leu	Pro	Thr	Glu	Ala	Glu	Ile	Lys	Leu	Ile	Asp			
				595					600					605				
Lys	Leu	Gln	His	Asn	Glu	Gln	Ser	Ala	Val	Gln	Ala	Ile	Met	Thr	Gly			
				610					615					620				
Asn	Tyr	Tyr	Trp	Asp	Ser	Tyr	Ser	Ala	Asn	Gly	Ser	Tyr	Lys	Met	Gln			
625					630					635					640			
Gly	Gly	Gly	Gly	Gln	Gly	Asn	Ser	Ser	Lys	Ala	Tyr	Val	Arg	Cys	Val			
				645					650					655				
Arg	Asp	Val	Lys	Lys	Pro	Ile	Arg	Asp	Lys	Lys	Ser	Gly	Lys					
				660					665					670				
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<211>		1282																
<212>		PRT																
<213>		Porphyromonas gingivalis																
<400>		465																
Met	Arg	Lys	Ile	Leu	Ser	Phe	Leu	Met	Met	Cys	Ser	Leu	His	Leu	Gly			
1					5					10					15			
Leu	Gln	Ser	Gln	Thr	Trp	His	Gly	Asp	Pro	Asp	Ser	Val	Ala	Ala	Leu			
				20					25					30				
Pro	Ser	Ile	Gly	Ile	Gln	Glu	Ser	Ser	Cys	Thr	Arg	Ile	Thr	Phe	Glu			
				35					40					45				
Val	Val	Phe	Pro	Gly	Phe	Tyr	Ser	Val	Glu	Lys	Arg	Glu	Gly	Asn	Gln			
				50					55					60				
Val	Phe	Gln	Arg	Ile	Ser	Met	Pro	Gly	Cys	Gly	Ser	Phe	Gly	Asn	Leu			
65					70					75					80			
Gly	Glu	Ala	Glu	Leu	Pro	Val	Leu	Lys	Lys	Met	Ile	Ala	Val	Pro	Glu			
				85					90					95				

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

Leu	Asn	Asn	Thr	Ser	Ser	Gln	Gly	Leu	Cys	Thr	Ser	Leu	Ser	Cys	Ser
		515					520					525			
Ser	Ala	Val	Ala	Asp	Ser	Thr	Ile	Arg	Ser	Leu	Gly	Glu	Val	Leu	Thr
		530					535					540			
Thr	Tyr	Ala	Pro	Asn	Lys	Gly	Phe	Ser	Ala	Phe	Leu	Gly	Gly	Ser	Arg
545					550					555					560
Ala	Thr	Gln	Tyr	Ala	Val	Tyr	Leu	Glu	Gly	Pro	Cys	Pro	Pro	Ser	Glu
					565					570					575
Phe	Tyr	Glu	Tyr	Leu	Pro	Tyr	Ser	Leu	Tyr	His	Asn	Leu	Ser	Thr	Val
					580					585				590	
Val	Gly	Glu	Met	Leu	Leu	Ser	Ser	Ile	Ile	Asn	Thr	Asn	Ser	Val	Asp
Thr	Tyr	Ser	Lys	Phe	Asn	Phe	Asn	Leu	Leu	Gly	Asp	Pro	Ala	Leu	Asn
Ile	Met	Ala	His	Gly	Met	Glu	Val	Ser	Asn	Cys	Ile	Thr	Leu	Pro	Asn
625					630						635				640
Asn	Thr	Ile	Ile	Ser	Ser	Pro	Ile	Thr	Ile	Lys	Asn	Gly	Gly	Cys	Leu
					645					650					655
Lys	Ile	Pro	Glu	Lys	Gly	Val	Leu	His	Phe	Thr	Asn	Asn	Gly	Ser	Ile
					660					665				670	
Gln	Val	Met	Ser	Gly	Gly	Thr	Leu	Glu	Ile	Gly	Asn	Gln	Ala	Lys	Ile
Ser	Gly	Glu	Thr	Gly	Ala	Asn	Pro	Thr	Phe	Ile	Thr	Val	Tyr	Gly	Asp
Gly	Leu	Ala	Ile	Asn	Lys	Gln	Val	Glu	Ile	Asp	Asn	Ile	Asp	Arg	Leu
705					710						715				720
Asn	Leu	Phe	Ser	Thr	His	Ser	Val	Met	Pro	Lys	Phe	His	Phe	Asp	Ser
					725					730					735
Val	Lys	Phe	Asn	Ser	Ala	Pro	Leu	Tyr	Thr	Thr	Asn	Cys	Ile	Val	Glu
Ile	Ser	Asn	Cys	Glu	Phe	Thr	Asn	Arg	Ser	Asp	Ile	Ile	Ser	Lys	Asn
Cys	Asp	Leu	Ser	Val	Glu	Asn	Ser	Met	Phe	Ser	Ser	Ser	Gly	Ile	Thr
Val	Phe	Lys	Pro	Met	Ala	Thr	Ser	Ser	Ile	Thr	Gly	Leu	Ser	Thr	Lys
785					790						795				800
Ala	Lys	Ile	Thr	Asp	Asn	Thr	Phe	Phe	Ala	Thr	Gly	Asn	Phe	Ala	Tyr
					805					810					815
His	Ile	Thr	Asn	Thr	Pro	Gly	Leu	Thr	Ala	Thr	Ser	Asn	Ala	Ala	Ile
Lys	Leu	Asp	Asn	Ile	Pro	Glu	Tyr	Tyr	Ile	Ser	Gly	Asn	Lys	Ile	Val
Asn	Cys	Asp	Glu	Ala	Leu	Val	Leu	Asn	Asn	Ser	Gly	Asn	Arg	Thr	Asn
Arg	Leu	His	Asn	Ile	Thr	Arg	Asn	Val	Ile	Lys	Asn	Cys	Arg	Ile	Gly
865					870	</									

Asn Arg Thr Trp Gln Leu Tyr Ser Ser Asn Gly Thr Phe Pro Leu Asn
 930 935 940
 Phe His Tyr Asn Ser Leu Gln Gly Gly Asp Thr Asp Thr Trp Ile Tyr
 945 950 955 960
 Asn Asp Thr Tyr Thr Asn Arg Tyr Ile Asp Val Ser Asn Asn His Trp
 965 970 975
 Gly Asn Asn Asp Leu Phe Asp Pro Asn Gln Val Phe Asn Thr Pro Asp
 980 985 990
 Leu Phe Ile Trp Ile Pro Phe Trp Asp Gly Leu Pro Asn Gly Arg Ser
 995 1000 1005
 Gly Asn Ser Ser Ala Glu Ala Val Glu Phe Gln Thr Ala Leu Asp Cys
 1010 1015 1020
 Ile Gly Asn Ser Asp Tyr Leu Ser Ala Lys Val Ala Leu Lys Met Met
 1025 1030 1035 1040
 Val Glu Thr Tyr Pro Glu Ser Asp Phe Ala Ile Ala Ala Leu Lys Glu
 1045 1050 1055
 Leu Phe Arg Ile Glu Lys Met Ser Gly Asn Asp Tyr Glu Gly Leu Lys
 1060 1065 1070
 Asp Tyr Phe Arg Ser Asn Pro Thr Ile Ile Ser Ser Gln Asn Leu Phe
 1075 1080 1085
 Pro Thr Ala Asp Phe Leu Ser Ala Arg Cys Asp Ile Val Cys Glu Asn
 1090 1095 1100
 Tyr Gln Ser Ala Ile Asp Trp Tyr Glu Asn Arg Leu Asn Ser Glu Ile
 1105 1110 1115 1120
 Ser Tyr Gln Asp Ser Val Phe Ala Val Ile Asp Leu Gly Asp Ile Tyr
 1125 1130 1135
 Trp Asn Met Gln Leu Asp Ser Leu Arg Gly Thr Gly Ile Asp Leu Asn
 1140 1145 1150
 Ile Leu Ser Cys Glu Gln Arg Lys Ser Leu Glu Ser His Gln Asn Val
 1155 1160 1165
 Lys Asn Tyr Leu Leu Ser Thr Leu Pro Glu Ser Thr Gly Thr Leu Leu
 1170 1175 1180
 Pro Pro Leu Glu Cys Asn Lys Ser Ser Leu Asp Lys Ser Lys Ile Ile
 1185 1190 1195 1200
 Ser Ile Ser Pro Asn Pro Ala Lys Ala Val Val Thr Ile Ile Tyr Tyr
 1205 1210 1215
 Thr Asp Asn Pro Ser Cys Ser Val Ile Lys Ile Tyr Gly Ile Asn Gly
 1220 1225 1230
 Ala Ser Ala Asp Ile Thr Gly Leu Pro Lys His Leu Ser Glu Gly Tyr
 1235 1240 1245
 Tyr Ser Ile Gln Phe Asn Thr Ser Asn Phe Asp Pro Gly Phe Tyr Leu
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 Ser Cys Thr Arg Ile Thr Phe Glu Val Val Phe Pro Gly Phe Tyr Ser
 35 40 45
 Val Glu Lys Arg Glu Gly Asn Gln Val Phe Gln Arg Ile Ser Met Pro
 50 55 60
 Gly Cys Gly Ser Phe Gly Asn Leu Gly Glu Ala Glu Leu Pro Val Leu
 65 70 75 80
 Lys Lys Met Ile Ala Val Pro Glu Phe Ser Thr Ala Asn Val Ala Val
 85 90 95
 Lys Ile Lys Glu Thr Glu Thr Phe Asp Asn Tyr Asn Ile Tyr Pro Asn
 100 105 110
 Pro Thr Tyr Val Val Glu Glu Leu Pro Glu Gly Gly Thr Tyr Leu Val
 115 120 125
 Glu Ala Phe Ala Ile Asn Asn Asp Tyr Tyr Ser Gln Asn Val Ser Leu
 130 135 140
 Pro Ser Thr His Tyr Val Tyr Ser Gln Asp Gly Tyr Phe Arg Ser Gln
 145 150 155 160
 Arg Phe Ile Glu Val Thr Leu Tyr Pro Phe Arg Tyr Asn Pro Val Arg
 165 170 175
 Gln Glu Ile Leu Phe Ala Lys Lys Ile Glu Val Thr Ile Thr Phe Asp
 180 185 190
 Asn Pro Gln Pro Pro Leu Gln Lys Asn Thr Gly Ile Phe Asn Lys Val
 195 200 205
 Ala Ser Ser Ala Phe Ile Asn Tyr Glu Ala Asp Gly Lys Ser Ala Ile
 210 215 220
 Glu Asn Asp Met Val Phe Ser Arg Gly Thr Thr Thr Tyr Ile Ser Gly
 225 230 235 240
 Asn Val Ala Ser Asn Leu Pro Gln Asn Cys Asp Tyr Leu Val Ile Tyr
 245 250 255
 Asp Asp Met Phe Asn Val Asn Gln Gln Pro His Asp Glu Ile Lys Arg
 260 265 270
 Leu Cys Glu His Arg Ala Phe Tyr Asn Gly Phe Asp Val Ala Ala Val
 275 280 285
 Ser Ile Lys Asp Val Leu Asn Ser Phe Pro Ser Asn Ala Thr Ser Tyr
 290 295 300
 Ile Asn Glu Thr Lys Leu Lys Asn Phe Ile Arg Ser Val Tyr Asn Gln
 305 310 315 320
 Ser Asn Ala Lys Arg Thr Leu Asp Gly Lys Leu Gly Tyr Val Leu Leu
 325 330 335
 Ile Gly Lys Pro Leu Ser Lys Tyr Leu Ala Asp Thr Asp Asn Thr Lys
 340 345 350
 Val Pro Thr Ser Phe Ile His Asn Val Ser Leu Ile Pro Ser His Pro
 355 360 365
 Thr Phe Gly Ser Ile Cys Ala Ser Asp Tyr Phe Phe Ser Cys Val Ser
 370 375 380
 Pro Leu Asp Thr Val Gly Asp Leu Phe Ile Gly Arg Phe Ser Val Thr
 385 390 395 400
 Asn Ala His Glu Leu His Asn Leu Ile Glu Lys Thr Ile Asn Lys Glu
 405 410 415
 Ile Ser Tyr Asn Pro Ile Ala His Lys Asn Ile Leu Tyr Ala Glu Gly
 420 425 430

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

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Asn Asn Ser Gly Asn Arg Thr Asn Arg Leu His Asn Ile Thr Arg Asn
 850                      855                      860
Val Ile Lys Asn Cys Arg Ile Gly Ser Thr Leu Tyr Asn Ser Tyr Gly
865                      870                      875                      880
Ile Tyr Asn Arg Asn Lys Ile Ser Asn Asn His Ile Gly Val Arg Leu
                      885                      890                      895
Leu Asn Asn Ser Cys Phe Tyr Phe Asp Asn Ala Pro Val Ile Asn Glu
 900                      905                      910
Glu Asp Lys Gln Thr Phe Ile Ser Asn Arg Thr Trp Gln Leu Tyr Ser
 915                      920                      925
Ser Asn Gly Thr Phe Pro Leu Asn Phe His Tyr Asn Ser Leu Gln Gly
 930                      935                      940
Gly Asp Thr Asp Thr Trp Ile Tyr Asn Asp Thr Tyr Thr Asn Arg Tyr
945                      950                      955                      960
Ile Asp Val Ser Asn Asn His Trp Gly Asn Asn Asp Leu Phe Asp Pro
 965                      970                      975
Asn Gln Val Phe Asn Thr Pro Asp Leu Phe Ile Trp Ile Pro Phe Trp
 980                      985                      990
Asp Gly Leu Pro Asn Gly Arg Ser Gly Asn Ser Ser Ala Glu Ala Val
 995                      1000                      1005
Glu Phe Gln Thr Ala Leu Asp Cys Ile Gly Asn Ser Asp Tyr Leu Ser
1010                      1015                      1020
Ala Lys Val Ala Leu Lys Met Met Val Glu Thr Tyr Pro Glu Ser Asp
1025                      1030                      1035                      1040
Phe Ala Ile Ala Ala Leu Lys Glu Leu Phe Arg Ile Glu Lys Met Ser
 1045                      1050                      1055
Gly Asn Asp Tyr Glu Gly Leu Lys Asp Tyr Phe Arg Ser Asn Pro Thr
1060                      1065                      1070
Ile Ile Ser Ser Gln Asn Leu Phe Pro Thr Ala Asp Phe Leu Ser Ala
 1075                      1080                      1085
Arg Cys Asp Ile Val Cys Glu Asn Tyr Gln Ser Ala Ile Asp Trp Tyr
1090                      1095                      1100
Glu Asn Arg Leu Asn Ser Glu Ile Ser Tyr Gln Asp Ser Val Phe Ala
1105                      1110                      1115                      1120
Val Ile Asp Leu Gly Asp Ile Tyr Trp Asn Met Gln Leu Asp Ser Leu
 1125                      1130                      1135
Arg Gly Thr Gly Ile Asp Leu Asn Ile Leu Ser Cys Glu Gln Arg Lys
 1140                      1145                      1150
Ser Leu Glu Ser His Gln Asn Val Lys Asn Tyr Leu Leu Ser Thr Leu
 1155                      1160                      1165
Pro Glu Ser Thr Gly Thr Leu Leu Pro Pro Leu Glu Cys Asn Lys Ser
 1170                      1175                      1180
Ser Leu Asp Lys Ser Lys Ile Ile Ser Ile Ser Pro Asn Pro Ala Lys
1185                      1190                      1195                      1200
Ala Val Val Thr Ile Ile Tyr Tyr Thr Asp Asn Pro Ser Cys Ser Val
 1205                      1210                      1215
Ile Lys Ile Tyr Gly Ile Asn Gly Ala Ser Ala Asp Ile Thr Gly Leu
 1220                      1225                      1230
Pro Lys His Leu Ser Glu Gly Tyr Tyr Ser Ile Gln Phe Asn Thr Ser
 1235                      1240                      1245
Asn Phe Asp Pro Gly Phe Tyr Leu Val Thr Leu Asn Val Asp Gln Lys
1250                      1255                      1260

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Ile Ile Asp Thr Glu Lys Leu Arg Ile Lys
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<211> 925
<212> PRT
<213> Porphyromonas gingivalis
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Met Ala Ile Met Met Lys Ser Ile Val Phe Arg Ala Phe Leu Thr Ile
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Leu Leu Ser Trp Ala Ala Ile Thr Asn Pro Thr Ala Gln Glu Ile Ser
20 25 30
Gly Met Asn Ala Ser Cys Leu Ala Ala Pro Ala Gln Pro Asp Thr Ile
35 40 45
Leu Tyr Glu Ser Phe Glu Asn Gly Pro Val Pro Asn Gly Trp Leu Glu
50 55 60
Ile Asp Ala Asp Ala Asp Gly Ala Thr Trp Gly Ser Pro Ser Gly Ser
65 70 75 80
Phe Ser Val Pro Tyr Gly His Asn Gly Leu Cys Thr Tyr Ser His Ile
85 90 95
Arg Ser Gly Ile Ser Thr Ala Gly Asn Tyr Leu Ile Thr Pro Asn Ile
100 105 110
Glu Gly Ala Lys Arg Val Lys Tyr Trp Val Cys Asn Gln Tyr Ser Thr
115 120 125
Asn Pro Glu His Tyr Ala Val Met Val Ser Thr Thr Gly Thr Ala Ile
130 135 140
Glu Asp Phe Val Leu Leu Phe Asp Asp Ser Ile Thr Gly Lys Pro Thr
145 150 155 160
Pro Leu Val Trp Arg Arg Arg Ile Val Asp Leu Pro Glu Gly Thr Lys
165 170 175
Tyr Ile Ala Trp Arg His Tyr Lys Val Thr Asp Ser His Thr Glu Phe
180 185 190
Leu Lys Leu Asp Asp Val Thr Val Tyr Arg Ser Ile Glu Gly Pro Glu
195 200 205
Pro Ala Thr Asp Phe Thr Val Ile Asn Ile Gly Gln Asn Val Gly Arg
210 215 220
Leu Thr Trp Asn Tyr Pro Glu Asp Tyr Gln Pro Glu Gly Lys Gly Asn
225 230 235 240
Glu Glu Leu Gln Leu Ser Gly Tyr Asn Ile Tyr Ala Asn Gly Thr Leu
245 250 255
Leu Ala Gln Ile Lys Asp Val Ser Ile Leu Glu Tyr Val Asp Ser Thr
260 265 270
Tyr Ser Leu Arg Asp Asn Pro Leu Gln Val Glu Tyr Cys Val Thr Ala
275 280 285
Val Tyr Asp Glu Ser Ile Glu Ser Ser Thr Val Cys Gly Thr Leu His
290 295 300
Tyr Ala Thr Asp Ala Ile Leu Tyr Glu Asn Phe Glu Asn Gly Pro Val
305 310 315 320
Pro Asn Gly Trp Leu Val Ile Asp Ala Asp Gly Asp Gly Phe Ser Trp
325 330 335
Gly His Tyr Leu Asn Ala Tyr Asp Ala Phe Pro Gly His Asn Gly Gly
340 345 350
His Cys Ser Leu Ser Ala Ser Tyr Val Pro Gly Ile Gly Pro Val Thr

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

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770              775              780
Gly Ser Leu Leu Val His Ile Gln Asp Pro Thr Val Leu Glu Tyr Ile
785              790              795              800
Asp Glu Thr Tyr Ser Ser Arg Asp Gly Gln Val Glu Met Glu Tyr Cys
805              810              815
Val Thr Ala Val Tyr Asn Asp Asn Ile Glu Ser Gln Ser Val Cys Asp
820              825              830
Lys Leu Asn Tyr Thr Ile Thr Ser Leu Asp Asn Ile Gln Ser Asp Thr
835              840              845
Ser Leu Lys Ile Tyr Pro Asn Pro Ala Ser Tyr Val Val Arg Ile Glu
850              855              860
Gly Leu Ser Arg Ser Lys Ser Thr Ile Glu Leu Tyr Asn Ala Leu Gly
865              870              875              880
Ile Cys Ile Leu Arg Glu Glu Thr His Ser Glu Lys Thr Glu Ile Asp
885              890              895
Val Ser Arg Leu Asn Asp Gly Val Tyr Leu Ile Lys Val Val Gly Gly
900              905              910
Asn Lys Thr Thr Thr Glu Lys Val Glu Ile Lys Arg Pro
915              920              925
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      20              25              30
Ala Ser Cys Leu Ala Ala Pro Ala Gln Pro Asp Thr Ile Leu Tyr Glu
      35              40              45
Ser Phe Glu Asn Gly Pro Val Pro Asn Gly Trp Leu Glu Ile Asp Ala
      50              55              60
Asp Ala Asp Gly Ala Thr Trp Gly Ser Pro Ser Gly Ser Phe Ser Val
      65              70              75              80
Pro Tyr Gly His Asn Gly Leu Cys Thr Tyr Ser His Ile Arg Ser Gly
      85              90              95
Ile Ser Thr Ala Gly Asn Tyr Leu Ile Thr Pro Asn Ile Glu Gly Ala
      100              105              110
Lys Arg Val Lys Tyr Trp Val Cys Asn Gln Tyr Ser Thr Asn Pro Glu
      115              120              125
His Tyr Ala Val Met Val Ser Thr Thr Gly Thr Ala Ile Glu Asp Phe
      130              135              140
Val Leu Leu Phe Asp Asp Ser Ile Thr Gly Lys Pro Thr Pro Leu Val
      145              150              155              160
Trp Arg Arg Arg Ile Val Asp Leu Pro Glu Gly Thr Lys Tyr Ile Ala
      165              170              175
Trp Arg His Tyr Lys Val Thr Asp Ser His Thr Glu Phe Leu Lys Leu
      180              185              190
Asp Asp Val Thr Val Tyr Arg Ser Ile Glu Gly Pro Glu Pro Ala Thr
      195              200              205
Asp Phe Thr Val Ile Asn Ile Gly Gln Asn Val Gly Arg Leu Thr Trp
      210              215              220

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

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Glu Gly Ala Lys Leu Val Lys Tyr Trp Val Ser Ala Gln Asp Ala Val
 645 650 655
 Tyr Ser Ala Glu His Tyr Ala Val Met Val Ser Thr Thr Gly Thr Ala
 660 665 670
 Val Glu Asp Phe Val Leu Leu Phe Glu Glu Thr Met Thr Ala Lys Ala
 675 680 685
 Asn Gly Ala Trp Tyr Glu Arg Thr Ile Thr Leu Pro Ala Gly Thr Lys
 690 695 700
 Tyr Ile Ala Trp Arg His Tyr Asp Cys Thr Asp Met Phe Phe Leu Leu
 705 710 715 720
 Leu Asp Asp Ile Thr Val Tyr Arg Ser Thr Glu Thr Val Pro Glu Pro
 725 730 735
 Val Thr Asp Phe Val Val Ser Leu Ile Glu Asn Asn Lys Gly Arg Leu
 740 745 750
 Lys Trp Asn Tyr Pro Asn Gly Tyr Glu Pro Asp Lys Thr Asp Asp Lys
 755 760 765
 Lys Pro Leu Gln Leu Thr Gly Tyr Asn Ile Tyr Ala Asn Gly Ser Leu
 770 775 780
 Leu Val His Ile Gln Asp Pro Thr Val Leu Glu Tyr Ile Asp Glu Thr
 785 790 795 800
 Tyr Ser Ser Arg Asp Gly Gln Val Glu Met Glu Tyr Cys Val Thr Ala
 805 810 815
 Val Tyr Asn Asp Asn Ile Glu Ser Gln Ser Val Cys Asp Lys Leu Asn
 820 825 830
 Tyr Thr Ile Thr Ser Leu Asp Asn Ile Gln Ser Asp Thr Ser Leu Lys
 835 840 845
 Ile Tyr Pro Asn Pro Ala Ser Tyr Val Val Arg Ile Glu Gly Leu Ser
 850 855 860
 Arg Ser Lys Ser Thr Ile Glu Leu Tyr Asn Ala Leu Gly Ile Cys Ile
 865 870 875 880
 Leu Arg Glu Glu Thr His Ser Glu Lys Thr Glu Ile Asp Val Ser Arg
 885 890 895
 Leu Asn Asp Gly Val Tyr Leu Ile Lys Val Val Gly Gly Asn Lys Thr
 900 905 910
 Thr Thr Glu Lys Val Glu Ile Lys Arg Pro
 915 920
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 <211> 921
 <212> PRT
 <213> Porphyromonas gingivalis
 <400> 469
 Met Lys Ser Ile Val Phe Arg Ala Phe Leu Thr Ile Leu Leu Ser Trp
 1 5 10 15
 Ala Ala Ile Thr Asn Pro Thr Ala Gln Glu Ile Ser Gly Met Asn Ala
 20 25 30
 Ser Cys Leu Ala Ala Pro Ala Gln Pro Asp Thr Ile Leu Tyr Glu Ser
 35 40 45
 Phe Glu Asn Gly Pro Val Pro Asn Gly Trp Leu Glu Ile Asp Ala Asp
 50 55 60
 Ala Asp Gly Ala Thr Trp Gly Ser Pro Ser Gly Ser Phe Ser Val Pro
 65 70 75 80
 Tyr Gly His Asn Gly Leu Cys Thr Tyr Ser His Ile Arg Ser Gly Ile

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

500				505				510							
Tyr	Ala	Asn	Gly	Ser	Leu	Leu	Val	His	Ile	Gln	Asp	Pro	Thr	Val	Leu
515				520				525							
Glu	Tyr	Ile	Asp	Glu	Thr	Tyr	Ser	Ser	Arg	Asp	Asp	Gln	Val	Glu	Val
530				535				540							
Glu	Tyr	Cys	Val	Thr	Ala	Val	Tyr	Asn	Asp	Asn	Ile	Glu	Ser	Gln	Ser
545				550				555				560			
Val	Cys	Asp	Lys	Leu	Ile	Tyr	Asp	Ser	Gln	Ser	Asp	Ile	Ile	Leu	Tyr
565				570				575							
Glu	Gly	Phe	Glu	Ala	Gly	Ser	Ile	Pro	Glu	Gly	Trp	Leu	Leu	Ile	Asp
580				585				590							
Ala	Asp	Gly	Asp	Asn	Val	Asn	Trp	Asp	Tyr	Tyr	Pro	Trp	Thr	Met	Tyr
595				600				605							
Gly	His	Asp	Ser	Glu	Lys	Cys	Ile	Ala	Ser	Pro	Ser	Tyr	Leu	Pro	Met
610				615				620							
Ile	Gly	Val	Leu	Thr	Pro	Asp	Asn	Tyr	Leu	Val	Thr	Pro	Arg	Leu	Glu
625				630				635				640			
Gly	Ala	Lys	Leu	Val	Lys	Tyr	Trp	Val	Ser	Ala	Gln	Asp	Ala	Val	Tyr
645				650				655							
Ser	Ala	Glu	His	Tyr	Ala	Val	Met	Val	Ser	Thr	Thr	Gly	Thr	Ala	Val
660				665				670							
Glu	Asp	Phe	Val	Leu	Leu	Phe	Glu	Glu	Thr	Met	Thr	Ala	Lys	Ala	Asn
675				680				685							
Gly	Ala	Trp	Tyr	Glu	Arg	Thr	Ile	Thr	Leu	Pro	Ala	Gly	Thr	Lys	Tyr
690				695				700							
Ile	Ala	Trp	Arg	His	Tyr	Asp	Cys	Thr	Asp	Met	Phe	Phe	Leu	Leu	Leu
705				710				715				720			
Asp	Asp	Ile	Thr	Val	Tyr	Arg	Ser	Thr	Glu	Thr	Val	Pro	Glu	Pro	Val
725				730				735							
Thr	Asp	Phe	Val	Val	Ser	Leu	Ile	Glu	Asn	Asn	Lys	Gly	Arg	Leu	Lys
740				745				750							
Trp	Asn	Tyr	Pro	Asn	Gly	Tyr	Glu	Pro	Asp	Lys	Thr	Asp	Asp	Lys	Lys
755				760				765							
Pro	Leu	Gln	Leu	Thr	Gly	Tyr	Asn	Ile	Tyr	Ala	Asn	Gly	Ser	Leu	Leu
770				775				780							
Val	His	Ile	Gln	Asp	Pro	Thr	Val	Leu	Glu	Tyr	Ile	Asp	Glu	Thr	Tyr
785				790				795				800			
Ser	Ser	Arg	Asp	Gly	Gln	Val	Glu	Met	Glu	Tyr	Cys	Val	Thr	Ala	Val
805				810				815							
Tyr	Asn	Asp	Asn	Ile	Glu	Ser	Gln	Ser	Val	Cys	Asp	Lys	Leu	Asn	Tyr
820				825				830							
Thr	Ile	Thr	Ser	Leu	Asp	Asn	Ile	Gln	Ser	Asp	Thr	Ser	Leu	Lys	Ile
835				840				845							
Tyr	Pro	Asn	Pro	Ala	Ser	Tyr	Val	Val	Arg	Ile	Glu	Gly	Leu	Ser	Arg
850				855				860							
Ser	Lys	Ser	Thr	Ile	Glu	Leu	Tyr	Asn	Ala	Leu	Gly	Ile	Cys	Ile	Leu
865				870				875				880			
Arg	Glu	Glu	Thr	His	Ser	Glu	Lys	Thr	Glu	Ile	Asp	Val	Ser	Arg	Leu
885				890				895							
Asn	Asp	Gly	Val	Tyr	Leu	Ile	Lys	Val	Val	Gly	Gly	Asn	Lys	Thr	Thr
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Thr	Glu	Lys	Val	Glu	Ile	Lys	Arg	Pro							

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

Gly Gly Val Ile Arg Asn Gly Leu Ala Asp Val Met Gln Glu Glu Met
370 375 380
Pro Tyr Leu Met Pro Asn Thr Ile Val Leu Pro Ser Arg Asn Ala Leu
385 390 395 400
Thr Ala Gln Leu Gly Val Lys Gly Asn Ile Ala Asp Val Val Arg Met
405 410 415
Glu Val Tyr Gly Asp Phe Ser Lys Leu Thr Gly Val Pro Phe Tyr Thr
420 425 430
Pro Thr Leu Pro Leu Tyr Asn Pro Ser Asp Leu Tyr Gln Tyr Asn Val
435 440 445
Ser Phe Leu Pro Ile Tyr Ala Asp Gly Ser Arg Trp Arg Ala Gly Gly
450 455 460
Lys Leu Glu Tyr Ser Tyr Arg Asp Met Leu Arg Phe Leu Val Asp Ala
465 470 475 480
Ser Tyr Gly Lys Trp Asn Leu Asp Gly Gly Leu Val Ala Ser Met Gln
485 490 495
Pro Asp Leu Ile Leu Lys Ala Glu Val Gly Val His Pro Ile Ala Pro
500 505 510
Leu Asp Val Arg Leu Arg Tyr Thr Gln Leu Asn Gly Arg Tyr Arg Tyr
515 520 525
Ser Phe Gly Ser Ala Gly Ser Glu Ala Leu Gly Ile Gly Asn Val His
530 535 540
Leu Leu Ser Ala Asp Val Ser Tyr Lys Leu Lys Lys Asn Leu Ser Leu
545 550 555 560
Tyr Leu Lys Ile Asp Asn Met Leu Ala Glu Thr Thr Glu Leu Ile Gly
565 570 575
Tyr Tyr Pro Met Gln Pro Phe His Cys Phe Ala Gly Phe Ser Trp Thr
580 585 590
Phe
<210> 471
<211> 589
<212> PRT
<213> Porphyromonas gingivalis
<400> 471
Met Lys Tyr Gln Leu Tyr Thr Ala Val Ile Met Ala Leu Ser Val Ser
1 5 10 15
Ser Val Cys Gly Gln Thr Pro Arg Asn Thr Glu Thr Lys Arg Pro Asp
20 25 30
Thr Leu Arg Arg Glu Leu Thr Ile Val Asn Asp Gln Thr Val Glu Met
35 40 45
Glu His Ala Asp Pro Leu Pro Ala Ala Tyr Lys Ala Ile Glu Pro Arg
50 55 60
Leu Lys Pro Phe Arg Pro Glu Tyr Asn Lys Arg Thr Phe Gly Phe Val
65 70 75 80
Pro Glu Val Ser Ser Ser Gly Arg Asn Asn Leu Pro Asn Ile Leu Pro
85 90 95
Thr Glu Gly His Met Lys His Arg Gly Tyr Leu Asn Ile Gly Ile Gly
100 105 110
His Thr Leu Asn Gln Arg Met Asp Ala Gly Tyr Arg Leu Ile Asp Ala
115 120 125
Glu Gln Glu Arg Leu Asn Leu Phe Leu Ser Tyr Arg Gly Met Lys Ser
130 135 140

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

Asp Asn Met Leu Ala Glu Thr Thr Glu Leu Ile Gly Tyr Tyr Pro Met
 565 570 575
 Gln Pro Phe His Cys Phe Ala Gly Phe Ser Trp Thr Phe
 580 585
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 <211> 346
 <212> PRT
 <213> Porphyromonas gingivalis
 <400> 472
 Met Met Glu Lys Cys Ile Phe Ala His Tyr Pro His Asn Leu Val Phe
 1 5 10 15
 Met Ile Arg Lys His Phe Gly Ile Ile Leu Gly Phe Leu Ser Leu Val
 20 25 30
 Phe Ser Ala Gly Ala Gln Gln Glu Lys Gln Val Phe His Phe Leu Asn
 35 40 45
 Leu Pro Ala Thr Ala Gln Ala Leu Ala Ala Gly Gly Lys Ala Ile Thr
 50 55 60
 Ile Val Asp Asp Asn Pro Gly Leu Ala Phe Glu Asn Pro Ala Leu Leu
 65 70 75 80
 Gly Tyr Glu Ser Gly Gly Arg Ala Phe Leu Ser Tyr Leu Tyr Tyr Met
 85 90 95
 Ser Gly Ser His Met Gly Asn Ala Cys Tyr Ala Ser Ser Val Gly Glu
 100 105 110
 Arg Gly Met Trp Gly Val Gly Met Arg Phe Leu Asn Tyr Gly Ser Met
 115 120 125
 Gln Gly Tyr Asp Gln Asn Ala Ile Ala Thr Gly Ser Phe Ser Ala Ser
 130 135 140
 Asp Ile Ala Val Gln Gly Phe Tyr Ser His Glu Leu Ser Asn His Phe
 145 150 155 160
 Arg Gly Gly Val Ser Leu Lys Ala Leu Tyr Ser Ser Ile Glu Thr Tyr
 165 170 175
 Ser Ser Phe Gly Leu Gly Val Asp Val Gly Ile Ser Tyr Tyr Asp Asp
 180 185 190
 Asp Lys Gly Tyr Ser Ala Ser Ala Leu Phe Lys Asn Val Gly Ala Gln
 195 200 205
 Leu Lys Gly Tyr Asn Glu Glu Arg Glu Pro Leu Asp Trp Asp Phe Gln
 210 215 220
 Leu Gly Phe Ser Arg Ser Phe Ile Asn Ala Pro Phe Arg Leu His Ile
 230 235 240
 Thr Leu Phe Asn Leu Asn Pro His Tyr Phe Lys Arg Leu Val Pro Arg
 245 250 255
 Asp Leu Ser Lys Met Gln Lys Phe Leu Arg His Phe Ser Ile Gly Ala
 260 265 270
 Glu Phe Thr Pro Ser Glu Arg Phe Trp Val Gly Leu Gly Tyr Thr Pro
 275 280 285
 Gln Ile Ala Gln Asp Phe Glu Val Glu Gly Gly Asn Lys Trp Gly Gly
 290 295 300
 Leu Ser Ala Gly Val Gly Phe Thr Ser Gly Val Val Arg Val Gly Val
 305 310 315 320
 Ser Ala Ala Thr Tyr His Pro Ala Ala Leu Ser Phe Met Cys Ser Val
 325 330 335
 Gly Ile Arg Leu Asp Asp Lys Ser Ile Phe

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                340                345
<210>      473
<211>      345
<212>      PRT
<213>      Porphyromonas gingivalis
<400>      473
Met Glu Lys Cys Ile Phe Ala His Tyr Pro His Asn Leu Val Phe Met
 1          5          10          15
Ile Arg Lys His Phe Gly Ile Ile Leu Gly Phe Leu Ser Leu Val Phe
          20          25          30
Ser Ala Gly Ala Gln Gln Glu Lys Gln Val Phe His Phe Leu Asn Leu
          35          40          45
Pro Ala Thr Ala Gln Ala Leu Ala Ala Gly Gly Lys Ala Ile Thr Ile
          50          55          60
Val Asp Asp Asn Pro Gly Leu Ala Phe Glu Asn Pro Ala Leu Leu Gly
 65          70          75          80
Tyr Glu Ser Gly Gly Arg Ala Phe Leu Ser Tyr Leu Tyr Tyr Met Ser
          85          90          95
Gly Ser His Met Gly Asn Ala Cys Tyr Ala Ser Ser Val Gly Glu Arg
          100          105          110
Gly Met Trp Gly Val Gly Met Arg Phe Leu Asn Tyr Gly Ser Met Gln
          115          120          125
Gly Tyr Asp Gln Asn Ala Ile Ala Thr Gly Ser Phe Ser Ala Ser Asp
          130          135          140
Ile Ala Val Gln Gly Phe Tyr Ser His Glu Leu Ser Asn His Phe Arg
          145          150          155          160
Gly Gly Val Ser Leu Lys Ala Leu Tyr Ser Ser Ile Glu Thr Tyr Ser
          165          170          175
Ser Phe Gly Leu Gly Val Asp Val Gly Ile Ser Tyr Tyr Asp Asp Asp
          180          185          190
Lys Gly Tyr Ser Ala Ser Ala Leu Phe Lys Asn Val Gly Ala Gln Leu
          195          200          205
Lys Gly Tyr Asn Glu Glu Arg Glu Pro Leu Asp Trp Asp Phe Gln Leu
          210          215          220
Gly Phe Ser Arg Ser Phe Ile Asn Ala Pro Phe Arg Leu His Ile Thr
          225          230          235          240
Leu Phe Asn Leu Asn Pro His Tyr Phe Lys Arg Leu Val Pro Arg Asp
          245          250          255
Leu Ser Lys Met Gln Lys Phe Leu Arg His Phe Ser Ile Gly Ala Glu
          260          265          270
Phe Thr Pro Ser Glu Arg Phe Trp Val Gly Leu Gly Tyr Thr Pro Gln
          275          280          285
Ile Ala Gln Asp Phe Glu Val Glu Gly Gly Asn Lys Trp Gly Gly Leu
          290          295          300
Ser Ala Gly Val Gly Phe Thr Ser Gly Val Val Arg Val Gly Val Ser
          305          310          315          320
Ala Ala Thr Tyr His Pro Ala Ala Leu Ser Phe Met Cys Ser Val Gly
          325          330          335
Ile Arg Leu Asp Asp Lys Ser Ile Phe
          340          345
<210>      474
<211>      330

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<212>      PRT
<213>      Porphyromonas gingivalis
<400>      474
Met Ile Arg Lys His Phe Gly Ile Ile Leu Gly Phe Leu Ser Leu Val
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Phe Ser Ala Gly Ala Gln Gln Glu Lys Gln Val Phe His Phe Leu Asn
      20              25              30
Leu Pro Ala Thr Ala Gln Ala Leu Ala Ala Gly Gly Lys Ala Ile Thr
      35              40              45
Ile Val Asp Asp Asn Pro Gly Leu Ala Phe Glu Asn Pro Ala Leu Leu
      50              55              60
Gly Tyr Glu Ser Gly Gly Arg Ala Phe Leu Ser Tyr Leu Tyr Tyr Met
      65              70              75              80
Ser Gly Ser His Met Gly Asn Ala Cys Tyr Ala Ser Ser Val Gly Glu
      85              90              95
Arg Gly Met Trp Gly Val Gly Met Arg Phe Leu Asn Tyr Gly Ser Met
      100             105             110
Gln Gly Tyr Asp Gln Asn Ala Ile Ala Thr Gly Ser Phe Ser Ala Ser
      115             120             125
Asp Ile Ala Val Gln Gly Phe Tyr Ser His Glu Leu Ser Asn His Phe
      130             135             140
Arg Gly Gly Val Ser Leu Lys Ala Leu Tyr Ser Ser Ile Glu Thr Tyr
      145             150             155             160
Ser Ser Phe Gly Leu Gly Val Asp Val Gly Ile Ser Tyr Tyr Asp Asp
      165             170             175
Asp Lys Gly Tyr Ser Ala Ser Ala Leu Phe Lys Asn Val Gly Ala Gln
      180             185             190
Leu Lys Gly Tyr Asn Glu Glu Arg Glu Pro Leu Asp Trp Asp Phe Gln
      195             200             205
Leu Gly Phe Ser Arg Ser Phe Ile Asn Ala Pro Phe Arg Leu His Ile
      210             215             220
Thr Leu Phe Asn Leu Asn Pro His Tyr Phe Lys Arg Leu Val Pro Arg
      225             230             235             240
Asp Leu Ser Lys Met Gln Lys Phe Leu Arg His Phe Ser Ile Gly Ala
      245             250             255
Glu Phe Thr Pro Ser Glu Arg Phe Trp Val Gly Leu Gly Tyr Thr Pro
      260             265             270
Gln Ile Ala Gln Asp Phe Glu Val Glu Gly Gly Asn Lys Trp Gly Gly
      275             280             285
Leu Ser Ala Gly Val Gly Phe Thr Ser Gly Val Val Arg Val Gly Val
      290             295             300
Ser Ala Ala Thr Tyr His Pro Ala Ala Leu Ser Phe Met Cys Ser Val
      305             310             315             320
Gly Ile Arg Leu Asp Asp Lys Ser Ile Phe
      325             330

<210>      475
<211>      324
<212>      PRT
<213>      Porphyromonas gingivalis
<400>      475
Met Cys Leu Glu Pro Ile Ile Ala Pro Ile Ser Ser Glu Leu Leu Glu
  1              5              10              15

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Gln Glu Leu Thr Ala Asp Arg Phe Leu Arg Met Thr Asn Lys Ala Gly
20 25 30
Asn Glu Ile Tyr Val Phe Thr Ala Glu Glu Ala Pro His Cys Met Lys
35 40 45
Glu Val Gly Arg Leu Arg Glu Glu Ala Phe Arg His Tyr Gly Gly Gly
50 55 60
Thr Gly Lys Ala Ile Asp Ile Asp Glu Phe Asp Thr Met Pro Gly Ser
65 70 75 80
Tyr Lys Gln Leu Ile Val Trp Asp Pro Gln Asn Lys Ala Ile Leu Gly
85 90 95
Gly Tyr Arg Phe Ile Tyr Gly Arg Asp Val Ala Phe Asp Thr Asp Gly
100 105 110
Lys Pro Leu Leu Ala Thr Ala Glu Met Phe Arg Phe Ser Asp Ala Phe
115 120 125
Leu His Asp Tyr Leu Pro Tyr Thr Val Glu Leu Gly Arg Ser Phe Val
130 135 140
Ser Leu Gln Tyr Gln Ser Thr Arg Met Gly Thr Lys Ala Ile Phe Val
145 150 155 160
Leu Asp Asn Leu Trp Asp Gly Ile Gly Ala Leu Thr Val Val Asn Pro
165 170 175
Glu Ala Leu Tyr Phe Tyr Gly Lys Val Thr Met Tyr Lys Asp Tyr Asp
180 185 190
Arg Arg Ala Arg Asn Leu Ile Leu Tyr Phe Leu Arg Lys His Phe Ser
195 200 205
Asp Pro Glu Gly Leu Val Lys Pro Ile His Pro Leu Pro Ile Glu Ile
210 215 220
Ser Ala Glu Asp Glu Ala Leu Phe Ser Ser Ser Asp Phe Asp Thr Asn
225 230 235 240
Tyr Lys Thr Leu Asn Ile Glu Val Arg Lys Leu Gly Ile Asn Ile Pro
245 250 255
Pro Leu Val Ser Ala Tyr Ile Ala Leu Ser Pro Glu Met Arg Val Phe
260 265 270
Gly Thr Ala Val Asn Glu Ser Phe Gly Glu Val Glu Glu Thr Gly Ile
275 280 285
Phe Ile Ala Val Gly Lys Ile Leu Glu Glu Lys Lys Gln Arg His Ile
290 295 300
Glu Ser Phe Ile Leu Ser Arg Asn Glu Lys Lys Gly Leu Asp Ser Ser
305 310 315 320
Asn Gly Arg Ser
<210> 476
<211> 547
<212> PRT
<213> Porphyromonas gingivalis
<400> 476
Met Lys Thr Ile Val Arg Tyr Ser Arg Leu Pro Val Ala Leu Phe Phe
1 5 10 15
Cys Leu Leu Gly Ala Val His Leu Ser Val Glu Ala Gln Met Leu Asn
20 25 30
Thr Pro Phe Glu Leu Ser Asp Gln Ile Val Leu Ser Pro Thr Glu Arg
35 40 45
Gln Tyr Arg Glu Ile Cys Val Gln Thr Lys Glu Lys Arg Gly Ala Asp
50 55 60

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

Ser Leu Tyr Val Ser Ile Pro Met Gln Asn Thr His Arg Leu Met Thr
485 490 495
Glu Leu Arg Leu Tyr Gly Asp Leu Met Lys Arg Lys Asp Gly Ile Ala
500 505 510
Tyr Gly Lys Thr Pro Gly Val Ile Ser His Ile Leu Ser Asp Pro Gln
515 520 525
Ala Glu Arg Thr Ser Gly His Thr Ile Gly Ala Ile Cys Asn Ile Ser
530 535 540
Tyr Leu Phe
545
<210> 477
<211> 750
<212> PRT
<213> Porphyromonas gingivalis
<400> 477
Met Lys Lys Leu His Met Ile Ala Ala Leu Ala Val Leu Pro Phe Cys
1 5 10 15
Leu Thr Ala Gln Ala Pro Val Ser Asn Ser Glu Ile Asp Ser Leu Ser
20 25 30
Asn Val Gln Leu Gln Thr Val Gln Val Val Ala Thr Arg Ala Thr Ala
35 40 45
Lys Thr Pro Val Ala Tyr Thr Asn Val Arg Lys Ala Glu Leu Ser Lys
50 55 60
Ser Asn Tyr Gly Arg Asp Ile Pro Tyr Leu Leu Met Leu Thr Pro Ser
65 70 75 80
Val Val Ala Thr Ser Asp Ala Gly Thr Gly Ile Gly Tyr Ser Gly Phe
85 90 95
Arg Val Arg Gly Thr Asp Ala Asn Arg Ile Asn Ile Thr Thr Asn Gly
100 105 110
Val Pro Leu Asn Asp Ser Glu Ser Gln Ser Val Phe Trp Val Asn Met
115 120 125
Pro Asp Phe Ala Ser Ser Ile Glu Asp Leu Gln Val Gln Arg Gly Val
130 135 140
Gly Thr Ser Thr Asn Gly Ala Gly Ala Phe Gly Ala Ser Val Asn Met
145 150 155 160
Arg Thr Asp Asn Leu Gly Leu Ala Pro Tyr Gly Arg Val Asp Leu Ser
165 170 175
Gly Gly Ser Phe Gly Thr Phe Arg Arg Ser Val Lys Leu Gly Ser Gly
180 185 190
Arg Ile Gly Arg His Trp Ala Val Asp Ala Arg Leu Ser Lys Ile Gly
195 200 205
Ser Asp Gly Tyr Val Asp Arg Gly Ser Val Asp Leu Lys Ser Tyr Phe
210 215 220
Ala Gln Val Gly Tyr Phe Gly Ser Asn Thr Ala Leu Arg Phe Ile Thr
225 230 235 240
Phe Gly Gly Lys Glu Val Thr Gly Ile Ala Trp Asn Gly Leu Ser Lys
245 250 255
Glu Asp Glu Ala Lys Tyr Gly Arg Arg Tyr Asn Ser Ala Gly Leu Met
260 265 270
Tyr Val Asp Ala Gln Gly Val Pro His Tyr Tyr His Asn Thr Asp Asn
275 280 285
Tyr Glu Gln Arg His Tyr His Ala Ile Met Thr His Ser Phe Ser Pro

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

705	710								715								720		
Gln	Ala	Ser	Gly	Glu	Leu	Ser	Ala	Tyr	Ala	Asp	Leu	Arg	Tyr	Tyr	Pro				
				725					730					735					
Gln	Ala	Gly	Phe	Asn	Ala	Leu	Gly	Ser	Leu	Thr	Ile	Asp	Phe						
				740					745					750					
<210>	478																		
<211>	494																		
<212>	PRT																		
<213>	Porphyromonas gingivalis																		
<400>	478																		
Met	Lys	Arg	Arg	Phe	Leu	Ser	Leu	Leu	Leu	Tyr	Ile	Leu	Ser	Ser					
1				5					10					15					
Ile	Ser	Leu	Ser	Ala	Gln	Arg	Phe	Pro	Met	Val	Gln	Gly	Ile	Glu	Leu				
				20					25					30					
Asp	Thr	Asp	Ser	Leu	Phe	Ser	Leu	Pro	Lys	Arg	Pro	Trp	Arg	Ala	Ile				
				35					40					45					
Gly	Lys	Thr	Ile	Gly	Val	Asn	Leu	Ala	Val	Trp	Gly	Phe	Asp	His	Phe				
				50					55					60					
Ile	Met	Asn	Glu	Asp	Phe	Ala	Asp	Ile	Ser	Trp	Gln	Thr	Ile	Lys	Ser				
65				70					75					80					
Asn	Phe	Gln	Thr	Gly	Phe	Gly	Trp	Asp	Asn	Asp	Lys	Phe	Val	Thr	Asn				
				85					90					95					
Leu	Phe	Ala	His	Pro	Tyr	His	Gly	Ser	Leu	Tyr	Phe	Asn	Ala	Ala	Arg				
				100					105					110					
Ser	Asn	Gly	Leu	Ser	Phe	Arg	His	Ser	Ala	Pro	Phe	Ala	Phe	Phe	Gly				
				115					120					125					
Ser	Leu	Met	Trp	Glu	Leu	Leu	Met	Glu	Asn	Glu	Pro	Pro	Ser	Ile	Asn				
				130					135					140					
Asp	Leu	Cys	Ala	Thr	Thr	Ile	Gly	Gly	Ile	Ala	Leu	Gly	Glu	Met	Gly				
145				150					155					160					
His	Arg	Leu	Ser	Asp	Leu	Leu	Ile	Asp	Asn	Arg	Thr	Thr	Gly	Trp	Glu				
				165					170					175					
Arg	Met	Gly	Arg	Glu	Val	Ala	Ile	Ala	Leu	Ile	Asn	Pro	Met	Arg	Phe				
				180					185					190					
Leu	Asn	Arg	Leu	Thr	Ala	Gly	Glu	Val	Thr	Ser	Val	Gly	Ser	Arg	Ser				
				195					200					205					
Gly	Gln	Ile	Phe	Gln	Ser	Val	Pro	Ile	Asn	Ile	Val	Val	Asp	Ala	Gly				
				210					215					220					
Phe	Arg	Phe	Leu	Ala	Asp	Lys	Arg	His	Ala	Arg	Thr	Gly	Ala	Thr	Ala				
225				230					235					240					
Leu	Thr	Leu	Asn	Leu	Arg	Phe	Asp	Tyr	Gly	Asp	Pro	Phe	Arg	Ser	Glu				
				245					250					255					
Thr	Phe	Ser	Pro	Tyr	Asp	Phe	Phe	Gln	Phe	Lys	Ala	Gly	Leu	Ser	Phe				
				260					265					270					
Ser	Glu	Ser	Gln	Pro	Leu	Leu	Ser	Gln	Ile	Asn	Leu	Ile	Gly	Ile	Leu				
				275					280					285					
Ser	Gly	Cys	Gln	Leu	Leu	Ala	His	Glu	Arg	Thr	Val	Leu	Val	Gly	Gly				
				290					295					300					
Leu	Phe	Gln	His	Phe	Asp	Tyr	Tyr	Asn	Ser	Glu	Lys	Arg	Ile	Ser	Lys				
305				310					315					320					
Asn	Ser	Glu	Glu	Val	Leu	Val	Thr	Pro	Tyr	Arg	Ile	Ser	Gln	Val	Ala				
				325					330					335					

Ala Leu Gly Gly Gly Leu Ile Phe Gln His His Gly Lys Phe Arg Arg
340 345 350
Arg Pro Leu Glu Leu Tyr Ala Glu Thr Tyr Leu Asn Val Val Pro Met
355 360 365
Gly Ala Ser Leu Ser Asp His Tyr Asn Val Asp Asn Arg Asp Tyr Asn
370 375 380
Leu Gly Ser Gly Leu Ser Gly Lys Leu Tyr Leu Gly Ala Thr Tyr Asn
385 390 395 400
Asp Leu Trp Ser Trp Leu Leu Gly Val Glu Ser Tyr Arg Leu Tyr Thr
405 410 415
Trp Ile Gly Tyr Glu Glu Pro His Gln Lys Asn Thr Asp Val Ser Ser
420 425 430
Phe Met Val Gln Gly Asp Glu Ser Lys Ala Arg Leu Leu Val Thr Ser
435 440 445
Ser Glu Phe Ala Phe His Pro Gly Pro Trp His Val Ala Ile Val Ala
450 455 460
Arg Arg Phe Ile Arg Lys Thr Ala Tyr Gln Phe Tyr Pro Asn Val Ser
465 470 475 480
Phe Asp Thr Gly Asp Ile Gln Leu Arg Val Gly Phe His Phe
485 490
<210> 479
<211> 294
<212> PRT
<213> Porphyromonas gingivalis
<400> 479
Met Lys Arg Leu Ile Val Phe Leu Ala Met Gly Gly Leu Leu Phe Thr
1 5 10 15
Leu Ala Asn Ala Gln Glu Ala Asn Thr Ala Ser Asp Thr Pro Lys Lys
20 25 30
Asp Trp Thr Ile Lys Gly Val Thr Gly Leu Asn Ala Ser Gln Thr Ser
35 40 45
Leu Thr Asn Trp Ala Ala Gly Gly Glu Asn Thr Val Ala Gly Asn Leu
50 55 60
Tyr Leu Asn Ile Asp Ala Asn Tyr Leu Lys Asp Lys Trp Ser Trp Asp
65 70 75 80
Asn Gly Leu Arg Thr Asp Phe Gly Leu Thr Tyr Thr Thr Ala Asn Lys
85 90 95
Trp Asn Lys Ser Val Asp Lys Ile Glu Leu Phe Thr Lys Ala Gly Tyr
100 105 110
Glu Ile Gly Lys His Trp Tyr Gly Ser Ala Leu Phe Thr Phe Leu Ser
115 120 125
Gln Tyr Ala Lys Gly Tyr Glu Lys Pro Ser Asp His Leu Thr Gly Val
130 135 140
Lys His Ile Ser Asn Phe Phe Ala Pro Ala Tyr Leu Thr Leu Gly Ile
145 150 155 160
Gly Ala Asp Tyr Lys Pro Asn Glu Lys Phe Ser Leu Tyr Leu Ser Pro
165 170 175
Thr Thr Gly Lys Leu Thr Val Val Ala Asp Asp Tyr Leu Ser Ser Leu
180 185 190
Gly Ala Phe Gly Val Lys Val Gly Glu Lys Thr Met Phe Glu Leu Gly
195 200 205
Ala Leu Val Val Gly Ser Ala Asn Ile Asn Leu Met Glu Asn Val Asn

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210                215                220
Leu Ile Thr Lys Ala Ser Phe Phe Ser Ala Tyr Thr His Asp Phe Gly
225                230                235                240
Asn Ile Asp Ile Asn Trp Glu Ala Met Leu Ala Met Lys Ile Asn Lys
245                250                255
Phe Leu Thr Ala Thr Ile Ala Thr Asn Leu Ile Tyr Asp Asp Asp Val
260                265                270
Lys Ile Asn Asp Gly Pro Lys Ile Gln Phe Lys Glu Val Val Gly Val
275                280                285
Gly Val Ala Tyr Thr Phe
290
<210>    480
<211>    204
<212>    PRT
<213>    Porphyromonas gingivalis
<400>    480
Met Lys Lys Met Ile Leu Ala Ala Thr Met Leu Leu Ala Thr Ile Gly
  1                5                10                15
Phe Ala Asn Ala Gln Ser Arg Pro Ala Leu Arg Leu Asp Ala Asn Phe
20                25                30
Val Gly Ser Asn Leu Met Gln Lys Val Ala Asn Thr Ser Val Asn Asn
35                40                45
Lys Met Ile Val Gly Leu Arg Val Gly Ala Ala Ala Glu Phe Ala Leu
50                55                60
Ser Asn Asp Gly Phe Tyr Leu Ala Pro Gly Leu Ala Tyr Thr Met Arg
65                70                75                80
Gly Ala Lys Met Glu Ser Leu Ser Glu Thr Thr Thr Arg Leu His Tyr
85                90                95
Leu Gln Ile Pro Val Asn Ala Gly Met Arg Phe Ser Phe Ala Asp Asn
100                105                110
Met Ala Ile Ser Leu Glu Ala Gly Pro Tyr Phe Ala Tyr Gly Val Ala
115                120                125
Gly Thr Ile Lys Thr Lys Val Ala Gly Val Thr Ala Ser Val Asp Ala
130                135                140
Phe Gly Asp Asn Gly Tyr Asn Arg Phe Asp Leu Gly Leu Gly Leu Ser
145                150                155                160
Ala Ala Leu Ser Tyr Asp Arg Tyr Tyr Val Gln Ile Gly Tyr Glu His
165                170                175
Gly Leu Leu Asn Met Leu Lys Asp Ala Pro Asp Lys Thr Ser Leu Arg
180                185                190
Asn His Asp Phe Phe Val Gly Leu Gly Val Arg Phe
195                200
<210>    481
<211>    243
<212>    PRT
<213>    Porphyromonas gingivalis
<400>    481
Met Lys Arg Ile Phe Thr Val Ala Leu Val Leu Leu Ala Ser Val Thr
  1                5                10                15
Met Ala Ile Gly Gln Ser Arg Pro Ala Leu Arg Val Asp Ala Asn Phe
20                25                30
Val Gly Ser Asn Gln Ser Met Lys Arg Asp Gly Tyr Val Trp Asp Thr

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35 40 45
 Lys Met Asn Val Gly Leu Arg Val Gly Ala Ala Ala Glu Phe Met Ile
 50 55 60
 Gly Ser Arg Gly Phe Tyr Leu Ala Pro Gly Leu Asn Tyr Thr Met Lys
 65 70 75 80
 Gly Ser Lys Thr Glu Trp Asp Ile Pro Glu Met Val Pro Gly Thr Tyr
 85 90 95
 Ile Thr Met Val Ser Thr Arg Leu His Tyr Leu Gln Leu Pro Ile Asn
 100 105 110
 Ala Gly Met Arg Phe Asp Leu Met Asn Asp Met Ala Val Ser Ile Glu
 115 120 125
 Ala Gly Pro Phe Leu Ala Tyr Gly Ile Tyr Gly Thr Tyr Arg Gln Lys
 130 135 140
 Leu Glu Gly Trp Lys Pro Asn Asn Tyr Ser Thr Glu Phe Phe Gly Pro
 145 150 155 160
 Thr Leu Gly Gly Pro Thr Asn Ile Arg Trp Asp Ile Gly Ala Asn Ile
 165 170 175
 Ile Ala Ala Phe His Tyr Lys Arg Tyr Tyr Ile Gln Ile Gly Tyr Glu
 180 185 190
 His Gly Phe Val Asp Ile Val Ser Gly Gly Gly Ser Asp Ile Pro Arg
 195 200 205
 Leu Asn Asp Asn Arg Gln Ser Ser Ser Thr Thr Ala Leu Arg Glu Lys
 210 215 220
 Gly Asn Asn Glu Tyr Ala Tyr Asn Arg Asp Phe Phe Val Gly Ile Gly
 225 230 235 240
 Tyr Arg Phe
 <210> 482
 <211> 207
 <212> PRT
 <213> Porphyromonas gingivalis
 <400> 482
 Met Lys Arg Met Leu Leu Leu Val Val Leu Leu Tyr Gly Ile Ala
 1 5 10 15
 Gly Arg Leu Ala Ala Gln Asp Val Ile Arg Pro Trp Ser Leu Gln Val
 20 25 30
 Gly Ala Gly Tyr Ser Asp Thr Glu Asn Ile Pro Gly Gly Phe Thr Tyr
 35 40 45
 Gly Phe Tyr Leu Gly Lys Arg Met Gly Ser Phe Leu Glu Val Gly Leu
 50 55 60
 Ser Met Tyr Asn Ser Thr Arg Gln Thr Ala Asn Asn Ala Asp Ser Phe
 65 70 75 80
 Ala Ser Asn Glu Gly Asp Gly Ser Phe Gln Val Asn Met Ser Ser Pro
 85 90 95
 Asn Glu Lys Trp Ser Phe Phe Asp Ala Gly Ser Ala Asn Cys Tyr Met
 100 105 110
 Ile Val Val Gly Val Asn Pro Leu His Leu Phe Trp Gln Asn Ser Arg
 115 120 125
 His Asn Leu Phe Leu Ala Val Gln Ala Gly Leu Ser Asn Lys His Asn
 130 135 140
 Ile His Phe Ile Tyr Gly Asp Lys Gly Ala Lys Val Ser Ile Tyr Thr
 145 150 155 160
 Asn Ser Asn Thr Tyr Ile Gly Tyr Gly Ala Arg Val Ala Tyr Glu Tyr


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                165                170                175
Gln Ile His Lys Asn Val Gly Ala Gly Ala Ala Val Met Tyr Asp His
                180                185                190
Gly Asn Lys Met Leu Thr Ala Met Ala Thr Leu Ser Thr His Phe
                195                200                205
<210>      483
<211>      951
<212>      PRT
<213>      Porphyromonas gingivalis
<400>      483
Met Arg Val Ser Asp Leu Cys Ser Arg Leu Ser Trp Leu Leu Pro Val
  1          5          10          15
Ile Leu Val Gly Leu Leu Cys Ala Thr Leu Val Ala Ala Glu Arg Pro
          20          25          30
Met Ala Gly Ala Val Gly Leu His His Arg Arg His Ala Ala Leu Ser
          35          40          45
Asp Ser Thr Ala Lys Asp Thr Val Pro Leu Ala Lys Pro Ile Pro Asp
          50          55          60
Ser Ala Phe Arg Asp Ser Leu Pro Ala Asp Ser Thr Gly Ser Met Arg
          65          70          75          80
Gln Asp Ser Val Tyr Asp Asp Glu Phe Glu Leu Glu Asp Ile Val Glu
          85          90          95
Tyr Glu Ala Ala Asp Ser Ile Val Leu Leu Gly Gln Asn Arg Ala Tyr
          100         105         110
Leu Phe Gly Lys Ser Tyr Val Ser Tyr Gln Lys Ser Arg Leu Glu Ala
          115         120         125
Asn Phe Met Tyr Leu Asn Thr Asp Ser Ser Thr Val Tyr Thr Arg Tyr
          130         135         140
Val Leu Asp Thr Ala Gly Tyr Pro Met Ala Phe Pro Val Phe Lys Asp
          145         150         155         160
Gly Glu Gln Ser Phe Glu Ala Lys Asn Phe Thr Tyr Asn Phe Arg Thr
          165         170         175
Glu Lys Gly Ile Ile Ser Gly Val Ile Thr Gln Gln Gly Glu Gly Tyr
          180         185         190
Leu Thr Ala Gly Lys Thr Lys Lys Met Pro Asp Asn Ile Met Phe Met
          195         200         205
Gln Gly Gly Arg Tyr Thr Thr Cys Asp Asn His Asp His Pro His Phe
          210         215         220
Tyr Ile Asn Leu Ser Lys Ala Lys Val His Pro Glu Lys Asp Ile Val
          225         230         235         240
Thr Gly Pro Val Asn Leu Val Ile Ala Asp Met Pro Leu Pro Ile Gly
          245         250         255
Leu Pro Phe Gly Tyr Phe Pro Phe Ser Asn Lys Tyr Ser Ser Gly Ile
          260         265         270
Leu Met Pro Thr Tyr Gly Glu Asp Asn Arg Tyr Gly Phe Tyr Leu Arg
          275         280         285
Asn Gly Gly Tyr Tyr Phe Ala Phe Ser Asp Tyr Ile Asp Leu Ala Leu
          290         295         300
Arg Gly Glu Ile Phe Ser Lys Gly Ser Trp Gly Ile Ser Ala Gln Ser
          305         310         315         320
Lys Tyr Lys Lys Arg Tyr Lys Tyr Asn Gly Ser Phe Glu Ala Asn Tyr
          325         330         335

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

Thr Gly Thr Ser Phe Ser Tyr Thr Leu Asn Lys Glu Ser Leu Ser Gly
 755 760 765
 Leu Ile Ala Leu Phe Ser Gly Lys Lys Glu Arg Arg Asp Glu Lys Lys
 770 775 780
 Asn Thr Gly Ala Thr Pro His Glu Gly Asp Asp Ala Ala Asp Ile Leu
 785 790 795 800
 Glu Gly Gly Arg Pro Gln Asn Glu Ser Gly Gly Ser Leu Leu Glu Arg
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 Asn Arg Gln Gly Gly Ala Val Asp Gln Asp Gly Tyr Phe Ala Tyr Ser
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 Phe Gly Phe Asn Ala Asn Tyr Asn Phe Asp Leu Lys Lys Ile Thr Ser
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 Asn Leu Arg Ala Ser Pro Pro Val Val Pro Val Ala Val Asp Lys Tyr
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 Ala Val Pro Val Ala Asn Pro Met Asp Pro Glu Asn Pro Asn Ala Trp
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 Asp Val Thr Leu Lys Ile Thr Thr Lys Ala Val Thr Val Pro Val Asp
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 Val Val Met Val Ile Asp Gln Ser Ser Ser Met Gly Gly Gln Asn Ile
 145 150 155 160
 Ala Arg Leu Lys Ser Ala Ile Ala Ser Gly Gln Arg Phe Val Lys Lys

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Gln	Tyr	Tyr	Ser	Val	Pro	Pro	Thr	Asn	Thr	Val	Ile	Thr	Thr	Ala	Asp									
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Gly	Lys	Arg	Tyr	Arg	Phe	Val	Glu	Val	Pro	Gly	Ser	Thr	Pro	Asn	Pro									
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Trp	Gln	Tyr	Phe	Gly	Ile	Pro	Val	Asn	Glu	Ser	Gly	Phe	Pro	Ile	Asn									
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Gly	Val	Tyr	Ser	Phe	Lys	Gly	Met	Ile	Cys	Val	Cys	Asp	Ala	Phe	Leu									
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Pro	Pro	Glu	Val	Glu	Gln	Thr	Val	Tyr	Leu	Phe	Asn	Thr	Gly	Thr	Arg									
915										920					925									
Asp	Gln	Trp	Arg	Lys	Leu	Asn	Gly	Ser	Thr	Val	Ser	Gly	Tyr	Arg	Ala									
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Phe Gly Phe Asp Asn Gly Trp Asp Gly Arg Lys Leu Thr Glu Lys Gly
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Leu Ser Gln Leu Tyr Ala Met Ser Asp Ile Gly Asn Asp Lys Phe Gln
          1060              1065              1070
Val Ala Gly Val Pro Glu Leu Asn Asn Leu Leu Ile Gly Phe Asp Ala
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Asp Lys Asp Gly Gln Tyr Thr Leu Glu Phe Ala Leu Ser Asp His Phe
          1090              1095              1100
Ala Lys Gly Ala Val Tyr Leu His Asp Leu Gln Ser Gly Ala Lys His
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Arg Ile Thr Asn Ser Thr Ser Tyr Ser Phe Asp Ala Lys Arg Gly Asp
          1125              1130              1135
Ser Gly Ala Arg Phe Arg Leu Ser Tyr Gly Cys Asp Glu Asn Val Asp
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Asp Ser His Val Val Ser Thr Asn Gly Arg Glu Ile Ile Ile Leu Asn
          1155              1160              1165
Gln Asp Ala Leu Asp Cys Thr Val Thr Leu Phe Thr Ile Glu Gly Lys
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Leu Leu Arg Arg Leu Lys Val Leu Ala Gly His Arg Glu Val Met Lys
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Val Glu Lys Pro Trp Ile Gln Lys His Ser Met Asp Ser Lys Leu Val
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Pro Ala Asn Lys Gly Asn Leu Ile Gln Ala Glu Ile Val Tyr Gln Ser
          50          55          60
Val Ser Glu His Ser Asp Leu Val Ile Ser Pro Val Asn Glu Ile Arg
          65          70          75          80
Pro Ala Asn Arg Phe Pro Ser His Arg Lys Ser Phe Phe Ala Glu Asn
          85          90          95
Leu Arg Ala Ser Pro Pro Val Val Pro Val Ala Val Asp Lys Tyr Ala
          100          105          110
Val Pro Val Ala Asn Pro Met Asp Pro Glu Asn Pro Asn Ala Trp Asp
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Val Thr Leu Lys Ile Thr Thr Lys Ala Val Thr Val Pro Val Asp Val
          130          135          140

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Leu	Pro	Lys	Gly	Thr	Ala	Thr	Glu	Gly	Val	Arg	Ile	Ala	Leu	Val	Ser	
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Tyr	Asp	His	Glu	Pro	His	Arg	Leu	Ser	Asp	Phe	Thr	Lys	Asp	Thr	Ala	
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Phe	Leu	Cys	Gln	Lys	Ile	Arg	Ala	Leu	Thr	Pro	Ile	Trp	Gly	Thr	His	
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Thr	Gln	Gly	Gly	Leu	Lys	Met	Ala	Arg	Asn	Ile	Met	Ala	Thr	Ser	Thr	
225					230					235					240	
Ala	Val	Asp	Lys	His	Ile	Ile	Leu	Met	Ser	Asp	Gly	Leu	Ala	Thr	Glu	
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Gln	Tyr	Pro	Val	Lys	Asn	Val	Thr	Thr	Ala	Asp	Phe	Ile	Gly	Lys	Thr	
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	290					295					300					
Asn	Tyr	Pro	Thr	His	Ser	Ser	Lys	Val	Gly	Arg	Arg	Asn	Leu	Pro	Glu	
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Ser	Lys	Phe	Asp	Tyr	Ser	Asn	Leu	Ser	Ala	Arg	Ile	Thr	Phe	Asp	Gly	
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Val	Ala	Gly	Ala	Leu	Val	Tyr	Glu	Pro	Arg	Phe	Pro	His	Pro	Tyr	Tyr	
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Tyr	Tyr	Phe	Pro	Cys	Asn	Ala	Ala	Ile	Asn	Glu	Ala	Gln	Phe	Ala	Lys	
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Val	Ala	Pro	Gly	Phe	Ile	Val	Lys	Asn	Leu	Thr	Gln	Ser	Gly	Asp	Val	
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Thr	His	Leu	Leu	Asn	Val	Ser	Asn	Gly	Thr	Val	His	Tyr	Asp	Val	Ser	
	450					455					460					
Thr	Lys	Lys	Leu	Thr	Trp	Thr	Thr	Gly	Thr	Ile	Leu	Ser	Ser	Ser	Glu	
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Ala	Thr	Ile	Thr	Tyr	Arg	Ile	Tyr	Ala	Asp	Leu	Asp	Tyr	Ile	Gln	Asn	
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Gly	Phe	Asp	Thr	Asn	Thr	Glu	Ala	Lys	Leu	Thr	Tyr	Thr	Asn	Ser	Asn	
	515						520					525				
Gly	Glu	Pro	Asn	Gln	Gln	Leu	Ile	Phe	Pro	Arg	Pro	Thr	Val	Lys	Leu	
	530					535				540						
Gly	Tyr	Gly	Val	Ile	Lys	Arg	His	Tyr	Val	Leu	Val	Asn	Lys	Asp	Gly	
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 His Val Leu Gln Ser Gln Asp Phe Phe Leu Pro Ser Gly Gly Gly His
 580 585 590
 Ile Val Pro Lys Trp Ile Lys Leu Asp Lys Thr Thr Glu Ala Leu Gln
 595 600 605
 Tyr Tyr Ser Val Pro Pro Thr Asn Thr Val Ile Thr Thr Ala Asp Gly
 610 615 620
 Lys Arg Tyr Arg Phe Val Glu Val Pro Gly Ser Thr Pro Asn Pro Gly
 625 630 635 640
 Gln Ile Gly Ile Ser Trp Lys Lys Pro Ala Gly Asn Ala Tyr Phe Ala
 645 650 655
 Tyr Lys Leu Leu Asn Tyr Trp Met Gly Gly Thr Thr Asp Gln Gln Ser
 660 665 670
 Glu Trp Asp Val Thr Ser Asn Trp Thr Gly Ala Gln Val Pro Leu Thr
 675 680 685
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 690 695 700
 Val Ala Asp Leu His Val Pro Thr Thr Asn Pro Lys Ile Ile Gly Asn
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 Leu Ile Asn Asn Ser Asp Lys Asp Leu Val Val Thr Thr Ser Ser Gln
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 Leu Thr Ile Asn Gly Val Val Glu Asp Asn Asn Pro Asn Val Gly Thr
 740 745 750
 Ile Val Val Lys Ser Ser Lys Asp Asn Pro Thr Gly Thr Leu Leu Phe
 755 760 765
 Ala Asn Pro Gly Tyr Asn Gln Asn Val Gly Gly Thr Val Glu Phe Tyr
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 Asp Lys Trp Arg Pro Ala Pro Tyr Ala Pro Asp Thr Glu Leu Gln Lys
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 Val Tyr Ser Phe Lys Gly Met Ile Cys Val Cys Asp Ala Phe Leu Asn
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 Pro Glu Val Glu Gln Thr Val Tyr Leu Phe Asn Thr Gly Thr Arg Asp
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 Gln Trp Arg Lys Leu Asn Gly Ser Thr Val Ser Gly Tyr Arg Ala Gly
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 Gln Tyr Leu Ser Val Pro Lys Asn Thr Ala Gly Gln Asp Asn Leu Pro
 945 950 955 960
 Asp Arg Ile Pro Ser Met His Ser Phe Leu Val Lys Met Gln Asn Gly
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Gly Phe Asp Asn Gly Trp Asp Gly Arg Lys Leu Thr Glu Lys Gly Leu
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Ala Gly Val Pro Glu Leu Asn Asn Leu Leu Ile Gly Phe Asp Ala Asp
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Lys Asp Gly Gln Tyr Thr Leu Glu Phe Ala Leu Ser Asp His Phe Ala
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Lys Gly Ala Val Tyr Leu His Asp Leu Gln Ser Gly Ala Lys His Arg
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Ala Val Arg Ser Ser Ser Pro Phe Asp Phe Met Ser Ser Arg Thr Arg
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Val Arg Gly Glu Leu Glu Arg Ser Phe Gly Asn Ser Lys Val Ala Val
65 70 75 80
Ser Val Asn Ala Thr Tyr Asn Ala Leu Leu Lys Asp Glu Thr Gly Leu
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Arg Leu Arg Glu Ala Phe Phe Glu His Gln Glu Glu His Trp Gly Leu
100 105 110
Arg Leu Gly Arg Gln Ile Val Ile Trp Gly Ala Ala Asp Gly Val Arg

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Ile Thr Asp Leu Ile Ser Pro Met Asp Met Thr Glu Phe Leu Ala Gln
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Asp Tyr Asp Asp Ile Arg Met Pro Val Asn Ala Leu Arg Phe Ser Val
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Phe Asn Glu Ser Met Lys Val Glu Val Val Val Leu Pro Val Phe Glu
165          170          175
Gly Tyr Arg Leu Pro Val Asp Pro Arg Asn Pro Trp Asn Ile Phe Ser
180          185          190
Leu Ser Pro Ile Ala Gln Gly Met Asn Ile Val Trp Lys Glu Glu Ala
195          200          205
Gly Lys Pro Ala Phe Lys Val Ala Asn Ile Glu Tyr Gly Ala Arg Trp
210          215          220
Ser Thr Thr Leu Ser Gly Ile Asp Phe Ala Leu Ala Ala Leu His Thr
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Trp Asn Lys Met Pro Val Ile Glu Val Gln Gly Ile Val Pro Thr Glu
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Ile Ile Val Ser Pro Arg Tyr Tyr Arg Met Gly Phe Val Gly Gly Asp
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Phe Gln Thr Ile Asn Trp Leu Ala Gly Ala Asp Trp Tyr Ala Pro Gly
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Arg Asp Phe Ile Ser Gln Arg Gln His Ser Thr Leu Ile Thr Leu Asn
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Val Ser Lys Lys Phe Phe Gly Ser Thr Leu Gln Leu Ser Asp Phe Thr
355          360          365
Tyr Tyr Asp Leu Thr Gly Lys Gly Trp Phe Ser Arg Phe Ala Ala Asp
370          375          380
Tyr Ala Leu Asn Asp Gln Ile His Leu Met Ala Gly Tyr Asp Trp Phe
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Leu Leu Asp Asn Ser Asn Gln Leu Leu Ala Thr Ile Leu Ile Gly Asn
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Asn Val Ile Asn Val Ala Ile Val Ile Leu Ser Asn Tyr Ala Ile Glu
50          55          60

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

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

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

545	550										555					560				
Leu	Lys	Leu	Ala	Tyr	Asn	Phe	Arg	Ile	Gln	Arg	Pro	Ala	Ile	Gly	Gln					
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Leu	Asn	Pro	Tyr	Arg	Leu	Gln	Thr	Asn	Asp	Tyr	Gln	Val	Gln	Tyr	Gly					
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Asn	Pro	Asp	Leu	Lys	Ser	Glu	Lys	Arg	His	His	Val	Gly	Leu	Ser	Tyr					
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Asn	Gln	Tyr	Gly	Ala	Lys	Val	Met	Leu	Thr	Ala	Ser	Leu	Asp	Tyr	Asp					
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Phe	Cys	Asn	Asn	Ala	Ile	Gln	Asn	Tyr	Thr	Phe	Ser	Asp	Pro	Ala	Asn					
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Pro	Asn	Leu	Phe	His	Gln	Thr	Tyr	Gly	Asn	Ile	Gly	Arg	Glu	His	Ser					
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Phe	Ser	Leu	Asn	Thr	Tyr	Ala	Met	Tyr	Thr	Pro	Ala	Val	Trp	Val	Arg					
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Ile	Met	Leu	Asn	Gly	Asn	Ile	Asp	Arg	Thr	Phe	Gln	Lys	Ser	Glu	Ala					
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Leu	Gly	Ile	Asp	Val	Asn	Ser	Trp	Ser	Gly	Met	Val	Tyr	Ser	Gly	Leu					
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Met	Phe	Thr	Leu	Pro	Lys	Asp	Trp	Thr	Val	Asn	Leu	Phe	Gly	Gly	Tyr					
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Tyr	His	Gly	Gly	Arg	Ser	Tyr	Gln	Thr	Lys	Tyr	Asp	Gly	Asn	Val	Phe					
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Asn	Asn	Ile	Gly	Ile	Ala	Lys	Gln	Leu	Phe	Asp	Lys	Lys	Leu	Arg	Val					
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Ser	Leu	Ser	Ala	Asn	Asn	Ile	His	Ala	Lys	Tyr	Ser	Thr	Trp	Lys	Ser					
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Arg	Thr	Ile	Gly	Asn	Gly	Phe	Thr	Ile	Tyr	Ser	Glu	Asn	Ala	Gly	Ile					
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Gln	Arg	Ser	Val	Ser	Leu	Ser	Leu	Thr	Tyr	Ser	Phe	Gly	Lys	Met	Asn					
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Thr	Gln	Val	Arg	Lys	Val	Glu	Arg	Thr	Ile	Val	Asn	Asp	Asp	Leu	Lys					
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Gln	Thr	Ser	Ser	Gln	Gly	Gln	Gln	Gly	Gly	Gly	Gln	Gly	Asn	Pro	Thr					
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Gly Asn																				
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Thr	Asp	Ser	Ile	Arg	Pro	Asn	Glu	Leu	Ser	Ala	Ser	Ile	Arg	Ser	Ala					
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Leu	Phe	Phe	Arg	Asn	Asn	Glu	Tyr	Asn	Ala	Arg	Ser	Val	Lys	Gly	Tyr					
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Thr	Leu	Pro	Gly	Ala	Arg	Val	Ser	Ala	Phe	Ala	Ser	Tyr	Ser	Leu	Pro					
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Ala	Ala	His	Gly	Val	Lys	Leu	Ser	Leu	Gly	Val	Ser	Thr	Leu	Asn	Tyr					

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


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

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Ser Leu Gly Phe Asn Val Lys Asn Ile Gly Thr Lys Ile Ser Tyr Asp
210 215 220
Gly Gly Val Thr Ser Phe Phe Ile Pro Thr Ser Leu Asn Leu Gly Thr
225 230 235 240
Gly Leu Leu Tyr Pro Ile Asp Asp Tyr Asn Ser Ile Asn Phe Asn Leu
245 250 255
Glu Leu Ser Lys Leu Leu Val Pro Thr Pro Pro Ile Met Asp Gln Asn
260 265 270
Asp Gln Ala Gly Tyr Glu Ala Ala Leu Lys Lys Tyr Gln Glu Thr Ser
275 280 285
Ser Ile Ser Gly Ile Phe Ser Ser Phe Gly Asp Ala Pro Gly Gly Leu
290 295 300
Lys Glu Glu Phe Arg Glu Ile Thr Trp Gly Leu Gly Ala Glu Tyr Ser
305 310 315 320
Tyr Asp Asp Lys Phe Phe Val Arg Ala Gly Tyr Ser Tyr Leu His Pro
325 330 335
Thr Lys Gly Asn Leu Gln Tyr Phe Thr Ala Gly Ala Gly Phe Lys Met
340 345 350
Asn Ile Phe Arg Ile Asp Ala Ser Tyr Leu Leu Ser Thr Ile Gln Ser
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Asn Pro Leu Asp Gln Thr Leu Arg Phe Thr Leu Ala Phe Asp Met Asp
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Gly Leu Arg Asn Leu Phe His
385 390
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Pro Pro Phe Ile Ser Asn Glu Pro Asn Val Lys Tyr Ile Ile Pro Asn
35 40 45
Met Gly Ile Asp Ser Lys Gly Thr Ile Tyr Val Thr Val Thr Lys Arg
50 55 60
Ile Gln Gln Gly Ala Asn Tyr Thr Ser Glu Gln Leu Gly Met Tyr Tyr
65 70 75 80
Arg Pro Leu Gly Asp Asn Glu Gln Trp Trp Lys His Asp Pro Tyr Phe
85 90 95
Asp Asp Lys Ile Val Ala Asp Ile Gln Thr Asp Ala Tyr Gly Arg Val
100 105 110
Tyr Val Cys Thr Thr Ser Ser Arg Asp Gln Glu Tyr Gln Leu Tyr Ile
115 120 125
Asn Glu Gln Asn Glu Trp Arg Cys Ile Phe Lys Thr Ser Val Ser Thr
130 135 140
Tyr Glu His Gly Met Ala Val Phe Arg Ser Ser Thr Gly Val Thr Tyr
145 150 155 160
Ile Gly Thr Arg His His Ile Phe Ala Ser Gly Val Asn Asp Phe Glu
165 170 175
Phe Asn Thr Ile Tyr Glu Asp Ser Thr Pro Met Ser Cys Arg Phe Ala

			180					185					190					
Glu	Ala	Thr	Asn	Ser	Gly	Thr	Ile	Tyr	Leu	Ala	Leu	Met	His	Glu	Thr			
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Thr	Met	Ser	Thr	Thr	Ile	Leu	Thr	Tyr	Gln	Asn	Gly	Glu	Phe	Val	Asp			
			210					215					220					
Ile	Ser	Glu	Ser	Glu	Leu	Ser	Asn	Ser	Ile	Ile	Ala	Ser	Met	Cys	Ser			
225			230					235					240					
Asn	Lys	Glu	Gly	Asp	Ile	Ile	Ala	Leu	Val	Thr	Ser	Tyr	Thr	Gly	Phe			
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Met	Ser	Gly	Thr	Leu	Ala	Ile	Arg	Lys	Ala	Asp	Glu	Gly	Lys	Trp	Gln			
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Leu	Val	Gly	Gly	Asp	Ile	Gln	Asn	Ala	Ile	Val	Gln	Asn	Ile	Cys	Met			
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Val	Asp	Gly	Arg	Thr	Arg	Val	Cys	Val	Ser	Asp	Ala	Ser	Val	Phe	Asp			
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Phe	Glu	Trp	Tyr	Glu	Asp	Glu	Ile	Tyr	Gly	Gly	Leu	Ile	Phe	Asp	Thr			
			325					330					335					
Phe	Phe	Tyr	Ser	Pro	Trp	Asp	Lys	Leu	Leu	Tyr	Ala	Lys	Phe	Gly	Gly			
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Ile	Met	Leu	Arg	Ser	Lys	Glu	Ser	Phe	Ile	Thr	Ser	Phe	Ile	Ser	Pro			
355			360					365										
Thr	Val	Val	Gln	Gly	Val	Asp	Val	Tyr	Thr	Leu	Ala	Gly	Lys	Ile	Arg			
370			375					380										
Ile	Glu	Ser	Glu	Thr	Pro	Val	Ser	Glu	Val	Leu	Leu	Phe	Asp	Leu	Ala			
385			390					395					400					
Gly	Arg	Met	Val	Leu	Arg	Gln	Thr	Ile	Asp	Asn	Lys	Ile	Tyr	Ser	Asp			
			405					410					415					
Ile	Asp	Thr	Asn	Gly	Leu	Lys	Arg	Ser	Gly	Ile	Tyr	Val	Val	Ser	Val			
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Arg	Leu	Ser	Ser	Gly	Gln	Val	Phe	Ser	His	Lys	Val	Gln	Val					
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Leu	Ile	Phe	Val	Val	Gly	Leu	Phe	Ser	Ala	Met	Ala	Gln	Glu	Lys	Lys			
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Asp	Ser	Leu	Ser	Thr	Val	Gln	Pro	Val	Pro	Asn	Ser	Ser	Met	Val	Glu			
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Gln	Thr	Pro	Leu	Leu	Ser	Ile	Asp	His	Pro	Val	Leu	Pro	Ala	Ser	Phe			
50			55					60										
Gln	Asn	Thr	Arg	Thr	Leu	Lys	Arg	Phe	Arg	Asp	Lys	His	Leu	Ser	Asp			
65			70					75					80					
Ala	Leu	Leu	Asn	Gly	Leu	Lys	Pro	His	Arg	Ser	Ser	Leu	Gln	Leu	Asn			
			85					90					95					
Glu	Glu	Leu	Asn	Phe	Ala	Ala	Glu	Arg	Arg	Asp	Phe	Val	Ser	Pro	Leu			
			100					105					110					

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

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                165                170                175
Tyr Thr Asn Ala Ile Ala Gln Ala Ser Ile Gly Tyr Tyr Val Pro Ser
                180                185                190
Glu Thr Phe Pro Leu Tyr Phe Arg Leu Leu Ser Gln Ile Asn Leu Phe
                195                200                205
Gly Ile Ala Tyr Gly Asn Gly Phe Gly Glu Ser Tyr Tyr Glu Asn Phe
                210                215                220
Leu Leu Asn Asn Gly Ile Ala Gly Ser Leu His Phe Thr Tyr Pro Gly
225                230                235                240
Lys Phe Thr Arg Phe Thr Thr Leu Ile Thr Ala Asp Ile Pro Ile Arg
                245                250                255
Asn Phe Cys Thr Leu Arg Val Gly Tyr Arg Tyr Ser His Leu Gly Ser
                260                265                270
Ser Leu Asn Ala Leu Asp Thr Arg Ile His Ser His Thr Ala Phe Ile
                275                280                285
Gly Phe Val Thr Glu Phe Tyr Arg Phe Arg Gly Arg Lys Ala Met Asn
                290                295                300
Thr Gly Arg Arg Thr Ser Leu Tyr Tyr His Asp
305                310                315
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<213>      Porphyromonas gingivalis
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Met Val Val Thr Leu Leu Val Ile Val Gly Ile Val Val Val Val Arg
  1                5                10                15
Tyr Ser Leu Arg Val His Val His Lys Thr Gly Thr Val Val Ser Ala
                20                25                30
Ala Ile Phe Gly Phe Ile Leu Leu Gly Lys Thr Val Pro Cys Asp Thr
                35                40                45
Arg Asn Phe Phe Ser Ser Glu Ser Asp Glu Pro Glu Ser Arg Val Ala
  50                55                60
Thr Glu Ile Ala His Leu Cys Glu Ile Gly Phe Gln Ile His Ala Ser
  65                70                75                80
Ser Ile His Val Ala Val Arg Thr Asp Phe Gly Gln Ala Gly Ile His
                85                90                95
Cys Pro Met Ala Thr Asp Ala Ser Ala Thr Glu Phe Asp Arg Ser Ala
                100                105                110
Glu Cys Ala Glu Arg Thr Ser Ala Gln Ile Asp Thr Ala Ile Arg Ser
                115                120                125
Gln Ser Gln Ile Ile Arg Thr His Ile Asp Thr Cys Pro Lys Ser Ser
                130                135                140
Gly Thr Ile Gly Gly Ser Thr His Thr Ser Leu His Leu Lys Val Phe
  145                150                155                160
Asp Gly Arg Gly Glu Val Gly His Ile His Pro Lys Asp Gly Leu Arg
                165                170                175
Phe Gly Val Val Glu Gly Tyr Ser Ile Gly Ser Tyr Val Asp Ala Ile
                180                185                190
Gly Ile Gly Ala Thr His Ala Lys Ala Gly Ile Ser Asp Thr Arg Thr
                195                200                205
Gly Ile Ala Gly Gly Tyr His Gly Gly Ser Gln His Gln Gln Ile Gly
                210                215                220

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Asp Val Thr Thr Ile Ile Gly Leu Gly Lys Phe Gly Leu Ala Asn Val
 225 230 235 240
 Gly Val Ser Asp Arg Gly Phe Arg Arg Gly Ala Ser Ser Tyr Asp Leu
 245 250 255
 Tyr Gly Leu Glu Leu His Ile Ala Lys Thr Ile Tyr Leu Ala Val Gly
 260 265 270
 Asp Gly Cys Leu Cys Arg Gln Ala Glu Arg Gln Asp Gly
 275 280 285
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 <213> Porphyromonas gingivalis
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 Glu Phe Glu Ala Gly Gly Val His Ala Ala Val Ser Arg Gln Glu Gln
 20 25 30
 Glu Ala Ala Tyr Asp Lys Thr Leu Asn Thr Ile Lys Glu Lys Glu Val
 35 40 45
 Val Met Gly Arg Val Thr Ala Ile Asn Lys Arg Glu Val Val Ile Asn
 50 55 60
 Val Gly Tyr Lys Ser Glu Gly Val Val Pro Ala Thr Glu Phe Arg Tyr
 65 70 75 80
 Asn Pro Glu Leu Lys Val Gly Asp Glu Val Glu Val Tyr Ile Glu Asn
 85 90 95
 Gln Glu Asp Lys Lys Gly Gln Leu Val Leu Ser His Arg Lys Gly Arg
 100 105 110
 Ala Ala Arg Ser Trp Glu Arg Val Asn Glu Ala Leu Glu Lys Asp Glu
 115 120 125
 Ile Val Lys Gly Tyr Val Lys Cys Arg Thr Lys Gly Gly Met Ile Val
 130 135 140
 Asp Val Phe Gly Ile Glu Ala Phe Leu Pro Gly Ser Gln Ile Asp Val
 145 150 155 160
 Arg Pro Ile Arg Asp Tyr Asp Ala Phe Val Glu Lys Thr Met Glu Phe
 165 170 175
 Lys Ile Val Lys Ile Asn Gln Glu Tyr Lys Asn Val Val Val Ser His
 180 185 190
 Lys Val Leu Ile Glu Ala Glu Leu Glu Gln Gln Lys Lys Glu Ile Ile
 195 200 205
 Gly Lys Leu Glu Lys Gly Gln Val Leu Glu Gly Ile Val Lys Asn Ile
 210 215 220
 Thr Ser Tyr Gly Val Phe Ile Asp Leu Gly Gly Val Asp Gly Leu Ile
 225 230 235 240
 His Ile Thr Asp Leu Ser Trp Gly Arg Val Ala His Pro Glu Glu Ile
 245 250 255
 Val Gln Leu Asp Gln Lys Ile Asn Val Val Ile Leu Asp Phe Asp Glu
 260 265 270
 Asp Arg Lys Arg Ile Ala Leu Gly Leu Lys Gln Leu Met Pro His Pro
 275 280 285
 Trp Asp Ala Leu Asp Ser Glu Leu Lys Val Gly Asp Lys Val Lys Gly
 290 295 300
 Lys Val Val Val Met Ala Asp Tyr Gly Ala Phe Val Glu Ile Ala Gln

305	310								315								320			
Gly	Val	Glu	Gly	Leu	Ile	His	Val	Ser	Glu	Met	Ser	Trp	Thr	Gln	His					
				325					330					335						
Leu	Arg	Ser	Ala	Gln	Asp	Phe	Leu	His	Val	Gly	Asp	Glu	Val	Glu	Ala					
				340					345					350						
Val	Ile	Leu	Thr	Leu	Asp	Arg	Glu	Glu	Arg	Lys	Met	Ser	Leu	Gly	Leu					
				355					360					365						
Lys	Gln	Leu	Lys	Pro	Asp	Pro	Trp	Ala	Asp	Ile	Glu	Thr	Arg	Phe	Pro					
				370					375					380						
Val	Gly	Ser	Arg	His	His	Ala	Arg	Val	Arg	Asn	Phe	Thr	Asn	Phe	Gly					
385					390					395					400					
Val	Phe	Val	Glu	Ile	Glu	Glu	Gly	Val	Asp	Gly	Leu	Ile	His	Ile	Ser					
				405					410					415						
Asp	Leu	Ser	Trp	Thr	Lys	Lys	Ile	Lys	His	Pro	Ser	Glu	Phe	Thr	Glu					
				420					425					430						
Val	Gly	Ala	Asp	Ile	Glu	Val	Gln	Val	Ile	Glu	Ile	Asp	Lys	Glu	Asn					
				435					440					445						
Arg	Arg	Leu	Ser	Leu	Gly	His	Lys	Gln	Leu	Glu	Glu	Asn	Pro	Trp	Asp					
				450					455					460						
Val	Phe	Glu	Thr	Val	Phe	Thr	Val	Gly	Ser	Ile	His	Glu	Gly	Thr	Val					
465					470					475					480					
Ile	Glu	Val	Met	Asp	Lys	Gly	Ala	Val	Val	Ser	Leu	Pro	Tyr	Gly	Val					
				485					490					495						
Glu	Gly	Phe	Ala	Thr	Pro	Lys	His	Met	Val	Lys	Glu	Asp	Gly	Ser	Gln					
				500					505					510						
Ala	Val	Leu	Glu	Glu	Lys	Leu	Pro	Phe	Lys	Val	Ile	Glu	Phe	Asn	Lys					
				515					520					525						
Asp	Ala	Lys	Arg	Ile	Ile	Val	Ser	His	Ser	Arg	Val	Phe	Glu	Asp	Glu					
				530					535					540						
Gln	Lys	Met	Ala	Gln	Arg	Glu	Ala	Asn	Ala	Glu	Arg	Lys	Ala	Glu	Ala					
545					550					555					560					
Lys	Ala	Ala	Gln	Lys	Glu	Ala	Ala	Ala	Glu	Ala	Ala	Asn	Pro	Ala	Gln					
				565					570					575						
Ala	Val	Glu	Lys	Ala	Thr	Leu	Gly	Asp	Leu	Gly	Glu	Leu	Ala	Ala	Leu					
				580					585					590						
Lys	Glu	Lys	Leu	Ser	Glu	Asn														
		595																		
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<212>		PRT																		
<213>		Porphyromonas gingivalis																		
<400>		499																		
Met	Gly	Arg	Val	Thr	Ala	Ile	Asn	Lys	Arg	Glu	Val	Val	Ile	Asn	Val					
1					5					10					15					
Gly	Tyr	Lys	Ser	Glu	Gly	Val	Val	Pro	Ala	Thr	Glu	Phe	Arg	Tyr	Asn					
				20					25					30						
Pro	Glu	Leu	Lys	Val	Gly	Asp	Glu	Val	Glu	Val	Tyr	Ile	Glu	Asn	Gln					
				35					40					45						
Glu	Asp	Lys	Lys	Gly	Gln	Leu	Val	Leu	Ser	His	Arg	Lys	Gly	Arg	Ala					
				50					55					60						
Ala	Arg	Ser	Trp	Glu	Arg	Val	Asn	Glu	Ala	Leu	Glu	Lys	Asp	Glu	Ile					
65					70					75					80					

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

Lys Met Ala Gln Arg Glu Ala Asn Ala Glu Arg Lys Ala Glu Ala Lys
 500 505 510
 Ala Ala Gln Lys Glu Ala Ala Ala Glu Ala Ala Asn Pro Ala Gln Ala
 515 520 525
 Val Glu Lys Ala Thr Leu Gly Asp Leu Gly Glu Leu Ala Ala Leu Lys
 530 535 540
 Glu Lys Leu Ser Glu Asn
 545 550
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 <212> PRT
 <213> Porphyromonas gingivalis
 <400> 500
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 Ile Asp Val Arg Pro Ile Arg Asp Tyr Asp Ala Phe Val Glu Lys Thr
 20 25 30
 Met Glu Phe Lys Ile Val Lys Ile Asn Gln Glu Tyr Lys Asn Val Val
 35 40 45
 Val Ser His Lys Val Leu Ile Glu Ala Glu Leu Glu Gln Gln Lys Lys
 50 55 60
 Glu Ile Ile Gly Lys Leu Glu Lys Gly Gln Val Leu Glu Gly Ile Val
 65 70 75 80
 Lys Asn Ile Thr Ser Tyr Gly Val Phe Ile Asp Leu Gly Gly Val Asp
 85 90 95
 Gly Leu Ile His Ile Thr Asp Leu Ser Trp Gly Arg Val Ala His Pro
 100 105 110
 Glu Glu Ile Val Gln Leu Asp Gln Lys Ile Asn Val Val Ile Leu Asp
 115 120 125
 Phe Asp Glu Asp Arg Lys Arg Ile Ala Leu Gly Leu Lys Gln Leu Met
 130 135 140
 Pro His Pro Trp Asp Ala Leu Asp Ser Glu Leu Lys Val Gly Asp Lys
 145 150 155 160
 Val Lys Gly Lys Val Val Val Met Ala Asp Tyr Gly Ala Phe Val Glu
 165 170 175
 Ile Ala Gln Gly Val Glu Gly Leu Ile His Val Ser Glu Met Ser Trp
 180 185 190
 Thr Gln His Leu Arg Ser Ala Gln Asp Phe Leu His Val Gly Asp Glu
 195 200 205
 Val Glu Ala Val Ile Leu Thr Leu Asp Arg Glu Glu Arg Lys Met Ser
 210 215 220
 Leu Gly Leu Lys Gln Leu Lys Pro Asp Pro Trp Ala Asp Ile Glu Thr
 225 230 235 240
 Arg Phe Pro Val Gly Ser Arg His His Ala Arg Val Arg Asn Phe Thr
 245 250 255
 Asn Phe Gly Val Phe Val Glu Ile Glu Glu Gly Val Asp Gly Leu Ile
 260 265 270
 His Ile Ser Asp Leu Ser Trp Thr Lys Lys Ile Lys His Pro Ser Glu
 275 280 285
 Phe Thr Glu Val Gly Ala Asp Ile Glu Val Gln Val Ile Glu Ile Asp
 290 295 300
 Lys Glu Asn Arg Arg Leu Ser Leu Gly His Lys Gln Leu Glu Glu Asn

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305          310          315          320
Pro Trp Asp Val Phe Glu Thr Val Phe Thr Val Gly Ser Ile His Glu
          325          330          335
Gly Thr Val Ile Glu Val Met Asp Lys Gly Ala Val Val Ser Leu Pro
          340          345          350
Tyr Gly Val Glu Gly Phe Ala Thr Pro Lys His Met Val Lys Glu Asp
          355          360          365
Gly Ser Gln Ala Val Leu Glu Glu Lys Leu Pro Phe Lys Val Ile Glu
          370          375          380
Phe Asn Lys Asp Ala Lys Arg Ile Ile Val Ser His Ser Arg Val Phe
385          390          395          400
Glu Asp Glu Gln Lys Met Ala Gln Arg Glu Ala Asn Ala Glu Arg Lys
          405          410          415
Ala Glu Ala Lys Ala Ala Gln Lys Glu Ala Ala Ala Glu Ala Ala Asn
          420          425          430
Pro Ala Gln Ala Val Glu Lys Ala Thr Leu Gly Asp Leu Gly Glu Leu
          435          440          445
Ala Ala Leu Lys Glu Lys Leu Ser Glu Asn
          450          455
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<213>      Porphyromonas gingivalis
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  1          5          10          15
Val Ser His Lys Val Leu Ile Glu Ala Glu Leu Glu Gln Gln Lys Lys
          20          25          30
Glu Ile Ile Gly Lys Leu Glu Lys Gly Gln Val Leu Glu Gly Ile Val
          35          40          45
Lys Asn Ile Thr Ser Tyr Gly Val Phe Ile Asp Leu Gly Gly Val Asp
          50          55          60
Gly Leu Ile His Ile Thr Asp Leu Ser Trp Gly Arg Val Ala His Pro
  65          70          75          80
Glu Glu Ile Val Gln Leu Asp Gln Lys Ile Asn Val Val Ile Leu Asp
          85          90          95
Phe Asp Glu Asp Arg Lys Arg Ile Ala Leu Gly Leu Lys Gln Leu Met
          100          105          110
Pro His Pro Trp Asp Ala Leu Asp Ser Glu Leu Lys Val Gly Asp Lys
          115          120          125
Val Lys Gly Lys Val Val Val Met Ala Asp Tyr Gly Ala Phe Val Glu
          130          135          140
Ile Ala Gln Gly Val Glu Gly Leu Ile His Val Ser Glu Met Ser Trp
145          150          155          160
Thr Gln His Leu Arg Ser Ala Gln Asp Phe Leu His Val Gly Asp Glu
          165          170          175
Val Glu Ala Val Ile Leu Thr Leu Asp Arg Glu Glu Arg Lys Met Ser
          180          185          190
Leu Gly Leu Lys Gln Leu Lys Pro Asp Pro Trp Ala Asp Ile Glu Thr
          195          200          205
Arg Phe Pro Val Gly Ser Arg His His Ala Arg Val Arg Asn Phe Thr
          210          215          220

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Asn Phe Gly Val Phe Val Glu Ile Glu Glu Gly Val Asp Gly Leu Ile
 225 230 235 240
 His Ile Ser Asp Leu Ser Trp Thr Lys Lys Ile Lys His Pro Ser Glu
 245 250 255
 Phe Thr Glu Val Gly Ala Asp Ile Glu Val Gln Val Ile Glu Ile Asp
 260 265 270
 Lys Glu Asn Arg Arg Leu Ser Leu Gly His Lys Gln Leu Glu Glu Asn
 275 280 285
 Pro Trp Asp Val Phe Glu Thr Val Phe Thr Val Gly Ser Ile His Glu
 290 295 300
 Gly Thr Val Ile Glu Val Met Asp Lys Gly Ala Val Val Ser Leu Pro
 305 310 315 320
 Tyr Gly Val Glu Gly Phe Ala Thr Pro Lys His Met Val Lys Glu Asp
 325 330 335
 Gly Ser Gln Ala Val Leu Glu Glu Lys Leu Pro Phe Lys Val Ile Glu
 340 345 350
 Phe Asn Lys Asp Ala Lys Arg Ile Ile Val Ser His Ser Arg Val Phe
 355 360 365
 Glu Asp Glu Gln Lys Met Ala Gln Arg Glu Ala Asn Ala Glu Arg Lys
 370 375 380
 Ala Glu Ala Lys Ala Ala Gln Lys Glu Ala Ala Ala Glu Ala Ala Asn
 385 390 395 400
 Pro Ala Gln Ala Val Glu Lys Ala Thr Leu Gly Asp Leu Gly Glu Leu
 405 410 415
 Ala Ala Leu Lys Glu Lys Leu Ser Glu Asn
 420 425
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 <213> Porphyromonas gingivalis
 <400> 502
 Met Lys Lys Ala Ile Leu Ser Gly Ala Ala Leu Leu Leu Gly Leu Cys
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 Ala Asn Ala Gln Asn Val Gln Leu His Tyr Asp Phe Gly His Ser Ile
 20 25 30
 Tyr Asp Glu Leu Asp Gly Arg Pro Lys Leu Thr Thr Thr Val Glu Asn
 35 40 45
 Phe Thr Pro Asp Lys Trp Gly Ser Thr Phe Phe Phe Ile Asp Met Asp
 50 55 60
 Tyr Thr Gly Lys Gly Ile Gln Ser Ala Tyr Trp Glu Ile Ser Arg Glu
 65 70 75 80
 Leu Lys Phe Trp Gln Ala Pro Val Ser Ile His Leu Glu Tyr Asn Gly
 85 90 95
 Gly Leu Ser Thr Ser Phe Thr Phe Gly His Asp Ala Leu Ile Gly Ala
 100 105 110
 Thr Tyr Thr Tyr Asn Asn Pro Ser Phe Thr Arg Gly Phe Thr Ile Thr
 115 120 125
 Pro Met Tyr Lys His Leu Gly Ala His Asp Phe His Thr Tyr Gln Ile
 130 135 140
 Thr Gly Thr Trp Tyr Met His Phe Leu Asp Gly Leu Leu Thr Phe Asn
 145 150 155 160
 Gly Phe Leu Asp Leu Trp Gly Phe Pro Gln Glu Asn Pro Ile Gly Gly

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                165                170                175
Pro Val Leu Lys Glu Gly Asp Lys Phe Val Phe Leu Ser Glu Pro Gln
                180                185                190
Phe Trp Ile Asn Leu Asn Arg Ile Lys Gly Ile Asp Lys Asp Phe Asn
                195                200                205
Leu Ser Ile Gly Thr Glu Met Glu Ile Ser Arg Asn Phe Ala Arg Met
                210                215                220
Asp Lys Phe Ser Cys Ile Pro Thr Leu Ala Val Lys Trp Thr Phe Asn
225                230                235                240
<210>      503
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<212>      PRT
<213>      Porphyromonas gingivalis
<400>      503
Met Tyr Lys Asp Tyr Lys Gly Leu Tyr Ala Ser Leu Arg Trp Tyr Ala
  1              5              10              15
Leu Ile Ile Gly Leu Leu Phe Ala Ala Asp Gly Ile Gln Ala Gln Asn
                20              25              30
Asn Asn Phe Thr Glu Ser Pro Tyr Thr Arg Phe Gly Leu Gly Arg Leu
                35              40              45
Gly Glu Arg Thr Thr Ile Ser Gly His Ser Met Gly Gly Leu Gly Val
                50              55              60
Gly Leu Arg Gln Gly Thr Tyr Val Asn Ala Val Asn Pro Ala Ser Tyr
  65              70              75              80
Ser Ala Val Asp Ser Met Thr Phe Ile Phe Asp Phe Gly Ala Ser Thr
                85              90              95
Gly Ile Thr Trp Tyr Ala Glu Asn Gly Lys Lys Asp Asn Arg Lys Met
                100             105             110
Gly Asn Ile Glu Tyr Phe Ala Met Leu Phe Pro Ile Ser Lys Ser Ile
                115             120             125
Ala Met Ser Ala Gly Val Leu Pro Tyr Ser Ala Ser Gly Tyr Gln Phe
  130             135             140
Gly Ser Val Asp Gln Val Glu Gly Gly Ser Val Gln Tyr Thr Arg Lys
145             150             155             160
Tyr Leu Gly Thr Gly Asn Leu Asn Asp Leu Tyr Val Gly Ile Gly Ala
                165             170             175
Thr Pro Phe Lys Asn Phe Ser Ile Gly Ala Asn Ala Ser Ser Leu Phe
                180             185             190
Gly Arg Phe Thr His Ser Arg Gln Val Ile Phe Ser Thr Glu Ala Pro
  195             200             205
Tyr Asn Pro Val His Leu Ser Thr Leu Tyr Leu Lys Ala Ala Lys Phe
  210             215             220
Asp Phe Gly Met Gln Tyr His Leu Leu Leu Lys Ser Asp Arg Ser Leu
225             230             235             240
Val Ile Gly Ala Val Tyr Ser Pro Arg Val Lys Met His Ser Glu Leu
                245             250             255
Thr Gln Ile Lys Asn Gln Val Gln Asn Gly Val Val Val Glu Ser Glu
                260             265             270
Thr Gln Glu Tyr Ile Lys Gly Met Asp Tyr Tyr Thr Leu Pro His Thr
                275             280             285
Leu Gly Ile Gly Phe Ser Tyr Glu Lys Lys Asp Lys Leu Leu Leu Gly
  290             295             300

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Ala Asp Val Gln Tyr Ser Lys Trp Lys Gly Glu Lys Phe Tyr Lys Ser
305 310 315 320
Asp Cys Lys Phe Gln Asp Arg Ile Arg Val Ser Leu Gly Gly Glu Ile
325 330 335
Ile Pro Asp Ile Asn Ala Val Gly Met Trp Pro Lys Val Arg Tyr Arg
340 345 350
Phe Gly Leu His Gly Glu Asn Ser Tyr Leu Lys Val Pro Thr Lys Gly
355 360 365
Gly Val Tyr Gln Gly Tyr His Ile Val Gly Ala Val Phe Gly Ile Gly
370 375 380
Ile Pro Leu Asn Asp Arg Arg Ser Phe Val Asn Val Ser Leu Glu Tyr
385 390 395 400
Asp Arg Leu Ile Pro Lys Glu Gly Met Ile Lys Glu Asn Ala Leu Lys
405 410 415
Leu Thr Phe Gly Leu Thr Phe Asn Glu Ser Trp Phe Lys Lys Leu Lys
420 425 430
Leu Asn
<210> 504
<211> 926
<212> PRT
<213> Porphyromonas gingivalis
<400> 504
Met Arg Ser Ile Tyr Gln Leu Leu Leu Ser Ile Leu Leu Ala Ser Leu
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Gly Phe Val Gly Leu Glu Ala Gln Gln Ala Gly Val Ala Gly Arg Val
20 25 30
Leu Asp Glu Glu Gly Asn Pro Met Ile Gln Ala Asn Val Gln Leu Val
35 40 45
Gln Ser Thr Gly Gln Val Ala Val Ala Ala Gly Ala Thr Asn Glu Lys
50 55 60
Gly Leu Phe Ser Leu Lys Thr Ser Gln Glu Gly Asp Tyr Ile Leu Arg
65 70 75 80
Val Ser Tyr Val Gly Tyr Thr Thr His Asp Glu Lys Ile Ser Leu Arg
85 90 95
Asn Gly Gln Thr Ile Thr Leu Lys Asp Ile Ser Met Asn Glu Asp Ala
100 105 110
Arg Leu Leu Gln Ser Val Thr Val Gln Ala Lys Ala Ala Glu Val Val
115 120 125
Val Arg Asn Asp Thr Leu Glu Phe Asn Ala Gly Ser Tyr Thr Val Ala
130 135 140
Gln Gly Ala Ser Ile Glu Glu Leu Ile Lys Lys Leu Pro Gly Ala Glu
145 150 155 160
Ile Gly Ser Asp Gly Lys Ile Thr Ile Asn Gly Lys Asp Ile Ser Lys
165 170 175
Ile Leu Val Asp Gly Lys Glu Phe Phe Ser Lys Asp Pro Gln Val Ala
180 185 190
Ile Lys Asn Leu Pro Ala Asp Met Val Asn Lys Val Gln Val Leu Asn
195 200 205
Lys Leu Ser Glu Leu Ser Arg Met Ser Gly Phe Asp Asp Gly Glu Glu
210 215 220
Glu Thr Val Ile Asn Leu Thr Val Lys Pro Glu Lys Lys Lys Gly Leu
225 230 235 240

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

Asn Val Met Ala Met Phe Ser Asp Phe Asp Ala Lys Ser Gln Arg Ala
 660 665 670
 Phe Asn Ile Val Phe Phe Gly Asn Tyr Thr Phe Asp Asp Ile Val Pro
 675 680 685
 Asn Thr His Tyr Asp Pro Ser Thr Gly Ile Arg Thr Thr Arg Tyr Glu
 690 695 700
 Asn Ala Ser Gly Thr Trp Gln Ala Asn Leu His Gly Thr Leu Ser Leu
 705 710 715 720
 Pro Leu Lys Asn Arg Ala Phe Ser Phe Arg Met Ser Leu Phe Asn Arg
 725 730 735
 Leu Ala Glu Gly Gln Ser Phe Ile Asn Asp Asp Lys Asn Lys Ala Leu
 740 745 750
 Ser Phe Arg Thr Arg Glu Arg Leu Thr Leu Thr Tyr Arg Asn Asn Trp
 755 760 765
 Ile Asp Thr Ser Ile Gly Gly Asn Ile Gly Phe Tyr Met Ala Asn Asn
 770 775 780
 Ser Leu Ser Gly Gln Lys Asp Ser Arg Thr Tyr Asp Phe Gly Gly Asn
 785 790 795 800
 Tyr Gln Val Ala Leu Thr Leu Pro Tyr Gly Phe Arg Ile Asp Ser Asp
 805 810 815
 Val Glu Tyr Asn Thr Asn Ser Gly Tyr Ser Gly Gly Phe Ser Leu Asp
 820 825 830
 Glu Trp Leu Trp Asn Ala Ser Leu Ser Tyr Ser Phe Leu Arg Asp Lys
 835 840 845
 Ala Gly Thr Leu Arg Val Asn Gly Tyr Asp Ile Leu Gly Gln Arg Ser
 850 855 860
 Ser Ile Ser Arg Ser Ala Ser Ala Ile Asn Ile Glu Glu Ser Met Ser
 865 870 875 880
 Asn Thr Ile Gly Arg Tyr Val Met Val Asp Phe Ile Tyr Arg Phe Asn
 885 890 895
 Ala Phe Ser Gly Gly Gly Ser Arg Ser Asp His Gln Arg Gly Asn Met
 900 905 910
 Asn Arg Pro Gly Pro Pro Phe Gly Gly Gly Arg Arg Pro Ser
 915 920 925
 <210> 505
 <211> 400
 <212> PRT
 <213> Porphyromonas gingivalis
 <400> 505
 Met Val Met Lys Leu Ile Lys Arg Ser Leu Leu Leu Leu Gly Ala Val
 1 5 10 15
 Leu Leu Ile Thr Leu Pro Ala Tyr Ser Gln Asn Asp Asp Ile Phe Glu
 20 25 30
 Asp Asp Ile Tyr Thr Ser Arg Lys Glu Ile Arg Lys Gln Asn Gln Val
 35 40 45
 Lys Asp Trp Gln Asn Gln Glu Asp Gly Tyr Gly Asp Asp Thr Glu Tyr
 50 55 60
 Thr Val Ala Ser Asp Arg Asp Ile Asp Ala Tyr Asn Arg Arg Asp Gly
 65 70 75 80
 Gln Ser Tyr Asp Gly Lys Lys Leu Ser Lys Asp Lys Lys Arg Asp Ser
 85 90 95
 Thr Arg Ser Ser Val Pro Gly Arg Tyr Ser Arg Arg Leu Ala Arg Phe

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100          105          110
Tyr Lys Pro Asn Thr Ile Val Ile Ser Gly Ala Asp Asn Val Tyr Val
115          120          125
Thr Asp Asp Gly Glu Tyr Phe Val Tyr Gly Asp Glu Tyr Tyr Asp Asp
130          135          140
Ala Ser Ser Val Asn Ile Tyr Ile Asn Ser Pro Trp Cys Asp Pro Phe
145          150          155          160
Pro Tyr Thr Ser Trp Tyr Pro Ser Phe Ser Gly Trp Tyr Asn Tyr Thr
165          170          175
Trp Asn Tyr Pro Trp Phe Tyr Tyr Gly Ser His Ile Gly Trp Gly Gly
180          185          190
Tyr Tyr Pro Gly Tyr Asn Trp Tyr Trp Ser Tyr Tyr Tyr Asp Pro Phe
195          200          205
Tyr Asn Pro Tyr Gly Ile Gly Met Gly Trp Gly Tyr Pro Tyr Gly Trp
210          215          220
Gly Ser Tyr Tyr Gly Trp Gly Gly Tyr Pro Gly Val Ile His His Tyr
225          230          235          240
His His Tyr Pro Lys Lys Thr Tyr Ser Asn Gly Gln His Ser Gly Ala
245          250          255
Tyr Tyr Ser Tyr Gly Arg Pro Asn Arg Ile Lys Gly Gly Thr Ser Gly
260          265          270
Ala Lys Leu Gly Thr Gly Arg Tyr Asp Arg Ile Gln Asn Ser Ser Ser
275          280          285
Gln Lys Asn Lys Phe Gly Leu Gln Ser Asn Lys Pro Asn Asn Asn Leu
290          295          300
Gln Asn Val Lys Ser Gly Arg Thr Gly Arg Ala Asn Arg Asp Arg Asn
305          310          315          320
Ile Glu Thr Val Thr Pro Asn Asn Gly Gln Lys Gln Asn Arg Pro Val
325          330          335
Phe Gln Gln Asn Gln Ser Gly Asn Asp Arg Pro Thr Gly Arg Asn Ile
340          345          350
Arg Ser Glu Arg Gln Gly Glu Asn Asn Asp Arg Thr Phe Ser Thr Pro
355          360          365
Ser Arg Ser Asn Ser Asn Gly Gly Phe Ser Thr Pro Ser Arg Ser Ser
370          375          380
Ser Gly Ser Met Ser Gly Gly Gly Gly Arg Ser Gly Arg Gly Arg Asn
385          390          395          400
<210>      506
<211>      398
<212>      PRT
<213>      Porphyromonas gingivalis
<400>      506
Met Lys Leu Ile Lys Arg Ser Leu Leu Leu Leu Gly Ala Val Leu Leu
1          5          10          15
Ile Thr Leu Pro Ala Tyr Ser Gln Asn Asp Asp Ile Phe Glu Asp Asp
20          25          30
Ile Tyr Thr Ser Arg Lys Glu Ile Arg Lys Gln Asn Gln Val Lys Asp
35          40          45
Trp Gln Asn Gln Glu Asp Gly Tyr Gly Asp Asp Thr Glu Tyr Thr Val
50          55          60
Ala Ser Asp Arg Asp Ile Asp Ala Tyr Asn Arg Arg Asp Gly Gln Ser
65          70          75          80

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Tyr Asp Gly Lys Lys Leu Ser Lys Asp Lys Lys Arg Asp Ser Thr Arg
 85 90 95
 Ser Ser Val Pro Gly Arg Tyr Ser Arg Arg Leu Ala Arg Phe Tyr Lys
 100 105 110
 Pro Asn Thr Ile Val Ile Ser Gly Ala Asp Asn Val Tyr Val Thr Asp
 115 120 125
 Asp Gly Glu Tyr Phe Val Tyr Gly Asp Glu Tyr Tyr Asp Asp Ala Ser
 130 135 140
 Ser Val Asn Ile Tyr Ile Asn Ser Pro Trp Cys Asp Pro Phe Pro Tyr
 145 150 155 160
 Thr Ser Trp Tyr Pro Ser Phe Ser Gly Trp Tyr Asn Tyr Thr Trp Asn
 165 170 175
 Tyr Pro Trp Phe Tyr Tyr Gly Ser His Ile Gly Trp Gly Gly Tyr Tyr
 180 185 190
 Pro Gly Tyr Asn Trp Tyr Trp Ser Tyr Tyr Tyr Asp Pro Phe Tyr Asn
 195 200 205
 Pro Tyr Gly Ile Gly Met Gly Trp Gly Tyr Pro Tyr Gly Trp Gly Ser
 210 215 220
 Tyr Tyr Gly Trp Gly Gly Tyr Pro Gly Val Ile His His Tyr His His
 225 230 235 240
 Tyr Pro Lys Lys Thr Tyr Ser Asn Gly Gln His Ser Gly Ala Tyr Tyr
 245 250 255
 Ser Tyr Gly Arg Pro Asn Arg Ile Lys Gly Gly Thr Ser Gly Ala Lys
 260 265 270
 Leu Gly Thr Gly Arg Tyr Asp Arg Ile Gln Asn Ser Ser Ser Gln Lys
 275 280 285
 Asn Lys Phe Gly Leu Gln Ser Asn Lys Pro Asn Asn Asn Leu Gln Asn
 290 295 300
 Val Lys Ser Gly Arg Thr Gly Arg Ala Asn Arg Asp Arg Asn Ile Glu
 305 310 315 320
 Thr Val Thr Pro Asn Asn Gly Gln Lys Gln Asn Arg Pro Val Phe Gln
 325 330 335
 Gln Asn Gln Ser Gly Asn Asp Arg Pro Thr Gly Arg Asn Ile Arg Ser
 340 345 350
 Glu Arg Gln Gly Glu Asn Asn Asp Arg Thr Phe Ser Thr Pro Ser Arg
 355 360 365
 Ser Asn Ser Asn Gly Gly Phe Ser Thr Pro Ser Arg Ser Ser Ser Gly
 370 375 380
 Ser Met Ser Gly Gly Gly Gly Arg Ser Gly Arg Gly Arg Asn
 385 390 395
 <210> 507
 <211> 581
 <212> PRT
 <213> Porphyromonas gingivalis
 <400> 507
 Met Ile Arg Lys Leu Ile Leu Leu Leu Ala Leu Met Pro Val Ala Ser
 1 5 10 15
 Val Ala Phe Ala Val Pro Thr Asp Ser Thr Glu Ser Lys Asp Asn Arg
 20 25 30
 Ile Leu Thr Ser Met Gln Ser Ser Ser Leu Asn Arg Asp Asp Ala Pro
 35 40 45
 Asp Lys Trp Gln Pro Met His Ala Asn Phe Ser Ile Gln Ser Asp Met

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

465 470 475 480
 Ser Asn Lys Val Ala Leu Arg Thr Glu Leu Gln Tyr Leu His Thr Lys
 485 490 495
 Gln Asp Gln Gly Asp Trp Ile Tyr Gly Met Ala Glu Leu Ser Ile Leu
 500 505 510
 Pro Ser Leu Met Leu Ser Leu Ser Glu Gln Tyr Asn Ile Gly Glu Thr
 515 520 525
 Lys Lys His Tyr Val Met Gly Ser Val Thr Tyr Thr His Gly Ala His
 530 535 540
 Arg Val Ala Phe Ser Ala Gly Lys Thr Arg Ala Gly Met Asn Cys Ser
 545 550 555 560
 Gly Gly Val Cys Arg Val Val Pro Glu Thr Gln Gly Phe Tyr Leu Ser
 565 570 575
 Tyr Ser Thr Asn Leu
 580
 <210> 508
 <211> 239
 <212> PRT
 <213> Porphyromonas gingivalis
 <400> 508
 Met Arg Ser Leu Phe Leu Ser Ala Leu Arg Ser Ser Ser Leu His Gly
 1 5 10 15
 Ser Glu Arg Arg Ser Arg Ile Ser Ser Ser Val Val Met Ser Ile Arg
 20 25 30
 Gln Lys Ile Arg Leu Phe His Leu Ser Val Cys Ala Gln Thr His Asp
 35 40 45
 His Leu Ile Glu Ile His Leu Val Cys Ile Glu Phe Gly Ala Ile Asp
 50 55 60
 Thr Asp Glu Phe Arg Leu Ser Ser His Ala Tyr Thr Thr Ser Pro Thr
 65 70 75 80
 His Thr Gly Ala Ile His His Asn Cys Ile Glu Arg Ser Tyr Gly Arg
 85 90 95
 Tyr Leu Val Thr Phe Gly Gln Glu Arg Asn Glu Leu His His His Ser
 100 105 110
 Arg Pro Asp Arg Asn Ala Glu Val Tyr Arg Phe Pro Phe Asp Asn Ala
 115 120 125
 Phe His Ser Ile Arg Tyr Glu Ala Phe Arg Pro Ile Arg Pro Ile Val
 130 135 140
 Cys His Asp Asp His Phe Ile Ala Ile Gly Ser His Leu Phe Phe Lys
 145 150 155 160
 Asp Asn Gln Ile Phe Ser Ser Gly Ser Gln Tyr Asp Asn Tyr Thr Val
 165 170 175
 Ala Cys Phe Val Glu Ser Leu His Asp Arg Glu Gln Arg Ser His Thr
 180 185 190
 His Thr Ala Ser Gly Thr Asn His Cys Ala Asp Leu Phe Asp Met Arg
 195 200 205
 Thr Leu Ser Gln Arg Thr Tyr His Ile Arg Asp Ile Val Ala Asp Phe
 210 215 220
 Glu Phe Gly Gln Phe Leu Gly Arg Phe Ala His Gly Leu Asn His
 225 230 235
 <210> 509
 <211> 211

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<212>      PRT
<213>      Porphyromonas gingivalis
<400>      509
Met Ser Ile Arg Gln Lys Ile Arg Leu Phe His Leu Ser Val Cys Ala
 1              5              10              15
Gln Thr His Asp His Leu Ile Glu Ile His Leu Val Cys Ile Glu Phe
              20              25              30
Gly Ala Ile Asp Thr Asp Glu Phe Arg Leu Ser Ser His Ala Tyr Thr
              35              40              45
Thr Ser Pro Thr His Thr Gly Ala Ile His His Asn Cys Ile Glu Arg
              50              55              60
Ser Tyr Gly Arg Tyr Leu Val Thr Phe Gly Gln Glu Arg Asn Glu Leu
              65              70              75              80
His His His Ser Arg Pro Asp Arg Asn Ala Glu Val Tyr Arg Phe Pro
              85              90              95
Phe Asp Asn Ala Phe His Ser Ile Arg Tyr Glu Ala Phe Arg Pro Ile
              100              105              110
Arg Pro Ile Val Cys His Asp Asp His Phe Ile Ala Ile Gly Ser His
              115              120              125
Leu Phe Phe Lys Asp Asn Gln Ile Phe Ser Ser Gly Ser Gln Tyr Asp
              130              135              140
Asn Tyr Thr Val Ala Cys Phe Val Glu Ser Leu His Asp Arg Glu Gln
              145              150              155              160
Arg Ser His Thr His Thr Ala Ser Gly Thr Asn His Cys Ala Asp Leu
              165              170              175
Phe Asp Met Arg Thr Leu Ser Gln Arg Thr Tyr His Ile Arg Asp Ile
              180              185              190
Val Ala Asp Phe Glu Phe Gly Gln Phe Leu Gly Arg Phe Ala His Gly
              195              200              205
Leu Asn His
              210
<210>      510
<211>      781
<212>      PRT
<213>      Porphyromonas gingivalis
<400>      510
Met Asp Arg Pro Lys Pro Ser Tyr Ile Val Arg Ile Ala Ala Ile Leu
 1              5              10              15
Cys Leu Phe Val Gly Arg Pro Leu Phe Ala Gln Ser Tyr Val Asp Tyr
              20              25              30
Val Asp Pro Leu Ile Gly Thr Leu Ser Ser Phe Glu Leu Ser Ala Gly
              35              40              45
Asn Thr Tyr Pro Val Ile Gly Leu Pro Trp Gly Met Asn Ser Trp Thr
              50              55              60
Pro Met Thr Gly Val Pro Gly Asp Gly Trp Gln Tyr Thr Tyr Ser Ala
              65              70              75              80
His Lys Ile Arg Gly Phe Lys Gln Thr His Gln Pro Ser Pro Trp Ile
              85              90              95
Asn Asp Tyr Gly Gln Phe Ser Leu Leu Pro Leu Thr Ala Pro Gln Lys
              100              105              110
Pro Ser Ser Asn Asp Ser Ile Ala Leu Thr Lys Trp Cys Lys Gln Leu
              115              120              125

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

Gly Asp Val Phe Thr Glu Gly Asn Ala Trp His Tyr Thr Trp Ser Val
 545 550 555 560
 Phe His Asp Val Gln Gly Leu Ile Asp Leu Met Gly Gly Asp Arg Pro
 565 570 575
 Phe Val Ser Met Leu Asp Ser Val Phe Asn Thr Pro Pro Met Phe Asp
 580 585 590
 Glu Ser Tyr Tyr Gly Phe Val Ile His Glu Ile Arg Glu Met Gln Ile
 595 600 605
 Ala Asp Met Gly Asn Tyr Ala His Gly Asn Gln Pro Ile Gln His Met
 610 615 620
 Ile Tyr Leu Tyr Asn His Ala Gly His Pro Trp Lys Ala Gln Glu Arg
 625 630 635 640
 Leu Arg Glu Val Met Gly Arg Leu Tyr Arg Pro Thr Pro Asp Gly Tyr
 645 650 655
 Cys Gly Asp Glu Asp Asn Gly Gln Thr Ser Ala Trp Tyr Val Phe Ser
 660 665 670
 Ala Leu Gly Phe Tyr Pro Val Thr Pro Ala Thr Asp Gln Tyr Val Leu
 675 680 685
 Gly Ser Pro Ile Phe Ser Lys Val Ile Leu Ser Phe Pro Asp Gly His
 690 695 700
 Lys Thr Val Leu His Ala Pro Ala Asn Ser Ala Asp Thr Pro Tyr Ile
 705 710 715 720
 Arg Ser Ile Ser Val Glu Gly Lys Glu Trp Ser Cys Asn Tyr Leu Thr
 725 730 735
 His Glu Gln Leu Arg Ser Ser Ala Ser Ile Gln Trp Met Met Asp Thr
 740 745 750
 Lys Pro Asn Tyr Asn Arg Gly Met Lys Glu Ser Asp Arg Pro Tyr Ser
 755 760 765
 Phe Ser Thr Glu Gln Gln Arg Arg Ala Asn His Ser Asn
 770 775 780
 <210> 511
 <211> 271
 <212> PRT
 <213> Porphyromonas gingivalis
 <400> 511
 Met Met Lys Ser Met Arg Ser Val Leu Leu Leu Leu Phe Pro Leu Ser
 1 5 10 15
 Leu Ile Thr Ala Leu Gly Cys Ser Asn Asn Lys Ala Ala Glu Ser Lys
 20 25 30
 Ser Val Ser Phe Asp Ser Ala Tyr Leu Glu Arg Tyr Ile Pro Leu Arg
 35 40 45
 Ala Asp Ile Asp Thr Pro Ser Leu His Val Met Ile Ser Tyr Val Tyr
 50 55 60
 Pro Ser Gly Asp Asp Met Leu Thr Glu Ile Phe Asn Gly Leu Leu Phe
 65 70 75 80
 Gly Asp Ser Leu Met Asp Ser Ser Ser Pro Glu Asn Ala Met Glu Gly
 85 90 95
 Tyr Ala Gln Met Leu Gly Glu Asp Tyr Arg Ser Asn Asn Ala Glu Ala
 100 105 110
 Asn Leu Gln Gly Leu Pro Ser Asp Leu Leu Asp Tyr Ile Tyr Lys Gln
 115 120 125
 Glu Asn Thr Ile Ala Tyr Cys Asp Thr Gly Leu Ile Ser Thr Arg Ile

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130          135          140
Asn Thr Tyr Thr Tyr Glu Gly Gly Ala His Thr Glu Asn Thr Val Arg
145          150          155          160
Phe Ala Asn Ile Leu Arg Thr Thr Gly Lys Val Leu Glu Glu Arg Asp
165          170          175
Ile Phe Lys Ile Asp Tyr Ala Glu Arg Leu Ser Ala Leu Ile Ile Gly
180          185          190
Gln Leu Val His Asp Phe Gly Lys Thr Thr Pro Ala Glu Leu Asp Ala
195          200          205
Ile Gly Phe Phe Asn Ala Glu Glu Ile Gln Pro Asn Gly Asn Phe Met
210          215          220
Ile Asp Asp Lys Gly Leu Thr Tyr Cys Phe Asn Glu Tyr Gln Ile Ala
225          230          235          240
Ala Tyr Ala Arg Gly Ala Val Tyr Val Arg Leu Gly Tyr Asp Val Leu
245          250          255
Ala Pro Leu Leu Arg Asp Asp Ser Pro Leu Lys Arg Tyr Leu Pro
260          265          270
<210> 512
<211> 270
<212> PRT
<213> Porphyromonas gingivalis
<400> 512
Met Lys Ser Met Arg Ser Val Leu Leu Leu Leu Phe Pro Leu Ser Leu
1 5 10 15
Ile Thr Ala Leu Gly Cys Ser Asn Asn Lys Ala Ala Glu Ser Lys Ser
20 25 30
Val Ser Phe Asp Ser Ala Tyr Leu Glu Arg Tyr Ile Pro Leu Arg Ala
35 40 45
Asp Ile Asp Thr Pro Ser Leu His Val Met Ile Ser Tyr Val Tyr Pro
50 55 60
Ser Gly Asp Asp Met Leu Thr Glu Ile Phe Asn Gly Leu Leu Phe Gly
65 70 75 80
Asp Ser Leu Met Asp Ser Ser Ser Pro Glu Asn Ala Met Glu Gly Tyr
85 90 95
Ala Gln Met Leu Gly Glu Asp Tyr Arg Ser Asn Asn Ala Glu Ala Asn
100 105 110
Leu Gln Gly Leu Pro Ser Asp Leu Leu Asp Tyr Ile Tyr Lys Gln Glu
115 120 125
Asn Thr Ile Ala Tyr Cys Asp Thr Gly Leu Ile Ser Thr Arg Ile Asn
130 135 140
Thr Tyr Thr Tyr Glu Gly Gly Ala His Thr Glu Asn Thr Val Arg Phe
145 150 155 160
Ala Asn Ile Leu Arg Thr Thr Gly Lys Val Leu Glu Glu Arg Asp Ile
165 170 175
Phe Lys Ile Asp Tyr Ala Glu Arg Leu Ser Ala Leu Ile Ile Gly Gln
180 185 190
Leu Val His Asp Phe Gly Lys Thr Thr Pro Ala Glu Leu Asp Ala Ile
195 200 205
Gly Phe Phe Asn Ala Glu Glu Ile Gln Pro Asn Gly Asn Phe Met Ile
210 215 220
Asp Asp Lys Gly Leu Thr Tyr Cys Phe Asn Glu Tyr Gln Ile Ala Ala
225 230 235 240

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

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

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Leu Thr Lys Leu Ser Leu Ser Asp Asn Gln Ile Ser Lys Leu Glu Gly
145                150                155                160
Leu Glu Arg Leu Thr Ser Leu Ala Glu Leu Tyr Leu Leu Asp Asn Gln
                165                170                175
Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Ala Thr Leu
                180                185                190
Glu Leu Ser Gly Asn Gln Ile Arg Lys Leu Glu Gly Leu Glu Arg Leu
                195                200                205
Thr Ser Leu Ala Thr Leu Glu Leu Ser Gly Asn Gln Ile Arg Lys Leu
                210                215                220
Glu Gly Leu Glu Arg Leu Thr Ser Leu Thr Lys Leu Arg Leu Arg Ser
225                230                235                240
Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Ala
                245                250                255
Thr Leu Glu Leu Ser Gly Asn Gln Ile Arg Lys Leu Glu Gly Leu Glu
                260                265                270
Arg Leu Thr Ser Leu Ala Thr Leu Glu Leu Ser Gly Asn Gln Ile Ser
                275                280                285
Lys Leu Glu Gly Leu Glu Arg Leu Ser Ser Leu Thr Lys Leu Arg Leu
                290                295                300
Arg Ser Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser
305                310                315                320
Leu Thr Lys Leu Ser Leu Ser Asp Asn Gln Ile Ser Lys Leu Glu Gly
                325                330                335
Leu Glu Arg Leu Thr Ser Leu Ala Glu Leu Tyr Leu Leu Asp Asn Gln
                340                345                350
Ile Arg Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Thr Lys Leu
                355                360                365
Arg Leu Arg Ser Asn Gln Ile Ser Lys Leu Glu Gly Leu Asp Ser Leu
                370                375                380
Thr Ser Leu Thr Lys Leu Ser Leu Ser Asp Asn Gln Ile Ser Lys Leu
385                390                395                400
Glu Gly Leu Glu Arg Leu Thr Ser Leu Ala Glu Leu Tyr Leu Leu Asp
                405                410                415
Asn Gln Ile Arg Lys Leu Glu Gly Leu Asp Gly Leu Ala Ser Leu Thr
                420                425                430
Arg Leu Ser Leu Arg Arg Asn Gln Ile Ser Lys Leu Glu Gly Leu Asp
                435                440                445
Arg Leu Lys Val Leu Arg Lys Leu Asp Val Ser Gly Asn Asp Ile Gln
450                455                460
Ser Ile Asp Asp Ile Lys Leu Leu Ala Pro Ile Leu Glu Gln Thr Leu
465                470                475                480
Glu Lys Leu Arg Ile His Asp Asn Pro Phe Val Ala Ser Ser Gly Leu
                485                490                495
Ile Leu Ser Pro Tyr Asp Asn His Leu Pro Glu Ile Lys Ala Leu Leu
                500                505                510
Glu Lys Glu Lys Glu Lys Gln Lys Lys Thr Ser Val Glu Tyr His Pro
515                520                525
Phe Cys Lys Val Met Leu Leu Gly Asn His Ser Ser Gly Lys Thr Thr
530                535                540
Phe Leu Ser Gln Tyr Asp Thr Asn Tyr Thr Tyr Gln Lys Asn Thr His
545                550                555                560

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

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Gln Arg Lys Thr Ser Ala Lys Asp Met Gln Arg Lys Glu Ala Thr Ile
980 985 990
Leu Ser Asp Met Leu Asp Met Tyr Trp Asn Asn Ile Pro Pro Arg Glu
995 1000 1005
Gln Ile Gly Asp Lys Asp Thr Glu Gln Thr Arg Ser Thr Ile Arg Glu
1010 1015 1020
Thr Asn Arg Lys Lys Arg Pro Ile Gln Asp Leu Tyr Leu Ser Cys Ala
1025 1030 1035 1040
Gln Ala Asp Lys Asp Leu Thr Glu Ser His Tyr Ile His Leu Gly Thr
1045 1050 1055
Leu Asp Asp Glu Ser Lys Thr Thr Ala Arg Ile Ala Ala Tyr Pro Leu
1060 1065 1070
Lys Asn Gly Val Ile Asp Lys Glu Arg Val Arg Glu Val Ser Thr Arg
1075 1080 1085
Pro Tyr Lys His Leu Ser Val Asn Lys Asn Leu Ala Thr Ala Lys Gln
1090 1095 1100
Ile Phe Ile Ser Tyr Ser Lys Glu Asp Gln Thr Glu Leu Glu Thr Cys
1105 1110 1115 1120
Leu Gln Phe Phe Lys Pro Leu Glu Lys Asn Gly Gln Ile Glu Ile Tyr
1125 1130 1135
Tyr Asp Lys Leu Thr Lys Phe Glu Thr Pro Ile His Pro Glu Ile Arg
1140 1145 1150
Lys Arg Ile Val Glu Ala Asp Cys Ile Ile Ala Leu Ile Ser Gln Arg
1155 1160 1165
Tyr Leu Ala Thr Asp Tyr Ile Leu Asp His Glu Leu Pro Val Phe Arg
1170 1175 1180
Glu Tyr Asn Lys Thr Ile Val Pro Ile Leu Ile Lys Pro Cys Thr Phe
1185 1190 1195 1200
Glu Asp Asp Glu Phe Leu Arg Glu Lys Tyr Phe Ala Gln Lys Ala Gln
1205 1210 1215
Ile Ile Asn Leu Gly Lys Glu Gly Lys Thr Ile Lys Ala Tyr Asp Ser
1220 1225 1230
Ile Thr Ala Ser Ala His Arg Asp Glu Asn Trp Val Ala Val Val Arg
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Asp Glu
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Val Asn Arg Tyr Phe Lys Gln Asp Ser Ser Gly Ala Val Val Glu Leu
35 40 45
Cys Leu Arg Glu Cys Gln Ile Glu Ser Met Thr Trp Leu Ile Asp Phe
50 55 60
Pro Ala Leu Lys Lys Leu Asp Leu Ser Tyr Asn Gln Ile Ser Lys Leu

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

900															905					910				
Glu	Gly	Leu	Pro	Lys	Thr	Asn	Ala	Glu	Asp	Tyr	Gln	Ile	Trp	Ile	Lys									
		915				920						925												
Leu	Asp	Phe	Thr	Asp	Leu	Ala	Ile	Ser	Val	Phe	Ile	Lys	Glu	Gln	Arg									
930						935				940														
Lys	Thr	Ser	Ala	Lys	Asp	Met	Gln	Arg	Lys	Glu	Ala	Thr	Ile	Leu	Ser									
945				950						955				960										
Asp	Met	Leu	Asp	Met	Tyr	Trp	Asn	Asn	Ile	Pro	Pro	Arg	Glu	Gln	Ile									
				965				970						975										
Gly	Asp	Lys	Asp	Thr	Glu	Gln	Thr	Arg	Ser	Thr	Ile	Arg	Glu	Thr	Asn									
		980						985				990												
Arg	Lys	Lys	Arg	Pro	Ile	Gln	Asp	Leu	Tyr	Leu	Ser	Cys	Ala	Gln	Ala									
		995				1000						1005												
Asp	Lys	Asp	Leu	Thr	Glu	Ser	His	Tyr	Ile	His	Leu	Gly	Thr	Leu	Asp									
1010						1015				1020														
Asp	Glu	Ser	Lys	Thr	Thr	Ala	Arg	Ile	Ala	Ala	Tyr	Pro	Leu	Lys	Asn									
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Gly	Val	Ile	Asp	Lys	Glu	Arg	Val	Arg	Glu	Val	Ser	Thr	Arg	Pro	Tyr									
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Lys	His	Leu	Ser	Val	Asn	Lys	Asn	Leu	Ala	Thr	Ala	Lys	Gln	Ile	Phe									
		1060				1065						1070												
Ile	Ser	Tyr	Ser	Lys	Glu	Asp	Gln	Thr	Glu	Leu	Glu	Thr	Cys	Leu	Gln									
1075						1080				1085														
Phe	Phe	Lys	Pro	Leu	Glu	Lys	Asn	Gly	Gln	Ile	Glu	Ile	Tyr	Tyr	Asp									
1090				1095						1100														
Lys	Leu	Thr	Lys	Phe	Glu	Thr	Pro	Ile	His	Pro	Glu	Ile	Arg	Lys	Arg									
1105				1110						1115				1120										
Ile	Val	Glu	Ala	Asp	Cys	Ile	Ile	Ala	Leu	Ile	Ser	Gln	Arg	Tyr	Leu									
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Ala	Thr	Asp	Tyr	Ile	Leu	Asp	His	Glu	Leu	Pro	Val	Phe	Arg	Glu	Tyr									
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Asn	Lys	Thr	Ile	Val	Pro	Ile	Leu	Ile	Lys	Pro	Cys	Thr	Phe	Glu	Asp									
1155						1160				1165														
Asp	Glu	Phe	Leu	Arg	Glu	Lys	Tyr	Phe	Ala	Gln	Lys	Ala	Gln	Ile	Ile									
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Ala	Ser	Ala	His	Arg	Asp	Glu	Asn	Trp	Val	Ala	Val	Val	Arg	Glu	Phe									
		1205						1210				1215												
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Tyr	Asn	Gln	Ile	Ser	Lys	Leu	Glu	Gly	Leu	Glu	Arg	Leu	Thr	Ser	Leu									

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

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Gln Lys Asn Thr His Val Leu Ser Ile His Arg Ser Asn Asn Pro Asn				
465		470		480
Ala Ile Phe Tyr Asp Phe Gly Gly Gln Asp Tyr Tyr His Gly Ile Tyr				
	485		490	495
Gln Ala Phe Phe Thr Thr Gln Ser Leu Tyr Leu Leu Phe Trp Asp Ala				
	500		505	510
Lys Lys Asp Arg Asn Phe Val Ser Val Asp Asp Lys Glu Tyr Gln Thr				
	515		520	525
Leu Asn Phe Asn Arg Pro Tyr Trp Leu Gly Gln Ile Ala Tyr Ala Cys				
	530		535	540
Asn Arg Cys Met Ser Val Gly Gly Asn Pro Asp Gly Lys Asp Thr Pro				
545		550		560
Gln Thr Thr Asp Asp Thr Ile Ile Ile Gln Thr His Ala Asp Glu Thr				
	565		570	575
Gly Ala Lys Gln Gln Thr Leu Gly Cys Ala Ala Glu Asn Gly Val Leu				
	580		585	590
Glu Glu Ile Tyr Val Ser Leu Glu Pro Lys Ala Asn Ser Ala Val His				
	595		600	605
Ala Leu Asn Tyr Leu Asn Glu Arg Val Arg Glu Val Val Ala Ser Arg				
	610		615	620
Ser Lys Ser Ile Gln Ile Thr Glu Lys Asp Lys Gly Leu Tyr Glu Ala				
625		630		640
Leu Pro Thr Ile Ala Gly Asp Asn Lys His Ile Pro Ile Ser Leu Glu				
	645		650	655
Ala Leu Ala Ala Gln Leu Asn Lys Gly Arg Ala Glu Asn Asp Leu Tyr				
	660		665	670
Thr Ile Glu Tyr Leu Gln Thr Glu Leu Asn Gln Leu Ser Leu Arg Gly				
	675		680	685
Glu Val Leu Tyr Tyr Arg Glu Asn Glu Lys Leu Asn Asn Tyr Val Trp				
	690		695	700
Leu Asp Pro Ala Ala Phe Val Gln Met Ile His Gly Glu Ile Leu Gln				
705		710		720
Lys Asp Asn Ile Asn Arg Gly Thr Val Pro Lys Asp Ile Phe Glu Cys				
	725		730	735
Lys Leu His Asn Leu Ser Ser Gly Ser Ile Phe Glu Glu Asp Gly Gln				
	740		745	750
Asn Gly Asn Met Ile Leu Gln Leu Leu Leu Glu Glu Leu Ile Val Tyr				
	755		760	765
Glu Asp Lys Asp Cys Tyr Val Ile Pro Gly Tyr Leu Pro Leu His Ser				
	770		775	780
Asp Asp Glu Ala Tyr Lys Trp Leu Thr Leu Gly Phe Glu Arg Pro Asn				
785		790		800
Phe Val Leu Lys Phe Glu Arg Phe Ile Pro Phe Gly Leu Ile Asn Gln				
	805		810	815
Ile Ile Ala Tyr Tyr Gly Arg Glu Glu Gly Ala Leu Lys Arg Tyr Trp				
	820		825	830
Arg Asp Gln Val Ile Phe Thr Ala Gly Arg Glu Met Asp Arg Gln Thr				
	835		840	845
Leu Glu Gln Glu Glu Glu Lys Glu Gly Leu Pro Lys Thr Asn Ala Glu				
	850		855	860
Asp Tyr Gln Ile Trp Ile Lys Leu Asp Phe Thr Asp Leu Ala Ile Ser				

865 870 875 880
 Val Phe Ile Lys Glu Gln Arg Lys Thr Ser Ala Lys Asp Met Gln Arg
 885 890 895
 Lys Glu Ala Thr Ile Leu Ser Asp Met Leu Asp Met Tyr Trp Asn Asn
 900 905 910
 Ile Pro Pro Arg Glu Gln Ile Gly Asp Lys Asp Thr Glu Gln Thr Arg
 915 920 925
 Ser Thr Ile Arg Glu Thr Asn Arg Lys Lys Arg Pro Ile Gln Asp Leu
 930 935 940
 Tyr Leu Ser Cys Ala Gln Ala Asp Lys Asp Leu Thr Glu Ser His Tyr
 945 950 955 960
 Ile His Leu Gly Thr Leu Asp Asp Glu Ser Lys Thr Thr Ala Arg Ile
 965 970 975
 Ala Ala Tyr Pro Leu Lys Asn Gly Val Ile Asp Lys Glu Arg Val Arg
 980 985 990
 Glu Val Ser Thr Arg Pro Tyr Lys His Leu Ser Val Asn Lys Asn Leu
 995 1000 1005
 Ala Thr Ala Lys Gln Ile Phe Ile Ser Tyr Ser Lys Glu Asp Gln Thr
 1010 1015 1020
 Glu Leu Glu Thr Cys Leu Gln Phe Phe Lys Pro Leu Glu Lys Asn Gly
 1025 1030 1035 1040
 Gln Ile Glu Ile Tyr Tyr Asp Lys Leu Thr Lys Phe Glu Thr Pro Ile
 1045 1050 1055
 His Pro Glu Ile Arg Lys Arg Ile Val Glu Ala Asp Cys Ile Ile Ala
 1060 1065 1070
 Leu Ile Ser Gln Arg Tyr Leu Ala Thr Asp Tyr Ile Leu Asp His Glu
 1075 1080 1085
 Leu Pro Val Phe Arg Glu Tyr Asn Lys Thr Ile Val Pro Ile Leu Ile
 1090 1095 1100
 Lys Pro Cys Thr Phe Glu Asp Asp Glu Phe Leu Arg Glu Lys Tyr Phe
 1105 1110 1115 1120
 Ala Gln Lys Ala Gln Ile Ile Asn Leu Gly Lys Glu Gly Lys Thr Ile
 1125 1130 1135
 Lys Ala Tyr Asp Ser Ile Thr Ala Ser Ala His Arg Asp Glu Asn Trp
 1140 1145 1150
 Val Ala Val Val Arg Glu Phe Lys Glu Lys Ile Leu Arg Ile Thr Lys
 1155 1160 1165
 Gln Glu Val Asn Thr Asp Glu
 1170 1175
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 <213> Porphyromonas gingivalis
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 Ser Phe Ser Ser Ser Ala Gln Thr Thr Thr Asn Ser Ser Arg Ser Tyr
 20 25 30
 Phe Thr Gly Arg Ile Glu Lys Val Ser Leu Asn Leu Gly Val Pro Pro
 35 40 45
 Val Ser Thr Glu Val Trp Gly Met Thr His Asp Ala Asn Gly Leu Pro
 50 55 60

Phe Glu Ile Pro Ile Ser Phe Ser Arg Phe Asn Ser Gln Gly Asp Ile
 65 70 75 80
 Ala Thr Thr Tyr Tyr Ile Ala Asn Ser Glu Ala Thr Leu Asn Glu Trp
 85 90 95
 Cys Asp Tyr Ala His Pro Gly Gly Ile Val Arg Val Glu Gly Arg Phe
 100 105 110
 Trp Lys Met Thr Tyr Asn Ile Pro Thr Tyr Asn Ala Val Cys Thr Arg
 115 120 125
 Ile Thr Phe Glu Asn Gln Glu Ile Glu Gly Thr Ile Val Leu Ile Pro
 130 135 140
 Lys Pro Lys Val Ser Leu Pro His Val Ser Glu Ser Val Pro Cys Ile
 145 150 155 160
 Arg Thr Glu Ala Gly Arg Glu Phe Ile Leu Cys Glu Glu Asp Asp Thr
 165 170 175
 Phe Val Ser His Asp Gly Asn Glu Val Thr Ile Gly Gly Lys Pro Phe
 180 185 190
 Leu Leu Asn Thr Asn Val Lys Ile Val Gly Asp Val Ser Gln Lys Tyr
 195 200 205
 Ala Val Gly Val Gly Glu Ile Arg Phe Leu Gln Ile Cys Ala Gln Thr
 210 215 220
 Val Ser Gln Gln Lys
 225
 <210> 519
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 Phe Ser Ser Ser Ala Gln Thr Thr Thr Asn Ser Ser Arg Ser Tyr Phe
 20 25 30
 Thr Gly Arg Ile Glu Lys Val Ser Leu Asn Leu Gly Val Pro Pro Val
 35 40 45
 Ser Thr Glu Val Trp Gly Met Thr His Asp Ala Asn Gly Leu Pro Phe
 50 55 60
 Glu Ile Pro Ile Ser Phe Ser Arg Phe Asn Ser Gln Gly Asp Ile Ala
 65 70 75 80
 Thr Thr Tyr Tyr Ile Ala Asn Ser Glu Ala Thr Leu Asn Glu Trp Cys
 85 90 95
 Asp Tyr Ala His Pro Gly Gly Ile Val Arg Val Glu Gly Arg Phe Trp
 100 105 110
 Lys Met Thr Tyr Asn Ile Pro Thr Tyr Asn Ala Val Cys Thr Arg Ile
 115 120 125
 Thr Phe Glu Asn Gln Glu Ile Glu Gly Thr Ile Val Leu Ile Pro Lys
 130 135 140
 Pro Lys Val Ser Leu Pro His Val Ser Glu Ser Val Pro Cys Ile Arg
 145 150 155 160
 Thr Glu Ala Gly Arg Glu Phe Ile Leu Cys Glu Glu Asp Asp Thr Phe
 165 170 175
 Val Ser His Asp Gly Asn Glu Val Thr Ile Gly Gly Lys Pro Phe Leu
 180 185 190
 Leu Asn Thr Asn Val Lys Ile Val Gly Asp Val Ser Gln Lys Tyr Ala

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195                200                205
Val Gly Val Gly Glu Ile Arg Phe Leu Gln Ile Cys Ala Gln Thr Val
210                215                220
Ser Gln Gln Lys
225
<210>      520
<211>      540
<212>      PRT
<213>      Porphyromonas gingivalis
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Met Lys Thr Lys Val Leu Arg Lys Phe Val Val Ala Ala Phe Ala Val
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Ala Thr Leu Cys Pro Leu Ala Gln Ala Gln Thr Met Gly Gly Asp Asp
20          25          30
Val Lys Val Val Gln Tyr Asn Gln Glu Lys Leu Val Gln Thr Arg Met
35          40          45
Ser Val Ala Asp Asn Gly Trp Ile Tyr Val Met Thr His Ser Gly Tyr
50          55          60
Asp Thr Gly Asn Ser Asn Val Lys Ile Phe Arg Ser Lys Asp Gln Gly
65          70          75          80
Ala Thr Tyr Gln Lys Leu Arg Asp Trp Asp Pro Ser Asp Asp Tyr Gln
85          90          95
Phe Gln Asp Phe Asp Ile Val Val Thr Gly Lys Asn Glu Ser Asp Ile
100         105         110
Lys Ile Trp Ser Val Glu Leu Met Asn Lys Pro Gly Gly Tyr Lys Ser
115         120         125
Arg Val Ala Val Phe Ser Arg Asp Ala Asn Ala Gln Asn Ala Lys Leu
130         135         140
Val Tyr Lys Glu Asp Phe Ser Asn Val Gln Leu Tyr Asp Val Asp Ile
145         150         155         160
Ala Ser Asn Tyr Arg Ser Pro Ser Ser Leu Asn Asn Gly Gly Asn Pro
165         170         175
Phe Ala Leu Ala Phe Ala Tyr Thr Gly Phe Asn Asn Thr His Lys Ile
180         185         190
Ser Phe Val Asp Tyr Val Phe Ser Leu Asn Gly Gly Gln Asn Phe Asn
195         200         205
Lys Asn Leu Leu Phe Ser Gln Asp Gly Glu Lys Lys Ile Asp Lys Val
210         215         220
Asp Leu Ser Leu Gly Ser Thr Ser Glu Ser Met Gly His Asn Ala Trp
225         230         235         240
Pro Leu Met Gly Val Val Phe Glu Met Asn Lys Gln Gly Gly Lys Ser
245         250         255
Asp Ile Gly Phe Leu Ser Asn Phe Val Asp Asn Asp Pro Glu Phe Gln
260         265         270
Trp Ser Gly Pro Ile Lys Val Ser Glu Ser Asp Met Ser Phe Ser Pro
275         280         285
Lys Ile Gln Met Leu Leu Asp Glu Asp Asn Asn Thr Ile Asn Gly Glu
290         295         300
Ser Cys His Asn Phe Met Ile Thr Tyr Ser Asp Tyr Asp Ser Glu Tyr
305         310         315         320
Ser Asp Trp Asp Ile Arg Tyr Val Tyr Pro Lys Lys Ser Phe Lys Tyr
325         330         335

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Glu Lys Gly Lys Thr Pro Thr Met Asp Asp Leu Val Glu Ala Phe Leu
 340 345 350
 Thr Ala Ser Tyr Gln Ser Glu Thr Asn Ser Gly Leu Gly Tyr Asp Lys
 355 360 365
 Asn Ala Asn His Tyr Leu Ile Thr Tyr Ala Lys Lys Glu Glu Asn Gly
 370 375 380
 Thr Asn Thr Leu Lys Tyr Arg Trp Ala Asn Tyr Asp Lys Ile His Asn
 385 390 395 400
 Lys Asp Leu Trp Ser Asp Thr Phe Thr Tyr Thr Ser Ser Ala Asn Ala
 405 410 415
 Leu Tyr Thr Pro Gln Val Asp Ile Asn Pro Thr Lys Gly Leu Val Cys
 420 425 430
 Trp Ser Trp Val Glu Tyr Leu Pro Gly Lys Arg Ile Val Trp Ser Asp
 435 440 445
 Thr Gln Trp Thr His Ala Asn Gly Val Glu Asp Ile Val Met Gln Glu
 450 455 460
 Gly Ser Met Lys Leu Tyr Pro Asn Pro Ala Gln Glu Tyr Ala Val Ile
 465 470 475 480
 Ser Leu Pro Thr Ala Ala Asn Cys Lys Ala Val Val Tyr Asp Met Gln
 485 490 495
 Gly Arg Val Val Ala Glu Ala Ser Phe Ser Gly Asn Glu Tyr Arg Leu
 500 505 510
 Asn Val Gln His Leu Ala Lys Gly Thr Tyr Ile Leu Lys Val Val Ser
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 Asp Thr Glu Arg Phe Val Glu Lys Leu Ile Val Glu
 530 535 540
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 Ala Phe Ala Ala Asp Ala Gln Ser Ser Val Ser Ser Gly Arg Arg Leu
 20 25 30
 Thr Glu Tyr Val Asn Pro Phe Ile Gly Thr Ala Asn Tyr Gly Thr Thr
 35 40 45
 Asn Pro Gly Ala Val Leu Pro Asn Gly Leu Met Ser Val Thr Pro Phe
 50 55 60
 Asn Val Ser Gly Ser Thr Glu Asn Arg Phe Asp Lys Asp Ser Arg Trp
 65 70 75 80
 Trp Ser Ala Pro Tyr Ser Ala Asp Asn Ser Tyr Cys Ile Gly Phe Ser
 85 90 95
 His Val Asn Leu Ser Gly Val Gly Cys Pro Glu Leu Ser Gly Ile Leu
 100 105 110
 Leu Met Ala Thr Ser Gly Thr Phe Asp Pro Asp Tyr Cys Cys Tyr Gly
 115 120 125
 Ser Ser Leu Ser Arg Glu Tyr Ala Arg Pro Gly Glu Tyr Lys Ala Val
 130 135 140
 Leu Asp Lys Tyr Gly Ile Asp Ala Ala Val Thr Val Thr Glu Arg Thr
 145 150 155 160
 Ala Leu Thr Glu Phe Ala Phe Pro Glu Gly Glu Gly His Ile Leu Leu

165																170				175							
Asn	Leu	Gly	180			Gln	Ala	Leu	Ser	Asn	185		Glu	Ser	Gly	Ala	Ser	Val	Arg	Phe							
Leu	Asn	Asp	Ser	Thr	Val	Val	Gly	Ser	Arg	Leu	Met	Gly	Thr	Phe	Cys												
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Tyr	Asn	Pro	Gln	Ala	Val	Phe	Arg	Gln	Tyr	Phe	Val	Leu	Gln	Val	Ser												
210																215				220							
Arg	Arg	Pro	Ile	Ser	Ala	Gly	Tyr	Trp	Lys	Lys	Gln	Pro	Pro	Met	Thr												
225																230				235				240			
Val	Glu	Ala	Gln	Trp	Asp	Ser	Thr	Ala	Gly	Lys	Tyr	Lys	Gln	Tyr	Asp												
245																250				255							
Gly	Tyr	Lys	Arg	Glu	Met	Ser	Gly	Asp	Asp	Ile	Gly	Val	Arg	Phe	Ser												
260																265				270							
Phe	Asn	Cys	Asp	Gln	Gly	Glu	Lys	Ile	Tyr	Val	Arg	Ser	Ala	Val	Ser												
275																280				285							
Phe	Val	Ser	Glu	Ala	Asn	Ala	Leu	Tyr	Asn	Leu	Glu	Ala	Glu	Gln	Glu												
290																295				300							
Glu	Val	Phe	Lys	Ser	Val	Gly	Gly	Asn	Pro	Ala	Lys	Ala	Phe	Ser	Ala												
305																310				315				320			
Ile	Arg	Ser	Arg	Ala	Ile	Glu	Arg	Trp	Glu	Glu	Ala	Leu	Gly	Thr	Val												
325																330				335							
Glu	Val	Glu	Gly	Gly	Thr	Pro	Asp	Glu	Lys	Thr	Ile	Phe	Tyr	Thr	Ala												
340																345				350							
Leu	Tyr	His	Leu	Leu	Ile	His	Pro	Asn	Ile	Leu	Gln	Asp	Ala	Asn	Gly												
355																360				365							
Glu	Tyr	Pro	Met	Met	Gly	Ser	Gly	Lys	Thr	Gly	Asn	Thr	Ala	His	Asp												
370																375				380							
Arg	Tyr	Thr	Val	Phe	Ser	Leu	Trp	Asp	Thr	Tyr	Arg	Asn	Val	His	Pro												
385																390				395				400			
Leu	Leu	Cys	Leu	Leu	Tyr	Pro	Glu	Lys	Gln	Leu	Asp	Met	Val	Arg	Thr												
405																410				415							
Leu	Ile	Asp	Met	Tyr	Arg	Glu	Ser	Gly	Trp	Leu	Pro	Arg	Trp	Glu	Leu												
420																425				430							
Tyr	Gly	Gln	Glu	Thr	Leu	Thr	Met	Glu	Gly	Asp	Pro	Ser	Leu	Ile	Val												
435																440				445							
Ile	Asn	Asp	Thr	Trp	Gln	Arg	Gly	Leu	Arg	Ala	Phe	Asp	Thr	Ala	Thr												
450																455				460							
Ala	Tyr	Glu	Ala	Met	Lys	Lys	Asn	Ala	Ser	Ser	Ala	Gly	Ala	Thr	His												
465																470				475				480			
Pro	Ile	Arg	Pro	Asp	Asn	Asp	Asp	Tyr	Leu	Thr	Leu	Gly	Phe	Val	Pro												
485																490				495							
Leu	Arg	Glu	Gln	Tyr	Asp	Asn	Ser	Val	Ser	His	Ala	Leu	Glu	Tyr	Tyr												
500																505				510							
Leu	Ala	Asp	Trp	Asn	Leu	Ser	Arg	Phe	Ala	His	Ala	Leu	Gly	His	Lys												
515																520				525							
Glu	Asp	Ala	Ala	Leu	Phe	Gly	Lys	Arg	Ser	Leu	Gly	Tyr	Arg	His	Tyr												
530																535				540							
Tyr	Asn	Lys	Glu	Tyr	Gly	Met	Leu	Cys	Pro	Leu	Leu	Pro	Asp	Gly	Ser												
545																550				555				560			
Phe	Leu	Thr	Pro	Phe	Asp	Pro	Lys	Gln	Gly	Glu	Asn	Phe	Glu	Pro	Asn												
565																570				575							
Pro	Gly	Phe	His	Glu	Gly	Ser	Ala	Tyr	Asn	Tyr	Ala	Phe	Phe	Val	Pro												

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                    580                      585                      590
His Asp Ile Gln Gly Leu Ala Arg Leu Met Gly Gly Ala Lys Val Phe
    595                      600                      605
Ser Glu Arg Leu Gln Lys Val Phe Asp Glu Gly Tyr Tyr Asp Pro Thr
    610                      615                      620
Asn Glu Pro Asp Ile Ala Tyr Pro Tyr Leu Phe Ser Tyr Phe Pro Lys
    625                      630                      635                      640
Glu Ala Trp Arg Thr Gln Lys Leu Thr Arg Glu Leu Ile Asp Lys His
    645                      650                      655
Phe Cys Asn Ala Pro Asn Gly Leu Pro Gly Asn Asp Asp Ala Gly Thr
    660                      665                      670
Met Ser Ala Trp Leu Val Tyr Ser Met Leu Gly Phe Tyr Pro Asp Cys
    675                      680                      685
Pro Gly Ser Pro Thr Tyr Thr Leu Thr Ser Pro Val Phe Pro Arg Val
    690                      695                      700
Arg Ile Arg Leu Asn Pro Gln Tyr Tyr Pro Gln Gly Glu Leu Ile Ile
    705                      710                      715                      720
Thr Thr Asn Thr Glu Asn Gln Pro Thr Asp Ser Ile Tyr Ile His Thr
    725                      730                      735
Val Ser Leu Gly Asn Lys Thr Leu Pro His Gly Thr Arg His Ile Ser
    740                      745                      750
His Ala Asp Leu Val Arg Cys Gly His Leu Arg Tyr Glu Leu Ser Asn
    755                      760                      765
Arg Pro Arg
    770
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<212>      PRT
<213>      Porphyromonas gingivalis
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Leu Phe Thr Ser Phe Ser Leu Gln Ala Gln Glu Glu Gly Ile Trp Asn
    20                      25                      30
Thr Leu Leu Ala Ile His Lys Thr Glu Lys Ala Val Glu Thr Pro Lys
    35                      40                      45
Lys Val Phe Ala Val Ala Asn Gly Val Leu Tyr Ser Val Gly Lys Glu
    50                      55                      60
Ala Pro His Glu Ala Lys Ile Phe Asp Arg Ile Ser Gly Leu Ser Asp
    65                      70                      75                      80
Thr Ser Val Ser Ser Ile Ala Tyr Ser Glu Gln Leu Lys Ser Leu Val
    85                      90                      95
Ile Tyr Tyr Ala Ser Gly Asn Ile Asp Ile Leu Asp Glu Ala Gly Arg
    100                      105                      110
Val Thr Asn Val Pro Ala Leu Lys Asp Asn Ile Asp Leu Ile Asp Lys
    115                      120                      125
Thr Leu Asn Arg Leu Leu Ile Val Gly Asn Arg Ala Tyr Leu Ala Gly
    130                      135                      140
Gly Phe Gly Leu Ser Val Leu Asp Val Ala Glu Ala Arg Ile Pro Ala
    145                      150                      155                      160
Thr Tyr Ala Lys Gly Thr Lys Val Thr Asp Val Ala Lys Leu Asp Asn
    165                      170                      175

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

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Gly Gly Glu Glu Pro Asn Leu Tyr Tyr Val Leu Asp Lys Val Thr Val
595 600 605
Thr Asp Ile Val Val Asp Lys Leu Asn His Lys Trp Val Ala Thr Gln
610 615 620
Gly Thr Gly Leu Tyr Leu Leu Ser Glu Asp Cys Ser Lys Ile Leu Ala
625 630 635 640
Gln Phe Thr Val Glu Asn Ser Pro Leu Leu Ser Asn Asn Ile Leu Ser
645 650 655
Leu Ala Leu Asn Asp Asp Asn Gly Leu Leu Tyr Ile Gly Thr Ala Asp
660 665 670
Gly Leu Met Thr Phe Gln Thr Gly Thr Gly Ser Gly Ser Ala Ser Glu
675 680 685
Leu Asp Gly Val Tyr Val Tyr Pro Asn Pro Leu Arg Pro Glu Tyr Pro
690 695 700
Asp Gly Val Thr Ile Ala Gly Leu Gln Ala Gly Cys Ser Val Lys Ile
705 710 715 720
Thr Asp Thr Thr Gly Arg Leu Leu Tyr Gln Thr Glu Ser Val Thr Thr
725 730 735
Glu Val Lys Trp Asn Ala Arg Gly Ala Asp Gly Asn Arg Val Ala Ser
740 745 750
Gly Val Tyr Ala Val Ala Val Tyr Asp Pro Val Ser Lys Lys Ser Lys
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Leu Ile Arg Phe Ala Val Ile Arg
770 775
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Leu Ala Leu Pro Ala Lys Ala Gln Arg Ala Met Gly Lys Thr Ala Asp
20 25 30
Arg Ser Leu Met Ala Ser Gly His Trp Val Lys Ile Arg Val Asp Ala
35 40 45
Ser Gly Val Tyr Arg Leu Thr Asp Glu Gln Leu Arg Ala Asn Gly Phe
50 55 60
Ser Asp Pro Ser Lys Val Gly Val Phe Gly Tyr Gly Gly Gly Val Leu
65 70 75 80
Pro Glu Asp Leu Ser Arg Ile Thr Thr Asp Asp Leu Pro Pro Val Pro
85 90 95
Val Leu Arg Gln Gly Asn Ala Leu Tyr Phe Tyr Ala Val Gly Pro Val
100 105 110
Thr Trp Phe Tyr Asn Pro Ala Lys Thr Thr Met Glu His Thr Val Asn
115 120 125
Thr Tyr Ser Thr His Gly Tyr Tyr Phe Leu Ser Asp Ala Ala Gly Ala
130 135 140
Pro Leu Gln Met Ser Gln Tyr Thr Gly Gly Gly Ala Ser Ala Glu Ala
145 150 155 160
Leu Ile Asp Tyr Tyr Asp Glu Leu Met Leu His Glu Gln Glu Leu Tyr
165 170 175
Ser Pro Lys Glu Ser Gly Arg Asp Leu Tyr Gly Glu Ser Phe Ser Ala

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

595	600	605
Tyr Ala Pro Ala Ile Met Pro Val Arg Ala Phe Gln Asp Val Tyr Pro		
610	615	620
His Val Ile Glu Asn Gly Leu His Ser Ile Pro Gly Ala Lys Lys Lys		
625	630	635
Met Leu Glu Thr Leu Gln Ser Gly Ile Ile Leu Leu Asn Tyr Ala Gly		
645	650	655
His Gly Gly Pro Ala Gly Trp Ser Asp Glu His Leu Leu Thr Leu Asn		
660	665	670
Asp Ile His Lys Phe Asn Tyr Lys His Met Pro Ile Trp Ile Thr Ala		
675	680	685
Thr Cys Asp Phe Ala Asn Tyr Asp Ser Gln Thr Thr Ser Ala Gly Glu		
690	695	700
Glu Val Phe Leu His Glu Lys Ser Gly Thr Pro Ile Met Phe Ser Thr		
705	710	715
Thr Arg Val Val Tyr Asn Thr Gln Asn Glu Lys Ile Asn Gly Phe Met		
725	730	735
Leu Arg Arg Met Phe Glu Lys Ala Lys Asp Gly Arg Tyr Arg Thr Met		
740	745	750
Gly Glu Ile Ile Arg Ser Ala Lys Gln Gly Met Leu Ser Thr Val Phe		
755	760	765
Pro Asp Ser Ile Asn Gln Leu Ser Phe Phe Leu Met Gly Asp Pro Ser		
770	775	780
Val Arg Met Asn Leu Pro Thr His Lys Val Gln Leu Thr Ala Ile Asn		
785	790	795
Gly Gln Asp Pro Glu Gly Gln Tyr Gly Thr Ile Met Leu Lys Ser Leu		
805	810	815
Glu Arg Val Ala Leu Lys Gly Lys Val Thr Asp Glu Lys Gly Thr Phe		
820	825	830
Asp Glu Thr Phe Ser Gly Lys Val Phe Leu Thr Val Phe Asp Gly Arg		
835	840	845
Lys Lys Met Thr Ala Leu Glu Glu Gly Asn Asp Leu Ser Leu Val		
850	855	860
Tyr Tyr Asp Tyr Pro Asn Val Met Tyr Ala Gly Ile Ala Glu Val Lys		
865	870	875
Asp Gly Leu Phe Glu Thr Ser Phe Ile Val Pro Lys Asp Val Asn Tyr		
885	890	895
Ser Glu His Glu Gly Arg Ile Asn Leu Tyr Ala Tyr Asn Glu Ser Thr		
900	905	910
Lys Ala Glu Ala Met Gly Val Asp Phe Ser Ile Arg Val Gln Pro Gly		
915	920	925
Ile Pro Asp Glu Val Thr Glu Asp Asn Thr Pro Pro Glu Ile Ile Ser		
930	935	940
Cys Phe Leu Asn Asp Ser Thr Phe Arg Ser Gly Asp Glu Val Asn Pro		
945	950	955
Thr Pro Leu Phe Met Ala Glu Val Phe Asp Leu Asn Gly Ile Asn Ile		
965	970	975
Thr Gly Ser Gly Val Gly His Asp Ile Thr Leu Cys Ile Asp Gly Arg		
980	985	990
Ala Asp Leu Thr Tyr Asn Leu Asn Ala Tyr Phe Thr Ser Ser Ala Thr		
995	1000	1005
Asp Ala Gly Val Gly Thr Ile Leu Phe Met Ile Pro Ala Leu Ala Glu		

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1010          1015          1020
Gly Asp His Thr Ala Arg Leu Thr Val Trp Asp Ile Phe Asn Asn Ala
1025          1030          1035          1040
Val His His Asp Phe Ser Phe Arg Val Val Asp Gly Ile Ala Pro Asp
          1045          1050          1055
Val Ala Asp Val Ile Leu Phe Pro Asn Pro Val Arg Glu Ser Ala Thr
          1060          1065          1070
Phe Arg Ile Phe His Asn Arg Pro Gly Ser Asp Leu Asn Val Ala Val
          1075          1080          1085
Glu Ile Tyr Asp Phe Thr Gly Arg Leu Val Asn Ser Leu Pro Val Lys
          1090          1095          1100
Thr Tyr Ser Ser Ser Tyr Gly Glu Pro Ile Glu Ile Lys Trp Asp Leu
1105          1110          1115          1120
Thr Ser Lys Tyr Gly Val Lys Ile Gly Asn Gly Phe Tyr Leu Tyr Arg
          1125          1130          1135
Cys Val Val Asn Ser Pro Gly Gly Gln Thr Ala Ser Met Ala Lys Lys
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Met Ile Val Val Gly Gln
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Lys Lys Arg Ile Thr Ala Leu Leu Tyr Glu Lys Glu Leu Pro Thr Asp
          35          40          45
Ser Val Lys Gln Leu Tyr Glu Asn Ser Val Gln Asn Lys Asn Leu Val
          50          55          60
Gly Gln Met Leu Phe Ala Ile Glu Val Gly Lys Arg Met Arg Asn Met
  65          70          75          80
Ser Gln Tyr Thr Asp Ala Met Leu Tyr His Gln Lys Gly Leu Asn Ala
          85          90          95
Ala Leu Asn Leu Arg Asp Thr Ile Val Ala Ala Gln Ala Trp Asn His
          100          105          110
Leu Gly Thr Asp Ser Arg Arg Ile Gly Ala Leu Ala Glu Ala Ser Asp
          115          120          125
Tyr His Tyr Lys Ala Leu Ser Leu Ile Glu Ser Phe Ser Gly Asn Gln
          130          135          140
Asn Arg Pro Ala Ile Lys Ala Arg Ser Ala Ala Leu Asn Gly Ile Gly
  145          150          155          160
Asn Ile Asn Leu Glu Leu Gly Tyr His Asp Glu Ala Glu Lys Asn Phe
          165          170          175
Leu Lys Ala Leu Gln Gly Glu Lys Glu Leu Asp Ser Pro Leu Gly Gln
          180          185          190
Ala Ile Asn Tyr Ala Asn Leu Gly Arg Ile Tyr Arg Gln Arg Lys Glu
          195          200          205
Tyr Asp Lys Ala Arg Thr Tyr Phe Leu Leu Ser Leu Glu Gln Asn Asn
  210          215          220

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Met Ala Glu Asn Leu Met Gly Ile Gly Leu Cys Ser Ile Asn Leu Gly
225                230                235                240
Glu Val Asp Glu Glu Lys Gly Asp Tyr Gln Lys Ala Leu Gln Glu Tyr
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Ala Thr Ala Tyr Lys Leu Met Glu Gln Leu Ser Asp Arg Trp His Trp
                260                265                270
Leu Asn Ser Cys Ile Pro Met Ala Arg Ile Asn Leu Lys Gln Gly Asn
                275                280                285
Glu Arg Leu Tyr Gln His Phe Ile Ser Leu Ala Glu Gly Thr Ala Lys
                290                295                300
Glu Ile Asn Ser Thr Ser His Leu Ile Glu Ile Tyr Asn Leu Gln Tyr
305                310                315                320
Glu Asn Leu Glu Arg Lys Lys Glu Tyr Lys Gln Ala Leu Glu Ala Phe
                325                330                335
Cys Leu Ser Lys Thr Leu Ser Asp Ser Met Ser Ile Ala His Lys Val
                340                345                350
Ser Ser Ile Gln Glu Thr Arg Phe Asn Tyr Glu Arg Asn Lys Ser Gln
                355                360                365
Lys Glu Leu Glu Glu Ile Gln Gln Val Ser Lys Ala Lys Gln Glu Lys
                370                375                380
Ser Lys Phe Ile Leu Leu Ser Thr Leu Phe Ala Leu Phe Ile Ser Ile
385                390                395                400
Leu Leu Ile Ser Val Leu Thr Tyr Ala Tyr Arg Gln Gly Lys Lys His
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Asn Lys Leu Ile Lys Glu Thr Asp Lys Leu Arg Ser Gly Phe Phe Thr
                420                425                430
Gly Ile Thr His Glu Phe Arg Thr Pro Ile Thr Val Ile Gln Gly Leu
                435                440                445
Asn Glu Lys Met Ser Ser Ser Pro Asp Leu Gln Ala Ser Asp Arg Thr
                450                455                460
Glu Leu His Lys Ile Ile Asp Arg Gln Ser Ser His Met Leu Asn Leu
465                470                475                480
Val Asn Gln Leu Leu Asp Ile Cys Lys Ile Arg Ser Gly Val Ser Thr
                485                490                495
Pro Glu Trp Arg Asn Gly Asp Ile Val Ser Phe Val Gln Ile Leu Ile
                500                505                510
Asp Ser Phe Ala Pro Tyr Ala Gln Ala Gln Asp Ile Thr Leu Glu Leu
                515                520                525
Gln Pro Glu Ser Lys Pro Ile Val Val Asp Phe Val Pro Ser Tyr Leu
530                535                540
Gln Lys Ile Ile Ser Asn Leu Leu Ser Asn Ala Ile Lys Tyr Ser Leu
545                550                555                560
Ala Gly Gly Arg Val Val Ile Ser Leu Ala Lys Thr Lys Asn Glu Lys
                565                570                575
Asn Leu Ile Ile Arg Val Ala Asp Asn Gly Ile Gly Ile Asp Lys Thr
                580                585                590
Asp Gln Ala His Ile Phe Asp Ile Phe Tyr Arg Gly Gln Ser Ala Thr
                595                600                605
Glu Lys His Gly Ser Gly Val Gly Leu Ser Phe Thr Asn Ile Leu Val
                610                615                620
Glu Asn Leu Arg Gly Thr Ile Lys Val Glu Ser Gln Pro Gly Lys Gly
625                630                635                640

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Ser Ala Phe Thr Ile Ser Ile Pro Thr Gln Asn Gln Ser Ser Ser Ala
645 650 655
Glu Ile Leu Pro Trp Leu Pro Ser Ser Asp Asp Ile Val Met Pro Val
660 665 670
His Ile Ala Pro Asp Asp Ser Pro Thr Ser Pro Met Val Ala Ala Leu
675 680 685
Asn His Arg Phe Glu Asp Glu Arg Pro Thr Ile Leu Val Glu Asp
690 695 700
Asn Lys Asp Ile Asn Leu Leu Val Lys Leu Leu Leu Cys Asp Arg Tyr
705 710 715 720
Asn Val Leu Ser Ala Ala Asn Gly Lys Glu Gly Ile Ala Leu Ala Thr
725 730 735
Glu His Ile Pro Asp Ile Ile Ile Thr Asp Ile Met Met Pro Ile Met
740 745 750
Asp Gly Ile Glu Met Thr Ile Arg Met Lys Gln Ser Pro Leu Leu Cys
755 760 765
His Ile Pro Ile Val Ala Leu Thr Ala Lys Ser Thr Glu Gln Asp Arg
770 775 780
Leu Glu Gly Ile Lys Ser Gly Val Val Ser Tyr Leu Cys Lys Pro Phe
785 790 795 800
Ser Pro Glu Glu Leu Leu Met Arg Ile Glu Gln Leu Leu Lys Asp Arg
805 810 815
Glu Leu Leu Lys Phe Tyr Met Gln Lys Leu Met Leu Asp Arg Lys
820 825 830
Pro Glu Glu Glu Pro Gln Pro Ile Asp Asp Ser Ser Met Gln Phe Leu
835 840 845
Leu Ala Ala Lys Asp Ala Val Ser Gly Gly Ile Lys Gln Asn Pro Asp
850 855 860
Phe Ser Ala Gln Asp Leu Ala Glu Lys Met Cys Met Ser Pro Ser Gln
865 870 875 880
Leu Asn Arg Lys Leu Thr Ser Val Val Gly Cys Ser Thr Ile Gly Tyr
885 890 895
Ile Gln Gln Ile Lys Ile Lys Leu Ala Cys Lys Leu Leu Ala Asp Glu
900 905 910
Ser Lys Asn Ile Ser Asp Ile Ser Ile Glu Ala Gly Phe Ser Asp Pro
915 920 925
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Gln Tyr Arg Gln Lys Leu Leu Ala Met Pro Gly Ser Asp Lys Glu Thr
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Asn Gly Gln Phe Ala Thr Glu Glu Met Gln Arg Ala Phe Gln Glu Thr
35 40 45

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

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Glu Thr Asn Thr Cys Thr Val Thr Gly Ala Ala Lys Ala Leu Arg Ala
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 Trp Phe Asn Ala Gly Arg Ser Glu Leu Ala Val Ser Val Ser Leu Asn
 485 490 495
 Ile Ala Gly Thr Tyr Arg Ile Lys Leu Tyr Asn Thr Ala Gly Glu Glu
 500 505 510
 Val Ala Ala Met Thr Lys Glu Leu Val Ala Gly Thr Ser Val Phe Ser
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 35 40 45
 Leu Leu Val His Ser Ile Glu Lys Lys Gly Ile Trp Ile Asp Leu Asn
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 Gly Asp Ala Thr Tyr Gln Gln Gly Glu Glu Ile Thr Val Phe Asp Glu
 65 70 75 80
 Ala Tyr His Glu Tyr Thr Ile Gly Thr Gln Thr Leu Thr Ile Tyr Gly
 85 90 95
 Asn Thr Thr Arg Leu Gly Cys Arg Ser Thr Gly Ala Thr Ala Val Asp
 100 105 110
 Val Thr Lys Asn Pro Asn Leu Thr Tyr Leu Ala Cys Pro Lys Asn Asn
 115 120 125
 Leu Lys Ser Leu Asp Leu Thr Gln Asn Pro Lys Leu Leu Arg Val Trp
 130 135 140
 Cys Asp Ser Asn Glu Ile Glu Ser Leu Asp Leu Ser Gly Asn Pro Ala
 145 150 155 160
 Leu Ile Ile Leu Gly Cys Asp Arg Asn Lys Leu Thr Glu Leu Lys Thr
 165 170 175
 Asp Asn Asn Pro Lys Leu Ala Ser Leu Trp Cys Ser Asp Asn Asn Leu
 180 185 190
 Thr Glu Leu Glu Leu Ser Ala Asn Pro Arg Leu Asn Asp Leu Trp Cys
 195 200 205
 Phe Gly Asn Arg Ile Thr Lys Leu Asp Leu Ser Ala Asn Pro Leu Leu
 210 215 220
 Val Thr Leu Trp Cys Ser Asp Asn Glu Leu Ser Thr Leu Asp Leu Ser
 225 230 235 240
 Lys Asn Ser Asp Val Ala Tyr Leu Trp Cys Ser Ser Asn Lys Leu Thr
 245 250 255
 Ser Leu Asn Leu Ser Gly Val Lys Gly Leu Ser Val Leu Val Cys His
 260 265 270
 Ser Asn Gln Ile Ala Gly Glu Glu Met Thr Lys Val Val Asn Ala Leu


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

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

275	280	285
Met Tyr Gly Phe Asn Ala Lys Arg Leu Lys Glu Thr Tyr Ser Ser Tyr		
290	295	300
Glu Gly Asp Val Ala Thr Pro Ile Phe Asp Tyr Ile Tyr Thr Tyr Lys		
305	310	315
Ala Leu Thr Ser Met Ala Thr Pro Ser Thr Glu Ala Gln Val Ala Val		
325	330	335
Tyr Leu Asn Pro Ser Thr Asp Arg Leu Val Ile Leu Ala Asn Gly Ile		
340	345	350
Thr His Leu Ser Met Tyr Asp Leu Gln Gly Lys Leu Ile Arg Asp Cys		
355	360	365
Ala Leu Ser Gly Asp Lys Val Glu Met Gly Val Gly Ser Leu Thr Lys		
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Lys Val Val Ile Arg		400
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Pro Glu Ala Ile Arg Gln Leu Val Gln Gly Ile Asn Glu Gly Met Pro
    20               25               30

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Ala	Asn	Val	Val	Ala	Ala	Val	Asn	Arg	Pro	Thr	Leu	Val	Leu	Ser	His
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Asn	Lys	Thr	Leu	Ala	Ala	Gln	Leu	Tyr	Gly	Glu	Phe	Lys	Ala	Phe	Phe
65						70						80			
Pro	Glu	Asn	Ala	Val	Glu	Tyr	Phe	Val	Ser	Tyr	Tyr	Asp	Tyr	Tyr	Gln
			85						90			95			
Pro	Glu	Ala	Tyr	Leu	Pro	Val	Thr	Asp	Thr	Tyr	Ile	Glu	Lys	Asp	Met
100						105						110			
Ala	Ile	Asn	Ala	Glu	Ile	Glu	Lys	Leu	Arg	Leu	Arg	Ala	Thr	Ala	Ser
115						120						125			
Leu	Leu	Ser	Gly	Arg	Lys	Asp	Val	Leu	Val	Val	Ser	Ser	Val	Ser	Cys
130						135						140			
Leu	Tyr	Gly	Met	Ala	Asn	Pro	Glu	Ala	Phe	Ser	Glu	Lys	Val	Ile	Ser
145			150						155			160			
Leu	His	Thr	Gly	Gln	Arg	Ala	Asp	Arg	Asp	His	Phe	Ile	Arg	Leu	Leu
			165						170			175			
Val	Glu	Ser	Tyr	Tyr	Thr	Asn	Asn	Lys	Val	Glu	Phe	Glu	Ser	Gly	Asn
180						185						190			
Phe	Arg	Val	Lys	Gly	Asp	Ser	Val	Asp	Ile	Phe	Pro	Ala	Val	Glu	Gly
195						200						205			
Tyr	Asp	Gly	Val	Ala	Tyr	Arg	Val	Glu	Phe	Trp	Asp	Gly	Glu	Val	Glu
210						215						220			
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225			230						235			240			
Ser	Glu	Leu	Lys	Ile	Tyr	Pro	Ala	Asn	Leu	Phe	Val	Thr	Thr	Lys	Glu
			245						250			255			
Gln	Val	Asp	Arg	Ala	Val	Gly	Lys	Ile	Asp	Val	Asp	Leu	Gly	Ala	Gln
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Tyr	Glu	Arg	Val	Thr	Tyr	Asp	Leu	Glu	Met	Ile	Arg	Glu	Leu	Gly	Tyr
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Cys	Ser	Gly	Ile	Glu	Asn	Tyr	Ser	Arg	Tyr	Phe	Asp	Gly	Arg	Asp	Ala
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Leu	Val	Ile	Asp	Glu	Ser	His	Val	Thr	Ile	Pro	Gln	Ile	Arg	Ala	Met
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Tyr	Gly	Gly	Asp	Arg	Ser	Arg	Lys	Glu	Asn	Leu	Val	Glu	Tyr	Gly	Phe
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Arg	Leu	Pro	Ala	Ala	Leu	Asp	Asn	Arg	Pro	Leu	Arg	Phe	Asp	Glu	Phe
370						375						380			
Glu	Ala	Leu	Thr	Pro	Arg	Thr	Leu	Tyr	Ile	Ser	Ala	Thr	Pro	Ala	Asp
385			390						395			400			
Tyr	Glu	Leu	Asn	Arg	Ser	Glu	Gly	Val	Ile	Val	Glu	Gln	Leu	Ile	Arg
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Pro	Thr	Gly	Leu	Leu	Asp	Pro	Ile	Ile	Asp	Val	Lys	Pro	Thr	Ala	Asn
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Gln	Val	Asp	Asp	Leu	Met	Glu	Glu	Ile	Ala	Arg	Cys	Ile	Glu	Lys	Lys
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Glu Arg Val Leu Val Thr Thr Leu Thr Lys Arg Met Ala Glu Glu Leu
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 Ser Glu Tyr Leu Leu Arg His Gly Ile Ser Thr Gly Tyr Ile His Ser
 465 470 475 480
 Asp Val Asp Thr Leu Glu Arg Val Arg Ile Met Glu Asp Leu Arg Lys
 485 490 495
 Gly Val Tyr Asp Ala Leu Ile Gly Val Asn Leu Leu Arg Glu Gly Leu
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 Asp Leu Pro Glu Val Ser Leu Val Ala Ile Leu Asp Ala Asp Lys Glu
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 Gly Phe Leu Arg Ser His Arg Ser Leu Thr Gln Thr Ala Gly Arg Ala
 530 535 540
 Ala Arg His Ile His Gly Arg Val Ile Phe Tyr Ala Asp Lys Ile Thr
 545 550 555 560
 Asp Ser Met Gln Leu Thr Met Asp Glu Thr Ala Arg Arg Arg Ala Lys
 565 570 575
 Gln Leu Ala Tyr Asn Glu Ala His Gly Ile Thr Pro Gln Gln Ile Val
 580 585 590
 Lys Asn Ser Ala Ala Ile Trp Gly Glu Gly Asp Val Ser Ala Leu Gln
 595 600 605
 Ser Asp Thr Glu Ser Gly Ala Tyr Ile Glu Glu Ser Ser Met Val Ala
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 Ala Asp Pro Leu Ala Asp Tyr Leu Ser Lys Pro Lys Leu Glu Ala Leu
 625 630 635 640
 Ile Ala Ser Thr Lys Lys Gln Met Leu Ala Ala Ala Lys Glu Leu Asp
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 Phe Leu Glu Ala Ala Arg Leu Arg Asp Glu Ala Ala Arg Leu Glu Lys
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 35 40 45
 Asn Val Val Ala Ala Val Asn Arg Pro Thr Leu Val Leu Ser His Asn
 50 55 60
 Lys Thr Leu Ala Ala Gln Leu Tyr Gly Glu Phe Lys Ala Phe Phe Pro
 65 70 75 80
 Glu Asn Ala Val Glu Tyr Phe Val Ser Tyr Tyr Asp Tyr Tyr Gln Pro
 85 90 95
 Glu Ala Tyr Leu Pro Val Thr Asp Thr Tyr Ile Glu Lys Asp Met Ala
 100 105 110
 Ile Asn Ala Glu Ile Glu Lys Leu Arg Leu Arg Ala Thr Ala Ser Leu
 115 120 125
 Leu Ser Gly Arg Lys Asp Val Leu Val Val Ser Ser Val Ser Cys Leu

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

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Ser Met Gln Leu Thr Met Asp Glu Thr Ala Arg Arg Arg Ala Lys Gln
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                595                600                605
Asp Thr Glu Ser Gly Ala Tyr Ile Glu Glu Ser Ser Met Val Ala Ala
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Asp Pro Leu Ala Asp Tyr Leu Ser Lys Pro Lys Leu Glu Ala Leu Ile
                625                630                635                640
Ala Ser Thr Lys Lys Gln Met Leu Ala Ala Ala Lys Glu Leu Asp Phe
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Leu Glu Ala Ala Arg Leu Arg Asp Glu Ala Ala Arg Leu Glu Lys Lys
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Leu Glu Gln Leu Thr Ala
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