



No. 10-025154- -00007-0000

Fecha: 2013-04-04 11:08:47 Dep. 2020 DIR.NUEVASCR
Tra. 11 PATENTEIYII Eve: 378 FASENACIONALI
Act. 523 RESPUESTA Follós: 218

Señor Director
DIRECCIÓN DE NUEVAS CREACIONES
Superintendencia de Industria y Comercio
E. S. D.

Trámite : 011
Evento : 378
Actuación : 444

Referencia Expediente No. 10025154
Asunto Solicitud de patente para
PROTEÍNAS DE STREPTOCOCCUS INMUNOGÉNICAS
Solicitante **BOEHRINGER INGELHEIM VETMEDICA GMBH**
Fecha de solicitud 3 de marzo de 2010

1. Yo, LUZ CLEMENCIA DE PÁEZ, obrando como apoderada del solicitante en el asunto antes identificado, me refiero al oficio No. **21635** notificado por fijación en lista de 27 de noviembre de 2012 y con solicitud de prórroga del 20 de Febrero de 2013
2. Mediante oficio No. **21635** se puso en conocimiento del solicitante el informe que contiene las observaciones hechas por su Despacho sobre la presente solicitud de patente. Atiendo a las observaciones de la manera siguiente:

2.1. **Modificaciones al Capítulo Reivindicatorio**

La solicitante desea presentar un nuevo capítulo reivindicatorio con el ánimo de superar las objeciones del Oficio 21635. El soporte a dichas modificaciones puede ser encontrado en el capítulo descriptivo como fue originalmente presentado.

"EXCELENCIA LEGAL EN UN MUNDO SIN FRONTERAS"

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Las modificaciones al capítulo reivindicatorio, corresponden a las admitidas en la aplicación de la Oficina Europea No 08793829.6, de la cual ya se ha recibido por parte de dicha oficina, la intención para otorgar su concesión. Se adjunta el documento en mención.

Las siguientes modificaciones se han realizado al capítulo reivindicatorio:

- Todas las reivindicaciones se han limitado a *Streptococcus uberis*
- Las antiguas reivindicaciones 13-21, han sido eliminadas.
- El término "factor de virulencia bacteriano" ha sido sustituido, por los números de identificación de las secuencias SEQ ID NO, enumerados en la Figura 4 de los aminoácidos o ácidos nucleicos correspondientes.
- En las reivindicaciones 1 y 8, la palabra "determinar" ha sido reemplazado por "probar".

Cabe destacar además, que durante el trámite de la solicitud de patente europea correspondiente, la numeración de las secuencias en la Figura 4 original no correspondía a la numeración de las mismas secuencias en el correspondiente listado de secuencias. Con el fin de superar este error en la presente solicitud, se ha modificado la Figura 4, tal y como se ha hecho en Europa, y en el que la numeración de las secuencias se ha adaptado a la Lista de Secuencias. Se adjunta la Figura 4 modificada con la lista de secuencias.

2.2. Excepción a la patentabilidad

El Examinador menciona que las reivindicaciones 20 – 21, no son patentables, de acuerdo con el Art 20, literal d).

Dado que dichas reivindicaciones han sido eliminadas del capítulo reivindicatorio se entiende por superada la objeción.

2.3. Claridad y concisión en las reivindicaciones

El examinador menciona que la reivindicación 1 carece de claridad, en la medida que el método que se desea proteger no especifica el procedimiento por medio del cual se identifica la proteína secretada, se selecciona y se determina su capacidad de unión a anticuerpo.

Según el examinador, además las reivindicaciones 15 y 16, las cuales se refieren a la proteína de *Streptococcus* y la molécula de ácido nucleico que codifica por lo menos dos proteínas, respectivamente, no se encuentran claramente definidas, ya que no se define de ninguna manera su estructura y que no se puede realizar la comparación con el estado de la técnica.

El Examinador además describe que la reivindicación 17, relacionada con el portador recombinante no se encuentra claro, porque no se hace mención al tipo de portador o depósito o acceso.

El Examinador menciona que la reivindicación 18 se encuentra caracterizada por un resultado a alcanzar.

Con el fin de superar el numeral de claridad y las anteriores objeciones descritas por el Examinador, el procedimiento reivindicado se ha modificado y se describe a continuación de manera detallada:

(1) La etapa a) de la reivindicación 1 se refiere a la identificación de (o parte de) una proteína secretada, una proteína asociada a superficie o una proteína que tiene el 80% de identidad de secuencia a secuencias específicas, las cuales se enumeran en la Figura 4 y en el Listado de Secuencias. Este paso es por ejemplo, realizado como se describe en la página 4, líneas 13-25 del documento PCT: los genes de *Streptococcus uberis* pueden ser identificados buscando el motivo de una proteína secretada y / o una proteína asociada a superficie. Por ejemplo, los genes pueden ser identificados buscando, un motivo de unión de lípidos (indicativo de una proteína asociada a superficie) o para un sitio de división de peptidasa señal (indicativo de una proteína secretada). Es comúnmente conocido, que las

proteínas secretadas contienen un péptido señal y un sitio de división de peptidasa señal en su extremo N-terminal. Debido a la presencia del péptido señal, la proteína se puede escindir en el sitio de división de peptidasa señal, de modo que tal la proteína será liberada. En la ausencia de dominios de transmembrana, la proteína entonces se secretará al exterior de la célula.

Las proteínas asociadas a superficie también pueden ser identificadas buscando genes con un sitio de unión de sortasa (indicativo para una proteína asociada a superficie), como se describe en el Ejemplo 1 de la presente solicitud. En este Ejemplo, las proteínas de *Streptococcus uberis* son identificadas basándose en motivos de firma en el genoma de *S. uberis*, tales como un motivo de sortasa LPxTGE, que es un sitio de unión a sortasa (ver descripción y la Tabla 1).

También es posible seleccionar proteínas o genes que tienen al menos 80% de identidad de secuencia a un número SEQ ID específica de una secuencia indicada, como las que se encuentran en la Figura 4.

Como se describe en la página 6, líneas 18-28 del documento PCT, los métodos y programas informáticos para la alineación de secuencias y la determinación de su identidad de secuencia, tales como "Align 2", son bien conocidos en la técnica.

- (2) La etapa b) de la reivindicación 1 comprende la selección de una proteína que fue identificada en el paso a) la cual es conservada sobre al menos dos cepas de *Streptococcus* y/o sus serotipos. En el Ejemplo 2, se evidencia cómo dicha identificación se puede realizar mediante hibridación de los productos de PCR, de los genes que codifican las proteínas identificadas en la etapa a). Estos productos de PCR se hibridizan con el ADN cromosómico de múltiples cepas de *S. uberis*. Si una proteína se hibridiza con múltiples cepas de *S. uberis*, indica que la proteína se encuentra conservada sobre de múltiples cepas de *S. uberis*.
- (3) Finalmente, en la etapa c) se comprueba si una proteína que es seleccionada en el paso b) se une a un anticuerpo o a una célula inmune de dos animales infectados por dos cepas diferentes de *Streptococcus* o sus serotipos.

La etapa c) tiene particular importancia, porque este paso implica probar si una proteína seleccionada se une a anticuerpos o células inmunes de al menos dos animales infectados, en los que los animales están infectados con por lo menos dos diferentes cepas o serotipos. Por lo tanto, los anticuerpos o células inmunes que se han planteado en contra de las bacterias cultivadas *in vivo*, se utilizan en el paso c).

Contrariamente a la afirmación del Examinador, este no es un procedimiento común para la producción de anticuerpos. Como se explica en la página 1, líneas 13-24 del documento PCT, hasta ahora muchas vacunas comerciales contra *Streptococcus* están basadas en bacterinas de células completas. Generalmente, dichas bacterinas producen una protección significativa contra el desafío a los serotipos homólogos, pero no protegen contra el desafío a los serotipos heterólogos. La vacunación con células completas de *Streptococcus*, a menudo resulta en una respuesta inmune, que se dirige contra la misma cepa de *Streptococcus*, pero la cual no es (suficientemente) dirigida contra otras cepas de *Streptococcus*, por no hablar además, de otros serotipos de *Streptococcus*. Como resultado, muchas vacunas proporcionan protección insuficiente frente a cepas heterólogas y/o serotipos, porque la vacunación contra una cepa de *Streptococcus*, no es generalmente eficaz en la lucha contra la infección por otra cepa de *Streptococcus*. Asimismo, la vacunación contra un serotipo *Streptococcus* generalmente no es eficaz en la lucha contra la infección por otro serotipo de *Streptococcus*.

Además, los procedimientos comunes para la producción de anticuerpos a menudo prueban la unión de anticuerpos a (inmovilizado) un antígeno o bacterias que se cultivan *in vitro*. La presente invención, sin embargo, difiere de tales procedimientos en los que los sueros de animales infectados son utilizados. Esto proporciona ventajas importantes, como se describe a continuación.

(4) Las diferencias entre las bacterias cultivadas *in vivo* e *in vitro*:

El hecho de que la etapa c) sea llevada a cabo usando animales infectados, es importante, porque la expresión de proteínas en la superficie celular de una bacteria *Streptococcus* que se cultiva *in vivo*, difiere de la expresión de proteínas que se cultivan *in vitro*. Como es conocido para un experto en la técnica, las bacterias

cultivadas *in vivo* se refieren a las bacterias que se cultivan en un animal después de la infección, mientras que las bacterias cultivadas *in vitro*, se refiere a bacterias que se cultivan, por ejemplo en caldo de cultivo en frascos de cultivo.

Muchas proteínas que se expresan en la superficie de la bacteria *Streptococcus* cultivadas *in vivo* pueden estar ausentes o ser expresadas en un menor grado que en las bacterias *Streptococcus* que se cultivan *in vitro*. La otra manera también es posible: la expresión de algunas proteínas en bacterias cultivadas *in vitro* puede ser mayor que su expresión en bacterias cultivadas *in vivo*. Tales diferencias en la expresión son principalmente un resultado del medio ambiente en el que las bacterias se cultivan. Por ejemplo, el contacto de las bacterias cultivadas *in vivo* con células eucariotas puede resultar en un aumento de las proteínas implicadas en la unión de células eucariotas. Como otro ejemplo, el contacto de las bacterias con compuestos ambientales, puede resultar en el aumento de la expresión de las proteínas capaces de degradar tales compuestos.

Además, la accesibilidad al sistema inmune de las proteínas expresadas en la superficie celular puede diferir entre las bacterias cultivadas *in vivo* e *in vitro*. La accesibilidad de las proteínas puede por ejemplo ser influenciada por el espesor de la cápsula bacteriana de polisacárido. Las bacterias pueden aumentar el grosor de la cápsula en respuesta a señales ambientales. Debido al aumento de espesor, la accesibilidad de las proteínas expresadas en la célula bacteriana al sistema inmunológico del animal infectado se reduce, aumentando así la resistencia de la bacteria a la fagocitosis y muerte por leucocitos.

En conclusión, la presente invención proporciona un enfoque diferente en comparación con los procedimientos comunes. Esto es debido al hecho de que un método de acuerdo con la presente invención incluye una etapa de prueba, en el que las proteínas seleccionadas se incuban con anticuerpos o células inmunes de los animales que están infectados por lo menos con dos diferentes cepas de *S. uberis* y/o serotipos, donde los métodos de la presente invención producirán proteínas diferentes en comparación con los procedimientos comunes *in vitro*. Las proteínas que se encuentran en la presente invención, por lo tanto, proporcionan una mejor respuesta

inmunogénica *in vivo* contra al menos dos cepas o serotipos de *S. uberis*, contrariamente a las vacunas conocidas actualmente de *S. uberis* que no protegen contra el desafío con cepas de *S. uberis* heterólogas.

2.4. **Análisis de novedad**

El Examinador refiere que el documento D1 afecta la novedad de las reivindicaciones 1-14.

Con el fin de superar esta objeción, la cepa de *Streptococcus* se ha limitado a *Streptococcus uberis*, la cual no está divulgada en el documento D1. El documento D1, describe la producción de la proteína SP36 de *Streptococcus pneumoniae*. Por lo tanto, las actuales reivindicaciones modificadas son novedosas e inventivas a la luz de D1, tal como la Oficina Europea ha reconocido.

3. **Modificación de la solicitud en trámite**

Con el objeto de subsanar las objeciones presentadas por su Despacho y de acuerdo con el artículo 34 de la Decisión 486 de la Comisión de la Comunidad Andina, donde se establece que la modificación de una solicitud es posible en cualquier momento del trámite mientras no implique una ampliación de la solicitud inicial, me permito presentar nuevo capítulo reivindicatorio modificado.

Sin embargo, la solicitante desearía señalar que cualquier materia divulgada borrada o no contenida en la presente serie de reclamaciones no debe ser considerada como abandonada. Así mismo, la solicitante se reserva su derecho a incluir tal materia en futuras series de reivindicaciones.

4. De acuerdo con los argumentos y modificaciones presentados con este escrito, la presente solicitud cumple a cabalidad con los requerimientos exigidos en la Decisión 486 y las objeciones formuladas por el Examinador se ven superadas.

Puesto que se ha dado respuesta a todas las objeciones formuladas por el Examinador, se solicita atentamente proceder al otorgamiento de la solicitud de patente. En este sentido, respetuosamente recordamos al Examinador que la patente no podrá ser negada con base en objeciones diferentes a las expuestas en la acción oficial No. **21635** toda vez que al no haber sido trasladadas a mi representada, dicha decisión violaría tanto el tenor literal del artículo 45 de la Decisión 486 como el derecho constitucional al debido proceso. En este evento, y con base en el inciso 2 del artículo 45, respetuosamente solicitamos al Examinador expedir una nueva acción oficial que permita a mi representada contra argumentar las mismas o modificar la solicitud con el fin de cumplir los requisitos de patentabilidad.

5. ANEXOS

- Nuevo pliego reivindicatorio conformado por 12 reivindicaciones
- Formulario para modificaciones.
- Copia de la intención de otorgar la patente correspondiente a la aplicación No 08793829.6 en Europa.
- Copia de la Figura 4 modificada
- Listado de secuencias correspondientes a la aplicación WO 2009/020391

Señor Director,


LUZ CLEMENCIA DE PÁEZ
C.C. 35.456.344 de Usaquén
T.P.A. No. 23.555

5 COLO-04484-0841-018-7
RBL\JMS\ID-238777\WPCL4484
No. M-2013-238777\IRBL

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DIRECCIÓN DE NUEVAS CREACIONES
MODIFICACIONES Y/O CORRECCIONES

1. Identificación del Trámite	
☐ Error material	☒ Modificación a una Solicitud en trámite
☒ Patente de Invención	
☐ Patente de Modelo de Utilidad	
☐ Registro de Diseño Industrial	
☐ Esquema de Trazado de Circuitos Integrados	

2. Datos del solicitante		
Persona Natural ☐	Persona Jurídica ☒	
BOEHRINGER INGELHEIM VETMEDICA GMBH		
Nombre o denominación / Nombre o razón social completa		
Nombre representante legal		
Tipo de empresa	Micro ☐ Pequeña ☐ Mediana ☐ Otra ☐	
Documento de identificación:	☐ C.C. ☐ C.E. ☐ NIT ☐ Otro Número _____	
Nacionalidad/País de constitución	Dirección y domicilio del titular	Ciudad
Alemania	Binger Strasse 173, 55216 Ingelheim Am Rhein, Alemania	Ingelheim Am Rhein
Dirección electrónica	No. Fax	Número telefónico
clientes@cavelier.com	2 11 86 50	3 47 36 11

☐ Autorizo expresamente a la Superintendencia de Industria y Comercio para que todas las comunicaciones sean enviadas a través de la dirección de correo electrónico

3. Datos del apoderado:		
Apellidos y Nombre De Páez Luz Clemencia	Documento de identificación C.C. 35.456.344	Tarjeta profesional T.P.A. 23.555
Dirección y domicilio	Ciudad	
Carrera 4ª No. 72 –35	Bogotá	
Dirección electrónica	No. Fax	Número telefónico
cavelier@cavelier.com	2 11 86 50	3 47 36 11
En caso de haber presentado poder general para asuntos que se adelanten ante la Delegatura de Propiedad Industrial, sírvase indicar el número de su radicación o protocolo de poder general		

4. Datos del trámite**Corrección:****Expediente No 10.025.154****Aparece****Debe ser****Modificación:****Modificación al capítulo reivindicatorio.**

Presento nuevo capítulo reivindicatorio compuesto por 12 reivindicaciones con el fin de superar las objeciones hechas por Su Despacho a la presente solicitud de patente y pido respetuosamente que el examen de patentabilidad sea realizado sobre estas nuevas reivindicaciones presentadas.

Respetuosamente manifiesto que a pesar de eliminar materia del pliego reivindicatorio originalmente presentado, mi representada no renuncia a la protección que pueda obtener sobre dicha materia y además se reserva el derecho de presentar una solicitud divisional que la contenga durante el trámite de la presente solicitud, beneficiándose de la fecha de prioridad inicialmente reivindicada.

**Modificación al capítulo descriptivo.****Modificación al resumen.****Modificación a los dibujos.**

Presento figura No 4 modificada.

**Modificación al Listado de Secuencias**

Presento nuevo listado de secuencias correspondiente a la aplicación WO 2009/020391.

5. Anexos

Poder, si fuere el caso.



Documento que contiene las modificaciones o correcciones.



Copia de la solicitud y sus anexos en formato magnético.

6. Firma		
Nombre y apellidos	Firma	
LUZ CLEMENCIA DE PAEZ	<i>Luz Clemencia De Paez</i>	
C.C. 35.456.344 DE Usaquén	Tarjeta Profesional 23.555	

RBLIRBLINCAID-AF239018\WPCL4484

REIVINDICACIONES

1. Un método para identificar una proteína de *Streptococcus uberis* que es capaz de provocar una respuesta inmunológica contra por lo menos dos cepas y/o serotipos de *Streptococcus uberis*, el método comprende:
 - a) identificar por lo menos parte de:
 - una proteína secretada, y/o
 - una proteína asociada con superficie, y/o
 - una proteína que tiene por lo menos 80% de identidad de secuencia con una proteína que tiene la secuencia de aminoácidos seleccionada del grupo que consiste de: SEQ ID NO: 110, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128, SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182, SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188 y SEQ ID NO: 190;
 - b) seleccionar por lo menos una proteína identificada en la etapa a) que se conserva sobre por lo menos dos cepas de *Streptococcus uberis* y/o serotipos; y
 - c) probar si por lo menos una proteína seleccionada en la etapa b) o una parte inmunogénica, derivado, y/o análogo de la misma es capaz de unir específicamente un anticuerpo y/o célula inmunológica de un animal infectado por una primera cepa de *Streptococcus uberis* y/o serotipo, y un anticuerpo y/o célula inmunológica de un animal infectado mediante una segunda cepa de *Streptococcus uberis* y/o serotipo.
2. Un método de acuerdo con la reivindicación 1, en donde dicha proteína secretada y/o proteína asociada con superficie se identifica al identificar en por lo menos parte de la secuencia genómica del *Streptococcus uberis* un gen que comprende un motivo de una proteína asociada con superficie y/o secretada.
3. Un método de acuerdo con la reivindicación 1 o 2, en donde dicha proteína que tiene por lo menos 80% de identidad de secuencia con una proteína que tiene la secuencia de aminoácidos del grupo que consiste de SEQ, ID NO: 110, SEQ. ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ, ID NO: 118, SEQ ID NO: 120,

SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128, SEQ. ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ. ID NO: 136, SEQ. ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164, SEQ ID NO: 166, SEQ. ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182, SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188 y SEQ ID NO: 190 se identifica al identificar en por lo menos parte de una secuencia genómica del *Streptococcus uberis* un gen que tiene por lo menos 80% de identidad de secuencia con una secuencia de ácido nucleico seleccionada del grupo que consiste de: SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187 y SEQ ID NO: 189.

4. Un método de acuerdo con la reivindicación 1 o 2 o 3, en donde dicha proteína que tiene por lo menos 80% de identidad de secuencia con una proteína que tiene la secuencia de aminoácidos seleccionados del grupo que consiste de SEQ. ID NO: 110, SEQ. ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ. ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128, SEQ. ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ. ID NO: 136, SEQ. ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164, SEQ ID NO: 166, SEQ. ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182, SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188 y SEQ ID NO: 190 se identifica al identificar en por lo menos parte de la secuencia genómica de *Streptococcus uberis* un gen que hibrida con la secuencia de nucleótido de longitud completa de cualquiera de las secuencias de ácido nucleico seleccionadas del grupo que consiste de SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ

ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187 y SEQ ID NO: 189 a 65° C en un amortiguador que tiene 0.5 M de fosfato de sodio, 1 mM EDTA, y 7% de dodecil sulfato de sodio en un pH de 7.2,

en donde la molécula de ácido nucleico permanece hibridada después de lavar dos veces con un amortiguador que contiene 40 mM de fosfato de sodio (pH 7.2), 1 mM EDTA y 5% de dodecil sulfato de sodio durante 30 minutos a 65° C y;

lavar dos veces con un amortiguador que contiene 40 mM de fosfato de sodio (pH 7.2), 1 mM EDTA y 1% de dodecil fosfato de sodio durante 30 minutos a 65° C.

5. Un método de acuerdo con la reivindicación 2, 3 o 4, que comprende adicionalmente seleccionar un gen que se conserva sobre por lo menos dos cepas de *Streptococcus uberis* y/o serotipos.
6. Un método de acuerdo con la reivindicación 5, que comprende adicionalmente obtener una proteína codificada mediante dicho gen, o una parte inmunogénica, derivado y/o análogo de dicha proteína.
7. Un método de acuerdo con una cualquiera de las reivindicaciones 2-6, en donde dicho gen se expresa en un sistema de expresión procariótico.
8. Un método de acuerdo con una cualquiera de las reivindicaciones 1-7, que comprende:
 - obtener proteínas aisladas y/o recombinantes de *Streptococcus uberis*;
 - incubar dichas proteínas con un anticuerpo y/o célula inmunológica de un animal infectado mediante una primera de *Streptococcus uberis* y/o serotipo y un anticuerpo y/o célula inmunológica de un animal infectado mediante una segunda cepa de *Streptococcus uberis* y/o serotipo, y
 - probar si una proteína es capaz de unirse un anticuerpo y/o célula inmunológica de un animal infectado mediante una primera cepa de *Streptococcus uberis* y/o serotipo y un anticuerpo y/o célula inmunológica de un animal infectado mediante una segunda cepa de *Streptococcus uberis* y/o serotipo.

9. Un método de acuerdo con la reivindicación 8, que comprende adicionalmente expresar dicha proteína utilizando una secuencia de ácido nucleico que codifica dicha proteína.
10. Un método de acuerdo con una cualquiera de las reivindicaciones 1-9, en donde dicho anticuerpo y/o célula inmunológica se deriva de un suero de convalescente.
11. Un método de acuerdo con una cualquiera de las reivindicaciones 1-10, en donde dicha proteína de *Streptococcus uberis* es capaz de provocar anticuerpos que inducen opsonofagocitosis.
12. Un método de acuerdo con una cualquiera de las reivindicaciones 1-11, en donde se identifican por lo menos dos proteínas de *Streptococcus uberis* capaces de provocar una respuesta inmunológica contra por lo menos dos cepas y/o serotipos de *Streptococcus uberis*.

RBL\RBL\ID-238774\WPCL4484



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Application No. 08 793 829.6 - 1405	Ref. P81948EP10	Date 15.02.2013
Applicant Boehringer Ingelheim Vetmedica GmbH		

Communication under Rule 71(3) EPC

1. Intention to grant

You are informed that the Examining Division intends to grant a European patent on the basis of the above application with the text and drawings and the related bibliographic data as indicated below.

A copy of the relevant documents is enclosed.

1.1 In the text for the Contracting States:

AT BE BG CH CY CZ DE DK EE ES FI FR GB GR HR HU IE IS IT LI LT LU LV MC MT NL NO PL PT RO SE
SI SK TR

Description, Pages

1, 13, 26, 27, 30, 32,	as published		
35, 37, 48-89			
2-12, 14-25, 28, 29,	received on	20-11-2012 with letter of	20-11-2012
31, 33, 34, 36, 38-47			
1a	introduction proposed by the Examining Division on		04-01-2013

Claims, Numbers

1-12	received on	31-10-2012 with letter of	31-10-2012
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Drawings, Sheets

1/45-15/45	as published		
16/45-45/45	received on	31-10-2012 with letter of	31-10-2012

With the following amendments to the above-mentioned documents proposed by the division

Description, Pages 1, 7-9, 11-14, 16, 17, 19, 20, 22-24, 28, 32-34, 37-39, 42-44, 47, 55, 67

Comments

Pages 1, 7-9, 11-14, 16, 17, 19, 20, 22-24, 28, 32-34, 37-39, 42-44, 47, 55, 67: Article 84 EPC; Rule 139 EPC. Page 1a: Rule 42(1)(b) EPC.

1.2 Bibliographic data

The title of the invention in the three official languages of the European Patent Office, the international patent classification, the designated Contracting States, the registered name(s) of the applicant(s) and the other bibliographic data are shown on **enclosed EPO Form 2056**.

2. Invitation

You are invited, **within a non-extendable period of four months** of notification of this communication,

2.1 to EITHER approve the text communicated above and verify the bibliographic data (R. 71(5) EPC)

(1) by filing a translation of the claim(s) in the two other official languages of the EPO

Fee code	EUR
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(2a) by paying the fee for grant including the fee for publication:
minus any amount already paid (R. 71a(5) EPC):

007	875.00 0.00
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Total amount:	875.00
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(3) by paying additional claims fees under Rule 71(4) EPC;
number of claims fees payable: 0
minus any amount already paid (R. 71a(5) EPC):

016	0.00 0.00
-----	--------------

Total amount:	0.00
---------------	------

Note 1: See "Important notes concerning fee payments" below.

Note 2: Any overpaid "minus" amounts will be refunded when the decision to grant (EPO Form 2006A) has been issued.

2.2 OR, in case of disapproval, to request reasoned amendments or corrections to the text communicated above or keep to the latest text submitted by you (R. 71(6) EPC).

In this case the claims translations and fee payments mentioned under point 2.1 above are NOT due.

The terms "amendment(s)" and "correction(s)" refer only to amendments or corrections of the application documents and not of other documents (e.g. bibliographic data, the designation of the inventor, etc.).

If filing amendments, you must identify them and indicate the basis for them in the application as filed. Failure to meet either requirement may lead to a communication from the Examining Division requesting that you correct this deficiency (R. 137(4) EPC).

2.3 Bibliographic data

Where the applicant requests a change or correction of bibliographic data in response to the Rule 71(3) communication, this will **not** cause the sending of a second communication under Rule 71(3) EPC. The applicant will still have to pay the fees and file translations in reply to the Rule 71(3) communication in case of 2.1 above, unless he also files a reasoned request for amendments or corrections in response to the Rule 71(3) communication (see case 2.2 above).

3. Loss of rights

If either of the two possible actions above (see points 2.1 or 2.2) is not performed in due time, the European patent application shall be deemed to be withdrawn (R. 71(7) EPC).

4. Further procedure

4.1 In case of point 2.1 above

- 4.1.1 The decision to grant the European patent shall be issued, and the **mention of the grant** of the patent shall be published in the European Patent Bulletin, if the requirements concerning the translation of the claims and the payment of all fees are fulfilled and there is agreement as to the text to be granted (R. 71a(1) EPC).

Note on payment of the renewal fee:

If a renewal fee becomes due before the next possible date for publication of the mention of the grant of the European patent, publication will be effected only after the renewal fee and any additional fee have been paid (R. 71a(4) EPC).

Under Article 86(2) EPC, the obligation to pay renewal fees to the European Patent Office terminates with the payment of the renewal fee due in respect of the year in which the mention of the grant of the European patent is published.

Note on payment of the designation fee(s):

If the designation fee(s) become(s) due after the communication under Rule 71(3) EPC, the mention of the grant of the European patent shall not be published until the designation fee(s) has/have been paid (R. 71a(3) EPC).

- 4.1.2 After publication, the **European patent specification** can be downloaded free of charge from the EPO publication server <https://data.epo.org/publication-server> or ordered from the Vienna sub-office upon payment of a fee (OJ EPO 2005, 126).

Upon request in writing each proprietor will receive the certificate for the European patent together with one copy of the patent specification provided that the request is filed within the time limit of Rule 71(3) EPC. If such request has been previously filed, it has to be confirmed within the time limit of Rule 71(3) EPC. The requested copy is free of charge. If the request is filed after expiry of the Rule 71(3) time limit, the certificate will be delivered without a copy of the patent specification (R. 74 EPC, Decision of the President of the EPO, Special edition No. 3, OJ EPO 2007, D.2).

4.1.3 Filing of translations in the Contracting States

As regards translation requirements prescribed by the Contracting States under Article 65(1) EPC, please consult the website of the European Patent Office

www.epo.org → Law & practice → All Legal texts → National law relating to the EPC

www.epo.org → Law & practice → All Legal texts → London Agreement

In case of a valid extension

As regards translation requirements prescribed by the Extension States, please consult the website of the European Patent Office

www.epo.org → Law & practice → All Legal texts → National law relating to the EPC

Failure to supply a prescribed translation in a Contracting State or an Extension State may result in the patent being deemed to be void *ab initio* in the State concerned (Art. 65(3) EPC).

4.2 In case of 2.2 above

If the present communication under Rule 71(3) EPC is based upon an auxiliary request, and within the time limit you maintain the main or higher ranking request which is not allowable, the application will be refused (Art. 97(2) EPC).

If the Examining Division gives its consent to the requested amendments or corrections, it shall issue a new communication under Rule 71(3) EPC; otherwise, it shall resume the examination proceedings (R. 71(6) EPC).

5. Filing of a divisional application

Any divisional application relating to this European patent application must be filed directly with the European Patent Office in Munich, The Hague or Berlin and shall be in the language of the proceedings for the present application, or if the latter was not in an official language of the EPO, the divisional application may be filed in the language of the present application as filed (cf. Art. 76(1) and R. 36(2) EPC). Any such divisional application must be filed while the present application is still pending and the time limit for filing divisional applications must be observed (R. 36(1) EPC; Guidelines A-IV, 1.1.1).

6. Important notes concerning fees payments

6.1 For all payments you are requested to refer to the relevant **fee code(s)**.

6.2 Automatic debiting procedure

The fee for grant including the fee for publication and any additional claims fees due under Rule 71(4) EPC will be debited automatically on the date of filing of the translations of the claims, or on the last day of the period of this communication. However, if the designation fee(s) become(s) due as set out in Rule 71a(3) EPC and/or a renewal fee becomes due as set out in Rule 71a(4) EPC, these should be paid separately by another permitted way of payment in order not to delay the publication of the mention of the grant. The same applies in these circumstances to the payment of extension fees. For further details see the Arrangements for the automatic debiting procedure (AAD) and accompanying information from the EPO concerning the automatic debiting procedure (Annexes A.1 and A.2 to the Arrangements for deposit accounts (ADA) in Supplement to OJ EPO 3/2009).

6.3 Fee amounts

Following any amendment to the Rules relating to Fees, the amount(s) mentioned in this communication may be different from the amount(s) **actually due on the date of payment**. The latest version of the Schedule of fees and expenses, published as a Supplement to the Official Journal of the EPO, is also available on the EPO website (www.epo.org) and can be found under www.epo.org/schedule-of-fees, which allows the viewing, downloading and searching for individual fee amounts, both current and previous.

6.4 **Payments by cheque** delivered or sent direct to the EPO are no longer accepted as from 1 April 2008 (see OJ EPO 2007, 626).

Date 15.02.2013

Sheet 5

Application No.: 08 793 829.6

Examining Division:

Chairman: Schulz, Regine
2nd Examiner: Adida, Anne
1st Examiner: Lunter, Pim



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Tel. No.: +31 70 340 - 4781

Branch at The Hague

Enclosure(s): 139 Copies of the relevant documents

EPO Form 2056

Registered Letter

EPO Form 2004C 04.12TRI



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Application No.:

08 793 829.6

14.01.2013
Date

R. Schulz
Schulz, Regine
Chairman

Enclosure(s):

P. Lunter
Lunter, Pim
1st examiner

A. Adida
Adida, Anne
2nd examiner

Figura 4.

Secuencias de ácidos nucleicos y secuencias de aminoácidos de las proteínas de S. uberis de la tabla 5

SEQ ID NO:109

atgactgagaacctaatacggaatttatcggtattcgaactttcaatcttattattacttattttgttgctgcatattt
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DDID

SEQ ID NO:111

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SEQ ID NO:114

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SEQ ID NO: 116

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 VQNNVQPIDRVEKMETSFSTELTKKAESSYNTNLQDLNYDPNVWEVREDGLYSNAVVGKGDN
 FLFSASTGENFIFQTDVTFQNTGAASLVFRSNDPENLNGYVNLNLDGNHSHKARLWRWAEAN
 LINDKEILASPDNKYFLKVATNGWISYYINGILIANLSDYTIQRDDLQTTYIKDGHFGLLNW
 NGEMVFQNTFYRELTNEELPLLNDVTVTSKNGPVEPKGQFFSESSVYIQYVSNDASTVDLSFD
 ANNSDALITVDAHGKVYSNPSAIPVTVGPNYLTVTSTYTTTDDGYVIPSTYRINVHRRQPQSVY
 YNENFRDQYHYSVKDGWANDPNGLVYNGVYHMFYQFYDDTKWGPMPHWAHATSTDLIHW
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 HTECPDLYPVLAEDQTVKWWLSRGGRYKVGDLQQADGNWKFIPDANYQETDSIMNFGKDS
 YAAMTYVQDFGTKANPTIPKIIELNWMNTWDNYCNLVADRLGQSFNFTNLNLELGLVKE
 GDKYVLTQTPVEAYESLRDNDNKVEYKNVVVGKENDLFKDFSGDYEIVAHFKPSDKTTKV
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 FSKNHTVAGANQIFTSAQSLGLEVLIDGEDAKADIVLYPLKSIWKNKIIDTTPQIVIPASEPKVR
 MNVGDSTTVKAYVSPVGASQDLIWNISNPSLVLDQISGNQVFLKAIKKGQVIVRAQ\$QSNPAV
 YQDFIIDILEDNFNTNVKDVNVFSGDWYVDGESLKVANHNSNDIYMSADKIPYENYQMDLDI
 KYGRGIVNIFFASGNPDANNAYTIQFGSNNSVRLFRFYRDTIFEAPMIDVINDNQFHHVRLVKS
 ANVIHVYVDNEMVMSYTFDQVEEFFNPNYLGGLWDGELAVQNFYVIDLDAQKPVFVEEHE
 KEKLLSELKKSVMKTSSYSTLKTETSSKTNSENLEAPT VSKKNLPMTSDSNNNLEELGILVIL
 TTLGAFLGRVILKKEK

SEQ ID NO: 117

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aataac

SEQ ID NO: 122

MKKHIVLKSSILGLVAGMSVLVSSVQADQVDVQILGVNDFHGDQDQTSAYMPDGKVSAGT
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AIKNIPVNNTSVNIGFIGVVTTEIPNLVLKQNYEQYNFLDEAETIAKYAKELQGQNVNALVLA
HIPATSGKDGIVGDEIATIMDKVNQLYPDNSIDIIFAGHNHQYTNGTIGSTRIVEALSQGKAYAD
VRGTLDTDTQDFIATPTAQVVAVAPGVLTGTAEIQAIVDEANTIVKQVTDQKIGTAASSELISRE
VNVDKESAVGNLITTAQLTVARETYPDVDFAITNNGGIRADLLVSSDQSITWGAAQAVQPFNGI
LQIVELTGQEIDALNEQYDEGQKYFLQMSGLRYAYTDSGSTDPLVPFKVVKAYKDNNGEIDP
NATYKLVINDFLYGGGDGFATFKKGKLLGAINPDTEVFIKYIKDLEAAGKPVTAITGVKTYVT
TALEPSTTTDASGTHEMINRVYRDRDGKIVATEVVSDFTPAPVEETETPKPAVNSIKIPVKTP
KYGQSLTAVKAGQQAQKASDKKQLPTTSSQEDTAILLSLLGASSLAMAVALKKENN

SEQ ID NO: 123

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SEQ ID NO: 124

MKKKQEMKYYLRKSAYGLAAVSVAVLAVGSPVSAQEKAASTEATPKVAPKVPEKPSKEVIK
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ETESEVKEESEEEKEDDPSESDTEVENVEAINLSEAEGNDSSKPETSEEVTAEEDRQETDRLA
EVKTEESAKEGDEDADKKDEAEKAKKGAELSRVKAELAKLEALNASRLMKKIVESGKTVE
GILSFMKESLPQLEAARASEQAKAPEVTQSPDHLPSKKAVHNPVQVAKRSESLEQKAENAK
TSTNLQNTQIPVQEAKRTQAQLPSTGEDYQAYLVAAAMALIASSGMVAYGSYRKKKQK

SEQ ID NO: 125

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caacagtttcacgctgacaaatacggatgtttctgctactgcggtcgctgcagattccattgcaagcccagtaacgact
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SEQ ID NO: 126

MTKNRSSHSTYADKVIKGLSASCFILGAFVFAQQVSAEEVVTATNTSLTAPT VTTVSPLTNTDV
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TSQTETLASQEIYMDKVNQVTINTTVNPATPMTWTIENYPNQTYNMQTGDFTGSPSYTVTSTS
PNNSSVQIEIPPLFGTDLRLWPNNIRRTYRDYMGSYTLKGISEDGLTIVTKELILRPYADYMT
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SLDANSPYTSGYAANSLYSNSGSWIEGVPTGFMTLANISASDFYVSGWWPNHEGLANKTVAI
SGLYQQQPMFIFAGNPVNKHTINFYRWVSNAIFGTNLTSFIEGQCTIPTDSETQVVRVNHNG
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SEQ ID NO: 127

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SEQ ID NO: 128

MKSYLKRRYGLITTSVLAATVLATGWQSTSVLAENPTTSPTTTVTSNGFNFNATLLDHNGKTV
SGKTVSLYDITDGNRTLVSQSAVSDQNGIASFSQPLNRLSVFVDNVAQGYTTRTSESGQVRS
SAFYIDGQGTNTPKYSDKTITISVLNEEAELPLANQKVTLTNPLKEVVGEAMTDADGHVVFKDKL
LEGVFYNYAVNGKAIDSAQPDSKRSVFLESNQLAKEGFTFTATILGKNGKTVAGKTVSLYDIT
DGNRTLVSQSAVSDQNGIASFSQPLNRLSVFIDDDVAQGYTTRTSENGQVRSSAFYVDGQGTN
TPKYSDKTITISVLNEEGEPLANQKVTLINPLKEVIGEANTDANGKVIFTDKLLDGVFYTYAVN
DQTIDATQPDTSRNVFLRADQILKESPKNTASEAATNLEKTTESKEGNMPQQNQSEAKEKAP
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SEQ ID NO: 129

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SEQ ID NO:130

MSKPMTKKKKAISIQKSVKPILGFTFGALLSTVFTPSVFEEVSSSLGHATSGLLSVSVPKEL
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SALISTALGLFLLKSNKND

27

SEQ ID NO: 131

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SEQ ID NO: 132

MEIKQKHGKHALRKAVTAAVLGTAFFSSLGGFAGAVTTVKAEDLFTINNSEVQDKLESKVQK
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SEQ ID NO: 133

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SEQ ID NO: 134

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 TDDL FKAMTMLFKKESFFLYPLKNDLNTNGISM MTSLVQFQAKDVKENIPLEWEIKTKASDS
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SEQ ID NO: 135

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SEQ ID NO: 136

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SEQ ID NO: 137

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SEQ ID NO: 138

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SEQ ID NO: 139

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SEQ ID NO: 140

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SEQ ID NO: 141

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SEQ ID NO: 142

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SEQ ID NO: 143

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SEQ ID NO: 144

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ADKMYTDQASIDSKKQLLGIERGQWINDKLPFYHDYTQGEESIDRNTYHGTHVAGIATASGLT
QKENKEQMKGIVPNAQLLFLKVGQPSVEGEREKHYAMA IKDAIALGATAINMSFGQVGKASH
ELNDDFKKALALAADKGVAVVAAGNDYAMGGSQTKPLAKNPDTGVIGTPATTEE VFTVAAY
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DFVTNSKEVAEKVEALGAAGVLVHNNQAKKPLIPLAYNGPLPMGFISKEDADWLKTM TSPQF
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VFLRNV RDIKAQVFASDDLQHP IWESPIKAFAKKDVNTNDIKESMLENTVWEGKDASGNPVT
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SEQ ID NO: 145

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SEQ ID NO: 146

MRFLKGKKVFLAVIGLAVMMTLVIMFQPQAKNKS VSAETLASGQTQAFINQIAGTASQIAAER
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SEQ ID NO: 147

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SEQ ID NO: 148

MKKIFQRKWFKRTSIVLGILLVALIALGSFYYSKSAVIDRYVVAKSCKNGGSFENIKAFVWDD
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 KTNVPNMDLLLNQKKVATSNSNFTELKRLPIADYSASINGTYKDKKIKVTKKYDGQKPV
 DLSVTFKNFTVSSNLTEGELYFDEDRVGTLLKNGQYQVTDYPITNGSKAFVKRNFDPGELKSE
 KADLEQVAEGSELKLTVDNLLDRTKAGEYLLAAFNQLMAYTSSRQDSTTVADVFNENND
 YKGLKESVKAKLETDSRKASSFAIPNVALNAMTQVGKESYLLDFAATYDFAYPKETDPEKGSS
 GNIIQELSGQLTLKSGDRYVISQAGTKNISVTSEKNNIKPSLLPDGIVGTWKGTKDDITYTLT
 ISEDGTVTRHIDFKDPKKADESRTAKITKTEKNPGDFQVIITPETDSSILIIGGGIGGANIKYAY
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SEQ ID NO: 149

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 aatttgcttctaataaaaaacaataccaacaatgctttaacaagttcagtaggtaaa

SEQ ID NO: 150

MNTSKKIVTGFVTLASVLTAAACSSTSDNTKVVTMKGDTITVTDYNEAKTSTAAQQSMLSLIL
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 AAKKELTDDNYKKAFESYTPMTTQVIAFDDEEKAKKVEETKAEGADFANIAKENTTEANK
 KIDYTFDSADTVLPSPVIKETAKLNEGEKSAVITVMDSRTYQKKYYVHLVKKAEEKADWKE
 YKSRLKEIIMNEKENDSNFQNKVISKTLKANVKIKDKAFANILSQFASNKNNTNNALTSSVGK

SEQ ID NO: 151

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SEQ ID NO: 152

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 DQAIVGAQYK GKTYAFPGIESQVLFYNKEKLSAEDIASYDAITSKATFGGTFKQANAYVTGPL
 FMSVGNTLFGENGEDTKGTNWGNEKGAAVLKWIADQKNNKGFVSLDANNVMSKFGDGSVA
 SFESGPWDYEAQAIGKDKLGVAVYPKVTIGGEEVQQKAFLGVKLYAVNQAPAKGDTKRIA
 ASYKLASYLTSAESQENQFKTRHIVPANKEIQSSEEVQSNELAKTVITMGSSKDYTVVMPKLS
 QMATFWTESAAILSDTFNGKIQEADYLT KLQQFDKDIAS TK

SEQ ID NO: 153

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SEQ ID NO: 154

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 NYIIVDDVIEGKDNVASVTFADNEAAYLAGIAAAKTTKTKVVG FVGGMEGTVITRFEKGFEAG
 VKSVDDSIQIKVDYAGSFGDAAGKGTIAAAQYAGGADVYQAAGGTGAGVFNEAKAVNEKKD
 EADKVVWIGVDRDQKEEGKYTSKDGKESNFVLASSIKQVGKSVQLINKLVTDKKFP GGKTTV
 YGLKGGVDIATTNLSDDAIKAVKEAKEKIISGDVKVPEK.

SEQ ID NO: 155

atgaaaaaattactgtcacattagtggtgatttcagcacattatcattgattgctgttcatcacaagcacaaagcaagaagatcataa
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SEQ ID NO: 156

MKKLLVTLVLIFSTLSLIACSSQSTKQEDHKTKLSQMPKISGFTYK GKVPENPKRVVSLSSSTYT
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EKDIYLF GKDWGRGGEIIHQAFQYQAPEKVKMEVFPKGYLSISQEVLPDYIGDYVVVAAEDEK
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SEQ ID NO: 157

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SEQ ID NO: 158

MNKKFIGLGLASVAILSLAACGNRGASKSDSKDAKTDLKAAIVTDTGGVDDKSFNQSAWEGL
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VKSVDDSIQIKVDYAGSFGDAAKGKTIAAAQYAGGADV IYQAAGGTGAGVFNEAKAVNEKKD
EADKVVVIGVDRDQKEEGKYTSKDGKESNFVLASSIKQVGKSVQLINKLVTDKKFPGGKTTV
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SEQ ID NO: 159

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SEQ ID NO: 160

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DDVIEGKDNVASITFADNEAAYLAGVAAAKTSKSKQVGVGGMEGTVVKRFEKGFEAGVKSV
DPSIKVSIAYAGSFADAAKGKSIAATQYASGADVIYQAAGGTGAGVFNEAKAINEKRAASDKV
WVLGVDRDQKAEGEYTDKDGQKGNFVLASSIKEVGKTMQKVIGMTEKGDFFGGKVNTFGLK
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SEQ ID NO: 161

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SEQ ID NO: 162

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WKRI VDPATASEYAYLATESHLLNAEDINTGKN TDLNSLG VKAEGNKVIFTL SAPAPQFKSLL
SFANFMPQKEEFVTKTGKDYGTSSEKQIYSGPYIVKDWNGTSGSFKLVKNDKYWD AKNVKM
KTINVQTVKKPDTAVQMYKQGKLDYANISGTS AIYNANKNNKDVVPVLEATTAYMVYNQTGS
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SEQ ID NO: 163

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SEQ ID NO: 164

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EESVSLEDTIQEYLLKGHVILRKRVEEPITHPTETANIEYKVQFATKDGFEHPLPIFVDYGEKHI
GEKLT\$DEFKIAEEKLLQLYPDYIMIDQKEYTIKHNSLGQLPRYYSYQDHF\$SYEIQDRQRIMA
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SEQ ID NO: 165

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SEQ ID NO: 166

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SQIKTKKAILNDLTQEKAKLTSAITTTEQQIVLLKNHLANQVANAPKISSIVQRSENNRVRPDV
SDTREKAVDTAQEATILAQAEITMAEEVITNSAKAIVANAQNVAAQIMKVAPEVTPDQGVVAKV
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SEQ ID NO: 167

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SEQ ID NO: 168

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QKDFTIYEEPLVKGVLPINSCLKPYSKVHVTKLSQTQHGNFYIENKGWVSEKYLKADNRM
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SEQ ID NO: 169

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SEQ ID NO: 170

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SEQ ID NO: 171

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SEQ ID NO: 172

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DKMTITIGKKARKTFNVVGSVDPKQVATGYELLSMDTGIDKVEVTSDESKIDLIDHVVAKLPD
DVKLNADYRGEVTLQAVSADGTVLASSISPAKTTLSVSVKKITKSVPIRVSMVGTMDLADIQ
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SEQ ID NO: 173

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SEQ ID NO: 174

MKPSNTEKFLILSLLTLILAGSFYLLFFARNHIGNALTQKETQTVQKSNMLSKAIDALEKAEKN
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AIDKIGNLTKKNELLNRLGAIVISDQAPESSTSSSEAASDTTISDANTGNAEQATIYESPVAPAE
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SEQ ID NO: 175

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SEQ ID NO: 176

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SEQ ID NO: 177

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SEQ ID NO: 178

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SEQ ID NO: 179

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SEQ ID NO: 188

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<140> PCT/NL2008/050537

<141> 2008-08-05

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<151> 2007-08-06

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<223> may be V, M, S, T, A, F, G

<220>
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<222> (39)..(39)
<223> may be G

<400> 5
Met Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Asp
1 5 10 15

Asp Asp Asp Asp Asp Asp Asp Asp Asp Asp Asp Asp Asp Asp Asp
20 25 30

Asp Asp Asp Leu Leu Ile Ala Cys
35 40

<210> 6
<211> 36
<212> PRT
<213> Streptococcus uberis

<400> 6
Leu Pro Met Thr Ser Asp Ser Asn Asn Asn Leu Glu Glu Leu Gly Ile
1 5 10 15

Leu Val Ile Leu Thr Thr Leu Gly Ala Phe Leu Gly Arg Val Ile Leu
20 25 30

Lys Lys Glu Lys
35

<210> 7
<211> 34
<212> PRT
<213> Streptococcus uberis

<400> 7

PCT_Sequence_listing (3)

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

Ala Ile Ile Leu Ser Val Leu Gly Leu Leu Gly Phe Lys Lys Arg Arg
20 25 30

Thr Tyr

<210> 8
<211> 35
<212> PRT
<213> Streptococcus uberis

<400> 8

Leu Pro Ser Thr Gly Asp Lys Ala Asn Pro Phe Phe Thr Ala Ala Ala
1 5 10 15

Leu Ala Val Met Ala Ser Ala Gly Met Val Ala Val Ser Arg Lys Arg
20 25 30

Lys Glu Asp
35

<210> 9
<211> 35
<212> PRT
<213> Streptococcus uberis

<400> 9

Leu Pro Ser Thr Gly Asp Lys Ala Asn Pro Phe Phe Thr Ala Ala Ala
1 5 10 15

Leu Ala Val Met Ala Ser Ala Gly Met Val Ala Val Ser Arg Lys Arg
20 25 30

Lys Glu Asp
35

<210> 10
<211> 34
<212> PRT
<213> Streptococcus uberis

<400> 10

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

Leu Gly Ala Ser Ser Leu Ala Met Ala Val Ala Leu Lys Lys Lys Glu
20 25 30

Asn Asn

<210> 11
<211> 37
<212> PRT
<213> Streptococcus uberis

PCT_Sequence_listing (3)

<400> 11

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

Met Ala Leu Ile Ala Ser Ser Gly Met Val Ala Tyr Gly Ser Tyr Arg
 20 25 30

Lys Lys Lys Gln Lys
 35

<210> 12

<211> 38

<212> PRT

<213> Streptococcus uberis

<400> 12

Leu Pro Ala Leu Ala Asp Gly Ser His Lys Asp Asp Ser Lys Leu Phe
 1 5 10 15

Trp Val Thr Gly Leu Leu Val Ala Ser Gly Gly Leu Phe Ala Ala Leu
 20 25 30

Lys Arg Arg Glu Glu Asp
 35

<210> 13

<211> 35

<212> PRT

<213> Streptococcus uberis

<400> 13

Leu Pro Met Ala Gly Glu Arg Gly Ser Arg Leu Phe Thr Phe Ile Gly
 1 5 10 15

Leu Ser Leu Ile Leu Gly Ile Ala Gly Tyr Leu Leu Lys His Lys Lys
 20 25 30

Val Lys Ser
 35

<210> 14

<211> 34

<212> PRT

<213> Streptococcus uberis

<400> 14

Leu Pro Pro Thr Gly Ser Gln Glu Ser Gly Ile Phe Ser Leu Phe Ser
 1 5 10 15

Ala Leu Ile Ser Thr Ala Leu Gly Leu Phe Leu Leu Lys Ser Asn Lys
 20 25 30

Asn Asp

<210> 15

<211> 36

<212> PRT

<213> Streptococcus uberis

PCT_Sequence_listing (3)

<400> 15

Leu Pro Ser Thr Gly Asp Lys Pro Val Asn Pro Leu Leu Val Ala Ser
1 5 10 15

Gly Leu Ser Leu Met Ile Gly Ala Gly Ala Phe Val Tyr Ala Gly Lys
20 25 30

Arg Lys Lys Gly
35

<210> 16

<211> 36

<212> PRT

<213> Streptococcus uberis

<400> 16

Leu Pro Glu Thr Arg Asp Ser Ser Ser Met Ala Asn Trp Ser Leu Ala
1 5 10 15

Phe Phe Leu Ser Ala Val Ile Cys Phe Phe Lys Gly Arg Arg Lys Arg
20 25 30

Leu Asn Lys Leu
35

<210> 17

<211> 37

<212> PRT

<213> Streptococcus uberis

<400> 17

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

Ile Gly Ala Leu Met Val Ser Phe Val Gly Phe Ser Ala Leu Lys Asp
20 25 30

Arg Lys Lys Glu Lys
35

<210> 18

<211> 33

<212> PRT

<213> Streptococcus uberis

<400> 18

Leu Pro His Thr Gly Glu Glu Lys Gly Phe Leu Ser Ile Ile Gly Gly
1 5 10 15

Thr Ile Leu Ser Phe Val Ala Phe Leu Phe Lys Lys Lys Ile Thr Leu
20 25 30

Asn

<210> 19

<211> 34

<212> PRT

PCT_Sequence_listing (3)

<213> Streptococcus uberis

<400> 19

Leu Pro His Thr Gly Glu Glu Gly Leu Ser Ile Leu Thr Val Ile Gly
1 5 10 15

Ala Ser Ile Leu Ser Val Leu Gly Leu Ser Val Leu Lys Lys Pro Lys
20 25 30

Glu Asn

<210> 20

<211> 33

<212> PRT

<213> Streptococcus uberis

<400> 20

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

Ser Leu Leu Leu Met Ser Leu Gly Leu Gly Leu Lys Lys Lys Glu Asp
20 25 30

Glu

<210> 21

<211> 34

<212> PRT

<213> Streptococcus uberis

<400> 21

Leu Pro Lys Thr Asp Ser Gln Lys Thr Met Thr Phe Leu Gly Ile Ala
1 5 10 15

Met Leu Phe Gly Gly Ile Leu Gln Val Leu Trp Ser Tyr Phe Lys Lys
20 25 30

Arg Asp

<210> 22

<211> 33

<212> PRT

<213> Streptococcus uberis

<400> 22

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

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

Gln

<210> 23

<211> 25

PCT_Sequence_listing (3)

<212> PRT
<213> Streptococcus uberis

<400> 23

Met Lys Ile Met Lys Met Asn Lys Met Leu Thr Leu Ala Val Leu Thr
1 5 10 15

Leu Ser Ser Phe Gly Leu Ala Ala Cys
20 25

<210> 24
<211> 22
<212> PRT
<213> Streptococcus uberis

<400> 24

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

Val Gly Leu Thr Ala Cys
20

<210> 25
<211> 25
<212> PRT
<213> Streptococcus uberis

<400> 25

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

Pro Phe Leu Val Gly Leu Ser Ala Cys
20 25

<210> 26
<211> 23
<212> PRT
<213> Streptococcus uberis

<400> 26

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

Val Leu Thr Leu Ala Ala Cys
20

<210> 27
<211> 24
<212> PRT
<213> Streptococcus uberis

<400> 27

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

Ala Ser Thr Leu Leu Val Gly Cys
20

<210> 28
<211> 21

PCT_Sequence_listing (3)

<212> PRT
<213> Streptococcus uberis

<400> 28

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

Leu Ser Val Leu Cys
20

<210> 29
<211> 22
<212> PRT
<213> Streptococcus uberis

<400> 29

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

Leu Phe Leu Val Ala Cys
20

<210> 30
<211> 21
<212> PRT
<213> Streptococcus uberis

<400> 30

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

Ser Leu Ala Ala Cys
20

<210> 31
<211> 20
<212> PRT
<213> Streptococcus uberis

<400> 31

Met Lys Lys Phe Phe Leu Val Gly Met Leu Thr Leu Ser Met Leu Thr
1 5 10 15

Leu Thr Ala Cys
20

<210> 32
<211> 20
<212> PRT
<213> Streptococcus uberis

<400> 32

Met Lys Lys Leu Phe Ile Tyr Leu Ser Leu Ala Phe Ser Leu Leu Val
1 5 10 15

Leu Gly Ala Cys
20

<210> 33
<211> 21

PCT_Sequence_listing (3)

<212> PRT
<213> Streptococcus uberis

<400> 33

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

Met Leu Gly Ala Cys
20

<210> 34
<211> 20
<212> PRT
<213> Streptococcus uberis

<400> 34

Met Lys Lys Leu Leu Val Thr Leu Val Leu Ile Phe Ser Thr Leu Ser
1 5 10 15

Leu Ile Ala Cys
20

<210> 35
<211> 24
<212> PRT
<213> Streptococcus uberis

<400> 35

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

Ile Leu Ile Thr Leu Thr Gly Cys
20

<210> 36
<211> 22
<212> PRT
<213> Streptococcus uberis

<400> 36

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

Ser Val Leu Val Ala Cys
20

<210> 37
<211> 23
<212> PRT
<213> Streptococcus uberis

<400> 37

Met Thr Leu Lys Lys Asn Leu Gly Ile Leu Ser Leu Thr Leu Gly Thr
1 5 10 15

Leu Ala Ile Leu Ala Ala Cys
20

<210> 38
<211> 22

PCT_Sequence_listing (3)

<212> PRT
<213> Streptococcus uberis

<400> 38

Met Ile Lys Phe Glu Thr Lys Lys Gly Gln Lys Leu Phe Leu Phe Gly
1 5 10 15

Leu Ile Leu Cys Phe Cys
20

<210> 39
<211> 22
<212> PRT
<213> Streptococcus uberis

<400> 39

Met Lys Val Lys Lys Asn Ile Lys Ile Ala Ala Leu Leu Pro Met Leu
1 5 10 15

Thr Leu Leu Ala Ala Cys
20

<210> 40
<211> 22
<212> PRT
<213> Streptococcus uberis

<400> 40

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

Ile Val Leu Gly Ala Cys
20

<210> 41
<211> 21
<212> PRT
<213> Streptococcus uberis

<400> 41

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

Pro Leu Ala Ala Cys
20

<210> 42
<211> 28
<212> PRT
<213> Streptococcus uberis

<400> 42

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

Val Thr Leu Ala Ser Ala Ala Leu Leu Met Ala Cys
20 25

<210> 43
<211> 22

PCT_Sequence_listing (3)

<212> PRT
<213> Streptococcus uberis

<400> 43

Met Lys Thr Lys Lys Ile Leu Lys Ala Ala Ile Gly Leu Met Thr Leu
1 5 10 15

Val Ser Met Thr Ala Cys
20

<210> 44
<211> 20
<212> PRT
<213> Streptococcus uberis

<400> 44

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

Leu Ser Ala Cys
20

<210> 45
<211> 20
<212> PRT
<213> Streptococcus uberis

<400> 45

Met Lys Lys Thr Phe Thr Ser Thr Leu Val Leu Leu Ser Ala Leu Met
1 5 10 15

Leu Thr Ala Cys
20

<210> 46
<211> 16
<212> PRT
<213> Streptococcus uberis

<400> 46

Met Lys Lys Trp Phe Leu Ile Leu Met Leu Leu Gly Ile Phe Gly Cys
1 5 10 15

<210> 47
<211> 20
<212> PRT
<213> Streptococcus uberis

<400> 47

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

Leu Val Ala Cys
20

<210> 48
<211> 23
<212> PRT
<213> Streptococcus uberis

<400> 48

PCT_Sequence_listing (3)

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

Met Phe Phe Leu Ser Ala Cys
 20

<210> 49
 <211> 21
 <212> PRT
 <213> Streptococcus uberis

<400> 49

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

Ser Leu Ala Ala Cys
 20

<210> 50
 <211> 19
 <212> PRT
 <213> Streptococcus uberis

<400> 50

Met Ile Asn Lys Lys Ile Ile Phe Thr Ser Leu Thr Val Ile Cys Ile
 1 5 10 15

Ser Asn Cys

<210> 51
 <211> 20
 <212> PRT
 <213> Streptococcus uberis

<400> 51

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

Leu Thr Ala Cys
 20

<210> 52
 <211> 23
 <212> PRT
 <213> Streptococcus uberis

<400> 52

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

Leu Leu Leu Leu Gly Ala Cys
 20

<210> 53
 <211> 22
 <212> PRT
 <213> Streptococcus uberis

<400> 53

PCT_Sequence_listing (3)

Met Lys Met Asn Lys Met Leu Thr Leu Ala Val Leu Thr Leu Ser Ser
1 5 10 15

Phe Gly Leu Ala Ala Cys
20

<210> 54
<211> 29
<212> PRT
<213> Streptococcus uberis

<400> 54

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

Ile Leu Ala Phe Phe Phe Leu Leu Thr Ala Ile Gly Ala
20 25

<210> 55
<211> 30
<212> PRT
<213> Streptococcus uberis

<400> 55

Met Lys Phe Ile Lys Ile Leu Leu Ser Gln Ile Val Ser Leu Phe Leu
1 5 10 15

Leu Leu Thr Ile Ser Leu His Ala Leu Glu Thr Val Asn Ala
20 25 30

<210> 56
<211> 29
<212> PRT
<213> Streptococcus uberis

<400> 56

Met Ser Asn Lys Tyr Pro Ser Gly Lys Lys Ile Ser Ala Ile Leu Ile
1 5 10 15

Ala Leu Leu Ile Thr Gly Leu Thr Ala Leu Ser Gln Gly
20 25

<210> 57
<211> 37
<212> PRT
<213> Streptococcus uberis

<400> 57

Met Lys Ile Ser Cys Cys His Ser Lys Ala Phe Thr Leu Ala Glu Ser
1 5 10 15

Leu Leu Cys Leu Ala Val Thr Thr Phe Thr Ile Leu Leu Leu Ser Ser
20 25 30

Ser Leu Ala Gly Val
35

<210> 58
<211> 32

62

PCT_Sequence_listing (3)

<212> PRT
<213> Streptococcus uberis

<400> 58

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

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

<210> 59
<211> 28
<212> PRT
<213> Streptococcus uberis

<400> 59

Met Lys Lys Ile Phe Gln Arg Lys Trp Phe Lys Arg Thr Ser Ile Val
1 5 10 15

Leu Gly Ile Leu Leu Val Ala Leu Ile Ala Leu Gly
20 25

<210> 60
<211> 31
<212> PRT
<213> Streptococcus uberis

<400> 60

Met Lys Lys Lys Phe Leu Lys Ile Met Thr Cys Ile Ile Ala Ile Cys
1 5 10 15

Ser Ile Phe Pro Tyr Leu Ser Ser Met Ala Ser Thr Val Tyr Ala
20 25 30

<210> 61
<211> 30
<212> PRT
<213> Streptococcus uberis

<400> 61

Met Met Lys Asn Asn Lys Leu Leu Ser Phe Leu Phe Gln Leu Leu Val
1 5 10 15

Ile Leu Leu Phe Ile Phe Cys Leu Phe Tyr Tyr Ile Lys Ala
20 25 30

<210> 62
<211> 31
<212> PRT
<213> Streptococcus uberis

<400> 62

Met Arg Asn Arg Leu Thr Phe Ser Tyr Phe Ile Gly Ile Phe Leu Thr
1 5 10 15

Phe Leu Phe Leu Leu Ile Thr Pro Leu Ile Val Asn Ser Gln Ala
20 25 30

<210> 63
<211> 25

PCT_Sequence_listing (3)

<212> PRT

<213> Streptococcus uberis

<400> 63

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

Leu Leu Val Leu Val Thr Ile Phe Ser
 20 25

<210> 64

<211> 36

<212> PRT

<213> Streptococcus uberis

<400> 64

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

Leu Thr Ser Thr Leu Ala Leu Leu Gly Thr Gly Val Gly Met Gly His
 20 25 30

Thr Val Asn Ala
 35

<210> 65

<211> 27

<212> PRT

<213> Streptococcus uberis

<400> 65

Met Lys Lys Leu Leu Ala Cys Met Leu Met Val Phe Phe Leu Ser Pro
 1 5 10 15

Ile Ser Val Ile Ser Thr Glu Lys Ser Ile Ser
 20 25

<210> 66

<211> 39

<212> PRT

<213> Streptococcus uberis

<400> 66

Met Pro Val Ser Lys Phe Lys His Phe Phe Lys Tyr Ile Met Ile Val
 1 5 10 15

Gly Leu Gly Phe Ile Gly Gly Ala Leu Ala Phe Phe Val Met Asn Leu
 20 25 30

Leu Pro His Pro Ser Ser Thr
 35

<210> 67

<211> 38

<212> PRT

<213> Streptococcus uberis

<400> 67

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

PCT_Sequence_listing (3)

Ile Leu Phe Gly Leu Leu Ala Leu Cys Val Arg Ile Met Gln Ser Lys
20 25 30

Met Leu Ile Ile Leu Ala
35

<210> 68
<211> 33
<212> PRT
<213> Streptococcus uberis

<400> 68

Met Lys Thr Trp Lys Lys Thr Ile Leu Ile Thr Ser Leu Cys Leu Leu
1 5 10 15

Ile Ser Gly Ala Ala Leu Ala Gly Phe Gly Phe Ile Arg Gly Gly Trp
20 25 30

Ser

<210> 69
<211> 30
<212> PRT
<213> Streptococcus uberis

<400> 69

Met Ile Arg Lys Glu Asn Phe Lys Lys Arg Tyr Ile Ser Phe Gly Ile
1 5 10 15

Leu Gly Phe Ala Val Ala Leu Leu Ala Leu Val Phe Ala Phe
20 25 30

<210> 70
<211> 29
<212> PRT
<213> Streptococcus uberis

<400> 70

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

Ile Val Ile Phe Ile Leu Leu Arg Ile Phe Val Phe Ser
20 25

<210> 71
<211> 26
<212> PRT
<213> Streptococcus uberis

<400> 71

Met Lys Ser Phe Phe Asn Ser Arg Ile Trp Leu Gly Leu Val Ser Val
1 5 10 15

Phe Phe Ala Ile Val Leu Phe Leu Thr Ala
20 25

<210> 72

PCT_Sequence_listing (3)

<211> 37
 <212> PRT
 <213> Streptococcus uberis

<400> 72

Met Arg Arg Gln Lys Lys Gln Gln Lys Lys Ile Ile Pro Leu Phe Leu
 1 5 10 15
 Ile Leu Leu Phe Ser Thr Leu Leu Leu Phe Thr Gly Phe Leu Phe Lys
 20 25 30
 Lys Glu Leu Arg Ala
 35

<210> 73
 <211> 24
 <212> PRT
 <213> Streptococcus uberis

<400> 73

Met Phe Lys Lys Lys Leu Met Leu Thr Gly Leu Ile Leu Phe Ser Gly
 1 5 10 15
 Met Thr Val Ser Thr Ala Ser Ala
 20

<210> 74
 <211> 36
 <212> PRT
 <213> Streptococcus uberis

<400> 74

Met Lys Pro Ser Asn Thr Glu Lys Leu Phe Leu Ile Leu Ser Leu Leu
 1 5 10 15
 Thr Leu Ile Leu Ala Gly Ser Phe Tyr Leu Phe Phe Ala Arg Asn His
 20 25 30
 Ile Gly Asn Ala
 35

<210> 75
 <211> 28
 <212> PRT
 <213> Streptococcus uberis

<400> 75

Met Lys Lys Ile Gln Lys Ile Phe Ile Ala Leu Ser Thr Met Ile Leu
 1 5 10 15
 Leu Leu Ser Asn Ile Phe Ser Thr Ile Ile Tyr Ala
 20 25

<210> 76
 <211> 26
 <212> PRT
 <213> Streptococcus uberis

<400> 76

Met Thr Lys Val Arg Lys Ala Ile Ile Pro Ala Ala Gly Leu Gly Thr
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PCT_Sequence_listing (3)

1 5 10 15

Arg Phe Leu Pro Ala Thr Lys Ala Leu Ala
20 25

<210> 77
<211> 28
<212> PRT
<213> Streptococcus uberis
<400> 77

Met Lys Lys Lys Thr Leu Val Met Met Gly Leu Ala Gly Leu Val Ala
1 5 10 15

Gly Gly Gln Leu Tyr Gln Ala Lys Ala Val Leu Ala
20 25

<210> 78
<211> 43
<212> PRT
<213> Streptococcus uberis
<400> 78

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

Ala Met Asn Gln Phe Lys Lys Trp Thr Phe Phe Cys Leu Met Thr Leu
20 25 30

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

<210> 79
<211> 43
<212> PRT
<213> Streptococcus uberis
<400> 79

Met Leu Leu Arg Lys Ala Arg His Ser Leu Lys Arg Arg His Met Met
1 5 10 15

Leu Glu Val Leu Leu Ile Val Ser Thr Phe Phe Leu Phe Ile Ile Phe
20 25 30

Ile Ser Leu Leu Ile Gly Ile Lys Arg Arg Ser
35 40

<210> 80
<211> 23
<212> PRT
<213> Streptococcus uberis
<400> 80

Met Asn Thr Lys Lys Phe Thr Leu Ala Thr Val Thr Val Met Thr Ala
1 5 10 15

Leu Ala Cys Tyr Ser Ser Ala
20

PCT_Sequence_listing (3)

<210> 81
 <211> 34
 <212> PRT
 <213> Streptococcus uberis

<400> 81

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

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

Ser Ala

<210> 82
 <211> 31
 <212> PRT
 <213> Streptococcus uberis

<400> 82

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

Ser Leu Ala Thr Phe Ser Ala Thr Gln Tyr Ser Lys Val Tyr Ala
 20 25 30

<210> 83
 <211> 27
 <212> PRT
 <213> Streptococcus uberis

<400> 83

Met Lys Ser Lys Lys Ser Tyr Val Leu Leu Leu Ala Pro Phe Val Leu
 1 5 10 15

Ala Ser Phe Trp Gln Ser Lys Met Val Ser Ala
 20 25

<210> 84
 <211> 39
 <212> PRT
 <213> Streptococcus uberis

<400> 84

Met Lys Lys Arg Lys Asn Lys Trp Arg Phe Phe Met Ile Lys Met Arg
 1 5 10 15

Lys Ser Gln Leu Ser Val Ser Leu Ala Leu Phe Ala Leu Leu Thr Phe
 20 25 30

Ala Ala Ser Pro Ile Tyr Ala
 35

<210> 85
 <211> 31
 <212> PRT
 <213> Streptococcus uberis

<400> 85

PCT_Sequence_listing (3)

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

Ala Ile Ile Ile Leu Ser Pro Val Leu Leu Ala Val Ala Ile Ala
20 25 30

<210> 86
<211> 33
<212> PRT
<213> Streptococcus uberis

<400> 86

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

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

Ala

<210> 87
<211> 38
<212> PRT
<213> Streptococcus uberis

<400> 87

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

Met Val Leu Ile Leu Phe Ala Leu Phe Phe Pro Leu Pro Tyr Tyr Ile
20 25 30

Glu Met Pro Gly Gly Ala
35

<210> 88
<211> 24
<212> PRT
<213> Streptococcus uberis

<400> 88

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

Gly Thr Ala Thr Thr Val Asn Ala
20

<210> 89
<211> 28
<212> PRT
<213> Streptococcus uberis

<400> 89

Met Arg Arg Arg Ile Lys Pro Ile Val Val Leu Val Phe Phe Leu Leu
1 5 10 15

Phe Ala Leu Leu Leu Ile Ile Gly Lys Thr His Ser
20 25

PCT_Sequence_listing (3)

<210> 90
 <211> 25
 <212> PRT
 <213> Streptococcus uberis

<400> 90

Met Lys Lys Phe Tyr Val Ile Val Gly Thr Leu Leu Ser Ile Phe Ile
 1 5 10 15

Leu Ser Val Ser Leu Phe Val Tyr Ser
 20 25

<210> 91
 <211> 20
 <212> PRT
 <213> Streptococcus uberis

<400> 91

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

Gly Thr Ala Leu
 20

<210> 92
 <211> 23
 <212> PRT
 <213> Streptococcus uberis

<400> 92

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

Ser Thr Ile Pro Val Ile Ala
 20

<210> 93
 <211> 24
 <212> PRT
 <213> Streptococcus uberis

<400> 93

Met Lys Lys Thr Ile Leu Ser Thr Ile Ile Val Gly Leu Phe Leu Trp
 1 5 10 15

Thr Leu Ser Thr Leu Val Leu Ala
 20

<210> 94
 <211> 22
 <212> PRT
 <213> Streptococcus uberis

<400> 94

Met Lys Lys Met Leu Leu Leu Cys Phe Ile Phe Leu Ile Leu Phe Pro
 1 5 10 15

Ile Asn Phe Val Asn Ala
 20

PCT_Sequence_listing (3)

<210> 95
 <211> 35
 <212> PRT
 <213> Streptococcus uberis

<400> 95

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

Val Leu Ile Phe Leu Cys Val Ser Leu Phe Leu Gly Leu Val Val Thr
 20 25 30

Val Ser Ala
 35

<210> 96
 <211> 23
 <212> PRT
 <213> Streptococcus uberis

<400> 96

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

Thr Thr Asn Ser Val Phe Ala
 20

<210> 97
 <211> 29
 <212> PRT
 <213> Streptococcus uberis

<400> 97

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

Val Ala Gly Thr Leu Ser Tyr Leu Ser Leu Ser His Ser
 20 25

<210> 98
 <211> 28
 <212> PRT
 <213> Streptococcus uberis

<400> 98

Met Thr Lys Lys Glu Lys Ile Ile Val Ile Val Gly Pro Thr Ala Val
 1 5 10 15

Gly Lys Thr Ala Leu Gly Ile Gln Val Ala Gln Ala
 20 25

<210> 99
 <211> 24
 <212> PRT
 <213> Streptococcus uberis

<400> 99

Met Thr Asn Ile Lys Thr Ile Gly Val Val Gly Ala Gly Ala Met Gly
 1 5 10 15

PCT_Sequence_listing (3)

Gly Gly Ile Ala Asn Leu Phe Ala
20

<210> 100
<211> 24
<212> PRT
<213> Streptococcus uberis

<400> 100

Met Thr Asn Ile Lys Thr Ile Gly Val Val Gly Ala Gly Ala Met Gly
1 5 10 15

Gly Gly Ile Ala Asn Leu Phe Ala
20

<210> 101
<211> 38
<212> PRT
<213> Streptococcus uberis

<400> 101

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

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

Lys Ser Val Ser Ala Glu
35

<210> 102
<211> 32
<212> PRT
<213> Streptococcus uberis

<400> 102

Met Arg Arg Leu Tyr Ser Phe Ile Ala Gly Val Leu Gly Ile Ile Leu
1 5 10 15

Ile Leu Ala Ser Ser Thr Phe Ile Leu Gln Lys Lys Thr Gly Ser Ala
20 25 30

<210> 103
<211> 29
<212> PRT
<213> Streptococcus uberis

<400> 103

Met Lys Lys Ile Phe Gln Arg Lys Trp Phe Lys Arg Thr Ser Ile Val
1 5 10 15

Leu Gly Ile Leu Leu Val Ala Leu Ile Ala Leu Gly Ser
20 25

<210> 104
<211> 42
<212> PRT
<213> Streptococcus uberis

<400> 104

PCT_Sequence_listing (3)

Met Lys Ser Asn Asp Pro Leu Ala Leu Leu Ala Lys Lys Arg Arg Arg
1 5 10 15

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

Leu Phe Ala Leu Cys Phe Lys Leu Leu Ser
35 40

<210> 105
<211> 35
<212> PRT
<213> Streptococcus uberis

<400> 105

Met Leu Ser Tyr Arg Val Val Lys Arg Arg Leu Gly Met Val Lys Lys
1 5 10 15

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

Ala Leu Ser
35

<210> 106
<211> 29
<212> PRT
<213> Streptococcus uberis

<400> 106

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

Leu Leu Ala Leu Asn Leu Ala Phe Val Cys Val Ile Ala
20 25

<210> 107
<211> 29
<212> PRT
<213> Streptococcus uberis

<400> 107

Met Arg Arg Arg Ile Lys Pro Ile Val Val Leu Val Phe Phe Leu Leu
1 5 10 15

Phe Ala Leu Leu Leu Ile Ile Gly Lys Thr His Ser Asp
20 25

<210> 108
<211> 33
<212> PRT
<213> Streptococcus uberis

<400> 108

Met Lys His Phe Phe Lys Glu Trp Gly Leu Phe Thr Leu Val Ile Leu
1 5 10 15

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

PCT_Sequence_listing (3)

Gly

<210> 109
<211> 1356
<212> DNA
<213> Streptococcus uberis

<220>
<221> CDS
<222> (1)..(1356)

<400> 109	
atg act gag aac cta atc gga aat tta tcg tta ttc gaa ctt tca atc	48
Met Thr Glu Asn Leu Ile Gly Asn Leu Ser Leu Phe Glu Leu Ser Ile	
1 5 10 15	
tta tta tta ctt att ttt gtt gct gca tat ttt att tat tta gca gtt	96
Leu Leu Leu Leu Ile Phe Val Ala Tyr Phe Ile Tyr Leu Ala Val	
20 25 30	
cgt gac tat cga aat gcc aaa att att cgg caa atg agt cat aaa atc	144
Arg Asp Tyr Arg Asn Ala Lys Ile Ile Arg Gln Met Ser His Lys Ile	
35 40 45	
cgt gac cta atc aat ggt cgt tac acg gat gaa atc aat gaa aaa gct	192
Arg Asp Leu Ile Asn Gly Arg Tyr Thr Asp Glu Ile Asn Glu Lys Ala	
50 55 60	
gat att gag ctc att gaa ctt tca gag caa ctc aat gat tta tcg gat	240
Asp Ile Glu Leu Ile Glu Leu Ser Glu Gln Leu Asn Asp Leu Ser Asp	
65 70 75 80	
gtc ttt cga ttg acc cat gaa aat ctt gcc cag gaa aaa aat cgc tta	288
Val Phe Arg Leu Thr His Glu Asn Leu Ala Gln Glu Lys Asn Arg Leu	
85 90 95	
gcc agt att ttg gcc tac atg agt gat ggg gtt ttg gca aca gac cga	336
Ala Ser Ile Leu Ala Tyr Met Ser Asp Gly Val Leu Ala Thr Asp Arg	
100 105 110	
act ggt caa atc atg atg att aac gaa acc gcc caa aaa caa ttg aat	384
Thr Gly Gln Ile Met Met Ile Asn Glu Thr Ala Gln Lys Gln Leu Asn	
115 120 125	
att tcg aaa gaa gaa gcc ctt tta atg aat atc acg gat ttg tta ggg	432
Ile Ser Lys Glu Glu Ala Leu Leu Met Asn Ile Thr Asp Leu Leu Gly	
130 135 140	
caa gac act ccc tat acc tac cgg gaa ttg gtt tcc aaa aca ccg att	480
Gln Asp Thr Pro Tyr Thr Tyr Arg Glu Leu Val Ser Lys Thr Pro Ile	
145 150 155 160	
gtt acc ttg aat aga cgc gat gag act ggt gaa ttt atc acc ctc agg	528
Val Thr Leu Asn Arg Arg Asp Glu Thr Gly Glu Phe Ile Thr Leu Arg	
165 170 175	
ctg cgc ttt gcc ttg aat aga aga gaa agt gga ttc att tcg ggg ctt	576
Leu Arg Phe Ala Leu Asn Arg Arg Glu Ser Gly Phe Ile Ser Gly Leu	
180 185 190	
gtt gtc gtc cta cat gac act acc gaa cag gaa aaa gaa gaa cgt gag	624
Val Val Val Leu His Asp Thr Thr Glu Gln Glu Lys Glu Glu Arg Glu	
195 200 205	
cgt cgc ctc ttt gtt tcg aat gtt agt cac gaa tta aga acg cca ttg	672
Arg Arg Leu Phe Val Ser Asn Val Ser His Glu Leu Arg Thr Pro Leu	
210 215 220	
aca tca gtc aaa tcc tat ttg gaa gcc ctg gat gag ggt gcc tta aaa	720
Thr Ser Val Lys Ser Tyr Leu Glu Ala Leu Asp Glu Gly Ala Leu Lys	

PCT_Sequence_listing (3)																
225				230				235				240				
gaa Glu	gat Asp	atc Ile	gca Ala	cca Pro 245	agt Ser	ttc Phe	atc Ile	aaa Lys	gtt Val 250	tca Ser	cta Leu	gat Asp	gaa Glu	acc Thr 255	aat Asn	768
cgg Arg	atg Met	atg Met	cga Arg 260	atg Met	att Ile	tcg Ser	gac Asp	ttg Leu 265	tta Leu	aac Asn	ctg Leu	tct Ser	cgt Arg 270	att Ile	gat Asp	816
aac Asn	caa Gln	gtc Val 275	aca Thr	gct Ala	cta Leu	gca Ala	gtt Val 280	gaa Glu	atg Met	acc Thr	aat Asn	ttc Phe 285	aca Thr	gcc Ala	ttt Phe	864
atg Met	act Thr 290	tct Ser	ata Ile	cta Leu	aat Asn	cgt Arg 295	ttt Phe	gat Asp	tta Leu	gtg Val	aga Arg 300	aac Asn	caa Gln	aat Asn	aca Thr	912
gtt Val 305	tca Ser	ggg Gly	aaa Lys	agc Ser	tat Tyr 310	gaa Glu	att Ile	ata Ile	cga Arg	gat Asp 315	tat Tyr	cct Pro	att Ile	act Thr	tct Ser 320	960
gtt Val	tgg Trp	cta Leu	gaa Glu	att Ile 325	gac Asp	aat Asn	gat Asp	aaa Lys	atg Met 330	aca Thr	caa Gln	gtc Val	att Ile	gaa Glu 335	aac Asn	1008
att Ile	tta Leu	aat Asn	aat Asn 340	gct Ala	atc Ile	aaa Lys	tat Tyr	tca Ser 345	cct Pro	gat Asp	ggg Gly	ggg Gly	aaa Lys 350	att Ile	cgt Arg	1056
gtt Val	aag Lys	atg Met 355	aaa Lys	aca Thr	aca Thr	gat Asp	agt Ser 360	caa Gln	ttg Leu	att Ile	atc Ile	tct Ser 365	att Ile	tcg Ser	gat Asp	1104
caa Gln	gga Gly 370	tta Leu	gga Gly	att Ile	cca Pro	aag Lys 375	aaa Lys	gat Asp	ctt Leu	cct Pro	ttg Leu 380	att Ile	ttt Phe	gac Asp	cga Arg	1152
ttt Phe 385	tat Tyr	cgg Arg	gtg Val	gat Asp	aaa Lys 390	gca Ala	cgc Arg	agt Ser	cgt Arg	gca Ala 395	caa Gln	ggg Gly	gga Gly	aca Thr	ggg Gly 400	1200
tta Leu	gga Gly	ctt Leu	gcc Ala	att Ile 405	gct Ala	aaa Lys	gaa Glu	att Ile	gta Val 410	aaa Lys	caa Gln	cat His	aat Asn	ggg Gly 415	ttt Phe	1248
ata Ile	tgg Trp	gca Ala	aaa Lys 420	agt Ser	gac Asp	tat Tyr	ggc Gly	aaa Lys 425	ggc Gly	tcg Ser	acc Thr	ttt Phe	aca Thr 430	att Ile	gta Val	1296
ttg Leu	cca Pro	tat Tyr 435	gaa Glu	aaa Lys	gat Asp	gtt Val	gtt Val 440	gca Ala	gga Gly	aca Thr	gat Asp	gat Asp 445	gaa Glu	tgg Trp	gag Glu	1344
gat Asp	gat Asp 450	att Ile	gac Asp													1356

<210> 110
<211> 452
<212> PRT
<213> Streptococcus uberis

<400> 110

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

Leu Leu Leu Leu Ile Phe Val Ala Ala Tyr Phe Ile Tyr Leu Ala Val
20 25 30

Arg Asp Tyr Arg Asn Ala Lys Ile Ile Arg Gln Met Ser His Lys Ile
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PCT_Sequence_listing (3)

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

PCT_Sequence_listing (3)

Ile Leu Asn Asn Ala Ile Lys Tyr Ser Pro Asp Gly Gly Lys Ile Arg
340 345 350

Val Lys Met Lys Thr Thr Asp Ser Gln Leu Ile Ile Ser Ile Ser Asp
355 360 365

Gln Gly Leu Gly Ile Pro Lys Lys Asp Leu Pro Leu Ile Phe Asp Arg
370 375 380

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

Leu Gly Leu Ala Ile Ala Lys Glu Ile Val Lys Gln His Asn Gly Phe
405 410 415

Ile Trp Ala Lys Ser Asp Tyr Gly Lys Gly Ser Thr Phe Thr Ile Val
420 425 430

Leu Pro Tyr Glu Lys Asp Val Val Ala Gly Thr Asp Asp Glu Trp Glu
435 440 445

Asp Asp Ile Asp
450

<210> 111
<211> 1086
<212> DNA
<213> Streptococcus uberis

<220>
<221> CDS
<222> (1)..(1086)

<400> 111	
atg aaa ttc ata aaa atc tta tta tct caa atc gtc agt cta ttt ttg	48
Met Lys Phe Ile Lys Ile Leu Leu Ser Gln Ile Val Ser Leu Phe Leu	
1 5 10 15	
ctc tta aca atc agt tta cat gct tta gag aca gtc aat gca gct gta	96
Leu Leu Thr Ile Ser Leu His Ala Leu Glu Thr Val Asn Ala Ala Val	
20 25 30	
ctg ggg gat gac tat ccc att gca tgg aaa tcc ggt tgg ggt aca gac	144
Leu Gly Asp Asp Tyr Pro Ile Ala Trp Lys Ser Gly Trp Gly Thr Asp	
35 40 45	
act tgg gga atg tac cga agg caa tgc acc tca ttt gtt gct ttt aga	192
Thr Trp Gly Met Tyr Arg Arg Gln Cys Thr Ser Phe Val Ala Phe Arg	
50 55 60	
ttg aat caa gta aat ggg ctt tca atc cct tct ggt tta gga aat gct	240
Leu Asn Gln Val Asn Gly Leu Ser Ile Pro Ser Gly Leu Gly Asn Ala	
65 70 75 80	
gat act tgg ggt cat att gct aga cga atg ggg tat cct gtt aat gat	288
Asp Thr Trp Gly His Ile Ala Arg Arg Met Gly Tyr Pro Val Asn Asp	
85 90 95	
atc cca gca gta gga gcc gtt gcc tgg ttt gat aaa gga ata aat ggt	336
Ile Pro Ala Val Gly Ala Val Ala Trp Phe Asp Lys Gly Ile Asn Gly	
100 105 110	
tct cat ctt gcc tat gga cat gtc tcc tgg gtt gcg gag gtt aat ggt	384
Ser His Leu Ala Tyr Gly His Val Ser Trp Val Ala Glu Val Asn Gly	
115 120 125	

PCT_Sequence_listing (3)

aat cta gtt acc tta gaa gaa tat aat ttt gat gcc gga caa ggt cct Asn Leu Val Thr Leu Glu Glu Tyr Asn Phe Asp Ala Gly Gln Gly Pro 130 135 140	432
gaa caa tat cat aga aga gtc att aac agt cat caa gtc agt ggt ttt Glu Gln Tyr His Arg Arg Val Ile Asn Ser His Gln Val Ser Gly Phe 145 150 155 160	480
att cat ttc aaa gat gtc gat act gga agt att ccc atc tct tct cct Ile His Phe Lys Asp Val Asp Thr Gly Ser Ile Pro Ile Ser Ser Pro 165 170 175	528
atg caa agc ccg aga tca aca att cca aac caa ggg agt tat cat ttt Met Gln Ser Pro Arg Ser Thr Ile Pro Asn Gln Gly Ser Tyr His Phe 180 185 190	576
acc gaa cag atg ccc ata aaa gct cag cct att gcc aat agc caa gca Thr Glu Gln Met Pro Ile Lys Ala Gln Pro Ile Ala Asn Ser Gln Ala 195 200 205	624
att gcc ttt tac cag gcc ggc caa atg gtt cac tat gat aaa acc gta Ile Ala Phe Tyr Gln Ala Gly Gln Met Val His Tyr Asp Lys Thr Val 210 215 220	672
att gct gat ggt tat caa tgg cta tca tac att gcc tat tct ggt caa Ile Ala Asp Gly Tyr Gln Trp Leu Ser Tyr Ile Ala Tyr Ser Gly Gln 225 230 235 240	720
aga cgc tac atc cca att gct aag gta act tct aag gaa agt tca aaa Arg Arg Tyr Ile Pro Ile Ala Lys Val Thr Ser Lys Glu Ser Ser Lys 245 250 255	768
cag gag gac ttt gcc cca ggt gac caa gtt act ttt tct ggt gtt tac Gln Glu Asp Phe Ala Pro Gly Asp Gln Val Thr Phe Ser Gly Val Tyr 260 265 270	816
caa gtc act caa att cat ggt agc ctg ctt tct agt aag gac tta gct Gln Val Thr Gln Ile His Gly Ser Leu Leu Ser Ser Lys Asp Leu Ala 275 280 285	864
ggt gga gag cct ggt cct cta aat tgg tta gat cca ggt cct gtc ctt Gly Gly Glu Pro Gly Pro Leu Asn Trp Leu Asp Pro Gly Pro Val Leu 290 295 300	912
gaa agc aac aga gac gga caa caa agt gga gat caa ata ctc tac ccc Glu Ser Asn Arg Asp Gly Gln Gln Ser Gly Asp Gln Ile Leu Tyr Pro 305 310 315 320	960
ggc gat ttc ttt atc att cca gga aac tac aaa gtt tta cag att cac Gly Asp Phe Phe Ile Ile Pro Gly Asn Tyr Lys Val Leu Gln Ile His 325 330 335	1008
aag gaa aca aaa ggt ctc ctt att caa ata gga aac cga caa act tgg Lys Glu Thr Lys Gly Leu Leu Ile Gln Ile Gly Asn Arg Gln Thr Trp 340 345 350	1056
gta tca atg aac aag gtt cag aaa tct aca Val Ser Met Asn Lys Val Gln Lys Ser Thr 355 360	1086

<210> 112
<211> 362
<212> PRT
<213> Streptococcus uberis

<400> 112

Met Lys Phe Ile Lys Ile Leu Leu Ser Gln Ile Val Ser Leu Phe Leu
1 5 10 15

Leu Leu Thr Ile Ser Leu His Ala Leu Glu Thr Val Asn Ala Ala Val
20 25 30

PCT_Sequence_listing (3)

Leu Gly Asp Asp Tyr Pro Ile Ala Trp Lys Ser Gly Trp Gly Thr Asp
35 40 45

Thr Trp Gly Met Tyr Arg Arg Gln Cys Thr Ser Phe Val Ala Phe Arg
50 55 60

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

Asp Thr Trp Gly His Ile Ala Arg Arg Met Gly Tyr Pro Val Asn Asp
85 90 95

Ile Pro Ala Val Gly Ala Val Ala Trp Phe Asp Lys Gly Ile Asn Gly
100 105 110

Ser His Leu Ala Tyr Gly His Val Ser Trp Val Ala Glu Val Asn Gly
115 120 125

Asn Leu Val Thr Leu Glu Glu Tyr Asn Phe Asp Ala Gly Gln Gly Pro
130 135 140

Glu Gln Tyr His Arg Arg Val Ile Asn Ser His Gln Val Ser Gly Phe
145 150 155 160

Ile His Phe Lys Asp Val Asp Thr Gly Ser Ile Pro Ile Ser Ser Pro
165 170 175

Met Gln Ser Pro Arg Ser Thr Ile Pro Asn Gln Gly Ser Tyr His Phe
180 185 190

Thr Glu Gln Met Pro Ile Lys Ala Gln Pro Ile Ala Asn Ser Gln Ala
195 200 205

Ile Ala Phe Tyr Gln Ala Gly Gln Met Val His Tyr Asp Lys Thr Val
210 215 220

Ile Ala Asp Gly Tyr Gln Trp Leu Ser Tyr Ile Ala Tyr Ser Gly Gln
225 230 235 240

Arg Arg Tyr Ile Pro Ile Ala Lys Val Thr Ser Lys Glu Ser Ser Lys
245 250 255

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

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

Gly Gly Glu Pro Gly Pro Leu Asn Trp Leu Asp Pro Gly Pro Val Leu
290 295 300

Glu Ser Asn Arg Asp Gly Gln Gln Ser Gly Asp Gln Ile Leu Tyr Pro
305 310 315 320

Gly Asp Phe Phe Ile Ile Pro Gly Asn Tyr Lys Val Leu Gln Ile His
325 330 335

PCT_Sequence_listing (3)

Lys Glu Thr Lys Gly Leu Leu Ile Gln Ile Gly Asn Arg Gln Thr Trp
340 345 350

Val Ser Met Asn Lys Val Gln Lys Ser Thr
355 360

<210> 113
<211> 435
<212> DNA
<213> Streptococcus uberis

<220>
<221> CDS
<222> (1)..(435)

<400> 113
atg act att atc aaa aac atc ctg gtg aaa ata agc tgt tgc cat agt 48
Met Thr Ile Ile Lys Asn Ile Leu Val Lys Ile Ser Cys Cys His Ser
1 5 10 15
aaa gcc ttc acc ctt gcg gag agt ctc ctg tgt ctg gca gtg acg acc 96
Lys Ala Phe Thr Leu Ala Glu Ser Leu Leu Cys Leu Ala Val Thr Thr
20 25 30
ttc acc att ctg ttg cta agt agc tct ctg gcg ggt gtt tat gaa agt 144
Phe Thr Ile Leu Leu Leu Ser Ser Ser Leu Ala Gly Val Tyr Glu Ser
35 40 45
gtg gaa aga gaa ttg ttt ttc att tcc ttt gaa cat ttt tat cgt cat 192
Val Glu Arg Glu Leu Phe Phe Ile Ser Phe Glu His Phe Tyr Arg His
50 55 60
tgt caa aaa atg agt gtt tta aaa caa gaa gaa agt gct ttg cac ttt 240
Cys Gln Lys Met Ser Val Leu Lys Gln Glu Glu Ser Ala Leu His Phe
65 70 75 80
aca gca cat cgt atc aaa tat ggt cag cgt gaa tta gtg att cca gat 288
Thr Ala His Arg Ile Lys Tyr Gly Gln Arg Glu Leu Val Ile Pro Asp
85 90 95
cat att cga ttg tta aat caa ggg act atc cct ttt aac aaa aca ggt 336
His Ile Arg Leu Leu Asn Gln Gly Thr Ile Pro Phe Asn Lys Thr Gly
100 105 110
ggg agt cat tcc tta gca aaa att gag tgg caa aca cca agg gag aaa 384
Gly Ser His Ser Leu Ala Lys Ile Glu Trp Gln Thr Pro Arg Glu Lys
115 120 125
ttg aca tac cag cta aat cta ggg agt gga aat tat caa aaa cga aga 432
Leu Thr Tyr Gln Leu Asn Leu Gly Ser Gly Asn Tyr Gln Lys Arg Arg
130 135 140
cat
His
145 435

<210> 114
<211> 145
<212> PRT
<213> Streptococcus uberis

<400> 114

Met Thr Ile Ile Lys Asn Ile Leu Val Lys Ile Ser Cys Cys His Ser
1 5 10 15

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

PCT_Sequence_listing (3)

Phe Thr Ile Leu Leu Leu Ser Ser Ser Leu Ala Gly Val Tyr Glu Ser
 35 40 45
 Val Glu Arg Glu Leu Phe Phe Ile Ser Phe Glu His Phe Tyr Arg His
 50 55 60
 Cys Gln Lys Met Ser Val Leu Lys Gln Glu Glu Ser Ala Leu His Phe
 65 70 75 80
 Thr Ala His Arg Ile Lys Tyr Gly Gln Arg Glu Leu Val Ile Pro Asp
 85 90 95
 His Ile Arg Leu Leu Asn Gln Gly Thr Ile Pro Phe Asn Lys Thr Gly
 100 105 110
 Gly Ser His Ser Leu Ala Lys Ile Glu Trp Gln Thr Pro Arg Glu Lys
 115 120 125
 Leu Thr Tyr Gln Leu Asn Leu Gly Ser Gly Asn Tyr Gln Lys Arg Arg
 130 135 140
 His
 145

<210> 115
 <211> 3861
 <212> DNA
 <213> Streptococcus uberis

<220>
 <221> CDS
 <222> (52)..(3861)

<400> 115
 atgatcaatc taaaggtaaa tactgtccct attcaaaagg agaaaggaat t atg aag 57
 Met Lys
 1
 caa gaa aag aaa tgt gtt aat tgg ttt atg cgc aag cgg ggg aaa caa 105
 Gln Glu Lys Lys Cys Val Asn Trp Phe Met Arg Lys Arg Gly Lys Gln
 5 10 15
 tgg att tat ggt tgt ggc att tta att tgt ggc ttg gtt ttc gga gtt 153
 Trp Ile Tyr Gly Cys Gly Ile Leu Ile Cys Gly Leu Val Phe Gly Val
 20 25 30
 gaa gct act tca gtc gct gct gag act att cca aca aca gca aca gtt 201
 Glu Ala Thr Ser Val Ala Ala Glu Thr Ile Pro Thr Thr Ala Thr Val
 35 40 45 50
 gag act tta aat tca gat gta aca agt aag aca tct caa gaa aca cag 249
 Glu Thr Leu Asn Ser Asp Val Thr Ser Lys Thr Ser Gln Glu Thr Gln
 55 60 65
 aag act act gaa ata gca aca cca gtt tca gaa ata gtt atg cca tct 297
 Lys Thr Thr Glu Ile Ala Thr Pro Val Ser Glu Ile Val Met Pro Ser
 70 75 80
 caa caa aaa gtt gtt gag gag gta act caa gaa gtt agc gta caa aat 345
 Gln Gln Lys Val Val Glu Glu Val Thr Gln Glu Val Ser Val Gln Asn
 85 90 95
 caa gag acg gtc ata aat atg cct gtg tta act caa gga gta aat ata 393
 Gln Glu Thr Val Ile Asn Met Pro Val Leu Thr Gln Gly Val Asn Ile

PCT_Sequence_listing (3)																
100				105				110								
gca Ala 115	gga Gly	cca Pro	aat Asn	gaa Glu	acg Thr 120	gct Ala	ata Ile	tta Leu	acg Thr 125	gat Asp	tcg Ser	att Ile	gtc Val	caa Gln	aac Asn 130	441
aat Asn	ggt Val	caa Gln	cct Pro	att Ile 135	gat Asp	aga Arg	ggt Val	gag Glu	aaa Lys 140	atg Met	gaa Glu	aca Thr	tcc Ser	ttt Phe 145	tct Ser	489
acc Thr	gaa Glu	ttg Leu	act Thr 150	aag Lys	aaa Lys	gct Ala	gaa Glu	agt Ser 155	agc Ser	tat Tyr	aat Asn	aca Thr	aat Asn 160	ctt Leu	caa Gln	537
gat Asp	ttg Leu	aat Asn 165	tat Tyr	gat Asp	cca Pro	aat Asn	ggt Val 170	tgg Trp	gaa Glu	ggt Val	cgt Arg	gaa Glu 175	gat Asp	ggt Gly	ttg Leu	585
tat Tyr	agt Ser 180	aac Asn	gct Ala	ggt Val	gga Gly	aaa Lys 185	ggt Gly	gac Asp	aat Asn	ttc Phe	cta Leu 190	ttt Phe	tca Ser	gca Ala	tca Ser	633
act Thr 195	ggt Gly	gaa Glu	aac Asn	ttt Phe	atc Ile 200	ttc Phe	caa Gln	aca Thr	gac Asp	gta Val 205	acc Thr	ttt Phe	ctt Leu	caa Gln	aat Asn 210	681
acc Thr	gga Gly	gca Ala	gct Ala	tca Ser 215	ctc Leu	ggt Val	ttc Phe	cgt Arg	tca Ser 220	aac Asn	aat Asn	gat Asp	cct Pro	gaa Glu 225	aat Asn	729
ctc Leu	aat Asn	ggt Gly	tat Tyr 230	ggt Val	ggt Val	aat Asn	ctt Leu	gat Asp 235	gga Gly	aat Asn	tca Ser	cac His	aaa Lys 240	gca Ala	agg Arg	777
tta Leu	tgg Trp	cgt Arg 245	tgg Trp	gct Ala	gaa Glu	gca Ala	aat Asn 250	tta Leu	att Ile	aat Asn	gac Asp	aaa Lys 255	gaa Glu	att Ile	cta Leu	825
gcc Ala 260	agt Ser	ccg Pro	gac Asp	aat Asn	aaa Lys	tat Tyr 265	ttc Phe	tta Leu	aaa Lys	gta Val	gtg Val 270	gcg Ala	act Thr	aac Asn	ggg Gly	873
tgg Trp 275	att Ile	tca Ser	tac Tyr	tac Tyr	att Ile 280	aat Asn	ggt Gly	att Ile	ttg Leu	att Ile 285	gca Ala	aac Asn	ttg Leu	agc Ser	gac Asp 290	921
tac Tyr	act Thr	ata Ile	caa Gln	cgt Arg 295	gat Asp	gac Asp	ctt Leu	ggt Gly	caa Gln 300	aca Thr	aca Thr	tat Tyr	att Ile	aaa Lys 305	gat Asp	969
ggt Gly	cat His	ttt Phe	ggt Gly 310	ctt Leu	ttg Leu	aac Asn	tgg Trp	aat Asn 315	ggt Gly	gaa Glu	atg Met	gtc Val	ttc Phe 320	caa Gln	aat Asn	1017
acc Thr	ttc Phe	tac Tyr 325	cgt Arg	gaa Glu	ttg Leu	aca Thr	aat Asn 330	gaa Glu	gag Glu	tta Leu	cct Pro	ctt Leu 335	ctt Leu	aat Asn	gat Asp	1065
gtg Val 340	acg Thr	gta Val	acg Thr	tca Ser	aaa Lys	aac Asn 345	ggt Gly	cca Pro	ggt Val	gaa Glu	cct Pro 350	aaa Lys	gga Gly	caa Gln	ttt Phe	1113
ttt Phe 355	tca Ser	gag Glu	agt Ser	tca Ser	ggt Val 360	tat Tyr	att Ile	caa Gln	tat Tyr	gta Val 365	tca Ser	aac Asn	gat Asp	gcc Ala	tca Ser 370	1161
acg Thr	gtg Val	gac Asp	ttg Leu	agc Ser 375	ttt Phe	gat Asp	gct Ala	aat Asn	aat Asn 380	tca Ser	gat Asp	gca Ala	cta Leu	ata Ile 385	aca Thr	1209
gtg Val	act Thr	gat Asp	gct Ala 390	cat His	ggt Gly	aaa Lys	ggt Val	tat Tyr 395	tca Ser	aat Asn	cca Pro	agc Ser	gca Ala 400	att Ile	cct Pro	1257
gta Leu	act Thr	ggt Val	gga Leu	cca Leu	aat Leu	tat Leu	ctc Leu	acg Leu	gtg Leu	aca Leu	agt Leu	act Leu	tac Leu	aca Leu	aca Leu	1305

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PCT_Sequence_listing (3)

Val	Thr	Val	Gly	Pro	Asn	Tyr	Leu	Thr	Val	Thr	Ser	Thr	Tyr	Thr	Thr	
		405					410					415				
aca	gat	ggc	tac	gta	atc	ccc	tca	aca	tac	cgt	att	aat	ggt	cac	cgg	1353
Thr	Asp	Gly	Tyr	Val	Ile	Pro	Ser	Thr	Tyr	Arg	Ile	Asn	Val	His	Arg	
	420					425					430					
cgt	caa	cca	cag	tca	ggt	tat	tat	aat	gaa	aac	ttc	cgt	gat	caa	tat	1401
Arg	Gln	Pro	Gln	Ser	Val	Tyr	Tyr	Asn	Glu	Asn	Phe	Arg	Asp	Gln	Tyr	
435					440					445					450	
cat	tac	tct	ggt	aaa	gat	ggc	tgg	gca	aat	gat	cct	aat	gga	tta	ggt	1449
His	Tyr	Ser	Val	Lys	Asp	Gly	Trp	Ala	Asn	Asp	Pro	Asn	Gly	Leu	Val	
				455					460					465		
tac	tat	aat	ggg	ggt	tat	cat	atg	ttt	tac	caa	ttc	tac	gat	gat	aca	1497
Tyr	Tyr	Asn	Gly	Val	Tyr	His	Met	Phe	Tyr	Gln	Phe	Tyr	Asp	Asp	Thr	
			470					475					480			
aaa	tgg	ggg	cca	atg	cat	tgg	gca	cat	gca	aca	agt	act	gat	ttg	att	1545
Lys	Trp	Gly	Pro	Met	His	Trp	Ala	His	Ala	Thr	Ser	Thr	Asp	Leu	Ile	
		485					490					495				
cat	tgg	gaa	gac	caa	cca	att	gct	ttt	tat	cca	gac	tat	aat	gga	acg	1593
His	Trp	Glu	Asp	Gln	Pro	Ile	Ala	Phe	Tyr	Pro	Asp	Tyr	Asn	Gly	Thr	
	500					505					510					
atg	ttc	tca	ggc	tgt	ata	gtg	gca	gat	ggt	aat	aat	tct	agt	gga	ctt	1641
Met	Phe	Ser	Gly	Cys	Ile	Val	Ala	Asp	Val	Asn	Asn	Ser	Ser	Gly	Leu	
515					520					525					530	
ttt	gat	agt	gaa	aat	ggg	gga	tta	gta	gct	ctc	att	acg	att	aac	ggg	1689
Phe	Asp	Ser	Glu	Asn	Gly	Gly	Leu	Val	Ala	Leu	Ile	Thr	Ile	Asn	Gly	
				535					540					545		
gaa	ggg	caa	cgc	att	aaa	ctt	gca	tat	agt	act	gat	gaa	ggg	aaa	acc	1737
Glu	Gly	Gln	Arg	Ile	Lys	Leu	Ala	Tyr	Ser	Thr	Asp	Glu	Gly	Lys	Thr	
			550					555					560			
tgg	caa	aaa	gtg	gat	gaa	att	gta	gcg	gat	tgg	act	aca	gac	cca	cta	1785
Trp	Gln	Lys	Val	Asp	Glu	Ile	Val	Ala	Asp	Trp	Thr	Thr	Asp	Pro	Leu	
		565					570					575				
caa	act	cgt	gat	ttt	cgt	gac	cct	aaa	ggt	ttc	cgt	tgg	gaa	aat	aaa	1833
Gln	Thr	Arg	Asp	Phe	Arg	Asp	Pro	Lys	Val	Phe	Arg	Trp	Glu	Asn	Lys	
	580					585					590					
tgg	ttt	atg	gta	att	gca	ggg	gga	cca	cta	cgt	ctt	tat	tca	tca	gat	1881
Trp	Phe	Met	Val	Ile	Ala	Gly	Gly	Pro	Leu	Arg	Leu	Tyr	Ser	Ser	Asp	
					600					605					610	
gat	ctt	aaa	aat	tgg	act	gtg	gaa	tca	acg	tat	cca	gat	ctt	cat	aca	1929
Asp	Leu	Lys	Asn	Trp	Thr	Val	Glu	Ser	Thr	Tyr	Pro	Asp	Leu	His	Thr	
				615					620					625		
gaa	tgt	cca	gat	ctt	tac	cca	gtc	ttg	gcg	gaa	gat	cag	aca	gtg	aaa	1977
Glu	Cys	Pro	Asp	Leu	Tyr	Pro	Val	Leu	Ala	Glu	Asp	Gln	Thr	Val	Lys	
			630					635					640			
tgg	ggt	ctt	tct	cgc	ggg	ggg	cgt	tat	tac	aaa	ggt	ggg	gat	tta	caa	2025
Trp	Val	Leu	Ser	Arg	Gly	Gly	Arg	Tyr	Tyr	Lys	Val	Gly	Asp	Leu	Gln	
		645					650					655				
caa	gct	gac	gga	aat	tgg	aaa	ttc	ata	cca	gat	gct	aat	tac	caa	gaa	2073
Gln	Ala	Asp	Gly	Asn	Trp	Lys	Phe	Ile	Pro	Asp	Ala	Asn	Tyr	Gln	Glu	
	660					665					670					
aca	gat	agt	atc	atg	aat	ttt	ggg	aaa	gat	tca	tat	gct	gcg	atg	aca	2121
Thr	Asp	Ser	Ile	Met	Asn	Phe	Gly	Lys	Asp	Ser	Tyr	Ala	Ala	Met	Thr	
					680					685					690	
tac	tat	gta	caa	gat	ttt	ggg	acc	aaa	gct	aat	cca	act	att	cca	aag	2169
Tyr	Tyr	Val	Gln	Asp	Phe	Gly	Thr	Lys	Ala	Asn	Pro	Thr	Ile	Pro	Lys	
				695					700					705		

PCT_Sequence_listing (3)																
att Ile	att Ile	gaa Glu	ttg Leu 710	aat Asn	tgg Trp	atg Met	aat Asn	act Thr 715	tgg Trp	gat Asp	aac Asn	tat Tyr	tgc Cys 720	aac Asn	ctt Leu	2217
gta Val	gct Ala	gat Asp 725	cgc Arg	tta Leu	ggt Gly	cag Gln	tca Ser 730	ttt Phe	aat Asn	ggg Gly	act Thr	ttt Phe 735	aac Asn	ctt Leu	aat Asn	2265
tta Leu	gaa Glu 740	ctt Leu	ggt Gly	ctt Leu	gtc Val	aaa Lys 745	gaa Glu	ggt Gly	gat Asp	aag Lys	tat Tyr 750	gtt Val	ctt Leu	act Thr	cag Gln	2313
aca Thr 755	ccg Pro	gtt Val	gaa Glu	gct Ala	tat Tyr 760	gaa Glu	agt Ser	tta Leu	cgt Arg	gat Asp 765	aat Asn	gac Asp	aac Asn	aaa Lys	gtt Val 770	2361
gaa Glu	tac Tyr	aaa Lys	aat Asn	gtt Val 775	gtc Val	gtt Val	ggt Gly	aaa Lys	gaa Glu 780	aat Asn	gac Asp	ctt Leu	ttt Phe	aaa Lys 785	gat Asp	2409
ttt Phe	tct Ser	gga Gly	gat Asp 790	act Thr	tat Tyr	gaa Glu	att Ile	gtt Val 795	gct Ala	cac His	ttt Phe	aaa Lys	ccg Pro 800	agt Ser	gac Asp	2457
aaa Lys	aca Thr 805	aca Thr	aaa Lys	gtt Val	ggt Gly	ttc Phe	aac Asn 810	ctt Leu	aga Arg	gtt Val	ggt Gly	tca Ser 815	ggg Gly	gag Glu	atg Met	2505
act Thr	aag Lys 820	gtt Val	tac Tyr	tat Tyr	gat Asp	ttg Leu 825	ata Ile	gca Ala	gga Gly	cga Arg	atc Ile 830	att Ile	atc Ile	gac Asp	cga Arg	2553
agt Ser 835	caa Gln	tca Ser	ggc Gly	att Ile	ata Ile 840	ttg Leu	acg Thr	gaa Glu	ctt Leu	ttt Phe 845	agt Ser	aat Asn	att Ile	gat Asp	agt Ser 850	2601
cag Gln	gct Ala	gta Val	aca Thr	cct Pro 855	aat Asn	att Ile	gat Asp	gga Gly	agt Ser 860	att Ile	gat Asp	cta Leu	cac His	att Ile 865	ttt Phe	2649
gtt Val	gat Asp	cgt Arg	gct Ala 870	agt Ser	gtt Val	gaa Glu	gtt Val	ttt Phe 875	tca Ser	aaa Lys	aat Asn	cat His	aca Thr 880	gta Val	gca Ala	2697
ggg Gly	gct Ala	aac Asn 885	caa Gln	att Ile	ttc Phe	aca Thr	tca Ser 890	gct Ala	caa Gln	agt Ser	cta Leu	gga Gly 895	ttg Leu	gaa Glu	gta Val	2745
ctc Leu	att Ile 900	gat Asp	ggt Gly	gaa Glu	gat Asp	gct Ala 905	aaa Lys	gca Ala	gat Asp	att Ile	gtc Val 910	tta Leu	tat Tyr	cca Pro	tta Leu	2793
aag Lys 915	agc Ser	atc Ile	tgg Trp	aaa Lys	aat Asn 920	aaa Lys	att Ile	att Ile	gat Asp	aca Thr 925	aca Thr	ccc Pro	caa Gln	att Ile	gtt Val 930	2841
att Ile	cca Pro	gct Ala	agt Ser	gaa Glu 935	cca Pro	aaa Lys	gta Val	cgg Arg	atg Met 940	aat Asn	gtg Val	ggt Gly	gat Asp	agc Ser 945	aca Thr	2889
acc Thr	gta Val	aaa Lys	gct Ala 950	tat Tyr	gtt Val	tca Ser	cca Pro	gtt Val 955	ggg Gly	gcg Ala	agt Ser	caa Gln	gat Asp 960	ctt Leu	att Ile	2937
tgg Trp	aat Asn	att Ile 965	agc Ser	aat Asn	cca Pro	agt Ser	cta Leu 970	gtt Val	tta Leu	gat Asp	caa Gln	ata Ile 975	tca Ser	ggt Gly	aat Asn	2985
cag Gln	gtt Val 980	ttt Phe	ctt Leu	aaa Lys	gcg Ala	att Ile 985	aag Lys	aaa Lys	gga Gly	caa Gln	gtt Val 990	att Ile	gta Val	aga Arg	gca Ala	3033
cag Gln 995	tca Ser	caa Gln	tct Ser	aat Asn	cca Pro 1000	gca Ala	gtt Val	tat Tyr	caa Gln	gat Asp 1005	ttt Phe	att Ile	att Ile	gat Asp		3078

PCT_Sequence_listing (3)

att Ile 1010	tta Leu	gaa Glu	gat Asp	aac Asn	ttc Phe 1015	aat Asn	aca Thr	aat Asn	gtt Val	aaa Lys 1020	gat Asp	gtg Val	aat Asn	gta Val	3123
ttt Phe 1025	tct Ser	ggc Gly	gat Asp	tgg Trp	tac Tyr 1030	gtt Val	gat Asp	ggc Gly	gaa Glu	tct Ser 1035	ttg Leu	aaa Lys	gtt Val	gca Ala	3168
aat Asn 1040	cac His	aat Asn	tca Ser	aac Asn	gac Asp 1045	att Ile	tac Tyr	atg Met	tca Ser	gca Ala 1050	gat Asp	aag Lys	ata Ile	cca Pro	3213
tat Tyr 1055	gaa Glu	aat Asn	tat Tyr	caa Gln	atg Met 1060	gac Asp	ttg Leu	gat Asp	ata Ile	aaa Lys 1065	tat Tyr	ggg Gly	cga Arg	gga Gly	3258
att Ile 1070	gta Val	aat Asn	atc Ile	ttc Phe	ttt Phe 1075	gct Ala	tca Ser	ggg Gly	aat Asn	cct Pro 1080	gac Asp	gct Ala	aac Asn	aac Asn	3303
gct Ala 1085	tat Tyr	act Thr	atc Ile	caa Gln	ttt Phe 1090	ggg Gly	agc Ser	aat Asn	aat Asn	tca Ser 1095	gtt Val	cgt Arg	ttg Leu	ttc Phe	3348
cgc Arg 1100	ttc Phe	tac Tyr	aga Arg	gat Asp	act Thr 1105	att Ile	ttt Phe	gag Glu	gcg Ala	cca Pro 1110	atg Met	ata Ile	gat Asp	gtg Val	3393
att Ile 1115	aat Asn	gac Asp	aat Asn	caa Gln	ttc Phe 1120	cac His	cat His	gtt Val	cga Arg	ttg Leu 1125	gtg Val	aaa Lys	tca Ser	gca Ala	3438
aat Asn 1130	gtc Val	atc Ile	cat His	gtt Val	tat Tyr 1135	gtt Val	gat Asp	aat Asn	gaa Glu	atg Met 1140	gta Val	atg Met	tct Ser	tac Tyr	3483
aca Thr 1145	ttt Phe	gat Asp	caa Gln	gtt Val	gaa Glu 1150	gag Glu	ttt Phe	ttc Phe	aac Asn	aat Asn 1155	cca Pro	tac Tyr	ctt Leu	ggc Gly	3528
cta Leu 1160	ggg Gly	ctt Leu	tgg Trp	gat Asp	ggc Gly 1165	gaa Glu	cta Leu	gct Ala	gtt Val	cag Gln 1170	aac Asn	ttt Phe	tat Tyr	gta Val	3573
att Ile 1175	gat Asp	tta Leu	gat Asp	gcg Ala	caa Gln 1180	aaa Lys	cct Pro	gtt Val	ttt Phe	gtt Val 1185	gaa Glu	gag Glu	cat His	gag Glu	3618
aaa Lys 1190	gag Glu	aaa Lys	cta Leu	cta Leu	tca Ser 1195	gaa Glu	tta Leu	aaa Lys	aaa Lys	tca Ser 1200	gtg Val	gtt Val	aaa Lys	aca Thr	3663
agt Ser 1205	tca Ser	tat Tyr	tca Ser	act Thr	cta Leu 1210	aaa Lys	aca Thr	ata Ile	gag Glu	acg Thr 1215	tct Ser	tca Ser	aaa Lys	aca Thr	3708
aat Asn 1220	tct Ser	gag Glu	aac Asn	tta Leu	gaa Glu 1225	gct Ala	ccg Pro	act Thr	gtt Val	tct Ser 1230	aag Lys	aaa Lys	aac Asn	tta Leu	3753
cct Pro 1235	atg Met	aca Thr	agt Ser	gat Asp	agt Ser 1240	aac Asn	aat Asn	aat Asn	tta Leu	gag Glu 1245	gaa Glu	ctg Leu	ggg Gly	ata Ile	3798
tta Leu 1250	gta Val	att Ile	cta Leu	acg Thr	act Thr 1255	tta Leu	gga Gly	gct Ala	ttt Phe	tta Leu 1260	gga Gly	cgc Arg	gtt Val	att Ile	3843
tta Leu 1265	aaa Lys	aaa Lys	gaa Glu	aaa Lys	taa										3861

<210> 116

PCT_Sequence_listing (3)

<211> 1269

<212> PRT

<213> Streptococcus uberis

<400> 116

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

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

Thr Gln Lys Thr Thr Glu Ile Ala Thr Pro Val Ser Glu Ile Val Met
 65 70 75 80

Pro Ser Gln Gln Lys Val Val Glu Glu Val Thr Gln Glu Val Ser Val
 85 90 95

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

Asn Ile Ala Gly Pro Asn Glu Thr Ala Ile Leu Thr Asp Ser Ile Val
 115 120 125

Gln Asn Asn Val Gln Pro Ile Asp Arg Val Glu Lys Met Glu Thr Ser
 130 135 140

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

Leu Gln Asp Leu Asn Tyr Asp Pro Asn Val Trp Glu Val Arg Glu Asp
 165 170 175

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

Ala Ser Thr Gly Glu Asn Phe Ile Phe Gln Thr Asp Val Thr Phe Leu
 195 200 205

Gln Asn Thr Gly Ala Ala Ser Leu Val Phe Arg Ser Asn Asn Asp Pro
 210 215 220

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

Ala Arg Leu Trp Arg Trp Ala Glu Ala Asn Leu Ile Asn Asp Lys Glu
 245 250 255

Ile Leu Ala Ser Pro Asp Asn Lys Tyr Phe Leu Lys Val Val Ala Thr
 260 265 270

Asn Gly Trp Ile Ser Tyr Tyr Ile Asn Gly Ile Leu Ile Ala Asn Leu
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PCT_Sequence_listing (3)
280 285

275

Ser Asp Tyr Thr Ile Gln Arg Asp Asp Leu Gly Gln Thr Thr Tyr Ile
290 295 300

Lys Asp Gly His Phe Gly Leu Leu Asn Trp Asn Gly Glu Met Val Phe
305 310 315 320

Gln Asn Thr Phe Tyr Arg Glu Leu Thr Asn Glu Glu Leu Pro Leu Leu
325 330 335

Asn Asp Val Thr Val Thr Ser Lys Asn Gly Pro Val Glu Pro Lys Gly
340 345 350

Gln Phe Phe Ser Glu Ser Ser Val Tyr Ile Gln Tyr Val Ser Asn Asp
355 360 365

Ala Ser Thr Val Asp Leu Ser Phe Asp Ala Asn Asn Ser Asp Ala Leu
370 375 380

Ile Thr Val Thr Asp Ala His Gly Lys Val Tyr Ser Asn Pro Ser Ala
385 390 395 400

Ile Pro Val Thr Val Gly Pro Asn Tyr Leu Thr Val Thr Ser Thr Tyr
405 410 415

Thr Thr Thr Asp Gly Tyr Val Ile Pro Ser Thr Tyr Arg Ile Asn Val
420 425 430

His Arg Arg Gln Pro Gln Ser Val Tyr Tyr Asn Glu Asn Phe Arg Asp
435 440 445

Gln Tyr His Tyr Ser Val Lys Asp Gly Trp Ala Asn Asp Pro Asn Gly
450 455 460

Leu Val Tyr Tyr Asn Gly Val Tyr His Met Phe Tyr Gln Phe Tyr Asp
465 470 475 480

Asp Thr Lys Trp Gly Pro Met His Trp Ala His Ala Thr Ser Thr Asp
485 490 495

Leu Ile His Trp Glu Asp Gln Pro Ile Ala Phe Tyr Pro Asp Tyr Asn
500 505 510

Gly Thr Met Phe Ser Gly Cys Ile Val Ala Asp Val Asn Asn Ser Ser
515 520 525

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

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

Lys Thr Trp Gln Lys Val Asp Glu Ile Val Ala Asp Trp Thr Thr Asp
565 570 575

PCT_Sequence_listing (3)

Pro Leu Gln Thr Arg Asp Phe Arg Asp Pro Lys Val Phe Arg Trp Glu
580 585 590

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

Ser Asp Asp Leu Lys Asn Trp Thr Val Glu Ser Thr Tyr Pro Asp Leu
610 615 620

His Thr Glu Cys Pro Asp Leu Tyr Pro Val Leu Ala Glu Asp Gln Thr
625 630 635 640

Val Lys Trp Val Leu Ser Arg Gly Gly Arg Tyr Tyr Lys Val Gly Asp
645 650 655

Leu Gln Gln Ala Asp Gly Asn Trp Lys Phe Ile Pro Asp Ala Asn Tyr
660 665 670

Gln Glu Thr Asp Ser Ile Met Asn Phe Gly Lys Asp Ser Tyr Ala Ala
675 680 685

Met Thr Tyr Tyr Val Gln Asp Phe Gly Thr Lys Ala Asn Pro Thr Ile
690 695 700

Pro Lys Ile Ile Glu Leu Asn Trp Met Asn Thr Trp Asp Asn Tyr Cys
705 710 715 720

Asn Leu Val Ala Asp Arg Leu Gly Gln Ser Phe Asn Gly Thr Phe Asn
725 730 735

Leu Asn Leu Glu Leu Gly Leu Val Lys Glu Gly Asp Lys Tyr Val Leu
740 745 750

Thr Gln Thr Pro Val Glu Ala Tyr Glu Ser Leu Arg Asp Asn Asp Asn
755 760 765

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

Lys Asp Phe Ser Gly Asp Thr Tyr Glu Ile Val Ala His Phe Lys Pro
785 790 795 800

Ser Asp Lys Thr Thr Lys Val Gly Phe Asn Leu Arg Val Gly Ser Gly
805 810 815

Glu Met Thr Lys Val Tyr Tyr Asp Leu Ile Ala Gly Arg Ile Ile Ile
820 825 830

Asp Arg Ser Gln Ser Gly Ile Ile Leu Thr Glu Leu Phe Ser Asn Ile
835 840 845

Asp Ser Gln Ala Val Thr Pro Asn Ile Asp Gly Ser Ile Asp Leu His
850 855 860

Ile Phe Val Asp Arg Ala Ser Val Glu Val Phe Ser Lys Asn His Thr
865 870 875 880

PCT_Sequence_listing (3)

Val Ala Gly Ala Asn Gln Ile Phe Thr Ser Ala Gln Ser Leu Gly Leu
 885 890 895
 Glu Val Leu Ile Asp Gly Glu Asp Ala Lys Ala Asp Ile Val Leu Tyr
 900 905 910
 Pro Leu Lys Ser Ile Trp Lys Asn Lys Ile Ile Asp Thr Thr Pro Gln
 915 920 925
 Ile Val Ile Pro Ala Ser Glu Pro Lys Val Arg Met Asn Val Gly Asp
 930 935 940
 Ser Thr Thr Val Lys Ala Tyr Val Ser Pro Val Gly Ala Ser Gln Asp
 945 950 955 960
 Leu Ile Trp Asn Ile Ser Asn Pro Ser Leu Val Leu Asp Gln Ile Ser
 965 970 975
 Gly Asn Gln Val Phe Leu Lys Ala Ile Lys Lys Gly Gln Val Ile Val
 980 985 990
 Arg Ala Gln Ser Gln Ser Asn Pro Ala Val Tyr Gln Asp Phe Ile Ile
 995 1000 1005
 Asp Ile Leu Glu Asp Asn Phe Asn Thr Asn Val Lys Asp Val Asn
 1010 1015 1020
 Val Phe Ser Gly Asp Trp Tyr Val Asp Gly Glu Ser Leu Lys Val
 1025 1030 1035
 Ala Asn His Asn Ser Asn Asp Ile Tyr Met Ser Ala Asp Lys Ile
 1040 1045 1050
 Pro Tyr Glu Asn Tyr Gln Met Asp Leu Asp Ile Lys Tyr Gly Arg
 1055 1060 1065
 Gly Ile Val Asn Ile Phe Phe Ala Ser Gly Asn Pro Asp Ala Asn
 1070 1075 1080
 Asn Ala Tyr Thr Ile Gln Phe Gly Ser Asn Asn Ser Val Arg Leu
 1085 1090 1095
 Phe Arg Phe Tyr Arg Asp Thr Ile Phe Glu Ala Pro Met Ile Asp
 1100 1105 1110
 Val Ile Asn Asp Asn Gln Phe His His Val Arg Leu Val Lys Ser
 1115 1120 1125
 Ala Asn Val Ile His Val Tyr Val Asp Asn Glu Met Val Met Ser
 1130 1135 1140
 Tyr Thr Phe Asp Gln Val Glu Glu Phe Phe Asn Asn Pro Tyr Leu
 1145 1150 1155
 Gly Leu Gly Leu Trp Asp Gly Glu Leu Ala Val Gln Asn Phe Tyr
 1160 1165 1170

PCT_Sequence_listing (3)

Val Ile Asp Leu Asp Ala Gln Lys Pro Val Phe Val Glu Glu His
1175 1180 1185

Glu Lys Glu Lys Leu Leu Ser Glu Leu Lys Lys Ser Val Val Lys
1190 1195 1200

Thr Ser Ser Tyr Ser Thr Leu Lys Thr Ile Glu Thr Ser Ser Lys
1205 1210 1215

Thr Asn Ser Glu Asn Leu Glu Ala Pro Thr Val Ser Lys Lys Asn
1220 1225 1230

Leu Pro Met Thr Ser Asp Ser Asn Asn Asn Leu Glu Glu Leu Gly
1235 1240 1245

Ile Leu Val Ile Leu Thr Thr Leu Gly Ala Phe Leu Gly Arg Val
1250 1255 1260

Ile Leu Lys Lys Glu Lys
1265

<210> 117
<211> 951
<212> DNA
<213> Streptococcus uberis

<220>
<221> CDS
<222> (1)..(951)

<400> 117
atg gct gaa ctt gaa aca caa aaa act cag tta act tct gcg gtt aat 48
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1 5 10 15

act aca aaa tct caa tta gac caa gct aag caa gta ttg agt aac tta 96
Thr Thr Lys Ser Gln Leu Asp Gln Ala Lys Gln Val Leu Ser Asn Leu
20 25 30

caa gca aca cct ctt caa act caa aat gct caa tct aaa ctt gat caa 144
Gln Ala Thr Pro Leu Gln Thr Gln Asn Ala Gln Ser Lys Leu Asp Gln
35 40 45

gcg aaa gta gag tta gca ctt gca caa gat aac tat gtt aaa gcc caa 192
Ala Lys Val Glu Leu Ala Leu Ala Gln Asp Asn Tyr Val Lys Ala Gln
50 55 60

gaa gct gtt aaa tta gct agt caa gaa tta gtt gtc aaa gaa gct aac 240
Glu Ala Val Lys Leu Ala Ser Gln Glu Leu Val Val Lys Glu Ala Asn
65 70 75 80

cta aaa aat gcc caa gcc gac cta tta gat aag caa aat att ttg aat 288
Leu Lys Asn Ala Gln Ala Asp Leu Leu Asp Lys Gln Asn Ile Leu Asn
85 90 95

gaa gca caa gca acc ctt gca gaa agt caa tta gta tta gct agt tta 336
Glu Ala Gln Ala Thr Leu Ala Glu Ser Gln Leu Val Leu Ala Ser Leu
100 105 110

caa tct aac ctt aaa gaa gca caa gca agt ttg gca gaa gct aaa aca 384
Gln Ser Asn Leu Lys Glu Ala Gln Ala Ser Leu Ala Glu Ala Lys Thr
115 120 125

tcg tta gat acc gct aaa aca aat ctt gca cag aaa caa gca tac tta 432
Ser Leu Asp Thr Ala Lys Thr Asn Leu Ala Gln Lys Gln Ala Tyr Leu

PCT_Sequence_listing (3)

130	135	140	
ctt tct ctt caa aat gcg cct aaa gtt cta gca gaa gct caa gct aaa Leu Ser Leu Gln Asn Ala Pro Lys Val Leu Ala Glu Ala Gln Ala Lys 145 150 155 160			480
ctt gtt act gct aaa agt gat tta gcc aaa aaa atg gct att tta gac Leu Val Thr Ala Lys Ser Asp Leu Ala Lys Lys Met Ala Ile Leu Asp 165 170 175			528
aaa gaa gta gcc aaa tta aaa gaa tta caa gct gtt caa gct gaa gct Lys Glu Val Ala Lys Leu Lys Glu Leu Gln Ala Val Gln Ala Glu Ala 180 185 190			576
caa aac caa tat agt att gtt ttt gaa gct ttt aaa gca gta caa gaa Gln Asn Gln Tyr Ser Ile Val Phe Glu Ala Phe Lys Ala Val Gln Glu 195 200 205			624
gct aag aaa caa gct gaa tta aca gaa atc tat gag cat att atc tca Ala Lys Lys Gln Ala Glu Leu Thr Glu Ile Tyr Glu His Ile Ile Ser 210 215 220			672
gaa gga gga gaa gca ata cca gtt gtt gac gaa aca ggt aaa ata act Glu Gly Gly Glu Ala Ile Pro Val Val Asp Glu Thr Gly Lys Ile Thr 225 230 235 240			720
ggt tat gta gat ggt agt aag aaa att gtt act aat gaa acg agt ttt Gly Tyr Val Asp Gly Ser Lys Lys Ile Val Thr Asn Glu Thr Ser Phe 245 250 255			768
gag cta att agt aca gat aaa tca cct gtt gaa tca cca gtc aat cag Glu Leu Ile Ser Thr Asp Lys Ser Pro Val Glu Ser Pro Val Asn Gln 260 265 270			816
gaa aac aaa tta gta agt tct tca act aat gat tta ccg aat act ggt Glu Asn Lys Leu Val Ser Ser Ser Thr Asn Asp Leu Pro Asn Thr Gly 275 280 285			864
gaa tca agc att gca cca ttc aca gca att gga gca att atc tta tca Glu Ser Ser Ile Ala Pro Phe Thr Ala Ile Gly Ala Ile Ile Leu Ser 290 295 300			912
gtt ctt gga cta tta ggg ttt aaa aaa cgt cgt act tat Val Leu Gly Leu Leu Gly Phe Lys Lys Arg Arg Thr Tyr 305 310 315			951

<210> 118
 <211> 317
 <212> PRT
 <213> Streptococcus uberis

<400> 118

Met Ala Glu Leu Glu Thr Gln Lys Thr Gln Leu Thr Ser Ala Val Asn
 1 5 10 15

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

Gln Ala Thr Pro Leu Gln Thr Gln Asn Ala Gln Ser Lys Leu Asp Gln
 35 40 45

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

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

Leu Lys Asn Ala Gln Ala Asp Leu Leu Asp Lys Gln Asn Ile Leu Asn

PCT_Sequence_listing (3)

85

90

95

Glu Ala Gln Ala Thr Leu Ala Glu Ser Gln Leu Val Leu Ala Ser Leu
100 105 110

Gln Ser Asn Leu Lys Glu Ala Gln Ala Ser Leu Ala Glu Ala Lys Thr
115 120 125

Ser Leu Asp Thr Ala Lys Thr Asn Leu Ala Gln Lys Gln Ala Tyr Leu
130 135 140

Leu Ser Leu Gln Asn Ala Pro Lys Val Leu Ala Glu Ala Gln Ala Lys
145 150 155 160

Leu Val Thr Ala Lys Ser Asp Leu Ala Lys Lys Met Ala Ile Leu Asp
165 170 175

Lys Glu Val Ala Lys Leu Lys Glu Leu Gln Ala Val Gln Ala Glu Ala
180 185 190

Gln Asn Gln Tyr Ser Ile Val Phe Glu Ala Phe Lys Ala Val Gln Glu
195 200 205

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

Glu Gly Gly Glu Ala Ile Pro Val Val Asp Glu Thr Gly Lys Ile Thr
225 230 235 240

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

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

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

Glu Ser Ser Ile Ala Pro Phe Thr Ala Ile Gly Ala Ile Ile Leu Ser
290 295 300

Val Leu Gly Leu Leu Gly Phe Lys Lys Arg Arg Thr Tyr
305 310 315

<210> 119
<211> 1695
<212> DNA
<213> Streptococcus uberis

<220>
<221> CDS
<222> (1)..(1695)

<400> 119
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Met Thr His Met Asn Lys Asn Gly Arg Tyr Lys Gln Arg Phe Ser Leu
1 5 10 15

cgc aag tac aaa ttt ggt gca gct tcc gtc ctc cta gga acc atc ttc 96
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PCT_Sequence_listing (3)															
Arg	Lys	Tyr	Lys	Phe	Gly	Ala	Ala	Ser	Val	Leu	Leu	Gly	Thr	Ile	Phe
			20					25					30		
gcc	cta	ggc	atg	acc	gga	aca	aca	gca	cag	gct	cag	gaa	gga	tgg	gct
Ala	Leu	Gly	Met	Thr	Gly	Thr	Thr	Ala	Gln	Ala	Gln	Glu	Gly	Trp	Ala
		35					40					45			
gga	agt	ggt	cta	gga	gta	cct	ggc	ggt	gga	gta	cct	ggc	ggt	gga	gta
Gly	Ser	Gly	Leu	Gly	Val	Pro	Gly	Val	Gly	Val	Pro	Gly	Val	Gly	Val
	50					55					60				
cct	ggc	ggt	gga	gta	cct	ggc	ggt	gga	gta	ccc	gga	gta	ggt	gta	cca
Pro	Gly	Val	Gly	Val	Pro	Gly	Val	Gly	Val	Pro	Gly	Val	Gly	Val	Pro
	65				70					75					80
ggt	gta	gga	gtc	cca	ggc	gta	ggt	gta	cct	ggt	gta	gga	gtc	cca	ggc
Gly	Val	Gly	Val	Pro	Gly	Val	Gly	Val	Pro	Gly	Val	Gly	Val	Pro	Gly
				85					90					95	
gta	ggc	gta	cca	gga	gta	gga	gta	cca	agt	ggt	tat	aat	aat	ggc	ttt
Val	Gly	Val	Pro	Gly	Val	Gly	Val	Pro	Ser	Gly	Tyr	Asn	Asn	Gly	Phe
			100					105					110		
gat	tat	gga	aca	ggt	tat	ggt	tca	ggg	tac	ggg	aat	tta	ggt	tat	cct
Asp	Tyr	Gly	Thr	Gly	Tyr	Gly	Ser	Gly	Tyr	Gly	Asn	Leu	Gly	Tyr	Pro
		115					120					125			
atg	ccc	gta	cct	gta	cca	gga	cct	atg	ggc	cct	ccg	gga	atg	cca	gga
Met	Pro	Val	Pro	Val	Pro	Gly	Pro	Met	Gly	Pro	Pro	Gly	Met	Pro	Gly
	130					135					140				
ttg	cct	gga	cca	gca	ggt	ccg	tca	gga	cca	ggt	gga	aga	aca	ggt	gag
Leu	Pro	Gly	Pro	Ala	Gly	Pro	Ser	Gly	Pro	Val	Gly	Arg	Thr	Gly	Glu
	145				150					155					160
gct	gga	caa	cct	gga	cca	gca	ggt	gct	cgc	gga	gag	caa	gga	cca	gca
Ala	Gly	Gln	Pro	Gly	Pro	Ala	Gly	Ala	Arg	Gly	Glu	Gln	Gly	Pro	Ala
				165					170					175	
gga	cca	aga	ggt	gag	gct	ggt	gca	act	gga	cca	aga	ggt	gaa	gca	ggt
Gly	Pro	Arg	Gly	Glu	Ala	Gly	Ala	Thr	Gly	Pro	Arg	Gly	Glu	Ala	Gly
			180					185					190		
cct	caa	ggt	aag	gaa	gga	ccg	gca	gga	cca	gca	ggt	gca	aaa	ggt	gaa
Pro	Gln	Gly	Lys	Glu	Gly	Pro	Ala	Gly	Pro	Ala	Gly	Ala	Lys	Gly	Glu
		195					200					205			
caa	ggt	ccc	cgt	ggt	caa	aaa	ggt	gaa	aaa	ggt	gat	cgc	gga	cgt	gat
Gln	Gly	Pro	Arg	Gly	Gln	Lys	Gly	Glu	Lys	Gly	Asp	Arg	Gly	Arg	Asp
	210					215					220				
gga	tta	caa	ggt	tta	caa	gga	aag	cca	ggt	aaa	gat	ggc	cgt	gat	gga
Gly	Leu	Gln	Gly	Leu	Gln	Gly	Lys	Pro	Gly	Lys	Asp	Gly	Arg	Asp	Gly
	225				230					235					240
caa	aag	gga	gaa	aaa	ggt	gat	cca	ggt	aaa	aat	ggt	aag	caa	ggc	cct
Gln	Lys	Gly	Glu	Lys	Gly	Asp	Pro	Gly	Lys	Asn	Gly	Lys	Gln	Gly	Pro
				245					250					255	
gca	gga	cgt	gat	ggc	ttg	aat	ggt	caa	aaa	ggt	gac	cca	ggt	aag	aac
Ala	Gly	Arg	Asp	Gly	Leu	Asn	Gly	Gln	Lys	Gly	Asp	Pro	Gly	Lys	Asn
			260					265					270		
ggt	cta	aat	ggt	aaa	cca	ggt	gct	aaa	ggt	gct	gat	ggt	caa	gat	ggt
Gly	Leu	Asn	Gly	Lys	Pro	Gly	Ala	Lys	Gly	Ala	Asp	Gly	Gln	Asp	Gly
		275					280					285			
cgc	gat	ggt	cgt	gac	ggt	aac	cca	ggt	aaa	cca	ggt	aag	aac	ggt	gct
Arg	Asp	Gly	Arg	Asp	Gly	Asn	Pro	Gly	Lys	Pro	Gly	Lys	Asn	Gly	Ala
	290					295					300				
aaa	gga	aca	cca	ggt	cgt	gac	ggt	gct	aaa	ggc	cgt	gat	ggt	aaa	gac
Lys	Gly	Thr	Pro	Gly	Arg	Asp	Gly	Ala	Lys	Gly	Arg	Asp	Gly	Lys	Asp
	305				310					315					320

PCT_Sequence_listing (3)

ggt acc aat ggt gta gcc ggt aaa aat ggt cgt gac ggt gcc aaa ggc Gly Thr Asn Gly Val Ala Gly Lys Asn Gly Arg Asp Gly Ala Lys Gly	1008
325	
330	
335	
cgt gat ggt aaa gat ggc gct aaa ggt caa gac ggt aaa cac ggt cgc Arg Asp Gly Lys Asp Gly Ala Lys Gly Gln Asp Gly Lys His Gly Arg	1056
340	
345	
350	
aac ggt caa gat ggc aga cat gga caa gac ggt gtc gat ggc cgt aat Asn Gly Gln Asp Gly Arg His Gly Gln Asp Gly Val Asp Gly Arg Asn	1104
355	
360	
365	
ggt cta gat ggt cgc cgt ggt cgt gac gga cgt gat ggt cgt gat ggt Gly Leu Asp Gly Arg Arg Gly Arg Asp Gly Arg Asp Gly Arg Asp Gly	1152
370	
375	
380	
atc gac ggt gtc gat ggt cgt gac ggt tta tca cca atc att aaa acc Ile Asp Gly Val Asp Gly Arg Asp Gly Leu Ser Pro Ile Ile Lys Thr	1200
385	
390	
395	
400	
atg aca cac tct gat gga agc cat act atc cac ttc ctc aac cca gat Met Thr His Ser Asp Gly Ser His Thr Ile His Phe Leu Asn Pro Asp	1248
405	
410	
415	
ggc aca cgt tca gaa atc acc ctt cgt gat ggt aag aac ggt caa gat Gly Thr Arg Ser Glu Ile Thr Leu Arg Asp Gly Lys Asn Gly Gln Asp	1296
420	
425	
430	
gga aaa gat ggc gct cca ggt cgt gac ggt gta gac ggt aaa gac ggt Gly Lys Asp Gly Ala Pro Gly Arg Asp Gly Val Asp Gly Lys Asp Gly	1344
435	
440	
445	
gca cca gga cgt gat ggc cgt gat ggt aaa gac ggt atg cca ggt cgt Ala Pro Gly Arg Asp Gly Arg Asp Gly Lys Asp Gly Met Pro Gly Arg	1392
450	
455	
460	
gac gga cgt gac ggt cac gat ggc aaa gac ggc atg cca gga cgc gat Asp Gly Arg Asp Gly His Asp Gly Lys Asp Gly Met Pro Gly Arg Asp	1440
465	
470	
475	
480	
ggc atg aac ggt aaa gat ggt caa gca gca gca ggc aac act gct ggc Gly Met Asn Gly Lys Asp Gly Gln Ala Ala Ala Gly Asn Thr Ala Gly	1488
485	
490	
495	
aaa ggc aat gct tca gac atg aaa cct aaa gct atg gca gca cct gca Lys Gly Asn Ala Ser Asp Met Lys Pro Lys Ala Met Ala Ala Pro Ala	1536
500	
505	
510	
gca atg act aac caa aac gct cat gca aat aac aaa ggt cca gct aca Ala Met Thr Asn Gln Asn Ala His Ala Asn Asn Lys Gly Pro Ala Thr	1584
515	
520	
525	
gcg caa ttg cca tca act ggt gac aag gct aac cca ttc ttc aca acc Ala Gln Leu Pro Ser Thr Gly Asp Lys Ala Asn Pro Phe Phe Thr Thr	1632
530	
535	
540	
gca gcc cta gca gtc atg gct tca gca gga atg gta gct gta tca cgc Ala Ala Leu Ala Val Met Ala Ser Ala Gly Met Val Ala Val Ser Arg	1680
545	
550	
555	
560	
aaa cgc aaa gaa gat Lys Arg Lys Glu Asp	1695
565	

<210> 120
 <211> 565
 <212> PRT
 <213> Streptococcus uberis
 <400> 120

Met Thr His Met Asn Lys Asn Gly Arg Tyr Lys Gln Arg Phe Ser Leu
1 5 10 15

PCT_Sequence_listing (3)

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

Ala Leu Gly Met Thr Gly Thr Thr Ala Gln Ala Gln Glu Gly Trp Ala
35 40 45

Gly ser Gly Leu Gly Val Pro Gly Val Gly Val Pro Gly Val Gly Val
50 55 60

Pro Gly Val Gly Val Pro Gly Val Gly Val Pro Gly Val Gly Val Pro
65 70 75 80

Gly Val Gly Val Pro Gly Val Gly Val Pro Gly Val Gly Val Pro Gly
85 90 95

Val Gly Val Pro Gly Val Gly Val Pro Ser Gly Tyr Asn Asn Gly Phe
100 105 110

Asp Tyr Gly Thr Gly Tyr Gly Ser Gly Tyr Gly Asn Leu Gly Tyr Pro
115 120 125

Met Pro Val Pro Val Pro Gly Pro Met Gly Pro Pro Gly Met Pro Gly
130 135 140

Leu Pro Gly Pro Ala Gly Pro Ser Gly Pro Val Gly Arg Thr Gly Glu
145 150 155 160

Ala Gly Gln Pro Gly Pro Ala Gly Ala Arg Gly Glu Gln Gly Pro Ala
165 170 175

Gly Pro Arg Gly Glu Ala Gly Ala Thr Gly Pro Arg Gly Glu Ala Gly
180 185 190

Pro Gln Gly Lys Glu Gly Pro Ala Gly Pro Ala Gly Ala Lys Gly Glu
195 200 205

Gln Gly Pro Arg Gly Gln Lys Gly Glu Lys Gly Asp Arg Gly Arg Asp
210 215 220

Gly Leu Gln Gly Leu Gln Gly Lys Pro Gly Lys Asp Gly Arg Asp Gly
225 230 235 240

Gln Lys Gly Glu Lys Gly Asp Pro Gly Lys Asn Gly Lys Gln Gly Pro
245 250 255

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

Gly Leu Asn Gly Lys Pro Gly Ala Lys Gly Ala Asp Gly Gln Asp Gly
275 280 285

Arg Asp Gly Arg Asp Gly Asn Pro Gly Lys Pro Gly Lys Asn Gly Ala
290 295 300

Lys Gly Thr Pro Gly Arg Asp Gly Ala Lys Gly Arg Asp Gly Lys Asp
305 310 315 320

95

PCT_Sequence_listing (3)

Gly Thr Asn Gly Val Ala Gly Lys Asn Gly Arg Asp Gly Ala Lys Gly
325 330 335

Arg Asp Gly Lys Asp Gly Ala Lys Gly Gln Asp Gly Lys His Gly Arg
340 345 350

Asn Gly Gln Asp Gly Arg His Gly Gln Asp Gly Val Asp Gly Arg Asn
355 360 365

Gly Leu Asp Gly Arg Arg Gly Arg Asp Gly Arg Asp Gly Arg Asp Gly
370 375 380

Ile Asp Gly Val Asp Gly Arg Asp Gly Leu Ser Pro Ile Ile Lys Thr
385 390 395 400

Met Thr His Ser Asp Gly Ser His Thr Ile His Phe Leu Asn Pro Asp
405 410 415

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

Gly Lys Asp Gly Ala Pro Gly Arg Asp Gly Val Asp Gly Lys Asp Gly
435 440 445

Ala Pro Gly Arg Asp Gly Arg Asp Gly Lys Asp Gly Met Pro Gly Arg
450 455 460

Asp Gly Arg Asp Gly His Asp Gly Lys Asp Gly Met Pro Gly Arg Asp
465 470 475 480

Gly Met Asn Gly Lys Asp Gly Gln Ala Ala Ala Gly Asn Thr Ala Gly
485 490 495

Lys Gly Asn Ala Ser Asp Met Lys Pro Lys Ala Met Ala Ala Pro Ala
500 505 510

Ala Met Thr Asn Gln Asn Ala His Ala Asn Asn Lys Gly Pro Ala Thr
515 520 525

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

Ala Ala Leu Ala Val Met Ala Ser Ala Gly Met Val Ala Val Ser Arg
545 550 555 560

Lys Arg Lys Glu Asp
565

<210> 121
<211> 2079
<212> DNA
<213> Streptococcus uberis

<220>
<221> CDS
<222> (1)..(2079)

PCT_Sequence_listing (3)

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1 5 10 15

gga atg tca gtt tta gta tca tct gta caa gct gat caa gtt gat gtt 96
Gly Met Ser Val Leu Val Ser Ser Val Gln Ala Asp Gln Val Asp Val
20 25 30

caa att tta gga gtt aat gat ttc cac ggt gca ctg gat caa act ggt 144
Gln Ile Leu Gly Val Asn Asp Phe His Gly Ala Leu Asp Gln Thr Gly
35 40 45

tca gct tat atg cct gat gga aaa gtg tct ggg gct ggg aca gcg gct 192
Ser Ala Tyr Met Pro Asp Gly Lys Val Ser Gly Ala Gly Thr Ala Ala
50 55 60

caa tta gat gca tac atg gat caa gcg caa gca gat ttt aac caa act 240
Gln Leu Asp Ala Tyr Met Asp Gln Ala Gln Ala Asp Phe Asn Gln Thr
65 70 75 80

agt cca act gga aca agt atc cgt gta caa gct ggt gat atg gtc ggt 288
Ser Pro Thr Gly Thr Ser Ile Arg Val Gln Ala Gly Asp Met Val Gly
85 90 95

gca agt cct gca aat tct gga tta cta caa gat gag cct aca gtc caa 336
Ala Ser Pro Ala Asn Ser Gly Leu Leu Gln Asp Glu Pro Thr Val Gln
100 105 110

gta ttt aat gaa atg ggc gtt gaa tac gga aca cta gga aac cat gaa 384
Val Phe Asn Glu Met Gly Val Glu Tyr Gly Thr Leu Gly Asn His Glu
115 120 125

ttt gat gaa gga tta gct gag tat aac cgt att atg act ggc act gca 432
Phe Asp Glu Gly Leu Ala Glu Tyr Asn Arg Ile Met Thr Gly Thr Ala
130 135 140

cct gca gct gat tca agc atc aac caa att aca aaa gat tat aca cac 480
Pro Ala Ala Asp Ser Ser Ile Asn Gln Ile Thr Lys Asp Tyr Thr His
145 150 155 160

att cca tcg gac caa aca att gtt atc gct aac gtg gtt gat aaa aca 528
Ile Pro Ser Asp Gln Thr Ile Val Ile Ala Asn Val Val Asp Lys Thr
165 170 175

act gga gag att ccg tat aac tgg caa cca tat gct ata aaa aat att 576
Thr Gly Glu Ile Pro Tyr Asn Trp Gln Pro Tyr Ala Ile Lys Asn Ile
180 185 190

cct gta aac aac act tct gtg aat atc ggt ttt att gga gtt gtt aca 624
Pro Val Asn Asn Thr Ser Val Asn Ile Gly Phe Ile Gly Val Val Thr
195 200 205

aca gaa att cca aat ctc gtc tta aaa caa aac tat gag caa tac aat 672
Thr Glu Ile Pro Asn Leu Val Leu Lys Gln Asn Tyr Glu Gln Tyr Asn
210 215 220

ttc tta gac gaa gcg gaa act att gcc aaa tat gcc aaa gaa tta caa 720
Phe Leu Asp Glu Ala Glu Thr Ile Ala Lys Tyr Ala Lys Glu Leu Gln
225 230 235 240

gga caa aat gtt aat gcc tta gtt gta tta gct cat att cct gca aca 768
Gly Gln Asn Val Asn Ala Leu Val Val Leu Ala His Ile Pro Ala Thr
245 250 255

agt ggt aaa gat ggt ata gta ggc gac gaa atc gct aca ata atg gat 816
Ser Gly Lys Asp Gly Ile Val Gly Asp Glu Ile Ala Thr Ile Met Asp
260 265 270

aag gtt aac caa tta tat cct gac aat agc att gat att att ttt gca 864
Lys Val Asn Gln Leu Tyr Pro Asp Asn Ser Ile Asp Ile Ile Phe Ala
275 280 285

ggt cat aat cac cag tat aca aat gga acc atc ggt tct act cga att 912

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9x

PCT_Sequence_listing (3)															
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ctt Leu	gac Asp	act Thr	gat Asp	aca Thr 325	caa Gln	gac Asp	ttt Phe	ata Ile	gct Ala 330	acc Thr	cct Pro	act Thr	gct Ala	caa Gln 335	ggt Val
ggt Val	gca Ala	ggt Val	gca Ala 340	cct Pro	ggc Gly	ggt Val	tta Leu	aca Thr 345	ggc Gly	aca Thr	gct Ala	gaa Glu	atc Ile 350	caa Gln	gct Ala
att Ile	ggt Val	gat Asp 355	gaa Glu	gct Ala	aat Asn	aca Thr	att Ile 360	ggt Val	aaa Lys	caa Gln	gtg Val	act Thr 365	gat Asp	caa Gln	aaa Lys
atc Ile	gga Gly 370	act Thr	gcc Ala	gca Ala	agt Ser	tca Ser 375	gaa Glu	tta Leu	att Ile	tca Ser	cgt Arg 380	gaa Glu	gta Val	aat Asn	gta Val
gat Asp 385	aaa Lys	gaa Glu	tct Ser	gca Ala	gta Val 390	gga Gly	aat Asn	ctc Leu	atc Ile	aca Thr 395	act Thr	gca Ala	caa Gln	ttg Leu	aca Thr 400
ggt Val	gct Ala	cgt Arg	gaa Glu	aca Thr 405	tat Tyr	cct Pro	gat Asp	ggt Val	gat Asp 410	ttt Phe	gct Ala	att Ile	aca Thr	aat Asn 415	aac Asn
gga Gly	gga Gly	atc Ile	cga Arg 420	gca Ala	gat Asp	tta Leu	cta Leu	gta Val 425	agt Ser	agt Ser	gat Asp	caa Gln	agc Ser 430	att Ile	act Thr
tgg Trp	ggt Gly	gct Ala 435	gct Ala	caa Gln	gca Ala	ggt Val	caa Gln 440	cct Pro	ttt Phe	gga Gly	aat Asn	atc Ile 445	cta Leu	caa Gln	ata Ile
ggt Val	gag Glu	cta Leu	act Thr	ggt Gly	caa Gln 455	gaa Glu	ata Ile	tac Tyr	gat Asp	gcc Ala 460	tta Leu	aat Asn	gaa Glu	cag Gln	tat Tyr
gat Asp 465	gag Glu	ggg Gly	caa Gln	aaa Lys	tac Tyr 470	ttc Phe	ctc Leu	caa Gln	atg Met	tca Ser 475	ggc Gly	tta Leu	cgc Arg	tat Tyr	gca Ala 480
tac Tyr	act Thr	gat Asp	agt Ser	ggc Gly 485	tca Ser	act Thr	gac Asp	cct Pro	ctt Leu 490	ggt Val	cca Pro	ttt Phe	aaa Lys	ggt Val 495	gtg Val
aaa Lys	gct Ala	tac Tyr	aaa Lys 500	gac Asp	aat Asn	gga Gly	gaa Glu	gaa Glu 505	atc Ile	gat Asp	cca Pro	aat Asn	gct Ala 510	act Thr	tat Tyr
aaa Lys	tta Leu	gtc Val 515	att Ile	aat Asn	gac Asp	ttc Phe	cta Leu 520	tat Tyr	ggt Gly	ggt Gly	ggt Gly	gat Asp 525	ggt Gly	ttt Phe	gca Ala
aca Thr	ttc Phe 530	aaa Lys	aaa Lys	ggg Gly	aaa Lys	tta Leu 535	tta Leu	gga Gly	gca Ala	att Ile	aat Asn 540	cct Pro	gat Asp	act Thr	gag Glu
gtc Val 545	ttt Phe	att Ile	aaa Lys	tat Tyr	atc Ile 550	aaa Lys	gac Asp	tta Leu	gaa Glu	gct Ala 555	gct Ala	ggc Gly	aaa Lys	cca Pro	gta Val 560
aca Thr	gct Ala	gca Ala	ata Ile	aca Thr 565	ggg Gly	ggt Val	aaa Lys	acc Thr	tat Tyr 570	ggt Val	aca Thr	acg Thr	gcc Ala	ctt Leu 575	gag Glu
cct Pro	tca Ser	aca Thr	act Thr 580	act Thr	gat Asp	gca Ala	agt Ser	ggt Gly 585	act Thr	cat His	gaa Glu	atg Met	atc Ile 590	aat Asn	cgt Arg

PCT_Sequence_listing (3)

ggt Val	tac Tyr	cgt Arg	gat Asp	cgt Arg	gat Asp	gga Gly	aaa Lys	att Ile	gtg Val	gct Ala	aca Thr	gaa Glu	gtc Val	ggt Val	tcc Ser	1824
gac Asp	ctc Leu	ttc Phe	act Thr	cca Pro	gct Ala	cct Pro	ggt Val	gaa Glu	gaa Glu	act Thr	gaa Glu	aca Thr	cct Pro	aaa Lys	cca Pro	1872
gct Ala	ggt Val	aac Asn	tct Ser	att Ile	aag Lys	att Ile	cct Pro	ggt Val	aaa Lys	aca Thr	cca Pro	aaa Lys	tat Tyr	ggt Gly	caa Gln	1920
agc Ser	tta Leu	aca Thr	gca Ala	gta Val	aaa Lys	gca Ala	ggt Gly	cag Gln	caa Gln	gca Ala	caa Gln	aaa Lys	gca Ala	agt Ser	gac Asp	1968
aaa Lys	aaa Lys	caa Gln	ttg Leu	cca Pro	act Thr	act Thr	tca Ser	agt Ser	caa Gln	gaa Glu	gac Asp	aca Thr	gca Ala	att Ile	cta Leu	2016
ctt Leu	tca Ser	tta Leu	ctt Leu	ggt Gly	gca Ala	tca Ser	agt Ser	cta Leu	gca Ala	atg Met	gcg Ala	gta Val	gca Ala	tta Leu	aag Lys	2064
aaa Lys	aaa Lys	gaa Glu	aat Asn	aac Asn												2079

<210> 122
<211> 693
<212> PRT
<213> Streptococcus uberis

<400> 122

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

PCT_Sequence_listing (3)

Ile Pro Ser Asp Gln Thr Ile Val Ile Ala Asn Val Val Asp Lys Thr
 165 170 175
 Thr Gly Glu Ile Pro Tyr Asn Trp Gln Pro Tyr Ala Ile Lys Asn Ile
 180 185 190
 Pro Val Asn Asn Thr Ser Val Asn Ile Gly Phe Ile Gly Val Val Thr
 195 200 205
 Thr Glu Ile Pro Asn Leu Val Leu Lys Gln Asn Tyr Glu Gln Tyr Asn
 210 215 220
 Phe Leu Asp Glu Ala Glu Thr Ile Ala Lys Tyr Ala Lys Glu Leu Gln
 225 230 235 240
 Gly Gln Asn Val Asn Ala Leu Val Val Leu Ala His Ile Pro Ala Thr
 245 250 255
 Ser Gly Lys Asp Gly Ile Val Gly Asp Glu Ile Ala Thr Ile Met Asp
 260 265 270
 Lys Val Asn Gln Leu Tyr Pro Asp Asn Ser Ile Asp Ile Ile Phe Ala
 275 280 285
 Gly His Asn His Gln Tyr Thr Asn Gly Thr Ile Gly Ser Thr Arg Ile
 290 295 300
 Val Glu Ala Leu Ser Gln Gly Lys Ala Tyr Ala Asp Val Arg Gly Thr
 305 310 315 320
 Leu Asp Thr Asp Thr Gln Asp Phe Ile Ala Thr Pro Thr Ala Gln Val
 325 330 335
 Val Ala Val Ala Pro Gly Val Leu Thr Gly Thr Ala Glu Ile Gln Ala
 340 345 350
 Ile Val Asp Glu Ala Asn Thr Ile Val Lys Gln Val Thr Asp Gln Lys
 355 360 365
 Ile Gly Thr Ala Ala Ser Ser Glu Leu Ile Ser Arg Glu Val Asn Val
 370 375 380
 Asp Lys Glu Ser Ala Val Gly Asn Leu Ile Thr Thr Ala Gln Leu Thr
 385 390 395 400
 Val Ala Arg Glu Thr Tyr Pro Asp Val Asp Phe Ala Ile Thr Asn Asn
 405 410 415
 Gly Gly Ile Arg Ala Asp Leu Leu Val Ser Ser Asp Gln Ser Ile Thr
 420 425 430
 Trp Gly Ala Ala Gln Ala Val Gln Pro Phe Gly Asn Ile Leu Gln Ile
 435 440 445
 Val Glu Leu Thr Gly Gln Glu Ile Tyr Asp Ala Leu Asn Glu Gln Tyr
 450 455 460

PCT_Sequence_listing (3)

Asp Glu Gly Gln Lys Tyr Phe Leu Gln Met Ser Gly Leu Arg Tyr Ala
465 470 475 480

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

Lys Ala Tyr Lys Asp Asn Gly Glu Glu Ile Asp Pro Asn Ala Thr Tyr
500 505 510

Lys Leu Val Ile Asn Asp Phe Leu Tyr Gly Gly Gly Asp Gly Phe Ala
515 520 525

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

Val Phe Ile Lys Tyr Ile Lys Asp Leu Glu Ala Ala Gly Lys Pro Val
545 550 555 560

Thr Ala Ala Ile Thr Gly Val Lys Thr Tyr Val Thr Thr Ala Leu Glu
565 570 575

Pro Ser Thr Thr Thr Asp Ala Ser Gly Thr His Glu Met Ile Asn Arg
580 585 590

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

Asp Leu Phe Thr Pro Ala Pro Val Glu Glu Thr Glu Thr Pro Lys Pro
610 615 620

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

Ser Leu Thr Ala Val Lys Ala Gly Gln Gln Ala Gln Lys Ala Ser Asp
645 650 655

Lys Lys Gln Leu Pro Thr Thr Ser Ser Gln Glu Asp Thr Ala Ile Leu
660 665 670

Leu Ser Leu Leu Gly Ala Ser Ser Leu Ala Met Ala Val Ala Leu Lys
675 680 685

Lys Lys Glu Asn Asn
690

<210> 123
<211> 1110
<212> DNA
<213> Streptococcus uberis

<220>
<221> CDS
<222> (1)..(1110)

<400> 123
atg aag aag aaa caa gaa atg aag tac tac ctc agg aaa tct gcc tat
Met Lys Lys Lys Gln Glu Met Lys Tyr Tyr Leu Arg Lys Ser Ala Tyr

PCT_Sequence_listing (3)

1	5	10	15	
ggc tta gca gcc gta tca gta gca gtc ctc gca gtc gga agt ccg gta				96
Gly Leu Ala Ala Val Ser Val Ala Val Leu Ala Val Gly Ser Pro Val	20	25	30	
tct gca cag gag aaa gct gca agc acc gaa gct acc cca aag gta gca				144
Ser Ala Gln Glu Lys Ala Ala Ser Thr Glu Ala Thr Pro Lys Val Ala	35	40	45	
cca aaa gtt cca gaa aaa cca agt aaa gaa gtt ata aaa aaa gct tta				192
Pro Lys Val Pro Glu Lys Pro Ser Lys Glu Val Ile Lys Lys Ala Leu	50	55	60	
aag aaa act gat gaa gaa aca aaa gaa aaa gag gaa gaa gcc aaa gaa				240
Lys Lys Thr Asp Glu Glu Thr Lys Glu Lys Glu Lys Glu Ala Lys Glu	65	70	75	80
aaa gta gaa aat tct gaa gaa tca acg gct atg gtt tca gag cta tct				288
Lys Val Glu Asn Ser Glu Glu Ser Thr Ala Met Val Ser Glu Leu Ser	85	90	95	
tcc acc aat gag gaa aca tcc tct gaa gaa gag aat aat act gat gaa				336
Ser Thr Asn Glu Glu Thr Ser Ser Glu Glu Glu Asn Asn Thr Asp Glu	100	105	110	
gag gaa aca gat ggt tta gaa agt gaa gaa tct gaa gaa aca gaa tcc				384
Glu Glu Thr Asp Gly Leu Glu Ser Glu Glu Ser Glu Glu Thr Glu Ser	115	120	125	
gaa gtc aaa gaa gaa tct gaa gaa gaa aaa gag gat gac cca tcc gaa				432
Glu Val Lys Glu Glu Ser Glu Glu Glu Lys Glu Asp Asp Pro Ser Glu	130	135	140	
tca gat aca gaa gtt gag aat gtt gaa gcg att aat ctt tct gaa gct				480
Ser Asp Thr Glu Val Glu Asn Val Glu Ala Ile Asn Leu Ser Glu Ala	145	150	155	160
gag gga aat gac tca tca aaa cct gaa act tca gaa gag gta act gct				528
Glu Gly Asn Asp Ser Ser Lys Pro Glu Thr Ser Glu Glu Val Thr Ala	165	170	175	
gaa gaa gac cgt caa gag act gat cgg ctt gca gaa gtc aaa aca gag				576
Glu Glu Asp Arg Gln Glu Thr Asp Arg Leu Ala Glu Val Lys Thr Glu	180	185	190	
gag agt gcc aaa gaa ggt gat gaa gat gct gat aaa aaa gat gag gct				624
Glu Ser Ala Lys Glu Gly Asp Glu Asp Ala Asp Lys Lys Asp Glu Ala	195	200	205	
gaa gaa aaa gcc aaa aaa gga gct gaa tta agc cgt gtg aaa gca gaa				672
Glu Glu Lys Ala Lys Lys Gly Ala Glu Leu Ser Arg Val Lys Ala Glu	210	215	220	
gca ctg gct aaa tta gaa gca ctt aat gct agt cgt ttg atg aag aaa				720
Ala Leu Ala Lys Leu Glu Ala Leu Asn Ala Ser Arg Leu Met Lys Lys	225	230	235	240
att gtt gaa tcg ggc aaa acg gta gaa ggc atc ctt tcc ttc atg aag				768
Ile Val Glu Ser Gly Lys Thr Val Glu Gly Ile Leu Ser Phe Met Lys	245	250	255	
gaa agc tta cct caa ctg gaa gct gct aga gca tct gaa caa gct aaa				816
Glu Ser Leu Pro Gln Leu Glu Ala Ala Arg Ala Ser Glu Gln Ala Lys	260	265	270	
gct ccg gaa gta act caa tct cct gat cac tta cca agt gag aaa aaa				864
Ala Pro Glu Val Thr Gln Ser Pro Asp His Leu Pro Ser Glu Lys Lys	275	280	285	
gca gtc cac aat cca gtc caa gta gct aaa aga agt gaa agc ttg gaa				912
Ala Val His Asn Pro Val Gln Val Ala Lys Arg Ser Glu Ser Leu Glu	290	295	300	
cag aaa gct gaa aat gct aag aca agc aca aat ctt caa aat act caa				960

102

PCT_Sequence_listing (3)

Gln Lys Ala Glu Asn Ala Lys Thr Ser Thr Asn Leu Gln Asn Thr Gln
305 310 315 320
att cca gta caa gag gca aaa aga act caa gcc caa ttg cca agt aca 1008
Ile Pro Val Gln Glu Ala Lys Arg Thr Gln Ala Gln Leu Pro Ser Thr
325 330 335
gga gaa gat tac caa gct tat ctt gtg gcc gca gca atg gcc ctt att 1056
Gly Glu Asp Tyr Gln Ala Tyr Leu Val Ala Ala Ala Met Ala Leu Ile
340 345 350
gcc tca tca ggc atg gtg gcc tat ggc agc tat cgc aag aaa aag caa 1104
Ala Ser Ser Gly Met Val Ala Tyr Gly Ser Tyr Arg Lys Lys Lys Gln
355 360 365
aaa tag 1110
Lys

<210> 124
<211> 369
<212> PRT
<213> Streptococcus uberis
<400> 124

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

PCT_Sequence_listing (3)
Glu Ser Ala Lys Glu Gly Asp Glu Asp Ala Asp Lys Lys Asp Glu Ala
195 200 205
Glu Glu Lys Ala Lys Lys Gly Ala Glu Leu Ser Arg Val Lys Ala Glu
210 215 220
Ala Leu Ala Lys Leu Glu Ala Leu Asn Ala Ser Arg Leu Met Lys Lys
225 230 235 240
Ile Val Glu Ser Gly Lys Thr Val Glu Gly Ile Leu Ser Phe Met Lys
245 250 255
Glu Ser Leu Pro Gln Leu Glu Ala Ala Arg Ala Ser Glu Gln Ala Lys
260 265 270
Ala Pro Glu Val Thr Gln Ser Pro Asp His Leu Pro Ser Glu Lys Lys
275 280 285
Ala Val His Asn Pro Val Gln Val Ala Lys Arg Ser Glu Ser Leu Glu
290 295 300
Gln Lys Ala Glu Asn Ala Lys Thr Ser Thr Asn Leu Gln Asn Thr Gln
305 310 315 320
Ile Pro Val Gln Glu Ala Lys Arg Thr Gln Ala Gln Leu Pro Ser Thr
325 330 335
Gly Glu Asp Tyr Gln Ala Tyr Leu Val Ala Ala Ala Met Ala Leu Ile
340 345 350
Ala Ser Ser Gly Met Val Ala Tyr Gly Ser Tyr Arg Lys Lys Lys Gln
355 360 365

Lys

<210> 125
<211> 3222
<212> DNA
<213> Streptococcus uberis

<220>
<221> CDS
<222> (1)..(3222)

<400> 125	
atg act aaa aat cgt tct agt cat tct acc tat gct gat aaa gtg att	48
Met Thr Lys Asn Arg Ser Ser His Ser Thr Tyr Ala Asp Lys Val Ile	
1 5 10 15	
aaa gga cta tca gct tca tgc ttc ata tta ggc gca ttc gtt ttt gca	96
Lys Gly Leu Ser Ala Ser Cys Phe Ile Leu Gly Ala Phe Val Phe Ala	
20 25 30	
caa cag gtt agt gca gaa gaa gtg gta act gct aca aac acg tct tta	144
Gln Gln Val Ser Ala Glu Glu Val Val Thr Ala Thr Asn Thr Ser Leu	
35 40 45	
act gca cca acc gtt aca aca gtt tca ccg ctg aca aat acg gat gtt	192
Thr Ala Pro Thr Val Thr Thr Val Ser Pro Leu Thr Asn Thr Asp Val	
50 55 60	

PCT_Sequence_listing (3)																
tct	gct	act	gcg	gtc	gct	gca	gat	tcc	att	gca	agc	cca	gta	acg	act	
Ser	Ala	Thr	Ala	Val	Ala	Ala	Asp	Ser	Ile	Ala	Ser	Pro	Val	Thr	Thr	240
65				70					75						80	
aca	gat	agt	aat	ctc	aat	tca	gct	cca	att	ata	gat	aca	agc	aat	cca	288
Thr	Asp	Ser	Asn	Leu	Asn	Ser	Ala	Pro	Ile	Ile	Asp	Thr	Ser	Asn	Pro	
				85					90					95		
tct	aat	ata	act	agt	cca	aca	gat	acc	aac	act	tca	aca	act	tca	tct	336
Ser	Asn	Ile	Thr	Ser	Pro	Thr	Asp	Thr	Asn	Thr	Ser	Thr	Thr	Ser	Ser	
			100					105					110			
gac	acg	act	tca	tca	cct	atc	ccc	gta	acc	tta	aat	aaa	gca	gca	att	384
Asp	Thr	Thr	Ser	Ser	Pro	Ile	Pro	Val	Thr	Leu	Asn	Lys	Ala	Ala	Ile	
			115				120					125				
gct	agc	cca	aca	agt	caa	acg	gaa	acc	cta	gca	agc	caa	gaa	att	tac	432
Ala	Ser	Pro	Thr	Ser	Gln	Thr	Glu	Thr	Leu	Ala	Ser	Gln	Glu	Ile	Tyr	
	130					135					140					
atg	gat	aag	gtc	aat	caa	gtg	acc	ata	aat	aca	aca	gta	aat	cca	gca	480
Met	Asp	Lys	Val	Asn	Gln	Val	Thr	Ile	Asn	Thr	Thr	Val	Asn	Pro	Ala	
				150					155						160	
act	cca	atg	acc	tgg	acg	att	gaa	aat	tat	cct	aat	caa	acc	tat	aat	528
Thr	Pro	Met	Thr	Trp	Thr	Ile	Glu	Asn	Tyr	Pro	Asn	Gln	Thr	Tyr	Asn	
				165					170					175		
atg	caa	acc	ggt	gat	ttt	act	gga	tct	cca	agt	tat	aca	gtt	aca	tca	576
Met	Gln	Thr	Gly	Asp	Phe	Thr	Gly	Ser	Pro	Ser	Tyr	Thr	Val	Thr	Ser	
			180					185					190			
act	agt	cca	aat	aat	agt	agt	gtt	caa	att	gaa	att	ccg	cca	ctt	ttt	624
Thr	Ser	Pro	Asn	Asn	Ser	Ser	Val	Gln	Ile	Glu	Ile	Pro	Pro	Leu	Phe	
			195				200					205				
gga	aca	gat	tta	agt	cta	cgt	tgg	cca	aac	aat	atc	aga	cgt	act	tac	672
Gly	Thr	Asp	Leu	Ser	Leu	Arg	Trp	Pro	Asn	Asn	Ile	Arg	Arg	Thr	Tyr	
			210			215					220					
cgt	gat	tat	atg	ggt	tcc	tat	aca	ctt	aaa	ggg	atc	agt	gaa	gat	ggt	720
Arg	Asp	Tyr	Met	Gly	Ser	Tyr	Thr	Leu	Lys	Gly	Ile	Ser	Glu	Asp	Gly	
				230						235					240	
ctt	acc	att	gtc	acc	aaa	gaa	ttg	att	cta	cga	cct	tat	gct	gat	tac	768
Leu	Thr	Ile	Val	Thr	Lys	Glu	Leu	Ile	Leu	Arg	Pro	Tyr	Ala	Asp	Tyr	
				245					250					255		
atg	aca	cat	gag	gaa	ctg	cta	aat	gaa	tta	aat	gct	att	gaa	gct	aat	816
Met	Thr	His	Glu	Glu	Leu	Leu	Asn	Glu	Leu	Asn	Ala	Ile	Glu	Ala	Asn	
			260					265					270			
cat	gca	aca	gac	cgt	ttg	gta	aca	ata	gaa	aca	atc	ggt	caa	agt	gct	864
His	Ala	Thr	Asp	Arg	Leu	Val	Thr	Ile	Glu	Thr	Ile	Gly	Gln	Ser	Ala	
			275			280						285				
tta	gga	aat	gct	att	aaa	atg	gga	att	gta	gct	aaa	gat	caa	gct	agc	912
Leu	Gly	Asn	Ala	Ile	Lys	Met	Gly	Ile	Val	Ala	Lys	Asp	Gln	Ala	Ser	
			290			295					300					
tta	gat	acc	tat	tta	aat	caa	aca	acc	cca	atg	atg	ttg	atg	gat	cct	960
Leu	Asp	Thr	Tyr	Leu	Asn	Gln	Thr	Thr	Pro	Met	Met	Leu	Met	Asp	Pro	
				310						315					320	
gac	caa	gca	ttg	aat	ctc	tta	gca	caa	gga	aaa	ttt	gat	tat	aaa	ctc	1008
Asp	Gln	Ala	Leu	Asn	Leu	Leu	Ala	Gln	Gly	Lys	Phe	Asp	Tyr	Lys	Leu	
				325					330					335		
cct	atc	tta	atc	aat	aat	acc	cat	gcg	gat	gaa	cag	cca	gga	att	gat	1056
Pro	Ile	Leu	Ile	Asn	Asn	Thr	His	Ala	Asp	Glu	Gln	Pro	Gly	Ile	Asp	
			340					345					350			
gtt	gtt	cgc	ggt	ctt	ttc	aaa	act	ttt	gca	aca	gag	tca	gtt	atc	aac	1104
Val	Val	Arg	Gly	Leu	Phe	Lys	Thr	Phe	Ala	Thr	Glu	Ser	Val	Ile	Asn	
		355					360					365				

PCT_Sequence_listing (3)

tat Tyr	caa Gln	act Thr	gtt Val	gat Asp	gcc Ala	gct Ala	aat Asn	aat Asn	cca Pro	aca Thr	aca Thr	gta Val	caa Gln	att Ile	gat Asp	1152
370						375					380					
atc Ile	aaa Lys	gct Ala	ctc Leu	tta Leu	gac Asp	aaa Lys	gtc Val	atc Ile	cta Leu	ctt Leu	ttc Phe	aac Asn	ttc Phe	aca Thr	gaa Glu	1200
385					390					395					400	
aat Asn	cct Pro	gat Asp	gga Gly	gac Asp	att Ile	gcc Ala	aat Asn	aca Thr	cgc Arg	gcc Ala	ctt Leu	aat Asn	aac Asn	gga Gly	tta Leu	1248
				405					410					415		
gat Asp	cca Pro	aac Asn	cgg Arg	gat Asp	act Thr	ggc Gly	tat Tyr	caa Gln	acc Thr	aat Asn	cca Pro	gaa Glu	acc Thr	cgt Arg	gcc Ala	1296
			420					425					430			
att Ile	gtt Val	gaa Glu	caa Gln	att Ile	aat Asn	aag Lys	tgg Trp	aat Asn	cct Pro	att Ile	tca Ser	att Ile	ttt Phe	gac Asp	gtg Val	1344
		435					440					445				
cat His	ggc Gly	ttt Phe	gtt Val	aaa Lys	gaa Glu	ttc Phe	ttg Leu	att Ile	gaa Glu	cca Pro	tgt Cys	aca Thr	cca Pro	cca Pro	cat His	1392
	450					455					460					
gat Asp	cct Pro	aac Asn	ttt Phe	gag Glu	tat Tyr	gat Asp	tta Leu	ttt Phe	gat Asp	gca Ala	agt Ser	ctc Leu	gtt Val	gaa Glu	ggt Gly	1440
					470					475					480	
gca Ala	cga Arg	gaa Glu	atg Met	gga Gly	aat Asn	gcc Ala	ggc Gly	atc Ile	aca Thr	aac Asn	tct Ser	gtt Val	tac Tyr	gac Asp	agc Ser	1488
				485					490					495		
tac Tyr	atc Ile	ata Ile	cca Pro	aaa Lys	ttt Phe	gat Asp	tat Tyr	ggc Gly	tca Ser	gga Gly	tgg Trp	gat Asp	gac Asp	tcc Ser	ttc Phe	1536
			500					505					510			
tca Ser	gga Gly	tac Tyr	aca Thr	gct Ala	gtt Val	tat Tyr	gga Gly	ttg Leu	tat Tyr	caa Gln	ggc Gly	atc Ile	tta Leu	gga Gly	cat His	1584
		515					520					525				
acc Thr	att Ile	gaa Glu	att Ile	cca Pro	gaa Glu	acc Thr	aac Asn	caa Gln	gaa Glu	tcc Ser	tat Tyr	aat Asn	gcg Ala	ggc Gly	tac Tyr	1632
		530				535					540					
ttc Phe	gca Ala	gtc Val	tta Leu	gca Ala	ggc Gly	att Ile	aat Asn	tat Tyr	gac Asp	ttg Leu	gca Ala	aat Asn	agt Ser	gac Asp	cag Gln	1680
		545			550					555					560	
cta Leu	atg Met	aaa Lys	aat Asn	aag Lys	tta Leu	acc Thr	ttc Phe	ttt Phe	tct Ser	cgt Arg	ggc Gly	atc Ile	cac His	aaa Lys	gca Ala	1728
				565					570					575		
gaa Glu	gtg Val	gct Ala	gcc Ala	gct Ala	gaa Glu	gaa Glu	gca Ala	ttg Leu	ctt Leu	aca Thr	gta Val	gac Asp	ggc Gly	tcc Ser	gtg Val	1776
			580					585					590			
aaa Lys	ggc Gly	aga Arg	att Ile	aaa Lys	gat Asp	ggc Gly	cac His	gat Asp	acc Thr	ttc Phe	ttc Phe	cca Pro	gat Asp	tat Tyr	tat Tyr	1824
		595					600					605				
atg Met	att Ile	cca Pro	atg Met	aca Thr	tta Leu	tca Ser	act Thr	gaa Glu	agt Ser	gat Asp	act Thr	gac Asp	caa Gln	gct Ala	ttc Phe	1872
		610				615					620					
aag Lys	atg Met	att Ile	gat Asp	tat Tyr	ttc Phe	aga Arg	aga Arg	aat Asn	ggg Gly	gtc Val	att Ile	tta Leu	aat Asn	gaa Glu	tta Leu	1920
					630				635						640	
aca Thr	gcg Ala	gat Asp	gtt Val	gct Ala	ggc Gly	tat Tyr	cat His	aaa Lys	ggc Gly	gat Asp	tta Leu	gtc Val	att Ile	gac Asp	atg Met	1968
				645					650					655		
gca Ala	caa Gln	gct Ala	aaa Lys	aga Arg	gga Gly	ttt Phe	gct Ala	aac Asn	cat His	gtt Val	ctc Leu	tac Tyr	aaa Lys	gga Gly	gca Ala	2016

PCT_Sequence_listing (3)

660	665	670	
aat gaa tct gaa tgg cca gct atg tat gca gaa tta gtg atg aat ttc Asn Glu Ser Glu Trp Pro Ala Met Tyr Ala Glu Leu Val Met Asn Phe 675 680 685			2064
cct gca atg cgt ggc ttt aaa gca gat gcc att tac gct gat agt tta Pro Ala Met Arg Gly Phe Lys Ala Asp Ala Ile Tyr Ala Asp Ser Leu 690 695 700			2112
ttt gct gga aat ctt gga gca gtt act tta aca agt gcc cca aga acc Phe Ala Gly Asn Leu Gly Ala Val Thr Leu Thr Ser Ala Pro Arg Thr 705 710 715 720			2160
gcg cct agt gat aaa gaa tac tat att gtt tca aat aat tca ctt gca Ala Pro Ser Asp Lys Glu Tyr Tyr Ile Val Ser Asn Asn Ser Leu Ala 725 730 735			2208
gca gtc caa gct gtc aat gct gct atc cgt gca gga aaa aat gtt tat Ala Val Gln Ala Val Asn Ala Ala Ile Arg Ala Gly Lys Asn Val Tyr 740 745 750			2256
ttg acc aat gat gga tat gtt atg gat aaa gcc act tat gaa agt gtc Leu Thr Asn Asp Gly Tyr Val Met Asp Lys Ala Thr Tyr Glu Ser Val 755 760 765			2304
att ggt aca tac cca tta ttt gct caa gca acc tgt atg aaa cca gtt Ile Gly Thr Tyr Pro Leu Phe Ala Gln Ala Thr Cys Met Lys Pro Val 770 775 780			2352
ggt gac act ttg aaa gct atc aaa gta tat gca cct gga aac cca aac Gly Asp Thr Leu Lys Ala Ile Lys Val Tyr Ala Pro Gly Asn Pro Asn 785 790 795 800			2400
ctc tat tta gga ttt aat tca cca tca gaa gtc agt ctt gct cta aat Leu Tyr Leu Gly Phe Asn Ser Pro Ser Glu Val Ser Leu Ala Leu Asn 805 810 815			2448
caa atg gga ttt gat gtg gtt cct tca gta gat cag gct gat gtc atc Gln Met Gly Phe Asp Val Val Pro Ser Val Asp Gln Ala Asp Val Ile 820 825 830			2496
gtg tta gac aat gat caa ttt gac gca agt att tta ggt aaa aaa cct Val Leu Asp Asn Asp Gln Phe Asp Ala Ser Ile Leu Gly Lys Lys Pro 835 840 845			2544
gtc atc att tta ggt ggc tct gca atg gct aag tta gaa agt ttg ggt Val Ile Ile Leu Gly Gly Ser 855 Ala Met Ala Lys Leu Glu Ser Leu Gly 850 855 860			2592
atc ttg aca ggt ttt gat gct gcc atg act agc gaa agc gat gga tca Ile Leu Thr Gly Phe Asp Ala Ala Met Thr Ser Glu Ser Asp Gly Ser 865 870 875 880			2640
agt tat gaa gga ctt atg aaa atc tct cta gat gcc aat agt cct tac Ser Tyr Glu Gly Leu Met Lys Ile Ser Leu Asp Ala Asn Ser Pro Tyr 885 890 895			2688
acg agt ggc tat gca gca aat tct tta tac tat tct aac tca ggt tct Thr Ser Gly Tyr Ala Ala Asn Ser Leu Tyr Tyr Ser Asn Ser Gly Ser 900 905 910			2736
tggt att gaa gga gtc cca aca gga ttt atg aca cta gcc aat att tct Trp Ile Glu Gly Val Pro Thr Gly Phe Met Thr Leu Ala Asn Ile Ser 915 920 925			2784
gca agt gat ttc tat gtt tca gga tgg tgg cca aat cat gaa gga tta Ala Ser Asp Phe Tyr Val Ser Gly Trp Trp Pro Asn His Glu Gly Leu 930 935 940			2832
gct aat aaa aca gtt gct att agt ggt ctt tat cag gga caa cca atg Ala Asn Lys Thr Val Ala Ile Ser Gly Leu Tyr Gln Gly Gln Pro Met 945 950 955 960			2880
ttt atc ttc gct gga aat cca gtg aat aag act cat acc att aat ttc			2928

PCT_Sequence_listing (3)

Phe Ile Phe Ala Gly Asn Pro Val Asn Lys Thr His Thr Ile Asn Phe	
965 970 975	
tac cgt tgg gtg agt aat gct att ttt gga aca aac tta acc agc ttc	2976
Tyr Arg Trp Val Ser Asn Ala Ile Phe Gly Thr Asn Leu Thr Ser Phe	
980 985 990	
att gaa ggt caa tgt act att cca act gac tct gaa aca caa gtt gta	3024
Ile Glu Gly Gln Cys Thr Ile Pro Thr Asp Ser Glu Thr Gln Val Val	
995 1000 1005	
agg gtt aac cat aat ggt caa aca gtg gca gtt tat caa caa gtg	3069
Arg Val Asn His Asn Gly Gln Thr Val Ala Val Tyr Gln Gln Val	
1010 1015 1020	
gct aat aag gaa gtt aat ggg aca gtg agt caa aat agc ttg cca	3114
Ala Asn Lys Glu Val Asn Gly Thr Val Ser Gln Asn Ser Leu Pro	
1025 1030 1035	
gca tta gct gat ggc agt cac aaa gat gac agc aaa ctc ttc tgg	3159
Ala Leu Ala Asp Gly Ser His Lys Asp Asp Ser Lys Leu Phe Trp	
1040 1045 1050	
gta act gga tta ttg gtt gca agt ggg gga tta ttt gca gct ctt	3204
Val Thr Gly Leu Leu Val Ala Ser Gly Gly Leu Phe Ala Ala Leu	
1055 1060 1065	
aaa cgc cgt gag gaa gac	3222
Lys Arg Arg Glu Glu Asp	
1070	

<210> 126
 <211> 1074
 <212> PRT
 <213> Streptococcus uberis

<400> 126

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

PCT_Sequence_listing (3)

Met Asp Lys Val Asn Gln Val Thr Ile Asn Thr Thr Val Asn Pro Ala
 145 150 155 160

Thr Pro Met Thr Trp Thr Ile Glu Asn Tyr Pro Asn Gln Thr Tyr Asn
 165 170 175

Met Gln Thr Gly Asp Phe Thr Gly Ser Pro Ser Tyr Thr Val Thr Ser
 180 185 190

Thr Ser Pro Asn Asn Ser Ser Val Gln Ile Glu Ile Pro Pro Leu Phe
 195 200 205

Gly Thr Asp Leu Ser Leu Arg Trp Pro Asn Asn Ile Arg Arg Thr Tyr
 210 215 220

Arg Asp Tyr Met Gly Ser Tyr Thr Leu Lys Gly Ile Ser Glu Asp Gly
 225 230 235 240

Leu Thr Ile Val Thr Lys Glu Leu Ile Leu Arg Pro Tyr Ala Asp Tyr
 245 250 255

Met Thr His Glu Glu Leu Leu Asn Glu Leu Asn Ala Ile Glu Ala Asn
 260 265 270

His Ala Thr Asp Arg Leu Val Thr Ile Glu Thr Ile Gly Gln Ser Ala
 275 280 285

Leu Gly Asn Ala Ile Lys Met Gly Ile Val Ala Lys Asp Gln Ala Ser
 290 295 300

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

Asp Gln Ala Leu Asn Leu Leu Ala Gln Gly Lys Phe Asp Tyr Lys Leu
 325 330 335

Pro Ile Leu Ile Asn Asn Thr His Ala Asp Glu Gln Pro Gly Ile Asp
 340 345 350

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

Tyr Gln Thr Val Asp Ala Ala Asn Asn Pro Thr Thr Val Gln Ile Asp
 370 375 380

Ile Lys Ala Leu Leu Asp Lys Val Ile Leu Leu Phe Asn Phe Thr Glu
 385 390 395 400

Asn Pro Asp Gly Asp Ile Ala Asn Thr Arg Ala Leu Asn Asn Gly Leu
 405 410 415

Asp Pro Asn Arg Asp Thr Gly Tyr Gln Thr Asn Pro Glu Thr Arg Ala
 420 425 430

Ile Val Glu Gln Ile Asn Lys Trp Asn Pro Ile Ser Ile Phe Asp Val
 435 440 445

PCT_Sequence_listing (3)

His Gly Phe Val Lys Glu Phe Leu Ile Glu Pro Cys Thr Pro Pro His
 450 455 460
 Asp Pro Asn Phe Glu Tyr Asp Leu Phe Asp Ala Ser Leu Val Glu Gly
 465 470 475 480
 Ala Arg Glu Met Gly Asn Ala Gly Ile Thr Asn Ser Val Tyr Asp Ser
 485 490 495
 Tyr Ile Ile Pro Lys Phe Asp Tyr Gly Ser Gly Trp Asp Asp Ser Phe
 500 505 510
 Ser Gly Tyr Thr Ala Val Tyr Gly Leu Tyr Gln Gly Ile Leu Gly His
 515 520 525
 Thr Ile Glu Ile Pro Glu Thr Asn Gln Glu Ser Tyr Asn Ala Gly Tyr
 530 535 540
 Phe Ala Val Leu Ala Gly Ile Asn Tyr Asp Leu Ala Asn Ser Asp Gln
 545 550 555 560
 Leu Met Lys Asn Lys Leu Thr Phe Phe Ser Arg Gly Ile His Lys Ala
 565 570 575
 Glu Val Ala Ala Glu Glu Ala Leu Leu Thr Val Asp Gly Ser Val
 580 585 590
 Lys Gly Arg Ile Lys Asp Gly His Asp Thr Phe Phe Pro Asp Tyr Tyr
 595 600 605
 Met Ile Pro Met Thr Leu Ser Thr Glu Ser Asp Thr Asp Gln Ala Phe
 610 615 620
 Lys Met Ile Asp Tyr Phe Arg Arg Asn Gly Val Ile Leu Asn Glu Leu
 625 630 635 640
 Thr Ala Asp Val Ala Gly Tyr His Lys Gly Asp Leu Val Ile Asp Met
 645 650 655
 Ala Gln Ala Lys Arg Gly Phe Ala Asn His Val Leu Tyr Lys Gly Ala
 660 665 670
 Asn Glu Ser Glu Trp Pro Ala Met Tyr Ala Glu Leu Val Met Asn Phe
 675 680 685
 Pro Ala Met Arg Gly Phe Lys Ala Asp Ala Ile Tyr Ala Asp Ser Leu
 690 695 700
 Phe Ala Gly Asn Leu Gly Ala Val Thr Leu Thr Ser Ala Pro Arg Thr
 705 710 715 720
 Ala Pro Ser Asp Lys Glu Tyr Tyr Ile Val Ser Asn Asn Ser Leu Ala
 725 730 735
 Ala Val Gln Ala Val Asn Ala Ala Ile Arg Ala Gly Lys Asn Val Tyr
 740 745 750

PCT_Sequence_listing (3)

Leu Thr Asn Asp Gly Tyr Val Met Asp Lys Ala Thr Tyr Glu Ser Val
755 760 765

Ile Gly Thr Tyr Pro Leu Phe Ala Gln Ala Thr Cys Met Lys Pro Val
770 775 780

Gly Asp Thr Leu Lys Ala Ile Lys Val Tyr Ala Pro Gly Asn Pro Asn
785 790 795 800

Leu Tyr Leu Gly Phe Asn Ser Pro Ser Glu Val Ser Leu Ala Leu Asn
805 810 815

Gln Met Gly Phe Asp Val Val Pro Ser Val Asp Gln Ala Asp Val Ile
820 825 830

Val Leu Asp Asn Asp Gln Phe Asp Ala Ser Ile Leu Gly Lys Lys Pro
835 840 845

Val Ile Ile Leu Gly Gly Ser Ala Met Ala Lys Leu Glu Ser Leu Gly
850 855 860

Ile Leu Thr Gly Phe Asp Ala Ala Met Thr Ser Glu Ser Asp Gly Ser
865 870 875 880

Ser Tyr Glu Gly Leu Met Lys Ile Ser Leu Asp Ala Asn Ser Pro Tyr
885 890 895

Thr Ser Gly Tyr Ala Ala Asn Ser Leu Tyr Tyr Ser Asn Ser Gly Ser
900 905 910

Trp Ile Glu Gly Val Pro Thr Gly Phe Met Thr Leu Ala Asn Ile Ser
915 920 925

Ala Ser Asp Phe Tyr Val Ser Gly Trp Trp Pro Asn His Glu Gly Leu
930 935 940

Ala Asn Lys Thr Val Ala Ile Ser Gly Leu Tyr Gln Gly Gln Pro Met
945 950 955 960

Phe Ile Phe Ala Gly Asn Pro Val Asn Lys Thr His Thr Ile Asn Phe
965 970 975

Tyr Arg Trp Val Ser Asn Ala Ile Phe Gly Thr Asn Leu Thr Ser Phe
980 985 990

Ile Glu Gly Gln Cys Thr Ile Pro Thr Asp Ser Glu Thr Gln Val Val
995 1000 1005

Arg Val Asn His Asn Gly Gln Thr Val Ala Val Tyr Gln Gln Val
1010 1015 1020

Ala Asn Lys Glu Val Asn Gly Thr Val Ser Gln Asn Ser Leu Pro
1025 1030 1035

Ala Leu Ala Asp Gly Ser His Lys Asp Asp Ser Lys Leu Phe Trp

PCT_Sequence_listing (3)

1040

1045

1050

Val Thr Gly Leu Leu Val Ala Ser Gly Gly Leu Phe Ala Ala Leu
1055 1060 1065

Lys Arg Arg Glu Glu Asp
1070

<210> 127
<211> 1497
<212> DNA
<213> Streptococcus uberis

<220>
<221> CDS
<222> (1)..(1497)

<400> 127
atg aaa tct tat ttg aaa cgt cgt tac ggt cta atc aca act tct gtt 48
Met Lys Ser Tyr Leu Lys Arg Arg Tyr Gly Leu Ile Thr Thr Ser Val
1 5 10 15
ctt gcc gca act gta tta gct act ggt tgg caa agc act tct gtt ttg 96
Leu Ala Ala Thr Val Leu Ala Thr Gly Trp Gln Ser Thr Ser Val Leu
20 25 30
gct gaa aat ccc aca aca tcc cca aca acc acc gtc act agt aat ggt 144
Ala Glu Asn Pro Thr Thr Ser Pro Thr Thr Thr Val Thr Ser Asn Gly
35 40 45
ttt aac ttt aat gca act ctt cta gat cac aat ggc aaa aca gtt tcc 192
Phe Asn Phe Asn Ala Thr Leu Leu Asp His Asn Gly Lys Thr Val Ser
50 55 60
ggg aaa aca gtt agt ctc tat gat att act gat ggt aac aga act ttg 240
Gly Lys Thr Val Ser Leu Tyr Asp Ile Thr Asp Gly Asn Arg Thr Leu
65 70 75 80
gtg cag agt gcc gtc tct gac caa aat ggt atc gca tca ttt tcc cag 288
Val Gln Ser Ala Val Ser Asp Gln Asn Gly Ile Ala Ser Phe Ser Gln
85 90 95
ttg cca ctc aac cga aat cta tcc gtt ttt gta gat aat gtc gct caa 336
Leu Pro Leu Asn Arg Asn Leu Ser Val Phe Val Asp Asn Val Ala Gln
100 105 110
ggc tac aca aca cgt act agt gaa agt gga caa gta cgc tcc tct gcc 384
Gly Tyr Thr Thr Arg Thr Ser Glu Ser Gly Gln Val Arg Ser Ser Ala
115 120 125
ttt tat att gat gga cag gga aca aac aca cca aaa tac agt gat aag 432
Phe Tyr Ile Asp Gly Gln Gly Thr Asn Thr Pro Lys Tyr Ser Asp Lys
130 135 140
aca atc act att agt gtc cta aat gag gaa gct gag cca ctt gcc aat 480
Thr Ile Thr Ile Ser Val Leu Asn Glu Glu Ala Glu Pro Leu Ala Asn
145 150 155 160
caa aaa gta acc tta acc aat ccc cta aaa gag gtt gtt ggc gaa gca 528
Gln Lys Val Thr Leu Thr Asn Pro Leu Lys Glu Val Val Gly Glu Ala
165 170 175
atg act gat gca gat ggt cat gtt gtt ttc aag gat aaa ctt tta gaa 576
Met Thr Asp Ala Asp Gly His Val Val Phe Lys Asp Lys Leu Leu Glu
180 185 190
ggt gtc ttt tac aac tat gct gtc aac gga aaa gca att gat tct gct 624
Gly Val Phe Tyr Asn Tyr Ala Val Asn Gly Lys Ala Ile Asp Ser Ala
195 200 205
cag cca gat tca aaa aga agt gtc ttt tta gag tcc aat caa cta gct 672

PCT_Sequence_listing (3)																
Gln 210	Pro	Asp	Ser	Lys	Arg	Ser 215	Val	Phe	Leu	Glu	Ser 220	Asn	Gln	Leu	Ala	
aaa Lys 225	gaa Glu	gga Gly	ttt Phe	act Thr	ttc Phe 230	aca Thr	gca Ala	act Thr	att Ile	tta Leu 235	gga Gly	aaa Lys	aac Asn	ggc Gly	aaa Lys 240	720
act Thr	gtc Val	gct Ala	ggt Gly	aaa Lys 245	acc Thr	gta Val	agt Ser	ctt Leu	tat Tyr 250	gac Asp	att Ile	act Thr	gat Asp	ggt Gly 255	aac Asn	768
aga Arg	act Thr	ttg Leu	gtg Val 260	cag Gln	agt Ser	gcc Ala	gtc Val	tct Ser 265	gat Asp	caa Gln	aat Asn	ggt Gly	atc Ile 270	gca Ala	tca Ser	816
ttt Phe	tct Ser	cag Gln 275	tta Leu	cca Pro	ctc Leu	aac Asn	cga Arg 280	aat Asn	cta Leu	tcc Ser	gtg Val	ttt Phe 285	att Ile	gat Asp	gat Asp	864
gtg Val	gct Ala	caa Gln	ggc Gly	tac Tyr	acc Thr	act Thr 295	cgt Arg	acc Thr	agt Ser	gaa Glu	aat Asn 300	gga Gly	caa Gln	gtg Val	cgt Arg	912
tca Ser 305	tct Ser	gcc Ala	ttc Phe	tat Tyr	gtc Val 310	gat Asp	gga Gly	cag Gln	gga Gly	aca Thr 315	aac Asn	aca Thr	cca Pro	aaa Lys	tac Tyr 320	960
agt Ser	gac Asp	aaa Lys	acc Thr	att Ile 325	acg Thr	att Ile	agc Ser	gtt Val	ctt Leu 330	aat Asn	gag Glu	gaa Glu	ggt Gly	gaa Glu 335	cct Pro	1008
cta Leu	gct Ala	aac Asn	caa Gln 340	aaa Lys	gtt Val	acc Thr	ttg Leu	atc Ile 345	aac Asn	ccc Pro	cta Leu	aaa Lys	gaa Glu 350	gtt Val	att Ile	1056
ggt Gly	gaa Glu	gca Ala 355	aat Asn	aca Thr	gat Asp	gca Ala	aat Asn 360	ggg Gly	aaa Lys	gtc Val	atc Ile	ttc Phe 365	aca Thr	gac Asp	aag Lys	1104
cta Leu	tta Leu 370	gat Asp	ggt Gly	gtc Val	ttt Phe 375	tac Tyr	acc Thr	tat Tyr	gct Ala	gta Val	aat Asn 380	gat Asp	caa Gln	aca Thr	att Ile	1152
gat Asp 385	gct Ala	act Thr	caa Gln	cca Pro	gat Asp 390	aca Thr	agc Ser	cgt Arg	aat Asn	gtc Val 395	ttt Phe	tta Leu	aga Arg	gct Ala	gat Asp 400	1200
caa Gln	atc Ile	ctg Leu	aag Lys	gaa Glu 405	agc Ser	cct Pro	aaa Lys	aat Asn	aca Thr 410	gca Ala	agc Ser	gag Glu	gct Ala	gct Ala 415	act Thr	1248
aat Asn	ttg Leu	gaa Glu	aaa Lys 420	acc Thr	act Thr	gaa Glu	agc Ser	aaa Lys 425	gaa Glu	ggt Gly	aac Asn	atg Met	cct Pro 430	cag Gln	caa Gln	1296
aac Asn	caa Gln	tca Ser 435	gaa Glu	gca Ala	aaa Lys	gaa Glu	aag Lys 440	gct Ala	cct Pro	gaa Glu	aaa Lys	caa Gln 445	gtc Val	gat Asp	gct Ala	1344
aat Asn 450	gct Ala	gcc Ala	aac Asn	aaa Lys	aaa Lys	gcg Ala 455	cca Pro	ggt Gly	cat His	gga Gly	gaa Glu 460	gcc Ala	aaa Lys	aaa Lys	ggc Gly	1392
cta Leu 465	cca Pro	atg Met	gct Ala	gga Gly	gaa Glu 470	aga Arg	gga Gly	agt Ser	cgc Arg	ttg Leu 475	ttc Phe	acc Thr	ttt Phe	att Ile	gga Gly 480	1440
ctt Leu	tca Ser	ctt Leu	att Ile	tta Leu 485	gga Gly	ata Ile	gcc Ala	ggt Gly	tac Tyr 490	tta Leu	ttg Leu	aaa Lys	cat His	aaa Lys 495	aaa Lys	1488
gtc Val	aaa Lys	tcc Ser														1497

PCT_Sequence_listing (3)

<210> 128
 <211> 499
 <212> PRT
 <213> Streptococcus uberis

<400> 128

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

PCT_Sequence_listing (3)

Phe Ser Gln Leu Pro Leu Asn Arg Asn Leu Ser Val Phe Ile Asp Asp
275 280 285

Val Ala Gln Gly Tyr Thr Thr Arg Thr Ser Glu Asn Gly Gln Val Arg
290 295 300

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

Ser Asp Lys Thr Ile Thr Ile Ser Val Leu Asn Glu Glu Gly Glu Pro
325 330 335

Leu Ala Asn Gln Lys Val Thr Leu Ile Asn Pro Leu Lys Glu Val Ile
340 345 350

Gly Glu Ala Asn Thr Asp Ala Asn Gly Lys Val Ile Phe Thr Asp Lys
355 360 365

Leu Leu Asp Gly Val Phe Tyr Thr Tyr Ala Val Asn Asp Gln Thr Ile
370 375 380

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

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

Asn Leu Glu Lys Thr Thr Glu Ser Lys Glu Gly Asn Met Pro Gln Gln
420 425 430

Asn Gln Ser Glu Ala Lys Glu Lys Ala Pro Glu Lys Gln Val Asp Ala
435 440 445

Asn Ala Ala Asn Lys Lys Ala Pro Gly His Gly Glu Ala Lys Lys Gly
450 455 460

Leu Pro Met Ala Gly Glu Arg Gly Ser Arg Leu Phe Thr Phe Ile Gly
465 470 475 480

Leu Ser Leu Ile Leu Gly Ile Ala Gly Tyr Leu Leu Lys His Lys Lys
485 490 495

Val Lys Ser

<210> 129
<211> 834
<212> DNA
<213> Streptococcus uberis

<220>
<221> CDS
<222> (1)..(834)

<400> 129
atg tct aag cca atg aca aag aaa aaa aag gct att tct att caa aag
Met Ser Lys Pro Met Thr Lys Lys Lys Lys Ala Ile Ser Ile Gln Lys
1 5 10 15

PCT_Sequence_listing (3)

tct gta aaa cca att tta ggt ttt acc ttc gga gcc cta tta tta tca Ser Val Lys Pro Ile Leu Gly Phe Thr Phe Gly Ala Leu Leu Leu Ser	96
act gtt ttt aca cct tcc gta ttt gct gaa gaa gta gtg tct tca tta Thr Val Phe Thr Pro Ser Val Phe Ala Glu Glu Val Val Ser Ser Leu	144
ggg cac gca aca agt ggt ttg ctg tct gta tca gtt ccc aaa gaa tta Gly His Ala Thr Ser Gly Leu Leu Ser Val Ser Val Pro Lys Glu Leu	192
acc agt ctt gag aca acg acc tac tta atg gca agt gag tct cca agt Thr Ser Leu Glu Thr Thr Thr Tyr Leu Met Ala Ser Glu Ser Pro Ser	240
aac act cta act tcg gat acc att tct agt gat aat gga ggg acg gct Asn Thr Leu Thr Ser Asp Thr Ile Ser Ser Asp Asn Gly Gly Thr Ala	288
tca aat cca aat gaa ata gta acc aca gag aca acc agc gag gcg att Ser Asn Pro Asn Glu Ile Val Thr Thr Thr Ser Glu Ala Ile	336
cct ttc gac aca gaa gtc att caa aat ccg gat tta cct ata ggt gag Pro Phe Asp Thr Glu Val Ile Gln Asn Pro Asp Leu Pro Ile Gly Glu	384
att aag gta gtt caa gaa gga gta gct ggt gaa gta acg gtt aca aag Ile Lys Val Val Gln Glu Gly Val Ala Gly Glu Val Thr Val Thr Lys	432
aca acc aca act att act cta aat ggt gtt tct cag tca act aca act Thr Thr Thr Thr Ile Thr Leu Asn Gly Val Ser Gln Ser Thr Thr Thr	480
gag tca agg gta cct gtc aaa aaa cct att aat aaa att att gaa gta Glu Ser Arg Val Pro Val Lys Lys Pro Ile Asn Lys Ile Ile Glu Val	528
ggt aca aaa gag att agt aca agt cca agt agt tct gat gtt att aca Gly Thr Lys Glu Ile Ser Thr Ser Pro Ser Ser Ser Asp Val Ile Thr	576
gtc agt cca tca ccc tct tca act tca tca gag tct aat cag caa ggt Val Ser Pro Ser Pro Ser Ser Thr Ser Ser Glu Ser Asn Gln Gln Gly	624
tcg tta act ccg gcc cct aaa tca cgt caa aat agt cag gaa aag aaa Ser Leu Thr Pro Ala Pro Lys Ser Arg Gln Asn Ser Gln Glu Lys Lys	672
ggt agt cag act aaa aaa tcc aaa gat gac gcc aaa gaa aaa gag ggt Gly Ser Gln Thr Lys Lys Ser Lys Asp Asp Ala Lys Glu Lys Glu Gly	720
gat aag aaa gaa ctt cct cca act ggc tca caa gaa agt ggt att ttt Asp Lys Lys Glu Leu Pro Pro Thr Gly Ser Gln Glu Ser Gly Ile Phe	768
tct cta ttt tct gca ctt att agc aca gct tta ggt ctt ttc cta tta Ser Leu Phe Ser Ala Leu Ile Ser Thr Ala Leu Gly Leu Phe Leu Leu	816
aaa tca aat aaa aat gat Lys Ser Asn Lys Asn Asp	834

<210> 130
 <211> 278
 <212> PRT
 <213> Streptococcus uberis

PCT_Sequence_listing (3)

<400> 130

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

Gly His Ala Thr Ser Gly Leu Leu Ser Val Ser Val Pro Lys Glu Leu
      50      55      60

Thr Ser Leu Glu Thr Thr Thr Tyr Leu Met Ala Ser Glu Ser Pro Ser
65      70      75      80

Asn Thr Leu Thr Ser Asp Thr Ile Ser Ser Asp Asn Gly Gly Thr Ala
      85      90      95

Ser Asn Pro Asn Glu Ile Val Thr Thr Glu Thr Thr Ser Glu Ala Ile
      100      105      110

Pro Phe Asp Thr Glu Val Ile Gln Asn Pro Asp Leu Pro Ile Gly Glu
      115      120      125

Ile Lys Val Val Gln Glu Gly Val Ala Gly Glu Val Thr Val Thr Lys
      130      135      140

Thr Thr Thr Thr Ile Thr Leu Asn Gly Val Ser Gln Ser Thr Thr Thr
145      150      155      160

Glu Ser Arg Val Pro Val Lys Lys Pro Ile Asn Lys Ile Ile Glu Val
      165      170      175

Gly Thr Lys Glu Ile Ser Thr Ser Pro Ser Ser Ser Asp Val Ile Thr
      180      185      190

Val Ser Pro Ser Pro Ser Ser Thr Ser Ser Glu Ser Asn Gln Gln Gly
      195      200      205

Ser Leu Thr Pro Ala Pro Lys Ser Arg Gln Asn Ser Gln Glu Lys Lys
      210      215      220

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

Asp Lys Lys Glu Leu Pro Pro Thr Gly Ser Gln Glu Ser Gly Ile Phe
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Ser Leu Phe Ser Ala Leu Ile Ser Thr Ala Leu Gly Leu Phe Leu Leu
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Lys Ser Asn Lys Asn Asp
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PCT_Sequence_listing (3)

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 <213> Streptococcus uberis

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acc gca gcg gtc tta gca ggg aca gct ttc tca agc cta gga gga ttc	96
Thr Ala Ala Val Leu Ala Gly Thr Ala Phe Ser Ser Leu Gly Gly Phe	
20 25 30	
gca gga gca gtc aca aca gtc aag gcg gaa gat tta ttt act ata aat	144
Ala Gly Ala Val Thr Thr Val Lys Ala Glu Asp Leu Phe Thr Ile Asn	
35 40 45	
aat tca gaa gtc caa gat aag tta gaa tca aag gta aaa caa ctt ttg	192
Asn Ser Glu Val Gln Asp Lys Leu Glu Ser Lys Val Lys Gln Leu Leu	
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gaa gcc caa cga aaa gga gaa gac att agc gaa aaa cta cga gag tta	240
Glu Ala Gln Arg Lys Gly Glu Asp Ile Ser Glu Lys Leu Arg Glu Leu	
65 70 75 80	
tta agt gaa ctt cca acc gat att tta aag gat att atg cta tca aat	288
Leu Ser Glu Leu Pro Thr Asp Ile Leu Lys Asp Ile Met Leu Ser Asn	
85 90 95	
att gaa gct gac tat ctt tta gga ttt cta aaa cca gct gtt gag gaa	336
Ile Glu Ala Asp Tyr Leu Leu Gly Phe Leu Lys Pro Ala Val Glu Glu	
100 105 110	
atg gtg aga aga tct gaa caa aat gac gag cgt tgg aaa gat att aca	384
Met Val Arg Arg Ser Glu Gln Asn Asp Glu Arg Trp Lys Asp Ile Thr	
115 120 125	
gaa aaa aca cta gct tta gag gct tta aaa gat tca gaa aga gaa att	432
Glu Lys Thr Leu Ala Leu Glu Ala Leu Lys Asp Ser Glu Arg Glu Ile	
130 135 140	
agg aaa gaa aaa gag aaa ctt gag gat gaa gtt caa ctt gca aag gta	480
Arg Lys Glu Lys Glu Lys Leu Glu Asp Glu Val Gln Leu Ala Lys Val	
145 150 155 160	
aaa ata gaa act aaa gaa tca gaa tta aat gat tta aaa aaa gat tat	528
Lys Ile Glu Thr Lys Glu Ser Glu Leu Asn Asp Leu Lys Lys Asp Tyr	
165 170 175	
att gat act agg gaa gaa tta gca gat act att gaa gaa cta gac gaa	576
Ile Asp Thr Arg Glu Glu Leu Ala Asp Thr Ile Glu Glu Leu Asp Glu	
180 185 190	
gtt aaa aat tca att gta gaa aaa gaa gca aaa gtt aaa ggc tta gaa	624
Val Lys Asn Ser Ile Val Glu Lys Glu Ala Lys Val Lys Gly Leu Glu	
195 200 205	
gaa aag tta cgt gat tta gaa aaa gaa tta ggt gac tac gat aaa aaa	672
Glu Lys Leu Arg Asp Leu Glu Lys Glu Leu Gly Asp Tyr Asp Lys Lys	
210 215 220	
tta agt gaa gct gct aag caa aat tca gat tta tca aat gaa aac aaa	720
Leu Ser Glu Ala Ala Lys Gln Asn Ser Asp Leu Ser Asn Glu Asn Lys	
225 230 235 240	
gag ttg aaa gaa aac tta gat act gct gag aat att act gtt gaa ctt	768
Glu Leu Lys Glu Asn Leu Asp Thr Ala Glu Asn Ile Thr Val Glu Leu	
245 250 255	
cag aaa aaa tct cat gaa ttg gaa aaa act aaa aaa gaa gtt gaa tta	816

PCT_Sequence_listing (3)															
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Glu	Leu	Lys	Ala	Glu	Lys	Glu	Ala	Leu	Glu	Ala	Glu	Lys	Val	Lys	Leu
		275					280					285			
gca	gaa	gct	aat	gaa	gca	aat	gat	aaa	cta	tct	gaa	gaa	cgt	gat	gct
Ala	Glu	Ala	Asn	Glu	Ala	Asn	Asp	Lys	Leu	Ser	Glu	Glu	Arg	Asp	Ala
	290					295					300				
gcc	aag	aaa	gaa	gct	gaa	aaa	gtt	cct	gaa	cta	gaa	ggg	caa	gtt	gaa
Ala	Lys	Lys	Glu	Ala	Glu	Lys	Val	Pro	Glu	Leu	Glu	Gly	Gln	Val	Glu
	305				310					315					320
aaa	tta	gtt	gaa	gaa	atc	act	gct	gct	aag	aaa	gaa	gca	gaa	gag	ctt
Lys	Leu	Val	Glu	Glu	Ile	Thr	Ala	Ala	Lys	Lys	Glu	Ala	Glu	Glu	Leu
				325					330					335	
caa	gct	aaa	gcc	gaa	ggc	ctt	gaa	aaa	gac	ttc	gaa	gct	gtt	aaa	gca
Gln	Ala	Lys	Ala	Glu	Gly	Leu	Glu	Lys	Asp	Phe	Glu	Ala	Val	Lys	Ala
			340					345					350		
gaa	aaa	gaa	gcc	ctt	gaa	gct	gaa	att	gct	aaa	ttg	aaa	gaa	gac	cac
Glu	Lys	Glu	Ala	Leu	Glu	Ala	Glu	Ile	Ala	Lys	Leu	Lys	Glu	Asp	His
		355					360					365			
caa	aaa	gaa	gtg	gac	gcg	ctt	aat	gct	ctc	ctt	gct	gat	aaa	gag	aaa
Gln	Lys	Glu	Val	Asp	Ala	Leu	Asn	Ala	Leu	Leu	Ala	Asp	Lys	Glu	Lys
	370					375					380				
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Met	Leu	Lys	Ser	Leu	Gln	Glu	Gln	Leu	Asp	Lys	Ala	Lys	Glu	Glu	Ala
	385				390				395						400
atg	aag	aac	gag	caa	atg	agc	caa	gaa	gaa	aaa	gct	aaa	ttg	caa	gct
Met	Lys	Asn	Glu	Gln	Met	Ser	Gln	Glu	Glu	Lys	Ala	Lys	Leu	Gln	Ala
				405					410					415	
gag	ttg	gac	aaa	gct	aaa	caa	gaa	ttg	gca	gaa	aaa	atc	aaa	gac	atg
Glu	Leu	Asp	Lys	Ala	Lys	Gln	Glu	Leu	Ala	Glu	Lys	Ile	Lys	Asp	Met
			420					425				430			
cca	aac	aaa	gtg	gct	cct	caa	gcc	gaa	ggc	aaa	gcc	aat	gca	ggt	caa
Pro	Asn	Lys	Val	Ala	Pro	Gln	Ala	Glu	Gly	Lys	Ala	Asn	Ala	Gly	Gln
		435					440					445			
gca	gct	cca	aat	caa	aac	caa	aac	aac	caa	gcg	caa	gca	aac	caa	gct
Ala	Ala	Pro	Asn	Gln	Asn	Gln	Asn	Asn	Gln	Ala	Gln	Ala	Asn	Gln	Ala
	450					455					460				
aag	aac	gca	aac	aac	ctc	cca	tca	aca	ggt	gac	aaa	cca	gtt	aac	cca
Lys	Asn	Ala	Asn	Asn	Leu	Pro	Ser	Thr	Gly	Asp	Lys	Pro	Val	Asn	Pro
	465				470				475						480
ctc	cta	gtg	gca	agt	ggt	ctc	tcc	ctc	atg	atc	gga	gca	ggt	gcc	ttc
Leu	Leu	Val	Ala	Ser	Gly	Leu	Ser	Leu	Met	Ile	Gly	Ala	Gly	Ala	Phe
				485					490					495	
gtc	tac	gcc	ggc	aaa	cgc	aaa	aaa	ggt	taa						
Val	Tyr	Ala	Gly	Lys	Arg	Lys	Lys	Gly							
			500					505							

<210> 132
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 <212> PRT
 <213> Streptococcus uberis
 <400> 132

Met Glu Ile Lys Gln Lys His Gly Lys His Ala Leu Arg Lys Ala Val
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PCT_Sequence_listing (3)

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

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

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

Leu Ser Glu Leu Pro Thr Asp Ile Leu Lys Asp Ile Met Leu Ser Asn
85 90 95

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

Met Val Arg Arg Ser Glu Gln Asn Asp Glu Arg Trp Lys Asp Ile Thr
115 120 125

Glu Lys Thr Leu Ala Leu Glu Ala Leu Lys Asp Ser Glu Arg Glu Ile
130 135 140

Arg Lys Glu Lys Glu Lys Leu Glu Asp Glu Val Gln Leu Ala Lys Val
145 150 155 160

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

Ile Asp Thr Arg Glu Glu Leu Ala Asp Thr Ile Glu Glu Leu Asp Glu
180 185 190

Val Lys Asn Ser Ile Val Glu Lys Glu Ala Lys Val Lys Gly Leu Glu
195 200 205

Glu Lys Leu Arg Asp Leu Glu Lys Glu Leu Gly Asp Tyr Asp Lys Lys
210 215 220

Leu Ser Glu Ala Ala Lys Gln Asn Ser Asp Leu Ser Asn Glu Asn Lys
225 230 235 240

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

Gln Lys Lys Ser His Glu Leu Glu Lys Thr Lys Lys Glu Val Glu Leu
260 265 270

Glu Leu Lys Ala Glu Lys Glu Ala Leu Glu Ala Glu Lys Val Lys Leu
275 280 285

Ala Glu Ala Asn Glu Ala Asn Asp Lys Leu Ser Glu Glu Arg Asp Ala
290 295 300

Ala Lys Lys Glu Ala Glu Lys Val Pro Glu Leu Glu Gly Gln Val Glu
305 310 315 320

PCT_Sequence_listing (3)

Lys Leu Val Glu Glu Ile Thr Ala Ala Lys Lys Glu Ala Glu Glu Leu
325 330 335

Gln Ala Lys Ala Glu Gly Leu Glu Lys Asp Phe Glu Ala Val Lys Ala
340 345 350

Glu Lys Glu Ala Leu Glu Ala Glu Ile Ala Lys Leu Lys Glu Asp His
355 360 365

Gln Lys Glu Val Asp Ala Leu Asn Ala Leu Leu Ala Asp Lys Glu Lys
370 375 380

Met Leu Lys Ser Leu Gln Glu Gln Leu Asp Lys Ala Lys Glu Glu Ala
385 390 395 400

Met Lys Asn Glu Gln Met Ser Gln Glu Glu Lys Ala Lys Leu Gln Ala
405 410 415

Glu Leu Asp Lys Ala Lys Gln Glu Leu Ala Glu Lys Ile Lys Asp Met
420 425 430

Pro Asn Lys Val Ala Pro Gln Ala Glu Gly Lys Ala Asn Ala Gly Gln
435 440 445

Ala Ala Pro Asn Gln Asn Gln Asn Asn Gln Ala Gln Ala Asn Gln Ala
450 455 460

Lys Asn Ala Asn Asn Leu Pro Ser Thr Gly Asp Lys Pro Val Asn Pro
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Val Tyr Ala Gly Lys Arg Lys Lys Gly
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<212> DNA
<213> Streptococcus uberis

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gaaaacagac aaattccaga agaaaaggta actgaggaag ctacaaatga tcagccggaa 240
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ggttctactt caaaaattcc ctttgtttat gattttctta gtggtgatac cagtgtgaga 480
gatgacgaag aagaacatgg tatgcatatt gcaggaatct tagttggtga ttctaaaaaa 540
ggtttcaaag ggatggcacc taaagcacag ctaattgcat atcgaacttg gagtaaaaaat 600

PCT_Sequence_Listing (3)

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tgggcaaagg	tattagaaga	agcgaaaaag	aaaaatgttg	ttgtcgttgc	agcaatggga	780
aactatggga	catcagcaac	aagtaatact	tttgatcaag	ttgttgatga	aactttccca	840
caaaccgata	gttccacttt	gctttctgta	tctgcaaatc	ccgaagtcac	tggtggtggc	900
tctatTTTTg	aaaaagaaat	gtattttacca	acactaaaaa	ttgatacttt	agaagtacct	960
tatgaaaata	tcaactggca	aaattattac	ctttttaagc	aagaaaagca	agaacgtatt	1020
tcttttaatg	aaatgttaat	aaccttaaac	caatcaaaaag	aagaaggaag	tttaaaagat	1080
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aaaaaaggtg	ctaaaggtgt	tatttttgatt	aaccaatcag	gaccaactac	ttatggtaac	1200
tatgagacag	ttccagaatt	aagaaatacc	ttattagatg	atgaagatgg	tgatttcaaa	1260
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22

PCT_Sequence_listing (3)

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aataagtta 4449

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<211> 1483
<212> PRT
<213> Streptococcus uberis

<400> 134

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Gln Ser Thr Leu Ile Met Ile Phe Ala Ser Ser Cys Val Asn His Phe
20 25 30

Lys Gly Thr Ile His Ala Asp Glu Lys Val Ile Asn Gly Ser Glu Ala
35 40 45

PCT_Sequence_listing (3)

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

Ile Pro Glu Glu Lys Val Thr Glu Glu Ala Thr Asn Asp Gln Pro Glu
65 70 75 80

Leu Leu Glu Lys Gln Ala Ala Phe Leu His Glu Gly Arg Glu Lys Asn
85 90 95

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

Asp Ser Gly Val Asp Ile Lys His Glu Ala Phe Ala Asn Asn Asp Asp
115 120 125

Asn His Asp Phe His Lys Glu Thr Glu Val Ser Glu Gly Ser Thr Ser
130 135 140

Lys Ile Pro Phe Val Tyr Asp Phe Leu Ser Gly Asp Thr Ser Val Arg
145 150 155 160

Asp Asp Glu Glu Glu His Gly Met His Ile Ala Gly Ile Leu Val Gly
165 170 175

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

Ala Tyr Arg Thr Trp Ser Lys Asn Asn Ser Glu Gly Tyr Gln Glu Ala
195 200 205

Asn Gln Phe Phe Ala Met Lys Asp Ala Ile Lys Arg Gly Ala Asp Val
210 215 220

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

Trp Ala Lys Val Leu Glu Glu Ala Lys Lys Lys Asn Val Val Val Val
245 250 255

Ala Ala Met Gly Asn Tyr Gly Thr Ser Ala Thr Ser Asn Thr Phe Asp
260 265 270

Gln Val Val Asp Glu Thr Phe Pro Gln Thr Asp Ser Ser Thr Leu Leu
275 280 285

Ser Val Ser Ala Asn Pro Glu Val Ile Gly Val Gly Ser Ile Phe Glu
290 295 300

Lys Glu Met Tyr Leu Pro Thr Leu Lys Ile Asp Thr Leu Glu Val Pro
305 310 315 320

Tyr Glu Asn Ile Asn Trp Gln Asn Tyr Tyr Leu Phe Lys Gln Glu Lys
325 330 335

Gln Glu Arg Ile Ser Phe Asn Glu Met Leu Ile Thr Leu Asn Gln Ser
340 345 350

PCT_Sequence_listing (3)

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

Ala Glu Asn Ile Phe Pro Gln Leu Lys Glu Val Met Lys Lys Gly Ala
370 375 380

Lys Gly Val Ile Leu Ile Asn Gln Ser Gly Pro Thr Thr Tyr Gly Asn
385 390 395 400

Tyr Glu Thr Val Pro Glu Leu Arg Asn Thr Leu Leu Asp Asp Glu Asp
405 410 415

Gly Asp Phe Lys Lys Thr Trp Ala Val Ser Ile Ser Ala Asn Asp Gly
420 425 430

Lys Ala Leu Lys Asp Tyr Leu Gln Lys Gln Asp Lys Lys Lys Ser Tyr
435 440 445

Ser Leu Val Phe Asn Thr Lys Pro Gln Leu Lys His Val Phe Lys Tyr
450 455 460

Pro Gly Val Ser Gly Phe Ser Thr Trp Gly Pro Gly Leu Asp Leu Thr
465 470 475 480

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

Asn Asp Asn Ser Tyr Phe Ile Ser Ser Gly Thr Ser Met Ser Ala Pro
500 505 510

Lys Val Ala Gly Ala Ser Ala Met Phe Leu Pro Val Thr Lys Lys Trp
515 520 525

Gln Lys Lys Trp Glu Lys Gln Asn Val Ser Met Ser Ile Pro Gln Leu
530 535 540

Thr Lys Leu Leu Phe Gln Asn Thr Ala Asp Ile Leu Tyr Asp His Ser
545 550 555 560

Val Pro Asn Gly Lys Pro Ile Leu Pro Tyr Ser Pro Arg Arg Gln Gly
565 570 575

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

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

Ser Arg Lys Glu Phe Asp Ile Val Ile Arg Asn Phe Ser Asp Gln Val
610 615 620

Arg Arg Phe Lys Ile Glu Pro Gly Ser Val Leu Gly Lys Ile Leu Tyr
625 630 635 640

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

125

PCT_Sequence_listing (3)

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

Gln Ile Ala Pro Asn Ser Ser Met Ile Leu Pro Leu Lys Leu Asn Val
675 680 685

Gly Lys Ala Val Glu Asn Glu Phe Val Glu Gly Phe Ile Lys Leu Arg
690 695 700

Ser Leu Glu Lys Asp Gln Pro Asp Leu Asn Ile Pro Phe Met Gly Phe
705 710 715 720

Tyr Gly Asp Trp Asn Ser Glu Asn Ile Leu Asp Pro Val Ala Trp Gln
725 730 735

Glu Gly Ser Lys Thr Arg Leu Thr Gly Ile Val His Pro Tyr Gly Leu
740 745 750

Gly Glu Asp Lys Phe Asp Ile Val Pro Trp Gly Val Asp Tyr Glu Lys
755 760 765

Trp Lys Gln Asp Pro Lys Ala Leu Asp Ala Asp Gln Arg Phe Tyr Val
770 775 780

Met Gln Ser Gln Ala Gly Ile Ala Asn His Ala Lys Met Arg Leu Arg
785 790 795 800

Leu Ile Phe Met Arg His Ala Lys Asp Tyr Arg Val Asp Ile Leu Asn
805 810 815

Ser Gln Lys Asp Lys Val Leu Lys Thr Leu Lys Thr Gly His Gln Ala
820 825 830

Pro Lys Tyr Met Glu Ser Ala Leu Leu Glu His Gly Asp Gln Tyr Gln
835 840 845

Met Gln Phe Ala Asp Phe Asp Pro Asp Leu Glu Trp Asp Gly Ser Val
850 855 860

Tyr Asn Pro Lys Thr Asn Thr Glu Asp Pro Leu Pro Asp Gly Asn Tyr
865 870 875 880

Phe Ile Arg Val Ser Ser Arg Ile Ser Lys Asn Arg Pro Tyr Gln Glu
885 890 895

His Ile Ile Pro Phe Ala Ile Asp Asn Gln Lys Pro Lys Val Lys Ile
900 905 910

Glu Glu Lys Thr Ala Leu Gln Val Val Phe His Val Asp Asp Ala His
915 920 925

Leu Gln Gly Ile Arg Leu Val Lys Asp Asn Lys Ile Ile Gln Thr Leu
930 935 940

Glu Thr Asp Thr Gln Gly Arg Phe Arg Leu Asn Leu Ala Asp Phe Gln

126

PCT_Sequence_listing (3)

945		950		955		960
Gly	Lys	Gly	Phe	Glu	Leu	Glu
		965		970		975
Ile	Ile	Asp	Leu	Asp	Ser	Leu
		980		985		990
Gly	Ala	Ser	Ser	Ser	Tyr	Asn
		995		1000		1005
Val	Ala	His	Lys	Asn	Ala	Glu
	1010					1015
Asp	Ile	Leu	His	Glu	Asn	Ser
				1020		
Glu	Ser	Glu	Glu	Ile	Ala	Ser
	1025					1030
Ala	Leu	Thr	Phe	Glu	Asp	Gly
				1035		
Asp	Phe	His	Asp	Gly	Lys	Lys
	1040					1045
Thr	Asn	Ala	Tyr	Ser	Glu	Ile
				1050		
Lys	Ser	Asn	Asp	Asn	Ser	Val
	1055					1060
His	Leu	Lys	Asp	Asn	Thr	Tyr
				1065		
Arg	Asp	Tyr	Tyr	Ile	His	Leu
	1070					1075
Lys	Glu	Gly	Gln	Arg	Leu	Leu
				1080		
Thr	Thr	Thr	Asn	Ala	Phe	His
	1085					1090
Asn	Ser	Lys	Gln	Gly	Asn	Asp
				1095		
Thr	Ala	Pro	Thr	Trp	Gln	Ala
	1100					1105
Asn	Tyr	Thr	Tyr	Asp	Pro	Ser
				1110		
Asn	Gln	Gly	Gln	Tyr	Tyr	Arg
	1115					1120
Lys	Ile	Ala	Ile	Pro	Ile	Tyr
				1125		
Gly	Ser	Asn	Thr	Ile	Asn	Val
	1130					1135
Lys	Ala	Phe	Tyr	Lys	Asp	Lys
				1140		
Ile	Phe	Asn	Lys	Gly	Tyr	Ala
	1145					1150
Val	Lys	Leu	Asp	Thr	Glu	Val
				1155		
Gln	Leu	Thr	Phe	Asp	Asn	Pro
	1160					1165
Asn	Ile	Ser	Phe	Thr	Ser	Asp
				1170		
Trp	Gln	Asn	Leu	Ser	Asp	Asp
	1175					1180
Glu	Tyr	Asp	Asp	Asp	Asn	Ile
				1185		
Gly	Thr	Ile	Thr	Ile	Pro	Asn
	1190					1195
Asn	Thr	Leu	Arg	Leu	Ser	Gly
				1200		
Ile	Arg	Asp	Gly	Leu	Asp	Gly
	1205					1210
Trp	Arg	Met	Phe	Ile	Asn	Gly
				1215		
Met	Val	Asp	Ser	Asp	Ile	Lys
	1220					1225
Leu	Gly	Glu	Tyr	Asp	Asp	Ile
				1230		

PCT_Sequence_listing (3)

Gln	Gln	Asn	Arg	Arg	Gln	Trp	Lys	Tyr	Glu	Lys	Gln	Val	Glu	Asn
1235						1240					1245			
Asp	Asp	Tyr	Val	Leu	Ile	Lys	Leu	Ser	Asp	His	Val	Lys	Asn	Ser
1250						1255					1260			
Arg	Ser	Tyr	Leu	Phe	Lys	Val	Lys	Ile	Asp	Pro	Thr	Val	Ser	Glu
1265						1270					1275			
Tyr	His	Phe	Thr	Asn	Lys	Asn	Asp	Ile	Ile	Asp	Asp	Asp	Lys	Thr
1280						1285					1290			
Leu	Leu	Thr	Leu	Asn	Thr	Leu	Thr	Asp	Ser	Ser	Leu	Gly	Tyr	Ala
1295						1300					1305			
Asn	Lys	Leu	Leu	Asn	Met	Pro	Lys	Asp	Leu	Val	Lys	Ser	Thr	Asp
1310						1315					1320			
Asp	Leu	Phe	Lys	Ala	Met	Thr	Met	Leu	Phe	Lys	Lys	Glu	Ser	Phe
1325						1330					1335			
Phe	Leu	Tyr	Pro	Leu	Lys	Asn	Asp	Leu	Asn	Thr	Asn	Gly	Ile	Ser
1340						1345					1350			
Met	Met	Thr	Ser	Leu	Val	Gln	Phe	Gln	Ala	Lys	Asp	Val	Lys	Glu
1355						1360					1365			
Asn	Ile	Pro	Leu	Glu	Trp	Glu	Ile	Lys	Thr	Lys	Ala	Ser	Asp	Ser
1370						1375					1380			
Arg	Gln	Leu	Leu	Tyr	Gln	Asn	Leu	Lys	Asn	Glu	Lys	Glu	Arg	Leu
1385						1390					1395			
Asp	Gln	Val	Ser	Thr	Asn	Pro	Leu	Ala	His	Gln	Leu	Pro	Leu	Glu
1400						1405					1410			
Asn	Ser	Asn	Gln	Glu	Asn	Gly	Gln	Asp	Ala	Ile	Leu	Thr	Ser	Thr
1415						1420					1425			
Lys	Val	Leu	Pro	Met	Ser	Lys	Ser	Ser	Ile	Phe	Arg	Asp	Ser	Leu
1430						1435					1440			
Arg	Glu	Thr	Ser	Leu	Pro	Glu	Thr	Arg	Asp	Ser	Ser	Ser	Met	Ala
1445						1450					1455			
Asn	Trp	Ser	Leu	Ala	Phe	Phe	Leu	Ser	Ala	Val	Ile	Cys	Phe	Phe
1460						1465					1470			
Lys	Gly	Arg	Arg	Lys	Arg	Leu	Asn	Lys	Leu					
1475						1480								

<210> 135
<211> 1368
<212> DNA
<213> Streptococcus uberis

<400> 135
gtgtcaaaag gtcaatctga tttaagccat gcggaacaag gtgttgatga tcaaattaca

PCT_Sequence_listing (3)

attgctaaaa aagatagtat ctacagtaaca actgattcaa aagatttaac gccaaaatac 120
attgatacaa aagggttgac tggttcagct ttaacaacag caatggaaaa aaacattgca 180
ctgtataatc aagcgggttaa tgatggcgta ggtattatgg atgcttcaag cgtccaaatg 240
aaaaaacaaa ttgctgatta tttaacagct ttgacaaatt atcaaaaggg tgtttcttca 300
aatacaggat tacaatggca aaatagtgtt gtcttagaag cgggctcagg tgcaagtaga 360
caaacaggca ctgaaaatgt tgttgatttt agtgatggaa cgattaaagc agcaggatatg 420
tatgcgacac aagggtcaaaa tttagaccaa aatactgatg caaatTTTga taatattttt 480
aagattgagg gaaccgggat tatttgggta aagaatacga ccaatggaga tgttaaattg 540
actttctctg aaattaatag tccatacaat acagggtactt acgttgctat ttgggggtgat 600
gacaaagggtg gtattgcttg gtcagtcttt gccttatact atgggtggtgc gagtggtgga 660
gctggtgaaa cagggttctaa tacaggttct ggtatcagtg gtcgcatttt aaattatgtg 720
aattcatata aagcaacagt agaaacaaca agagggtgttt cagttgtaac ttttaatgac 780
attgataatc aacagacagt taaaatgtcg ggacttgata atgccaaagt aacaacagggt 840
gagaatatta atcagacagg aaatgatttt gttgcagggt cgggtgacgt ttctcaaagt 900
tcagcaggag ttttaggaac caatggtgtt aaatggactt ttacaagtgc tgataggcgt 960
ttattctcat ttactcattc tacagcagga actaaaaaca catcaatcgt aggtggtatt 1020
tttgatcag cgtctaactg acctcaaaag ccagtaattc ctaaactaac cgctcataaa 1080
gcaatcgta caggaccaa gggccaagc atccctgtta atcaaaaagt gacggttcac 1140
tactataagg tttcggttac acctacacca gaaaatccag ttactccaca aaaaaacatt 1200
acttataaac caattacaac cactccacaa acaccagtaa gccaaagcaa tgtgggactt 1260
ccaacaactg gtgataaagc agatggttct attgttcaaa tggttaattgg tgcattaatg 1320
gtatcatttg ttgggttttc agcattaaaa gatcggaataa aagaaaaa 1368

<210> 136
<211> 456
<212> PRT
<213> Streptococcus uberis

<400> 136

Met Ser Lys Gly Gln Ser Asp Leu Ser His Ala Glu Gln Gly Val Asp
1 5 10 15

Asp Gln Ile Thr Ile Ala Lys Lys Asp Ser Ile Ser Val Thr Thr Asp
20 25 30

Ser Lys Asp Leu Thr Pro Lys Tyr Ile Asp Thr Lys Gly Leu Thr Gly
35 40 45

Ser Ala Leu Thr Thr Ala Met Glu Lys Asn Ile Ala Leu Tyr Asn Gln
50 55 60

Ala Val Asn Asp Gly Val Gly Ile Met Asp Ala Ser Ser Val Gln Met
65 70 75 80

Lys Lys Gln Ile Ala Asp Tyr Leu Thr Ala Leu Thr Asn Tyr Gln Lys
85 90 95

109

PCT_Sequence_listing (3)

Gly Val Ser Ser Asn Thr Gly Leu Gln Trp Gln Asn Ser Val Val Leu
100 105 110

Glu Ala Gly Ser Gly Ala Ser Arg Gln Thr Gly Thr Glu Asn Val Val
115 120 125

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

Gly Gln Asn Leu Asp Gln Asn Thr Asp Ala Asn Phe Asp Asn Ile Phe
145 150 155 160

Lys Ile Glu Gly Thr Gly Ile Ile Trp Val Lys Asn Thr Thr Asn Gly
165 170 175

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

Thr Tyr Val Ala Ile Trp Gly Asp Asp Lys Gly Gly Ile Ala Trp Ser
195 200 205

Val Phe Ala Leu Tyr Tyr Gly Gly Ala Ser Gly Gly Ala Gly Glu Thr
210 215 220

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

Asn Ser Tyr Lys Ala Thr Val Glu Thr Thr Arg Gly Val Ser Val Val
245 250 255

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

Asp Asn Ala Lys Val Thr Thr Gly Glu Asn Ile Asn Gln Thr Gly Asn
275 280 285

Asp Phe Val Ala Gly Ser Gly Asp Val Ser Gln Ser Ser Ala Gly Val
290 295 300

Leu Gly Thr Asn Gly Val Lys Trp Thr Phe Thr Ser Ala Asp Arg Arg
305 310 315 320

Leu Phe Ser Phe Thr His Ser Thr Ala Gly Thr Lys Asn Thr Ser Ile
325 330 335

Val Gly Gly Ile Phe Gly Ser Ala Ser Asn Val Pro Gln Lys Pro Val
340 345 350

Ile Pro Lys Leu Thr Ala His Lys Ala Ile Val Thr Gly Pro Lys Gly
355 360 365

Pro Ser Ile Pro Val Asn Gln Lys Val Thr Val His Tyr Tyr Lys Val
370 375 380

Ser Val Thr Pro Thr Pro Glu Asn Pro Val Thr Pro Gln Lys Asn Ile

PCT_Sequence_listing (3)

385		390		395		400
Thr Tyr Lys Pro	Ile Thr Thr Thr Pro Gln Thr Pro Val Ser Gln Ala					
	405			410		415
Asn Val Gly Leu Pro Thr Thr Gly Asp Lys Ala Asp Gly Ser Ile Val						
	420			425		430
Gln Met Val Ile Gly Ala Leu Met Val Ser Phe Val Gly Phe Ser Ala						
	435			440		445
Leu Lys Asp Arg Lys Lys Glu Lys						
	450			455		

<210> 137
 <211> 714
 <212> DNA
 <213> Streptococcus uberis

<220>
 <221> CDS
 <222> (1)..(714)

<400> 137	
atg tta aaa aaa caa tta tta gtc cta act tgt gtt tca act ctt gga	48
Met Leu Lys Lys Gln Leu Leu Val Leu Thr Cys Val Ser Thr Leu Gly	
1 5 10 15	
cta gta ggg acc aca gct ttt gct gaa gat gta gtc ccg gta gat cca	96
Leu Val Gly Thr Thr Ala Phe Ala Glu Asp Val Val Pro Val Asp Pro	
20 25 30	
act acc cca tca aca gaa gtg att aca cca tca acc cca ata gat act	144
Thr Thr Pro Ser Thr Glu Val Ile Thr Pro Ser Thr Pro Ile Asp Thr	
35 40 45	
ggg tta ccg tct gat act act gac cct agc act ccg gtt gaa ccc gag	192
Gly Leu Pro Ser Asp Thr Thr Asp Pro Ser Thr Pro Val Glu Pro Glu	
50 55 60	
act cct act aat cct act aat cct agt act ccg ata gat cca gga act	240
Thr Pro Thr Asn Pro Thr Asn Pro Ser Thr Pro Ile Asp Pro Gly Thr	
65 70 75 80	
cca act gat acg aca acg cca aca gat gat aca aca aca cct gga aca	288
Pro Thr Asp Thr Thr Pro Thr Asp Asp Thr Thr Thr Pro Gly Thr	
85 90 95	
tct act agt ccc tca gat tca gag tca act aac aca aat cca ggc aca	336
Ser Thr Ser Pro Ser Asp Ser Glu Ser Thr Asn Thr Asn Pro Gly Thr	
100 105 110	
aaa cca aca gat gaa gta aaa cca gtt acc cca tct act cct gaa gtg	384
Lys Pro Thr Asp Glu Val Lys Pro Val Thr Pro Ser Thr Pro Glu Val	
115 120 125	
cct tca act gtt act cca gga gta gtt gat aat gtt gat aaa gaa aca	432
Pro Ser Thr Val Thr Pro Gly Val Val Asp Asn Val Asp Lys Glu Thr	
130 135 140	
ggg aat att acc att aaa cca atc cca att agc cca gat aaa aca gtt	480
Gly Asn Ile Thr Ile Lys Pro Ile Pro Ile Ser Pro Asp Lys Thr Val	
145 150 155 160	
ggt ggg act cag aat ggg aat gtg ctt att caa gat cgc tca gga agg	528
Val Gly Thr Gln Asn Gly Asn Val Leu Ile Gln Asp Arg Ser Gly Arg	
165 170 175	
tat tta gta tct gct agt gaa ctt ggt ggt cga ctt aat gat gat gga	576

PCT_Sequence_listing (3)

Tyr	Leu	Val	Ser	Ala	Ser	Glu	Leu	Gly	Gly	Arg	Leu	Asn	Asp	Asp	Gly		
			180					185					190				
act	gta	aca	atc	aaa	gat	tcg	gaa	gga	aaa	gaa	aaa	aca	ctt	cct	cat	624	
Thr	Val	Thr	Ile	Lys	Asp	Ser	Glu	Gly	Lys	Glu	Lys	Thr	Leu	Pro	His		
		195					200					205					
aca	ggt	gaa	gaa	aaa	gga	ttt	tta	agt	atc	att	ggt	gga	aca	atc	tta	672	
Thr	Gly	Glu	Glu	Lys	Gly	Phe	Leu	Ser	Ile	Ile	Gly	Gly	Thr	Ile	Leu		
	210					215					220						
tct	ttt	gta	gcc	ttc	tta	ttc	aag	aaa	aaa	ata	act	tta	aat			714	
Ser	Phe	Val	Ala	Phe	Leu	Phe	Lys	Lys	Lys	Ile	Thr	Leu	Asn				
					230					235							
225																	

<210> 138
<211> 238
<212> PRT
<213> Streptococcus uberis

<400> 138

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

PCT_Sequence_listing (3)

Thr Gly Glu Glu Lys Gly Phe Leu Ser Ile Ile Gly Gly Thr Ile Leu
 210 215 220

Ser Phe Val Ala Phe Leu Phe Lys Lys Lys Ile Thr Leu Asn
 225 230 235

<210> 139
 <211> 2628
 <212> DNA
 <213> Streptococcus uberis

<220>
 <221> CDS
 <222> (1)..(2628)

<400> 139	
atg aat tca aac aca aaa gga cat ggt ttt ttc aga aaa tca aaa gca	48
Met Asn Ser Asn Thr Lys Gly His Gly Phe Arg Lys Ser Lys Ala	
1 5 10 15	
tac ggt tta gta tgt gga atc gca cta gca ggt gct ttt gct ttt agt	96
Tyr Gly Leu Val Cys Gly Ile Ala Leu Ala Gly Ala Phe Ala Phe Ser	
20 25 30	
gga ggg aat gta tcg gca gat gaa gtt act gct cca gca gaa cgt caa	144
Gly Gly Asn Val Ser Ala Asp Glu Val Thr Ala Pro Ala Glu Arg Gln	
35 40 45	
act gtt gta aca acc tta aca gag cca aca aat aac caa gca caa gca	192
Thr Val Val Thr Thr Leu Thr Glu Pro Thr Asn Asn Gln Ala Gln Ala	
50 55 60	
gtt acg tca gaa gca ctt aat aca gca gtt tca aca gct aaa gaa gca	240
Val Thr Ser Glu Ala Leu Asn Thr Ala Val Ser Thr Ala Lys Glu Ala	
65 70 75 80	
gga gta act gtt aac aca aca gga gca gtt agt cat aca gat gtt cca	288
Gly Val Thr Val Asn Thr Thr Gly Ala Val Ser His Thr Asp Val Pro	
85 90 95	
agt gca caa tct gat tta gct agt caa aca caa act gtt aaa gat gcg	336
Ser Ala Gln Ser Asp Leu Ala Ser Gln Thr Gln Thr Val Lys Asp Ala	
100 105 110	
act gct aaa gca gaa gct aat aca cag gct att aaa gat gcg act gcg	384
Thr Ala Lys Ala Glu Ala Asn Thr Gln Ala Ile Lys Asp Ala Thr Ala	
115 120 125	
caa aat gct caa att gat gct caa aat cag gca gaa gct aca cgt gtt	432
Gln Asn Ala Gln Ile Asp Ala Gln Asn Gln Ala Glu Ala Thr Arg Val	
130 135 140	
gct gaa ata aat aaa gca agt caa ctt gcg gtt gat caa aaa aat gcc	480
Ala Glu Ile Asn Lys Ala Ser Gln Leu Ala Val Asp Gln Lys Asn Ala	
145 150 155 160	
caa ggt caa gca ctc gtt gat aaa caa aat gct gat gca caa gca caa	528
Gln Gly Gln Ala Leu Val Asp Lys Gln Asn Ala Asp Ala Gln Ala Gln	
165 170 175	
gca gat gcg aca aat gca caa ctt aaa gca gat tat gaa gct aaa tta	576
Ala Asp Ala Thr Asn Ala Gln Leu Lys Ala Asp Tyr Glu Ala Lys Leu	
180 185 190	
gct gaa att aaa act gtt gaa gac tac aac aaa gca gta gct gaa cgc	624
Ala Glu Ile Lys Thr Val Glu Asp Tyr Asn Lys Ala Val Ala Glu Arg	
195 200 205	
aat gct tta gct aaa caa caa gca gat gcg aca aat gca caa ctt aaa	672
Asn Ala Leu Ala Lys Gln Gln Ala Asp Ala Thr Asn Ala Gln Leu Lys	
210 215 220	

PCT_Sequence_listing (3)

gcg gat tat caa act aaa ctt gat gca tat aac aaa gcg tta gct gat Ala Asp Tyr Gln Thr Lys Leu Asp Ala Tyr Asn Lys Ala Leu Ala Asp 225 230 235 240	720
aaa atc aat cta ata gct aat gat gtt act ttt aaa ggt tat ggt aaa Lys Ile Asn Leu Ile Ala Asn Asp Val Thr Phe Lys Gly Tyr Gly Lys 245 250 255	768
tca gaa gat tta aat gct tat ggt ata gta act tct gat act ata aca Ser Glu Asp Leu Asn Ala Tyr Gly Ile Val Thr Ser Asp Thr Ile Thr 260 265 270	816
att gat ggt gca gga aac ttt ata tta aaa gaa cca atg tct gat cca Ile Asp Gly Ala Gly Asn Phe Ile Leu Lys Glu Pro Met Ser Asp Pro 275 280 285	864
aca ggg gtt att ggt tat atc act aca aaa ggt aaa tta aac tat tct Thr Gly Val Ile Gly Tyr Ile Thr Thr Lys Gly Lys Leu Asn Tyr Ser 290 295 300	912
agt gtt tat gat cca aca ctt aat aaa gcg aat att acg att gat tca Ser Val Tyr Asp Pro Thr Lys Ala Asn Ile Thr Ile Asp Ser 305 310 315 320	960
att act tta aat aca tgg cag tta gat ttg aat cgc ccc tca att tca Ile Thr Leu Asn Thr Trp Gln Leu Asp Leu Asn Arg Pro Ser Ile Ser 325 330 335	1008
gga aat act aat gca ttt gca gaa tac att ggg tta gac gga act tcg Gly Asn Thr Asn Ala Phe Ala Glu Tyr Ile Gly Leu Asp Gly Thr Ser 340 345 350	1056
tta ttt aag caa gct tat aca ggt cta acc tca atg tca ccg att act Leu Phe Lys Gln Ala Tyr Thr Gly Leu Thr Ser Met Ser Pro Ile Thr 355 360 365	1104
atc ggt aaa act agt caa att gga aag aca ttc act gtg gca agc ggg Ile Gly Lys Thr Ser Gln Ile Gly Lys Thr Phe Thr Val Ala Ser Gly 370 375 380	1152
gaa aca aca cca gaa ttt atg ttc ttg aaa aca aat ccg ttc tgg gag Glu Thr Thr Pro Glu Phe Met Phe Leu Lys Thr Asn Pro Phe Trp Glu 385 390 395 400	1200
ttt ttc gca cca tct tct tta ttt gcg gaa tta acc tat aat aca gca Phe Phe Ala Pro Ser Ser Leu Phe Ala Glu Leu Thr Tyr Asn Thr Ala 405 410 415	1248
cca tta cca aat aaa cct att gaa cca aca ttg gtt act gtt acc cca Pro Leu Pro Asn Lys Pro Ile Glu Pro Thr Leu Val Thr Val Thr Pro 420 425 430	1296
gaa gca ctt aaa cca gtt cca caa aca ccc cca act cca gtt tat gtg Glu Ala Leu Lys Pro Val Pro Gln Thr Pro Pro Thr Pro Val Tyr Val 435 440 445	1344
aca cca aat ctc aaa tcc ttc aca cct gaa gtt tac acc cca atc aaa Thr Pro Asn Leu Lys Ser Phe Thr Pro Glu Val Tyr Thr Pro Ile Lys 450 455 460	1392
cca act gtt aaa ccc cac gtt gct gta cct gat aaa tta gtt gtc aca Pro Thr Val Lys Pro His Val Ala Val Pro Asp Lys Leu Val Val Thr 465 470 475 480	1440
gta tca gta cat cct gtt gtg gtt cca gtt gcg aat cct tct aaa gac Val Ser Val His Pro Val Val Val Pro Val Ala Asn Pro Ser Lys Asp 485 490 495	1488
gtt gta gat caa gca ggt aaa tca att aat ggt tta tca gtg tta cct Val Val Asp Gln Ala Gly Lys Ser Ile Asn Gly Leu Ser Val Leu Pro 500 505 510	1536
aat tct gac tta aac tac gtg gct tta caa gac ttt agt caa tat aag Asn Ser Asp Leu Asn Tyr Val Ala Leu Gln Asp Phe Ser Gln Tyr Lys 515 520 525	1584

PCT_Sequence_listing (3)

gga atg agt gct tca caa gat aaa atc gcc aaa aac ttt atc ttt att Gly Met Ser Ala Ser Gln Asp Lys Ile Ala Lys Asn Phe Ile Phe Ile	1632
530 535 540	
gat gac tac aaa gat gaa gca cta gac gga aaa tca atg gtt gtt aat Asp Asp Tyr Lys Asp Glu Ala Leu Asp Gly Lys Ser Met Val Val Asn	1680
545 550 555 560	
agc att aaa gct aaa aat ggt gat gat gtg tca cat ctt tta gaa atg Ser Ile Lys Ala Lys Asn Gly Asp Asp Val Ser His Leu Leu Glu Met	1728
565 570 575	
cat cat gta tta tct aaa gat ggc tta gat gtc aaa ctt caa gct atc His His Val Leu Ser Lys Asp Gly Leu Asp Val Lys Leu Gln Ala Ile	1776
580 585 590	
ttg gct gaa agt gga tta tct cca gtt ggt gaa ttc tat atg tgg gta Leu Ala Glu Ser Gly Leu Ser Pro Val Gly Glu Phe Tyr Met Trp Val	1824
595 600 605	
gct aag gat cca aca agc ttc tat aaa gct tat gtg caa aaa ggt tta Ala Lys Asp Pro Thr Ser Phe Tyr Lys Ala Tyr Val Gln Lys Gly Leu	1872
610 615 620	
gat att act tac aac ctc tca ttc aaa gta cat caa aca ttt act gaa Asp Ile Thr Tyr Asn Leu Ser Phe Lys Val His Gln Thr Phe Thr Glu	1920
625 630 635 640	
agt gaa att gtt aat ggt gtt gct caa att gat ttt ggc aat ggc tat Ser Glu Ile Val Asn Gly Val Ala Gln Ile Asp Phe Gly Asn Gly Tyr	1968
645 650 655	
ctt gga aat ctt gta gtt aat gat tta cca aaa cca gaa gtt cat aaa Leu Gly Asn Leu Val Val Asn Asp Leu Pro Lys Pro Glu Val His Lys	2016
660 665 670	
gac gtc ata gat gaa gca gga aaa tct att aac aac ggt act gta aaa Asp Val Ile Asp Glu Ala Gly Lys Ser Ile Asn Asn Gly Thr Val Lys	2064
675 680 685	
ctt ggt gat gaa gtc act tac aag cta gaa ggt tgg gtc gtt cca act Leu Gly Asp Glu Val Thr Tyr Lys Leu Glu Gly Trp Val Val Pro Thr	2112
690 695 700	
gga cgt tca tac gat tta ttc gag tac aaa ttt gta gat cag tta caa Gly Arg Ser Tyr Asp Leu Phe Glu Tyr Lys Phe Val Asp Gln Leu Gln	2160
705 710 715 720	
aat aca cat gat ctt tat ttg aaa gat agt gtt gtt gcc aaa gtt gat Asn Thr His Asp Leu Tyr Leu Lys Asp Ser Val Val Ala Lys Val Asp	2208
725 730 735	
att act cta tca gac ggt aca gtc att aca aaa ggt tct gat tta gca Ile Thr Leu Ser Asp Gly Thr Val Ile Thr Lys Gly Ser Asp Leu Ala	2256
740 745 750	
caa tat act gag aca gtt tac aac aaa gaa act gga cgc tat gaa tta Gln Tyr Thr Glu Thr Val Tyr Asn Lys Glu Thr Gly Arg Tyr Glu Leu	2304
755 760 765	
gcg ttc aag aaa gat ttc ttg gct aaa gtt gta cgt tct agt gaa ttt Ala Phe Lys Lys Asp Phe Leu Ala Lys Val Val Arg Ser Ser Glu Phe	2352
770 775 780	
gga gca gat gcc ttc tta gtt gtt aag cgt att aaa gca ggt gat gtc Gly Ala Asp Ala Phe Leu Val Val Lys Arg Ile Lys Ala Gly Asp Val	2400
785 790 795 800	
tat aac aca act gat cta tat gtt aat ggt aac aaa gtg aag tct gaa Tyr Asn Thr Thr Asp Leu Tyr Val Asn Gly Asn Lys Val Lys Ser Glu	2448
805 810 815	
aca gtt gtg aca cat acc cct gaa gca cca aaa cca gtc act cca act Thr Val Val Thr His Thr Pro Glu Ala Pro Lys Pro Val Thr Pro Thr	2496

PCT_Sequence_listing (3)

820															825	830															
aaa	gaa	gtg	cca	aaa	aca	cct	gaa	aaa	gta	ctt	cca	cac	aca	gga	gaa	2544															
Lys	Glu	Val	Pro	Lys	Thr	Pro	Glu	Lys	Val	Leu	Pro	His	Thr	Gly	Glu																
		835					840					845																			
gaa	ggg	ctt	tca	att	ttg	acc	gtt	att	ggt	gca	agt	att	ctt	tca	gta	2592															
Glu	Gly	Leu	Ser	Ile	Leu	Thr	Val	Ile	Gly	Ala	Ser	Ile	Leu	Ser	Val																
	850					855					860																				
ctt	ggt	ctt	tca	gta	ctt	aaa	aaa	cct	aaa	gaa	aat					2628															
Leu	Gly	Leu	Ser	Val	Leu	Lys	Lys	Pro	Lys	Glu	Asn																				
865					870					875																					
<210> 140																															
<211> 876																															
<212> PRT																															
<213> Streptococcus uberis																															
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Met	Asn	Ser	Asn	Thr	Lys	Gly	His	Gly	Phe	Phe	Arg	Lys	Ser	Lys	Ala																
1				5					10					15																	
Tyr	Gly	Leu	Val	Cys	Gly	Ile	Ala	Leu	Ala	Gly	Ala	Phe	Ala	Phe	Ser																
			20					25					30																		
Gly	Gly	Asn	Val	Ser	Ala	Asp	Glu	Val	Thr	Ala	Pro	Ala	Glu	Arg	Gln																
		35					40					45																			
Thr	Val	Val	Thr	Thr	Leu	Thr	Glu	Pro	Thr	Asn	Asn	Gln	Ala	Gln	Ala																
	50					55					60																				
Val	Thr	Ser	Glu	Ala	Leu	Asn	Thr	Ala	Val	Ser	Thr	Ala	Lys	Glu	Ala																
65					70				75					80																	
Gly	Val	Thr	Val	Asn	Thr	Thr	Gly	Ala	Val	Ser	His	Thr	Asp	Val	Pro																
				85					90					95																	
Ser	Ala	Gln	Ser	Asp	Leu	Ala	Ser	Gln	Thr	Gln	Thr	Val	Lys	Asp	Ala																
			100					105					110																		
Thr	Ala	Lys	Ala	Glu	Ala	Asn	Thr	Gln	Ala	Ile	Lys	Asp	Ala	Thr	Ala																
		115					120					125																			
Gln	Asn	Ala	Gln	Ile	Asp	Ala	Gln	Asn	Gln	Ala	Glu	Ala	Thr	Arg	Val																
	130					135					140																				
Ala	Glu	Ile	Asn	Lys	Ala	Ser	Gln	Leu	Ala	Val	Asp	Gln	Lys	Asn	Ala																
145					150					155					160																
Gln	Gly	Gln	Ala	Leu	Val	Asp	Lys	Gln	Asn	Ala	Asp	Ala	Gln	Ala	Gln																
				165					170					175																	
Ala	Asp	Ala	Thr	Asn	Ala	Gln	Leu	Lys	Ala	Asp	Tyr	Glu	Ala	Lys	Leu																
			180					185					190																		
Ala	Glu	Ile	Lys	Thr	Val	Glu	Asp	Tyr	Asn	Lys	Ala	Val	Ala	Glu	Arg																
		195					200					205																			
Asn	Ala	Leu	Ala	Lys	Gln	Gln	Ala	Asp	Ala	Thr	Asn	Ala	Gln	Leu	Lys																

PCT_Sequence_listing (3)

210		215		220	
Ala 225	Asp	Tyr	Gln	Thr	Lys 230
Leu	Asp	Ala	Tyr	Asn 235	Lys
Ala	Leu	Ala	Asp	240	
Lys	Ile	Asn	Leu	Ile 245	Ala
Asn	Asp	Val	Thr	Phe	Lys
Gly	Tyr	Gly	255	Lys	
Ser	Glu	Asp	Leu	Asn	Ala
Tyr	Gly	Ile	Val	Thr	Ser
Asp	Thr	Ile	Thr	270	
Ile	Asp	Gly	Ala	Gly	Asn
Phe	Ile	Leu	Lys	Glu	Pro
Met	Ser	Asp	Pro	285	
Thr	Gly	Val	Ile	Gly	Tyr
Ile	Thr	Thr	Lys	Gly	Lys
Leu	Asn	Tyr	Ser	300	
Ser	Val	Tyr	Asp	Pro	Thr
Leu	Asn	Lys	Ala	Asn	Ile
Thr	Ile	Asp	Ser	320	
Ile	Thr	Leu	Asn	Thr	Trp
Gln	Leu	Asp	Leu	Asn	Arg
Pro	Ser	Ile	Ser	335	
Gly	Asn	Thr	Asn	Ala	Phe
Ala	Glu	Tyr	Ile	Gly	Leu
Asp	Gly	Thr	Ser	350	
Leu	Phe	Lys	Gln	Ala	Tyr
Thr	Gly	Leu	Thr	Ser	Met
Ser	Pro	Ile	Thr	365	
Ile	Gly	Lys	Thr	Ser	Gln
Ile	Gly	Lys	Thr	Phe	Thr
Val	Ala	Ser	Gly	380	
Glu	Thr	Thr	Pro	Glu	Phe
Met	Phe	Leu	Lys	Thr	Asn
Pro	Phe	Trp	Glu	400	
Phe	Phe	Ala	Pro	Ser	Ser
Leu	Phe	Ala	Glu	Leu	Thr
Tyr	Asn	Thr	Ala	415	
Pro	Leu	Pro	Asn	Lys	Pro
Ile	Glu	Pro	Thr	Leu	Val
Thr	Val	Thr	Pro	430	
Glu	Ala	Leu	Lys	Pro	Val
Pro	Gln	Thr	Pro	Pro	Thr
Pro	Val	Tyr	Val	445	
Thr	Pro	Asn	Leu	Lys	Ser
Phe	Thr	Pro	Glu	Val	Tyr
Thr	Pro	Ile	Lys	460	
Pro	Thr	Val	Lys	Pro	His
Val	Ala	Val	Pro	Asp	Lys
Leu	Val	Val	Thr	480	
Val	Ser	Val	His	Pro	Val
Val	Val	Val	Pro	Val	Ala
Asn	Pro	Ser	Lys	495	
Val	Val	Asp	Gln	Ala	Gly
Lys	Ser	Ile	Asn	Gly	Leu
Ser	Val	Leu	Pro	510	

PCT_Sequence_listing (3)

Asn Ser Asp Leu Asn Tyr Val Ala Leu Gln Asp Phe Ser Gln Tyr Lys
515 520 525

Gly Met Ser Ala Ser Gln Asp Lys Ile Ala Lys Asn Phe Ile Phe Ile
530 535 540

Asp Asp Tyr Lys Asp Glu Ala Leu Asp Gly Lys Ser Met Val Val Asn
545 550 555 560

Ser Ile Lys Ala Lys Asn Gly Asp Asp Val Ser His Leu Leu Glu Met
565 570 575

His His Val Leu Ser Lys Asp Gly Leu Asp Val Lys Leu Gln Ala Ile
580 585 590

Leu Ala Glu Ser Gly Leu Ser Pro Val Gly Glu Phe Tyr Met Trp Val
595 600 605

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

Asp Ile Thr Tyr Asn Leu Ser Phe Lys Val His Gln Thr Phe Thr Glu
625 630 635 640

Ser Glu Ile Val Asn Gly Val Ala Gln Ile Asp Phe Gly Asn Gly Tyr
645 650 655

Leu Gly Asn Leu Val Val Asn Asp Leu Pro Lys Pro Glu Val His Lys
660 665 670

Asp Val Ile Asp Glu Ala Gly Lys Ser Ile Asn Asn Gly Thr Val Lys
675 680 685

Leu Gly Asp Glu Val Thr Tyr Lys Leu Glu Gly Trp Val Val Pro Thr
690 695 700

Gly Arg Ser Tyr Asp Leu Phe Glu Tyr Lys Phe Val Asp Gln Leu Gln
705 710 715 720

Asn Thr His Asp Leu Tyr Leu Lys Asp Ser Val Val Ala Lys Val Asp
725 730 735

Ile Thr Leu Ser Asp Gly Thr Val Ile Thr Lys Gly Ser Asp Leu Ala
740 745 750

Gln Tyr Thr Glu Thr Val Tyr Asn Lys Glu Thr Gly Arg Tyr Glu Leu
755 760 765

Ala Phe Lys Lys Asp Phe Leu Ala Lys Val Val Arg Ser Ser Glu Phe
770 775 780

Gly Ala Asp Ala Phe Leu Val Val Lys Arg Ile Lys Ala Gly Asp Val
785 790 795 800

Tyr Asn Thr Thr Asp Leu Tyr Val Asn Gly Asn Lys Val Lys Ser Glu
805 810 815

PCT_Sequence_listing (3)

Thr Val Val Thr His Thr Pro Glu Ala Pro Lys Pro Val Thr Pro Thr
820 825 830

Lys Glu Val Pro Lys Thr Pro Glu Lys Val Leu Pro His Thr Gly Glu
835 840 845

Glu Gly Leu Ser Ile Leu Thr Val Ile Gly Ala Ser Ile Leu Ser Val
850 855 860

Leu Gly Leu Ser Val Leu Lys Lys Pro Lys Glu Asn
865 870 875

<210> 141
<211> 1947
<212> DNA
<213> Streptococcus uberis

<220>
<221> CDS
<222> (1)..(1947)

<400> 141
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Met Gly Glu Thr Thr Leu Gly Leu Ala Asn Ser Ala Asp Gln Thr Ile
1 5 10 15
gcc tta aaa tat gaa gcc aat aat ctg aac ttg gtt tca aca gtg ctt 96
Ala Leu Lys Tyr Glu Ala Asn Asn Leu Asn Leu Val Ser Thr Val Leu
20 25 30
cat gaa atg acg cat att atc gac ttt aag agt ggc ctc tat tca gaa 144
His Glu Met Thr His Ile Ile Asp Phe Lys Ser Gly Leu Tyr Ser Glu
35 40 45
acg act gac cgt aat aca gat ggt agt ctt agt acg gtc atg gcc ttt 192
Thr Thr Asp Arg Asn Thr Asp Gly Ser Leu Ser Thr Val Met Ala Phe
50 55 60
tca gat acc caa gag ttc tta gat gtc tac cat acc tat ttt gac cga 240
Ser Asp Thr Gln Glu Phe Leu Asp Val Tyr His Thr Tyr Phe Asp Arg
65 70 75 80
ccg gat gtt tgg tct tac tat cgt gat aac agc gaa gaa gct ttt gct 288
Pro Asp Val Trp Ser Tyr Tyr Arg Asp Asn Ser Glu Glu Ala Phe Ala
85 90 95
gaa ggg ctc agt cag tat atc atg cac cgt ctc ttt gga aca cca tac 336
Glu Gly Leu Ser Gln Tyr Ile Met His Arg Leu Phe Gly Thr Pro Tyr
100 105 110
tcg aca tat att gcc aat cct tat act gga gat gcc tac aat cca ggt 384
Ser Thr Tyr Ile Ala Asn Pro Tyr Thr Gly Asp Ala Tyr Asn Pro Gly
115 120 125
gat ggt tca ggt tat agc cca ttt gcg gaa aca gaa ttt tat ttt gcc 432
Asp Gly Ser Gly Tyr Ser Pro Phe Ala Glu Thr Glu Phe Tyr Phe Ala
130 135 140
agc tta tac aac cgt tta ttt gaa tac ccg aga aca gct caa gtt gtt 480
Ser Leu Tyr Asn Arg Leu Phe Glu Tyr Pro Arg Thr Ala Gln Val Val
145 150 155 160
cca tat ctt gtc act act acg aca aca gct cca gta aat ggt caa gtt 528
Pro Tyr Leu Val Thr Thr Thr Thr Ala Pro Val Asn Gly Gln Val
165 170 175
att tac gga gca atg cca gag gaa aca act aca aca aca cct tac aca 576
Ile Tyr Gly Ala Met Pro Glu Glu Thr Thr Thr Thr Pro Tyr Thr
180 185 190

PCT_Sequence_listing (3)

aca gtt tat gtg gga gat acc agt ttc gcc tat gac cct act gga cag Thr Val Tyr Val Gly Asp Thr Ser Phe Ala Tyr Asp Pro Thr Gly Gln 195 200 205	624
act gac cgt gta caa gca ggt gtc gat ggg aca gaa acc att cgc acg Thr Asp Arg Val Gln Ala Gly Val Asp Gly Thr Glu Thr Ile Arg Thr 210 215 220	672
acc tac tca cta gat agc aat aac cag ttg gta gca act cag acg gtt Thr Tyr Ser Leu Asp Ser Asn Asn Gln Leu Val Ala Thr Gln Thr Val 225 230 235 240	720
att tca tct act cct gtt caa aat caa att att aca aaa ggc act caa Ile Ser Ser Thr Pro Val Gln Asn Gln Ile Ile Thr Lys Gly Thr Gln 245 250 255	768
cct acc gtt gtt gac act agt gtt cca atg act att gtt tat caa gaa Pro Thr Val Val Asp Thr Ser Val Pro Met Thr Ile Val Tyr Gln Glu 260 265 270	816
gtc aca gat ggt tca ttg ggt gac tgg caa gtt aac gtt ttg gat gca Val Thr Asp Gly Ser Leu Gly Asp Trp Gln Val Asn Val Leu Asp Ala 275 280 285	864
ggt caa gat ggc tta atc cgt agc aca aca acc tat agt gtt gat cct Gly Gln Asp Gly Leu Ile Arg Ser Thr Thr Thr Tyr Ser Val Asp Pro 290 295 300	912
gtg aca ggt att gtg aca cca agt aca aca gaa gct act atc aca gca Val Thr Gly Ile Val Thr Pro Ser Thr Thr Glu Ala Thr Ile Thr Ala 305 310 315 320	960
atg aga cca atg att gtt caa tac caa gtt ggt tcc gaa aaa gtg aca Met Arg Pro Met Ile Val Gln Tyr Gln Val Gly Ser Glu Lys Val Thr 325 330 335	1008
gct att cct tac caa acc cgt tat gtt ata gat act agt tta gca act Ala Ile Pro Tyr Gln Thr Arg Tyr Val Ile Asp Thr Ser Leu Ala Thr 340 345 350	1056
gga aca caa gtt att gta caa gaa ggt gtc aac ggt agc tca acc gag Gly Thr Gln Val Ile Val Gln Glu Gly Val Asn Gly Ser Thr Thr Glu 355 360 365	1104
agt gtt cag tct tat aac ttt atc caa gat ggc tca aat agt cga ttt Ser Val Gln Ser Tyr Asn Phe Ile Gln Asp Gly Ser Asn Ser Arg Phe 370 375 380	1152
gac gct att gtc tat gct agt cca gtt gtt gta gct gcc caa gac cag Asp Ala Ile Val Tyr Ala Ser Pro Val Val Val Ala Ala Gln Asp Gln 385 390 395 400	1200
gtg ata gca gta gga ggt caa gac caa gta act gac caa gct gtc gca Val Ile Ala Val Gly Gly Gln Asp Gln Val Thr Asp Gln Ala Val Ala 405 410 415	1248
aaa acg att ttc tat caa gaa gtt act gat ggt tca ttg ggc gac tgg Lys Thr Ile Phe Tyr Gln Glu Val Thr Asp Gly Ser Leu Gly Asp Trp 420 425 430	1296
cag gtt aaa gtc tta gat gca ggt caa gat ggt ttg gtt cgt aca acg Gln Val Lys Val Leu Asp Ala Gly Gln Asp Gly Leu Val Arg Thr Thr 435 440 445	1344
aca agc tat agc gtt gac cct gtg aca ggt att gtg aca cca agt aca Thr Ser Tyr Ser Val Asp Pro Val Thr Gly Ile Val Thr Pro Ser Thr 450 455 460	1392
aca gaa gca act atc acc gcg atg aaa cca atg att gtt caa tat caa Thr Glu Ala Thr Ile Thr Ala Met Lys Pro Met Ile Val Gln Tyr Gln 465 470 475 480	1440
gtt ggt aaa tct aaa ctt agt gcc att cct ttc ttg aca gag tat ata Val Gly Lys Ser Lys Leu Ser Ala Ile Pro Phe Leu Thr Glu Tyr Ile 485 490 495	1488

PCT_Sequence_listing (3)

PCF_Sequence_Listing (3)																
485				490				495								
act	gat	gat	agc	tta	gct	ggt	ggc	tta	gaa	aaa	gtc	att	caa	gaa	ggc	1536
Thr	Asp	Asp	Ser	Leu	Ala	Val	Gly	Leu	Glu	Lys	Val	Ile	Gln	Glu	Gly	
500				505				510								
gtc	gga	ggg	act	caa	atc	gag	aca	ggt	caa	tcc	ttt	aat	ttt	att	caa	1584
Val	Gly	Gly	Thr	Gln	Ile	Glu	Thr	Val	Gln	Ser	Phe	Asn	Phe	Ile	Gln	
515				520				525								
gat	ggt	gca	aat	tct	cat	ttt	gaa	aac	att	gtc	tac	agt	tcc	cca	act	1632
Asp	Gly	Ala	Asn	Ser	His	Phe	Glu	Asn	Ile	Val	Tyr	Ser	Ser	Pro	Thr	
530				535				540								
att	ggt	ggt	gct	gct	ggt	gat	caa	gtc	ata	gcg	cgt	gga	acg	aaa	gta	1680
Ile	Val	Val	Ala	Ala	Val	Asp	Gln	Val	Ile	Ala	Arg	Gly	Thr	Lys	Val	
545				550				555				560				
ggt	gaa	ggt	gta	ggt	gca	gta	cca	gaa	ggt	gta	aca	ccg	aaa	cca	gaa	1728
Val	Glu	Val	Val	Val	Ala	Val	Pro	Glu	Val	Val	Thr	Pro	Lys	Pro	Glu	
565				570				575				580				
aca	tcg	gaa	gtg	ata	agt	cct	gaa	aaa	ggc	caa	aca	gct	cct	act	att	1776
Thr	Ser	Glu	Val	Ile	Ser	Pro	Glu	Lys	Gly	Gln	Thr	Ala	Pro	Thr	Ile	
580				585				590								
aca	ggt	gaa	gct	att	aaa	gcc	ccg	gct	cag	aaa	aag	gct	aaa	ggt	gaa	1824
Thr	Val	Glu	Ala	Ile	Lys	Ala	Pro	Ala	Gln	Lys	Lys	Ala	Lys	Val	Glu	
595				600				605				610				
ggt	ggt	aca	act	cca	aaa	gaa	agt	ttg	cca	aca	act	ggt	gat	gat	caa	1872
Val	Val	Thr	Thr	Pro	Lys	Glu	Ser	Leu	Pro	Thr	Thr	Gly	Asp	Asp	Gln	
610				615				620								
aat	cta	ctc	gtg	act	ctc	atg	tca	agt	ctc	tta	tta	atg	agt	cta	ggt	1920
Asn	Leu	Leu	Val	Thr	Leu	Met	Ser	Ser	Leu	Leu	Leu	Met	Ser	Leu	Gly	
625				630				635				640				
tta	gga	ctt	aag	aaa	aaa	gaa	gac	gaa								1947
Leu	Gly	Leu	Lys	Lys	Lys	Glu	Asp	Glu								
645																

<210> 142
<211> 649
<212> PRT
<213> Streptococcus uberis

<400> 142															
Met	Gly	Glu	Thr	Thr	Leu	Gly	Leu	Ala	Asn	Ser	Ala	Asp	Gln	Thr	Ile
1				5					10				15		
Ala	Leu	Lys	Tyr	Glu	Ala	Asn	Asn	Leu	Asn	Leu	Val	Ser	Thr	Val	Leu
			20					25					30		
His	Glu	Met	Thr	His	Ile	Ile	Asp	Phe	Lys	Ser	Gly	Leu	Tyr	Ser	Glu
		35					40					45			
Thr	Thr	Asp	Arg	Asn	Thr	Asp	Gly	Ser	Leu	Ser	Thr	Val	Met	Ala	Phe
	50					55					60				
Ser	Asp	Thr	Gln	Glu	Phe	Leu	Asp	Val	Tyr	His	Thr	Tyr	Phe	Asp	Arg
65					70					75				80	
Pro	Asp	Val	Trp	Ser	Tyr	Tyr	Arg	Asp	Asn	Ser	Glu	Glu	Ala	Phe	Ala
				85					90					95	
Glu	Gly	Leu	Ser	Gln	Tyr	Ile	Met	His	Arg	Leu	Phe	Gly	Thr	Pro	Tyr

PCT_Sequence_listing (3)

Val Ile Ala Val Gly Gly Gln Asp Gln Val Thr Asp Gln Ala Val Ala
405 410 415

Lys Thr Ile Phe Tyr Gln Glu Val Thr Asp Gly Ser Leu Gly Asp Trp
420 425 430

Gln Val Lys Val Leu Asp Ala Gly Gln Asp Gly Leu Val Arg Thr Thr
435 440 445

Thr Ser Tyr Ser Val Asp Pro Val Thr Gly Ile Val Thr Pro Ser Thr
450 455 460

Thr Glu Ala Thr Ile Thr Ala Met Lys Pro Met Ile Val Gln Tyr Gln
465 470 475 480

Val Gly Lys Ser Lys Leu Ser Ala Ile Pro Phe Leu Thr Glu Tyr Ile
485 490 495

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

Val Gly Gly Thr Gln Ile Glu Thr Val Gln Ser Phe Asn Phe Ile Gln
515 520 525

Asp Gly Ala Asn Ser His Phe Glu Asn Ile Val Tyr Ser Ser Pro Thr
530 535 540

Ile Val Val Ala Ala Val Asp Gln Val Ile Ala Arg Gly Thr Lys Val
545 550 555 560

Val Glu Val Val Val Ala Val Pro Glu Val Val Thr Pro Lys Pro Glu
565 570 575

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

Thr Val Glu Ala Ile Lys Ala Pro Ala Gln Lys Lys Ala Lys Val Glu
595 600 605

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

Asn Leu Leu Val Thr Leu Met Ser Ser Leu Leu Leu Met Ser Leu Gly
625 630 635 640

Leu Gly Leu Lys Lys Lys Glu Asp Glu
645

<210> 143
<211> 3432
<212> DNA
<213> Streptococcus uberis

<220>
<221> CDS
<222> (1)..(3432)
<400> 143

PCT_Sequence_listing (3)																
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Met	Val	Lys	Asn	Asn	Ile	His	Ser	Arg	Lys	Lys	His	Ile	Leu	Lys	Ile	48
1				5					10					15		
tca	tta	tta	gca	aca	agt	gta	tta	acg	aca	aca	ggt	tca	aca	gtc	tca	96
Ser	Leu	Leu	Ala	Thr	Ser	Val	Leu	Thr	Thr	Thr	Val	Ser	Thr	Val	Ser	
			20					25					30			
gca	gag	caa	ttg	caa	aat	gaa	aag	cag	tcg	gat	ttg	ctt	agt	aag	atg	144
Ala	Glu	Gln	Leu	Gln	Asn	Glu	Lys	Gln	Ser	Asp	Leu	Leu	Ser	Lys	Met	
		35					40					45				
aca	gaa	aca	tct	acg	cct	cat	act	atc	ata	agt	tca	gaa	gac	ctc	tca	192
Thr	Glu	Thr	Ser	Thr	Pro	His	Thr	Ile	Ile	Ser	Ser	Glu	Asp	Leu	Ser	
	50					55					60					
aac	tca	aat	caa	gag	gcc	aat	caa	aag	gat	gag	act	gcc	tca	aaa	agc	240
Asn	Ser	Asn	Gln	Glu	Ala	Asn	Gln	Lys	Asp	Glu	Thr	Ala	Ser	Lys	Ser	
65				70					75						80	
tta	caa	cct	atg	att	gaa	aaa	gtc	gat	cca	tct	cat	atc	cag	gct	ctt	288
Leu	Gln	Pro	Met	Ile	Glu	Lys	Val	Asp	Pro	Ser	His	Ile	Gln	Ala	Leu	
				85					90					95		
tgg	gaa	aaa	gtt	ggc	aca	ggg	gaa	gga	gat	gtc	tta	gct	gtc	ata	gat	336
Trp	Glu	Lys	Val	Gly	Thr	Gly	Glu	Gly	Asp	Val	Leu	Ala	Val	Ile	Asp	
			100					105					110			
tca	gga	att	gaa	acc	aaa	cat	tcc	atg	cta	cag	ctt	cca	gag	gat	gct	384
Ser	Gly	Ile	Glu	Thr	Lys	His	Ser	Met	Leu	Gln	Leu	Pro	Glu	Asp	Ala	
		115					120					125				
gac	aaa	atg	tac	aca	gat	caa	gcc	agc	att	gac	agt	aag	aaa	caa	tta	432
Asp	Lys	Met	Tyr	Thr	Asp	Gln	Ala	Ser	Ile	Asp	Ser	Lys	Lys	Gln	Leu	
	130					135					140					
tta	ggt	att	gaa	cga	gga	cag	tgg	ata	aat	gat	aag	ctc	cca	ttt	tac	480
Leu	Gly	Ile	Glu	Arg	Gly	Gln	Trp	Ile	Asn	Asp	Lys	Leu	Pro	Phe	Tyr	
145				150					155						160	
cat	gat	tac	aca	caa	ggg	gaa	gag	tct	att	gac	aga	aat	acc	tac	cat	528
His	Asp	Tyr	Thr	Gln	Gly	Glu	Glu	Ser	Ile	Asp	Arg	Asn	Thr	Tyr	His	
				165					170					175		
gga	acc	cac	gtc	gca	ggg	att	gca	act	gct	tca	ggc	cta	aca	cag	aaa	576
Gly	Thr	His	Val	Ala	Gly	Ile	Ala	Thr	Ala	Ser	Gly	Leu	Thr	Gln	Lys	
			180					185					190			
gaa	aat	aag	gag	caa	atg	caa	ggc	att	gtt	ccc	aat	gct	caa	tta	tta	624
Glu	Asn	Lys	Glu	Gln	Met	Gln	Gly	Ile	Val	Pro	Asn	Ala	Gln	Leu	Leu	
		195					200					205				
ttt	tta	aaa	gta	ggg	caa	cca	agt	gta	gaa	ggt	gaa	aga	gaa	aag	cat	672
Phe	Leu	Lys	Val	Gly	Gln	Pro	Ser	Val	Glu	Gly	Glu	Arg	Glu	Lys	His	
210						215					220					
tat	gcc	atg	gct	att	aaa	gat	gct	att	gct	tta	gga	gca	aca	gct	att	720
Tyr	Ala	Met	Ala	Ile	Lys	Asp	Ala	Ile	Ala	Leu	Gly	Ala	Thr	Ala	Ile	
225				230						235					240	
aat	atg	agt	ttt	gga	caa	gtt	gga	aaa	gct	agc	cat	gaa	ctt	aat	gat	768
Asn	Met	Ser	Phe	Gly	Gln	Val	Gly	Lys	Ala	Ser	His	Glu	Leu	Asn	Asp	
				245					250					255		
gat	ttc	aaa	aaa	gcc	tta	gca	tta	gca	gca	gat	aaa	ggc	gtc	gct	att	816
Asp	Phe	Lys	Lys	Ala	Leu	Ala	Leu	Ala	Ala	Asp	Lys	Gly	Val	Ala	Ile	
			260				265						270			
gtt	gtt	gct	gca	gga	aat	gat	tat	gcc	atg	ggc	ggc	agc	cag	acg	aaa	864
Val	Val	Ala	Ala	Gly	Asn	Asp	Tyr	Ala	Met	Gly	Gly	Ser	Gln	Thr	Lys	
		275					280					285				
cct	ctt	gcg	aaa	aat	cct	gat	aca	ggt	gtc	att	gga	act	cca	gca	act	912
Pro	Leu	Ala	Lys	Asn	Pro	Asp	Thr	Gly	Val	Ile	Gly	Thr	Pro	Ala	Thr	
	290					295					300					

PCT_Sequence_listing (3)

acg Thr 305	gag Glu	gag Glu	gtt Val	ttt Phe	aca Thr 310	gta Val	gca Ala	gca Ala	tat Tyr	gtt Val 315	gca Ala	ccg Pro	cac His	tat Tyr	tgg Trp 320	960
agc Ser	aga Arg	gta Val	cta Leu	tcg Ser 325	gtt Val	act Thr	gac Asp	ggg Gly	agc Ser 330	aca Thr	tca Ser	aaa Lys	gcc Ala	ttg Leu 335	gcg Ala	1008
ctt Leu	gaa Glu	atg Met	gct Ala 340	agt Ser	cca Pro	ttt Phe	gca Ala	gaa Glu 345	aat Asn	aag Lys	gac Asp	tat Tyr	gag Glu 350	ctc Leu	att Ile	1056
ttc Phe	tta Leu	gaa Glu 355	aag Lys	gga Gly	tta Leu	gaa Glu	acg Thr 360	gaa Glu	gag Glu	aat Asn	gca Ala	gaa Glu 365	aga Arg	ctg Leu	aaa Lys	1104
aat Asn 370	aag Lys	gtt Val	tta Leu	gtc Val	ttg Leu	aat Asn 375	tat Tyr	gac Asp	ttt Phe	gtt Val	acc Thr 380	aat Asn	tcc Ser	aaa Lys	gaa Glu	1152
gtt Val 385	gct Ala	gaa Glu	aaa Lys	gtt Val	gag Glu 390	gct Ala	ttg Leu	gga Gly	gca Ala	gct Ala 395	ggg Gly	gta Val	ctt Leu	gtc Val	cac His 400	1200
aat Asn	aat Asn	caa Gln	gct Ala	aaa Lys 405	aaa Lys	ccg Pro	ctc Leu	att Ile	cct Pro 410	tta Leu	gct Ala	tat Tyr	aat Asn	ggg Gly 415	cct Pro	1248
tta Leu	cct Pro	atg Met	ggc Gly 420	ttt Phe	atc Ile	agt Ser	aaa Lys	gag Glu 425	gat Asp	gca Ala	gat Asp	tgg Trp	tta Leu 430	aaa Lys	acg Thr	1296
atg Met	aca Thr	agt Ser	cca Pro	cag Gln	ttt Phe	aga Arg	tta Leu 440	aaa Lys	aaa Lys	gag Glu	aag Lys	caa Gln 445	tta Leu	gtt Val	gag Glu	1344
gtg Val 450	cct Pro	ggg Gly	ggc Gly	aga Arg	caa Gln	atg Met 455	aca Thr	aac Asn	ttt Phe	tca Ser	agc Ser 460	tgg Trp	ggc Gly	tta Leu	tca Ser	1392
gtt Val 465	gat Asp	ggc Gly	aat Asn	atg Met	aaa Lys 470	cct Pro	gat Asp	ttt Phe	gct Ala	gca Ala 475	cct Pro	ggc Gly	tat Tyr	gaa Glu	att Ile 480	1440
tat Tyr	tca Ser	cct Pro	act Thr	cca Pro 485	gga Gly	aac Asn	gac Asp	tac Tyr	tca Ser 490	aag Lys	atg Met	tca Ser	gga Gly 495	act Thr	agt Ser	1488
gct Ala	gca Ala	agt Ser	cca Pro 500	cat His	gct Ala	atg Met	gga Gly	att Ile 505	att Ile	cat His	tta Leu	gtc Val	cgt Arg 510	aaa Lys	cac His	1536
att Ile	cag Gln	aaa Lys 515	gaa Glu	tac Tyr	cct Pro	cac His	tta Leu 520	agt Ser	gct Ala	aag Lys	gaa Glu	cag Gln 525	tta Leu	cag Gln	tta Leu	1584
gtt Val 530	aag Lys	aac Asn	tta Leu	tta Leu	atg Met	tct Ser 535	act Thr	gcc Ala	agt Ser	cca Pro	att Ile 540	tat Tyr	tca Ser	gag Glu	tta Leu	1632
gat Asp 545	cac His	agt Ser	tac Tyr	tat Tyr	tct Ser 550	cct Pro	agg Arg	gtt Val	caa Gln	gga Gly 555	gca Ala	ggg Gly	gca Ala	ctg Leu	gat Asp 560	1680
gcc Ala	aaa Lys	aag Lys	gcc Ala	ctt Leu 565	gaa Glu	aca Thr	gat Asp	gtt Val	tat Tyr 570	gta Val	aca Thr	gct Ala	gcg Ala	gat Asp 575	ggg Gly	1728
ctt Leu	tca Ser	aaa Lys	att Ile 580	caa Gln	tta Leu	ggg Gly	gat Asp	gtc Val 585	aat Asn	aat Asn	cag Gln	ttc Phe	gaa Glu 590	tta Leu	aga Arg	1776
gta Val	acc Thr	tta Leu	cat His	aat Asn	tta Leu	agc Ser	aat Asn	cag Gln	gaa Glu	aaa Lys	aac Asn	ttt Phe	act Thr	tac Tyr	ttt Phe	1824

PCT_Sequence_listing (3)																
595				600				605								
gca Ala	agg Arg 610	gtg Val	ctt Leu	act Thr	gac Asp	aaa Lys 615	gtt Val	gaa Glu	aag Lys	ggg Gly	cgt Arg 620	att Ile	ctc Leu	ttg Leu	cgt Arg	1872
cca Pro 625	caa Gln	gag Glu	cta Leu	tat Tyr	caa Gln 630	acg Thr	aga Arg	ccc Pro	ctc Leu	caa Gln 635	gta Val	aaa Lys	cta Leu	gct Ala	ccg Pro 640	1920
aat Asn	caa Gln	aag Lys	caa Gln	gaa Glu 645	gtg Val	gtt Val	atc Ile	aag Lys	gtt Val 650	gat Asp	att Ile	tct Ser	aac Asn	ttt Phe 655	gat Asp	1968
caa Gln	cag Gln	ctt Leu	aaa Lys 660	gct Ala	caa Gln	atg Met	cct Pro	aac Asn 665	ggg Gly	tat Tyr	ttt Phe	cta Leu	gat Asp 670	ggg Gly	ttt Phe	2016
gta Val	gta Val	ttt Phe 675	cag Gln	tct Ser	aag Lys	gaa Glu	ggg Gly 680	gct Ala	caa Gln	aaa Lys	gac Asp	tta Leu 685	tct Ser	att Ile	ccc Pro	2064
ttt Phe	atc Ile 690	gct Ala	ttc Phe	aaa Lys	gga Gly	aaa Lys 695	ttt Phe	gca Ala	gat Asp	tta Leu	gag Glu 700	gct Ala	ctt Leu	gat Asp	agt Ser	2112
cca Pro 705	att Ile	tat Tyr	cga Arg	aat Asn	tta Leu 710	gat Asp	ggg Gly	acg Thr	ttt Phe	tac Tyr 715	tac Tyr	agc Ser	ccc Pro	aaa Lys	gaa Glu 720	2160
ggc Gly	caa Gln	gac Asp	cct Pro	tat Tyr 725	gac Asp	ttt Phe	gaa Glu	gtg Val	gat Asp 730	agt Ser	atc Ile	caa Gln	caa Gln	att Ile 735	aaa Lys	2208
gaa Glu	caa Gln	tat Tyr	atg Met 740	act Thr	ggg Gly	ctt Leu	ata Ile	aca Thr 745	aca Thr	ttt Phe	acg Thr	cct Pro	tgg Trp 750	tca Ser	ctg Leu	2256
gtt Val	gaa Glu	gga Gly 755	agt Ser	aaa Lys	ata Ile	gat Asp	ggc Gly 760	ttt Phe	tca Ser	cca Pro	gag Glu	atg Met 765	gct Ala	tct Ser	gaa Glu	2304
ttt Phe	agc Ser 770	acg Thr	act Thr	gat Asp	tac Tyr	ctc Leu 775	ggg Gly	tcc Ser	tat Tyr	aat Asn	aaa Lys 780	gaa Glu	gga Gly	gat Asp	aat Asn	2352
aca Thr 785	gtt Val	cgt Arg	cga Arg	ttc Phe	cga Arg 790	ttt Phe	gtc Val	gaa Glu	ggc Gly	aaa Lys 795	cct Pro	tat Tyr	cta Leu	gca Ala	ctt Leu 800	2400
tca Ser	cct Pro	aat Asn	ggc Gly	gat Asp 805	gat Asp	aat Asn	atg Met	gat Asp	aaa Lys 810	gtg Val	gga Gly	ttt Phe	aga Arg	ggg Gly 815	gtt Val	2448
ttc Phe	tta Leu	aga Arg	aat Asn 820	gtc Val	aga Arg	gac Asp	atc Ile	aaa Lys 825	gca Ala	cag Gln	gta Val	ttt Phe	gca Ala 830	agt Ser	gat Asp	2496
gat Asp	ttg Leu	caa Gln 835	cat His	ccg Pro	att Ile	tgg Trp	gag Glu 840	agt Ser	cct Pro	ata Ile	aaa Lys	gct Ala 845	ttt Phe	gct Ala	aaa Lys	2544
aaa Lys	gat Asp 850	gtg Val	aat Asn	aca Thr	aat Asn	gat Asp 855	atc Ile	aaa Lys	gaa Glu	agc Ser	atg Met 860	ctt Leu	gaa Glu	aat Asn	acc Thr	2592
gtt Val 865	tgg Trp	gaa Glu	ggg Gly	aaa Lys	gat Asp 870	gct Ala	tct Ser	gga Gly	aat Asn	ccg Pro 875	gtt Val	aca Thr	gag Glu	gga Gly	tta Leu 880	2640
tat Tyr	cga Arg	tat Tyr	cgt Arg	gta Val 885	act Thr	tat Tyr	acg Thr	cca Pro	ctt Leu 890	gct Ala	gaa Glu	ggg Gly	gcc Ala	aaa Lys 895	gaa Glu	2688
cag	ttt	att	gat	ttt	gat	att	cta	gtt	gat	tta	acc	ccg	tca	aaa	ctg	2736

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PCT_Sequence_listing (3)

Gln	Phe	Ile	Asp	Phe	Asp	Ile	Leu	Val	Asp	Leu	Thr	Pro	Ser	Lys	Leu		
			900					905					910				
cca	caa	agt	gca	atc	ttg	atg	cta	gcc	gaa	aga	cgg	att	gag	cta	aca	2784	
Pro	Gln	Ser	Ala	Ile	Leu	Met	Leu	Ala	Glu	Arg	Arg	Ile	Glu	Leu	Thr		
		915					920					925					
gaa	tca	aga	gac	tat	tta	tct	cat	gat	act	tat	cgt	gat	cga	ctt	tac	2832	
Glu	Ser	Arg	Asp	Tyr	Leu	Ser	His	Asp	Thr	Tyr	Arg	Asp	Arg	Leu	Tyr		
	930					935					940						
tat	aaa	tat	gga	aca	gat	gat	att	aat	ttc	acc	act	ttt	gaa	aaa	gat	2880	
Tyr	Lys	Tyr	Gly	Thr	Asp	Asp	Ile	Asn	Phe	Thr	Thr	Phe	Glu	Lys	Asp		
	945				950					955					960		
gat	atg	gga	cat	ttt	gtg	atc	cca	aac	caa	ggt	gaa	gat	gaa	ctc	agt	2928	
Asp	Met	Gly	His	Phe	Val	Ile	Pro	Asn	Gln	Val	Glu	Asp	Glu	Leu	Ser		
				965					970					975			
gga	gag	aag	att	act	atc	aat	ctt	gat	aaa	act	gat	cat	ttc	ttc	ttt	2976	
Gly	Glu	Lys	Ile	Thr	Ile	Asn	Leu	Asp	Lys	Thr	Asp	His	Phe	Phe	Phe		
			980					985					990				
gtc	aga	gaa	gat	ttc	tca	ggt	aat	ttt	agt	ggt	att	agc	ctg	tca	caa	3024	
Val	Arg	Glu	Asp	Phe	Ser	Gly	Asn	Phe	Ser	Val	Ile	Ser	Leu	Ser	Gln		
		995					1000					1005					
tta	ttg	aac	aat	cat	tca	gat	caa	atg	cat	tca	ctt	gaa	gag	agt		3069	
Leu	Leu	Asn	Asn	His	Ser	Asp	Gln	Met	His	Ser	Leu	Glu	Glu	Ser			
	1010					1015					1020						
aag	agt	gat	aga	aaa	gaa	tct	aat	aca	ggt	gat	att	aga	cac	gaa		3114	
Lys	Ser	Asp	Arg	Lys	Glu	Ser	Asn	Thr	Gly	Asp	Ile	Arg	His	Glu			
	1025					1030					1035						
aag	caa	gaa	aat	ctt	agt	caa	caa	act	cta	cta	tcg	aca	cca	tca		3159	
Lys	Gln	Glu	Asn	Leu	Ser	Gln	Gln	Thr	Leu	Leu	Ser	Thr	Pro	Ser			
	1040					1045					1050						
att	gat	ggc	caa	aaa	caa	aat	gac	caa	tta	atg	ggt	gaa	aaa	gag		3204	
Ile	Asp	Gly	Gln	Lys	Gln	Asn	Asp	Gln	Leu	Met	Val	Glu	Lys	Glu			
	1055					1060					1065						
aaa	gac	att	atg	gat	gaa	agt	aag	tct	gaa	aga	agt	gag	aaa	aat		3249	
Lys	Asp	Ile	Met	Asp	Glu	Ser	Lys	Ser	Glu	Arg	Ser	Glu	Lys	Asn			
	1070					1075					1080						
aag	ttt	cca	aaa	ggt	ccc	gct	tca	atc	acg	ctt	aag	gat	gga	act		3294	
Lys	Phe	Pro	Lys	Val	Pro	Ala	Ser	Ile	Thr	Leu	Lys	Asp	Gly	Thr			
	1085					1090					1095						
ctt	tat	ccg	cag	tca	ata	agc	caa	aaa	aca	agt	ctt	cct	aaa	aca		3339	
Leu	Tyr	Pro	Gln	Ser	Ile	Ser	Gln	Lys	Thr	Ser	Leu	Pro	Lys	Thr			
	1100					1105					1110						
ggt	gat	tca	caa	aag	aca	atg	aca	ttt	tta	ggg	att	gcc	atg	tta		3384	
Val	Asp	Ser	Gln	Lys	Thr	Met	Thr	Phe	Leu	Gly	Ile	Ala	Met	Leu			
	1115					1120					1125						
ttt	ggt	ggc	ata	tta	caa	gtc	cta	tgg	tca	tac	ttt	aaa	aag	aga		3429	
Phe	Gly	Gly	Ile	Leu	Gln	Val	Leu	Trp	Ser	Tyr	Phe	Lys	Lys	Arg			
	1130					1135					1140						
gat																3432	
Asp																	

<210> 144
 <211> 1144
 <212> PRT
 <213> Streptococcus uberis
 <400> 144

PCT_Sequence_listing (3)

Met Val Lys Asn Asn Ile His Ser Arg Lys Lys His Ile Leu Lys Ile
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Ser Leu Leu Ala Thr Ser Val Leu Thr Thr Thr Val Ser Thr Val Ser
20 25 30

Ala Glu Gln Leu Gln Asn Glu Lys Gln Ser Asp Leu Leu Ser Lys Met
35 40 45

Thr Glu Thr Ser Thr Pro His Thr Ile Ile Ser Ser Glu Asp Leu Ser
50 55 60

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

Leu Gln Pro Met Ile Glu Lys Val Asp Pro Ser His Ile Gln Ala Leu
85 90 95

Trp Glu Lys Val Gly Thr Gly Glu Gly Asp Val Leu Ala Val Ile Asp
100 105 110

Ser Gly Ile Glu Thr Lys His Ser Met Leu Gln Leu Pro Glu Asp Ala
115 120 125

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

Leu Gly Ile Glu Arg Gly Gln Trp Ile Asn Asp Lys Leu Pro Phe Tyr
145 150 155 160

His Asp Tyr Thr Gln Gly Glu Glu Ser Ile Asp Arg Asn Thr Tyr His
165 170 175

Gly Thr His Val Ala Gly Ile Ala Thr Ala Ser Gly Leu Thr Gln Lys
180 185 190

Glu Asn Lys Glu Gln Met Gln Gly Ile Val Pro Asn Ala Gln Leu Leu
195 200 205

Phe Leu Lys Val Gly Gln Pro Ser Val Glu Gly Glu Arg Glu Lys His
210 215 220

Tyr Ala Met Ala Ile Lys Asp Ala Ile Ala Leu Gly Ala Thr Ala Ile
225 230 235 240

Asn Met Ser Phe Gly Gln Val Gly Lys Ala Ser His Glu Leu Asn Asp
245 250 255

Asp Phe Lys Lys Ala Leu Ala Leu Ala Ala Asp Lys Gly Val Ala Ile
260 265 270

Val Val Ala Ala Gly Asn Asp Tyr Ala Met Gly Gly Ser Gln Thr Lys
275 280 285

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

PCT_Sequence_listing (3)

Thr Glu Glu Val Phe Thr Val Ala Ala Tyr Val Ala Pro His Tyr Trp
305 310 315 320

Ser Arg Val Leu Ser Val Thr Asp Gly Ser Thr Ser Lys Ala Leu Ala
325 330 335

Leu Glu Met Ala Ser Pro Phe Ala Glu Asn Lys Asp Tyr Glu Leu Ile
340 345 350

Phe Leu Glu Lys Gly Leu Glu Thr Glu Glu Asn Ala Glu Arg Leu Lys
355 360 365

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

Val Ala Glu Lys Val Glu Ala Leu Gly Ala Ala Gly Val Leu Val His
385 390 395 400

Asn Asn Gln Ala Lys Lys Pro Leu Ile Pro Leu Ala Tyr Asn Gly Pro
405 410 415

Leu Pro Met Gly Phe Ile Ser Lys Glu Asp Ala Asp Trp Leu Lys Thr
420 425 430

Met Thr Ser Pro Gln Phe Arg Leu Lys Lys Glu Lys Gln Leu Val Glu
435 440 445

Val Pro Gly Gly Arg Gln Met Thr Asn Phe Ser Ser Trp Gly Leu Ser
450 455 460

Val Asp Gly Asn Met Lys Pro Asp Phe Ala Ala Pro Gly Tyr Glu Ile
465 470 475 480

Tyr Ser Pro Thr Pro Gly Asn Asp Tyr Ser Lys Met Ser Gly Thr Ser
485 490 495

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

Ile Gln Lys Glu Tyr Pro His Leu Ser Ala Lys Glu Gln Leu Gln Leu
515 520 525

Val Lys Asn Leu Leu Met Ser Thr Ala Ser Pro Ile Tyr Ser Glu Leu
530 535 540

Asp His Ser Tyr Tyr Ser Pro Arg Val Gln Gly Ala Gly Ala Leu Asp
545 550 555 560

Ala Lys Lys Ala Leu Glu Thr Asp Val Tyr Val Thr Ala Ala Asp Gly
565 570 575

Leu Ser Lys Ile Gln Leu Gly Asp Val Asn Asn Gln Phe Glu Leu Arg
580 585 590

Val Thr Leu His Asn Leu Ser Asn Gln Glu Lys Asn Phe Thr Tyr Phe
595 600 605

PCT_Sequence_listing (3)

Ala Arg Val Leu Thr Asp Lys Val Glu Lys Gly Arg Ile Leu Leu Arg
610 615 620

Pro Gln Glu Leu Tyr Gln Thr Arg Pro Leu Gln Val Lys Leu Ala Pro
625 630 635 640

Asn Gln Lys Gln Glu Val Val Ile Lys Val Asp Ile Ser Asn Phe Asp
645 650 655

Gln Gln Leu Lys Ala Gln Met Pro Asn Gly Tyr Phe Leu Asp Gly Phe
660 665 670

Val Val Phe Gln Ser Lys Glu Gly Ala Gln Lys Asp Leu Ser Ile Pro
675 680 685

Phe Ile Ala Phe Lys Gly Lys Phe Ala Asp Leu Glu Ala Leu Asp Ser
690 695 700

Pro Ile Tyr Arg Asn Leu Asp Gly Thr Phe Tyr Tyr Ser Pro Lys Glu
705 710 715 720

Gly Gln Asp Pro Tyr Asp Phe Glu Val Asp Ser Ile Gln Gln Ile Lys
725 730 735

Glu Gln Tyr Met Thr Gly Leu Ile Thr Thr Phe Thr Pro Trp Ser Leu
740 745 750

Val Glu Gly Ser Lys Ile Asp Gly Phe Ser Pro Glu Met Ala Ser Glu
755 760 765

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

Thr Val Arg Arg Phe Arg Phe Val Glu Gly Lys Pro Tyr Leu Ala Leu
785 790 795 800

Ser Pro Asn Gly Asp Asp Asn Met Asp Lys Val Gly Phe Arg Gly Val
805 810 815

Phe Leu Arg Asn Val Arg Asp Ile Lys Ala Gln Val Phe Ala Ser Asp
820 825 830

Asp Leu Gln His Pro Ile Trp Glu Ser Pro Ile Lys Ala Phe Ala Lys
835 840 845

Lys Asp Val Asn Thr Asn Asp Ile Lys Glu Ser Met Leu Glu Asn Thr
850 855 860

Val Trp Glu Gly Lys Asp Ala Ser Gly Asn Pro Val Thr Glu Gly Leu
865 870 875 880

Tyr Arg Tyr Arg Val Thr Tyr Thr Pro Leu Ala Glu Gly Ala Lys Glu
885 890 895

Gln Phe Ile Asp Phe Asp Ile Leu Val Asp Leu Thr Pro Ser Lys Leu

PCT_Sequence_listing (3)
905 910

900

Pro Gln Ser Ala Ile Leu Met Leu Ala Glu Arg Arg Ile Glu Leu Thr
915 920 925

Glu Ser Arg Asp Tyr Leu Ser His Asp Thr Tyr Arg Asp Arg Leu Tyr
930 935 940

Tyr Lys Tyr Gly Thr Asp Asp Ile Asn Phe Thr Thr Phe Glu Lys Asp
945 950 955 960

Asp Met Gly His Phe Val Ile Pro Asn Gln Val Glu Asp Glu Leu Ser
965 970 975

Gly Glu Lys Ile Thr Ile Asn Leu Asp Lys Thr Asp His Phe Phe Phe
980 985 990

Val Arg Glu Asp Phe Ser Gly Asn Phe Ser Val Ile Ser Leu Ser Gln
995 1000 1005

Leu Leu Asn Asn His Ser Asp Gln Met His Ser Leu Glu Glu Ser
1010 1015 1020

Lys Ser Asp Arg Lys Glu Ser Asn Thr Gly Asp Ile Arg His Glu
1025 1030 1035

Lys Gln Glu Asn Leu Ser Gln Gln Thr Leu Leu Ser Thr Pro Ser
1040 1045 1050

Ile Asp Gly Gln Lys Gln Asn Asp Gln Leu Met Val Glu Lys Glu
1055 1060 1065

Lys Asp Ile Met Asp Glu Ser Lys Ser Glu Arg Ser Glu Lys Asn
1070 1075 1080

Lys Phe Pro Lys Val Pro Ala Ser Ile Thr Leu Lys Asp Gly Thr
1085 1090 1095

Leu Tyr Pro Gln Ser Ile Ser Gln Lys Thr Ser Leu Pro Lys Thr
1100 1105 1110

Val Asp Ser Gln Lys Thr Met Thr Phe Leu Gly Ile Ala Met Leu
1115 1120 1125

Phe Gly Gly Ile Leu Gln Val Leu Trp Ser Tyr Phe Lys Lys Arg
1130 1135 1140

Asp

<210> 145
<211> 738
<212> DNA
<213> Streptococcus uberis

<220>
<221> CDS

PCT_Sequence_listing (3)

<222> (1)..(738)

<400> 145

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1 5 10 15	
gca gtc atg atg aca ctt gtc ata atg ttc caa cca caa gca aaa aat	96
Ala Val Met Met Thr Leu Val Ile Met Phe Gln Pro Gln Ala Lys Asn	
20 25 30	
aag agt gta tct gct gaa acc cta gct tca ggg caa aca caa gca ttt	144
Lys Ser Val Ser Ala Glu Thr Leu Ala Ser Gly Gln Thr Gln Ala Phe	
35 40 45	
atc aat caa atc gcg ggt act gca agc caa atc gca gct gaa cga gat	192
Ile Asn Gln Ile Ala Gly Thr Ala Ser Gln Ile Ala Ala Glu Arg Asp	
50 55 60	
tta tat gcg tca gtc atg att gcc caa gcg gtt tta gaa tct agt agt	240
Leu Tyr Ala Ser Val Met Ile Ala Gln Ala Val Leu Glu Ser Ser Ser	
65 70 75 80	
ggc caa tca ggt tta agt cag gcg cca tat tat aat ttt ttt ggg att	288
Gly Gln Ser Gly Leu Ser Gln Ala Pro Tyr Tyr Asn Phe Phe Gly Ile	
85 90 95	
aaa gga agt tat aat ggt ggc tca gtt aca atg aaa act tgg gaa gat	336
Lys Gly Ser Tyr Asn Gly Gly Ser Val Thr Met Lys Thr Trp Glu Asp	
100 105 110	
gat gga ttg gga aat cct tat gaa att gat cag gct ttc cgt gcc tat	384
Asp Gly Leu Gly Asn Pro Tyr Glu Ile Asp Gln Ala Phe Arg Ala Tyr	
115 120 125	
cca agt att tat gat tcc ctt tat gat tat gct aat ttg tta agt tca	432
Pro Ser Ile Tyr Asp Ser Leu Tyr Asp Tyr Ala Asn Leu Leu Ser Ser	
130 135 140	
cca act tat gtc gga gca aga cga tct aat acc tta tct tac caa gat	480
Pro Thr Tyr Val Gly Ala Arg Arg Ser Asn Thr Leu Ser Tyr Gln Asp	
145 150 155 160	
gca aca gct gct tta acg gga tta tat gca aca gat act tcc tat aat	528
Ala Thr Ala Ala Leu Thr Gly Leu Tyr Ala Thr Asp Thr Ser Tyr Asn	
165 170 175	
gtt aaa ttg aat gcc att ata caa aat tat ggc ttg aca gca tat gat	576
Val Lys Leu Asn Ala Ile Ile Gln Asn Tyr Gly Leu Thr Ala Tyr Asp	
180 185 190	
gtt gtt aat cct gca gtt gca act tcc aca aca gat gtc cct agt gat	624
Val Val Asn Pro Ala Val Ala Thr Ser Thr Thr Asp Val Pro Ser Asp	
195 200 205	
agt gtt gca act gtt gat act agc caa tac gtt tgg aac aaa cac aga	672
Ser Val Ala Thr Val Asp Thr Ser Gln Tyr Val Trp Asn Lys His Arg	
210 215 220	
gga agt tac aca gat act agc act tta gca caa gac gat gct tgg tct	720
Gly Ser Tyr Thr Asp Thr Ser Thr Leu Ala Gln Asp Asp Ala Trp Ser	
225 230 235 240	
ctt ttc ata aaa ggc tat	738
Leu Phe Ile Lys Gly Tyr	
245	

<210> 146

<211> 246

<212> PRT

<213> Streptococcus uberis

<400> 146

PCT_Sequence_listing (3)

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

Lys Ser Val Ser Ala Glu Thr Leu Ala Ser Gly Gln Thr Gln Ala Phe
35      40      45

Ile Asn Gln Ile Ala Gly Thr Ala Ser Gln Ile Ala Ala Glu Arg Asp
50      55      60

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

Gly Gln Ser Gly Leu Ser Gln Ala Pro Tyr Tyr Asn Phe Phe Gly Ile
85      90      95

Lys Gly Ser Tyr Asn Gly Gly Ser Val Thr Met Lys Thr Trp Glu Asp
100     105     110

Asp Gly Leu Gly Asn Pro Tyr Glu Ile Asp Gln Ala Phe Arg Ala Tyr
115     120     125

Pro Ser Ile Tyr Asp Ser Leu Tyr Asp Tyr Ala Asn Leu Leu Ser Ser
130     135     140

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

Ala Thr Ala Ala Leu Thr Gly Leu Tyr Ala Thr Asp Thr Ser Tyr Asn
165     170     175

Val Lys Leu Asn Ala Ile Ile Gln Asn Tyr Gly Leu Thr Ala Tyr Asp
180     185     190

Val Val Asn Pro Ala Val Ala Thr Ser Thr Thr Asp Val Pro Ser Asp
195     200     205

Ser Val Ala Thr Val Asp Thr Ser Gln Tyr Val Trp Asn Lys His Arg
210     215     220

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

Leu Phe Ile Lys Gly Tyr
245

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<210> 147
<211> 1635
<212> DNA
<213> Streptococcus uberis

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<220>
<221> CDS
<222> (1)..(1635)

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<400> 147

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PCT_Sequence_listing (3)

atg Met 1	aaa Lys	aag Lys	ata Ile	ttt Phe 5	caa Gln	aga Arg	aaa Lys	tgg Trp 10	ttc Phe	aaa Lys	cga Arg	aca Thr	tcc Ser	att Ile 15	gtt Val	48
tta Leu	ggt Gly	att Ile	ttg Leu 20	ctt Leu	gta Val	gct Ala	ctg Leu	att Ile 25	gcc Ala	tta Leu	ggt Gly	tct Ser	ttt Phe 30	tat Tyr	tat Tyr	96
tca Ser	aag Lys	tca Ser 35	gcc Ala	gtg Val	att Ile	gat Asp	cgt Arg 40	tat Tyr	gtt Val	gtt Val	gct Ala	aaa Lys 45	agt Ser	aaa Lys	aag Lys	144
aat Asn	ggc Gly 50	ggg Gly	tcc Ser	ttt Phe	gaa Glu	aat Asn 55	att Ile	aaa Lys	gct Ala	ttt Phe	tta Leu 60	gtc Val	tgg Trp	gat Asp	gat Asp	192
acc Thr 65	gat Asp	gaa Glu	atc Ile	att Ile	aca Thr 70	aat Asn	gat Asp	caa Gln	gca Ala	gct Ala 75	ttt Phe	gct Ala	tca Ser	ttc Phe	acg Thr 80	240
cca Pro	ctt Leu	cca Pro	aaa Lys	tca Ser 85	gag Glu	att Ile	tcc Ser	tcg Ser	tta Leu 90	aaa Lys	aaa Lys	gag Glu	ctc Leu	aaa Lys 95	agt Ser	288
gca Ala	aca Thr	gcc Ala	tct Ser 100	gat Asp	cca Pro	gta Val	tac Tyr	att Ile 105	aag Lys	tcc Ser	att Ile	ggt Gly	cat His 110	cgt Arg	ttt Phe	336
tgg Trp	att Ile	ttt Phe 115	ccg Pro	gat Asp	tat Tyr	cgg Arg	gta Val 120	gcc Ala	atg Met	aaa Lys	cca Pro	atg Met 125	tca Ser	cta Leu	acc Thr	384
tta Leu 130	aaa Lys	acg Thr	aat Asn	gtc Val	cct Pro	aat Asn 135	atg Met	gat Asp	ctg Leu	ctc Leu	tta Leu 140	aat Asn	cag Gln	aaa Lys	aaa Lys	432
gta Val 145	gca Ala	aca Thr	tct Ser	aat Asn	tcg Ser 150	gaa Glu	aat Asn	ttt Phe	acg Thr	aca Thr 155	gaa Glu	tta Leu	aaa Lys	agg Arg	tta Leu 160	480
cca Pro	att Ile	gct Ala	gac Asp	tac Tyr 165	agt Ser	gca Ala	agt Ser	atc Ile	aat Asn 170	ggg Gly	act Thr	tac Tyr	aaa Lys	gat Asp 175	aaa Lys	528
aaa Lys	atc Ile	aaa Lys	gtt Val 180	act Thr	aaa Lys	aaa Lys	tat Tyr	gat Asp 185	ggg Gly	caa Gln	aaa Lys	cca Pro	gta Val 190	cta Leu	gat Asp	576
tta Leu	tct Ser	gtt Val 195	aca Thr	ttt Phe	aag Lys	aat Asn	ttt Phe 200	aca Thr	gta Val	agc Ser	agt Ser	aat Asn 205	ctt Leu	aca Thr	gaa Glu	624
ggt Gly 210	gag Glu	ctt Leu	tat Tyr	ttt Phe	gac Asp	gag Glu 215	gat Asp	cgc Arg	gtc Val	ggt Gly	act Thr 220	cta Leu	aaa Lys	aat Asn	ggt Gly	672
cag Gln 225	tat Tyr	caa Gln	gtc Val	aca Thr	gac Asp 230	tat Tyr	ccc Pro	att Ile	act Thr	aat Asn 235	ggt Gly	agc Ser	aaa Lys	gct Ala	ttt Phe 240	720
gta Val	aaa Lys	cga Arg	aat Asn	ttc Phe 245	cca Pro	gat Asp	ggt Gly	gag Glu	ctc Leu 250	aag Lys	agt Ser	gaa Glu	aaa Lys	gct Ala 255	gac Asp	768
ctt Leu	gaa Glu	cag Gln	gtt Val 260	gct Ala	gaa Glu	ggt Gly	tct Ser	gaa Glu 265	ctg Leu	aag Lys	tta Leu	acg Thr	gtc Val 270	gat Asp	aat Asn	816
ctc Leu	tta Leu	gat Asp 275	cgc Arg	act Thr	aaa Lys	gct Ala	gga Gly 280	gaa Glu	tat Tyr	ctt Leu	tta Leu	gct Ala 285	gct Ala	ttt Phe	aat Asn	864
caa Gln	ctg Leu 290	atg Met	gca Ala	tat Tyr	aca Thr	agt Ser 295	agc Ser	cga Arg	caa Gln	gat Asp	tca Ser 300	acg Thr	aca Thr	gtt Val	gca Ala	912

PCT_Sequence_listing (3)

gat Asp 305	gtc Val	ttc Phe	gaa Glu	aat Asn	ggc Gly 310	gta Val	aat Asn	aac Asn	gat Asp	ttt Phe 315	tat Tyr	aaa Lys	ggg Gly	tta Leu	aaa Lys 320	960
gaa Glu	agt Ser	gtg Val	aaa Lys	gca Ala 325	aaa Lys	ttg Leu	gaa Glu	aca Thr	gat Asp 330	agt Ser	cgc Arg	aag Lys	gct Ala	tct Ser 335	agt Ser	1008
ttt Phe	gcc Ala	att Ile	cca Pro 340	aat Asn	gtt Val	gcc Ala	cta Leu	aat Asn 345	gcc Ala	atg Met	acg Thr	caa Gln	gtc Val 350	ggc Gly	aag Lys	1056
gag Glu	tct Ser	tac Tyr 355	ctc Leu	tta Leu	gat Asp	ttt Phe	gcg Ala 360	gct Ala	aca Thr	tat Tyr	gat Asp	ttt Phe 365	gcc Ala	tat Tyr	cca Pro	1104
aaa Lys 370	gaa Glu	aca Thr	gac Asp	cct Pro	gaa Glu	aaa Lys 375	ggc Gly	agt Ser	tca Ser	ggg Gly 380	aac Asn	atc Ile	att Ile	caa Gln	gag Glu	1152
tta Leu 385	agt Ser	gga Gly	caa Gln	cta Leu	acg Thr 390	ctc Leu	aaa Lys	aaa Lys	tca Ser	gga Gly 395	gat Asp	cgt Arg	tat Tyr	gtg Val	att Ile 400	1200
agt Ser	caa Gln	gct Ala	ggg Gly	aca Thr 405	aaa Lys	aat Asn	atc Ile	tct Ser	gtg Val 410	acc Thr	agt Ser	gaa Glu	aaa Lys	aat Asn 415	aat Asn	1248
att Ile	aaa Lys	aaa Lys	ccg Pro 420	tca Ser	tta Leu	ctg Leu	cca Pro	gat Asp 425	ggc Gly	ata Ile	gtt Val	gga Gly	act Thr 430	tgg Trp	aag Lys	1296
gga Gly	act Thr	aaa Lys 435	gac Asp	gac Asp	att Ile	acc Thr	tat Tyr 440	acg Thr	ttg Leu	acc Thr	att Ile	tct Ser 445	gag Glu	gat Asp	gga Gly	1344
aca Thr 450	gta Val	aca Thr	cgt Arg	cat His	atc Ile	gat Asp 455	ttc Phe	aaa Lys	gat Asp	ccg Pro	aaa Lys 460	aaa Lys	gct Ala	gat Asp	gaa Glu	1392
agt Ser 465	aga Arg	aca Thr	gca Ala	aaa Lys	atc Ile 470	acg Thr	aag Lys	acc Thr	gaa Glu	gaa Glu 475	aag Lys	aat Asn	cca Pro	gga Gly	gat Asp 480	1440
ttc Phe	cag Gln	gtt Val	att Ile	atc Ile 485	acc Thr	cca Pro	gaa Glu	act Thr	gat Asp 490	agc Ser	tca Ser	att Ile	ctc Leu	atc Ile 495	att Ile	1488
ggg Gly	ggg Gly	ggg Gly	att Ile 500	ggg Gly	ggg Gly	gct Ala	aac Asn	atc Ile 505	aag Lys	tat Tyr	gcc Ala	tat Tyr	ggc Gly 510	ctt Leu	cat His	1536
tta Leu	gat Asp	ggc Gly 515	aat Asn	caa Gln	tta Leu	aca Thr	ccg Pro 520	att Ile	att Ile	tgg Trp	caa Gln	aca Thr 525	ggg Gly	atg Met	gat Asp	1584
aag Lys	gac Asp 530	ttt Phe	gat Asp	ttt Phe	tcg Ser	aaa Lys 535	ccg Pro	gca Ala	cca Pro	ggg Gly	tta Leu 540	cct Pro	tta Leu	acg Thr	aaa Lys	1632
caa Gln 545																1635

<210> 148
<211> 545
<212> PRT
<213> Streptococcus uberis

<400> 148

Met Lys Lys Ile phe Gln Arg Lys Trp Phe Lys Arg Thr Ser Ile Val
1 5 10 15

PCT_Sequence_listing (3)

Leu Gly Ile Leu Leu Val Ala Leu Ile Ala Leu Gly Ser Phe Tyr Tyr
 20 25 30
 Ser Lys Ser Ala Val Ile Asp Arg Tyr Val Val Ala Lys Ser Lys Lys
 35 40 45
 Asn Gly Gly Ser Phe Glu Asn Ile Lys Ala Phe Leu Val Trp Asp Asp
 50 55 60
 Thr Asp Glu Ile Ile Thr Asn Asp Gln Ala Ala Phe Ala Ser Phe Thr
 65 70 75 80
 Pro Leu Pro Lys Ser Glu Ile Ser Ser Leu Lys Lys Glu Leu Lys Ser
 85 90 95
 Ala Thr Ala Ser Asp Pro Val Tyr Ile Lys Ser Ile Gly His Arg Phe
 100 105 110
 Trp Ile Phe Pro Asp Tyr Arg Val Ala Met Lys Pro Met Ser Leu Thr
 115 120 125
 Leu Lys Thr Asn Val Pro Asn Met Asp Leu Leu Leu Asn Gln Lys Lys
 130 135 140
 Val Ala Thr Ser Asn Ser Glu Asn Phe Thr Thr Glu Leu Lys Arg Leu
 145 150 155 160
 Pro Ile Ala Asp Tyr Ser Ala Ser Ile Asn Gly Thr Tyr Lys Asp Lys
 165 170 175
 Lys Ile Lys Val Thr Lys Lys Tyr Asp Gly Gln Lys Pro Val Leu Asp
 180 185 190
 Leu Ser Val Thr Phe Lys Asn Phe Thr Val Ser Ser Asn Leu Thr Glu
 195 200 205
 Gly Glu Leu Tyr Phe Asp Glu Asp Arg Val Gly Thr Leu Lys Asn Gly
 210 215 220
 Gln Tyr Gln Val Thr Asp Tyr Pro Ile Thr Asn Gly Ser Lys Ala Phe
 225 230 235 240
 Val Lys Arg Asn Phe Pro Asp Gly Glu Leu Lys Ser Glu Lys Ala Asp
 245 250 255
 Leu Glu Gln Val Ala Glu Gly Ser Glu Leu Lys Leu Thr Val Asp Asn
 260 265 270
 Leu Leu Asp Arg Thr Lys Ala Gly Glu Tyr Leu Leu Ala Ala Phe Asn
 275 280 285
 Gln Leu Met Ala Tyr Thr Ser Ser Arg Gln Asp Ser Thr Thr Val Ala
 290 295 300
 Asp Val Phe Glu Asn Gly Val Asn Asn Asp Phe Tyr Lys Gly Leu Lys
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PCT_Sequence_listing (3)

305 310 315 320

Glu Ser Val Lys Ala Lys Leu Glu Thr Asp Ser Arg Lys Ala Ser Ser
325 330 335

Phe Ala Ile Pro Asn Val Ala Leu Asn Ala Met Thr Gln Val Gly Lys
340 345 350

Glu Ser Tyr Leu Leu Asp Phe Ala Ala Thr Tyr Asp Phe Ala Tyr Pro
355 360 365

Lys Glu Thr Asp Pro Glu Lys Gly Ser Ser Gly Asn Ile Ile Gln Glu
370 375 380

Leu Ser Gly Gln Leu Thr Leu Lys Lys Ser Gly Asp Arg Tyr Val Ile
385 390 395 400

Ser Gln Ala Gly Thr Lys Asn Ile Ser Val Thr Ser Glu Lys Asn Asn
405 410 415

Ile Lys Lys Pro Ser Leu Leu Pro Asp Gly Ile Val Gly Thr Trp Lys
420 425 430

Gly Thr Lys Asp Asp Ile Thr Tyr Thr Leu Thr Ile Ser Glu Asp Gly
435 440 445

Thr Val Thr Arg His Ile Asp Phe Lys Asp Pro Lys Lys Ala Asp Glu
450 455 460

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

Phe Gln Val Ile Ile Thr Pro Glu Thr Asp Ser Ser Ile Leu Ile Ile
485 490 495

Gly Gly Gly Ile Gly Gly Ala Asn Ile Lys Tyr Ala Tyr Gly Leu His
500 505 510

Leu Asp Gly Asn Gln Leu Thr Pro Ile Ile Trp Gln Thr Gly Met Asp
515 520 525

Lys Asp Phe Asp Phe Ser Lys Pro Ala Pro Gly Leu Pro Leu Thr Lys
530 535 540

Gln
545

<210> 149
<211> 942
<212> DNA
<213> Streptococcus uberis

<220>
<221> CDS
<222> (1)..(942)

<400> 149
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PCT_Sequence_listing (3)

Met 1	Asn	Thr	Ser	Lys 5	Lys	Ile	Val	Thr	Gly 10	Phe	Val	Thr	Leu	Ala 15	Ser		
gtc Val	ctt Leu	acc Thr	ctt Leu 20	gca Ala	gca Ala	tgt Cys	tct Ser	tca Ser 25	aca Thr	agt Ser	gac Asp	aat Asn	aca Thr 30	aaa Lys	gta Val	96	
gtt Val	acc Thr	atg Met 35	aaa Lys	ggt Gly	gat Asp	acc Thr	att Ile 40	aca Thr	gta Val	act Thr	gat Asp	ttt Phe 45	tat Tyr	aat Asn	gaa Glu	144	
gct Ala	aaa Lys 50	acg Thr	tca Ser	aca Thr	gca Ala	gca Ala 55	caa Gln	caa Gln	tcc Ser	atg Met	ttg Leu 60	agt Ser	ttg Leu	att Ile	tta Leu	192	
tca Ser 65	cgt Arg	gtc Val	ttt Phe	gaa Glu 70	aaa Lys	gaa Glu	tat Tyr	ggt Gly	aaa Lys	agt Ser 75	gtc Val	cct Pro	gag Glu	aaa Lys	aag Lys 80	240	
gtt Val	gag Glu	gaa Glu	tct Ser	tat Tyr 85	aat Asn	aaa Lys	aca Thr	gct Ala 90	aag Lys	cag Gln	tac Tyr	ggt Gly	tct Ser 95	tct Ser	ttc Phe	288	
tcc Ser	gat Asp	gct Ala	tta Leu 100	gca Ala	cag Gln	gca Ala	gga Gly	ctg Leu 105	aca Thr	acg Thr	gac Asp	acc Thr	tat Tyr 110	aaa Lys	aaa Lys	336	
caa Gln	att Ile	cgc Arg 115	act Thr	aca Thr	atg Met	tta Leu	ggt Val 120	gaa Glu	tat Tyr	gca Ala	gta Val	aaa Lys 125	caa Gln	gct Ala	gcc Ala	384	
aaa Lys 130	aaa Lys	gaa Glu	cta Leu	aca Thr	gat Asp	gat Asp 135	aat Asn	tat Tyr	aaa Lys	aaa Lys	gct Ala 140	ttt Phe	gaa Glu	tca Ser	tat Tyr	432	
acc Thr 145	cct Pro	gaa Glu	atg Met	aca Thr	aca Thr 150	caa Gln	ggt Val	att Ile	gct Ala	ttt Phe 155	gat Asp	gat Asp	gaa Glu	gaa Glu	aaa Lys 160	480	
gcc Ala	aaa Lys	aaa Lys	ggt Val	tta Leu 165	gaa Glu	gaa Glu	aca Thr	aaa Lys	gct Ala 170	gaa Glu	ggt Gly	gct Ala	gac Asp	ttt Phe 175	gct Ala	528	
aac Asn	atc Ile	gca Ala	aaa Lys 180	gaa Glu	aac Asn	acg Thr	act Thr	gaa Glu 185	gcc Ala	aat Asn	aaa Lys	aaa Lys	att Ile 190	gat Asp	tac Tyr	576	
acc Thr	ttt Phe	gat Asp 195	tca Ser	gcc Ala	gac Asp	act Thr	ggt Val 200	tta Leu	cca Pro	agt Ser	gat Asp	gtc Val 205	att Ile	aaa Lys	gaa Glu	624	
aca Thr 210	gca Ala	aaa Lys	tta Leu	aat Asn	gaa Glu	ggt Gly 215	gaa Glu	aaa Lys	tca Ser	gct Ala	ggt Val 220	att Ile	aca Thr	ggt Val	atg Met	672	
gat Asp 225	tca Ser	aga Arg	act Thr	tat Tyr	cag Gln 230	aaa Lys	aaa Lys	tat Tyr	tat Tyr	gtg Val 235	ggt Val	cat His	tta Leu	gtc Val	aag Lys 240	720	
aaa Lys	gct Ala	gag Glu	aaa Lys	aaa Lys 245	gcc Ala	gat Asp	tgg Trp	aaa Lys	gaa Glu 250	tac Tyr	aaa Lys	tca Ser	cga Arg	cta Leu 255	aaa Lys	768	
gaa Glu	atc Ile	att Ile	atg Met 260	aat Asn	gaa Glu	aag Lys	gaa Glu	aac Asn 265	gac Asp	agt Ser	aac Asn	ttc Phe	caa Gln 270	aac Asn	aaa Lys	816	
gtg Val	att Ile	tca Ser 275	aaa Lys	act Thr	tta Leu	gat Asp	aag Lys 280	gca Ala	aat Asn	ggt Val	aaa Lys	att Ile 285	aaa Lys	gac Asp	aaa Lys	864	
gcc Ala 290	ttt Phe	gca Ala	aat Asn	atc Ile	ttg Leu	tca Ser 295	caa Gln	ttt Phe	gct Ala	tct Ser	aat Asn 300	aaa Lys	aac Asn	aat Asn	acc Thr	912	

PCT_Sequence_listing (3)

942

aac aat gct tta aca agt tca gta ggt aaa
 Asn Asn Ala Leu Thr Ser Ser Val Gly Lys
 305 310

<210> 150
 <211> 314
 <212> PRT
 <213> Streptococcus uberis

<400> 150

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

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

Ala Lys Thr Ser Thr Ala Ala Gln Gln Ser Met Leu Ser Leu Ile Leu
 50 55 60

Ser Arg Val Phe Glu Lys Glu Tyr Gly Lys Ser Val Pro Glu Lys Lys
 65 70 75 80

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

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

Gln Ile Arg Thr Thr Met Leu Val Glu Tyr Ala Val Lys Gln Ala Ala
 115 120 125

Lys Lys Glu Leu Thr Asp Asp Asn Tyr Lys Lys Ala Phe Glu Ser Tyr
 130 135 140

Thr Pro Glu Met Thr Thr Gln Val Ile Ala Phe Asp Asp Glu Glu Lys
 145 150 155 160

Ala Lys Lys Val Leu Glu Glu Thr Lys Ala Glu Gly Ala Asp Phe Ala
 165 170 175

Asn Ile Ala Lys Glu Asn Thr Thr Glu Ala Asn Lys Lys Ile Asp Tyr
 180 185 190

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

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

Asp Ser Arg Thr Tyr Gln Lys Lys Tyr Tyr Val Val His Leu Val Lys
 225 230 235 240

Lys Ala Glu Lys Lys Ala Asp Trp Lys Glu Tyr Lys Ser Arg Leu Lys
 245 250 255

PCT_Sequence_listing (3)

Glu Ile Ile Met Asn Glu Lys Glu Asn Asp Ser Asn Phe Gln Asn Lys
260 265 270

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

Ala Phe Ala Asn Ile Leu Ser Gln Phe Ala Ser Asn Lys Asn Asn Thr
290 295 300

Asn Asn Ala Leu Thr Ser Ser Val Gly Lys
305 310

<210> 151
<211> 1248
<212> DNA
<213> Streptococcus uberis

<220>
<221> CDS
<222> (1)..(1248)

<400> 151
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Met Lys Ser Trp Gln Lys Ile Ile Val Ser Gly Ala Ser Leu Thr Leu
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gca agt aca ctt tta gtg ggc tgt gct tct gac tca aaa gga aaa aca 96
Ala Ser Thr Leu Leu Val Gly Cys Ala Ser Asp Ser Lys Gly Lys Thr
20 25 30
gaa tca gca tca tca gat tca aaa aca att aaa ttg tgg gtt cca act 144
Glu Ser Ala Ser Ser Asp Ser Lys Thr Ile Lys Leu Trp Val Pro Thr
35 40 45
ggg gct aaa aaa tct tat gca gat act gtt gct aaa ttt gag aaa gat 192
Gly Ala Lys Lys Ser Tyr Ala Asp Thr Val Ala Lys Phe Glu Lys Asp
50 55 60
tct ggt tat aaa gta aaa gtt att gaa tca gaa gat cca aaa gct caa 240
Ser Gly Tyr Lys Val Lys Val Ile Glu Ser Glu Asp Pro Lys Ala Gln
65 70 75 80
gaa aaa atc aaa aaa gat gct act act gct gct gac gta ttt tca ctt 288
Glu Lys Ile Lys Lys Asp Ala Thr Thr Ala Ala Asp Val Phe Ser Leu
85 90 95
cct cac gac caa ctt ggt caa tta gta gaa tct gga act att caa gaa 336
Pro His Asp Gln Leu Gly Gln Leu Val Glu Ser Gly Thr Ile Gln Glu
100 105 110
gta cca gaa caa tac act aaa gat att gct gca act gcg act gat caa 384
Val Pro Glu Gln Tyr Thr Lys Asp Ile Ala Ala Thr Ala Thr Asp Gln
115 120 125
gca att gta ggt gct caa tat aaa ggc aaa act tat gct ttc cca ttt 432
Ala Ile Val Gly Ala Gln Tyr Lys Gly Lys Thr Tyr Ala Phe Pro Phe
130 135 140
gga att gaa tca caa gtt ctt ttc tat aat aaa gaa aaa tta agc gct 480
Gly Ile Glu Ser Gln Val Leu Phe Tyr Asn Lys Glu Lys Leu Ser Ala
145 150 155 160
gaa gat atc gca tct tat gat gca att aca agc aaa gca aca ttt ggt 528
Glu Asp Ile Ala Ser Tyr Asp Ala Ile Thr Ser Lys Ala Thr Phe Gly
165 170 175
ggt acc ttc aaa caa gct aat gct tac gta act ggt cct tta ttc atg 576
Gly Thr Phe Lys Gln Ala Asn Ala Tyr Val Thr Gly Pro Leu Phe Met
180 185 190

PCT_Sequence_listing (3)

tct gtt ggt aac aca ttg ttt ggt gaa aac ggt gaa gat act aaa gga Ser Val Gly Asn Thr Leu Phe Gly Glu Asn Gly Glu Asp Thr Lys Gly	624
act aac tgg ggt aac gaa aaa ggt gct gca gta ctt aaa tgg att gct Thr Asn Trp Gly Asn Glu Lys Gly Ala Ala Val Leu Lys Trp Ile Ala	672
gat caa aag aac aac aaa gga ttt gtt agc tta gat gct aat aac gtt Asp Gln Lys Asn Asn Lys Gly Phe Val Ser Leu Asp Ala Asn Asn Val	720
atg tct aaa ttc ggt gac ggt tct gta gcc tca ttt gaa tca ggt cct Met Ser Lys Phe Gly Asp Gly Ser Val Ala Ser Phe Glu Ser Gly Pro	768
tgg gat tac gaa gct gca caa aaa gct atc ggt aaa gac aaa ctt ggt Trp Asp Tyr Glu Ala Ala Gln Lys Ala Ile Gly Lys Asp Lys Leu Gly	816
gtt gct gtt tat cca aaa gtg act atc ggt ggt gaa gaa gtt caa caa Val Ala Val Tyr Pro Lys Val Thr Ile Gly Gly Glu Glu Val Gln Gln	864
aaa gca ttc ctt ggt gtt aaa tta tac gct gtt aac caa gca cct gct Lys Ala Phe Leu Gly Val Lys Leu Tyr Ala Val Asn Gln Ala Pro Ala	912
aaa ggt gat act aaa cgt att gca gca agc tat aaa ctt gct tct tac Lys Gly Asp Thr Lys Arg Ile Ala Ala Ser Tyr Lys Leu Ala Ser Tyr	960
tta acg agt gct gaa agc caa gaa aat caa ttt aaa aca cgt cat atc Leu Thr Ser Ala Glu Ser Gln Glu Asn Gln Phe Lys Thr Arg His Ile	1008
gta cct gct aac aaa gag att caa tca tca gaa gaa gtt cag tca aat Val Pro Ala Asn Lys Glu Ile Gln Ser Ser Glu Glu Val Gln Ser Asn	1056
gaa ctt gct aaa aca gtt att aca atg gga tct tca aaa gat tac aca Glu Leu Ala Lys Thr Val Ile Thr Met Gly Ser Ser Lys Asp Tyr Thr	1104
gtt gta atg cct aaa tta agc caa atg gca aca ttc tgg act gaa agt Val Val Met Pro Lys Leu Ser Gln Met Ala Thr Phe Trp Thr Glu Ser	1152
gca gct att tta agt gat act ttc aat ggt aaa att caa gaa gct gat Ala Ala Ile Leu Ser Asp Thr Phe Asn Gly Lys Ile Gln Glu Ala Asp	1200
tac cta act aaa tta caa caa ttt gat aaa gat atc gct tct aca aaa Tyr Leu Thr Lys Leu Gln Gln Phe Asp Lys Asp Ile Ala Ser Thr Lys	1248

<210> 152
<211> 416
<212> PRT
<213> Streptococcus uberis

<400> 152

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

PCT_Sequence_listing (3)

Gly Ala Lys Lys Ser Tyr Ala Asp Thr Val Ala Lys Phe Glu Lys Asp
50 55 60

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

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

Pro His Asp Gln Leu Gly Gln Leu Val Glu Ser Gly Thr Ile Gln Glu
100 105 110

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

Ala Ile Val Gly Ala Gln Tyr Lys Gly Lys Thr Tyr Ala Phe Pro Phe
130 135 140

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

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

Gly Thr Phe Lys Gln Ala Asn Ala Tyr Val Thr Gly Pro Leu Phe Met
180 185 190

Ser Val Gly Asn Thr Leu Phe Gly Glu Asn Gly Glu Asp Thr Lys Gly
195 200 205

Thr Asn Trp Gly Asn Glu Lys Gly Ala Ala Val Leu Lys Trp Ile Ala
210 215 220

Asp Gln Lys Asn Asn Lys Gly Phe Val Ser Leu Asp Ala Asn Asn Val
225 230 235 240

Met Ser Lys Phe Gly Asp Gly Ser Val Ala Ser Phe Glu Ser Gly Pro
245 250 255

Trp Asp Tyr Glu Ala Ala Gln Lys Ala Ile Gly Lys Asp Lys Leu Gly
260 265 270

Val Ala Val Tyr Pro Lys Val Thr Ile Gly Gly Glu Glu Val Gln Gln
275 280 285

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

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

Leu Thr Ser Ala Glu Ser Gln Glu Asn Gln Phe Lys Thr Arg His Ile
325 330 335

Val Pro Ala Asn Lys Glu Ile Gln Ser Ser Glu Glu Val Gln Ser Asn
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PCT_Sequence_listing (3)

340 345 350

Glu Leu Ala Lys Thr Val Ile Thr Met Gly Ser Ser Lys Asp Tyr Thr
 355 360 365
 Val Val Met Pro Lys Leu Ser Gln Met Ala Thr Phe Trp Thr Glu Ser
 370 375 380
 Ala Ala Ile Leu Ser Asp Thr Phe Asn Gly Lys Ile Gln Glu Ala Asp
 385 390 395 400
 Tyr Leu Thr Lys Leu Gln Gln Phe Asp Lys Asp Ile Ala Ser Thr Lys
 405 410 415

<210> 153
 <211> 1056
 <212> DNA
 <213> Streptococcus uberis

<220>
 <221> CDS
 <222> (1)..(1056)

<400> 153
 atg aac aag aaa ttt att ggt ctt ggt tta gct tca gta gct ata tta 48
 Met Asn Lys Lys Phe Ile Gly Leu Gly Leu Ala Ser Val Ala Ile Leu
 1 5 10
 agt tta gct gca tgt ggc aac cgt ggt gct tca aaa tct gat agc aaa 96
 Ser Leu Ala Ala Cys Gly Asn Arg Gly Ala Ser Lys Ser Asp Ser Lys
 20 25 30
 gat gct aaa aca gat tta aaa gct gct att gtt act gat aca ggt ggt 144
 Asp Ala Lys Thr Asp Leu Lys Ala Ala Ile Val Thr Asp Thr Gly Gly
 35 40 45
 gtt gat gat aaa tca ttt aac caa tct gct tgg gaa ggt tta gaa gct 192
 Val Asp Asp Lys Ser Phe Asn Gln Ser Ala Trp Glu Gly Leu Glu Ala
 50 55 60
 tgg ggt aaa gaa aat ggg ctt aaa aaa ggt gct ggt ttc gac tac ttc 240
 Trp Gly Lys Glu Asn Gly Leu Lys Lys Gly Ala Gly Phe Asp Tyr Phe
 65 70 75 80
 caa tca aat agt gaa tca gaa tat gct act aat ctt gac act gct gtc 288
 Gln Ser Asn Ser Glu Ser Glu Tyr Ala Thr Asn Leu Asp Thr Ala Val
 85 90 95
 tca agt ggt tat aac gta gta tat gga atc gga ttt gcc ctt aaa gat 336
 Ser Ser Gly Tyr Asn Val Val Tyr Gly Ile Gly Phe Ala Leu Lys Asp
 100 105 110
 gca att gat aaa gct gct ggt gac aat agt gat gtt aac tat att atc 384
 Ala Ile Asp Lys Ala Ala Gly Asp Asn Ser Asp Val Asn Tyr Ile Ile
 115 120 125
 gtt gac gat gtc atc gaa gga aaa gat aat gtt gca agt gta act ttt 432
 Val Asp Asp Val Ile Glu Gly Lys Asp Asn Val Ala Ser Val Thr Phe
 130 135 140
 gcg gat aac gaa gct gct tat ctt gct ggt att gct gca gct aaa act 480
 Ala Asp Asn Glu Ala Ala Tyr Leu Ala Gly Ile Ala Ala Ala Lys Thr
 145 150 155 160
 aca aaa act aaa gta gta ggt ttt gta ggt ggt atg gaa ggt act gtt 528
 Thr Lys Thr Lys Val Val Gly Phe Val Gly Gly Met Glu Gly Thr Val
 165 170 175
 atc act cgt ttt gaa aaa ggt ttt gag gcg gga gtg aaa tca gtt gat 576

PCT_Sequence_listing (3)															
Ile	Thr	Arg	Phe 180	Glu	Lys	Gly	Phe 185	Glu	Ala	Gly	Val	Lys	Ser 190	Val	Asp
gat Asp	tct Ser	atc Ile 195	caa Gln	atc Ile	aaa Lys	gtt Val	gac Asp 200	tac Tyr	gct Ala	gga Gly	tca Ser	ttt Phe 205	ggt Gly	gat Asp	gct Ala
624															
gct Ala	aaa Lys 210	ggt Gly	aaa Lys	aca Thr	att Ile	gcc Ala 215	gca Ala	gct Ala	caa Gln	tat Tyr	gca Ala 220	ggt Gly	ggt Gly	gct Ala	gac Asp
672															
gtt Val 225	att Ile	tat Tyr	caa Gln	gcc Ala	gct Ala 230	ggt Gly	ggt Gly	act Thr	gga Gly	gca Ala 235	ggt Gly	gtc Val	ttc Phe	aat Asn	gaa Glu 240
720															
gct Ala	aaa Lys	gct Ala	gta Val	aat Asn 245	gag Glu	aaa Lys	aaa Lys	gat Asp	gaa Glu 250	gct Ala	gat Asp	aaa Lys	gtt Val	tgg Trp 255	gta Val
768															
atc Ile	ggt Gly	gta Val	gac Asp 260	cgt Arg	gac Asp	caa Gln	aaa Lys	gag Glu 265	gaa Glu	ggt Gly	aaa Lys	tac Tyr	act Thr 270	tca Ser	aaa Lys
816															
gac Asp	ggt Gly	aaa Lys 275	gaa Glu	tct Ser	aac Asn	ttt Phe	gtt Val 280	cta Leu	gca Ala	tct Ser	tca Ser	att Ile 285	aaa Lys	caa Gln	gtt Val
864															
ggt Gly 290	aaa Lys	tct Ser	gta Val	caa Gln	ctg Leu	att Ile 295	aac Asn	aaa Lys	ctt Leu	gtt Val	act Thr 300	gat Asp	aaa Lys	aaa Lys	ttc Phe
912															
cct Pro 305	ggt Gly	gga Gly	aaa Lys	aca Thr	act Thr 310	gtt Val	tat Tyr	gga Gly	tta Leu	aaa Lys 315	gat Asp	ggt Gly	ggt Gly	gtt Val	gat Asp 320
960															
att Ile	gca Ala	aca Thr	aca Thr	aac Asn 325	ctt Leu	tct Ser	gat Asp	gat Asp	gct Ala 330	ata Ile	aaa Lys	gct Ala	gtt Val	aaa Lys 335	gaa Glu
1008															
gct Ala	aaa Lys	gaa Glu	aaa Lys 340	att Ile	att Ile	tct Ser	ggc Gly	gat Asp 345	gta Val	aaa Lys	gtt Val	cct Pro	gaa Glu 350	aaa Lys	taa
1056															

<210> 154
 <211> 351
 <212> PRT
 <213> Streptococcus uberis
 <400> 154

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

PCT_Sequence_listing (3)

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

Ala Ile Asp Lys Ala Ala Gly Asp Asn Ser Asp Val Asn Tyr Ile Ile
115 120 125

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

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

Thr Lys Thr Lys Val Val Gly Phe Val Gly Gly Met Glu Gly Thr Val
165 170 175

Ile Thr Arg Phe Glu Lys Gly Phe Glu Ala Gly Val Lys Ser Val Asp
180 185 190

Asp Ser Ile Gln Ile Lys Val Asp Tyr Ala Gly Ser Phe Gly Asp Ala
195 200 205

Ala Lys Gly Lys Thr Ile Ala Ala Ala Gln Tyr Ala Gly Gly Ala Asp
210 215 220

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

Ala Lys Ala Val Asn Glu Lys Lys Asp Glu Ala Asp Lys Val Trp Val
245 250 255

Ile Gly Val Asp Arg Asp Gln Lys Glu Glu Gly Lys Tyr Thr Ser Lys
260 265 270

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

Gly Lys Ser Val Gln Leu Ile Asn Lys Leu Val Thr Asp Lys Lys Phe
290 295 300

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

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

Ala Lys Glu Lys Ile Ile Ser Gly Asp Val Lys Val Pro Glu Lys
340 345 350

<210> 155
<211> 933
<212> DNA
<213> Streptococcus uberis

<220>
<221> CDS
<222> (1)..(933)
<400> 155

PCT_Sequence_listing (3)

atg Met 1	aaa Lys	aaa Lys	tta Leu	ctt Leu 5	gtc Val	aca Thr	tta Leu	gtg Val 10	ttg Leu 10	att Ile	ttc Phe	agc Ser	aca Thr	tta Leu 15	tca Ser	48
ttg Leu	att Ile	gct Ala	tgt Cys 20	tca Ser	tca Ser	caa Gln	agc Ser	aca Thr 25	aag Lys	caa Gln	gaa Glu	gat Asp	cat His 30	aaa Lys	aca Thr	96
aaa Lys	cta Leu	tca Ser 35	caa Gln	atg Met	cca Pro	aag Lys	atc Ile 40	tct Ser	ggg Gly	ttt Phe	acc Thr	tat Tyr 45	aaa Lys	ggg Gly	aag Lys	144
gta Val 50	cca Pro	gaa Glu	aac Asn	cct Pro	aaa Lys	aga Arg 55	gta Val	gtt Val	agt Ser	tta Leu	tct Ser 60	tca Ser	acc Thr	tac Tyr	acc Thr	192
ggg Gly 65	tat Tyr	ttg Leu	gca Ala	aag Lys	ctc Leu 70	gat Asp	atc Ile	cca Pro	cta Leu	gtt Val 75	gga Gly	atc Ile	act Thr	tct Ser	tat Tyr 80	240
gat Asp	cac His	aaa Lys	aat Asn	ccc Pro 85	gtc Val	tta Leu	aag Lys	aaa Lys	tac Tyr 90	atc Ile	aag Lys	gat Asp	gct Ala	aaa Lys 95	gtt Val	288
gtc Val	tct Ser	gca Ala	acc Thr 100	gac Asp	cta Leu	gaa Glu	agc Ser	att Ile 105	acg Thr	gcc Ala	ttg Leu	gaa Glu	cct Pro 110	gat Asp	tta Leu	336
att Ile	att Ile	gtg Val 115	ggg Gly	tca Ser	aat Asn	gaa Glu	gaa Glu 120	aat Asn	atc Ile	agt Ser	caa Gln	tta Leu 125	gct Ala	gaa Glu	atc Ile	384
gct Ala	ccc Pro 130	ctt Leu	att Ile	tcc Ser	att Ile	gaa Glu 135	tac Tyr	cgc Arg	aaa Lys	cat His	gac Asp 140	tat Tyr	tta Leu	cag Gln	gta Val	432
ttc Phe 145	tca Ser	gat Asp	ttt Phe	ggg Gly 150	aaa Lys	gtc Val	ttt Phe	aac Asn	aaa Lys	acc Thr 155	aaa Lys	gaa Glu	acc Thr	gac Asp	aaa Lys 160	480
tgg Trp	tta Leu	cag Gln	gaa Glu 165	tgg Trp	aaa Lys	aca Thr	aaa Lys	aca Thr	gct Ala 170	tct Ser	ttt Phe	gaa Glu	agt Ser	gac Asp 175	gtt Val	528
aaa Lys	gca Ala	gtt Val	aca Thr 180	ggg Gly	aat Asn	aat Asn	gct Ala	acc Thr 185	ttt Phe	acc Thr	ata Ile	atg Met	gga Gly 190	tta Leu	tat Tyr	576
gag Glu	aaa Lys	gat Asp 195	atc Ile	tat Tyr	ctt Leu	ttc Phe	ggg Gly 200	aaa Lys	gat Asp	tgg Trp	ggg Gly 205	cgt Arg 205	ggg Gly	ggg Gly	gaa Glu	624
atc Ile	att Ile 210	cac His	caa Gln	gcc Ala	ttc Phe	caa Gln 215	tat Tyr	caa Gln	gct Ala	cca Pro	gaa Glu 220	aaa Lys	gta Val	aaa Lys	atg Met	672
gag Glu 225	gtt Val	ttc Phe	cca Pro	aaa Lys	ggg Gly 230	tat Tyr	ttg Leu	tcc Ser	att Ile	tca Ser 235	caa Gln	gaa Glu	gtt Val	ctt Leu	cca Pro 240	720
gat Asp	tat Tyr	att Ile	ggg Gly	gat Asp 245	tat Tyr	gtc Val	gtt Val	gtc Val	gct Ala 250	gca Ala	gag Glu	gat Asp	gaa Glu	aaa Lys 255	aca Thr	768
ggg Gly	tct Ser	tct Ser	ctt Leu 260	tat Tyr	gaa Glu	agt Ser	gac Asp	ctt Leu 265	tgg Trp	aaa Lys	aat Asn	ata Ile	cca Pro 270	gcc Ala	gtt Val	816
caa Gln	aaa Lys	aat Asn 275	cat His	gtc Val	ata Ile	aat Asn	gtt Val 280	aat Asn	gcg Ala	aat Asn	acc Thr	ttt Phe 285	tat Tyr	ttc Phe	act Thr	864
gac Asp	cct Pro 290	ctg Leu	tca Ser	tta Leu	gag Glu	tat Tyr 295	gaa Glu	tta Leu	aaa Lys	acc Thr	tta Leu 300	acg Thr	gat Asp	gct Ala	atc Ile	912

PCT_Sequence_listing (3)

933

ttg act cag aaa act cac aac
Leu Thr Gln Lys Thr His Asn
305 310

<210> 156
<211> 311
<212> PRT
<213> Streptococcus uberis
<400> 156

Met Lys Lys Leu Leu Val Thr Leu Val Leu Ile Phe Ser Thr Leu Ser
1 5 10 15

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

Lys Leu Ser Gln Met Pro Lys Ile Ser Gly Phe Thr Tyr Lys Gly Lys
35 40 45

Val Pro Glu Asn Pro Lys Arg Val Val Ser Leu Ser Ser Thr Tyr Thr
50 55 60

Gly Tyr Leu Ala Lys Leu Asp Ile Pro Leu Val Gly Ile Thr Ser Tyr
65 70 75 80

Asp His Lys Asn Pro Val Leu Lys Lys Tyr Ile Lys Asp Ala Lys Val
85 90 95

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

Ile Ile Val Gly Ser Asn Glu Glu Asn Ile Ser Gln Leu Ala Glu Ile
115 120 125

Ala Pro Leu Ile Ser Ile Glu Tyr Arg Lys His Asp Tyr Leu Gln Val
130 135 140

Phe Ser Asp Phe Gly Lys Val Phe Asn Lys Thr Lys Glu Thr Asp Lys
145 150 155 160

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

Lys Ala Val Thr Gly Asn Asn Ala Thr Phe Thr Ile Met Gly Leu Tyr
180 185 190

Glu Lys Asp Ile Tyr Leu Phe Gly Lys Asp Trp Gly Arg Gly Gly Glu
195 200 205

Ile Ile His Gln Ala Phe Gln Tyr Gln Ala Pro Glu Lys Val Lys Met
210 215 220

Glu Val Phe Pro Lys Gly Tyr Leu Ser Ile Ser Gln Glu Val Leu Pro
225 230 235 240

Asp Tyr Ile Gly Asp Tyr Val Val Val Ala Ala Glu Asp Glu Lys Thr
245 250 255

PCT_Sequence_listing (3)

Gly Ser Ser Leu Tyr Glu Ser Asp Leu Trp Lys Asn Ile Pro Ala Val
260 265 270

Gln Lys Asn His Val Ile Asn Val Asn Ala Asn Thr Phe Tyr Phe Thr
275 280 285

Asp Pro Leu Ser Leu Glu Tyr Glu Leu Lys Thr Leu Thr Asp Ala Ile
290 295 300

Leu Thr Gln Lys Thr His Asn
305 310

<210> 157
<211> 1056
<212> DNA
<213> Streptococcus uberis

<220>
<221> CDS
<222> (1)..(1056)

<400> 157
atg aac aag aaa ttt att ggt ctt ggt tta gct tca gta gct ata tta 48
Met Asn Lys Lys Phe Ile Gly Leu Gly Leu Ala Ser Val Ala Ile Leu
1 5 10
agt tta gct gca tgt ggc aac cgt ggt gct tca aaa tct gat agc aaa 96
Ser Leu Ala Ala Cys Gly Asn Arg Gly Ala Ser Lys Ser Asp Ser Lys
20 25 30
gat gct aaa aca gat tta aaa gct gct att gtt act gat aca ggt ggt 144
Asp Ala Lys Thr Asp Leu Lys Ala Ala Ile Val Thr Asp Thr Gly Gly
35 40 45
gtt gat gat aaa tca ttt aac caa tct gct tgg gaa ggt tta caa gct 192
Val Asp Asp Lys Ser Phe Asn Gln Ser Ala Trp Glu Gly Leu Gln Ala
50 55 60
tgg ggt aaa gaa aat ggg ctt aaa aaa ggt gct ggt ttc gac tac ttc 240
Trp Gly Lys Glu Asn Gly Leu Lys Lys Gly Ala Gly Phe Asp Tyr Phe
65 70 75 80
caa tca aat agt gaa tca gaa tat gct act aat ctt gac act gct gtc 288
Gln Ser Asn Ser Glu Ser Glu Tyr Ala Thr Asn Leu Asp Thr Ala Val
85 90 95
tca agt ggt tat aac gta gta tat gga atc gga ttt gcc ctt aaa gat 336
Ser Ser Gly Tyr Asn Val Val Tyr Gly Ile Gly Phe Ala Leu Lys Asp
100 105 110
gca att gat aaa gct gct ggt gac aat agt gat gtt aac tat gtt atc 384
Ala Ile Asp Lys Ala Ala Gly Asp Asn Ser Asp Val Asn Tyr Val Ile
115 120 125
gtt gac gat gtc atc gaa gga aaa gac aat gtt gca agt gta act ttt 432
Val Asp Asp Val Ile Glu Gly Lys Asp Asn Val Ala Ser Val Thr Phe
130 135 140
gcg gat aac gaa gct gct tat ctt gct ggt att gct gca gct aaa act 480
Ala Asp Asn Glu Ala Ala Tyr Leu Ala Gly Ile Ala Ala Ala Lys Thr
145 150 155 160
aca aaa act aaa gta gta ggt ttt gta ggt ggt atg gaa ggt act gtt 528
Thr Lys Thr Lys Val Val Gly Phe Val Gly Gly Met Glu Gly Thr Val
165 170 175
atc act cgt ttt gaa aaa ggt ttt gag gcg gga gtg aaa tca gtt gat 576
Ile Thr Arg Phe Glu Lys Gly Phe Glu Ala Gly Val Lys Ser Val Asp

148

PCT_Sequence_listing (3)

180	185	190	
gat tct atc caa atc aaa gtt gac tac gct gga tca ttt ggt gat gct Asp Ser Ile Gln Ile Lys Val Asp Tyr Ala Gly Ser Phe Gly Asp Ala	195	200	205
gct aaa ggt aaa aca att gcc gca gct caa tat gca ggt ggt gct gac Ala Lys Gly Lys Thr Ile Ala Ala Ala Gln Tyr Ala Gly Gly Ala Asp	210	215	220
gtt att tat caa gcc gct ggt ggt act gga gca ggt gtc ttc aat gaa Val Ile Tyr Gln Ala Ala Gly Gly Thr Gly Ala Gly Val Phe Asn Glu	225	230	235
gct aaa gct gta aat gag aaa aaa gat gaa gct gat aaa gtt tgg gta Ala Lys Ala Val Asn Glu Lys Lys Asp Glu Ala Asp Lys Val Trp Val	245	250	255
atc ggt gta gac cgt gac caa aaa gag gaa ggt aaa tac act tca aaa Ile Gly Val Asp Arg Asp Gln Lys Glu Glu Gly Lys Tyr Thr Ser Lys	260	265	270
gac ggt aaa gaa tct aac ttt gtt cta gca tct tca att aaa caa gtt Asp Gly Lys Glu Ser Asn Phe Val Leu Ala Ser Ser Ile Lys Gln Val	275	280	285
ggt aaa tct gta caa ctg att aac aaa ctt gtt act gat aaa aaa ttc Gly Lys Ser Val Gln Leu Ile Asn Lys Leu Val Thr Asp Lys Lys Phe	290	295	300
cct ggt gga aaa aca act gtt tat gga tta aaa gat ggt ggt gtt gat Pro Gly Gly Lys Thr Thr Val Tyr Gly Leu Lys Asp Gly Gly Val Asp	305	310	315
att gca aca aca aac ctt tct gat gat gct ata aaa gct gtt aaa gaa Ile Ala Thr Thr Asn Leu Ser Asp Asp Ala Ile Lys Ala Val Lys Glu	325	330	335
gct aaa gaa aaa att att tct ggc gat gta aaa gtt cct gaa aaa taa Ala Lys Glu Lys Ile Ile Ser Gly Asp Val Lys Val Pro Glu Lys	340	345	350

<210> 158
<211> 351
<212> PRT
<213> Streptococcus uberis

<400> 158
Met Asn Lys Lys Phe Ile Gly Leu Gly Leu Ala Ser Val Ala Ile Leu 1 5 10 15
Ser Leu Ala Ala Cys Gly Asn Arg Gly Ala Ser Lys Ser Asp Ser Lys 20 25 30
Asp Ala Lys Thr Asp Leu Lys Ala Ala Ile Val Thr Asp Thr Gly Gly 35 40 45
Val Asp Asp Lys Ser Phe Asn Gln Ser Ala Trp Glu Gly Leu Gln Ala 50 55 60
Trp Gly Lys Glu Asn Gly Leu Lys Lys Gly Ala Gly Phe Asp Tyr Phe 65 70 75 80
Gln Ser Asn Ser Glu Ser Glu Tyr Ala Thr Asn Leu Asp Thr Ala Val 85 90 95
ser ser Gly Tyr Asn Val Val Tyr Gly Ile Gly Phe Ala Leu Lys Asp

PCT_Sequence_listing (3)

100

105

110

Ala Ile Asp Lys Ala Ala Gly Asp Asn Ser Asp Val Asn Tyr Val Ile
115 120 125

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

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

Thr Lys Thr Lys Val Val Gly Phe Val Gly Gly Met Glu Gly Thr Val
165 170 175

Ile Thr Arg Phe Glu Lys Gly Phe Glu Ala Gly Val Lys Ser Val Asp
180 185 190

Asp Ser Ile Gln Ile Lys Val Asp Tyr Ala Gly Ser Phe Gly Asp Ala
195 200 205

Ala Lys Gly Lys Thr Ile Ala Ala Ala Gln Tyr Ala Gly Gly Ala Asp
210 215 220

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

Ala Lys Ala Val Asn Glu Lys Lys Asp Glu Ala Asp Lys Val Trp Val
245 250 255

Ile Gly Val Asp Arg Asp Gln Lys Glu Glu Gly Lys Tyr Thr Ser Lys
260 265 270

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

Gly Lys Ser Val Gln Leu Ile Asn Lys Leu Val Thr Asp Lys Lys Phe
290 295 300

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

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

Ala Lys Glu Lys Ile Ile Ser Gly Asp Val Lys Val Pro Glu Lys
340 345 350

<210> 159
<211> 1041
<212> DNA
<213> Streptococcus uberis

<220>
<221> CDS
<222> (1)..(1041)

<400> 159
atg aat aaa aaa tta aca tcc ctt gcc tta tta tca gct gct att atc

1-30

PCT_Sequence_listing (3)

Met 1	Asn	Lys	Lys	Leu 5	Thr	Ser	Leu	Ala 10	Leu	Ser	Ala	Ala	Ile 15	Ile		
cca Pro	tta Leu	gcg Ala	gca Ala 20	tgt Cys	tct Ser	cat His	aaa Lys	ggc Gly 25	caa Gln	aaa Lys	tct Ser	gct Ala 30	tct Ser	tta Leu	tca Ser	96
gat Asp	tta Leu	aaa Lys 35	gta Val	gcc Ala	atg Met	att Ile	act Thr 40	gac Asp	caa Gln	ggg Gly	ggt Gly	ggt Val 45	gat Asp	gat Asp	aaa Lys	144
tcc Ser	ttt Phe 50	aac Asn	caa Gln	tca Ser	gct Ala	tgg Trp 55	gaa Glu	ggg Gly	cta Leu	caa Gln	gct Ala 60	tgg Trp	ggc Gly	aaa Lys	tca Ser	192
aaa Lys 65	aat Asn	ttg Leu	aaa Lys	aaa Lys	gga Gly 70	agt Ser	gat Asp	ttt Phe	aat Asn	tat Tyr 75	ttc Phe	caa Gln	tca Ser	acc Thr	aat Asn 80	240
gaa Glu	tca Ser	gaa Glu	tat Tyr	gtg Val 85	aca Thr	aac Asn	ctt Leu	gat Asp	act Thr 90	gca Ala	aag Lys	tca Ser	aat Asn	ggt Gly 95	ttt Phe	288
aat Asn	gtc Val	atc Ile	ttt Phe 100	ggg Gly	att Ile	ggc Gly	ttt Phe	aac Asn 105	ctg Leu	act Thr	gat Asp	tct Ser	att Ile 110	aaa Lys	aaa Lys	336
gcg Ala	tct Ser	tct Ser 115	gat Asp	aac Asn	gca Ala	gat Asp	aca Thr 120	aaa Lys	tac Tyr	gct Ala	att Ile	gtc Val 125	gat Asp	gat Asp	gtc Val	384
att Ile	gaa Glu 130	gga Gly	aaa Lys	gac Asp	aat Asn	gtt Val 135	gca Ala	agt Ser	atc Ile	act Thr	ttt Phe 140	gcc Ala	gac Asp	aac Asn	gaa Glu	432
gca Ala 145	gct Ala	tac Tyr	tta Leu	gct Ala	ggg Gly 150	gtt Val	gcg Ala	gct Ala	gct Ala	aaa Lys 155	acc Thr	agc Ser	aaa Lys	agc Ser	aaa Lys 160	480
caa Gln	gtt Val	ggg Gly	ttt Phe	gta Val 165	ggg Gly	ggg Gly	atg Met	gaa Glu	gga Gly 170	acc Thr	gtt Val	gtt Val	aaa Lys	cgt Arg 175	ttt Phe	528
gaa Glu	aaa Lys	ggc Gly	ttt Phe 180	gaa Glu	gca Ala	ggg Gly	gtt Val	aaa Lys 185	tca Ser	gtt Val	gat Asp	cct Pro	tct Ser 190	atc Ile	aaa Lys	576
gta Val	tca Ser	atc Ile 195	gct Ala	tac Tyr	gca Ala	ggg Gly	tca Ser 200	ttt Phe	gcg Ala	gat Asp	gct Ala	gct Ala 205	aaa Lys	gga Gly	aaa Lys	624
tca Ser	att Ile 210	gca Ala	gca Ala	aca Thr	caa Gln	tat Tyr 215	gca Ala	agt Ser	ggg Gly	gct Ala	gat Asp 220	gtc Val	atc Ile	tat Tyr	caa Gln	672
gca Ala 225	gca Ala	ggg Gly	gga Gly	acg Thr	ggg Gly 230	gct Ala	ggg Gly	gtc Val	ttc Phe	aac Asn 235	gaa Glu	gcc Ala	aaa Lys	gct Ala	att Ile 240	720
aat Asn	gaa Glu	aaa Lys	cgt Arg	gcc Ala 245	gct Ala	tca Ser	gat Asp	aaa Lys	gtt Val 250	tgg Trp	gtc Val	ctt Leu	ggg Gly	gta Val 255	gac Asp	768
cgt Arg	gac Asp	caa Gln	aaa Lys 260	gct Ala	gaa Glu	ggg Gly	gaa Glu	tac Tyr 265	act Thr	gat Asp	aaa Lys	gat Asp	ggg Gly 270	caa Gln	aaa Lys	816
gga Gly	aac Asn	ttt Phe 275	gtc Val	ctt Leu	gct Ala	tca Ser	agt Ser 280	atc Ile	aaa Lys	gaa Glu	gtt Val	ggg Gly 285	aaa Lys	acc Thr	atg Met	864
caa Gln	aaa Lys 290	gtc Val	att Ile	ggg Gly	atg Met	act Thr 295	gaa Glu	aaa Lys	ggg Gly	gac Asp	ttc Phe 300	cct Pro	ggg Gly	ggg Gly	aaa Lys	912

PCT_Sequence_listing (3)

gtc aat acc ttt ggt tta aaa gaa tca ggt gtt aac ctc acc aca aaa	960
Val Asn Thr Phe Gly Leu Lys Glu Ser Gly Val Asn Leu Thr Thr Lys	
305 310 315 320	
gat ctt cca gaa gat gtt aaa aaa gca gtt gaa aca gca cgc caa gac	1008
Asp Leu Pro Glu Asp Val Lys Lys Ala Val Glu Thr Ala Arg Gln Asp	
325 330 335	
att atc tca ggt aaa atc aaa gtc cca gaa aaa	1041
Ile Ile Ser Gly Lys Ile Lys Val Pro Glu Lys	
340 345	
 <210> 160	
<211> 347	
<212> PRT	
<213> Streptococcus uberis	
 <400> 160	
Met Asn Lys Lys Leu Thr Ser Leu Ala Leu Leu Ser Ala Ala Ile Ile	
1 5 10 15	
Pro Leu Ala Ala Cys Ser His Lys Gly Gln Lys Ser Ala Ser Leu Ser	
20 25 30	
Asp Leu Lys Val Ala Met Ile Thr Asp Gln Gly Gly Val Asp Asp Lys	
35 40 45	
Ser Phe Asn Gln Ser Ala Trp Glu Gly Leu Gln Ala Trp Gly Lys Ser	
50 55 60	
Lys Asn Leu Lys Lys Gly Ser Asp Phe Asn Tyr Phe Gln Ser Thr Asn	
65 70 75 80	
Glu Ser Glu Tyr Val Thr Asn Leu Asp Thr Ala Lys Ser Asn Gly Phe	
85 90 95	
Asn Val Ile Phe Gly Ile Gly Phe Asn Leu Thr Asp Ser Ile Lys Lys	
100 105 110	
Ala Ser Ser Asp Asn Ala Asp Thr Lys Tyr Ala Ile Val Asp Asp Val	
115 120 125	
Ile Glu Gly Lys Asp Asn Val Ala Ser Ile Thr Phe Ala Asp Asn Glu	
130 135 140	
Ala Ala Tyr Leu Ala Gly Val Ala Ala Ala Lys Thr Ser Lys Ser Lys	
145 150 155 160	
Gln Val Gly Phe Val Gly Gly Met Glu Gly Thr Val Val Lys Arg Phe	
165 170 175	
Glu Lys Gly Phe Glu Ala Gly Val Lys Ser Val Asp Pro Ser Ile Lys	
180 185 190	
Val Ser Ile Ala Tyr Ala Gly Ser Phe Ala Asp Ala Ala Lys Gly Lys	
195 200 205	
Ser Ile Ala Ala Thr Gln Tyr Ala Ser Gly Ala Asp Val Ile Tyr Gln	
210 215 220	

PCT_Sequence_listing (3)

Ala Ala Gly Gly Thr Gly Ala Gly Val Phe Asn Glu Ala Lys Ala Ile
225 230 235 240

Asn Glu Lys Arg Ala Ala Ser Asp Lys Val Trp Val Leu Gly Val Asp
245 250 255

Arg Asp Gln Lys Ala Glu Gly Glu Tyr Thr Asp Lys Asp Gly Gln Lys
260 265 270

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

Gln Lys Val Ile Gly Met Thr Glu Lys Gly Asp Phe Pro Gly Gly Lys
290 295 300

Val Asn Thr Phe Gly Leu Lys Glu Ser Gly Val Asn Leu Thr Thr Lys
305 310 315 320

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

Ile Ile Ser Gly Lys Ile Lys Val Pro Glu Lys
340 345

<210> 161
<211> 1656
<212> DNA
<213> Streptococcus uberis

<220>
<221> CDS
<222> (1)..(1656)

<400> 161	
atg aca gta gca caa aaa tct aca ttt aag cgc ttc ggc cta gga gct	48
Met Thr Val Ala Gln Lys Ser Thr Phe Lys Arg Phe Gly Leu Gly Ala	
1 5 10 15	

gta aca ctt gct tca gca gcc cta ttg atg gct tgt ggt aac aag aca	96
Val Thr Leu Ala Ser Ala Ala Leu Leu Met Ala Cys Gly Asn Lys Thr	
20 25 30	

gca gca aaa aat gat aac aaa aat gag att aac tgg tac aca cca aca	144
Ala Ala Lys Asn Asp Asn Lys Asn Glu Ile Asn Trp Tyr Thr Pro Thr	
35 40 45	

gaa ctc atc act tta gac att tca aaa aat act gac act tat tct ggt	192
Glu Leu Ile Thr Leu Asp Ile Ser Lys Asn Thr Asp Thr Tyr Ser Gly	
50 55 60	

ctt gca atc ggt aac tca gaa agt aac tta ctt cgt gtt gac gga aaa	240
Leu Ala Ile Gly Asn Ser Glu Ser Asn Leu Leu Arg Val Asp Gly Lys	
65 70 75 80	

ggg aaa ttg caa cca gac tta gct aaa aaa gta gaa gtt tca gaa gat	288
Gly Lys Leu Gln Pro Asp Leu Ala Lys Lys Val Glu Val Ser Glu Asp	
85 90 95	

ggt tta act tat act gca acc ttg aga gat ggt ttg aaa tgg tct gac	336
Gly Leu Thr Tyr Thr Ala Thr Leu Arg Asp Gly Leu Lys Trp Ser Asp	
100 105 110	

gga agt gaa tta aca gca gag gac ttt gtt tac act tgg aaa cgt att	384
Gly Ser Glu Leu Thr Ala Glu Asp Phe Val Tyr Thr Trp Lys Arg Ile	
115 120 125	

PCT_Sequence_listing (3)

gta Val	gac Asp 130	cca Pro	gca Ala	act Thr	gct Ala 135	tca Ser	gaa Glu	tat Tyr	gct Ala	tac Tyr	tta Leu 140	gca Ala	act Thr	gaa Glu	tca Ser	432
cat His 145	tta Leu	tta Leu	aat Asn	gct Ala	gaa Glu 150	gat Asp	att Ile	aat Asn	aca Thr	ggg Gly 155	aaa Lys	aac Asn	act Thr	gat Asp	tta Leu 160	480
aat Asn	tct Ser	ctt Leu	ggg Gly	gtt Val 165	aaa Lys	gcc Ala	gaa Glu	ggc Gly	aac Asn 170	aaa Lys	gtt Val	atc Ile	ttt Phe	aca Thr 175	ttg Leu	528
agt Ser	gca Ala	cct Pro	gct Ala 180	cct Pro	caa Gln	ttc Phe	aag Lys	agc Ser 185	tta Leu	ttg Leu	tca Ser	ttt Phe	gct Ala 190	aac Asn	ttc Phe	576
atg Met	cct Pro	caa Gln 195	aaa Lys	gaa Glu	gaa Glu	ttt Phe	gtt Val 200	act Thr	aaa Lys	aca Thr	gga Gly 205	aaa Lys	gac Asp	tat Tyr	ggg Gly	624
act Thr	tct Ser 210	tct Ser	gaa Glu	aaa Lys	caa Gln	att Ile 215	tat Tyr	tct Ser	ggg Gly	cca Pro	tac Tyr 220	att Ile	gta Val	aaa Lys	gat Asp	672
tgg Trp 225	aat Asn	ggg Gly	aca Thr	agt Ser	ggg Gly 230	tca Ser	ttc Phe	aaa Lys	tta Leu	gtt Val 235	aag Lys	aat Asn	gac Asp	aaa Lys	tat Tyr 240	720
tgg Trp	gat Asp	gct Ala	aaa Lys	aac Asn 245	gtt Val	aaa Lys	atg Met	aaa Lys	act Thr 250	att Ile	aac Asn	gtt Val	caa Gln	aca Thr 255	gtt Val	768
aaa Lys	aaa Lys	cca Pro	gat Asp 260	aca Thr	gcc Ala	gtt Val	caa Gln	atg Met 265	tat Tyr	aaa Lys	caa Gln	gga Gly 270	aaa Lys	ctt Leu	gat Asp	816
tat Tyr	gca Ala	aac Asn 275	att Ile	tca Ser	gga Gly	aca Thr	tct Ser 280	gct Ala	ata Ile	tac Tyr	aat Asn	gca Ala 285	aac Asn	aaa Lys	aac Asn	864
aac Asn	aaa Lys 290	gac Asp	gtt Val	gtt Val	ccc Pro	gta Val 295	tta Leu	gaa Glu	gca Ala	aca Thr	act Thr 300	gct Ala	tat Tyr	atg Met	gta Val	912
tac Tyr 305	aat Asn	caa Gln	aca Thr	ggg Gly	tct Ser 310	gta Val	cca Pro	gca Ala	ttg Leu	agc Ser 315	aac Asn	ctt Leu	aag Lys	att Ile	cgt Arg 320	960
caa Gln	gca Ala	ttg Leu	aat Asn	tta Leu 325	gca Ala	aca Thr	gac Asp	cgt Arg	aaa Lys 330	gga Gly	att Ile	gtg Val	tct Ser	gca Ala 335	gca Ala	1008
gtg Val	gat Asp	act Thr	ggg Gly 340	tct Ser	aaa Lys	cca Pro	gca Ala	aca Thr 345	gca Ala	att Ile	gct Ala	cct Pro	act Thr 350	gga Gly	ctt Leu	1056
gca Ala	aaa Lys	ctt Leu 355	aaa Lys	gat Asp	gga Gly	tct Ser	gat Asp 360	tta Leu	act Thr	aaa Lys	ttt Phe	gta Val 365	gct Ala	cct Pro	ggg Gly	1104
tat Tyr	aaa Lys 370	tat Tyr	gat Asp	gaa Glu	aaa Lys	gaa Glu 375	gca Ala	gga Gly	aaa Lys	ctt Leu	ttc Phe 380	aaa Lys	gaa Glu	gga Gly	ctt Leu	1152
gct Ala 385	gaa Glu	ctc Leu	gga Gly	aaa Lys	gat Asp 390	tct Ser	ctt Leu	aaa Lys	att Ile	aca Thr 395	att Ile	acc Thr	gct Ala	gat Asp	gcg Ala 400	1200
gat Asp	gca Ala	cca Pro	gca Ala	gct Ala 405	aaa Lys	tct Ser	tca Ser	gtt Val	gac Asp 410	tac Tyr	att Ile	aaa Lys	gaa Glu	act Thr 415	tgg Trp	1248
gaa Glu	aaa Lys	gct Ala	tta Leu	cca Pro	gga Gly	tta Leu	aca Thr	gtt Val	gaa Glu	gaa Glu	aaa Lys	ttt Phe	gtt Val	cca Pro	ttt Phe	1296

PCT_Sequence_listing (3)

420	425	430	
aaa caa cgt tta gaa gat aca aaa aat caa aac ttt gaa gtt gct gta Lys Gln Arg Leu Glu Asp Thr Lys Asn Gln Asn Phe Glu Val Ala Val	435	440	445
gca ctt tgg ggt ggt gac tat cca gaa gga tca act ttc tat ggt ttg Ala Leu Trp Gly Gly Asp Tyr Pro Glu Gly Ser Thr Phe Tyr Gly Leu	450	455	460
ttt aaa tca ggt tct gca tat aac tac ggt aaa ttc acc aat gca aaa Phe Lys Ser Gly Ser Ala Tyr Asn Tyr Gly Lys Phe Thr Asn Ala Lys	465	470	475
ttt gat gct gct tat gaa aaa gct tta aca acc gat gca tta gat aca Phe Asp Ala Ala Tyr Glu Lys Ala Leu Thr Thr Asp Ala Leu Asp Thr	485	490	495
gac gcc gca gct aat gat tat aaa gaa gca gaa aaa gct ctt tat gat Asp Ala Ala Ala Asn Asp Tyr Lys Glu Ala Glu Lys Ala Leu Tyr Asp	500	505	510
gaa gca aac tat aac cca ctt tac ttc cgt agc gga gaa gga tta caa Glu Ala Asn Tyr Asn Pro Leu Tyr Phe Arg Ser Gly Glu Gly Leu Gln	515	520	525
aat cca agt att aaa ggg tta att cgt aat tca aca ggt ctt aat gtt Asn Pro Ser Ile Lys Gly Leu Ile Arg Asn Ser Thr Gly Leu Asn Val	530	535	540
gac ttt acc tat gct tat aaa aaa Asp Phe Thr Tyr Ala Tyr Lys Lys	545	550	

<210> 162
<211> 552
<212> PRT
<213> Streptococcus uberis

<400> 162

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

PCT_Sequence_listing (3)

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

PCT_Sequence_listing (3)

Lys Gln Arg Leu Glu Asp Thr Lys Asn Gln Asn Phe Glu Val Ala Val
435 440 445

Ala Leu Trp Gly Gly Asp Tyr Pro Glu Gly Ser Thr Phe Tyr Gly Leu
450 455 460

Phe Lys Ser Gly Ser Ala Tyr Asn Tyr Gly Lys Phe Thr Asn Ala Lys
465 470 475 480

Phe Asp Ala Ala Tyr Glu Lys Ala Leu Thr Thr Asp Ala Leu Asp Thr
485 490 495

Asp Ala Ala Ala Asn Asp Tyr Lys Glu Ala Glu Lys Ala Leu Tyr Asp
500 505 510

Glu Ala Asn Tyr Asn Pro Leu Tyr Phe Arg Ser Gly Glu Gly Leu Gln
515 520 525

Asn Pro Ser Ile Lys Gly Leu Ile Arg Asn Ser Thr Gly Leu Asn Val
530 535 540

Asp Phe Thr Tyr Ala Tyr Lys Lys
545 550

<210> 163
<211> 858
<212> DNA
<213> Streptococcus uberis

<220>
<221> CDS
<222> (1)..(858)

<400> 163	
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Met Lys Lys Trp Phe Leu Ile Leu Met Leu Leu Gly Ile Phe Gly Cys	
1 5 10 15	
gct act caa cca tca aag gtt gca gca ata acc ggt tat gat tcc gac	96
Ala Thr Gln Pro Ser Lys Val Ala Ala Ile Thr Gly Tyr Asp Ser Asp	
20 25 30	
tac tac gct aga tat att gat ccc gat gaa aat aaa ata aca ttt gcc	144
Tyr Tyr Ala Arg Tyr Ile Asp Pro Asp Glu Asn Lys Ile Thr Phe Ala	
35 40 45	
ata aat gtt gat ggt ttt gtc gaa ggt agt aat caa gaa atc ctt att	192
Ile Asn Val Asp Gly Phe Val Glu Gly Ser Asn Gln Glu Ile Leu Ile	
50 55 60	
aga gga att cat cat gtt tta aca gat caa aac caa aag att gtt aca	240
Arg Gly Ile His His Val Leu Thr Asp Gln Asn Gln Lys Ile Val Thr	
65 70 75 80	
aag gcc gag ttg tta gac gct att aga cat caa atg gtt ctt cta caa	288
Lys Ala Glu Leu Leu Asp Ala Ile Arg His Gln Met Val Leu Leu Gln	
85 90 95	
ttg gat tat tcc tat gaa cta gtc gac ttt gcg cct gat gca caa tta	336
Leu Asp Tyr Ser Tyr Glu Leu Val Asp Phe Ala Pro Asp Ala Gln Leu	
100 105 110	
tta aca caa gat cga cgg ctt tta ttt gcc aat caa aat ttt gag gaa	384
Leu Thr Gln Asp Arg Arg Leu Leu Phe Ala Asn Gln Asn Phe Glu Glu	
115 120 125	

PCT_Sequence_listing (3)

tcc gta tca ctt gaa gat act att caa gaa tac ctt tta aaa ggg cat	432
Ser Val Ser Leu Glu Asp Thr Ile Gln Glu Tyr Leu Leu Lys Gly His	
130 135 140	
ggt att ctc aga aaa cgg gtt gaa gaa cct atc act cat cct act gag	480
Val Ile Leu Arg Lys Arg Val Glu Glu Pro Ile Thr His Pro Thr Glu	
145 150 155 160	
act gct aat att gag tat aaa gtt caa ttc gcg act aaa gat ggg gaa	528
Thr Ala Asn Ile Glu Tyr Lys Val Gln Phe Ala Thr Lys Asp Gly Glu	
165 170 175	
ttc cac cca cta cct att ttt gta gac tac gga gaa aaa cat att gga	576
Phe His Pro Leu Pro Ile Phe Val Asp Tyr Gly Glu Lys His Ile Gly	
180 185 190	
gaa aaa tta acc tct gac gag ttt cga aaa att gca gaa gaa aag ctt	624
Glu Lys Leu Thr Ser Asp Glu Phe Arg Lys Ile Ala Glu Glu Lys Leu	
195 200 205	
ttg caa ctc tac cct gac tat atg att gat caa aaa gaa tat act atc	672
Leu Gln Leu Tyr Pro Asp Tyr Met Ile Asp Gln Lys Glu Tyr Thr Ile	
210 215 220	
att aaa cac aat tct ctt ggt caa ctt cca aga tat tat tct tat caa	720
Ile Lys His Asn Ser Leu Gly Gln Leu Pro Arg Tyr Tyr Ser Tyr Gln	
225 230 235 240	
gat cat ttc agc tac gaa att caa gat agg caa cgt atc atg gct aag	768
Asp His Phe Ser Tyr Glu Ile Gln Asp Arg Gln Arg Ile Met Ala Lys	
245 250 255	
gac cca aaa tcc gga aaa gaa ctc ggt gaa act caa agt att gat aat	816
Asp Pro Lys Ser Gly Lys Glu Leu Gly Glu Thr Gln Ser Ile Asp Asn	
260 265 270	
ggt ttt gag aaa tac ctt att acc aaa aaa agt tat aaa cct	858
Val Phe Glu Lys Tyr Leu Ile Thr Lys Lys Ser Tyr Lys Pro	
275 280 285	

<210> 164
<211> 286
<212> PRT
<213> Streptococcus uberis

<400> 164

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

PCT_Sequence_listing (3)

Leu Thr Gln Asp Arg Arg Leu Leu Phe Ala Asn Gln Asn Phe Glu Glu
115 120 125

Ser Val Ser Leu Glu Asp Thr Ile Gln Glu Tyr Leu Leu Lys Gly His
130 135 140

Val Ile Leu Arg Lys Arg Val Glu Glu Pro Ile Thr His Pro Thr Glu
145 150 155 160

Thr Ala Asn Ile Glu Tyr Lys Val Gln Phe Ala Thr Lys Asp Gly Glu
165 170 175

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

Glu Lys Leu Thr Ser Asp Glu Phe Arg Lys Ile Ala Glu Glu Lys Leu
195 200 205

Leu Gln Leu Tyr Pro Asp Tyr Met Ile Asp Gln Lys Glu Tyr Thr Ile
210 215 220

Ile Lys His Asn Ser Leu Gly Gln Leu Pro Arg Tyr Tyr Ser Tyr Gln
225 230 235 240

Asp His Phe Ser Tyr Glu Ile Gln Asp Arg Gln Arg Ile Met Ala Lys
245 250 255

Asp Pro Lys Ser Gly Lys Glu Leu Gly Glu Thr Gln Ser Ile Asp Asn
260 265 270

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

<210> 165
<211> 2637
<212> DNA
<213> Streptococcus uberis

<220>
<221> CDS
<222> (1)..(2637)

<400> 165
atg gaa ttc gaa aac aca aaa tct aat cag att aaa aca aca ctt gct 48
Met Glu Phe Glu Asn Thr Lys Ser Asn Gln Ile Lys Thr Thr Leu Ala
1 5 10 15

tta acg tca aca ctc gca ctt ctt gga act ggt gtt ggt atg gga cat 96
Leu Thr Ser Thr Leu Ala Leu Leu Gly Thr Gly Val Gly Met Gly His
20 25 30

acc gtt aat gcg gat gac atg aca act gct gat caa tca cct aaa tta 144
Thr Val Asn Ala Asp Asp Met Thr Thr Ala Asp Gln Ser Pro Lys Leu
35 40 45

caa ggt gaa gaa gca aca ttg gcg cct aca aac att gaa gat act aaa 192
Gln Gly Glu Glu Ala Thr Leu Ala Pro Thr Asn Ile Glu Asp Thr Lys
50 55 60

gca gcc att gat att aaa aca gct aca tta gca gaa caa acc gat gct 240
Ala Ala Ile Asp Ile Lys Thr Ala Thr Leu Ala Glu Gln Thr Asp Ala
65 70 75 80

PCT_Sequence_listing (3)

ctt aat act gta aat gag aca atc aca agc aca aat gaa gaa tta gct Leu Asn Thr Val Asn Glu Thr Ile Thr Ser Thr Asn Glu Glu Leu Ala 85 90	288
act tta gaa gga ggc tta gct gat aaa gaa aca gca gtt gca gat gct Thr Leu Glu Gly Gly Leu Ala Asp Lys Glu Thr Ala Val Ala Asp Ala 100 105 110	336
gaa aaa aca ttg gag tct gtt tca aat gcc tca gaa gaa gaa ttt aat Glu Lys Thr Leu Glu Ser Val Ser Asn Ala Ser Glu Glu Glu Phe Asn 115 120 125	384
caa tta gca gaa caa aat aaa gct gac tta gct aaa act caa gag gag Gln Leu Ala Glu Gln Asn Lys Ala Asp Leu Ala Lys Thr Gln Glu Glu 130 135 140	432
cta aaa ctt gct gaa gca aca aaa gaa gaa gtt gca aca cag gta ttg Leu Lys Leu Ala Glu Ala Thr Lys Glu Glu Val Ala Thr Gln Val Leu 145 150 155 160	480
aca caa tct gac gag gta aca gct gca gct aat gaa gct aaa aaa atg Thr Gln Ser Asp Glu Val Thr Ala Ala Asn Glu Ala Lys Lys Met 165 170 175	528
gct gaa aaa gtt gca caa gca gag aca aaa gtt tca gac ttg acg aaa Ala Glu Lys Val Ala Gln Ala Glu Thr Lys Val Ser Asp Leu Thr Lys 180 185 190	576
atg gtc aat caa cca gaa gca ata aca gct caa gtt gaa ata gaa caa Met Val Asn Gln Pro Glu Ala Ile Thr Ala Gln Val Glu Ile Glu Gln 195 200 205	624
aac aat gtc aaa atc att tcg gaa gat tta gca aaa gcc aaa act gat Asn Asn Val Lys Ile Ile Ser Glu Asp Leu Ala Lys Ala Lys Thr Asp 210 215 220	672
tta gtt gct gta aca gat aat aca aaa aca caa tta gca aat gat tta Leu Val Ala Val Thr Asp Asn Thr Lys Thr Gln Leu Ala Asn Asp Leu 225 230 235 240	720
gcg act gct caa tct agc tta agt gcc aaa caa aat gaa tta gct aaa Ala Thr Ala Gln Ser Ser Leu Ser Ala Lys Gln Asn Glu Leu Ala Lys 245 250 255	768
gta cag tca caa aca agt aat gtc gca gtg aat gtt atg ggt gct aat Val Gln Ser Gln Thr Ser Asn Val Ala Val Asn Val Met Gly Ala Asn 260 265 270	816
aaa atg gtt gct cca act aat tac cca att aat gaa atc aaa aaa tta Lys Met Val Ala Pro Thr Asn Tyr Pro Ile Asn Glu Ile Lys Lys Leu 275 280 285	864
atg tca agt ggt tac att ggg aca caa tct tat cta aat aca ttc tat Met Ser Ser Gly Tyr Ile Gly Thr Gln Ser Tyr Leu Asn Thr Phe Tyr 290 295 300	912
gct tta aaa gat caa ctg gtt tct aaa gca gaa gtt ggg gca tac tta Ala Leu Lys Asp Gln Leu Val Ser Lys Ala Glu Val Gly Ala Tyr Leu 305 310 315 320	960
aat cat tac gtt gat atc gca agt gac tta aac cgt atc gtt aac cca Asn His Tyr Val Asp Ile Ala Ser Asp Leu Asn Arg Ile Val Asn Pro 325 330 335	1008
gat aac tta tca gtt gag gtt caa aat gaa ttg gct gta ttt gca gca Asp Asn Leu Ser Val Glu Val Gln Asn Glu Leu Ala Val Phe Ala Ala 340 345 350	1056
aca ttg att aat tct gtt cgt caa caa ttt ggt ctt tct gca gtc gaa Thr Leu Ile Asn Ser Val Arg Gln Gln Phe Gly Leu Ser Ala Val Glu 355 360 365	1104
gtg acg caa ggt gct caa gag ttt gct cgc act ttg act cga aac tat Val Thr Gln Gly Ala Gln Glu Phe Ala Arg Thr Leu Thr Arg Asn Tyr 370 375 380 385 390	1152

PCT_Sequence_listing (3)

370	375	380	
aaa gta aca cat gga aac act gtt cct ttc ttt aat tac aat caa cct Lys Val Thr His Gly Asn Thr Val Pro Phe Phe Asn Tyr Asn Gln Pro 385 390 395 400			1200
ggc aag aat ggt cat ata ggc att ggt cca cac gat aga aca att atc Gly Lys Asn Gly His Ile Gly Ile Gly Pro His Asp Arg Thr Ile Ile 405 410 415			1248
gaa caa gca gct aca agt gtt ggc tta aaa gct aat gat gat aat atg Glu Gln Ala Ala Thr Ser Val Gly Leu Lys Ala Asn Asp Asp Asn Met 420 425 430			1296
tat gaa aac atc gga ttc ttt gat gat gtt cat act gtt aat ggt atc Tyr Glu Asn Ile Gly Phe Phe Asp Asp Val His Thr Val Asn Gly Ile 435 440 445			1344
aaa cgt agt att tat aac agt att aag tac atg ctg ttt aca gac ttc Lys Arg Ser Ile Tyr Asn Ser Ile Lys Tyr Met Leu Phe Thr Asp Phe 450 455 460			1392
acc tat gga aat aca ttt gga cat acg gtt aac ttg ttg cgt tct gat Thr Tyr Gly Asn Thr Phe Gly His Thr Val Asn Leu Leu Arg Ser Asp 465 470 475 480			1440
aaa aca aac cca agt gct ccg gtc tat tta gga gtt tca aca gaa act Lys Thr Asn Pro Ser Ala Pro Val Tyr Leu Gly Val Ser Thr Glu Thr 485 490 495			1488
gtt ggt ggt tta aat acc cac tat gtt atc ttc ccg gca agc aat att Val Gly Gly Leu Asn Thr His Tyr Val Ile Phe Pro Ala Ser Asn Ile 500 505 510			1536
gta aat gcc agc caa ttc agc aaa caa gtg gtt tca ggt cca tta aca Val Asn Ala Ser Gln Phe Ser Lys Gln Val Val Ser Gly Pro Leu Thr 515 520 525			1584
aca gtt gat aac agt gct aaa att agc act ctt caa gca agt att act Thr Val Asp Asn Ser Ala Lys Ile Ser Thr Leu Gln Ala Ser Ile Thr 530 535 540			1632
tct gtt gag tct aaa att caa acc tta caa aaa cgt att gca aat att Ser Val Glu Ser Lys Ile Gln Thr Leu Gln Lys Arg Ile Ala Asn Ile 545 550 555 560			1680
tct tca gaa gca cta gtt gtc tct gca cag aga aaa gta gat ggt tta Ser Ser Glu Ala Leu Val Val Ser Ala Gln Arg Lys Val Asp Gly Leu 565 570 575			1728
gct gca aaa ctt caa aaa gct gaa tct aac gtt gaa aaa gca aaa gct Ala Ala Lys Leu Gln Lys Ala Glu Ser Asn Val Glu Lys Ala Lys Ala 580 585 590			1776
caa ctt caa cag tta caa gat tca aaa gaa gat tta cat aaa caa ctt Gln Leu Gln Gln Leu Gln Asp Ser Lys Glu Asp Leu His Lys Gln Leu 595 600 605			1824
gct ttt tcc ctt tca act cgt aag gat tta aaa ggt caa ctt gac gaa Ala Phe Ser Leu Ser Thr Arg Lys Asp Leu Lys Gly Gln Leu Asp Glu 610 615 620			1872
tcg ctt gtt cac cta aat cag tct aaa att ctt tta cat agc tta gaa Ser Leu Val His Leu Asn Gln Ser Lys Ile Leu Leu His Ser Leu Glu 625 630 635 640			1920
gaa aaa caa agt caa gtg gca agt caa att aac gtc ttg aca ttg aag Glu Lys Gln Ser Gln Val Ala Ser Gln Ile Asn Val Leu Thr Leu Lys 645 650 655			1968
aag gca caa ctt gaa aaa gaa cta gcc ttt aac tct cat cca aat cgt Lys Ala Gln Leu Glu Lys Glu Leu Ala Phe Asn Ser His Pro Asn Arg 660 665 670			2016
gaa aaa gtt gca aaa gaa aaa gtt gaa gag gct caa aaa gca tta aca 675 680 685 690			2064

PCT_Sequence_listing (3)

Glu	Lys	Val	Ala	Lys	Glu	Lys	Val	Glu	Glu	Ala	Gln	Lys	Ala	Leu	Thr	
		675					680					685				
gaa	acc	tta	tct	caa	att	aaa	act	aaa	aaa	gct	atc	tta	aat	gat	tta	2112
Glu	Thr	Leu	Ser	Gln	Ile	Lys	Thr	Lys	Lys	Ala	Ile	Leu	Asn	Asp	Leu	
	690					695					700					
aca	caa	gaa	aaa	gca	aaa	ttg	acg	tca	gca	atc	aca	aca	act	gaa	caa	2160
Thr	Gln	Glu	Lys	Ala	Lys	Leu	Thr	Ser	Ala	Ile	Thr	Thr	Thr	Glu	Gln	
	705				710					715					720	
caa	att	gtt	ttg	ttg	aag	aat	cat	tta	gca	aat	caa	gtg	gcg	aat	gct	2208
Gln	Ile	Val	Leu	Leu	Lys	Asn	His	Leu	Ala	Asn	Gln	Val	Ala	Asn	Ala	
			725						730					735		
cca	aaa	atc	agc	agt	att	gtc	caa	aga	tca	gaa	aac	aat	aga	gta	aga	2256
Pro	Lys	Ile	Ser	Ser	Ile	Val	Gln	Arg	Ser	Glu	Asn	Asn	Arg	Val	Arg	
			740					745					750			
cct	gat	gtt	tct	gat	aca	aga	gag	aag	gca	gta	gat	act	gct	caa	gaa	2304
Pro	Asp	Val	Ser	Asp	Thr	Arg	Glu	Lys	Ala	Val	Asp	Thr	Ala	Gln	Glu	
		755					760					765				
gcg	aca	att	ctt	gct	caa	gca	gaa	aca	atg	gct	gaa	gaa	gtc	att	aca	2352
Ala	Thr	Ile	Leu	Ala	Gln	Ala	Glu	Thr	Met	Ala	Glu	Glu	Val	Ile	Thr	
	770					775					780					
aat	tct	gca	aaa	gcc	att	gtt	gca	aat	gct	caa	aat	gtt	gca	caa	gag	2400
Asn	Ser	Ala	Lys	Ala	Ile	Val	Ala	Asn	Ala	Gln	Asn	Val	Ala	Gln	Glu	
	785				790					795					800	
att	atg	aaa	gta	gca	cct	gaa	gta	aca	cct	gat	caa	gga	gtt	gtt	gca	2448
Ile	Met	Lys	Val	Ala	Pro	Glu	Val	Thr	Pro	Asp	Gln	Gly	Val	Val	Ala	
				805					810					815		
aaa	gtt	gca	gat	aat	att	aag	aaa	aat	aat	gcc	cca	gca	agt	aaa	tca	2496
Lys	Val	Ala	Asp	Asn	Ile	Lys	Lys	Asn	Asn	Ala	Pro	Ala	Ser	Lys	Ser	
			820					825					830			
tat	ggc	gca	agt	tca	tca	acg	gta	gga	aat	gct	act	tct	tca	cga	gat	2544
Tyr	Gly	Ala	Ser	Ser	Ser	Thr	Val	Gly	Asn	Ala	Thr	Ser	Ser	Arg	Asp	
		835					840					845				
gaa	agt	aca	aaa	cgt	gct	tta	aga	gca	gga	att	gtt	atg	ctg	gca	gca	2592
Glu	Ser	Thr	Lys	Arg	Ala	Leu	Arg	Ala	Gly	Ile	Val	Met	Leu	Ala	Ala	
	850					855					860					
gca	gga	ctt	act	ggc	tac	aaa	ctc	aga	aga	gat	ggc	aaa	aaa	taa		2637
Ala	Gly	Leu	Thr	Gly	Tyr	Lys	Leu	Arg	Arg	Asp	Gly	Lys	Lys			
	865				870					875						

<210> 166
<211> 878
<212> PRT
<213> Streptococcus uberis

<400> 166

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

PCT_Sequence_listing (3)

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

PCT_Sequence_listing (3)

Val Thr Gln Gly Ala Gln Glu Phe Ala Arg Thr Leu Thr Arg Asn Tyr
370 375 380

Lys Val Thr His Gly Asn Thr Val Pro Phe Phe Asn Tyr Asn Gln Pro
385 390 395 400

Gly Lys Asn Gly His Ile Gly Ile Gly Pro His Asp Arg Thr Ile Ile
405 410 415

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

Tyr Glu Asn Ile Gly Phe Phe Asp Asp Val His Thr Val Asn Gly Ile
435 440 445

Lys Arg Ser Ile Tyr Asn Ser Ile Lys Tyr Met Leu Phe Thr Asp Phe
450 455 460

Thr Tyr Gly Asn Thr Phe Gly His Thr Val Asn Leu Leu Arg Ser Asp
465 470 475 480

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

Val Gly Gly Leu Asn Thr His Tyr Val Ile Phe Pro Ala Ser Asn Ile
500 505 510

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

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

Ser Val Glu Ser Lys Ile Gln Thr Leu Gln Lys Arg Ile Ala Asn Ile
545 550 555 560

Ser Ser Glu Ala Leu Val Val Ser Ala Gln Arg Lys Val Asp Gly Leu
565 570 575

Ala Ala Lys Leu Gln Lys Ala Glu Ser Asn Val Glu Lys Ala Lys Ala
580 585 590

Gln Leu Gln Gln Leu Gln Asp Ser Lys Glu Asp Leu His Lys Gln Leu
595 600 605

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

Ser Leu Val His Leu Asn Gln Ser Lys Ile Leu Leu His Ser Leu Glu
625 630 635 640

Glu Lys Gln Ser Gln Val Ala Ser Gln Ile Asn Val Leu Thr Leu Lys
645 650 655

Lys Ala Gln Leu Glu Lys Glu Leu Ala Phe Asn Ser His Pro Asn Arg
660 665 670

PCT_Sequence_listing (3)

Glu Lys Val Ala Lys Glu Lys Val Glu Glu Ala Gln Lys Ala Leu Thr
675 680 685

Glu Thr Leu Ser Gln Ile Lys Thr Lys Lys Ala Ile Leu Asn Asp Leu
690 695 700

Thr Gln Glu Lys Ala Lys Leu Thr Ser Ala Ile Thr Thr Thr Glu Gln
705 710 715 720

Gln Ile Val Leu Leu Lys Asn His Leu Ala Asn Gln Val Ala Asn Ala
725 730 735

Pro Lys Ile Ser Ser Ile Val Gln Arg Ser Glu Asn Asn Arg Val Arg
740 745 750

Pro Asp Val Ser Asp Thr Arg Glu Lys Ala Val Asp Thr Ala Gln Glu
755 760 765

Ala Thr Ile Leu Ala Gln Ala Glu Thr Met Ala Glu Glu Val Ile Thr
770 775 780

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

Ile Met Lys Val Ala Pro Glu Val Thr Pro Asp Gln Gly Val Val Ala
805 810 815

Lys Val Ala Asp Asn Ile Lys Lys Asn Asn Ala Pro Ala Ser Lys Ser
820 825 830

Tyr Gly Ala Ser Ser Ser Thr Val Gly Asn Ala Thr Ser Ser Arg Asp
835 840 845

Glu Ser Thr Lys Arg Ala Leu Arg Ala Gly Ile Val Met Leu Ala Ala
850 855 860

Ala Gly Leu Thr Gly Tyr Lys Leu Arg Arg Asp Gly Lys Lys
865 870 875

<210> 167
<211> 1284
<212> DNA
<213> Streptococcus uberis

<220>
<221> CDS
<222> (1)..(1284)

<400> 167	
atg aaa aaa tta tta gct tgt atg tta atg gtc ttt ttt cta tct cct	48
Met Lys Lys Leu Leu Ala Cys Met Leu Met Val Phe Phe Leu Ser Pro	
1 5 10 15	
att tct gtt att agt act gaa aaa tct ata tca ttt cca agt aca acc	96
Ile Ser Val Ile Ser Thr Glu Lys Ser Ile Ser Phe Pro Ser Thr Thr	
20 25 30	
att cat caa ttg tct caa aac gtg cta act tct agt acg tat ttt aat	144
Ile His Gln Leu Ser Gln Asn Val Leu Thr Ser Ser Thr Tyr Phe Asn	

285

PCT_Sequence_listing (3)

35	40	45	
gca att cct aaa aat cca aat gtc tac gat gag ctt caa aca tat agt Ala Ile Pro Lys Asn Pro Asn Val Tyr Asp Glu Leu Gln Thr Tyr Ser 50 55 60			192
gat caa tct tta aca att cca agt gga gtt ctt aaa cca aat gat gat Asp Gln Ser Leu Thr Ile Pro Ser Gly Val Leu Lys Pro Asn Asp Asp 65 70 75 80			240
ttt ata atc aat aat ctt ttg tta aat caa aat aat tta cca att ttt Phe Ile Ile Asn Asn Leu Leu Leu Asn Gln Asn Asn Leu Pro Ile Phe 85 90 95			288
caa tta gca aat gga caa ttt att ttg gca aat aaa aag ttc att tat Gln Leu Ala Asn Gly Gln Phe Ile Leu Ala Asn Lys Lys Phe Ile Tyr 100 105 110			336
gaa gac gaa aca act aat caa acc aat ctc aat agt tgg ttg tgg cta Glu Asp Glu Thr Thr Asn Gln Thr Asn Leu Asn Ser Trp Leu Trp Leu 115 120 125			384
caa aaa gat ttt aca atc tat gaa gaa cct ctt gta aaa gga gtt tta Gln Lys Asp Phe Thr Ile Tyr Glu Glu Pro Leu Val Lys Gly Val Leu 130 135 140			432
cct att aat agt gat tta aaa cct tat tca aaa gtt cat gtt aca aaa Pro Ile Asn Ser Asp Leu Lys Pro Tyr Ser Lys Val His Val Thr Lys 145 150 155 160			480
cta tca caa aca cag cat gga aat ttt tat tat att gaa aac aaa ggt Leu Ser Gln Thr Gln His Gly Asn Phe Tyr Tyr Ile Glu Asn Lys Gly 165 170 175			528
tgg gtt tct gag aaa tat ctc tca aaa gct gat aac aga atg gta aaa Trp Val Ser Glu Lys Tyr Leu Ser Lys Ala Asp Asn Arg Met Val Lys 180 185 190			576
gtt caa gaa atg ctg agt caa aaa tat aat aaa gaa aat tat tct att Val Gln Glu Met Leu Ser Gln Lys Tyr Asn Lys Glu Asn Tyr Ser Ile 195 200 205			624
ttt gtt aaa caa tta aca aca cag aca agt gca gga atc aat gcc gat Phe Val Lys Gln Leu Thr Thr Gln Thr Ser Ala Gly Ile Asn Ala Asp 210 215 220			672
aaa tta atg tat tct gca agt att gct aaa tta gca acc tta tac tat Lys Leu Met Tyr Ser Ala Ser Ile Ala Lys Leu Ala Thr Leu Tyr Tyr 225 230 235 240			720
gtt caa aat aag att gaa act ggt aaa act tct ctt aat cag acc tta Val Gln Asn Lys Ile Glu Thr Gly Lys Thr Ser Leu Asn Gln Thr Leu 245 250 255			768
aaa tat act gat caa gta aac cat ttt aaa ggt gac tat gat cca tca Lys Tyr Thr Asp Gln Val Asn His Phe Lys Gly Asp Tyr Asp Pro Ser 260 265 270			816
ggg agt ggt aaa ctt cca aaa acg tca gat aat gag aat tat act gtt Gly Ser Gly Lys Leu Pro Lys Thr Ser Asp Asn Glu Asn Tyr Thr Val 275 280 285			864
gat gat tta tta aaa gca gtt gcc cag cat tct gat aat gtt gct aca Asp Asp Leu Leu Lys Ala Val Ala Gln His Ser Asp Asn Val Ala Thr 290 295 300			912
aat ata ctt ggc tat tat cta gct aat caa tat gat aga gat ttc tct Asn Ile Leu Gly Tyr Tyr Leu Ala Asn Gln Tyr Asp Arg Asp Phe Ser 305 310 315 320			960
act caa atg aca gct att tct ggt att aat tgg gat atg gaa gaa cgg Thr Gln Met Thr Ala Ile Ser Gly Ile Asn Trp Asp Met Glu Glu Arg 325 330 335			1008
atg tta tct tca aaa gca gca gca aat gta atg gaa tct att tac tat			1056

PCT_Sequence_listing (3)

Met	Leu	Ser	Ser	Lys	Ala	Ala	Ala	Asn	Val	Met	Glu	Ser	Ile	Tyr	Tyr		
			340					345					350				
caa	aat	gga	cct	att	gtt	tct	tat	tta	aca	aat	act	gat	ttt	gac	aat	1104	
Gln	Asn	Gly	Pro	Ile	Val	Ser	Tyr	Leu	Thr	Asn	Thr	Asp	Phe	Asp	Asn		
		355					360					365					
caa	cgt	att	tct	aaa	aat	att	gct	gta	cca	gta	gct	cat	aaa	att	ggg	1152	
Gln	Arg	Ile	Ser	Lys	Asn	Ile	Ala	Val	Pro	Val	Ala	His	Lys	Ile	Gly		
	370					375					380						
gat	gcc	tat	gat	tat	aaa	cat	gat	gtt	gca	ata	gtt	tat	agt	gac	tcg	1200	
Asp	Ala	Tyr	Asp	Tyr	Lys	His	Asp	Val	Ala	Ile	Val	Tyr	Ser	Asp	Ser		
	385				390					395					400		
cca	ttc	att	cta	tcg	att	ttt	agt	gag	aac	gca	tcc	tat	gat	gat	att	1248	
Pro	Phe	Ile	Leu	Ser	Ile	Phe	Ser	Glu	Asn	Ala	Ser	Tyr	Asp	Asp	Ile		
			405					410						415			
act	gca	atc	gcc	gat	ggg	att	tat	tct	ata	ttg	aaa					1284	
Thr	Ala	Ile	Ala	Asp	Gly	Ile	Tyr	Ser	Ile	Leu	Lys						
			420					425									

<210> 168
 <211> 428
 <212> PRT
 <213> Streptococcus uberis

<400> 168

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

PCT_Sequence_listing (3)

Trp Val Ser Glu Lys Tyr Leu Ser Lys Ala Asp Asn Arg Met Val Lys
 180 185 190

Val Gln Glu Met Leu Ser Gln Lys Tyr Asn Lys Glu Asn Tyr Ser Ile
 195 200 205

Phe Val Lys Gln Leu Thr Thr Gln Thr Ser Ala Gly Ile Asn Ala Asp
 210 215 220

Lys Leu Met Tyr Ser Ala Ser Ile Ala Lys Leu Ala Thr Leu Tyr Tyr
 225 230 235 240

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

Lys Tyr Thr Asp Gln Val Asn His Phe Lys Gly Asp Tyr Asp Pro Ser
 260 265 270

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

Asp Asp Leu Leu Lys Ala Val Ala Gln His Ser Asp Asn Val Ala Thr
 290 295 300

Asn Ile Leu Gly Tyr Tyr Leu Ala Asn Gln Tyr Asp Arg Asp Phe Ser
 305 310 315 320

Thr Gln Met Thr Ala Ile Ser Gly Ile Asn Trp Asp Met Glu Glu Arg
 325 330 335

Met Leu Ser Ser Lys Ala Ala Ala Asn Val Met Glu Ser Ile Tyr Tyr
 340 345 350

Gln Asn Gly Pro Ile Val Ser Tyr Leu Thr Asn Thr Asp Phe Asp Asn
 355 360 365

Gln Arg Ile Ser Lys Asn Ile Ala Val Pro Val Ala His Lys Ile Gly
 370 375 380

Asp Ala Tyr Asp Tyr Lys His Asp Val Ala Ile Val Tyr Ser Asp Ser
 385 390 395 400

Pro Phe Ile Leu Ser Ile Phe Ser Glu Asn Ala Ser Tyr Asp Asp Ile
 405 410 415

Thr Ala Ile Ala Asp Gly Ile Tyr Ser Ile Leu Lys
 420 425

<210> 169
 <211> 651
 <212> DNA
 <213> Streptococcus uberis

<220>
 <221> CDS
 <222> (1)..(651)
 <400> 169

PCT_Sequence_listing (3)																	
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1 5 10 15																	
ttg gga ttt gca gtg gca ttg tta gct ctt gtt ttt gct ttt tca agt	Leu	Gly	Phe	Ala	Val	Ala	Leu	Leu	Ala	Leu	Val	Phe	Ala	Phe	Ser	Ser	96
20 25 30																	
aag aaa gta gat aca gaa tca tat gct aaa aaa tca gaa tct aaa gtt	Lys	Lys	Val	Asp	Thr	Glu	Ser	Tyr	Ala	Lys	Lys	Ser	Glu	Ser	Lys	Val	144
35 40 45																	
gtt aaa aat gta aca aaa tca caa tca aca tca tct tca act caa aaa	Val	Lys	Asn	Val	Thr	Lys	Ser	Gln	Ser	Thr	Ser	Ser	Ser	Thr	Gln	Lys	192
50 55 60																	
gtt gaa gca tca aca gaa caa agt tct tca agt caa gaa caa gct aca	Val	Glu	Ala	Ser	Thr	Glu	Gln	Ser	Ser	Ser	Ser	Gln	Glu	Gln	Ala	Thr	240
65 70 75 80																	
cct gat act tca gtg gct act caa tca gta cct gta gaa cag gtt gct	Pro	Asp	Thr	Ser	Val	Ala	Thr	Gln	Ser	Val	Pro	Val	Glu	Gln	Val	Ala	288
85 90 95																	
caa cca aca ccg aca cct tca act gag gtt gca caa cag gtt gta cca	Gln	Pro	Thr	Pro	Thr	Pro	Ser	Thr	Glu	Val	Ala	Gln	Gln	Val	Val	Pro	336
100 105 110																	
gct cag cct agt gtt cca aca act caa tat gct gca act cca gta act	Ala	Gln	Pro	Ser	Val	Pro	Thr	Thr	Gln	Tyr	Ala	Ala	Thr	Pro	Val	Thr	384
115 120 125																	
tat tat caa tca aat gga aat act gcc gga gct att ggt agt cag gct	Tyr	Tyr	Gln	Ser	Asn	Gly	Asn	Thr	Ala	Gly	Ala	Ile	Gly	Ser	Gln	Ala	432
130 135 140																	
gct gct caa atg gct gca gca aca ggt gtt cct caa tca act tgg gaa	Ala	Ala	Gln	Met	Ala	Ala	Ala	Thr	Gly	Val	Pro	Gln	Ser	Thr	Trp	Glu	480
145 150 155 160																	
gct att att gct cgc gaa tca aac ggt aac cca tat gta agt aat gca	Ala	Ile	Ile	Ala	Arg	Glu	Ser	Asn	Gly	Asn	Pro	Tyr	Val	Ser	Asn	Ala	528
165 170 175																	
tct ggt gcc tct ggt ttg ttt caa aca atg cca gga tgg ggt tca act	Ser	Gly	Ala	Ser	Gly	Leu	Phe	Gln	Thr	Met	Pro	Gly	Trp	Gly	Ser	Thr	576
180 185 190																	
gca act gta caa gat caa atc aat tct gct att tca gca tat aat gca	Ala	Thr	Val	Gln	Asp	Gln	Ile	Asn	Ser	Ala	Ile	Ser	Ala	Tyr	Asn	Ala	624
195 200 205																	
caa ggc tta tca gct tgg ggt tat taa	Gln	Gly	Leu	Ser	Ala	Trp	Gly	Tyr									651
210 215																	

<210> 170
<211> 216
<212> PRT
<213> Streptococcus uberis

<400> 170

Met Ile Arg Lys Glu Asn Phe Lys Lys Arg Tyr Ile Ser Phe Gly Ile	1	5	10	15												
Leu Gly Phe Ala Val Ala Leu Leu Ala Leu Val Phe Ala Phe Ser Ser		20					25					30				
Lys Lys Val Asp Thr Glu Ser Tyr Ala Lys Lys Ser Glu Ser Lys Val		35					40					45				

PCT_Sequence_listing (3)

Val Lys Asn Val Thr Lys Ser Gln Ser Thr Ser Ser Ser Thr Gln Lys
50 55 60

Val Glu Ala Ser Thr Glu Gln Ser Ser Ser Ser Gln Glu Gln Ala Thr
65 70 75 80

Pro Asp Thr Ser Val Ala Thr Gln Ser Val Pro Val Glu Gln Val Ala
85 90 95

Gln Pro Thr Pro Thr Pro Ser Thr Glu Val Ala Gln Gln Val Val Pro
100 105 110

Ala Gln Pro Ser Val Pro Thr Thr Gln Tyr Ala Ala Thr Pro Val Thr
115 120 125

Tyr Tyr Gln Ser Asn Gly Asn Thr Ala Gly Ala Ile Gly Ser Gln Ala
130 135 140

Ala Ala Gln Met Ala Ala Ala Thr Gly Val Pro Gln Ser Thr Trp Glu
145 150 155 160

Ala Ile Ile Ala Arg Glu Ser Asn Gly Asn Pro Tyr Val Ser Asn Ala
165 170 175

Ser Gly Ala Ser Gly Leu Phe Gln Thr Met Pro Gly Trp Gly Ser Thr
180 185 190

Ala Thr Val Gln Asp Gln Ile Asn Ser Ala Ile Ser Ala Tyr Asn Ala
195 200 205

Gln Gly Leu Ser Ala Trp Gly Tyr
210 215

<210> 171
<211> 954
<212> DNA
<213> Streptococcus uberis

<220>
<221> CDS
<222> (1)..(954)

<400> 171
atg aaa tca ttt ttt aat agt cgg att tgg ctt gga ctt gtt tcg gtg 48
Met Lys Ser Phe Phe Asn Ser Arg Ile Trp Leu Gly Leu Val Ser Val
1 5 10 15

ttt ttt gct att gtc ctc ttt tta aca gca gct tca aat agt tat cga 96
Phe Phe Ala Ile Val Leu Phe Leu Thr Ala Ala Ser Asn Ser Tyr Arg
20 25 30

aac tct gca aac caa gca tac agc cca atc gaa acc tat acc cac aac 144
Asn Ser Ala Asn Gln Ala Tyr Ser Pro Ile Glu Thr Tyr Thr His Asn
35 40 45

cta tca gat gtt cct atc gat atc aaa tat gac agc gac aag tac ttt 192
Leu Ser Asp Val Pro Ile Asp Ile Lys Tyr Asp Ser Asp Lys Tyr Phe
50 55 60

atc agt gag tac tcc tac ggg gca caa gtc tat ttg acc tca acc aac 240
Ile Ser Glu Tyr Ser Tyr Gly Ala Gln Val Tyr Leu Thr Ser Thr Asn
65 70 75 80

PCT_Sequence_listing (3)

cgg Arg	gtt Val	aaa Lys	ctg Leu	gat Asp 85	tcc Ser	gag Glu	gtt Val	aac Asn	act Thr 90	gat Asp	acc Thr	cgt Arg	aat Asn	ttt Phe 95	aaa Lys	288
atc Ile	gtc Val	gca Ala	gac Asp 100	tta Leu	aca Thr	gat Asp	agc Ser	aag Lys 105	cct Pro	gga Gly	aaa Lys	gca Ala	act Thr 110	gtt Val	cct Pro	336
ctt Leu	aaa Lys	gtc Val 115	aat Asn	aac Asn	cta Leu	cct Pro	tct Ser 120	ggc Gly	gtg Val	gca Ala	gcc Ala	aaa Lys 125	gtg Val	acc Thr	cca Pro	384
gat Asp	aaa Lys 130	atg Met	acc Thr	atc Ile	acc Thr	atc Ile 135	ggc Gly	aag Lys	aaa Lys	gca Ala	cgt Arg 140	aag Lys	acc Thr	ttt Phe	aat Asn	432
gtc Val 145	gta Val	gga Gly	agt Ser	gtc Val	gat Asp 150	cca Pro	aaa Lys	caa Gln	gtg Val	gca Ala 155	aca Thr	ggt Gly	tat Tyr	gaa Glu	ttg Leu 160	480
ctc Leu	tca Ser	atg Met	gac Asp	aca Thr 165	ggc Gly	att Ile	gac Asp	aaa Lys	gtt Val 170	gaa Glu	gtg Val	acc Thr	agt Ser	gac Asp 175	gag Glu	528
tct Ser	aag Lys	att Ile	gat Asp 180	ttg Leu	att Ile	gat Asp	cat His	gtc Val 185	gtt Val	gcc Ala	aaa Lys	cta Leu	cct Pro 190	gac Asp	gat Asp	576
gtt Val	aaa Lys	tta Leu 195	aat Asn	gca Ala	gac Asp	tac Tyr	cga Arg 200	gga Gly	gaa Glu	gtg Val	act Thr	ctt Leu 205	caa Gln	gca Ala	gtc Val	624
tca Ser	gca Ala 210	gat Asp	gga Gly	acg Thr	gtt Val	tta Leu 215	gcc Ala	agc Ser	tcc Ser	att Ile	tca Ser 220	cca Pro	gcc Ala	aaa Lys	acg Thr	672
acc Thr 225	tta Leu	tcg Ser	gtt Val	tca Ser	gtc Val 230	aaa Lys	aaa Lys	atc Ile	acc Thr	aag Lys 235	tct Ser	gtt Val	cca Pro	ata Ile	aga Arg 240	720
gtt Val	tca Ser	atg Met	gta Val	gga Gly 245	acc Thr	atg Met	gat Asp	gaa Glu	agc Ser 250	ttg Leu	gcg Ala	gat Asp	att Ile	cag Gln 255	cca Pro	768
aaa Lys	ctt Leu	gga Gly	aaa Lys 260	gaa Glu	aca Thr	gct Ala	gtc Val	att Ile 265	tca Ser	ggg Gly	cca Pro	aga Arg	gaa Glu 270	gtt Val	ctg Leu	816
gat Asp	acc Thr	att Ile 275	aat Asn	gaa Glu	gtg Val	gta Val	gcg Ala 280	gaa Glu	gtc Val	aat Asn	att Ile	agt Ser 285	ggt Gly	gtg Val	act Thr	864
aaa Lys	gat Asp 290	acg Thr	gaa Glu	aaa Lys	acg Thr	gtt Val 295	agc Ser	ctc Leu	cat His	tcg Ser	gat Asp 300	att Ile	gta Val	tcc Ser	att Ile	912
gaa Glu 305	cct Pro	tct Ser	tcc Ser	gtg Val	ccg Pro 310	gtt Val	cag Gln	ttg Leu	aca Thr	acc Thr 315	aaa Lys	aag Lys	aaa Lys			954

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<210> 172
<211> 318
<212> PRT
<213> Streptococcus uberis
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<400> 172

Met Lys Ser Phe Phe Asn Ser Arg Ile Trp Leu Gly Leu Val Ser Val
1 5 10 15

Phe Phe Ala Ile Val Leu Phe Leu Thr Ala Ala Ser Asn Ser Tyr Arg
20 25 30

PCT_Sequence_listing (3)

Asn Ser Ala Asn Gln Ala Tyr Ser Pro Ile Glu Thr Tyr Thr His Asn
35 40 45

Leu Ser Asp Val Pro Ile Asp Ile Lys Tyr Asp Ser Asp Lys Tyr Phe
50 55 60

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

Arg Val Lys Leu Asp Ser Glu Val Asn Thr Asp Thr Arg Asn Phe Lys
85 90 95

Ile Val Ala Asp Leu Thr Asp Ser Lys Pro Gly Lys Ala Thr Val Pro
100 105 110

Leu Lys Val Asn Asn Leu Pro Ser Gly Val Ala Ala Lys Val Thr Pro
115 120 125

Asp Lys Met Thr Ile Thr Ile Gly Lys Lys Ala Arg Lys Thr Phe Asn
130 135 140

Val Val Gly Ser Val Asp Pro Lys Gln Val Ala Thr Gly Tyr Glu Leu
145 150 155 160

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

Ser Lys Ile Asp Leu Ile Asp His Val Val Ala Lys Leu Pro Asp Asp
180 185 190

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

Ser Ala Asp Gly Thr Val Leu Ala Ser Ser Ile Ser Pro Ala Lys Thr
210 215 220

Thr Leu Ser Val Ser Val Lys Lys Ile Thr Lys Ser Val Pro Ile Arg
225 230 235 240

Val Ser Met Val Gly Thr Met Asp Glu Ser Leu Ala Asp Ile Gln Pro
245 250 255

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

Asp Thr Ile Asn Glu Val Val Ala Glu Val Asn Ile Ser Gly Val Thr
275 280 285

Lys Asp Thr Glu Lys Thr Val Ser Leu His Ser Asp Ile Val Ser Ile
290 295 300

Glu Pro Ser Ser Val Pro Val Gln Leu Thr Thr Lys Lys Lys
305 310 315

<210> 173

PCT_Sequence_listing (3)

<211> 723
<212> DNA
<213> Streptococcus uberis

<220>
<221> CDS
<222> (1)..(723)

<400> 173
atg aag cca tca aat acg gaa aaa cta ttt ctc att ttg agt ctt tta 48
Met Lys Pro Ser Asn Thr Glu Lys Leu Phe Leu Ile Leu Ser Leu Leu
1 5 10 15
aca tta att ctt gca ggt agt ttt tat tta ttc ttt gca aga aac cat 96
Thr Leu Ile Leu Ala Gly Ser Phe Tyr 25 Leu Phe Phe Ala Arg Asn His
20 30
atc gga aac gcc tta aca caa aaa gaa aca caa aca gtt caa aaa agt 144
Ile Gly Asn Ala Leu Thr Gln Lys Glu Thr Gln Thr Val Gln Lys Ser
35 40 45
aat atg tta agc aag gcc att gac gcc cta gaa aaa gct gag aaa aat 192
Asn Met Leu Ser Lys Ala Ile Asp Ala Leu Glu Lys Ala Glu Lys Asn
50 55 60
cca agt ctt gaa gca att gaa aaa gct gag aaa gcc att aat cag ttg 240
Pro Ser Leu Glu Ala Ile Glu Lys Ala Glu Lys Ala Ile Asn Gln Leu
65 70 75 80
aaa aaa act gat act aag tta cgt ctc caa gag cga cta aat caa cta 288
Lys Lys Thr Asp Thr Lys Leu Arg Leu Gln Glu Arg Leu Asn Gln Leu
85 90 95
aaa aaa gct ttc tcc att gaa aag gaa gcc att aaa gca ctt gag gag 336
Lys Lys Ala Phe Ser Ile Glu Lys Glu Ala Ile Lys Ala Leu Glu Glu
100 105 110
gct gaa aaa aat cct agt ctt gaa acc aaa gac aaa gct aaa gaa gcc 384
Ala Glu Lys Asn Pro Ser Leu Glu Thr Lys Asp Lys Ala Lys Glu Ala
115 120 125
att gat aaa att gga aat ctc acc aaa aaa aat gag ctc tta aat cga 432
Ile Asp Lys Ile Gly Asn Leu Thr Lys Lys Asn Glu Leu Leu Asn Arg
130 135 140
tta gga gca att gtc att tca gat caa gca cct gaa tca agc tcc aca 480
Leu Gly Ala Ile Val Ile Ser Asp Gln Ala Pro 155 Glu Ser Ser Ser Thr
145 150 155 160
tcg tca gaa gct gca agt gac acg act ata agt gat gca aac aca gga 528
Ser Ser Glu Ala Ala Ser Asp Thr Thr Ile Ser Asp Ala Asn Thr Gly
165 170 175
aat gca gaa caa gca acc att tat gaa agt ccg gtt gca cca gct gaa 576
Asn Ala Glu Gln Ala Thr Ile Tyr Glu Ser Pro Val Ala Pro Ala Glu
180 185 190
agc tat gtt cct caa gcc ccc gct caa agt gtt gga gaa cct gtc caa 624
Ser Tyr Val Pro Gln Ala Pro Ala Gln Ser Val Gly Glu Pro Val Gln
195 200 205
ccc gca aca cca agt act cct gcg cca agc cct gag gct cca agt act 672
Pro Ala Thr Pro Ser Thr Pro Ala Pro Ser Pro Glu Ala Pro Ser Thr
210 215 220
cct cca act gtt cct gcg aca gat acc cca agt gaa tca acc cct aat 720
Pro Pro Thr Val Pro Ala Thr Asp Thr Pro Ser Glu Ser Thr Pro Asn
225 230 235 240
cca 723
Pro

PCT_Sequence_listing (3)

<210> 174
<211> 241
<212> PRT
<213> Streptococcus uberis

<400> 174

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

<210> 175
<211> 1554
<212> DNA
<213> Streptococcus uberis

PCT_Sequence_listing (3)

<220>
<221> CDS
<222> (1)..(1554)

<400> 175	
atg aag aaa aaa aca ctt gtc atg atg gga ttg gca gga cta gta gca Met Lys Lys Lys Thr Leu Val Met Met Gly Leu Ala Gly Leu Val Ala 1 5 10 15	48
ggc ggt caa ctc tat caa gcc aaa gca gtt tta gca gac caa gaa aaa Gly Gly Gln Leu Tyr Gln Ala Lys Ala Val Leu Ala Asp Gln Glu Lys 20 25 30	96
ctc aaa gtg gta acc act ttt tat cct gtt tat gaa ttt aca aaa ggt Leu Lys Val Val Thr Thr Phe Tyr Pro Val Tyr Glu Phe Thr Lys Gly 35 40 45	144
gtg gta ggt aaa gag gga gat gtt tcc atg ctg atg aag gct gga act Val Val Gly Lys Glu Gly Asp Val Ser Met Leu Met Lys Ala Gly Thr 50 55 60	192
gag cca cat gac ttt gaa ccc tca aca aaa gac att aaa aaa ata caa Glu Pro His Asp Phe Glu Pro Ser Thr Lys Asp Ile Lys Lys Ile Gln 65 70 75 80	240
gat tcg caa gcc ttt att tat atg gat gac aac atg gaa act tgg att Asp Ser Gln Ala Phe Ile Tyr Met Asp Asp Asn Met Glu Thr Trp Ile 85 90 95	288
cca gaa gtg aaa aaa gct att aag tcg aaa aaa gta gcc tat att gaa Pro Glu Val Lys Lys Ala Ile Lys Ser Lys Lys Val Ala Tyr Ile Glu 100 105 110	336
ggc act ggc gac atg tta tta gca gct gga acg gaa gaa ggt cac gat Gly Thr Gly Asp Met Leu Leu Ala Ala Gly Thr Glu Glu Gly His Asp 115 120 125	384
cat gaa gga gaa gat gat cat cat cat gat ggt gaa gac aaa cat ggt His Glu Gly Glu Asp Asp His His His Asp Gly Glu Asp Lys His Gly 130 135 140	432
cat gaa gaa cat agt cat aaa ttt gat cca cat gtt tgg tta tct cca His Glu Glu His Ser His Lys Phe Asp Pro His Val Trp Leu Ser Pro 145 150 155 160	480
tat cgc agt att tct gtc gtt gaa cat ata cgt gat tca ctt tct aaa Tyr Arg Ser Ile Ser Val Val Glu His Ile Arg Asp Ser Leu Ser Lys 165 170 175	528
aaa tat cca gaa aaa gca gaa aag ttt aat gcc aac gct caa gcc tat Lys Tyr Pro Glu Lys Ala Glu Lys Phe Asn Ala Asn Ala Gln Ala Tyr 180 185 190	576
att gaa aaa ttg aaa aag ctt gat tcg gaa tat aca gaa act tta tca Ile Glu Lys Leu Lys Lys Leu Asp Ser Glu Tyr Thr Glu Thr Leu Ser 195 200 205	624
tct gct aaa cag aag agt ttt gtg acg caa cac gcg gca ttt gga tat Ser Ala Lys Gln Lys Ser Phe Val Thr Gln His Ala Phe Gly Tyr 210 215 220	672
atg gca ttg gat tat ggc ttg aat cag gtt gct att aat ggt atc tca Met Ala Leu Asp Tyr Gly Leu Asn Gln Val Ala Ile Asn Gly Ile Ser 225 230 235 240	720
gca gag agt gaa cca tca gct aag cgt att gct gaa ttg tct aaa tat Ala Glu Ser Glu Pro Ser Ala Lys Arg Ile Ala Glu Leu Ser Lys Tyr 245 250 255	768
gtt aaa aaa tat gat att aac tat atc tat ttt gaa gaa aat gct tca Val Lys Lys Tyr Asp Ile Asn Tyr Ile Tyr Phe Glu Glu Asn Ala Ser 260 265 270	816

PCT_Sequence_listing (3)

aat aaa gta gct aag act ctt gca aat gaa gca ggt gtc aaa gct gtt Asn Lys Val Ala Lys Thr Leu Ala Asn Glu Ala Gly Val Lys Ala Val 275 280 285	864
gtt tta agc cct ctt gaa ggt ttg acc caa aaa gaa atg gat aag gga Val Leu Ser Pro Leu Glu Gly Leu Thr Gln Lys Glu Met Asp Lys Gly 290 295 300	912
gaa gat tac ttc tct gtc atg cgt gat aat tta aaa gcc ctt cag ttg Glu Asp Tyr Phe Ser Val Met Arg Asp Asn Leu Lys Ala Leu Gln Leu 305 310 315 320	960
aca acc gaa cgc gaa ggt aag gaa att gac cca gaa gaa gat gca agt Thr Thr Glu Arg Glu Gly Lys Glu Ile Asp Pro Glu Glu Asp Ala Ser 325 330 335	1008
aaa tct gtt tat aat ggt tat ttc aaa gat tct gaa gtc aaa gac cgt Lys Ser Val Tyr Asn Gly Tyr Phe Lys Asp Ser Glu Val Lys Asp Arg 340 345 350	1056
aaa tta agc gat tgg tct ggt gat tgg cag tcc gta tat cca tac tta Lys Leu Ser Asp Trp Ser Gly Asp Trp Gln Ser Val Tyr Pro Tyr Leu 355 360 365	1104
caa gat ggt acc ctt gat cag gtt atg gat tac aaa gct aaa aag tct Gln Asp Gly Thr Leu Asp Gln Val Met Asp Tyr Lys Ala Lys Lys Ser 370 375 380	1152
aaa ggt gaa aaa tct gcg aaa gaa ttc aaa gac tat tac gaa aca ggt Lys Gly Glu Lys Ser Ala Lys Glu Phe Lys Asp Tyr Tyr Glu Thr Gly 385 390 400	1200
tat aaa aca gat gtc aac aag att caa att gat ggc aaa aag aaa acc Tyr Lys Thr Asp Val Asn Lys Ile Gln Ile Asp Gly Lys Lys Lys Thr 405 410 415	1248
atc acc ttt gaa aga aat ggg gac aag aaa acc ttt act tat cag tac Ile Thr Phe Glu Arg Asn Gly Asp Lys Lys Thr Phe Thr Tyr Gln Tyr 420 425 430	1296
tca ggc aag aaa atc tta aca tat gaa aaa gga aac cgt ggt gtc cgt Ser Gly Lys Lys Ile Leu Thr Tyr Glu Lys Gly Asn Arg Gly Val Arg 435 440 445	1344
tat atg ttt gaa act aag gat aaa gat gcg ggc gaa ttc aaa tac att Tyr Met Phe Glu Thr Lys Asp Lys Asp Ala Gly Glu Phe Lys Tyr Ile 450 455 460	1392
caa ttt agt gat cat ggc att gct ccc gaa aaa gca gga cat ttc cac Gln Phe Ser Asp His Gly Ile Ala Pro Glu Lys Ala Gly His Phe His 465 470 475 480	1440
att tat tgg ggt gat caa gga cat gat gcc att gct tca aaa tgg gat Ile Tyr Trp Gly Asp Gln Gly His Asp Ala Ile Ala Ser Lys Trp Asp 485 490 495	1488
cat tgg cca act tac tat ggt tct gat tta agt ggt cgt gaa att gcc His Trp Pro Thr Tyr Tyr Gly Ser Asp Leu Ser Gly Arg Glu Ile Ala 500 505 510	1536
caa gaa atg aat gct cat Gln Glu Met Asn Ala His 515	1554

<210> 176
 <211> 518
 <212> PRT
 <213> Streptococcus uberis
 <400> 176

Met Lys Lys Lys Thr Leu Val Met Met Gly Leu Ala Gly Leu Val Ala
 1 5 10 15

PCT_Sequence_listing (3)

Gly Gly Gln Leu Tyr Gln Ala Lys Ala Val Leu Ala Asp Gln Glu Lys
20 25 30

Leu Lys Val Val Thr Thr Phe Tyr Pro Val Tyr Glu Phe Thr Lys Gly
35 40 45

Val Val Gly Lys Glu Gly Asp Val Ser Met Leu Met Lys Ala Gly Thr
50 55 60

Glu Pro His Asp Phe Glu Pro Ser Thr Lys Asp Ile Lys Lys Ile Gln
65 70 75 80

Asp Ser Gln Ala Phe Ile Tyr Met Asp Asp Asn Met Glu Thr Trp Ile
85 90 95

Pro Glu Val Lys Lys Ala Ile Lys Ser Lys Lys Val Ala Tyr Ile Glu
100 105 110

Gly Thr Gly Asp Met Leu Leu Ala Ala Gly Thr Glu Glu Gly His Asp
115 120 125

His Glu Gly Glu Asp Asp His His His Asp Gly Glu Asp Lys His Gly
130 135 140

His Glu Glu His Ser His Lys Phe Asp Pro His Val Trp Leu Ser Pro
145 150 155 160

Tyr Arg Ser Ile Ser Val Val Glu His Ile Arg Asp Ser Leu Ser Lys
165 170 175

Lys Tyr Pro Glu Lys Ala Glu Lys Phe Asn Ala Asn Ala Gln Ala Tyr
180 185 190

Ile Glu Lys Leu Lys Lys Leu Asp Ser Glu Tyr Thr Glu Thr Leu Ser
195 200 205

Ser Ala Lys Gln Lys Ser Phe Val Thr Gln His Ala Ala Phe Gly Tyr
210 215 220

Met Ala Leu Asp Tyr Gly Leu Asn Gln Val Ala Ile Asn Gly Ile Ser
225 230 235 240

Ala Glu Ser Glu Pro Ser Ala Lys Arg Ile Ala Glu Leu Ser Lys Tyr
245 250 255

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

Asn Lys Val Ala Lys Thr Leu Ala Asn Glu Ala Gly Val Lys Ala Val
275 280 285

Val Leu Ser Pro Leu Glu Gly Leu Thr Gln Lys Glu Met Asp Lys Gly
290 295 300

Glu Asp Tyr Phe Ser Val Met Arg Asp Asn Leu Lys Ala Leu Gln Leu
305 310 315 320

PCT_Sequence_listing (3)

Thr Thr Glu Arg Glu Gly Lys Glu Ile Asp Pro Glu Glu Asp Ala Ser
325 330 335

Lys Ser Val Tyr Asn Gly Tyr Phe Lys Asp Ser Glu Val Lys Asp Arg
340 345 350

Lys Leu Ser Asp Trp Ser Gly Asp Trp Gln Ser Val Tyr Pro Tyr Leu
355 360 365

Gln Asp Gly Thr Leu Asp Gln Val Met Asp Tyr Lys Ala Lys Lys Ser
370 375 380

Lys Gly Glu Lys Ser Ala Lys Glu Phe Lys Asp Tyr Tyr Glu Thr Gly
385 390 395 400

Tyr Lys Thr Asp Val Asn Lys Ile Gln Ile Asp Gly Lys Lys Lys Thr
405 410 415

Ile Thr Phe Glu Arg Asn Gly Asp Lys Lys Thr Phe Thr Tyr Gln Tyr
420 425 430

Ser Gly Lys Lys Ile Leu Thr Tyr Glu Lys Gly Asn Arg Gly Val Arg
435 440 445

Tyr Met Phe Glu Thr Lys Asp Lys Asp Ala Gly Glu Phe Lys Tyr Ile
450 455 460

Gln Phe Ser Asp His Gly Ile Ala Pro Glu Lys Ala Gly His Phe His
465 470 475 480

Ile Tyr Trp Gly Asp Gln Gly His Asp Ala Ile Ala Ser Lys Trp Asp
485 490 495

His Trp Pro Thr Tyr Tyr Gly Ser Asp Leu Ser Gly Arg Glu Ile Ala
500 505 510

Gln Glu Met Asn Ala His
515

<210> 177
<211> 603
<212> DNA
<213> Streptococcus uberis

<220>
<221> CDS
<222> (1)..(603)

<400> 177
atg gca aac tac aaa aaa ata aca tct tta tca ctt ttg acc ctt tta 48
Met Ala Asn Tyr Lys Lys Ile Thr Ser Leu Ser Leu Leu Thr Leu Leu
1 5 10 15

tca ctt gct acc ttt tca gca act caa tat tct aaa gtc tat gca caa 96
Ser Leu Ala Thr Phe Ser Ala Thr Gln Tyr Ser Lys Val Tyr Ala Gln
20 25 30

gat cct gag tca tcc tca tca gtc aat att aaa acc att gat ggt cag 144
Asp Pro Glu Ser Ser Ser Ser Val Asn Ile Lys Thr Ile Asp Gly Gln

PCT_Sequence_listing (3)

35	40	45	
tta gct att gct gac aaa gag gca gag cca tta tac aaa gaa atg gat Leu Ala Ile Ala Asp Lys Glu Ala Glu Pro Leu Tyr Lys Glu Met Asp	192		
50	55	60	
agt att caa atg agt ata gaa aaa att aag gca agc cgc ttt aaa cct Ser Ile Gln Met Ser Ile Glu Lys Ile Lys Ala Ser Arg Phe Lys Pro	240		
65	70	75	80
gct gaa ata gct att aca aca gaa att caa caa ctg gaa aat ctt aat Ala Glu Ile Ala Ile Thr Thr Glu Ile Gln Gln Leu Glu Asn Leu Asn	288		
85	90		95
gaa act cta tta gaa aag ttt tat cag aaa att ggc aat cgt atc tgg Glu Thr Leu Leu Glu Lys Phe Tyr Gln Lys Ile Gly Asn Arg Ile Trp	336		
100	105	110	
aat act aaa gaa gaa gca ctc aat tta att agt aag aca act ctt tca Asn Thr Lys Glu Glu Ala Leu Asn Leu Ile Ser Lys Thr Thr Leu Ser	384		
115	120	125	
cct tct gaa aaa gag cta tta aag gac tac ttt aat aaa gat gag gta Pro Ser Glu Lys Glu Leu Leu Lys Asp Tyr Phe Asn Lys Asp Glu Val	432		
130	135	140	
ttg caa aaa aaa tta aaa gaa aat gac tta ctc att gat caa gag aca Leu Gln Lys Lys Leu Lys Glu Asn Asp Leu Leu Ile Asp Gln Glu Thr	480		
145	150	155	160
gct caa tac aac gca aaa ctg gct atc cta act cag caa gct gat aaa Ala Gln Tyr Asn Ala Lys Leu Ala Ile Leu Thr Gln Gln Ala Asp Lys	528		
165	170	175	
att tat gaa aaa cac ggg att acc aaa gat atc ttg gca gct tac tat Ile Tyr Glu Lys His Gly Ile Thr Lys Asp Ile Leu Ala Ala Tyr Tyr	576		
180	185	190	
atg caa aca gga atg gaa gca gat taa Met Gln Thr Gly Met Glu Ala Asp	603		
195	200		

<210> 178
 <211> 200
 <212> PRT
 <213> Streptococcus uberis

<400> 178
Met Ala Asn Tyr Lys Lys Ile Thr Ser Leu Ser Leu Leu Thr Leu Leu
1 5 10 15
Ser Leu Ala Thr Phe Ser Ala Thr Gln Tyr Ser Lys Val Tyr Ala Gln
20 25 30
Asp Pro Glu Ser Ser Ser Ser Val Asn Ile Lys Thr Ile Asp Gly Gln
35 40 45
Leu Ala Ile Ala Asp Lys Glu Ala Glu Pro Leu Tyr Lys Glu Met Asp
50 55 60
Ser Ile Gln Met Ser Ile Glu Lys Ile Lys Ala Ser Arg Phe Lys Pro
65 70 75 80
Ala Glu Ile Ala Ile Thr Thr Glu Ile Gln Gln Leu Glu Asn Leu Asn
85 90 95
Glu Thr Leu Leu Glu Lys Phe Tyr Gln Lys Ile Gly Asn Arg Ile Trp

PCT_Sequence_listing (3)

100

105

110

Asn Thr Lys Glu Glu Ala Leu Asn Leu Ile Ser Lys Thr Thr Leu Ser
115 120 125

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

Leu Gln Lys Lys Leu Lys Glu Asn Asp Leu Leu Ile Asp Gln Glu Thr
145 150 155 160

Ala Gln Tyr Asn Ala Lys Leu Ala Ile Leu Thr Gln Gln Ala Asp Lys
165 170 175

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

Met Gln Thr Gly Met Glu Ala Asp
195 200

<210> 179
<211> 2274
<212> DNA
<213> Streptococcus uberis

<400> 179
ttgaaatcta aaaagtctta tgttttatta ttagcaccgt ttgttctggc ttcattttgg 60
cagtcaaaga tgggtgtctgc ttcagaaatc gccaatcaaa acgtgacagt tgattcaagt 120
gcaaataata acatgtcatc taagttgtct acttcaaatt tagatacaat tccagaaagt 180
acttctgaag taactgtttt ggatcagtcg acaaatttag taacagaaaa tgtagtccaa 240
gaaaaggcgc tagcatcatc agaaatacaa acagatgaga gtatcatagt atcatctcca 300
tcaggtgacc tcagtgtctc agaagataac acactttctg aagggaatgc tttatcagca 360
gtaggggagcag taaaatctag ttttcaatca gttaatactg atgtatcaag caatctcaaa 420
actgctaaac aggaaacggt cgtttcttta gctgctcaag tagcagagcc cgtaactgca 480
actgtagatg acaaaggat tagcattcaa tataatgagg cgattccaca agatacaagc 540
attttatttg ctgtctgggg tgataaacia gatcagaatg atttgggtctg gtataatgca 600
tcatcaactg gctatgccta tgttgatttt tcacgccata aagaatatgg attataccat 660
attcatactt atgcaaaacg caatggcaat atgtatggaa ttagcgctct tcaagtcaca 720
cttttgacac caciaaattac tagtcaaatc gctcaaaagg atgccaactc tttcacaatt 780
acagtatcca atgtcccttc tacaatcacc agtggttaaga ttccagtttg gacagataaa 840
gatgaccaa atgatttgat ttggtataat gcccgctcaag tgtcaaaagg aacctatcaa 900
gtactgggtga atacagctaa tcataataat gaaaaaggtc tttatcacat tcatatttat 960
ggctatagta caattttggg tagtcagatt ggacttgag ccaaaacctt caataatgtg 1020
gatagtcgcc caaatgctac agtatcagtt gttaaattatg ccgaaaacia aaccaccttt 1080
accgttaatg ttgtcggttc taciaaataa aaagtattaa caggtgttca aatcgagta 1140
tggtctgaaa caaatgggtc ggatgattta aaatgggtata agcctcttgt ttctgggaat 1200
agtgtagtc aagtgttgta tgttgctaata catagtaata ccagtgatca atatattatt 1260

PCT_Sequence_listing (3)

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cacgtttata cggattatac tgatggaagt cgtgttgga cgaatttagg ggcctataaa 1320
attgttaaag aaattctgcc tgtcgtaaaa cctaacgtaa cagttcaaaa ttaccaagct 1380
gacaaggggt tacttgaagt caagggtcag gaaggtagta aagcaatctc aaaaataagc 1440
gtagcagcat ggtcgacttc taatcaaaca aatctccatt ggtatcaaga aattccaata 1500
gctgggtcaag agacgattat taaagtcaat caagcctacc atgatttttt agttggaaat 1560
tacctgttc atacttatat tgattatacg gacaagtcac gagatggctt caatctagga 1620
aattatgaat ttcctgttaa agttggcctt tctgcttcac aaggaaatta tgatattgtc 1680
aataagggtca ttacctaga tgctgggtcat ggcgggttatg atccaggagc agtttttttt 1740
gggacatctg aaaaaacctt gaatttgcaa atgcaaactt tggtaaaaag taaattagaa 1800
tctcaaggct acacagtcgt aactacaaga acagatgact cttttacaga ttgctttcca 1860
cgttcggaaa aagcaaataa cagtctttca gatctctttg ttagcctcca ttttaatgcc 1920
tctacaagtt cgcaagcctc tggaattgaa acttattact atgaatacta cgaagagtat 1980
ccttcacgca ttaatgagat ttttcataat gatcctgaac gtttgagtcg aagtagtggt 2040
ttagccgaag ctattcaggc ggcgaccact gctaaaactg gcgctaaaaa caatggtggt 2100
ttgagaaata catttgagcgt attaagagaa acaacagccc cagcagtgct agtagaatta 2160
ggttacatgt caaatgctag cgagttccaa aatattagca atgtgaacta tcaagaaaaa 2220
ttagcacaag gaattgtttc agggatttta tcctattatc aaacctacag tggtt 2274

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<210> 180
<211> 758
<212> PRT
<213> Streptococcus uberis

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<400> 180

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Met Lys Ser Lys Lys Ser Tyr Val Leu Leu Leu Ala Pro Phe Val Leu
1      5      10

```

```

Ala Ser Phe Trp Gln Ser Lys Met Val Ser Ala Ser Glu Ile Ala Asn
20      25      30

```

```

Gln Asn Val Thr Val Asp Ser Ser Ala Asn Asn Asn Met Ser Ser Lys
35      40      45

```

```

Leu Ser Thr Ser Asn Leu Asp Thr Ile Pro Glu Ser Thr Ser Glu Val
50      55      60

```

```

Thr Val Leu Asp Gln Ser Thr Asn Leu Val Thr Glu Asn Val Val Gln
65      70      75      80

```

```

Glu Lys Ala Leu Ala Ser Ser Glu Ile Gln Thr Asp Glu Ser Ile Ile
85      90      95

```

```

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

```

```

Ser Glu Gly Asn Ala Leu Ser Ala Val Gly Ala Val Lys Ser Ser Phe
115     120     125

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```

Gln Ser Val Asn Thr Asp Val Ser Ser Asn Leu Lys Thr Ala Lys Gln

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PCT_Sequence_listing (3)

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

PCT_Sequence_listing (3)

Gly Thr Asn Leu Gly Ala Tyr Lys Ile Val Lys Glu Ile Leu Pro Val
 435 440 445
 Val Lys Pro Asn Val Thr Val Gln Asn Tyr Gln Ala Asp Lys Gly Leu
 450 455 460
 Leu Glu Val Lys Val Gln Glu Gly Ser Lys Ala Ile Ser Lys Ile Ser
 465 470 475 480
 Val Ala Ala Trp Ser Thr Ser Asn Gln Thr Asn Leu His Trp Tyr Gln
 485 490 495
 Glu Ile Pro Ile Ala Gly Gln Glu Thr Ile Ile Lys Val Asn Gln Ala
 500 505 510
 Tyr His Asp Phe Leu Val Gly Asn Tyr Thr Val His Thr Tyr Ile Asp
 515 520 525
 Tyr Thr Asp Lys Ser Arg Asp Gly Phe Asn Leu Gly Asn Tyr Glu Phe
 530 535 540
 Pro Val Lys Val Gly Leu Ser Ala Ser Gln Gly Asn Tyr Asp Ile Val
 545 550 555 560
 Asn Lys Val Ile Tyr Leu Asp Ala Gly His Gly Gly Tyr Asp Pro Gly
 565 570 575
 Ala Val Tyr Phe Gly Thr Ser Glu Lys Thr Leu Asn Leu Gln Met Gln
 580 585 590
 Thr Leu Val Lys Ser Lys Leu Glu Ser Gln Gly Tyr Thr Val Val Thr
 595 600 605
 Thr Arg Thr Asp Asp Ser Phe Thr Asp Leu Leu Pro Arg Ser Glu Lys
 610 615 620
 Ala Asn Asn Ser Leu Ser Asp Leu Phe Val Ser Leu His Phe Asn Ala
 625 630 635 640
 Ser Thr Ser Ser Gln Ala Ser Gly Ile Glu Thr Tyr Tyr Tyr Glu Tyr
 645 650 655
 Tyr Glu Glu Tyr Pro Ser Arg Ile Asn Glu Ile Phe His Asn Asp Pro
 660 665 670
 Glu Arg Leu Ser Arg Ser Ser Val Leu Ala Glu Ala Ile Gln Ala Ala
 675 680 685
 Thr Thr Ala Lys Thr Gly Ala Lys Asn Asn Gly Val Leu Arg Asn Thr
 690 695 700
 Phe Ala Val Leu Arg Glu Thr Thr Ala Pro Ala Val Leu Val Glu Leu
 705 710 715 720
 Gly Tyr Met Ser Asn Ala Ser Glu Phe Gln Asn Ile Ser Asn Val Asn
 725 730 735

PCT_Sequence_listing (3)

Tyr Gln Glu Lys Leu Ala Gln Gly Ile Val Ser Gly Ile Leu Ser Tyr
740 745 750

Tyr Gln Thr Tyr Ser Val
755

<210> 181
<211> 432
<212> DNA
<213> Streptococcus uberis

<220>
<221> CDS
<222> (1)..(432)

<400> 181
atg aaa aaa aga aag aat aaa tgg agg ttt ttt atg att aaa atg aga 48
Met Lys Lys Arg Lys Asn Lys Trp Arg Phe Phe Met Ile Lys Met Arg
1 5 10 15
aaa tca cag ttg tca gtc agt ctt gcc ctt ttt gcc tta cta act ttt 96
Lys Ser Gln Leu Ser Val Ser Leu Ala Leu Phe Ala Leu Leu Thr Phe
20 25 30
gcg gct tca cct att tat gcc tta caa acg aat caa aac caa gct ggg 144
Ala Ala Ser Pro Ile Tyr Ala Leu Gln Thr Asn Gln Asn Gln Ala Gly
35 40 45
caa gaa gtc caa caa gat agt ctt gct gtc acg gct cat tta caa gct 192
Gln Glu Val Gln Gln Asp Ser Leu Ala Val Thr Ala His Leu Gln Ala
50 55 60
cag aaa cct ctt tta gat att gct att cag ata cca gct caa ctg gct 240
Gln Lys Pro Leu Leu Asp Ile Ala Ile Gln Ile Pro Ala Gln Leu Ala
65 70 75 80
aag gga ggt caa gca aaa gtg gaa ttg ctt gat caa aca ggt cag gtc 288
Lys Gly Gly Gln Ala Lys Val Glu Leu Leu Asp Gln Thr Gly Gln Val
85 90 95
aaa aat acc att agc tat gac ttg caa gca gga tgg aca caa atg tca 336
Lys Asn Thr Ile Ser Tyr Asp Leu Gln Ala Gly Trp Thr Gln Met Ser
100 105 110
gcc tgg ttt gac atg aca ggt tac cca agt ggt gat tat agt gtt aag 384
Ala Trp Phe Asp Met Thr Gly Tyr Pro Ser Gly Asp Tyr Ser Val Lys
115 120 125
gtt acc tac aat ggc atc agc caa caa tca tca cct att cac tat taa 432
Val Thr Tyr Asn Gly Ile Ser Gln Gln Ser Ser Pro Ile His Tyr
130 135 140

<210> 182
<211> 143
<212> PRT
<213> Streptococcus uberis

<400> 182

Met Lys Lys Arg Lys Asn Lys Trp Arg Phe Phe Met Ile Lys Met Arg
1 5 10 15

Lys Ser Gln Leu Ser Val Ser Leu Ala Leu Phe Ala Leu Leu Thr Phe
20 25 30

Ala Ala Ser Pro Ile Tyr Ala Leu Gln Thr Asn Gln Asn Gln Ala Gly
35 40 45

204

PCT_Sequence_listing (3)

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

Gln Lys Pro Leu Leu Asp Ile Ala Ile Gln Ile Pro Ala Gln Leu Ala
65 70 75 80

Lys Gly Gly Gln Ala Lys Val Glu Leu Leu Asp Gln Thr Gly Gln Val
85 90 95

Lys Asn Thr Ile Ser Tyr Asp Leu Gln Ala Gly Trp Thr Gln Met Ser
100 105 110

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

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

<210> 183
<211> 507
<212> DNA
<213> Streptococcus uberis

<220>
<221> CDS
<222> (1)..(507)

<400> 183	
atg aat acc aaa aaa ata atg caa ttt ata ctt gca att acc gtg act	48
Met Asn Thr Lys Lys Ile Met Gln Phe Ile Leu Ala Ile Thr Val Thr	
1 5 10 15	
cta ttt gca act gtc ggt atg aaa acg gta gct gaa agt ttt tgg gct	96
Leu Phe Ala Thr Val Gly Met Lys Thr Val Ala Glu Ser Phe Trp Ala	
20 25 30	
ggg cat cat gat att gaa atg att aat cga aac ata gac act ttg tct	144
Gly His His Asp Ile Glu Met Ile Asn Arg Asn Ile Asp Thr Leu Ser	
35 40 45	
aat cgc att aaa aca aaa aat cag aaa att tca gat tta aac gca agc	192
Asn Arg Ile Lys Thr Lys Asn Gln Lys Ile Ser Asp Leu Asn Ala Ser	
50 55 60	
att tca act tta aaa tca gat att gct tct caa aac agc caa gtg agc	240
Ile Ser Thr Leu Lys Ser Asp Ile Ala Ser Gln Asn Ser Gln Val Ser	
65 70 75 80	
gca ctg caa caa caa tta atc caa gct aat att gat aaa caa aat gag	288
Ala Leu Gln Gln Gln Leu Ile Gln Ala Asn Ile Asp Lys Gln Asn Glu	
85 90 95	
atc aat caa aaa att aat gaa atc aac gct aaa att gca gaa ggt aat	336
Ile Asn Gln Lys Ile Asn Glu Ile Asn Ala Lys Ile Ala Glu Gly Asn	
100 105 110	
caa aag gtt gcc gaa aaa caa ctt gaa gtg gat gcc gcc aat caa aaa	384
Gln Lys Val Ala Glu Lys Gln Leu Glu Val Asp Ala Asn Gln Lys	
115 120 125	
ata gca gaa ttg aat caa caa gta tcc tca tta caa gat aaa ttg aat	432
Ile Ala Glu Leu Asn Gln Gln Val Ser Ser Leu Gln Asp Lys Leu Asn	
130 135 140	
caa aat gat tct caa gca tta aga gat gtt caa aac act cgt caa aaa	480
Gln Asn Asp Ser Gln Ala Leu Arg Asp Val Gln Asn Thr Arg Gln Lys	
145 150 155 160	

205

PCT_Sequence_listing (3)

507

tct gat aaa gct gtt tta gaa acg gaa
Ser Asp Lys Ala Val Leu Glu Thr Glu
165

<210> 184
<211> 169
<212> PRT
<213> Streptococcus uberis

<400> 184

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

Leu Phe Ala Thr Val Gly Met Lys Thr Val Ala Glu Ser Phe Trp Ala
20 25 30

Gly His His Asp Ile Glu Met Ile Asn Arg Asn Ile Asp Thr Leu Ser
35 40 45

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

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

Ala Leu Gln Gln Gln Leu Ile Gln Ala Asn Ile Asp Lys Gln Asn Glu
85 90 95

Ile Asn Gln Lys Ile Asn Glu Ile Asn Ala Lys Ile Ala Glu Gly Asn
100 105 110

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

Ile Ala Glu Leu Asn Gln Gln Val Ser Ser Leu Gln Asp Lys Leu Asn
130 135 140

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

Ser Asp Lys Ala Val Leu Glu Thr Glu
165

<210> 185
<211> 2181
<212> DNA
<213> Streptococcus uberis

<220>
<221> CDS
<222> (1)..(2181)

<400> 185
atg aag aaa aaa act tat tta ttt gtt gct gga atc act gta acc tgt
Met Lys Lys Lys Thr Tyr Leu Phe Val Ala Gly Ile Thr Val Thr Cys
1 5 10 15

48

ggt act gca ttg gcg att cat tta tca caa cca aag tca ata cca atg
Gly Thr Ala Leu Ala Ile His Leu Ser Gln Pro Lys Ser Ile Pro Met
20 25 30

96

PCT_Sequence_listing (3)

aca Thr	aaa Lys	tca Ser 35	gga Gly	cat His	gag Glu	aaa Lys	atg Met 40	att Ile	tca Ser	aaa Lys	tcc Ser 45	cca Pro	act Thr	aat Asn	agt Ser	144
gat Asp	gat Asp 50	aaa Lys	tct Ser	agg Arg	aaa Lys	aaa Lys 55	gat Asp	aag Lys	ggg Gly	att Ile	gct Ala 60	ggg Gly	att Ile	gat Asp	tat Tyr	192
cct Pro 65	act Thr	agt Ser	gat Asp	gga Gly	ttt Phe 70	aaa Lys	cta Leu	gat Asp	aag Lys	caa Gln 75	tct Ser	aaa Lys	atc Ile	att Ile	tct Ser 80	240
aaa Lys	aca Thr	gac Asp	aca Thr	gga Gly 85	att Ile	att Ile	gtt Val	gct Ala	cat His 90	gga Gly	gat Asp	cat His	tct Ser	cac His 95	ttt Phe	288
att Ile	ttt Phe	tat Tyr	aaa Lys 100	gat Asp	ttg Leu	aaa Lys	ggg Gly	act Thr 105	gca Ala	ttt Phe	gca Ala	tat Tyr	tta Leu 110	ata Ile	cca Pro	336
aat Asn	ggc Gly	gtt Val 115	caa Gln	ata Ile	act Thr	aaa Lys	cct Pro 120	tta Leu	ata Ile	ggg Gly	gat Asp	aca Thr 125	aat Asn	gaa Glu	tcg Ser	384
ata Ile 130	aat Asn	gga Gly	cat His	ggg Gly	cat His	cat His 135	tat Tyr	gtt Val	ttc Phe	aat Asn	cca Pro 140	aag Lys	gat Asp	att Ile	gtt Val	432
gca Ala 145	gaa Glu	gat Asp	gct Ala	ttt Phe	ggg Gly 150	tat Tyr	act Thr	gtc Val	aga Arg	cat His 155	gat Asp	gat Asp	cat His	ttc Phe	cat His 160	480
tat Tyr	att Ile	tta Leu	aaa Lys	tct Ser 165	agt Ser	cta Leu	gga Gly	atg Met	acc Thr 170	cct Pro	atg Met	ttg Leu	acc Thr	aac Asn	tat Tyr 175	528
aat Asn	caa Gln	ggc Gly	cgt Arg 180	cat His	ttc Phe	caa Gln	agg Arg	gat Asp 185	agt Ser	cat His	tac Tyr	aaa Lys	cct Pro 190	aat Asn	gtt Val	576
caa Gln	gga Gly	att Ile 195	cca Pro	ggg Gly	ctt Leu	gat Asp	ttt Phe 200	gct Ala	acc Thr	tct Ser	gat Asp	ggg Gly 205	ttt Phe	caa Gln	ttt Phe	624
gat Asp	ggg Gly 210	agc Ser	gga Gly	att Ile	gta Val	ggg Gly 215	aaa Lys	aca Thr	aat Asn	gat Asp	agt Ser 220	att Ile	ttg Leu	gtt Val	agt Ser	672
cac His 225	gat Asp	gac Asp	cat His	ctt Leu	cat His 230	ccc Pro	att Ile	tcg Ser	ttt Phe	gat Asp 235	gat Asp	tta Leu	agg Arg	aaa Lys	aca Thr 240	720
ggg Gly	tgg Trp	gga Gly	gag Glu	ata Ile 245	gtc Val	aaa Lys	att Ile	tat Tyr	gag Glu 250	aaa Lys	aga Arg	gaa Glu	att Ile	gca Ala 255	act Thr	768
ccc Pro	ctt Leu	agt Ser	cat His 260	gta Val	gca Ala	agc Ser	aag Lys	gag Glu 265	gac Asp	ttg Leu	gtt Val	caa Gln	aag Lys 270	acc Thr	ata Ile	816
gaa Glu	tat Tyr	tta Leu 275	gcg Ala	aaa Lys	tca Ser	ttg Leu	gcc Ala 280	tta Leu	cca Pro	tta Leu	tca Ser	tct Ser 285	att Ile	gaa Glu	ata Ile	864
atc Ile	aaa Lys 290	act Thr	gac Asp	gat Asp	ggg Gly 295	aaa Lys 295	att Ile	ggg Gly	ttt Phe	aaa Lys	tat Tyr 300	cct Pro	cat His	cat His	gat Asp	912
cat His 305	agc Ser	cat His	gtc Val	atc Ile	atg Met 310	tta Leu	gaa Glu	gat Asp	atc Ile	gaa Glu 315	atc Ile	ggg Gly	aaa Lys	cca Pro	att Ile 320	960
cca Pro	gat Asp	cct Pro	cat His	caa Gln	ctt Leu	cat His	cat His	gcc Ala	aaa Lys	gaa Glu	ttg Leu	gaa Glu	aag Lys	cat His	cgc Arg	1008

PCT_Sequence_listing (3)

PCT_Sequence_listing (3)																
325				330				335								
att ggc atg aat aca tta agg gag atc ggc ttt gat gaa gaa gtc att	Ile Gly Met Asn Thr Leu Arg Glu Ile Gly Phe Asp Glu Glu Val Ile															1056
340				345				350								
ctt gat att gtt aga acc cat gat gca aaa aca gaa ttt cca tca aat	Leu Asp Ile Val Arg Thr His Asp Ala Lys Thr Glu Phe Pro Ser Asn															1104
355				360				365								
gaa aaa aat ccg gaa aag atg aag gag tgg ttg acc aca gtt aca aaa	Glu Lys Asn Pro Glu Lys Met Lys Glu Trp Leu Thr Thr Val Thr Lys															1152
370				375				380								
ttg gat tta gga agc cga aaa gac ccc ttg aat cga ttt gga ctt cat	Leu Asp Leu Gly Ser Arg Lys Asp Pro Leu Asn Arg Phe Gly Leu His															1200
385				390				395								
tta tta cct aat cta gag aat tta gga atc ggc ttt aca cct atc aaa	Leu Leu Pro Asn Leu Glu Asn Leu Gly Ile Gly Phe Thr Pro Ile Lys															1248
405				410				415								
aat atg gag cct gtt cta caa ttt aaa aaa tta aaa cga ctg tta atg	Asn Met Glu Pro Val Leu Gln Phe Lys Lys Leu Lys Arg Leu Leu Met															1296
420				425				430								
aca gca act ggt gtt aaa aac tat gat ttt ctg aag tac atg cca aat	Thr Ala Thr Gly Val Lys Asn Tyr Asp Phe Leu Lys Tyr Met Pro Asn															1344
435				440				445								
ctt gag gga tta gat att tca caa aac aac tta aag gat ttg agc ttt	Leu Glu Gly Leu Asp Ile Ser Gln Asn Asn Leu Lys Asp Leu Ser Phe															1392
450				455				460								
ttg acg cct tat aaa caa ctc aat cta tta gct gcc gca gat aac caa	Leu Thr Pro Tyr Lys Gln Leu Asn Leu Leu Ala Ala Asp Asn Gln															1440
465				470				475								
tta tca aca ttg caa cca tta gcg gaa ctg cca aag tta caa ttt tta	Leu Ser Thr Leu Gln Pro Leu Ala Glu Leu Pro Lys Leu Gln Phe Leu															1488
485				490				495								
gta tta agt aat aat aag ata aaa gat ttg agt cca ttg aaa aat tta	Val Leu Ser Asn Asn Lys Ile Lys Asp Leu Ser Pro Leu Lys Asn Leu															1536
500				505				510								
aca agg ctt caa gaa gtt cat att gag aac aat ctg gtc aga gat tta	Thr Arg Leu Gln Glu Val His Ile Glu Asn Asn Leu Val Arg Asp Leu															1584
515				520				525								
acc cct tta aat gac aaa gaa aac tta aaa gtt tta aat cta tcc gaa	Thr Pro Leu Asn Asp Lys Glu Asn Leu Lys Val Leu Asn Leu Ser Glu															1632
530				535				540								
aat agg gga gtt gac tta aag act ttg agg tta ccg ctt ctt gag aca	Asn Arg Gly Val Asp Leu Lys Thr Leu Arg Leu Pro Leu Leu Glu Thr															1680
545				550				555								
ctt acc gta aat aaa gca tct ttg acg gat tta aac ttt ttt gaa gct	Leu Thr Val Asn Lys Ala Ser Leu Thr Asp Leu Asn Phe Phe Glu Ala															1728
565				570				575								
aat cct aac ctg act gaa gta aca gca aca aaa aat gct att cag aaa	Asn Pro Asn Leu Thr Glu Val Thr Ala Thr Lys Asn Ala Ile Gln Lys															1776
580				585				590								
tta gat ggc att gag aaa gca aag aaa ttg caa ttt tta gat ttg caa	Leu Asp Gly Ile Glu Lys Ala Lys Lys Leu Gln Phe Leu Asp Leu Gln															1824
595				600				605								
gaa aat aag gtt aat cat tta aac att aag gaa aaa caa gag tca cta	Glu Asn Lys Val Asn His Leu Asn Ile Lys Glu Lys Gln Glu Ser Leu															1872
610				615				620								
act ttc ttg aat ctt tct gat aat gca ttg gaa tcg ctc gaa ggg gta																1920

PCT_Sequence_listing (3)

Thr 625	Phe	Leu	Asn	Leu	Ser 630	Asp	Asn	Ala	Leu	Glu 635	Ser	Leu	Glu	Gly	Val 640	
aat Asn	gac Asp	ttt Phe	aca Thr	gct Ala	ttg Leu	gag Glu	aca Thr	tta Leu	aga Arg	gtg Val	gca Ala	tca Ser	aat Asn	aaa Lys	att Ile	1968
tcg Ser	agc Ser	tta Leu	cac His	ctt Leu	gaa Glu	gaa Glu	agc Ser	aat Asn	cag Gln	caa Gln	gta Val	aaa Lys	agc Ser	tta Leu	gat Asp	2016
gtc Val	agt Ser	tat Tyr	aat Asn	caa Gln	ttg Leu	cca Pro	aag Lys	gag Glu	gaa Glu	tta Leu	aca Thr	tta Leu	aat Asn	gaa Glu	aac Asn	2064
gac Asp	ata Ile	ccc Pro	ctt Leu	ggt Gly	gtt Val	gct Ala	cat His	cat His	ttt Phe	aca Thr	gcg Ala	ggt Val	aag Lys	gaa Glu	ggg Gly	2112
tca Ser	ata Ile	gag Glu	ggg Gly	aat Asn	ccc Pro	tct Ser	cta Leu	aat Asn	gat Asp	gtt Val	tta Leu	gaa Glu	agt Ser	caa Gln	aat Asn	2160
caa Gln	aag Lys	aat Asn	aat Asn	aaa Lys	aaa Lys	gaa Glu										2181

<210> 186
 <211> 727
 <212> PRT
 <213> Streptococcus uberis
 <400> 186

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

PCT_Sequence_listing (3)

Tyr Ile Leu Lys Ser Ser Leu Gly Met Thr Pro Met Leu Thr Asn Tyr
165 170 175

Asn Gln Gly Arg His Phe Gln Arg Asp Ser His Tyr Lys Pro Asn Val
180 185 190

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

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

His Asp Asp His Leu His Pro Ile Ser Phe Asp Asp Leu Arg Lys Thr
225 230 235 240

Gly Trp Gly Glu Ile Val Lys Ile Tyr Glu Lys Arg Glu Ile Ala Thr
245 250 255

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

Glu Tyr Leu Ala Lys Ser Leu Ala Leu Pro Leu Ser Ser Ile Glu Ile
275 280 285

Ile Lys Thr Asp Asp Gly Lys Ile Gly Phe Lys Tyr Pro His His Asp
290 295 300

His Ser His Val Ile Met Leu Glu Asp Ile Glu Ile Gly Lys Pro Ile
305 310 315 320

Pro Asp Pro His Gln Leu His His Ala Lys Glu Leu Glu Lys His Arg
325 330 335

Ile Gly Met Asn Thr Leu Arg Glu Ile Gly Phe Asp Glu Glu Val Ile
340 345 350

Leu Asp Ile Val Arg Thr His Asp Ala Lys Thr Glu Phe Pro Ser Asn
355 360 365

Glu Lys Asn Pro Glu Lys Met Lys Glu Trp Leu Thr Thr Val Thr Lys
370 375 380

Leu Asp Leu Gly Ser Arg Lys Asp Pro Leu Asn Arg Phe Gly Leu His
385 390 395 400

Leu Leu Pro Asn Leu Glu Asn Leu Gly Ile Gly Phe Thr Pro Ile Lys
405 410 415

Asn Met Glu Pro Val Leu Gln Phe Lys Lys Leu Lys Arg Leu Leu Met
420 425 430

Thr Ala Thr Gly Val Lys Asn Tyr Asp Phe Leu Lys Tyr Met Pro Asn
435 440 445

Leu Glu Gly Leu Asp Ile Ser Gln Asn Asn Leu Lys Asp Leu Ser Phe
450 455 460

PCT_Sequence_listing (3)

Leu Thr Pro Tyr Lys Gln Leu Asn Leu Leu Ala Ala Ala Asp Asn Gln
465 470 475 480

Leu Ser Thr Leu Gln Pro Leu Ala Glu Leu Pro Lys Leu Gln Phe Leu
485 490 495

Val Leu Ser Asn Asn Lys Ile Lys Asp Leu Ser Pro Leu Lys Asn Leu
500 505 510

Thr Arg Leu Gln Glu Val His Ile Glu Asn Asn Leu Val Arg Asp Leu
515 520 525

Thr Pro Leu Asn Asp Lys Glu Asn Leu Lys Val Leu Asn Leu Ser Glu
530 535 540

Asn Arg Gly Val Asp Leu Lys Thr Leu Arg Leu Pro Leu Leu Glu Thr
545 550 555 560

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

Asn Pro Asn Leu Thr Glu Val Thr Ala Thr Lys Asn Ala Ile Gln Lys
580 585 590

Leu Asp Gly Ile Glu Lys Ala Lys Lys Leu Gln Phe Leu Asp Leu Gln
595 600 605

Glu Asn Lys Val Asn His Leu Asn Ile Lys Glu Lys Gln Glu Ser Leu
610 615 620

Thr Phe Leu Asn Leu Ser Asp Asn Ala Leu Glu Ser Leu Glu Gly Val
625 630 635 640

Asn Asp Phe Thr Ala Leu Glu Thr Leu Arg Val Ala Ser Asn Lys Ile
645 650 655

Ser Ser Leu His Leu Glu Glu Ser Asn Gln Gln Val Lys Ser Leu Asp
660 665 670

Val Ser Tyr Asn Gln Leu Pro Lys Glu Glu Leu Thr Leu Asn Glu Asn
675 680 685

Asp Ile Pro Leu Gly Val Ala His His Phe Thr Ala Val Lys Glu Gly
690 695 700

Ser Ile Glu Gly Asn Pro Ser Leu Asn Asp Val Leu Glu Ser Gln Asn
705 710 715 720

Gln Lys Asn Asn Lys Lys Glu
725

<210> 187
<211> 606
<212> DNA
<213> Streptococcus uberis

PCT_Sequence_listing (3)

<220>

<221> CDS

<222> (1)..(606)

<400> 187

atg gca att att tta cct gac ctt cca tat gca tat gat gct ctt gag 48
 Met Ala Ile Ile Leu Pro Asp Leu Pro Tyr Ala Tyr Asp Ala Leu Glu
 1 5 10 15

cca caa att gat aaa gaa aca atg act ctt cat cat gac aaa cat cat 96
 Pro Gln Ile Asp Lys Glu Thr Met Thr Leu His His Asp Lys His His
 20 25 30

gcg aca tat gtt gct aat gcc aat gct gcg ctt gaa aaa cat cca gaa 144
 Ala Thr Tyr Val Ala Asn Ala Asn Ala Ala Leu Glu Lys His Pro Glu
 35 40 45

att ggt gaa gat ttg gtg gcg tta tta tct gat gtg tca tca att cca 192
 Ile Gly Glu Asp Leu Val Ala Leu Leu Ser Asp Val Ser Ser Ile Pro
 50 55 60

gaa gat att cgt caa gct ctt atc aat aat gga ggc gga cat ctt aac 240
 Glu Asp Ile Arg Gln Ala Leu Ile Asn Asn Gly Gly Gly His Leu Asn
 65 70 75 80

cat gca ctt ttt tgg gaa ctt ctt tca cct gag aaa aca gaa atc act 288
 His Ala Leu Phe Trp Glu Leu Leu Ser Pro Glu Lys Thr Glu Ile Thr
 85 90 95

tcg gaa gta gct tct gct att gat gaa gca ttt ggt tct ttt gat gca 336
 Ser Glu Val Ala Ser Ala Ile Asp Glu Ala Phe Gly Ser Phe Asp Ala
 100 105 110

ttt aaa gaa aaa ttt aca gca gca gca acg gga cgt ttt gga tct ggt 384
 Phe Lys Glu Lys Phe Thr Ala Ala Ala Thr Gly Arg Phe Gly Ser Gly
 115 120 125

tgg gct tgg tta gtt gtc aat aaa gaa gga aaa ctt gaa gta act tca 432
 Trp Ala Trp Leu Val Val Asn Lys Glu Gly Lys Leu Glu Val Thr Ser
 130 135 140

act gca aac caa gat aca cca att tct gaa ggt aaa cag cct att ttg 480
 Thr Ala Asn Gln Asp Thr Pro Ile Ser Glu Gly Lys Gln Pro Ile Leu
 145 150 155 160

ggt ctt gat gta tgg gaa cat gct tat tac tta aat tat cgt aat gta 528
 Gly Leu Asp Val Trp Glu His Ala Tyr Tyr Leu Asn Tyr Arg Asn Val
 165 170 175

cgt cca aat tac att aaa gct ttc ttt gaa att att aat tgg aaa aag 576
 Arg Pro Asn Tyr Ile Lys Ala Phe Phe Glu Ile Ile Asn Trp Lys Lys
 180 185 190

gtt gat gag ctt tat aaa gca gca aaa gcg 606
 Val Asp Glu Leu Tyr Lys Ala Ala Lys Ala
 195 200

<210> 188

<211> 202

<212> PRT

<213> Streptococcus uberis

<400> 188

Met Ala Ile Ile Leu Pro Asp Leu Pro Tyr Ala Tyr Asp Ala Leu Glu
 1 5 10 15

Pro Gln Ile Asp Lys Glu Thr Met Thr Leu His His Asp Lys His His
 20 25 30

Ala Thr Tyr Val Ala Asn Ala Asn Ala Ala Leu Glu Lys His Pro Glu
 35 40 45

PCT_Sequence_listing (3)

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

Glu Asp Ile Arg Gln Ala Leu Ile Asn Asn Gly Gly Gly His Leu Asn
65 70 75 80

His Ala Leu Phe Trp Glu Leu Leu Ser Pro Glu Lys Thr Glu Ile Thr
85 90 95

Ser Glu Val Ala Ser Ala Ile Asp Glu Ala Phe Gly Ser Phe Asp Ala
100 105 110

Phe Lys Glu Lys Phe Thr Ala Ala Ala Thr Gly Arg Phe Gly Ser Gly
115 120 125

Trp Ala Trp Leu Val Val Asn Lys Glu Gly Lys Leu Glu Val Thr Ser
130 135 140

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

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

Arg Pro Asn Tyr Ile Lys Ala Phe Phe Glu Ile Ile Asn Trp Lys Lys
180 185 190

Val Asp Glu Leu Tyr Lys Ala Ala Lys Ala
195 200

<210> 189
<211> 2454
<212> DNA
<213> Streptococcus uberis

<220>
<221> CDS
<222> (1)..(2454)

<400> 189
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Met Arg Lys His Tyr Val Ser Lys Ser Ala Ile Phe Leu Ala Met Leu
1 5 10 15

gtt gca aca ggt tca gct caa ttc gta aaa gct gag aca cca aca act 96
Val Ala Thr Gly Ser Ala Gln Phe Val Lys Ala Glu Thr Pro Thr Thr
20 25 30

aca act agc cca gca aca agt ctt act gat gcc tct gca agt acg act 144
Thr Thr Ser Pro Ala Thr Ser Leu Thr Asp Ala Ser Ala Ser Thr Thr
35 40 45

cca aca acg aac acg acg tca act gtg aca cct gct ctt gat cca aat 192
Pro Thr Thr Asn Thr Thr Ser Thr Val Thr Pro Ala Leu Asp Pro Asn
50 55 60

act aat ttc acc gtt gat tct agt gct aca aca agt act act act cca 240
Thr Asn Phe Thr Val Asp Ser Ser Ala Thr Thr Ser Thr Thr Thr Pro
65 70 75 80

agt cca gtg gag gca gca gcc atc tct cct gtg ata gca act gct caa 288
Ser Pro Val Glu Ala Ala Ala Ile Ser Pro Val Ile Ala Thr Ala Gln
85 90 95

PCT_Sequence_listing (3)

PCI_Sequence_Firsting (3)																
85				90				95								
cct Pro	aca Thr	act Thr	aat Asn 100	gtc Val	act Thr	agt Ser	gct Ala	agc Ser 105	ctt Leu	gcg Ala	cca Pro	gca Ala	gct Ala 110	aac Asn	aca Thr	336
atg Met	gca Ala	aca Thr 115	act Thr	cca Pro	gtt Val	gaa Glu	ggc Gly 120	caa Gln	aca Thr	gtt Val	gat Asp	gtg Val 125	cgc Arg	atc Ile	atc Ile	384
tca Ser	acc Thr 130	act Thr	gac Asp	ctt Leu	cac His	tct Ser 135	aac Asn	tta Leu	gtc Val	aac Asn	tat Tyr 140	gat Asp	tac Tyr	tat Tyr	caa Gln	432
gat Asp 145	aaa Lys	gca Ala	tct Ser	caa Gln	act Thr 150	atc Ile	ggc Gly	tta Leu	gcg Ala	aaa Lys 155	gct Ala	gcc Ala	gtt Val	ctt Leu	atc Ile 160	480
gat Asp	caa Gln	gca Ala	aaa Lys	gct Ala 165	gaa Glu	aat Asn	cct Pro	aat Asn	gct Ala 170	gtt Val	ctt Leu	gtt Val	gat Asp	aac Asn 175	ggc Gly	528
gat Asp	atc Ile	tta Leu	caa Gln 180	ggc Gly	aca Thr	cca Pro	ctc Leu	gga Gly 185	act Thr	tat Tyr	gaa Glu	gca Ala	ttg Leu 190	att Ile	gat Asp	576
cct Pro	tta Leu	caa Gln 195	cca Pro	ggc Gly	gaa Glu	gtg Val	cac His 200	cca Pro	atg Met	tac Tyr	gca Ala	gcc Ala 205	ctt Leu	gat Asp	aaa Lys	624
ctt Leu	ggc Gly 210	ttt Phe	gac Asp	gct Ala	tca Ser	act Thr 215	tta Leu	ggc Gly	aac Asn	cac His	gaa Glu 220	ttc Phe	aac Asn	tat Tyr	ggc Gly	672
ctt Leu 225	acc Thr	ttc Phe	atc Ile	gaa Glu	aat Asn 230	gcc Ala	att Ile	gct Ala	tca Ser	gcc Ala 235	gga Gly	cta Leu	cca Pro	atc Ile	cta Leu 240	720
aat Asn	gct Ala	aac Asn	gtc Val	ttt Phe 245	gat Asp	gca Ala	gca Ala	acg Thr	gga Gly 250	gaa Glu	tac Tyr	ctt Leu	ttc Phe	caa Gln 255	cct Pro	768
tac Tyr	gct Ala	atc Ile	gtt Val 260	acg Thr	aaa Lys	agc Ser	ttt Phe	acg Thr 265	gat Asp	gct Ala	aat Asn	ggc Gly	caa Gln 270	gct Ala	gtc Val	816
gac Asp	cta Leu	aaa Lys 275	atc Ile	ggc Gly	atc Ile	aca Thr	ggc Gly 280	att Ile	gtg Val	cca Pro	cct Pro	caa Gln 285	atc Ile	atg Met	ctt Leu	864
tgg Trp	gat Asp 290	aag Lys	gct Ala	aac Asn	ctc Leu	gaa Glu 295	ggc Gly	aaa Lys	gtt Val	acg Thr	gtc Val 300	aaa Lys	gat Asp	gcc Ala	gtg Val	912
caa Gln 305	gct Ala	gtg Val	aca Thr	gaa Glu	atc Ile 310	att Ile	cct Pro	acc Thr	atc Ile	aaa Lys 315	aat Asn	gct Ala	ggc Gly	gct Ala	gac Asp 320	960
atc Ile	gtt Val	tta Leu	gtc Val	ctt Leu 325	gcc Ala	cac His	act Thr	ggc Gly	atc Ile 330	ggc Gly	gat Asp	gat Asp	gtt Val	tat Tyr 335	gaa Glu	1008
act Thr	ggc Gly	gaa Glu	gaa Glu 340	aat Asn	gtc Val	ggc Gly	tac Tyr	cag Gln 345	att Ile	gca Ala	agt Ser	ctt Leu	gct Ala 350	ggc Gly	gtt Val	1056
gac Asp	gcg Ala	gtc Val 355	gta Val	aca Thr	ggc Gly	cac His	tca Ser 360	cat His	gca Ala	gaa Glu	ttc Phe	cct Pro 365	tca Ser	gga Gly	caa Gln	1104
gat Asp	acc Thr 370	ggc Gly	ttc Phe	tac Tyr	gaa Glu	tcc Ser 375	tat Tyr	aat Asn	ggc Gly	gtc Val	gac Asp 380	ggg Gly	gtg Val	tct Ser	ggc Gly	1152
tta	att	aac	gga	aca	cct	gtt	acc	atg	gca	gga	aaa	tac	ggg	gat	cat	1200

PCT_Sequence_listing (3)

Leu 385	Ile	Asn	Gly	Thr	Pro 390	Val	Thr	Met	Ala	Gly 395	Lys	Tyr	Gly	Asp	His 400	
atc Ile	ggt Gly	att Ile	att Ile	gat Asp 405	tta Leu	aat Asn	gtg Val	tcc Ser	tat Tyr 410	aca Thr	ggt Gly	ggt Gly	aaa Lys	tgg Trp 415	act Thr	1248
gtt Val	aat Asn	cgc Arg	gat Asp 420	aaa Lys	aac Asn	cat His	gca Ala	gaa Glu 425	atc Ile	cgt Arg	aaa Lys	att Ile	gat Asp 430	acc Thr	aaa Lys	1296
tca Ser	acc Thr	atc Ile 435	gcc Ala	gat Asp	gct Ala	gat Asp	att Ile 440	tta Leu	gct Ala	ttg Leu	gct Ala	caa Gln 445	gca Ala	tct Ser	cac His	1344
ctt Leu	gga Gly 450	aca Thr	att Ile	gat Asp	tac Tyr	gtg Val 455	cgt Arg	caa Gln	act Thr	gtt Val	ggt Gly 460	gaa Glu	aca Thr	act Thr	gca Ala	1392
cca Pro 465	att Ile	aac Asn	agt Ser	tac Tyr	ttc Phe 470	gct Ala	tta Leu	gtc Val	aaa Lys	gat Asp 475	gat Asp	cca Pro	tct Ser	gtt Val	caa Gln 480	1440
att Ile	gtc Val	aat Asn	aat Asn	gca Ala 485	caa Gln	ctt Leu	tggt Trp	tat Tyr	gcc Ala 490	aaa Lys	caa Gln	caa Gln	tta Leu	gct Ala 495	ggt Gly	1488
act Thr	cca Pro	gaa Glu 500	gct Ala	gac Asp	tta Leu	cct Pro	ctt Leu 505	tca Ser	gca Ala	gca Ala	gca Ala	cca Pro 510	ttt Phe	aaa Lys		1536
gct Ala	ggt Gly	act Thr 515	cgt Arg	aat Asn	gac Asp	cca Pro	acc Thr 520	gct Ala	tat Tyr	act Thr	gat Asp	atc Ile 525	ccg Pro	gct Ala	gga Gly	1584
cca Pro	att Ile 530	gcc Ala	att Ile	aaa Lys	aac Asn	gtt Val 535	gcc Ala	gac Asp	cta Leu	tac Tyr	tta Leu 540	tat Tyr	gat Asp	aat Asn	gtc Val	1632
act Thr 545	gct Ala	atc Ile	cta Leu	aaa Lys	ctg Leu 550	aca Thr	ggt Gly	gca Ala	gat Asp	atc Ile 555	aaa Lys	gaa Glu	tgg Trp	tta Leu	gag Glu 560	1680
atg Met	tca Ser	gca Ala	gga Gly	caa Gln 565	ttt Phe	aat Asn	acc Thr	atc Ile	gac Asp 570	cca Pro	aat Asn	gta Val	gct Ala	gga Gly 575	cct Pro	1728
caa Gln	aac Asn	cta Leu	gtc Val 580	aat Asn	acg Thr	gat Asp	tat Tyr	aga Arg 585	act Thr	tac Tyr	aac Asn	ttt Phe	gat Asp 590	gtg Val	att Ile	1776
gat Asp	ggc Gly	gtt Val 595	act Thr	tac Tyr	gag Glu	ttt Phe	gat Asp 600	gta Val	aca Thr	caa Gln	cct Pro	aac Asn 605	aag Lys	tat Tyr	gat Asp	1824
gcc Ala 610	aaa Lys	ggt Gly	aat Asn	ctt Leu	ctt Leu	aac Asn 615	cct Pro	aat Asn	gct Ala	agt Ser	cgt Arg 620	gtt Val	cgt Arg	aac Asn	ctt Leu	1872
aaa Lys 625	ttc Phe	caa Gln	ggt Gly	aaa Lys	gaa Glu 630	atc Ile	gat Asp	cca Pro	aat Asn	caa Gln 635	gaa Glu	ttc Phe	atg Met	gtt Val	gtc Val 640	1920
act Thr	aat Asn	aac Asn	tac Tyr	cgt Arg 645	gct Ala	agt Ser	gga Gly	agt Ser	ttc Phe 650	cca Pro	ggg Gly	gta Val	aaa Lys	aat Asn 655	gca Ala	1968
acc Thr	att Ile	aat Asn	cga Arg 660	ttg Leu	ctt Leu	aac Asn	ctt Leu	gaa Glu 665	aat Asn	cga Arg	caa Gln	gcc Ala	atc Ile 670	atc Ile	aat Asn	2016
tat Tyr	atc Ile	gtt Val 675	tct Ser	gaa Glu	aaa Lys	acc Thr	att Ile 680	aac Asn	cca Pro	agt Ser	gca Ala	gat Asp 685	aac Asn	aac Asn	tggt Trp	2064

PCT_Sequence_listing (3)

tac Tyr	ttt Phe	gca Ala	gat Asp	acc Thr	att Ile	caa Gln	gga Gly	ctt Leu	gat Asp	tta Leu	cac His	ttc Phe	tta Leu	agt Ser	gca Ala	2112
690						695				700						
gat Asp	act Thr	tct Ser	aag Lys	aat Asn	tta Leu	att Ile	ggt Gly	gac Asp	aaa Lys	gct Ala	gat Asp	att Ile	tct Ser	tat Tyr	acc Thr	2160
705					710					715					720	
ggc Gly	cct Pro	tct Ser	act Thr	att Ile	gaa Glu	ggt Gly	ttt Phe	ggt Gly	gac Asp	ttc Phe	gtc Val	ttt Phe	aca Thr	tat Tyr	gtt Val	2208
				725					730					735		
aaa Lys	cca Pro	gaa Glu	tta Leu	cca Pro	gta Val	gcc Ala	act Thr	ccg Pro	gaa Glu	aca Thr	cca Pro	caa Gln	gaa Glu	act Thr	ggt Gly	2256
			740					745					750			
agc Ser	caa Gln	ttg Leu	act Thr	gaa Glu	aac Asn	cgt Arg	cgt Arg	caa Gln	gaa Glu	att Ile	cat His	caa Gln	tta Leu	gct Ala	acg Thr	2304
		755					760					765				
cgt Arg	gtt Val	tac Tyr	aat Asn	caa Gln	aca Thr	aaa Lys	gcg Ala	aca Thr	tca Ser	tca Ser	agt Ser	act Thr	act Thr	aag Lys	gct Ala	2352
	770					775					780					
gaa Glu	tta Leu	cca Pro	aaa Lys	gct Ala	ggt Gly	agc Ser	caa Gln	gag Glu	tct Ser	aaa Lys	ggt Gly	tta Leu	ttc Phe	ttc Phe	atg Met	2400
	785				790					795					800	
ggc Gly	tta Leu	agc Ser	tta Leu	ctt Leu	ggt Gly	tta Leu	gcc Ala	gga Gly	tta Leu	atc Ile	acg Thr	aaa Lys	aaa Lys	gaa Glu	gaa Glu	2448
				805					810					815		
aga Arg	caa Gln															2454

<210> 190
<211> 818
<212> PRT
<213> Streptococcus uberis

<400> 190

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

PCT_Sequence_listing (3)

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

PCT_Sequence_listing (3)

Ser Thr Ile Ala Asp Ala Asp Ile Leu Ala Leu Ala Gln Ala Ser His
435 440 445

Leu Gly Thr Ile Asp Tyr Val Arg Gln Thr Val Gly Glu Thr Thr Ala
450 455 460

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

Ile Val Asn Asn Ala Gln Leu Trp Tyr Ala Lys Gln Gln Leu Ala Gly
485 490 495

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

Ala Gly Thr Arg Asn Asp Pro Thr Ala Tyr Thr Asp Ile Pro Ala Gly
515 520 525

Pro Ile Ala Ile Lys Asn Val Ala Asp Leu Tyr Leu Tyr Asp Asn Val
530 535 540

Thr Ala Ile Leu Lys Leu Thr Gly Ala Asp Ile Lys Glu Trp Leu Glu
545 550 555 560

Met Ser Ala Gly Gln Phe Asn Thr Ile Asp Pro Asn Val Ala Gly Pro
565 570 575

Gln Asn Leu Val Asn Thr Asp Tyr Arg Thr Tyr Asn Phe Asp Val Ile
580 585 590

Asp Gly Val Thr Tyr Glu Phe Asp Val Thr Gln Pro Asn Lys Tyr Asp
595 600 605

Ala Lys Gly Asn Leu Leu Asn Pro Asn Ala Ser Arg Val Arg Asn Leu
610 615 620

Lys Phe Gln Gly Lys Glu Ile Asp Pro Asn Gln Glu Phe Met Val Val
625 630 635 640

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

Thr Ile Asn Arg Leu Leu Asn Leu Glu Asn Arg Gln Ala Ile Ile Asn
660 665 670

Tyr Ile Val Ser Glu Lys Thr Ile Asn Pro Ser Ala Asp Asn Asn Trp
675 680 685

Tyr Phe Ala Asp Thr Ile Gln Gly Leu Asp Leu His Phe Leu Ser Ala
690 695 700

Asp Thr Ser Lys Asn Leu Ile Gly Asp Lys Ala Asp Ile Ser Tyr Thr
705 710 715 720

Gly Pro Ser Thr Ile Glu Gly Phe Gly Asp Phe Val Phe Thr Tyr Val

