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(54)【発明の名称】歯周疾患の診断、治療、およびモニタリングのためのアクチノバチルス・アクチノミセテムコミタンス抗原の同定

(57)【要約】
アクチノバチルス・アクチノミセテムコミタンスに起因する疾病の検出、予防、改善、および治療のための、抗体、ポリペプチド、およびポリヌクレオチドが提供される。

【特許請求の範囲】

【請求項１】

以下からなる群から選択されるアミノ酸配列の少なくとも５個の連続するアミノ酸を含有する精製免疫原性ポリペプチド：配列番号2、配列番号4、配列番号6、配列番号8、配列番号10、配列番号12、配列番号14、配列番号16、配列番号18、配列番号20、配列番号22、配列番号24、配列番号26、配列番号28、配列番号30、配列番号32、配列番号34、配列番号36、配列番号38、配列番号40、配列番号42、配列番号44、配列番号46、配列番号48、配列番号50、配列番号52、配列番号54、配列番号56、配列番号58、配列番号60、配列番号62、配列番号64、配列番号66、配列番号68、配列番号70、配列番号72、配列番号74、配列番号76、配列番号78、配列番号80、配列番号82、配列番号84、配列番号86、配列番号88、配列番号90、配列番号92、配列番号94、配列番号96、配列番号98、配列番号100、配列番号102、配列番号103、配列番号104、配列番号105、配列番号107、配列番号109、配列番号110、配列番号111、配列番号112、配列番号113、配列番号114、配列番号116、配列番号118、配列番号120、配列番号122、配列番号124、配列番号126、配列番号128、配列番号130、配列番号132、配列番号134、配列番号136、配列番号138、配列番号140、配列番号142、配列番号144、配列番号146、配列番号148、配列番号150、配列番号152、配列番号154、配列番号156、配列番号158、配列番号160、配列番号162、配列番号164、配列番号166、配列番号168、配列番号170、配列番号172、配列番号174、配列番号176、配列番号178、配列番号180、配列番号182、配列番号184、配列番号186、配列番号188、配列番号190、配列番号192、配列番号194、配列番号196、配列番号198、配列番号200、配列番号202、配列番号204、配列番号206、配列番号208、配列番号210、配列番号212、配列番号214、配列番号216、配列番号218、配列番号220、配列番号222、および配列番号224。

【請求項２】

以下からなる群から選択されるアミノ酸配列を含有する精製ポリペプチド：配列番号2、配列番号4、配列番号6、配列番号8、配列番号10、配列番号12、配列番号14、配列番号16、配列番号18、配列番号20、配列番号22、配列番号24、配列番号26、配列番号28、配列番号30、配列番号32、配列番号34、配列番号36、配列番号38、配列番号40、配列番号42、配列番号44、配列番号46、配列番号48、配列番号50、配列番号52、配列番号54、配列番号56、配列番号58、配列番号60、配列番号62、配列番号64、配列番号66、配列番号68、配列番号70、配列番号72、配列番号74、配列番号76、配列番号78、配列番号80、配列番号82、配列番号84、配列番号86、配列番号88、配列番号90、配列番号92、配列番号94、配列番号96、配列番号98、配列番号100、配列番号102、配列番号103、配列番号104、配列番号105、配列番号107、配列番号109、配列番号110、配列番号111、配列番号112、配列番号113、配列番号114、配列番号116、配列番号118、配列番号120、配列番号122、配列番号124、配列番号126、配列番号128、配列番号130、配列番号132、配列番号134、配列番号136、配列番号138、配列番号140、配列番号142、配列番号144、配列番号146、配列番号148、配列番号150、配列番号152、配列番号154、配列番号156、配列番号158、配列番号160、配列番号162、配列番号164、配列番号166、配列番号168、配列番号170、配列番号172、配列番号174、配列番号176、配列番号178、配列番号180、配列番号182、配列番号184、配列番号186、配列番号188、配列番号190、配列番号192、配列番号194、配列番号196、配列番号198、配列番号200、配列番号202、配列番号204、配列番号206、配列番号208、配列番号210、配列番号212、配列番号214、配列番号216、配列番号218、配列番号220、配列番号222、および配列番号224。

【請求項３】

請求項１記載のポリペプチドをコードする配列を含有する精製ポリヌクレオチド。

【請求項４】

以下からなる群から選択される配列の少なくとも約１５個の連続した核酸を含有する精製ポリヌクレオチド、またはその縮重変異体：配列番号1、配列番号3、配列番号5、配列番号7、配列番号9、配列番号11、配列番号13、配列番号15、配列番号17、配列番号19、配列番号21、配列番号23、配列番号25、配列番号27、配列番号29、配列番号31、配列番号33

、配列番号35、配列番号37、配列番号39、配列番号41、配列番号43、配列番号45、配列番号47、配列番号49、配列番号51、配列番号53、配列番号55、配列番号57、配列番号59、配列番号61、配列番号63、配列番号65、配列番号67、配列番号69、配列番号71、配列番号73、配列番号75、配列番号77、配列番号79、配列番号81、配列番号83、配列番号85、配列番号87、配列番号89、配列番号91、配列番号93、配列番号95、配列番号97、配列番号99、配列番号101、配列番号106、配列番号108、配列番号115、配列番号117、配列番号119、配列番号121、配列番号123、配列番号125、配列番号127、配列番号129、配列番号131、配列番号133、配列番号135、配列番号137、配列番号139、配列番号141、配列番号143、配列番号145、配列番号147、配列番号149、配列番号151、配列番号153、配列番号155、配列番号157、配列番号159、配列番号161、配列番号163、配列番号165、配列番号167、配列番号169、配列番号171、配列番号173、配列番号175、配列番号177、配列番号179、配列番号181、配列番号183、配列番号185、配列番号187、配列番号189、配列番号191、配列番号193、配列番号195、配列番号197、配列番号199、配列番号201、配列番号203、配列番号205、配列番号207、配列番号209、配列番号211、配列番号213、配列番号215、配列番号217、配列番号219、配列番号221、および配列番号223。

【請求項５】

以下のヌクレオチド配列を含有する精製ポリヌクレオチド、またはその縮重変異体：配列番号1、配列番号3、配列番号5、配列番号7、配列番号9、配列番号11、配列番号13、配列番号15、配列番号17、配列番号19、配列番号21、配列番号23、配列番号25、配列番号27、配列番号29、配列番号31、配列番号33、配列番号35、配列番号37、配列番号39、配列番号41、配列番号43、配列番号45、配列番号47、配列番号49、配列番号51、配列番号53、配列番号55、配列番号57、配列番号59、配列番号61、配列番号63、配列番号65、配列番号67、配列番号69、配列番号71、配列番号73、配列番号75、配列番号77、配列番号79、配列番号81、配列番号83、配列番号85、配列番号87、配列番号89、配列番号91、配列番号93、配列番号95、配列番号97、配列番号99、配列番号101、配列番号106、配列番号108、配列番号115、配列番号117、配列番号119、配列番号121、配列番号123、配列番号125、配列番号127、配列番号129、配列番号131、配列番号133、配列番号135、配列番号137、配列番号139、配列番号141、配列番号143、配列番号145、配列番号147、配列番号149、配列番号151、配列番号153、配列番号155、配列番号157、配列番号159、配列番号161、配列番号163、配列番号165、配列番号167、配列番号169、配列番号171、配列番号173、配列番号175、配列番号177、配列番号179、配列番号181、配列番号183、配列番号185、配列番号187、配列番号189、配列番号191、配列番号193、配列番号195、配列番号197、配列番号199、配列番号201、配列番号203、配列番号205、配列番号207、配列番号209、配列番号211、配列番号213、配列番号215、配列番号217、配列番号219、配列番号221、および配列番号223。

【請求項６】

発現制御配列に動作可能なように連結された請求項４記載のポリヌクレオチドを含有する発現ベクター。

【請求項７】

請求項６記載のベクターを含有する培養細胞。

【請求項８】

ポリヌクレオチドが発現制御配列に動作可能なように連結されている、請求項４記載のポリヌクレオチドを含有する培養細胞。

【請求項９】

請求項１記載のポリペプチドに特異的に結合する抗体またはそのフラグメント。

【請求項１０】

フラグメントがFabおよび$F(ab')_2$からなる群から選択される、請求項９記載の抗体またはそのフラグメント。

【請求項１１】

抗体がモノクローナル抗体またはポリクローナル抗体である、請求項９記載の抗体。

【請求項１２】

請求項９記載の抗体および医薬的に許容されるキャリアーを含有する組成物。

【請求項１３】

A.アクチノミセテムコミタンスに起因する疾病を治療、改善、または予防する方法であって、請求項９記載の抗体またはそのフラグメントを動物に投与し、それによってA.アクチノミセテムコミタンスに起因する疾病を治療、改善、または予防することを含む上記方法。

【請求項１４】

疾病が局所性思春期前歯周炎、汎発性思春期前歯周炎、局所性若年性歯周炎、汎発性若年性歯周炎、急速進行性成人歯周炎、抗療性成人歯周炎、心内膜炎、甲状腺膿瘍、尿路感染症、脳膿瘍、および椎骨髄炎からなる群から選択される、請求項１３記載の方法。

【請求項１５】

試験サンプル中のA.アクチノミセテムコミタンスまたはA.アクチノミセテムコミタンス抗原の存在を検出する方法であって、

試験サンプルを、A.アクチノミセテムコミタンスまたはA.アクチノミセテムコミタンス抗原に特異的に結合する請求項９記載の抗体と、抗体とA.アクチノミセテムコミタンスまたはA.アクチノミセテムコミタンス抗原との間の免疫複合体の生成が可能な条件下で接触させ；そして

免疫複合体を検出する、

ことを含み、ここで、免疫複合体の検出は試験サンプル中のA.アクチノミセテムコミタンスまたはA.アクチノミセテムコミタンス抗原の存在を示す、上記方法。

【請求項１６】

A.アクチノミセテムコミタンス抗原が動物感染の際にインビボで発現される、請求項１５記載の方法。

【請求項１７】

請求項１記載のポリペプチドおよび医薬的に許容されるキャリアーを含有する医薬組成物。

【請求項１８】

動物に請求項１記載の精製ポリペプチドを投与して免疫応答を誘発することを含む、免疫応答を誘発する方法。

【請求項１９】

A.アクチノミセテムコミタンスに起因する疾病または感染を治療、予防、または改善する方法であって、請求項１記載の精製ポリペプチドを動物に投与して疾病または感染を治療、予防、または改善することを含む上記方法。

【請求項２０】

疾病が、局所性思春期前歯周炎、汎発性思春期前歯周炎、局所性若年性歯周炎、汎発性若年性歯周炎、急速進行性成人歯周炎、抗療性成人歯周炎、心内膜炎、甲状腺膿瘍、尿路感染症、脳膿瘍、および椎骨髄炎からなる群から選択される、請求項１９記載の方法。

【請求項２１】

請求項４記載のポリヌクレオチドおよび医薬的に許容されるキャリアーを含有する組成物。

【請求項２２】

ポリヌクレオチドがDNAである、請求項２１記載の組成物。

【請求項２３】

ポリヌクレオチドがプラスミド中に存在する、請求項２１記載の組成物。

【請求項２４】

請求項４記載の精製ポリヌクレオチドを動物に投与して免疫応答を誘発することを含む、免疫応答を誘発する方法。

【請求項２５】

A.アクチノミセテムコミタンスに起因する疾病または感染を治療、予防、または改善する方法であって、請求項４記載の精製ポリヌクレオチドを動物に投与して、疾病または感

染を治療、予防、または改善する上記方法。

【請求項２６】

疾病が局所性思春期前歯周炎、汎発性思春期前歯周炎、局所性若年性歯周炎、汎発性若年性歯周炎、急速進行性成人歯周炎、抗療性成人歯周炎、心内膜炎、甲状腺膿瘍、尿路感染症、脳膿瘍、および椎骨髄炎からなる群から選択される、請求項２５記載の方法。

【請求項２７】

試験サンプル中の第１のA.アクチノミセテムコミタンス・ポリヌクレオチドの存在を同定する方法であって、

第１のポリヌクレオチドを含有する疑いのある試験サンプルを第２のポリヌクレオチドとハイブリダイゼーション条件下で接触させ、ここで、第２のポリヌクレオチドは請求項４記載のポリヌクレオチドであり；そして

ハイブリダイズした第１および第２のポリヌクレオチドの複合体を検出する、

ことを含み、ここで、ハイブリダイズした第１および第２のポリヌクレオチドの存在は試験サンプル中の第１のポリヌクレオチドの存在を示す、上記方法。

【発明の詳細な説明】

【技術分野】

【０００１】

政府の権利

本発明は国立保健研究所（National Institutes of Health）（国立歯／頭蓋顔面研究所（National Institute for Dental and Craniofacial Research、NIDCR））による助成金番号R01 DE 13523下での政府の援助によるものである。政府は本発明において一定の権利を有する。

【０００２】

技術分野

本発明はアクチノバチルス・アクチノミセテムコミタンス（Actinobacillus actinomycetemcomitans）に起因する疾病の診断、治療、予防、および改善のための方法および組成物を提供する。

【背景技術】

【０００３】

発明の背景

アクチノバチルス・アクチノミセテムコミタンス（Aa）は、早期発症型歯周炎（例えば、局所性および汎発性歯周炎、局所性および汎発性若年性歯周炎、および急速進行性または抗療性成人歯周炎等）の主要な原因微生物である。現在、これらの疾病の診断は、通常、疾病の発症後長時間を経て、支持する骨格および組織のかなりの損傷が起こってから、Ｘ線分析によってなされる。歯の喪失は破壊性歯周疾患の最も有害な影響である。米国の国民調査により、局所性若年性歯周炎の罹患率は0.53％、汎発性若年性歯周炎では0.13％であることが明かとなった（LoeおよびBrown、J. Periodontol. 62:608－616（1991））。多くの研究からの知見により、早期発症型疾患は他の先進国でも同様であり、発展途上国ではより頻度が高いという結論が裏付けてられている（LoeおよびBrown、J. Periodontol. 62:608－616（1991））。従って、早期発症型歯周炎、局所性および汎発性若年性歯周炎、および急速進行性または抗療性成人歯周炎の早期診断法が当該分野で必要とされている。更に、一般に成人集団の半数以上が罹患している非常に一般的な症状である、ある種の成人歯周炎は、Aaによって起こると考えられる。また、Aaは口腔外疾患、例えば心内膜炎、甲状腺膿瘍、尿路感染症、脳膿瘍、および椎骨髄炎（vertebral osteomyelitis）を引き起こしうる。

【０００４】

Aa誘導型歯周炎の治療には、抗生物質療法、外科療法、および機械的治療法があるが、予防の方法はない。テトラサイクリンは早期発症型歯周炎の治療に広範に使用されてきた

。しかしながら、テトラサイクリンへの耐性を獲得する株の懸念、並びに他の病原微生物の過剰増殖の可能性が残っている。これらの疾病の発生があるとすれば、Aaの安全なワクチンが必要とされる。ワクチンは例えば多価ワクチンであってもよい。歯周疾患の制御は、最近注目されている全身性疾患（例えば虚血性心疾患）のリスク因子としての歯周感染症の役割の可能性の点からも非常に重要である。

【０００５】

ほとんどの人はその歯垢の正常なメンバーとしてAaを有するが、これは通常、疾病の原因とならない。しかしながら、Aaが疾病の原因となる時、宿主は著しい免疫応答を開始し、これは当然無駄に終わるが、それはおそらく免疫応答が誤ったAa抗原に向けられるためである。最も好適な歯周疾患治療を提供するためには、正確な診断を行い、最適な治療を実施し、そして治療に対する患者の反応をモニタリングすることが必要である。

【０００６】

現在、Aaの標準的な微生物学的試験は、歯垢中のAaの存在のみを検出するものであり、疾病の活性を特異的に同定するものではない。この理由から、これらの試験は、予測的な価値が低い。Aaは健康な個体の歯垢中にも一般的に見られるので、これらの試験の適用の有用性は、一定の疾病の臨床的兆候を示す人、例えば２５才未満の進行性付着器官（attachment）喪失および骨喪失患者、約２５－３５才の相対的に短時間で付着器官および骨が急速破壊される（急速進行性歯周炎）患者、および厳密な治療にも関わらず付着器官を喪失し続ける（抗療性歯周炎）患者に限定される。

【０００７】

歯垢中のAaの存在を同定するためにDNAプローブ技術が開発されているが、この技術は歯垢群集の正常な一部分であるAaと実際の疾病過程に関与するAaを識別することができない。従って、これらのDNAプローブは疾病過程に関与するAaを同定しない。

【０００８】

従って、Aaに起因する疾病の診断、モニタリング、治療、予防、または改善の方法が当該分野で必要とされている。

【発明の開示】

【課題を解決するための手段】

【０００９】

発明の概要

本発明の目的は、Aaに起因する疾病の治療、改善、および予防のための方法および組成物を提供することである。本発明のこの目的および他の目的は、下記の態様の１またはそれ以上によって提供される。

【００１０】

本発明の１つの態様は、以下からなる群から選択されるアミノ酸配列の少なくとも５個の連続するアミノ酸を含有する精製免疫原性ポリペプチドを提供する：配列番号2、配列番号4、配列番号6、配列番号8、配列番号10、配列番号12、配列番号14、配列番号16、配列番号18、配列番号20、配列番号22、配列番号24、配列番号26、配列番号28、配列番号30、配列番号32、配列番号34、配列番号36、配列番号38、配列番号40、配列番号42、配列番号44、配列番号46、配列番号48、配列番号50、配列番号52、配列番号54、配列番号56、配列番号58、配列番号60、配列番号62、配列番号64、配列番号66、配列番号68、配列番号70、配列番号72、配列番号74、配列番号76、配列番号78、配列番号80、配列番号82、配列番号84、配列番号86、配列番号88、配列番号90、配列番号92、配列番号94、配列番号96、配列番号98、配列番号100、配列番号102、配列番号103、配列番号104、配列番号105、配列番号107、配列番号109、配列番号110、配列番号111、配列番号112、配列番号113、配列番号114、配列番号116、配列番号118、配列番号120、配列番号122、配列番号124、配列番号126、配列番号128、配列番号130、配列番号132、配列番号134、配列番号,136、配列番号138、配列番号140、配列番号142、配列番号144、配列番号146、配列番号148、配列番号150、配列番号152、配列番号154、配列番号156、配列番号158、配列番号160、配列番号162、配列番号164、配列番号166、配列番号168、配列番号170、配列番号172、配列番号174、配

列番号176、配列番号178、配列番号180、配列番号182、配列番号184、配列番号186、配列番号188、配列番号190、配列番号192、配列番号194、配列番号196、配列番号198、配列番号200、配列番号202、配列番号204、配列番号206、配列番号208、配列番号210、配列番号212、配列番号214、配列番号216、配列番号218、配列番号220、配列番号222、配列番号224、配列番号226、配列番号228、配列番号230、配列番号232、および配列番号234（“ポリペプチド配列番号”）。これらのポリペプチド配列のそれぞれを集合的に“ポリペプチド配列番号”と呼び、合わせて一群として表すが、これらの配列のそれぞれは、個別に考慮し特許請求することができる。

【００１１】

本発明の別の態様は、“ポリペプチド配列番号”からなる群から選択されるアミノ酸配列を含有する精製ポリペプチドを提供する。

【００１２】

本発明の更に別の態様は、“ポリペプチド配列番号”をコードする配列を含有する精製ポリヌクレオチドを提供する。

【００１３】

本発明の更に別の態様は、以下からなる群から選択される配列の少なくとも約１５個の連続する核酸を含有する精製ポリヌクレオチドを提供する：配列番号1、配列番号3、配列番号5、配列番号7、配列番号9、配列番号11、配列番号13、配列番号15、配列番号17、配列番号19、配列番号21、配列番号23、配列番号25、配列番号27、配列番号29、配列番号31、配列番号33、配列番号35、配列番号37、配列番号39、配列番号41、配列番号43、配列番号45、配列番号47、配列番号49、配列番号51、配列番号53、配列番号55、配列番号57、配列番号59、配列番号61、配列番号63、配列番号65、配列番号67、配列番号69、配列番号71、配列番号73、配列番号75、配列番号77、配列番号79、配列番号81、配列番号83、配列番号85、配列番号87、配列番号89、配列番号91、配列番号93、配列番号95、配列番号97、配列番号99、配列番号101、配列番号106、配列番号108、配列番号115、配列番号117、配列番号119、配列番号121、配列番号123、配列番号125、配列番号127、配列番号129、配列番号131、配列番号133、配列番号135、配列番号137、配列番号139、配列番号141、配列番号143、配列番号145、配列番号147、配列番号149、配列番号151、配列番号153、配列番号155、配列番号157、配列番号159、配列番号161、配列番号163、配列番号165、配列番号167、配列番号169、配列番号171、配列番号173、配列番号175、配列番号177、配列番号179、配列番号181、配列番号183、配列番号185、配列番号187、配列番号189、配列番号191、配列番号193、配列番号195、配列番号197、配列番号199、配列番号201、配列番号203、配列番号205、配列番号207、配列番号209、配列番号211、配列番号213、配列番号215、配列番号217、配列番号219、配列番号221、配列番号223、配列番号225、配列番号227、配列番号229,配列番号231、および配列番号233（“ポリヌクレオチド配列番号”）。これらのポリヌクレオチド配列のそれぞれを集合的に“ポリヌクレオチド配列番号”と呼び、合わせて一群として表すが、これらの配列はそれぞれ個別に考慮し特許請求することができる。

【００１４】

本発明の別の態様は、“ポリヌクレオチド配列番号”のヌクレオチド配列またはそれらの縮重変異体を含有する精製ポリヌクレオチドを提供する。

【００１５】

本発明の別の態様は、発現制御配列に動作可能なように連結された“ポリヌクレオチド配列番号”を含有する発現ベクターを提供する。ベクターは培養細胞中に存在してもよい。

【００１６】

本発明の更に別の態様は、“ポリペプチド配列番号”のポリペプチドに特異的に結合する抗体またはそのフラグメントを提供する。抗体フラグメントは、例えばFabまたはF(ab')$_2$フラグメントであってもよい。抗体はモノクローナル抗体またはポリクローナル抗体であってもよい。抗体は医薬的に許容されるキャリアーと共に医薬組成物中に存在してもよい。

【００１７】

本発明の更に別の態様は、A.アクチノミセテムコミタンスに起因する疾病の治療、改善、または予防の方法を提供する。方法は本発明の抗体またはそのフラグメントを動物に投与することを含む。それによって、A.アクチノミセテムコミタンスに起因する疾病を治療、改善、または予防する。A.アクチノミセテムコミタンスに起因する疾病は以下からなる群から選択することができる：局所性思春期前歯周炎、汎発性思春期前歯周炎、局所性若年性歯周炎、汎発性若年性歯周炎、急速進行性成人歯周炎、抗療性成人歯周炎、心内膜炎（endiocarditis）、甲状腺膿瘍、尿路感染症、脳膿瘍、および椎骨髄炎。

【００１８】

本発明の更に別の態様は、試験サンプル中のA.アクチノミセテムコミタンスまたはA.アクチノミセテムコミタンス抗原の存在を検出する方法を提供する。方法は、試験サンプルとA.アクチノミセテムコミタンスまたはA.アクチノミセテムコミタンス抗原に特異的に結合する本発明の抗体を、抗体とA.アクチノミセテムコミタンスまたはA.アクチノミセテムコミタンス抗原との間の免疫複合体の生成が可能な条件下で接触させ、そして免疫複合体を検出することを含む。免疫複合体の検出は、試験サンプル中のA.アクチノミセテムコミタンスまたはA.アクチノミセテムコミタンス抗原の存在を示す。検出されるA.アクチノミセテムコミタンス抗原は、動物の感染の際にインビボで発現される抗原であってもよい。

【００１９】

本発明の別の態様は、本発明のポリペプチドを医薬的に許容されるキャリアーと共に含有する医薬組成物を提供する。

【００２０】

本発明の更に別の態様は、免疫応答を誘発する方法を提供する。方法は本発明のポリペプチドを動物に投与して免疫応答を誘発することを含む。

【００２１】

本発明の更に別の態様は、A.アクチノミセテムコミタンスに起因する疾病または感染の治療、予防、または改善の方法を提供する。方法は本発明のポリペプチドを動物に投与して疾病または感染を治療、予防、または改善することを含む。

【００２２】

本発明の更に別の態様は、本発明のポリヌクレオチドおよび医薬的に許容されるキャリアーを含有する組成物を提供する。ポリヌクレオチドはDNAであってもよい。ポリヌクレオチドはプラスミド中に存在してもよい。

【００２３】

本発明の別の方法は、免疫応答を誘発する方法を提供し、方法は本発明の精製ポリヌクレオチドを動物に投与して免疫応答を誘発することを含む。本発明の更に別の態様は、A.アクチノミセテムコミタンスに起因する疾病または感染の治療、予防、または改善の方法を提供する。方法は本発明の精製ポリヌクレオチドを動物に投与して疾病または感染を治療、予防、または改善することを含む。

【００２４】

本発明の更に別の態様は、第１のA.アクチノミセテムコミタンス・ポリヌクレオチドの存在を同定する方法を提供する。この方法は、ハイブリダイゼーション条件下で第１のA.アクチノミセテムコミタンス・ポリヌクレオチドを含有する疑いのある試験サンプルを第２のポリヌクレオチドと接触させることを含み、ここで第２のポリヌクレオチドは本発明のポリヌクレオチドである。ハイブリダイズした第１および第２のポリヌクレオチドの複合体を検出する。ハイブリダイズした第１および第２ポリヌクレオチド複合体の存在は、試験サンプル中の第１のポリヌクレオチドの存在を示す。

【発明を実施するための最良の形態】

【００２５】

発明の詳細な説明

ポリヌクレオチドおよびポリペプチドの同定法

微生物が疾病を誘発する能力にとって重要なヌクレオチド配列を同定する方法を、早期

発症型歯周炎（例えば、局所性思春期前歯周炎、汎発性思春期前歯周炎、局所性若年性歯周炎、汎発性若年性歯周炎、急速進行性成人歯周炎、および抗療性成人歯周炎等）の主要な原因微生物であるAaに適用する。Aaはまた、心内膜炎、甲状腺膿瘍、尿路感染症、脳膿瘍、および椎骨髄炎も引き起こしうる。本発明のポリヌクレオチドおよびポリペプチド配列を同定するのに使用される方法は、インビボ誘導型抗原法（in vivo induced antigen technology；IVIAT）と呼ばれる（Handfieldら、Trends Microbiol. 336:336－339 (2000)；国際特許公開WO 01/11081参照）。

【００２６】

簡単には、IVIATは、インビボおよびインビトロでAaによって発現されるAa抗原に対する抗体のサンプルを得、インビトロで増殖させたAaの細胞または細胞抽出物に抗体を吸収させることを含む。使用できる抗体のサンプルの例は、Aaに感染したことのある、または感染している患者由来の血清である。未吸収の抗体を単離し、これを使用してAa DNAの発現ライブラリーを探索する。反応性クローンを単離し、クローニングしたフラグメントの配列を確認する。

【００２７】

IVIATを使用して、Aaが動物（特にヒト）において実際に疾病を引き起こすことに携わる場合にのみ発現されるAaのポリヌクレオチドを同定した。通常、感染の際にAaによる毒性遺伝子の刺激を引き起こす重要な環境シグナルは、細菌を実験室で増殖させた場合は見られない。従って、診断およびワクチン戦略のための最も優れた標的の多くは未知であった。IVIAT方法論を使用して、ヒト宿主におけるAaの増殖の際には特異的に刺激されるが、日常的な実験室での増殖の際には刺激されないポリヌクレオチドを同定した。これらのポリヌクレオチド、および対応するポリペプチドおよび抗体は、例えば感染の初期段階にある被験体の同定および治療への反応のモニタリングのためのAaの診断試験の開発、および疑いのある動物におけるAaに起因する疾病を予防または治療するためのワクチンまたは治療の開発に有用である。

【００２８】

IVIATによって同定される抗原は、Aaに起因する疾病（例えば歯周疾患）に関して、予測的な価値が非常に高い。Aaの診断試験は、母親が歯周炎の病歴を有する小児をスクリーニングして、小児がその疾病に罹患しやすい傾向を有するかどうかを確認するような適用に有用でありうる。思春期前の歯周炎に関係することが知られている疾病には以下がある：パピヨン・ルフェーブル症候群（PLS）、低ホスファターゼ血症、好中球減少症、白血球付着欠損症（leukocyte adhesion deficiency；LAD）、チェディアック・ヒガシ症候群、ダウン症候群、白血病、ヒスチオサイトーシスＸ、早期発症型Ｉ型糖尿病、および先端疼痛症。これらの疾病を有する小児はAa試験の候補者である。更に、歯周炎の傾向がより低い他の思春期前小児にもAa診断試験は有益であり、これは、他の予測方法、または既知のリスク因子がないためである。

【００２９】

ポリペプチド

本発明の精製ポリペプチドは、完全長のポリペプチドまたはポリペプチドのフラグメントのいずれであってもよい。例えば本発明のポリペプチドのフラグメントは、本発明のポリペプチドの約５、１０、２５、５０、１００、または２００アミノ酸を含有してもよい。本発明のポリペプチドの例には以下に示すものがある：配列番号2、配列番号4、配列番号6、配列番号8、配列番号10、配列番号12、配列番号14、配列番号16、配列番号18、配列番号20、配列番号22、配列番号24、配列番号26、配列番号28、配列番号30、配列番号32、配列番号34、配列番号36、配列番号38、配列番号40、配列番号42、配列番号44、配列番号46、配列番号48、配列番号50、配列番号52、配列番号54、配列番号56、配列番号58、配列番号60、配列番号62、配列番号64、配列番号66、配列番号68、配列番号70、配列番号72、配列番号74、配列番号76、配列番号78、配列番号80、配列番号82、配列番号84、配列番号86、配列番号88、配列番号90、配列番号92、配列番号94、配列番号96、配列番号98、配列番号100、配列番号102、配列番号103、配列番号104、配列番号105、配列番号107、配列番

号109、配列番号110、配列番号111、配列番号112、配列番号113、配列番号114、配列番号116、配列番号118、配列番号120、配列番号122、配列番号124、配列番号126、配列番号128、配列番号130、配列番号132、配列番号134、配列番号136、配列番号138、配列番号140、配列番号142、配列番号144、配列番号146、配列番号148、配列番号150、配列番号152、配列番号154、配列番号156、配列番号158、配列番号160、配列番号162、配列番号164、配列番号166、配列番号168、配列番号170、配列番号172、配列番号174、配列番号176、配列番号178、配列番号180、配列番号182、配列番号184、配列番号186、配列番号188、配列番号190、配列番号192、配列番号194、配列番号196、配列番号198、配列番号200、配列番号202、配列番号204、配列番号206、配列番号208、配列番号210、配列番号212、配列番号214、配列番号216、配列番号218、配列番号220、配列番号222、配列番号224、配列番号226、配列番号228、配列番号230、配列番号232、および配列番号234。これらのポリペプチドを“ポリペプチド配列番号”と呼ぶ。ポリペプチド配列番号に示すポリペプチド配列と少なくとも約７５、または約９０、９６、９８、もしくは９９％の同一性を示す相同アミノ酸配列もAaポリペプチドである。相同なアミノ酸配列は生体活性を保持し、すなわち生体機能的に同等である。

【００３０】

配列同一性のパーセンテージは当該分野で認識される意味を持ち、２つのポリペプチドまたはポリヌクレオチド配列間の同一性を測定するための多くの方法がある。例えば以下を参照されたい：Lesk編, Computational Molecular Biology, Oxford University Press, New York, (1988)；Smith編, Biocomputing: Informatics And Genome Projects, Academic Press, New York, (1993)；GriffinおよびGriffin編, Computer Analysis Of Sequence Data, Part I, Humana Press, New Jersey, (1994)；von Heinje, Sequence Analysis In Molecular Biology, Academic Press, (1987)；そして、GribskovおよびDevereux編, Sequence Analysis Primer, M Stockton Press, New York, (1991)。ポリヌクレオチドまたはポリペプチドをアラインメントする方法は以下のようなコンピュータープログラムにコーディングされている：GCGプログラムパッケージ（Devereuxら, Nuc. Acids Res. 12:387 (1984)）、BLASTP、BLASTN、FASTA（Atschul ら, J. Molec. Biol. 215:403 (1990)）、およびBestfitプログラム（Wisconsin Sequence Analysis Package, Version 8 for Unix, Genetics Computer Group, University Research Park, 575 Science Drive, Madison, WI 53711）（これはSmithおよびWatermanの局所相同性アルゴリズムを使用する（Adv. App. Math., 2:482－489 (1981)））。例えば、FASTAアルゴリズムを使用するコンピュータープログラムALIGNを、ギャップオープンペナルティー－１２、ギャップ伸長ペナルティー－２のアフィンギャップサーチと共に使用できる。

【００３１】

配列アラインメントプログラムを使用して、特定の配列が例えば参照配列と約９５％の同一性を有するかどうかを確認する場合、同一性のパーセンテージが参照ポリヌクレオチドの完全長にわたって計算されるように、そして同一性のギャップが参照ポリヌクレオチド中のヌクレオチド総数の５％までとなるように、パラメーターを設定する。

【００３２】

ポリペプチド配列番号に示すポリペプチド変異体およびそのフラグメントも本発明に含まれる。変異体は、保存的置換および／または修飾においてのみ、ポリペプチド配列番号またはそのフラグメントと異なるポリペプチドであり、そのためポリペプチドの抗原性は元のポリペプチドと実質的に同じである。一般に変異体の同定は、本発明のポリペプチド配列の１つを修飾し、修飾されたポリペプチドの抗原性を、例えば免疫組織化学的アッセイ、酵素結合免疫吸着アッセイ（ELISA）、ラジオイムノアッセイ（RIA）、またはウェスタンブロットアッセイを使用して評価することによって行うことができる。本発明のポリペプチドは少なくとも１、５、１０、２５、５０、または１００個の保存的アミノ酸置換を含むことができる。

【００３３】

保存的置換は、アミノ酸が同様の特性を有する別のアミノ酸で置換され、そのためペプ

チド化学分野の当業者によってポリペプチドの２次構造およびハイドロパシー特性が実質的に変化しないことが予期されるものである。一般に、以下のアミノ酸群は保存的変化を示す：（１）ala、pro、gly、glu、asp、gln、asn、ser、thr；（２）cys、ser、tyr、thr；（３）val、ile、leu、met、ala、phe；（４）lys、arg、his；および（５）phe、tyr、trp、his。

【００３４】

変異体は更に（または代わりに）、例えばポリペプチドの抗原性、２次構造、およびハイドロパシー特性に最小限の影響しか与えないアミノ酸の欠失または添加によって修飾することもできる。例えばポリペプチドをタンパク質のN－末端でシグナル（またはリーダー）配列にコンジュゲートさせることができ、これは翻訳時に、または翻訳後にタンパク質を移動させる。また、ポリペプチドを、ポリペプチドの合成、精製、もしくは同定を容易にするため（例えばポリHis）、または固体支持体へのポリペプチドの結合を向上するために、リンカーまたは他の配列にコンジュゲートさせることもできる。例えばポリペプチドを免疫グロブリンのFc領域にコンジュゲートさせることができる。

【００３５】

本発明のポリペプチドはポリペプチド配列番号に示すポリペプチドの少なくとも約５、１０、２５、５０、１００、または２００アミノ酸の生体機能的同等物を更に含んでもよい。ポリペプチドがアッセイ（例えば免疫組織化学的アッセイ、ELISA、RIA、またはウェスタンブロットアッセイ）において本発明のポリペプチドと実質的に同じように反応し、例えば元のポリペプチドの９０－１１０％の活性を有する場合、これは生物学的同等物である。ある態様では、アッセイは競合アッセイであり、ここでは、生物学的に同等であるポリペプチドは、本発明のポリペプチドの対応する反応性抗原または抗体への結合を約８０、９５、９９、または１００％低下させる能力を有する。

【００３６】

本発明のポリペプチドは、Aaに対して反応性を有する抗体によって認識される抗原を含むことができる。抗原は１またはそれ以上のエピトープ（または抗原決定基）を含むことができる。エピトープは直鎖エピトープ、連続エピトープ（sequential epitope）、またはコンフォメーションエピトープであってもよい。本発明のポリペプチド内のエピトープはいくつかの方法によって同定できる。例えば米国特許第4,554,101号；JamesonおよびWolf, CABIOS 4:181－186 (1988)参照。例えば、本発明のポリペプチドを単離およびスクリーニングすることができる。合わせると全ポリペプチド配列を網羅するような一連の短鎖ペプチドを、タンパク分解による開裂によって調製することができる。例えば１００量体ポリペプチドフラグメントから出発して、ELISAで認識されるエピトープの存在について各フラグメントを試験できる。例えばELISAアッセイで、Aaポリペプチド（例えば１００量体ポリペプチドフラグメント）を固体支持体（例えばプラスチック製のマルチウェルプレートのウェル）に結合させる。抗体集団を標識し、固体支持体に添加し、非特異的吸収が阻害されるような条件下で未標識の抗原に結合させ、未結合の抗体および他のタンパク質を洗浄除去する。抗体結合を、例えば無色の基質を着色された反応生成物に変換する反応によって検出する。次いで、同定された１００量体から次第に小さくした重複するフラグメントを試験し、興味のエピトープのマッピングを行う。

【００３７】

本発明のポリペプチドは組換え技術によって生成することができる。本発明のポリペプチドをコードするポリヌクレオチドを組換え発現ベクターに導入することができ、これを当業界で周知の技術を使用して好適な発現宿主細胞系で発現させることができる。種々の細菌、酵母、植物、哺乳動物、および昆虫発現系が当業界で利用されており、それらの発現系のいずれを使用してもよい。必要により、ポリペプチドをコードするポリヌクレオチドを、細胞を使用しない翻訳系において翻訳することができる。また、ポリペプチドは化学的に合成することもできる。

【００３８】

必要により、ポリペプチドを融合タンパク質として生成することができ、これは他のア

ミノ酸配列（例えばアミノ酸リンカーまたはシグナル配列）、並びにタンパク質の精製に有用なリガンド（例えばグルタチオン－Ｓ－トランスフェラーゼ、ヒスチジンタグ、およびブドウ球菌プロテインＡ（staphylococcal protein A））を含むこともできる。融合タンパク質中には２個以上の本発明のポリペプチドが存在してもよい。

【００３９】

ポリヌクレオチド

本発明のポリヌクレオチドは、微生物ゲノム全体より少ないものを含有し、１本鎖または２本鎖のDNAまたはRNAであってもよい。ポリヌクレオチドは他の成分（例えばタンパク質および脂質）が含有されないように精製することができる。本発明のポリヌクレオチドは上記のポリペプチドをコードする。本発明のポリヌクレオチドは他のヌクレオチド配列、例えばリンカーをコードする配列、シグナル配列、異種シグナル配列、TMR転写停止配列、膜貫通ドメイン、またはタンパク質精製に有用なリガンド、例えばグルタチオン－Ｓ－トランスフェラーゼ、ヒスチジンタグ、およびブドウ球菌プロテインＡを含むこともできる。

【００４０】

本発明のポリヌクレオチドは、配列番号1、配列番号3、配列番号5、配列番号7、配列番号9、配列番号11、配列番号13、配列番号15、配列番号17、配列番号19、配列番号21、配列番号23、配列番号25、配列番号27、配列番号29、配列番号31、配列番号33、配列番号35、配列番号37、配列番号39、配列番号41、配列番号43、配列番号45、配列番号47、配列番号49、配列番号51、配列番号53、配列番号55、配列番号57、配列番号59、配列番号61、配列番号63、配列番号65、配列番号67、配列番号69、配列番号71、配列番号73、配列番号75、配列番号77、配列番号79、配列番号81、配列番号83、配列番号85、配列番号87、配列番号89、配列番号91、配列番号93、配列番号95、配列番号97、配列番号99、配列番号101、配列番号106、配列番号108、配列番号115、配列番号117、配列番号119、配列番号121、配列番号123、配列番号125、配列番号127、配列番号129、配列番号131、配列番号133、配列番号135、配列番号137、配列番号139、配列番号141、配列番号143、配列番号145、配列番号147、配列番号149、配列番号151、配列番号153、配列番号155、配列番号157、配列番号159、配列番号161、配列番号163、配列番号165、配列番号167、配列番号169、配列番号171、配列番号173、配列番号175、配列番号177、配列番号179、配列番号181、配列番号183、配列番号185、配列番号187、配列番号189、配列番号191、配列番号193、配列番号195、配列番号197、配列番号199、配列番号201、配列番号203、配列番号205、配列番号207、配列番号209、配列番号211、配列番号213、配列番号215、配列番号217、配列番号219、配列番号221、配列番号223、配列番号225、配列番号227、配列番号229、配列番号231、および配列番号233で示される。これらのポリヌクレオチドを“ポリヌクレオチド配列番号”と呼ぶ。

【００４１】

本発明のポリペプチドをコードする縮重ヌクレオチド配列、並びにポリヌクレオチド配列番号 に示すヌクレオチド配列と少なくとも約７５％、または約９０、９６、９８、もしくは９９％の同一性を有する相同ヌクレオチド配列およびそれらの相補体も本発明のポリヌクレオチドである。配列同一性のパーセンテージを“ポリペプチド”の項に記載するように算出できる。縮重ヌクレオチド配列は、ポリペプチド配列番号に示すポリペプチドまたはそのフラグメントをコードするポリヌクレオチドであるが、遺伝子コードの縮重により、ポリヌクレオチド配列番号に示される配列と核酸配列が異なる。相補DNA（cDNA）分子、種間相同体、および生体機能的Aaポリペプチドをコードする Aaポリヌクレオチドの変異体もAaポリヌクレオチドである。本発明のポリヌクレオチドはポリヌクレオチド配列番号に示す核酸配列の約５、１０、１５、５０、１００、または２００ヌクレオチドを含有することができる。

【００４２】

本発明のポリヌクレオチドは、例えば、感染した個体由来の生体サンプル、例えば歯垢、唾液、歯肉滲出液、痰、血液、血清、血漿、尿、便、脳脊髄液、羊水、創傷滲出液、ま

たは組織中に存在する核酸配列から単離できる。ポリヌクレオチドは、例えば自動合成装置を使用して、実験室で合成することもできる。PCRのような増幅法を使用して、ポリペプチドをコードするゲノムDNAまたはcDNAのいずれかからポリヌクレオチドを増幅することができる。

【００４３】

本発明のポリヌクレオチドは天然に存在するポリペプチドのコーディング配列を含んでいてもよく、または天然には存在しない変更された配列をコードしてもよい。必要により、発現制御要素を含む発現ベクター中にポリヌクレオチドをクローニングすることができ、それらの要素には、例えば複製開始点、プロモーター、エンハンサー、または宿主細胞において本発明のポリヌクレオチドの発現を誘導する他の要素がある。発現ベクターは、例えばプラスミド（例えばpBR322、pUC、またはColE1）またはアデノウィルスベクター（例えばアデノウィルスII型ベクターまたはＶ型ベクター）であってもよい。必要により他のベクターを使用することができ、それらには、限定される訳ではないが、シンドビスウィルス、シミアンウィルス４０、アルファウィルスベクター、ポックスウィルスベクター、およびサイトメガロウィルスおよびレトロウィルスベクター、例えばマウス肉腫ウィルス、マウス乳腺癌ウィルス、マウスモロニー白血病ウィルス、およびラウス肉腫ウィルス等が含まれる。ミニクロモソーム、例えばMCおよびMC1、バクテリオファージ、ファージミド、人工酵母染色体、人工細菌染色体、ウィルス粒子、ウィルス様粒子、コスミド（λファージのcos部位を挿入したプラスミド）、およびレプリコン（細胞中でそれら独自の制御下で複製する能力を有する遺伝要素）を使用することもできる。

【００４４】

発現制御配列に動作可能なように連結されたポリヌクレオチドの調製および宿主細胞でのそれらの発現の方法は当該分野で周知である。例えば米国特許第4,366,246号を参照されたい。本発明のポリヌクレオチドは、ポリヌクレオチドの転写および／または翻訳を指示する１またはそれ以上の発現制御要素に隣接して配置されている場合、動作可能なように連結されている。

【００４５】

本発明のポリヌクレオチドを含有するベクターを、例えば細菌、酵母、昆虫、または哺乳動物細胞に形質転換し、本発明のポリペプチドを細胞培養液中で発現させ、そこから単離することができる。当該分野で可能な方法のいずれかを使用して、宿主細胞にポリヌクレオチドを導入することができる。これらには、限定されるわけではないが、裸の、またはカプセルに封入された核酸でのトランスフェクション、細胞融合、プロトプラスト融合、ウィルス感染、およびエレクトロポレーション等がある。

【００４６】

本発明のポリヌクレオチドを、例えばプローブまたはプライマー（例えばPCRプライマー）として使用し、サンプル（例えば生体サンプル）中のAaポリヌクレオチドの存在を検出することができる。それらのプローブおよびプライマーがAaポリヌクレオチド配列に特異的にハイブリダイズする能力により、それらを使用して所定のサンプル中の相補配列の存在を検出することが可能となる。本発明のポリヌクレオチドプローブおよびプライマーを、サンプル（例えば生体サンプル（例えば歯垢、唾液、歯肉滲出液、痰、血液、尿、便、脳脊髄液、羊水、創傷滲出液、または組織））中の相補配列にハイブリダイズさせることができる。サンプル由来のポリヌクレオチドを、例えばゲル電気泳動もしくは他のサイズ分離法に適用するか、またはサイズ分離を行わずに固定化することができる。ポリヌクレオチドプローブまたはプライマーを標識することができる。好適な標識、およびプローブおよびプライマーを標識する方法は当業界で周知であり、それらには、例えば、ニックトランスレーションまたはキナーゼによって導入する放射線標識、ビオチン標識、蛍光標識、化学発光標識、生物発光標識、金属キレート剤標識、および酵素標識がある。サンプル由来のポリヌクレオチドを、好適なストリンジェンシーのハイブリダイゼーション条件下でプローブまたはプライマーと接触させる。

【００４７】

用途によって、種々のハイブリダイゼーション条件を使用して、プローブまたはプライマーの標的配列に対する選択性を種々の程度にすることができる。高度の選択性を必要とする用途では、相対的にストリンジェントな条件（例えば低塩および／または高温条件、例えば約０．０２Ｍから約０．１５Ｍの塩濃度で、約５０℃から約７０℃の温度）が使用される。より低い選択性が必要とされる適用では、より低いストリンジェンシーのハイブリダイゼーション条件を使用できる。例えば約０．１４Ｍから約０．９Ｍの塩濃度で約２０℃から約５５℃の温度範囲である。プローブまたはプライマーおよび試験サンプル由来の相補ポリヌクレオチドを含有するハイブリッド複合体の存在は、サンプル中のAaまたはAaポリヌクレオチド配列の存在を示す。

【００４８】

抗体

本発明の抗体は、本発明のAaポリペプチドまたはそのフラグメントに特異的かつ安定に結合する抗体分子である。本発明の抗体はポリクローナル抗体、モノクローナル抗体、１本鎖抗体（scFv）、または抗体のフラグメントであってもよい。抗体のフラグメントは無傷の抗体の抗原結合部位または可変領域を含む無傷の抗体の一部であり、この部分は無傷の抗体のFc領域の定常領域重鎖ドメインを含まない。抗体フラグメントの例にはFab、Fab'、Fab'－SH、F(ab')$_2$、およびF$_v$フラグメントがある。

【００４９】

本発明の抗体は、例えばIgG、IgM、IgA、IgD、およびIgEを含むいずれのクラスの抗体であってもよい。抗体またはそのフラグメントは本発明のポリペプチドのエピトープに結合する。抗体は、好適な実験動物においてインビボで生成するか、または組換えDNA技術を使用してインビトロで生成できる。抗体を調製および特性決定する方法は当該分野で周知である。例えば以下を参照されたい：Methods Mol. Biol. 80:23－37 (1998)；Dean, Methods Mol. Biol. 32:361－79 (1994)；Baileg, Methods Mol. Biol. 32:381－88 (1994)；Gullick, Methods Mol. Biol. 32:389－99 (1994)；Drenckhahnら Methods Cell. Biol. 37:7－56 (1993)；Morrison, Ann. Rev. Immunol. 10:239－65 (1992)；Wrightら Crit. Rev. Immunol. 12:125－68(1992)。例えば、ポリクローナル抗体の生成は、本発明のポリペプチドを動物（例えばヒトもしくは他の霊長類、マウス、ラット、ウサギ、モルモット、ヤギ、ブタ、ウシ、ヒツジ、ロバ、またはウマ）に投与することによって行ってもよい。免疫化した動物からの血清を回収し、例えば硫酸アンモニウムによる沈殿、次いでクロマトグラフィー（例えばアフィニティークロマトグラフィー）によって、抗体を血漿から精製する。ポリクローナル抗体を生成および加工する技術は当該分野で周知である。

【００５０】

更に、本発明のポリペプチド上に存在するエピトープに対するモノクローナル抗体も容易に生成できる。例えば本発明のポリペプチドで免疫化した哺乳動物（例えばマウス）由来の正常Ｂ細胞を、例えばHAT感受性マウス骨髄腫細胞と融合させてハイブリドーマを生成することができる。Aa特異的抗体を生成するハイブリドーマは、RIAまたはELISAを使用して同定し、半流動寒天中でクローニングするか、または限界希釈によって単離することができる。Aa特異的抗体を生成するクローンを、更なるラウンドのスクリーニングによって単離する。モノクローナル抗体の特異性に関するスクリーニングは、標準的な技術、例えば本発明のポリペプチドをマイクロタイタープレートに結合させ、ELISAアッセイによってモノクローナル抗体の結合を測定することによって行うことができる。モノクローナル抗体の生成および加工の技術は当該分野で周知である。例えばKohlerおよびMilstein, Nature, 256:495 (1975)を参照されたい。モノクローナル抗体の特定のアイソタイプの調製は、異なるアイソタイプのモノクローナル抗体を分泌する親ハイブリドーマから直接、初めの融合体からの選択によって、または二次的に行うことができ、これは同胞選択法（sib selection technique）を使用してクラススイッチ変異体を単離することによって行う。Steplewskiら., P.N.A.S. U.S.A. 82:8653 1985；Spriaら, J. Immunolog. Meth. 74:307, 1984参照。本発明のモノクローナル抗体は組換えモノクローナル抗体であってもよい。例えば米国特許第4,474,893号；米国特許第4,816,567号参照。本発明の抗体は化学的

に構築することもできる。例えば米国特許第4,676,980号参照。

【００５１】

本発明の抗体はキメラ（例えば米国特許第5,482,856号参照）、ヒト化（例えばJonesら，Nature 321:522 (1986)；Reichmannら，Nature 332:323 (1988)；Presta, Curr. Op. Struct. Biol. 2:593 (1992)参照）、またはヒト抗体であってもよい。ヒト抗体は、例えば直接不死化、ファージディスプレイ、トランスジェニックマウス、またはトリメラ（Trimera）法によって生成することができる。例えばReisenerら、Trends Biotechnol. 16:242－246 (1998)参照。

【００５２】

Aa抗原に対する抗体（モノクローナル抗体およびポリクローナル抗体のいずれも）は、サンプル（例えばAa感染したヒト由来の血清サンプル）中のAaまたはAa抗原の存在を検出するのに特に有用である。AaまたはAa抗原に関する免疫アッセイは１つの抗体、またはいくつかの抗体を利用することができる。AaまたはAa抗原に関する免疫アッセイは、例えば以下を使用することができる：Aaエピトープ（単数）に対するモノクローナル抗体（単数）、１つのAaポリペプチドのエピトープ（複数）に対するモノクローナル抗体（複数）の組み合わせ、異なるAaポリペプチド（複数）のエピトープ（複数）に対するモノクローナル抗体（複数）、同じAa抗原（単数）に対するポリクローナル抗体（複数）、異なるAa抗原（複数）に対するポリクローナル抗体（複数）、またはモノクローナルおよびポリクローナル抗体の組み合わせ。免疫アッセイのプロトコールは、例えば競合、直接反応、またはサンドイッチ型アッセイ（例えば標識した抗体を使用する）に基づくものであってもよい。本発明の抗体は、当該分野で周知の型の標識、例えば蛍光、化学発光、放射能、酵素、コロイド金属、放射性同位元素、および生体発光標識で標識することができる。

【００５３】

本発明の抗体またはそのフラグメントを支持体に結合させ、AaまたはAa抗原の存在を検出することができる。支持体には、例えばガラス、ポリスチレン、ポリプロピレン、ポリエチレン、デキストラン、ナイロン、アミラーゼ、天然および修飾セルロース、ポリアクリルアミド、アガロース、およびマグネタイトがある。

【００５４】

本発明のポリクローナルまたはモノクローナル抗体は、更に免疫アフィニティーカラムによるAa生体またはAa抗原の単離に使用することができる。抗体がその免疫選択活性を保持するように、例えば吸収または共有結合によって固体支持体に抗体を固定化することができる。必要により、スペーサー基を含有させて、抗体の抗原結合部位を利用可能な状態に保持することができる。その後、固定化した抗体を使用してサンプル由来のAa生体またはAa抗原を結合させることができるが、それらのサンプルは例えば唾液、歯垢、歯肉滲出液、痰、血液、尿、便、脳脊髄液、羊水、創傷滲出液、または組織を含む生体サンプルである。結合したAa生体またはAa抗原を、カラムマトリクスから（例えばpH変化によって）回収する。

【００５５】

本発明の抗体を免疫局在化の研究に使用し、種々の細胞事象または生理学的状態の際の本発明のポリペプチドの存在および分布を分析することもできる。抗体を使用して、受動免疫に関係する分子の同定および非タンパク質抗原の生合成に関係する分子の同定を行うこともできる。それらの分子の同定はワクチンの開発に有用でありうる。本発明の抗体（例えばモノクローナル抗体および１本鎖抗体を含む）を使用して、Aaに起因する疾病の回復の経過をモニタリングすることができる。動物由来の試験サンプル中のAaタンパク質に対するAa抗体の増加または減少を測定することによって、障害を改善することを目的とする特定の治療計画が有効かどうかを確認することができる。抗体は、例えば直接結合アッセイ（例えばRIA、ELISA、またはウェスタンブロットアッセイ）を使用して検出および／または定量することができる。

【００５６】

Aaに感染している疑いのある動物由来の試験サンプルを得ることにより、本発明の抗体

をAa感染の診断法に使用することができる。試験サンプルを、抗体－抗原複合体（すなわち免疫複合体）の生成が可能な条件下で、本発明の抗体と接触させる。抗体－抗原複合体の量は、当該分野で周知の方法によって測定できる。コントロールサンプルで生成されたものよりレベルが高ければ、Aa感染を示している。あるいはまた、本発明のポリペプチドを試験サンプルと接触させることができる。陽性生体サンプル中のAa抗体は、好適な条件下で抗原－抗体複合体を生成する。抗体－抗原複合体の量は、当該分野で周知の方法によって測定できる。

【００５７】

Aaに起因する疾病の治療、改善、または予防の方法

本発明のポリペプチド、ポリヌクレオチド、および抗体を使用して、Aaに起因する疾病（例えば早期発症型歯周炎（例えば局所性および汎発性思春期前歯周炎、局所性および汎発性若年性歯周炎、および急速進行性または抗療性成人歯周炎、心内膜炎、甲状腺膿瘍、尿路感染症、脳膿瘍、および椎骨髄炎を含む）を治療、改善、または予防することができる。

【００５８】

例えば本発明のモノクローナル抗体のような抗体またはそのフラグメントを動物（例えばヒト）に投与することができる。本発明のある態様では、抗体またはそのフラグメントを、医薬的に許容されるキャリアーを含む医薬組成物で動物に投与する。医薬組成物は治療的有効量の抗体またはそのフラグメントを含有する。治療的有効量は、被験体においてAa感染の症状を改善する、またはAa生体の量を低減するのに有効な量である。

【００５９】

本発明のポリペプチドまたはポリヌクレオチドを使用して、宿主において免疫応答を誘発することができる。免疫原性ポリペプチドまたはポリヌクレオチドは、動物において免疫応答を誘導する能力のある本発明のポリペプチドまたはポリヌクレオチドである。本発明の免疫原性ポリペプチドまたはポリヌクレオチドは、動物の免疫系を感作するのに特に有用であり、その結果として免疫応答が起こり、これによってAa感染の影響が改善または予防される。動物モデルにおける免疫応答の誘発は、例えば最適な投与量または投与経路を決定するのに有用でありうる。免疫応答の誘発は、Aaに起因する疾病または感染を治療、予防、または改善するのにも有用でありうる。免疫応答には体液性免疫応答もしくは細胞介在型免疫応答、またはそれらの組み合わせがある。免疫応答は、例えばディフェンシンの生成の促進による、全身性宿主応答の促進を含んでもよい。

【００６０】

動物によるAaに対する抗体価の生成は、感染からの防御および感染のクリアランスに重要でありうる。ポリペプチドまたはポリヌクレオチドをデリバリーした後の抗体の検出および／または定量を使用して、抗体価の誘発に特に有効なエピトープを同定することができる。Aaに対する強い抗体反応に関与するエピトープは、異なる長さのAaポリペプチドに対する抗体を誘発させることによって同定できる。その後、特定のポリペプチドエピトープによって誘発される抗体を、例えばELISAアッセイを使用して試験し、いずれのポリペプチドが強い反応の生成に最も有効なエピトープを含有するかを確認できる。次いで、これらのエピトープまたはエピトープをコードするポリヌクレオチドを含有するポリペプチドまたは融合タンパク質を構築し、強い抗体反応を誘発するために使用できる。

【００６１】

本発明のポリペプチド、ポリヌクレオチド、または抗体を、哺乳動物（例えばマウス、ウサギ、モルモット、マカク、ヒヒ、チンパンジー、ヒト、ウシ、ヒツジ、ブタ、ウマ、イヌ、ネコ）またはニワトリもしくはアヒルのような動物に投与して、インビボにおいて抗体を誘発することができる。ポリヌクレオチドの注射は構築および修飾の簡易化に実用上、有益である。更に、ポリヌクレオチドの注射によって、宿主におけるポリペプチドの合成が起こる。従って、ポリペプチドは天然の翻訳後修飾、構造、およびコンフォメーションで宿主免疫系に存在する。ポリヌクレオチドは“裸DNA”として被験体に送達することができる。

【００６２】

　ポリヌクレオチド、ポリペプチド、または抗体の投与は当該分野で知られるいずれの方法によってもよく、例えば、筋肉内、静脈内、肺内、筋肉内、皮内、腹膜内、または皮下注射、エアロゾル、鼻腔内、輸液ポンプ、坐薬、粘膜、局所、および経口（生物学的弾道銃（biological ballistic gun；“遺伝子銃”）を使用する注射を含む）が挙げられる。ポリヌクレオチド、ポリペプチド、または抗体は経口投与のためのタンパク質キャリアーを伴うことができる。投与方法を併用して免疫応答を誘発することもできる。抗体を約０．５ｍｇから約２００ｍｇの日用量で投与することができる。本発明のある態様では、抗体を約２０から約１００mgの日用量で投与する。

【００６３】

　治療に使用するための医薬的に許容されるキャリアーおよび希釈剤は当該分野で周知であり、例えばレミントンの薬学（Remington's Pharmaceutical Sciences, Mack Publishing 社 (A.R. Gennaro編 (1985)）に記載されている。キャリアーそのものは宿主に有害な抗体の生成を誘導すべきではない。それらのキャリアーには、限定されるわけではないが、大型で代謝が遅い巨大分子（例えばタンパク質、多糖、例えばラテックス機能性化セファロース、アガロース、セルロース、セルロースビーズなど）、ポリ乳酸、ポリグリコール酸、重合アミノ酸（例えばポリグルタミン酸、ポリリジンなど）、アミノ酸コポリマー、ペプトイド、リピトイド、および不活性無毒性ウィルス粒子または細菌細胞等が含まれる。リポソーム、ヒドロゲル、シクロデキストリン、生分解性ナノカプセル、および生物接着性剤（bioadhesive）も本発明の組成物のキャリアーとして使用できる。

【００６４】

　医薬的に許容される塩も本発明の組成物に使用することができ、それらは例えば、金属塩（例えば塩酸塩、臭化水素酸塩、リン酸塩、または硫酸塩）、並びに有機酸の塩（例えば酢酸塩、プロピオン酸塩、マロン酸塩、または安息香酸塩）である。特に有用なタンパク質基質は、血清アルブミン、キーホールリンペットヘモシアニン、免疫グロブリン分子、サイログロブリン、オボアルブミン、破傷風トキソイド、および当業者に周知の他のタンパク質である。本発明の組成物は液体または添加剤、例えば水、食塩水、リン酸バッファー液、リンガー液、ハンクス液、グルコース、グリセロール、デキストロース、マロデキストリン、エタノールなど（単独で、または組み合わせて）、並びに基質、例えば湿潤剤、乳化剤、浸透圧調整剤、界面活性剤、またはpH調整剤を含有することもできる。更なる活性剤、例えば殺菌剤を使用することもできる。

【００６５】

　必要により、リンパ球に対する免疫原性提示を向上する共刺激分子（例えばB7－1またはB7－2）、またはサイトカイン（MIP1α、GM－CSF、IL－2、およびIL－12）を本発明の組成物に含有させることができる。必要により、アジュバントを組成物に含有させることもできる。アジュバントは特異的免疫応答を非特異に増加させるために使用できる物質である。一般に、本発明のアジュバントおよびポリペプチドは混合した後に免疫系に提示するか、または別々に、しかし動物の同じ部位に提示する。アジュバントは、例えば以下を含有することができる：オイルアジュバント（例えばフロイントの完全および不完全アジュバント）金属塩（例えば$AlK(SO_4)_2$；$AlNa(SO_4)_2$、$AlNH_4(SO_4)$、シリカ、アラム、$Al(OH)_3$、および$Ca_3(PO_4)_2$）、ポリヌクレオチド（すなわちPolyicおよびポリAU酸）、およびある種の天然物質（例えば結核菌（Mycobacterium tuberculosis）由来のワックスD、並びにコリネバクテリウム・パルヴム（Corynebacterium parvum）、百日咳菌（Bordetella pertussis）、およびブルセラ菌属のメンバーに見られる物質）。使用できるアジュバントには、限定される訳ではないが以下がある：MF59－0、水酸化アルミニウム、N－アセチルームラミールーL－トレオニルーD－イソグルタミン（thr－MDP）、N－アセチルーノルームラミルーL－アラニルーD－イソグルタミン（CGP 11637、ノルーMDPとも呼ばれる)、N－アセチルムラミールーL－アラニルーD－イソグルタミニルーL－アラニン－2－(1'－2'－ジパルミトイルーsn－グリセロ－3－ヒドロキシホスホリルオキシ)－エチルアミン（CGP 19835A、MTP－PEと呼ばれる）、およびRIBIで、細菌から抽出された３つの成分、モノ

ホスホリルリピッドA、トレハロースジミコレート、および細胞壁骨格（MPL+TDM+CWS）を2%スクアレン／ツイーン80エマルジョンに混合して含有するもの。

【００６６】

本発明の組成物は、経口錠剤、バッカル錠、トローチ、カプセル、エリキシル、懸濁液、シロップ、オブラート、注射用製剤、マウスウォッシュ、歯磨き粉などに調製することができる。それらの組成物および製剤中の１またはそれ以上の本発明のポリペプチド、ポリヌクレオチド、または抗体のパーセンテージは単位重量の0.１%から60%で様々でありうる。

【００６７】

ポリペプチドまたはポリヌクレオチドの投与によって動物における免疫応答を誘発することができ、これは少なくとも１週間、１ヶ月、３ヶ月、６ヶ月、１年、またはそれ以上の間持続する。必要により、初期注射後１ヶ月、３ヶ月、６ヶ月、１年、またはそれ以上の時点でポリペプチドまたはポリヌクレオチドを１回以上追加注射し、動物における免疫応答を保持することができる。必要により、共刺激分子またはアジュバントを組成物の前、後、または共に与えてもよい。

【００６８】

ポリペプチド、ポリヌクレオチド、またはそれらを組み合わせたものを含有する本発明の組成物を、使用される特定の組成物に適合する方法で、ELISA等により検出される免疫応答を誘発するのに有効な量で投与する。ポリヌクレオチドを大型哺乳動物（例えばヒヒ、チンパンジー、またはヒト）に、1ng/kg、10ng/kg、100ng/kg、1000ng/kg、0.001mg/kg、0.1mg/kg、または0.5 mg/kgの用量で筋肉内注射することができる。ポリペプチドを大型哺乳動物（例えばヒト）に、0.01、0.05、0.5、0.75、1.0、1.5、2.0、2.5、5、または10mg/kgの用量で筋肉内注射することができる。

【００６９】

ポリペプチド、ポリヌクレオチド、もしくは抗体、またはその組み合わせをAaに感染していない動物、またはAa感染した動物のいずれにも投与できる。組成物中のポリヌクレオチド、ポリペプチド、または抗体の特定の用量は多くの因子に依存し、それらには、限定されるわけではないが、組成物を投与する哺乳動物の種、年齢、性別、併用する医薬品、一般的な状態、および組成物の投与方法等が含まれる。本発明の組成物の有効量は、日常的な実験のみを用いることにより容易に決定できる。

【００７０】

本発明の方法に使用する原料はキットの形態であってもよい。キットは方法に使用される１またはそれ以上の要素を含むことができる。例えば、キットは容器内に本発明の抗体を含み、別の容器内にAaポリペプチドを含むことができる。キットおよび容器にラベルを付け、キットは容器内の要素の使用説明書を含む。キットの成分は、例えば液体または凍結乾燥した形態であってもよい。

【００７１】

本明細書に引用する全ての文献は、参照により本明細書に組み込まれる。

【配列表】

```
                         SEQUENCE LISTING

<110>  Handfield, Martin
       Hillman, Jeffrey
       Progulske-Fox, Ann

<120>  Identification of Actinobacillus actinomycetemcomitans Antigens for
Use in the Diagnosis, Treatment, and Monitoring of Periodontal Diseases

<130>  MBHB01-662B

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    35                      40                  45

ccg ata aaa gaa acc ggt acg cgt tta ggt gaa gtg act tca gaa gtt       192
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gca caa caa acc ggt tta ata cag ggc aca ccg gtt gtg gtc ggc ggc       240
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ggg gac gtg cag tta ggt tgt att ggt tta ggc gtc acc gag ccc gct       288
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                85                  90                  95

caa gcg gca gtt atc ggc ggt acg ttc tgg caa caa gtg gtg aat tta       336
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            100                 105                 110

ccg cag gcg gtg acc gac ccg gaa atg aat gta cgt att aac ccg cac       384
Pro Gln Ala Val Thr Asp Pro Glu Met Asn Val Arg Ile Asn Pro His
    115                     120                 125

gtt atc ccg ccg tta gta cag gcg gaa tcc att agc ttt ttc acc aga       432
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145                 150                 155                 160

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Pro Ile Lys Glu Thr Gly Thr Arg Leu Gly Glu Val Thr Ser Glu Val
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Ala Gln Gln Thr Gly Leu Ile Gln Gly Thr Pro Val Val Val Gly Gly
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Gly Asp Val Gln Leu Gly Cys Ile Gly Leu Gly Val Thr Glu Pro Ala
                85                  90                  95


Gln Ala Ala Val Ile Gly Gly Thr Phe Trp Gln Gln Val Val Asn Leu
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Pro Gln Ala Val Thr Asp Pro Glu Met Asn Val Arg Ile Asn Pro His
        115                 120                 125


Val Ile Pro Pro Leu Val Gln Ala Glu Ser Ile Ser Phe Phe Thr Arg
    130                 135                 140


Leu Thr Met Arg Trp Phe Arg Asp Ala Phe Cys Glu Glu Glu Lys Arg
145                 150                 155                 160
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Asn Pro Arg Pro Ser Asn Asp Lys Ile Asn Gly Ala Thr Ile Asp Val
            20                  25                  30

cgt ttg ggc aat tcc ttc cgc gta ttt cgt gaa cat tcc gcc cct tac       144
Arg Leu Gly Asn Ser Phe Arg Val Phe Arg Glu His Ser Ala Pro Tyr
        35                  40                  45

att gat ttg agc ggt ccg aaa gaa gaa gtg tcg gcg cag ttg gaa tcg       192
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gtc atg agc gat gaa atg att atc ggt gat gac gaa gcc ttc ttt tta       240
Val Met Ser Asp Glu Met Ile Ile Gly Asp Asp Glu Ala Phe Phe Leu
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cat ccc ggc gtg ctg gcg ctt gcc acg act ttg gaa tca gta aaa ctg       288
His Pro Gly Val Leu Ala Leu Ala Thr Thr Leu Glu Ser Val Lys Leu
                85                  90                  95

ccg gcg aat att atc ggt tgg ctg gac ggg cgt tct tct ttg gcg cgt       336
Pro Ala Asn Ile Ile Gly Trp Leu Asp Gly Arg Ser Ser Leu Ala Arg
            100                 105                 110

ttg ggg ttg atg gta cac gtc acc gcc cat cgt atc gac cca ggc tgg       384
Leu Gly Leu Met Val His Val Thr Ala His Arg Ile Asp Pro Gly Trp
        115                 120                 125

gaa ggc aaa atc gtg ttg gaa ttt tac aat tcc ggc aaa tta ccg tta       432
Glu Gly Lys Ile Val Leu Glu Phe Tyr Asn Ser Gly Lys Leu Pro Leu
    130                 135                 140

gcg tta cgc ccg aat atg att atc ggc gcc ttg agt ttc gaa gtg tta       480
Ala Leu Arg Pro Asn Met Ile Ile Gly Ala Leu Ser Phe Glu Val Leu
145                 150                 155                 160

agc gga ccg gcg gcg cgt ccg tac agc agc cgc aaa gac gca aaa tac       528
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Ser Gly Pro Ala Ala Arg Pro Tyr Ser Ser Arg Lys Asp Ala Lys Tyr
                165                 170                 175

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            180                 185                 190


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Arg Leu Gly Asn Ser Phe Arg Val Phe Arg Glu His Ser Ala Pro Tyr
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Ile Asp Leu Ser Gly Pro Lys Glu Glu Val Ser Ala Gln Leu Glu Ser
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Val Met Ser Asp Glu Met Ile Ile Gly Asp Asp Glu Ala Phe Phe Leu
65                  70                  75                  80


His Pro Gly Val Leu Ala Leu Ala Thr Thr Leu Glu Ser Val Lys Leu
                85                  90                  95


Pro Ala Asn Ile Ile Gly Trp Leu Asp Gly Arg Ser Ser Leu Ala Arg
            100                 105                 110


Leu Gly Leu Met Val His Val Thr Ala His Arg Ile Asp Pro Gly Trp
        115                 120                 125


Glu Gly Lys Ile Val Leu Glu Phe Tyr Asn Ser Gly Lys Leu Pro Leu
    130                 135                 140


Ala Leu Arg Pro Asn Met Ile Ile Gly Ala Leu Ser Phe Glu Val Leu
145                 150                 155                 160


Ser Gly Pro Ala Ala Arg Pro Tyr Ser Ser Arg Lys Asp Ala Lys Tyr
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Lys Asn Gln Gln Asn Ala Val Ala Ser Arg Ile Asp Glu Asp Lys
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aga tca aaa ata cat tta att gac ggc aag ctt cct ttc ggc aat gcc          96
Arg Ser Lys Ile His Leu Ile Asp Gly Lys Leu Pro Phe Gly Asn Ala
            20                  25                  30

acc gaa ctg ggt ttc gtc ggg ctt cat gct atg cgc atc ggc gaa tgg         144
Thr Glu Leu Gly Phe Val Gly Leu His Ala Met Arg Ile Gly Glu Trp
        35                  40                  45

ctg gag caa ccg tta tat ttg gtg gaa acc caa ccg aac gac aac cgc         192
Leu Glu Gln Pro Leu Tyr Leu Val Glu Thr Gln Pro Asn Asp Asn Arg
    50                  55                  60

acc tat ttt tct tta cgc gat caa ctg ccg ctg ccg caa gcg caa ttt         240
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65                  70                  75                  80

aat ctg ttg agc tgc ggc gtg gag tta aat cat ttc tat cag acc cat         288
Asn Leu Leu Ser Cys Gly Val Glu Leu Asn His Phe Tyr Gln Thr His
                85                  90                  95

caa ttc tgc gga aag tgc ggt gga aaa acc gag caa atg cag gag gaa         336
Gln Phe Cys Gly Lys Cys Gly Gly Lys Thr Glu Gln Met Gln Glu Glu
            100                 105                 110

tgg gcg gta aaa tgc cgt gcc tgc ggt ttt cat acc tat ccc gtc att         384
Trp Ala Val Lys Cys Arg Ala Cys Gly Phe His Thr Tyr Pro Val Ile
        115                 120                 125

tgc cct tcc att atc gtt gca gta cga cac gat tca caa atc ctg ctg         432
Cys Pro Ser Ile Ile Val Ala Val Arg His Asp Ser Gln Ile Leu Leu
    130                 135                 140

gca aat cat atg cgc cac aaa ggc ggc att tac acc acg ttg gcg ggt         480
Ala Asn His Met Arg His Lys Gly Gly Ile Tyr Thr Thr Leu Ala Gly
145                 150                 155                 160

ttt gtg gaa gta ggc gaa acc ttt gag gat gcg gta cat cgc gaa att         528
Phe Val Glu Val Gly Glu Thr Phe Glu Asp Ala Val His Arg Glu Ile
                165                 170                 175

tgg gag gaa acc caa atc aaa gta aaa aat ttg cgt tat ttc gac agc         576
Trp Glu Glu Thr Gln Ile Lys Val Lys Asn Leu Arg Tyr Phe Asp Ser
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tat gaa gga ggc gag att act att cag cgt gaa gaa ctt tat gac gca       672
Tyr Glu Gly Gly Glu Ile Thr Ile Gln Arg Glu Glu Leu Tyr Asp Ala
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caa tgg ttt gat tgc gac caa ccg ttg ccc gaa ctg cca ccg cac ggc       720
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225                 230                 235                 240

acc atc gca cgc aaa tta att gaa acc aca ctt gaa ttg tgt aaa cag       768
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Thr Glu Leu Gly Phe Val Gly Leu His Ala Met Arg Ile Gly Glu Trp
        35                  40                  45


Leu Glu Gln Pro Leu Tyr Leu Val Glu Thr Gln Pro Asn Asp Asn Arg
    50                  55                  60


Thr Tyr Phe Ser Leu Arg Asp Gln Leu Pro Leu Pro Gln Ala Gln Phe
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Asn Leu Leu Ser Cys Gly Val Glu Leu Asn His Phe Tyr Gln Thr His
                85                  90                  95


Gln Phe Cys Gly Lys Cys Gly Gly Lys Thr Glu Gln Met Gln Glu Glu
            100                 105                 110


Trp Ala Val Lys Cys Arg Ala Cys Gly Phe His Thr Tyr Pro Val Ile
        115                 120                 125


Cys Pro Ser Ile Ile Val Ala Val Arg His Asp Ser Gln Ile Leu Leu
    130                 135                 140
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Ala Asn His Met Arg His Lys Gly Gly Ile Tyr Thr Thr Leu Ala Gly
145                 150                 155                 160

Phe Val Glu Val Gly Glu Thr Phe Glu Asp Ala Val His Arg Glu Ile
                165                 170                 175

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

Gln Pro Trp Ala Phe Pro Asn Ser Gln Met Val Gly Phe Leu Ala Asp
        195                 200                 205

Tyr Glu Gly Gly Glu Ile Thr Ile Gln Arg Glu Glu Leu Tyr Asp Ala
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Gln Trp Phe Asp Cys Asp Gln Pro Leu Pro Glu Leu Pro Pro His Gly
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Thr Ile Ala Arg Lys Leu Ile Glu Thr Thr Leu Glu Leu Cys Lys Gln
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aac ccg att tcc gtt gaa atg tcc gcc atg cgt gtt tca tta ttg acc        96
Asn Pro Ile Ser Val Glu Met Ser Ala Met Arg Val Ser Leu Leu Thr
            20                  25                  30

ggt tta ttg ggc gca gtg att tat aat caa aac cgc caa caa agt cgc       144
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gtg cgt ttg ttt gag cac ggt tta cgt ttt att ccg gac gaa aag gcc       192
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gaa ttc ggc gtg cac caa gag ccg gtt ttt gcc gcg gtg atg aca ggg       240
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                85                  90                  95

tac gac tta aaa ggc tac att gaa aac tta ctt tcg tta agt tct gct       336
Tyr Asp Leu Lys Gly Tyr Ile Glu Asn Leu Leu Ser Leu Ser Ser Ala
            100                 105                 110

gga aat cgg gca aaa ttt gta gca aaa tca tac aca gca ttg cat ccg       384
Gly Asn Arg Ala Lys Phe Val Ala Lys Ser Tyr Thr Ala Leu His Pro
        115                 120                 125

ggt caa tct gcg gcc att atg ctg gat ggt gaa gaa atc gga ttt att       432
Gly Gln Ser Ala Ala Ile Met Leu Asp Gly Glu Glu Ile Gly Phe Ile
    130                 135                 140

ggt caa ctt cac ccg act atc gcg caa aaa att ggt ctt acc gga aaa       480
Gly Gln Leu His Pro Thr Ile Ala Gln Lys Ile Gly Leu Thr Gly Lys
145                 150                 155                 160

gca ttt gtt tgt gaa att tcg gtc gca cac att tct cga cga gaa gtc       528
Ala Phe Val Cys Glu Ile Ser Val Ala His Ile Ser Arg Arg Glu Val
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gcc cgt gcc aaa gaa att tcc cgt ttc cct gct aat cgt cgt gat ttg       576
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gcg gtt gtg gtt gcg gat aat atc cct gca aat gac gtg ctg gaa gtg       624
Ala Val Val Val Ala Asp Asn Ile Pro Ala Asn Asp Val Leu Glu Val
        195                 200                 205

tgt cgt aca gca ggc gga gat aaa tta acc caa atc aat tta ttt gat       672
Cys Arg Thr Ala Gly Gly Asp Lys Leu Thr Gln Ile Asn Leu Phe Asp
    210                 215                 220

gtt tac cac gga acc ggt gtt gct gca ggg cat aag agc tta gct atc       720
Val Tyr His Gly Thr Gly Val Ala Ala Gly His Lys Ser Leu Ala Ile
225                 230                 235                 240

agc tta gta att caa gat aat gaa aaa acc ctt gaa gaa gat gaa att       768
Ser Leu Val Ile Gln Asp Asn Glu Lys Thr Leu Glu Glu Asp Glu Ile
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<213>  Actinobacillus actinomycetemcomitans

<400>  8

Lys Ile Gln Ser Leu Leu His Pro Asp Val Lys Pro Met Val Leu Pro
1               5                   10                  15
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```
Asn Pro Ile Ser Val Glu Met Ser Ala Met Arg Val Ser Leu Leu Thr
            20                  25                  30

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

Val Arg Leu Phe Glu His Gly Leu Arg Phe Ile Pro Asp Glu Lys Ala
    50                  55                  60

Glu Phe Gly Val His Gln Glu Pro Val Phe Ala Ala Val Met Thr Gly
65                  70                  75                  80

Leu Lys Ser Asn Glu Gln Trp Ser Glu Lys Ala Val Pro Ala Asp Phe
                85                  90                  95

Tyr Asp Leu Lys Gly Tyr Ile Glu Asn Leu Leu Ser Leu Ser Ser Ala
            100                 105                 110

Gly Asn Arg Ala Lys Phe Val Ala Lys Ser Tyr Thr Ala Leu His Pro
        115                 120                 125

Gly Gln Ser Ala Ala Ile Met Leu Asp Gly Glu Glu Ile Gly Phe Ile
    130                 135                 140

Gly Gln Leu His Pro Thr Ile Ala Gln Lys Ile Gly Leu Thr Gly Lys
145                 150                 155                 160

Ala Phe Val Cys Glu Ile Ser Val Ala His Ile Ser Arg Arg Glu Val
                165                 170                 175

Ala Arg Ala Lys Glu Ile Ser Arg Phe Pro Ala Asn Arg Arg Asp Leu
            180                 185                 190

Ala Val Val Val Ala Asp Asn Ile Pro Ala Asn Asp Val Leu Glu Val
        195                 200                 205

Cys Arg Thr Ala Gly Gly Asp Lys Leu Thr Gln Ile Asn Leu Phe Asp
    210                 215                 220

Val Tyr His Gly Thr Gly Val Ala Ala Gly His Lys Ser Leu Ala Ile
225                 230                 235                 240

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

<210>  9
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<211>  141
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(141)

<400>  9
gat cag cct gat tat gtc aac gcc gtc gct tgc ctg gaa acg gcg ctt       48
Asp Gln Pro Asp Tyr Val Asn Ala Val Ala Cys Leu Glu Thr Ala Leu
1               5                   10                  15

tct ccc ttc gca ttg ctt gat gaa tta caa cgt att gaa cag gaa caa       96
Ser Pro Phe Ala Leu Leu Asp Glu Leu Gln Arg Ile Glu Gln Glu Gln
            20                  25                  30

ggg cgt gtc cgt ctt cgt cgt tgg ggt gag cgc aca tta gat ctg          141
Gly Arg Val Arg Leu Arg Arg Trp Gly Glu Arg Thr Leu Asp Leu
        35                  40                  45


<210>  10
<211>  47
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  10

Asp Gln Pro Asp Tyr Val Asn Ala Val Ala Cys Leu Glu Thr Ala Leu
1               5                   10                  15


Ser Pro Phe Ala Leu Leu Asp Glu Leu Gln Arg Ile Glu Gln Glu Gln
            20                  25                  30


Gly Arg Val Arg Leu Arg Arg Trp Gly Glu Arg Thr Leu Asp Leu
        35                  40                  45


<210>  11
<211>  597
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(597)

<400>  11
ggt ctg agt ttt act ttc ctt tca tca ttg gct ttt gca gaa tct tgg       48
Gly Leu Ser Phe Thr Phe Leu Ser Ser Leu Ala Phe Ala Glu Ser Trp
1               5                   10                  15

act atg cat att tcc gaa gat ggc gtg ata acc gat aaa acc gct caa       96
Thr Met His Ile Ser Glu Asp Gly Val Ile Thr Asp Lys Thr Ala Gln
            20                  25                  30

cag ctt aat ccg gct agg tat gcc gga gct gtg tac aaa caa caa ttt      144
Gln Leu Asn Pro Ala Arg Tyr Ala Gly Ala Val Tyr Lys Gln Gln Phe
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```
        35                  40                  45

tct ttt tct gac agc ggc ggg caa ggt aaa acc act tac att aat caa        192
Ser Phe Ser Asp Ser Gly Gly Gln Gly Lys Thr Thr Tyr Ile Asn Gln
    50                  55                  60

aat aac ggc aag aaa ttc gat cct aaa aat gct gct gat gtg agt gaa        240
Asn Asn Gly Lys Lys Phe Asp Pro Lys Asn Ala Ala Asp Val Ser Glu
65                  70                  75                  80

ttg ggt aaa agc atc gcc ttt gaa gtg ttt gag att aaa gaa aat aaa        288
Leu Gly Lys Ser Ile Ala Phe Glu Val Phe Glu Ile Lys Glu Asn Lys
                85                  90                  95

gac tct cac tca gta ttt gaa tcc ggc gcc ggc att tgt tac ggc ttc        336
Asp Ser His Ser Val Phe Glu Ser Gly Ala Gly Ile Cys Tyr Gly Phe
            100                 105                 110

aaa tat acc gat ggc gtc gcg ttc acc gat tct aca acc tat tat gta        384
Lys Tyr Thr Asp Gly Val Ala Phe Thr Asp Ser Thr Thr Tyr Tyr Val
        115                 120                 125

gat aaa tcc aag cag caa tat tac gcc agt atc atc ggc gcc acc gta        432
Asp Lys Ser Lys Gln Gln Tyr Tyr Ala Ser Ile Ile Gly Ala Thr Val
    130                 135                 140

tct tct gac gtg gaa ccg aaa aac gtg caa tat gcg ccg gtg ttt aat        480
Ser Ser Asp Val Glu Pro Lys Asn Val Gln Tyr Ala Pro Val Phe Asn
145                 150                 155                 160

att cag gat ccc gag tta gat aaa gaa gta aag tcg gaa gaa caa cga        528
Ile Gln Asp Pro Glu Leu Asp Lys Glu Val Lys Ser Glu Glu Gln Arg
                165                 170                 175

aac ggt aaa acc ttg att aat aaa aat ttg caa aag agc aga gaa att        576
Asn Gly Lys Thr Leu Ile Asn Lys Asn Leu Gln Lys Ser Arg Glu Ile
            180                 185                 190

ctt tct aac gta gtt tgt aag                                            597
Leu Ser Asn Val Val Cys Lys
        195


<210>  12
<211>  199
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  12

Gly Leu Ser Phe Thr Phe Leu Ser Ser Leu Ala Phe Ala Glu Ser Trp
1               5                   10                  15


Thr Met His Ile Ser Glu Asp Gly Val Ile Thr Asp Lys Thr Ala Gln
            20                  25                  30


Gln Leu Asn Pro Ala Arg Tyr Ala Gly Ala Val Tyr Lys Gln Gln Phe
        35                  40                  45
```

```
Ser Phe Ser Asp Ser Gly Gly Gln Gly Lys Thr Thr Tyr Ile Asn Gln
    50                  55                  60

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

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

Asp Ser His Ser Val Phe Glu Ser Gly Ala Gly Ile Cys Tyr Gly Phe
            100                 105                 110

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

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

Ser Ser Asp Val Glu Pro Lys Asn Val Gln Tyr Ala Pro Val Phe Asn
145                 150                 155                 160

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

Asn Gly Lys Thr Leu Ile Asn Lys Asn Leu Gln Lys Ser Arg Glu Ile
            180                 185                 190

Leu Ser Asn Val Val Cys Lys
        195


<210>  13
<211>  288
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(288)

<400>  13
atg caa aaa ttg tta ctc gtc aca gtg att agt ggt gtt tta gtt gct        48
Met Gln Lys Leu Leu Leu Val Thr Val Ile Ser Gly Val Leu Val Ala
1               5                   10                  15

tgt tct tct aag gct cca caa atc aat caa gct cct tta gat aag cag        96
Cys Ser Ser Lys Ala Pro Gln Ile Asn Gln Ala Pro Leu Asp Lys Gln
            20                  25                  30

aca gtt gaa gct tat caa gcg aaa gtg tat agc ggt aat acg gtg tcg       144
Thr Val Glu Ala Tyr Gln Ala Lys Val Tyr Ser Gly Asn Thr Val Ser
```

```
            35                  40                  45

aag aaa tat caa gta aga gac gtt aaa ccg gaa gac aat gtg tta aat        192
Lys Lys Tyr Gln Val Arg Asp Val Lys Pro Glu Asp Asn Val Leu Asn
    50                  55                  60

gct agt gat tcg gaa ccg aaa acc gtg att tat cgc gag cgt cag cca        240
Ala Ser Asp Ser Glu Pro Lys Thr Val Ile Tyr Arg Glu Arg Gln Pro
65                  70                  75                  80

aga ctg gtt gtg aca ccg agc att ggc tat tat cgc ggt tgg cac tgg        288
Arg Leu Val Val Thr Pro Ser Ile Gly Tyr Tyr Arg Gly Trp His Trp
                85                  90                  95


<210>  14
<211>  96
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  14

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


Cys Ser Ser Lys Ala Pro Gln Ile Asn Gln Ala Pro Leu Asp Lys Gln
            20                  25                  30


Thr Val Glu Ala Tyr Gln Ala Lys Val Tyr Ser Gly Asn Thr Val Ser
        35                  40                  45


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


Ala Ser Asp Ser Glu Pro Lys Thr Val Ile Tyr Arg Glu Arg Gln Pro
65                  70                  75                  80


Arg Leu Val Val Thr Pro Ser Ile Gly Tyr Tyr Arg Gly Trp His Trp
                85                  90                  95


<210>  15
<211>  403
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(402)

<400>  15
cca aac tgg ttg cgc cgg caa gtc ggt gtc gtc ttg caa gat aat gtg        48
Pro Asn Trp Leu Arg Arg Gln Val Gly Val Val Leu Gln Asp Asn Val
1               5                   10                  15

ttg ctt aat cga agt atc aga gag aat att gcg tta acc aat ccg gga        96
```

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

atg cca atg gaa aag gtt att gcc gcg gca aaa ctt gcg gga gcg cac      144
Met Pro Met Glu Lys Val Ile Ala Ala Ala Lys Leu Ala Gly Ala His
        35                  40                  45

gat ttt att tct gaa tta aga gaa ggt tat aac acg gtt gtg ggg gaa      192
Asp Phe Ile Ser Glu Leu Arg Glu Gly Tyr Asn Thr Val Val Gly Glu
    50                  55                  60

cag gga gcc ggt ttg tcc gga gga caa cgt caa cgg atc gcg ata gca      240
Gln Gly Ala Gly Leu Ser Gly Gly Gln Arg Gln Arg Ile Ala Ile Ala
65                  70                  75                  80

agg gca cta gtc aat aac cca agg att ttg att ttt gat gaa gca acc      288
Arg Ala Leu Val Asn Asn Pro Arg Ile Leu Ile Phe Asp Glu Ala Thr
                85                  90                  95

agt gca ctt gat tac gaa tct gaa aat atc att atg cat aat atg cat      336
Ser Ala Leu Asp Tyr Glu Ser Glu Asn Ile Ile Met His Asn Met His
            100                 105                 110

aaa att tgc caa aat cgt act gtg ctt atc att gct cac cgc ctt tct      384
Lys Ile Cys Gln Asn Arg Thr Val Leu Ile Ile Ala His Arg Leu Ser
        115                 120                 125

act gta aaa aat gct gat c                                            403
Thr Val Lys Asn Ala Asp
    130


<210>  16
<211>  134
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  16

Pro Asn Trp Leu Arg Arg Gln Val Gly Val Val Leu Gln Asp Asn Val
1               5                   10                  15


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


Met Pro Met Glu Lys Val Ile Ala Ala Ala Lys Leu Ala Gly Ala His
        35                  40                  45


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


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


Arg Ala Leu Val Asn Asn Pro Arg Ile Leu Ile Phe Asp Glu Ala Thr
                85                  90                  95
```

```
Ser Ala Leu Asp Tyr Glu Ser Glu Asn Ile Ile Met His Asn Met His
            100                 105                 110


Lys Ile Cys Gln Asn Arg Thr Val Leu Ile Ile Ala His Arg Leu Ser
        115                 120                 125


Thr Val Lys Asn Ala Asp
    130


<210>  17
<211>  374
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(372)

<400>  17
cac cgt tta ccg gaa atg att aac caa att cgc ggt ggc aaa agt gct        48
His Arg Leu Pro Glu Met Ile Asn Gln Ile Arg Gly Gly Lys Ser Ala
1               5                   10                  15

gtg gtg gat att agt ttc ccg gaa atc gaa aaa ttc gac cgg ttg ccg        96
Val Val Asp Ile Ser Phe Pro Glu Ile Glu Lys Phe Asp Arg Leu Pro
            20                  25                  30

gaa ccg cgc gca gaa ggc ccg act gcc ttt gtt tct atc atg gaa ggc       144
Glu Pro Arg Ala Glu Gly Pro Thr Ala Phe Val Ser Ile Met Glu Gly
        35                  40                  45

tgt aat aaa tac tgt act tac tgc gtg gtg cct tat acc cgt ggc gag       192
Cys Asn Lys Tyr Cys Thr Tyr Cys Val Val Pro Tyr Thr Arg Gly Glu
    50                  55                  60

gaa gtt agc cgt ccg gtg gat gat att tta ttt gaa att gcc cag ttg       240
Glu Val Ser Arg Pro Val Asp Asp Ile Leu Phe Glu Ile Ala Gln Leu
65                  70                  75                  80

gcg gag caa ggc gtg cgc gaa gtg aat ttg ctc ggc cag aac gtg aac       288
Ala Glu Gln Gly Val Arg Glu Val Asn Leu Leu Gly Gln Asn Val Asn
                85                  90                  95

gcc tat cgt ggt ccg aca ttt gat ggc gat att tgc acc ttc gcc gaa       336
Ala Tyr Arg Gly Pro Thr Phe Asp Gly Asp Ile Cys Thr Phe Ala Glu
            100                 105                 110

ttg ttg cgt ttg gta gcg gcc att gac ggt atc gat cg                    374
Leu Leu Arg Leu Val Ala Ala Ile Asp Gly Ile Asp
        115                 120


<210>  18
<211>  124
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans
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```
<400>  18

His Arg Leu Pro Glu Met Ile Asn Gln Ile Arg Gly Gly Lys Ser Ala
1               5                   10                  15


Val Val Asp Ile Ser Phe Pro Glu Ile Glu Lys Phe Asp Arg Leu Pro
            20                  25                  30


Glu Pro Arg Ala Glu Gly Pro Thr Ala Phe Val Ser Ile Met Glu Gly
        35                  40                  45


Cys Asn Lys Tyr Cys Thr Tyr Cys Val Val Pro Tyr Thr Arg Gly Glu
    50                  55                  60


Glu Val Ser Arg Pro Val Asp Asp Ile Leu Phe Glu Ile Ala Gln Leu
65                  70                  75                  80


Ala Glu Gln Gly Val Arg Glu Val Asn Leu Leu Gly Gln Asn Val Asn
                85                  90                  95


Ala Tyr Arg Gly Pro Thr Phe Asp Gly Asp Ile Cys Thr Phe Ala Glu
            100                 105                 110


Leu Leu Arg Leu Val Ala Ala Ile Asp Gly Ile Asp
        115                 120


<210>  19
<211>  158
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(156)

<400>  19
cta agc gta ttc aac tac gcc cat ttg ccg agc cgt ttt gcc gga cag       48
Leu Ser Val Phe Asn Tyr Ala His Leu Pro Ser Arg Phe Ala Gly Gln
1               5                   10                  15

gcg aaa atc aag gat tgg cag ttg ccg aaa ccg gaa gcg aaa ctg gaa       96
Ala Lys Ile Lys Asp Trp Gln Leu Pro Lys Pro Glu Ala Lys Leu Glu
            20                  25                  30

att ctg caa aaa acc atc gaa acg ctg ggc aac gcc ggt tac aaa ttt      144
Ile Leu Gln Lys Thr Ile Glu Thr Leu Gly Asn Ala Gly Tyr Lys Phe
        35                  40                  45

atc ggc atg gat ca                                                   158
Ile Gly Met Asp
    50
```

```
<210>  20
<211>  52
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  20

Leu Ser Val Phe Asn Tyr Ala His Leu Pro Ser Arg Phe Ala Gly Gln
1               5                   10                  15


Ala Lys Ile Lys Asp Trp Gln Leu Pro Lys Pro Glu Ala Lys Leu Glu
            20                  25                  30


Ile Leu Gln Lys Thr Ile Glu Thr Leu Gly Asn Ala Gly Tyr Lys Phe
        35                  40                  45


Ile Gly Met Asp
    50


<210>  21
<211>  1098
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(1095)

<400>  21
aat cag atg aat aaa acc tta aaa att tca ttg ttt gcc atg att tcc       48
Asn Gln Met Asn Lys Thr Leu Lys Ile Ser Leu Phe Ala Met Ile Ser
1               5                   10                  15

gcg tta gct ttt aat acc atg gca aat aca caa ccg tta gcc gtg ttg       96
Ala Leu Ala Phe Asn Thr Met Ala Asn Thr Gln Pro Leu Ala Val Leu
            20                  25                  30

gaa ccg cag gta aac tat caa cag tta ctc acc caa cgg cag gtg gtg      144
Glu Pro Gln Val Asn Tyr Gln Gln Leu Leu Thr Gln Arg Gln Val Val
        35                  40                  45

gat gat tta atc gcg cag gcg gtg aaa atc caa aat tca ccg gcg cgg      192
Asp Asp Leu Ile Ala Gln Ala Val Lys Ile Gln Asn Ser Pro Ala Arg
    50                  55                  60

gtg tcc aat gcg ggc ttt acc gca aaa ttg cca agc aac atg gaa cgc      240
Val Ser Asn Ala Gly Phe Thr Ala Lys Leu Pro Ser Asn Met Glu Arg
65                  70                  75                  80

att gcc gcg att ttg ttg gaa gcc tat gaa ttg gaa cct tac cgc gtt      288
Ile Ala Ala Ile Leu Leu Glu Ala Tyr Glu Leu Glu Pro Tyr Arg Val
                85                  90                  95

gat ttt ctg ttc ggc gca gca aat gcc aac att tac aac ggc aat acg      336
Asp Phe Leu Phe Gly Ala Ala Asn Ala Asn Ile Tyr Asn Gly Asn Thr
            100                 105                 110
```

```
gac aaa gcc atc gag ctt tac caa aaa gtg ctc acg gtg gcg cct gat        384
Asp Lys Ala Ile Glu Leu Tyr Gln Lys Val Leu Thr Val Ala Pro Asp
        115                 120                 125

gat gtg aaa gca cat att tat tta acc gcg tgg aat cgt ttt aaa caa        432
Asp Val Lys Ala His Ile Tyr Leu Thr Ala Trp Asn Arg Phe Lys Gln
    130                 135                 140

aac caa ggg gaa acc gac aaa tac ttc acc cgc tta aaa gcg ctg gca        480
Asn Gln Gly Glu Thr Asp Lys Tyr Phe Thr Arg Leu Lys Ala Leu Ala
145                 150                 155                 160

ccg caa aaa gca gcg gaa ctg gag cag gtc ttc aag att att gat aac        528
Pro Gln Lys Ala Ala Glu Leu Glu Gln Val Phe Lys Ile Ile Asp Asn
                165                 170                 175

gcc gca agc caa ccg att agc gat aaa ttg gcg aat aaa ttg ccg gcg        576
Ala Ala Ser Gln Pro Ile Ser Asp Lys Leu Ala Asn Lys Leu Pro Ala
            180                 185                 190

gat tcc gcc att att acc ttg ggt tat gcg tta aat ccg gac ggc agt        624
Asp Ser Ala Ile Ile Thr Leu Gly Tyr Ala Leu Asn Pro Asp Gly Ser
        195                 200                 205

atg cac gac att ttg att cag cgt ttg gaa aaa acc ttg gaa atc gcc        672
Met His Asp Ile Leu Ile Gln Arg Leu Glu Lys Thr Leu Glu Ile Ala
    210                 215                 220

aaa caa aat cct gat gca ttg att att gtc acc ggc ggc atg ccg caa        720
Lys Gln Asn Pro Asp Ala Leu Ile Ile Val Thr Gly Gly Met Pro Gln
225                 230                 235                 240

aat aat cgt acg gaa ggg gca tta atg aaa caa tgg ctg att aac aaa        768
Asn Asn Arg Thr Glu Gly Ala Leu Met Lys Gln Trp Leu Ile Asn Lys
                245                 250                 255

ggc atc gat gcc aaa cgc att tat gcc gac aat tac gcc cgt tca acg        816
Gly Ile Asp Ala Lys Arg Ile Tyr Ala Asp Asn Tyr Ala Arg Ser Thr
            260                 265                 270

gtg gaa aat gcg tta ttt tcc cgt tac gcc ttg gcg aaa cac cat atc        864
Val Glu Asn Ala Leu Phe Ser Arg Tyr Ala Leu Ala Lys His His Ile
        275                 280                 285

aaa cac gcc tcc ctc atc agc tcc ggt agc cat gtg cgg cgc ggt cag        912
Lys His Ala Ser Leu Ile Ser Ser Gly Ser His Val Arg Arg Gly Gln
    290                 295                 300

gcg ttg ttt gaa atc gcc gcc ttg gaa tcc ggt ccg caa aac atc aaa        960
Ala Leu Phe Glu Ile Ala Ala Leu Glu Ser Gly Pro Gln Asn Ile Lys
305                 310                 315                 320

atc gaa acg gtg gcg gcg cta gac aaa ccg tta gac gaa tta caa aaa       1008
Ile Glu Thr Val Ala Ala Leu Asp Lys Pro Leu Asp Glu Leu Gln Lys
                325                 330                 335

gtg agt gaa aaa gat tta ttg gga atc tat cgc gac agc ctg aaa acc       1056
Val Ser Glu Lys Asp Leu Leu Gly Ile Tyr Arg Asp Ser Leu Lys Thr
            340                 345                 350
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```
atg ggc ttg cca atg ttt aat agc gga gca cta caa gat taa             1098
Met Gly Leu Pro Met Phe Asn Ser Gly Ala Leu Gln Asp
        355                 360                 365


<210>  22
<211>  365
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  22

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

Ala Leu Ala Phe Asn Thr Met Ala Asn Thr Gln Pro Leu Ala Val Leu
            20                  25                  30

Glu Pro Gln Val Asn Tyr Gln Gln Leu Leu Thr Gln Arg Gln Val Val
        35                  40                  45

Asp Asp Leu Ile Ala Gln Ala Val Lys Ile Gln Asn Ser Pro Ala Arg
    50                  55                  60

Val Ser Asn Ala Gly Phe Thr Ala Lys Leu Pro Ser Asn Met Glu Arg
65                  70                  75                  80

Ile Ala Ala Ile Leu Leu Glu Ala Tyr Glu Leu Glu Pro Tyr Arg Val
                85                  90                  95

Asp Phe Leu Phe Gly Ala Ala Asn Ala Asn Ile Tyr Asn Gly Asn Thr
            100                 105                 110

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

Asp Val Lys Ala His Ile Tyr Leu Thr Ala Trp Asn Arg Phe Lys Gln
    130                 135                 140

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

Pro Gln Lys Ala Ala Glu Leu Glu Gln Val Phe Lys Ile Ile Asp Asn
                165                 170                 175

Ala Ala Ser Gln Pro Ile Ser Asp Lys Leu Ala Asn Lys Leu Pro Ala
            180                 185                 190

Asp Ser Ala Ile Ile Thr Leu Gly Tyr Ala Leu Asn Pro Asp Gly Ser
```

```
        195                 200                 205

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

Lys Gln Asn Pro Asp Ala Leu Ile Ile Val Thr Gly Gly Met Pro Gln
225                 230                 235                 240

Asn Asn Arg Thr Glu Gly Ala Leu Met Lys Gln Trp Leu Ile Asn Lys
                245                 250                 255

Gly Ile Asp Ala Lys Arg Ile Tyr Ala Asp Asn Tyr Ala Arg Ser Thr
            260                 265                 270

Val Glu Asn Ala Leu Phe Ser Arg Tyr Ala Leu Ala Lys His His Ile
        275                 280                 285

Lys His Ala Ser Leu Ile Ser Ser Gly Ser His Val Arg Arg Gly Gln
    290                 295                 300

Ala Leu Phe Glu Ile Ala Ala Leu Glu Ser Gly Pro Gln Asn Ile Lys
305                 310                 315                 320

Ile Glu Thr Val Ala Ala Leu Asp Lys Pro Leu Asp Glu Leu Gln Lys
                325                 330                 335

Val Ser Glu Lys Asp Leu Leu Gly Ile Tyr Arg Asp Ser Leu Lys Thr
            340                 345                 350

Met Gly Leu Pro Met Phe Asn Ser Gly Ala Leu Gln Asp
        355                 360                 365


<210>  23
<211>  134
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(132)

<400>  23
ttg gat caa ttc ccg tcc gac gtt tat caa ggc ggc gcg ggc act tcc        48
Leu Asp Gln Phe Pro Ser Asp Val Tyr Gln Gly Gly Ala Gly Thr Ser
1               5                   10                  15

gtc aac atg aat acg aac gaa gtg gtt gcg aat ctg gca ttg gaa att        96
Val Asn Met Asn Thr Asn Glu Val Val Ala Asn Leu Ala Leu Glu Ile
            20                  25                  30
```

```
tta gga cac aaa aaa ggc gaa tat aat tat ttg gat cc                  134
Leu Gly His Lys Lys Gly Glu Tyr Asn Tyr Leu Asp
        35                  40


<210>  24
<211>  44
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  24

Leu Asp Gln Phe Pro Ser Asp Val Tyr Gln Gly Gly Ala Gly Thr Ser
1               5                   10                  15


Val Asn Met Asn Thr Asn Glu Val Val Ala Asn Leu Ala Leu Glu Ile
            20                  25                  30


Leu Gly His Lys Lys Gly Glu Tyr Asn Tyr Leu Asp
        35                  40


<210>  25
<211>  380
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(378)

<400>  25
gat ccg aac agc ttc aaa ctg cgc ggc gaa ttg agc cac ggc aaa gac       48
Asp Pro Asn Ser Phe Lys Leu Arg Gly Glu Leu Ser His Gly Lys Asp
1               5                   10                  15

gtg gaa atc gac atg aac gtg att tta aac ggc aaa gtg cgg tta gga       96
Val Glu Ile Asp Met Asn Val Ile Leu Asn Gly Lys Val Arg Leu Gly
            20                  25                  30

aat cgg gtg aaa atc ggt gca ggt tgt gtg ttg act aac tgc gac atc      144
Asn Arg Val Lys Ile Gly Ala Gly Cys Val Leu Thr Asn Cys Asp Ile
        35                  40                  45

ggc gat gac gtg gaa atc aaa ccg tat tcc gtg ctg gaa gat gcc tcc      192
Gly Asp Asp Val Glu Ile Lys Pro Tyr Ser Val Leu Glu Asp Ala Ser
    50                  55                  60

gta ggc gcc aat gcc gcc atc gga ccg ttc tcc cgc tta cgt ccg ggc      240
Val Gly Ala Asn Ala Ala Ile Gly Pro Phe Ser Arg Leu Arg Pro Gly
65                  70                  75                  80

gcc gac ttg gcg gaa aac acc cac gtg ggc aat ttc gtg gaa atc aaa      288
Ala Asp Leu Ala Glu Asn Thr His Val Gly Asn Phe Val Glu Ile Lys
                85                  90                  95

aaa gcg tac atc ggc aaa ggc tcc aaa gtg aac cac tta acc tat gtg      336
Lys Ala Tyr Ile Gly Lys Gly Ser Lys Val Asn His Leu Thr Tyr Val
            100                 105                 110
```

```
ggc gac gcg gaa atc ggc aaa gat tgt aac ata ggc gca ggc gt           380
Gly Asp Ala Glu Ile Gly Lys Asp Cys Asn Ile Gly Ala Gly
        115                 120                 125


<210>  26
<211>  126
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  26

Asp Pro Asn Ser Phe Lys Leu Arg Gly Glu Leu Ser His Gly Lys Asp
1               5                   10                  15


Val Glu Ile Asp Met Asn Val Ile Leu Asn Gly Lys Val Arg Leu Gly
            20                  25                  30


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


Gly Asp Asp Val Glu Ile Lys Pro Tyr Ser Val Leu Glu Asp Ala Ser
    50                  55                  60


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


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


Lys Ala Tyr Ile Gly Lys Gly Ser Lys Val Asn His Leu Thr Tyr Val
            100                 105                 110


Gly Asp Ala Glu Ile Gly Lys Asp Cys Asn Ile Gly Ala Gly
        115                 120                 125


<210>  27
<211>  468
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(468)

<400>  27
att ggt cgc caa ctt gct cag ttg ctc aac atg gat ttt gta gat acc       48
Ile Gly Arg Gln Leu Ala Gln Leu Leu Asn Met Asp Phe Val Asp Thr
1               5                   10                  15

gac gca gaa att gaa gaa cgc gcc ggc gca gat att ggc tgg att ttt       96
Asp Ala Glu Ile Glu Glu Arg Ala Gly Ala Asp Ile Gly Trp Ile Phe
```

```
            20                  25                  30

gat gtt gag ggc gaa gcc ggt ttc cgt aaa aga gaa gaa cgt att att         144
Asp Val Glu Gly Glu Ala Gly Phe Arg Lys Arg Glu Glu Arg Ile Ile
        35                  40                  45

aac gaa tta acg caa cgc caa ggc atc gtg tta tct acc ggc ggc ggt         192
Asn Glu Leu Thr Gln Arg Gln Gly Ile Val Leu Ser Thr Gly Gly Gly
    50                  55                  60

gca gtg tta tct aag gac aat cga aac cag ctt gcc gcg cgc ggt att         240
Ala Val Leu Ser Lys Asp Asn Arg Asn Gln Leu Ala Ala Arg Gly Ile
65                  70                  75                  80

gtg att tat ctg gaa acc act gtt gaa aag caa tat caa cgc acc cag         288
Val Ile Tyr Leu Glu Thr Thr Val Glu Lys Gln Tyr Gln Arg Thr Gln
                85                  90                  95

cgg gat aaa aag cgc ccg ctt ttg caa gat gtt gcc gat ccg cgt cag         336
Arg Asp Lys Lys Arg Pro Leu Leu Gln Asp Val Ala Asp Pro Arg Gln
            100                 105                 110

gtg ttg gaa gat ttg gcg aaa atc cgc aat ccg ctg tat gaa gac gta         384
Val Leu Glu Asp Leu Ala Lys Ile Arg Asn Pro Leu Tyr Glu Asp Val
        115                 120                 125

gca gac att acc ctc cct act gat gac caa agt gcc aag gta atg gca         432
Ala Asp Ile Thr Leu Pro Thr Asp Asp Gln Ser Ala Lys Val Met Ala
    130                 135                 140

acg cag att atc gac ttg att gat aac tat aac ggt                         468
Thr Gln Ile Ile Asp Leu Ile Asp Asn Tyr Asn Gly
145                 150                 155


<210>  28
<211>  156
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  28

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


Asp Ala Glu Ile Glu Glu Arg Ala Gly Ala Asp Ile Gly Trp Ile Phe
            20                  25                  30


Asp Val Glu Gly Glu Ala Gly Phe Arg Lys Arg Glu Glu Arg Ile Ile
        35                  40                  45


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


Ala Val Leu Ser Lys Asp Asn Arg Asn Gln Leu Ala Ala Arg Gly Ile
65                  70                  75                  80
```

```
Val Ile Tyr Leu Glu Thr Thr Val Glu Lys Gln Tyr Gln Arg Thr Gln
                85                  90                  95

Arg Asp Lys Lys Arg Pro Leu Leu Gln Asp Val Ala Asp Pro Arg Gln
            100                 105                 110

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

Ala Asp Ile Thr Leu Pro Thr Asp Asp Gln Ser Ala Lys Val Met Ala
    130                 135                 140

Thr Gln Ile Ile Asp Leu Ile Asp Asn Tyr Asn Gly
145                 150                 155


<210>  29
<211>  307
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(306)

<400>  29
gcc tcc cgc agt ggc gat gcc gat gag cgt gtc atg gat tcc aac gat          48
Ala Ser Arg Ser Gly Asp Ala Asp Glu Arg Val Met Asp Ser Asn Asp
1               5                   10                  15

tta gaa aaa gag cgc ggc atc act att tta gcg aaa aat act gcc att          96
Leu Glu Lys Glu Arg Gly Ile Thr Ile Leu Ala Lys Asn Thr Ala Ile
            20                  25                  30

aac tgg aat agc tac cgt att aac att gta gac acc ccg ggg cac gcg         144
Asn Trp Asn Ser Tyr Arg Ile Asn Ile Val Asp Thr Pro Gly His Ala
        35                  40                  45

gac ttc ggt ggc gaa gtg gaa cgc gta ctt tcc atg gtg gat tcc gta         192
Asp Phe Gly Gly Glu Val Glu Arg Val Leu Ser Met Val Asp Ser Val
    50                  55                  60

tta ttg atg gtg gat gcc ttc gac ggc ccg atg ccg caa acc cgt ttt         240
Leu Leu Met Val Asp Ala Phe Asp Gly Pro Met Pro Gln Thr Arg Phe
65                  70                  75                  80

gtt acg caa aaa gcc ttc tcc cac ggt tta aaa cct atc gta gtc atc         288
Val Thr Gln Lys Ala Phe Ser His Gly Leu Lys Pro Ile Val Val Ile
                85                  90                  95

aat aaa gtt gac cgc ccg g                                               307
Asn Lys Val Asp Arg Pro
            100


<210>  30
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```
<211>  102
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  30

Ala Ser Arg Ser Gly Asp Ala Asp Glu Arg Val Met Asp Ser Asn Asp
1               5                   10                  15


Leu Glu Lys Glu Arg Gly Ile Thr Ile Leu Ala Lys Asn Thr Ala Ile
            20                  25                  30


Asn Trp Asn Ser Tyr Arg Ile Asn Ile Val Asp Thr Pro Gly His Ala
        35                  40                  45


Asp Phe Gly Gly Glu Val Glu Arg Val Leu Ser Met Val Asp Ser Val
    50                  55                  60


Leu Leu Met Val Asp Ala Phe Asp Gly Pro Met Pro Gln Thr Arg Phe
65                  70                  75                  80


Val Thr Gln Lys Ala Phe Ser His Gly Leu Lys Pro Ile Val Val Ile
                85                  90                  95


Asn Lys Val Asp Arg Pro
            100


<210>  31
<211>  891
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(891)

<220>
<221>  misc_feature
<222>  (182)..(182)
<223>  n is any nucleotide a, g, c, or t.


<220>
<221>  misc_feature
<222>  (188)..(188)
<223>  n is any nucleotide a, g, c, or t.


<400>  31
atg gct atc gta caa tcc aaa tct gcc cgc tac cgt tta tgg gtg acc        48
Met Ala Ile Val Gln Ser Lys Ser Ala Arg Tyr Arg Leu Trp Val Thr
1               5                   10                  15

cat ttg ctg ctg att gca ttt att tgt ctg att att ttc ccg tta ctg        96
```

```
His Leu Leu Leu Ile Ala Phe Ile Cys Leu Ile Ile Phe Pro Leu Leu
            20                  25                  30

atg gtg atc ggc att tcc ctg cgc ccg ggc aac ctc gct ttg ggc gat        144
Met Val Ile Gly Ile Ser Leu Arg Pro Gly Asn Leu Ala Leu Gly Asp
        35                  40                  45

ttg att ccg aaa caa att tcc tgg gaa cac tgg cag gcg gcg ctt ggc        192
Leu Ile Pro Lys Gln Ile Ser Trp Glu His Trp Gln Ala Ala Leu Gly
    50                  55                  60

ttt tat gtg gta cac gcc gac ggt tct gtc aca cca ccg ccg ttc ccg        240
Phe Tyr Val Val His Ala Asp Gly Ser Val Thr Pro Pro Pro Phe Pro
65                  70                  75                  80

gtg ttg ttg tgg ttg tgg aac tcc att aaa gtg gcg acc atc acc tcc        288
Val Leu Leu Trp Leu Trp Asn Ser Ile Lys Val Ala Thr Ile Thr Ser
                85                  90                  95

gtg ggt atc gtt gtt atg tcc acc act tgc gcc tac gct ttc gcg cgg        336
Val Gly Ile Val Val Met Ser Thr Thr Cys Ala Tyr Ala Phe Ala Arg
            100                 105                 110

atg aaa ttc aaa ggc aaa aaa acc atc ttg caa ggc atg tta att ttc        384
Met Lys Phe Lys Gly Lys Lys Thr Ile Leu Gln Gly Met Leu Ile Phe
        115                 120                 125

caa atg ttc cct gcg gtg ttg tct ttg gtc gcc tta tac gcc tta ttc        432
Gln Met Phe Pro Ala Val Leu Ser Leu Val Ala Leu Tyr Ala Leu Phe
    130                 135                 140

gat cgc ctc ggt caa tat atc ccg ttc ctc ggc tta aac acc cac ggc        480
Asp Arg Leu Gly Gln Tyr Ile Pro Phe Leu Gly Leu Asn Thr His Gly
145                 150                 155                 160

ggc gtg att ttc gct tac ttg ggc ggt atc gcc ttg cac gtt tgg acc        528
Gly Val Ile Phe Ala Tyr Leu Gly Gly Ile Ala Leu His Val Trp Thr
                165                 170                 175

atc aaa ggc tat ttt gaa acc atc gac gga tcc ctg gaa gaa gct gcc        576
Ile Lys Gly Tyr Phe Glu Thr Ile Asp Gly Ser Leu Glu Glu Ala Ala
            180                 185                 190

gcc tta gac ggc gct acc cca tgg cag gca ttc cgc tta att tta cta        624
Ala Leu Asp Gly Ala Thr Pro Trp Gln Ala Phe Arg Leu Ile Leu Leu
        195                 200                 205

cct ctc tcc gta ccg att ctg gcg gtg gtc ttc att ctt tcc ttc atc        672
Pro Leu Ser Val Pro Ile Leu Ala Val Val Phe Ile Leu Ser Phe Ile
    210                 215                 220

gcc gcc att acc gaa gtg ccg gtc gcc tcg cta tta tta cgc gat gtc        720
Ala Ala Ile Thr Glu Val Pro Val Ala Ser Leu Leu Leu Arg Asp Val
225                 230                 235                 240

aac agc tac acc ctg gcg gtg gga atg caa caa tat ctc tac ccg caa        768
Asn Ser Tyr Thr Leu Ala Val Gly Met Gln Gln Tyr Leu Tyr Pro Gln
                245                 250                 255

aac tac ctt tgg ggc gac ttc gcc gct gca gcg gtg ctt tcc gct att        816
Asn Tyr Leu Trp Gly Asp Phe Ala Ala Ala Ala Val Leu Ser Ala Ile
```

```
            260                 265                 270

cct att acc ctc gtg ttc tta ctg gca caa cgc tgg tta atc ggc gga       864
Pro Ile Thr Leu Val Phe Leu Leu Ala Gln Arg Trp Leu Ile Gly Gly
        275                 280                 285

tta acg gca ggt ggg gtn aar ggn tga                                   891
Leu Thr Ala Gly Gly Val Lys Gly
    290                 295


<210>  32
<211>  296
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  misc_feature
<222>  (182)..(182)
<223>  n is any nucleotide a, g, c, or t.

<220>
<221>  misc_feature
<222>  (188)..(188)
<223>  n is any nucleotide a, g, c, or t.

<400>  32

Met Ala Ile Val Gln Ser Lys Ser Ala Arg Tyr Arg Leu Trp Val Thr
1               5                   10                  15


His Leu Leu Leu Ile Ala Phe Ile Cys Leu Ile Ile Phe Pro Leu Leu
            20                  25                  30


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


Leu Ile Pro Lys Gln Ile Ser Trp Glu His Trp Gln Ala Ala Leu Gly
    50                  55                  60


Phe Tyr Val Val His Ala Asp Gly Ser Val Thr Pro Pro Pro Phe Pro
65                  70                  75                  80


Val Leu Leu Trp Leu Trp Asn Ser Ile Lys Val Ala Thr Ile Thr Ser
                85                  90                  95


Val Gly Ile Val Val Met Ser Thr Thr Cys Ala Tyr Ala Phe Ala Arg
            100                 105                 110


Met Lys Phe Lys Gly Lys Lys Thr Ile Leu Gln Gly Met Leu Ile Phe
        115                 120                 125


Gln Met Phe Pro Ala Val Leu Ser Leu Val Ala Leu Tyr Ala Leu Phe
```

```
    130                 135                 140

Asp Arg Leu Gly Gln Tyr Ile Pro Phe Leu Gly Leu Asn Thr His Gly
145                 150                 155                 160

Gly Val Ile Phe Ala Tyr Leu Gly Gly Ile Ala Leu His Val Trp Thr
                165                 170                 175

Ile Lys Gly Tyr Phe Glu Thr Ile Asp Gly Ser Leu Glu Glu Ala Ala
            180                 185                 190

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

Pro Leu Ser Val Pro Ile Leu Ala Val Val Phe Ile Leu Ser Phe Ile
    210                 215                 220

Ala Ala Ile Thr Glu Val Pro Val Ala Ser Leu Leu Leu Arg Asp Val
225                 230                 235                 240

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

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

Pro Ile Thr Leu Val Phe Leu Leu Ala Gln Arg Trp Leu Ile Gly Gly
        275                 280                 285

Leu Thr Ala Gly Gly Val Lys Gly
    290                 295

<210>  33
<211>  323
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(321)

<400>  33
aat gtt tat ggc ggt acc aaa gcc ttt gta aaa caa ttt agc tta aac       48
Asn Val Tyr Gly Gly Thr Lys Ala Phe Val Lys Gln Phe Ser Leu Asn
1               5                   10                  15

cta cgt gcc gat ctt gcc gga acc aat att cgc gtt tcc aat gta gaa       96
Leu Arg Ala Asp Leu Ala Gly Thr Asn Ile Arg Val Ser Asn Val Glu
            20                  25                  30
```

```
ccg gga ctg tgc ggc ggc acg gaa ttt tct aac gta cgt ttt aaa ggc        144
Pro Gly Leu Cys Gly Gly Thr Glu Phe Ser Asn Val Arg Phe Lys Gly
        35                  40                  45

gat aac gcc cgc gcg gaa aaa ctc tac gaa aac gta caa tat gtt acg        192
Asp Asn Ala Arg Ala Glu Lys Leu Tyr Glu Asn Val Gln Tyr Val Thr
    50                  55                  60

cca caa gat att gcc aat atc gtg ttg tgg ctc aat caa caa ccg gaa        240
Pro Gln Asp Ile Ala Asn Ile Val Leu Trp Leu Asn Gln Gln Pro Glu
65                  70                  75                  80

cac gtc aac att aac cgc att gaa gtg atg ccg acg gcg caa acc ttc        288
His Val Asn Ile Asn Arg Ile Glu Val Met Pro Thr Ala Gln Thr Phe
                85                  90                  95

gcc ccg ctt aat gta gca agg aat tta aat tta ga                         323
Ala Pro Leu Asn Val Ala Arg Asn Leu Asn Leu
            100                 105


<210>  34
<211>  107
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  34

Asn Val Tyr Gly Gly Thr Lys Ala Phe Val Lys Gln Phe Ser Leu Asn
1               5                   10                  15


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


Pro Gly Leu Cys Gly Gly Thr Glu Phe Ser Asn Val Arg Phe Lys Gly
        35                  40                  45


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


Pro Gln Asp Ile Ala Asn Ile Val Leu Trp Leu Asn Gln Gln Pro Glu
65                  70                  75                  80


His Val Asn Ile Asn Arg Ile Glu Val Met Pro Thr Ala Gln Thr Phe
                85                  90                  95


Ala Pro Leu Asn Val Ala Arg Asn Leu Asn Leu
            100                 105


<210>  35
<211>  585
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans
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<220>
<221>  CDS
<222>  (1)..(585)

<400>  35
atg gcg gaa acg att tta aac ccg tat ttc ggg gaa ttc ggc gga atg       48
Met Ala Glu Thr Ile Leu Asn Pro Tyr Phe Gly Glu Phe Gly Gly Met
1               5                   10                  15

tat gtg ccg gaa att cta gtg ccg gtg ttg caa cag ttg gaa aaa gcg       96
Tyr Val Pro Glu Ile Leu Val Pro Val Leu Gln Gln Leu Glu Lys Ala
            20                  25                  30

ttt gta gaa gcc aag gcg gat cct gca ttt cag cgc gaa ttt cag gat      144
Phe Val Glu Ala Lys Ala Asp Pro Ala Phe Gln Arg Glu Phe Gln Asp
        35                  40                  45

tta ttg aaa aat tat gcc ggc aga ccc acc gca ctt acc ctt tgt cgc      192
Leu Leu Lys Asn Tyr Ala Gly Arg Pro Thr Ala Leu Thr Leu Cys Arg
    50                  55                  60

aat ctc acc aaa ggc acc aac gcc aaa atc tat tta aaa cgg gaa gat      240
Asn Leu Thr Lys Gly Thr Asn Ala Lys Ile Tyr Leu Lys Arg Glu Asp
65                  70                  75                  80

tta tta cac ggc ggc gca cat aaa acc aac cag gta tta ggt cag att      288
Leu Leu His Gly Gly Ala His Lys Thr Asn Gln Val Leu Gly Gln Ile
                85                  90                  95

ttg ctt gcc aaa cgc atg ggc aaa acc cgc att att gcc gaa acc ggc      336
Leu Leu Ala Lys Arg Met Gly Lys Thr Arg Ile Ile Ala Glu Thr Gly
            100                 105                 110

gcg gga cag cac ggt gtc gcc act gct ctc gcc tgc gcc atg ttg gat      384
Ala Gly Gln His Gly Val Ala Thr Ala Leu Ala Cys Ala Met Leu Asp
        115                 120                 125

atg ccg tgc cgt gtt tat atg ggc gcg aaa gat gtg gaa cgc caa tcg      432
Met Pro Cys Arg Val Tyr Met Gly Ala Lys Asp Val Glu Arg Gln Ser
    130                 135                 140

ccg aat gtg ttt cgt atg cgt tta atg ggc acg gaa gtg gta ccg gtg      480
Pro Asn Val Phe Arg Met Arg Leu Met Gly Thr Glu Val Val Pro Val
145                 150                 155                 160

caa aaa ggt tcc tgt tct ttg aaa gac gct tgc tgc gaa gcc atg cgt      528
Gln Lys Gly Ser Cys Ser Leu Lys Asp Ala Cys Cys Glu Ala Met Arg
                165                 170                 175

gac tgg tcg gca aat tat gaa aat acg cac tat ttg ctc ggc aca gcg      576
Asp Trp Ser Ala Asn Tyr Glu Asn Thr His Tyr Leu Leu Gly Thr Ala
            180                 185                 190

gca ggt ccg                                                          585
Ala Gly Pro
        195


<210>  36
<211>  195
<212>  PRT
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<213>  Actinobacillus actinomycetemcomitans

<400>  36

Met Ala Glu Thr Ile Leu Asn Pro Tyr Phe Gly Glu Phe Gly Gly Met
1               5                   10                  15


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


Phe Val Glu Ala Lys Ala Asp Pro Ala Phe Gln Arg Glu Phe Gln Asp
        35                  40                  45


Leu Leu Lys Asn Tyr Ala Gly Arg Pro Thr Ala Leu Thr Leu Cys Arg
    50                  55                  60


Asn Leu Thr Lys Gly Thr Asn Ala Lys Ile Tyr Leu Lys Arg Glu Asp
65                  70                  75                  80


Leu Leu His Gly Gly Ala His Lys Thr Asn Gln Val Leu Gly Gln Ile
                85                  90                  95


Leu Leu Ala Lys Arg Met Gly Lys Thr Arg Ile Ile Ala Glu Thr Gly
            100                 105                 110


Ala Gly Gln His Gly Val Ala Thr Ala Leu Ala Cys Ala Met Leu Asp
        115                 120                 125


Met Pro Cys Arg Val Tyr Met Gly Ala Lys Asp Val Glu Arg Gln Ser
    130                 135                 140


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


Gln Lys Gly Ser Cys Ser Leu Lys Asp Ala Cys Cys Glu Ala Met Arg
                165                 170                 175


Asp Trp Ser Ala Asn Tyr Glu Asn Thr His Tyr Leu Leu Gly Thr Ala
            180                 185                 190


Ala Gly Pro
        195


<210>  37
<211>  543
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans
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<220>
<221>  CDS
<222>  (1)..(543)

<400>  37
atg tcg cac gta ttt caa atc tca aga gaa att atg aca gct tta aat        48
Met Ser His Val Phe Gln Ile Ser Arg Glu Ile Met Thr Ala Leu Asn
1               5                   10                  15

gta ctt att tac ccg gaa gag cac ctt aaa gtg gtt tgc gat ccg gtc        96
Val Leu Ile Tyr Pro Glu Glu His Leu Lys Val Val Cys Asp Pro Val
            20                  25                  30

gtg gaa gtc aat gac aac acg cgt aag att att gat aat atg ttt gat       144
Val Glu Val Asn Asp Asn Thr Arg Lys Ile Ile Asp Asn Met Phe Asp
        35                  40                  45

acc atg tat cag gaa ggc ggt atc ggc cta gcg gca ccg cag gtg gat       192
Thr Met Tyr Gln Glu Gly Gly Ile Gly Leu Ala Ala Pro Gln Val Asp
    50                  55                  60

att tta cag cgt att atc act att gat att gag ggt gac aaa caa aac       240
Ile Leu Gln Arg Ile Ile Thr Ile Asp Ile Glu Gly Asp Lys Gln Asn
65                  70                  75                  80

cag tta gtg ttg att aac cct gaa att ttg gaa tcg gaa ggt gaa acc       288
Gln Leu Val Leu Ile Asn Pro Glu Ile Leu Glu Ser Glu Gly Glu Thr
                85                  90                  95

gga att gaa gag ggt tgt ttg tcg att ccc gga ttt cgt gcg tta gtg       336
Gly Ile Glu Glu Gly Cys Leu Ser Ile Pro Gly Phe Arg Ala Leu Val
            100                 105                 110

cca cgt aaa gag aaa gtg act gta aaa gcg ctg gat cgt cat ggt aaa       384
Pro Arg Lys Glu Lys Val Thr Val Lys Ala Leu Asp Arg His Gly Lys
        115                 120                 125

gaa ttc acc tta aaa gcc gat ggt ctg ttg gca att tgt att cag cat       432
Glu Phe Thr Leu Lys Ala Asp Gly Leu Leu Ala Ile Cys Ile Gln His
    130                 135                 140

gaa att gat cat tta aac ggt att ctt ttt gtg gat tat ctc tct cca       480
Glu Ile Asp His Leu Asn Gly Ile Leu Phe Val Asp Tyr Leu Ser Pro
145                 150                 155                 160

ttg aaa cgt cag cgg att aaa gaa aag ctg att aaa atg aaa aag cag       528
Leu Lys Arg Gln Arg Ile Lys Glu Lys Leu Ile Lys Met Lys Lys Gln
                165                 170                 175

atg gaa aag caa aaa                                                   543
Met Glu Lys Gln Lys
            180


<210>  38
<211>  181
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  38
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Met Ser His Val Phe Gln Ile Ser Arg Glu Ile Met Thr Ala Leu Asn
1               5                   10                  15


Val Leu Ile Tyr Pro Glu Glu His Leu Lys Val Val Cys Asp Pro Val
            20                  25                  30


Val Glu Val Asn Asp Asn Thr Arg Lys Ile Ile Asp Asn Met Phe Asp
        35                  40                  45


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


Ile Leu Gln Arg Ile Ile Thr Ile Asp Ile Glu Gly Asp Lys Gln Asn
65                  70                  75                  80


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


Gly Ile Glu Glu Gly Cys Leu Ser Ile Pro Gly Phe Arg Ala Leu Val
            100                 105                 110


Pro Arg Lys Glu Lys Val Thr Val Lys Ala Leu Asp Arg His Gly Lys
        115                 120                 125


Glu Phe Thr Leu Lys Ala Asp Gly Leu Leu Ala Ile Cys Ile Gln His
    130                 135                 140


Glu Ile Asp His Leu Asn Gly Ile Leu Phe Val Asp Tyr Leu Ser Pro
145                 150                 155                 160


Leu Lys Arg Gln Arg Ile Lys Glu Lys Leu Ile Lys Met Lys Lys Gln
                165                 170                 175


Met Glu Lys Gln Lys
            180


<210>  39
<211>  353
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(351)

<400>  39
cgc ggc gtg aca ccg gaa cta ttc gcc gac tgg tta aaa cag tta cat        48
Arg Gly Val Thr Pro Glu Leu Phe Ala Asp Trp Leu Lys Gln Leu His
1               5                   10                  15
```

```
cag gcg ggc gta aaa gtg gtg ttg gac agc agt aac gcc gca ttg acc         96
Gln Ala Gly Val Lys Val Val Leu Asp Ser Ser Asn Ala Ala Leu Thr
            20                  25                  30

gcc ggc tta acg gcg caa cct tgg ttg gtt aaa ccg aat cat cgt gag        144
Ala Gly Leu Thr Ala Gln Pro Trp Leu Val Lys Pro Asn His Arg Glu
        35                  40                  45

ttg gaa gcc tgg att ggt cat gcg ctg ccg acc ttg gac gac att atc        192
Leu Glu Ala Trp Ile Gly His Ala Leu Pro Thr Leu Asp Asp Ile Ile
    50                  55                  60

gcg gcg gcg aaa aaa ctg aaa gca caa ggc att gct aac gtg att att        240
Ala Ala Ala Lys Lys Leu Lys Ala Gln Gly Ile Ala Asn Val Ile Ile
65                  70                  75                  80

tcc atg ggc gcc aac ggt tcg ttg tgg ttg agc gat aca gcc gtc gta        288
Ser Met Gly Ala Asn Gly Ser Leu Trp Leu Ser Asp Thr Ala Val Val
                85                  90                  95

cag gcg caa ccg ccg aaa tgc gaa aac gtg gtc agc acc gtg ggc gcg        336
Gln Ala Gln Pro Pro Lys Cys Glu Asn Val Val Ser Thr Val Gly Ala
            100                 105                 110

ggc gat tct atg gtg gc                                                 353
Gly Asp Ser Met Val
        115


<210>  40
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<213>  Actinobacillus actinomycetemcomitans

<400>  40

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


Gln Ala Gly Val Lys Val Val Leu Asp Ser Ser Asn Ala Ala Leu Thr
            20                  25                  30


Ala Gly Leu Thr Ala Gln Pro Trp Leu Val Lys Pro Asn His Arg Glu
        35                  40                  45


Leu Glu Ala Trp Ile Gly His Ala Leu Pro Thr Leu Asp Asp Ile Ile
    50                  55                  60


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


Ser Met Gly Ala Asn Gly Ser Leu Trp Leu Ser Asp Thr Ala Val Val
                85                  90                  95
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Gln Ala Gln Pro Pro Lys Cys Glu Asn Val Val Ser Thr Val Gly Ala
            100                 105                 110


Gly Asp Ser Met Val
        115


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atg aaa aaa tgg ttt atg ctg tta ctt ccg ctg aca ttt atc ggc agc         48
Met Lys Lys Trp Phe Met Leu Leu Leu Pro Leu Thr Phe Ile Gly Ser
1               5                   10                  15

ctt tgg gcg cag gaa gcg cct tcc ccc ttt ctt gcc ggg gaa tta ccg         96
Leu Trp Ala Gln Glu Ala Pro Ser Pro Phe Leu Ala Gly Glu Leu Pro
            20                  25                  30

gca gcg caa aaa atc gaa aaa gtc tta agc gcc ggt aat ccg agt gat        144
Ala Ala Gln Lys Ile Glu Lys Val Leu Ser Ala Gly Asn Pro Ser Asp
        35                  40                  45

gcg tta ttg ctg gcc gcc gcg ccg caa aaa atg gtc gga ctg gcg ggc        192
Ala Leu Leu Leu Ala Ala Ala Pro Gln Lys Met Val Gly Leu Ala Gly
    50                  55                  60

ttt aag atg gca tcc aaa ggc ggc aaa tta ttt cct gtg caa caa caa        240
Phe Lys Met Ala Ser Lys Gly Gly Lys Leu Phe Pro Val Gln Gln Gln
65                  70                  75                  80

gcg ttg ccg acc atc ggc aaa att gcc gga aag ggc agt acg ttt tcc        288
Ala Leu Pro Thr Ile Gly Lys Ile Ala Gly Lys Gly Ser Thr Phe Ser
                85                  90                  95

gcc gaa aaa atc gtg gcg ctt caa ccg aat ttg att att gat gtg ggc        336
Ala Glu Lys Ile Val Ala Leu Gln Pro Asn Leu Ile Ile Asp Val Gly
            100                 105                 110

aat gtg gcg ccg aat tac atc gat cag gca a                              367
Asn Val Ala Pro Asn Tyr Ile Asp Gln Ala
        115                 120


<210>  42
<211>  122
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  42

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


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


Ala Leu Leu Leu Ala Ala Ala Pro Gln Lys Met Val Gly Leu Ala Gly
    50                  55                  60


Phe Lys Met Ala Ser Lys Gly Gly Lys Leu Phe Pro Val Gln Gln Gln
65                  70                  75                  80


Ala Leu Pro Thr Ile Gly Lys Ile Ala Gly Lys Gly Ser Thr Phe Ser
                85                  90                  95


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


Asn Val Ala Pro Asn Tyr Ile Asp Gln Ala
        115                 120


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gtc ttt aaa gta atc tgg tgt aaa aca tct cag aca tgg att gcc gta         48
Val Phe Lys Val Ile Trp Cys Lys Thr Ser Gln Thr Trp Ile Ala Val
1               5                   10                  15

tct gaa cta tct aaa gct ttt tcc ctt tct acc act aca gat ata cct         96
Ser Glu Leu Ser Lys Ala Phe Ser Leu Ser Thr Thr Thr Asp Ile Pro
            20                  25                  30

aaa aaa act aaa ata ttc att gct gca gcc ccg tta tta ttt ctc tcc        144
Lys Lys Thr Lys Ile Phe Ile Ala Ala Ala Pro Leu Leu Phe Leu Ser
        35                  40                  45

ttt aat acc aac gct tac att gct ata ggt tct gtt gaa aac aat tct        192
Phe Asn Thr Asn Ala Tyr Ile Ala Ile Gly Ser Val Glu Asn Asn Ser
    50                  55                  60

gtg aaa tcc gag ggg gca gaa gcc tcc cca aac aag aga aag gga agc        240
Val Lys Ser Glu Gly Ala Glu Ala Ser Pro Asn Lys Arg Lys Gly Ser
65                  70                  75                  80

caa gca tta aat tat tac aac ccc ggt agt aaa tca tat gat gat aaa        288
Gln Ala Leu Asn Tyr Tyr Asn Pro Gly Ser Lys Ser Tyr Asp Asp Lys
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                85                  90                  95

gac aaa ccg agc aat cct gaa aga aga tac agc aat ggg gag gca tat         336
Asp Lys Pro Ser Asn Pro Glu Arg Arg Tyr Ser Asn Gly Glu Ala Tyr
            100                 105                 110

ggt atc gct atc ggt aaa aat acc gat gtt cgt gac tca agt aag gat         384
Gly Ile Ala Ile Gly Lys Asn Thr Asp Val Arg Asp Ser Ser Lys Asp
        115                 120                 125

tca aat ggt atc gcc tta ggc gat tat tct aaa gct acc ggt ggg ctt         432
Ser Asn Gly Ile Ala Leu Gly Asp Tyr Ser Lys Ala Thr Gly Gly Leu
    130                 135                 140

gcc atg gcc tta ggt tca ttt tcc aga gca gaa aaa aat ggc ggt att         480
Ala Met Ala Leu Gly Ser Phe Ser Arg Ala Glu Lys Asn Gly Gly Ile
145                 150                 155                 160

gca atc ggt ata gct tcc aga tca tca gga att aat tct ctt gcg atg         528
Ala Ile Gly Ile Ala Ser Arg Ser Ser Gly Ile Asn Ser Leu Ala Met
                165                 170                 175

atg cgt caa tct gca gca acc ggg gat tat tct act gcc att ggt tct         576
Met Arg Gln Ser Ala Ala Thr Gly Asp Tyr Ser Thr Ala Ile Gly Ser
            180                 185                 190

gtc gca tgg gct gca ggt caa tca agc ttc gca ctg ggg gct tct gct         624
Val Ala Trp Ala Ala Gly Gln Ser Ser Phe Ala Leu Gly Ala Ser Ala
        195                 200                 205

act gct aaa ggc aac caa tcc att gca att ggc agc ttg gaa caa aaa         672
Thr Ala Lys Gly Asn Gln Ser Ile Ala Ile Gly Ser Leu Glu Gln Lys
    210                 215                 220

ata tct ccg aat ggt tct ggt gtg cca atc aca aaa tac aac ggg tta         720
Ile Ser Pro Asn Gly Ser Gly Val Pro Ile Thr Lys Tyr Asn Gly Leu
225                 230                 235                 240

gac aac aca caa acc aat ggt aac cgt tcc atg gca ttg ggt acg gca         768
Asp Asn Thr Gln Thr Asn Gly Asn Arg Ser Met Ala Leu Gly Thr Ala
                245                 250                 255

gct aaa acc aat ggt gat gat tca ttt gct att ggt tat aaa gca cac         816
Ala Lys Thr Asn Gly Asp Asp Ser Phe Ala Ile Gly Tyr Lys Ala His
            260                 265                 270

acc ggt gag ttt aaa gtg gaa cat gac aac tat cta aaa gag aat gtt         864
Thr Gly Glu Phe Lys Val Glu His Asp Asn Tyr Leu Lys Glu Asn Val
        275                 280                 285

acc tct ccg gat ctg tct aaa aaa gct gat aaa gcc att gct gtc ggt         912
Thr Ser Pro Asp Leu Ser Lys Lys Ala Asp Lys Ala Ile Ala Val Gly
    290                 295                 300

acg agt gcc ctt gcg caa aaa gaa tct gct atc gca ttt ggc tac caa         960
Thr Ser Ala Leu Ala Gln Lys Glu Ser Ala Ile Ala Phe Gly Tyr Gln
305                 310                 315                 320

gct aat gct tcc ggc att aat gca att tct ctt ggc gca aat gca aaa        1008
Ala Asn Ala Ser Gly Ile Asn Ala Ile Ser Leu Gly Ala Asn Ala Lys
                325                 330                 335
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gca tct caa gat aac gtt gta gca ata ggt aaa tat gct aca gcc act        1056
Ala Ser Gln Asp Asn Val Val Ala Ile Gly Lys Tyr Ala Thr Ala Thr
            340                 345                 350

gaa tct ggt tca atg gcc att ggt cag gga gct aaa tct acc ttt aaa        1104
Glu Ser Gly Ser Met Ala Ile Gly Gln Gly Ala Lys Ser Thr Phe Lys
        355                 360                 365

aac tca ttg gca tta ggt aca ggt acc att gtc aac agt gtc gat ggc        1152
Asn Ser Leu Ala Leu Gly Thr Gly Thr Ile Val Asn Ser Val Asp Gly
    370                 375                 380

ggg caa tct aaa ttt act gca caa aat tat gat gct aat aat ggt gtt        1200
Gly Gln Ser Lys Phe Thr Ala Gln Asn Tyr Asp Ala Asn Asn Gly Val
385                 390                 395                 400

gta gct gtt gca aac gcc ggt aaa gag cgt cga att att aat gtt gcc        1248
Val Ala Val Ala Asn Ala Gly Lys Glu Arg Arg Ile Ile Asn Val Ala
                405                 410                 415

ggt ggt cgt aat gat act gat gca gtg aat att gcc cag tta aaa ttc        1296
Gly Gly Arg Asn Asp Thr Asp Ala Val Asn Ile Ala Gln Leu Lys Phe
            420                 425                 430

gtg aat gat aac tta gcc aag tcc atc gca ggc gcc ggt tat aac ggc        1344
Val Asn Asp Asn Leu Ala Lys Ser Ile Ala Gly Ala Gly Tyr Asn Gly
        435                 440                 445

tat gaa aca gac gga cat act tac aaa gca ccg gta ttt agt att aaa        1392
Tyr Glu Thr Asp Gly His Thr Tyr Lys Ala Pro Val Phe Ser Ile Lys
    450                 455                 460

aat acc aac tat cac gat gtc aaa aca gct gtt gaa gcg gca caa acc        1440
Asn Thr Asn Tyr His Asp Val Lys Thr Ala Val Glu Ala Ala Gln Thr
465                 470                 475                 480

aat tat gta agt gta aat agc act aat aca gca gcc gat agt aat tac        1488
Asn Tyr Val Ser Val Asn Ser Thr Asn Thr Ala Ala Asp Ser Asn Tyr
                485                 490                 495

gac aat aaa ggg gct aaa gca gta ggt tct att gcg tta ggc gaa aaa        1536
Asp Asn Lys Gly Ala Lys Ala Val Gly Ser Ile Ala Leu Gly Glu Lys
            500                 505                 510

gcc aca aca gga acg gcg gca atg aac tct att gcc att ggt tta aac        1584
Ala Thr Thr Gly Thr Ala Ala Met Asn Ser Ile Ala Ile Gly Leu Asn
        515                 520                 525

agc aat gtt agc ggc caa aat acc gtt gca ttg ggt gcc aat atc acc        1632
Ser Asn Val Ser Gly Gln Asn Thr Val Ala Leu Gly Ala Asn Ile Thr
    530                 535                 540

gcg aca acc aac ggt tcc gtc att tta gga aat tcc tcc acc acg gaa        1680
Ala Thr Thr Asn Gly Ser Val Ile Leu Gly Asn Ser Ser Thr Thr Glu
545                 550                 555                 560

ggt tca cat cct gtt tca aat gtt agc agt gcg act gtt aac gga tat        1728
Gly Ser His Pro Val Ser Asn Val Ser Ser Ala Thr Val Asn Gly Tyr
                565                 570                 575
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acc tac tca ggt ttt acc ggc acg gta aaa gag tcg gga cat ttt gtg        1776
Thr Tyr Ser Gly Phe Thr Gly Thr Val Lys Glu Ser Gly His Phe Val
            580                 585                 590

agc att ggt tca aaa ggc aat gag cgt caa att aaa aat gtg gca gca        1824
Ser Ile Gly Ser Lys Gly Asn Glu Arg Gln Ile Lys Asn Val Ala Ala
        595                 600                 605

ggt aat gtt gcg gca aac tca acc gat gcc gtt aat ggc tct caa tta        1872
Gly Asn Val Ala Ala Asn Ser Thr Asp Ala Val Asn Gly Ser Gln Leu
    610                 615                 620

ttt gct gtc gcc agt cgt gta gaa caa ggt tgg caa atc act tcc ggc        1920
Phe Ala Val Ala Ser Arg Val Glu Gln Gly Trp Gln Ile Thr Ser Gly
625                 630                 635                 640

gta gaa aat ggt ggt act caa aat ggc gca gcc tca aca gca aca atc        1968
Val Glu Asn Gly Gly Thr Gln Asn Gly Ala Ala Ser Thr Ala Thr Ile
                645                 650                 655

aaa ccg agt aac caa gtg aag cta ctg gca gga aag aat tta gca gtc        2016
Lys Pro Ser Asn Gln Val Lys Leu Leu Ala Gly Lys Asn Leu Ala Val
            660                 665                 670

aaa caa aac ggc act aac ttc acc ttc tca acc caa gaa aat gtc acg        2064
Lys Gln Asn Gly Thr Asn Phe Thr Phe Ser Thr Gln Glu Asn Val Thr
        675                 680                 685

ttc act aat gtt acg acc caa gat cta act gca aca ggc aac acc act        2112
Phe Thr Asn Val Thr Thr Gln Asp Leu Thr Ala Thr Gly Asn Thr Thr
    690                 695                 700

gtt aag aac ttc agc gtt caa aat ggc gga acc atc aat atg gga aat        2160
Val Lys Asn Phe Ser Val Gln Asn Gly Gly Thr Ile Asn Met Gly Asn
705                 710                 715                 720

aat cgc att acc ggt gtc gct gaa ggc act caa gat gac gac gcg gtt        2208
Asn Arg Ile Thr Gly Val Ala Glu Gly Thr Gln Asp Asp Asp Ala Val
                725                 730                 735

aac ttt aaa caa tta aaa agc ctt ctt ggt ggc tcc gca tca acg gaa        2256
Asn Phe Lys Gln Leu Lys Ser Leu Leu Gly Gly Ser Ala Ser Thr Glu
            740                 745                 750

att gtt gag aaa aaa gca gct caa gcc gga gat gaa aac ctg gcg gat        2304
Ile Val Glu Lys Lys Ala Ala Gln Ala Gly Asp Glu Asn Leu Ala Asp
        755                 760                 765

att agc gta gca aat ggt aaa aac gcc ggc gat atg ggt gcg aaa tac        2352
Ile Ser Val Ala Asn Gly Lys Asn Ala Gly Asp Met Gly Ala Lys Tyr
    770                 775                 780

gaa gta tct gta tcc aaa aaa gcc gta caa agt gcc gca aaa gaa gcg        2400
Glu Val Ser Val Ser Lys Lys Ala Val Gln Ser Ala Ala Lys Glu Ala
785                 790                 795                 800

gtt aaa gtg aca ggt tcg gca ccg att aat gta aac aaa aca gat gta        2448
Val Lys Val Thr Gly Ser Ala Pro Ile Asn Val Asn Lys Thr Asp Val
                805                 810                 815

aat ggc gtt gat act tat gcc gta acc ttt aat ggc aca gaa gcg gcg        2496
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Asn Gly Val Asp Thr Tyr Ala Val Thr Phe Asn Gly Thr Glu Ala Ala
            820                 825                 830

aaa tct atc cca tta act tat aaa gct aac ggt agc ggt gat aaa acc      2544
Lys Ser Ile Pro Leu Thr Tyr Lys Ala Asn Gly Ser Gly Asp Lys Thr
        835                 840                 845

gtc atg ttg gat aaa gga tta aac ttt acc aat ggt atg atg aca acc      2592
Val Met Leu Asp Lys Gly Leu Asn Phe Thr Asn Gly Met Met Thr Thr
    850                 855                 860

gct tcc gtg gca aat gac ggt gtg gtg aaa tat gac gtc aat tta tcc      2640
Ala Ser Val Ala Asn Asp Gly Val Val Lys Tyr Asp Val Asn Leu Ser
865                 870                 875                 880

acc att aaa gta gaa gat ggc aag gct gcc gta gcc ggt aca ccg ggc      2688
Thr Ile Lys Val Glu Asp Gly Lys Ala Ala Val Ala Gly Thr Pro Gly
                885                 890                 895

aca aat ggc gcc aac ggc act gat ggc aaa gat ggc gta gcg acg gtt      2736
Thr Asn Gly Ala Asn Gly Thr Asp Gly Lys Asp Gly Val Ala Thr Val
            900                 905                 910

aaa aat gtg gta gag gcg tta aat aat gcc gca tgg aca ata act gcc      2784
Lys Asn Val Val Glu Ala Leu Asn Asn Ala Ala Trp Thr Ile Thr Ala
        915                 920                 925

tct aaa tct gac ggc gaa gtc gtc agc aat gca tct aat tcc gtt aaa      2832
Ser Lys Ser Asp Gly Glu Val Val Ser Asn Ala Ser Asn Ser Val Lys
    930                 935                 940

aat ggg gat acg gtg act tat gat gcc ggc aaa aac atc aaa att act      2880
Asn Gly Asp Thr Val Thr Tyr Asp Ala Gly Lys Asn Ile Lys Ile Thr
945                 950                 955                 960

caa aga gat aaa aaa ttc tct ttt gcc acc aaa gat aat gtt gaa ttt      2928
Gln Arg Asp Lys Lys Phe Ser Phe Ala Thr Lys Asp Asn Val Glu Phe
                965                 970                 975

act tct gtg acc acg ggc aat acc aaa tta acc ggt aat ggt gta gaa      2976
Thr Ser Val Thr Thr Gly Asn Thr Lys Leu Thr Gly Asn Gly Val Glu
            980                 985                 990

atc acc aac ggc cct aaa ctt acc  caa tca ggt gtg gat  gca ggc ggt    3024
Ile Thr Asn Gly Pro Lys Leu Thr  Gln Ser Gly Val Asp  Ala Gly Gly
        995                 1000                 1005

aag aaa  atc acc aat gta gca  gat ggc gtt att gca  gct aac agc       3069
Lys Lys  Ile Thr Asn Val Ala  Asp Gly Val Ile Ala  Ala Asn Ser
    1010                 1015                 1020

aaa gat  gcc gtg aat ggc ggt  caa tta ttc gct gaa  act gca aaa       3114
Lys Asp  Ala Val Asn Gly Gly  Gln Leu Phe Ala Glu  Thr Ala Lys
    1025                 1030                 1035

gcc aaa  act acg gtt gag aaa  ggt gat gat aat att  caa atc aca       3159
Ala Lys  Thr Thr Val Glu Lys  Gly Asp Asp Asn Ile  Gln Ile Thr
    1040                 1045                 1050

tca gaa  act gca acg gac gga  cat att aac tat aaa  gtg gca tta       3204
Ser Glu  Thr Ala Thr Asp Gly  His Ile Asn Tyr Lys  Val Ala Leu
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    1055                1060                1065

aat cct  agc ttg acc gtc gga  cca aga aca aat ggt  cac ccg atc        3249
Asn Pro  Ser Leu Thr Val Gly  Pro Arg Thr Asn Gly  His Pro Ile
    1070                1075                1080

acc att  gat ggt aat aac ggc  tat att acc ggt tta  acc aat aca        3294
Thr Ile  Asp Gly Asn Asn Gly  Tyr Ile Thr Gly Leu  Thr Asn Thr
    1085                1090                1095

agc tgg  acg ggc gcg cca aca  acc ggt cgt gca gca  acg gaa gat        3339
Ser Trp  Thr Gly Ala Pro Thr  Thr Gly Arg Ala Ala  Thr Glu Asp
    1100                1105                1110

caa tta  tct ata gtc gat aaa  aaa ttc gat aat aag  gtt tct tta        3384
Gln Leu  Ser Ile Val Asp Lys  Lys Phe Asp Asn Lys  Val Ser Leu
    1115                1120                1125

ggc ggt  gac aac ggt agt acc  aca gag aaa tcc ttg  tct cac aac        3429
Gly Gly  Asp Asn Gly Ser Thr  Thr Glu Lys Ser Leu  Ser His Asn
    1130                1135                1140

ggc gga  atc aaa ttt aat atc  aaa ggc gga gac agc  caa aaa tat        3474
Gly Gly  Ile Lys Phe Asn Ile  Lys Gly Gly Asp Ser  Gln Lys Tyr
    1145                1150                1155

gtg acg  aca tca gga tcc ggc  gat gat gtc acg gtg  gat ctt gcc        3519
Val Thr  Thr Ser Gly Ser Gly  Asp Asp Val Thr Val  Asp Leu Ala
    1160                1165                1170

caa acc  aca aaa aat aag atc  gac aat gcg gca gat  aaa gat ctc        3564
Gln Thr  Thr Lys Asn Lys Ile  Asp Asn Ala Ala Asp  Lys Asp Leu
    1175                1180                1185

gcc aac  att acc gat aat ggt  aaa aaa gtt att acc  gct tta ggc        3609
Ala Asn  Ile Thr Asp Asn Gly  Lys Lys Val Ile Thr  Ala Leu Gly
    1190                1195                1200

gct gta  gtg aaa gcg gct gat  tct acg att acg gta  act gac gaa        3654
Ala Val  Val Lys Ala Ala Asp  Ser Thr Ile Thr Val  Thr Asp Glu
    1205                1210                1215

acc gat  aat acg aca gga caa  aaa acc tac aaa atc  aaa gcc aat        3699
Thr Asp  Asn Thr Thr Gly Gln  Lys Thr Tyr Lys Ile  Lys Ala Asn
    1220                1225                1230

att cca  aca ccg gaa aaa aca  gca atg gct ccc ggc  aac aat aca        3744
Ile Pro  Thr Pro Glu Lys Thr  Ala Met Ala Pro Gly  Asn Asn Thr
    1235                1240                1245

acc att  gaa ggt gat ggc tca  gcc gcc aat ccg ttt  aaa gtg aat        3789
Thr Ile  Glu Gly Asp Gly Ser  Ala Ala Asn Pro Phe  Lys Val Asn
    1250                1255                1260

ctg aaa  gat gat tta gcg cta  ggt caa aaa gac gct  aac ggc gta        3834
Leu Lys  Asp Asp Leu Ala Leu  Gly Gln Lys Asp Ala  Asn Gly Val
    1265                1270                1275

acc ggt  aaa gat tct tcc att  aaa gtg aac ggc aaa  gat ggc tcc        3879
Thr Gly  Lys Asp Ser Ser Ile  Lys Val Asn Gly Lys  Asp Gly Ser
    1280                1285                1290
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ggt gtg  gcg att aac ggt aaa  gac ggt tcc att gca  tta aat ggc      3924
Gly Val  Ala Ile Asn Gly Lys  Asp Gly Ser Ile Ala  Leu Asn Gly
    1295                 1300                 1305

aaa gac  ggt gcg aat cct gtc  acc atc aaa acg gcg  caa ggt cct      3969
Lys Asp  Gly Ala Asn Pro Val  Thr Ile Lys Thr Ala  Gln Gly Pro
    1310                 1315                 1320

gcc ggt  gtg aat gaa acc aat  ccc aaa gac cgt tta  atg gtg aat      4014
Ala Gly  Val Asn Glu Thr Asn  Pro Lys Asp Arg Leu  Met Val Asn
    1325                 1330                 1335

aac gac  gct gtt gca acc ctt  aaa gac ggc tta aaa  ttc gcc gga      4059
Asn Asp  Ala Val Ala Thr Leu  Lys Asp Gly Leu Lys  Phe Ala Gly
    1340                 1345                 1350

gat aac  agc acc gaa gtc atc  act aaa acc tta aat  caa aaa ctg      4104
Asp Asn  Ser Thr Glu Val Ile  Thr Lys Thr Leu Asn  Gln Lys Leu
    1355                 1360                 1365

gaa att  gtg ggt ggt gca gat  aaa aac aaa tta tct  gac aac aat      4149
Glu Ile  Val Gly Gly Ala Asp  Lys Asn Lys Leu Ser  Asp Asn Asn
    1370                 1375                 1380

atc ggc  gta aat gcc aat aac  ggc aaa ctg gaa gtg  aaa tta gcc      4194
Ile Gly  Val Asn Ala Asn Asn  Gly Lys Leu Glu Val  Lys Leu Ala
    1385                 1390                 1395

aaa gag  ttg aat gag tta acc  agt gcg caa ttc aag  aat ggc gac      4239
Lys Glu  Leu Asn Glu Leu Thr  Ser Ala Gln Phe Lys  Asn Gly Asp
    1400                 1405                 1410

aac aca  acg gtt atc aat ggc  aat ggc ata aca att  acc ccg aaa      4284
Asn Thr  Thr Val Ile Asn Gly  Asn Gly Ile Thr Ile  Thr Pro Lys
    1415                 1420                 1425

gat ccg  aca aag gcg gtc agc  tta acg gat aaa gga  cta aac aat      4329
Asp Pro  Thr Lys Ala Val Ser  Leu Thr Asp Lys Gly  Leu Asn Asn
    1430                 1435                 1440

ggt ggt  aat caa att gtg aac  att gac agc gga tta  aaa caa gcc      4374
Gly Gly  Asn Gln Ile Val Asn  Ile Asp Ser Gly Leu  Lys Gln Ala
    1445                 1450                 1455

gac ggt  tca aca gtt gct tta  aaa gac gcc tca ggt  gat acc tta      4419
Asp Gly  Ser Thr Val Ala Leu  Lys Asp Ala Ser Gly  Asp Thr Leu
    1460                 1465                 1470

aaa aat  gcg gcg aat atc ggc  gat tta caa aaa tcc  att aac gac      4464
Lys Asn  Ala Ala Asn Ile Gly  Asp Leu Gln Lys Ser  Ile Asn Asp
    1475                 1480                 1485

att acc  gac gca agt aaa aac  ggc ggc ttc ggt tta  agc gat gac      4509
Ile Thr  Asp Ala Ser Lys Asn  Gly Gly Phe Gly Leu  Ser Asp Asp
    1490                 1495                 1500

aat ggc  gca acc gct aaa gcc  aac tta ggt gaa acc  cgt gaa agt      4554
Asn Gly  Ala Thr Ala Lys Ala  Asn Leu Gly Glu Thr  Arg Glu Ser
    1505                 1510                 1515
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gaa agg  cga tgg cag tgt tat  tac aaa agt agt tac  cga            4593
Glu Arg  Arg Trp Gln Cys Tyr  Tyr Lys Ser Ser Tyr  Arg
    1520                 1525                 1530


<210>  44
<211>  1531
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  44

Val Phe Lys Val Ile Trp Cys Lys Thr Ser Gln Thr Trp Ile Ala Val
1               5                   10                  15


Ser Glu Leu Ser Lys Ala Phe Ser Leu Ser Thr Thr Thr Asp Ile Pro
            20                  25                  30


Lys Lys Thr Lys Ile Phe Ile Ala Ala Ala Pro Leu Leu Phe Leu Ser
        35                  40                  45


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


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


Gln Ala Leu Asn Tyr Tyr Asn Pro Gly Ser Lys Ser Tyr Asp Asp Lys
                85                  90                  95


Asp Lys Pro Ser Asn Pro Glu Arg Arg Tyr Ser Asn Gly Glu Ala Tyr
            100                 105                 110


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


Ser Asn Gly Ile Ala Leu Gly Asp Tyr Ser Lys Ala Thr Gly Gly Leu
    130                 135                 140


Ala Met Ala Leu Gly Ser Phe Ser Arg Ala Glu Lys Asn Gly Gly Ile
145                 150                 155                 160


Ala Ile Gly Ile Ala Ser Arg Ser Ser Gly Ile Asn Ser Leu Ala Met
                165                 170                 175


Met Arg Gln Ser Ala Ala Thr Gly Asp Tyr Ser Thr Ala Ile Gly Ser
            180                 185                 190


Val Ala Trp Ala Ala Gly Gln Ser Ser Phe Ala Leu Gly Ala Ser Ala
```

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        195                 200                 205

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

Ile Ser Pro Asn Gly Ser Gly Val Pro Ile Thr Lys Tyr Asn Gly Leu
225                 230                 235                 240

Asp Asn Thr Gln Thr Asn Gly Asn Arg Ser Met Ala Leu Gly Thr Ala
                245                 250                 255

Ala Lys Thr Asn Gly Asp Asp Ser Phe Ala Ile Gly Tyr Lys Ala His
            260                 265                 270

Thr Gly Glu Phe Lys Val Glu His Asp Asn Tyr Leu Lys Glu Asn Val
        275                 280                 285

Thr Ser Pro Asp Leu Ser Lys Lys Ala Asp Lys Ala Ile Ala Val Gly
    290                 295                 300

Thr Ser Ala Leu Ala Gln Lys Glu Ser Ala Ile Ala Phe Gly Tyr Gln
305                 310                 315                 320

Ala Asn Ala Ser Gly Ile Asn Ala Ile Ser Leu Gly Ala Asn Ala Lys
                325                 330                 335

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

Glu Ser Gly Ser Met Ala Ile Gly Gln Gly Ala Lys Ser Thr Phe Lys
        355                 360                 365

Asn Ser Leu Ala Leu Gly Thr Gly Thr Ile Val Asn Ser Val Asp Gly
    370                 375                 380

Gly Gln Ser Lys Phe Thr Ala Gln Asn Tyr Asp Ala Asn Asn Gly Val
385                 390                 395                 400

Val Ala Val Ala Asn Ala Gly Lys Glu Arg Arg Ile Ile Asn Val Ala
                405                 410                 415

Gly Gly Arg Asn Asp Thr Asp Ala Val Asn Ile Ala Gln Leu Lys Phe
            420                 425                 430

Val Asn Asp Asn Leu Ala Lys Ser Ile Ala Gly Ala Gly Tyr Asn Gly
        435                 440                 445
```

```
Tyr Glu Thr Asp Gly His Thr Tyr Lys Ala Pro Val Phe Ser Ile Lys
    450                 455                 460

Asn Thr Asn Tyr His Asp Val Lys Thr Ala Val Glu Ala Ala Gln Thr
465                 470                 475                 480

Asn Tyr Val Ser Val Asn Ser Thr Asn Thr Ala Ala Asp Ser Asn Tyr
                485                 490                 495

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

Ala Thr Thr Gly Thr Ala Ala Met Asn Ser Ile Ala Ile Gly Leu Asn
        515                 520                 525

Ser Asn Val Ser Gly Gln Asn Thr Val Ala Leu Gly Ala Asn Ile Thr
    530                 535                 540

Ala Thr Thr Asn Gly Ser Val Ile Leu Gly Asn Ser Ser Thr Thr Glu
545                 550                 555                 560

Gly Ser His Pro Val Ser Asn Val Ser Ser Ala Thr Val Asn Gly Tyr
                565                 570                 575

Thr Tyr Ser Gly Phe Thr Gly Thr Val Lys Glu Ser Gly His Phe Val
            580                 585                 590

Ser Ile Gly Ser Lys Gly Asn Glu Arg Gln Ile Lys Asn Val Ala Ala
        595                 600                 605

Gly Asn Val Ala Ala Asn Ser Thr Asp Ala Val Asn Gly Ser Gln Leu
    610                 615                 620

Phe Ala Val Ala Ser Arg Val Glu Gln Gly Trp Gln Ile Thr Ser Gly
625                 630                 635                 640

Val Glu Asn Gly Gly Thr Gln Asn Gly Ala Ala Ser Thr Ala Thr Ile
                645                 650                 655

Lys Pro Ser Asn Gln Val Lys Leu Leu Ala Gly Lys Asn Leu Ala Val
            660                 665                 670

Lys Gln Asn Gly Thr Asn Phe Thr Phe Ser Thr Gln Glu Asn Val Thr
        675                 680                 685
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```
Phe Thr Asn Val Thr Thr Gln Asp Leu Thr Ala Thr Gly Asn Thr Thr
    690                 695                 700

Val Lys Asn Phe Ser Val Gln Asn Gly Gly Thr Ile Asn Met Gly Asn
705                 710                 715                 720

Asn Arg Ile Thr Gly Val Ala Glu Gly Thr Gln Asp Asp Asp Ala Val
                725                 730                 735

Asn Phe Lys Gln Leu Lys Ser Leu Leu Gly Gly Ser Ala Ser Thr Glu
            740                 745                 750

Ile Val Glu Lys Lys Ala Ala Gln Ala Gly Asp Glu Asn Leu Ala Asp
        755                 760                 765

Ile Ser Val Ala Asn Gly Lys Asn Ala Gly Asp Met Gly Ala Lys Tyr
    770                 775                 780

Glu Val Ser Val Ser Lys Lys Ala Val Gln Ser Ala Ala Lys Glu Ala
785                 790                 795                 800

Val Lys Val Thr Gly Ser Ala Pro Ile Asn Val Asn Lys Thr Asp Val
                805                 810                 815

Asn Gly Val Asp Thr Tyr Ala Val Thr Phe Asn Gly Thr Glu Ala Ala
            820                 825                 830

Lys Ser Ile Pro Leu Thr Tyr Lys Ala Asn Gly Ser Gly Asp Lys Thr
        835                 840                 845

Val Met Leu Asp Lys Gly Leu Asn Phe Thr Asn Gly Met Met Thr Thr
    850                 855                 860

Ala Ser Val Ala Asn Asp Gly Val Val Lys Tyr Asp Val Asn Leu Ser
865                 870                 875                 880

Thr Ile Lys Val Glu Asp Gly Lys Ala Ala Val Ala Gly Thr Pro Gly
                885                 890                 895

Thr Asn Gly Ala Asn Gly Thr Asp Gly Lys Asp Gly Val Ala Thr Val
            900                 905                 910

Lys Asn Val Val Glu Ala Leu Asn Asn Ala Ala Trp Thr Ile Thr Ala
        915                 920                 925
```

Ser Lys Ser Asp Gly Glu Val Val Ser Asn Ala Ser Asn Ser Val Lys
930 935 940

Asn Gly Asp Thr Val Thr Tyr Asp Ala Gly Lys Asn Ile Lys Ile Thr
945 950 955 960

Gln Arg Asp Lys Lys Phe Ser Phe Ala Thr Lys Asp Asn Val Glu Phe
965 970 975

Thr Ser Val Thr Thr Gly Asn Thr Lys Leu Thr Gly Asn Gly Val Glu
980 985 990

Ile Thr Asn Gly Pro Lys Leu Thr Gln Ser Gly Val Asp Ala Gly Gly
995 1000 1005

Lys Lys Ile Thr Asn Val Ala Asp Gly Val Ile Ala Ala Asn Ser
1010 1015 1020

Lys Asp Ala Val Asn Gly Gly Gln Leu Phe Ala Glu Thr Ala Lys
1025 1030 1035

Ala Lys Thr Thr Val Glu Lys Gly Asp Asp Asn Ile Gln Ile Thr
1040 1045 1050

Ser Glu Thr Ala Thr Asp Gly His Ile Asn Tyr Lys Val Ala Leu
1055 1060 1065

Asn Pro Ser Leu Thr Val Gly Pro Arg Thr Asn Gly His Pro Ile
1070 1075 1080

Thr Ile Asp Gly Asn Asn Gly Tyr Ile Thr Gly Leu Thr Asn Thr
1085 1090 1095

Ser Trp Thr Gly Ala Pro Thr Thr Gly Arg Ala Ala Thr Glu Asp
1100 1105 1110

Gln Leu Ser Ile Val Asp Lys Lys Phe Asp Asn Lys Val Ser Leu
1115 1120 1125

Gly Gly Asp Asn Gly Ser Thr Thr Glu Lys Ser Leu Ser His Asn
1130 1135 1140

Gly Gly Ile Lys Phe Asn Ile Lys Gly Gly Asp Ser Gln Lys Tyr
1145 1150 1155

Val Thr Thr Ser Gly Ser Gly Asp Asp Val Thr Val Asp Leu Ala

```
        1160                   1165                   1170

Gln Thr  Thr Lys Asn Lys Ile  Asp Asn Ala Ala Asp  Lys Asp Leu
    1175                 1180                 1185

Ala Asn  Ile Thr Asp Asn Gly  Lys Lys Val Ile Thr  Ala Leu Gly
    1190                 1195                 1200

Ala Val  Val Lys Ala Ala Asp  Ser Thr Ile Thr Val  Thr Asp Glu
    1205                 1210                 1215

Thr Asp  Asn Thr Thr Gly Gln  Lys Thr Tyr Lys Ile  Lys Ala Asn
    1220                 1225                 1230

Ile Pro  Thr Pro Glu Lys Thr  Ala Met Ala Pro Gly  Asn Asn Thr
    1235                 1240                 1245

Thr Ile  Glu Gly Asp Gly Ser  Ala Ala Asn Pro Phe  Lys Val Asn
    1250                 1255                 1260

Leu Lys  Asp Asp Leu Ala Leu  Gly Gln Lys Asp Ala  Asn Gly Val
    1265                 1270                 1275

Thr Gly  Lys Asp Ser Ser Ile  Lys Val Asn Gly Lys  Asp Gly Ser
    1280                 1285                 1290

Gly Val  Ala Ile Asn Gly Lys  Asp Gly Ser Ile Ala  Leu Asn Gly
    1295                 1300                 1305

Lys Asp  Gly Ala Asn Pro Val  Thr Ile Lys Thr Ala  Gln Gly Pro
    1310                 1315                 1320

Ala Gly  Val Asn Glu Thr Asn  Pro Lys Asp Arg Leu  Met Val Asn
    1325                 1330                 1335

Asn Asp  Ala Val Ala Thr Leu  Lys Asp Gly Leu Lys  Phe Ala Gly
    1340                 1345                 1350

Asp Asn  Ser Thr Glu Val Ile  Thr Lys Thr Leu Asn  Gln Lys Leu
    1355                 1360                 1365

Glu Ile  Val Gly Gly Ala Asp  Lys Asn Lys Leu Ser  Asp Asn Asn
    1370                 1375                 1380

Ile Gly  Val Asn Ala Asn Asn  Gly Lys Leu Glu Val  Lys Leu Ala
    1385                 1390                 1395
```

```
Lys Glu Leu Asn Glu Leu Thr Ser Ala Gln Phe Lys Asn Gly Asp
    1400                1405                1410

Asn Thr Thr Val Ile Asn Gly Asn Gly Ile Thr Ile Thr Pro Lys
    1415                1420                1425

Asp Pro Thr Lys Ala Val Ser Leu Thr Asp Lys Gly Leu Asn Asn
    1430                1435                1440

Gly Gly Asn Gln Ile Val Asn Ile Asp Ser Gly Leu Lys Gln Ala
    1445                1450                1455

Asp Gly Ser Thr Val Ala Leu Lys Asp Ala Ser Gly Asp Thr Leu
    1460                1465                1470

Lys Asn Ala Ala Asn Ile Gly Asp Leu Gln Lys Ser Ile Asn Asp
    1475                1480                1485

Ile Thr Asp Ala Ser Lys Asn Gly Gly Phe Gly Leu Ser Asp Asp
    1490                1495                1500

Asn Gly Ala Thr Ala Lys Ala Asn Leu Gly Glu Thr Arg Glu Ser
    1505                1510                1515

Glu Arg Arg Trp Gln Cys Tyr Tyr Lys Ser Ser Tyr Arg
    1520                1525                1530


<210>  45
<211>  565
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(564)

<400>  45
caa gaa atc att aac cta gcg cct aaa ggc tta att acc gcc gcc agc        48
Gln Glu Ile Ile Asn Leu Ala Pro Lys Gly Leu Ile Thr Ala Ala Ser
1               5                   10                  15

cct tat tta tac ggt gta acc cgt agt gat ttg gaa aaa atc gtc atc        96
Pro Tyr Leu Tyr Gly Val Thr Arg Ser Asp Leu Glu Lys Ile Val Ile
            20                  25                  30

atg ggc gtg tgg ttt gaa gac atg aaa acc ctc gcg ccc tac tgg caa       144
Met Gly Val Trp Phe Glu Asp Met Lys Thr Leu Ala Pro Tyr Trp Gln
        35                  40                  45

atc acc ggc acg ccc acc ggt gtc aac ttt gac gaa cgc aac gcc atg       192
```

```
Ile Thr Gly Thr Pro Thr Gly Val Asn Phe Asp Glu Arg Asn Ala Met
    50                  55                  60

atc ggc aaa acc ctc gcc gaa cgc tta aac ctg aaa gtg ggc agt aag      240
Ile Gly Lys Thr Leu Ala Glu Arg Leu Asn Leu Lys Val Gly Ser Lys
65                  70                  75                  80

ctg acc tta agc ctg aat tcg gta gat aaa cac cag ttt acg att aaa      288
Leu Thr Leu Ser Leu Asn Ser Val Asp Lys His Gln Phe Thr Ile Lys
                85                  90                  95

gcc atc gtg gaa gcg ggc gac gcc acc gac aat atg ctc atc gtg agc      336
Ala Ile Val Glu Ala Gly Asp Ala Thr Asp Asn Met Leu Ile Val Ser
            100                 105                 110

ctg gat ttc gcg caa aac tgg ctg gaa aaa gaa aac ttt gcc acc aat      384
Leu Asp Phe Ala Gln Asn Trp Leu Glu Lys Glu Asn Phe Ala Thr Asn
        115                 120                 125

gcc ctg ctt aac gtg aaa aat gat cag ggg caa gtg gaa caa ttc gca      432
Ala Leu Leu Asn Val Lys Asn Asp Gln Gly Gln Val Glu Gln Phe Ala
    130                 135                 140

cag caa ctt cag caa caa tat ccc gat ttg gat att cat ccg atc cgc      480
Gln Gln Leu Gln Gln Gln Tyr Pro Asp Leu Asp Ile His Pro Ile Arg
145                 150                 155                 160

aaa gtc tcc gcc tcc gaa ggg caa att ctg gat aag att aaa ggc ttg      528
Lys Val Ser Ala Ser Glu Gly Gln Ile Leu Asp Lys Ile Lys Gly Leu
                165                 170                 175

atg ggc ttg att tcc gtg gtg att ctg att tta gcc a                    565
Met Gly Leu Ile Ser Val Val Ile Leu Ile Leu Ala
            180                 185


<210>  46
<211>  188
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  46

Gln Glu Ile Ile Asn Leu Ala Pro Lys Gly Leu Ile Thr Ala Ala Ser
1               5                   10                  15


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


Met Gly Val Trp Phe Glu Asp Met Lys Thr Leu Ala Pro Tyr Trp Gln
        35                  40                  45


Ile Thr Gly Thr Pro Thr Gly Val Asn Phe Asp Glu Arg Asn Ala Met
    50                  55                  60


Ile Gly Lys Thr Leu Ala Glu Arg Leu Asn Leu Lys Val Gly Ser Lys
65                  70                  75                  80
```

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

Ala Ile Val Glu Ala Gly Asp Ala Thr Asp Asn Met Leu Ile Val Ser
            100                 105                 110

Leu Asp Phe Ala Gln Asn Trp Leu Glu Lys Glu Asn Phe Ala Thr Asn
        115                 120                 125

Ala Leu Leu Asn Val Lys Asn Asp Gln Gly Gln Val Glu Gln Phe Ala
    130                 135                 140

Gln Gln Leu Gln Gln Gln Tyr Pro Asp Leu Asp Ile His Pro Ile Arg
145                 150                 155                 160

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

Met Gly Leu Ile Ser Val Val Ile Leu Ile Leu Ala
            180                 185


<210>  47
<211>  668
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(666)

<400>  47
gcc aat cgg atc att gaa atc aaa gat ggt gaa att atc agt gat acg       48
Ala Asn Arg Ile Ile Glu Ile Lys Asp Gly Glu Ile Ile Ser Asp Thr
1               5                   10                  15

caa aaa cgt cag gta aaa agt gcg gtt aaa aat cca agt gtt ttt aaa       96
Gln Lys Arg Gln Val Lys Ser Ala Val Lys Asn Pro Ser Val Phe Lys
            20                  25                  30

ggt cgt ttc ggt ttc agc aaa gat caa ctt atg gaa gcc ttc cgt atg      144
Gly Arg Phe Gly Phe Ser Lys Asp Gln Leu Met Glu Ala Phe Arg Met
        35                  40                  45

tcc gtc agt gcc att gta gcg cac aaa atg cgc tca ttg ctg acc atg      192
Ser Val Ser Ala Ile Val Ala His Lys Met Arg Ser Leu Leu Thr Met
    50                  55                  60

ctg gga att atc atc ggg atc act tcc gtc gtt tcc gtg gtg gcg tta      240
Leu Gly Ile Ile Ile Gly Ile Thr Ser Val Val Ser Val Val Ala Leu
65                  70                  75                  80

gga aat ggt tca caa caa aag att ttg gaa aat att cgc ggt atc ggc      288
```

```
Gly Asn Gly Ser Gln Gln Lys Ile Leu Glu Asn Ile Arg Gly Ile Gly
                85                  90                  95

aca aac aca atg acg att ttt aac ggt aat ggt ttc ggt gac cgt cgt       336
Thr Asn Thr Met Thr Ile Phe Asn Gly Asn Gly Phe Gly Asp Arg Arg
            100                 105                 110

tca cgg cac att caa aac cta aaa atc agc gat gcc aat acg tta tcg       384
Ser Arg His Ile Gln Asn Leu Lys Ile Ser Asp Ala Asn Thr Leu Ser
        115                 120                 125

aaa caa agt tat att caa agc gtt act cca aat acc tct tcc agc ggc       432
Lys Gln Ser Tyr Ile Gln Ser Val Thr Pro Asn Thr Ser Ser Ser Gly
    130                 135                 140

att tta gtg gtc ggt aac aaa tcc ttc aca tcc gcc aat tta tat ggt       480
Ile Leu Val Val Gly Asn Lys Ser Phe Thr Ser Ala Asn Leu Tyr Gly
145                 150                 155                 160

atc ggt gaa caa tat ttt gat gta gaa ggc ttg aag tta aaa cag ggc       528
Ile Gly Glu Gln Tyr Phe Asp Val Glu Gly Leu Lys Leu Lys Gln Gly
                165                 170                 175

cgt tta tta acc gag gac gat gtg gat caa agc aac cag gtg gtc gtg       576
Arg Leu Leu Thr Glu Asp Asp Val Asp Gln Ser Asn Gln Val Val Val
            180                 185                 190

ctg gac gaa agt gca aaa aaa gcc att ttt gcc aac gaa aat ccc ctt       624
Leu Asp Glu Ser Ala Lys Lys Ala Ile Phe Ala Asn Glu Asn Pro Leu
        195                 200                 205

ggc aaa acg gtg att ttt aat aag cga cca ttt cgt gtc att gg            668
Gly Lys Thr Val Ile Phe Asn Lys Arg Pro Phe Arg Val Ile
    210                 215                 220


<210>  48
<211>  222
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  48

Ala Asn Arg Ile Ile Glu Ile Lys Asp Gly Glu Ile Ile Ser Asp Thr
1               5                   10                  15


Gln Lys Arg Gln Val Lys Ser Ala Val Lys Asn Pro Ser Val Phe Lys
            20                  25                  30


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


Ser Val Ser Ala Ile Val Ala His Lys Met Arg Ser Leu Leu Thr Met
    50                  55                  60


Leu Gly Ile Ile Ile Gly Ile Thr Ser Val Val Ser Val Val Ala Leu
65                  70                  75                  80
```

```
Gly Asn Gly Ser Gln Gln Lys Ile Leu Glu Asn Ile Arg Gly Ile Gly
                85                  90                  95

Thr Asn Thr Met Thr Ile Phe Asn Gly Asn Gly Phe Gly Asp Arg Arg
            100                 105                 110

Ser Arg His Ile Gln Asn Leu Lys Ile Ser Asp Ala Asn Thr Leu Ser
        115                 120                 125

Lys Gln Ser Tyr Ile Gln Ser Val Thr Pro Asn Thr Ser Ser Ser Gly
    130                 135                 140

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

Ile Gly Glu Gln Tyr Phe Asp Val Glu Gly Leu Lys Leu Lys Gln Gly
                165                 170                 175

Arg Leu Leu Thr Glu Asp Asp Val Asp Gln Ser Asn Gln Val Val Val
            180                 185                 190

Leu Asp Glu Ser Ala Lys Lys Ala Ile Phe Ala Asn Glu Asn Pro Leu
        195                 200                 205

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


<210>  49
<211>  276
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(276)

<400>  49
atg aga atg cac aat cct cca cac ccg gga gaa ctg tta aaa gaa tat         48
Met Arg Met His Asn Pro Pro His Pro Gly Glu Leu Leu Lys Glu Tyr
1               5                   10                  15

att gat ggc gtg agt gtc acg aag gtt gcc caa aaa tta ggt gtt tcg         96
Ile Asp Gly Val Ser Val Thr Lys Val Ala Gln Lys Leu Gly Val Ser
            20                  25                  30

cgt gtt acg ctt tcc cgc att ctt aat ggg aaa gca agt ata acg cct        144
Arg Val Thr Leu Ser Arg Ile Leu Asn Gly Lys Ala Ser Ile Thr Pro
        35                  40                  45

gaa atg gct gtg cga tta agc gaa tta ttg aat acc aca aca ccg aaa        192
```

```
Glu Met Ala Val Arg Leu Ser Glu Leu Leu Asn Thr Thr Thr Pro Lys
    50                  55                  60

tta tgg ctg ggt atg caa gca gac tac gat tta tgg caa att gaa caa        240
Leu Trp Leu Gly Met Gln Ala Asp Tyr Asp Leu Trp Gln Ile Glu Gln
65                  70                  75                  80

caa cac gcc gta ttc aac atc caa cca tta ttt aat                        276
Gln His Ala Val Phe Asn Ile Gln Pro Leu Phe Asn
                85                  90


<210>  50
<211>  92
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  50

Met Arg Met His Asn Pro Pro His Pro Gly Glu Leu Leu Lys Glu Tyr
1               5                   10                  15


Ile Asp Gly Val Ser Val Thr Lys Val Ala Gln Lys Leu Gly Val Ser
            20                  25                  30


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


Glu Met Ala Val Arg Leu Ser Glu Leu Leu Asn Thr Thr Thr Pro Lys
    50                  55                  60


Leu Trp Leu Gly Met Gln Ala Asp Tyr Asp Leu Trp Gln Ile Glu Gln
65                  70                  75                  80


Gln His Ala Val Phe Asn Ile Gln Pro Leu Phe Asn
                85                  90


<210>  51
<211>  537
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(537)

<400>  51
caa cat aat ggt gta cta ggt cct tat atc ggt aaa ggc agt tta acc         48
Gln His Asn Gly Val Leu Gly Pro Tyr Ile Gly Lys Gly Ser Leu Thr
1               5                   10                  15

tta aaa tta ccg gct tac tgg gaa cta tca gga ttc cat caa tta acc         96
Leu Lys Leu Pro Ala Tyr Trp Glu Leu Ser Gly Phe His Gln Leu Thr
            20                  25                  30
```

```
gat caa tgg gct atc cac tat agc tat aaa tat aca gaa tgg agt cgt        144
Asp Gln Trp Ala Ile His Tyr Ser Tyr Lys Tyr Thr Glu Trp Ser Arg
        35                  40                  45

ttt aaa gaa tta cgc ggc aaa tat caa gat ggt tcc ggc tat gag gcc        192
Phe Lys Glu Leu Arg Gly Lys Tyr Gln Asp Gly Ser Gly Tyr Glu Ala
    50                  55                  60

ttt acc aag aaa gag gaa tac aaa gac aac tcc cgt ttt gct att ggt        240
Phe Thr Lys Lys Glu Glu Tyr Lys Asp Asn Ser Arg Phe Ala Ile Gly
65                  70                  75                  80

aca aca tat agc cta aat gat gct tta aca tta cgt gca ggt ttg gct        288
Thr Thr Tyr Ser Leu Asn Asp Ala Leu Thr Leu Arg Ala Gly Leu Ala
                85                  90                  95

tac gat aaa gcc gcg agt aaa acg cat tta tct gcg tcc att cct gat        336
Tyr Asp Lys Ala Ala Ser Lys Thr His Leu Ser Ala Ser Ile Pro Asp
            100                 105                 110

acc gac cgt atg tgg tat agt ata gga gcc acc tat aaa ttc acc ccg        384
Thr Asp Arg Met Trp Tyr Ser Ile Gly Ala Thr Tyr Lys Phe Thr Pro
        115                 120                 125

aat tta tct gtt gat gtc ggc ttc gct cat tta cgt ggt aag aag aaa        432
Asn Leu Ser Val Asp Val Gly Phe Ala His Leu Arg Gly Lys Lys Lys
    130                 135                 140

cat ttt gtt gag acc caa aat atc aag ggg tta ttg ctt gtt gag gcg        480
His Phe Val Glu Thr Gln Asn Ile Lys Gly Leu Leu Leu Val Glu Ala
145                 150                 155                 160

gat tac acc act aaa gcc acc gct aac ctc tac ggt ttg aat cta aat        528
Asp Tyr Thr Thr Lys Ala Thr Ala Asn Leu Tyr Gly Leu Asn Leu Asn
                165                 170                 175

tac cgt ttc                                                            537
Tyr Arg Phe


<210>  52
<211>  179
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  52

Gln His Asn Gly Val Leu Gly Pro Tyr Ile Gly Lys Gly Ser Leu Thr
1               5                   10                  15


Leu Lys Leu Pro Ala Tyr Trp Glu Leu Ser Gly Phe His Gln Leu Thr
            20                  25                  30


Asp Gln Trp Ala Ile His Tyr Ser Tyr Lys Tyr Thr Glu Trp Ser Arg
        35                  40                  45


Phe Lys Glu Leu Arg Gly Lys Tyr Gln Asp Gly Ser Gly Tyr Glu Ala
```

```
    50                  55                  60

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

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

Tyr Asp Lys Ala Ala Ser Lys Thr His Leu Ser Ala Ser Ile Pro Asp
            100                 105                 110

Thr Asp Arg Met Trp Tyr Ser Ile Gly Ala Thr Tyr Lys Phe Thr Pro
        115                 120                 125

Asn Leu Ser Val Asp Val Gly Phe Ala His Leu Arg Gly Lys Lys Lys
    130                 135                 140

His Phe Val Glu Thr Gln Asn Ile Lys Gly Leu Leu Leu Val Glu Ala
145                 150                 155                 160

Asp Tyr Thr Thr Lys Ala Thr Ala Asn Leu Tyr Gly Leu Asn Leu Asn
                165                 170                 175

Tyr Arg Phe


<210>  53
<211>  548
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(546)

<400>  53
gga cca agt gtc acc aag gac ggc att cac gcc aat gat aag aaa atc         48
Gly Pro Ser Val Thr Lys Asp Gly Ile His Ala Asn Asp Lys Lys Ile
1               5                   10                  15

acc ggt gta aaa gac ggt gaa att tca gcc cat agt aaa gag gcg gtg         96
Thr Gly Val Lys Asp Gly Glu Ile Ser Ala His Ser Lys Glu Ala Val
            20                  25                  30

aac ggt agc caa tta cat caa acc aac caa aat gtg acg aat tta gcc        144
Asn Gly Ser Gln Leu His Gln Thr Asn Gln Asn Val Thr Asn Leu Ala
        35                  40                  45

aac aat gtg gac aaa ggg ctg aat ttc caa gga gac aat caa gaa gtc        192
Asn Asn Val Asp Lys Gly Leu Asn Phe Gln Gly Asp Asn Gln Glu Val
    50                  55                  60
```

```
aca gtt aat cgt aaa tta ggc gat caa ctt aac att cgc ggc ggt gcg        240
Thr Val Asn Arg Lys Leu Gly Asp Gln Leu Asn Ile Arg Gly Gly Ala
65                  70                  75                  80

gat ccg aag aaa tta aca caa aat aat atc ggc gtg acc gca gat aaa        288
Asp Pro Lys Lys Leu Thr Gln Asn Asn Ile Gly Val Thr Ala Asp Lys
                85                  90                  95

aac ggc acc atg acc gtt cag ctg gcg aag gaa gtt aat ctc ggc gca        336
Asn Gly Thr Met Thr Val Gln Leu Ala Lys Glu Val Asn Leu Gly Ala
            100                 105                 110

gat ggc agc ctt act gta ggc aat acc acg gtc aat aac gac ggt gtt        384
Asp Gly Ser Leu Thr Val Gly Asn Thr Thr Val Asn Asn Asp Gly Val
        115                 120                 125

acg att aaa gac ggt cca agc atg aca agc cac ggc atc aac gcc ggc        432
Thr Ile Lys Asp Gly Pro Ser Met Thr Ser His Gly Ile Asn Ala Gly
    130                 135                 140

ggc aaa cga att gct aac gtt gcg aaa ggg aaa gca ccg acg gat gca        480
Gly Lys Arg Ile Ala Asn Val Ala Lys Gly Lys Ala Pro Thr Asp Ala
145                 150                 155                 160

gta aat atg agt cag ctt caa gac gtc ggc agt gcc att aat aat cgc        528
Val Asn Met Ser Gln Leu Gln Asp Val Gly Ser Ala Ile Asn Asn Arg
                165                 170                 175

att gat aac att gat aag cg                                             548
Ile Asp Asn Ile Asp Lys
            180


<210>  54
<211>  182
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  54

Gly Pro Ser Val Thr Lys Asp Gly Ile His Ala Asn Asp Lys Lys Ile
1               5                   10                  15


Thr Gly Val Lys Asp Gly Glu Ile Ser Ala His Ser Lys Glu Ala Val
            20                  25                  30


Asn Gly Ser Gln Leu His Gln Thr Asn Gln Asn Val Thr Asn Leu Ala
        35                  40                  45


Asn Asn Val Asp Lys Gly Leu Asn Phe Gln Gly Asp Asn Gln Glu Val
    50                  55                  60


Thr Val Asn Arg Lys Leu Gly Asp Gln Leu Asn Ile Arg Gly Gly Ala
65                  70                  75                  80


Asp Pro Lys Lys Leu Thr Gln Asn Asn Ile Gly Val Thr Ala Asp Lys
```

```
                85                  90                  95

Asn Gly Thr Met Thr Val Gln Leu Ala Lys Glu Val Asn Leu Gly Ala
            100                 105                 110

Asp Gly Ser Leu Thr Val Gly Asn Thr Thr Val Asn Asn Asp Gly Val
        115                 120                 125

Thr Ile Lys Asp Gly Pro Ser Met Thr Ser His Gly Ile Asn Ala Gly
    130                 135                 140

Gly Lys Arg Ile Ala Asn Val Ala Lys Gly Lys Ala Pro Thr Asp Ala
145                 150                 155                 160

Val Asn Met Ser Gln Leu Gln Asp Val Gly Ser Ala Ile Asn Asn Arg
                165                 170                 175

Ile Asp Asn Ile Asp Lys
            180


<210>  55
<211>  168
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(168)

<400>  55
atg gat cac ttt ccg ccg ctt tgg ctt ttt cgg tta aac agc tta atg       48
Met Asp His Phe Pro Pro Leu Trp Leu Phe Arg Leu Asn Ser Leu Met
1               5                   10                  15

ctt ctt ttg ctg ctt ctt ccg ttg cat aaa cct gtt caa aat cca ccg       96
Leu Leu Leu Leu Leu Leu Pro Leu His Lys Pro Val Gln Asn Pro Pro
            20                  25                  30

tgc agt cag aac cgt caa tca ccg tac cca cct cga cac aac agc aaa      144
Cys Ser Gln Asn Arg Gln Ser Pro Tyr Pro Pro Arg His Asn Ser Lys
        35                  40                  45

ctt ttg ctt ctt ccg cct gac att                                      168
Leu Leu Leu Leu Pro Pro Asp Ile
    50                  55


<210>  56
<211>  56
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  56
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```
Met Asp His Phe Pro Pro Leu Trp Leu Phe Arg Leu Asn Ser Leu Met
1               5                   10                  15


Leu Leu Leu Leu Leu Leu Pro Leu His Lys Pro Val Gln Asn Pro Pro
            20                  25                  30


Cys Ser Gln Asn Arg Gln Ser Pro Tyr Pro Pro Arg His Asn Ser Lys
        35                  40                  45


Leu Leu Leu Leu Pro Pro Asp Ile
    50                  55


<210>  57
<211>  492
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(492)

<400>  57
atg acg aac aaa cca aaa tcc ggg ctc tca ttt ttg tgg tta agt acg        48
Met Thr Asn Lys Pro Lys Ser Gly Leu Ser Phe Leu Trp Leu Ser Thr
1               5                   10                  15

ctg gca ttt atc gcc gat att ttt acc aaa tac tta atc gta agc cat        96
Leu Ala Phe Ile Ala Asp Ile Phe Thr Lys Tyr Leu Ile Val Ser His
            20                  25                  30

ttt gaa tac ggc gaa agc gta aat atc ctg ccg att ttt aat ttg acc       144
Phe Glu Tyr Gly Glu Ser Val Asn Ile Leu Pro Ile Phe Asn Leu Thr
        35                  40                  45

tat gtg ggt aac ttt ggc gcc gct ttt agt ttc ctg gcg gat cat gac       192
Tyr Val Gly Asn Phe Gly Ala Ala Phe Ser Phe Leu Ala Asp His Asp
    50                  55                  60

ggt tgg caa aaa ttc ttt ttc ctt gcg ttg gca gtg ggg att tcc gcc       240
Gly Trp Gln Lys Phe Phe Phe Leu Ala Leu Ala Val Gly Ile Ser Ala
65                  70                  75                  80

atg ttg gtt tat ttt tta atg aaa aat cgc cat gaa caa aaa ctg ctg       288
Met Leu Val Tyr Phe Leu Met Lys Asn Arg His Glu Gln Lys Leu Leu
                85                  90                  95

aat gcc gcc tac gct ttg att atc ggc ggc gct ttg ggc aat gcg gcg       336
Asn Ala Ala Tyr Ala Leu Ile Ile Gly Gly Ala Leu Gly Asn Ala Ala
            100                 105                 110

gat cgt ctg tat cac ggc tat gtg gtg gat ttt tta gat ttc tat tgg       384
Asp Arg Leu Tyr His Gly Tyr Val Val Asp Phe Leu Asp Phe Tyr Trp
        115                 120                 125

cgg gat tgg cat tat ccc gtg ttt aac ctg gcg gat att gcc att tgt       432
Arg Asp Trp His Tyr Pro Val Phe Asn Leu Ala Asp Ile Ala Ile Cys
    130                 135                 140
```

```
gtg ggt gcc ggt ttg att gcc ttg gat gcg ttc aaa aac ggc aat aaa       480
Val Gly Ala Gly Leu Ile Ala Leu Asp Ala Phe Lys Asn Gly Asn Lys
145                 150                 155                 160

cag gaa tgt aaa                                                       492
Gln Glu Cys Lys



<210>  58
<211>  164
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  58

Met Thr Asn Lys Pro Lys Ser Gly Leu Ser Phe Leu Trp Leu Ser Thr
1               5                   10                  15


Leu Ala Phe Ile Ala Asp Ile Phe Thr Lys Tyr Leu Ile Val Ser His
            20                  25                  30


Phe Glu Tyr Gly Glu Ser Val Asn Ile Leu Pro Ile Phe Asn Leu Thr
        35                  40                  45


Tyr Val Gly Asn Phe Gly Ala Ala Phe Ser Phe Leu Ala Asp His Asp
    50                  55                  60


Gly Trp Gln Lys Phe Phe Phe Leu Ala Leu Ala Val Gly Ile Ser Ala
65                  70                  75                  80


Met Leu Val Tyr Phe Leu Met Lys Asn Arg His Glu Gln Lys Leu Leu
                85                  90                  95


Asn Ala Ala Tyr Ala Leu Ile Ile Gly Gly Ala Leu Gly Asn Ala Ala
            100                 105                 110


Asp Arg Leu Tyr His Gly Tyr Val Val Asp Phe Leu Asp Phe Tyr Trp
        115                 120                 125


Arg Asp Trp His Tyr Pro Val Phe Asn Leu Ala Asp Ile Ala Ile Cys
    130                 135                 140


Val Gly Ala Gly Leu Ile Ala Leu Asp Ala Phe Lys Asn Gly Asn Lys
145                 150                 155                 160


Gln Glu Cys Lys
```

```
<210>  59
<211>  453
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(453)

<400>  59
atg gct aaa ttg tat ttt tac tat tcc acc atg aat gca gga aaa tcc        48
Met Ala Lys Leu Tyr Phe Tyr Tyr Ser Thr Met Asn Ala Gly Lys Ser
1               5                   10                  15

acc acc ttg ttg caa tct tcc tat aat tac cgc gaa cgt aac atg aac        96
Thr Thr Leu Leu Gln Ser Ser Tyr Asn Tyr Arg Glu Arg Asn Met Asn
            20                  25                  30

acg ctg gtt tat aca gcg gcg ata gac gat cgt ttc ggc gta ggg cag       144
Thr Leu Val Tyr Thr Ala Ala Ile Asp Asp Arg Phe Gly Val Gly Gln
        35                  40                  45

gtg act tcc cgc atc ggg att agc gaa cgg gcg aat acc ttt acc cgc       192
Val Thr Ser Arg Ile Gly Ile Ser Glu Arg Ala Asn Thr Phe Thr Arg
    50                  55                  60

aat acg aat ttg ttc gct gaa att gaa caa cat ctg gcg cag gag ccg       240
Asn Thr Asn Leu Phe Ala Glu Ile Glu Gln His Leu Ala Gln Glu Pro
65                  70                  75                  80

ctt cat tgt att ttg gtg gat gag gca cag ttt tta acc aaa gaa cag       288
Leu His Cys Ile Leu Val Asp Glu Ala Gln Phe Leu Thr Lys Glu Gln
                85                  90                  95

gtt tat caa ctg agc gat gtg gtg gat aaa cta cat att ccc gtg ttg       336
Val Tyr Gln Leu Ser Asp Val Val Asp Lys Leu His Ile Pro Val Leu
            100                 105                 110

tgc tac ggt ttg cgc acc gat ttc caa gcg gaa tta ttt gaa ggc agt       384
Cys Tyr Gly Leu Arg Thr Asp Phe Gln Ala Glu Leu Phe Glu Gly Ser
        115                 120                 125

cgc tat tta ctg gcg tgg gcg gat cag ctg gaa gaa ctc aaa acc att       432
Arg Tyr Leu Leu Ala Trp Ala Asp Gln Leu Glu Glu Leu Lys Thr Ile
    130                 135                 140

tgt tac tgc ggt cgc aaa gcc                                           453
Cys Tyr Cys Gly Arg Lys Ala
145                 150


<210>  60
<211>  151
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  60

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

```
Thr Thr Leu Leu Gln Ser Ser Tyr Asn Tyr Arg Glu Arg Asn Met Asn
            20                  25                  30

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

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

Asn Thr Asn Leu Phe Ala Glu Ile Glu Gln His Leu Ala Gln Glu Pro
65                  70                  75                  80

Leu His Cys Ile Leu Val Asp Glu Ala Gln Phe Leu Thr Lys Glu Gln
                85                  90                  95

Val Tyr Gln Leu Ser Asp Val Val Asp Lys Leu His Ile Pro Val Leu
            100                 105                 110

Cys Tyr Gly Leu Arg Thr Asp Phe Gln Ala Glu Leu Phe Glu Gly Ser
        115                 120                 125

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

Cys Tyr Cys Gly Arg Lys Ala
145                 150


<210>  61
<211>  643
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(642)

<400>  61
tat aac gaa aaa act tac gaa aat gac tta acc gca aaa gaa atc ttc         48
Tyr Asn Glu Lys Thr Tyr Glu Asn Asp Leu Thr Ala Lys Glu Ile Phe
1               5                   10                  15

gta act tat gta ttg aaa aac aaa ttg tta tgg tac atc gcc att gct         96
Val Thr Tyr Val Leu Lys Asn Lys Leu Leu Trp Tyr Ile Ala Ile Ala
            20                  25                  30

aac gtg ttc gtt tac tta atc cgc tac ggc gta ttg aaa tgg tct ccg        144
Asn Val Phe Val Tyr Leu Ile Arg Tyr Gly Val Leu Lys Trp Ser Pro
        35                  40                  45

gtt tac ttg agt gaa gtg aaa cac ttc aac atc aaa ggt acc gca tgg        192
Val Tyr Leu Ser Glu Val Lys His Phe Asn Ile Lys Gly Thr Ala Trp
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    50                  55                  60

gca tac acc att tat gaa ttg gcg gcc gtt ccg ggt aca tta ctt tgc      240
Ala Tyr Thr Ile Tyr Glu Leu Ala Ala Val Pro Gly Thr Leu Leu Cys
65                  70                  75                  80

ggt tgg gta tct gac cat gta ttc aaa ggt aaa cgt ggc tta acc ggt      288
Gly Trp Val Ser Asp His Val Phe Lys Gly Lys Arg Gly Leu Thr Gly
                85                  90                  95

ttc atc ttt atg att tta acc acc gca gcg gta gcc aca tac tgg atg      336
Phe Ile Phe Met Ile Leu Thr Thr Ala Ala Val Ala Thr Tyr Trp Met
            100                 105                 110

aac cct gca aca ccg gaa gct gag ctt gca aac tac agc gca tgg tat      384
Asn Pro Ala Thr Pro Glu Ala Glu Leu Ala Asn Tyr Ser Ala Trp Tyr
        115                 120                 125

gaa aac cca tac caa tta acc gac ttt att ttg atg acc tta atc ggt      432
Glu Asn Pro Tyr Gln Leu Thr Asp Phe Ile Leu Met Thr Leu Ile Gly
    130                 135                 140

ttc tta atc tac ggc cct gtg atg cta atc ggc ttg cac gcc ctt gaa      480
Phe Leu Ile Tyr Gly Pro Val Met Leu Ile Gly Leu His Ala Leu Glu
145                 150                 155                 160

ctt gca ccg aaa aaa gcg gca ggt acc gca gca ggt ttc acc ggt tta      528
Leu Ala Pro Lys Lys Ala Ala Gly Thr Ala Ala Gly Phe Thr Gly Leu
                165                 170                 175

ttc ggt tac tta ggc ggt acc gtg tct gca tca gca gtt atc ggt tgg      576
Phe Gly Tyr Leu Gly Gly Thr Val Ser Ala Ser Ala Val Ile Gly Trp
            180                 185                 190

gca gcc caa cac tac ggc tgg gac ggc ggt ttt tac gtg atg atc ggc      624
Ala Ala Gln His Tyr Gly Trp Asp Gly Gly Phe Tyr Val Met Ile Gly
        195                 200                 205

ggt ggt atc tta ccg gtc a                                            643
Gly Gly Ile Leu Pro Val
    210


<210>  62
<211>  214
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  62

Tyr Asn Glu Lys Thr Tyr Glu Asn Asp Leu Thr Ala Lys Glu Ile Phe
1               5                   10                  15


Val Thr Tyr Val Leu Lys Asn Lys Leu Leu Trp Tyr Ile Ala Ile Ala
            20                  25                  30


Asn Val Phe Val Tyr Leu Ile Arg Tyr Gly Val Leu Lys Trp Ser Pro
        35                  40                  45
```

```
Val Tyr Leu Ser Glu Val Lys His Phe Asn Ile Lys Gly Thr Ala Trp
    50                  55                  60

Ala Tyr Thr Ile Tyr Glu Leu Ala Ala Val Pro Gly Thr Leu Leu Cys
65                  70                  75                  80

Gly Trp Val Ser Asp His Val Phe Lys Gly Lys Arg Gly Leu Thr Gly
                85                  90                  95

Phe Ile Phe Met Ile Leu Thr Thr Ala Ala Val Ala Thr Tyr Trp Met
            100                 105                 110

Asn Pro Ala Thr Pro Glu Ala Glu Leu Ala Asn Tyr Ser Ala Trp Tyr
        115                 120                 125

Glu Asn Pro Tyr Gln Leu Thr Asp Phe Ile Leu Met Thr Leu Ile Gly
    130                 135                 140

Phe Leu Ile Tyr Gly Pro Val Met Leu Ile Gly Leu His Ala Leu Glu
145                 150                 155                 160

Leu Ala Pro Lys Lys Ala Ala Gly Thr Ala Ala Gly Phe Thr Gly Leu
                165                 170                 175

Phe Gly Tyr Leu Gly Gly Thr Val Ser Ala Ser Ala Val Ile Gly Trp
            180                 185                 190

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

Gly Gly Ile Leu Pro Val
    210


<210>  63
<211>  333
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(333)

<400>  63
gaa tgg gcg gga acg cct tat cgt atc ggc gga caa agt cgc agt ggc      48
Glu Trp Ala Gly Thr Pro Tyr Arg Ile Gly Gly Gln Ser Arg Ser Gly
1               5                   10                  15

gtg gat tgc tcc ggt ttc gtg caa acc acc ttt ttc gat cgc ttc ggc      96
Val Asp Cys Ser Gly Phe Val Gln Thr Thr Phe Phe Asp Arg Phe Gly
```

```
            20                  25                  30

ata aaa ttg ccg cga caa acc aaa gat cag gca aat tac ggt cag tat       144
Ile Lys Leu Pro Arg Gln Thr Lys Asp Gln Ala Asn Tyr Gly Gln Tyr
        35                  40                  45

att gaa aaa ggc gat att caa acc ggt gat ttg gtg ttc ttt aaa acc       192
Ile Glu Lys Gly Asp Ile Gln Thr Gly Asp Leu Val Phe Phe Lys Thr
    50                  55                  60

ggt cgc ggt cct cat ggc tat cat gtg ggc att tat gtg aag gaa gac       240
Gly Arg Gly Pro His Gly Tyr His Val Gly Ile Tyr Val Lys Glu Asp
65                  70                  75                  80

aaa ttt ctg cac gcg tct act aag ggt ggc gtg att tat tcc tcg ttg       288
Lys Phe Leu His Ala Ser Thr Lys Gly Gly Val Ile Tyr Ser Ser Leu
                85                  90                  95

aac agc gat tat tgg cgt aag gca tat tgg cag gca aga cga att           333
Asn Ser Asp Tyr Trp Arg Lys Ala Tyr Trp Gln Ala Arg Arg Ile
            100                 105                 110


<210>  64
<211>  111
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  64

Glu Trp Ala Gly Thr Pro Tyr Arg Ile Gly Gly Gln Ser Arg Ser Gly
1               5                   10                  15


Val Asp Cys Ser Gly Phe Val Gln Thr Thr Phe Phe Asp Arg Phe Gly
            20                  25                  30


Ile Lys Leu Pro Arg Gln Thr Lys Asp Gln Ala Asn Tyr Gly Gln Tyr
        35                  40                  45


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


Gly Arg Gly Pro His Gly Tyr His Val Gly Ile Tyr Val Lys Glu Asp
65                  70                  75                  80


Lys Phe Leu His Ala Ser Thr Lys Gly Gly Val Ile Tyr Ser Ser Leu
                85                  90                  95


Asn Ser Asp Tyr Trp Arg Lys Ala Tyr Trp Gln Ala Arg Arg Ile
            100                 105                 110


<210>  65
<211>  423
<212>  DNA
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<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(423)

<400>  65
atg aaa aaa cgt tgc aca tgg gcg gaa aac tca caa att tat cag gat       48
Met Lys Lys Arg Cys Thr Trp Ala Glu Asn Ser Gln Ile Tyr Gln Asp
1               5                   10                  15

tac cac gac aac gaa tgg ggt aaa cca caa ttt gat gat cgc aaa tta       96
Tyr His Asp Asn Glu Trp Gly Lys Pro Gln Phe Asp Asp Arg Lys Leu
            20                  25                  30

ttt gaa aaa ctg tgt ctg gaa ggg cag caa gcg ggc ctg tcg tgg att      144
Phe Glu Lys Leu Cys Leu Glu Gly Gln Gln Ala Gly Leu Ser Trp Ile
        35                  40                  45

acg gta tta aaa aaa cgg gaa gct tat cgg cag gcg ttt ttc cat ttt      192
Thr Val Leu Lys Lys Arg Glu Ala Tyr Arg Gln Ala Phe Phe His Phe
    50                  55                  60

gat ccg cac aaa gtc gca gca atg act gat gcc gat atc gat cac tgt      240
Asp Pro His Lys Val Ala Ala Met Thr Asp Ala Asp Ile Asp His Cys
65                  70                  75                  80

atg caa aat aca ggc tta att cgc cat cgc gct aaa tta cag gca atc      288
Met Gln Asn Thr Gly Leu Ile Arg His Arg Ala Lys Leu Gln Ala Ile
                85                  90                  95

gtc acc aat gcg cgg gcg ttt ctt gcc atg caa aag tgc ggt gaa aat      336
Val Thr Asn Ala Arg Ala Phe Leu Ala Met Gln Lys Cys Gly Glu Asn
            100                 105                 110

ttc agt cat ttt att tgg tct ttc gtg aat cat cag ccg caa att cat      384
Phe Ser His Phe Ile Trp Ser Phe Val Asn His Gln Pro Gln Ile His
        115                 120                 125

gac gtg ccc gag tta agc cat gtg ccg gcg caa acg gca                  423
Asp Val Pro Glu Leu Ser His Val Pro Ala Gln Thr Ala
    130                 135                 140


<210>  66
<211>  141
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  66

Met Lys Lys Arg Cys Thr Trp Ala Glu Asn Ser Gln Ile Tyr Gln Asp
1               5                   10                  15


Tyr His Asp Asn Glu Trp Gly Lys Pro Gln Phe Asp Asp Arg Lys Leu
            20                  25                  30


Phe Glu Lys Leu Cys Leu Glu Gly Gln Gln Ala Gly Leu Ser Trp Ile
        35                  40                  45
```

```
Thr Val Leu Lys Lys Arg Glu Ala Tyr Arg Gln Ala Phe Phe His Phe
    50                  55                  60

Asp Pro His Lys Val Ala Ala Met Thr Asp Ala Asp Ile Asp His Cys
65                  70                  75                  80

Met Gln Asn Thr Gly Leu Ile Arg His Arg Ala Lys Leu Gln Ala Ile
                85                  90                  95

Val Thr Asn Ala Arg Ala Phe Leu Ala Met Gln Lys Cys Gly Glu Asn
            100                 105                 110

Phe Ser His Phe Ile Trp Ser Phe Val Asn His Gln Pro Gln Ile His
        115                 120                 125

Asp Val Pro Glu Leu Ser His Val Pro Ala Gln Thr Ala
    130                 135                 140


<210>  67
<211>  375
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(375)

<400>  67
gac atc gtt aca ttt acc caa aaa cgc tgc ccg ttt aat cac atg acg        48
Asp Ile Val Thr Phe Thr Gln Lys Arg Cys Pro Phe Asn His Met Thr
1               5                   10                  15

gtg gcg tat caa aaa agt gcg gtc ata aat tgc ggc gga tat gag gat        96
Val Ala Tyr Gln Lys Ser Ala Val Ile Asn Cys Gly Gly Tyr Glu Asp
            20                  25                  30

tta cag gaa gat tat tat ttg tgg atc aaa ctg gtg gcg caa ggg cag       144
Leu Gln Glu Asp Tyr Tyr Leu Trp Ile Lys Leu Val Ala Gln Gly Gln
        35                  40                  45

cgc gta gca aat tta ccc gat att ttg gtc tat gcg cgc gtc ggc aac       192
Arg Val Ala Asn Leu Pro Asp Ile Leu Val Tyr Ala Arg Val Gly Asn
    50                  55                  60

ggc atg gta ggg cga cgc cgt ggt tta aac caa gcc aaa gcg gaa tgg       240
Gly Met Val Gly Arg Arg Arg Gly Leu Asn Gln Ala Lys Ala Glu Trp
65                  70                  75                  80

cgc tta ttt aag cta aaa cac cat ctt ggc att cag gga ttt tta tcc       288
Arg Leu Phe Lys Leu Lys His His Leu Gly Ile Gln Gly Phe Leu Ser
                85                  90                  95

ggg cta ttc act ttt gtc ctg cgt tcc ggt gcc aga tta ttg ccg aca       336
```

```
Gly Leu Phe Thr Phe Val Leu Arg Ser Gly Ala Arg Leu Leu Pro Thr
            100                 105                 110

tca tta ctg aaa aac atc tat caa acc ttt tta aga aaa                  375
Ser Leu Leu Lys Asn Ile Tyr Gln Thr Phe Leu Arg Lys
        115                 120                 125


<210>  68
<211>  125
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  68

Asp Ile Val Thr Phe Thr Gln Lys Arg Cys Pro Phe Asn His Met Thr
1               5                   10                  15


Val Ala Tyr Gln Lys Ser Ala Val Ile Asn Cys Gly Gly Tyr Glu Asp
            20                  25                  30


Leu Gln Glu Asp Tyr Tyr Leu Trp Ile Lys Leu Val Ala Gln Gly Gln
        35                  40                  45


Arg Val Ala Asn Leu Pro Asp Ile Leu Val Tyr Ala Arg Val Gly Asn
    50                  55                  60


Gly Met Val Gly Arg Arg Arg Gly Leu Asn Gln Ala Lys Ala Glu Trp
65                  70                  75                  80


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


Gly Leu Phe Thr Phe Val Leu Arg Ser Gly Ala Arg Leu Leu Pro Thr
            100                 105                 110


Ser Leu Leu Lys Asn Ile Tyr Gln Thr Phe Leu Arg Lys
        115                 120                 125


<210>  69
<211>  1005
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(1005)

<400>  69
tcc ggt aaa tcc gtc ggc gta aat acc atg att tta agc ctg ctt tac      48
Ser Gly Lys Ser Val Gly Val Asn Thr Met Ile Leu Ser Leu Leu Tyr
1               5                   10                  15
```

```
cgc gtt aaa ccg gaa gaa gtg aaa ttc atc atg att gac ccg aaa gtg      96
Arg Val Lys Pro Glu Glu Val Lys Phe Ile Met Ile Asp Pro Lys Val
            20                  25                  30

gtg gaa ttg tct att tat aat gat att ccg cat ctt tta acg gaa gtg      144
Val Glu Leu Ser Ile Tyr Asn Asp Ile Pro His Leu Leu Thr Glu Val
        35                  40                  45

gtc acg gac atg aaa aaa gcg gca aac gcg ttg cgc tgg tgt gta gac      192
Val Thr Asp Met Lys Lys Ala Ala Asn Ala Leu Arg Trp Cys Val Asp
    50                  55                  60

gaa atg gag cgc cgt tat caa tta ttg tct gct ttg cgg gtg cgt aat      240
Glu Met Glu Arg Arg Tyr Gln Leu Leu Ser Ala Leu Arg Val Arg Asn
65                  70                  75                  80

att gaa gga ttt aac gag aaa gtt gat gaa tat gag gcc tta aat atg      288
Ile Glu Gly Phe Asn Glu Lys Val Asp Glu Tyr Glu Ala Leu Asn Met
                85                  90                  95

ccg att ccg aac ccg tta tgg aag ccg ggc gat tcc atg gat act ttg      336
Pro Ile Pro Asn Pro Leu Trp Lys Pro Gly Asp Ser Met Asp Thr Leu
            100                 105                 110

ccg cca cca tta gaa aaa ctg agt tac att gtg gtg att gtg gat gaa      384
Pro Pro Pro Leu Glu Lys Leu Ser Tyr Ile Val Val Ile Val Asp Glu
        115                 120                 125

ttc gcc gat ttg atg atg gtg gca ggc aaa cag gtg gaa gag ctt atc      432
Phe Ala Asp Leu Met Met Val Ala Gly Lys Gln Val Glu Glu Leu Ile
    130                 135                 140

gca cgt ttg gcg caa aaa gcc cgt gcg gtg ggg att cac tta att ttg      480
Ala Arg Leu Ala Gln Lys Ala Arg Ala Val Gly Ile His Leu Ile Leu
145                 150                 155                 160

gca acc caa cgc cct tcc gta gat gtg att acc ggt ttg att aaa gcg      528
Ala Thr Gln Arg Pro Ser Val Asp Val Ile Thr Gly Leu Ile Lys Ala
                165                 170                 175

aac gta ccg agt cga att gcg ttt act gtg gcg act aaa att gac tcg      576
Asn Val Pro Ser Arg Ile Ala Phe Thr Val Ala Thr Lys Ile Asp Ser
            180                 185                 190

cgt act att ctt gat gca ggc ggt gcg gaa tcc tta ttg ggt aaa ggt      624
Arg Thr Ile Leu Asp Ala Gly Gly Ala Glu Ser Leu Leu Gly Lys Gly
        195                 200                 205

gat atg ctg tat tcc cca cag ggt tct acc gaa tta gtc cgt att cac      672
Asp Met Leu Tyr Ser Pro Gln Gly Ser Thr Glu Leu Val Arg Ile His
    210                 215                 220

ggt gcc ttt atg act gat gac gaa gtc gtg cgc gtg gta gat gat tgg      720
Gly Ala Phe Met Thr Asp Asp Glu Val Val Arg Val Val Asp Asp Trp
225                 230                 235                 240

aaa gca cgc ggt aaa ccg aat tac att gat ggt att tta gag ggt gat      768
Lys Ala Arg Gly Lys Pro Asn Tyr Ile Asp Gly Ile Leu Glu Gly Asp
                245                 250                 255

gaa gaa gat gcc ggt gcg gaa cgc tta agt gag cgt ggc ggc gaa acc      816
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```
Glu Glu Asp Ala Gly Ala Glu Arg Leu Ser Glu Arg Gly Gly Glu Thr
            260                 265                 270

gac ggg ttg ttt gat gaa gtg gta gag ttt gtg gtc agc aca ggc acc       864
Asp Gly Leu Phe Asp Glu Val Val Glu Phe Val Val Ser Thr Gly Thr
        275                 280                 285

acg tct att tct gcg att caa cgc cgt ttc cga gta ggc ttt aac cgt       912
Thr Ser Ile Ser Ala Ile Gln Arg Arg Phe Arg Val Gly Phe Asn Arg
    290                 295                 300

gcc gcc aat att atg gat cag ctg gaa gag cag ggc att gtt tcg ccg       960
Ala Ala Asn Ile Met Asp Gln Leu Glu Glu Gln Gly Ile Val Ser Pro
305                 310                 315                 320

gtg caa aac ggt aaa cgt gaa gtg ttg gcg cgc agt gcg gat tat          1005
Val Gln Asn Gly Lys Arg Glu Val Leu Ala Arg Ser Ala Asp Tyr
                325                 330                 335


<210>  70
<211>  335
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  70

Ser Gly Lys Ser Val Gly Val Asn Thr Met Ile Leu Ser Leu Leu Tyr
1               5                   10                  15


Arg Val Lys Pro Glu Glu Val Lys Phe Ile Met Ile Asp Pro Lys Val
            20                  25                  30


Val Glu Leu Ser Ile Tyr Asn Asp Ile Pro His Leu Leu Thr Glu Val
        35                  40                  45


Val Thr Asp Met Lys Lys Ala Ala Asn Ala Leu Arg Trp Cys Val Asp
    50                  55                  60


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


Ile Glu Gly Phe Asn Glu Lys Val Asp Glu Tyr Glu Ala Leu Asn Met
                85                  90                  95


Pro Ile Pro Asn Pro Leu Trp Lys Pro Gly Asp Ser Met Asp Thr Leu
            100                 105                 110


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


Phe Ala Asp Leu Met Met Val Ala Gly Lys Gln Val Glu Glu Leu Ile
    130                 135                 140
```

```
Ala Arg Leu Ala Gln Lys Ala Arg Ala Val Gly Ile His Leu Ile Leu
145                 150                 155                 160

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

Asn Val Pro Ser Arg Ile Ala Phe Thr Val Ala Thr Lys Ile Asp Ser
            180                 185                 190

Arg Thr Ile Leu Asp Ala Gly Gly Ala Glu Ser Leu Leu Gly Lys Gly
        195                 200                 205

Asp Met Leu Tyr Ser Pro Gln Gly Ser Thr Glu Leu Val Arg Ile His
    210                 215                 220

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

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

Glu Glu Asp Ala Gly Ala Glu Arg Leu Ser Glu Arg Gly Gly Glu Thr
            260                 265                 270

Asp Gly Leu Phe Asp Glu Val Val Glu Phe Val Val Ser Thr Gly Thr
        275                 280                 285

Thr Ser Ile Ser Ala Ile Gln Arg Arg Phe Arg Val Gly Phe Asn Arg
    290                 295                 300

Ala Ala Asn Ile Met Asp Gln Leu Glu Glu Gln Gly Ile Val Ser Pro
305                 310                 315                 320

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

<210>  71
<211>  426
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(426)

<400>  71
atg tcg cct aat tat cct tat att aaa aca ttg gtt ata ttt cct ctg        48
```

```
Met Ser Pro Asn Tyr Pro Tyr Ile Lys Thr Leu Val Ile Phe Pro Leu
1               5                   10                  15

ctt gct caa ctt atc ggc acc atc atc agc att tgt gtg gat gac aat       96
Leu Ala Gln Leu Ile Gly Thr Ile Ile Ser Ile Cys Val Asp Asp Asn
            20                  25                  30

act gac agt ttt ctc ggc act gcc gac gtg atc ctt ttt agt ctg tta      144
Thr Asp Ser Phe Leu Gly Thr Ala Asp Val Ile Leu Phe Ser Leu Leu
        35                  40                  45

tcg act ttt atc gtg gca acc gtg ccc gct ttt ttg att gca ctg tgg      192
Ser Thr Phe Ile Val Ala Thr Val Pro Ala Phe Leu Ile Ala Leu Trp
    50                  55                  60

aca aaa att tat cgc tat acg cgc tat aac atg atg gcg att gtg tta      240
Thr Lys Ile Tyr Arg Tyr Thr Arg Tyr Asn Met Met Ala Ile Val Leu
65                  70                  75                  80

atc tcg ctg att atc gct ttt tgt tat ggc aac gta gct agc ttt atc      288
Ile Ser Leu Ile Ile Ala Phe Cys Tyr Gly Asn Val Ala Ser Phe Ile
                85                  90                  95

tac atg acg ttc tct cag cca aac atg acg ttt ggt att tgg ctg cgt      336
Tyr Met Thr Phe Ser Gln Pro Asn Met Thr Phe Gly Ile Trp Leu Arg
            100                 105                 110

agc ggc ggc att gat atg gcg ttt tta ctg agt ttc ggc atg gcg ttg      384
Ser Gly Gly Ile Asp Met Ala Phe Leu Leu Ser Phe Gly Met Ala Leu
        115                 120                 125

tat tca gtt ctt gtc ttg cct ttg ttg tta ccg caa acc aga              426
Tyr Ser Val Leu Val Leu Pro Leu Leu Leu Pro Gln Thr Arg
    130                 135                 140


<210>  72
<211>  142
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  72

Met Ser Pro Asn Tyr Pro Tyr Ile Lys Thr Leu Val Ile Phe Pro Leu
1               5                   10                  15


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


Thr Asp Ser Phe Leu Gly Thr Ala Asp Val Ile Leu Phe Ser Leu Leu
        35                  40                  45


Ser Thr Phe Ile Val Ala Thr Val Pro Ala Phe Leu Ile Ala Leu Trp
    50                  55                  60


Thr Lys Ile Tyr Arg Tyr Thr Arg Tyr Asn Met Met Ala Ile Val Leu
65                  70                  75                  80
```

```
Ile Ser Leu Ile Ile Ala Phe Cys Tyr Gly Asn Val Ala Ser Phe Ile
                85                  90                  95

Tyr Met Thr Phe Ser Gln Pro Asn Met Thr Phe Gly Ile Trp Leu Arg
            100                 105                 110

Ser Gly Gly Ile Asp Met Ala Phe Leu Leu Ser Phe Gly Met Ala Leu
        115                 120                 125

Tyr Ser Val Leu Val Leu Pro Leu Leu Leu Pro Gln Thr Arg
    130                 135                 140


<210>  73
<211>  600
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(600)

<400>  73
gta tct caa caa aac cgc tgc gga ttc cac cac gga ttc aat aat gaa       48
Val Ser Gln Gln Asn Arg Cys Gly Phe His His Gly Phe Asn Asn Glu
1               5                   10                  15

aga gga aaa ata atc atg ttg gca aga atg tta ttt caa tcc tgg cgt       96
Arg Gly Lys Ile Ile Met Leu Ala Arg Met Leu Phe Gln Ser Trp Arg
            20                  25                  30

tat gat tta aag cgc aaa ctc ctc gcc att gtg acc att ttc ctc gct      144
Tyr Asp Leu Lys Arg Lys Leu Leu Ala Ile Val Thr Ile Phe Leu Ala
        35                  40                  45

gcc gga tta att tcc gcc ttg ctt gcg gtg tcc atc gac atc ggc gac      192
Ala Gly Leu Ile Ser Ala Leu Leu Ala Val Ser Ile Asp Ile Gly Asp
    50                  55                  60

aaa atg gcg aaa gag ctt aaa tcc tac ggc gcc aat att ctg gtg gag      240
Lys Met Ala Lys Glu Leu Lys Ser Tyr Gly Ala Asn Ile Leu Val Glu
65                  70                  75                  80

ccc gcc agc agc gcc att ttg cct gat gaa gtg agc cgt aat aat tct      288
Pro Ala Ser Ser Ala Ile Leu Pro Asp Glu Val Ser Arg Asn Asn Ser
                85                  90                  95

ctc gcc acg caa gat ttt ttg gac gaa aaa gaa ctg ccg aac att aaa      336
Leu Ala Thr Gln Asp Phe Leu Asp Glu Lys Glu Leu Pro Asn Ile Lys
            100                 105                 110

gac att ttt tgg cgt aac aat att gta ggc ttc gcc ccg tta ctc agc      384
Asp Ile Phe Trp Arg Asn Asn Ile Val Gly Phe Ala Pro Leu Leu Ser
        115                 120                 125

gca caa gtc aaa gcc gat gga cca aac ggc aag gcg caa gac atc gac      432
```

```
Ala Gln Val Lys Ala Asp Gly Pro Asn Gly Lys Ala Gln Asp Ile Asp
    130                 135                 140

att ctc ggc acg ttt ttt gat cat caa atc gcc gtg ccg gat gaa gac       480
Ile Leu Gly Thr Phe Phe Asp His Gln Ile Ala Val Pro Asp Glu Asp
145                 150                 155                 160

gat tac cac acc ggg caa aaa atc atc aac cct tat tgg cag gtg gaa       528
Asp Tyr His Thr Gly Gln Lys Ile Ile Asn Pro Tyr Trp Gln Val Glu
                165                 170                 175

ggc gaa tgg gtg aac gat gcc acc gat gat ttc agc gaa cag gtt cct       576
Gly Glu Trp Val Asn Asp Ala Thr Asp Asp Phe Ser Glu Gln Val Pro
            180                 185                 190

gcg tta ctc ggc gca caa ctt gcc                                       600
Ala Leu Leu Gly Ala Gln Leu Ala
        195                 200


<210>  74
<211>  200
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  74

Val Ser Gln Gln Asn Arg Cys Gly Phe His His Gly Phe Asn Asn Glu
1               5                   10                  15


Arg Gly Lys Ile Ile Met Leu Ala Arg Met Leu Phe Gln Ser Trp Arg
            20                  25                  30


Tyr Asp Leu Lys Arg Lys Leu Leu Ala Ile Val Thr Ile Phe Leu Ala
        35                  40                  45


Ala Gly Leu Ile Ser Ala Leu Leu Ala Val Ser Ile Asp Ile Gly Asp
    50                  55                  60


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


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


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


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


Ala Gln Val Lys Ala Asp Gly Pro Asn Gly Lys Ala Gln Asp Ile Asp
    130                 135                 140
```

```
Ile Leu Gly Thr Phe Phe Asp His Gln Ile Ala Val Pro Asp Glu Asp
145                 150                 155                 160


Asp Tyr His Thr Gly Gln Lys Ile Ile Asn Pro Tyr Trp Gln Val Glu
                165                 170                 175


Gly Glu Trp Val Asn Asp Ala Thr Asp Asp Phe Ser Glu Gln Val Pro
            180                 185                 190


Ala Leu Leu Gly Ala Gln Leu Ala
        195                 200


<210>  75
<211>  603
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(603)

<400>  75
gaa cct cga atc act gca ttg cac caa gaa aat caa ggc aaa gcc agt        48
Glu Pro Arg Ile Thr Ala Leu His Gln Glu Asn Gln Gly Lys Ala Ser
1               5                   10                  15

gca ttg aat cat ggt tta acg gtt gcc aag gga aaa tac gtt gcc tgt        96
Ala Leu Asn His Gly Leu Thr Val Ala Lys Gly Lys Tyr Val Ala Cys
            20                  25                  30

atc gac ggt gat gcg gta ttg gat tac tac gcg ctg gac tac atg gtt       144
Ile Asp Gly Asp Ala Val Leu Asp Tyr Tyr Ala Leu Asp Tyr Met Val
        35                  40                  45

caa gcc tta gag caa gat ccg aaa tat gct gct acc aca ggt aat ccg       192
Gln Ala Leu Glu Gln Asp Pro Lys Tyr Ala Ala Thr Thr Gly Asn Pro
    50                  55                  60

cgt gta cgt aac cgt agt act att ttg ggg cgt tta cag gta tcc gag       240
Arg Val Arg Asn Arg Ser Thr Ile Leu Gly Arg Leu Gln Val Ser Glu
65                  70                  75                  80

ttc agc tcc atc atc ggt cta att aag cgg gca caa ggt cta atg ggc       288
Phe Ser Ser Ile Ile Gly Leu Ile Lys Arg Ala Gln Gly Leu Met Gly
                85                  90                  95

aca atc ttt acc gtt tcc ggc gtg tgt tgt tta ttc cgt aaa gat gtc       336
Thr Ile Phe Thr Val Ser Gly Val Cys Cys Leu Phe Arg Lys Asp Val
            100                 105                 110

atg gaa gaa atc ggt gga tgg agt act aac atg atc acc gaa gac att       384
Met Glu Glu Ile Gly Gly Trp Ser Thr Asn Met Ile Thr Glu Asp Ile
        115                 120                 125

gat att agc tgg aaa att caa att gcc ggt tac aac atc atg tac gaa       432
```

```
Asp Ile Ser Trp Lys Ile Gln Ile Ala Gly Tyr Asn Ile Met Tyr Glu
    130                 135                 140

cca cgc gca ctc tgc tgg gtg ctt atg ccg gaa agc ata aaa ggg ctt        480
Pro Arg Ala Leu Cys Trp Val Leu Met Pro Glu Ser Ile Lys Gly Leu
145                 150                 155                 160

tat aaa cag cgt ttg cgt tgg gca caa ggc ggt gcg gaa act atc atg        528
Tyr Lys Gln Arg Leu Arg Trp Ala Gln Gly Gly Ala Glu Thr Ile Met
                165                 170                 175

aag tat ttt tcg aaa ata tgg cat tgg cgg aat cgt cgc ttg tgg cca        576
Lys Tyr Phe Ser Lys Ile Trp His Trp Arg Asn Arg Arg Leu Trp Pro
            180                 185                 190

atg tat att gag tat ttt gct acc gtt                                    603
Met Tyr Ile Glu Tyr Phe Ala Thr Val
        195                 200


<210>  76
<211>  201
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  76

Glu Pro Arg Ile Thr Ala Leu His Gln Glu Asn Gln Gly Lys Ala Ser
1               5                   10                  15


Ala Leu Asn His Gly Leu Thr Val Ala Lys Gly Lys Tyr Val Ala Cys
            20                  25                  30


Ile Asp Gly Asp Ala Val Leu Asp Tyr Tyr Ala Leu Asp Tyr Met Val
        35                  40                  45


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


Arg Val Arg Asn Arg Ser Thr Ile Leu Gly Arg Leu Gln Val Ser Glu
65                  70                  75                  80


Phe Ser Ser Ile Ile Gly Leu Ile Lys Arg Ala Gln Gly Leu Met Gly
                85                  90                  95


Thr Ile Phe Thr Val Ser Gly Val Cys Cys Leu Phe Arg Lys Asp Val
            100                 105                 110


Met Glu Glu Ile Gly Gly Trp Ser Thr Asn Met Ile Thr Glu Asp Ile
        115                 120                 125


Asp Ile Ser Trp Lys Ile Gln Ile Ala Gly Tyr Asn Ile Met Tyr Glu
    130                 135                 140
```

```
Pro Arg Ala Leu Cys Trp Val Leu Met Pro Glu Ser Ile Lys Gly Leu
145                 150                 155                 160


Tyr Lys Gln Arg Leu Arg Trp Ala Gln Gly Gly Ala Glu Thr Ile Met
                165                 170                 175


Lys Tyr Phe Ser Lys Ile Trp His Trp Arg Asn Arg Arg Leu Trp Pro
            180                 185                 190


Met Tyr Ile Glu Tyr Phe Ala Thr Val
    195                 200


<210>  77
<211>  759
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(759)

<400>  77
atg cga tat ttg aaa caa aca aca att tca ctg tta att ttg acc gca        48
Met Arg Tyr Leu Lys Gln Thr Thr Ile Ser Leu Leu Ile Leu Thr Ala
1               5                   10                  15

ctt tcc tcc tcc ttt gcc aat cag cac aag gcg aca acg cat aaa gcg        96
Leu Ser Ser Ser Phe Ala Asn Gln His Lys Ala Thr Thr His Lys Ala
            20                  25                  30

aat gtt gcc cat acg cac gcc aaa ccg gag caa cac cac gca gaa tta       144
Asn Val Ala His Thr His Ala Lys Pro Glu Gln His His Ala Glu Leu
        35                  40                  45

gaa cgg cta aaa cag cgt gca act ttt ctg cag tta gaa agc ctg ctg       192
Glu Arg Leu Lys Gln Arg Ala Thr Phe Leu Gln Leu Glu Ser Leu Leu
    50                  55                  60

aaa agt gcg gtc aaa aat aac ggc gtt ttt atc aac caa act gta ttc       240
Lys Ser Ala Val Lys Asn Asn Gly Val Phe Ile Asn Gln Thr Val Phe
65                  70                  75                  80

ctg aaa ctg att gag gat ttg aaa ggc tat ccg ttg caa aca gat gcc       288
Leu Lys Leu Ile Glu Asp Leu Lys Gly Tyr Pro Leu Gln Thr Asp Ala
                85                  90                  95

ata gcg gct tat ttc gac gcc tgc att aaa agc gta aat cac gac aca       336
Ile Ala Ala Tyr Phe Asp Ala Cys Ile Lys Ser Val Asn His Asp Thr
            100                 105                 110

tcg aag gga gaa gtt aag gcg cta aaa cag gac att gag caa ttt atc       384
Ser Lys Gly Glu Val Lys Ala Leu Lys Gln Asp Ile Glu Gln Phe Ile
        115                 120                 125

gaa aag cat ccg act cat ttt cta cgg gaa aaa ttg gaa caa aga ctt       432
```

```
Glu Lys His Pro Thr His Phe Leu Arg Glu Lys Leu Glu Gln Arg Leu
    130                 135                 140

ttt acc tta ttt atc aac acg gaa gat ctt gaa ggc tta gtt ggt tac      480
Phe Thr Leu Phe Ile Asn Thr Glu Asp Leu Glu Gly Leu Val Gly Tyr
145                 150                 155                 160

gcg caa cgg gtt aaa ccg aaa ggg ttg gaa gcc caa ctt gca gtg ttg      528
Ala Gln Arg Val Lys Pro Lys Gly Leu Glu Ala Gln Leu Ala Val Leu
                165                 170                 175

aat gcc gaa tat caa ctg ggg cgc aaa cgt gcc gaa tct gat aaa aat      576
Asn Ala Glu Tyr Gln Leu Gly Arg Lys Arg Ala Glu Ser Asp Lys Asn
            180                 185                 190

ccg aat gcg aat gtg tcg aaa atc atc gcc cgt tat gag caa ctt tgg      624
Pro Asn Ala Asn Val Ser Lys Ile Ile Ala Arg Tyr Glu Gln Leu Trp
        195                 200                 205

tta aac aat agt gaa ctg cca aac gat gcg cag cta cgg gca aaa tgg      672
Leu Asn Asn Ser Glu Leu Pro Asn Asp Ala Gln Leu Arg Ala Lys Trp
    210                 215                 220

tat tcc gac ggc ggc aga atg gca gaa aaa gtg tat caa aaa gct gag      720
Tyr Ser Asp Gly Gly Arg Met Ala Glu Lys Val Tyr Gln Lys Ala Glu
225                 230                 235                 240

aat ctc ttt atc aaa aac aat gta aaa ggc ttg gaa ttg                  759
Asn Leu Phe Ile Lys Asn Asn Val Lys Gly Leu Glu Leu
                245                 250


<210>  78
<211>  253
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  78

Met Arg Tyr Leu Lys Gln Thr Thr Ile Ser Leu Leu Ile Leu Thr Ala
1               5                   10                  15


Leu Ser Ser Ser Phe Ala Asn Gln His Lys Ala Thr Thr His Lys Ala
            20                  25                  30


Asn Val Ala His Thr His Ala Lys Pro Glu Gln His His Ala Glu Leu
        35                  40                  45


Glu Arg Leu Lys Gln Arg Ala Thr Phe Leu Gln Leu Glu Ser Leu Leu
    50                  55                  60


Lys Ser Ala Val Lys Asn Asn Gly Val Phe Ile Asn Gln Thr Val Phe
65                  70                  75                  80


Leu Lys Leu Ile Glu Asp Leu Lys Gly Tyr Pro Leu Gln Thr Asp Ala
                85                  90                  95
```

```
Ile Ala Ala Tyr Phe Asp Ala Cys Ile Lys Ser Val Asn His Asp Thr
            100                 105                 110

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

Glu Lys His Pro Thr His Phe Leu Arg Glu Lys Leu Glu Gln Arg Leu
    130                 135                 140

Phe Thr Leu Phe Ile Asn Thr Glu Asp Leu Glu Gly Leu Val Gly Tyr
145                 150                 155                 160

Ala Gln Arg Val Lys Pro Lys Gly Leu Glu Ala Gln Leu Ala Val Leu
                165                 170                 175

Asn Ala Glu Tyr Gln Leu Gly Arg Lys Arg Ala Glu Ser Asp Lys Asn
            180                 185                 190

Pro Asn Ala Asn Val Ser Lys Ile Ile Ala Arg Tyr Glu Gln Leu Trp
        195                 200                 205

Leu Asn Asn Ser Glu Leu Pro Asn Asp Ala Gln Leu Arg Ala Lys Trp
    210                 215                 220

Tyr Ser Asp Gly Gly Arg Met Ala Glu Lys Val Tyr Gln Lys Ala Glu
225                 230                 235                 240

Asn Leu Phe Ile Lys Asn Asn Val Lys Gly Leu Glu Leu
                245                 250


<210>  79
<211>  624
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(624)

<400>  79
gtc ggt caa tgg acg gag aaa ggt aac caa acg gaa aat cgc gat aat        48
Val Gly Gln Trp Thr Glu Lys Gly Asn Gln Thr Glu Asn Arg Asp Asn
1               5                   10                  15

tcc gat ccg tcc ggt tta ggt tgt act ctt ggt tgg ggc ttt gca tgg        96
Ser Asp Pro Ser Gly Leu Gly Cys Thr Leu Gly Trp Gly Phe Ala Trp
            20                  25                  30

cca gca aac cgc cgc gtg ctt tat agc cgc gcc tct ttg gat att aac       144
```

```
Pro Ala Asn Arg Arg Val Leu Tyr Ser Arg Ala Ser Leu Asp Ile Asn
        35                  40                  45

ggt aat cct tgg gat aaa cac cgt caa ctg atc aaa tgg aac ggt aaa      192
Gly Asn Pro Trp Asp Lys His Arg Gln Leu Ile Lys Trp Asn Gly Lys
    50                  55                  60

aac tgg aac tgg ttt gat att gcc gac tac ggc act caa cca cca ggt      240
Asn Trp Asn Trp Phe Asp Ile Ala Asp Tyr Gly Thr Gln Pro Pro Gly
65                  70                  75                  80

tcc gat acc aga cca ttt atg atg tca gcc gaa ggt gtt gga cgc tta      288
Ser Asp Thr Arg Pro Phe Met Met Ser Ala Glu Gly Val Gly Arg Leu
                85                  90                  95

ttt gcc gtt gat aaa att aat agc gga ccg ttc ccg gaa cac tat gaa      336
Phe Ala Val Asp Lys Ile Asn Ser Gly Pro Phe Pro Glu His Tyr Glu
            100                 105                 110

ccg att gaa agt ccg att gat acg aat ccg ctt cat ccg aat gtg gta      384
Pro Ile Glu Ser Pro Ile Asp Thr Asn Pro Leu His Pro Asn Val Val
        115                 120                 125

tca gat ccg acg gtg cgt att tac aaa gaa gat cgc gag ttt atc ggc      432
Ser Asp Pro Thr Val Arg Ile Tyr Lys Glu Asp Arg Glu Phe Ile Gly
    130                 135                 140

tca aat aaa gaa tat ccg ttt gtg gca aca act tat cgt cta acc gaa      480
Ser Asn Lys Glu Tyr Pro Phe Val Ala Thr Thr Tyr Arg Leu Thr Glu
145                 150                 155                 160

cat ttc cac agt tgg acc gcg caa tct gcc att aac atc atc gca caa      528
His Phe His Ser Trp Thr Ala Gln Ser Ala Ile Asn Ile Ile Ala Gln
                165                 170                 175

ccg caa caa ttt gtg gaa atc ggt gaa aaa ttg gca gaa gaa aaa ggt      576
Pro Gln Gln Phe Val Glu Ile Gly Glu Lys Leu Ala Glu Glu Lys Gly
            180                 185                 190

atc caa aaa ggc gat atg gta cgt att acc tcc aaa cgg ggc tat att      624
Ile Gln Lys Gly Asp Met Val Arg Ile Thr Ser Lys Arg Gly Tyr Ile
        195                 200                 205


<210>  80
<211>  208
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  80

Val Gly Gln Trp Thr Glu Lys Gly Asn Gln Thr Glu Asn Arg Asp Asn
1               5                   10                  15


Ser Asp Pro Ser Gly Leu Gly Cys Thr Leu Gly Trp Gly Phe Ala Trp
            20                  25                  30


Pro Ala Asn Arg Arg Val Leu Tyr Ser Arg Ala Ser Leu Asp Ile Asn
        35                  40                  45
```

```
Gly Asn Pro Trp Asp Lys His Arg Gln Leu Ile Lys Trp Asn Gly Lys
    50                  55                  60


Asn Trp Asn Trp Phe Asp Ile Ala Asp Tyr Gly Thr Gln Pro Pro Gly
65                  70                  75                  80


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


Phe Ala Val Asp Lys Ile Asn Ser Gly Pro Phe Pro Glu His Tyr Glu
            100                 105                 110


Pro Ile Glu Ser Pro Ile Asp Thr Asn Pro Leu His Pro Asn Val Val
        115                 120                 125


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


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


His Phe His Ser Trp Thr Ala Gln Ser Ala Ile Asn Ile Ile Ala Gln
                    165                 170                 175


Pro Gln Gln Phe Val Glu Ile Gly Glu Lys Leu Ala Glu Glu Lys Gly
            180                 185                 190


Ile Gln Lys Gly Asp Met Val Arg Ile Thr Ser Lys Arg Gly Tyr Ile
        195                 200                 205


<210>  81
<211>  534
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(534)

<400>  81
att cct ggc tta att gaa ggc gca tcg gaa gga gca ggc ttg ggt atc        48
Ile Pro Gly Leu Ile Glu Gly Ala Ser Glu Gly Ala Gly Leu Gly Ile
1               5                   10                  15

cgc ttc ctg aaa cac ttg gaa cgt tgc cgc gtg ttg att cat ttg gtg        96
Arg Phe Leu Lys His Leu Glu Arg Cys Arg Val Leu Ile His Leu Val
            20                  25                  30

gat atc aac cca att gat gat tcc aac ccg gcg gat aac gtg gcg att       144
```

```
Asp Ile Asn Pro Ile Asp Asp Ser Asn Pro Ala Asp Asn Val Ala Ile
        35                  40                  45

atc gaa tcg gaa ttg ttc caa tac agc gag tcc ttg gcg gaa aaa ccg      192
Ile Glu Ser Glu Leu Phe Gln Tyr Ser Glu Ser Leu Ala Glu Lys Pro
    50                  55                  60

cgc tgg ctg gtg ttc aac aaa atc gat acg ctc agt gat gaa gaa gcc      240
Arg Trp Leu Val Phe Asn Lys Ile Asp Thr Leu Ser Asp Glu Glu Ala
65                  70                  75                  80

cat gcg cga gcg aaa gag atc acc gaa cgt ctg ggc cgg gag gaa ggt      288
His Ala Arg Ala Lys Glu Ile Thr Glu Arg Leu Gly Arg Glu Glu Gly
                85                  90                  95

tat tat tta att tcc gcc gcc acc ggt aaa aac gcc ccg caa ctg tgc      336
Tyr Tyr Leu Ile Ser Ala Ala Thr Gly Lys Asn Ala Pro Gln Leu Cys
            100                 105                 110

cgc gat att atg gac ttc ctg gaa gcc cac ccg cgc aaa aca gaa aaa      384
Arg Asp Ile Met Asp Phe Leu Glu Ala His Pro Arg Lys Thr Glu Lys
        115                 120                 125

acg ccg gta gaa aat gaa gaa gtc aaa ttc aaa tgg gaa gat tat cat      432
Thr Pro Val Glu Asn Glu Glu Val Lys Phe Lys Trp Glu Asp Tyr His
    130                 135                 140

cag gag caa ttg gaa aat gcc gat gtt gat gat gaa gag gat aat gac      480
Gln Glu Gln Leu Glu Asn Ala Asp Val Asp Asp Glu Glu Asp Asn Asp
145                 150                 155                 160

tgg gat gac tgg tcg gaa gac gat gaa gaa ggc gtg gaa att atc tat      528
Trp Asp Asp Trp Ser Glu Asp Asp Glu Glu Gly Val Glu Ile Ile Tyr
                165                 170                 175

aag cct                                                              534
Lys Pro


<210>  82
<211>  178
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  82

Ile Pro Gly Leu Ile Glu Gly Ala Ser Glu Gly Ala Gly Leu Gly Ile
1               5                   10                  15


Arg Phe Leu Lys His Leu Glu Arg Cys Arg Val Leu Ile His Leu Val
            20                  25                  30


Asp Ile Asn Pro Ile Asp Asp Ser Asn Pro Ala Asp Asn Val Ala Ile
        35                  40                  45


Ile Glu Ser Glu Leu Phe Gln Tyr Ser Glu Ser Leu Ala Glu Lys Pro
    50                  55                  60
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```
Arg Trp Leu Val Phe Asn Lys Ile Asp Thr Leu Ser Asp Glu Glu Ala
65                  70                  75                  80


His Ala Arg Ala Lys Glu Ile Thr Glu Arg Leu Gly Arg Glu Glu Gly
                85                  90                  95


Tyr Tyr Leu Ile Ser Ala Ala Thr Gly Lys Asn Ala Pro Gln Leu Cys
            100                 105                 110


Arg Asp Ile Met Asp Phe Leu Glu Ala His Pro Arg Lys Thr Glu Lys
        115                 120                 125


Thr Pro Val Glu Asn Glu Glu Val Lys Phe Lys Trp Glu Asp Tyr His
    130                 135                 140


Gln Glu Gln Leu Glu Asn Ala Asp Val Asp Asp Glu Glu Asp Asn Asp
145                 150                 155                 160


Trp Asp Asp Trp Ser Glu Asp Asp Glu Glu Gly Val Glu Ile Ile Tyr
                165                 170                 175


Lys Pro


<210>  83
<211>  372
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(372)

<400>  83
atg tta acg gaa agt gcg gtc gtt att gag tac gaa tcc ggc aga gcc        48
Met Leu Thr Glu Ser Ala Val Val Ile Glu Tyr Glu Ser Gly Arg Ala
1               5                   10                  15

aaa gtg aaa tgc caa tca caa agc gca tgc ggc gct tgc gcg gca aaa        96
Lys Val Lys Cys Gln Ser Gln Ser Ala Cys Gly Ala Cys Ala Ala Lys
            20                  25                  30

ccg gcg tgc ggt aat tct gcc ttg tcg gaa tta gcc agc agc ggc gcg       144
Pro Ala Cys Gly Asn Ser Ala Leu Ser Glu Leu Ala Ser Ser Gly Ala
        35                  40                  45

cgc ggc gaa cat att ttc acc atc gag acc att acg cca ctg aaa atc       192
Arg Gly Glu His Ile Phe Thr Ile Glu Thr Ile Thr Pro Leu Lys Ile
    50                  55                  60

ggg caa cgg gtg gaa atc ggt ttg tcc gaa cgt tcc tta atc aaa tcc       240
```

```
Gly Gln Arg Val Glu Ile Gly Leu Ser Glu Arg Ser Leu Ile Lys Ser
65                  70                  75                  80

gcc ttg ctc atg tat tgc gtg ccg cta ttt act tta tta ttc agc acg        288
Ala Leu Leu Met Tyr Cys Val Pro Leu Phe Thr Leu Leu Phe Ser Thr
                85                  90                  95

tta tta ttt gat tcg ctg ttt gcc cat gag ctc gtc agc gtc ttt ttt        336
Leu Leu Phe Asp Ser Leu Phe Ala His Glu Leu Val Ser Val Phe Phe
            100                 105                 110

atc ttc att tcc act gca ctt tct ttc ctt ggt gtg                        372
Ile Phe Ile Ser Thr Ala Leu Ser Phe Leu Gly Val
        115                 120


<210>  84
<211>  124
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  84

Met Leu Thr Glu Ser Ala Val Val Ile Glu Tyr Glu Ser Gly Arg Ala
1               5                   10                  15


Lys Val Lys Cys Gln Ser Gln Ser Ala Cys Gly Ala Cys Ala Ala Lys
            20                  25                  30


Pro Ala Cys Gly Asn Ser Ala Leu Ser Glu Leu Ala Ser Ser Gly Ala
    35                  40                  45


Arg Gly Glu His Ile Phe Thr Ile Glu Thr Ile Thr Pro Leu Lys Ile
    50                  55                  60


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


Ala Leu Leu Met Tyr Cys Val Pro Leu Phe Thr Leu Leu Phe Ser Thr
                85                  90                  95


Leu Leu Phe Asp Ser Leu Phe Ala His Glu Leu Val Ser Val Phe Phe
            100                 105                 110


Ile Phe Ile Ser Thr Ala Leu Ser Phe Leu Gly Val
        115                 120


<210>  85
<211>  629
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
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<221>  CDS
<222>  (1)..(627)

<400>  85
att tct tcc ggt tcc tta ttg ctt gcc gtg ctt tat aaa cgc aat cgc       48
Ile Ser Ser Gly Ser Leu Leu Leu Ala Val Leu Tyr Lys Arg Asn Arg
1               5                   10                  15

aaa ccg gaa aaa aca agc gaa aac tgg att att cgc agt gct gcg atc       96
Lys Pro Glu Lys Thr Ser Glu Asn Trp Ile Ile Arg Ser Ala Ala Ile
            20                  25                  30

tta gcg cct ggc acg gtg att atc ggt tta ttg ctg ttg att ttc cac      144
Leu Ala Pro Gly Thr Val Ile Ile Gly Leu Leu Leu Leu Ile Phe His
        35                  40                  45

ttg gcg cgc cct tgg acg ttc tgg tat ttg atg ttt aac tac cag ttc      192
Leu Ala Arg Pro Trp Thr Phe Trp Tyr Leu Met Phe Asn Tyr Gln Phe
    50                  55                  60

aat tcc gtg atg tcc atg ggg gta ctg tta ttc caa atc tat atg gcg      240
Asn Ser Val Met Ser Met Gly Val Leu Leu Phe Gln Ile Tyr Met Ala
65                  70                  75                  80

gcg gtt ctc ctc tgg att gcg att ctc ttt aaa aat gaa ctt gcc gcc      288
Ala Val Leu Leu Trp Ile Ala Ile Leu Phe Lys Asn Glu Leu Ala Ala
                85                  90                  95

ttg ctc gat aga ttt tta ccg aaa tta aaa ttt atc gtg aaa tgg att      336
Leu Leu Asp Arg Phe Leu Pro Lys Leu Lys Phe Ile Val Lys Trp Ile
            100                 105                 110

ttc gcc tgt gaa cgc att acc aac ccg ttg gaa ctg ttc ctg ttg ttc      384
Phe Ala Cys Glu Arg Ile Thr Asn Pro Leu Glu Leu Phe Leu Leu Phe
        115                 120                 125

ctt gcg gtg ttg cta ggc gct tat acc ggt ttc tta ttg tcg gcg tta      432
Leu Ala Val Leu Leu Gly Ala Tyr Thr Gly Phe Leu Leu Ser Ala Leu
    130                 135                 140

atc agc tac ccg atg cta aac aat ccc gta ttg ccg gca tta ttc ctc      480
Ile Ser Tyr Pro Met Leu Asn Asn Pro Val Leu Pro Ala Leu Phe Leu
145                 150                 155                 160

gct tcg ggc acg tct tcc ggt atc gcg gcg gta ttc tta acc atc ctg      528
Ala Ser Gly Thr Ser Ser Gly Ile Ala Ala Val Phe Leu Thr Ile Leu
                165                 170                 175

att gtg ggc aaa tta aaa ggg cat tcc gac gaa gtg aat ttc atg cat      576
Ile Val Gly Lys Leu Lys Gly His Ser Asp Glu Val Asn Phe Met His
            180                 185                 190

aaa ttt gaa gtg ccg atc atg ctc gcc gaa ctc ttt tgc atc ggc tgc      624
Lys Phe Glu Val Pro Ile Met Leu Ala Glu Leu Phe Cys Ile Gly Cys
        195                 200                 205

ttc tt                                                               629
Phe
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<210>  86
<211>  209
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  86

Ile Ser Ser Gly Ser Leu Leu Leu Ala Val Leu Tyr Lys Arg Asn Arg
1               5                   10                  15


Lys Pro Glu Lys Thr Ser Glu Asn Trp Ile Ile Arg Ser Ala Ala Ile
            20                  25                  30


Leu Ala Pro Gly Thr Val Ile Ile Gly Leu Leu Leu Leu Ile Phe His
        35                  40                  45


Leu Ala Arg Pro Trp Thr Phe Trp Tyr Leu Met Phe Asn Tyr Gln Phe
    50                  55                  60


Asn Ser Val Met Ser Met Gly Val Leu Leu Phe Gln Ile Tyr Met Ala
65                  70                  75                  80


Ala Val Leu Leu Trp Ile Ala Ile Leu Phe Lys Asn Glu Leu Ala Ala
                85                  90                  95


Leu Leu Asp Arg Phe Leu Pro Lys Leu Lys Phe Ile Val Lys Trp Ile
            100                 105                 110


Phe Ala Cys Glu Arg Ile Thr Asn Pro Leu Glu Leu Phe Leu Leu Phe
        115                 120                 125


Leu Ala Val Leu Leu Gly Ala Tyr Thr Gly Phe Leu Leu Ser Ala Leu
    130                 135                 140


Ile Ser Tyr Pro Met Leu Asn Asn Pro Val Leu Pro Ala Leu Phe Leu
145                 150                 155                 160


Ala Ser Gly Thr Ser Ser Gly Ile Ala Ala Val Phe Leu Thr Ile Leu
                165                 170                 175


Ile Val Gly Lys Leu Lys Gly His Ser Asp Glu Val Asn Phe Met His
            180                 185                 190


Lys Phe Glu Val Pro Ile Met Leu Ala Glu Leu Phe Cys Ile Gly Cys
        195                 200                 205


Phe
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<210>  87
<211>  266
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(264)

<400>  87
tgg gat gcc att gag aaa tgt att cag gaa tgg caa ccg gcg cgt att        48
Trp Asp Ala Ile Glu Lys Cys Ile Gln Glu Trp Gln Pro Ala Arg Ile
1               5                   10                  15

gtg gtc ggt ttg cca ctg aat atg gat ggt acg gaa cag ccc tta acg        96
Val Val Gly Leu Pro Leu Asn Met Asp Gly Thr Glu Gln Pro Leu Thr
            20                  25                  30

ttg cgt gcc aaa aag ttt gct aag cgt ttg cac gga cgt ttt aac gtg       144
Leu Arg Ala Lys Lys Phe Ala Lys Arg Leu His Gly Arg Phe Asn Val
        35                  40                  45

ccg gtg gat tta cag gac gaa cgt ctt acc acc acc gaa gcg cgt agc       192
Pro Val Asp Leu Gln Asp Glu Arg Leu Thr Thr Thr Glu Ala Arg Ser
    50                  55                  60

gaa att ttc agt cgt ggt ggt tat cgc gcc tta aat aaa agc aaa gtg       240
Glu Ile Phe Ser Arg Gly Gly Tyr Arg Ala Leu Asn Lys Ser Lys Val
65                  70                  75                  80

gac ggc att tcc gcc tgt ttg att tt                                    266
Asp Gly Ile Ser Ala Cys Leu Ile
                85


<210>  88
<211>  88
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  88

Trp Asp Ala Ile Glu Lys Cys Ile Gln Glu Trp Gln Pro Ala Arg Ile
1               5                   10                  15


Val Val Gly Leu Pro Leu Asn Met Asp Gly Thr Glu Gln Pro Leu Thr
            20                  25                  30


Leu Arg Ala Lys Lys Phe Ala Lys Arg Leu His Gly Arg Phe Asn Val
        35                  40                  45


Pro Val Asp Leu Gln Asp Glu Arg Leu Thr Thr Thr Glu Ala Arg Ser
    50                  55                  60


Glu Ile Phe Ser Arg Gly Gly Tyr Arg Ala Leu Asn Lys Ser Lys Val
```

65 70 75 80

Asp Gly Ile Ser Ala Cys Leu Ile
85

<210> 89
<211> 567
<212> DNA
<213> Actinobacillus actinomycetemcomitans

<220>
<221> CDS
<222> (1)..(567)

<400> 89
caa caa gta aaa gcg ccg gga gaa gcc aaa tcc gac gta tgg caa ttg 48
Gln Gln Val Lys Ala Pro Gly Glu Ala Lys Ser Asp Val Trp Gln Leu
1 5 10 15

gta gaa ttc tcc aaa tat ttc acc acc gat gaa atg tgg ccg gcg gaa 96
Val Glu Phe Ser Lys Tyr Phe Thr Thr Asp Glu Met Trp Pro Ala Glu
20 25 30

att ctg gac aaa aat ccg gaa tac aaa ggc aaa acc tta tat gac gtg 144
Ile Leu Asp Lys Asn Pro Glu Tyr Lys Gly Lys Thr Leu Tyr Asp Val
35 40 45

tta tac cgc aac ggt caa gta gat aaa ttc ccg tta agc gaa ttg gcg 192
Leu Tyr Arg Asn Gly Gln Val Asp Lys Phe Pro Leu Ser Glu Leu Ala
50 55 60

gaa gga caa ttg aat gat gag tcc tat cac ttc ggt ttc tac ttg caa 240
Glu Gly Gln Leu Asn Asp Glu Ser Tyr His Phe Gly Phe Tyr Leu Gln
65 70 75 80

aaa ggc tta ttt gag gaa tac gcc tcc ttc ggt cgc ggt cac gga cat 288
Lys Gly Leu Phe Glu Glu Tyr Ala Ser Phe Gly Arg Gly His Gly His
85 90 95

gac ttg gca tcg ttc gat act tac cac aaa gca cgc ggt tta cgc tgg 336
Asp Leu Ala Ser Phe Asp Thr Tyr His Lys Ala Arg Gly Leu Arg Trp
100 105 110

ccg gtg gtg gac ggc aaa gaa acc tta tgg cgt tat cgc gaa ggc tac 384
Pro Val Val Asp Gly Lys Glu Thr Leu Trp Arg Tyr Arg Glu Gly Tyr
115 120 125

gac ccg tat gtc aaa gaa ggg gaa ggt gtg gcg ttc tac ggc tat ccg 432
Asp Pro Tyr Val Lys Glu Gly Glu Gly Val Ala Phe Tyr Gly Tyr Pro
130 135 140

gat aaa aaa gcg att att ctt gcc gtg cct tat gag ccg cct gcg gaa 480
Asp Lys Lys Ala Ile Ile Leu Ala Val Pro Tyr Glu Pro Pro Ala Glu
145 150 155 160

tca ccg gac gaa gaa tac gat ttg tgg tta tgt acc ggt cgc gtg ttg 528
Ser Pro Asp Glu Glu Tyr Asp Leu Trp Leu Cys Thr Gly Arg Val Leu
165 170 175

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gaa cac tgg cac acc ggc acc atg acc cgt cgt gta cca                 567
Glu His Trp His Thr Gly Thr Met Thr Arg Arg Val Pro
            180                 185


<210>  90
<211>  189
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  90

Gln Gln Val Lys Ala Pro Gly Glu Ala Lys Ser Asp Val Trp Gln Leu
1               5                   10                  15


Val Glu Phe Ser Lys Tyr Phe Thr Thr Asp Glu Met Trp Pro Ala Glu
            20                  25                  30


Ile Leu Asp Lys Asn Pro Glu Tyr Lys Gly Lys Thr Leu Tyr Asp Val
        35                  40                  45


Leu Tyr Arg Asn Gly Gln Val Asp Lys Phe Pro Leu Ser Glu Leu Ala
    50                  55                  60


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


Lys Gly Leu Phe Glu Glu Tyr Ala Ser Phe Gly Arg Gly His Gly His
                85                  90                  95


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


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


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


Asp Lys Lys Ala Ile Ile Leu Ala Val Pro Tyr Glu Pro Pro Ala Glu
145                 150                 155                 160


Ser Pro Asp Glu Glu Tyr Asp Leu Trp Leu Cys Thr Gly Arg Val Leu
                165                 170                 175


Glu His Trp His Thr Gly Thr Met Thr Arg Arg Val Pro
            180                 185


<210>  91
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<211>  563
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(561)

<400>  91
ccg aaa cct ttc tat ttt tcc gct gaa aaa gat ggc att ggt gta gaa          48
Pro Lys Pro Phe Tyr Phe Ser Ala Glu Lys Asp Gly Ile Gly Val Glu
1               5                   10                  15

att gcg ttg caa tgg aac gac ggt tac gcg gaa aac att tat tgt ttc          96
Ile Ala Leu Gln Trp Asn Asp Gly Tyr Ala Glu Asn Ile Tyr Cys Phe
            20                  25                  30

acc aac aac att ccg caa cgg gac ggc ggt acg cac tta gcc ggt ttc         144
Thr Asn Asn Ile Pro Gln Arg Asp Gly Gly Thr His Leu Ala Gly Phe
        35                  40                  45

cgt ggc gca atg acc cgc acc ttg aac aac tac atg gaa aac gaa ggc         192
Arg Gly Ala Met Thr Arg Thr Leu Asn Asn Tyr Met Glu Asn Glu Gly
    50                  55                  60

tac acc aag aaa tcc aaa gtg gcg act tcc ggt gat gat gcc cgt gaa         240
Tyr Thr Lys Lys Ser Lys Val Ala Thr Ser Gly Asp Asp Ala Arg Glu
65                  70                  75                  80

ggc ttg gtg gcg gtg att tcc gtg aaa gta ccg gat ccg aaa ttc tct         288
Gly Leu Val Ala Val Ile Ser Val Lys Val Pro Asp Pro Lys Phe Ser
                85                  90                  95

tct caa aca aaa gac aaa ctg gtt tcc tcc gaa gtg aaa agt gcg gtg         336
Ser Gln Thr Lys Asp Lys Leu Val Ser Ser Glu Val Lys Ser Ala Val
            100                 105                 110

gaa tcc ctg atg aac gaa tat tta caa acc tat ttg ttg gaa aac ccg         384
Glu Ser Leu Met Asn Glu Tyr Leu Gln Thr Tyr Leu Leu Glu Asn Pro
        115                 120                 125

aac gat gta aaa atc atc gtg acc aaa att att gat gcc gcg cgt gcc         432
Asn Asp Val Lys Ile Ile Val Thr Lys Ile Ile Asp Ala Ala Arg Ala
    130                 135                 140

cgt gaa gcc gcc cgc aaa gcc cgc gaa atg acc cgt cgt aaa ggc gcg         480
Arg Glu Ala Ala Arg Lys Ala Arg Glu Met Thr Arg Arg Lys Gly Ala
145                 150                 155                 160

ttg gat tta ggc ggc ttg ccg ggc aaa ttg gcg gat tgt cag gaa cgc         528
Leu Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp Cys Gln Glu Arg
                165                 170                 175

gat ccg gcg tta tcc gag ctt tac atc gtg gag gg                          563
Asp Pro Ala Leu Ser Glu Leu Tyr Ile Val Glu
            180                 185


<210>  92
<211>  187
<212>  PRT
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<213>  Actinobacillus actinomycetemcomitans

<400>  92

Pro Lys Pro Phe Tyr Phe Ser Ala Glu Lys Asp Gly Ile Gly Val Glu
1               5                   10                  15


Ile Ala Leu Gln Trp Asn Asp Gly Tyr Ala Glu Asn Ile Tyr Cys Phe
            20                  25                  30


Thr Asn Asn Ile Pro Gln Arg Asp Gly Gly Thr His Leu Ala Gly Phe
        35                  40                  45


Arg Gly Ala Met Thr Arg Thr Leu Asn Asn Tyr Met Glu Asn Glu Gly
    50                  55                  60


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


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


Ser Gln Thr Lys Asp Lys Leu Val Ser Ser Glu Val Lys Ser Ala Val
            100                 105                 110


Glu Ser Leu Met Asn Glu Tyr Leu Gln Thr Tyr Leu Leu Glu Asn Pro
        115                 120                 125


Asn Asp Val Lys Ile Ile Val Thr Lys Ile Ile Asp Ala Ala Arg Ala
    130                 135                 140


Arg Glu Ala Ala Arg Lys Ala Arg Glu Met Thr Arg Arg Lys Gly Ala
145                 150                 155                 160


Leu Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp Cys Gln Glu Arg
                165                 170                 175


Asp Pro Ala Leu Ser Glu Leu Tyr Ile Val Glu
            180                 185


<210>  93
<211>  627
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(627)
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```
<400>  93
aaa cag caa tta gcc gct gca ctt gcc cga caa gaa caa aaa caa att       48
Lys Gln Gln Leu Ala Ala Ala Leu Ala Arg Gln Glu Gln Lys Gln Ile
1               5                   10                  15

atc gtt tta caa aaa aag tta acg tct ttg tct tcc cta tcc cca caa       96
Ile Val Leu Gln Lys Lys Leu Thr Ser Leu Ser Ser Leu Ser Pro Gln
            20                  25                  30

cgt ctt gcg caa caa att cgg act acc gaa aaa att ctg acc cgt att      144
Arg Leu Ala Gln Gln Ile Arg Thr Thr Glu Lys Ile Leu Thr Arg Ile
        35                  40                  45

ttt aaa aca gag aaa aat ctg aca ccc aaa ttt att gat tac ctg tat      192
Phe Lys Thr Glu Lys Asn Leu Thr Pro Lys Phe Ile Asp Tyr Leu Tyr
    50                  55                  60

ttt gag cca att gaa acg gct gat gac acc tta atg cag gaa atg aaa      240
Phe Glu Pro Ile Glu Thr Ala Asp Asp Thr Leu Met Gln Glu Met Lys
65                  70                  75                  80

aaa aat ctt ttg atc tct ttc ttg gca aat gaa cgc gct caa atc tat      288
Lys Asn Leu Leu Ile Ser Phe Leu Ala Asn Glu Arg Ala Gln Ile Tyr
                85                  90                  95

att aaa gac atg cca aac gct aat caa ttt gtt cag ctt tta aca gaa      336
Ile Lys Asp Met Pro Asn Ala Asn Gln Phe Val Gln Leu Leu Thr Glu
            100                 105                 110

aaa gga gca aag act acg caa ata tcc gta ttg gca gaa cct gct aaa      384
Lys Gly Ala Lys Thr Thr Gln Ile Ser Val Leu Ala Glu Pro Ala Lys
        115                 120                 125

acc att ttc cag cga atc cgc gaa caa atg tac caa gat ttt cct aat      432
Thr Ile Phe Gln Arg Ile Arg Glu Gln Met Tyr Gln Asp Phe Pro Asn
    130                 135                 140

aaa aaa cag ttt act atc act gaa aat cga gta agt gtt att gcc cct      480
Lys Lys Gln Phe Thr Ile Thr Glu Asn Arg Val Ser Val Ile Ala Pro
145                 150                 155                 160

tcc tcc gtt att aag cca cgc ctt gcc ttg gca gct gca att ttt gat      528
Ser Ser Val Ile Lys Pro Arg Leu Ala Leu Ala Ala Ala Ile Phe Asp
                165                 170                 175

cag cag ttt aaa ggg gtt gaa gtt gat gat ttt tct tac ttg gat caa      576
Gln Gln Phe Lys Gly Val Glu Val Asp Asp Phe Ser Tyr Leu Asp Gln
            180                 185                 190

ccg cgt gaa aat ttg caa cac aat aat gat aca acc cgt tat aaa acc      624
Pro Arg Glu Asn Leu Gln His Asn Asn Asp Thr Thr Arg Tyr Lys Thr
        195                 200                 205

ttt                                                                  627
Phe


<210>  94
<211>  209
<212>  PRT
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```
<213>  Actinobacillus actinomycetemcomitans

<400>  94

Lys Gln Gln Leu Ala Ala Ala Leu Ala Arg Gln Glu Gln Lys Gln Ile
1               5                   10                  15

Ile Val Leu Gln Lys Lys Leu Thr Ser Leu Ser Ser Leu Ser Pro Gln
            20                  25                  30

Arg Leu Ala Gln Gln Ile Arg Thr Thr Glu Lys Ile Leu Thr Arg Ile
        35                  40                  45

Phe Lys Thr Glu Lys Asn Leu Thr Pro Lys Phe Ile Asp Tyr Leu Tyr
    50                  55                  60

Phe Glu Pro Ile Glu Thr Ala Asp Asp Thr Leu Met Gln Glu Met Lys
65                  70                  75                  80

Lys Asn Leu Leu Ile Ser Phe Leu Ala Asn Glu Arg Ala Gln Ile Tyr
                85                  90                  95

Ile Lys Asp Met Pro Asn Ala Asn Gln Phe Val Gln Leu Leu Thr Glu
            100                 105                 110

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

Thr Ile Phe Gln Arg Ile Arg Glu Gln Met Tyr Gln Asp Phe Pro Asn
    130                 135                 140

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

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

Gln Gln Phe Lys Gly Val Glu Val Asp Asp Phe Ser Tyr Leu Asp Gln
            180                 185                 190

Pro Arg Glu Asn Leu Gln His Asn Asn Asp Thr Thr Arg Tyr Lys Thr
        195                 200                 205

Phe


<210>  95
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<211>  270
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(270)

<400>  95
tct gac aat acg caa tat ttt tgc ccg gcg gga tta agc gag gag cgt        48
Ser Asp Asn Thr Gln Tyr Phe Cys Pro Ala Gly Leu Ser Glu Glu Arg
1               5                   10                  15

gaa cag gag ctc cgc cgt ttg gta aaa cag gcc tat gat gtg gtg ggc        96
Glu Gln Glu Leu Arg Arg Leu Val Lys Gln Ala Tyr Asp Val Val Gly
            20                  25                  30

tgt cgt ggt tgg agc cgt att gat gtg atg gcg gat gcg gaa gga aag       144
Cys Arg Gly Trp Ser Arg Ile Asp Val Met Ala Asp Ala Glu Gly Lys
        35                  40                  45

ttc cgt ttg gtg gaa gtt aat acc aac cct ggc atg acc agc cac agt       192
Phe Arg Leu Val Glu Val Asn Thr Asn Pro Gly Met Thr Ser His Ser
    50                  55                  60

tta ttc ccg aaa tcg gcg gca acg gtc ggc tat tct ttt gcg cag ttg       240
Leu Phe Pro Lys Ser Ala Ala Thr Val Gly Tyr Ser Phe Ala Gln Leu
65                  70                  75                  80

gtt gag aaa att tta gag ttg agc gcg gaa                               270
Val Glu Lys Ile Leu Glu Leu Ser Ala Glu
                85                  90


<210>  96
<211>  90
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  96

Ser Asp Asn Thr Gln Tyr Phe Cys Pro Ala Gly Leu Ser Glu Glu Arg
1               5                   10                  15


Glu Gln Glu Leu Arg Arg Leu Val Lys Gln Ala Tyr Asp Val Val Gly
            20                  25                  30


Cys Arg Gly Trp Ser Arg Ile Asp Val Met Ala Asp Ala Glu Gly Lys
        35                  40                  45


Phe Arg Leu Val Glu Val Asn Thr Asn Pro Gly Met Thr Ser His Ser
    50                  55                  60


Leu Phe Pro Lys Ser Ala Ala Thr Val Gly Tyr Ser Phe Ala Gln Leu
65                  70                  75                  80
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```
Val Glu Lys Ile Leu Glu Leu Ser Ala Glu
                85                  90


<210>  97
<211>  379
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(378)

<400>  97
ggg gaa tat ttc ggt cct tat ccg aat gcc ggt gca gtg cgc gaa acc        48
Gly Glu Tyr Phe Gly Pro Tyr Pro Asn Ala Gly Ala Val Arg Glu Thr
1               5                   10                  15

ctg tct tta tta caa aaa ctg ttc ccc att cgg cag tgt gaa aac tcc        96
Leu Ser Leu Leu Gln Lys Leu Phe Pro Ile Arg Gln Cys Glu Asn Ser
            20                  25                  30

gtg tat aac aac cgt tcg cgc ccc tgt ttg cag tat caa atc ggg cgt       144
Val Tyr Asn Asn Arg Ser Arg Pro Cys Leu Gln Tyr Gln Ile Gly Arg
        35                  40                  45

tgt ctg gcg cct tgc gta aag ggc tat gtg acc gat gaa gcc tat gcg       192
Cys Leu Ala Pro Cys Val Lys Gly Tyr Val Thr Asp Glu Ala Tyr Ala
    50                  55                  60

cag cag gtc aat ttc gcc cgc ttg ttt tta caa gga aaa gat caa cag       240
Gln Gln Val Asn Phe Ala Arg Leu Phe Leu Gln Gly Lys Asp Gln Gln
65                  70                  75                  80

gtg ctg gat cat ttg gtg aag caa atg gaa cag gca agt cag caa ctg       288
Val Leu Asp His Leu Val Lys Gln Met Glu Gln Ala Ser Gln Gln Leu
                85                  90                  95

aat ttt gaa gaa gcg gca cgc gtt cgt gat caa att cag gca gtg cgg       336
Asn Phe Glu Glu Ala Ala Arg Val Arg Asp Gln Ile Gln Ala Val Arg
            100                 105                 110

gca gta att gaa aaa caa ttt gtc gcc aac gat cgc cat gac g             379
Ala Val Ile Glu Lys Gln Phe Val Ala Asn Asp Arg His Asp
        115                 120                 125


<210>  98
<211>  126
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  98

Gly Glu Tyr Phe Gly Pro Tyr Pro Asn Ala Gly Ala Val Arg Glu Thr
1               5                   10                  15


Leu Ser Leu Leu Gln Lys Leu Phe Pro Ile Arg Gln Cys Glu Asn Ser
            20                  25                  30
```

```
Val Tyr Asn Asn Arg Ser Arg Pro Cys Leu Gln Tyr Gln Ile Gly Arg
        35                  40                  45

Cys Leu Ala Pro Cys Val Lys Gly Tyr Val Thr Asp Glu Ala Tyr Ala
    50                  55                  60

Gln Gln Val Asn Phe Ala Arg Leu Phe Leu Gln Gly Lys Asp Gln Gln
65                  70                  75                  80

Val Leu Asp His Leu Val Lys Gln Met Glu Gln Ala Ser Gln Gln Leu
                85                  90                  95

Asn Phe Glu Glu Ala Ala Arg Val Arg Asp Gln Ile Gln Ala Val Arg
            100                 105                 110

Ala Val Ile Glu Lys Gln Phe Val Ala Asn Asp Arg His Asp
        115                 120                 125


<210>  99
<211>  625
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(624)

<400>  99
gca aaa acc tta gat ttt cag tcc gca ggg ccg gaa aaa ctc ccg aaa       48
Ala Lys Thr Leu Asp Phe Gln Ser Ala Gly Pro Glu Lys Leu Pro Lys
1               5                   10                  15

ttt caa ccg cac ttt ttg gcg caa agc caa caa tta atc gac att tgc       96
Phe Gln Pro His Phe Leu Ala Gln Ser Gln Gln Leu Ile Asp Ile Cys
            20                  25                  30

cgc cgc ctg aca ccg gcg gat att gct tcg ctc atg tct atc agc gac      144
Arg Arg Leu Thr Pro Ala Asp Ile Ala Ser Leu Met Ser Ile Ser Asp
        35                  40                  45

aaa ctt gcc ggg ttg aat gcc gca cgt ttc gcc gaa tgg cag ttg gaa      192
Lys Leu Ala Gly Leu Asn Ala Ala Arg Phe Ala Glu Trp Gln Leu Glu
    50                  55                  60

cat aac gaa cac aat gcc aaa gcg gcg gtg tat gcc ttt aga ggc gat      240
His Asn Glu His Asn Ala Lys Ala Ala Val Tyr Ala Phe Arg Gly Asp
65                  70                  75                  80

gtt tac acc ggc ttg gac gtg gat tcc tta agc aat gac gat atg ttg      288
Val Tyr Thr Gly Leu Asp Val Asp Ser Leu Ser Asn Asp Asp Met Leu
                85                  90                  95

ttt gca caa cag cat ttg cgc att ttg tcc ggg tta tat ggg ctg tta      336
Phe Ala Gln Gln His Leu Arg Ile Leu Ser Gly Leu Tyr Gly Leu Leu
```

```
            100                 105                 110

acg ccg ctg gat ttg att cag cct tat cgt ttg gaa atg ggc acc aaa      384
Thr Pro Leu Asp Leu Ile Gln Pro Tyr Arg Leu Glu Met Gly Thr Lys
        115                 120                 125

tta gcc aac ggc aaa ggc gcc gat ttg tat gcc ttt tgg cat ggt ttg      432
Leu Ala Asn Gly Lys Gly Ala Asp Leu Tyr Ala Phe Trp His Gly Leu
    130                 135                 140

gtg atg cag gcg tta caa cag gcg att gat gaa caa cag gac gat gtt      480
Val Met Gln Ala Leu Gln Gln Ala Ile Asp Glu Gln Gln Asp Asp Val
145                 150                 155                 160

ttg gtg aat ctg gcg tcc gat gaa tat tat aaa tcg gta caa ccg tcg      528
Leu Val Asn Leu Ala Ser Asp Glu Tyr Tyr Lys Ser Val Gln Pro Ser
                165                 170                 175

aat tta acg gcg caa atc att aaa ccg gtg ttc ctg gat aat aaa aac      576
Asn Leu Thr Ala Gln Ile Ile Lys Pro Val Phe Leu Asp Asn Lys Asn
            180                 185                 190

ggc aaa tat aaa att atc agt ttc tac gcg aaa aaa gcc cgc ggt tta a    625
Gly Lys Tyr Lys Ile Ile Ser Phe Tyr Ala Lys Lys Ala Arg Gly Leu
        195                 200                 205


<210>  100
<211>  208
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  100

Ala Lys Thr Leu Asp Phe Gln Ser Ala Gly Pro Glu Lys Leu Pro Lys
1               5                   10                  15


Phe Gln Pro His Phe Leu Ala Gln Ser Gln Gln Leu Ile Asp Ile Cys
            20                  25                  30


Arg Arg Leu Thr Pro Ala Asp Ile Ala Ser Leu Met Ser Ile Ser Asp
        35                  40                  45


Lys Leu Ala Gly Leu Asn Ala Ala Arg Phe Ala Glu Trp Gln Leu Glu
    50                  55                  60


His Asn Glu His Asn Ala Lys Ala Ala Val Tyr Ala Phe Arg Gly Asp
65                  70                  75                  80


Val Tyr Thr Gly Leu Asp Val Asp Ser Leu Ser Asn Asp Asp Met Leu
                85                  90                  95


Phe Ala Gln Gln His Leu Arg Ile Leu Ser Gly Leu Tyr Gly Leu Leu
            100                 105                 110
```

```
Thr Pro Leu Asp Leu Ile Gln Pro Tyr Arg Leu Glu Met Gly Thr Lys
        115                 120                 125


Leu Ala Asn Gly Lys Gly Ala Asp Leu Tyr Ala Phe Trp His Gly Leu
    130                 135                 140


Val Met Gln Ala Leu Gln Gln Ala Ile Asp Glu Gln Gln Asp Asp Val
145                 150                 155                 160


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


Asn Leu Thr Ala Gln Ile Ile Lys Pro Val Phe Leu Asp Asn Lys Asn
            180                 185                 190


Gly Lys Tyr Lys Ile Ile Ser Phe Tyr Ala Lys Lys Ala Arg Gly Leu
        195                 200                 205


<210>  101
<211>  500
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(498)

<400>  101
cac tgc ttt ata ccg cca tcg cta tgg ctt gct tac cgg cgt atg ccg       48
His Cys Phe Ile Pro Pro Ser Leu Trp Leu Ala Tyr Arg Arg Met Pro
1               5                   10                  15

aag aag ttt tta ccc ttg ggc aaa ttg agg tga ttg ccg ata gat caa       96
Lys Lys Phe Leu Pro Leu Gly Lys Leu Arg     Leu Pro Ile Asp Gln
        20                  25                          30

cgg att taa gca cca cac gca ttg aac agg ctg act tac aga aaa aca      144
Arg Ile     Ala Pro His Ala Leu Asn Arg Leu Thr Tyr Arg Lys Thr
                35                  40                  45

atc aaa cca atg tcg ccg agg tgg cga aaa cca cac cgg gcg tat ttt      192
Ile Lys Pro Met Ser Pro Arg Trp Arg Lys Pro His Arg Ala Tyr Phe
            50                  55                  60

tgg atc gta gcg gcg cac gca atg aac ata att tgt tgg tac gcg gat      240
Trp Ile Val Ala Ala His Ala Met Asn Ile Ile Cys Trp Tyr Ala Asp
    65                  70                  75

tta aag cca atc gcg tgc cag tgt tta ttg acg gca ttc cgg tgt atg      288
Leu Lys Pro Ile Ala Cys Gln Cys Leu Leu Thr Ala Phe Arg Cys Met
    80                  85                  90

tgc cct atg acg gca ata tgg aca ttg gtc gct tca cca cct tcg att      336
Cys Pro Met Thr Ala Ile Trp Thr Leu Val Ala Ser Pro Pro Ser Ile
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95                  100                 105                 110

tat ccc gca ttg ata ttt cca agg gcg caa gtt ccg tgc ttt atg gcg       384
Tyr Pro Ala Leu Ile Phe Pro Arg Ala Gln Val Pro Cys Phe Met Ala
                115                 120                 125

cca aca cgc tgg gcg gtg cgg taa atc tca tta cgc aaa aac cga cca       432
Pro Thr Arg Trp Ala Val Arg     Ile Ser Leu Arg Lys Asn Arg Pro
            130                     135                 140

aac cgt ttg aag gca cta tcg gct acg gat ttg ctc acg gta gaa gcg       480
Asn Arg Leu Lys Ala Leu Ser Ala Thr Asp Leu Leu Thr Val Glu Ala
            145                 150                 155

gca gca cgg gca cca atc aa                                            500
Ala Ala Arg Ala Pro Ile
        160


<210>  102
<211>  26
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  102

His Cys Phe Ile Pro Pro Ser Leu Trp Leu Ala Tyr Arg Arg Met Pro
1               5                   10                  15


Lys Lys Phe Leu Pro Leu Gly Lys Leu Arg
            20                  25


<210>  103
<211>  7
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  103

Leu Pro Ile Asp Gln Arg Ile
1               5


<210>  104
<211>  100
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  104

Ala Pro His Ala Leu Asn Arg Leu Thr Tyr Arg Lys Thr Ile Lys Pro
1               5                   10                  15


Met Ser Pro Arg Trp Arg Lys Pro His Arg Ala Tyr Phe Trp Ile Val
            20                  25                  30


Ala Ala His Ala Met Asn Ile Ile Cys Trp Tyr Ala Asp Leu Lys Pro
```

```
        35                  40                  45

Ile Ala Cys Gln Cys Leu Leu Thr Ala Phe Arg Cys Met Cys Pro Met
    50                  55                  60

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

Leu Ile Phe Pro Arg Ala Gln Val Pro Cys Phe Met Ala Pro Thr Arg
                85                  90                  95

Trp Ala Val Arg
            100


<210>  105
<211>  30
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  105

Ile Ser Leu Arg Lys Asn Arg Pro Asn Arg Leu Lys Ala Leu Ser Ala
1               5                   10                  15

Thr Asp Leu Leu Thr Val Glu Ala Ala Ala Arg Ala Pro Ile
            20                  25                  30


<210>  106
<211>  303
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(303)

<400>  106
gca ttc ttc tcc tta ttt tcc att atc atg agc ggc aga tta aaa gaa         48
Ala Phe Phe Ser Leu Phe Ser Ile Ile Met Ser Gly Arg Leu Lys Glu
1               5                   10                  15

ttg ggc gaa cac tta aac gaa acc ggc tct ttc aaa gtg ggc atg att         96
Leu Gly Glu His Leu Asn Glu Thr Gly Ser Phe Lys Val Gly Met Ile
            20                  25                  30

tgg aaa gct ttt atc gtc atc acc acc ggt gta ctg gct ttc atg cta        144
Trp Lys Ala Phe Ile Val Ile Thr Thr Gly Val Leu Ala Phe Met Leu
        35                  40                  45

tac aaa gaa gca ggc aaa gtg ctc acc aaa ggc tac gaa ggc tat ccg        192
Tyr Lys Glu Ala Gly Lys Val Leu Thr Lys Gly Tyr Glu Gly Tyr Pro
    50                  55                  60

gac cgg ttc gtc aac acc ttc ggc tgg ggc atg gca atc gct ttg gtg        240
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```
Asp Arg Phe Val Asn Thr Phe Gly Trp Gly Met Ala Ile Ala Leu Val
65                  70                  75                  80

atc atc gca ttc ctg ctt tcc cgc ctg ccg tgg aaa cac tta acg caa         288
Ile Ile Ala Phe Leu Leu Ser Arg Leu Pro Trp Lys His Leu Thr Gln
                85                  90                  95

aca caa gga gaa aaa                                                     303
Thr Gln Gly Glu Lys
            100


<210>  107
<211>  101
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  107

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


Leu Gly Glu His Leu Asn Glu Thr Gly Ser Phe Lys Val Gly Met Ile
            20                  25                  30


Trp Lys Ala Phe Ile Val Ile Thr Thr Gly Val Leu Ala Phe Met Leu
        35                      40                  45


Tyr Lys Glu Ala Gly Lys Val Leu Thr Lys Gly Tyr Glu Gly Tyr Pro
    50                  55                  60


Asp Arg Phe Val Asn Thr Phe Gly Trp Gly Met Ala Ile Ala Leu Val
65                  70                  75                  80


Ile Ile Ala Phe Leu Leu Ser Arg Leu Pro Trp Lys His Leu Thr Gln
                85                  90                  95


Thr Gln Gly Glu Lys
            100


<210>  108
<211>  465
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(465)

<400>  108
gtg ttt ata acc gct tgc aac aat ata aac ttc ccg aga tcg gtc tcg          48
Val Phe Ile Thr Ala Cys Asn Asn Ile Asn Phe Pro Arg Ser Val Ser
1               5                   10                  15
```

```
gga ggc ttc agg ttt acg aac ttt gac tac act aaa cag aga acg gat        96
Gly Gly Phe Arg Phe Thr Asn Phe Asp Tyr Thr Lys Gln Arg Thr Asp
            20                  25                  30

ctc ttt taa gta ttc atc aaa acc ttc ccc ctg aaa aac ttt tac tac       144
Leu Phe     Val Phe Ile Lys Thr Phe Pro Leu Lys Asn Phe Tyr Tyr
            35                  40                  45

aaa act tcc ttt att agc gag aat ctg ctt gca cat atc aag cgc aag       192
Lys Thr Ser Phe Ile Ser Glu Asn Leu Leu Ala His Ile Lys Arg Lys
        50                  55                  60

ttc tac caa ata cat cgc acg cgg aat atc cac tga tgg cat ccc act       240
Phe Tyr Gln Ile His Arg Thr Arg Asn Ile His     Trp His Pro Thr
    65                  70                      75

gaa att cgg tgc cat atc tga cat cac cac atc tac ttt gcc ttc acc       288
Glu Ile Arg Cys His Ile     His His His Ile Tyr Phe Ala Phe Thr
    80                      85                  90

gac ccg ctc caa taa aat gtt taa cac att ttc atc acg gaa atc gcc       336
Asp Pro Leu Gln     Asn Val     His Ile Phe Ile Thr Glu Ile Ala
    95                          100                 105

ttg tag aaa atc cac gcc tac aat agg atc cat ttc cag aag atc aca       384
Leu     Lys Ile His Ala Tyr Asn Arg Ile His Phe Gln Lys Ile Thr
            110                 115                 120

ggc aat aat ccg tcc att gcg ccc aat ttg gct tac cac ata ctg cga       432
Gly Asn Asn Pro Ser Ile Ala Pro Asn Leu Ala Tyr His Ile Leu Arg
        125                 130                 135

cca tcc gcc cgg cgc tgc acc taa atc aac cac                           465
Pro Ser Ala Arg Arg Cys Thr     Ile Asn His
    140                 145


<210>  109
<211>  34
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  109

Val Phe Ile Thr Ala Cys Asn Asn Ile Asn Phe Pro Arg Ser Val Ser
1               5                   10                  15


Gly Gly Phe Arg Phe Thr Asn Phe Asp Tyr Thr Lys Gln Arg Thr Asp
            20                  25                  30


Leu Phe



<210>  110
<211>  40
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans
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```
<400>  110

Val Phe Ile Lys Thr Phe Pro Leu Lys Asn Phe Tyr Tyr Lys Thr Ser
1               5                   10                  15


Phe Ile Ser Glu Asn Leu Leu Ala His Ile Lys Arg Lys Phe Tyr Gln
            20                  25                  30


Ile His Arg Thr Arg Asn Ile His
        35                  40


<210>  111
<211>  10
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  111

Trp His Pro Thr Glu Ile Arg Cys His Ile
1               5                   10


<210>  112
<211>  13
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  112

His His His Ile Tyr Phe Ala Phe Thr Asp Pro Leu Gln
1               5                   10


<210>  113
<211>  9
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  113

His Ile Phe Ile Thr Glu Ile Ala Leu
1               5


<210>  114
<211>  37
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  114

Lys Ile His Ala Tyr Asn Arg Ile His Phe Gln Lys Ile Thr Gly Asn
1               5                   10                  15


Asn Pro Ser Ile Ala Pro Asn Leu Ala Tyr His Ile Leu Arg Pro Ser
            20                  25                  30
```

```
Ala Arg Arg Cys Thr
        35


<210>  115
<211>  630
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(630)

<400>  115
gaa ctg ggc tgg gga ggt tgg tgg ttc tgg gat ccg gtg gaa aat gcg         48
Glu Leu Gly Trp Gly Gly Trp Trp Phe Trp Asp Pro Val Glu Asn Ala
1               5                   10                  15

tcg ctc atg ccg tgg ttg ctc ggc ttg gca ttg ttg cac agt tta atc         96
Ser Leu Met Pro Trp Leu Leu Gly Leu Ala Leu Leu His Ser Leu Ile
            20                  25                  30

gtc agc gaa aaa cgc gga att ttt aat tac tgg acg acc tta ttt tcc        144
Val Ser Glu Lys Arg Gly Ile Phe Asn Tyr Trp Thr Thr Leu Phe Ser
        35                  40                  45

ttg ttg gca ttt gcc ttc agc gta tta ggc acg ttt atc gtg cgc tcc        192
Leu Leu Ala Phe Ala Phe Ser Val Leu Gly Thr Phe Ile Val Arg Ser
    50                  55                  60

ggc gcg ctt acc tcc gta cac gct ttc gct gtg gac agc caa cgc ggc        240
Gly Ala Leu Thr Ser Val His Ala Phe Ala Val Asp Ser Gln Arg Gly
65                  70                  75                  80

tcg gca tta tta ctg att ttc ttc ctg ctc acc gtg ggt tct ctc ggt        288
Ser Ala Leu Leu Leu Ile Phe Phe Leu Leu Thr Val Gly Ser Leu Gly
                85                  90                  95

tta ttc gcg ttc aaa gcc aat ttg cag caa cgc cgc gtc aaa tta acg        336
Leu Phe Ala Phe Lys Ala Asn Leu Gln Gln Arg Arg Val Lys Leu Thr
            100                 105                 110

ctg ctt tcc aaa gaa agt gcg gtg ctt ttt ttg aat gtt tta ttg agt        384
Leu Leu Ser Lys Glu Ser Ala Val Leu Phe Leu Asn Val Leu Leu Ser
        115                 120                 125

atc gcc acc gtt agc acc ttt ctc ggc acc ttt tat ccc atg ctg ttc        432
Ile Ala Thr Val Ser Thr Phe Leu Gly Thr Phe Tyr Pro Met Leu Phe
    130                 135                 140

caa gcc atg aat tgg ggt tcc att tcc gtc ggt gcg cct tat ttc aac        480
Gln Ala Met Asn Trp Gly Ser Ile Ser Val Gly Ala Pro Tyr Phe Asn
145                 150                 155                 160

agt att ttc ttg ccg ctg ctt acg ctg att tta atc gcc atg gtg ttt        528
Ser Ile Phe Leu Pro Leu Leu Thr Leu Ile Leu Ile Ala Met Val Phe
                165                 170                 175

tcc ctc ggc ttg cac tgg gcg aag gcg gac aaa ggc att ttg ttt aaa        576
Ser Leu Gly Leu His Trp Ala Lys Ala Asp Lys Gly Ile Leu Phe Lys
```

```
            180                 185                 190

cgc gcg gcg ttg tta ctg ccg tct ttg ttg atc gct tat ttt atg att      624
Arg Ala Ala Leu Leu Leu Pro Ser Leu Leu Ile Ala Tyr Phe Met Ile
        195                 200                 205

cgt cag                                                              630
Arg Gln
    210


<210>  116
<211>  210
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  116

Glu Leu Gly Trp Gly Gly Trp Trp Phe Trp Asp Pro Val Glu Asn Ala
1               5                   10                  15


Ser Leu Met Pro Trp Leu Leu Gly Leu Ala Leu Leu His Ser Leu Ile
            20                  25                  30


Val Ser Glu Lys Arg Gly Ile Phe Asn Tyr Trp Thr Thr Leu Phe Ser
        35                  40                  45


Leu Leu Ala Phe Ala Phe Ser Val Leu Gly Thr Phe Ile Val Arg Ser
    50                  55                  60


Gly Ala Leu Thr Ser Val His Ala Phe Ala Val Asp Ser Gln Arg Gly
65                  70                  75                  80


Ser Ala Leu Leu Leu Ile Phe Phe Leu Leu Thr Val Gly Ser Leu Gly
                85                  90                  95


Leu Phe Ala Phe Lys Ala Asn Leu Gln Gln Arg Arg Val Lys Leu Thr
            100                 105                 110


Leu Leu Ser Lys Glu Ser Ala Val Leu Phe Leu Asn Val Leu Leu Ser
        115                 120                 125


Ile Ala Thr Val Ser Thr Phe Leu Gly Thr Phe Tyr Pro Met Leu Phe
    130                 135                 140


Gln Ala Met Asn Trp Gly Ser Ile Ser Val Gly Ala Pro Tyr Phe Asn
145                 150                 155                 160


Ser Ile Phe Leu Pro Leu Leu Thr Leu Ile Leu Ile Ala Met Val Phe
                165                 170                 175
```

```
Ser Leu Gly Leu His Trp Ala Lys Ala Asp Lys Gly Ile Leu Phe Lys
            180                 185                 190


Arg Ala Ala Leu Leu Leu Pro Ser Leu Leu Ile Ala Tyr Phe Met Ile
        195                 200                 205


Arg Gln
    210


<210>  117
<211>  876
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(876)

<400>  117
act cac cct gtg cat att tcg atg caa tat atg gca gat gaa gtt aaa         48
Thr His Pro Val His Ile Ser Met Gln Tyr Met Ala Asp Glu Val Lys
1               5                   10                  15

aaa tta aca aat ggt gaa gtg gtg atc cga att tac cca aat agc cag         96
Lys Leu Thr Asn Gly Glu Val Val Ile Arg Ile Tyr Pro Asn Ser Gln
            20                  25                  30

ctt ggt agc cag cgt gaa tca atg gaa tta ttg caa tcc ggg tca cta        144
Leu Gly Ser Gln Arg Glu Ser Met Glu Leu Leu Gln Ser Gly Ser Leu
        35                  40                  45

gat atg gca aaa tca aac gca agt gaa tta gaa gca ttt gag cca tct        192
Asp Met Ala Lys Ser Asn Ala Ser Glu Leu Glu Ala Phe Glu Pro Ser
    50                  55                  60

tat ggt gca tac aat att ccg tat ctt ttc cat aat gtt gat cat tat        240
Tyr Gly Ala Tyr Asn Ile Pro Tyr Leu Phe His Asn Val Asp His Tyr
65                  70                  75                  80

tat cgt gct cta ctt gat cct gaa gtt ggg caa aaa att ctt gat tca        288
Tyr Arg Ala Leu Leu Asp Pro Glu Val Gly Gln Lys Ile Leu Asp Ser
                85                  90                  95

tca aag ggc aaa ggt ttc att ggg ttg act tat tat gat ggt ggt gcg        336
Ser Lys Gly Lys Gly Phe Ile Gly Leu Thr Tyr Tyr Asp Gly Gly Ala
            100                 105                 110

cgt agt ttc tat gcg ggt aag gca att aaa tcg cct gcg gac ctc aaa        384
Arg Ser Phe Tyr Ala Gly Lys Ala Ile Lys Ser Pro Ala Asp Leu Lys
        115                 120                 125

ggt atg aaa att cgc gtt caa cca agc cca acc gca gta gaa atg atc        432
Gly Met Lys Ile Arg Val Gln Pro Ser Pro Thr Ala Val Glu Met Ile
    130                 135                 140

aaa tta atg ggt gct tct cca aca cct tta gct tat ggt gaa ctc tat        480
Lys Leu Met Gly Ala Ser Pro Thr Pro Leu Ala Tyr Gly Glu Leu Tyr
```

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145                 150                 155                 160

acc gca ctc caa caa aaa gtg gtt gat ggc gcg gaa aat aac caa aca       528
Thr Ala Leu Gln Gln Lys Val Val Asp Gly Ala Glu Asn Asn Gln Thr
                165                 170                 175

gca tta acc tta tct cgt cat ggt gaa gtg gct aaa ttc ttt agt gaa       576
Ala Leu Thr Leu Ser Arg His Gly Glu Val Ala Lys Phe Phe Ser Glu
            180                 185                 190

gat gaa cat act atg att cct gat gtg ctc gta att ggt caa aaa tct       624
Asp Glu His Thr Met Ile Pro Asp Val Leu Val Ile Gly Gln Lys Ser
        195                 200                 205

tgg gat aaa tta act cca gaa caa caa aat gca ctt aaa aaa gcc gct       672
Trp Asp Lys Leu Thr Pro Glu Gln Gln Asn Ala Leu Lys Lys Ala Ala
    210                 215                 220

gat gat tca atg atg tat cac aaa gat tta tgg caa aaa atg att gct       720
Asp Asp Ser Met Met Tyr His Lys Asp Leu Trp Gln Lys Met Ile Ala
225                 230                 235                 240

gaa acc act caa gaa gct aaa gat aaa ttg ggt gta gaa ttt gtg aaa       768
Glu Thr Thr Gln Glu Ala Lys Asp Lys Leu Gly Val Glu Phe Val Lys
                245                 250                 255

gta gat aaa caa cct ttc att gat gca aca aaa agc atg cat gat gcg       816
Val Asp Lys Gln Pro Phe Ile Asp Ala Thr Lys Ser Met His Asp Ala
            260                 265                 270

gca aaa gcc aat cct ttg ctt aaa gaa tac att gaa cgt att gat agt       864
Ala Lys Ala Asn Pro Leu Leu Lys Glu Tyr Ile Glu Arg Ile Asp Ser
        275                 280                 285

ttg gca acc aag                                                       876
Leu Ala Thr Lys
    290


<210>  118
<211>  292
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  118

Thr His Pro Val His Ile Ser Met Gln Tyr Met Ala Asp Glu Val Lys
1               5                   10                  15


Lys Leu Thr Asn Gly Glu Val Val Ile Arg Ile Tyr Pro Asn Ser Gln
            20                  25                  30


Leu Gly Ser Gln Arg Glu Ser Met Glu Leu Leu Gln Ser Gly Ser Leu
        35                  40                  45


Asp Met Ala Lys Ser Asn Ala Ser Glu Leu Glu Ala Phe Glu Pro Ser
    50                  55                  60
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```
Tyr Gly Ala Tyr Asn Ile Pro Tyr Leu Phe His Asn Val Asp His Tyr
65                  70                  75                  80

Tyr Arg Ala Leu Leu Asp Pro Glu Val Gly Gln Lys Ile Leu Asp Ser
                85                  90                  95

Ser Lys Gly Lys Gly Phe Ile Gly Leu Thr Tyr Tyr Asp Gly Gly Ala
            100                 105                 110

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

Gly Met Lys Ile Arg Val Gln Pro Ser Pro Thr Ala Val Glu Met Ile
    130                 135                 140

Lys Leu Met Gly Ala Ser Pro Thr Pro Leu Ala Tyr Gly Glu Leu Tyr
145                 150                 155                 160

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

Ala Leu Thr Leu Ser Arg His Gly Glu Val Ala Lys Phe Phe Ser Glu
            180                 185                 190

Asp Glu His Thr Met Ile Pro Asp Val Leu Val Ile Gly Gln Lys Ser
        195                 200                 205

Trp Asp Lys Leu Thr Pro Glu Gln Gln Asn Ala Leu Lys Lys Ala Ala
    210                 215                 220

Asp Asp Ser Met Met Tyr His Lys Asp Leu Trp Gln Lys Met Ile Ala
225                 230                 235                 240

Glu Thr Thr Gln Glu Ala Lys Asp Lys Leu Gly Val Glu Phe Val Lys
                245                 250                 255

Val Asp Lys Gln Pro Phe Ile Asp Ala Thr Lys Ser Met His Asp Ala
            260                 265                 270

Ala Lys Ala Asn Pro Leu Leu Lys Glu Tyr Ile Glu Arg Ile Asp Ser
        275                 280                 285

Leu Ala Thr Lys
    290
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<210>  119
<211>  303
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(303)

<400>  119
atg agt gtt tta agt tat gcc caa aaa atc ggg caa gcc tta atg gta        48
Met Ser Val Leu Ser Tyr Ala Gln Lys Ile Gly Gln Ala Leu Met Val
1               5                   10                  15

ccc gtt gcc gtt ttg ccg gca gcc gcc gta tta atg ggg atc ggc tat        96
Pro Val Ala Val Leu Pro Ala Ala Ala Val Leu Met Gly Ile Gly Tyr
            20                  25                  30

tgg ctt gac ccg gac ggc tgg ggc gca aac agc caa ctt gcc gcc tta       144
Trp Leu Asp Pro Asp Gly Trp Gly Ala Asn Ser Gln Leu Ala Ala Leu
        35                  40                  45

tta atc aag tcc ggc gcg gca atc atc gat aac atg ggc tta tta ttc       192
Leu Ile Lys Ser Gly Ala Ala Ile Ile Asp Asn Met Gly Leu Leu Phe
    50                  55                  60

gcc gtg ggc gta gca ttc ggg ttg tcc aaa gac aag cac ggt tct gct       240
Ala Val Gly Val Ala Phe Gly Leu Ser Lys Asp Lys His Gly Ser Ala
65                  70                  75                  80

gcg ctt tcc ggt tta gtg ggc tat tat gtg gtc act acc cta ctc gcc       288
Ala Leu Ser Gly Leu Val Gly Tyr Tyr Val Val Thr Thr Leu Leu Ala
                85                  90                  95

cct ggc ggc gta gcg                                                   303
Pro Gly Gly Val Ala
            100


<210>  120
<211>  101
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  120

Met Ser Val Leu Ser Tyr Ala Gln Lys Ile Gly Gln Ala Leu Met Val
1               5                   10                  15


Pro Val Ala Val Leu Pro Ala Ala Ala Val Leu Met Gly Ile Gly Tyr
            20                  25                  30


Trp Leu Asp Pro Asp Gly Trp Gly Ala Asn Ser Gln Leu Ala Ala Leu
        35                  40                  45


Leu Ile Lys Ser Gly Ala Ala Ile Ile Asp Asn Met Gly Leu Leu Phe
    50                  55                  60
```

```
Ala Val Gly Val Ala Phe Gly Leu Ser Lys Asp Lys His Gly Ser Ala
65                  70                  75                  80


Ala Leu Ser Gly Leu Val Gly Tyr Tyr Val Val Thr Thr Leu Leu Ala
                85                  90                  95


Pro Gly Gly Val Ala
            100


<210>  121
<211>  590
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(588)

<400>  121
gaa tat aaa aat ctt gct gtt gct tat atc cgt atg tct acg gag cat        48
Glu Tyr Lys Asn Leu Ala Val Ala Tyr Ile Arg Met Ser Thr Glu His
1               5                   10                  15

cag gaa ttt tca ccg gat ata caa cgt cgc ttc att caa aaa tat gct        96
Gln Glu Phe Ser Pro Asp Ile Gln Arg Arg Phe Ile Gln Lys Tyr Ala
            20                  25                  30

aag gaa caa ggg ctt ata ctc act agg gaa tac cta gat gag gga agg       144
Lys Glu Gln Gly Leu Ile Leu Thr Arg Glu Tyr Leu Asp Glu Gly Arg
        35                  40                  45

agt gga tta agc gca gaa aaa cgt cct cag ttt tta tca ctc att aat       192
Ser Gly Leu Ser Ala Glu Lys Arg Pro Gln Phe Leu Ser Leu Ile Asn
    50                  55                  60

ttt gta caa tcc ggt aat gct gat ttt tca cat att ctt gtt tat gac       240
Phe Val Gln Ser Gly Asn Ala Asp Phe Ser His Ile Leu Val Tyr Asp
65                  70                  75                  80

att agc cga tgg ggg cgc ttt cta aat att gat gaa tct gca cat tat       288
Ile Ser Arg Trp Gly Arg Phe Leu Asn Ile Asp Glu Ser Ala His Tyr
                85                  90                  95

gaa caa att tgt tca aaa atg ggg att aaa gtg cat tac tgt gca gaa       336
Glu Gln Ile Cys Ser Lys Met Gly Ile Lys Val His Tyr Cys Ala Glu
            100                 105                 110

cct ttt aag gga aac gac att ggt tct caa att ttt aaa gcg gta aaa       384
Pro Phe Lys Gly Asn Asp Ile Gly Ser Gln Ile Phe Lys Ala Val Lys
        115                 120                 125

cgt tgg tct gcc gga gaa tac tgt cgt gag cta ggt gaa aaa gtt ttt       432
Arg Trp Ser Ala Gly Glu Tyr Cys Arg Glu Leu Gly Glu Lys Val Phe
    130                 135                 140

aat ggg cag aag aat ttg att gag cgc gga ttt cgt caa ggt gga cca       480
Asn Gly Gln Lys Asn Leu Ile Glu Arg Gly Phe Arg Gln Gly Gly Pro
```

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145                 150                 155                 160

gct gga ttt ggg tta aga cgc cta tta tta agt gct gat ggt tcg cca        528
Ala Gly Phe Gly Leu Arg Arg Leu Leu Leu Ser Ala Asp Gly Ser Pro
                165                 170                 175

aaa ttt gaa cta aaa acg ggt gac agg aag agt ttg cag tcg gat cgt        576
Lys Phe Glu Leu Lys Thr Gly Asp Arg Lys Ser Leu Gln Ser Asp Arg
            180                 185                 190

gtc att ctt att gc                                                     590
Val Ile Leu Ile
        195


<210>  122
<211>  196
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  122

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


Gln Glu Phe Ser Pro Asp Ile Gln Arg Arg Phe Ile Gln Lys Tyr Ala
            20                  25                  30


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


Ser Gly Leu Ser Ala Glu Lys Arg Pro Gln Phe Leu Ser Leu Ile Asn
    50                  55                  60


Phe Val Gln Ser Gly Asn Ala Asp Phe Ser His Ile Leu Val Tyr Asp
65                  70                  75                  80


Ile Ser Arg Trp Gly Arg Phe Leu Asn Ile Asp Glu Ser Ala His Tyr
                85                  90                  95


Glu Gln Ile Cys Ser Lys Met Gly Ile Lys Val His Tyr Cys Ala Glu
            100                 105                 110


Pro Phe Lys Gly Asn Asp Ile Gly Ser Gln Ile Phe Lys Ala Val Lys
        115                 120                 125


Arg Trp Ser Ala Gly Glu Tyr Cys Arg Glu Leu Gly Glu Lys Val Phe
    130                 135                 140


Asn Gly Gln Lys Asn Leu Ile Glu Arg Gly Phe Arg Gln Gly Gly Pro
145                 150                 155                 160
```

```
Ala Gly Phe Gly Leu Arg Arg Leu Leu Leu Ser Ala Asp Gly Ser Pro
                165                 170                 175


Lys Phe Glu Leu Lys Thr Gly Asp Arg Lys Ser Leu Gln Ser Asp Arg
            180                 185                 190


Val Ile Leu Ile
        195


<210>  123
<211>  531
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(531)

<400>  123
ttt tta acc aaa gat aaa atc aag cag gca ata cag gca cag caa cag        48
Phe Leu Thr Lys Asp Lys Ile Lys Gln Ala Ile Gln Ala Gln Gln Gln
1               5                   10                  15

gaa ctg tta cta caa gtg atc ccg cag gat tac ttc aat aat gat ctg        96
Glu Leu Leu Leu Gln Val Ile Pro Gln Asp Tyr Phe Asn Asn Asp Leu
            20                  25                  30

acg cag gct tgt tat gca ccg caa gcg ggg aca tta caa gtc gtg gag       144
Thr Gln Ala Cys Tyr Ala Pro Gln Ala Gly Thr Leu Gln Val Val Glu
        35                  40                  45

ata agc aaa ata tgc acg gca aag aaa gac ggc gtg act act gcc tat       192
Ile Ser Lys Ile Cys Thr Ala Lys Lys Asp Gly Val Thr Thr Ala Tyr
    50                  55                  60

gcc ttt gaa agc acg gcg cat gat ggc tat tcc ggc gat att cat att       240
Ala Phe Glu Ser Thr Ala His Asp Gly Tyr Ser Gly Asp Ile His Ile
65                  70                  75                  80

ttg gtg ggc atg aaa cct gat ggc gaa gtg ctt ggc gtg cgc att acg       288
Leu Val Gly Met Lys Pro Asp Gly Glu Val Leu Gly Val Arg Ile Thr
                85                  90                  95

gaa cac cac gaa acc ccg gga tta ggc gat aaa att gaa acc cgc att       336
Glu His His Glu Thr Pro Gly Leu Gly Asp Lys Ile Glu Thr Arg Ile
            100                 105                 110

tcc aac tgg gtt tta agt ttt gat cat cag gtt atc agc aac gaa aat       384
Ser Asn Trp Val Leu Ser Phe Asp His Gln Val Ile Ser Asn Glu Asn
        115                 120                 125

gcc gca gaa tgg gcg gtg aaa aaa gac ggc ggt aaa ttc gat caa ttc       432
Ala Ala Glu Trp Ala Val Lys Lys Asp Gly Gly Lys Phe Asp Gln Phe
    130                 135                 140

gcc ggt gcc acc atc acg ccc cgc gct gtg gtt aac caa gtg aaa cgg       480
Ala Gly Ala Thr Ile Thr Pro Arg Ala Val Val Asn Gln Val Lys Arg
```

```
145                 150                 155                 160

gcg gca ttg gct atg ctg gat aat ctg ccg aaa gag aga gaa agt gat         528
Ala Ala Leu Ala Met Leu Asp Asn Leu Pro Lys Glu Arg Glu Ser Asp
                165                 170                 175

gga                                                                     531
Gly


<210>  124
<211>  177
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  124

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


Glu Leu Leu Leu Gln Val Ile Pro Gln Asp Tyr Phe Asn Asn Asp Leu
            20                  25                  30


Thr Gln Ala Cys Tyr Ala Pro Gln Ala Gly Thr Leu Gln Val Val Glu
        35                  40                  45


Ile Ser Lys Ile Cys Thr Ala Lys Lys Asp Gly Val Thr Thr Ala Tyr
    50                  55                  60


Ala Phe Glu Ser Thr Ala His Asp Gly Tyr Ser Gly Asp Ile His Ile
65                  70                  75                  80


Leu Val Gly Met Lys Pro Asp Gly Glu Val Leu Gly Val Arg Ile Thr
                85                  90                  95


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


Ser Asn Trp Val Leu Ser Phe Asp His Gln Val Ile Ser Asn Glu Asn
        115                 120                 125


Ala Ala Glu Trp Ala Val Lys Lys Asp Gly Gly Lys Phe Asp Gln Phe
    130                 135                 140


Ala Gly Ala Thr Ile Thr Pro Arg Ala Val Val Asn Gln Val Lys Arg
145                 150                 155                 160


Ala Ala Leu Ala Met Leu Asp Asn Leu Pro Lys Glu Arg Glu Ser Asp
                165                 170                 175
```

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Gly


<210>  125
<211>  783
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(783)

<400>  125
atg gat aaa tta gac gaa aca caa gaa ctg caa caa acc gaa gcc aaa        48
Met Asp Lys Leu Asp Glu Thr Gln Glu Leu Gln Gln Thr Glu Ala Lys
1               5                   10                  15

agt gcg gtt gac aaa aaa caa cat ttt ttg aac gtt ggt tct gcc aac        96
Ser Ala Val Asp Lys Lys Gln His Phe Leu Asn Val Gly Ser Ala Asn
            20                  25                  30

ggc ccc gaa ggg gtg aat aag cga aca agt gag ctt atg aat aat att       144
Gly Pro Glu Gly Val Asn Lys Arg Thr Ser Glu Leu Met Asn Asn Ile
        35                  40                  45

tca aat gaa aaa agc att tgg aaa acg att ttc att cag ggc atc tgg       192
Ser Asn Glu Lys Ser Ile Trp Lys Thr Ile Phe Ile Gln Gly Ile Trp
    50                  55                  60

acc aac aat tcc acc gtg gtg caa ctg ctt ggg ttg tgt ccg ctg ctg       240
Thr Asn Asn Ser Thr Val Val Gln Leu Leu Gly Leu Cys Pro Leu Leu
65                  70                  75                  80

gcg gtg tcc aac tcc gtg acc aac gcc ctc ggg ctg ggt tta gcc acc       288
Ala Val Ser Asn Ser Val Thr Asn Ala Leu Gly Leu Gly Leu Ala Thr
                85                  90                  95

atg ctt gtg ctg acg tgt acg aac acg gta gtt tct ctt ttc cgt aag       336
Met Leu Val Leu Thr Cys Thr Asn Thr Val Val Ser Leu Phe Arg Lys
            100                 105                 110

cac atc ccc aat gaa atc cgc att ccg att tat gtg atg atc atc gca       384
His Ile Pro Asn Glu Ile Arg Ile Pro Ile Tyr Val Met Ile Ile Ala
        115                 120                 125

acc acg gta acc gct gtg caa tta ttg atg aat gcc tat acc tac gcg       432
Thr Thr Val Thr Ala Val Gln Leu Leu Met Asn Ala Tyr Thr Tyr Ala
    130                 135                 140

ctt tat caa tct ctc ggg att ttt att ccg ctc atc gtc acc aac tgt       480
Leu Tyr Gln Ser Leu Gly Ile Phe Ile Pro Leu Ile Val Thr Asn Cys
145                 150                 155                 160

att gtg atc ggt cgc gcc gaa gcc ttt gct tcc aag aac agc att tcc       528
Ile Val Ile Gly Arg Ala Glu Ala Phe Ala Ser Lys Asn Ser Ile Ser
                165                 170                 175

cat tcc gcc ttt gac ggt ttt tcc atg gga tta ggg atg tta ttc agt       576
His Ser Ala Phe Asp Gly Phe Ser Met Gly Leu Gly Met Leu Phe Ser
```

```
                180                 185                 190

tta gta gcg ctc ggc ggc atc cgc gaa atc atc ggc aac ggt act tta         624
Leu Val Ala Leu Gly Gly Ile Arg Glu Ile Ile Gly Asn Gly Thr Leu
        195                 200                 205

ttt gac ggc atc gaa aat ttg ctg ggc gat tgg gct aaa ttc atg cgg         672
Phe Asp Gly Ile Glu Asn Leu Leu Gly Asp Trp Ala Lys Phe Met Arg
    210                 215                 220

att gaa ttt ttc cac aat gac agt aat ctg tta ctt gcg att ttg cct         720
Ile Glu Phe Phe His Asn Asp Ser Asn Leu Leu Leu Ala Ile Leu Pro
225                 230                 235                 240

ccc ggc gca ttt att ggt tta gct ttg ttg tta gcc tta aaa aat gta         768
Pro Gly Ala Phe Ile Gly Leu Ala Leu Leu Leu Ala Leu Lys Asn Val
                245                 250                 255

ata gat aca aaa aag                                                     783
Ile Asp Thr Lys Lys
            260


<210>  126
<211>  261
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  126

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


Ser Ala Val Asp Lys Lys Gln His Phe Leu Asn Val Gly Ser Ala Asn
            20                  25                  30


Gly Pro Glu Gly Val Asn Lys Arg Thr Ser Glu Leu Met Asn Asn Ile
        35                  40                  45


Ser Asn Glu Lys Ser Ile Trp Lys Thr Ile Phe Ile Gln Gly Ile Trp
    50                  55                  60


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


Ala Val Ser Asn Ser Val Thr Asn Ala Leu Gly Leu Gly Leu Ala Thr
                85                  90                  95


Met Leu Val Leu Thr Cys Thr Asn Thr Val Val Ser Leu Phe Arg Lys
            100                 105                 110


His Ile Pro Asn Glu Ile Arg Ile Pro Ile Tyr Val Met Ile Ile Ala
        115                 120                 125
```

```
Thr Thr Val Thr Ala Val Gln Leu Leu Met Asn Ala Tyr Thr Tyr Ala
    130                 135                 140

Leu Tyr Gln Ser Leu Gly Ile Phe Ile Pro Leu Ile Val Thr Asn Cys
145                 150                 155                 160

Ile Val Ile Gly Arg Ala Glu Ala Phe Ala Ser Lys Asn Ser Ile Ser
                165                 170                 175

His Ser Ala Phe Asp Gly Phe Ser Met Gly Leu Gly Met Leu Phe Ser
            180                 185                 190

Leu Val Ala Leu Gly Gly Ile Arg Glu Ile Ile Gly Asn Gly Thr Leu
        195                 200                 205

Phe Asp Gly Ile Glu Asn Leu Leu Gly Asp Trp Ala Lys Phe Met Arg
    210                 215                 220

Ile Glu Phe Phe His Asn Asp Ser Asn Leu Leu Leu Ala Ile Leu Pro
225                 230                 235                 240

Pro Gly Ala Phe Ile Gly Leu Ala Leu Leu Leu Ala Leu Lys Asn Val
                245                 250                 255

Ile Asp Thr Lys Lys
            260


<210>  127
<211>  627
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(627)

<400>  127
atg aat ttt act aaa acg cta tat att ttt aaa tat act ggc gaa ctt        48
Met Asn Phe Thr Lys Thr Leu Tyr Ile Phe Lys Tyr Thr Gly Glu Leu
1               5                   10                  15

ttc gcg att ttt att tat aat gaa gac gct atg ttt tta aat ata cat        96
Phe Ala Ile Phe Ile Tyr Asn Glu Asp Ala Met Phe Leu Asn Ile His
            20                  25                  30

cgt tat att ttt ctc aca ttc tgt tgg ggt aac atc atg aaa ttt gaa       144
Arg Tyr Ile Phe Leu Thr Phe Cys Trp Gly Asn Ile Met Lys Phe Glu
        35                  40                  45

gtc att tac aaa ttc ctg ttg ttg tgt gtg ctg att atc agt ttg ttg       192
Val Ile Tyr Lys Phe Leu Leu Leu Cys Val Leu Ile Ile Ser Leu Leu
```

```
    50                  55                  60

tgt gtt gtg ata agc ggc gcc gga tta ttc tac ggt tgg caa ttg agc       240
Cys Val Val Ile Ser Gly Ala Gly Leu Phe Tyr Gly Trp Gln Leu Ser
65                  70                  75                  80

atg ctg ttc aat att cat gtg agc ttt gcc gtt ttg ctg gtc gcc gcg       288
Met Leu Phe Asn Ile His Val Ser Phe Ala Val Leu Leu Val Ala Ala
                85                  90                  95

ttg tta ctg cat att ctg aac cgc aaa aat aaa ttg gcg aaa atc aat       336
Leu Leu Leu His Ile Leu Asn Arg Lys Asn Lys Leu Ala Lys Ile Asn
            100                 105                 110

acc caa ttt gcc gat ttg gtc tta cac aat aaa tac ccg agt tat tgc       384
Thr Gln Phe Ala Asp Leu Val Leu His Asn Lys Tyr Pro Ser Tyr Cys
        115                 120                 125

aat tta gac cgc ttg atc atg acg ttc gag cat ttt tcc gtt gtg caa       432
Asn Leu Asp Arg Leu Ile Met Thr Phe Glu His Phe Ser Val Val Gln
    130                 135                 140

att gcc gaa cag tta aac ctg gat ttg gat gcg ctg cta aaa gaa ctc       480
Ile Ala Glu Gln Leu Asn Leu Asp Leu Asp Ala Leu Leu Lys Glu Leu
145                 150                 155                 160

gcc gaa gga aaa ata aac gtc aaa aat tcc cac agc act tta cgg gag       528
Ala Glu Gly Lys Ile Asn Val Lys Asn Ser His Ser Thr Leu Arg Glu
                165                 170                 175

aat ttt ccc cat aat gat gaa aag att ttt gct gcg atc acc atc gtg       576
Asn Phe Pro His Asn Asp Glu Lys Ile Phe Ala Ala Ile Thr Ile Val
            180                 185                 190

ctg caa ctt cgt tta att aat cct atc cct gct ttt aac tta aaa gga       624
Leu Gln Leu Arg Leu Ile Asn Pro Ile Pro Ala Phe Asn Leu Lys Gly
        195                 200                 205

cat                                                                   627
His


<210>  128
<211>  209
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  128

Met Asn Phe Thr Lys Thr Leu Tyr Ile Phe Lys Tyr Thr Gly Glu Leu
1               5                   10                  15


Phe Ala Ile Phe Ile Tyr Asn Glu Asp Ala Met Phe Leu Asn Ile His
            20                  25                  30


Arg Tyr Ile Phe Leu Thr Phe Cys Trp Gly Asn Ile Met Lys Phe Glu
        35                  40                  45
```

```
Val Ile Tyr Lys Phe Leu Leu Leu Cys Val Leu Ile Ile Ser Leu Leu
    50                  55                  60


Cys Val Val Ile Ser Gly Ala Gly Leu Phe Tyr Gly Trp Gln Leu Ser
65                  70                  75                  80


Met Leu Phe Asn Ile His Val Ser Phe Ala Val Leu Leu Val Ala Ala
                85                  90                  95


Leu Leu Leu His Ile Leu Asn Arg Lys Asn Lys Leu Ala Lys Ile Asn
            100                 105                 110


Thr Gln Phe Ala Asp Leu Val Leu His Asn Lys Tyr Pro Ser Tyr Cys
        115                 120                 125


Asn Leu Asp Arg Leu Ile Met Thr Phe Glu His Phe Ser Val Val Gln
    130                 135                 140


Ile Ala Glu Gln Leu Asn Leu Asp Leu Asp Ala Leu Leu Lys Glu Leu
145                 150                 155                 160


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


Asn Phe Pro His Asn Asp Glu Lys Ile Phe Ala Ala Ile Thr Ile Val
            180                 185                 190


Leu Gln Leu Arg Leu Ile Asn Pro Ile Pro Ala Phe Asn Leu Lys Gly
        195                 200                 205


His


<210>  129
<211>  663
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(663)

<400>  129
gtg caa tct tac gag cag caa agt aat aac ggc gtg ccg att caa ttc        48
Val Gln Ser Tyr Glu Gln Gln Ser Asn Asn Gly Val Pro Ile Gln Phe
1                   5                   10                  15

cag cag tta gac caa tca caa acc gtt gaa ccg acc gtg ttg gat aat        96
Gln Gln Leu Asp Gln Ser Gln Thr Val Glu Pro Thr Val Leu Asp Asn
```

```
            20                  25                  30

ctg acc ccg caa acc gat aac act gtc gcg caa caa cct gct gcg gaa       144
Leu Thr Pro Gln Thr Asp Asn Thr Val Ala Gln Gln Pro Ala Ala Glu
        35                  40                  45

acc aat acg caa aat gtc aat gcc ggc gcc ata gaa ccg caa gcg gtg       192
Thr Asn Thr Gln Asn Val Asn Ala Gly Ala Ile Glu Pro Gln Ala Val
    50                  55                  60

gaa caa ggg gca acc acc tcc gtt gct gag caa acg aca act gcg gcg       240
Glu Gln Gly Ala Thr Thr Ser Val Ala Glu Gln Thr Thr Thr Ala Ala
65                  70                  75                  80

gta gaa aat aaa ccg gca gaa gtc aaa ccg gaa gag gtc gaa acc gtt       288
Val Glu Asn Lys Pro Ala Glu Val Lys Pro Glu Glu Val Glu Thr Val
            85                  90                  95

aaa ccg agt gag cct gca aaa gcg caa gaa gcc gtc aaa ccg cgt caa       336
Lys Pro Ser Glu Pro Ala Lys Ala Gln Glu Ala Val Lys Pro Arg Gln
            100                 105                 110

cat cag gaa agc gtg aaa aaa gag ccg gtg aaa acc gat aaa gtg aaa       384
His Gln Glu Ser Val Lys Lys Glu Pro Val Lys Thr Asp Lys Val Lys
        115                 120                 125

cag gct gaa aaa gcg act gct aaa aat caa ccg act aaa tcg gca aaa       432
Gln Ala Glu Lys Ala Thr Ala Lys Asn Gln Pro Thr Lys Ser Ala Lys
    130                 135                 140

acc gaa aaa gaa gta cgg gat att tta gaa ggc aaa aca acg act atc       480
Thr Glu Lys Glu Val Arg Asp Ile Leu Glu Gly Lys Thr Thr Thr Ile
145                 150                 155                 160

acc aaa gca gca gcc ggt agc aaa acc tta acc att ccg caa ggc gtg       528
Thr Lys Ala Ala Ala Gly Ser Lys Thr Leu Thr Ile Pro Gln Gly Val
                165                 170                 175

acc tta atg cag gtg ttc cgt gac aac cat cta cct gtc ggt gat gtg       576
Thr Leu Met Gln Val Phe Arg Asp Asn His Leu Pro Val Gly Asp Val
            180                 185                 190

aat gcc atg acc aaa gcc aaa ggc gta ggc aag gtg tta agc agc ttc       624
Asn Ala Met Thr Lys Ala Lys Gly Val Gly Lys Val Leu Ser Ser Phe
        195                 200                 205

aag ccg ggt gat aag gta cag gtt tcc ctg aat gca caa                   663
Lys Pro Gly Asp Lys Val Gln Val Ser Leu Asn Ala Gln
    210                 215                 220


<210>  130
<211>  221
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  130

Val Gln Ser Tyr Glu Gln Gln Ser Asn Asn Gly Val Pro Ile Gln Phe
1               5                   10                  15
```

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Gln Gln Leu Asp Gln Ser Gln Thr Val Glu Pro Thr Val Leu Asp Asn
            20                  25                  30

Leu Thr Pro Gln Thr Asp Asn Thr Val Ala Gln Gln Pro Ala Ala Glu
        35                  40                  45

Thr Asn Thr Gln Asn Val Asn Ala Gly Ala Ile Glu Pro Gln Ala Val
    50                  55                  60

Glu Gln Gly Ala Thr Thr Ser Val Ala Glu Gln Thr Thr Thr Ala Ala
65                  70                  75                  80

Val Glu Asn Lys Pro Ala Glu Val Lys Pro Glu Glu Val Glu Thr Val
                85                  90                  95

Lys Pro Ser Glu Pro Ala Lys Ala Gln Glu Ala Val Lys Pro Arg Gln
            100                 105                 110

His Gln Glu Ser Val Lys Lys Glu Pro Val Lys Thr Asp Lys Val Lys
        115                 120                 125

Gln Ala Glu Lys Ala Thr Ala Lys Asn Gln Pro Thr Lys Ser Ala Lys
    130                 135                 140

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

Thr Lys Ala Ala Ala Gly Ser Lys Thr Leu Thr Ile Pro Gln Gly Val
                165                 170                 175

Thr Leu Met Gln Val Phe Arg Asp Asn His Leu Pro Val Gly Asp Val
            180                 185                 190

Asn Ala Met Thr Lys Ala Lys Gly Val Gly Lys Val Leu Ser Ser Phe
        195                 200                 205

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


<210>  131
<211>  478
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(477)
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<400>  131
atg tta aaa aaa atc tta cat tcc gca ctc atc ggt ttg gtt acg gca        48
Met Leu Lys Lys Ile Leu His Ser Ala Leu Ile Gly Leu Val Thr Ala
1               5                   10                  15

ggt gtg att ttg ttt gtg cta ccg aaa atc acc ggg aaa tcc gtg tta        96
Gly Val Ile Leu Phe Val Leu Pro Lys Ile Thr Gly Lys Ser Val Leu
            20                  25                  30

ccg gag caa gaa atc gcc tct tat aaa gat gca gtg cgt att gct tcg       144
Pro Glu Gln Glu Ile Ala Ser Tyr Lys Asp Ala Val Arg Ile Ala Ser
        35                  40                  45

ccg gcg gtt gtg aac gtt tat aat cag gcg ttt act tct tcg tcc gcg       192
Pro Ala Val Val Asn Val Tyr Asn Gln Ala Phe Thr Ser Ser Ser Ala
    50                  55                  60

caa ttg cag gtg aat aac ctc ggt tcg ggc gtg atc atg tca aaa gac       240
Gln Leu Gln Val Asn Asn Leu Gly Ser Gly Val Ile Met Ser Lys Asp
65                  70                  75                  80

ggt tat att ctg acg aac aaa cac gtt att caa aat gcc gat caa att       288
Gly Tyr Ile Leu Thr Asn Lys His Val Ile Gln Asn Ala Asp Gln Ile
                85                  90                  95

gta gta gcg ttg caa aac ggg cat att ttt gat gcg gcg ctc att ggt       336
Val Val Ala Leu Gln Asn Gly His Ile Phe Asp Ala Ala Leu Ile Gly
            100                 105                 110

tcc gat tct tta acg gat ttg gca gta tta aaa att aaa gcg gat aat       384
Ser Asp Ser Leu Thr Asp Leu Ala Val Leu Lys Ile Lys Ala Asp Asn
        115                 120                 125

tta tcc acg att ccg caa aat ctc agc cgt ccg gtg cat gtg gga gat       432
Leu Ser Thr Ile Pro Gln Asn Leu Ser Arg Pro Val His Val Gly Asp
    130                 135                 140

gtg gcg ctg gca atc ggc aat ccg tat aac ctg ggg caa agc gtg t         478
Val Ala Leu Ala Ile Gly Asn Pro Tyr Asn Leu Gly Gln Ser Val
145                 150                 155


<210>  132
<211>  159
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  132

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


Gly Val Ile Leu Phe Val Leu Pro Lys Ile Thr Gly Lys Ser Val Leu
            20                  25                  30


Pro Glu Gln Glu Ile Ala Ser Tyr Lys Asp Ala Val Arg Ile Ala Ser
        35                  40                  45
```

```
Pro Ala Val Val Asn Val Tyr Asn Gln Ala Phe Thr Ser Ser Ser Ala
    50                  55                  60


Gln Leu Gln Val Asn Asn Leu Gly Ser Gly Val Ile Met Ser Lys Asp
65              70                  75                  80


Gly Tyr Ile Leu Thr Asn Lys His Val Ile Gln Asn Ala Asp Gln Ile
                85                  90                  95


Val Val Ala Leu Gln Asn Gly His Ile Phe Asp Ala Ala Leu Ile Gly
            100                 105                 110


Ser Asp Ser Leu Thr Asp Leu Ala Val Leu Lys Ile Lys Ala Asp Asn
        115                 120                 125


Leu Ser Thr Ile Pro Gln Asn Leu Ser Arg Pro Val His Val Gly Asp
    130                 135                 140


Val Ala Leu Ala Ile Gly Asn Pro Tyr Asn Leu Gly Gln Ser Val
145                 150                 155


<210>  133
<211>  537
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(537)

<400>  133
gcc ggc tgg cag ata aaa aat aac aaa cct ttt gac ggt aaa gac tgg        48
Ala Gly Trp Gln Ile Lys Asn Asn Lys Pro Phe Asp Gly Lys Asp Trp
1               5                   10                  15

acc cgt tgg gtc gat gcg aga gaa tcc gga gcc att gcc ggt gca gta        96
Thr Arg Trp Val Asp Ala Arg Glu Ser Gly Ala Ile Ala Gly Ala Val
            20                  25                  30

gaa ttt aac aat tat gtc aat tct cat aaa ggc aaa atg ttc tat gtg       144
Glu Phe Asn Asn Tyr Val Asn Ser His Lys Gly Lys Met Phe Tyr Val
        35                  40                  45

tca aat cgc aaa gac agt aat gaa aaa gca ggt acc att gat gac atg       192
Ser Asn Arg Lys Asp Ser Asn Glu Lys Ala Gly Thr Ile Asp Asp Met
    50                  55                  60

aaa cgt tta ggc ttt acc ggt gtt gat gaa tca tcc ctt tat ctg aaa       240
Lys Arg Leu Gly Phe Thr Gly Val Asp Glu Ser Ser Leu Tyr Leu Lys
65                  70                  75                  80

aaa gat aaa tcc gcc aaa tct gcc cgt ttt gca gaa att gaa agt caa       288
Lys Asp Lys Ser Ala Lys Ser Ala Arg Phe Ala Glu Ile Glu Ser Gln
```

```
            85                  90                  95

ggc tat gac atc gtg ctt tat gta ggc gac aac ctg gat gat ttc ggt      336
Gly Tyr Asp Ile Val Leu Tyr Val Gly Asp Asn Leu Asp Asp Phe Gly
            100                 105                 110

gat gca aca cac ggt aaa tta aat gcg gat cgt cga gac ttt gtt gct      384
Asp Ala Thr His Gly Lys Leu Asn Ala Asp Arg Arg Asp Phe Val Ala
        115                 120                 125

aaa aac cag gcg aaa ttc ggt aaa act tat atc gtt tta cct aat ccg      432
Lys Asn Gln Ala Lys Phe Gly Lys Thr Tyr Ile Val Leu Pro Asn Pro
    130                 135                 140

aat tac ggt ggt tgg gaa ggc ggt tta gcc aaa gac tac ttt aaa ggt      480
Asn Tyr Gly Gly Trp Glu Gly Gly Leu Ala Lys Asp Tyr Phe Lys Gly
145                 150                 155                 160

gat tcc caa agc aaa gtt gat gcc cgc tta aat gta att aag gca tgg      528
Asp Ser Gln Ser Lys Val Asp Ala Arg Leu Asn Val Ile Lys Ala Trp
                165                 170                 175

agt gga aaa                                                          537
Ser Gly Lys


<210>  134
<211>  179
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  134

Ala Gly Trp Gln Ile Lys Asn Asn Lys Pro Phe Asp Gly Lys Asp Trp
1               5                   10                  15


Thr Arg Trp Val Asp Ala Arg Glu Ser Gly Ala Ile Ala Gly Ala Val
            20                  25                  30


Glu Phe Asn Asn Tyr Val Asn Ser His Lys Gly Lys Met Phe Tyr Val
        35                  40                  45


Ser Asn Arg Lys Asp Ser Asn Glu Lys Ala Gly Thr Ile Asp Asp Met
    50                  55                  60


Lys Arg Leu Gly Phe Thr Gly Val Asp Glu Ser Ser Leu Tyr Leu Lys
65                  70                  75                  80


Lys Asp Lys Ser Ala Lys Ser Ala Arg Phe Ala Glu Ile Glu Ser Gln
                85                  90                  95


Gly Tyr Asp Ile Val Leu Tyr Val Gly Asp Asn Leu Asp Asp Phe Gly
            100                 105                 110
```

```
Asp Ala Thr His Gly Lys Leu Asn Ala Asp Arg Arg Asp Phe Val Ala
        115                 120                 125


Lys Asn Gln Ala Lys Phe Gly Lys Thr Tyr Ile Val Leu Pro Asn Pro
    130                 135                 140


Asn Tyr Gly Gly Trp Glu Gly Gly Leu Ala Lys Asp Tyr Phe Lys Gly
145                 150                 155                 160


Asp Ser Gln Ser Lys Val Asp Ala Arg Leu Asn Val Ile Lys Ala Trp
                165                 170                 175


Ser Gly Lys


<210>  135
<211>  765
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(765)

<400>  135
atg tgg ata ttt tac aac acc cgg aca ttc gtg ccg aat tac cgg ctt        48
Met Trp Ile Phe Tyr Asn Thr Arg Thr Phe Val Pro Asn Tyr Arg Leu
1               5                   10                  15

atg cca act ggc cga cat tcc cgc aat tat ggg tgg aag gcg agc tca        96
Met Pro Thr Gly Arg His Ser Arg Asn Tyr Gly Trp Lys Ala Ser Ser
            20                  25                  30

tcg gtg gtt gcg aca tcg tgt tgg aaa tgt acc aac aag gtg agc tta       144
Ser Val Val Ala Thr Ser Cys Trp Lys Cys Thr Asn Lys Val Ser Leu
        35                  40                  45

aaa cct tgt tac aag agg ttg ccg caa gac atc cgc aag cgt aaa aac       192
Lys Pro Cys Tyr Lys Arg Leu Pro Gln Asp Ile Arg Lys Arg Lys Asn
    50                  55                  60

gcg ttt caa aat gac cgt act ttg gtt tcc gga gtg cgg ttt ttt gct       240
Ala Phe Gln Asn Asp Arg Thr Leu Val Ser Gly Val Arg Phe Phe Ala
65                  70                  75                  80

gct tgg cgc agg gaa aaa cag gcg gtt tgt gct ata att ctc cgc aaa       288
Ala Trp Arg Arg Glu Lys Gln Ala Val Cys Ala Ile Ile Leu Arg Lys
                85                  90                  95

ttt tta ccg cac ttt agg atc aat atg tcg ttt caa ttc aac gcg atc       336
Phe Leu Pro His Phe Arg Ile Asn Met Ser Phe Gln Phe Asn Ala Ile
            100                 105                 110

gcc tta ctt ttg gtg att tta att tta tta ggt gta ctc agc cac aac       384
Ala Leu Leu Leu Val Ile Leu Ile Leu Leu Gly Val Leu Ser His Asn
```

```
        115                 120                 125

agt tcc atc acc att tcc gct gcc gta ttg ctc atc atg caa caa acc       432
Ser Ser Ile Thr Ile Ser Ala Ala Val Leu Leu Ile Met Gln Gln Thr
    130                 135                 140

ttg ctc gca aaa tat att cct tac ttg gaa aaa tac ggc ttg agc atc       480
Leu Leu Ala Lys Tyr Ile Pro Tyr Leu Glu Lys Tyr Gly Leu Ser Ile
145                 150                 155                 160

ggt atc gta att tta acc atc ggc gta cta agc ccg ttg gtt tcc ggc       528
Gly Ile Val Ile Leu Thr Ile Gly Val Leu Ser Pro Leu Val Ser Gly
                165                 170                 175

aga att caa ctg cct ggc ttg tcg gca ttt ttt agc tgg cga atg ttt       576
Arg Ile Gln Leu Pro Gly Leu Ser Ala Phe Phe Ser Trp Arg Met Phe
            180                 185                 190

gtt gcc att ggc gtc ggc gta tta gtg gcg tgg ctt gcc ggc aaa ggc       624
Val Ala Ile Gly Val Gly Val Leu Val Ala Trp Leu Ala Gly Lys Gly
        195                 200                 205

gtt ccg ctc atg ggg gaa gag cct gtt ctg gta acc ggc ttg gtt atc       672
Val Pro Leu Met Gly Glu Glu Pro Val Leu Val Thr Gly Leu Val Ile
    210                 215                 220

ggc acc att atc ggc gtt tct ttt ctc ggt ggt att ccc gtt ggt ccc       720
Gly Thr Ile Ile Gly Val Ser Phe Leu Gly Gly Ile Pro Val Gly Pro
225                 230                 235                 240

ctt att gcg gca ggg att ttg gca tta tta ata gga aaa ttt taa           765
Leu Ile Ala Ala Gly Ile Leu Ala Leu Leu Ile Gly Lys Phe
                245                 250


<210>  136
<211>  254
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  136

Met Trp Ile Phe Tyr Asn Thr Arg Thr Phe Val Pro Asn Tyr Arg Leu
1               5                   10                  15


Met Pro Thr Gly Arg His Ser Arg Asn Tyr Gly Trp Lys Ala Ser Ser
            20                  25                  30


Ser Val Val Ala Thr Ser Cys Trp Lys Cys Thr Asn Lys Val Ser Leu
        35                  40                  45


Lys Pro Cys Tyr Lys Arg Leu Pro Gln Asp Ile Arg Lys Arg Lys Asn
    50                  55                  60


Ala Phe Gln Asn Asp Arg Thr Leu Val Ser Gly Val Arg Phe Phe Ala
65                  70                  75                  80
```

```
Ala Trp Arg Arg Glu Lys Gln Ala Val Cys Ala Ile Ile Leu Arg Lys
                85                  90                  95

Phe Leu Pro His Phe Arg Ile Asn Met Ser Phe Gln Phe Asn Ala Ile
            100                 105                 110

Ala Leu Leu Leu Val Ile Leu Ile Leu Leu Gly Val Leu Ser His Asn
        115                 120                 125

Ser Ser Ile Thr Ile Ser Ala Ala Val Leu Leu Ile Met Gln Gln Thr
    130                 135                 140

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

Gly Ile Val Ile Leu Thr Ile Gly Val Leu Ser Pro Leu Val Ser Gly
                165                 170                 175

Arg Ile Gln Leu Pro Gly Leu Ser Ala Phe Phe Ser Trp Arg Met Phe
            180                 185                 190

Val Ala Ile Gly Val Gly Val Leu Val Ala Trp Leu Ala Gly Lys Gly
        195                 200                 205

Val Pro Leu Met Gly Glu Glu Pro Val Leu Val Thr Gly Leu Val Ile
    210                 215                 220

Gly Thr Ile Ile Gly Val Ser Phe Leu Gly Gly Ile Pro Val Gly Pro
225                 230                 235                 240

Leu Ile Ala Ala Gly Ile Leu Ala Leu Leu Ile Gly Lys Phe
                245                 250


<210>  137
<211>  387
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(387)

<400>  137
atg aaa aac aaa tgg tta ttg att gcc gcc gtg agc ggt ttt tta tgt       48
Met Lys Asn Lys Trp Leu Leu Ile Ala Ala Val Ser Gly Phe Leu Cys
1               5                   10                  15

gtg act atc ggt gcg ttt gcg gcg cac ggt tta agc caa gtg ttg gac       96
Val Thr Ile Gly Ala Phe Ala Ala His Gly Leu Ser Gln Val Leu Asp
```

```
            20                  25                  30

gcg aaa gcc tta gcg tgg att gac acc ggc gtg aaa tat caa atg ttc       144
Ala Lys Ala Leu Ala Trp Ile Asp Thr Gly Val Lys Tyr Gln Met Phe
        35                  40                  45

cac acc ctc gcc atc atg gga atc ggc atc gca caa tta tgt cgc gaa       192
His Thr Leu Ala Ile Met Gly Ile Gly Ile Ala Gln Leu Cys Arg Glu
    50                  55                  60

cca ttt gcc gcc aac aaa agc gcc aat gtt gcc gcc ggc gcg tgg tca       240
Pro Phe Ala Ala Asn Lys Ser Ala Asn Val Ala Ala Gly Ala Trp Ser
65                  70                  75                  80

ttc gga atc ctt ctc ttt agc ggc agt tta tac gcc ctc gca ctt ggc       288
Phe Gly Ile Leu Leu Phe Ser Gly Ser Leu Tyr Ala Leu Ala Leu Gly
                85                  90                  95

tca ggt aaa ttt atg gtt tgg ctc acg ccc atc ggc ggc acg cta ttt       336
Ser Gly Lys Phe Met Val Trp Leu Thr Pro Ile Gly Gly Thr Leu Phe
            100                 105                 110

tta atc ggc tgg ctt ggt tta gct tac ggc gct ttc aaa agt aaa tca       384
Leu Ile Gly Trp Leu Gly Leu Ala Tyr Gly Ala Phe Lys Ser Lys Ser
        115                 120                 125

gaa                                                                   387
Glu


<210>  138
<211>  129
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  138

Met Lys Asn Lys Trp Leu Leu Ile Ala Ala Val Ser Gly Phe Leu Cys
1               5                   10                  15


Val Thr Ile Gly Ala Phe Ala Ala His Gly Leu Ser Gln Val Leu Asp
            20                  25                  30


Ala Lys Ala Leu Ala Trp Ile Asp Thr Gly Val Lys Tyr Gln Met Phe
        35                  40                  45


His Thr Leu Ala Ile Met Gly Ile Gly Ile Ala Gln Leu Cys Arg Glu
    50                  55                  60


Pro Phe Ala Ala Asn Lys Ser Ala Asn Val Ala Ala Gly Ala Trp Ser
65                  70                  75                  80


Phe Gly Ile Leu Leu Phe Ser Gly Ser Leu Tyr Ala Leu Ala Leu Gly
                85                  90                  95
```

```
Ser Gly Lys Phe Met Val Trp Leu Thr Pro Ile Gly Gly Thr Leu Phe
            100                 105                 110

Leu Ile Gly Trp Leu Gly Leu Ala Tyr Gly Ala Phe Lys Ser Lys Ser
        115                 120                 125

Glu


<210>  139
<211>  684
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(684)

<400>  139
atc aat ttg gca cat aat tat cag caa aaa tgg cag gcg gac atc ggt        48
Ile Asn Leu Ala His Asn Tyr Gln Gln Lys Trp Gln Ala Asp Ile Gly
1               5                   10                  15

cgg cac gcc gtg cag tat ttt gct tac gat aac ccg cgg gcg gat ttt        96
Arg His Ala Val Gln Tyr Phe Ala Tyr Asp Asn Pro Arg Ala Asp Phe
            20                  25                  30

tac gcc gaa caa att cat ttc tcc gaa caa ggc gcc tat ttc tta ctc       144
Tyr Ala Glu Gln Ile His Phe Ser Glu Gln Gly Ala Tyr Phe Leu Leu
        35                  40                  45

cac acg ccg caa ggc cgc gtg caa atc aat tca ccg tat ttg ggt gag       192
His Thr Pro Gln Gly Arg Val Gln Ile Asn Ser Pro Tyr Leu Gly Glu
    50                  55                  60

cat aat atc tct aat gcg ttg gcg gca act gcc ttg gcg atg aac gtg       240
His Asn Ile Ser Asn Ala Leu Ala Ala Thr Ala Leu Ala Met Asn Val
65                  70                  75                  80

ggt gcc acc acg gcg cag gtg aaa aaa ggg ttg gaa acg ccc tct ttg       288
Gly Ala Thr Thr Ala Gln Val Lys Lys Gly Leu Glu Thr Pro Ser Leu
                85                  90                  95

gtg aaa ggg cgt ttg ttc ccg att cag cct tgt gaa aat ctg tta ttg       336
Val Lys Gly Arg Leu Phe Pro Ile Gln Pro Cys Glu Asn Leu Leu Leu
            100                 105                 110

ctg gac gat act tac aac gcc aat gtg gga tct atg aaa tcg gcg att       384
Leu Asp Asp Thr Tyr Asn Ala Asn Val Gly Ser Met Lys Ser Ala Ile
        115                 120                 125

tcc gtg tta caa aaa tat cct gct ttt cgc gtc ttt gtt gtt ggt gat       432
Ser Val Leu Gln Lys Tyr Pro Ala Phe Arg Val Phe Val Val Gly Asp
    130                 135                 140

atg ggc gaa tta ggc gat aat gcg caa ctt tgc cat caa gag gtg ggg       480
Met Gly Glu Leu Gly Asp Asn Ala Gln Leu Cys His Gln Glu Val Gly
```

```
145                 150                 155                 160

gag ttc gct cat gcc gcc aag tta gac tta gtg ctt tct ttc ggg tgt         528
Glu Phe Ala His Ala Ala Lys Leu Asp Leu Val Leu Ser Phe Gly Cys
                165                 170                 175

tcc agt ggc gtt ata agt gcg gtt aat tcg gga cgc cat ttt acc gat         576
Ser Ser Gly Val Ile Ser Ala Val Asn Ser Gly Arg His Phe Thr Asp
            180                 185                 190

aaa acg gaa ctt gta act tat tta aca ccg att att caa caa caa tta         624
Lys Thr Glu Leu Val Thr Tyr Leu Thr Pro Ile Ile Gln Gln Gln Leu
        195                 200                 205

gca caa caa aaa gtc gtt gtt ttg gtg aaa gga tca cgc agc atg aaa         672
Ala Gln Gln Lys Val Val Val Leu Val Lys Gly Ser Arg Ser Met Lys
    210                 215                 220

atg gaa gaa gtg                                                         684
Met Glu Glu Val
225


<210>  140
<211>  228
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  140

Ile Asn Leu Ala His Asn Tyr Gln Gln Lys Trp Gln Ala Asp Ile Gly
1               5                   10                  15


Arg His Ala Val Gln Tyr Phe Ala Tyr Asp Asn Pro Arg Ala Asp Phe
            20                  25                  30


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


His Thr Pro Gln Gly Arg Val Gln Ile Asn Ser Pro Tyr Leu Gly Glu
    50                  55                  60


His Asn Ile Ser Asn Ala Leu Ala Ala Thr Ala Leu Ala Met Asn Val
65                  70                  75                  80


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


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


Leu Asp Asp Thr Tyr Asn Ala Asn Val Gly Ser Met Lys Ser Ala Ile
        115                 120                 125
```

```
Ser Val Leu Gln Lys Tyr Pro Ala Phe Arg Val Phe Val Val Gly Asp
    130                 135                 140

Met Gly Glu Leu Gly Asp Asn Ala Gln Leu Cys His Gln Glu Val Gly
145                 150                 155                 160

Glu Phe Ala His Ala Ala Lys Leu Asp Leu Val Leu Ser Phe Gly Cys
                165                 170                 175

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

Lys Thr Glu Leu Val Thr Tyr Leu Thr Pro Ile Ile Gln Gln Gln Leu
        195                 200                 205

Ala Gln Gln Lys Val Val Val Leu Val Lys Gly Ser Arg Ser Met Lys
    210                 215                 220

Met Glu Glu Val
225


<210>  141
<211>  267
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(267)

<400>  141
gat ggc ggt aag gcg ggt tcg agg tat gca ggt att atc tat aaa tct       48
Asp Gly Gly Lys Ala Gly Ser Arg Tyr Ala Gly Ile Ile Tyr Lys Ser
1               5                   10                  15

gtg aag cca tat ttt cgt ggt gat agt cgt ttt ttt ggt aag gtc tgt       96
Val Lys Pro Tyr Phe Arg Gly Asp Ser Arg Phe Phe Gly Lys Val Cys
            20                  25                  30

gat att aga att gag ctt tct agt gat ggc act att tta tct tac caa      144
Asp Ile Arg Ile Glu Leu Ser Ser Asp Gly Thr Ile Leu Ser Tyr Gln
        35                  40                  45

aag gtc tcc ggg cca aat gat tta tgt ggg gcg gct tta aat gct att      192
Lys Val Ser Gly Pro Asn Asp Leu Cys Gly Ala Ala Leu Asn Ala Ile
    50                  55                  60

ggt caa acc aga aaa atg aac gaa ccg cct acg ccg gaa gaa tat gaa      240
Gly Gln Thr Arg Lys Met Asn Glu Pro Pro Thr Pro Glu Glu Tyr Glu
65                  70                  75                  80

ata ttt aaa agg tcc att gta acc ttt                                  267
Ile Phe Lys Arg Ser Ile Val Thr Phe
```

```
                85

<210>  142
<211>  89
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  142

Asp Gly Gly Lys Ala Gly Ser Arg Tyr Ala Gly Ile Ile Tyr Lys Ser
1               5                   10                  15


Val Lys Pro Tyr Phe Arg Gly Asp Ser Arg Phe Phe Gly Lys Val Cys
            20                  25                  30


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


Lys Val Ser Gly Pro Asn Asp Leu Cys Gly Ala Ala Leu Asn Ala Ile
    50                  55                  60


Gly Gln Thr Arg Lys Met Asn Glu Pro Pro Thr Pro Glu Glu Tyr Glu
65                  70                  75                  80


Ile Phe Lys Arg Ser Ile Val Thr Phe
                85


<210>  143
<211>  683
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(681)

<400>  143
ggt gcc tta tat ttt gta ttc agt ctg atg ggc gtg ttc gcc agt ttg        48
Gly Ala Leu Tyr Phe Val Phe Ser Leu Met Gly Val Phe Ala Ser Leu
1               5                   10                  15

tta tcc acc gcg cgc ggc ggc tgg att ggt atc cct ttt gtt ctc ctg        96
Leu Ser Thr Ala Arg Gly Gly Trp Ile Gly Ile Pro Phe Val Leu Leu
            20                  25                  30

tta atc ctc ttt gct tat cgt cgt tat tta tcg aaa aaa ttc gtc gcc       144
Leu Ile Leu Phe Ala Tyr Arg Arg Tyr Leu Ser Lys Lys Phe Val Ala
        35                  40                  45

ggc ttt ttt att gtg ctt gcc ctg att gta aca acc gtt gcg atg ttg       192
Gly Phe Phe Ile Val Leu Ala Leu Ile Val Thr Thr Val Ala Met Leu
    50                  55                  60

cca aat acc aaa att aaa gaa cgc att gcc gcc gca gaa tac gac atc       240
```

```
Pro Asn Thr Lys Ile Lys Glu Arg Ile Ala Ala Ala Glu Tyr Asp Ile
65                  70                  75                  80

atc gcc tat ttt caa caa aat aac ggt tct acc tcc gtc ggc gcc cgt      288
Ile Ala Tyr Phe Gln Gln Asn Asn Gly Ser Thr Ser Val Gly Ala Arg
                85                  90                  95

ttt gat atg tgg aaa agc gtg atg tta atg acg cag gaa aaa ccg att      336
Phe Asp Met Trp Lys Ser Val Met Leu Met Thr Gln Glu Lys Pro Ile
            100                 105                 110

ttc ggt tgg ggc gta caa ggg gtc agc gaa aaa cgc aaa ctg caa tat      384
Phe Gly Trp Gly Val Gln Gly Val Ser Glu Lys Arg Lys Leu Gln Tyr
        115                 120                 125

gag caa ggt ttg ata agc caa tat gcc gcc gcc ttt aac cac gcg cac      432
Glu Gln Gly Leu Ile Ser Gln Tyr Ala Ala Ala Phe Asn His Ala His
    130                 135                 140

aac caa tat ttt gat gat tta tcc aaa cgc ggc gca tta ggt tta ctc      480
Asn Gln Tyr Phe Asp Asp Leu Ser Lys Arg Gly Ala Leu Gly Leu Leu
145                 150                 155                 160

gcc tta ctc ggc gta ttt tta gtg ccg ttg cgt ttc ttt ata cgg cat      528
Ala Leu Leu Gly Val Phe Leu Val Pro Leu Arg Phe Phe Ile Arg His
                165                 170                 175

ctc aaa agc gtc gat tta gaa ctg aaa ctc gtt tcg ttg tta ggt gcg      576
Leu Lys Ser Val Asp Leu Glu Leu Lys Leu Val Ser Leu Leu Gly Ala
            180                 185                 190

gtt cat att gtc tcc gtg atg ttc tac tgt ttc agc caa ggc ttt ttc      624
Val His Ile Val Ser Val Met Phe Tyr Cys Phe Ser Gln Gly Phe Phe
        195                 200                 205

agc cat aac tcg ggc aat att ttc tat ttt ttc ccg gtg att gtg ttt      672
Ser His Asn Ser Gly Asn Ile Phe Tyr Phe Phe Pro Val Ile Val Phe
    210                 215                 220

tac gcc ttg gt                                                       683
Tyr Ala Leu
225


<210>  144
<211>  227
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  144

Gly Ala Leu Tyr Phe Val Phe Ser Leu Met Gly Val Phe Ala Ser Leu
1               5                   10                  15


Leu Ser Thr Ala Arg Gly Gly Trp Ile Gly Ile Pro Phe Val Leu Leu
            20                  25                  30


Leu Ile Leu Phe Ala Tyr Arg Arg Tyr Leu Ser Lys Lys Phe Val Ala
        35                  40                  45
```

```
Gly Phe Phe Ile Val Leu Ala Leu Ile Val Thr Thr Val Ala Met Leu
    50                  55                  60

Pro Asn Thr Lys Ile Lys Glu Arg Ile Ala Ala Ala Glu Tyr Asp Ile
65                  70                  75                  80

Ile Ala Tyr Phe Gln Gln Asn Asn Gly Ser Thr Ser Val Gly Ala Arg
                85                  90                  95

Phe Asp Met Trp Lys Ser Val Met Leu Met Thr Gln Glu Lys Pro Ile
            100                 105                 110

Phe Gly Trp Gly Val Gln Gly Val Ser Glu Lys Arg Lys Leu Gln Tyr
        115                 120                 125

Glu Gln Gly Leu Ile Ser Gln Tyr Ala Ala Ala Phe Asn His Ala His
    130                 135                 140

Asn Gln Tyr Phe Asp Asp Leu Ser Lys Arg Gly Ala Leu Gly Leu Leu
145                 150                 155                 160

Ala Leu Leu Gly Val Phe Leu Val Pro Leu Arg Phe Phe Ile Arg His
                165                 170                 175

Leu Lys Ser Val Asp Leu Glu Leu Lys Leu Val Ser Leu Leu Gly Ala
            180                 185                 190

Val His Ile Val Ser Val Met Phe Tyr Cys Phe Ser Gln Gly Phe Phe
        195                 200                 205

Ser His Asn Ser Gly Asn Ile Phe Tyr Phe Phe Pro Val Ile Val Phe
    210                 215                 220

Tyr Ala Leu
225

<210>  145
<211>  408
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(408)

<400>  145
gcc gat tat ggc atc gac tat ggt aac gat ttc gta ggt atc att gaa        48
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Ala Asp Tyr Gly Ile Asp Tyr Gly Asn Asp Phe Val Gly Ile Ile Glu
1               5                   10                  15

gga aaa ttg aag tta aac aaa tca acg tta cat gat aat aac gcc tcc       96
Gly Lys Leu Lys Leu Asn Lys Ser Thr Leu His Asp Asn Asn Ala Ser
            20                  25                  30

ggc tac cgt ggc aaa ctg aac gaa aag gca cgt ttg ggc gta agt tac      144
Gly Tyr Arg Gly Lys Leu Asn Glu Lys Ala Arg Leu Gly Val Ser Tyr
        35                  40                  45

tta caa ggc tat cgc gta aca cca agc att ctt cct tat gcc aaa gtt      192
Leu Gln Gly Tyr Arg Val Thr Pro Ser Ile Leu Pro Tyr Ala Lys Val
    50                  55                  60

ggg gtg caa act gct aaa ttt gaa agt gag gtt cgt aca cgc aac tac      240
Gly Val Gln Thr Ala Lys Phe Glu Ser Glu Val Arg Thr Arg Asn Tyr
65                  70                  75                  80

tca gct acg cat agt gat acc aaa aac ggt ata ggt ttt ggt gcg ggt      288
Ser Ala Thr His Ser Asp Thr Lys Asn Gly Ile Gly Phe Gly Ala Gly
                85                  90                  95

gtt aag gtc aat ctg gta ccg gac ttt gag cta agc ttg gaa tat tta      336
Val Lys Val Asn Leu Val Pro Asp Phe Glu Leu Ser Leu Glu Tyr Leu
            100                 105                 110

agg act cat aac aaa ttt gat ggt caa aag tta aga ggt aat gta tat      384
Arg Thr His Asn Lys Phe Asp Gly Gln Lys Leu Arg Gly Asn Val Tyr
        115                 120                 125

agc acc aac gct aca tat cgt ttc                                      408
Ser Thr Asn Ala Thr Tyr Arg Phe
    130                 135


<210>  146
<211>  136
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  146

Ala Asp Tyr Gly Ile Asp Tyr Gly Asn Asp Phe Val Gly Ile Ile Glu
1               5                   10                  15


Gly Lys Leu Lys Leu Asn Lys Ser Thr Leu His Asp Asn Asn Ala Ser
            20                  25                  30


Gly Tyr Arg Gly Lys Leu Asn Glu Lys Ala Arg Leu Gly Val Ser Tyr
        35                  40                  45


Leu Gln Gly Tyr Arg Val Thr Pro Ser Ile Leu Pro Tyr Ala Lys Val
    50                  55                  60


Gly Val Gln Thr Ala Lys Phe Glu Ser Glu Val Arg Thr Arg Asn Tyr
65                  70                  75                  80
```

```
Ser Ala Thr His Ser Asp Thr Lys Asn Gly Ile Gly Phe Gly Ala Gly
                85                  90                  95

Val Lys Val Asn Leu Val Pro Asp Phe Glu Leu Ser Leu Glu Tyr Leu
            100                 105                 110

Arg Thr His Asn Lys Phe Asp Gly Gln Lys Leu Arg Gly Asn Val Tyr
        115                 120                 125

Ser Thr Asn Ala Thr Tyr Arg Phe
    130                 135


<210>  147
<211>  426
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(426)

<400>  147
atg aaa aaa att ctt acc gca ctt ttt tgc agt tgt ctc att tcc cct        48
Met Lys Lys Ile Leu Thr Ala Leu Phe Cys Ser Cys Leu Ile Ser Pro
1               5                   10                  15

ctc aca aac gct gaa acc ttg tct gat ggt tta cca cca cag gca gct        96
Leu Thr Asn Ala Glu Thr Leu Ser Asp Gly Leu Pro Pro Gln Ala Ala
            20                  25                  30

ggt gat tat gtg ttc ttg gac ccg cat caa aac aat acg gat ata caa       144
Gly Asp Tyr Val Phe Leu Asp Pro His Gln Asn Asn Thr Asp Ile Gln
        35                  40                  45

ttt cgt tta aaa ctt aaa ggc aaa caa tgg ctg gca gac ggt tcc caa       192
Phe Arg Leu Lys Leu Lys Gly Lys Gln Trp Leu Ala Asp Gly Ser Gln
    50                  55                  60

aat gcc ggc aaa agc tgg tcg cct gtg tgc gaa gtc agt ggc gaa tgc       240
Asn Ala Gly Lys Ser Trp Ser Pro Val Cys Glu Val Ser Gly Glu Cys
65                  70                  75                  80

aaa ctg gag aca tcc tcc aaa gcg gaa atc gaa cgc ttc ttt gag caa       288
Lys Leu Glu Thr Ser Ser Lys Ala Glu Ile Glu Arg Phe Phe Glu Gln
                85                  90                  95

tat ccg caa gta cta aac cga aca gat gtc agc tgc att cac aat atg       336
Tyr Pro Gln Val Leu Asn Arg Thr Asp Val Ser Cys Ile His Asn Met
            100                 105                 110

gcg ttc gct ttc tgc ggg tta act tta gat aaa aaa acc gat tat gtg       384
Ala Phe Ala Phe Cys Gly Leu Thr Leu Asp Lys Lys Thr Asp Tyr Val
        115                 120                 125

atg gtc gca tta gtg acc aat ccg cca caa gtc aca tcg tat               426
```

```
Met Val Ala Leu Val Thr Asn Pro Pro Gln Val Thr Ser Tyr
    130                 135                 140


<210>  148
<211>  142
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  148

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


Leu Thr Asn Ala Glu Thr Leu Ser Asp Gly Leu Pro Pro Gln Ala Ala
            20                  25                  30


Gly Asp Tyr Val Phe Leu Asp Pro His Gln Asn Asn Thr Asp Ile Gln
        35                  40                  45


Phe Arg Leu Lys Leu Lys Gly Lys Gln Trp Leu Ala Asp Gly Ser Gln
    50                  55                  60


Asn Ala Gly Lys Ser Trp Ser Pro Val Cys Glu Val Ser Gly Glu Cys
65                  70                  75                  80


Lys Leu Glu Thr Ser Ser Lys Ala Glu Ile Glu Arg Phe Phe Glu Gln
                85                  90                  95


Tyr Pro Gln Val Leu Asn Arg Thr Asp Val Ser Cys Ile His Asn Met
            100                 105                 110


Ala Phe Ala Phe Cys Gly Leu Thr Leu Asp Lys Lys Thr Asp Tyr Val
        115                 120                 125


Met Val Ala Leu Val Thr Asn Pro Pro Gln Val Thr Ser Tyr
    130                 135                 140


<210>  149
<211>  679
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(678)

<400>  149
cgc cga att att ggc aca acg aca aca gga tat tca cta atg cgc gca       48
Arg Arg Ile Ile Gly Thr Thr Thr Thr Gly Tyr Ser Leu Met Arg Ala
1               5                   10                  15
```

```
tta ttg cct ttt ctt cgt tta ttt aaa ttc gcc aaa ctg ccg tta att         96
Leu Leu Pro Phe Leu Arg Leu Phe Lys Phe Ala Lys Leu Pro Leu Ile
        20                  25                  30

tta ggc ggc ttg ctg atg att tta ggg ctg gcg tcc agt atc ggg ttg        144
Leu Gly Gly Leu Leu Met Ile Leu Gly Leu Ala Ser Ser Ile Gly Leu
        35                  40                  45

ctc acc ctt tcc ggc tgg ttt ctt gcc gcc acc gcc atc gcc ggt ttc        192
Leu Thr Leu Ser Gly Trp Phe Leu Ala Ala Thr Ala Ile Ala Gly Phe
    50                  55                  60

ggc tcg cta ttt aac ttt ttc tac cca tcc gcc agc gta cgc ggt ttg        240
Gly Ser Leu Phe Asn Phe Phe Tyr Pro Ser Ala Ser Val Arg Gly Leu
65                  70                  75                  80

gca atc ggg cgt acc gtg gcg cgc tac ctt gaa aaa gtg gtc acc cat        288
Ala Ile Gly Arg Thr Val Ala Arg Tyr Leu Glu Lys Val Val Thr His
                85                  90                  95

gac gcc acc ttc cgc gta ttg gca aaa ctg cgt gtg cag gtg ttt gac        336
Asp Ala Thr Phe Arg Val Leu Ala Lys Leu Arg Val Gln Val Phe Asp
            100                 105                 110

aaa atc att ccg tta agc cct gcg ctg ctc aac cgt tat cgt aac agc        384
Lys Ile Ile Pro Leu Ser Pro Ala Leu Leu Asn Arg Tyr Arg Asn Ser
        115                 120                 125

gat tta tta aac cgc ttg gtt gcc gat gtg gac acc ctc gac agc cta        432
Asp Leu Leu Asn Arg Leu Val Ala Asp Val Asp Thr Leu Asp Ser Leu
    130                 135                 140

tat ctt cgc ctc att gcg ccc ttt atc agc gcc ata gtg gtg att gcg        480
Tyr Leu Arg Leu Ile Ala Pro Phe Ile Ser Ala Ile Val Val Ile Ala
145                 150                 155                 160

ttc att acc ttt ggc ttg agt ttt att aat gcc ccg ctc gcg ctg ttt        528
Phe Ile Thr Phe Gly Leu Ser Phe Ile Asn Ala Pro Leu Ala Leu Phe
                165                 170                 175

atc ggt ttc aca tta ctg gcg ctc ttg ctg gtt atc ccg acg att ttt        576
Ile Gly Phe Thr Leu Leu Ala Leu Leu Leu Val Ile Pro Thr Ile Phe
            180                 185                 190

tac cat ttg ggt aac aaa ttc ggc gcc aaa ctt acc caa tcc cgc gcc        624
Tyr His Leu Gly Asn Lys Phe Gly Ala Lys Leu Thr Gln Ser Arg Ala
        195                 200                 205

ctt tac cgc acg caa ttt atc gaa ttt att cag gcg caa gcg gaa tta        672
Leu Tyr Arg Thr Gln Phe Ile Glu Phe Ile Gln Ala Gln Ala Glu Leu
    210                 215                 220

ttg ctg t                                                              679
Leu Leu
225


<210>  150
<211>  226
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans
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<400>  150

Arg Arg Ile Ile Gly Thr Thr Thr Thr Gly Tyr Ser Leu Met Arg Ala
1               5                   10                  15

Leu Leu Pro Phe Leu Arg Leu Phe Lys Phe Ala Lys Leu Pro Leu Ile
            20                  25                  30

Leu Gly Gly Leu Leu Met Ile Leu Gly Leu Ala Ser Ser Ile Gly Leu
        35                  40                  45

Leu Thr Leu Ser Gly Trp Phe Leu Ala Ala Thr Ala Ile Ala Gly Phe
    50                  55                  60

Gly Ser Leu Phe Asn Phe Phe Tyr Pro Ser Ala Ser Val Arg Gly Leu
65                  70                  75                  80

Ala Ile Gly Arg Thr Val Ala Arg Tyr Leu Glu Lys Val Val Thr His
                85                  90                  95

Asp Ala Thr Phe Arg Val Leu Ala Lys Leu Arg Val Gln Val Phe Asp
            100                 105                 110

Lys Ile Ile Pro Leu Ser Pro Ala Leu Leu Asn Arg Tyr Arg Asn Ser
        115                 120                 125

Asp Leu Leu Asn Arg Leu Val Ala Asp Val Asp Thr Leu Asp Ser Leu
    130                 135                 140

Tyr Leu Arg Leu Ile Ala Pro Phe Ile Ser Ala Ile Val Val Ile Ala
145                 150                 155                 160

Phe Ile Thr Phe Gly Leu Ser Phe Ile Asn Ala Pro Leu Ala Leu Phe
                165                 170                 175

Ile Gly Phe Thr Leu Leu Ala Leu Leu Leu Val Ile Pro Thr Ile Phe
            180                 185                 190

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

Leu Tyr Arg Thr Gln Phe Ile Glu Phe Ile Gln Ala Gln Ala Glu Leu
    210                 215                 220

Leu Leu
225
```

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<210>  151
<211>  323
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(321)

<400>  151
cct tcc aaa ttg acg tta gct ctt gct att gca agt ggc tta agt gta       48
Pro Ser Lys Leu Thr Leu Ala Leu Ala Ile Ala Ser Gly Leu Ser Val
1               5                   10                  15

aca aat tta agc tat gcc act aac gat act att caa gcg ggc aac ggc       96
Thr Asn Leu Ser Tyr Ala Thr Asn Asp Thr Ile Gln Ala Gly Asn Gly
            20                  25                  30

att gcc gtg gta caa acc caa tcg ggt gaa atc caa ggt tat att cat      144
Ile Ala Val Val Gln Thr Gln Ser Gly Glu Ile Gln Gly Tyr Ile His
        35                  40                  45

aac gat att ttg acc tat aaa ggc att ccg tat gcc aca gca gaa cgt      192
Asn Asp Ile Leu Thr Tyr Lys Gly Ile Pro Tyr Ala Thr Ala Glu Arg
    50                  55                  60

ttt atg cca cca aaa ccg gtg gag aat tgg caa ggg aca aaa atg gcg      240
Phe Met Pro Pro Lys Pro Val Glu Asn Trp Gln Gly Thr Lys Met Ala
65                  70                  75                  80

ttg act tat ggc gat gtc tgc ccg caa gtg ccg atg ggc ggt cgt agt      288
Leu Thr Tyr Gly Asp Val Cys Pro Gln Val Pro Met Gly Gly Arg Ser
                85                  90                  95

ttc ttc ttt acc gga cct gaa atg acg gaa agt ga                       323
Phe Phe Phe Thr Gly Pro Glu Met Thr Glu Ser
            100                 105


<210>  152
<211>  107
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  152

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


Thr Asn Leu Ser Tyr Ala Thr Asn Asp Thr Ile Gln Ala Gly Asn Gly
            20                  25                  30


Ile Ala Val Val Gln Thr Gln Ser Gly Glu Ile Gln Gly Tyr Ile His
        35                  40                  45


Asn Asp Ile Leu Thr Tyr Lys Gly Ile Pro Tyr Ala Thr Ala Glu Arg
```

```
    50                  55                  60

Phe Met Pro Pro Lys Pro Val Glu Asn Trp Gln Gly Thr Lys Met Ala
65                  70                  75                  80

Leu Thr Tyr Gly Asp Val Cys Pro Gln Val Pro Met Gly Gly Arg Ser
                85                  90                  95

Phe Phe Phe Thr Gly Pro Glu Met Thr Glu Ser
            100                 105


<210>  153
<211>  177
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(177)

<400>  153
ggc ggc ggt gcc tgg gtt cag gcg gat ttg aag atg ttc caa atg cac        48
Gly Gly Gly Ala Trp Val Gln Ala Asp Leu Lys Met Phe Gln Met His
1               5                   10                  15

agg atg tcg ttt ggt tca tcg gtg gcc gcg caa aat acc ttg aac gtg        96
Arg Met Ser Phe Gly Ser Ser Val Ala Ala Gln Asn Thr Leu Asn Val
            20                  25                  30

gtt gat att tac gcc gtg tca ctc aaa acc atc caa tgt cag ctg aaa       144
Val Asp Ile Tyr Ala Val Ser Leu Lys Thr Ile Gln Cys Gln Leu Lys
        35                  40                  45

gcc att gtg aca gat ttt gat att tcg cac ctt                           177
Ala Ile Val Thr Asp Phe Asp Ile Ser His Leu
    50                  55


<210>  154
<211>  59
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  154

Gly Gly Gly Ala Trp Val Gln Ala Asp Leu Lys Met Phe Gln Met His
1               5                   10                  15

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

Val Asp Ile Tyr Ala Val Ser Leu Lys Thr Ile Gln Cys Gln Leu Lys
        35                  40                  45
```

```
Ala Ile Val Thr Asp Phe Asp Ile Ser His Leu
    50                  55


<210>  155
<211>  469
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(468)

<400>  155
atg gag aaa aaa caa acc tca cgg gta caa aaa ctg gaa ttt ttg ctc        48
Met Glu Lys Lys Gln Thr Ser Arg Val Gln Lys Leu Glu Phe Leu Leu
1               5                   10                  15

aaa caa aca gat aaa atc cat ctg cgc gac gcg gca caa atg ctt gat        96
Lys Gln Thr Asp Lys Ile His Leu Arg Asp Ala Ala Gln Met Leu Asp
            20                  25                  30

gtg tcg gaa atg act tta cgt cgg gat tta agt tcc gac agc ggc aat       144
Val Ser Glu Met Thr Leu Arg Arg Asp Leu Ser Ser Asp Ser Gly Asn
        35                  40                  45

gtg gtg tta ttg ggc ggc tat atc gtg atg aac cca caa aaa agc ggc       192
Val Val Leu Leu Gly Gly Tyr Ile Val Met Asn Pro Gln Lys Ser Gly
    50                  55                  60

aat cat tat cag att ttt gac caa caa acg cgc cac att acg gaa aaa       240
Asn His Tyr Gln Ile Phe Asp Gln Gln Thr Arg His Ile Thr Glu Lys
65                  70                  75                  80

atg tgg ctc ggt aaa ctc gcc gcc aat ctc gtc aag gac gga gat acc       288
Met Trp Leu Gly Lys Leu Ala Ala Asn Leu Val Lys Asp Gly Asp Thr
                85                  90                  95

gtg ttc ttc gat tgc ggt agc acc att ccg ttt atc att tcg caa atc       336
Val Phe Phe Asp Cys Gly Ser Thr Ile Pro Phe Ile Ile Ser Gln Ile
            100                 105                 110

gat ccg cag ata aaa ttc acc gca ctt ttt tgc tcc atc aat agt ttt       384
Asp Pro Gln Ile Lys Phe Thr Ala Leu Phe Cys Ser Ile Asn Ser Phe
        115                 120                 125

atg gcg ttg cag gac aaa ccg cac tgc gaa gtg att ctg tgc ggc gga       432
Met Ala Leu Gln Asp Lys Pro His Cys Glu Val Ile Leu Cys Gly Gly
    130                 135                 140

cat tat tcg cgc cac aat tct ttc ctg act tcc gtg c                     469
His Tyr Ser Arg His Asn Ser Phe Leu Thr Ser Val
145                 150                 155


<210>  156
<211>  156
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  156
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Met Glu Lys Lys Gln Thr Ser Arg Val Gln Lys Leu Glu Phe Leu Leu
1               5                   10                  15

Lys Gln Thr Asp Lys Ile His Leu Arg Asp Ala Ala Gln Met Leu Asp
            20                  25                  30

Val Ser Glu Met Thr Leu Arg Arg Asp Leu Ser Ser Asp Ser Gly Asn
        35                  40                  45

Val Val Leu Leu Gly Gly Tyr Ile Val Met Asn Pro Gln Lys Ser Gly
    50                  55                  60

Asn His Tyr Gln Ile Phe Asp Gln Gln Thr Arg His Ile Thr Glu Lys
65                  70                  75                  80

Met Trp Leu Gly Lys Leu Ala Ala Asn Leu Val Lys Asp Gly Asp Thr
                85                  90                  95

Val Phe Phe Asp Cys Gly Ser Thr Ile Pro Phe Ile Ile Ser Gln Ile
            100                 105                 110

Asp Pro Gln Ile Lys Phe Thr Ala Leu Phe Cys Ser Ile Asn Ser Phe
        115                 120                 125

Met Ala Leu Gln Asp Lys Pro His Cys Glu Val Ile Leu Cys Gly Gly
    130                 135                 140

His Tyr Ser Arg His Asn Ser Phe Leu Thr Ser Val
145                 150                 155


<210>  157
<211>  340
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(339)

<400>  157
atg aca tat cca ggt gga aaa ggt aaa tgt ttc caa aaa atc att aat         48
Met Thr Tyr Pro Gly Gly Lys Gly Lys Cys Phe Gln Lys Ile Ile Asn
1               5                   10                  15

tta atg cct ccg cat gac gta tat att gaa act cat ctt ggt agt ggt         96
Leu Met Pro Pro His Asp Val Tyr Ile Glu Thr His Leu Gly Ser Gly
            20                  25                  30

gca gta cta cga aat aaa aaa cca gca cta aaa aat att gga ata gat        144
Ala Val Leu Arg Asn Lys Lys Pro Ala Leu Lys Asn Ile Gly Ile Asp
```

```
        35                  40                  45

cta gat ttt gat gtt att caa tca tgg att ggt tat tct cct gaa aat       192
Leu Asp Phe Asp Val Ile Gln Ser Trp Ile Gly Tyr Ser Pro Glu Asn
    50                  55                  60

cat aag ttt ttt aat aat gat gca ttg gcg ttt cta act aag tac ctg       240
His Lys Phe Phe Asn Asn Asp Ala Leu Ala Phe Leu Thr Lys Tyr Leu
65                  70                  75                  80

ttt act ggg aaa gag tta gta tat tgt gat cct cca tat gtt ctt tca       288
Phe Thr Gly Lys Glu Leu Val Tyr Cys Asp Pro Pro Tyr Val Leu Ser
                85                  90                  95

act aga aga aga caa aaa ata tat aaa tat gaa tac act gat gag cag       336
Thr Arg Arg Arg Gln Lys Ile Tyr Lys Tyr Glu Tyr Thr Asp Glu Gln
            100                 105                 110

cat g                                                                 340
His


<210>  158
<211>  113
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  158

Met Thr Tyr Pro Gly Gly Lys Gly Lys Cys Phe Gln Lys Ile Ile Asn
1               5                   10                  15


Leu Met Pro Pro His Asp Val Tyr Ile Glu Thr His Leu Gly Ser Gly
            20                  25                  30


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


Leu Asp Phe Asp Val Ile Gln Ser Trp Ile Gly Tyr Ser Pro Glu Asn
    50                  55                  60


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


Phe Thr Gly Lys Glu Leu Val Tyr Cys Asp Pro Pro Tyr Val Leu Ser
                85                  90                  95


Thr Arg Arg Arg Gln Lys Ile Tyr Lys Tyr Glu Tyr Thr Asp Glu Gln
            100                 105                 110


His
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<210>  159
<211>  771
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(771)

<400>  159
atc gac gct ttt ttc tct cgc caa aac aat caa ttt cac ttg gaa caa          48
Ile Asp Ala Phe Phe Ser Arg Gln Asn Asn Gln Phe His Leu Glu Gln
1               5                   10                  15

caa agc cat tgc gtt aac caa att atc gag caa tgg cgt tat aac ggg          96
Gln Ser His Cys Val Asn Gln Ile Ile Glu Gln Trp Arg Tyr Asn Gly
            20                  25                  30

caa att atc ggg cgt gaa att ccg caa ttt gtc gcc gaa cag aaa aac         144
Gln Ile Ile Gly Arg Glu Ile Pro Gln Phe Val Ala Glu Gln Lys Asn
        35                  40                  45

caa caa ggc ttg gca gtg cgt gtc acc tgc ccc gag caa acc tct ctt         192
Gln Gln Gly Leu Ala Val Arg Val Thr Cys Pro Glu Gln Thr Ser Leu
    50                  55                  60

tta gcg gaa ttt aac aat caa ccg gtg aac gat gcc ctt caa acg gca         240
Leu Ala Glu Phe Asn Asn Gln Pro Val Asn Asp Ala Leu Gln Thr Ala
65                  70                  75                  80

gaa aag tgc ggt gta tct ttt gag agt ttt cat att gtg gcg gaa gat         288
Glu Lys Cys Gly Val Ser Phe Glu Ser Phe His Ile Val Ala Glu Asp
                85                  90                  95

ctc aat tct gaa atc acc gcc acg gaa aca ccc gct tgg caa ctg ctc         336
Leu Asn Ser Glu Ile Thr Ala Thr Glu Thr Pro Ala Trp Gln Leu Leu
            100                 105                 110

tac acc acc tat ttg cag tct tgt tct ccc ctg caa agc ggt gaa tcc         384
Tyr Thr Thr Tyr Leu Gln Ser Cys Ser Pro Leu Gln Ser Gly Glu Ser
        115                 120                 125

ctg caa ccg att ccg ctg tat aaa caa ctg aaa aac ata ccg cac tta         432
Leu Gln Pro Ile Pro Leu Tyr Lys Gln Leu Lys Asn Ile Pro His Leu
    130                 135                 140

gca atg gat ttg gtt aaa tgg cag gaa aat tgg cag gcg tgc gat caa         480
Ala Met Asp Leu Val Lys Trp Gln Glu Asn Trp Gln Ala Cys Asp Gln
145                 150                 155                 160

ttg caa atg aac ggt tcc gtg ttg gaa caa cag gct ttg gtg caa att         528
Leu Gln Met Asn Gly Ser Val Leu Glu Gln Gln Ala Leu Val Gln Ile
                165                 170                 175

tca gac acc caa agc acg ctg ttt aag cat ggt tac cat cta acg cag         576
Ser Asp Thr Gln Ser Thr Leu Phe Lys His Gly Tyr His Leu Thr Gln
            180                 185                 190

gaa att gag cga cac agc ggc att cct act tac tat tat tta tac cgc         624
Glu Ile Glu Arg His Ser Gly Ile Pro Thr Tyr Tyr Tyr Leu Tyr Arg
```

```
        195                 200                 205

atc ggt gga aaa agc tgt gaa gcg gag ctg caa tca cgc tgt ccg tta      672
Ile Gly Gly Lys Ser Cys Glu Ala Glu Leu Gln Ser Arg Cys Pro Leu
    210                 215                 220

tgt aaa aga aaa tgg acg tta agc cac ccg ctt ttt gac ttc tta tat      720
Cys Lys Arg Lys Trp Thr Leu Ser His Pro Leu Phe Asp Phe Leu Tyr
225                 230                 235                 240

ttt aaa tgt gat cat tgt cgc ctc gtt tca aac ctc tca tgg cat tgg      768
Phe Lys Cys Asp His Cys Arg Leu Val Ser Asn Leu Ser Trp His Trp
                245                 250                 255

caa                                                                  771
Gln


<210>  160
<211>  257
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  160

Ile Asp Ala Phe Phe Ser Arg Gln Asn Asn Gln Phe His Leu Glu Gln
1               5                   10                  15


Gln Ser His Cys Val Asn Gln Ile Ile Glu Gln Trp Arg Tyr Asn Gly
            20                  25                  30


Gln Ile Ile Gly Arg Glu Ile Pro Gln Phe Val Ala Glu Gln Lys Asn
        35                  40                  45


Gln Gln Gly Leu Ala Val Arg Val Thr Cys Pro Glu Gln Thr Ser Leu
    50                  55                  60


Leu Ala Glu Phe Asn Asn Gln Pro Val Asn Asp Ala Leu Gln Thr Ala
65                  70                  75                  80


Glu Lys Cys Gly Val Ser Phe Glu Ser Phe His Ile Val Ala Glu Asp
                85                  90                  95


Leu Asn Ser Glu Ile Thr Ala Thr Glu Thr Pro Ala Trp Gln Leu Leu
            100                 105                 110


Tyr Thr Thr Tyr Leu Gln Ser Cys Ser Pro Leu Gln Ser Gly Glu Ser
        115                 120                 125


Leu Gln Pro Ile Pro Leu Tyr Lys Gln Leu Lys Asn Ile Pro His Leu
    130                 135                 140
```

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Ala Met Asp Leu Val Lys Trp Gln Glu Asn Trp Gln Ala Cys Asp Gln
145                 150                 155                 160

Leu Gln Met Asn Gly Ser Val Leu Glu Gln Gln Ala Leu Val Gln Ile
                165                 170                 175

Ser Asp Thr Gln Ser Thr Leu Phe Lys His Gly Tyr His Leu Thr Gln
            180                 185                 190

Glu Ile Glu Arg His Ser Gly Ile Pro Thr Tyr Tyr Tyr Leu Tyr Arg
        195                 200                 205

Ile Gly Gly Lys Ser Cys Glu Ala Glu Leu Gln Ser Arg Cys Pro Leu
    210                 215                 220

Cys Lys Arg Lys Trp Thr Leu Ser His Pro Leu Phe Asp Phe Leu Tyr
225                 230                 235                 240

Phe Lys Cys Asp His Cys Arg Leu Val Ser Asn Leu Ser Trp His Trp
                245                 250                 255

Gln


<210>  161
<211>  330
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(330)

<400>  161
gag gcg gat aaa ttt aaa gtg gat att ccg tct atg gca aga ctg aga          48
Glu Ala Asp Lys Phe Lys Val Asp Ile Pro Ser Met Ala Arg Leu Arg
1               5                   10                  15

atc agc ccg aat atc gac atc agt gcg aca ccg aag ctg ttg gaa ctt          96
Ile Ser Pro Asn Ile Asp Ile Ser Ala Thr Pro Lys Leu Leu Glu Leu
            20                  25                  30

tcc ggc aat att gat att ccc tgg gcg cgc att gcc att gaa aac ctg         144
Ser Gly Asn Ile Asp Ile Pro Trp Ala Arg Ile Ala Ile Glu Asn Leu
        35                  40                  45

ccg gac agt gca gtg gcg gtc agc tcc gat gaa gtg att tta aat ggc         192
Pro Asp Ser Ala Val Ala Val Ser Ser Asp Glu Val Ile Leu Asn Gly
    50                  55                  60

aat aag aag agt act ctg ccg aaa aca ttg ccg agc gaa acc caa agc         240
Asn Lys Lys Ser Thr Leu Pro Lys Thr Leu Pro Ser Glu Thr Gln Ser
```

```
65                  70                  75                  80

ggc atg gca att cgt tct gat tta aga atc aat atc ggc gat gat gtc       288
Gly Met Ala Ile Arg Ser Asp Leu Arg Ile Asn Ile Gly Asp Asp Val
                85                  90                  95

agt tta aat gcc tat ggc ttg aaa acc cat ctc cac ggg ttg               330
Ser Leu Asn Ala Tyr Gly Leu Lys Thr His Leu His Gly Leu
            100                 105                 110


<210>  162
<211>  110
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  162

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


Ile Ser Pro Asn Ile Asp Ile Ser Ala Thr Pro Lys Leu Leu Glu Leu
            20                  25                  30


Ser Gly Asn Ile Asp Ile Pro Trp Ala Arg Ile Ala Ile Glu Asn Leu
        35                  40                  45


Pro Asp Ser Ala Val Ala Val Ser Ser Asp Glu Val Ile Leu Asn Gly
    50                  55                  60


Asn Lys Lys Ser Thr Leu Pro Lys Thr Leu Pro Ser Glu Thr Gln Ser
65                  70                  75                  80


Gly Met Ala Ile Arg Ser Asp Leu Arg Ile Asn Ile Gly Asp Asp Val
                85                  90                  95


Ser Leu Asn Ala Tyr Gly Leu Lys Thr His Leu His Gly Leu
            100                 105                 110


<210>  163
<211>  625
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(624)

<400>  163
gat aag aca gaa acg atg caa caa aat gaa gaa aaa atc acg ccg tca        48
Asp Lys Thr Glu Thr Met Gln Gln Asn Glu Glu Lys Ile Thr Pro Ser
1               5                   10                  15

gag caa aaa ccg atc gtg cat gaa acc gtt gtg gtg aag aaa acc ggt        96
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```
Glu Gln Lys Pro Ile Val His Glu Thr Val Val Val Lys Lys Thr Gly
            20                  25                  30

tcc gcg tta ggt ttg ctg gca ctt tta att gcg ttg ggt tta ggc ggc      144
Ser Ala Leu Gly Leu Leu Ala Leu Leu Ile Ala Leu Gly Leu Gly Gly
        35                  40                  45

gcg ggc tat tat ttc ggt cag cta cag gtt gac gaa ata cag caa aaa      192
Ala Gly Tyr Tyr Phe Gly Gln Leu Gln Val Asp Glu Ile Gln Gln Lys
    50                  55                  60

ctg acc gca ctt gaa aac caa ttg caa caa aaa ggc act tcc gcc gat      240
Leu Thr Ala Leu Glu Asn Gln Leu Gln Gln Lys Gly Thr Ser Ala Asp
65                  70                  75                  80

gtt gcc ggc atg ccg gat ttt agt gca gag aaa aat cag ctg gcg aaa      288
Val Ala Gly Met Pro Asp Phe Ser Ala Glu Lys Asn Gln Leu Ala Lys
                85                  90                  95

tta acg gaa ttt tcc caa gtg gca agt gat caa atc agc gcc ttg aat      336
Leu Thr Glu Phe Ser Gln Val Ala Ser Asp Gln Ile Ser Ala Leu Asn
            100                 105                 110

cag aat ttg tcc gcc aaa gaa caa agc ctg tcg gca ttg caa caa cag      384
Gln Asn Leu Ser Ala Lys Glu Gln Ser Leu Ser Ala Leu Gln Gln Gln
        115                 120                 125

gtg caa cgt ttg tcc aat caa gcc aaa gcg gag cag ccg aat gac tgg      432
Val Gln Arg Leu Ser Asn Gln Ala Lys Ala Glu Gln Pro Asn Asp Trp
    130                 135                 140

tta ctg acc gaa gcg gat ttt ctg tta aat aac gct ttg cgc aaa ctg      480
Leu Leu Thr Glu Ala Asp Phe Leu Leu Asn Asn Ala Leu Arg Lys Leu
145                 150                 155                 160

gtg ttg gat aac gac gtg gat acc agt gtg tcc ttg ttg aaa gtt gcc      528
Val Leu Asp Asn Asp Val Asp Thr Ser Val Ser Leu Leu Lys Val Ala
                165                 170                 175

gat gaa acc ctt tcc aaa gtc gcc atg cca caa gtg gcg cag gtg cgt      576
Asp Glu Thr Leu Ser Lys Val Ala Met Pro Gln Val Ala Gln Val Arg
            180                 185                 190

agc gcc att aac gcc gat tta aaa cag ttg ttg tcc ctg aac aat gtg g    625
Ser Ala Ile Asn Ala Asp Leu Lys Gln Leu Leu Ser Leu Asn Asn Val
        195                 200                 205


<210>  164
<211>  208
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  164

Asp Lys Thr Glu Thr Met Gln Gln Asn Glu Glu Lys Ile Thr Pro Ser
1               5                   10                  15


Glu Gln Lys Pro Ile Val His Glu Thr Val Val Val Lys Lys Thr Gly
            20                  25                  30
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```
Ser Ala Leu Gly Leu Leu Ala Leu Leu Ile Ala Leu Gly Leu Gly Gly
        35                  40                  45

Ala Gly Tyr Tyr Phe Gly Gln Leu Gln Val Asp Glu Ile Gln Gln Lys
    50                  55                  60

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

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

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

Gln Asn Leu Ser Ala Lys Glu Gln Ser Leu Ser Ala Leu Gln Gln Gln
        115                 120                 125

Val Gln Arg Leu Ser Asn Gln Ala Lys Ala Glu Gln Pro Asn Asp Trp
    130                 135                 140

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

Val Leu Asp Asn Asp Val Asp Thr Ser Val Ser Leu Leu Lys Val Ala
                165                 170                 175

Asp Glu Thr Leu Ser Lys Val Ala Met Pro Gln Val Ala Gln Val Arg
            180                 185                 190

Ser Ala Ile Asn Ala Asp Leu Lys Gln Leu Leu Ser Leu Asn Asn Val
        195                 200                 205


<210>  165
<211>  684
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(684)

<400>  165
atg acg att tta gtt ctg ggt atc aat cac aaa act gct tcc gtg gca       48
Met Thr Ile Leu Val Leu Gly Ile Asn His Lys Thr Ala Ser Val Ala
1               5                   10                  15

ttg cgg gaa aag gtg gcg ttt tcc gac gaa aag cgc act ttt gct ttg       96
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```
Leu Arg Glu Lys Val Ala Phe Ser Asp Glu Lys Arg Thr Phe Ala Leu
            20                  25                  30

cgt cac att caa caa acg cag ttg gcg gaa agt gcg gtg att tta tcc       144
Arg His Ile Gln Gln Thr Gln Leu Ala Glu Ser Ala Val Ile Leu Ser
        35                  40                  45

acc tgt aat cgc acg gaa gtt tat ctg cac aat aaa agc gtt ccg ccg       192
Thr Cys Asn Arg Thr Glu Val Tyr Leu His Asn Lys Ser Val Pro Pro
50                  55                  60

caa gag acg caa acc tgg atc aca ctg gcg gtg cag tgg ttt gcc ggc       240
Gln Glu Thr Gln Thr Trp Ile Thr Leu Ala Val Gln Trp Phe Ala Gly
65                  70                  75                  80

att cat caa cta gcg ttg gcg gag ctg cag cac tgt gtt tat act cac       288
Ile His Gln Leu Ala Leu Ala Glu Leu Gln His Cys Val Tyr Thr His
                85                  90                  95

gaa aat ctt cag gcg gcg aat cat tta atg gaa gtg gcg tgc ggt ttg       336
Glu Asn Leu Gln Ala Ala Asn His Leu Met Glu Val Ala Cys Gly Leu
            100                 105                 110

gat tcg ctg att tta ggc gaa ccg cag att ttg ggg cag gtg aag caa       384
Asp Ser Leu Ile Leu Gly Glu Pro Gln Ile Leu Gly Gln Val Lys Gln
        115                 120                 125

gcc tac cac atg agc gag cag cat tat caa cag gaa ggg caa acc att       432
Ala Tyr His Met Ser Glu Gln His Tyr Gln Gln Glu Gly Gln Thr Ile
    130                 135                 140

tcc ggc gaa cta tcc cgt tta ttc caa aaa acc ttt gct acc gct aaa       480
Ser Gly Glu Leu Ser Arg Leu Phe Gln Lys Thr Phe Ala Thr Ala Lys
145                 150                 155                 160

cgg gtg cgc acc gaa acc aac atc ggc gag agt gcg gtg tcc gtt gcc       528
Arg Val Arg Thr Glu Thr Asn Ile Gly Glu Ser Ala Val Ser Val Ala
                165                 170                 175

tat gcc gcc tgt agc cta gca cgt cag att ttt gaa tcc ctg cgt gac       576
Tyr Ala Ala Cys Ser Leu Ala Arg Gln Ile Phe Glu Ser Leu Arg Asp
            180                 185                 190

ttg acg att tta tta gtg ggc gca ggt gaa acc att gaa ctg gtg aac       624
Leu Thr Ile Leu Leu Val Gly Ala Gly Glu Thr Ile Glu Leu Val Asn
        195                 200                 205

cgc cat ttg tta cgt cac ggc gtg aaa aac tta ttt atc gcc aac cgt       672
Arg His Leu Leu Arg His Gly Val Lys Asn Leu Phe Ile Ala Asn Arg
    210                 215                 220

aca ttg gcg cgc                                                       684
Thr Leu Ala Arg
225


<210>  166
<211>  228
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans
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<400>  166

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

Leu Arg Glu Lys Val Ala Phe Ser Asp Glu Lys Arg Thr Phe Ala Leu
            20                  25                  30

Arg His Ile Gln Gln Thr Gln Leu Ala Glu Ser Ala Val Ile Leu Ser
        35                  40                  45

Thr Cys Asn Arg Thr Glu Val Tyr Leu His Asn Lys Ser Val Pro Pro
    50                  55                  60

Gln Glu Thr Gln Thr Trp Ile Thr Leu Ala Val Gln Trp Phe Ala Gly
65                  70                  75                  80

Ile His Gln Leu Ala Leu Ala Glu Leu Gln His Cys Val Tyr Thr His
                85                  90                  95

Glu Asn Leu Gln Ala Ala Asn His Leu Met Glu Val Ala Cys Gly Leu
            100                 105                 110

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

Ala Tyr His Met Ser Glu Gln His Tyr Gln Gln Glu Gly Gln Thr Ile
    130                 135                 140

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

Arg Val Arg Thr Glu Thr Asn Ile Gly Glu Ser Ala Val Ser Val Ala
                165                 170                 175

Tyr Ala Ala Cys Ser Leu Ala Arg Gln Ile Phe Glu Ser Leu Arg Asp
            180                 185                 190

Leu Thr Ile Leu Leu Val Gly Ala Gly Glu Thr Ile Glu Leu Val Asn
        195                 200                 205

Arg His Leu Leu Arg His Gly Val Lys Asn Leu Phe Ile Ala Asn Arg
    210                 215                 220

Thr Leu Ala Arg
225
```

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<210>  167
<211>  138
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(138)

<400>  167
atg cgc cgt tgg aag ctg aaa atc ttc cgc aaa atg aac cgc act ttg       48
Met Arg Arg Trp Lys Leu Lys Ile Phe Arg Lys Met Asn Arg Thr Leu
1               5                   10                  15

cgc gtt cgc ctt tcg ttc cca atg cac cga ttc gtg ccg gac ctt aat       96
Arg Val Arg Leu Ser Phe Pro Met His Arg Phe Val Pro Asp Leu Asn
            20                  25                  30

tta ttt aac ttc gat ctt tgt ata ttc cgt cgt tta att cgt              138
Leu Phe Asn Phe Asp Leu Cys Ile Phe Arg Arg Leu Ile Arg
        35                  40                  45


<210>  168
<211>  46
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  168

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


Arg Val Arg Leu Ser Phe Pro Met His Arg Phe Val Pro Asp Leu Asn
            20                  25                  30


Leu Phe Asn Phe Asp Leu Cys Ile Phe Arg Arg Leu Ile Arg
        35                  40                  45


<210>  169
<211>  1950
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(1950)

<400>  169
atg gct gat gta tta acc cgt ttc aac agt ggc aag ctt tgg gaa ttc       48
Met Ala Asp Val Leu Thr Arg Phe Asn Ser Gly Lys Leu Trp Glu Phe
1               5                   10                  15

gat ggc ggc att cat ccg ccc gac atg aaa tcc caa tcc aac cgc gcg       96
Asp Gly Gly Ile His Pro Pro Asp Met Lys Ser Gln Ser Asn Arg Ala
            20                  25                  30
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```
cct att cgt acc ttg ccg ttg ccc gat aat ttc tac gtt ctt ctg aaa       144
Pro Ile Arg Thr Leu Pro Leu Pro Asp Asn Phe Tyr Val Leu Leu Lys
        35                  40                  45

caa cac gcc ggc aca gcg ggc aat tta ttg gta aaa tgc ggc gat cat       192
Gln His Ala Gly Thr Ala Gly Asn Leu Leu Val Lys Cys Gly Asp His
    50                  55                  60

gtt ttg aaa ggt caa ccg ctc acc cag ggg gac ggt ttg cgt tcg ctg       240
Val Leu Lys Gly Gln Pro Leu Thr Gln Gly Asp Gly Leu Arg Ser Leu
65                  70                  75                  80

ccg gtt cat gcg cct act tca ggc acg gtc att gat gtg atg cct tat       288
Pro Val His Ala Pro Thr Ser Gly Thr Val Ile Asp Val Met Pro Tyr
                85                  90                  95

gtc acc gcc cat cct tcc ggt cta ccg gaa acc tgt gtg cat att aaa       336
Val Thr Ala His Pro Ser Gly Leu Pro Glu Thr Cys Val His Ile Lys
            100                 105                 110

gcg gat gga tta gat caa tgg cgc gag caa acc ccg ttg gag gat ttc       384
Ala Asp Gly Leu Asp Gln Trp Arg Glu Gln Thr Pro Leu Glu Asp Phe
        115                 120                 125

ctt agc caa acg ccg gaa cag tta atc gaa aaa att tat cag gcg ggc       432
Leu Ser Gln Thr Pro Glu Gln Leu Ile Glu Lys Ile Tyr Gln Ala Gly
    130                 135                 140

att gcc ggt ctg ggt ggc gcg gta ttc ccg acc gcg gca aaa att cat       480
Ile Ala Gly Leu Gly Gly Ala Val Phe Pro Thr Ala Ala Lys Ile His
145                 150                 155                 160

tcc gcc gag aaa cag gtg aaa tta ctg att att aac ggc gcg gaa tgt       528
Ser Ala Glu Lys Gln Val Lys Leu Leu Ile Ile Asn Gly Ala Glu Cys
                165                 170                 175

gaa cct tac att acc tgc gac gat cgc tta atg cat gat tat gct gat       576
Glu Pro Tyr Ile Thr Cys Asp Asp Arg Leu Met His Asp Tyr Ala Asp
            180                 185                 190

gaa att atc gaa ggc gtg cgt att ttg cgc tac att tta cgc cct gag       624
Glu Ile Ile Glu Gly Val Arg Ile Leu Arg Tyr Ile Leu Arg Pro Glu
        195                 200                 205

aaa gtg gtg atc gcc gtt gaa gat aat aaa cca aaa gcg gtg aaa tcc       672
Lys Val Val Ile Ala Val Glu Asp Asn Lys Pro Lys Ala Val Lys Ser
    210                 215                 220

ttg gaa cgc gcc tta cac ggc gcc aac gat att gaa atc cga gtg att       720
Leu Glu Arg Ala Leu His Gly Ala Asn Asp Ile Glu Ile Arg Val Ile
225                 230                 235                 240

ccg acc aaa tac cct tcc ggc gcg gca aaa cag tta att caa gtg ctg       768
Pro Thr Lys Tyr Pro Ser Gly Ala Ala Lys Gln Leu Ile Gln Val Leu
                245                 250                 255

acc ggc atg gag gta cct agc ggt caa cgc tcc tcc ggt atc ggc gtg       816
Thr Gly Met Glu Val Pro Ser Gly Gln Arg Ser Ser Gly Ile Gly Val
            260                 265                 270

ctg atg caa aac atc ggc acc gct ttt gct att aaa cgc gca gtg atg       864
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```
Leu Met Gln Asn Ile Gly Thr Ala Phe Ala Ile Lys Arg Ala Val Met
        275                 280                 285

gat gat gaa ccg ctg att gag cgc gtc gtc acc ctc acc ggt gat aaa        912
Asp Asp Glu Pro Leu Ile Glu Arg Val Val Thr Leu Thr Gly Asp Lys
    290                 295                 300

atc gcc gat aaa ggc aac tat tgg gcg cgt ttt gga acg ccg att tat        960
Ile Ala Asp Lys Gly Asn Tyr Trp Ala Arg Phe Gly Thr Pro Ile Tyr
305                 310                 315                 320

cac ttg ttg cgc gaa acg ggc tat caa tac gac gat cgt ttc ccg gtc       1008
His Leu Leu Arg Glu Thr Gly Tyr Gln Tyr Asp Asp Arg Phe Pro Val
                325                 330                 335

ttc atg ggc ggt ccg atg atg ggc ttt att ctg ccc gat tta aat gcg       1056
Phe Met Gly Gly Pro Met Met Gly Phe Ile Leu Pro Asp Leu Asn Ala
            340                 345                 350

ccg atg acc aaa gtg acc aac tgc ctg ttg gcg ccg gat cat ttt gaa       1104
Pro Met Thr Lys Val Thr Asn Cys Leu Leu Ala Pro Asp His Phe Glu
        355                 360                 365

tac gcc ccg ccg gaa gaa gaa aaa aat tgt att cgc tgt tct gcc tgt       1152
Tyr Ala Pro Pro Glu Glu Glu Lys Asn Cys Ile Arg Cys Ser Ala Cys
    370                 375                 380

tcc gat gcc tgc ccg gtg aaa ctc atg ccg cag caa ttg tat tgg ttt       1200
Ser Asp Ala Cys Pro Val Lys Leu Met Pro Gln Gln Leu Tyr Trp Phe
385                 390                 395                 400

gca cgc agc gaa gat cac gaa aaa tcg gaa gaa tat tcc ctc aaa gat       1248
Ala Arg Ser Glu Asp His Glu Lys Ser Glu Glu Tyr Ser Leu Lys Asp
                405                 410                 415

tgt att gaa tgc ggc gtg tgc gct tat gtt tgc cca agt cac att ccg       1296
Cys Ile Glu Cys Gly Val Cys Ala Tyr Val Cys Pro Ser His Ile Pro
            420                 425                 430

tta att caa tat ttc cgc cgg gaa aaa gct aaa atc tgg gaa atc aaa       1344
Leu Ile Gln Tyr Phe Arg Arg Glu Lys Ala Lys Ile Trp Glu Ile Lys
        435                 440                 445

cac aaa gcc aaa ttg gcg gaa gaa gct aaa ata cgt ttt gaa caa cgc       1392
His Lys Ala Lys Leu Ala Glu Glu Ala Lys Ile Arg Phe Glu Gln Arg
    450                 455                 460

caa gcc cgt ttg gaa cgg gaa gaa cag gaa cgc aaa gat cgc tca caa       1440
Gln Ala Arg Leu Glu Arg Glu Glu Gln Glu Arg Lys Asp Arg Ser Gln
465                 470                 475                 480

cgt gct gca gcc gcc cgt cgt gaa gaa ttg gcg caa caa aaa ggc gtg       1488
Arg Ala Ala Ala Ala Arg Arg Glu Glu Leu Ala Gln Gln Lys Gly Val
                485                 490                 495

gat ccg gtg gct gcc gcc tta gcg cgc tta aaa gcg aaa aaa gcc gaa       1536
Asp Pro Val Ala Ala Ala Leu Ala Arg Leu Lys Ala Lys Lys Ala Glu
            500                 505                 510

acg acg gaa gct acg cag gca gaa cag aaa acc att gtt gac gaa aaa       1584
Thr Thr Glu Ala Thr Gln Ala Glu Gln Lys Thr Ile Val Asp Glu Lys
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        515                 520                 525

ggt cat atc ctg cct gac aac agc gac atc atg gca caa cgc aaa gcc        1632
Gly His Ile Leu Pro Asp Asn Ser Asp Ile Met Ala Gln Arg Lys Ala
    530                 535                 540

cgt cgt tta gcc cgt cag gcg gaa gcg gca cac tcg ccg tcg cag aaa        1680
Arg Arg Leu Ala Arg Gln Ala Glu Ala Ala His Ser Pro Ser Gln Lys
545                 550                 555                 560

aca gaa aaa acg cta gaa aaa acg cta gaa aaa acc acc gca ctt gag        1728
Thr Glu Lys Thr Leu Glu Lys Thr Leu Glu Lys Thr Thr Ala Leu Glu
                565                 570                 575

gat aaa aaa tct acc gtt gcc gcc gcc att gcc cgt gcg aaa gcc aag        1776
Asp Lys Lys Ser Thr Val Ala Ala Ala Ile Ala Arg Ala Lys Ala Lys
            580                 585                 590

aaa gcg gcg cag caa acg gaa gcc gtc gaa gca aac gaa cct gaa acg        1824
Lys Ala Ala Gln Gln Thr Glu Ala Val Glu Ala Asn Glu Pro Glu Thr
        595                 600                 605

gca aaa agt gcg gtc aat att tcc ggt gaa aat ggc gca gag aac gat        1872
Ala Lys Ser Ala Val Asn Ile Ser Gly Glu Asn Gly Ala Glu Asn Asp
    610                 615                 620

ccg cgc aaa gcc gct gtt gcc gcc gct att gcc cgt gcg aaa gcg aag        1920
Pro Arg Lys Ala Ala Val Ala Ala Ala Ile Ala Arg Ala Lys Ala Lys
625                 630                 635                 640

aaa gcc caa cgt gaa aac acg caa caa gat                                1950
Lys Ala Gln Arg Glu Asn Thr Gln Gln Asp
                645                 650


<210>  170
<211>  650
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  170

Met Ala Asp Val Leu Thr Arg Phe Asn Ser Gly Lys Leu Trp Glu Phe
1               5                   10                  15


Asp Gly Gly Ile His Pro Pro Asp Met Lys Ser Gln Ser Asn Arg Ala
            20                  25                  30


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


Gln His Ala Gly Thr Ala Gly Asn Leu Leu Val Lys Cys Gly Asp His
    50                  55                  60


Val Leu Lys Gly Gln Pro Leu Thr Gln Gly Asp Gly Leu Arg Ser Leu
65                  70                  75                  80
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Pro Val His Ala Pro Thr Ser Gly Thr Val Ile Asp Val Met Pro Tyr
                85                  90                  95

Val Thr Ala His Pro Ser Gly Leu Pro Glu Thr Cys Val His Ile Lys
            100                 105                 110

Ala Asp Gly Leu Asp Gln Trp Arg Glu Gln Thr Pro Leu Glu Asp Phe
        115                 120                 125

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

Ile Ala Gly Leu Gly Gly Ala Val Phe Pro Thr Ala Ala Lys Ile His
145                 150                 155                 160

Ser Ala Glu Lys Gln Val Lys Leu Leu Ile Ile Asn Gly Ala Glu Cys
                165                 170                 175

Glu Pro Tyr Ile Thr Cys Asp Asp Arg Leu Met His Asp Tyr Ala Asp
            180                 185                 190

Glu Ile Ile Glu Gly Val Arg Ile Leu Arg Tyr Ile Leu Arg Pro Glu
        195                 200                 205

Lys Val Val Ile Ala Val Glu Asp Asn Lys Pro Lys Ala Val Lys Ser
    210                 215                 220

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

Pro Thr Lys Tyr Pro Ser Gly Ala Ala Lys Gln Leu Ile Gln Val Leu
                245                 250                 255

Thr Gly Met Glu Val Pro Ser Gly Gln Arg Ser Ser Gly Ile Gly Val
            260                 265                 270

Leu Met Gln Asn Ile Gly Thr Ala Phe Ala Ile Lys Arg Ala Val Met
        275                 280                 285

Asp Asp Glu Pro Leu Ile Glu Arg Val Val Thr Leu Thr Gly Asp Lys
    290                 295                 300

Ile Ala Asp Lys Gly Asn Tyr Trp Ala Arg Phe Gly Thr Pro Ile Tyr
305                 310                 315                 320
```

```
His Leu Leu Arg Glu Thr Gly Tyr Gln Tyr Asp Asp Arg Phe Pro Val
                325                 330                 335

Phe Met Gly Gly Pro Met Met Gly Phe Ile Leu Pro Asp Leu Asn Ala
            340                 345                 350

Pro Met Thr Lys Val Thr Asn Cys Leu Leu Ala Pro Asp His Phe Glu
        355                 360                 365

Tyr Ala Pro Pro Glu Glu Glu Lys Asn Cys Ile Arg Cys Ser Ala Cys
    370                 375                 380

Ser Asp Ala Cys Pro Val Lys Leu Met Pro Gln Gln Leu Tyr Trp Phe
385                 390                 395                 400

Ala Arg Ser Glu Asp His Glu Lys Ser Glu Glu Tyr Ser Leu Lys Asp
                405                 410                 415

Cys Ile Glu Cys Gly Val Cys Ala Tyr Val Cys Pro Ser His Ile Pro
            420                 425                 430

Leu Ile Gln Tyr Phe Arg Arg Glu Lys Ala Lys Ile Trp Glu Ile Lys
        435                 440                 445

His Lys Ala Lys Leu Ala Glu Glu Ala Lys Ile Arg Phe Glu Gln Arg
    450                 455                 460

Gln Ala Arg Leu Glu Arg Glu Glu Gln Glu Arg Lys Asp Arg Ser Gln
465                 470                 475                 480

Arg Ala Ala Ala Ala Arg Arg Glu Glu Leu Ala Gln Gln Lys Gly Val
                485                 490                 495

Asp Pro Val Ala Ala Ala Leu Ala Arg Leu Lys Ala Lys Lys Ala Glu
            500                 505                 510

Thr Thr Glu Ala Thr Gln Ala Glu Gln Lys Thr Ile Val Asp Glu Lys
        515                 520                 525

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

Arg Arg Leu Ala Arg Gln Ala Glu Ala Ala His Ser Pro Ser Gln Lys
545                 550                 555                 560

Thr Glu Lys Thr Leu Glu Lys Thr Leu Glu Lys Thr Thr Ala Leu Glu
```

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                565                 570                 575

Asp Lys Lys Ser Thr Val Ala Ala Ala Ile Ala Arg Ala Lys Ala Lys
            580                 585                 590

Lys Ala Ala Gln Gln Thr Glu Ala Val Glu Ala Asn Glu Pro Glu Thr
        595                 600                 605

Ala Lys Ser Ala Val Asn Ile Ser Gly Glu Asn Gly Ala Glu Asn Asp
    610                 615                 620

Pro Arg Lys Ala Ala Val Ala Ala Ala Ile Ala Arg Ala Lys Ala Lys
625                 630                 635                 640

Lys Ala Gln Arg Glu Asn Thr Gln Gln Asp
                645                 650


<210>  171
<211>  525
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(525)

<400>  171
atg aag ttt aaa acg cta ctt ggc gcg ctc tta ttg agc gtg ttt tcc         48
Met Lys Phe Lys Thr Leu Leu Gly Ala Leu Leu Leu Ser Val Phe Ser
1               5                   10                  15

act tcc gtt tgg gct gat cgc gtg att acc gat caa ctt gat cga caa         96
Thr Ser Val Trp Ala Asp Arg Val Ile Thr Asp Gln Leu Asp Arg Gln
            20                  25                  30

gtg acc atc ccc gac cat att cat cgc gct gtg ata tta cag cac cag        144
Val Thr Ile Pro Asp His Ile His Arg Ala Val Ile Leu Gln His Gln
        35                  40                  45

acc tta aat ctc gcg gtg caa ctg gat gcc acc aaa caa att gcg ggc        192
Thr Leu Asn Leu Ala Val Gln Leu Asp Ala Thr Lys Gln Ile Ala Gly
    50                  55                  60

gtg ctt tcc aac tgg caa aaa cag ctg ggc aaa gac ttc gtg cgc ctt        240
Val Leu Ser Asn Trp Gln Lys Gln Leu Gly Lys Asp Phe Val Arg Leu
65                  70                  75                  80

gcg ccg gaa ttg gca aat tta ccg atg ccc ggt gat ttg aat acg gtc        288
Ala Pro Glu Leu Ala Asn Leu Pro Met Pro Gly Asp Leu Asn Thr Val
                85                  90                  95

aat att gaa agc cta atg gaa atc aaa ccg gat gtt gtt ttc gtg acc        336
Asn Ile Glu Ser Leu Met Glu Ile Lys Pro Asp Val Val Phe Val Thr
            100                 105                 110
```

```
aat tac gcg ccg aaa gaa atg att gaa aaa atc agc caa atg aac gtg       384
Asn Tyr Ala Pro Lys Glu Met Ile Glu Lys Ile Ser Gln Met Asn Val
        115                 120                 125

ccg gtg att gcc att tcg tta cgc agc ggc gat aaa acc gaa caa agc       432
Pro Val Ile Ala Ile Ser Leu Arg Ser Gly Asp Lys Thr Glu Gln Ser
    130                 135                 140

aaa ctc aac ccg acc ctt gcc gat gaa aac aat gcc tac aac gaa ggg       480
Lys Leu Asn Pro Thr Leu Ala Asp Glu Asn Asn Ala Tyr Asn Glu Gly
145                 150                 155                 160

tta aaa cgc ggg att gaa att att gcc gat gtt ttt gat aaa aaa           525
Leu Lys Arg Gly Ile Glu Ile Ile Ala Asp Val Phe Asp Lys Lys
                165                 170                 175


<210>  172
<211>  175
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  172

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


Thr Ser Val Trp Ala Asp Arg Val Ile Thr Asp Gln Leu Asp Arg Gln
            20                  25                  30


Val Thr Ile Pro Asp His Ile His Arg Ala Val Ile Leu Gln His Gln
        35                  40                  45


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


Val Leu Ser Asn Trp Gln Lys Gln Leu Gly Lys Asp Phe Val Arg Leu
65                  70                  75                  80


Ala Pro Glu Leu Ala Asn Leu Pro Met Pro Gly Asp Leu Asn Thr Val
                85                  90                  95


Asn Ile Glu Ser Leu Met Glu Ile Lys Pro Asp Val Val Phe Val Thr
            100                 105                 110


Asn Tyr Ala Pro Lys Glu Met Ile Glu Lys Ile Ser Gln Met Asn Val
        115                 120                 125


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


Lys Leu Asn Pro Thr Leu Ala Asp Glu Asn Asn Ala Tyr Asn Glu Gly
```

```
145                 150                 155                 160

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


<210>  173
<211>  391
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(390)

<400>  173
atg gcg gag ttg gtg tat aaa ccg ctt gag caa cct gtg gaa gca cca       48
Met Ala Glu Leu Val Tyr Lys Pro Leu Glu Gln Pro Val Glu Ala Pro
1               5                   10                  15

aat ccg aat cta aaa att gaa gcg gta aac gaa cag ttt gcg gca aaa       96
Asn Pro Asn Leu Lys Ile Glu Ala Val Asn Glu Gln Phe Ala Ala Lys
            20                  25                  30

tac ccg aaa caa ttt gcg tct tgg aaa gcc acc gaa aaa ggc gac aag      144
Tyr Pro Lys Gln Phe Ala Ser Trp Lys Ala Thr Glu Lys Gly Asp Lys
        35                  40                  45

att att tat gca gat gag gaa aat cca cgt tta atc ata tta tgg ggc      192
Ile Ile Tyr Ala Asp Glu Glu Asn Pro Arg Leu Ile Ile Leu Trp Gly
    50                  55                  60

ggt tat gcc ttt gcg aaa gaa tat aac gca ccg cgc gga cac att tat      240
Gly Tyr Ala Phe Ala Lys Glu Tyr Asn Ala Pro Arg Gly His Ile Tyr
65                  70                  75                  80

gcc att aaa gat tta cgc aat att ttg cgt acc ggt gcg ccg aaa acc      288
Ala Ile Lys Asp Leu Arg Asn Ile Leu Arg Thr Gly Ala Pro Lys Thr
                85                  90                  95

gct aac gac ggt cca caa ccg atg gcg tgt tgg acc tgt aaa ggt ccg      336
Ala Asn Asp Gly Pro Gln Pro Met Ala Cys Trp Thr Cys Lys Gly Pro
            100                 105                 110

gat gtg ccg cgt tta atc gcc gaa tgg gga gaa gaa ggc tat ttc aat      384
Asp Val Pro Arg Leu Ile Ala Glu Trp Gly Glu Glu Gly Tyr Phe Asn
        115                 120                 125

ggt aaa t                                                            391
Gly Lys
    130


<210>  174
<211>  130
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  174
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Met Ala Glu Leu Val Tyr Lys Pro Leu Glu Gln Pro Val Glu Ala Pro
1               5                   10                  15

Asn Pro Asn Leu Lys Ile Glu Ala Val Asn Glu Gln Phe Ala Ala Lys
            20                  25                  30

Tyr Pro Lys Gln Phe Ala Ser Trp Lys Ala Thr Glu Lys Gly Asp Lys
        35                  40                  45

Ile Ile Tyr Ala Asp Glu Glu Asn Pro Arg Leu Ile Ile Leu Trp Gly
    50                  55                  60

Gly Tyr Ala Phe Ala Lys Glu Tyr Asn Ala Pro Arg Gly His Ile Tyr
65                  70                  75                  80

Ala Ile Lys Asp Leu Arg Asn Ile Leu Arg Thr Gly Ala Pro Lys Thr
                85                  90                  95

Ala Asn Asp Gly Pro Gln Pro Met Ala Cys Trp Thr Cys Lys Gly Pro
            100                 105                 110

Asp Val Pro Arg Leu Ile Ala Glu Trp Gly Glu Glu Gly Tyr Phe Asn
        115                 120                 125

Gly Lys
    130


<210>  175
<211>  540
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(540)

<400>  175
aaa gcc atg ccg gca tta gac tta aat aaa gac ggc aaa atc caa tat        48
Lys Ala Met Pro Ala Leu Asp Leu Asn Lys Asp Gly Lys Ile Gln Tyr
1               5                   10                  15

gtg tta tta aaa ggc gaa ccg ggc cac cct gat gcg gaa gca cgt acc        96
Val Leu Leu Lys Gly Glu Pro Gly His Pro Asp Ala Glu Ala Arg Thr
            20                  25                  30

aag tat gtg att gag caa cta aac gcg caa ggc att cca acg gaa caa       144
Lys Tyr Val Ile Glu Gln Leu Asn Ala Gln Gly Ile Pro Thr Glu Gln
        35                  40                  45

ctc ttt atc gac acc ggg atg tgg gat gcg gca ctg gca aaa gac aaa       192
Leu Phe Ile Asp Thr Gly Met Trp Asp Ala Ala Leu Ala Lys Asp Lys
    50                  55                  60
```

```
atg gat gcg tgg tta tcc agc tct aaa gcc aat gac att gaa gtc att         240
Met Asp Ala Trp Leu Ser Ser Ser Lys Ala Asn Asp Ile Glu Val Ile
65                  70                  75                  80

att tcc aac aac gac ggc atg gcg atg ggc gca ttg gaa gca acc aaa         288
Ile Ser Asn Asn Asp Gly Met Ala Met Gly Ala Leu Glu Ala Thr Lys
                85                  90                  95

gca cac ggc aaa aaa tta ccg att ttc ggg gta gat gcg ttg cct gaa         336
Ala His Gly Lys Lys Leu Pro Ile Phe Gly Val Asp Ala Leu Pro Glu
            100                 105                 110

gta tta caa ctc atc aag aaa ggc gac att gca ggt acc gta ttg aat         384
Val Leu Gln Leu Ile Lys Lys Gly Asp Ile Ala Gly Thr Val Leu Asn
        115                 120                 125

gac ggc gcg act caa ggt aaa gcg att gtg gat tta tcc aac aac ctg         432
Asp Gly Ala Thr Gln Gly Lys Ala Ile Val Asp Leu Ser Asn Asn Leu
    130                 135                 140

gca aac ggc aaa ccg gct acc gaa ggc acc aaa tgg gag ctt aaa gat         480
Ala Asn Gly Lys Pro Ala Thr Glu Gly Thr Lys Trp Glu Leu Lys Asp
145                 150                 155                 160

cgc gtt gtg cgc att cct tat gtt ggc gta gat aaa gac aac ttg tct         528
Arg Val Val Arg Ile Pro Tyr Val Gly Val Asp Lys Asp Asn Leu Ser
                165                 170                 175

caa ttc tta aaa                                                         540
Gln Phe Leu Lys
            180


<210>  176
<211>  180
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  176

Lys Ala Met Pro Ala Leu Asp Leu Asn Lys Asp Gly Lys Ile Gln Tyr
1               5                   10                  15


Val Leu Leu Lys Gly Glu Pro Gly His Pro Asp Ala Glu Ala Arg Thr
            20                  25                  30


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


Leu Phe Ile Asp Thr Gly Met Trp Asp Ala Ala Leu Ala Lys Asp Lys
    50                  55                  60


Met Asp Ala Trp Leu Ser Ser Ser Lys Ala Asn Asp Ile Glu Val Ile
65                  70                  75                  80
```

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

Ala His Gly Lys Lys Leu Pro Ile Phe Gly Val Asp Ala Leu Pro Glu
            100                 105                 110

Val Leu Gln Leu Ile Lys Lys Gly Asp Ile Ala Gly Thr Val Leu Asn
        115                 120                 125

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

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

Arg Val Val Arg Ile Pro Tyr Val Gly Val Asp Lys Asp Asn Leu Ser
                165                 170                 175

Gln Phe Leu Lys
            180


<210>  177
<211>  1071
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(1071)

<400>  177
atg gca gga aat acc atc gga caa tta ttt cgc gtc acc acc ttc ggc       48
Met Ala Gly Asn Thr Ile Gly Gln Leu Phe Arg Val Thr Thr Phe Gly
1               5                   10                  15

gag tcc cac ggc att gcc ttg ggt tgc att gtg gac ggc gta ccg ccg       96
Glu Ser His Gly Ile Ala Leu Gly Cys Ile Val Asp Gly Val Pro Pro
            20                  25                  30

aac atg gca tta tcg gaa gcg gat att caa ccg gat ttg gat cgt cgt      144
Asn Met Ala Leu Ser Glu Ala Asp Ile Gln Pro Asp Leu Asp Arg Arg
        35                  40                  45

aaa ccc ggc acc tcg cgc tat acc aca ccg cgc cgc gaa gac gat gaa      192
Lys Pro Gly Thr Ser Arg Tyr Thr Thr Pro Arg Arg Glu Asp Asp Glu
    50                  55                  60

gtg cag att tta tcc ggt gtc ttt gaa gga aaa acc acc ggc acc agt      240
Val Gln Ile Leu Ser Gly Val Phe Glu Gly Lys Thr Thr Gly Thr Ser
65                  70                  75                  80

att ggc ata atc att aag aac ggc gat caa cgc tcg cag gac tat ggc      288
Ile Gly Ile Ile Ile Lys Asn Gly Asp Gln Arg Ser Gln Asp Tyr Gly
                85                  90                  95
```

```
gaa att aaa gat cgc ttc cgt ccg gga cat gca gat ttt act tat caa       336
Glu Ile Lys Asp Arg Phe Arg Pro Gly His Ala Asp Phe Thr Tyr Gln
            100                 105                 110

caa aaa tac ggc att cgt gat tat cgc ggc ggc ggt cgt tct tcc gcc       384
Gln Lys Tyr Gly Ile Arg Asp Tyr Arg Gly Gly Gly Arg Ser Ser Ala
        115                 120                 125

cgc gaa act gcc atg cgc gtg gcg gcg ggt gcc atc gcg aaa aaa tat       432
Arg Glu Thr Ala Met Arg Val Ala Ala Gly Ala Ile Ala Lys Lys Tyr
    130                 135                 140

tta cgc gaa caa ttc ggc att gaa gtg cgt ggt ttc tta agc caa atc       480
Leu Arg Glu Gln Phe Gly Ile Glu Val Arg Gly Phe Leu Ser Gln Ile
145                 150                 155                 160

ggc gat gtc aaa att gcg ccg caa tcc gtg gaa cat att gat tgg gca       528
Gly Asp Val Lys Ile Ala Pro Gln Ser Val Glu His Ile Asp Trp Ala
                165                 170                 175

gaa gta aat agc aat ctg ttt ttc tgc ccc gat aaa agt gcg gtg gaa       576
Glu Val Asn Ser Asn Leu Phe Phe Cys Pro Asp Lys Ser Ala Val Glu
            180                 185                 190

aaa ttc gat gaa tta att cgt gat ctg aaa aaa caa ggg gat tct atc       624
Lys Phe Asp Glu Leu Ile Arg Asp Leu Lys Lys Gln Gly Asp Ser Ile
        195                 200                 205

ggt gct aaa ttg acc gtg gtg gcg gaa aac gtc ccc gtc ggg ttg ggc       672
Gly Ala Lys Leu Thr Val Val Ala Glu Asn Val Pro Val Gly Leu Gly
    210                 215                 220

gaa ccg gtg ttt gat cgt ttg gat gcg gat tta gcc cac gca tta atg       720
Glu Pro Val Phe Asp Arg Leu Asp Ala Asp Leu Ala His Ala Leu Met
225                 230                 235                 240

agc att aat gcg gta aaa ggc gtg gaa att ggt gac ggt ttc gct gtg       768
Ser Ile Asn Ala Val Lys Gly Val Glu Ile Gly Asp Gly Phe Ala Val
                245                 250                 255

gta gaa caa aaa ggt agc caa cat cgt gac gaa atg atc ccg caa gga       816
Val Glu Gln Lys Gly Ser Gln His Arg Asp Glu Met Ile Pro Gln Gly
            260                 265                 270

ttt ctt tcc aac tat gcc ggc ggg att ttg ggc ggc atc agt tca gga       864
Phe Leu Ser Asn Tyr Ala Gly Gly Ile Leu Gly Gly Ile Ser Ser Gly
        275                 280                 285

caa ccg att atc gcc acg att gcc ctc aaa ccc act tcc agc att acc       912
Gln Pro Ile Ile Ala Thr Ile Ala Leu Lys Pro Thr Ser Ser Ile Thr
    290                 295                 300

att ccg ggg cgc tcg gtg aat ctc gac aat gaa tct gtc gaa gtt gtt       960
Ile Pro Gly Arg Ser Val Asn Leu Asp Asn Glu Ser Val Glu Val Val
305                 310                 315                 320

act aaa ggt cgc cac gat cct tgt gtc ggc atc cgc gcc gtg ccg att      1008
Thr Lys Gly Arg His Asp Pro Cys Val Gly Ile Arg Ala Val Pro Ile
                325                 330                 335
```

```
gcg gaa gct atg acg gcg att gta ttg ttg gat cat ttg ttg cgt ttt      1056
Ala Glu Ala Met Thr Ala Ile Val Leu Leu Asp His Leu Leu Arg Phe
            340                 345                 350

aaa gcg caa tgc cga                                                  1071
Lys Ala Gln Cys Arg
        355


<210>  178
<211>  357
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  178

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


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


Asn Met Ala Leu Ser Glu Ala Asp Ile Gln Pro Asp Leu Asp Arg Arg
        35                  40                  45


Lys Pro Gly Thr Ser Arg Tyr Thr Thr Pro Arg Arg Glu Asp Asp Glu
    50                  55                  60


Val Gln Ile Leu Ser Gly Val Phe Glu Gly Lys Thr Thr Gly Thr Ser
65                  70                  75                  80


Ile Gly Ile Ile Ile Lys Asn Gly Asp Gln Arg Ser Gln Asp Tyr Gly
                85                  90                  95


Glu Ile Lys Asp Arg Phe Arg Pro Gly His Ala Asp Phe Thr Tyr Gln
            100                 105                 110


Gln Lys Tyr Gly Ile Arg Asp Tyr Arg Gly Gly Gly Arg Ser Ser Ala
        115                 120                 125


Arg Glu Thr Ala Met Arg Val Ala Ala Gly Ala Ile Ala Lys Lys Tyr
    130                 135                 140


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


Gly Asp Val Lys Ile Ala Pro Gln Ser Val Glu His Ile Asp Trp Ala
                165                 170                 175


Glu Val Asn Ser Asn Leu Phe Phe Cys Pro Asp Lys Ser Ala Val Glu
```

```
            180                 185                 190


Lys Phe Asp Glu Leu Ile Arg Asp Leu Lys Lys Gln Gly Asp Ser Ile
        195                 200                 205


Gly Ala Lys Leu Thr Val Val Ala Glu Asn Val Pro Val Gly Leu Gly
    210                 215                 220


Glu Pro Val Phe Asp Arg Leu Asp Ala Asp Leu Ala His Ala Leu Met
225                 230                 235                 240


Ser Ile Asn Ala Val Lys Gly Val Glu Ile Gly Asp Gly Phe Ala Val
                245                 250                 255


Val Glu Gln Lys Gly Ser Gln His Arg Asp Glu Met Ile Pro Gln Gly
            260                 265                 270


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


Gln Pro Ile Ile Ala Thr Ile Ala Leu Lys Pro Thr Ser Ser Ile Thr
    290                 295                 300


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


Thr Lys Gly Arg His Asp Pro Cys Val Gly Ile Arg Ala Val Pro Ile
                325                 330                 335


Ala Glu Ala Met Thr Ala Ile Val Leu Leu Asp His Leu Leu Arg Phe
            340                 345                 350


Lys Ala Gln Cys Arg
        355


<210>  179
<211>  633
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(633)

<400>  179
gac ctc ttg gtg gat tcc tac gtg aaa tgg cgt atc aat gat tta ggt        48
Asp Leu Leu Val Asp Ser Tyr Val Lys Trp Arg Ile Asn Asp Leu Gly
1               5                   10                  15
```

```
cgt ttc ttc acc acg acc ggt ggt ggc gat tat gca caa gca gcc aac         96
Arg Phe Phe Thr Thr Thr Gly Gly Gly Asp Tyr Ala Gln Ala Ala Asn
            20                  25                  30

tta tta cgt cgt aaa gtc aat gac cgt ttg cgt tcc gaa atc ggt tcc        144
Leu Leu Arg Arg Lys Val Asn Asp Arg Leu Arg Ser Glu Ile Gly Ser
        35                  40                  45

cgc acc att aaa gac atc gtt tcc ggt aca cga ggc gaa ctc atg gta        192
Arg Thr Ile Lys Asp Ile Val Ser Gly Thr Arg Gly Glu Leu Met Val
    50                  55                  60

ggc acg aaa aaa gcg ctc aac agt ggg caa gac agc acc gcc gaa ctg        240
Gly Thr Lys Lys Ala Leu Asn Ser Gly Gln Asp Ser Thr Ala Glu Leu
65                  70                  75                  80

ggg att gaa gtg ctc gac gta cgg att aaa caa att aac ttg ccg gat        288
Gly Ile Glu Val Leu Asp Val Arg Ile Lys Gln Ile Asn Leu Pro Asp
                85                  90                  95

gaa gtg tct tcc tcc att tac cag cgt atg cgc gcc gaa cgg gat gcg        336
Glu Val Ser Ser Ser Ile Tyr Gln Arg Met Arg Ala Glu Arg Asp Ala
            100                 105                 110

gta gcc cgt gaa cac cgc tct caa ggt aaa gaa aaa gcg gca ttt att        384
Val Ala Arg Glu His Arg Ser Gln Gly Lys Glu Lys Ala Ala Phe Ile
        115                 120                 125

cag gcg gat gta gat cgt aaa gtc acc tta att atc gcc aat gcg gaa        432
Gln Ala Asp Val Asp Arg Lys Val Thr Leu Ile Ile Ala Asn Ala Glu
    130                 135                 140

aaa acc gca cag gaa tta cgc ggt gac ggc gac gcg acc gca gcc aaa        480
Lys Thr Ala Gln Glu Leu Arg Gly Asp Gly Asp Ala Thr Ala Ala Lys
145                 150                 155                 160

atc ttt gcc gat gcc ttt ggt aaa gag cct gaa ttt tac agc ttc att        528
Ile Phe Ala Asp Ala Phe Gly Lys Glu Pro Glu Phe Tyr Ser Phe Ile
                165                 170                 175

cgt agc ctg aaa gcc tat gaa agc agc ttc gcc gac tcg gac aat ttg        576
Arg Ser Leu Lys Ala Tyr Glu Ser Ser Phe Ala Asp Ser Asp Asn Leu
            180                 185                 190

ttg att tta aaa ccg gac agt gac ttc ttc cgt ttt atg caa tca cca        624
Leu Ile Leu Lys Pro Asp Ser Asp Phe Phe Arg Phe Met Gln Ser Pro
        195                 200                 205

agt aaa taa                                                            633
Ser Lys
    210


<210>  180
<211>  210
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  180

Asp Leu Leu Val Asp Ser Tyr Val Lys Trp Arg Ile Asn Asp Leu Gly
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1               5                   10                  15

Arg Phe Phe Thr Thr Thr Gly Gly Gly Asp Tyr Ala Gln Ala Ala Asn
            20                  25                  30

Leu Leu Arg Arg Lys Val Asn Asp Arg Leu Arg Ser Glu Ile Gly Ser
        35                  40                  45

Arg Thr Ile Lys Asp Ile Val Ser Gly Thr Arg Gly Glu Leu Met Val
    50                  55                  60

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

Gly Ile Glu Val Leu Asp Val Arg Ile Lys Gln Ile Asn Leu Pro Asp
                85                  90                  95

Glu Val Ser Ser Ser Ile Tyr Gln Arg Met Arg Ala Glu Arg Asp Ala
            100                 105                 110

Val Ala Arg Glu His Arg Ser Gln Gly Lys Glu Lys Ala Ala Phe Ile
        115                 120                 125

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

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

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

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

Leu Ile Leu Lys Pro Asp Ser Asp Phe Phe Arg Phe Met Gln Ser Pro
        195                 200                 205

Ser Lys
    210


<210>  181
<211>  582
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
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<221>  CDS
<222>  (1)..(582)

<400>  181
atg atc gac aac atc aac gaa ctt cgc acc ttt atc acc gcg gcg caa        48
Met Ile Asp Asn Ile Asn Glu Leu Arg Thr Phe Ile Thr Ala Ala Gln
1               5                   10                  15

gaa ggc agt ttc acc aaa gcc gcc gca aaa tta aac gtt tcc acc tcc        96
Glu Gly Ser Phe Thr Lys Ala Ala Ala Lys Leu Asn Val Ser Thr Ser
            20                  25                  30

gca tta agc cat tcc att cgc aag ctg gaa gaa cag ctc aac atc aaa       144
Ala Leu Ser His Ser Ile Arg Lys Leu Glu Glu Gln Leu Asn Ile Lys
        35                  40                  45

ctg ttc aac cgc acc aca cgc agc att gcc acc acg gag gcg ggc gag       192
Leu Phe Asn Arg Thr Thr Arg Ser Ile Ala Thr Thr Glu Ala Gly Glu
    50                  55                  60

cag ttg ttt caa aat ctc ttg ccg ttg ttt gaa agt att gaa gat aat       240
Gln Leu Phe Gln Asn Leu Leu Pro Leu Phe Glu Ser Ile Glu Asp Asn
65                  70                  75                  80

ctc aac gca tta agc acc ttt cgc aac acg ttg aaa ggg aaa tta tgc       288
Leu Asn Ala Leu Ser Thr Phe Arg Asn Thr Leu Lys Gly Lys Leu Cys
                85                  90                  95

att aac ggt aac gat cat gtt ttt tta tcc att ttg tgg gat aaa ttg       336
Ile Asn Gly Asn Asp His Val Phe Leu Ser Ile Leu Trp Asp Lys Leu
            100                 105                 110

atg gcg ttc gcg gaa caa tac ccc gaa atg gaa ttg gaa ttg acc agt       384
Met Ala Phe Ala Glu Gln Tyr Pro Glu Met Glu Leu Glu Leu Thr Ser
        115                 120                 125

gac acc aaa ttt gtg gat atc gtg gcg ggg cgg ttt gat gcg ggt att       432
Asp Thr Lys Phe Val Asp Ile Val Ala Gly Arg Phe Asp Ala Gly Ile
    130                 135                 140

cgc tta gga tcg gac gtg gca caa gat atg atc gcc gtg aga tta agc       480
Arg Leu Gly Ser Asp Val Ala Gln Asp Met Ile Ala Val Arg Leu Ser
145                 150                 155                 160

gac aaa atg caa atg gcg gtg gtc ggc acg cca gag tat ttc gcc aaa       528
Asp Lys Met Gln Met Ala Val Val Gly Thr Pro Glu Tyr Phe Ala Lys
                165                 170                 175

aaa gcc aca ccg aag aaa gta gaa gac ttg ggc gaa cac gag tgc ttg       576
Lys Ala Thr Pro Lys Lys Val Glu Asp Leu Gly Glu His Glu Cys Leu
            180                 185                 190

ctg gtg                                                               582
Leu Val


<210>  182
<211>  194
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans
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<400>  182

Met Ile Asp Asn Ile Asn Glu Leu Arg Thr Phe Ile Thr Ala Ala Gln
1               5                   10                  15


Glu Gly Ser Phe Thr Lys Ala Ala Ala Lys Leu Asn Val Ser Thr Ser
            20                  25                  30


Ala Leu Ser His Ser Ile Arg Lys Leu Glu Glu Gln Leu Asn Ile Lys
        35                  40                  45


Leu Phe Asn Arg Thr Thr Arg Ser Ile Ala Thr Thr Glu Ala Gly Glu
    50                  55                  60


Gln Leu Phe Gln Asn Leu Leu Pro Leu Phe Glu Ser Ile Glu Asp Asn
65                  70                  75                  80


Leu Asn Ala Leu Ser Thr Phe Arg Asn Thr Leu Lys Gly Lys Leu Cys
                85                  90                  95


Ile Asn Gly Asn Asp His Val Phe Leu Ser Ile Leu Trp Asp Lys Leu
            100                 105                 110


Met Ala Phe Ala Glu Gln Tyr Pro Glu Met Glu Leu Glu Leu Thr Ser
        115                 120                 125


Asp Thr Lys Phe Val Asp Ile Val Ala Gly Arg Phe Asp Ala Gly Ile
    130                 135                 140


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


Asp Lys Met Gln Met Ala Val Val Gly Thr Pro Glu Tyr Phe Ala Lys
                165                 170                 175


Lys Ala Thr Pro Lys Lys Val Glu Asp Leu Gly Glu His Glu Cys Leu
            180                 185                 190


Leu Val


<210>  183
<211>  662
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
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<221>  CDS
<222>  (1)..(660)

<400>  183
taa tct cgg caa tgt tcg cca cct tgc ttt ttt tgc ctg cat tat ttc        48
    Ser Arg Gln Cys Ser Pro Pro Cys Phe Phe Cys Leu His Tyr Phe
    1               5                   10                  15

gcc gtt atc aaa aca aac cgc gca ccc cga acc caa aag tgc ggt gga        96
Ala Val Ile Lys Thr Asn Arg Ala Pro Arg Thr Gln Lys Cys Gly Gly
                20                  25                  30

ttt tgg atg cgt ttt tta cgc atg ggc gtg gtt tca atc ctg tta ggg       144
Phe Trp Met Arg Phe Leu Arg Met Gly Val Val Ser Ile Leu Leu Gly
            35                  40                  45

ggg att ttt atc gtc ggc ggt ttg tat cgt tcc gaa tgg cgt gat gat       192
Gly Ile Phe Ile Val Gly Gly Leu Tyr Arg Ser Glu Trp Arg Asp Asp
        50                  55                  60

att cgt caa tgg gtt tct atg ccg cag gtg atg tta gac gag gcg aag       240
Ile Arg Gln Trp Val Ser Met Pro Gln Val Met Leu Asp Glu Ala Lys
    65                  70                  75

caa atc gct gac ttg acc ggc gtg gat ttg ggc aac cgt tat ttc ctg       288
Gln Ile Ala Asp Leu Thr Gly Val Asp Leu Gly Asn Arg Tyr Phe Leu
80                  85                  90                  95

gtg ctt gcc gac aac gac gat gcc tta ctg gaa aaa gaa cgg gcg ctg       336
Val Leu Ala Asp Asn Asp Asp Ala Leu Leu Glu Lys Glu Arg Ala Leu
                100                 105                 110

aca aca aaa ctg gat gaa cag cac atc cct tat cgc gcc ctt tcc caa       384
Thr Thr Lys Leu Asp Glu Gln His Ile Pro Tyr Arg Ala Leu Ser Gln
            115                 120                 125

tgg atg atg tcg gaa gcg caa cag cgg caa ttt ata gtg gaa ttg cag       432
Trp Met Met Ser Glu Ala Gln Gln Arg Gln Phe Ile Val Glu Leu Gln
        130                 135                 140

gca aaa ctc aaa ccg cag gat tat gcc gta ttg gat gag att ggc gtg       480
Ala Lys Leu Lys Pro Gln Asp Tyr Ala Val Leu Asp Glu Ile Gly Val
    145                 150                 155

ccg tcg gaa aga tta caa cag gca ctg cgg gaa ttg aac acg cag ccg       528
Pro Ser Glu Arg Leu Gln Gln Ala Leu Arg Glu Leu Asn Thr Gln Pro
160                 165                 170                 175

ccg tta tcc ttg cag cag gcg ttg caa tct acc gtc ggg caa gca tgg       576
Pro Leu Ser Leu Gln Gln Ala Leu Gln Ser Thr Val Gly Gln Ala Trp
                180                 185                 190

ctg ccg ctc tat tta ggc aaa tta gcg gaa aat cag gtg gct ggc atc       624
Leu Pro Leu Tyr Leu Gly Lys Leu Ala Glu Asn Gln Val Ala Gly Ile
            195                 200                 205

gtg cag gta agc gga cac agt gcc gtt tcc ctt gcg ca                    662
Val Gln Val Ser Gly His Ser Ala Val Ser Leu Ala
        210                 215
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<210>  184
<211>  219
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  184

Ser Arg Gln Cys Ser Pro Pro Cys Phe Phe Cys Leu His Tyr Phe Ala
1               5                   10                  15


Val Ile Lys Thr Asn Arg Ala Pro Arg Thr Gln Lys Cys Gly Gly Phe
            20                  25                  30


Trp Met Arg Phe Leu Arg Met Gly Val Val Ser Ile Leu Leu Gly Gly
        35                  40                  45


Ile Phe Ile Val Gly Gly Leu Tyr Arg Ser Glu Trp Arg Asp Asp Ile
    50                  55                  60


Arg Gln Trp Val Ser Met Pro Gln Val Met Leu Asp Glu Ala Lys Gln
65                  70                  75                  80


Ile Ala Asp Leu Thr Gly Val Asp Leu Gly Asn Arg Tyr Phe Leu Val
                85                  90                  95


Leu Ala Asp Asn Asp Asp Ala Leu Leu Glu Lys Glu Arg Ala Leu Thr
            100                 105                 110


Thr Lys Leu Asp Glu Gln His Ile Pro Tyr Arg Ala Leu Ser Gln Trp
        115                 120                 125


Met Met Ser Glu Ala Gln Gln Arg Gln Phe Ile Val Glu Leu Gln Ala
    130                 135                 140


Lys Leu Lys Pro Gln Asp Tyr Ala Val Leu Asp Glu Ile Gly Val Pro
145                 150                 155                 160


Ser Glu Arg Leu Gln Gln Ala Leu Arg Glu Leu Asn Thr Gln Pro Pro
                165                 170                 175


Leu Ser Leu Gln Gln Ala Leu Gln Ser Thr Val Gly Gln Ala Trp Leu
            180                 185                 190


Pro Leu Tyr Leu Gly Lys Leu Ala Glu Asn Gln Val Ala Gly Ile Val
        195                 200                 205


Gln Val Ser Gly His Ser Ala Val Ser Leu Ala
    210                 215
```

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<210>  185
<211>  247
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(246)

<400>  185
ggg gtg ttt atg tcc gcg cat aat ttc ccg aaa tcc cgt gaa acc cgt       48
Gly Val Phe Met Ser Ala His Asn Phe Pro Lys Ser Arg Glu Thr Arg
1               5                   10                  15

gca cct aaa gtg gcg gaa ttg gcg tta tat cgt gag cgg ctg ccg gaa       96
Ala Pro Lys Val Ala Glu Leu Ala Leu Tyr Arg Glu Arg Leu Pro Glu
            20                  25                  30

aaa tta agc tat ctg gct gac gca cca caa acg gat ccg gaa ggc agt      144
Lys Leu Ser Tyr Leu Ala Asp Ala Pro Gln Thr Asp Pro Glu Gly Ser
        35                  40                  45

gaa gcc atc att cgc ttt agt cgt aaa gaa aaa cgt caa tat gtc acc      192
Glu Ala Ile Ile Arg Phe Ser Arg Lys Glu Lys Arg Gln Tyr Val Thr
    50                  55                  60

tcc gaa aag aat ggc aag gcg aca aaa tgg ata gtg gat ttt gtt gat      240
Ser Glu Lys Asn Gly Lys Ala Thr Lys Trp Ile Val Asp Phe Val Asp
65                  70                  75                  80

ggg aag t                                                            247
Gly Lys


<210>  186
<211>  82
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  186

Gly Val Phe Met Ser Ala His Asn Phe Pro Lys Ser Arg Glu Thr Arg
1               5                   10                  15


Ala Pro Lys Val Ala Glu Leu Ala Leu Tyr Arg Glu Arg Leu Pro Glu
            20                  25                  30


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


Glu Ala Ile Ile Arg Phe Ser Arg Lys Glu Lys Arg Gln Tyr Val Thr
    50                  55                  60


Ser Glu Lys Asn Gly Lys Ala Thr Lys Trp Ile Val Asp Phe Val Asp
```

```
65                  70                  75                  80

Gly Lys


<210>  187
<211>  357
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(357)

<400>  187
tgc gtc cac tcc ggt cct ctc gta cta gga gca gcc cca acc aat tct        48
Cys Val His Ser Gly Pro Leu Val Leu Gly Ala Ala Pro Thr Asn Ser
1               5                   10                  15

cct acg ccc acg gca gat agg gac cga act gtc tca cga cgt tct aaa        96
Pro Thr Pro Thr Ala Asp Arg Asp Arg Thr Val Ser Arg Arg Ser Lys
            20                  25                  30

ccc agc tcg cgt acc act tta aat ggc gaa cag cca tac cct tgg gac       144
Pro Ser Ser Arg Thr Thr Leu Asn Gly Glu Gln Pro Tyr Pro Trp Asp
        35                  40                  45

cta ctt cag ccc cag gat gtg atg agc cga cat cga ggt gcc aaa cac       192
Leu Leu Gln Pro Gln Asp Val Met Ser Arg His Arg Gly Ala Lys His
    50                  55                  60

cgc cgt cga tat gaa ctc ttg ggc ggt atc agc ctg tta tcc ccg gag       240
Arg Arg Arg Tyr Glu Leu Leu Gly Gly Ile Ser Leu Leu Ser Pro Glu
65                  70                  75                  80

tac ctt tta tcc gtt gag cga tgg ccc ttc cat gca gaa cca ccg gat       288
Tyr Leu Leu Ser Val Glu Arg Trp Pro Phe His Ala Glu Pro Pro Asp
                85                  90                  95

cac tat gac cta ctt tcg tac ctg ccc gac ctg tcc gtc tcg cag tta       336
His Tyr Asp Leu Leu Ser Tyr Leu Pro Asp Leu Ser Val Ser Gln Leu
            100                 105                 110

agc ttg ctt ata cca ttg cac                                           357
Ser Leu Leu Ile Pro Leu His
        115


<210>  188
<211>  119
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  188

Cys Val His Ser Gly Pro Leu Val Leu Gly Ala Ala Pro Thr Asn Ser
1               5                   10                  15
```

```
Pro Thr Pro Thr Ala Asp Arg Asp Arg Thr Val Ser Arg Arg Ser Lys
            20                  25                  30


Pro Ser Ser Arg Thr Thr Leu Asn Gly Glu Gln Pro Tyr Pro Trp Asp
        35                  40                  45


Leu Leu Gln Pro Gln Asp Val Met Ser Arg His Arg Gly Ala Lys His
    50                  55                  60


Arg Arg Arg Tyr Glu Leu Leu Gly Gly Ile Ser Leu Leu Ser Pro Glu
65                  70                  75                  80


Tyr Leu Leu Ser Val Glu Arg Trp Pro Phe His Ala Glu Pro Pro Asp
                85                  90                  95


His Tyr Asp Leu Leu Ser Tyr Leu Pro Asp Leu Ser Val Ser Gln Leu
            100                 105                 110


Ser Leu Leu Ile Pro Leu His
        115


<210>  189
<211>  222
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(222)

<400>  189
gaa acc gtg tgc tat gaa atc atg cgc gaa atc att cgc gta cac cat         48
Glu Thr Val Cys Tyr Glu Ile Met Arg Glu Ile Ile Arg Val His His
1               5                   10                  15

gta ttt gcc agc gaa caa ttc gtg gtt tat gcc tct cac gcc gtc gcc         96
Val Phe Ala Ser Glu Gln Phe Val Val Tyr Ala Ser His Ala Val Ala
            20                  25                  30

gat tat ctg att aac gaa gaa tcc cac ggc tta ctg gct gaa ctg gaa        144
Asp Tyr Leu Ile Asn Glu Glu Ser His Gly Leu Leu Ala Glu Leu Glu
        35                  40                  45

gtg ttc atc ggc aaa caa atc caa gta aaa act gaa gtg ttt tat act        192
Val Phe Ile Gly Lys Gln Ile Gln Val Lys Thr Glu Val Phe Tyr Thr
    50                  55                  60

cag gaa cag ttt gat gtg gtg gtg atg tag                                222
Gln Glu Gln Phe Asp Val Val Val Met
65                  70


<210>  190
<211>  73
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<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  190

Glu Thr Val Cys Tyr Glu Ile Met Arg Glu Ile Ile Arg Val His His
1               5                   10                  15


Val Phe Ala Ser Glu Gln Phe Val Val Tyr Ala Ser His Ala Val Ala
            20                  25                  30


Asp Tyr Leu Ile Asn Glu Glu Ser His Gly Leu Leu Ala Glu Leu Glu
        35                  40                  45


Val Phe Ile Gly Lys Gln Ile Gln Val Lys Thr Glu Val Phe Tyr Thr
    50                  55                  60


Gln Glu Gln Phe Asp Val Val Val Met
65                  70


<210>  191
<211>  1670
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(1668)

<400>  191
atc gaa cgt tat caa cgt tat aac aac acc tca tac aat ctt gag ccg        48
Ile Glu Arg Tyr Gln Arg Tyr Asn Asn Thr Ser Tyr Asn Leu Glu Pro
1               5                   10                  15

gac atc aaa tac agt ccg ggc ggg ttg cgc gat ttg cat ttg ttg tat        96
Asp Ile Lys Tyr Ser Pro Gly Gly Leu Arg Asp Leu His Leu Leu Tyr
            20                  25                  30

tgg atc gcg ttg cgc cat aac ggg gct aaa aat tta cag gaa att tta       144
Trp Ile Ala Leu Arg His Asn Gly Ala Lys Asn Leu Gln Glu Ile Leu
        35                  40                  45

cag gcg ggg ttt att cat ccg gca gaa cac gcc ttg tta cta aaa agc       192
Gln Ala Gly Phe Ile His Pro Ala Glu His Ala Leu Leu Leu Lys Ser
    50                  55                  60

cag caa ttt ctg ttt aaa gtg cgg tac gct ttg cac tta att tta aag       240
Gln Gln Phe Leu Phe Lys Val Arg Tyr Ala Leu His Leu Ile Leu Lys
65                  70                  75                  80

cgt tat gac aac cgc ctg ttg ttt gat cgc caa ctg aaa gtc agc gaa       288
Arg Tyr Asp Asn Arg Leu Leu Phe Asp Arg Gln Leu Lys Val Ser Glu
                85                  90                  95

ttg ttg ggt ttc cag ggg gaa ggc aat caa ggc gtg gaa gcc atg atg       336
Leu Leu Gly Phe Gln Gly Glu Gly Asn Gln Gly Val Glu Ala Met Met
```

```
            100                 105                 110

aag cgc ttt ttt cag gcg ttg cat tcc att tcg tta cta agc gaa ttg         384
Lys Arg Phe Phe Gln Ala Leu His Ser Ile Ser Leu Leu Ser Glu Leu
        115                 120                 125

ttg gta aaa cat tat cag gaa cat ttt tta acc cgt cat gca gtg gtg         432
Leu Val Lys His Tyr Gln Glu His Phe Leu Thr Arg His Ala Val Val
    130                 135                 140

agc gag caa ata ctc gat gac aat ttc agc ctg atc aat caa tcc att         480
Ser Glu Gln Ile Leu Asp Asp Asn Phe Ser Leu Ile Asn Gln Ser Ile
145                 150                 155                 160

tgc tta cgt aat cat caa tgc ttt gag cag cag ccg gaa agc att ctt         528
Cys Leu Arg Asn His Gln Cys Phe Glu Gln Gln Pro Glu Ser Ile Leu
                165                 170                 175

gac ctt ttt tat cat tta acc caa tat ccg cag gcg gaa att cat tcc         576
Asp Leu Phe Tyr His Leu Thr Gln Tyr Pro Gln Ala Glu Ile His Ser
            180                 185                 190

ttt gtc ttg cgc gag ctt tat ttg gcg ctg gag caa cgg cag ggc tat         624
Phe Val Leu Arg Glu Leu Tyr Leu Ala Leu Glu Gln Arg Gln Gly Tyr
        195                 200                 205

ttg tgt gat ttg cca gcg gcg cgg gaa aaa ttc gtg cgc ctg ttt aat         672
Leu Cys Asp Leu Pro Ala Ala Arg Glu Lys Phe Val Arg Leu Phe Asn
    210                 215                 220

cag ccg aat gcg att aaa cgt gct ttt ttc cct atg cac caa tac ggc         720
Gln Pro Asn Ala Ile Lys Arg Ala Phe Phe Pro Met His Gln Tyr Gly
225                 230                 235                 240

gtg ctt acc gcc tat tta ccg caa tgg ggc aac gtc gtc ggt tta atg         768
Val Leu Thr Ala Tyr Leu Pro Gln Trp Gly Asn Val Val Gly Leu Met
                245                 250                 255

cag ttt gat tta ttt cat tgt tac acc gtg gac gag cat att ctg cgc         816
Gln Phe Asp Leu Phe His Cys Tyr Thr Val Asp Glu His Ile Leu Arg
            260                 265                 270

gtg atg tta aaa ctg gaa agt ttt tta gag ggc gct tcg gca caa agc         864
Val Met Leu Lys Leu Glu Ser Phe Leu Glu Gly Ala Ser Ala Gln Ser
        275                 280                 285

cat ccc att tgc cat caa ata ttc agc cga att tcc gac cgc act ttg         912
His Pro Ile Cys His Gln Ile Phe Ser Arg Ile Ser Asp Arg Thr Leu
    290                 295                 300

ttg tat att gcc gct tta ttt cac gac atc gcc aaa ggg cgc ggc ggt         960
Leu Tyr Ile Ala Ala Leu Phe His Asp Ile Ala Lys Gly Arg Gly Gly
305                 310                 315                 320

tct cat gaa tta ttg ggt gcg gtg gat gtg cgc gaa ttt gcc gtt cgg        1008
Ser His Glu Leu Leu Gly Ala Val Asp Val Arg Glu Phe Ala Val Arg
                325                 330                 335

cac ggt ttt gat caa cgg gaa acg gaa acc atg gtg tgg ctg gtg gag        1056
His Gly Phe Asp Gln Arg Glu Thr Glu Thr Met Val Trp Leu Val Glu
            340                 345                 350
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cag cat ttg ctt atg tcg gtc acg gca caa cgg cgg gat att cat gat       1104
Gln His Leu Leu Met Ser Val Thr Ala Gln Arg Arg Asp Ile His Asp
        355                 360                 365

ccg gaa att gta ctg aat ttc gcc gaa ctg gtg cgt aat cag gtg cgt       1152
Pro Glu Ile Val Leu Asn Phe Ala Glu Leu Val Arg Asn Gln Val Arg
    370                 375                 380

ttg gat tat tta acc tgc ctg acc gtc gcc gat att gtg gcg acc aat       1200
Leu Asp Tyr Leu Thr Cys Leu Thr Val Ala Asp Ile Val Ala Thr Asn
385                 390                 395                 400

gaa act ttg tgg aat agc tgg aag cgt tct ttg ctg gcg act ttg tac       1248
Glu Thr Leu Trp Asn Ser Trp Lys Arg Ser Leu Leu Ala Thr Leu Tyr
                405                 410                 415

gat tac gcc acc caa caa ttc gcc caa ggg ctg gaa agt atc ttg gat       1296
Asp Tyr Ala Thr Gln Gln Phe Ala Gln Gly Leu Glu Ser Ile Leu Asp
            420                 425                 430

aat caa gcg aaa gcg aaa gga cac cgc cga tta gca ctg cag gaa ata       1344
Asn Gln Ala Lys Ala Lys Gly His Arg Arg Leu Ala Leu Gln Glu Ile
        435                 440                 445

cgt gaa aaa acc acc gca ctt tcc gac aaa cac atc gaa aaa ttg tgg       1392
Arg Glu Lys Thr Thr Ala Leu Ser Asp Lys His Ile Glu Lys Leu Trp
    450                 455                 460

cag cgt ttt ccg ata gat tat ttc ttg cgc aat tcg cca caa caa att       1440
Gln Arg Phe Pro Ile Asp Tyr Phe Leu Arg Asn Ser Pro Gln Gln Ile
465                 470                 475                 480

ggt tgg cat acc cgt ttg ctt gcc gaa ttt gaa ggg gaa ttg ttg gtg       1488
Gly Trp His Thr Arg Leu Leu Ala Glu Phe Glu Gly Glu Leu Leu Val
                485                 490                 495

aaa gtc agt aac cgg ttt tct gcc ggc ggc acg gaa att ttc att tat       1536
Lys Val Ser Asn Arg Phe Ser Ala Gly Gly Thr Glu Ile Phe Ile Tyr
            500                 505                 510

acc aaa gac cga ccg aac ctg ttt cac aaa gtg gta agt act atc ggc       1584
Thr Lys Asp Arg Pro Asn Leu Phe His Lys Val Val Ser Thr Ile Gly
        515                 520                 525

gcg aaa aaa ctc agt atc cat gat gcg caa att atc acc gcc aaa gac       1632
Ala Lys Lys Leu Ser Ile His Asp Ala Gln Ile Ile Thr Ala Lys Asp
    530                 535                 540

ggc tat gtg ttg gac agt ttt att gtg acg gaa tta ga                    1670
Gly Tyr Val Leu Asp Ser Phe Ile Val Thr Glu Leu
545                 550                 555


<210>  192
<211>  556
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  192
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Ile Glu Arg Tyr Gln Arg Tyr Asn Asn Thr Ser Tyr Asn Leu Glu Pro
1               5                   10                  15

Asp Ile Lys Tyr Ser Pro Gly Gly Leu Arg Asp Leu His Leu Leu Tyr
            20                  25                  30

Trp Ile Ala Leu Arg His Asn Gly Ala Lys Asn Leu Gln Glu Ile Leu
        35                  40                  45

Gln Ala Gly Phe Ile His Pro Ala Glu His Ala Leu Leu Leu Lys Ser
    50                  55                  60

Gln Gln Phe Leu Phe Lys Val Arg Tyr Ala Leu His Leu Ile Leu Lys
65                  70                  75                  80

Arg Tyr Asp Asn Arg Leu Leu Phe Asp Arg Gln Leu Lys Val Ser Glu
                85                  90                  95

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

Lys Arg Phe Phe Gln Ala Leu His Ser Ile Ser Leu Leu Ser Glu Leu
        115                 120                 125

Leu Val Lys His Tyr Gln Glu His Phe Leu Thr Arg His Ala Val Val
    130                 135                 140

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

Cys Leu Arg Asn His Gln Cys Phe Glu Gln Gln Pro Glu Ser Ile Leu
                165                 170                 175

Asp Leu Phe Tyr His Leu Thr Gln Tyr Pro Gln Ala Glu Ile His Ser
            180                 185                 190

Phe Val Leu Arg Glu Leu Tyr Leu Ala Leu Glu Gln Arg Gln Gly Tyr
        195                 200                 205

Leu Cys Asp Leu Pro Ala Ala Arg Glu Lys Phe Val Arg Leu Phe Asn
    210                 215                 220

Gln Pro Asn Ala Ile Lys Arg Ala Phe Phe Pro Met His Gln Tyr Gly
225                 230                 235                 240

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

Gln Phe Asp Leu Phe His Cys Tyr Thr Val Asp Glu His Ile Leu Arg
            260                 265                 270

Val Met Leu Lys Leu Glu Ser Phe Leu Glu Gly Ala Ser Ala Gln Ser
        275                 280                 285

His Pro Ile Cys His Gln Ile Phe Ser Arg Ile Ser Asp Arg Thr Leu
    290                 295                 300

Leu Tyr Ile Ala Ala Leu Phe His Asp Ile Ala Lys Gly Arg Gly Gly
305                 310                 315                 320

Ser His Glu Leu Leu Gly Ala Val Asp Val Arg Glu Phe Ala Val Arg
                325                 330                 335

His Gly Phe Asp Gln Arg Glu Thr Glu Thr Met Val Trp Leu Val Glu
            340                 345                 350

Gln His Leu Leu Met Ser Val Thr Ala Gln Arg Arg Asp Ile His Asp
        355                 360                 365

Pro Glu Ile Val Leu Asn Phe Ala Glu Leu Val Arg Asn Gln Val Arg
    370                 375                 380

Leu Asp Tyr Leu Thr Cys Leu Thr Val Ala Asp Ile Val Ala Thr Asn
385                 390                 395                 400

Glu Thr Leu Trp Asn Ser Trp Lys Arg Ser Leu Leu Ala Thr Leu Tyr
                405                 410                 415

Asp Tyr Ala Thr Gln Gln Phe Ala Gln Gly Leu Glu Ser Ile Leu Asp
            420                 425                 430

Asn Gln Ala Lys Ala Lys Gly His Arg Arg Leu Ala Leu Gln Glu Ile
        435                 440                 445

Arg Glu Lys Thr Thr Ala Leu Ser Asp Lys His Ile Glu Lys Leu Trp
    450                 455                 460

Gln Arg Phe Pro Ile Asp Tyr Phe Leu Arg Asn Ser Pro Gln Gln Ile
465                 470                 475                 480

Gly Trp His Thr Arg Leu Leu Ala Glu Phe Glu Gly Glu Leu Leu Val
                485                 490                 495
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Lys Val Ser Asn Arg Phe Ser Ala Gly Gly Thr Glu Ile Phe Ile Tyr
            500                 505                 510


Thr Lys Asp Arg Pro Asn Leu Phe His Lys Val Val Ser Thr Ile Gly
        515                 520                 525


Ala Lys Lys Leu Ser Ile His Asp Ala Gln Ile Ile Thr Ala Lys Asp
    530                 535                 540


Gly Tyr Val Leu Asp Ser Phe Ile Val Thr Glu Leu
545                 550                 555


<210>  193
<211>  567
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(567)

<400>  193
gtc aac cat tcg ctt tat tcc gta ttg aga ccg att aat ggc gaa agc       48
Val Asn His Ser Leu Tyr Ser Val Leu Arg Pro Ile Asn Gly Glu Ser
1               5                   10                  15

acc ctt att aaa ggt caa gcg aag tgg gtg att tca aga ggt tcg cgt       96
Thr Leu Ile Lys Gly Gln Ala Lys Trp Val Ile Ser Arg Gly Ser Arg
            20                  25                  30

aat cgc act ttt cgt gtc ggt caa tct tat tgt cct tgt tgt tta ggg      144
Asn Arg Thr Phe Arg Val Gly Gln Ser Tyr Cys Pro Cys Cys Leu Gly
        35                  40                  45

gaa aca cct tat ttg cgt aat gaa tgg cgt ttt gcg tgg cat ttt ggt      192
Glu Thr Pro Tyr Leu Arg Asn Glu Trp Arg Phe Ala Trp His Phe Gly
    50                  55                  60

tgt tcg aaa cat caa gtt tta ctt gaa tct aaa tgc cct tgt tgt ggc      240
Cys Ser Lys His Gln Val Leu Leu Glu Ser Lys Cys Pro Cys Cys Gly
65                  70                  75                  80

gaa ctg tat caa cct cat ttg ctt tcc gca gaa aaa cga cac tta aat      288
Glu Leu Tyr Gln Pro His Leu Leu Ser Ala Glu Lys Arg His Leu Asn
                85                  90                  95

tac tgt cat caa tgt ggt gag aaa tta cag gtt gtt aca aca ccg ctt      336
Tyr Cys His Gln Cys Gly Glu Lys Leu Gln Val Val Thr Thr Pro Leu
            100                 105                 110

aat gaa gta gaa att gca aca atg gaa aca ctt aat aac gta ttt atg      384
Asn Glu Val Glu Ile Ala Thr Met Glu Thr Leu Asn Asn Val Phe Met
        115                 120                 125

act aac tca ggt gaa tgt ttc agg aaa cgt gtg aat gca caa gtg tac      432
```

```
Thr Asn Ser Gly Glu Cys Phe Arg Lys Arg Val Asn Ala Gln Val Tyr
    130                 135                 140

ttt gct ata ttg cgt tac ttc atc aat ctt att cgg cgt gct acg gtc      480
Phe Ala Ile Leu Arg Tyr Phe Ile Asn Leu Ile Arg Arg Ala Thr Val
145                 150                 155                 160

gta aaa tct act cac gct ttt gca aaa ttt gtg gaa gaa tgt ggt att      528
Val Lys Ser Thr His Ala Phe Ala Lys Phe Val Glu Glu Cys Gly Ile
                165                 170                 175

tct caa gcg gaa ata tgc caa acc aaa acc gcc ctt gca                  567
Ser Gln Ala Glu Ile Cys Gln Thr Lys Thr Ala Leu Ala
            180                 185


<210>  194
<211>  189
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  194

Val Asn His Ser Leu Tyr Ser Val Leu Arg Pro Ile Asn Gly Glu Ser
1               5                   10                  15


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


Asn Arg Thr Phe Arg Val Gly Gln Ser Tyr Cys Pro Cys Cys Leu Gly
        35                  40                  45


Glu Thr Pro Tyr Leu Arg Asn Glu Trp Arg Phe Ala Trp His Phe Gly
    50                  55                  60


Cys Ser Lys His Gln Val Leu Leu Glu Ser Lys Cys Pro Cys Cys Gly
65                  70                  75                  80


Glu Leu Tyr Gln Pro His Leu Leu Ser Ala Glu Lys Arg His Leu Asn
                85                  90                  95


Tyr Cys His Gln Cys Gly Glu Lys Leu Gln Val Val Thr Thr Pro Leu
            100                 105                 110


Asn Glu Val Glu Ile Ala Thr Met Glu Thr Leu Asn Asn Val Phe Met
        115                 120                 125


Thr Asn Ser Gly Glu Cys Phe Arg Lys Arg Val Asn Ala Gln Val Tyr
    130                 135                 140


Phe Ala Ile Leu Arg Tyr Phe Ile Asn Leu Ile Arg Arg Ala Thr Val
145                 150                 155                 160
```

```
Val Lys Ser Thr His Ala Phe Ala Lys Phe Val Glu Glu Cys Gly Ile
                165                 170                 175


Ser Gln Ala Glu Ile Cys Gln Thr Lys Thr Ala Leu Ala
            180                 185


<210>  195
<211>  492
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(492)

<400>  195
acc ttg gat gtg ctt cgt tcc gaa act ttc gtt tcc gaa tta aaa ggc          48
Thr Leu Asp Val Leu Arg Ser Glu Thr Phe Val Ser Glu Leu Lys Gly
1               5                   10                  15

tta aat gct tat cgc acc acc gtg cct gtc atc ggc gga cac tcc ggt          96
Leu Asn Ala Tyr Arg Thr Thr Val Pro Val Ile Gly Gly His Ser Gly
            20                  25                  30

gtg act att ctt ccg tta tta tct caa gtg caa tac gtt gaa tgg aaa         144
Val Thr Ile Leu Pro Leu Leu Ser Gln Val Gln Tyr Val Glu Trp Lys
        35                  40                  45

gag gac gaa att gaa ccg tta acc aaa cgc att caa aat gcc ggc acc         192
Glu Asp Glu Ile Glu Pro Leu Thr Lys Arg Ile Gln Asn Ala Gly Thr
    50                  55                  60

gaa gta gta aac gcg aaa gcc ggc ggc ggt tcc gca acc tta tcc atg         240
Glu Val Val Asn Ala Lys Ala Gly Gly Gly Ser Ala Thr Leu Ser Met
65                  70                  75                  80

gcg cag gcg gca gcc cgt ttt gct aat gct gta gtc cgc ggt tta caa         288
Ala Gln Ala Ala Ala Arg Phe Ala Asn Ala Val Val Arg Gly Leu Gln
                85                  90                  95

ggt gaa acc gtc gta gaa tgc agc tat gtg gaa ggc gac ggc aaa tac         336
Gly Glu Thr Val Val Glu Cys Ser Tyr Val Glu Gly Asp Gly Lys Tyr
            100                 105                 110

gcc cgc ttc ttc gca caa ccg gtt cgc ttc ggc aag gaa ggt gtg gaa         384
Ala Arg Phe Phe Ala Gln Pro Val Arg Phe Gly Lys Glu Gly Val Glu
        115                 120                 125

gaa atc cta cca atc ggt aaa ctc agc gcc ttg gaa caa cag gct tta         432
Glu Ile Leu Pro Ile Gly Lys Leu Ser Ala Leu Glu Gln Gln Ala Leu
    130                 135                 140

gaa acc atg tta ccg aca ttg cgt gca gat att gaa tta ggt gag aag         480
Glu Thr Met Leu Pro Thr Leu Arg Ala Asp Ile Glu Leu Gly Glu Lys
145                 150                 155                 160

ttt att aat cca                                                         492
```

```
Phe Ile Asn Pro


<210>  196
<211>  164
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  196

Thr Leu Asp Val Leu Arg Ser Glu Thr Phe Val Ser Glu Leu Lys Gly
1               5                   10                  15

Leu Asn Ala Tyr Arg Thr Thr Val Pro Val Ile Gly Gly His Ser Gly
            20                  25                  30

Val Thr Ile Leu Pro Leu Leu Ser Gln Val Gln Tyr Val Glu Trp Lys
        35                  40                  45

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

Glu Val Val Asn Ala Lys Ala Gly Gly Gly Ser Ala Thr Leu Ser Met
65                  70                  75                  80

Ala Gln Ala Ala Ala Arg Phe Ala Asn Ala Val Val Arg Gly Leu Gln
                85                  90                  95

Gly Glu Thr Val Val Glu Cys Ser Tyr Val Glu Gly Asp Gly Lys Tyr
            100                 105                 110

Ala Arg Phe Phe Ala Gln Pro Val Arg Phe Gly Lys Glu Gly Val Glu
        115                 120                 125

Glu Ile Leu Pro Ile Gly Lys Leu Ser Ala Leu Glu Gln Gln Ala Leu
    130                 135                 140

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

Phe Ile Asn Pro


<210>  197
<211>  667
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
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<221>  CDS
<222>  (1)..(666)

<400>  197
gca tta agc ctg caa agt ttc aac ctt gaa gtg ccg gtt gat gat aaa          48
Ala Leu Ser Leu Gln Ser Phe Asn Leu Glu Val Pro Val Asp Asp Lys
1               5                   10                  15

gaa cgt atc gaa aac atc aaa cgt tac acc ggt gaa aaa tta gat acg          96
Glu Arg Ile Glu Asn Ile Lys Arg Tyr Thr Gly Glu Lys Leu Asp Thr
            20                  25                  30

gcg ttt gtc aac gga tta gtg gaa gcc tcg agc cgt tta cgt cgc tta         144
Ala Phe Val Asn Gly Leu Val Glu Ala Ser Ser Arg Leu Arg Arg Leu
        35                  40                  45

tcc ccg ccg gca ttc cgt ttc caa tta acc gaa tta gcc cgc gcc gcc         192
Ser Pro Pro Ala Phe Arg Phe Gln Leu Thr Glu Leu Ala Arg Ala Ala
    50                  55                  60

caa aaa cgc atc gtc tta ccg gaa ggc gac gaa ccg cgc acc att aaa         240
Gln Lys Arg Ile Val Leu Pro Glu Gly Asp Glu Pro Arg Thr Ile Lys
65                  70                  75                  80

gcg gcg att tta tgt gcc gaa cgc ggt atc gca gaa tgt gtg ctg tta         288
Ala Ala Ile Leu Cys Ala Glu Arg Gly Ile Ala Glu Cys Val Leu Leu
                85                  90                  95

gcc aaa ccg gaa gac gta caa cgc gtg gcg gaa tcc caa ggc gtt aag         336
Ala Lys Pro Glu Asp Val Gln Arg Val Ala Glu Ser Gln Gly Val Lys
            100                 105                 110

ttg gta aac ggc att acc gtt atc gac ccg gcg agc gtg cgt gaa aac         384
Leu Val Asn Gly Ile Thr Val Ile Asp Pro Ala Ser Val Arg Glu Asn
        115                 120                 125

tat gtg gca cgt ttg gtt gag cta cgc aaa gcc aaa ggc atg acc gaa         432
Tyr Val Ala Arg Leu Val Glu Leu Arg Lys Ala Lys Gly Met Thr Glu
    130                 135                 140

acc atg gcg cgt gaa caa ttg gaa gac aat gtt gtg ctc ggt acc atg         480
Thr Met Ala Arg Glu Gln Leu Glu Asp Asn Val Val Leu Gly Thr Met
145                 150                 155                 160

atg ttg gaa gcc aac caa gta gac ggt ttg gta tcc ggc gcc gta cac         528
Met Leu Glu Ala Asn Gln Val Asp Gly Leu Val Ser Gly Ala Val His
                165                 170                 175

acc acc gcc aac acc att cgc ccg cca atg caa atc atc aaa acc gca         576
Thr Thr Ala Asn Thr Ile Arg Pro Pro Met Gln Ile Ile Lys Thr Ala
            180                 185                 190

ccg ggc agc tcc att att tct tcc atc ttc ttc atg ttg cta ccg gat         624
Pro Gly Ser Ser Ile Ile Ser Ser Ile Phe Phe Met Leu Leu Pro Asp
        195                 200                 205

caa gta ttg gtc tat ggc gat tgc gca gtg aac ccg gat ccg a               667
Gln Val Leu Val Tyr Gly Asp Cys Ala Val Asn Pro Asp Pro
    210                 215                 220
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<210>  198
<211>  222
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  198

Ala Leu Ser Leu Gln Ser Phe Asn Leu Glu Val Pro Val Asp Asp Lys
1               5                   10                  15


Glu Arg Ile Glu Asn Ile Lys Arg Tyr Thr Gly Glu Lys Leu Asp Thr
            20                  25                  30


Ala Phe Val Asn Gly Leu Val Glu Ala Ser Ser Arg Leu Arg Arg Leu
        35                  40                  45


Ser Pro Pro Ala Phe Arg Phe Gln Leu Thr Glu Leu Ala Arg Ala Ala
    50                  55                  60


Gln Lys Arg Ile Val Leu Pro Glu Gly Asp Glu Pro Arg Thr Ile Lys
65                  70                  75                  80


Ala Ala Ile Leu Cys Ala Glu Arg Gly Ile Ala Glu Cys Val Leu Leu
                85                  90                  95


Ala Lys Pro Glu Asp Val Gln Arg Val Ala Glu Ser Gln Gly Val Lys
            100                 105                 110


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


Tyr Val Ala Arg Leu Val Glu Leu Arg Lys Ala Lys Gly Met Thr Glu
    130                 135                 140


Thr Met Ala Arg Glu Gln Leu Glu Asp Asn Val Val Leu Gly Thr Met
145                 150                 155                 160


Met Leu Glu Ala Asn Gln Val Asp Gly Leu Val Ser Gly Ala Val His
                165                 170                 175


Thr Thr Ala Asn Thr Ile Arg Pro Pro Met Gln Ile Ile Lys Thr Ala
            180                 185                 190


Pro Gly Ser Ser Ile Ile Ser Ser Ile Phe Phe Met Leu Leu Pro Asp
        195                 200                 205


Gln Val Leu Val Tyr Gly Asp Cys Ala Val Asn Pro Asp Pro
    210                 215                 220
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```
<210>  199
<211>  267
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(267)

<400>  199
ggt ata cgc cct gag cat tta att ccg tct gat gag gca gaa gtt acg       48
Gly Ile Arg Pro Glu His Leu Ile Pro Ser Asp Glu Ala Glu Val Thr
1               5                   10                  15

ttg cgc agc aat gtg cag gtg gtg gaa ttg ctt ggt aac gaa acg caa       96
Leu Arg Ser Asn Val Gln Val Val Glu Leu Leu Gly Asn Glu Thr Gln
            20                  25                  30

att cac ctt gaa atc cct gaa att aaa caa ccg acc tta att tat cgc      144
Ile His Leu Glu Ile Pro Glu Ile Lys Gln Pro Thr Leu Ile Tyr Arg
        35                  40                  45

caa aat gat gtg gtg ttg gtg aag gag ggg gaa acg atg gac atc ggc      192
Gln Asn Asp Val Val Leu Val Lys Glu Gly Glu Thr Met Asp Ile Gly
    50                  55                  60

atc att ccg gaa cgt tgc cat ctg ttt aaa gaa gac ggc acc gcc tgc      240
Ile Ile Pro Glu Arg Cys His Leu Phe Lys Glu Asp Gly Thr Ala Cys
65                  70                  75                  80

caa cgt ttg tat aaa gaa aaa ggc gtt                                  267
Gln Arg Leu Tyr Lys Glu Lys Gly Val
                85


<210>  200
<211>  89
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  200

Gly Ile Arg Pro Glu His Leu Ile Pro Ser Asp Glu Ala Glu Val Thr
1               5                   10                  15


Leu Arg Ser Asn Val Gln Val Val Glu Leu Leu Gly Asn Glu Thr Gln
            20                  25                  30


Ile His Leu Glu Ile Pro Glu Ile Lys Gln Pro Thr Leu Ile Tyr Arg
        35                  40                  45


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


Ile Ile Pro Glu Arg Cys His Leu Phe Lys Glu Asp Gly Thr Ala Cys
```

```
65                  70                  75                  80


Gln Arg Leu Tyr Lys Glu Lys Gly Val
                85


<210>  201
<211>  219
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(219)

<400>  201
tac atc gtc atc gcc ttt gtg gtg tca cag tta ttg gac gga aat ctg       48
Tyr Ile Val Ile Ala Phe Val Val Ser Gln Leu Leu Asp Gly Asn Leu
1               5                   10                  15

ctg gtg ccg ttt ttg ttc tcc gaa gcg gtc aat ctg cac ccg ttg gtg       96
Leu Val Pro Phe Leu Phe Ser Glu Ala Val Asn Leu His Pro Leu Val
            20                  25                  30

atc atc att gcc gtt ttg att ttc ggt ggc ttg tgg gga ttc tgg ggc      144
Ile Ile Ile Ala Val Leu Ile Phe Gly Gly Leu Trp Gly Phe Trp Gly
        35                  40                  45

gta ttt ttt gcc att ccg ctg gcg act ttg gtg aaa gcg gtg gtg aac      192
Val Phe Phe Ala Ile Pro Leu Ala Thr Leu Val Lys Ala Val Val Asn
    50                  55                  60

gct tgg cct tcc aat gaa gcg gtg gaa                                  219
Ala Trp Pro Ser Asn Glu Ala Val Glu
65                  70


<210>  202
<211>  73
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  202

Tyr Ile Val Ile Ala Phe Val Val Ser Gln Leu Leu Asp Gly Asn Leu
1               5                   10                  15


Leu Val Pro Phe Leu Phe Ser Glu Ala Val Asn Leu His Pro Leu Val
            20                  25                  30


Ile Ile Ile Ala Val Leu Ile Phe Gly Gly Leu Trp Gly Phe Trp Gly
        35                  40                  45


Val Phe Phe Ala Ile Pro Leu Ala Thr Leu Val Lys Ala Val Val Asn
    50                  55                  60
```

```
Ala Trp Pro Ser Asn Glu Ala Val Glu
65                  70


<210>  203
<211>  631
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(630)

<400>  203
cct ttc gcc atc gaa agt gac gag aaa ttt gcc tcc gcc tgc att cgt       48
Pro Phe Ala Ile Glu Ser Asp Glu Lys Phe Ala Ser Ala Cys Ile Arg
1               5                   10                  15

tgc ggt cag tgc gtg caa gcc tgc cct tat gat atg ttg cat ttg gca       96
Cys Gly Gln Cys Val Gln Ala Cys Pro Tyr Asp Met Leu His Leu Ala
            20                  25                  30

tcg ttg cta tca cca atg gaa gcg ggg acg ccg tat ttt atc gcg cgc      144
Ser Leu Leu Ser Pro Met Glu Ala Gly Thr Pro Tyr Phe Ile Ala Arg
        35                  40                  45

gat aaa cct tgc gaa atg tgt ccg gat att cct tgc gcc cat gcg tgt      192
Asp Lys Pro Cys Glu Met Cys Pro Asp Ile Pro Cys Ala His Ala Cys
    50                  55                  60

ccg agc ggt gcg tta gat cgt gag gcg cag gat att aat caa tcc cgt      240
Pro Ser Gly Ala Leu Asp Arg Glu Ala Gln Asp Ile Asn Gln Ser Arg
65                  70                  75                  80

atg ggg ctg gcg gtg ttg ctg gat cat gaa acc tgc ttg aac tgg caa      288
Met Gly Leu Ala Val Leu Leu Asp His Glu Thr Cys Leu Asn Trp Gln
                85                  90                  95

ggc ttg cgt tgc gat gtg tgt tat cgg gtt tgt ccg ttg att gat aaa      336
Gly Leu Arg Cys Asp Val Cys Tyr Arg Val Cys Pro Leu Ile Asp Lys
            100                 105                 110

gcc att acg ctg gaa agc cat cgt aat gag cgc acc ggc aag cac gcg      384
Ala Ile Thr Leu Glu Ser His Arg Asn Glu Arg Thr Gly Lys His Ala
        115                 120                 125

gtg ttt att ccg acg gtg cat tcc gat ggc tgt acc ggc tgt ggc aaa      432
Val Phe Ile Pro Thr Val His Ser Asp Gly Cys Thr Gly Cys Gly Lys
    130                 135                 140

tgc gaa caa gcg tgt gtc ttg gaa gaa gcg gca atc aaa gta tta ccg      480
Cys Glu Gln Ala Cys Val Leu Glu Glu Ala Ala Ile Lys Val Leu Pro
145                 150                 155                 160

atg cat ttg gcg aaa ggc atg tta ggc aaa cat tat cgt ttg ggt tgg      528
Met His Leu Ala Lys Gly Met Leu Gly Lys His Tyr Arg Leu Gly Trp
                165                 170                 175

gaa gaa aag gcg aaa gcc gga cat tcc ttg gcg ccg aaa gat ttg att      576
Glu Glu Lys Ala Lys Ala Gly His Ser Leu Ala Pro Lys Asp Leu Ile
            180                 185                 190
```

```
tcg atg ccg acc cgt atg ccg gaa gcc aca atg ccg gta atg ggc gca        624
Ser Met Pro Thr Arg Met Pro Glu Ala Thr Met Pro Val Met Gly Ala
        195                 200                 205

gaa gac a                                                              631
Glu Asp
    210


<210>  204
<211>  210
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  204

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


Cys Gly Gln Cys Val Gln Ala Cys Pro Tyr Asp Met Leu His Leu Ala
            20                  25                  30


Ser Leu Leu Ser Pro Met Glu Ala Gly Thr Pro Tyr Phe Ile Ala Arg
        35                  40                  45


Asp Lys Pro Cys Glu Met Cys Pro Asp Ile Pro Cys Ala His Ala Cys
    50                  55                  60


Pro Ser Gly Ala Leu Asp Arg Glu Ala Gln Asp Ile Asn Gln Ser Arg
65                  70                  75                  80


Met Gly Leu Ala Val Leu Leu Asp His Glu Thr Cys Leu Asn Trp Gln
                85                  90                  95


Gly Leu Arg Cys Asp Val Cys Tyr Arg Val Cys Pro Leu Ile Asp Lys
            100                 105                 110


Ala Ile Thr Leu Glu Ser His Arg Asn Glu Arg Thr Gly Lys His Ala
        115                 120                 125


Val Phe Ile Pro Thr Val His Ser Asp Gly Cys Thr Gly Cys Gly Lys
    130                 135                 140


Cys Glu Gln Ala Cys Val Leu Glu Glu Ala Ala Ile Lys Val Leu Pro
145                 150                 155                 160


Met His Leu Ala Lys Gly Met Leu Gly Lys His Tyr Arg Leu Gly Trp
                165                 170                 175
```

```
Glu Glu Lys Ala Lys Ala Gly His Ser Leu Ala Pro Lys Asp Leu Ile
            180                 185                 190


Ser Met Pro Thr Arg Met Pro Glu Ala Thr Met Pro Val Met Gly Ala
        195                 200                 205


Glu Asp
    210


<210>  205
<211>  354
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(354)

<400>  205
tgc ctg gaa cgg gtg aaa cgg ttg gag aag caa ggg gtg att atg ggg       48
Cys Leu Glu Arg Val Lys Arg Leu Glu Lys Gln Gly Val Ile Met Gly
1               5                   10                  15

tat cgt gct ttg ctg aat ccc gca tta ttg gat tcg ccg ttg ttg gtg       96
Tyr Arg Ala Leu Leu Asn Pro Ala Leu Leu Asp Ser Pro Leu Leu Val
            20                  25                  30

atc gtg gaa att acg ctg gta cgt ggc aag ccc gat gtg ttt gaa gaa      144
Ile Val Glu Ile Thr Leu Val Arg Gly Lys Pro Asp Val Phe Glu Glu
        35                  40                  45

ttt aac gcg gcg gtg cag cag tta gat gaa att cag gaa tgc cat ttg      192
Phe Asn Ala Ala Val Gln Gln Leu Asp Glu Ile Gln Glu Cys His Leu
    50                  55                  60

gtt tcc ggt gat ttc gat tat tta ttg aaa aca cgg gtg gcg gat atg      240
Val Ser Gly Asp Phe Asp Tyr Leu Leu Lys Thr Arg Val Ala Asp Met
65                  70                  75                  80

gcg gcg tat cgt aaa ttg ctg ggg acc acc ttg ctg cgc ctg ccc ggg      288
Ala Ala Tyr Arg Lys Leu Leu Gly Thr Thr Leu Leu Arg Leu Pro Gly
                85                  90                  95

gtg aac gac acg cgc act tat gtg gtg atg gaa gaa gtg aaa caa acg      336
Val Asn Asp Thr Arg Thr Tyr Val Val Met Glu Glu Val Lys Gln Thr
            100                 105                 110

aat ttt tta cag tta aaa                                              354
Asn Phe Leu Gln Leu Lys
        115


<210>  206
<211>  118
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  206
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```
Cys Leu Glu Arg Val Lys Arg Leu Glu Lys Gln Gly Val Ile Met Gly
1               5                   10                  15

Tyr Arg Ala Leu Leu Asn Pro Ala Leu Leu Asp Ser Pro Leu Leu Val
            20                  25                  30

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

Phe Asn Ala Ala Val Gln Gln Leu Asp Glu Ile Gln Glu Cys His Leu
    50                  55                  60

Val Ser Gly Asp Phe Asp Tyr Leu Leu Lys Thr Arg Val Ala Asp Met
65                  70                  75                  80

Ala Ala Tyr Arg Lys Leu Leu Gly Thr Thr Leu Leu Arg Leu Pro Gly
                85                  90                  95

Val Asn Asp Thr Arg Thr Tyr Val Val Met Glu Glu Val Lys Gln Thr
            100                 105                 110

Asn Phe Leu Gln Leu Lys
        115

<210>  207
<211>  613
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(612)

<400>  207
atg agt tta aaa ata tta tta aat cag ccg caa tac gat ccg att cgt          48
Met Ser Leu Lys Ile Leu Leu Asn Gln Pro Gln Tyr Asp Pro Ile Arg
1               5                   10                  15

gac aaa aaa gcc gag cgc aac tta ttt gcc cgt cgc gct ttg gtg tca          96
Asp Lys Lys Ala Glu Arg Asn Leu Phe Ala Arg Arg Ala Leu Val Ser
            20                  25                  30

ttt atc ggc gtg ttg gtg ttg tcg gtg gtg tta att tta aac ttg tat         144
Phe Ile Gly Val Leu Val Leu Ser Val Val Leu Ile Leu Asn Leu Tyr
        35                  40                  45

gat ttg cag gtg gtc aat tat gac ggt tat caa acc cgt tcc aac ggc         192
Asp Leu Gln Val Val Asn Tyr Asp Gly Tyr Gln Thr Arg Ser Asn Gly
    50                  55                  60

aat cgt att aag ttg ttg ccg ctg ccg ccg act cgc ggg ttg att tat         240
Asn Arg Ile Lys Leu Leu Pro Leu Pro Pro Thr Arg Gly Leu Ile Tyr
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65                  70                  75                  80

gat cgc aac ggc aaa ctg ctg gcg gaa aat ctg acc ttt ttc ggg ctt       288
Asp Arg Asn Gly Lys Leu Leu Ala Glu Asn Leu Thr Phe Phe Gly Leu
                85                  90                  95

tat atc gtg cct gaa aag gtg gaa aat tta gac cgc act ttt gag gag       336
Tyr Ile Val Pro Glu Lys Val Glu Asn Leu Asp Arg Thr Phe Glu Glu
            100                 105                 110

ctg agg gtg ttg gta ggc tta act gat gaa gat att gcg aat ttt aac       384
Leu Arg Val Leu Val Gly Leu Thr Asp Glu Asp Ile Ala Asn Phe Asn
        115                 120                 125

aag gaa cgg cgt cgc tcc tcc cgt tat atg ccg att atg ctg aaa cga       432
Lys Glu Arg Arg Arg Ser Ser Arg Tyr Met Pro Ile Met Leu Lys Arg
    130                 135                 140

aat cta acg gaa gag caa att gcc cgt ttt gcg gtg aat caa tac aat       480
Asn Leu Thr Glu Glu Gln Ile Ala Arg Phe Ala Val Asn Gln Tyr Asn
145                 150                 155                 160

ttc cag agt ttg gat gtg aaa ccc tac ttt aag cgc cat tat tta tac       528
Phe Gln Ser Leu Asp Val Lys Pro Tyr Phe Lys Arg His Tyr Leu Tyr
                165                 170                 175

ggc gaa ccg ctg acc cat gtt ttg ggc tat gtg tca aaa att aac gat       576
Gly Glu Pro Leu Thr His Val Leu Gly Tyr Val Ser Lys Ile Asn Asp
            180                 185                 190

cgt gat gta gaa cgc ttg aaa aaa gag gaa aag tac g                    613
Arg Asp Val Glu Arg Leu Lys Lys Glu Glu Lys Tyr
        195                 200


<210>  208
<211>  204
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  208

Met Ser Leu Lys Ile Leu Leu Asn Gln Pro Gln Tyr Asp Pro Ile Arg
1               5                   10                  15


Asp Lys Lys Ala Glu Arg Asn Leu Phe Ala Arg Arg Ala Leu Val Ser
            20                  25                  30


Phe Ile Gly Val Leu Val Leu Ser Val Val Leu Ile Leu Asn Leu Tyr
        35                  40                  45


Asp Leu Gln Val Val Asn Tyr Asp Gly Tyr Gln Thr Arg Ser Asn Gly
    50                  55                  60


Asn Arg Ile Lys Leu Leu Pro Leu Pro Pro Thr Arg Gly Leu Ile Tyr
65                  70                  75                  80
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Asp Arg Asn Gly Lys Leu Leu Ala Glu Asn Leu Thr Phe Phe Gly Leu
                85                  90                  95

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

Leu Arg Val Leu Val Gly Leu Thr Asp Glu Asp Ile Ala Asn Phe Asn
        115                 120                 125

Lys Glu Arg Arg Arg Ser Ser Arg Tyr Met Pro Ile Met Leu Lys Arg
    130                 135                 140

Asn Leu Thr Glu Glu Gln Ile Ala Arg Phe Ala Val Asn Gln Tyr Asn
145                 150                 155                 160

Phe Gln Ser Leu Asp Val Lys Pro Tyr Phe Lys Arg His Tyr Leu Tyr
                165                 170                 175

Gly Glu Pro Leu Thr His Val Leu Gly Tyr Val Ser Lys Ile Asn Asp
            180                 185                 190

Arg Asp Val Glu Arg Leu Lys Lys Glu Glu Lys Tyr
        195                 200


<210>  209
<211>  631
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(630)

<400>  209
cgc tta gca caa cat tca tcg gaa aaa ctg acc gca ctt tcc cat gca       48
Arg Leu Ala Gln His Ser Ser Glu Lys Leu Thr Ala Leu Ser His Ala
1               5                   10                  15

acc acg cat tct gac gcc caa agt gcg gta gaa aat cag agt gaa tct       96
Thr Thr His Ser Asp Ala Gln Ser Ala Val Glu Asn Gln Ser Glu Ser
            20                  25                  30

gat agc gac gaa act gat gcg gat gtg ttg tta ggc gag gat tat cgt      144
Asp Ser Asp Glu Thr Asp Ala Asp Val Leu Leu Gly Glu Asp Tyr Arg
        35                  40                  45

tgg gag tgg agc aac ccc gag ctt gcc aat att gag caa ggc cct aag      192
Trp Glu Trp Ser Asn Pro Glu Leu Ala Asn Ile Glu Gln Gly Pro Lys
    50                  55                  60

ccc tcc gaa atc aaa gcc gcc att ttg cag gac atc act cct gaa tta      240
Pro Ser Glu Ile Lys Ala Ala Ile Leu Gln Asp Ile Thr Pro Glu Leu
```

```
65                  70                  75                  80

cag caa aaa atc gtc aat tta act caa acg caa gat cgc tgg gcg cag        288
Gln Gln Lys Ile Val Asn Leu Thr Gln Thr Gln Asp Arg Trp Ala Gln
                85                  90                  95

ctg att gag caa agc ggt gta gaa aat ctc acc aaa gag ttc gcc tta        336
Leu Ile Glu Gln Ser Gly Val Glu Asn Leu Thr Lys Glu Phe Ala Leu
            100                 105                 110

aat acc ttc att tgg cag gaa aat gac gcg gag ttt aaa ctt ggt gtg        384
Asn Thr Phe Ile Trp Gln Glu Asn Asp Ala Glu Phe Lys Leu Gly Val
        115                 120                 125

cgt tcc agc cac ggg cat tta aat cag gat aag cat cgg aag ctg tta        432
Arg Ser Ser His Gly His Leu Asn Gln Asp Lys His Arg Lys Leu Leu
    130                 135                 140

caa cag gca ctt tca gtg gtg tta cag aaa gaa att gca ctg acc gtg        480
Gln Gln Ala Leu Ser Val Val Leu Gln Lys Glu Ile Ala Leu Thr Val
145                 150                 155                 160

gaa att aac gac gac gaa caa tat ctg acg ccg acg gat tat cgc cgt        528
Glu Ile Asn Asp Asp Glu Gln Tyr Leu Thr Pro Thr Asp Tyr Arg Arg
                165                 170                 175

aaa acc tat gct caa ttg cgt gag cag gcg aaa cag gat ttg ttg caa        576
Lys Thr Tyr Ala Gln Leu Arg Glu Gln Ala Lys Gln Asp Leu Leu Gln
            180                 185                 190

gat gaa aag ttg caa cta ttg gag cgt gaa ttt gat tgt cag gtt gat        624
Asp Glu Lys Leu Gln Leu Leu Glu Arg Glu Phe Asp Cys Gln Val Asp
        195                 200                 205

gtg aaa a                                                              631
Val Lys
    210


<210>  210
<211>  210
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  210

Arg Leu Ala Gln His Ser Ser Glu Lys Leu Thr Ala Leu Ser His Ala
1               5                   10                  15


Thr Thr His Ser Asp Ala Gln Ser Ala Val Glu Asn Gln Ser Glu Ser
            20                  25                  30


Asp Ser Asp Glu Thr Asp Ala Asp Val Leu Leu Gly Glu Asp Tyr Arg
        35                  40                  45


Trp Glu Trp Ser Asn Pro Glu Leu Ala Asn Ile Glu Gln Gly Pro Lys
    50                  55                  60
```

```
Pro Ser Glu Ile Lys Ala Ala Ile Leu Gln Asp Ile Thr Pro Glu Leu
65                  70                  75                  80

Gln Gln Lys Ile Val Asn Leu Thr Gln Thr Gln Asp Arg Trp Ala Gln
                85                  90                  95

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

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

Arg Ser Ser His Gly His Leu Asn Gln Asp Lys His Arg Lys Leu Leu
    130                 135                 140

Gln Gln Ala Leu Ser Val Val Leu Gln Lys Glu Ile Ala Leu Thr Val
145                 150                 155                 160

Glu Ile Asn Asp Asp Glu Gln Tyr Leu Thr Pro Thr Asp Tyr Arg Arg
                165                 170                 175

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

Asp Glu Lys Leu Gln Leu Leu Glu Arg Glu Phe Asp Cys Gln Val Asp
        195                 200                 205

Val Lys
    210


<210>  211
<211>  1155
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(1155)

<400>  211
ccc gaa cat ata aaa gac aag gta tcg aga ggt ttc att atg gca agt        48
Pro Glu His Ile Lys Asp Lys Val Ser Arg Gly Phe Ile Met Ala Ser
1               5                   10                  15

gta aca ttg cgc aat gtg ggc aaa tct tac gga aac gta cat att tcc        96
Val Thr Leu Arg Asn Val Gly Lys Ser Tyr Gly Asn Val His Ile Ser
            20                  25                  30

aaa gat att aat ttg gat att gaa gaa ggc gaa ttt gtc gtc ttt gtc       144
Lys Asp Ile Asn Leu Asp Ile Glu Glu Gly Glu Phe Val Val Phe Val
```

```
        35                  40                  45

gga ccg tcc ggt tgc ggt aaa tcc aca tta ttg cga atg att gcc gga       192
Gly Pro Ser Gly Cys Gly Lys Ser Thr Leu Leu Arg Met Ile Ala Gly
    50                  55                  60

ctt gag gat att acc acc ggt gaa ctt tac atc ggt gaa aaa cgg atg       240
Leu Glu Asp Ile Thr Thr Gly Glu Leu Tyr Ile Gly Glu Lys Arg Met
65                  70                  75                  80

aac gat gtg ccg ccg gca aag cgc ggt atc ggt atg gtg ttc caa tct       288
Asn Asp Val Pro Pro Ala Lys Arg Gly Ile Gly Met Val Phe Gln Ser
                85                  90                  95

tac gcc ctg tac ccg cac ttg gat gtg gca gaa aat atg tct ttc ggg       336
Tyr Ala Leu Tyr Pro His Leu Asp Val Ala Glu Asn Met Ser Phe Gly
            100                 105                 110

ctg aaa tta gcc ggt gta aat aaa acg gaa cgg gat cag cgc gtt aat       384
Leu Lys Leu Ala Gly Val Asn Lys Thr Glu Arg Asp Gln Arg Val Asn
        115                 120                 125

cag gtt gcc gaa att tta cag ctt gcc cat ttg ctt gaa cgt aaa ccg       432
Gln Val Ala Glu Ile Leu Gln Leu Ala His Leu Leu Glu Arg Lys Pro
    130                 135                 140

aaa gcc ttg tcg ggc ggt cag cgt caa cgt gtg gcg att ggg cga acc       480
Lys Ala Leu Ser Gly Gly Gln Arg Gln Arg Val Ala Ile Gly Arg Thr
145                 150                 155                 160

ctt gtt tcc cag cca gaa gta ttc ttg ctg gac gaa ccg ctt tcc aac       528
Leu Val Ser Gln Pro Glu Val Phe Leu Leu Asp Glu Pro Leu Ser Asn
                165                 170                 175

tta gat gcc gcc ttg cgc gta caa atg cgg gtg gaa atc tcc aaa tta       576
Leu Asp Ala Ala Leu Arg Val Gln Met Arg Val Glu Ile Ser Lys Leu
            180                 185                 190

cac aaa aaa ctc aac cgc acc atg att tat gtt acc cat gac caa gtg       624
His Lys Lys Leu Asn Arg Thr Met Ile Tyr Val Thr His Asp Gln Val
        195                 200                 205

gaa gcc atg acc ctg gcg gac aaa atc gtg gtg ttg aat gcg ggc ggt       672
Glu Ala Met Thr Leu Ala Asp Lys Ile Val Val Leu Asn Ala Gly Gly
    210                 215                 220

att gcg cag gtg ggg aaa ccg ctg gaa ctt tac cat tat ccg caa aat       720
Ile Ala Gln Val Gly Lys Pro Leu Glu Leu Tyr His Tyr Pro Gln Asn
225                 230                 235                 240

cgt ttc gtg gcc ggt ttt atc ggt tca ccg aaa atg aat ttc ctg ccg       768
Arg Phe Val Ala Gly Phe Ile Gly Ser Pro Lys Met Asn Phe Leu Pro
                245                 250                 255

gtg aaa gtg act gct gtg gaa aaa gag cgg gtg caa atc gaa ttg ccc       816
Val Lys Val Thr Ala Val Glu Lys Glu Arg Val Gln Ile Glu Leu Pro
            260                 265                 270

gac gcc aac cat cat aac ttc tgg atc ccg gtt tcc ggt aat ggc gtg       864
Asp Ala Asn His His Asn Phe Trp Ile Pro Val Ser Gly Asn Gly Val
        275                 280                 285
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aaa gtg ggt gaa aac ctt tca tta ggt ata cgc cct gag cat tta att         912
Lys Val Gly Glu Asn Leu Ser Leu Gly Ile Arg Pro Glu His Leu Ile
    290                 295                 300

ccg tct gat gag gca gaa gtt acg ttg cgc agc aat gtg cag gtg gtg         960
Pro Ser Asp Glu Ala Glu Val Thr Leu Arg Ser Asn Val Gln Val Val
305                 310                 315                 320

gaa ttg ctt ggt aac gaa acg caa att cac ctt gaa atc cct gaa att        1008
Glu Leu Leu Gly Asn Glu Thr Gln Ile His Leu Glu Ile Pro Glu Ile
                325                 330                 335

aaa caa ccg acc tta att tat cgc caa aat gat gtg gtg ttg gtg aag        1056
Lys Gln Pro Thr Leu Ile Tyr Arg Gln Asn Asp Val Val Leu Val Lys
            340                 345                 350

gag ggg gaa acg atg gac atc ggc atc att ccg gaa cgt tgc cat ctg        1104
Glu Gly Glu Thr Met Asp Ile Gly Ile Ile Pro Glu Arg Cys His Leu
        355                 360                 365

ttt aaa gaa gac ggc acc gcc tgc caa cgt ttg tat aaa gaa aaa ggc        1152
Phe Lys Glu Asp Gly Thr Ala Cys Gln Arg Leu Tyr Lys Glu Lys Gly
    370                 375                 380

gtt                                                                    1155
Val
385


<210>  212
<211>  385
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  212

Pro Glu His Ile Lys Asp Lys Val Ser Arg Gly Phe Ile Met Ala Ser
1               5                   10                  15


Val Thr Leu Arg Asn Val Gly Lys Ser Tyr Gly Asn Val His Ile Ser
            20                  25                  30


Lys Asp Ile Asn Leu Asp Ile Glu Glu Gly Glu Phe Val Val Phe Val
        35                  40                  45


Gly Pro Ser Gly Cys Gly Lys Ser Thr Leu Leu Arg Met Ile Ala Gly
    50                  55                  60


Leu Glu Asp Ile Thr Thr Gly Glu Leu Tyr Ile Gly Glu Lys Arg Met
65                  70                  75                  80


Asn Asp Val Pro Pro Ala Lys Arg Gly Ile Gly Met Val Phe Gln Ser
                85                  90                  95
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Tyr Ala Leu Tyr Pro His Leu Asp Val Ala Glu Asn Met Ser Phe Gly
            100                 105                 110

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

Gln Val Ala Glu Ile Leu Gln Leu Ala His Leu Leu Glu Arg Lys Pro
    130                 135                 140

Lys Ala Leu Ser Gly Gly Gln Arg Gln Arg Val Ala Ile Gly Arg Thr
145                 150                 155                 160

Leu Val Ser Gln Pro Glu Val Phe Leu Leu Asp Glu Pro Leu Ser Asn
                165                 170                 175

Leu Asp Ala Ala Leu Arg Val Gln Met Arg Val Glu Ile Ser Lys Leu
            180                 185                 190

His Lys Lys Leu Asn Arg Thr Met Ile Tyr Val Thr His Asp Gln Val
        195                 200                 205

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

Ile Ala Gln Val Gly Lys Pro Leu Glu Leu Tyr His Tyr Pro Gln Asn
225                 230                 235                 240

Arg Phe Val Ala Gly Phe Ile Gly Ser Pro Lys Met Asn Phe Leu Pro
                245                 250                 255

Val Lys Val Thr Ala Val Glu Lys Glu Arg Val Gln Ile Glu Leu Pro
            260                 265                 270

Asp Ala Asn His His Asn Phe Trp Ile Pro Val Ser Gly Asn Gly Val
        275                 280                 285

Lys Val Gly Glu Asn Leu Ser Leu Gly Ile Arg Pro Glu His Leu Ile
    290                 295                 300

Pro Ser Asp Glu Ala Glu Val Thr Leu Arg Ser Asn Val Gln Val Val
305                 310                 315                 320

Glu Leu Leu Gly Asn Glu Thr Gln Ile His Leu Glu Ile Pro Glu Ile
                325                 330                 335

Lys Gln Pro Thr Leu Ile Tyr Arg Gln Asn Asp Val Val Leu Val Lys
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            340                 345                 350

Glu Gly Glu Thr Met Asp Ile Gly Ile Ile Pro Glu Arg Cys His Leu
        355                 360                 365

Phe Lys Glu Asp Gly Thr Ala Cys Gln Arg Leu Tyr Lys Glu Lys Gly
    370                 375                 380

Val
385


<210>  213
<211>  447
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(447)

<400>  213
atg cca aaa aat gcg caa ttc tac ctg ctt tcc gat gcc tct ccc gca        48
Met Pro Lys Asn Ala Gln Phe Tyr Leu Leu Ser Asp Ala Ser Pro Ala
1               5                   10                  15

cag acg aat ttg tct gcg gtg gaa agc ctt gcc tgc aat ttg gcg gcg        96
Gln Thr Asn Leu Ser Ala Val Glu Ser Leu Ala Cys Asn Leu Ala Ala
            20                  25                  30

tcc gcc tgg cgt ttg gga aaa cgg gtt ctg ttg gcg tgt gaa aat gaa       144
Ser Ala Trp Arg Leu Gly Lys Arg Val Leu Leu Ala Cys Glu Asn Glu
        35                  40                  45

gcg cag gcg ctc aat att gat gaa gcc ctt tgg caa cgg gaa ccg gac       192
Ala Gln Ala Leu Asn Ile Asp Glu Ala Leu Trp Gln Arg Glu Pro Asp
    50                  55                  60

gaa ttc gtc ccg cac aac ctt tcc ggc gaa gcc acc acg tat gcc acg       240
Glu Phe Val Pro His Asn Leu Ser Gly Glu Ala Thr Thr Tyr Ala Thr
65                  70                  75                  80

ccc atc gaa atc agc tgg acg ggc aaa cgc aac gca caa agc cgc gat       288
Pro Ile Glu Ile Ser Trp Thr Gly Lys Arg Asn Ala Gln Ser Arg Asp
                85                  90                  95

ttg ctg att aat tta caa ccg cag ctg ccg gaa ttc atc aac agc ttt       336
Leu Leu Ile Asn Leu Gln Pro Gln Leu Pro Glu Phe Ile Asn Ser Phe
            100                 105                 110

aac caa att atc gat ttc gta ccc gcc gaa gaa caa caa aaa gct tta       384
Asn Gln Ile Ile Asp Phe Val Pro Ala Glu Glu Gln Gln Lys Ala Leu
        115                 120                 125

gcg cgg gaa cgt tat aaa caa ttg agg cag ttg ggc tgg gaa ttg agt       432
Ala Arg Glu Arg Tyr Lys Gln Leu Arg Gln Leu Gly Trp Glu Leu Ser
    130                 135                 140
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acg gag cag gcg ggg 447
Thr Glu Gln Ala Gly
145

<210> 214
<211> 149
<212> PRT
<213> Actinobacillus actinomycetemcomitans

<400> 214

Met Pro Lys Asn Ala Gln Phe Tyr Leu Leu Ser Asp Ala Ser Pro Ala
1 5 10 15

Gln Thr Asn Leu Ser Ala Val Glu Ser Leu Ala Cys Asn Leu Ala Ala
20 25 30

Ser Ala Trp Arg Leu Gly Lys Arg Val Leu Leu Ala Cys Glu Asn Glu
35 40 45

Ala Gln Ala Leu Asn Ile Asp Glu Ala Leu Trp Gln Arg Glu Pro Asp
50 55 60

Glu Phe Val Pro His Asn Leu Ser Gly Glu Ala Thr Thr Tyr Ala Thr
65 70 75 80

Pro Ile Glu Ile Ser Trp Thr Gly Lys Arg Asn Ala Gln Ser Arg Asp
85 90 95

Leu Leu Ile Asn Leu Gln Pro Gln Leu Pro Glu Phe Ile Asn Ser Phe
100 105 110

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

Ala Arg Glu Arg Tyr Lys Gln Leu Arg Gln Leu Gly Trp Glu Leu Ser
130 135 140

Thr Glu Gln Ala Gly
145

<210> 215
<211> 774
<212> DNA
<213> Actinobacillus actinomycetemcomitans

<220>
<221> CDS
<222> (1)..(774)

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<400>  215
aaa gac aac aaa atc tgg cac ttc acc tta cga aaa gaa gca ata tgg        48
Lys Asp Asn Lys Ile Trp His Phe Thr Leu Arg Lys Glu Ala Ile Trp
1               5                   10                  15

tct aac ggc gaa ccg gtg act gcg cag caa ttt gtt gca agc tgg caa        96
Ser Asn Gly Glu Pro Val Thr Ala Gln Gln Phe Val Ala Ser Trp Gln
            20                  25                  30

cgg ctg gcg caa tcg gat tct cct tta aag cac tat tta cgc tac ctt       144
Arg Leu Ala Gln Ser Asp Ser Pro Leu Lys His Tyr Leu Arg Tyr Leu
        35                  40                  45

aac tta gtc aac gcg gag aaa gtg tta cag caa act ctg ctg cca gag       192
Asn Leu Val Asn Ala Glu Lys Val Leu Gln Gln Thr Leu Leu Pro Glu
    50                  55                  60

cag ttg gga att gtc gcg gaa aat gac cgc act tta cgc tta act tta       240
Gln Leu Gly Ile Val Ala Glu Asn Asp Arg Thr Leu Arg Leu Thr Leu
65                  70                  75                  80

gat aaa gcg acc cct tac ttg ccg caa atg ctg gcg cat atc agc ctg       288
Asp Lys Ala Thr Pro Tyr Leu Pro Gln Met Leu Ala His Ile Ser Leu
                85                  90                  95

ttg cca caa tat ttg tcg cca cat gaa ggc att gtg acc aac ggg gcg       336
Leu Pro Gln Tyr Leu Ser Pro His Glu Gly Ile Val Thr Asn Gly Ala
            100                 105                 110

tat caa gtg atg ggg cag caa ggc aat ctc atc cat ttg gaa aag aac       384
Tyr Gln Val Met Gly Gln Gln Gly Asn Leu Ile His Leu Glu Lys Asn
        115                 120                 125

ccg caa tat tgg gcg aaa gaa aaa gtg gcg ttt aaa aat gtg gat tat       432
Pro Gln Tyr Trp Ala Lys Glu Lys Val Ala Phe Lys Asn Val Asp Tyr
    130                 135                 140

cag aaa atc gca ctg caa cag gac gtc agc gcc tta gat gtg gtg tgg       480
Gln Lys Ile Ala Leu Gln Gln Asp Val Ser Ala Leu Asp Val Val Trp
145                 150                 155                 160

cag ccg cag caa caa acg gat caa acg caa tac ttc ccg caa ctt tgc       528
Gln Pro Gln Gln Gln Thr Asp Gln Thr Gln Tyr Phe Pro Gln Leu Cys
                165                 170                 175

acc tat ttt tac acc ttt aat ttt aac atg cca caa ctg gcg caa agc       576
Thr Tyr Phe Tyr Thr Phe Asn Phe Asn Met Pro Gln Leu Ala Gln Ser
            180                 185                 190

ccg gtg cgt aag gca ttg gca atg atg aca tct gcc cgc agt tta ttg       624
Pro Val Arg Lys Ala Leu Ala Met Met Thr Ser Ala Arg Ser Leu Leu
        195                 200                 205

ccg gaa agt aaa aac agg att cct tta acg gat aat ttt tta cca att       672
Pro Glu Ser Lys Asn Arg Ile Pro Leu Thr Asp Asn Phe Leu Pro Ile
    210                 215                 220

tcc atg caa acc atc gat agc cgg tgg gag caa acg ccg gtt gaa caa       720
Ser Met Gln Thr Ile Asp Ser Arg Trp Glu Gln Thr Pro Val Glu Gln
225                 230                 235                 240
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tta tta agc caa gcg cga att gga gag aag gca ccg ctc aaa ctg acc       768
Leu Leu Ser Gln Ala Arg Ile Gly Glu Lys Ala Pro Leu Lys Leu Thr
                245                 250                 255

cta agt                                                               774
Leu Ser



<210>  216
<211>  258
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  216

Lys Asp Asn Lys Ile Trp His Phe Thr Leu Arg Lys Glu Ala Ile Trp
1               5                   10                  15


Ser Asn Gly Glu Pro Val Thr Ala Gln Gln Phe Val Ala Ser Trp Gln
            20                  25                  30


Arg Leu Ala Gln Ser Asp Ser Pro Leu Lys His Tyr Leu Arg Tyr Leu
        35                  40                  45


Asn Leu Val Asn Ala Glu Lys Val Leu Gln Gln Thr Leu Leu Pro Glu
    50                  55                  60


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


Asp Lys Ala Thr Pro Tyr Leu Pro Gln Met Leu Ala His Ile Ser Leu
                85                  90                  95


Leu Pro Gln Tyr Leu Ser Pro His Glu Gly Ile Val Thr Asn Gly Ala
            100                 105                 110


Tyr Gln Val Met Gly Gln Gln Gly Asn Leu Ile His Leu Glu Lys Asn
        115                 120                 125


Pro Gln Tyr Trp Ala Lys Glu Lys Val Ala Phe Lys Asn Val Asp Tyr
    130                 135                 140


Gln Lys Ile Ala Leu Gln Gln Asp Val Ser Ala Leu Asp Val Val Trp
145                 150                 155                 160


Gln Pro Gln Gln Gln Thr Asp Gln Thr Gln Tyr Phe Pro Gln Leu Cys
                165                 170                 175


Thr Tyr Phe Tyr Thr Phe Asn Phe Asn Met Pro Gln Leu Ala Gln Ser
```

```
            180                 185                 190

Pro Val Arg Lys Ala Leu Ala Met Met Thr Ser Ala Arg Ser Leu Leu
    195                 200                 205

Pro Glu Ser Lys Asn Arg Ile Pro Leu Thr Asp Asn Phe Leu Pro Ile
    210                 215                 220

Ser Met Gln Thr Ile Asp Ser Arg Trp Glu Gln Thr Pro Val Glu Gln
225                 230                 235                 240

Leu Leu Ser Gln Ala Arg Ile Gly Glu Lys Ala Pro Leu Lys Leu Thr
                245                 250                 255

Leu Ser


<210>  217
<211>  363
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(363)

<400>  217
atc cgt att caa ccg gac gaa ggc att tct atg cgt ttt ggc ttg aaa        48
Ile Arg Ile Gln Pro Asp Glu Gly Ile Ser Met Arg Phe Gly Leu Lys
1               5                   10                  15

aaa ccg ggc gcc ggc ttt gaa gcc aaa gaa gtg tcg atg gat ttc cgc        96
Lys Pro Gly Ala Gly Phe Glu Ala Lys Glu Val Ser Met Asp Phe Arg
            20                  25                  30

tat gcc gat ctt gcg ggt gcc acc gtc atg acc gct tat gag cgt tta       144
Tyr Ala Asp Leu Ala Gly Ala Thr Val Met Thr Ala Tyr Glu Arg Leu
        35                  40                  45

ttg ctt gat gcc atg aaa ggc gac gcg acc cta ttt gcg cgt acc gat       192
Leu Leu Asp Ala Met Lys Gly Asp Ala Thr Leu Phe Ala Arg Thr Asp
    50                  55                  60

gcc gta cac gcc gcc tgg aaa ttc gtt caa ccg att ttg aac tat aaa       240
Ala Val His Ala Ala Trp Lys Phe Val Gln Pro Ile Leu Asn Tyr Lys
65                  70                  75                  80

gcc caa ggc ggc aga ctt tat gat tac gag gcc ggc acc tgg gga ccg       288
Ala Gln Gly Gly Arg Leu Tyr Asp Tyr Glu Ala Gly Thr Trp Gly Pro
                85                  90                  95

acg gca gcc gat aaa ctc atc gcc aaa agc ggt cgt gta tgg cgc cgc       336
Thr Ala Ala Asp Lys Leu Ile Ala Lys Ser Gly Arg Val Trp Arg Arg
            100                 105                 110
```

```
cca agc ggg ttg atg aag aaa aaa gtg                                  363
Pro Ser Gly Leu Met Lys Lys Lys Val
        115                 120


<210>  218
<211>  121
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  218

Ile Arg Ile Gln Pro Asp Glu Gly Ile Ser Met Arg Phe Gly Leu Lys
1               5                   10                  15


Lys Pro Gly Ala Gly Phe Glu Ala Lys Glu Val Ser Met Asp Phe Arg
            20                  25                  30


Tyr Ala Asp Leu Ala Gly Ala Thr Val Met Thr Ala Tyr Glu Arg Leu
        35                  40                  45


Leu Leu Asp Ala Met Lys Gly Asp Ala Thr Leu Phe Ala Arg Thr Asp
    50                  55                  60


Ala Val His Ala Ala Trp Lys Phe Val Gln Pro Ile Leu Asn Tyr Lys
65                  70                  75                  80


Ala Gln Gly Gly Arg Leu Tyr Asp Tyr Glu Ala Gly Thr Trp Gly Pro
                85                  90                  95


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


Pro Ser Gly Leu Met Lys Lys Lys Val
        115                 120


<210>  219
<211>  159
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(159)

<400>  219
atg gca aca ggc aaa agc att att tta atg gga gtt tcc agt aca gga      48
Met Ala Thr Gly Lys Ser Ile Ile Leu Met Gly Val Ser Ser Thr Gly
1               5                   10                  15

aaa aca tca gtg ggg acg gaa gta gca cgt cgt ttg gag ata aaa ctg      96
Lys Thr Ser Val Gly Thr Glu Val Ala Arg Arg Leu Glu Ile Lys Leu
            20                  25                  30
```

```
att gat ggc gat gat ctg cac ccg cgc gcc aat atc ata aaa atg ggc        144
Ile Asp Gly Asp Asp Leu His Pro Arg Ala Asn Ile Ile Lys Met Gly
        35                  40                  45

gaa gga cat ccg ctc                                                    159
Glu Gly His Pro Leu
    50


<210>  220
<211>  53
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  220

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


Lys Thr Ser Val Gly Thr Glu Val Ala Arg Arg Leu Glu Ile Lys Leu
            20                  25                  30


Ile Asp Gly Asp Asp Leu His Pro Arg Ala Asn Ile Ile Lys Met Gly
        35                  40                  45


Glu Gly His Pro Leu
    50


<210>  221
<211>  289
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(288)

<400>  221
aac att gct tat gcg gcg aaa gac aaa tac agt cgt gaa gaa atc atc        48
Asn Ile Ala Tyr Ala Ala Lys Asp Lys Tyr Ser Arg Glu Glu Ile Ile
1               5                   10                  15

aaa gcg gca aaa gcg gcg cac gcc atg gaa ttt atc gag cat ttg gaa        96
Lys Ala Ala Lys Ala Ala His Ala Met Glu Phe Ile Glu His Leu Glu
            20                  25                  30

aac ggt ctg gat acg gtt atc ggc gaa aac ggc gcc agc tta tcc ggc       144
Asn Gly Leu Asp Thr Val Ile Gly Glu Asn Gly Ala Ser Leu Ser Gly
        35                  40                  45

ggt caa cgc cag cgt tta gcc atc gcc cgc gcc ttg ttg cgt aac tcg       192
Gly Gln Arg Gln Arg Leu Ala Ile Ala Arg Ala Leu Leu Arg Asn Ser
    50                  55                  60

ccg gta ttg att tta gat gaa gcc acc tcg gca ttg gat acg gaa tcc       240
Pro Val Leu Ile Leu Asp Glu Ala Thr Ser Ala Leu Asp Thr Glu Ser
```

```
65                  70                  75                  80

gaa cgc gca att caa gcg gca ttg gaa gaa atc caa aaa gat cgc acg g     289
Glu Arg Ala Ile Gln Ala Ala Leu Glu Glu Ile Gln Lys Asp Arg Thr
                85                  90                  95


<210>  222
<211>  96
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  222

Asn Ile Ala Tyr Ala Ala Lys Asp Lys Tyr Ser Arg Glu Glu Ile Ile
1               5                   10                  15


Lys Ala Ala Lys Ala Ala His Ala Met Glu Phe Ile Glu His Leu Glu
            20                  25                  30


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


Gly Gln Arg Gln Arg Leu Ala Ile Ala Arg Ala Leu Leu Arg Asn Ser
    50                  55                  60


Pro Val Leu Ile Leu Asp Glu Ala Thr Ser Ala Leu Asp Thr Glu Ser
65                  70                  75                  80


Glu Arg Ala Ile Gln Ala Ala Leu Glu Glu Ile Gln Lys Asp Arg Thr
                85                  90                  95


<210>  223
<211>  353
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(351)

<400>  223
tcg aac atc aac cct gat gat cca agt gcg att atc gaa ggc aac gaa       48
Ser Asn Ile Asn Pro Asp Asp Pro Ser Ala Ile Ile Glu Gly Asn Glu
1               5                   10                  15

aaa gtg gtt cgc cct cgt tta acc gac gcg gaa ttc ttc tcc aaa acc       96
Lys Val Val Arg Pro Arg Leu Thr Asp Ala Glu Phe Phe Ser Lys Thr
            20                  25                  30

gac tta aaa caa aaa tta gtg gat cgc tta ccg cgc ttg gaa act gtg      144
Asp Leu Lys Gln Lys Leu Val Asp Arg Leu Pro Arg Leu Glu Thr Val
        35                  40                  45

ttg ttc caa caa caa ctt ggc aca ttg cgt gat aaa acc gac cgc atc      192
```

```
Leu Phe Gln Gln Gln Leu Gly Thr Leu Arg Asp Lys Thr Asp Arg Ile
    50                  55                  60

gaa caa ctt gcg ggt gca atc gcc aaa caa atc ggt gcc gac gaa gcg      240
Glu Gln Leu Ala Gly Ala Ile Ala Lys Gln Ile Gly Ala Asp Glu Ala
65                  70                  75                  80

aaa gca aaa cgt gcg ggc ttg ctg tca aaa tgc gat ttg atg acc aat      288
Lys Ala Lys Arg Ala Gly Leu Leu Ser Lys Cys Asp Leu Met Thr Asn
                85                  90                  95

atg gtg ttt gaa ttc acc gac acc caa ggc gta atg ggt atg cac tat      336
Met Val Phe Glu Phe Thr Asp Thr Gln Gly Val Met Gly Met His Tyr
            100                 105                 110

gcc cgt cac gac ggc ga                                               353
Ala Arg His Asp Gly
        115


<210>  224
<211>  117
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  224

Ser Asn Ile Asn Pro Asp Asp Pro Ser Ala Ile Ile Glu Gly Asn Glu
1               5                   10                  15


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


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


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


Glu Gln Leu Ala Gly Ala Ile Ala Lys Gln Ile Gly Ala Asp Glu Ala
65                  70                  75                  80


Lys Ala Lys Arg Ala Gly Leu Leu Ser Lys Cys Asp Leu Met Thr Asn
                85                  90                  95


Met Val Phe Glu Phe Thr Asp Thr Gln Gly Val Met Gly Met His Tyr
            100                 105                 110


Ala Arg His Asp Gly
        115


<210>  225
<211>  366
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<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(366)

<400>  225
cta ttg gaa aaa caa ggg tta att aaa tta aaa gat ccg acc aac ctg        48
Leu Leu Glu Lys Gln Gly Leu Ile Lys Leu Lys Asp Pro Thr Asn Leu
1               5                   10              15

ttc tcc act tct ata gat atc att gaa aat ccg aaa aat tta caa atc        96
Phe Ser Thr Ser Ile Asp Ile Ile Glu Asn Pro Lys Asn Leu Gln Ile
            20                  25                  30

aaa gaa gtg gat acc tcc gtt gcg gca cgt gcc tta gat gac gtt gat       144
Lys Glu Val Asp Thr Ser Val Ala Ala Arg Ala Leu Asp Asp Val Asp
        35                  40                  45

ttg gcg gta gtg aat aac aac tac gcc ggt caa gta ggc tta aat gcg       192
Leu Ala Val Val Asn Asn Asn Tyr Ala Gly Gln Val Gly Leu Asn Ala
    50                  55                  60

caa gat cac ggc gta ttt gtg gaa gat aaa gat tca ccg tat gta aat       240
Gln Asp His Gly Val Phe Val Glu Asp Lys Asp Ser Pro Tyr Val Asn
65                  70                  75                  80

att atc gtg gca cgg acc gat aac aaa gac agc aaa gcc gta cag act       288
Ile Ile Val Ala Arg Thr Asp Asn Lys Asp Ser Lys Ala Val Gln Thr
                85                  90                  95

ttc gtg aaa gcc tac caa acc ccg gaa gtg gaa caa gaa gcg aaa aaa       336
Phe Val Lys Ala Tyr Gln Thr Pro Glu Val Glu Gln Glu Ala Lys Lys
            100                 105                 110

cac ttt aaa gac ggc gtg gta aaa ggc tgg                               366
His Phe Lys Asp Gly Val Val Lys Gly Trp
        115                 120


<210>  226
<211>  122
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  226

Leu Leu Glu Lys Gln Gly Leu Ile Lys Leu Lys Asp Pro Thr Asn Leu
1               5                   10                  15


Phe Ser Thr Ser Ile Asp Ile Ile Glu Asn Pro Lys Asn Leu Gln Ile
            20                  25                  30


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


Leu Ala Val Val Asn Asn Asn Tyr Ala Gly Gln Val Gly Leu Asn Ala
```

```
    50                  55                  60


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


Ile Ile Val Ala Arg Thr Asp Asn Lys Asp Ser Lys Ala Val Gln Thr
                85                  90                  95


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


His Phe Lys Asp Gly Val Val Lys Gly Trp
        115                 120


<210>  227
<211>  465
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(465)

<400>  227
atg act tgg caa aac gtg tcg atc atc gtt agt tat cct caa act gac        48
Met Thr Trp Gln Asn Val Ser Ile Ile Val Ser Tyr Pro Gln Thr Asp
1               5                   10                  15

ata aaa agg gga tct ttt atg aac ttg aaa aaa tta tta ggc gtc gca        96
Ile Lys Arg Gly Ser Phe Met Asn Leu Lys Lys Leu Leu Gly Val Ala
            20                  25                  30

aca tta gcc tcc gta ttc gcc tta acg gct tgt aat gaa gag aaa aaa       144
Thr Leu Ala Ser Val Phe Ala Leu Thr Ala Cys Asn Glu Glu Lys Lys
        35                  40                  45

ccg gaa gcc gca ccg gca gac aaa ccg gcg gca gaa gcc ccg gca aca       192
Pro Glu Ala Ala Pro Ala Asp Lys Pro Ala Ala Glu Ala Pro Ala Thr
    50                  55                  60

atc aaa gtg ggc gtg atg gca gga ccg gaa cac caa gtg gct gaa atc       240
Ile Lys Val Gly Val Met Ala Gly Pro Glu His Gln Val Ala Glu Ile
65                  70                  75                  80

gca gcg aaa gtg gca aaa gaa aaa tac aac tta gac gta gaa tac gtt       288
Ala Ala Lys Val Ala Lys Glu Lys Tyr Asn Leu Asp Val Glu Tyr Val
                85                  90                  95

tta ttc aat gac tac gcc ttg cca aac act gca gtg tct aaa ggt gat       336
Leu Phe Asn Asp Tyr Ala Leu Pro Asn Thr Ala Val Ser Lys Gly Asp
            100                 105                 110

tta gac gtt aac gca atg caa cat aaa ccg tat tta gac aaa gat tcc       384
Leu Asp Val Asn Ala Met Gln His Lys Pro Tyr Leu Asp Lys Asp Ser
        115                 120                 125
```

```
caa gcg aaa gga ttg aac aac tta gtg atc gtg ggt aat acc ttc gtt       432
Gln Ala Lys Gly Leu Asn Asn Leu Val Ile Val Gly Asn Thr Phe Val
    130                 135                 140

tac ccg tta gcc ggc tat tca aaa aaa atc aaa                           465
Tyr Pro Leu Ala Gly Tyr Ser Lys Lys Ile Lys
145                 150                 155


<210>  228
<211>  155
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  228

Met Thr Trp Gln Asn Val Ser Ile Ile Val Ser Tyr Pro Gln Thr Asp
1               5                   10                  15


Ile Lys Arg Gly Ser Phe Met Asn Leu Lys Lys Leu Leu Gly Val Ala
            20                  25                  30


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


Pro Glu Ala Ala Pro Ala Asp Lys Pro Ala Ala Glu Ala Pro Ala Thr
    50                  55                  60


Ile Lys Val Gly Val Met Ala Gly Pro Glu His Gln Val Ala Glu Ile
65                  70                  75                  80


Ala Ala Lys Val Ala Lys Glu Lys Tyr Asn Leu Asp Val Glu Tyr Val
                85                  90                  95


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


Leu Asp Val Asn Ala Met Gln His Lys Pro Tyr Leu Asp Lys Asp Ser
        115                 120                 125


Gln Ala Lys Gly Leu Asn Asn Leu Val Ile Val Gly Asn Thr Phe Val
    130                 135                 140


Tyr Pro Leu Ala Gly Tyr Ser Lys Lys Ile Lys
145                 150                 155


<210>  229
<211>  1008
<212>  DNA
<213>  Actinobacillus actinomycetemcomitans
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<220>
<221>  CDS
<222>  (1)..(1008)

<400>  229
atg atg gaa ctc gcc tat ttg caa aaa acg ccg cca aaa cag acc gca          48
Met Met Glu Leu Ala Tyr Leu Gln Lys Thr Pro Pro Lys Gln Thr Ala
1               5                   10                  15

ctt tta aaa gcg gaa tgc gcg gat ttt gtc gtc aaa gag caa ctg ggc          96
Leu Leu Lys Ala Glu Cys Ala Asp Phe Val Val Lys Glu Gln Leu Gly
            20                  25                  30

tac gac atg agc ggc gac ggc gaa ttc gtg gcg gtg aaa ata cgc aaa         144
Tyr Asp Met Ser Gly Asp Gly Glu Phe Val Ala Val Lys Ile Arg Lys
        35                  40                  45

acc gat tgc aac acc ttg ttt gta ggc gag caa ctg gcg aaa ttc gcc         192
Thr Asp Cys Asn Thr Leu Phe Val Gly Glu Gln Leu Ala Lys Phe Ala
    50                  55                  60

ggc att tcg gca cgc aac atg agt tat gcc ggt ttg aaa gat cgc aaa         240
Gly Ile Ser Ala Arg Asn Met Ser Tyr Ala Gly Leu Lys Asp Arg Lys
65                  70                  75                  80

gct gtc acc gaa caa tgg ttc agc ctg caa atg ccc ggg caa ccg acg         288
Ala Val Thr Glu Gln Trp Phe Ser Leu Gln Met Pro Gly Gln Pro Thr
                85                  90                  95

ccg gat ttc agc caa ttt cac ctt gac ggc gtg gat att ctt gaa gtg         336
Pro Asp Phe Ser Gln Phe His Leu Asp Gly Val Asp Ile Leu Glu Val
            100                 105                 110

acc cgc cac caa cgc aaa atc cgt atc ggc agc ctg caa ggc aat cat         384
Thr Arg His Gln Arg Lys Ile Arg Ile Gly Ser Leu Gln Gly Asn His
        115                 120                 125

ttt gag att ttg ctg cgc cac gcg gaa gaa acc gac gag ctc aaa gtg         432
Phe Glu Ile Leu Leu Arg His Ala Glu Glu Thr Asp Glu Leu Lys Val
    130                 135                 140

cgg ttg gat ttt ctg gca aaa aac ggc ttc ccc aat tat ttc acc gaa         480
Arg Leu Asp Phe Leu Ala Lys Asn Gly Phe Pro Asn Tyr Phe Thr Glu
145                 150                 155                 160

cag cgt ttc ggg cgc gac ggc aac aat ctc acc caa gcc cta cgc tgg         528
Gln Arg Phe Gly Arg Asp Gly Asn Asn Leu Thr Gln Ala Leu Arg Trp
                165                 170                 175

gcg gcg ggc gaa atc aaa gtg aaa gat cgc aac aag cgc agt ttc tat         576
Ala Ala Gly Glu Ile Lys Val Lys Asp Arg Asn Lys Arg Ser Phe Tyr
            180                 185                 190

att tcc gcc gcc cgc agt gag att ttc aat tta atc gtt gcc aaa cgt         624
Ile Ser Ala Ala Arg Ser Glu Ile Phe Asn Leu Ile Val Ala Lys Arg
        195                 200                 205

att gaa ctc agt ctg gcg cag cag gtc tta aat gga gac gtt ttg caa         672
Ile Glu Leu Ser Leu Ala Gln Gln Val Leu Asn Gly Asp Val Leu Gln
    210                 215                 220
```

```
ctg aac ggt tcg cac agt tgg ttt gtg gcg gac gca tcg gaa gat ttg        720
Leu Asn Gly Ser His Ser Trp Phe Val Ala Asp Ala Ser Glu Asp Leu
225                 230                 235                 240

acg caa ctg caa caa cgc ttg gca caa cgg gat att ttg ctt acc gca        768
Thr Gln Leu Gln Gln Arg Leu Ala Gln Arg Asp Ile Leu Leu Thr Ala
                245                 250                 255

ccg ctt atc ggc gaa gag gac aaa agt gcg gtg gat ttt gag aat gaa        816
Pro Leu Ile Gly Glu Glu Asp Lys Ser Ala Val Asp Phe Glu Asn Glu
            260                 265                 270

att ttt gtc gcg cac caa gcc ttg ttc cat ttg atg cgg caa gaa cgc        864
Ile Phe Val Ala His Gln Ala Leu Phe His Leu Met Arg Gln Glu Arg
        275                 280                 285

gtg aaa gcc gcc cgc cgt ccg att tta atg cag gcg caa cag ttt caa        912
Val Lys Ala Ala Arg Arg Pro Ile Leu Met Gln Ala Gln Gln Phe Gln
    290                 295                 300

tgg caa ttt gaa ccg aac ggt ttg cgc ctt aaa ttt tat ttg ccg gca        960
Trp Gln Phe Glu Pro Asn Gly Leu Arg Leu Lys Phe Tyr Leu Pro Ala
305                 310                 315                 320

ggc agt tac gcc acg gcg ttg gta cgc gag ctg gtg aat gtt gaa aac       1008
Gly Ser Tyr Ala Thr Ala Leu Val Arg Glu Leu Val Asn Val Glu Asn
                325                 330                 335


<210>  230
<211>  336
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  230

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


Leu Leu Lys Ala Glu Cys Ala Asp Phe Val Val Lys Glu Gln Leu Gly
            20                  25                  30


Tyr Asp Met Ser Gly Asp Gly Glu Phe Val Ala Val Lys Ile Arg Lys
        35                  40                  45


Thr Asp Cys Asn Thr Leu Phe Val Gly Glu Gln Leu Ala Lys Phe Ala
    50                  55                  60


Gly Ile Ser Ala Arg Asn Met Ser Tyr Ala Gly Leu Lys Asp Arg Lys
65                  70                  75                  80


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


Pro Asp Phe Ser Gln Phe His Leu Asp Gly Val Asp Ile Leu Glu Val
```

```
            100                 105                 110

Thr Arg His Gln Arg Lys Ile Arg Ile Gly Ser Leu Gln Gly Asn His
        115                 120                 125

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

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

Gln Arg Phe Gly Arg Asp Gly Asn Asn Leu Thr Gln Ala Leu Arg Trp
                165                 170                 175

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

Ile Ser Ala Ala Arg Ser Glu Ile Phe Asn Leu Ile Val Ala Lys Arg
        195                 200                 205

Ile Glu Leu Ser Leu Ala Gln Gln Val Leu Asn Gly Asp Val Leu Gln
    210                 215                 220

Leu Asn Gly Ser His Ser Trp Phe Val Ala Asp Ala Ser Glu Asp Leu
225                 230                 235                 240

Thr Gln Leu Gln Gln Arg Leu Ala Gln Arg Asp Ile Leu Leu Thr Ala
                245                 250                 255

Pro Leu Ile Gly Glu Glu Asp Lys Ser Ala Val Asp Phe Glu Asn Glu
            260                 265                 270

Ile Phe Val Ala His Gln Ala Leu Phe His Leu Met Arg Gln Glu Arg
        275                 280                 285

Val Lys Ala Ala Arg Arg Pro Ile Leu Met Gln Ala Gln Gln Phe Gln
    290                 295                 300

Trp Gln Phe Glu Pro Asn Gly Leu Arg Leu Lys Phe Tyr Leu Pro Ala
305                 310                 315                 320

Gly Ser Tyr Ala Thr Ala Leu Val Arg Glu Leu Val Asn Val Glu Asn
                325                 330                 335

<210>  231
<211>  738
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<212>  DNA
<213>  Actinobacillus actinomycetemcomitans

<220>
<221>  CDS
<222>  (1)..(738)

<400>  231
atg aat att tta tta agt aac gat gac ggc att cac gcg ccg ggc att       48
Met Asn Ile Leu Leu Ser Asn Asp Asp Gly Ile His Ala Pro Gly Ile
1               5                   10                  15

cgt gtg atg gca gaa gca ttg cgt aag att gcc aat gtg acc atc gtc       96
Arg Val Met Ala Glu Ala Leu Arg Lys Ile Ala Asn Val Thr Ile Val
            20                  25                  30

gcg ccg gac agc aac cgc agc gcc gcc tcc agt tcc tta acc ttg gtg      144
Ala Pro Asp Ser Asn Arg Ser Ala Ala Ser Ser Ser Leu Thr Leu Val
        35                  40                  45

aag ccg ttg tat ccg tta cat ttg gaa agc ggt gat tat tgc gtc aac      192
Lys Pro Leu Tyr Pro Leu His Leu Glu Ser Gly Asp Tyr Cys Val Asn
    50                  55                  60

ggc acg ccg gcg gat tgc gtg cat att gcg ctg aac ggt ttt ctt tcc      240
Gly Thr Pro Ala Asp Cys Val His Ile Ala Leu Asn Gly Phe Leu Ser
65                  70                  75                  80

ggg cgc atc gat ttg gtg att tcc ggc atc aac gcc ggg gcg aac ctg      288
Gly Arg Ile Asp Leu Val Ile Ser Gly Ile Asn Ala Gly Ala Asn Leu
                85                  90                  95

ggc gat gat gtg cta tat tcc ggc acg gtc gcg gca gca ttt gaa ggg      336
Gly Asp Asp Val Leu Tyr Ser Gly Thr Val Ala Ala Ala Phe Glu Gly
            100                 105                 110

cgt cat ctg ggc ttg ccg tct att gcg gta tcg ctc gat ggt cgt caa      384
Arg His Leu Gly Leu Pro Ser Ile Ala Val Ser Leu Asp Gly Arg Gln
        115                 120                 125

cat ttt gaa acg gcg gcg cgc gtg gta tgc gat ttg gtg ccg aaa tta      432
His Phe Glu Thr Ala Ala Arg Val Val Cys Asp Leu Val Pro Lys Leu
    130                 135                 140

cac gcc caa tta tta ggc aaa cac gaa att ctg aat att aac gtg ccc      480
His Ala Gln Leu Leu Gly Lys His Glu Ile Leu Asn Ile Asn Val Pro
145                 150                 155                 160

gat gtg cct tac gaa gaa ctg aaa ggc att aaa gtg tgc cat ttg ggc      528
Asp Val Pro Tyr Glu Glu Leu Lys Gly Ile Lys Val Cys His Leu Gly
                165                 170                 175

tac cgt tct tcc gct tct gaa gtg att aaa cag caa agc ccg cgt ggc      576
Tyr Arg Ser Ser Ala Ser Glu Val Ile Lys Gln Gln Ser Pro Arg Gly
            180                 185                 190

gaa gac atg tat tgg atc ggg ctc agc ggc ttg ccg gaa tat gaa agc      624
Glu Asp Met Tyr Trp Ile Gly Leu Ser Gly Leu Pro Glu Tyr Glu Ser
        195                 200                 205

gaa ggc acc gat ttc cac gcg gtg aaa aac ggc tat gtt tcc att acg      672
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Glu Gly Thr Asp Phe His Ala Val Lys Asn Gly Tyr Val Ser Ile Thr
    210                 215                 220

ccg att cag gtg gac atg acc gcg cac cac tca atc aac gct tta caa       720
Pro Ile Gln Val Asp Met Thr Ala His His Ser Ile Asn Ala Leu Gln
225                 230                 235                 240

cgt tgg tta gaa agt gaa                                               738
Arg Trp Leu Glu Ser Glu
                245


<210>  232
<211>  246
<212>  PRT
<213>  Actinobacillus actinomycetemcomitans

<400>  232

Met Asn Ile Leu Leu Ser Asn Asp Asp Gly Ile His Ala Pro Gly Ile
1               5                   10                  15


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


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


Lys Pro Leu Tyr Pro Leu His Leu Glu Ser Gly Asp Tyr Cys Val Asn
    50                  55                  60


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


Gly Arg Ile Asp Leu Val Ile Ser Gly Ile Asn Ala Gly Ala Asn Leu
                85                  90                  95


Gly Asp Asp Val Leu Tyr Ser Gly Thr Val Ala Ala Ala Phe Glu Gly
            100                 105                 110


Arg His Leu Gly Leu Pro Ser Ile Ala Val Ser Leu Asp Gly Arg Gln
        115                 120                 125


His Phe Glu Thr Ala Ala Arg Val Val Cys Asp Leu Val Pro Lys Leu
    130                 135                 140


His Ala Gln Leu Leu Gly Lys His Glu Ile Leu Asn Ile Asn Val Pro
145                 150                 155                 160


Asp Val Pro Tyr Glu Glu Leu Lys Gly Ile Lys Val Cys His Leu Gly
                165                 170                 175
```

```
Tyr Arg Ser Ser Ala Ser Glu Val Ile Lys Gln Gln Ser Pro Arg Gly
        180                 185                 190

Glu Asp Met Tyr Trp Ile Gly Leu Ser Gly Leu Pro Glu Tyr Glu Ser
    195                 200                 205

Glu Gly Thr Asp Phe His Ala Val Lys Asn Gly Tyr Val Ser Ile Thr
    210                 215                 220

Pro Ile Gln Val Asp Met Thr Ala His His Ser Ile Asn Ala Leu Gln
225                 230                 235                 240

Arg Trp Leu Glu Ser Glu
                245


<210>  233
<211>  426
<212>  DNA
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1               5                   10                  15

gtg gaa aaa gaa acc ggc att gct gca gaa cgc cca caa gtg gcg tcg       96
Val Glu Lys Glu Thr Gly Ile Ala Ala Glu Arg Pro Gln Val Ala Ser
            20                  25                  30

gta ttc att aat cgg tta aaa gcc aaa atg aag ctg caa acc gat ccg      144
Val Phe Ile Asn Arg Leu Lys Ala Lys Met Lys Leu Gln Thr Asp Pro
        35                  40                  45

acc gtc att tac ggc atg ggc gac gac tac aac ggc aat att cgc aaa      192
Thr Val Ile Tyr Gly Met Gly Asp Asp Tyr Asn Gly Asn Ile Arg Lys
    50                  55                  60

aaa gat ttg gaa acg cca acg cct tat aac acc tat gtg att gac ggc      240
Lys Asp Leu Glu Thr Pro Thr Pro Tyr Asn Thr Tyr Val Ile Asp Gly
65                  70                  75                  80

ttg ccg ccg aca ccg att gcg atg ccg agt gaa gag gcg tta cag gcg      288
Leu Pro Pro Thr Pro Ile Ala Met Pro Ser Glu Glu Ala Leu Gln Ala
                85                  90                  95

gtg gca cat ccg gcg caa acg gcg ttt tat tat ttc gtg gca gac ggc      336
Val Ala His Pro Ala Gln Thr Ala Phe Tyr Tyr Phe Val Ala Asp Gly
            100                 105                 110

acg ggg gga cac aaa ttc agt cgt aat tta aac gaa cat aac aaa gcg      384
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Thr Gly Gly His Lys [illegible] Ser Arg Asn Leu Asn Glu His Asn Lys Ala
        115                 120                 125

gtg cag caa tat ttg cgc tgg tac cgc gaa caa aac gga aaa                     426
Val Gln Gln Tyr Leu Arg Trp Tyr Arg Glu Gln Asn Gly Lys
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<400>  234

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1               5                   10                  15


Val Glu Lys Glu Thr Gly Ile Ala Ala Glu Arg Pro Gln Val Ala Ser
            20                  25                  30


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


Thr Val Ile Tyr Gly Met Gly Asp Asp Tyr Asn Gly Asn Ile Arg Lys
    50                  55                  60


Lys Asp Leu Glu Thr Pro Thr Pro Tyr Asn Thr Tyr Val Ile Asp Gly
65                  70                  75                  80


Leu Pro Pro Thr Pro Ile Ala Met Pro Ser Glu Glu Ala Leu Gln Ala
                85                  90                  95


Val Ala His Pro Ala Gln Thr Ala Phe Tyr Tyr Phe Val Ala Asp Gly
            100                 105                 110


Thr Gly Gly His Lys Phe Ser Arg Asn Leu Asn Glu His Asn Lys Ala
        115                 120                 125


Val Gln Gln Tyr Leu Arg Trp Tyr Arg Glu Gln Asn Gly Lys
    130                 135                 140




1
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【国際調査報告】

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US03/32645

A. CLASSIFICATION OF SUBJECT MATTER
IPC(7) : A61K 38/00; C07K 1/00, 14/00, 17/00
US CL : 530/330, 300, 350; 424/190.1
According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
U.S. : 530/330, 300, 350; 424/190.1

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
Please See Continuation Sheet

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X --- A	WO 02/077183 A2 (ELITRA PHARM INC.) 03 October 2002 (03.10.02), see SEQ ID NO:67236 in particular residues 73-91 are identical to residues 236-254 of SEQ ID NO:2 of claim 1 herein.	1, 17 ---------- 2

☐ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:	"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"A" document defining the general state of the art which is not considered to be of particular relevance	"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"E" earlier application or patent published on or after the international filing date	
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"O" document referring to an oral disclosure, use, exhibition or other means	
"P" document published prior to the international filing date but later than the priority date claimed	"&" document member of the same patent family

Date of the actual completion of the international search 20 July 2004 (20.07.2004)	Date of mailing of the international search report 03 NOV 2004
Name and mailing address of the ISA/US Mail Stop PCT, Attn: ISA/US Commissioner for Patents P.O. Box 1450 Alexandria, Virginia 22313-1450 Facsimile No. (703) 305-3230	Authorized officer Patricia A. Duffy Telephone No. 703-308-0196

Form PCT/ISA/210 (second sheet) (July 1998)

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US03/32645

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claim Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claim Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claim Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:
Please See Continuation Sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 1, 2 and 17 (in part as drawn to SEQ ID NO:2)

Remark on Protest ☐ The additional search fees were accompanied by the applicant's protest.
☐ No protest accompanied the payment of additional search fees.

PCT/US03/32645

INTERNATIONAL SEARCH REPORT

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING

The inventions listed as Groups 1-1052 do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: in the instant case the technical features are defined as recited below.

Groups 1-116, claims 1, 2 and 17 (in part), drawn to polypeptides (the first appearing technical feature each represented by a unique sequence identifier).

Groups 117-233, claims 3-8 and 21-23 (in part), drawn to nucleic acids, vectors and host cells (the second appearing technical feature each represented by a unique sequence identifier)..

Groups 234-350, claims 9-12 (in part), drawn to antibodies (the third appearing technical feature each represented by and antibody binding a unique sequence identifier)..

Groups 351-467, claims 13 and 14 (in part), drawn to methods of treatment using the antibodies (the first method of use of the third technical feature).

Groups 468-584, claims 15 and 16 (in part) , drawn to methods of detecting using the antibodies (the second method of use of the third technical feature).

Groups 585-701 , claims 18-20 (in part), drawn to methods of using the polypeptides to elicit an immune response (the first method of use of the first appearing technical feature).

Groups 702-818, claims 24-26 (in part), drawn to methods of using the nucleic acids to elicit an immune response (the first method of use of the second technical feature).

Groups 819-935, claim 27 (in part), drawn to methods of detection of a microbe using the nucleic acid (the second method of use of the second technical feature).

Groups 936-1052, claim 28 (in part), drawn to methods of detection of antibodies using the polypeptides (the second method of use of the first technical feature).

Each of the polypeptides of Groups 1-116 fail to share a common technical feature that defines the polypeptides over the art. The polypeptides do not share a common core sequence / structure and therefore do not relate to a single general inventive concept within the meaning of PCT Rule 13.1. Further, the first appearing technical feature of the polypeptide comprising at least contiguous 5 amino acids of SEQ ID NO:2 of claim 1 is anticipated by the disclosure of the polypeptide sequence of SEQ ID NO:67236 of WO200277183, published 03 October 2002. SEQ ID NO:67236 of the prior art has 19 consecutive amino acids in common with the claimed polypeptide of SEQ ID NO:2 and meets the limitations of the claimed invention. Therefore, the groups of inventions (1, 117, 234, 351, 468, 585, 702, 819 and 936) as they relate to the polypeptide of SEQ ID NO:2, do not recite a technical feature that is "special" within the meaning of PCT Rule 13.2 because the claims do not recite a technical feature that provides for a novel contribution over the prior art. As such, the polypeptides, nucleic acids, antibodies and associated methods of use as drawn to the polypeptide of SEQ ID NO:2, do not share a single general inventive concept because the first appearing technical feature defined by claim 1 is not "special".

INTERNATIONAL SEARCH REPORT

PCT/US03/32645

Continuation of B. FIELDS SEARCHED Item 3:
BIOTECH SEQUENCE SEARCH: SEQ ID NO:2 and oligomers thereof. WEST, MEDLINE, EMBASE, WIPO, JAPIO: search terms: actinomycetemcomitans, Actinobacillus, antigens, vaccines, polypeptides, isolate, purify.

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(51)Int.Cl.			ＦＩ			テーマコード（参考）
C12N	**1/21**	**(2006.01)**	C12N	1/21		４Ｃ０８５
C12N	**5/10**	**(2006.01)**	C12N	5/00	A	４Ｃ０８６
C12Q	**1/02**	**(2006.01)**	C12Q	1/02		４Ｈ０４５
C12Q	**1/68**	**(2006.01)**	C12Q	1/68	A	
A61K	**39/395**	**(2006.01)**	A61K	39/395	D	
A61P	**1/02**	**(2006.01)**	A61K	39/395	R	
A61P	**31/04**	**(2006.01)**	A61P	1/02		
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			C12P	21/08		

(81)指定国　AP(GH,GM,KE,LS,MW,MZ,SD,SL,SZ,TZ,UG,ZM,ZW),EA(AM,AZ,BY,KG,KZ,MD,RU,TJ,TM),EP(AT,BE,BG,CH,CY,CZ,DE,DK,EE,ES,FI,FR,GB,GR,HU,IE,IT,LU,MC,NL,PT,RO,SE,SI,SK,TR),OA(BF,BJ,CF,CG,CI,CM,GA,GN,GQ,GW,ML,MR,NE,SN,TD,TG),AE,AG,AL,AM,AT,AU,AZ,BA,BB,BG,BR,BY,BZ,CA,CH,CN,CO,CR,CU,CZ,DE,DK,DM,DZ,EC,EE,ES,FI,GB,GD,GE,GH,GM,HR,HU,ID,IL,IN,IS,JP,KE,KG,KP,KR,KZ,LC,LK,LR,LS,LT,LU,LV,MA,MD,MG,MK,MN,MW,MX,MZ,NI,NO,NZ,OM,PG,PH,PL,PT,RO,RU,SC,SD,SE,SG,SK,SL,SY,TJ,TM,TN,TR,TT,TZ,UA,UG,US,UZ,VC,VN,YU,ZA,ZM,ZW

（特許庁注：以下のものは登録商標）
ＵＮＩＸ

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Ｆターム(参考)
4B024 AA01 AA11 AA13 BA31 CA02 EA02 EA04 HA17
4B063 QA01 QA18 QA19 QQ06 QQ43 QR32 QR39 QR48 QR55 QR62 QS33 QS34 QX02
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申请号	JP2004553443	申请日	2003-10-15
[标]申请(专利权)人(译)	佛罗里达州研究基金会股份有限公司雷开球德大学		
申请(专利权)人(译)	佛罗里达州研究基金会大学，Incorporated的雷开球德		
[标]发明人	ハンドフィールドマーティン ヒルマンジェフリーダニエル プログルスクフォックスアン		
发明人	ハンドフィールド,マーティン ヒルマン,ジェフリー,ダニエル プログルスク-フォックス,アン		
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代理人(译)	森田浩二 田中玲子 北野 健		
优先权	02/37235 2002-11-20 US		
其他公开文献	JP2006519586A		

摘要(译)

设置引起的放线放线杆菌病，预防，改善和治疗为，抗体，多肽和多核苷酸的检测。