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权利要求书2页 说明书25页
序列表222页

(54)发明名称

从另选的蔗糖源制备葡聚糖聚合物

(57)摘要

本文公开一种反应溶液,所述反应溶液包含水、不完全精制的蔗糖和葡糖基转移酶,所述反应溶液合成不溶性聚α-1,3-葡聚糖,其具有至少50%的α-1,3糖苷键和至少100的重均聚合度(DP_w)。本文的反应溶液的聚α-1,3-葡聚糖的收率是在所述反应溶液中被转化的蔗糖的重量的至少7%。还公开利用不完全精制的蔗糖制备聚α-1,3-葡聚糖的方法和通过这些方法制备的聚α-1,3-葡聚糖。

CN 106661598 B

权 利 要 求 书

1.一种反应溶液,所述反应溶液包含水、蔗糖和葡糖基转移酶,所述反应溶液合成不溶性聚α-1,3-葡聚糖,其具有至少50%的α-1,3糖苷键和至少100的重均聚合度(DP_w),其中所述蔗糖是未精制或部分精制的且具有大于150的ICUMSA(国际糖统一分析法委员会)值;

其中通过所述反应溶液的聚α-1,3-葡聚糖的收率是在所述反应溶液中转化为产物的蔗糖的重量的至少7%。

2.根据权利要求1所述的反应溶液,其中所述蔗糖来自糖用甜菜,并且尚未结晶。

3.根据权利要求1所述的反应溶液,其中所述蔗糖来自甘蔗,并且(i)尚未结晶,或(ii)已经利用不超过三个结晶步骤结晶。

4.根据权利要求1-3中任一项所述的反应溶液,其中所述蔗糖具有大于400的ICUMSA值。

5.根据权利要求1-3中任一项所述的反应溶液,其中相对于包含水、白色精制蔗糖和所述葡糖基转移酶的反应溶液的反应速率,所述反应溶液的相对反应速率为至少0.8。

6.根据权利要求1-3中任一项所述的反应溶液,其中由所述反应溶液产生的聚α-1,3-葡聚糖具有小于93的L*值。

7.根据权利要求6所述的反应溶液,其中由所述反应溶液产生的聚α-1,3-葡聚糖具有小于90的L*值。

8.根据权利要求1-3中任一项所述的反应溶液,其中所述葡糖基转移酶由SEQ ID NO:4、SEQ ID NO:8、SEQ ID NO:10、SEQ ID NO:12、SEQ ID NO:14、SEQ ID NO:20、SEQ ID NO:26、SEQ ID NO:28、SEQ ID NO:30或SEQ ID NO:34的氨基酸序列组成。

9.根据权利要求1-3中任一项所述的反应溶液,其中所述聚α-1,3-葡聚糖具有至少90%的α-1,3糖苷键。

10.一种用于生产不溶性聚α-1,3-葡聚糖的方法,所述方法包括:

使至少水、蔗糖和葡糖基转移酶接触,其中所述蔗糖是未精制或部分精制的且具有大于150的ICUMSA(国际糖统一分析法委员会)值,

由此生产聚α-1,3-葡聚糖,其具有至少50%的α-1,3糖苷键和至少100的重均聚合度(DP_w)。

11.根据权利要求10所述的方法,其中所述蔗糖来自糖用甜菜,并且尚未结晶。

12.根据权利要求10所述的方法,其中所述蔗糖来自甘蔗,并且(i)尚未结晶,或(ii)已经利用不超过三个结晶步骤结晶。

13.根据权利要求10-12中任一项所述的方法,其中所述蔗糖具有大于400的ICUMSA值。

14.根据权利要求10-12中任一项所述的方法,其中相对于使用白色精制蔗糖替代所述未精制或部分精制蔗糖时的反应速率,生产聚α-1,3-葡聚糖的相对反应速率为至少0.8。

15.根据权利要求10-12中任一项所述的方法,其进一步包括分离接触步骤中产生的聚α-1,3-葡聚糖的步骤。

16.根据权利要求15所述的方法,其中已经分离的聚α-1,3-葡聚糖具有小于93的L*值。

17.根据权利要求16所述的方法,其中已经分离的聚α-1,3-葡聚糖具有小于90的L*值。

18.根据权利要求10-12中任一项所述的方法,其中所述葡糖基转移酶由SEQ ID NO:4、SEQ ID NO:8、SEQ ID NO:10、SEQ ID NO:12、SEQ ID NO:14、SEQ ID NO:20、SEQ ID NO:26、SEQ ID NO:28、SEQ ID NO:30或SEQ ID NO:34的氨基酸序列组成。

19.分离的聚α-1,3-葡聚糖,其具有小于93的L*值,其中所述聚α-1,3-葡聚糖具有至少90%的α-1,3糖苷键和至少100的重均聚合度。

20.根据权利要求19所述的分离的聚α-1,3-葡聚糖,其具有小于90的L*值。

从另选的蔗糖源制备葡聚糖聚合物

[0001] 本申请要求美国临时申请61/969,958(2014年3月25日提交)的优先权，该申请全文以引用方式并入本文。

技术领域

[0002] 本发明属于多糖合成领域。例如，本发明涉及利用未完全精制的蔗糖制备不溶性聚α-1,3-葡聚糖。

[0003] 以电子方式递交的序列表的引用

[0004] 通过EFS-Web以电子方式将序列表的正式文本作为ASCII格式的序列表递交，该文件名称为“20150324_CL6221USNP_SequenceListing”，创建日期为2015年3月16日，文件大小为569千字节，并且该文件与本说明书同时提交。在这一ASCII格式的文件中包含的序列表为所述说明书的一部分并且全文以引用方式并入本文。

背景技术

[0005] 受到利用酶法合成或微生物的基因工程寻找新结构多糖愿望的驱使，研究人员已经发现可以生物降解且可以从可再生资源原料经济地制造的多糖。一种此类多糖是聚α-1,3-葡聚糖，一种特征为具有α-1,3-糖苷键的葡聚糖聚合物。

[0006] 已经通过使蔗糖的水性溶液与从唾液链球菌(Streptococcus salivarius)分离的葡糖基转移酶(gtf)接触来分离聚α-1,3-葡聚糖(Simpson等人，Microbiology 141:1451-1460,1995)。美国专利7,000,000公开利用唾液链球菌gtfJ酶制备多糖纤维。这种纤维的聚合物中至少50％己糖单元是通过α-1,3-糖苷键连接。本发明所公开的聚合物当它在溶剂或包含溶剂的混合物中以高于临界浓度的浓度溶解时形成液晶溶液。从这一溶液中纺出高度适用于纺织品的连续的、高强度的、棉花样纤维，并且使用。

[0007] 先前已经利用白色精制蔗糖进行聚α-1,3-葡聚糖的酶法合成。因为这种形式的蔗糖相对昂贵，希望开发出利用未精制或以其它方式不完全精制的蔗糖合成聚α-1,3-葡聚糖的新型酶法工艺。

发明内容

[0008] 在一个实施方案中，本公开涉及一种反应溶液，所述溶液包含水、蔗糖和葡糖基转移酶，所述溶液合成不溶性聚α-1,3-葡聚糖，其具有至少50％的α-1,3糖苷键和至少100的重均聚合度(DP_w)，其中所述蔗糖是未精制或部分精制的。所述反应溶液的聚α-1,3-葡聚糖的收率是在所述反应溶液中转化为产物的蔗糖的重量的至少7％。

[0009] 在反应溶液的另一个实施方案中，蔗糖来自糖用甜菜，且尚未结晶。

[0010] 在反应溶液的另一个实施方案中，蔗糖来自甘蔗，且(i)尚未结晶，或(ii)已经利用不超过三个结晶步骤结晶。

[0011] 在反应溶液的另一个实施方案中，蔗糖具有大于150的ICUMSA值。

[0012] 在反应溶液的另一个实施方案中，反应溶液的相对反应速率为至少0.8，这是相对

于包含水、白色精制蔗糖和葡糖基转移酶的反应溶液的反应速率而言。

[0013] 在反应溶液的另一个实施方案中，由反应溶液制备的聚α-1,3-葡聚糖具有小于93的L*值。

[0014] 在另一个实施方案中，葡糖基转移酶包含与SEQ ID NO:4、SEQ ID NO:8、SEQ ID NO:10、SEQ ID NO:12、SEQ ID NO:14、SEQ ID NO:20、SEQ ID NO:26、SEQ ID NO:28、SEQ ID NO:30或SEQ ID NO:34具有至少90％同一性的氨基酸序列。

[0015] 在另一个实施方案中，本公开涉及一种用于制备聚α-1,3-葡聚糖的方法，所述方法包括接触水、蔗糖和葡糖基转移酶的步骤，其中蔗糖是未精制或部分精制的。所述接触步骤中制备的聚α-1,3-葡聚糖具有至少50％的α-1,3糖苷键和至少100的重均聚合度(DP_w)。所述方法中制备的聚α-1,3-葡聚糖的收率是在所述接触步骤中转化为产物的蔗糖的重量的至少7％。所述方法任选地包括分离所述接触步骤中制备的聚α-1,3-葡聚糖。

[0016] 在另一个实施方案中，所述方法中使用的蔗糖来自糖用甜菜，且尚未结晶。

[0017] 在另一个实施方案中，所述方法中使用的蔗糖来自甘蔗，且(i)尚未结晶，或(ii)已经利用不超过三个结晶步骤结晶。

[0018] 在另一个实施方案中，所述方法中使用的蔗糖具有大于150的ICUMSA值。

[0019] 在另一个实施方案中，所述方法的接触步骤中制备聚α-1,3-葡聚糖的相对反应速率为至少0.8，这是相对于使用白色精制蔗糖替代未精制或部分精制蔗糖时的接触步骤的反应速率而言。

[0020] 在另一个实施方案中，所述方法中任选地分离的聚α-1,3-葡聚糖具有小于93的L*值。

[0021] 在另一个实施方案中，所述方法中使用的葡糖基转移酶包含与SEQ ID NO:4、SEQ ID NO:8、SEQ ID NO:10、SEQ ID NO:12、SEQ ID NO:14、SEQ ID NO:20、SEQ ID NO:26、SEQ ID NO:28、SEQ ID NO:30或SEQ ID NO:34具有至少90％同一性的氨基酸序列。

[0022] 在另一个实施方案中，本公开涉及通过以上方法制备的分离的聚α-1,3-葡聚糖，其中聚α-1,3-葡聚糖具有小于93的L*值。

[0023] 序列简述

[0024] 表1.核酸和蛋白质序列识别号概述

[0025]

说明	核酸 SEQ ID NO.	蛋白质 SEQ ID NO.
“0874 gtf”，远缘链球菌（*Streptococcus sobrinus*）。DNA 密码子经优化以在大肠杆菌（E. coli）中表达。与 GENBANK 识别号 450874 相比，所述蛋白的最初 156 个氨基酸缺失；包括起始甲硫氨酸。	1	2 (1435 aa)
“6855 gtf”，唾液链球菌（*Streptococcus salivarius*）SK126。DNA 密码子经优化以在大肠杆菌中表达。与 GENBANK 识别号 228476855 相比，所述蛋白的最初 178 个氨基酸缺失；包括了起始甲硫氨酸。	3	4 (1341 aa)
“2379 gtf”，唾液链球菌。DNA 密码子经优化以在大肠杆菌中表达。与 GENBANK 识别号 662379 相比，所述蛋白的最初 203 个氨基酸缺失；包括起始甲硫氨酸。	5	6 (1247 aa)
“7527”或“gtfJ”，唾液链球菌。DNA 密码子经优化以在大肠杆菌中表达。与 GENBANK 识别号 47527 相比，所述蛋白的最初 42 个氨基酸缺失；包括起始甲硫氨酸。	7	8 (1477 aa)
“1724 gtf”，汗毛链球菌（*Streptococcus downei*）。DNA 密码子经优化以在大肠杆菌中表达。与 GENBANK	9	10 (1436 aa)

[0026]

识别号 121724 相比，所述蛋白的最初 162 个氨基酸缺失；包括起始甲硫氨酸。		
“0544 gtf”，变异链球菌（*Streptococcus mutans*）。DNA 密码子经优化以在大肠杆菌中表达。与 GENBANK 识别号 290580544 相比，所述蛋白的最初 164 个氨基酸缺失；包括起始甲硫氨酸。	11	12 (1313 aa)
“5926 gtf”，蝙蝠齿链球菌（*Streptococcus dentirousetti*）。DNA 密码子经优化以在大肠杆菌中表达。与 GENBANK 识别号 167735926 相比，所述蛋白的最初 144 个氨基酸缺失；包括起始甲硫氨酸。	13	14 (1323 aa)
“4297 gtf”，口腔链球菌（*Streptococcus oralis*）。DNA 密码子经优化以在大肠杆菌中表达。与 GENBANK 识别号 7684297 相比，所述蛋白的最初 228 个氨基酸缺失；包括起始甲硫氨酸。	15	16 (1348 aa)
“5618 gtf”，血链球菌（*Streptococcus sanguinis*）。DNA 密码子经优化以在大肠杆菌中表达。与 GENBANK 识别号 328945618 相比，所述蛋白的最初 223 个氨基酸缺失；包括起始甲硫氨酸。	17	18 (1348 aa)
“2765 gtf”，未知链球菌属物种（*Streptococcus sp.*）C150。DNA 密码子经优化以在大肠杆菌中表达。与 GENBANK 识别号 322372765 相比，所述蛋白的最初 193 个氨基酸缺失；包括起始甲硫氨酸。	19	20 (1340 aa)
“4700 gtf”，肠膜明串珠菌（*Leuconostoc mesenteroides*）。DNA 密码子经优化以在大肠杆菌中表达。与 GENBANK 识别号 21654700 相比，所述蛋白的最初 36 个氨基酸缺失；包括起始甲硫氨酸。	21	22 (1492 aa)
“1366 gtf”，仓鼠链球菌（*Streptococcus criceti*）。DNA 密码子经优化以在大肠杆菌中表达。与 GENBANK 识别号 146741366 相比，所述蛋白的最初 139 个氨基酸缺失；包括起始甲硫氨酸。	23	24 (1323 aa)
“0427 gtf”，远缘链球菌（*Streptococcus sobrinus*）。DNA 密码子经优化以在大肠杆菌中表达。与 GENBANK 识别号 940427 相比，所述蛋白的最初 156 个氨基酸缺失；包括起始甲硫氨酸。	25	26 (1435 aa)
“2919 gtf”，唾液链球菌 PS4。DNA 密码子经优化以在大肠杆菌中表达。与 GENBANK 识别号 383282919 相比，所述蛋白的最初 92 个氨基酸缺失；包括起始甲硫氨酸。	27	28 (1340 aa)
“2678 gtf”，唾液链球菌 K12。DNA 密码子经优化以在大肠杆菌中表达。与 GENBANK 识别号 400182678 相比，所述蛋白的最初 188 个氨基酸缺失；包括起始甲硫氨酸。	29	30 (1341 aa)
“2381 gtf”，唾液链球菌。DNA 密码子经优化以在大肠	31	32

[0027]

杆菌中表达。与GENBANK识别号662381相比，所述蛋白的最初273个氨基酸缺失；包括起始甲硫氨酸。		(1305 aa)
“3929 gtf”，唾液链球菌JIM8777。DNA密码子经优化以在大肠杆菌中表达。与GENBANK识别号387783929相比，所述蛋白的最初178个氨基酸缺失；包括起始甲硫氨酸。	33	34 (1341 aa)
“6907 gtf”，唾液链球菌SK126。DNA密码子经优化以在大肠杆菌中表达。与GENBANK识别号228476907相比，所述蛋白的最初161个氨基酸缺失；包括起始甲硫氨酸。	35	36 (1331 aa)
“6661 gtf”，唾液链球菌SK126。DNA密码子经优化以在大肠杆菌中表达。与GENBANK识别号228476661相比，所述蛋白的最初265个氨基酸缺失；包括起始甲硫氨酸。	37	38 (1305 aa)
“0339 gtf”，解没食子酸链球菌（Streptococcus gallolyticus）ATCC 43143。DNA密码子经优化以在大肠杆菌中表达。与GENBANK识别号334280339相比，所述蛋白的最初213个氨基酸缺失；包括起始甲硫氨酸。	39	40 (1310 aa)
“0088 gtf”，变异链球菌（*Streptococcus mutans*）。DNA密码子经优化以在大肠杆菌中表达。与GENBANK识别号3130088相比，所述蛋白的最初189个氨基酸缺失；包括起始甲硫氨酸。	41	42 (1267 aa)
“9358 gtf”，变异链球菌UA159。DNA密码子经优化以在大肠杆菌中表达。与GENBANK识别号24379358相比，所述蛋白的最初176个氨基酸缺失；包括起始甲硫氨酸。	43	44 (1287 aa)
“8242 gtf”，解没食子酸链球菌ATCC BAA-2069。DNA密码子经优化以在大肠杆菌中表达。与GENBANK识别号325978242相比，所述蛋白的最初191个氨基酸缺失；包括起始甲硫氨酸。	45	46 (1355 aa)
“3442 gtf”，血链球菌SK405。DNA密码子经优化以在大肠杆菌中表达。与GENBANK识别号324993442相比，所述蛋白的最初228个氨基酸缺失；包括起始甲硫氨酸。	47	48 (1348 aa)
“7528 gtf”，唾液链球菌。DNA密码子经优化以在大肠杆菌中表达。与GENBANK识别号47528相比，所述蛋白的最初173个氨基酸缺失；包括起始甲硫氨酸。	49	50 (1427 aa)
“3279 gtf”，链球菌属物种（*Streptococcus sp.*）C150。DNA密码子经优化以在大肠杆菌中表达。与GENBANK识别号322373279相比，所述蛋白的最初178个氨基酸缺失；包括起始甲硫氨酸。	51	52 (1393 aa)
“6491 gtf”，柠檬明串珠菌（*Leuconostoc citreum*）KM20。DNA密码子经优化以在大肠杆菌中表达。与	53	54 (1262 aa)

[0028]

GENBANK 识别号 170016491 相比，所述蛋白的最初 244 个氨基酸缺失；包括起始甲硫氨酸。		
“6889 gtf”，唾液链球菌 SK126。DNA 密码子经优化以在大肠杆菌中表达。与 GENBANK 识别号 228476889 相比，所述蛋白的最初 173 个氨基酸缺失；包括起始甲硫氨酸。	55	56 (1427 aa)
“4154 gtf”，罗伊氏乳杆菌（*Lactobacillus reuteri*）。DNA 密码子经优化以在大肠杆菌中表达。与 GENBANK 识别号 51574154 相比，所述蛋白的最初 38 个氨基酸缺失；包括起始甲硫氨酸。	57	58 (1735 aa)
“3298 gtf”，链球菌属物种（*Streptococcus sp.*）C150。与 GENBANK 识别号 322373298 相比，所述蛋白的最初 209 个氨基酸缺失；包括起始甲硫氨酸。		59 (1242 aa)
“野生型 gtfJ”，唾液链球菌。GENBANK 识别号 47527。		60 (1518 aa)
对应 2678 gtf 的野生型 gtf，唾液链球菌 K12。GENBANK 识别号 400182678。		61 (1528 aa)
对应 6855 gtf 的野生型 gtf，唾液链球菌 SK126。GENBANK 识别号 228476855。		62 (1518 aa)
对应 2919 gtf 的野生型 gtf，唾液链球菌 PS4。GENBANK 识别号 383282919。		63 (1431 aa)
对应 2765 gtf 的野生型 gtf，链球菌属物种（*Streptococcus sp.*）C150。GENBANK 识别号 322372765。		64 (1532 aa)

具体实施方式

[0029] 所有引用的专利和非专利文献的公开全文以引用方式并入本文。

[0030] 如本文所用，术语“发明”或“本发明所公开的”不旨在限制但一般适用于权利要求中所限定的或本文所述的任何发明。这些术语在本文中可互换使用。

[0031] 术语“聚α-1,3-葡聚糖”、“α-1,3-葡聚糖聚合物”等在本文中可互换使用。聚α-1,3-葡聚糖是包含由糖苷键(即葡糖苷键)连接在一起的葡萄糖单体单元的聚合物，其中至少约50％的糖苷键是α-1,3-糖苷键。聚α-1,3-葡聚糖是一类多糖。如本文所用，术语“α-1,3-糖苷键”是指通过在邻近α-D-葡萄糖环上的碳1和碳3彼此接合α-D-葡萄糖分子的一类共价键。

[0032] 术语“糖苷键(glycosidic linkage)”和“糖苷键(glycosidic bond)”在本文中可以互换使用，且是指将碳水化合物(糖)分子接合至另一基团诸如另一碳水化合物的一类共价键。如本文所用，术语“α-1,3-糖苷键”是指通过在邻近α-D-葡萄糖环上的碳1和碳3彼此接合α-D-葡萄糖分子的一类共价键。

[0033] “α-D-葡萄糖”在本文中也可以指“葡萄糖”。

[0034] 术语“蔗糖”在本文中指由通过α-1,2-糖苷键连接的α-D-葡萄糖分子和β-D-果糖分子组成的非还原二糖。已知蔗糖常作为食糖。

[0035] “白色精制”蔗糖在本文中是指包含至少99.0重量％蔗糖的蔗糖。此外或另选地，白色精制蔗糖可以指具有150或更小(例如，45或更小)的ICUMSA值、99.70％的最小偏振和/或至少87.0的L*值的蔗糖。

[0036] “ICUMSA”(国际食糖统一分析法委员会)值或“标准ICUMSA”值是用于表示溶液中蔗糖样品纯度的国际单位,且与蔗糖的颜色直接相关。蔗糖样品的ICUMSA值越大,蔗糖样品越深。测定蔗糖样品的ICUMSA值的方法是本领域中所熟知的,且由国际食糖统一分析法委员会公开在例如ICUMSA Methods of Sugar Analvsis:Official and Tentative Methods Recommended by the International Commission for Uniform Methods of Sugar Analysis(ICUMSA)(Ed.H.C.S.de Whalley,Elsevier Pub.Co.,1964)中,该文献以引用的方式并入本文。ICUMSA可以例如通过如由R.J.McCowage、R.M.Urquhart和M.L.Burge(Determination of the Solution Colour of Raw Sugars,Brown Sugars and Coloured Syrups at pH 7.0-Official,Verlag Dr Albert Bartens,2011 revision)所述的ICUMSA方法GS1/3-7测定,该文献以引用的方式并入本文。ICUMSA值可以表示为“参考基本单位”(RBU)。

[0037] 本文的ICUMSA值可以通过极其类似于ICUMSA方法GS1/3-7的方法测定,但不同的是利用醋酸纤维素过滤器替代硝酸纤维素过滤器。因此,本文所公开的ICUMSA值可以另外称作“改良ICUMSA”值。考虑到ICUMSA是如何测定的,应理解,本文针对固体糖样品(例如,原蔗糖)提供的ICUMSA值是利用糖样品的水性溶液(约200g/L)获得的。

[0038] 蔗糖样品的“偏振”(“pol”)在本文中称为样品中的表观蔗糖含量,表示为通过在20℃下穿过含蔗糖样品的溶液的偏振光的旋光度测量的质量百分比。蔗糖样品的偏振越大,样品中的蔗糖纯度越大。

[0039] “未完全精制的”蔗糖(“不完全精制的”蔗糖)在本文中称为尚未加工成白色精制蔗糖的蔗糖。因此,不完全精制的蔗糖可以是完全未精制或部分精制的。未精制蔗糖的示例是“原蔗糖”(“原糖”)和它的溶液。部分精制的蔗糖的示例尚未经历一个、两个、三个或更多个结晶步骤。不完全精制的蔗糖的ICUMSA在本文中大于150。

[0040] 术语蔗糖“结晶”“结晶步骤”、“分步结晶”等在本文中可互换使用,且是指从含不完全精制的蔗糖的溶液结晶出蔗糖,并从上清液(母液)分离蔗糖晶体的过程。由这个过程产生的晶体通常代表比在结晶步骤之前存在的蔗糖纯的蔗糖。然而,需要重点注意的是,已经经历一个、两个、三个或更多个结晶步骤的不完全精制的蔗糖仍然可以构成不完全精制的蔗糖(即,结晶蔗糖可以不具有白色精制蔗糖的纯度)。蔗糖通常需要三个或更多个结晶步骤来制备白色精制糖,而甜菜汁在一些实施方案中可能只需要一个结晶步骤就可以达到这种纯度。本领域中已知用于使蔗糖结晶的各种方式,诸如蒸发、沸腾和/或真空干燥工艺。

[0041] 如本文中所用,术语“L*值”是指由国际照明委员会(CIE,Vienna,Austria)指定的CIE 1976(L*,a*,b*)(“CIELAB”)三维色彩空间的明度分量。L*a*b*色彩空间的三个坐标分别代表固体颜色的明度(L*=0指黑色,且L*=100指漫射白色)、对象沿着红色/品红色与绿色间的标度的颜色(a*,负值指绿色,而正值指品红色)和对象沿着黄色与蓝色间的标度的颜色(b*,负值指蓝色,且正值指黄色)。用于指对象的L*a*b*色彩空间的星号(*)的发音为“星号”(例如,L*是“L-星号”),且作用是将这个色彩空间与Hunter的L,a,b色彩系统区分开来。对象的CIELAB色彩空间的L*、a*和b*分量可以利用J.Schwiegerling(Field Guide to Visual and Ophthalmic Optics,SPIE Press,Bellingham,WA,2004)所公开的公式计算,该文献以引用的方式并入本文。L*、a*、b*值在本文中是针对固体材料诸如干燥蔗糖或干燥聚α-1,3-葡聚糖来说。

[0042] 如本文所用，“干燥”蔗糖可以表征含不超过2.0、1.5、1.0、0.5、0.25、0.10、0.05或0.01重量％水的蔗糖。

[0043] 聚α-1,3-葡聚糖的“分子量”在本文中可以表示为数均分子量(M_n)或重均分子量(M_w)。另选地，分子量可以表示为道尔顿、克/摩尔、DP_w(重均聚合度)或DP_n(数均聚合度)。本领域中已知用于计算这些分子量测量值的各种方式，诸如利用高压液相色谱法(HPLC)、尺寸排阻色谱法(SEC)或凝胶渗透色谱法(GPC)。

[0044] 术语“葡糖基转移酶”、“gtf酶”、“gtf酶催化剂”、“gtf”、“葡聚糖蔗糖酶”等在本文中可互换使用。本文gtf酶的活性催化底物蔗糖反应以制备产物聚α-1,3-葡聚糖和果糖。gtf反应的其它产物(副产物)可以包括葡萄糖(当葡萄糖从葡糖基-gtf酶中间复合物水解时产生)、各种可溶性低聚糖(例如，DP2-DP7)和明串珠菌二糖(当葡糖基-gtf酶中间复合物的葡萄糖连接至果糖时产生)。明串珠菌二糖是由通过α-1,5键连接的葡萄糖和果糖组成的二糖。野生型形式的葡糖基转移酶通常包含(在N-末端至C-末端方向上)信号肽、可变结构域、催化结构域和葡聚糖结合结构域。本文的gtf根据CAZy(碳水化合物活性酶)数据库(Cantarel等人，Nucleic Acids Res.37:D233-238,2009)归类在配糖水解酶家族70(GH70)下。

[0045] 如本文所用，“反应溶液”通常是指包含蔗糖、水、至少一种活性葡糖基转移酶、和可选的其它组分的溶液。另选地，反应溶液可以在本文中称为例如“葡聚糖合成反应”、“葡聚糖反应”或“gtf反应”。可用在葡聚糖合成反应中的其它组分包括果糖、葡萄糖、明串珠菌二糖和可溶性低聚糖(例如，DP2-DP7)。应当理解，某些葡聚糖产物(诸如聚合度(DP)为至少8或9的聚α-1,3-葡聚糖)是水不溶性的，且因此在葡聚糖合成反应中不溶解，而是存在于溶液之外。正是在反应溶液中进行使水、蔗糖和葡糖基转移酶接触的步骤。如本文所用，术语“在合适反应条件下”是指支持蔗糖通过葡糖基转移酶活性转化为聚α-1,3-葡聚糖的反应条件。

[0046] 如本文所用，“对照”反应溶液可以指包含白色精制蔗糖而非不完全精制的蔗糖的反应溶液。对照反应溶液的所有其它特征(例如，蔗糖浓度、温度、pH、gtf类型)可以与所比较的反应溶液相同。

[0047] 葡聚糖合成反应的“干燥固体百分比”是指葡聚糖合成反应中所有糖的重量％。gtf反应的干燥固体百分比可以例如基于用于制备反应的蔗糖的量计算。

[0048] 本文反应溶液的聚α-1,3-葡聚糖的“收率”表示聚α-1,3-葡聚糖产物的重量，表示为反应中被转化的蔗糖底物的重量百分比。例如，如果反应溶液中100g蔗糖转化为产物，且10g产物是聚α-1,3-葡聚糖，那么聚α-1,3-葡聚糖的收率将是10％。这个收率计算可以视为反应针对聚α-1,3-葡聚糖的选择性的量度。

[0049] 如本文所用，术语“相对反应速率”是指特定葡聚糖合成反应与另一种葡聚糖合成反应相比的速率。例如，如果反应A的速率为x，且反应B的速率为y，那么反应A相对于反应B的反应速率的相对反应速率可以表示为x/y(x除以y)。术语“反应速率”和“反应的速率”在本文中可以互换地指代在单位时间内每单位酶下，反应物的浓度/量的变化或者产物的浓度/量的变化。葡聚糖合成反应在本文中的优选反应物和产物分别是蔗糖和聚α-1,3-葡聚糖。

[0050] 本文葡聚糖合成反应的“馏分”是指葡聚糖合成反应的液体溶液部分。馏分可以是

葡聚糖合成反应的一部分或全部液体溶液，且已经从反应中合成的固体葡聚糖产物分离出来。馏分也可以称为“母液”。馏分的示例是葡聚糖合成反应的滤液。因为馏分可以包含溶解的糖，诸如蔗糖、果糖、葡萄糖、明串珠菌二糖、可溶性低聚糖(例如，DP2-DP7)，馏分也可以称为来源于葡聚糖合成反应的“混合糖溶液”。

[0051] 术语“滤液”、“葡聚糖反应滤液”、“葡聚糖滤液”等在本文中可互换使用，且是指已经从葡聚糖合成反应中合成的固体葡聚糖产物过滤出的馏分。

[0052] 术语“体积％”、“体积百分比”、“vol％”、“体积/体积％”等在本文中可互换使用。溶液中溶质的体积％可以利用下式测定：[(溶质体积)/(溶液体积)]×100％。

[0053] 术语“重量％”、“重量百分比(wt％)”以及“重量-重量百分比(重量/重量％)”等在本文中可互换使用。重量％是指物质在其被包含在组合物、混合物或溶液中时以质量计的百分比。

[0054] 术语“提高的”、“增强的”和“改善的”在本文中可互换使用。这些术语是指更大的数量或活性，诸如略大于原始数量或活性的数量或活性、或大大超出原始数量或活性的数量或活性，且包括其间的所有数量或活性。另选地，这些术语可以指例如该数量或活性与和它相比较的数量或活性相比，提高至少1％、2％、3％、4％、5％、6％、7％、8％、9％、10％、11％、12％、13％、14％、15％、16％、17％、18％、19％或20％。

[0055] 如本文所用，相对于多核苷酸或多肽序列的术语“序列同一性”或“同一性”是指在指定的比较窗范围为获得最大对应而比对时两条序列中相同的核酸碱基或氨基酸残基。因此，“序列同一性百分比”或“同一性百分比”指通过在比较窗口上比较两个最佳比对的序列而测定的值，其中在与参考序列(其不包含添加或缺失)进行比较时，比较窗口中的多核苷酸或多肽序列的部分可包含添加或缺失(即缺口)以实现两个序列的最佳比对。通过以下方式计算这种百分比：确定在两个序列中出现相同核酸碱基或氨基酸残基的位置的数目以得到匹配的位置的数目，将匹配的位置的数目除以比较窗口中位置的总数目，然后将结果乘以100以得到序列同一性百分比。

[0056] 在National Center for Biotechnology Information(NCBI)网站在线可用的Basic Local Alignment Search Tool(BLAST)算法可用于例如测量本文所公开的两个或更多个多核苷酸序列(BLASTN算法)或多肽序列(BLASTP算法)之间的百分比同一性。另选地，序列间的百分比同一性可使用Clustal算法(例如ClustalW或ClustalV)进行计算。对于使用Clustal比对方法的多重比对，默认值可对应于GAP PENALTY＝10、以及GAP LENGTH PENALTY＝10。用Clustal方法进行成对比对和蛋白质序列的百分比同一性计算的默认参数可为KTUPLE＝1、GAP PENALTY＝3、WINDOW＝5、以及DIAGONALS SAVED＝5。对于核酸，这些参数可为KTUPLE＝2，GAP PENALTY＝5，WINDOW＝4、以及DIAGONALS SAVED＝4。另选地，序列间的百分比同一性可以利用EMBOSS算法(例如，needle)进行，其中参数诸如GAP OPEN＝10、GAP EXTEND＝0.5、END GAP PENALTY＝false、END GAP OPEN＝10、END GAP EXTEND＝0.5，利用BLOSUM矩阵(例如，BLOSUM62)。

[0057] 本文公开了多种多核苷酸和多肽序列作为某些实施方案的特征。可使用与本文所公开的序列具有至少约70-85％、85-90％或90％-95％同一性的这些序列的变体。另选地，变体氨基酸序列可与本文所公开的序列具有至少70％、71％、72％、73％、74％、75％、76％、77％、78％、79％、80％、81％、82％、83％、84％、85％、86％、87％、88％、89％、90％、91％、

92％、93％、94％、95％、96％、97％、98％或99％的同一性。变体核苷酸或氨基酸序列具有与本发明所公开的序列相同的功能/活性，或者具有本发明所公开的序列的至少约85％、86％、87％、88％、89％、90％、91％、92％、93％、94％、95％、96％、97％、98％或99％的功能/活性。

[0058] 如某些实施方案中所用，术语“分离的”是指完全从其原始来源分离的任何细胞组分(例如，分离的多核苷酸或多肽分子)。在一些情况下，分离的多核苷酸或多肽分子是较大组合物、缓冲体系或试剂混合物的一部分。例如，分离的多核苷酸或多肽分子可以异源方式包含在细胞或生物内。其它的示例是分离的葡糖基转移酶和分离的聚α-1,3-葡聚糖。据信，本文所公开的葡糖基转移酶反应过程是合成、非天然存在的过程。

[0059] 先前已经利用白色精制蔗糖进行聚α-1,3-葡聚糖的酶法合成。因为这种形式的蔗糖相对昂贵，希望开发出利用未精制或以其它方式不完全精制的蔗糖合成聚α-1,3-葡聚糖的新型酶法工艺。

[0060] 本公开的实施方案涉及一种反应溶液，所述反应溶液包含至少水、蔗糖和葡糖基转移酶，所述反应溶液合成不溶性聚α-1,3-葡聚糖，其具有至少50％的α-1,3糖苷键和至少100的重均聚合度(DP_w)，其中所述蔗糖是未精制或部分精制的(即，未完全精制的)。反应溶液制备具有至少50％的α-1,3糖苷键和至少100的DP_w的不溶性聚α-1,3-葡聚糖。所述反应溶液的聚α-1,3-葡聚糖的收率是在所述反应溶液中转化为产物的蔗糖的重量的至少7％。

[0061] 显著地，这种反应溶液的实施方案制备收率和分子量与通过使用白色精制蔗糖而非不完全精制的蔗糖的反应溶液制备的葡聚糖收率和分子量相当的聚α-1,3-葡聚糖。这些结果表明，不完全精制的蔗糖中存在的污染物一般不会阻碍它通过葡糖基转移酶用于使聚α-1,3-葡聚糖聚合。

[0062] 未完全精制的蔗糖可以用在当前公开的反应溶液中。此类蔗糖尚未加工成白色精制蔗糖。示例包括含原蔗糖(原糖)的未精制蔗糖组合物。可用于本文中的其它形式的不完全精制的蔗糖包括以下形式：来源于例如甘蔗(甘蔗属物种(*Saccharum spp.*)，诸如甘蔗(*S.officenarum*))、糖用甜菜(甜菜属物种(*Beta spp.*)，诸如甜菜(*B.vulgaris*))(也可以在本文中称为“beet”)、枣椰(date palm)(海枣(*Phoenix dactylifera*))、高粱(高粱属物种(*Sorghum spp.*)，诸如高粱(*S.vulgare*)和双色高粱(*S.bicolor*))、糖枫(sugar maple)(糖槭(*Acer saccharum*))、木薯(cassava)(木薯(*Manihot esculenta*))或玉米的蔗糖。甘蔗和/或糖用甜菜的蔗糖的不完全精制形式可以用在本文中的优选实施方案中。甘蔗汁中含约20％蔗糖，而糖用甜菜汁中含约10％至15％蔗糖。

[0063] 在某些实施方案中，不完全精制的蔗糖可以来自产蔗糖和任选地种植用于产蔗糖的植物。此类植物(诸如上文所列的那些)可以来自世界上通常种植植物的任何地区。例如，本文的蔗糖可以来自种植在南美洲(例如，巴西、哥伦比亚、阿根廷、圭亚那)、北美洲(例如，美国、墨西哥、西印度群岛、中美洲[例如，伯利兹城])、澳洲、亚洲(例如，印度、中国、俄罗斯、土耳其、泰国、巴基斯坦、菲律宾、印度尼西亚)、非洲(例如，埃及、莫桑比克、津巴布韦)和欧洲(例如，法国、德国、乌克兰、俄罗斯、土耳其)的植物。

[0064] 不完全精制的蔗糖可以作为在从含蔗糖的植物(例如，甘蔗或糖用甜菜)的汁纯化蔗糖工艺的任何阶段获得的组合物提供。此类工艺公开在例如Handbook of Sugar Refining:A Manual for the Design and Operation of Sugar Refining Facilities

(Ed.C.C.Chou,John Wiley&Sons,Inc.,2000)、Chen and Chou(Cane Sugar Handbook:A Manual for Cane Sugar Manufacturers and Their Chemists,第12版,John Wiley&Sons,Inc.,1993)和Asadi(Beet-Sugar Handbook,第1版,Wiley-Interscience,2006)中,这些文献全部以引用的方式并入本文。如下讨论来自这些参考文献的一些优选组合物和工艺。

[0065] 本文的不完全精制的蔗糖可以作为蔗糖-纯化工艺的任何步骤所产生的组合物提供,诸如(i)初始提取(例如,热水提取)植物材料的“原汁”;(ii)通过碳酸化纯化汁(即,利用石灰和二氧化碳形成使杂质共沉淀的碳酸钙沉淀物),得到“稀汁”;(iii)蒸发稀汁的水,得到“浓汁”,和/或(iv)使浓汁沸腾或进行真空浓缩,以使蔗糖结晶(此类一次结晶蔗糖通常不是白色精制糖)(可以例如通过离心从上清液去除晶体)。例如,在某些实施方案中,步骤(i)和(ii)的产物可以在进一步加工前过滤。结晶(iv)的上清液可以再循环,并与其它上清液和/或浓汁混合,然后使它经历结晶(得到如步骤[iv]中的晶体,它们也可以用在本文中)。上清液的再循环最终得到“糖蜜”。因此,不完全精制的蔗糖可以作为原汁、稀汁、浓汁、糖蜜和/或已经经历例如不超过一次结晶的蔗糖晶体提供。这些形式的不完全精制的蔗糖和用于获得它们的相应工艺步骤优选地表征从糖用甜菜获得的不完全精制的蔗糖的示例,而且可以表征从其它来源诸如甘蔗获得的蔗糖。

[0066] 可用在本文中的来自糖用甜菜的不完全精制的蔗糖的示例包括甜菜原汁、甜菜稀汁(含约10重量%-20重量%蔗糖)、甜菜浓汁(含约60重量%-90重量%蔗糖)和糖用甜菜糖蜜(约50重量%-60重量%蔗糖)。在某些实施方案中使用甜菜稀汁和/或浓汁。本文的ICUMSA值:例如对于甜菜稀汁可以是至少1000(例如,～1000-1300),对于甜菜浓汁可以是至少1300(例如,～1300-1800),和/或对于甜菜糖蜜可以是至少50000(例如,～50000-60000)。

[0067] 另选地,本文的不完全精制的蔗糖可以是“原蔗糖”(“原糖”),它是通过去除原汁的所有水提供(即,原蔗糖是固体)。另选地,本文的不完全精制的蔗糖可以是“VHP蔗糖”(“VHP”、“VHP糖”、“极高偏振”蔗糖),它是如下提供:首先碳酸化,并过滤原汁,接着蒸发原汁,以使其中蔗糖的一部分结晶;从上清液去除的结晶蔗糖是VHP蔗糖。因此,VHP蔗糖已经经历一次结晶。另选地,本文的不完全精制的蔗糖可以是“VVHP蔗糖”(“VVHP”、“VVHP糖”、“极其极其高偏振”蔗糖),它是通过将VHP蔗糖溶解在水中,并使蔗糖重结晶而提供。因此,VVHP蔗糖已经经历两次结晶。这些形式的不完全精制的蔗糖(原蔗糖、VHP、VVHP)和用于获得它们的相应工艺步骤优选地表征从甘蔗获得的不完全精制的蔗糖的示例,而且可以表征从其它来源诸如糖用甜菜获得的蔗糖。

[0068] 本文的原蔗糖(例如,“原蔗糖”)可以具有94%至97%的偏振值、约600至1200的ICUMSA值和/或低于87.0(例如,小于85、80、75、70、65、60、55或50)的L*值,应当理解,原蔗糖不是“红糖”,红糖是混合糖蜜糖浆与白色精制糖,接着干燥所得的产物。本文的VHP蔗糖可以具有例如至少99.30%的偏振值和/或约300至1000的ICUMSA值。VHP蔗糖可以任选地具有以下特性中的任一种:0.15%最大含水量、0.15%最大灰分含量、97%水中溶解度和/或金棕色。本文的VVHP蔗糖可以具有例如至少99.50%的偏振值和/或超过150至约400的ICUMSA值。

[0069] 本文的不完全精制的蔗糖不是白色精制蔗糖。白色精制蔗糖在本文中是指含至少

99.0重量％蔗糖(例如,至少99.5重量％或99.9重量％)的蔗糖。此外或另选地,白色精制蔗糖可以指具有150或更小(例如,45或更小)的ICUMSA值、99.70％(例如,至少99.80％)的最小偏振和/或至少87.0(例如,至少87.5、88.0或88.5)的L*值的蔗糖。在某些实施方案中,白色精制蔗糖也可以具有以下特性中的任一种:0.04％最大含水量、0.04％最大灰分含量、100％水中溶解度、亮白色和/或细化颗粒。

[0070]　在某些实施方案中,不完全精制的蔗糖尚未结晶。可以提到从糖用甜菜包括例如甜菜原汁、甜菜稀汁和甜菜浓汁获得的不完全精制的蔗糖。另选地,本文的不完全精制的蔗糖已经具有不超过一个、两个、三个或更多个结晶步骤。例如,可以使用来自甘蔗且已经具有不超过两次或三次结晶的不完全精制的蔗糖。另选地,如果已经经历一次、两次、三次或更多次结晶但具有大于150的ICUMSA,可以使用不完全精制的蔗糖。结晶步骤可以包括例如使含蔗糖的水性溶液至少沸腾和/或真空干燥至使溶解的蔗糖开始作为晶体析出溶液的程度。

[0071]　本文的不完全精制的蔗糖的ICUMSA值可以大于例如150。另选地,不完全精制的蔗糖可以具有例如至少约200、300、400、500、600、700、800、900、1000、1100、1200、1300、1400、1500、2000、2500、3000、4000、5000、6000、7000、8000、9000、10000、20000、30000、40000、50000或60000(或介于151和60000之间的任何整数值)的ICUMSA值。在某些实施方案中,ICUMSA可在约1000-1300的范围内,诸如当不完全精制的蔗糖是甜菜稀汁时。在其它实施方案中,本文的ICUMSA可在约1300-1800的范围内,诸如当不完全精制的蔗糖是甜菜浓汁时,或约50000至60000的范围内,诸如当不完全精制的蔗糖是甜菜糖蜜时。在其它实施方案中,ICUMSA可在约600-1200的范围内,诸如当不完全精制的蔗糖是原蔗糖时;约300-1000的范围内,诸如当不完全精制的蔗糖是VHP蔗糖时;或超过150至约400的范围内,诸如当不完全精制的蔗糖是VVHP蔗糖时。

[0072]　据信,本文的蔗糖组合物的ICUMSA值(“改良ICUMSA”)与针对所述组合物利用其它ICUMSA方法测得的ICUMSA值相同或极其类似。

[0073]　本文的反应溶液是指至少包含不完全精制的蔗糖、水和活性葡糖基转移酶和任选的其它组分的溶液。可以用在葡聚糖合成反应中的其它组分包括例如果糖、葡萄糖、明串珠菌二糖、可溶性低聚糖(例如,DP2-DP7)。应当理解,某些葡聚糖产物(诸如DP为至少8或9的聚α-1,3-葡聚糖)可以是水不溶性的,且因此在葡聚糖合成反应中不溶解,而是存在于溶液之外。本文的反应溶液可以是一种除制备不溶性葡聚糖产物以外,制备副产物诸如明串珠菌二糖和/或可溶性低聚糖的溶液。

[0074]　如本文所公开的反应溶液包含制备具有至少50％的α-1,3糖苷键和至少100的DP_w的聚α-1,3-葡聚糖的葡糖基转移酶。此类可用于本文中的葡糖基转移酶的示例公开在美国专利7000000和美国专利申请公布2013/0244288和2013/0244287(所有这些文献以引用的方式并入本文)中。可以用在本文的反应溶液中制备聚α-1,3-葡聚糖的葡糖基转移酶的其它示例公开在美国专利申请公布2014/0087431(美国专利申请14/036,049)中,该文献以引用的方式并入本文。例如,本文的葡糖基转移酶可以(i)包含与SEQ ID NO:4、8、10、12、14、20、26、28、30或34具有100％同一性或至少90％、91％、92％、93％、94％、95％、96％、97％、98％或99％同一性的氨基酸序列,或由其组成,且(ii)具有葡糖基转移酶活性。

[0075]　在某些其它实施方案中,反应溶液包含这样的葡糖基转移酶,其(i)包含与SEQ ID

NO:2、4、6、8、10、12、14、16、18、20、22、24、26、28、30、32、34、36、38、40、42、44、46、48、50、52、54、56、58、59、60、61、62、63或64具有100％同一性或至少90％、91％、92％、93％、94％、95％、96％、97％、98％或99％同一性的氨基酸序列，或由其组成，且(ii)具有葡糖基转移酶活性。

[0076] 本文的葡糖基转移酶可以来源于任何微生物来源，诸如细菌或真菌。细菌葡糖基转移酶的示例是来源于链球菌属(Streptococcus)菌种、明串珠菌属(Leuconostoc)菌种或乳杆菌属(Lactobacillus)菌种的那些葡糖基转移酶。链球菌属菌种的示例包括唾液链球菌(S.salivarius)、远缘链球菌(S.sobrinus)、蝙蝠齿链球菌(S.dentirousetti)、汗毛链球菌(S.downei)、变异链球菌(S.mutans)、口腔链球菌(S.oralis)、解没食子酸链球菌(S.gallolyticus)和血链球菌(S.sanguinis)。明串珠菌属菌种的示例包括肠膜明串珠菌(L.mesenteroides)、蜜二糖明串珠菌(L.amelibiosum)、阿根廷明串珠菌(L.argentinum)、肠系膜状明串珠菌(L.carnosum)、柠檬明串珠菌(L.citreum)、乳脂明串珠菌(L.cremoris)、葡聚糖明串珠菌(L.dextranicum)和果糖明串珠菌(L.fructosum。乳杆菌属菌种的示例包括嗜酸乳杆菌(L.acidophilus)、德氏乳酸杆菌(L.delbrueckii)、瑞士乳杆菌(L.helveticus)、唾液乳杆菌(L.salivarius)、干酪乳杆菌(L.casei)、弯曲乳杆菌(L.curvatus)、植物乳杆菌(L.plantarum)、清酒乳杆菌(L.sakei)、短乳杆菌(L.brevis)、布氏乳杆菌(L.buchneri)、发酵乳杆菌(L.fermentum)和罗伊氏乳杆菌(L.reuteri)。

[0077] 在一些方面，本文的葡糖基转移酶在葡聚糖合成反应中制备具有至少50％的α-1，3糖苷键的聚α-1,3-葡聚糖，其中使用不完全精制的蔗糖。据信，在某些实施方案中，葡糖基转移酶合成这样的聚α-1,3-葡聚糖，其中至少约60％、70％、80％、90％、95％、96％、97％、98％、99％或100％(或介于60％和100％之间的任何整数)的组成糖苷键是α-1,3键。因此，葡糖基转移酶在上述实施方案中合成这样的聚α-1,3-葡聚糖，其中少于约50％、40％、30％、20％、10％、5％、4％、3％、2％、1％或0％(或介于0％和50％之间的任何整数值)的糖苷键不是α-1,3。

[0078] 在本文的其它方面，葡糖基转移酶可以合成不具有分支点或具有占聚合物中糖苷键的百分比少于约10％、9％、8％、7％、6％、5％、4％、3％、2％或1％分支点的聚α-1,3-葡聚糖。分支点的示例包括α-1,6分支点，诸如存在于突变聚合物中的那些分支点。

[0079] 在本文的一些方面，葡糖基转移酶可以合成分子量以DP_n或DP_w计为至少约100的聚α-1,3-葡聚糖。另选地，葡糖基转移酶可以合成分子量以DP_n或DP_w计为至少约400的聚α-1,3-葡聚糖。另选地，葡糖基转移酶可以合成分子量以DP_n或DP_w计为至少约100、150、200、250、300、350、400、450、500、550、600、650、700、750、800、850、900、950或1000(或介于100和1000之间的任何整数)的聚α-1,3-葡聚糖。

[0080] 在某些方面，可以使用一种或多种不同的葡糖基转移酶。在某些实施方案中，葡糖基转移酶不具有或具有极小(小于1％的)的葡聚糖蔗糖酶活性、罗伊糖蔗糖酶活性、或交替糖蔗糖酶活性。本文的反应溶液可以包含例如一种、两种或更多种葡糖基转移酶。

[0081] 本文的葡糖基转移酶可以是不依赖引物的或依赖引物的。不依赖引物的葡糖基转移酶不需要存在引物来实施葡聚糖合成。在葡聚糖聚合物合成期间，依赖引物的葡糖基转移酶需要反应溶液中存在引发分子充当酶引物。如本文所用的术语“引物”是指能够用作葡糖基转移酶的引发剂的任何分子。可以用在某些实施方案中的引物包括例如右旋糖酐和其

它基于碳水化合物的引物，诸如水解的葡聚糖。用作引物的右旋糖酐可以是例如右旋糖酐T10(即，分子量为10kD的右旋糖酐)。

[0082] 本文的葡糖基转移酶的示例可以具有本文所公开的任何氨基酸序列，且其还在N-末端和/或C末端包括1-300(或其中的任何整数[例如，10、15、20、25、30、35、40、45或50])个残基。此类附加残基可以来自得到葡糖基转移酶的相应野生型序列，或者可以是例如异源序列，诸如表位标记(在N-末端或C-末端)或异源信号肽(在N-末端)。

[0083] 本文的葡糖基转移酶通常不含N-末端信号肽。用于产生本文的葡糖基转移酶的表达系统可以采用酶编码多核苷酸，如果需要，其还包含编码指导胞外分泌的N-末端信号肽的序列。在此类实施方案中，信号肽在分泌过程中从所述酶裂解。信号肽可以与葡糖基转移酶同源或异源。可用于本文中的信号肽的示例是一种来自细菌(例如，芽孢杆菌属菌种，诸如枯草芽孢杆菌(B.subtilis))或真菌菌种的信号肽。细菌信号肽的示例是aprE信号肽，诸如一种来自芽孢杆菌属的信号肽(例如，枯草芽孢杆菌，参见Vogtentanz等人，Protein Expr.Purif.55:40-52，该文献以引用的方式并入本文)。

[0084] 本文所公开的若干种葡糖基转移酶序列不含N-末端信号肽(以及可变结构域)(参考表1)。为了进行细胞内表达，已经向每条序列添加N-末端起始甲硫氨酸(氨基酸位置1)(表达的酶可以在例如细胞裂解液中得到)。本领域的技术人员应理解，可以任选地在起始甲硫氨酸与葡糖基转移酶序列之间添加居间异源氨基酸序列诸如表位和/或信号肽。因此，例如，本文的葡糖基转移酶可以包含这样的氨基酸序列，或由其组成：(i)与SEQ ID NO:2、4、6、8、10、12、14、16、18、20、22、24、26、28、30、32、34、36、38、40、42、44、46、48、50、52、54、56、58、59、60、61、62、63或64的从位置2开始的氨基酸序列具有100％同一性或至少90％、91％、92％、93％、94％、95％、96％、97％、98％或99％同一性的氨基酸序列，且(ii)具有葡糖基转移酶活性。

[0085] 用于本文葡聚糖合成反应的葡糖基转移酶可以通过本领域内已知的任何方式制备。例如，葡糖基转移酶可以在异源表达系统中重组产生，诸如微生物异源表达系统。异源表达系统的示例包括细菌(例如，大肠杆菌，诸如TOP10或MG1655；芽孢杆菌属物种)和真核(例如，酵母，诸如毕赤酵母属物种(Pichia sp.)和酵母属物种(Saccharomyces sp.))表达系统。

[0086] 在某些实施方案中，异源性基因表达系统可以是一种设计用于蛋白质分泌的表达系统。在此类实施方案中，葡糖基转移酶包含信号肽(信号序列)。信号肽可以是其天然信号肽或异源信号肽。

[0087] 本文所述葡糖基转移酶可以以任何纯化状态(例如，纯化或非纯化)使用。例如，葡糖基转移酶可以在使用前纯化和/或分离。非纯化葡糖基转移酶的示例包括形式为细胞裂解液的那些葡糖基转移酶。细胞裂解液或提取物可以由用于异源表达酶的细菌(例如，大肠杆菌)制备。例如，细菌可以利用弗氏压碎器经受破坏。在另选的实施方案中，细菌可以借助匀化器(例如，APV、Rannie、Gaulin)匀化。葡糖基转移酶通常在这些类型的制剂中可溶。本文的细菌细胞裂解液、提取物、均化物可以在用于从蔗糖制备聚α-1,3-葡聚糖的反应溶液中以约0.15％-0.3％(v/v)使用。

[0088] 本文葡糖基转移酶的活性可以利用本领域已知的任何方法测定。例如，葡糖基转移酶活性可以通过测量含蔗糖(50g/L)、右旋糖酐T10(1mg/mL)和磷酸钾缓冲液(pH 6.5， 50mM)的反应溶液中的还原糖(果糖和葡萄糖)的产量来测定,其中将所述溶液保持在22-25℃下持续24-30小时。可以通过向含1N NaOH和0.1%氯化三苯基四唑的混合物中添加0.01mL反应溶液测量还原糖,然后监测OD_{480nm}下的吸光度在五分钟内的增加来测量还原糖。

[0089] 如果需要,可以控制本文的反应溶液的温度。在某些实施方案中,反应温度在介于约5℃至约50℃之间。在某些其它实施方案中,温度在介于约20℃至约40℃,或约20℃至约30℃之间(例如,约25℃)。

[0090] 本文的反应溶液中的蔗糖的初始浓度可以为例如约20g/L至约400g/L。另选地,蔗糖的初始浓度可以为约75g/L至约175g/L,或约50g/L至约150g/L。另选地,蔗糖的初始浓度可以为例如约40g/L、50g/L、60g/L、70g/L、80g/L、90g/L、100g/L、110g/L、120g/L、130g/L、140g/L、150g/L或160g/L(或介于40g/L和160g/L之间的任何整数值)。“蔗糖的初始浓度”是指刚添加完所有反应溶液组分(至少水、不完全精制的蔗糖、gtf酶)后gtf反应溶液中的蔗糖浓度。反应溶液中的所有或一部分蔗糖可以来自添加到所述溶液中的不完全精制的蔗糖。虽然优选地是所有蔗糖都是不完全精制的,但是可以另外将白色精制蔗糖用于反应溶液中。

[0091] 应理解,借助某些液体形式的不完全精制的蔗糖组合物(例如,甜菜稀汁、甜菜浓汁、糖蜜),因此可将此类组合物添加到反应溶液中,以在特定反应体积中达到蔗糖的特定初始浓度。例如,可将来自糖用甜菜(例如,甜菜稀汁、甜菜浓汁、糖蜜)的不完全精制的蔗糖组合物稀释在反应溶液中,使得反应的初始蔗糖浓度为约70g/L-90g/L或80g/L-85g/L。

[0092] 在某些实施方案中,葡聚糖合成反应的pH可以在介于约4.0至约8.0之间。另选地,pH可为约4.0、4.5、5.0、5.5、6.0、6.5、7.0、7.5或8.0。可通过添加或掺入合适的缓冲液来调节或控制pH,包括但不限于磷酸盐、tris、柠檬酸盐或它们的组合。葡聚糖合成反应中的缓冲液浓度可为例如0mM至约100mM、或约10mM、20mM或50mM。可任选地将适量DTT(二硫苏糖醇,例如,约1.0mM)添加到反应溶液中。

[0093] 本文的反应溶液可以包含在任何适合施加本文所公开的一个或多个反应条件的容器。例如,本文的反应溶液可以在尺寸适合容纳特定反应的不锈钢、塑料或玻璃容器中。此类容器可以任选地配备有搅拌装置。

[0094] 适合进行本文反应溶液的其它条件和组分的示例公开在美国专利7000000和美国专利申请公布2013/0244288、2013/0244287、2013/0196384、2013/0157316和2014/0087431中,所有这些专利均以引用方式并入本文。

[0095] 本公开的反应溶液的聚α-1,3-葡聚糖的收率是在反应溶液中转化为产物的蔗糖的重量的至少7%。另选地,聚α-1,3-葡聚糖的收率可为至少约8%、9%、10%、11%、12%、13%、14%、15%、16%、17%、18%、19%、20%、21%、22%、23%、24%、25%、26%、27%、28%、29%、30%、31%、32%、33%、34%、35%、36%、37%、38%、39%、40%、41%、42%、43%、44%、45%、46%或47%。在某些实施方案中,聚α-1,3-葡聚糖在本文的反应溶液中的收率与通过对照反应溶液的聚α-1,3-葡聚糖的收率大致相同,在对照反应溶液中,使用白色精制蔗糖替代不完全精制的蔗糖。所有上述收率都可以利用保持在约20-30℃(例如,25℃)的温度下的反应溶液和/或利用含例如SEQ ID NO:8的gtf获得。这些实施方案中的某些实施方案可以使用浓甜菜汁或稀甜菜汁作为不完全精制的蔗糖。

[0096] 在某些实施方案中,反应溶液的相对反应速率是至少约0.8,这是相对于包含水、

白色精制蔗糖和葡糖基转移酶的反应溶液的反应速率而言。例如，反应溶液的相对反应速率是至少约0.8，这是相对于对照反应而言(即，本文的反应溶液的反应速率是对照反应的速率的至少80％)。本文的相对反应速率也可以是例如至少约0.82、0.84、0.86、0.88、0.90、0.92、0.94、0.96、0.98、1.00、1.02或1.04。反应溶液的反应速率可以依据在单位时间内每单位浓度的活性葡糖基转移酶下，反应物(例如，蔗糖)的浓度/量的变化和/或产物(例如，聚α-1,3-葡聚糖)的浓度/量的变化来表示。

[0097] 本文的反应溶液可以制备L*值小于例如93的聚α-1,3-葡聚糖。另选地，由本文的反应溶液制备的聚α-1,3-葡聚糖的L*值可以小于92、90、88、86、84、82、80、78、76、74、72、70、68、66、64、62或60。本文的聚α-1,3-葡聚糖产物的L*值的范围的示例可为约82-87(例如，当反应溶液中使用甜菜稀汁或甜菜浓汁时)或80-82(例如，当反应溶液中使用VHP蔗糖时)。可以测定L*值，例如，对于已经从反应溶液去除的聚α-1,3-葡聚糖而言，在两次置换洗涤中用至少一半反应体积的水洗涤(例如，如果反应体积的2L，用至少一份1-L的水洗涤)，然后干燥、碾碎并经过60-目筛网筛分。干燥应该在不使聚α-1,3-葡聚糖变色的温度下进行。因此，聚α-1,3-葡聚糖的任何颜色都应该源自不完全精制的蔗糖。

[0098] 本文的反应溶液产生具有至少50％的α-1,3糖苷键的聚α-1,3-葡聚糖。据信，在某些实施方案中，制备这样的聚α-1,3-葡聚糖，其中至少约60％、70％、80％、90％、95％、96％、97％、98％、99％或100％(或介于60％和100％之间的任何整数)的组成糖苷键是α-1,3键。因此，上述实施方案中制备的聚α-1,3-葡聚糖具有少于约50％、40％、30％、20％、10％、5％、4％、3％、2％、1％或0％(或介于0％和50％之间的任何整数值)的非α-1,3糖苷键。

[0099] 本文的聚α-1,3-葡聚糖产物的糖苷键分布可以利用本领域已知的任何方法测定。例如，键分布可以利用使用核磁共振(NMR)光谱法(例如，^{13}C NMR或^{1}H NMR)的方法测定。这些方法和可以使用的其它方法公开在Food Carbohydrates:Chemistry,Phsical Properties,and Applications(S.W.Cui编辑，第3章，S.W.Cui,Structural Analysis of Polysaccharides,Taylor&Francis Group LLC,Boca Raton,FL,2005)中，所述文献以引用方式并入本文。

[0100] 本文的反应溶液产生以DP_n或DP_w计的分子量为至少约100的聚α-1,3-葡聚糖。另选地，本文的反应溶液中制备的聚α-1,3-葡聚糖可以具有以DP_n或DP_w计为至少约400的分子量。另选地，聚α-1,3-葡聚糖可以具有以DP_n或DP_w计为至少约100、150、200、250、300、350、400、450、500、550、600、650、700、750、800、850、900、950或1000(或介于100和1000之间的任何整数)的分子量。

[0101] 本文的聚α-1,3-葡聚糖的分子量可以利用本领域已知的若干方法中的任一种测量。例如，葡聚糖聚合物的分子量可以利用高压液相色谱法(HPLC)、尺寸排阻色谱法(SEC)或凝胶渗透色谱法(GPC)测量。

[0102] 本公开还涉及一种用于制备聚α-1,3-葡聚糖的方法，所述方法包括使至少水、蔗糖和葡糖基转移酶接触的步骤，其中蔗糖是未精制或部分精制的(即，不完全精制的)。这种方法中制备的，且可任选地分离的聚α-1,3-葡聚糖具有至少50％的α-1,3糖苷键和至少100的重均聚合度(DP_w)。另外，所述方法中制备的聚α-1,3-葡聚糖的收率是通过与水和葡糖基转移酶接触转化为产物的蔗糖的重量的至少7％。如上文和实施例中所公开的本文反应溶

液的任何特征都可以表征所述方法。所述方法的以下特征是示例。

[0103] 在所述方法的某些实施方案中，不完全精制的蔗糖可以来自糖用甜菜(例如，甜菜稀汁或甜菜浓汁)且尚未结晶。在另一个示例中，不完全精制的蔗糖来自甘蔗(例如，原蔗糖、VHP或VVHP蔗糖)且已经具有不超过两个或三个结晶步骤。

[0104] 所公开的方法中使用的不完全精制的蔗糖可以具有大于例如150的ICUMSA值。

[0105] 所述方法的某些实施方案中制备的聚α-1,3-葡聚糖具有小于93的L*值。可以针对例如已经从反应溶液去除的聚α-1,3-葡聚糖测定本文的L*值；任选地用水洗涤一次、两次或更多次；并干燥。

[0106] 所述方法的接触步骤中制备聚α-1,3-葡聚糖的相对反应速率为至少0.8，这是相对于使用白色精制蔗糖替代不完全精制蔗糖时的反应速率而言。

[0107] 本公开的方法包括使至少水、不完全精制的蔗糖和葡糖基转移酶接触。该接触步骤可以包括提供包含水、不完全精制的蔗糖和葡糖基转移酶的反应溶液。应当理解，当葡糖基转移酶合成聚α-1,3-葡聚糖时，考虑到不溶性聚α-1,3-葡聚糖从溶液中析出，如反应变浑浊所指示，反应溶液变成反应混合物。本公开的方法的接触步骤可以以任意种方式进行。例如，可以首先将所需量的不完全精制的蔗糖溶解或混合在水(任选地，也可以在这个制备阶段添加其它组分，诸如缓冲液组分)中，接着添加葡糖基转移酶。溶液可以保持静置，或经由例如搅拌或回转式振荡搅动。反应可以是且通常是不含细胞的。

[0108] 在某些实施方案中，可以通过视觉地(不溶性聚α-1,3-葡聚糖不再累积)和/或通过测量溶液中留下的蔗糖的量(残余蔗糖)确定反应的完成，其中蔗糖消耗百分比超过约90％可以视为反应完成。通常，本发明所公开的工艺的反应将需要约12、24、36、48、60、72、84或96小时完成，这取决于某些参数，诸如用于所述反应中的蔗糖和葡糖基转移酶的量。

[0109] 在本文所公开的方法的某些实施方案中，反应的蔗糖消耗百分比是起初接触水和葡糖基转移酶的蔗糖的至少90％、91％、92％、93％、94％、95％、96％、97％、98％、99％或100％。另选地，蔗糖消耗百分比可以＞90％或＞95％。

[0110] 在本文的葡聚糖合成方法的一些方面中制备的聚α-1,3-葡聚糖的收率基于所述反应中转化的蔗糖的重量计可为至少约7％、8％、9％、10％、11％、12％、13％、14％、15％、16％、17％、18％、19％、20％、21％、22％、23％、24％、25％、26％、27％、28％、29％、30％、31％、32％、33％、34％、35％、36％、37％、38％、39％、40％、41％、42％、43％、44％、45％、46％或47％。

[0111] 可以任选地分离本公开的方法中制备的聚α-1,3-葡聚糖。例如，可以通过离心或过滤分离不溶性聚α-1,3-葡聚糖。这样，分离大部分反应溶液的聚α-1,3-葡聚糖，所述反应溶液可包含水、果糖和某些副产物(例如，明串珠菌二糖、可溶性低聚糖DP2-DP7)。该溶液也可包含残余蔗糖和果糖单体。分离还可以任选地包括用水洗涤聚α-1,3-葡聚糖一次、两次或更多次，和/或干燥聚α-1,3-葡聚糖。

[0112] 本公开还涉及通过本文所公开的反应溶液或方法制备的聚α-1,3-葡聚糖。这种聚α-1,3-葡聚糖具有小于93的L*值。如上文和实施例中所公开的聚α-1,3-葡聚糖的任何特征都可以表征该实施方案的聚α-1,3-葡聚糖。以下特征是示例。

[0113] 可以分离本文的聚α-1,3-葡聚糖产物，且可以任选地以例如干燥形式提供。在某些实施方案中，聚α-1,3-葡聚糖产物是以至少1克(例如，至少100g或500g)的分离的干燥量

提供。“干燥”聚α-1,3-葡聚糖包含不超过例如2.0重量％、1.5重量％、1.0重量％、0.5重量％、0.25重量％、0.10重量％、0.05重量％或0.01重量％的水。

[0114] 据信,在某些实施方案中,聚α-1,3-葡聚糖产物可包含以下化合物中的一种或多种:焦糖、蛋白黑素、己糖碱性降解产物(HADP)(在碱性条件下形成的聚合C6糖缩合产物)、多酚-铁络合物(例如,铁儿茶酚络合物)、黑色素。据信,与仅使用白色精制蔗糖的反应溶液赋予聚α-1,3-葡聚糖产物的着色(如果有的话)相比,这些化合物中的一种或多种还为聚α-1,3-葡聚糖产物提供更深的着色。此类着色差异可以利用例如L*值测定。

[0115] 本文所公开的组合物和方法的非限制性示例包括：

[0116] 1.一种反应溶液,所述反应溶液包含水、蔗糖和葡糖基转移酶,所述反应溶液合成不溶性聚α-1,3-葡聚糖,其具有至少50％的α-1,3糖苷键和至少100的重均聚合度(DP_w),其中所述蔗糖是未精制或部分精制的；

[0117] 其中所述反应溶液的聚α-1,3-葡聚糖的收率是在所述反应溶液中转化为产物的蔗糖的重量的至少7％。

[0118] 2.根据实施方案1所述的反应溶液,其中所述蔗糖来自糖用甜菜,并且尚未结晶。

[0119] 3.根据实施方案1所述的反应溶液,其中所述蔗糖来自甘蔗,并且(i)尚未结晶,或(ii)已经利用不超过三个结晶步骤结晶。

[0120] 4.根据实施方案1、3或3所述的反应溶液,其中所述蔗糖具有大于150的ICUMSA值。

[0121] 5.根据实施方案1、2、3或4所述的反应溶液,其中所述反应溶液的相对反应速率为至少0.8,这是相对于包含水、白色精制蔗糖和葡糖基转移酶的反应溶液的反应速率而言。

[0122] 6.根据实施方案1、2、3、4或5所述的反应溶液,其中由所述反应溶液制备的聚α-1,3-葡聚糖具有小于93的L*值。

[0123] 7.根据实施方案1、2、3、4、5或6所述的反应溶液,其中所述葡糖基转移酶包含与SEQ ID NO:4、SEQ ID NO:8、SEQ ID NO:10、SEQ ID NO:12、SEQ ID NO:14、SEQ ID NO:20、SEQ ID NO:26、SEQ ID NO:28、SEQ ID NO:30或SEQ ID NO:34具有至少90％同一性的氨基酸序列。

[0124] 8.一种用于制备不溶性聚α-1,3-葡聚糖的方法,所述方法包括：

[0125] (a)使至少水、蔗糖和葡糖基转移酶接触,其中所述蔗糖是未精制或部分精制的,

[0126] 由此制备聚α-1,3-葡聚糖,其具有至少50％的α-1,3糖苷键和至少100的重均聚合度(DP_w);以及

[0127] b)任选地,分离步骤(a)中制备的聚α-1,3-葡聚糖；

[0128] 其中聚α-1,3-葡聚糖的收率是在步骤(a)中转化为产物的蔗糖的重量的至少7％。

[0129] 9.根据实施方案8所述的方法,其中所述蔗糖来自糖用甜菜,并且尚未结晶。

[0130] 10.根据实施方案8所述的方法,其中所述蔗糖来自甘蔗,并且(i)尚未结晶,或(ii)已经利用不超过三个结晶步骤结晶。

[0131] 11.根据实施方案8、9或10所述的方法,其中所述蔗糖具有大于150的ICUMSA值。

[0132] 12.根据实施方案8、9、10或11所述的方法,其中步骤(a)中制备聚α-1,3-葡聚糖的相对反应速率是至少0.8,这是相对于使用白色精制蔗糖替代所述未精制或部分精制的蔗糖时的步骤(a)的反应速率而言。

[0133] 13.根据实施方案8、9、10、11或12所述的方法,其中步骤(b)中分离的聚α-1,3-葡

聚糖具有小于93的L*值。

[0134] 14.根据实施方案8、9、10、11、12或13所述的方法，其中所述葡糖基转移酶包含与SEQ ID NO:4、SEQ ID NO:8、SEQ ID NO:10、SEQ ID NO:12、SEQ ID NO:14、SEQ ID NO:20、SEQ ID NO:26、SEQ ID NO:28、SEQ ID NO:30或SEQ ID NO:34具有至少90％同一性的氨基酸序列。

[0135] 15.一种通过根据实施方案8、9、10、11、12、13或14所述的方法制备的分离的聚α-1,3-葡聚糖，其中所述聚α-1,3-葡聚糖具有小于93的L*值。

[0136] 实施例

[0137] 本公开还在下文提供的实施例2-12中进一步举例说明。应该理解，尽管这些实施例说明了本文的某些优选方面，但仅是以例证的方式给出的。通过上述论述和这些实施例，本领域的技术人员可确定本发明所公开的实施方案的必要特征，并且在不脱离其实质和范围的前提下，可对本发明所公开的实施方案进行各种变化和修改以适应多种用途和条件。

[0138] 一般方法

[0139] 蔗糖ICUMSA测量

[0140] 密切根据ICUMSA方法GS1/3-7进行ICUMSA测量(R.J.McCowage、R.M.Urquhart和M.L.Burge(Determination of the Solution Colour of Raw Sugars,Brown Sugars and Coloured Syrups at pH 7.0-Official,Verlag Dr Albert Bartens,2011版)，该文献以引用的方式并入本文。蔗糖样品的ICUMSA颜色测量的基本步骤如下。将蔗糖添加至到离子水(如果是固体形式诸如蔗糖被溶解，如果是液体形式诸如甜菜汁被稀释)中至基于预期ICUMSA范围的指定浓度，如ICUMSA方法GS1/3-7中所指定。过滤蔗糖溶液，以去除任何未溶解的杂质，并测量过滤后的蔗糖溶液的吸光度。然后根据公式1计算溶液的ICUMSA颜色：

[0141]
$$\boxed{\text{颜色ICUMSA}(UI)=\frac{\text{吸光度}}{bxc}\times 100}$$

[0142] 其中吸光度(Abs)＝样品溶液吸光度读数；b＝光学单元路径(cm)；c＝蔗糖浓度，以g/mL计。

[0143] 上文ICUMSA方法沿循ICUMSA方法GS1/3-7，但作了以下修改：

[0144] 1.使用醋酸纤维素0.45-微米过滤器(正方形50mm)替代硝酸纤维素0.45-微米过滤器。

[0145] 2.不计算RDS(“折光干物质”)和密度，通过以下步骤测定样品的蔗糖浓度：利用折射计测量有效ppt盐度，并利用从公布的数据获得的线性关系转化为％Brix(％Brix＝0.1258ppt盐度+0.0152)。对另外稀释的样品进行折射率测量，并将Brix值变回用于UV测量的标准浓度。

[0146] 使用去离子水溶解蔗糖。蔗糖溶液样品未脱气，因为溶液中没观察到泡沫或气泡。将醋酸纤维素过滤器预先放置在用于无菌过滤应用的塑料漏斗中。

[0147] 聚α-1,3-葡聚糖的L*a*b*颜色测量

[0148] 利用CIE L*a*b*测量系统测量聚α-1,3-葡聚糖颜色。两种样品制备方法的使用取决于可用聚α-1,3-葡聚糖的量。两种方法得出相同L*a*b*测量值。

[0149] 在第一方法中，在咖啡研磨机中将干燥的聚α-1,3-葡聚糖磨成细粉。将0.77g粉末转移至可排空的13-mm KBr制粒模，并在7000磅下使聚α-1,3-葡聚糖形成颗粒。利用Konica

Minolta 2600D分光光度计测量颗粒颜色。

[0150] 在第二方法中，在咖啡研磨机中将干燥聚α-1，3-葡聚糖磨成细粉。使研磨过的聚α-1，3-葡聚糖经过60-目筛网筛分，并填充到1-cm比色管中。利用HUNTERLAB COLORQUEST XE分光光度计测量研磨过的聚α-1，3-葡聚糖的颜色。

[0151] 制备葡糖基转移酶(gtf)的粗提物

[0152] 如下制备gtf酶(例如，SEQ ID NO:8))。用含特定gtf-编码DNA序列的基于pJexpress404®的构建体使大肠杆菌TOP10®细胞(Invitrogen，Carlsbad California)转化。每条序列经密码子优化以在大肠杆菌中表达gtf酶。使表达特定gtf酶的单个的大肠杆菌菌株在37℃的含氨苄青霉素(100μg/mL)的LB(Luria发酵液)培养基(Becton，Dickinson and Company，Franklin Lakes，NJ)中生长，同时振荡，至OD_{600}＝0.4-0.5，此时添加IPTG(异丙基β-D-1-硫代半乳糖苷，Cat.No.I6758，Sigma-Aldrich，St.Louis，MO)，至最终浓度为0.5mM。IPTG诱导后，在37℃下培养培养物2-4小时。通过以5，000×g离心15分钟收获细胞，并将细胞(以20％重量体积比)重悬于补充有二硫苏糖醇(DTT，1.0mM)的50mM磷酸盐缓冲液(pH 7.0)中。使得重悬细胞两次通过弗氏压碎器(SLM Instruments，Rochester，NY)以确保＞95％的细胞裂解。在4℃下以12，000×g对裂解细胞离心30分钟。通过BCA(二喹啉甲酸)蛋白质分析(Sigma-Aldrich)和SDS-PAGE分析所得上清液，以确认表达gtf酶，并将上清液保存在-20℃下。

[0153] Gtf的相对反应速率

[0154] 蔗糖通过葡糖基转移酶得到聚α-1，3-葡聚糖的酶促反应遵循Michaelis-Menten动力学。在高蔗糖浓度下，蔗糖的反应速率是零阶。在整个反应期间通过HPLC定期测量蔗糖浓度。将反应速率计算为零阶反应期间蔗糖消耗速率。即，将反应速率计算为蔗糖浓度-时间图的线性区域的负斜率。然后反应速率除以加载到反应器的酶活性，得到归一化反应速率，这消除了因为酶浓度变动引起的反应速率差异。最后，归一化反应速率除以白色精制糖的归一化反应速率，得到相对反应速率。

[0155] 测定Gtf酶活性

[0156] 按照诸如以下的方案确认gtf酶(例如，SEQ ID NO:8)活性，所述方案测量gtf反应溶液中的还原糖(果糖和葡萄糖)的产量。通过将gtf粗提物添加到含蔗糖(50g/L或150g/L)、磷酸钾缓冲液(pH 6.5，50mM)和任选的右旋糖酐(1mg/mL，右旋糖酐T10，Cat.No.D9260，Sigma-Aldrich)的混合物中制备反应溶液；添加gtf提取物至2.5体积％-5体积％。然后在22℃-25℃下培养反应溶液24-30小时，然后进行离心。将上清液(0.01mL)添加至包含1N NaOH和0.1％氯化三苯基四唑(Sigma-Aldrich)的混合物中。温育混合物五分钟，然后利用ULTROSPEC分光光度计(Pharmacia LKB，New York，NY)测定其OD_{480nm}，以估计还原糖果糖和葡萄糖的存在。

[0157] 测定重均聚合度(DP_W)

[0158] 利用尺寸排阻色谱法(SEC)测定通过gtf酶(例如，SEQ ID NO:8)合成的葡聚糖产物的DP_W。示例性SEC方案如下。以5mg/mL将干燥聚α-1，3-葡聚糖聚合物溶解于N，N-二甲基-乙酰胺(DMAc)和5％LiCl，同时在100℃下振荡过夜。SEC系统是来自Waters Corporation(Milford，MA)的耦接三个在线检测器的Alliance™2695分离模块：来自Waters的差示折射计2410、来自Wyatt Technologies(Santa Barbara，CA)的多角度散光光度计Heleos™8+和

来自Wyatt的差示毛细管粘度计ViscoStar™。用于SEC的柱是四个来自Shodex(Japan)的苯乙烯-二乙烯基苯柱和两个线性KD-806M、KD-802和KD-801柱，以改善在聚合物分布的低分子量区域下的分辨率。移动相是具有0.11％LiCl的DMAc。所用的色谱分离条件是50℃柱和检测器隔室，40℃样品和注射器隔室，流量0.5mL/min，和注射体积100μL。用于数据还原的软件包是来自Waters的Empower™版本3(用广泛葡聚糖聚合物标准进行校正)和来自Wyatt的Astra®版本6(具有柱校正的三重检测方法)。

[0159] 测定糖苷键

[0160] 由gtf酶(例如，SEQ ID NO:8)合成的葡聚糖产物中的糖苷键可以按照诸如以下的^{13}C NMR(核磁共振)测定。在50℃下在搅拌下将干燥葡聚糖聚合物(25-30mg)溶解于1mL含3重量％LiCl的氘代二甲基亚砜(DMSO)。利用玻璃吸移管，将0.8mL溶液转移至5-mm NMR管中。利用配备有CPDUL冷冻探针的Bruker Avance 500-MHz NMR光谱仪(Billerica，MA)，在125.76MHz的光谱频率下，利用26041.7Hz的光谱窗采集定量^{13}C NMR光谱。利用waltz解耦的反向门控解耦脉冲序列，采集时间为0.629秒，脉冲间延迟为5秒，并且脉冲为6000。利用2.0Hz的指数倍增转化时域数据。

[0161] 实施例1(比较例)

[0162] 利用白色精制蔗糖制备聚α-1,3-葡聚糖

[0163] 该实施例描述在gtf-催化的反应中利用白色精制蔗糖制备α-1,3-葡聚糖。

[0164] 80g/L蔗糖溶液如下制备。将1500g去离子水充入控制在23℃下的带夹套搅动的2-L玻璃反应器中。将2.7g KH_2PO_4缓冲液加入到反应器中。接下来，将160g白色精制蔗糖(ICUMSA 47;United Sugars Corporation，Bloomington，MN)添加至反应器，此后，用更多去离子水将反应器中的体积调节至2L。然后添加FermaSure®(DuPont)(1mL/L反应)，并利用5重量％氢氧化钠水溶液或5重量％硫酸水溶液将pH调节至5.5。通过添加0.3体积％gtf酶(SEQ ID NO:8)粗提物(一般方法)引发葡聚糖聚合反应，并保持在23℃下。

[0165] 通过完全消耗蔗糖或测量间的蔗糖浓度无变化确定反应完成后，利用FILTRATEST(Bokela GmbH Karlsruhe，Germany)过滤200mL反应浆液。此过滤操作使母液(滤液)与聚α-1,3-葡聚糖湿饼分离。用去离子水两次置换洗涤(每次200-L)洗出湿饼中的残余糖。然后在80℃下将湿饼在对流烘箱中干燥约24小时。用干燥聚合物的最终重量除以反应的蔗糖量计算聚合收率。

[0166] 通过SEC(一般方法)测量聚α-1,3-葡聚糖产物的分子量，并表示为DP_w(表2)，计算方法为用平均聚合物分子量除以单体分子量。根据一般方法测量干燥葡聚糖聚合物产物的颜色，并在表2中表示为L*。

[0167] 实施例2

[0168] 利用VHP蔗糖制备聚α-1,3-葡聚糖

[0169] 该实施例描述在gtf-催化的反应中利用VHP制备α-1,3-葡聚糖，VHP是一类不完全精制的蔗糖。

[0170] 遵循实施例1的聚合过程，不同的是使用VHP蔗糖(ICUMSA 501，Iracema Mill，Brazil)替代白色精制蔗糖。

[0171] 通过完全消耗蔗糖或测量间的蔗糖浓度无变化确定反应完成后，利用布氏漏斗和真空烧瓶过滤反应浆液。此过滤操作使母液(滤液)与聚α-1,3-葡聚糖湿饼分离。用去离子

水两次置换洗涤(每次1-L)洗出湿饼中的残余糖。然后在40℃和360mm Hg下将湿饼在真空烘箱中干燥约48小时。用干燥聚合物的最终重量除以反应的蔗糖量计算聚合收率。该过程中制备的聚α-1,3-葡聚糖的分子量、收率和颜色呈现在表2中。

[0172] 因此,可以在含不完全精制的蔗糖的gtf反应溶液中合成聚α-1,3-葡聚糖。

[0173] 实施例3

[0174] 利用VVHP蔗糖制备聚α-1,3-葡聚糖

[0175] 该实施例描述在gtf-催化的反应中利用VVHP制备α-1,3-葡聚糖,VVHP是一类不完全精制的蔗糖。

[0176] 遵循实施例2的聚合和聚合物分离过程,不同的是使用VVHP蔗糖(ICUMSA 421,Ferrari Mill,Brazil)替代VHP蔗糖。这个过程中制备的聚α-1,3-葡聚糖的分子量、收率和颜色呈现在表2中。

[0177] 因此,可在包含不完全精制的蔗糖的gtf反应溶液中合成聚α-1,3-葡聚糖。

[0178] 实施例4

[0179] 利用甜菜浓汁制备聚α-1,3-葡聚糖

[0180] 该实施例描述在gtf-催化的反应中利用甜菜浓汁制备α-1,3-葡聚糖,甜菜浓汁是一类不完全精制的蔗糖。

[0181] 总体上遵循实施例2的聚合和聚合物分离过程,不同的是使用甜菜浓汁蔗糖(ICUMSA 1414,Southern Minnesota Beet Sugar Cooperative)替代VHP蔗糖。聚合过程如下进行。将235g甜菜浓汁添加到反应器中,并用去离子水稀释,直到蔗糖浓度为80g/L(添加约1765mL水)。添加2.72g KH_2PO_4缓冲液,并用5重量%氢氧化钠将pH调节至5.5。通过添加0.3体积%gtf酶(SEQ ID NO:8)粗提物(一般方法)引发葡聚糖聚合反应,并保持在23℃下。该过程中制备的聚α-1,3-葡聚糖的分子量、收率和颜色呈现在表2中。

[0182] 因此,可在包含不完全精制的蔗糖的gtf反应溶液中合成聚α-1,3-葡聚糖。

[0183] 实施例5

[0184] 利用甜菜稀汁制备聚α-1,3-葡聚糖

[0185] 该实施例描述在gtf-催化的反应中利用甜菜稀汁制备α-1,3-葡聚糖,甜菜稀汁是一类不完全精制的蔗糖。

[0186] 总体上遵循实施例2的聚合和聚合物分离过程,不同的是使用甜菜稀汁蔗糖(ICUMSA 1158,Southern Minnesota Beet Sugar Cooperative)替代VHP蔗糖,且一次1-L洗涤后接着500-mL水洗涤,而不是两次1-L洗涤。将1229mL甜菜稀汁添加至771mL去离子水,以制备80g/L的起始蔗糖浓度。添加2.72g KH_2PO_4缓冲液,并用5重量%硫酸将pH调节至5.5。通过添加0.3体积%gtf酶(SEQ ID NO:8)粗提物(一般方法)引发葡聚糖聚合反应,并保持在23℃下。该过程中制备的聚α-1,3-葡聚糖的分子量、收率和颜色呈现在表2中。

[0187] 因此,可在包含不完全精制的蔗糖的gtf反应溶液中合成聚α-1,3-葡聚糖。

[0188] 实施例6

[0189] 利用甜菜糖蜜制备聚α-1,3-葡聚糖

[0190] 该实施例描述在gtf-催化的反应中利用甜菜糖蜜制备α-1,3-葡聚糖,甜菜糖蜜是一类不完全精制的蔗糖。

[0191] 总体上遵循实施例2的聚合和聚合物分离过程,不同的是使用甜菜糖蜜(ICUMSA

57781,Southern Minnesota Beet Sugar Cooperative)替代VHP蔗糖,并且使用三次1-L水洗涤替代两次1-L洗涤。将291mL甜菜糖蜜添加至1709mL去离子水,以制备83.4g/L的起始蔗糖浓度。添加2.72g KH_2PO_4缓冲液,并用5重量%氢氧化钠将pH调节至5.5。通过添加0.3体积%gtf酶(SEQ ID NO:8)粗提物(一般方法)引发葡聚糖聚合反应,并保持在23℃下。该过程中制备的聚α-1,3-葡聚糖的分子量、收率和颜色呈现在表2中。

[0192] 因此,可在包含不完全精制的蔗糖的gtf反应溶液中合成聚α-1,3-葡聚糖。

[0193] 实施例7

[0194] 利用巴西原蔗糖制备聚α-1,3-葡聚糖

[0195] 该实施例描述在gtf-催化的反应中利用巴西原蔗糖制备α-1,3-葡聚糖,巴西原蔗糖是一类不完全精制的蔗糖。

[0196] 在一个1-升锥形瓶中,将75g巴西原蔗糖(ICUMSA 2655)溶解于约500mL去离子水中。添加1.02g KH_2PO_4和0.15mL FermaSure®,此后添加水,直到体积为750mL。使用5重量%氢氧化钠将pH调节至5.5。将烧瓶置于25℃温育搅拌烘箱中。通过添加0.3体积%gtf酶(SEQ ID NO:8)粗提物(一般方法)引发葡聚糖聚合反应,并保持在25℃下。反应在30小时内完成。反应完成后,用布氏漏斗和真空烧瓶过滤反应。用两次800-mL水洗涤和一次200-mL水洗涤对所得滤饼进行置换洗涤。在40℃真空烘箱中干燥聚α-1,3-葡聚糖。该过程中制备的聚α-1,3-葡聚糖的分子量、收率和颜色呈现在表2中。

[0197] 因此,可在包含不完全精制的蔗糖的gtf反应溶液中合成聚α-1,3-葡聚糖。

[0198] 实施例8

[0199] 利用新奥尔良原蔗糖制备聚α-1,3-葡聚糖

[0200] 这个实施例描述在gtf-催化的反应中利用新奥尔良原蔗糖制备α-1,3-葡聚糖,新奥尔良原蔗糖是一类不完全精制的蔗糖。

[0201] 遵循实施例7的聚合和聚合物分离过程,不同的是使用新奥尔良原蔗糖(ICUMSA 2850)作为蔗糖组分。该过程中制备的聚α-1,3-葡聚糖的分子量、收率和颜色呈现在表2中。

[0202] 因此,可在包含不完全精制的蔗糖的gtf反应溶液中合成聚α-1,3-葡聚糖。

[0203] 实施例9

[0204] 利用莫桑比克原蔗糖制备聚α-1,3-葡聚糖

[0205] 该实施例描述在gtf-催化的反应中利用莫桑比克原蔗糖制备α-1,3-葡聚糖,莫桑比克原蔗糖是一类不完全精制的蔗糖。

[0206] 遵循实施例7的聚合和聚合物分离过程,不同的是使用莫桑比克原蔗糖(ICUMSA 3022)作为蔗糖组分。该过程中制备的聚α-1,3-葡聚糖的分子量、收率和颜色呈现在表2中。

[0207] 因此,可在包含不完全精制的蔗糖的gtf反应溶液中合成聚α-1,3-葡聚糖。

[0208] 实施例10

[0209] 利用津巴布韦原蔗糖制备聚α-1,3-葡聚糖

[0210] 该实施例描述在gtf-催化的反应中利用津巴布韦原蔗糖制备α-1,3-葡聚糖,津巴布韦原蔗糖是一类不完全精制的蔗糖。

[0211] 遵循实施例7的聚合和聚合物分离过程,不同的是使用津巴布韦原蔗糖(ICUMSA 4183)作为蔗糖组分。该过程中制备的聚α-1,3-葡聚糖的分子量、收率和颜色呈现在表2中。

[0212] 因此,可在包含不完全精制的蔗糖的gtf反应溶液中合成聚α-1,3-葡聚糖。

[0213] 实施例11

[0214] 利用伯利兹原蔗糖制备聚α-1,3-葡聚糖

[0215] 该实施例描述在gtf-催化的反应中利用伯利兹原蔗糖制备α-1,3-葡聚糖，伯利兹原蔗糖是一类不完全精制的蔗糖。

[0216] 遵循实施例7的聚合和聚合物分离过程，不同的是使用伯利兹原蔗糖(ICUMSA 5150)作为蔗糖组分。该过程中制备的聚α-1,3-葡聚糖的分子量、收率和颜色呈现在表2中。

[0217] 因此，可在包含不完全精制的蔗糖的gtf反应溶液中合成聚α-1,3-葡聚糖。

[0218] 实施例12

[0219] 利用圭亚那原蔗糖制备聚α-1,3-葡聚糖

[0220] 该实施例描述在gtf-催化的反应中利用圭亚那原蔗糖制备α-1,3-葡聚糖，圭亚那原蔗糖是一类不完全精制的蔗糖。

[0221] 遵循实施例7的聚合和聚合物分离过程，不同的是使用圭亚那原蔗糖(ICUMSA 8153)作为蔗糖组分。该过程中制备的聚α-1,3-葡聚糖的分子量、收率和颜色呈现在表2中。

[0222] 因此，可在包含不完全精制的蔗糖的gtf反应溶液中合成聚α-1,3-葡聚糖。

[0223] 表2

[0224] 利用各类不完全精制的蔗糖制备聚α-1,3-葡聚糖

[0225]

	用于反应中的蔗糖			相对反应速率^{a}	聚α-1,3-葡聚糖产物		
实施例	来源	类型	ICUMSA		DP$_{W}$	L*	收率
1	United Sugars Corporation	白色精制	47	1.00	708	93.9^{b}	18%
2	Iracema Mill, Brazil	VHP	501	0.88	765	78	21%
3	Ferrari Mill, Brazil	VVHP	421	0.88	876	88	17%
4	Southern Minnesota Beet Sugar Cooperative	甜菜浓汁	1414	0.97	760	86	21%
5	Southern Minnesota Beet Sugar Cooperative	甜菜稀汁	1158	1.01	781	83	13%
6	Southern Minnesota Beet Sugar Cooperative	甜菜糖蜜	57781	0.92	756	65	8%
7	巴西	原蔗糖	2655	1.00	565	78	16%
8	新奥尔良	原蔗糖	2850	0.92	573	86	17%
9	莫桑比克	原蔗糖	3022	1.01	532	82	16%
10	津巴布韦	原蔗糖	4183	0.88	553	71	16%
11	伯利兹	原蔗糖	5150	0.74	721	62	11%
12	圭亚那	原蔗糖	8153	0.95	577	62	16%

[0226]

[0227] ^{a}实施例2-12中的相对反应速率是相对于实施例1中的反应速率计算的。

[0228] ^{b}该L*是针对遵循实施例1过程制备的聚合物测定，不同的是使用500-mL反应替代2-L，且产物在40℃和360mm Hg烘箱中干燥约48小时。

[0229] 表2中的数据总体上表明，包含不完全精制的蔗糖的gtf反应溶液(实施例2-12)可表现出水平与包含白色精制蔗糖的gtf反应溶液(实施例1)相比相同或甚至更佳的水平。大多数情况下，包含不完全精制的蔗糖的反应的反应速率接近或完全等同于包含白色精制蔗

糖的反应的速率。同样,包含不完全精制的蔗糖的若干反应产生DP_w和/或收率大于利用白色精制蔗糖观察到的DP_w和/或收率的葡聚糖(例如,实施例2-6)。

[0230] 因此,可以使用多种不同类型的不完全精制的蔗糖以用酶促方法制备聚α-1,3-葡聚糖。

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Fake, Dean

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        Asn Pro Val Val Gln Ala Glu Gln Leu Asn Trp Leu His Tyr Leu Leu
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        Asn Phe Gly Ser Ile Tyr Ala Asn Asp Ala Asp Ala Asn Phe Asp Ser
                275                 280                 285

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

Glu Asn Gly Tyr Leu Tyr Phe Leu Asn Asp Asp Leu Lys Gly Val Ala
    610                 615                 620

Asn Pro Gln Val Ser Gly Phe Leu Gln Val Trp Val Pro Val Gly Ala
625                 630                 635                 640

Ala Asp Asp Gln Asp Ile Arg Val Ala Ala Ser Asp Thr Ala Ser Thr
                645                 650                 655

Asp Gly Lys Ser Leu His Gln Asp Ala Ala Met Asp Ser Arg Val Met
            660                 665                 670
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[0005]

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Phe Glu Gly Phe Ser Asn Phe Gln Ser Phe Ala Thr Lys Glu Glu Glu
        675                 680                 685

Tyr Thr Asn Val Val Ile Ala Asn Asn Val Asp Lys Phe Val Ser Trp
    690                 695                 700

Gly Ile Thr Asp Phe Glu Met Ala Pro Gln Tyr Val Ser Ser Thr Asp
705                 710                 715                 720

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

Arg Tyr Asp Leu Gly Met Ser Lys Ala Asn Lys Tyr Gly Thr Ala Asp
            740                 745                 750

Gln Leu Val Lys Ala Ile Lys Ala Leu His Ala Lys Gly Leu Lys Val
        755                 760                 765

Met Ala Asp Trp Val Pro Asp Gln Met Tyr Thr Phe Pro Lys Gln Glu
    770                 775                 780

Val Val Thr Val Thr Arg Thr Asp Lys Phe Gly Lys Pro Ile Ala Gly
785                 790                 795                 800

Ser Gln Ile Asn His Ser Leu Tyr Val Thr Asp Thr Lys Ser Ser Gly
                805                 810                 815

Asp Asp Tyr Gln Ala Lys Tyr Gly Gly Ala Phe Leu Asp Glu Leu Lys
            820                 825                 830
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Glu Lys Tyr Pro Glu Leu Phe Thr Lys Lys Gln Ile Ser Thr Gly Gln
835 840 845

Ala Ile Asp Pro Ser Val Lys Ile Lys Gln Trp Ser Ala Lys Tyr Phe
850 855 860

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

Gln Val Ser Asn Lys Tyr Phe Asn Val Ala Ser Asp Thr Leu Phe Leu
885 890 895

Pro Ser Ser Leu Leu Gly Lys Val Val Glu Ser Gly Ile Arg Tyr Asp
900 905 910

Gly Lys Gly Tyr Ile Tyr Asn Ser Ser Ala Thr Gly Asp Gln Val Lys
915 920 925

Ala Ser Phe Ile Thr Glu Ala Gly Asn Leu Tyr Tyr Phe Gly Lys Asp
930 935 940

Gly Tyr Met Val Thr Gly Ala Gln Thr Ile Asn Gly Ala Asn Tyr Phe
945 950 955 960

Phe Leu Glu Asn Gly Thr Ala Leu Arg Asn Thr Ile Tyr Thr Asp Ala
965 970 975

[0006] Gln Gly Asn Ser His Tyr Tyr Ala Asn Asp Gly Lys Arg Tyr Glu Asn
980 985 990

Gly Tyr Gln Gln Phe Gly Asn Asp Trp Arg Tyr Phe Lys Asp Gly Asn
995 1000 1005

Met Ala Val Gly Leu Thr Thr Val Asp Gly Asn Val Gln Tyr Phe
1010 1015 1020

Asp Lys Asp Gly Val Gln Ala Lys Asp Lys Ile Ile Val Thr Arg
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Asp Gly Lys Val Arg Tyr Phe Asp Gln His Asn Gly Asn Ala Ala
1040 1045 1050

Thr Asn Thr Phe Ile Ala Asp Lys Thr Gly His Trp Tyr Tyr Leu
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Gly Lys Asp Gly Val Ala Val Thr Gly Ala Gln Thr Val Gly Lys
1070 1075 1080

Gln Lys Leu Tyr Phe Glu Ala Asn Gly Gln Gln Val Lys Gly Asp
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Phe Val Thr Ser Asp Glu Gly Lys Leu Tyr Phe Tyr Asp Val Asp
1100 1105 1110

Ser Gly Asp Met Trp Thr Asp Thr Phe Ile Glu Asp Lys Ala Gly
1115 1120 1125

Asn Trp Phe Tyr Leu Gly Lys Asp Gly Ala Ala Val Thr Gly Ala
1130 1135 1140

Gln Thr Ile Arg Gly Gln Lys Leu Tyr Phe Lys Ala Asn Gly Gln
1145 1150 1155

Gln Val Lys Gly Asp Ile Val Lys Gly Thr Asp Gly Lys Ile Arg
1160 1165 1170

Tyr Tyr Asp Ala Lys Ser Gly Glu Gln Val Phe Asn Lys Thr Val
1175 1180 1185

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

Ala Val Asp Pro Ser Val Val Lys Gly Gln Thr Phe Lys Asp Ala
1205 1210 1215

Ser Gly Ala Leu Arg Phe Tyr Asn Leu Lys Gly Gln Leu Val Thr
1220 1225 1230

Gly Ser Gly Trp Tyr Glu Thr Ala Asn His Asp Trp Val Tyr Ile
1235 1240 1245

Gln Ser Gly Lys Ala Leu Thr Gly Glu Gln Thr Ile Asn Gly Gln
1250 1255 1260

[0007] His Leu Tyr Phe Lys Glu Asp Gly His Gln Val Lys Gly Gln Leu
1265 1270 1275

Val Thr Gly Thr Asp Gly Lys Val Arg Tyr Tyr Asp Ala Asn Ser
1280 1285 1290

Gly Asp Gln Ala Phe Asn Lys Ser Val Thr Val Asn Gly Lys Thr
1295 1300 1305

Tyr Tyr Phe Gly Asn Asp Gly Thr Ala Gln Thr Ala Gly Asn Pro
1310 1315 1320

Lys Gly Gln Thr Phe Lys Asp Gly Ser Asp Ile Arg Phe Tyr Ser
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Met Glu Gly Gln Leu Val Thr Gly Ser Gly Trp Tyr Glu Asn Ala
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Gln Gly Gln Trp Leu Tyr Val Lys Asn Gly Lys Val Leu Thr Gly
1355 1360 1365

Leu Gln Thr Val Gly Ser Gln Arg Val Tyr Phe Asp Glu Asn Gly
1370 1375 1380

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

Arg Tyr Phe Asp Glu Asn Ser Gly Ser Met Ile Thr Asn Gln Trp
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Lys Phe Val Tyr Gly Gln Tyr Tyr Tyr Phe Gly Asn Asp Gly Ala
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Arg Ile Tyr Arg Gly Trp Asn
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<213> 唾液链球菌（Streptococcus salivarius）

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aattaa 4026

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

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

Ser Glu Ala Ser Phe Glu Leu Ile Asp Gly Tyr Leu Thr Ala Asp Ser
65                  70                  75                  80

Trp Tyr Arg Pro Ala Ser Ile Ile Lys Asp Gly Val Thr Trp Gln Ala
                85                  90                  95

Ser Thr Ala Glu Asp Phe Arg Pro Leu Leu Met Ala Trp Trp Pro Asn
            100                 105                 110

Val Asp Thr Gln Val Asn Tyr Leu Asn Tyr Met Ser Lys Val Phe Asn
        115                 120                 125

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

Ala Ala Lys Asp Ile Gln Ile Lys Ile Glu Gln Lys Ile Gln Ala Glu
145                 150                 155                 160

Lys Ser Thr Gln Trp Leu Arg Glu Thr Ile Ser Ala Phe Val Lys Thr
                165                 170                 175

Gln Pro Gln Trp Asn Lys Glu Thr Glu Asn Tyr Ser Lys Gly Gly Gly
            180                 185                 190

Glu Asp His Leu Gln Gly Gly Ala Leu Leu Tyr Val Asn Asp Ser Arg
        195                 200                 205

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

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

Pro Asn His Met Gly Gly Phe Asp Phe Leu Leu Ala Asn Asp Val Asp
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Leu Ser Asn Pro Val Val Gln Ala Glu Gln Leu Asn Gln Ile His Tyr
            260                 265                 270
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       Leu Met Asn Trp Gly Ser Ile Val Met Gly Asp Lys Asp Ala Asn Phe
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       Asp Gly Ile Arg Val Asp Ala Val Asp Asn Val Asp Ala Asp Met Leu
           290                 295                 300

       Gln Leu Tyr Thr Asn Tyr Phe Arg Glu Tyr Tyr Gly Val Asn Lys Ser
       305                 310                 315                 320

       Glu Ala Asn Ala Leu Ala His Ile Ser Val Leu Glu Ala Trp Ser Leu
                       325                 330                 335

       Asn Asp Asn His Tyr Asn Asp Lys Thr Asp Gly Ala Ala Leu Ala Met
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       Glu Asn Lys Gln Arg Leu Ala Leu Leu Phe Ser Leu Ala Lys Pro Ile
               355                 360                 365

       Lys Glu Arg Thr Pro Ala Val Ser Pro Leu Tyr Asn Asn Thr Phe Asn
           370                 375                 380

       Thr Thr Gln Arg Asp Glu Lys Thr Asp Trp Ile Asn Lys Asp Gly Ser
       385                 390                 395                 400

       Lys Ala Tyr Asn Glu Asp Gly Thr Val Lys Gln Ser Thr Ile Gly Lys
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[0011] Tyr Asn Glu Lys Tyr Gly Asp Ala Ser Gly Asn Tyr Val Phe Ile Arg
                   420                 425                 430

       Ala His Asp Asn Asn Val Gln Asp Ile Ile Ala Glu Ile Ile Lys Lys
               435                 440                 445

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

       Lys Gln Ala Phe Glu Ile Tyr Asn Lys Asp Met Leu Ser Ser Asp Lys
       465                 470                 475                 480

       Lys Tyr Thr Leu Asn Asn Ile Pro Ala Ala Tyr Ala Val Met Leu Gln
                       485                 490                 495

       Asn Met Glu Thr Ile Thr Arg Val Tyr Tyr Gly Asp Leu Tyr Thr Asp
                   500                 505                 510

       Asp Gly His Tyr Met Glu Thr Lys Ser Pro Tyr Tyr Asp Thr Ile Val
               515                 520                 525

       Asn Leu Met Lys Ser Arg Ile Lys Tyr Val Ser Gly Gly Gln Ala Gln
           530                 535                 540

       Arg Ser Tyr Trp Leu Pro Thr Asp Gly Lys Met Asp Asn Ser Asp Val
       545                 550                 555                 560

       Glu Leu Tyr Arg Thr Asn Glu Val Tyr Thr Ser Val Arg Tyr Gly Lys
                       565                 570                 575
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Asp Ile Met Thr Ala Asn Asp Thr Glu Gly Ser Lys Tyr Ser Arg Thr
580 585 590

Ser Gly Gln Val Thr Leu Val Ala Asn Asn Pro Lys Leu Thr Leu Asp
595 600 605

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

Lys Tyr Arg Ala Leu Ile Val Gly Thr Ala Asp Gly Ile Lys Asn Phe
625 630 635 640

Thr Ser Asp Ala Asp Ala Ile Ala Ala Gly Tyr Val Lys Glu Thr Asp
645 650 655

Ser Asn Gly Val Leu Thr Phe Gly Ala Asn Asp Ile Lys Gly Tyr Glu
660 665 670

Thr Phe Asp Met Ser Gly Phe Val Ala Val Trp Val Pro Val Gly Ala
675 680 685

Ser Asp Asp Gln Asp Ile Arg Val Ala Pro Ser Thr Glu Ala Lys Lys
690 695 700

Glu Gly Glu Leu Thr Leu Lys Ala Thr Glu Ala Tyr Asp Ser Gln Leu
705 710 715 720

[0012] Ile Tyr Glu Gly Phe Ser Asn Phe Gln Thr Ile Pro Asp Gly Ser Asp
725 730 735

Pro Ser Val Tyr Thr Asn Arg Lys Ile Ala Glu Asn Val Asp Leu Phe
740 745 750

Lys Ser Trp Gly Val Thr Ser Phe Glu Met Ala Pro Gln Phe Val Ser
755 760 765

Ala Asp Asp Gly Thr Phe Leu Asp Ser Val Ile Gln Asn Gly Tyr Ala
770 775 780

Phe Ala Asp Arg Tyr Asp Leu Ala Met Ser Lys Asn Asn Lys Tyr Gly
785 790 795 800

Ser Lys Glu Asp Leu Arg Asp Ala Leu Lys Ala Leu His Lys Ala Gly
805 810 815

Ile Gln Ala Ile Ala Asp Trp Val Pro Asp Gln Ile Tyr Gln Leu Pro
820 825 830

Gly Lys Glu Val Val Thr Ala Thr Arg Thr Asp Gly Ala Gly Arg Lys
835 840 845

Ile Ala Asp Ala Ile Ile Asp His Ser Leu Tyr Val Ala Asn Thr Lys
850 855 860

Ser Ser Gly Lys Asp Tyr Gln Ala Lys Tyr Gly Gly Glu Phe Leu Ala
865 870 875 880

Glu Leu Lys Ala Lys Tyr Pro Glu Met Phe Lys Val Asn Met Ile Ser
885 890 895

Thr Gly Lys Pro Ile Asp Asp Ser Val Lys Leu Lys Gln Trp Lys Ala
900 905 910

Glu Tyr Phe Asn Gly Thr Asn Val Leu Glu Arg Gly Val Gly Tyr Val
915 920 925

Leu Ser Asp Glu Ala Thr Gly Lys Tyr Phe Thr Val Thr Lys Asp Gly
930 935 940

Asn Phe Ile Pro Leu Gln Leu Thr Gly Asn Glu Lys Val Val Thr Gly
945 950 955 960

Phe Ser Asn Asp Gly Lys Gly Ile Thr Tyr Phe Gly Thr Ser Gly Thr
965 970 975

Gln Ala Lys Ser Ala Phe Val Thr Phe Asn Gly Asn Thr Tyr Tyr Phe
980 985 990

Asp Ala Arg Gly His Met Val Thr Asn Gly Glu Tyr Ser Pro Asn Gly
995 1000 1005

Lys Asp Val Tyr Arg Phe Leu Pro Asn Gly Ile Met Leu Ser Asn
1010 1015 1020

[0013] Ala Phe Tyr Val Asp Ala Asn Gly Asn Thr Tyr Leu Tyr Asn Ser
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Lys Gly Gln Met Tyr Lys Gly Gly Tyr Thr Lys Phe Asp Val Thr
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Glu Thr Asp Lys Asp Gly Lys Glu Ser Lys Val Val Lys Phe Arg
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Tyr Phe Thr Asn Glu Gly Val Met Ala Lys Gly Val Thr Val Ile
1070 1075 1080

Asp Gly Phe Thr Gln Tyr Phe Gly Glu Asp Gly Phe Gln Ala Lys
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Asp Lys Leu Val Thr Phe Lys Gly Lys Thr Tyr Tyr Phe Asp Ala
1100 1105 1110

His Thr Gly Asn Ala Ile Lys Asp Thr Trp Arg Asn Ile Asn Gly
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Lys Trp Tyr His Phe Asp Ala Asn Gly Val Ala Ala Thr Gly Ala
1130 1135 1140

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

Gln Val Lys Gly Gly Val Val Lys Asn Ala Asp Gly Thr Tyr Ser
1160 1165 1170

Lys Tyr Lys Glu Gly Ser Gly Glu Leu Val Thr Asn Glu Phe Phe
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Thr Thr Asp Gly Asn Val Trp Tyr Tyr Ala Gly Ala Asn Gly Lys
1190 1195 1200

Thr Val Thr Gly Ala Gln Val Ile Asn Gly Gln His Leu Tyr Phe
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Asn Ala Asp Gly Ser Gln Val Lys Gly Gly Val Val Lys Asn Ala
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Asp Gly Thr Tyr Ser Lys Tyr Asp Ala Ser Thr Gly Glu Arg Leu
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Thr Asn Glu Phe Phe Thr Thr Gly Asp Asn Asn Trp Tyr Tyr Ile
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Gly Ala Asn Gly Lys Ser Val Thr Gly Glu Val Lys Ile Gly Asp
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Asp Thr Tyr Phe Phe Ala Lys Asp Gly Lys Gln Val Lys Gly Gln
1280 1285 1290

Thr Val Ser Ala Gly Asn Gly Arg Ile Ser Tyr Tyr Tyr Gly Asp
1295 1300 1305

[0014] Ser Gly Lys Arg Ala Val Ser Thr Trp Ile Glu Ile Gln Pro Gly
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Val Tyr Val Tyr Phe Asp Lys Asn Gly Ile Ala Tyr Pro Pro Arg
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Val Leu Asn
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aaagacaaca aatatggttc gctggcggat ttgaaggcag cactgaagag cttgcatgcc 2340

gttggtatta gcgcaatcgc ggattgggtt cctgatcaga tctacaatct gccaggcgac 2400

gaggtcgtca ccgcaacccg cgttaacaac tacggcgaaa ccaaagatgg tgcaatcatt 2460

gatcactctt tgtacgcggc caaaacccgt acttttggta acgactacca gggtaagtat 2520

ggtggtgcgt tcctggacga gctgaaacgt ctgtatccgc agatctttga ccgcgttcag 2580

atttctaccg gtaagcgcat gaccacggac gagaagatca cccaatggtc tgcaaagtat 2640

atgaacggta cgaacatctt ggaccgtggc tctgaatacg ttttgaagaa tggtctgaat 2700

ggttactatg gcaccaatgg tggcaaagtt tcgctgccga aagttgtggg tagcaatcaa 2760

agcacgaatg gcgacaatca aaacggcgac ggtagcggca agtttgaaaa gcgtctgttc 2820

agcgtgcgtt accgttataa caatggccag tacgcgaaaa atgcctttat caaagataac 2880

gacggcaatg tttactattt cgacaatagc ggtcgtatgg ctgtcggtga gaaaacgatt 2940 gacggcaagc agtacttctt cctggctaat ggcgttcagc tgcgtgacgg ctaccgtcaa 3000

aatcgtcgcg gtcaggtgtt ttactacgac cagaatggtg tgctgaacgc aaacggtaaa 3060

caagacccga agcctgacaa caataacaat gcgagcggcc gtaatcaatt cgtccagatc 3120

ggtaacaacg tgtgggcgta ttatgatggc aatggtaaac gtgtcaccgg tcaccagaac 3180

atcaacggtc aggagttgtt tttcgataac aacggtgtcc aggttaaggg tcgtacggtg 3240

aatgagaacg gtgcaattcg ctactatgac gcgaatagcg gtgagatggc acgcaatcgt 3300

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gcggtgaagg gtatggtcaa tatcaacggc caaaatctgt tgtttgacaa taacggcaaa 3600

cagattaagg gtcatctggt ccgcgtcaac ggcgtcgtgc gctattttga tccgaactct 3660

ggtgaaatgg cggttaatcg ttgggttgag gtgagcccag gttggtgggt ttactttgac 3720

ggtgaaggtc gtggtcagat ctaa 3744

<210> 6
<211> 1247
<212> PRT
<213> 唾液链球菌（Streptococcus salivarius）

<400> 6

[0016] Met Pro Ser His Ile Lys Thr Ile Asn Gly Lys Gln Tyr Tyr Val Glu
1 5 10 15

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

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

Tyr Arg Phe Asp Lys Asn Gly Gly Thr Gly Ser Ser Ala Asp Ser Thr
50 55 60

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

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

Trp Tyr Arg Pro Lys Glu Ile Leu Lys Asp Gly Lys Glu Trp Thr Ala
100 105 110

Ser Thr Glu Asn Asp Lys Arg Pro Leu Leu Thr Val Trp Trp Pro Ser
115 120 125

Lys Ala Ile Gln Ala Ser Tyr Leu Asn Tyr Met Lys Glu Gln Gly Leu
130 135 140

Gly Thr Asn Gln Thr Tyr Thr Ser Phe Ser Ser Gln Thr Gln Met Asp
145 150 155 160

Gln Ala Ala Leu Glu Val Gln Lys Arg Ile Glu Glu Arg Ile Ala Arg
165 170 175

Glu Gly Asn Thr Asp Trp Leu Arg Thr Thr Ile Lys Asn Phe Val Lys
180 185 190

Thr Gln Pro Gly Trp Asn Ser Thr Ser Glu Asn Leu Asp Asn Asn Asp
195 200 205

His Leu Gln Gly Gly Ala Leu Leu Tyr Asn Asn Asp Ser Arg Thr Ser
210 215 220

His Ala Asn Ser Asp Tyr Arg Leu Leu Asn Arg Thr Pro Thr Ser Gln
225 230 235 240

Thr Gly Lys His Asn Pro Lys Tyr Thr Lys Asp Thr Ser Asn Gly Gly
245 250 255

Phe Glu Phe Leu Leu Ala Asn Asp Ile Asp Asn Ser Asn Pro Ala Val
260 265 270

Gln Ala Glu Gln Leu Asn Trp Leu His Tyr Ile Met Asn Ile Gly Thr
275 280 285

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

[0017] Ala Val Asp Asn Val Asn Ala Asp Leu Leu Gln Ile Ala Ser Asp Tyr
305 310 315 320

Phe Lys Ala Lys Tyr Gly Ala Asp Gln Ser Gln Asp Gln Ala Ile Lys
325 330 335

His Leu Ser Ile Leu Glu Ala Trp Ser His Asn Asp Ala Tyr Tyr Asn
340 345 350

Glu Asp Thr Lys Gly Ala Gln Leu Pro Met Asp Asp Pro Met His Leu
355 360 365

Ala Leu Val Tyr Ser Leu Leu Arg Pro Ile Gly Asn Arg Ser Gly Val
370 375 380

Glu Pro Leu Ile Ser Asn Ser Leu Asn Asp Arg Ser Glu Ser Gly Lys
385 390 395 400

Asn Ser Lys Arg Met Ala Asn Tyr Ala Phe Val Arg Ala His Asp Ser
405 410 415

Glu Val Gln Ser Ile Ile Gly Gln Ile Ile Lys Asn Glu Ile Asn Pro
420 425 430

Gln Ser Thr Gly Asn Thr Phe Thr Leu Asp Glu Met Lys Lys Ala Phe
435 440 445

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

```
       Tyr Asn Ile Pro Ser Ala Tyr Ala Leu Met Leu Thr His Lys Asp Thr
       465                 470                 475                 480

       Val Pro Arg Val Tyr Tyr Gly Asp Met Tyr Thr Asp Asp Gly Gln Tyr
                       485                 490                 495

       Met Ala Gln Lys Ser Pro Tyr Tyr Asp Ala Ile Glu Thr Leu Leu Lys
                   500                 505                 510

       Gly Arg Ile Arg Tyr Ala Ala Gly Gly Gln Asp Met Lys Val Asn Tyr
               515                 520                 525

       Ile Gly Tyr Gly Asn Thr Asn Gly Trp Asp Ala Ala Gly Val Leu Thr
           530                 535                 540

       Ser Val Arg Tyr Gly Thr Gly Ala Asn Ser Ala Ser Asp Thr Gly Thr
       545                 550                 555                 560

       Ala Glu Thr Arg Asn Gln Gly Met Ala Val Ile Val Ser Asn Gln Pro
                       565                 570                 575

       Ala Leu Arg Leu Thr Ser Asn Leu Thr Ile Asn Met Gly Ala Ala His
                   580                 585                 590

       Arg Asn Gln Ala Tyr Arg Pro Leu Leu Leu Thr Thr Asn Asp Gly Val
               595                 600                 605

[0018] Ala Thr Tyr Leu Asn Asp Ser Asp Ala Asn Gly Ile Val Lys Tyr Thr
           610                 615                 620

       Asp Gly Asn Gly Asn Leu Thr Phe Ser Ala Asn Glu Ile Arg Gly Ile
       625                 630                 635                 640

       Arg Asn Pro Gln Val Asp Gly Tyr Leu Ala Val Trp Val Pro Val Gly
                       645                 650                 655

       Ala Ser Glu Asn Gln Asp Val Arg Val Ala Pro Ser Lys Glu Lys Asn
                   660                 665                 670

       Ser Ser Gly Leu Val Tyr Glu Ser Asn Ala Ala Leu Asp Ser Gln Val
               675                 680                 685

       Ile Tyr Glu Gly Phe Ser Asn Phe Gln Asp Phe Val Gln Asn Pro Ser
           690                 695                 700

       Gln Tyr Thr Asn Lys Lys Ile Ala Glu Asn Ala Asn Leu Phe Lys Ser
       705                 710                 715                 720

       Trp Gly Ile Thr Ser Phe Glu Phe Ala Pro Gln Tyr Val Ser Ser Asp
                       725                 730                 735

       Asp Gly Ser Phe Leu Asp Ser Val Ile Gln Asn Gly Tyr Ala Phe Thr
                   740                 745                 750

       Asp Arg Tyr Asp Ile Gly Met Ser Lys Asp Asn Lys Tyr Gly Ser Leu
               755                 760                 765
```

Ala Asp Leu Lys Ala Ala Leu Lys Ser Leu His Ala Val Gly Ile Ser
770 775 780

Ala Ile Ala Asp Trp Val Pro Asp Gln Ile Tyr Asn Leu Pro Gly Asp
785 790 795 800

Glu Val Val Thr Ala Thr Arg Val Asn Asn Tyr Gly Glu Thr Lys Asp
805 810 815

Gly Ala Ile Ile Asp His Ser Leu Tyr Ala Ala Lys Thr Arg Thr Phe
820 825 830

Gly Asn Asp Tyr Gln Gly Lys Tyr Gly Gly Ala Phe Leu Asp Glu Leu
835 840 845

Lys Arg Leu Tyr Pro Gln Ile Phe Asp Arg Val Gln Ile Ser Thr Gly
850 855 860

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

Met Asn Gly Thr Asn Ile Leu Asp Arg Gly Ser Glu Tyr Val Leu Lys
885 890 895

Asn Gly Leu Asn Gly Tyr Tyr Gly Thr Asn Gly Gly Lys Val Ser Leu
900 905 910

[0019] Pro Lys Val Val Gly Ser Asn Gln Ser Thr Asn Gly Asp Asn Gln Asn
915 920 925

Gly Asp Gly Ser Gly Lys Phe Glu Lys Arg Leu Phe Ser Val Arg Tyr
930 935 940

Arg Tyr Asn Asn Gly Gln Tyr Ala Lys Asn Ala Phe Ile Lys Asp Asn
945 950 955 960

Asp Gly Asn Val Tyr Tyr Phe Asp Asn Ser Gly Arg Met Ala Val Gly
965 970 975

Glu Lys Thr Ile Asp Gly Lys Gln Tyr Phe Phe Leu Ala Asn Gly Val
980 985 990

Gln Leu Arg Asp Gly Tyr Arg Gln Asn Arg Arg Gly Gln Val Phe Tyr
995 1000 1005

Tyr Asp Gln Asn Gly Val Leu Asn Ala Asn Gly Lys Gln Asp Pro
1010 1015 1020

Lys Pro Asp Asn Asn Asn Asn Ala Ser Gly Arg Asn Gln Phe Val
1025 1030 1035

Gln Ile Gly Asn Asn Val Trp Ala Tyr Tyr Asp Gly Asn Gly Lys
1040 1045 1050

Arg Val Thr Gly His Gln Asn Ile Asn Gly Gln Glu Leu Phe Phe
1055 1060 1065

Asp Asn Asn Gly Val Gln Val Lys Gly Arg Thr Val Asn Glu Asn
1070 1075 1080

Gly Ala Ile Arg Tyr Tyr Asp Ala Asn Ser Gly Glu Met Ala Arg
1085 1090 1095

Asn Arg Phe Ala Glu Ile Glu Pro Gly Val Trp Ala Tyr Phe Asn
1100 1105 1110

Asn Asp Gly Thr Ala Val Lys Gly Ser Gln Asn Ile Asn Gly Gln
1115 1120 1125

Asp Leu Tyr Phe Asp Gln Asn Gly Arg Gln Val Lys Gly Ala Leu
1130 1135 1140

Ala Asn Val Asp Gly Asn Leu Arg Tyr Tyr Asp Val Asn Ser Gly
1145 1150 1155

Glu Leu Tyr Arg Asn Arg Phe His Glu Ile Asp Gly Ser Trp Tyr
1160 1165 1170

Tyr Phe Asp Gly Asn Gly Asn Ala Val Lys Gly Met Val Asn Ile
1175 1180 1185

Asn Gly Gln Asn Leu Leu Phe Asp Asn Asn Gly Lys Gln Ile Lys
1190 1195 1200

[0020] Gly His Leu Val Arg Val Asn Gly Val Val Arg Tyr Phe Asp Pro
1205 1210 1215

Asn Ser Gly Glu Met Ala Val Asn Arg Trp Val Glu Val Ser Pro
1220 1225 1230

Gly Trp Trp Val Tyr Phe Asp Gly Glu Gly Arg Gly Gln Ile
1235 1240 1245

<210> 7
<211> 4434
<212> DNA
<213> 唾液链球菌（Streptococcus salivarius）

<400> 7
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gtcactagcc ctgaagccac gaaagaggcg gacaaacgca cgaacactaa agaggccgac 120

gttctgacgc ctgcaaaaga aacgaacgca gtcgagactg cgaccaccac taacacccag 180

gcgacggcgg aggccgccac gaccgcgacc accgcggacg tcgcggtggc tgcggtgccg 240

aacaaagaag cggtcgttac cacggatgct ccggcggtca cgaccgagaa agcggaagaa 300

cagccggcta ccgttaaagc agaagtcgtc aatacggaag tgaaagcgcc ggaagcggct 360

ctgaaagaca gcgaggttga ggcagcgctg agcctgaaga acatcaagaa cattgatggc 420

aagtattact atgttaatga ggatggcagc cacaaagaga atttcgctat taccgtgaat 480

ggccagctgc tgtactttgg taaagacggt gcgctgacgt cctctagcac gtattctttt 540

accccaggca ctaccaatat cgtggacggt tttagcatta acaaccgcgc ttacgacagc 600

agcgaggcga gctttgagct gatcgacggt tacttgaccg cagacagctg gtatcgtccg 660 gctagcatca tcaaagatgg tgttacgtgg caagcgtcca ccgccgagga ttttcgtccg 720

ctgctgatgg catggtggcc gaatgtggat acgcaggtga actatttgaa ttacatgtcc 780

aaagttttca acctggacgc gaaatactct agcaccgaca aacaggaaac cctgaaagtg 840

gcagcaaaag acattcaaat caagattgaa caaaagattc aagcggagaa gagcacgcag 900

tggctgcgtg aaactatcag cgcctttgtg aaaacccagc cgcagtggaa caaagaaacc 960

gagaattaca gcaagggtgg tggtgaggac cacctgcaag gtggcgcact gctgtatgtt 1020

aacgacagcc gtaccccttg ggcgaatagc gattaccgtc gtctgaatcg caccgcaacc 1080

aatcagacgg gcacgatcga taagtctatt ctggacgagc agtctgaccc aaaccacatg 1140

ggcggtttcg actttctgct ggcgaacgac gtcgacctga gcaatccggt cgtgcaggct 1200

gagcagctga atcaaatcca ctatctgatg aattggggtt ccattgtgat gggtgacaag 1260

gatgcgaact ttgacggcat tcgtgtcgat gcagttgaca acgtggacgc ggacatgttg 1320

caactgtata ccaattactt ccgtgagtac tacggtgtga acaagagcga agctaacgca 1380

ctggctcaca tcagcgttct ggaggcgtgg agcctgaatg ataatcatta caatgacaag 1440

accgatggtg cggcactggc aatggagaat aagcaacgtc tggcgctgtt gttttcgttg 1500

gcgaaaccga tcaaagagcg taccccggca gtgagcccgc tgtataacaa caccttcaat 1560

accacccagc gtgatgaaaa gaccgattgg attaacaaag acggtagcaa ggcttacaac 1620

gaagatggca cggtcaaaca atcgaccatc ggtaagtaca acgagaaata cggtgacgca 1680

tccggtaact acgttttcat ccgtgcccac gataacaacg tccaggacat catcgccgag 1740

atcatcaaga aagagatcaa cccgaaaagc gacggcttca ccatcaccga cgccgaaatg 1800

[0021] aagcaagcct ttgaaatcta taacaaagat atgctgtcga gcgacaaaaa gtataccctg 1860

aataacattc cggcagcgta tgccgtgatg ttgcagaata tggaaacgat tacccgcgtc 1920

tattacggtg atctgtatac ggacgacggt cactacatgg aaaccaaatc tccgtattac 1980

gataccatcg tgaatttgat gaagagccgt atcaagtatg tttcgggtgg ccaggcgcaa 2040

cgtagctatt ggctgccgac cgacggtaag atggacaata gcgacgttga gctgtaccgc 2100

acgaatgagg tttacacgag cgtgcgctat ggtaaggata tcatgaccgc taatgatacc 2160

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ccggtgggtg catctgacaa tcaggacatt cgtgttgcgc cgagcaccga ggcaaagaaa 2520

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caatttgtct cggcggatga tggcaccttt ctggatagcg ttattcagaa tggctacgcc 2760

ttcgccgacc gttatgacct ggccatgtcc aagaacaaca agtatggtag caaagaggac 2820

ctgcgtgatg cactgaaagc actgcataag gcgggtattc aagctatcgc agactgggtt 2880

ccagaccaga tctaccagct gccgggcaaa gaagttgtca ccgccacccg tacggatggt 2940

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gctggccgta agatcgcaga cgcgattatc gaccattctc tgtatgttgc aaacagcaaa      3000

agcagcggca aagattatca agcaaagtac ggtggcgagt tcctggccga gctgaaagcc      3060

aaatacccgg aaatgttcaa agttaacatg attagcacgg gtaagccgat tgatgactcc      3120

gtgaaattga agcaatggaa agccgagtac ttcaatggca ccaacgtttt ggaacgtggt      3180

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aatttcattc cgctgcaact gacgggtaaa gagaaagtta tcacgggttt ctccagcgat      3300

ggtaagggta tcacctattt cggtacgagc ggtacgcagg cgaagtctgc gtttgttacc      3360

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agcccgaatg gcaaggacgt ctaccgtttt ctgccgaacg gtatcatgct gagcaatgcg      3480

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ggcggttaca cgaaattcga tgtttctgaa acggataagg acggtaaaga gtccaaggtc      3600

gtcaagttcc gctactttac gaacgaaggc gtcatggcca agggtgttac cgtcattgat      3660

ggttttaccc aatacttcgg tgaggacggc tttcaagcga aggataagct ggtcaccttc      3720

aagggcaaga cgtattactt cgacgcacac actggtaatg gtatcaaaga tacctggcgc      3780

aatatcaatg gtaaatggta ctatttcgac gcgaatggcg ttgctgcgac cggtgcgcag      3840

gtgattaacg gccagaaact gtacttcaac gaggatggct cccaagtcaa aggcggcgtg      3900

gttaagaacg cagacggcac ctatagcaaa tacaaagaag gttttggtga gctggttact      3960

aacgagtttt tcacgactga tggcaatgtt tggtactacg ccggtgcaaa tggtaaaacc      4020

gttaccggtg cacaagtgat caacggccaa catttgtact tcaatgcgga cggttcccag      4080
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[0022]

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gtgaagggtg gcgttgtcaa gaacgcggat ggcacctaca gcaagtacaa tgctagcact      4140

ggtgaacgtc tgacgaacga gttctttacg accggtgata acaattggta ttacattggc      4200

gcaaacggta agagcgtgac gggtgaggtc aagattggtg atgatactta ctttttcgcg      4260

aaggatggca aacaagttaa aggtcaaacc gtcagcgccg gtaatggtcg cattagctac      4320

tactacggtg acagcggcaa gcgtgcggtt agcacctgga ttgagattca gccgggtgtt      4380

tatgtgtatt tcgacaaaaa cggtttggcg taccctccgc gtgttctgaa ttaa            4434
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<210> 8
<211> 1477
<212> PRT
<213> 唾液链球菌（Streptococcus salivarius）

<400> 8

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


Arg Thr Asn Thr Lys Glu Ala Asp Val Leu Thr Pro Ala Lys Glu Thr
    35                  40                  45


Asn Ala Val Glu Thr Ala Thr Thr Thr Asn Thr Gln Ala Thr Ala Glu
    50                  55                  60


Ala Ala Thr Thr Ala Thr Thr Ala Asp Val Ala Val Ala Ala Val Pro
65                  70                  75                  80
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Asn Lys Glu Ala Val Val Thr Thr Asp Ala Pro Ala Val Thr Thr Glu
85 90 95

Lys Ala Glu Glu Gln Pro Ala Thr Val Lys Ala Glu Val Val Asn Thr
100 105 110

Glu Val Lys Ala Pro Glu Ala Ala Leu Lys Asp Ser Glu Val Glu Ala
115 120 125

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

Val Asn Glu Asp Gly Ser His Lys Glu Asn Phe Ala Ile Thr Val Asn
145 150 155 160

Gly Gln Leu Leu Tyr Phe Gly Lys Asp Gly Ala Leu Thr Ser Ser Ser
165 170 175

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

Ile Asn Asn Arg Ala Tyr Asp Ser Ser Glu Ala Ser Phe Glu Leu Ile
195 200 205

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

[0023] Lys Asp Gly Val Thr Trp Gln Ala Ser Thr Ala Glu Asp Phe Arg Pro
225 230 235 240

Leu Leu Met Ala Trp Trp Pro Asn Val Asp Thr Gln Val Asn Tyr Leu
245 250 255

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

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

Ile Glu Gln Lys Ile Gln Ala Glu Lys Ser Thr Gln Trp Leu Arg Glu
290 295 300

Thr Ile Ser Ala Phe Val Lys Thr Gln Pro Gln Trp Asn Lys Glu Thr
305 310 315 320

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

Leu Leu Tyr Val Asn Asp Ser Arg Thr Pro Trp Ala Asn Ser Asp Tyr
340 345 350

Arg Arg Leu Asn Arg Thr Ala Thr Asn Gln Thr Gly Thr Ile Asp Lys
355 360 365

Ser Ile Leu Asp Glu Gln Ser Asp Pro Asn His Met Gly Gly Phe Asp
370 375 380

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

Glu Gln Leu Asn Gln Ile His Tyr Leu Met Asn Trp Gly Ser Ile Val
                405                 410                 415

Met Gly Asp Lys Asp Ala Asn Phe Asp Gly Ile Arg Val Asp Ala Val
            420                 425                 430

Asp Asn Val Asp Ala Asp Met Leu Gln Leu Tyr Thr Asn Tyr Phe Arg
        435                 440                 445

Glu Tyr Tyr Gly Val Asn Lys Ser Glu Ala Asn Ala Leu Ala His Ile
    450                 455                 460

Ser Val Leu Glu Ala Trp Ser Leu Asn Asp Asn His Tyr Asn Asp Lys
465                 470                 475                 480

Thr Asp Gly Ala Ala Leu Ala Met Glu Asn Lys Gln Arg Leu Ala Leu
                485                 490                 495

Leu Phe Ser Leu Ala Lys Pro Ile Lys Glu Arg Thr Pro Ala Val Ser
            500                 505                 510

Pro Leu Tyr Asn Asn Thr Phe Asn Thr Thr Gln Arg Asp Glu Lys Thr
        515                 520                 525
```

[0024]

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Asp Trp Ile Asn Lys Asp Gly Ser Lys Ala Tyr Asn Glu Asp Gly Thr
    530                 535                 540

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

Ser Gly Asn Tyr Val Phe Ile Arg Ala His Asp Asn Asn Val Gln Asp
                565                 570                 575

Ile Ile Ala Glu Ile Ile Lys Lys Glu Ile Asn Pro Lys Ser Asp Gly
            580                 585                 590

Phe Thr Ile Thr Asp Ala Glu Met Lys Gln Ala Phe Glu Ile Tyr Asn
        595                 600                 605

Lys Asp Met Leu Ser Ser Asp Lys Lys Tyr Thr Leu Asn Asn Ile Pro
    610                 615                 620

Ala Ala Tyr Ala Val Met Leu Gln Asn Met Glu Thr Ile Thr Arg Val
625                 630                 635                 640

Tyr Tyr Gly Asp Leu Tyr Thr Asp Asp Gly His Tyr Met Glu Thr Lys
                645                 650                 655

Ser Pro Tyr Tyr Asp Thr Ile Val Asn Leu Met Lys Ser Arg Ile Lys
            660                 665                 670

Tyr Val Ser Gly Gly Gln Ala Gln Arg Ser Tyr Trp Leu Pro Thr Asp
        675                 680                 685
```

Gly Lys Met Asp Asn Ser Asp Val Glu Leu Tyr Arg Thr Asn Glu Val
690 695 700

Tyr Thr Ser Val Arg Tyr Gly Lys Asp Ile Met Thr Ala Asn Asp Thr
705 710 715 720

Glu Gly Ser Lys Tyr Ser Arg Thr Ser Gly Gln Val Thr Leu Val Ala
725 730 735

Asn Asn Pro Lys Leu Asn Leu Asp Gln Ser Ala Lys Leu Asn Val Glu
740 745 750

Met Gly Lys Ile His Ala Asn Gln Lys Tyr Arg Ala Leu Ile Val Gly
755 760 765

Thr Ala Asp Gly Ile Lys Asn Phe Thr Ser Asp Ala Asp Ala Ile Ala
770 775 780

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

Ala Asn Asp Ile Lys Gly Tyr Glu Thr Phe Asp Met Ser Gly Phe Val
805 810 815

Ala Val Trp Val Pro Val Gly Ala Ser Asp Asn Gln Asp Ile Arg Val
820 825 830

[0025] Ala Pro Ser Thr Glu Ala Lys Lys Glu Gly Glu Leu Thr Leu Lys Ala
835 840 845

Thr Glu Ala Tyr Asp Ser Gln Leu Ile Tyr Glu Gly Phe Ser Asn Phe
850 855 860

Gln Thr Ile Pro Asp Gly Ser Asp Pro Ser Val Tyr Thr Asn Arg Lys
865 870 875 880

Ile Ala Glu Asn Val Asp Leu Phe Lys Ser Trp Gly Val Thr Ser Phe
885 890 895

Glu Met Ala Pro Gln Phe Val Ser Ala Asp Asp Gly Thr Phe Leu Asp
900 905 910

Ser Val Ile Gln Asn Gly Tyr Ala Phe Ala Asp Arg Tyr Asp Leu Ala
915 920 925

Met Ser Lys Asn Asn Lys Tyr Gly Ser Lys Glu Asp Leu Arg Asp Ala
930 935 940

Leu Lys Ala Leu His Lys Ala Gly Ile Gln Ala Ile Ala Asp Trp Val
945 950 955 960

Pro Asp Gln Ile Tyr Gln Leu Pro Gly Lys Glu Val Val Thr Ala Thr
965 970 975

Arg Thr Asp Gly Ala Gly Arg Lys Ile Ala Asp Ala Ile Ile Asp His
980 985 990

Ser Leu Tyr Val Ala Asn Ser Lys Ser Ser Gly Lys Asp Tyr Gln Ala
995 1000 1005

Lys Tyr Gly Gly Glu Phe Leu Ala Glu Leu Lys Ala Lys Tyr Pro
1010 1015 1020

Glu Met Phe Lys Val Asn Met Ile Ser Thr Gly Lys Pro Ile Asp
1025 1030 1035

Asp Ser Val Lys Leu Lys Gln Trp Lys Ala Glu Tyr Phe Asn Gly
1040 1045 1050

Thr Asn Val Leu Glu Arg Gly Val Gly Tyr Val Leu Ser Asp Glu
1055 1060 1065

Ala Thr Gly Lys Tyr Phe Thr Val Thr Lys Glu Gly Asn Phe Ile
1070 1075 1080

Pro Leu Gln Leu Thr Gly Lys Glu Lys Val Ile Thr Gly Phe Ser
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Ser Asp Gly Lys Gly Ile Thr Tyr Phe Gly Thr Ser Gly Thr Gln
1100 1105 1110

Ala Lys Ser Ala Phe Val Thr Phe Asn Gly Asn Thr Tyr Tyr Phe
1115 1120 1125

[0026] Asp Ala Arg Gly His Met Val Thr Asn Ser Glu Tyr Ser Pro Asn
1130 1135 1140

Gly Lys Asp Val Tyr Arg Phe Leu Pro Asn Gly Ile Met Leu Ser
1145 1150 1155

Asn Ala Phe Tyr Ile Asp Ala Asn Gly Asn Thr Tyr Leu Tyr Asn
1160 1165 1170

Ser Lys Gly Gln Met Tyr Lys Gly Gly Tyr Thr Lys Phe Asp Val
1175 1180 1185

Ser Glu Thr Asp Lys Asp Gly Lys Glu Ser Lys Val Val Lys Phe
1190 1195 1200

Arg Tyr Phe Thr Asn Glu Gly Val Met Ala Lys Gly Val Thr Val
1205 1210 1215

Ile Asp Gly Phe Thr Gln Tyr Phe Gly Glu Asp Gly Phe Gln Ala
1220 1225 1230

Lys Asp Lys Leu Val Thr Phe Lys Gly Lys Thr Tyr Tyr Phe Asp
1235 1240 1245

Ala His Thr Gly Asn Gly Ile Lys Asp Thr Trp Arg Asn Ile Asn
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Gly Lys Trp Tyr Tyr Phe Asp Ala Asn Gly Val Ala Ala Thr Gly
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Ala Gln Val Ile Asn Gly Gln Lys Leu Tyr Phe Asn Glu Asp Gly
1280 1285 1290

Ser Gln Val Lys Gly Gly Val Val Lys Asn Ala Asp Gly Thr Tyr
1295 1300 1305

Ser Lys Tyr Lys Glu Gly Phe Gly Glu Leu Val Thr Asn Glu Phe
1310 1315 1320

Phe Thr Thr Asp Gly Asn Val Trp Tyr Tyr Ala Gly Ala Asn Gly
1325 1330 1335

Lys Thr Val Thr Gly Ala Gln Val Ile Asn Gly Gln His Leu Tyr
1340 1345 1350

Phe Asn Ala Asp Gly Ser Gln Val Lys Gly Gly Val Val Lys Asn
1355 1360 1365

Ala Asp Gly Thr Tyr Ser Lys Tyr Asn Ala Ser Thr Gly Glu Arg
1370 1375 1380

Leu Thr Asn Glu Phe Phe Thr Thr Gly Asp Asn Asn Trp Tyr Tyr
1385 1390 1395

Ile Gly Ala Asn Gly Lys Ser Val Thr Gly Glu Val Lys Ile Gly
1400 1405 1410

[0027] Asp Asp Thr Tyr Phe Phe Ala Lys Asp Gly Lys Gln Val Lys Gly
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Gln Thr Val Ser Ala Gly Asn Gly Arg Ile Ser Tyr Tyr Tyr Gly
1430 1435 1440

Asp Ser Gly Lys Arg Ala Val Ser Thr Trp Ile Glu Ile Gln Pro
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Gly Val Tyr Val Tyr Phe Asp Lys Asn Gly Leu Ala Tyr Pro Pro
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<213> 汗毛链球菌（Streptococcus downei）

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<212> PRT
<213> 汗毛链球菌（Streptococcus downei）

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Thr Gly Ala Tyr Lys Asp Thr Ser Lys Val Glu Ala Asp Lys Ser Gly
35 40 45

Ser Asp Ile Ser Lys Glu Glu Thr Thr Phe Ala Ala Asn Asn Arg Ala
50 55 60

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

Ala Asp Ser Trp Tyr Arg Pro Lys Ser Ile Leu Lys Asp Gly Lys Thr
85 90 95

Trp Thr Glu Ser Ser Lys Asp Asp Phe Arg Pro Leu Leu Met Ala Trp
100 105 110

Trp Pro Asp Thr Glu Thr Lys Arg Asn Tyr Val Asn Tyr Met Asn Lys
115 120 125

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

Leu Thr Ala Ala Ala Glu Leu Val Gln Ala Arg Ile Glu Gln Lys Ile
145 150 155 160

Thr Thr Glu Gln Asn Thr Lys Trp Leu Arg Glu Ala Ile Ser Ala Phe
165 170 175

Val Lys Thr Gln Pro Gln Trp Asn Gly Glu Ser Glu Lys Pro Tyr Asp
180 185 190

[0030] Asp His Leu Gln Asn Gly Ala Leu Lys Phe Asp Asn Gln Ser Asp Leu
195 200 205

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

Asn Gln Thr Gly Ser Leu Asp Ser Arg Phe Thr Tyr Asn Ala Asn Asp
225 230 235 240

Pro Leu Gly Gly Tyr Glu Leu Leu Leu Ala Asn Asp Val Asp Asn Ser
245 250 255

Asn Pro Ile Val Gln Ala Glu Gln Leu Asn Trp Leu His Tyr Leu Leu
260 265 270

Asn Phe Gly Thr Ile Tyr Ala Lys Asp Ala Asp Ala Asn Phe Asp Ser
275 280 285

Ile Arg Val Asp Ala Val Asp Asn Val Asp Ala Asp Leu Leu Gln Ile
290 295 300

Ser Ser Asp Tyr Leu Lys Ala Ala Tyr Gly Ile Asp Lys Asn Asn Lys
305 310 315 320

Asn Ala Asn Asn His Val Ser Ile Val Glu Ala Trp Ser Asp Asn Asp
325 330 335

Thr Pro Tyr Leu His Asp Asp Gly Asp Asn Leu Met Asn Met Asp Asn
340 345 350

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Lys Phe Arg Leu Ser Met Leu Trp Ser Leu Ala Lys Pro Leu Asp Lys
        355                 360                 365

Arg Ser Gly Leu Asn Pro Leu Ile His Asn Ser Leu Val Asp Arg Glu
    370                 375                 380

Val Asp Asp Arg Glu Val Glu Thr Val Pro Ser Tyr Ser Phe Ala Arg
385                 390                 395                 400

Ala His Asp Ser Glu Val Gln Asp Leu Ile Arg Asp Ile Ile Lys Ala
                405                 410                 415

Glu Ile Asn Pro Asn Ala Phe Gly Tyr Ser Phe Thr Gln Asp Glu Ile
            420                 425                 430

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

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

Asn Lys Gly Ser Ile Pro Arg Val Tyr Tyr Gly Asp Met Phe Thr Asp
465                 470                 475                 480

Asp Gly Gln Tyr Met Ala Asn Lys Thr Val Asn Tyr Asp Ala Ile Glu
                485                 490                 495
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[0031]

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Ser Leu Leu Lys Ala Arg Met Lys Tyr Val Ala Gly Gly Gln Ala Met
            500                 505                 510

Gln Asn Tyr Gln Ile Gly Asn Gly Glu Ile Leu Thr Ser Val Arg Tyr
        515                 520                 525

Gly Lys Gly Ala Leu Lys Gln Ser Asp Lys Gly Asp Ala Thr Thr Arg
    530                 535                 540

Thr Ser Gly Val Gly Val Val Met Gly Asn Gln Pro Asn Phe Ser Leu
545                 550                 555                 560

Asp Gly Lys Val Val Ala Leu Asn Met Gly Ala Ala His Ala Asn Gln
                565                 570                 575

Glu Tyr Arg Ala Leu Met Val Ser Thr Lys Asp Gly Val Ala Thr Tyr
            580                 585                 590

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

Glu Asn Gly Tyr Leu Tyr Phe Leu Asn Asp Asp Leu Lys Gly Val Ala
    610                 615                 620

Asn Pro Gln Val Ser Gly Phe Leu Gln Val Trp Val Pro Val Gly Ala
625                 630                 635                 640

Ala Asp Asp Gln Asp Ile Arg Val Ala Ala Ser Asp Thr Ala Ser Thr
                645                 650                 655
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Asp Gly Lys Ser Leu His Gln Asp Ala Ala Met Asp Ser Arg Val Met
660 665 670

Phe Glu Gly Phe Ser Asn Phe Gln Ser Phe Ala Thr Lys Glu Glu Glu
675 680 685

Tyr Thr Asn Val Val Ile Ala Asn Asn Val Asp Lys Phe Val Ser Trp
690 695 700

Gly Ile Thr Asp Phe Glu Met Ala Pro Gln Tyr Val Ser Ser Thr Asp
705 710 715 720

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

Arg Tyr Asp Leu Gly Met Ser Lys Ala Asn Lys Tyr Gly Thr Ala Asp
740 745 750

Gln Leu Val Lys Ala Ile Lys Ala Leu His Ala Lys Gly Leu Lys Val
755 760 765

Met Ala Asp Trp Val Pro Asp Gln Met Tyr Thr Phe Pro Lys Gln Glu
770 775 780

Val Val Thr Val Thr Arg Thr Asp Lys Phe Gly Lys Pro Ile Ala Gly
785 790 795 800

[0032] Ser Gln Ile Asn His Ser Leu Tyr Val Thr Asp Thr Lys Ser Ser Gly
805 810 815

Asp Asp Tyr Gln Ala Lys Tyr Gly Gly Ala Phe Leu Asp Glu Leu Lys
820 825 830

Glu Lys Tyr Pro Glu Leu Phe Thr Lys Lys Gln Ile Ser Thr Gly Gln
835 840 845

Ala Ile Asp Pro Ser Val Lys Ile Lys Gln Trp Ser Ala Lys Tyr Phe
850 855 860

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

Gln Ala Ser Asn Lys Tyr Leu Asn Val Ser Asp Asp Lys Leu Phe Leu
885 890 895

Pro Lys Thr Leu Leu Gly Gln Val Val Glu Ser Gly Ile Arg Phe Asp
900 905 910

Gly Thr Gly Tyr Val Tyr Asn Ser Ser Thr Thr Gly Glu Lys Val Thr
915 920 925

Asp Ser Phe Ile Thr Glu Ala Gly Asn Leu Tyr Tyr Phe Gly Gln Asp
930 935 940

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

Phe Leu Ala Asn Gly Ala Ala Leu Arg Asn Thr Val Tyr Thr Asp Ala
965 970 975

Gln Gly Gln Asn His Tyr Tyr Gly Asn Asp Gly Lys Arg Tyr Glu Asn
980 985 990

Gly Tyr Gln Gln Phe Gly Asn Asp Ser Trp Arg Tyr Phe Lys Asn Gly
995 1000 1005

Val Met Ala Leu Gly Leu Thr Thr Val Asp Gly His Val Gln Tyr
1010 1015 1020

Phe Asp Lys Asp Gly Val Gln Ala Lys Asp Lys Ile Ile Val Thr
1025 1030 1035

Arg Asp Gly Lys Val Arg Tyr Phe Asp Gln His Asn Gly Asn Ala
1040 1045 1050

Val Thr Asn Thr Phe Val Ala Asp Lys Thr Gly His Trp Tyr Tyr
1055 1060 1065

Leu Gly Lys Asp Gly Val Ala Val Thr Gly Ala Gln Thr Val Gly
1070 1075 1080

Lys Gln His Leu Tyr Phe Glu Ala Asn Gly Gln Gln Val Lys Gly
1085 1090 1095

[0033] Asp Phe Val Thr Ala Lys Asp Gly Lys Leu Tyr Phe Tyr Asp Val
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Asp Ser Gly Asp Met Trp Thr Asn Thr Phe Ile Glu Asp Lys Ala
1115 1120 1125

Gly Asn Trp Phe Tyr Leu Gly Lys Asp Gly Ala Ala Val Thr Gly
1130 1135 1140

Ala Gln Thr Ile Lys Gly Gln Lys Leu Tyr Phe Lys Ala Asn Gly
1145 1150 1155

Gln Gln Val Lys Gly Asp Ile Val Lys Asp Ala Asp Gly Lys Ile
1160 1165 1170

Arg Tyr Tyr Asp Ala Gln Thr Gly Glu Gln Val Phe Asn Lys Ser
1175 1180 1185

Val Ser Val Asn Gly Lys Thr Tyr Tyr Phe Gly Ser Asp Gly Thr
1190 1195 1200

Ala Gln Thr Gln Ala Asn Pro Lys Gly Gln Thr Phe Lys Asp Gly
1205 1210 1215

Ser Gly Val Leu Arg Phe Tyr Asn Leu Glu Gly Gln Tyr Val Ser
1220 1225 1230

Gly Ser Gly Trp Tyr Glu Thr Ala Glu His Glu Trp Val Tyr Val
1235 1240 1245

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Lys Ser Gly Lys Val Leu Thr Gly Ala Gln Thr Ile Gly Asn Gln
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Arg Val Tyr Phe Lys Asp Asn Gly His Gln Val Lys Gly Gln Leu
    1265                1270                1275

Val Thr Gly Asn Asp Gly Lys Leu Arg Tyr Tyr Asp Ala Asn Ser
    1280                1285                1290

Gly Asp Gln Ala Phe Asn Lys Ser Val Thr Val Asn Gly Lys Thr
    1295                1300                1305

Tyr Tyr Phe Gly Ser Asp Gly Thr Ala Gln Thr Gln Ala Asn Pro
    1310                1315                1320

Lys Gly Gln Thr Phe Lys Asp Gly Ser Gly Val Leu Arg Phe Tyr
    1325                1330                1335

Asn Leu Glu Gly Gln Tyr Val Ser Gly Ser Gly Trp Tyr Lys Asn
    1340                1345                1350

Ala Gln Gly Gln Trp Leu Tyr Val Lys Asp Gly Lys Val Leu Thr
    1355                1360                1365

Gly Leu Gln Thr Val Gly Asn Gln Lys Val Tyr Phe Asp Lys Asn
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[0034]

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Gly Ile Gln Ala Lys Gly Lys Ala Val Arg Thr Ser Asp Gly Lys
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Val Arg Tyr Phe Asp Glu Asn Ser Gly Ser Met Ile Thr Asn Gln
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Trp Lys Phe Val Tyr Gly Gln Tyr Tyr Tyr Phe Gly Ser Asp Gly
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Ala Ala Val Tyr Arg Gly Trp Asn
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caagtgtatg atcgcagcgc gcagagcttc gagcatgttg atcactacct gacggcggaa     240

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ctgaagaaca ccgattggct gcgtcaaacg atcagcgcgt tcgtcaaaac ccaaagcgct     540
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aatgatggtc gccgctacga gaatggctat tatcagttta tgagcggtgt ttggcgccat      3000
ttcaataatg gcgagatgtc cgttggtctg accgtcattg acggtcaagt tcaatacttt      3060
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tacttcgata agcagagcgg caatatgtat cgtaatcgtt tcattgagaa cgaagagggc      3180
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cagcacctgt attttcgtgc taacggcgtt caggttaagg gtgagttcgt gaccgatcgt      3300
catggccgca tctcttatta cgacggcaac agcggtgatc agatccgcaa ccgtttcgtc      3360
cgcaatgcgc aaggccagtg gttttacttt gacaacaatg gctatgcagt aactggtgct      3420
cgtacgatca acggccagca cctgtatttc cgcgcgaacg gtgttcaggt aaaaggtgag      3480
tttgttacgg accgccacgg ccgcattagc tattatgatg gtaatagcgg tgaccaaatt      3540
cgcaatcgtt tcgtgcgtaa tgcacagggt cagtggttct acttcgacaa taatggttat      3600
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caagtgaaag gcgaatttgt tactgatcgt tatggtcgta tcagctacta tgatggcaat      3720
tctggcgacc aaattcgcaa tcgctttgtt cgtaacgccc aaggtcaatg gttctatttc      3780
gacaacaacg gttacgcggt gaccggtgcc cgcacgatta atggtcaaca cttgtacttc      3840
cgtgccaacg gtgtccaggt gaagggtgaa tttgtgaccg accgctatgg tcgcatttct      3900
tactacgacg caaattccgg tgaacgcgtc cgtatcaatt aa                         3942
```

[0036]

<210> 12
<211> 1313
<212> PRT
<213> 变异链球菌(Streptococcus mutans)

<400> 12

```
Met Ile Asp Gly Lys Tyr Tyr Tyr Tyr Asp Asn Asn Gly Lys Val Arg
1               5                   10                  15

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

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

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

Arg Ser Ala Gln Ser Phe Glu His Val Asp His Tyr Leu Thr Ala Glu
65                  70                  75                  80

Ser Trp Tyr Arg Pro Lys Tyr Ile Leu Lys Asp Gly Lys Thr Trp Thr
                85                  90                  95

Gln Ser Thr Glu Lys Asp Phe Arg Pro Leu Leu Met Thr Trp Trp Pro
            100                 105                 110

Ser Gln Glu Thr Gln Arg Gln Tyr Val Asn Phe Met Asn Ala Gln Leu
        115                 120                 125
```

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

Ile Ala Ala Ala Thr Ile Gln Ala Lys Ile Glu Ala Lys Ile Thr Thr
145 150 155 160

Leu Lys Asn Thr Asp Trp Leu Arg Gln Thr Ile Ser Ala Phe Val Lys
165 170 175

Thr Gln Ser Ala Trp Asn Ser Asp Ser Glu Lys Pro Phe Asp Asp His
180 185 190

Leu Gln Asn Gly Ala Val Leu Tyr Asp Asn Glu Gly Lys Leu Thr Pro
195 200 205

Tyr Ala Asn Ser Asn Tyr Arg Ile Leu Asn Arg Thr Pro Thr Asn Gln
210 215 220

Thr Gly Lys Lys Asp Pro Arg Tyr Thr Ala Asp Asn Thr Ile Gly Gly
225 230 235 240

Tyr Glu Phe Leu Leu Ala Asn Asp Val Asp Asn Ser Asn Pro Val Val
245 250 255

Gln Ala Glu Gln Leu Asn Trp Leu His Phe Leu Met Asn Phe Gly Asn
260 265 270

[0037] Ile Tyr Ala Asn Asp Pro Asp Ala Asn Phe Asp Ser Ile Arg Val Asp
275 280 285

Ala Val Asp Asn Val Asp Ala Asp Leu Leu Gln Ile Ala Gly Asp Tyr
290 295 300

Leu Lys Ala Ala Lys Gly Ile His Lys Asn Asp Lys Ala Ala Asn Asp
305 310 315 320

His Leu Ser Ile Leu Glu Ala Trp Ser Asp Asn Asp Thr Pro Tyr Leu
325 330 335

His Asp Asp Gly Asp Asn Met Ile Asn Met Asp Asn Lys Leu Arg Leu
340 345 350

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

Asn Pro Leu Ile Thr Asn Ser Leu Val Asn Arg Thr Asp Asp Asn Ala
370 375 380

Glu Thr Ala Ala Val Pro Ser Tyr Ser Phe Ile Arg Ala His Asp Ser
385 390 395 400

Glu Val Gln Asp Leu Ile Arg Asp Ile Ile Lys Ala Glu Ile Asn Pro
405 410 415

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

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

Tyr Asn Thr Ala Leu Ser Tyr Ala Leu Leu Leu Thr Asn Lys Ser Ser
    450                 455                 460

Val Pro Arg Val Tyr Tyr Gly Asp Met Phe Thr Asp Asp Gly Gln Tyr
465                 470                 475                 480

Met Ala His Lys Thr Ile Asn Tyr Glu Ala Ile Glu Thr Leu Leu Lys
                485                 490                 495

Ala Arg Ile Lys Tyr Val Ser Gly Gly Gln Ala Met Arg Asn Gln Gln
            500                 505                 510

Val Gly Asn Ser Glu Ile Ile Thr Ser Val Arg Tyr Gly Lys Gly Ala
        515                 520                 525

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

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

Arg Val Val Val Asn Met Gly Ala Ala His Lys Asn Gln Ala Tyr Arg
                565                 570                 575
```

[0038]

```
Pro Leu Leu Leu Thr Thr Asp Asn Gly Ile Lys Ala Tyr His Ser Asp
            580                 585                 590

Gln Glu Ala Ala Gly Leu Val Arg Tyr Thr Asn Asp Arg Gly Glu Leu
        595                 600                 605

Ile Phe Thr Ala Ala Asp Ile Lys Gly Tyr Ala Asn Pro Gln Val Ser
    610                 615                 620

Gly Tyr Leu Gly Val Trp Val Pro Val Gly Ala Ala Ala Asp Gln Asp
625                 630                 635                 640

Val Arg Val Ala Ala Ser Thr Ala Pro Ser Thr Asp Gly Lys Ser Val
                645                 650                 655

His Gln Asn Ala Ala Leu Asp Ser Arg Val Met Phe Glu Gly Phe Ser
            660                 665                 670

Asn Phe Gln Ala Phe Ala Thr Lys Lys Glu Glu Tyr Thr Asn Val Val
        675                 680                 685

Ile Ala Lys Asn Val Asp Lys Phe Ala Glu Trp Gly Val Thr Asp Phe
    690                 695                 700

Glu Met Ala Pro Gln Tyr Val Ser Ser Thr Asp Gly Ser Phe Leu Asp
705                 710                 715                 720

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

Ile Ser Lys Pro Asn Lys Tyr Gly Thr Ala Asp Asp Leu Val Lys Ala
740 745 750

Ile Lys Ala Leu His Ser Lys Gly Ile Lys Val Met Ala Asp Trp Val
755 760 765

Pro Asp Gln Met Tyr Ala Leu Pro Glu Lys Glu Val Val Thr Ala Thr
770 775 780

Arg Val Asp Lys Tyr Gly Thr Pro Val Ala Gly Ser Gln Ile Lys Asn
785 790 795 800

Thr Leu Tyr Val Val Asp Gly Lys Ser Ser Gly Lys Asp Gln Gln Ala
805 810 815

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

Leu Phe Ala Arg Lys Gln Ile Ser Thr Gly Val Pro Met Asp Pro Ser
835 840 845

Val Lys Ile Lys Gln Trp Ser Ala Lys Tyr Phe Asn Gly Thr Asn Ile
850 855 860

Leu Gly Arg Gly Ala Gly Tyr Val Leu Lys Asp Gln Ala Thr Asn Thr
865 870 875 880

[0039] Tyr Phe Asn Ile Ser Asp Asn Lys Glu Ile Asn Phe Leu Pro Lys Thr
885 890 895

Leu Leu Asn Gln Asp Ser Gln Val Gly Phe Ser Tyr Asp Gly Lys Gly
900 905 910

Tyr Val Tyr Tyr Ser Thr Ser Gly Tyr Gln Ala Lys Asn Thr Phe Ile
915 920 925

Ser Glu Gly Asp Lys Trp Tyr Tyr Phe Asp Asn Asn Gly Tyr Met Val
930 935 940

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

Gly Leu Gln Leu Arg Asp Ala Ile Leu Lys Asn Glu Asp Gly Thr Tyr
965 970 975

Ala Tyr Tyr Gly Asn Asp Gly Arg Arg Tyr Glu Asn Gly Tyr Tyr Gln
980 985 990

Phe Met Ser Gly Val Trp Arg His Phe Asn Asn Gly Glu Met Ser Val
995 1000 1005

Gly Leu Thr Val Ile Asp Gly Gln Val Gln Tyr Phe Asp Glu Met
1010 1015 1020

Gly Tyr Gln Ala Lys Gly Lys Phe Val Thr Thr Ala Asp Gly Lys
1025 1030 1035

Ile Arg Tyr Phe Asp Lys Gln Ser Gly Asn Met Tyr Arg Asn Arg
1040 1045 1050

Phe Ile Glu Asn Glu Glu Gly Lys Trp Leu Tyr Leu Gly Glu Asp
1055 1060 1065

Gly Ala Ala Val Thr Gly Ser Gln Thr Ile Asn Gly Gln His Leu
1070 1075 1080

Tyr Phe Arg Ala Asn Gly Val Gln Val Lys Gly Glu Phe Val Thr
1085 1090 1095

Asp Arg His Gly Arg Ile Ser Tyr Tyr Asp Gly Asn Ser Gly Asp
1100 1105 1110

Gln Ile Arg Asn Arg Phe Val Arg Asn Ala Gln Gly Gln Trp Phe
1115 1120 1125

Tyr Phe Asp Asn Asn Gly Tyr Ala Val Thr Gly Ala Arg Thr Ile
1130 1135 1140

Asn Gly Gln His Leu Tyr Phe Arg Ala Asn Gly Val Gln Val Lys
1145 1150 1155

Gly Glu Phe Val Thr Asp Arg His Gly Arg Ile Ser Tyr Tyr Asp
1160 1165 1170

[0040] Gly Asn Ser Gly Asp Gln Ile Arg Asn Arg Phe Val Arg Asn Ala
1175 1180 1185

Gln Gly Gln Trp Phe Tyr Phe Asp Asn Asn Gly Tyr Ala Val Thr
1190 1195 1200

Gly Ala Arg Thr Ile Asn Gly Gln His Leu Tyr Phe Arg Ala Asn
1205 1210 1215

Gly Val Gln Val Lys Gly Glu Phe Val Thr Asp Arg Tyr Gly Arg
1220 1225 1230

Ile Ser Tyr Tyr Asp Gly Asn Ser Gly Asp Gln Ile Arg Asn Arg
1235 1240 1245

Phe Val Arg Asn Ala Gln Gly Gln Trp Phe Tyr Phe Asp Asn Asn
1250 1255 1260

Gly Tyr Ala Val Thr Gly Ala Arg Thr Ile Asn Gly Gln His Leu
1265 1270 1275

Tyr Phe Arg Ala Asn Gly Val Gln Val Lys Gly Glu Phe Val Thr
1280 1285 1290

Asp Arg Tyr Gly Arg Ile Ser Tyr Tyr Asp Ala Asn Ser Gly Glu
1295 1300 1305

Arg Val Arg Ile Asn
1310

<210> 13
<211> 3972
<212> DNA
<213> 蝙蝠齿链球菌（Streptococcus dentirousetti）

<400> 13
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gttagcgttg gcgatgccat tttctatttt gatgaaacgg gtgcctacaa agataccagc 120

aaagttgatg cggataagac cagctctagc gtcaatcaga ccacggaaac gttcgcagcg 180

aataaccgtg cgtatagcac cgcagccgag aactttgaag cgattgataa ctacctgact 240

gcggatagct ggtatcgtcc gaagtctatc ttgaaagatg gtacgacgtg gaccgaaagc 300

accaaggatg attttcgccc gctgctgatg gcgtggtggc cggataccga aaccaaacgt 360

aactacgtga actatatgaa caaggtggtc ggtatcgaca aaacgtacac cgcggaaacg 420

tcccaagctg acctgacggc ggcagccgaa ctggtgcagg cgcgtatcga gcagaaaatc 480

actagcgaaa agaatacgaa gtggctgcgt gaggcgattt ccgcgttcgt taagactcaa 540

ccgcagtgga atggcgagag cgagaaacct tatgatgacc acctgcaaaa tggtgcgctg 600

aagttcgaca atgaaaccag cctgaccccg gatacgcaga gcggctatcg catcctgaac 660

cgtaccccga cgaatcaaac cggtagcctg gacccgcgct tcacctttaa tcagaatgac 720

ccgctgggtg gttatgagta tttgctggct aatgatgtcg ataacagcaa cccggtcgtt 780

caggccgaga gcctgaactg gctgcattac ctgctgaatt ttggtagcat ttacgcgaat 840

gatccggagg ccaatttcga cagcatccgt gtggacgcgg tggacaatgt tgacgcagac 900

[0041] ctgctgcaaa ttagctcgga ttacctgaaa tcggcgtaca aaattgacaa gaacaacaaa 960

aatgcgaacg accacgttag catcgtcgag gcgtggagcg acaatgatac cccgtacctg 1020

aatgatgatg gcgacaatct gatgaacatg gataacaagt ttcgtctgag catgctgtgg 1080

agcctggcga agccaaccaa tgtccgtagc ggcttgaatc cgctgatcca caacagcgtg 1140

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ctgctgctga cgaacaaggg cagcattcca cgcatttact acggtgacat gtttacggat 1440

gacggtcagt atatggccaa caaaaccgtt aactatgacg ccattgagag cctgctgaaa 1500

gcacgtatga agtatgttag cggtggccaa gcgatgcaga attacaacat cggcaacggc 1560

gagattctga ccagcgtccg ttacggtaag ggtgccctga aacagagcga caaaggcgat 1620

aagactactc gtaccagcgg tattggcgtt gtgatgggta accagagcaa tttcagcctg 1680

gagggcaagg tggtggccct gaatatgggt gcaacgcata ccaaacagaa gtatcgtgca 1740

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gcaggcctga tcaaaacgac cgatgagaat ggttatttgt actttctgaa tgacgatctg 1860

aagggcgtgg ctaacccgca ggtcagcggc ttcctgcaag tgtgggttcc ggttggtgca 1920

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cctaagaagg aagtggttac cgttacccgt acggacaaat ttggcaatcc agtggcaggc 2400

agccaaatca accacacctt gtacgtcact gatactaagg gtagcggtga cgactaccag 2460

gcgaagtacg gtggcgcatt cctggatgaa ctgaaagaaa agtacccgga gctgtttacc 2520

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gcgaagtact tcaacggtag caatatcttg ggtcgcggtg cgaactacgt gctgtccgac 2640

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ctgggtaagg tcgtcgagag cggtatccgt ttcgacggta aaggttatat ctataacagc 2760

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[0042] gatcaagccg gccattggta ctacctgggt aaagatggtg tcgccgtgac gggtgcgcag 3240

accgttggca agcaacacct gtacttcgag gctaacggcc aacaagtaaa aggcgatttt 3300

gttaccgcca aggacggtaa gttgtatttt ctggacggtg actctggcga catgtggacc 3360

gataccttcg tccaggataa ggctggtcat tggttctatc tgggcaaaga cggtgcggcg 3420

gtaaccggtg cccagaccgt ccgtggtcag aagctgtact tcaaagcgaa tggccagcag 3480

gttaagggtg acattgtgaa aggcgcggat ggtaaaatcc gttactatga tgcaaattcc 3540

ggtgaccagg tttacaatcg cacggtgaaa ggctccgacg gcaagaccta tatcattggt 3600

aatgacggcg tcgcaatcac gcaaaccatc gccaaaggcc agaccatcaa ggatggcagc 3660

gttctgcgct tctatagcat ggagggtcag ctggtgaccg gcagcggctg gtattccaac 3720

gcgaaaggtc aatggttgta tgtcaagaac ggtcaagtcc tgacgggttt gcagacggtg 3780

ggcagccagc gtgtgtactt tgacgcaaat ggtattcaag cgaaaggtaa agcagtgcgt 3840

acctccgatg gcaaactgcg ttacttcgat gcgaacagcg gcagcatgat caccaatcag 3900

tggaaagaag ttaatggtca gtactactat ttcgacaaca acggtgttgc gatctatcgc 3960

ggttggaact aa 3972

<210> 14
<211> 1323
<212> PRT
<213> 蝙蝠齿链球菌（Streptococcus dentirousetti）

<400> 14

Met Val Asp Gly Lys Tyr Tyr Tyr Tyr Asp Ala Asp Gly Asn Val Lys
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Lys Asn Phe Ala Val Ser Val Gly Asp Ala Ile Phe Tyr Phe Asp Glu
20 25 30

Thr Gly Ala Tyr Lys Asp Thr Ser Lys Val Asp Ala Asp Lys Thr Ser
35 40 45

Ser Ser Val Asn Gln Thr Thr Glu Thr Phe Ala Ala Asn Asn Arg Ala
50 55 60

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

Ala Asp Ser Trp Tyr Arg Pro Lys Ser Ile Leu Lys Asp Gly Thr Thr
85 90 95

Trp Thr Glu Ser Thr Lys Asp Asp Phe Arg Pro Leu Leu Met Ala Trp
100 105 110

Trp Pro Asp Thr Glu Thr Lys Arg Asn Tyr Val Asn Tyr Met Asn Lys
115 120 125

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

Leu Thr Ala Ala Ala Glu Leu Val Gln Ala Arg Ile Glu Gln Lys Ile
145 150 155 160

[0043] Thr Ser Glu Lys Asn Thr Lys Trp Leu Arg Glu Ala Ile Ser Ala Phe
165 170 175

Val Lys Thr Gln Pro Gln Trp Asn Gly Glu Ser Glu Lys Pro Tyr Asp
180 185 190

Asp His Leu Gln Asn Gly Ala Leu Lys Phe Asp Asn Glu Thr Ser Leu
195 200 205

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

Asn Gln Thr Gly Ser Leu Asp Pro Arg Phe Thr Phe Asn Gln Asn Asp
225 230 235 240

Pro Leu Gly Gly Tyr Glu Tyr Leu Leu Ala Asn Asp Val Asp Asn Ser
245 250 255

Asn Pro Val Val Gln Ala Glu Ser Leu Asn Trp Leu His Tyr Leu Leu
260 265 270

Asn Phe Gly Ser Ile Tyr Ala Asn Asp Pro Glu Ala Asn Phe Asp Ser
275 280 285

Ile Arg Val Asp Ala Val Asp Asn Val Asp Ala Asp Leu Leu Gln Ile
290 295 300

Ser Ser Asp Tyr Leu Lys Ser Ala Tyr Lys Ile Asp Lys Asn Asn Lys
305 310 315 320

Asn Ala Asn Asp His Val Ser Ile Val Glu Ala Trp Ser Asp Asn Asp
325 330 335

Thr Pro Tyr Leu Asn Asp Asp Gly Asp Asn Leu Met Asn Met Asp Asn
340 345 350

Lys Phe Arg Leu Ser Met Leu Trp Ser Leu Ala Lys Pro Thr Asn Val
355 360 365

Arg Ser Gly Leu Asn Pro Leu Ile His Asn Ser Val Val Asp Arg Glu
370 375 380

Val Asp Asp Arg Glu Val Glu Ala Thr Pro Asn Tyr Ser Phe Ala Arg
385 390 395 400

Ala His Asp Ser Glu Val Gln Asp Leu Ile Arg Asp Ile Ile Lys Ala
405 410 415

Glu Ile Asn Pro Asn Ser Phe Gly Tyr Ser Phe Thr Gln Glu Glu Ile
420 425 430

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

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

[0044] Asn Lys Gly Ser Ile Pro Arg Ile Tyr Tyr Gly Asp Met Phe Thr Asp
465 470 475 480

Asp Gly Gln Tyr Met Ala Asn Lys Thr Val Asn Tyr Asp Ala Ile Glu
485 490 495

Ser Leu Leu Lys Ala Arg Met Lys Tyr Val Ser Gly Gly Gln Ala Met
500 505 510

Gln Asn Tyr Asn Ile Gly Asn Gly Glu Ile Leu Thr Ser Val Arg Tyr
515 520 525

Gly Lys Gly Ala Leu Lys Gln Ser Asp Lys Gly Asp Lys Thr Thr Arg
530 535 540

Thr Ser Gly Ile Gly Val Val Met Gly Asn Gln Ser Asn Phe Ser Leu
545 550 555 560

Glu Gly Lys Val Val Ala Leu Asn Met Gly Ala Thr His Thr Lys Gln
565 570 575

Lys Tyr Arg Ala Leu Met Val Ser Thr Glu Thr Gly Val Ala Ile Tyr
580 585 590

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

Glu Asn Gly Tyr Leu Tyr Phe Leu Asn Asp Asp Leu Lys Gly Val Ala
610 615 620

```
Asn Pro Gln Val Ser Gly Phe Leu Gln Val Trp Val Pro Val Gly Ala
625                 630                 635                 640

Pro Ala Asp Gln Asp Ile Arg Val Ala Ala Thr Asp Ala Ala Ser Thr
                645                 650                 655

Asp Gly Lys Ser Leu His Gln Asp Ala Ala Leu Asp Ser Arg Val Met
            660                 665                 670

Phe Glu Gly Phe Ser Asn Phe Gln Ser Phe Ala Thr Lys Glu Glu Glu
        675                 680                 685

Tyr Thr Asn Val Val Ile Ala Lys Asn Val Asp Lys Phe Val Ser Trp
    690                 695                 700

Gly Ile Thr Asp Phe Glu Met Ala Pro Gln Tyr Val Ser Ser Thr Asp
705                 710                 715                 720

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

Arg Tyr Asp Leu Gly Met Ser Lys Ala Asn Lys Tyr Gly Thr Ala Asp
            740                 745                 750

Gln Leu Val Ala Ala Ile Lys Ala Leu His Ala Lys Gly Leu Arg Val
        755                 760                 765
```

[0045]

```
Met Ala Asp Trp Val Pro Asp Gln Met Tyr Thr Phe Pro Lys Lys Glu
    770                 775                 780

Val Val Thr Val Thr Arg Thr Asp Lys Phe Gly Asn Pro Val Ala Gly
785                 790                 795                 800

Ser Gln Ile Asn His Thr Leu Tyr Val Thr Asp Thr Lys Gly Ser Gly
                805                 810                 815

Asp Asp Tyr Gln Ala Lys Tyr Gly Gly Ala Phe Leu Asp Glu Leu Lys
            820                 825                 830

Glu Lys Tyr Pro Glu Leu Phe Thr Lys Lys Gln Ile Ser Thr Gly Gln
        835                 840                 845

Ala Ile Asp Pro Ser Val Lys Ile Lys Gln Trp Ser Ala Lys Tyr Phe
    850                 855                 860

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

Gln Ala Ser Asn Lys Tyr Phe Asn Val Ala Glu Gly Lys Val Phe Leu
                885                 890                 895

Pro Ala Ala Met Leu Gly Lys Val Val Glu Ser Gly Ile Arg Phe Asp
            900                 905                 910

Gly Lys Gly Tyr Ile Tyr Asn Ser Ser Thr Thr Gly Glu Gln Val Lys
        915                 920                 925
```

Asp Ser Phe Ile Thr Glu Ala Gly Asn Leu Tyr Tyr Phe Gly Lys Asp
930 935 940

Gly Tyr Met Val Met Gly Ala Gln Asn Ile Gln Gly Ala Asn Tyr Tyr
945 950 955 960

Phe Leu Ala Asn Gly Ala Ala Leu Arg Asn Ser Ile Leu Thr Asp Gln
965 970 975

Asp Gly Lys Ser His Tyr Tyr Ala Asn Asp Gly Lys Arg Tyr Glu Asn
980 985 990

Gly Tyr Tyr Gln Phe Gly Asn Asp Ser Trp Arg Tyr Phe Glu Asn Gly
995 1000 1005

Val Met Ala Val Gly Leu Thr Arg Val Ala Gly His Asp Gln Tyr
1010 1015 1020

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

Arg Asp Gly Lys Val Arg Tyr Phe Asp Glu His Asn Gly Asn Ala
1040 1045 1050

Ala Thr Asn Thr Phe Ile Ser Asp Gln Ala Gly His Trp Tyr Tyr
1055 1060 1065

[0046] Leu Gly Lys Asp Gly Val Ala Val Thr Gly Ala Gln Thr Val Gly
1070 1075 1080

Lys Gln His Leu Tyr Phe Glu Ala Asn Gly Gln Gln Val Lys Gly
1085 1090 1095

Asp Phe Val Thr Ala Lys Asp Gly Lys Leu Tyr Phe Leu Asp Gly
1100 1105 1110

Asp Ser Gly Asp Met Trp Thr Asp Thr Phe Val Gln Asp Lys Ala
1115 1120 1125

Gly His Trp Phe Tyr Leu Gly Lys Asp Gly Ala Ala Val Thr Gly
1130 1135 1140

Ala Gln Thr Val Arg Gly Gln Lys Leu Tyr Phe Lys Ala Asn Gly
1145 1150 1155

Gln Gln Val Lys Gly Asp Ile Val Lys Gly Ala Asp Gly Lys Ile
1160 1165 1170

Arg Tyr Tyr Asp Ala Asn Ser Gly Asp Gln Val Tyr Asn Arg Thr
1175 1180 1185

Val Lys Gly Ser Asp Gly Lys Thr Tyr Ile Ile Gly Asn Asp Gly
1190 1195 1200

Val Ala Ile Thr Gln Thr Ile Ala Lys Gly Gln Thr Ile Lys Asp
1205 1210 1215

Gly Ser Val Leu Arg Phe Tyr Ser Met Glu Gly Gln Leu Val Thr
1220 1225 1230

Gly Ser Gly Trp Tyr Ser Asn Ala Lys Gly Gln Trp Leu Tyr Val
1235 1240 1245

Lys Asn Gly Gln Val Leu Thr Gly Leu Gln Thr Val Gly Ser Gln
1250 1255 1260

Arg Val Tyr Phe Asp Ala Asn Gly Ile Gln Ala Lys Gly Lys Ala
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Val Arg Thr Ser Asp Gly Lys Leu Arg Tyr Phe Asp Ala Asn Ser
1280 1285 1290

Gly Ser Met Ile Thr Asn Gln Trp Lys Glu Val Asn Gly Gln Tyr
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Tyr Tyr Phe Asp Asn Asn Gly Val Ala Ile Tyr Arg Gly Trp Asn
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<210> 15
<211> 4047
<212> DNA
<213> 口腔链球菌（Streptococcus oralis）

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agctggtatc gcccgaaatt catcctgaag gatggcaaga cgtggaccgc gagcacggaa 300

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ctgaactaca tgaaccagca gggtctgggt gcgggtgcgt ttgagaacaa agtggagcag 420

gccctgctga cgggtgcaag ccaacaggta caacgcaaga tcgaagagaa gattggtaaa 480

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<210> 16
<211> 1348
<212> PRT
<213> 口腔链球菌（Streptococcus oralis）

<400> 16

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Lys Asn Phe Ala Val Glu Leu Asn Gly Arg Ile Leu Tyr Phe Asp Ala
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[0049] Glu Thr Gly Ala Leu Val Asp Ser Asn Glu Tyr Gln Phe Gln Gln Gly
35 40 45

Thr Ser Ser Leu Asn Asn Glu Phe Ser Gln Lys Asn Ala Phe Tyr Gly
50 55 60

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

Ser Trp Tyr Arg Pro Lys Phe Ile Leu Lys Asp Gly Lys Thr Trp Thr
85 90 95

Ala Ser Thr Glu Thr Asp Leu Arg Pro Leu Leu Met Ala Trp Trp Pro
100 105 110

Asp Lys Arg Thr Gln Ile Asn Tyr Leu Asn Tyr Met Asn Gln Gln Gly
115 120 125

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

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

Glu Gly Asp Thr Lys Trp Leu Arg Thr Leu Met Gly Ala Phe Val Lys
165 170 175

Thr Gln Pro Asn Trp Asn Ile Lys Thr Glu Ser Glu Thr Thr Gly Thr
180 185 190

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

Lys Ser Pro His Ala Asp Ser Lys Phe Arg Leu Leu Asn Arg Thr Pro
    210                 215                 220

Thr Ser Gln Thr Gly Thr Pro Lys Tyr Phe Ile Asp Lys Ser Asn Gly
225                 230                 235                 240

Gly Tyr Glu Phe Leu Leu Ala Asn Asp Phe Asp Asn Ser Asn Pro Ala
                245                 250                 255

Val Gln Ala Glu Gln Leu Asn Trp Leu His Tyr Met Met Asn Phe Gly
            260                 265                 270

Ser Ile Val Ala Asn Asp Pro Thr Ala Asn Phe Asp Gly Val Arg Val
        275                 280                 285

Asp Ala Val Asp Asn Val Asn Ala Asp Leu Leu Gln Ile Ala Ser Asp
    290                 295                 300

Tyr Phe Lys Ser Arg Tyr Lys Val Gly Glu Ser Glu Glu Glu Ala Ile
305                 310                 315                 320

Lys His Leu Ser Ile Leu Glu Ala Trp Ser Asp Asn Asp Pro Asp Tyr
                325                 330                 335
```

[0050]

```
Asn Lys Asp Thr Lys Gly Ala Gln Leu Ala Ile Asp Asn Lys Leu Arg
            340                 345                 350

Leu Ser Leu Leu Tyr Ser Phe Met Arg Asn Leu Ser Ile Arg Ser Gly
        355                 360                 365

Val Glu Pro Thr Ile Thr Asn Ser Leu Asn Asp Arg Ser Ser Glu Lys
    370                 375                 380

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

Ser Glu Val Gln Thr Val Ile Ala Asp Ile Ile Arg Glu Asn Ile Asn
                405                 410                 415

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

Phe Lys Ile Tyr Asn Glu Asp Met Arg Lys Ala Asp Lys Lys Tyr Thr
        435                 440                 445

Gln Phe Asn Ile Pro Thr Ala His Ala Leu Met Leu Ser Asn Lys Asp
    450                 455                 460

Ser Ile Thr Arg Val Tyr Tyr Gly Asp Leu Tyr Thr Asp Asp Gly Gln
465                 470                 475                 480

Tyr Met Glu Lys Lys Ser Pro Tyr His Asp Ala Ile Asp Ala Leu Leu
                485                 490                 495
```

```
Arg Ala Arg Ile Lys Tyr Val Ala Gly Gly Gln Asp Met Lys Val Thr
            500                 505                 510

Tyr Met Gly Val Pro Arg Glu Ala Asp Lys Trp Ser Tyr Asn Gly Ile
        515                 520                 525

Leu Thr Ser Val Arg Tyr Gly Thr Gly Ala Asn Glu Ala Thr Asp Glu
    530                 535                 540

Gly Thr Ala Glu Thr Arg Thr Gln Gly Met Ala Val Ile Ala Ser Asn
545                 550                 555                 560

Asn Pro Asn Leu Lys Leu Asn Glu Trp Asp Lys Leu Gln Val Asn Met
                565                 570                 575

Gly Ala Ala His Lys Asn Gln Tyr Tyr Arg Pro Val Leu Leu Thr Thr
            580                 585                 590

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

Leu Trp Lys Lys Thr Asp Ala Asn Gly Ile Leu Thr Phe Asp Met Asn
    610                 615                 620

Asp Ile Ala Gly Tyr Ser Asn Val Gln Val Ser Gly Tyr Leu Ala Val
625                 630                 635                 640
```

[0051]

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Trp Val Pro Val Gly Ala Lys Ala Asp Gln Asp Ala Arg Thr Thr Ala
                645                 650                 655

Ser Lys Lys Lys Asn Ala Ser Gly Gln Val Tyr Glu Ser Ser Ala Ala
            660                 665                 670

Leu Asp Ser Gln Leu Ile Tyr Glu Gly Phe Ser Asn Phe Gln Asp Phe
        675                 680                 685

Ala Thr Arg Asp Asp Gln Tyr Thr Asn Lys Val Ile Ala Lys Asn Val
    690                 695                 700

Asn Leu Phe Lys Glu Trp Gly Val Thr Ser Phe Glu Leu Pro Pro Gln
705                 710                 715                 720

Tyr Val Ser Ser Gln Asp Gly Thr Phe Leu Asp Ser Ile Ile Gln Asn
                725                 730                 735

Gly Tyr Ala Phe Glu Asp Arg Tyr Asp Met Ala Met Ser Lys Asn Asn
            740                 745                 750

Lys Tyr Gly Ser Leu Lys Asp Leu Leu Asn Ala Leu Arg Ala Leu His
        755                 760                 765

Ser Val Asn Ile Gln Ala Ile Ala Asp Trp Val Pro Asp Gln Ile Tyr
    770                 775                 780

Asn Leu Pro Gly Lys Glu Val Val Thr Ala Thr Arg Val Asn Asn Tyr
785                 790                 795                 800
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Gly Thr Tyr Arg Glu Gly Ala Glu Ile Lys Glu Lys Leu Tyr Val Ala
805 810 815

Asn Ser Lys Thr Asn Glu Thr Asp Phe Gln Gly Lys Tyr Gly Gly Ala
820 825 830

Phe Leu Asp Glu Leu Lys Ala Lys Tyr Pro Glu Ile Phe Glu Arg Val
835 840 845

Gln Ile Ser Asn Gly Gln Lys Met Thr Thr Asp Glu Lys Ile Thr Lys
850 855 860

Trp Ser Ala Lys Tyr Phe Asn Gly Thr Asn Ile Leu Gly Arg Gly Ala
865 870 875 880

Tyr Tyr Val Leu Lys Asp Trp Ala Ser Asn Asp Tyr Leu Thr Asn Arg
885 890 895

Asn Gly Glu Ile Val Leu Pro Lys Gln Leu Val Asn Lys Asn Ser Tyr
900 905 910

Thr Gly Phe Val Ser Asp Ala Asn Gly Thr Lys Phe Tyr Ser Thr Ser
915 920 925

Gly Tyr Gln Ala Lys Asn Ser Phe Ile Gln Asp Glu Asn Gly Asn Trp
930 935 940

[0052] Tyr Tyr Phe Asp Lys Arg Gly Tyr Leu Val Thr Gly Ala His Glu Ile
945 950 955 960

Asp Gly Lys His Val Tyr Phe Leu Lys Asn Gly Ile Gln Leu Arg Asp
965 970 975

Ser Ile Arg Glu Asp Glu Asn Gly Asn Gln Tyr Tyr Tyr Asp Gln Thr
980 985 990

Gly Ala Gln Val Leu Asn Arg Tyr Tyr Thr Thr Asp Gly Gln Asn Trp
995 1000 1005

Arg Tyr Phe Asp Ala Lys Gly Val Met Ala Arg Gly Leu Val Lys
1010 1015 1020

Ile Gly Asp Gly Gln Gln Phe Phe Asp Glu Asn Gly Tyr Gln Val
1025 1030 1035

Lys Gly Lys Ile Val Ser Ala Lys Asp Gly Lys Leu Arg Tyr Phe
1040 1045 1050

Asp Lys Asp Ser Gly Asn Ala Val Ile Asn Arg Phe Ala Gln Gly
1055 1060 1065

Asp Asn Pro Ser Asp Trp Tyr Tyr Phe Gly Val Glu Phe Ala Lys
1070 1075 1080

Leu Thr Gly Leu Gln Lys Ile Gly Gln Gln Thr Leu Tyr Phe Asp
1085 1090 1095

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Gln Asp  Gly Lys Gln Val Lys  Gly Lys Ile Val Thr  Leu Ser Asp
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Lys Ser  Ile Arg Tyr Phe Asp  Ala Asn Ser Gly Glu  Met Ala Val
    1115                 1120                 1125

Gly Lys  Phe Ala Glu Gly Ala  Lys Asn Glu Trp Tyr  Tyr Phe Asp
    1130                 1135                 1140

Lys Thr  Gly Lys Ala Val Thr  Gly Leu Gln Lys Ile  Gly Lys Gln
    1145                 1150                 1155

Thr Leu  Tyr Phe Asp Gln Asp  Gly Lys Gln Val Lys  Gly Lys Val
    1160                 1165                 1170

Val Thr  Leu Ala Asp Lys Ser  Ile Arg Tyr Phe Asp  Ala Asp Ser
    1175                 1180                 1185

Gly Glu  Met Ala Val Gly Lys  Phe Ala Glu Gly Ala  Lys Asn Glu
    1190                 1195                 1200

Trp Tyr  Tyr Phe Asp Gln Thr  Gly Lys Ala Val Thr  Gly Leu Gln
    1205                 1210                 1215

Lys Ile  Asp Lys Gln Thr Leu  Tyr Phe Asp Gln Asp  Gly Lys Gln
    1220                 1225                 1230

Val Lys  Gly Lys Ile Val Thr  Leu Ser Asp Lys Ser  Ile Arg Tyr
    1235                 1240                 1245

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

Gly Ser  Gln Asn Glu Trp Tyr  Tyr Phe Asp Gln Ala  Gly Lys Ala
    1265                 1270                 1275

Val Thr  Gly Leu Gln Gln Val  Gly Gln Gln Thr Leu  Tyr Phe Thr
    1280                 1285                 1290

Gln Asp  Gly Lys Gln Val Lys  Gly Lys Val Val Asp  Val Asn Gly
    1295                 1300                 1305

Val Ser  Arg Tyr Phe Asp Ala  Asn Ser Gly Asp Met  Ala Arg Ser
    1310                 1315                 1320

Lys Trp  Ile Gln Leu Glu Asp  Gly Ser Trp Met Tyr  Phe Asp Arg
    1325                 1330                 1335

Asp Gly  Arg Gly Gln Asn Phe  Gly Arg Asn
    1340                 1345
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[0053]

<210> 17
<211> 4047
<212> DNA
<213> 血链球菌（Streptococcus sanguinis）

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cgtggtcgtc gtttcggttg gaactaa 4047

<210> 18
<211> 1348
<212> PRT
<213> 血链球菌（Streptococcus sanguinis）

<400> 18

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Glu Thr Gly Ala Leu Ile Asp Ser Ala Glu Tyr Gln Phe Gln Gln Gly
35 40 45

Thr Ser Ser Leu Asn Asn Glu Phe Thr Gln Lys Asn Ala Phe Tyr Gly
50 55 60

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

Ser Trp Tyr Arg Pro Lys Phe Ile Leu Lys Asp Gly Lys Thr Trp Thr
85 90 95

Ala Ser Thr Glu Ile Asp Leu Arg Pro Leu Leu Met Ala Trp Trp Pro
100 105 110

Asp Lys Gln Thr Gln Val Ser Tyr Leu Asn Tyr Met Asn Gln Gln Gly
115 120 125

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

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

Glu Gly Asp Thr Lys Trp Leu Arg Thr Leu Met Gly Ala Phe Val Lys
165 170 175

Thr Gln Pro Asn Trp Asn Ile Lys Thr Glu Ser Glu Thr Thr Gly Thr
180 185 190

[0056] Asn Lys Asp His Leu Gln Gly Gly Ala Leu Leu Tyr Ser Asn Ser Asp
195 200 205

Lys Thr Ser His Ala Asn Ser Lys Tyr Arg Ile Leu Asn Arg Thr Pro
210 215 220

Thr Asn Gln Thr Gly Thr Pro Lys Tyr Phe Ile Asp Lys Ser Asn Gly
225 230 235 240

Gly Tyr Glu Phe Leu Leu Ala Asn Asp Phe Asp Asn Ser Asn Pro Ala
245 250 255

Val Gln Ala Glu Gln Leu Asn Trp Leu His Phe Met Met Asn Phe Gly
260 265 270

Ser Ile Val Ala Asn Asp Pro Thr Ala Asn Phe Asp Gly Val Arg Val
275 280 285

Asp Ala Val Asp Asn Val Asn Ala Asp Leu Leu Gln Ile Ala Ser Asp
290 295 300

Tyr Phe Lys Ser Arg Tyr Lys Val Gly Glu Ser Glu Glu Glu Ala Ile
305 310 315 320

Lys His Leu Ser Ile Leu Glu Ala Trp Ser Asp Asn Asp Pro Asp Tyr
325 330 335

Asn Lys Asp Thr Lys Gly Ala Gln Leu Pro Ile Asp Asn Lys Leu Arg
340 345 350

Leu Ser Leu Leu Tyr Ser Phe Met Arg Lys Leu Ser Ile Arg Ser Gly
355 360 365

Val Glu Pro Thr Ile Thr Asn Ser Leu Asn Asp Arg Ser Thr Glu Lys
370 375 380

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

Ser Glu Val Gln Thr Val Ile Ala Asp Ile Ile Arg Glu Asn Ile Asn
405 410 415

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

Phe Lys Ile Tyr Asn Glu Asp Met Arg Lys Ala Asp Lys Lys Tyr Thr
435 440 445

Gln Phe Asn Ile Pro Thr Ala His Ala Leu Met Leu Ser Asn Lys Asp
450 455 460

Ser Ile Thr Arg Val Tyr Tyr Gly Asp Leu Tyr Thr Asp Asp Gly Gln
465 470 475 480

Tyr Met Glu Lys Lys Ser Pro Tyr His Asp Ala Ile Asp Ala Leu Leu
485 490 495

[0057] Arg Ala Arg Ile Lys Tyr Val Ala Gly Gly Gln Asp Met Lys Val Thr
500 505 510

Tyr Met Gly Val Pro Arg Glu Ala Asp Lys Trp Ser Tyr Asn Gly Ile
515 520 525

Leu Thr Ser Val Arg Tyr Gly Thr Gly Ala Asn Glu Ala Thr Asp Glu
530 535 540

Gly Thr Ala Glu Thr Arg Thr Gln Gly Met Ala Val Ile Ala Ser Asn
545 550 555 560

Asn Pro Asn Leu Lys Leu Asn Glu Trp Asp Lys Leu Gln Val Asn Met
565 570 575

Gly Ala Ala His Lys Asn Gln Tyr Tyr Arg Pro Val Leu Leu Thr Thr
580 585 590

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

Leu Trp Lys Lys Thr Asp Ala Asn Gly Ile Leu Thr Phe Asp Met Asn
610 615 620

Asp Ile Ala Gly Tyr Ser Asn Val Gln Val Ser Gly Tyr Leu Ala Val
625 630 635 640

Trp Val Pro Val Gly Ala Lys Ala Asp Gln Asp Ala Arg Val Thr Ala
645 650 655

Ser Lys Lys Lys Asn Ala Ser Gly Gln Val Tyr Glu Ser Ser Ala Ala
660 665 670

Leu Asp Ser Gln Leu Ile Tyr Glu Gly Phe Ser Asn Phe Gln Asp Phe
675 680 685

Ala Thr Arg Asp Asp Gln Tyr Thr Asn Lys Val Ile Ala Lys Asn Val
690 695 700

Asn Leu Phe Lys Glu Trp Gly Val Thr Ser Phe Glu Leu Pro Pro Gln
705 710 715 720

Tyr Val Ser Ser Gln Asp Gly Thr Phe Leu Asp Ser Ile Ile Gln Asn
725 730 735

Gly Tyr Ala Phe Glu Asp Arg Tyr Asp Met Ala Met Ser Lys Asn Asn
740 745 750

Lys Tyr Gly Ser Leu Asn Asp Leu Leu Asn Ala Leu Arg Ala Leu His
755 760 765

Ser Val Asn Ile Gln Ala Ile Ala Asp Trp Val Pro Asp Gln Ile Tyr
770 775 780

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

[0058] Gly Thr Tyr Arg Glu Gly Ser Glu Ile Lys Glu Asn Leu Tyr Val Ala
805 810 815

Asn Thr Lys Thr Asn Gly Thr Asp Tyr Gln Gly Lys Tyr Gly Gly Ala
820 825 830

Phe Leu Asp Glu Leu Lys Ala Lys Tyr Pro Glu Ile Phe Glu Arg Val
835 840 845

Gln Ile Ser Asn Gly Gln Lys Met Thr Thr Asp Glu Lys Ile Thr Lys
850 855 860

Trp Ser Ala Lys His Phe Asn Gly Thr Asn Ile Leu Gly Arg Gly Ala
865 870 875 880

Tyr Tyr Val Leu Lys Asp Trp Ala Ser Asn Glu Tyr Leu Asn Asn Lys
885 890 895

Asn Gly Glu Met Val Leu Pro Lys Gln Leu Val Asn Lys Asn Ala Tyr
900 905 910

Thr Gly Phe Val Ser Asp Ala Ser Gly Thr Lys Tyr Tyr Ser Thr Ser
915 920 925

Gly Tyr Gln Ala Arg Asn Ser Phe Ile Gln Asp Glu Asn Gly Asn Trp
930 935 940

Tyr Tyr Phe Asn Asn Arg Gly Tyr Leu Val Thr Gly Ala Gln Glu Ile
945 950 955 960

Asp Gly Lys Gln Leu Tyr Phe Leu Lys Asn Gly Ile Gln Leu Arg Asp
965 970 975

Ser Leu Arg Glu Asp Glu Asn Gly Asn Gln Tyr Tyr Tyr Asp Lys Thr
980 985 990

Gly Ala Gln Val Leu Asn Arg Tyr Tyr Thr Thr Asp Gly Gln Asn Trp
995 1000 1005

Arg Tyr Phe Asp Val Lys Gly Val Met Ala Arg Gly Leu Val Thr
1010 1015 1020

Met Gly Gly Asn Gln Gln Phe Phe Asp Gln Asn Gly Tyr Gln Val
1025 1030 1035

Lys Gly Lys Ile Ala Arg Ala Lys Asp Gly Lys Leu Arg Tyr Phe
1040 1045 1050

Asp Lys Asp Ser Gly Asn Ala Ala Ala Asn Arg Phe Ala Gln Gly
1055 1060 1065

Asp Asn Pro Ser Asp Trp Tyr Tyr Phe Gly Ala Asp Gly Val Ala
1070 1075 1080

Val Thr Gly Leu Gln Lys Val Gly Gln Gln Thr Leu Tyr Phe Asp
1085 1090 1095

[0059] Gln Asp Gly Lys Gln Val Lys Gly Lys Val Val Thr Leu Ala Asp
1100 1105 1110

Lys Ser Ile Arg Tyr Phe Asp Ala Asn Ser Gly Glu Met Ala Val
1115 1120 1125

Asn Lys Phe Val Glu Gly Ala Lys Asn Val Trp Tyr Tyr Phe Asp
1130 1135 1140

Gln Ala Gly Lys Ala Val Thr Gly Leu Gln Thr Ile Asn Lys Gln
1145 1150 1155

Val Leu Tyr Phe Asp Gln Asp Gly Lys Gln Val Lys Gly Lys Val
1160 1165 1170

Val Thr Leu Ala Asp Lys Ser Ile Arg Tyr Phe Asp Ala Asn Ser
1175 1180 1185

Gly Glu Met Ala Val Gly Lys Phe Ala Glu Gly Ala Lys Asn Glu
1190 1195 1200

Trp Tyr Tyr Phe Asp Gln Ala Gly Lys Ala Val Thr Gly Leu Gln
1205 1210 1215

Lys Ile Gly Gln Gln Thr Leu Tyr Phe Asp Gln Asn Gly Lys Gln
1220 1225 1230

Val Lys Gly Lys Val Val Thr Leu Ala Asp Lys Ser Ile Arg Tyr
1235 1240 1245

Phe Asp Ala Asn Ser Gly Glu Met Ala Ser Asn Lys Phe Val Glu
1250 1255 1260

Gly Ala Lys Asn Glu Trp Tyr Tyr Phe Asp Gln Ala Gly Lys Ala
1265 1270 1275

Val Thr Gly Leu Gln Gln Ile Gly Gln Gln Thr Leu Tyr Phe Asp
1280 1285 1290

Gln Asn Gly Lys Gln Val Lys Gly Lys Ile Val Tyr Val Asn Gly
1295 1300 1305

Ala Asn Arg Tyr Phe Asp Ala Asn Ser Gly Glu Met Ala Arg Asn
1310 1315 1320

Lys Trp Ile Gln Leu Glu Asp Gly Ser Trp Met Tyr Phe Asp Arg
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Asn Gly Arg Gly Arg Arg Phe Gly Trp Asn
1340 1345

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acgtacagct tcacccaagg cactaccaat attgtggacg gttttagcat taacaaccgt 180

gcgtatgact ccagcgaggc ctctttcgag ctgattgacg gttatctgac tgcggactct 240

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aagtccacgc aatggctgcg tgaaacgatc agcgcctttg taaaaaccca gccgcaatgg 540

aacaaagaga ctgagaacta cagcaagggc ggtggtgagg accatctgca aggtggtgcc 600

ctgctgtatg ttaatgactc tcgtaccccg tgggcgaaca gcaactatcg tttgctgaac 660

cgcacggcga ccaaccagac cggtacgatc gacaagagca tcctggacga gcagagcgat 720

ccgaatcaca tgggtggttt tgatttcttg ctggctaatg acgttgactt gagcaatccg 780

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gcggacatgc tgcaattgta caccaactat ttccgcgaat actatggtgt caacaaaagc 960

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accagcgacg cagaggctat tgccgcaggc tatgtcaaag aaaccgatgg caatggcgtg 1980

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tga 4023

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[0062] Glu Asn Phe Ala Ile Thr Val Asn Gly Gln Leu Leu Tyr Phe Gly Lys
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Asp Gly Ala Leu Thr Ser Ser Ser Thr Tyr Ser Phe Thr Gln Gly Thr
35 40 45

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

Ser Glu Ala Ser Phe Glu Leu Ile Asp Gly Tyr Leu Thr Ala Asp Ser
65 70 75 80

Trp Tyr Arg Pro Ala Ser Ile Ile Lys Asp Gly Val Thr Trp Gln Ala
85 90 95

Ser Thr Ala Glu Asp Phe Arg Pro Leu Leu Met Ala Trp Trp Pro Asn
100 105 110

Val Asp Thr Gln Val Asn Tyr Leu Asn Tyr Met Ser Lys Val Phe Asn
115 120 125

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

Ala Ala Lys Asp Ile Gln Ile Lys Ile Glu Gln Lys Ile Gln Ala Glu
145 150 155 160

Lys Ser Thr Gln Trp Leu Arg Glu Thr Ile Ser Ala Phe Val Lys Thr
165 170 175

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Gln Pro Gln Trp Asn Lys Glu Thr Glu Asn Tyr Ser Lys Gly Gly Gly
            180                 185                 190

Glu Asp His Leu Gln Gly Gly Ala Leu Leu Tyr Val Asn Asp Ser Arg
        195                 200                 205

Thr Pro Trp Ala Asn Ser Asn Tyr Arg Leu Leu Asn Arg Thr Ala Thr
    210                 215                 220

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

Pro Asn His Met Gly Gly Phe Asp Phe Leu Leu Ala Asn Asp Val Asp
                245                 250                 255

Leu Ser Asn Pro Val Val Gln Ala Glu Gln Leu Asn Gln Ile His Tyr
            260                 265                 270

Leu Met Asn Trp Gly Ser Ile Val Met Gly Asp Lys Asp Ala Asn Phe
        275                 280                 285

Asp Gly Ile Arg Val Asp Ala Val Asp Asn Val Asp Ala Asp Met Leu
    290                 295                 300

Gln Leu Tyr Thr Asn Tyr Phe Arg Glu Tyr Tyr Gly Val Asn Lys Ser
305                 310                 315                 320
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[0063]

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Glu Ala Asn Ala Leu Ala His Ile Ser Val Leu Glu Ala Trp Ser Leu
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Asn Asp Asn His Tyr Asn Asp Lys Thr Asp Val Ala Ala Leu Ala Met
            340                 345                 350

Glu Asn Lys Gln Arg Leu Ala Leu Leu Phe Ser Leu Ala Lys Pro Ile
        355                 360                 365

Lys Glu Arg Thr Pro Ala Val Ser Pro Leu Tyr Asn Asn Thr Phe Asn
    370                 375                 380

Thr Thr Gln Arg Asp Glu Lys Thr Asp Trp Ile Asn Lys Asp Gly Ser
385                 390                 395                 400

Lys Ala Tyr Asn Glu Asp Gly Thr Val Lys Lys Ser Thr Ile Gly Lys
                405                 410                 415

Tyr Asn Glu Lys Tyr Gly Asp Ala Ser Gly Asn Tyr Val Phe Ile Arg
            420                 425                 430

Ala His Asp Asn Asn Val Gln Asp Ile Ile Ala Glu Ile Ile Lys Lys
        435                 440                 445

Glu Ile Asn Glu Lys Ser Asp Gly Phe Thr Ile Thr Asp Ser Glu Met
    450                 455                 460

Lys Arg Ala Phe Glu Ile Tyr Asn Lys Asp Met Leu Ser Asn Asp Lys
465                 470                 475                 480
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Lys Tyr Thr Leu Asn Asn Ile Pro Ala Ala Tyr Ala Val Met Leu Gln
485 490 495

Asn Met Glu Thr Ile Thr Arg Val Tyr Tyr Gly Asp Leu Tyr Thr Asp
500 505 510

Asp Gly Asn Tyr Met Glu Ala Lys Ser Pro Tyr Tyr Asp Thr Ile Val
515 520 525

Asn Leu Met Lys Ser Arg Ile Lys Tyr Val Ser Gly Gly Gln Ala Gln
530 535 540

Arg Ser Tyr Trp Leu Pro Thr Asp Gly Lys Met Asp Lys Ser Asp Val
545 550 555 560

Glu Leu Tyr Arg Thr Asn Glu Val Tyr Thr Ser Val Arg Tyr Gly Lys
565 570 575

Asp Ile Met Thr Ala Asp Asp Thr Gln Gly Ser Lys Tyr Ser Arg Thr
580 585 590

Ser Gly Gln Val Thr Leu Val Val Asn Asn Pro Lys Leu Thr Leu Asp
595 600 605

Gln Ser Ala Lys Leu Asn Val Val Met Gly Lys Ile His Ala Asn Gln
610 615 620

[0064] Lys Tyr Arg Ala Leu Ile Val Gly Thr Pro Asn Gly Ile Lys Asn Phe
625 630 635 640

Thr Ser Asp Ala Glu Ala Ile Ala Ala Gly Tyr Val Lys Glu Thr Asp
645 650 655

Gly Asn Gly Val Leu Thr Phe Gly Ala Asn Asp Ile Lys Gly Tyr Glu
660 665 670

Thr Phe Asp Met Ser Gly Phe Val Ala Val Trp Val Pro Val Gly Ala
675 680 685

Ser Asp Asp Gln Asp Ile Arg Val Ala Ala Ser Thr Ala Ala Lys Lys
690 695 700

Glu Gly Glu Leu Thr Leu Lys Ala Thr Glu Ala Tyr Asp Ser Gln Leu
705 710 715 720

Ile Tyr Glu Gly Phe Ser Asn Phe Gln Thr Ile Pro Asp Gly Ser Asp
725 730 735

Pro Ser Val Tyr Thr Asn Arg Lys Ile Ala Glu Asn Val Asp Leu Phe
740 745 750

Lys Ser Trp Gly Val Thr Ser Phe Glu Met Ala Pro Gln Phe Val Ser
755 760 765

Ala Asp Asp Gly Thr Phe Leu Asp Ser Val Ile Gln Asn Gly Tyr Ala
770 775 780

Phe Ala Asp Arg Tyr Asp Leu Ala Met Ser Lys Asn Asn Lys Tyr Gly
785 790 795 800

Ser Lys Glu Asp Leu Arg Asn Ala Leu Lys Ala Leu His Lys Ala Gly
805 810 815

Ile Gln Ala Ile Ala Asp Trp Val Pro Asp Gln Ile Tyr Gln Leu Pro
820 825 830

Gly Lys Glu Val Val Thr Ala Thr Arg Thr Asp Gly Ala Gly Arg Lys
835 840 845

Ile Ser Asp Ala Ile Ile Asp His Ser Leu Tyr Val Ala Asn Ser Lys
850 855 860

Ser Ser Gly Lys Asp Tyr Gln Ala Lys Tyr Gly Gly Glu Phe Leu Ala
865 870 875 880

Glu Leu Lys Ala Lys Tyr Pro Glu Met Phe Lys Val Asn Met Ile Ser
885 890 895

Thr Gly Lys Pro Ile Asp Asp Ser Val Lys Leu Lys Gln Trp Lys Ala
900 905 910

Glu Tyr Phe Asn Gly Thr Asn Val Leu Asp Arg Gly Val Gly Tyr Val
915 920 925

[0065] Leu Ser Asp Glu Ala Thr Gly Lys Tyr Phe Thr Val Thr Lys Glu Gly
930 935 940

Asn Phe Ile Pro Leu Gln Leu Lys Gly Asn Lys Lys Val Ile Thr Gly
945 950 955 960

Phe Ser Ser Asp Gly Lys Gly Ile Thr Tyr Phe Gly Thr Ser Gly Asn
965 970 975

Gln Ala Lys Ser Ala Phe Val Thr Phe Asn Gly Asn Thr Tyr Tyr Phe
980 985 990

Asp Ala Arg Gly His Met Val Thr Asn Gly Glu Tyr Ser Pro Asn Gly
995 1000 1005

Lys Asp Val Tyr Arg Phe Leu Pro Asn Gly Ile Met Leu Ser Asn
1010 1015 1020

Ala Phe Tyr Val Asp Gly Asn Gly Asn Thr Tyr Leu Tyr Asn Ser
1025 1030 1035

Lys Gly Gln Met Tyr Lys Gly Gly Tyr Ser Lys Phe Asp Val Thr
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Glu Thr Lys Asp Gly Lys Glu Ser Lys Val Val Lys Phe Arg Tyr
1055 1060 1065

Phe Thr Asn Glu Gly Val Met Ala Lys Gly Val Thr Val Val Asp
1070 1075 1080

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Gly Phe  Thr Gln Tyr Phe Asn  Glu Asp Gly Ile Gln  Ser Lys Asp
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Glu Leu  Val Thr Tyr Asn Gly  Lys Thr Tyr Tyr Phe  Glu Ala His
    1100                 1105                 1110

Thr Gly  Asn Ala Ile Lys Asn  Thr Trp Arg Asn Ile  Lys Gly Lys
    1115                 1120                 1125

Trp Tyr  His Phe Asp Ala Asn  Gly Val Ala Ala Thr  Gly Ala Gln
    1130                 1135                 1140

Val Ile  Asn Gly Gln His Leu  Tyr Phe Asn Glu Asp  Gly Ser Gln
    1145                 1150                 1155

Val Lys  Gly Ser Ile Val Lys  Asn Ala Asp Gly Thr  Phe Ser Lys
    1160                 1165                 1170

Tyr Lys  Asp Ser Ser Gly Asp  Leu Val Val Asn Glu  Phe Phe Thr
    1175                 1180                 1185

Thr Gly  Asp Asn Val Trp Tyr  Tyr Ala Gly Ala Asn  Gly Lys Thr
    1190                 1195                 1200

Val Thr  Gly Ala Gln Val Ile  Asn Gly Gln His Leu  Phe Phe Lys
    1205                 1210                 1215
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[0066]

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Glu Asp  Gly Ser Gln Val Lys  Gly Asp Phe Val Lys  Asn Ser Asp
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Gly Thr  Tyr Ser Lys Tyr Asp  Ala Ala Ser Gly Glu  Arg Leu Thr
    1235                 1240                 1245

Asn Glu  Phe Phe Thr Thr Gly  Asp Asn His Trp Tyr  Tyr Ile Gly
    1250                 1255                 1260

Ala Asn  Gly Lys Thr Val Thr  Gly Glu Val Lys Ile  Gly Asp Asp
    1265                 1270                 1275

Thr Tyr  Phe Phe Ala Lys Asp  Gly Lys Gln Leu Lys  Gly Gln Ile
    1280                 1285                 1290

Val Thr  Thr Arg Ser Gly Arg  Ile Ser Tyr Tyr Phe  Gly Asp Ser
    1295                 1300                 1305

Gly Lys  Lys Ala Ile Ser Thr  Trp Val Glu Ile Gln  Pro Gly Val
    1310                 1315                 1320

Phe Val  Phe Phe Asp Lys Asn  Gly Leu Ala Tyr Pro  Pro Glu Asn
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Met Asn
    1340

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agcgccgata acaacgttac cgagaaacaa tctgatgatc acgcgctgga taatgaaaag 240

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<213>  肠膜明串珠菌（Leuconostoc mesenteroides）

<400>  22

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

Asp Asn Val Thr Thr Ala Ala Ser Asp Thr Thr Gln Ser Ala Asp Asn
    50                  55                  60

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

Val Asp Asn Lys Gln Asp Glu Val Ala Gln Thr Asn Val Thr Ser Lys
                85                  90                  95

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

[0069]
Thr Thr Asp Glu Thr Gln Gln Val Ser Gly Lys Tyr Val Glu Lys Asp
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Gly Ser Trp Tyr Tyr Tyr Phe Asp Asp Gly Lys Asn Ala Lys Gly Leu
    130                 135                 140

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

Val Lys Gly Gln Tyr Val Thr Ile Asp Asn Gln Thr Tyr Tyr Phe Asp
                165                 170                 175

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

Ile Val Ala Phe Asn Asp Glu Gly Gln Gln Ile Phe Asn Gln Tyr Tyr
        195                 200                 205

Gln Ser Glu Asn Gly Thr Thr Tyr Tyr Phe Asp Asp Lys Gly His Ala
    210                 215                 220

Ala Thr Gly Ile Lys Asn Ile Glu Gly Lys Asn Tyr Tyr Phe Asp Asn
225                 230                 235                 240

Leu Gly Gln Leu Lys Lys Gly Phe Ser Gly Val Ile Asp Gly Gln Ile
                245                 250                 255

Met Thr Phe Asp Gln Glu Thr Gly Gln Glu Val Ser Asn Thr Thr Ser
            260                 265                 270
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Glu Ile Lys Glu Gly Leu Thr Thr Gln Asn Thr Asp Tyr Ser Glu His
        275                 280                 285

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

Gly Thr Asp Trp Glu Pro Ser Thr Asp Thr Asp Phe Arg Pro Ile Leu
                325                 330                 335

Ser Val Trp Trp Pro Asp Lys Asn Thr Gln Val Asn Tyr Leu Asn Tyr
            340                 345                 350

Met Ala Asp Leu Gly Phe Ile Ser Asn Ala Asp Ser Phe Glu Thr Gly
        355                 360                 365

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

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

Ala Met Ala Ala Phe Ile Val Thr Gln Pro Gln Trp Asn Glu Thr Ser
                405                 410                 415
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[0070]

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Glu Asp Met Ser Asn Asp His Leu Gln Asn Gly Ala Leu Thr Tyr Val
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Arg Thr Pro Thr Asn Gln Thr Gly Glu Gln Ala Tyr Asn Leu Asp Asn
    450                 455                 460

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

Asn Pro Val Val Gln Ala Glu Gln Leu Asn Trp Leu Tyr Tyr Leu Met
                485                 490                 495

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

Ile Arg Val Asp Ala Val Asp Asn Val Asp Ala Asp Leu Leu Gln Ile
        515                 520                 525

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

Thr Ala Asn Gln His Leu Ser Ile Leu Glu Asp Trp Ser His Asn Asp
545                 550                 555                 560

Pro Leu Tyr Val Thr Asp Gln Gly Ser Asp Gln Leu Thr Met Asp Asp
                565                 570                 575
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Tyr Val His Thr Gln Leu Ile Trp Ser Leu Thr Lys Ser Ser Asp Ile
580 585 590

Arg Gly Thr Met Gln Arg Phe Val Asp Tyr Tyr Met Val Asp Arg Ser
595 600 605

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

Ala His Asp Ser Glu Val Gln Thr Val Ile Ala Gln Ile Val Ser Asp
625 630 635 640

Leu Tyr Pro Asp Val Glu Asn Ser Leu Ala Pro Thr Thr Glu Gln Leu
645 650 655

Ala Ala Ala Phe Lys Val Tyr Asn Glu Asp Glu Lys Leu Ala Asp Lys
660 665 670

Lys Tyr Thr Gln Tyr Asn Met Ala Ser Ala Tyr Ala Met Leu Leu Thr
675 680 685

Asn Lys Asp Thr Val Pro Arg Val Tyr Tyr Gly Asp Leu Tyr Thr Asp
690 695 700

Asp Gly Gln Tyr Met Ala Thr Lys Ser Pro Tyr Tyr Asp Ala Ile Asn
705 710 715 720

[0071] Thr Leu Leu Lys Ala Arg Val Gln Tyr Val Ala Gly Gly Gln Ser Met
725 730 735

Ser Val Asp Ser Asn Asp Val Leu Thr Ser Val Arg Tyr Gly Lys Asp
740 745 750

Ala Met Thr Ala Ser Asp Thr Gly Thr Ser Glu Thr Arg Thr Glu Gly
755 760 765

Val Gly Val Ile Val Ser Asn Asn Ala Glu Leu Gln Leu Glu Asp Gly
770 775 780

His Thr Val Thr Leu His Met Gly Ala Ala His Lys Asn Gln Ala Tyr
785 790 795 800

Arg Ala Leu Leu Ser Thr Thr Ala Asp Gly Leu Ala Tyr Tyr Asp Thr
805 810 815

Asp Glu Asn Ala Pro Val Ala Tyr Thr Asp Ala Asn Gly Asp Leu Ile
820 825 830

Phe Thr Asn Glu Ser Ile Tyr Gly Val Gln Asn Pro Gln Val Ser Gly
835 840 845

Tyr Leu Ala Val Trp Val Pro Val Gly Ala Gln Gln Asp Gln Asp Ala
850 855 860

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

Ser Asn Ala Ala Leu Asp Ser Gln Val Ile Tyr Glu Gly Phe Ser Asn
885 890 895

Phe Gln Ala Phe Ala Thr Asp Ser Ser Glu Tyr Thr Asn Val Val Ile
900 905 910

Ala Gln Asn Ala Asp Gln Phe Lys Gln Trp Gly Val Thr Ser Phe Gln
915 920 925

Leu Ala Pro Gln Tyr Arg Ser Ser Thr Asp Thr Ser Phe Leu Asp Ser
930 935 940

Ile Ile Gln Asn Gly Tyr Ala Phe Thr Asp Arg Tyr Asp Leu Gly Tyr
945 950 955 960

Gly Thr Pro Thr Lys Tyr Gly Thr Ala Asp Gln Leu Arg Asp Ala Ile
965 970 975

Lys Ala Leu His Ala Ser Gly Ile Gln Ala Ile Ala Asp Trp Val Pro
980 985 990

Asp Gln Ile Tyr Asn Leu Pro Glu Gln Glu Leu Ala Thr Val Thr Arg
995 1000 1005

Thr Asn Ser Phe Gly Asp Asp Asp Thr Asp Ser Asp Ile Asp Asn
1010 1015 1020

[0072] Ala Leu Tyr Val Val Gln Ser Arg Gly Gly Gly Gln Tyr Gln Glu
1025 1030 1035

Met Tyr Gly Gly Ala Phe Leu Glu Glu Leu Gln Ala Leu Tyr Pro
1040 1045 1050

Ser Leu Phe Lys Val Asn Gln Ile Ser Thr Gly Val Pro Ile Asp
1055 1060 1065

Gly Ser Val Lys Ile Thr Glu Trp Ala Ala Lys Tyr Phe Asn Gly
1070 1075 1080

Ser Asn Ile Gln Gly Lys Gly Ala Gly Tyr Val Leu Lys Asp Met
1085 1090 1095

Gly Ser Asn Lys Tyr Phe Lys Val Val Ser Asn Thr Glu Asp Gly
1100 1105 1110

Asp Tyr Leu Pro Lys Gln Leu Thr Asn Asp Leu Ser Glu Thr Gly
1115 1120 1125

Phe Thr His Asp Asp Lys Gly Ile Ile Tyr Tyr Thr Leu Ser Gly
1130 1135 1140

Tyr Arg Ala Gln Asn Ala Phe Ile Gln Asp Asp Asp Asn Asn Tyr
1145 1150 1155

Tyr Tyr Phe Asp Lys Thr Gly His Leu Val Thr Gly Leu Gln Lys
1160 1165 1170

Ile Asn Asn His Thr Tyr Phe Phe Leu Pro Asn Gly Ile Glu Leu
1175 1180 1185

Val Lys Ser Phe Leu Gln Asn Glu Asp Gly Thr Ile Val Tyr Phe
1190 1195 1200

Asp Lys Lys Gly His Gln Val Phe Asp Gln Tyr Ile Thr Asp Gln
1205 1210 1215

Asn Gly Asn Ala Tyr Tyr Phe Asp Asp Ala Gly Val Met Leu Lys
1220 1225 1230

Ser Gly Leu Ala Thr Ile Asp Gly His Gln Gln Tyr Phe Asp Gln
1235 1240 1245

Asn Gly Val Gln Val Lys Asp Lys Phe Val Ile Gly Thr Asp Gly
1250 1255 1260

Tyr Lys Tyr Tyr Phe Glu Pro Gly Cys Gly Asn Leu Ala Ile Leu
1265 1270 1275

Arg Tyr Val Gln Asn Ser Lys Asn Gln Trp Phe Tyr Phe Asp Gly
1280 1285 1290

Asn Gly His Ala Val Thr Gly Phe Gln Thr Ile Asn Gly Lys Lys
1295 1300 1305

[0073] Gln Tyr Phe Tyr Asn Asp Gly His Gln Ser Lys Gly Glu Phe Ile
1310 1315 1320

Asn Ala Asp Gly Asp Thr Phe Tyr Thr Ser Ala Thr Asp Gly Arg
1325 1330 1335

Leu Val Thr Gly Val Gln Lys Ile Asn Gly Ile Thr Tyr Ala Phe
1340 1345 1350

Asp Asn Thr Gly Asn Leu Ile Thr Asn Gln Tyr Tyr Gln Leu Ala
1355 1360 1365

Asp Gly Lys Tyr Met Leu Leu Asp Asp Ser Gly Arg Ala Lys Thr
1370 1375 1380

Gly Phe Val Leu Gln Asp Gly Val Leu Arg Tyr Phe Asp Gln Asn
1385 1390 1395

Gly Glu Gln Val Lys Asp Ala Ile Ile Val Asp Pro Asp Thr Asn
1400 1405 1410

Leu Ser Tyr Tyr Phe Asn Ala Thr Gln Gly Val Ala Val Lys Asn
1415 1420 1425

Asp Tyr Phe Glu Tyr Gln Gly Asn Trp Tyr Leu Thr Asp Ala Asn
1430 1435 1440

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

His Phe Asp Glu Val Thr Gly Val Gln Thr Lys Glu Ser Ala Leu
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Ile Ser Ala Gln Gly Lys Val Tyr Gln Phe Asp Asn Asn Gly Asn
1475 1480 1485

Ala Val Ser Ala
1490

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<211> 3972
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<213> 仓鼠链球菌（Streptococcus criceti）

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<213>  仓鼠链球菌（Streptococcus criceti）

<400>  24

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

Ser Ser Ala Asn Gln Thr Thr Ala Thr Phe Ala Ala Asn Asn Arg Ala
    50                  55                  60

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

Ala Asp Ser Trp Tyr Arg Pro Lys Ser Ile Leu Lys Asp Gly Lys Thr
                85                  90                  95

Trp Thr Glu Ser Thr Lys Asp Asp Phe Arg Pro Leu Leu Met Ala Trp
            100                 105                 110

[0076]
Trp Pro Asp Thr Glu Thr Lys Arg Asn Tyr Val Asn Tyr Met Asn Lys
        115                 120                 125

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

Leu Thr Ala Ala Ala Glu Leu Val Gln Ala Arg Ile Glu Gln Arg Ile
145                 150                 155                 160

Thr Ser Glu Lys Asn Thr Lys Trp Leu Arg Glu Ala Ile Ser Ala Phe
                165                 170                 175

Val Lys Thr Gln Pro Gln Trp Asn Gly Glu Ser Glu Lys Pro Tyr Asp
            180                 185                 190

Asp His Leu Gln Asn Gly Ala Leu Lys Phe Asp Asn Glu Thr Ser Leu
        195                 200                 205

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

Asn Gln Thr Gly Ser Leu Asp Pro Arg Phe Thr Phe Asn Gln Asn Asp
225                 230                 235                 240

Pro Leu Gly Gly Tyr Glu Tyr Leu Leu Ala Asn Asp Val Asp Asn Ser
                245                 250                 255

Asn Pro Val Val Gln Ala Glu Ser Leu Asn Trp Leu His Tyr Leu Leu
            260                 265                 270
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Asn Phe Gly Ser Ile Tyr Ala Asn Asp Pro Glu Ala Asn Phe Asp Ser
275 280 285

Ile Arg Val Asp Ala Val Asp Asn Val Asp Ala Asp Leu Leu Gln Ile
290 295 300

Ser Ser Asp Tyr Leu Lys Ser Ala Tyr Lys Ile Asp Lys Asn Asn Lys
305 310 315 320

Asn Ala Asn Asp His Val Ser Ile Val Glu Ala Trp Ser Asp Asn Asp
325 330 335

Thr Pro Tyr Leu His Asp Glu Gly Asp Asn Leu Met Asn Met Asp Asn
340 345 350

Lys Phe Arg Leu Ser Met Leu Arg Ser Leu Ala Lys Pro Leu Asp Lys
355 360 365

Arg Ser Gly Leu Asn Pro Leu Ile His Asn Ser Val Val Asp Arg Glu
370 375 380

Val Asp Asp Arg Glu Val Glu Lys Ile Pro Ser Tyr Ser Phe Ala Arg
385 390 395 400

Ala His Asp Ser Glu Val Gln Asp Leu Ile Arg Asp Ile Ile Lys Ala
405 410 415

[0077] Glu Ile Asn Pro Asn Ser Phe Gly Tyr Ser Phe Thr Gln Glu Glu Ile
420 425 430

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

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

Asn Lys Gly Ser Ile Pro Arg Ile Tyr Tyr Gly Asp Met Phe Thr Asp
465 470 475 480

Asp Gly Gln Tyr Met Ala Asn Lys Thr Val Asn Tyr Asn Ala Ile Glu
485 490 495

Ser Leu Leu Lys Ala Arg Met Lys Tyr Val Ser Gly Gly Gln Ala Met
500 505 510

Gln Asn Tyr Gln Ile Gly Asn Gly Glu Ile Leu Thr Ser Val Arg Tyr
515 520 525

Gly Lys Gly Ala Leu Lys Gln Ser Asp Lys Gly Asp Ala Thr Thr Arg
530 535 540

Thr Ser Gly Ile Gly Ile Val Met Gly Asn Gln Pro Asn Phe Ser Leu
545 550 555 560

Glu Gly Lys Val Val Ala Leu Asn Met Gly Ala Ala His Ala Asn Gln
565 570 575

Glu Tyr Arg Ala Leu Met Val Ser Thr Lys Asp Gly Val Ala Thr Tyr
580 585 590

Ala Thr Asp Ala Asp Ala Ser Lys Ala Gly Met Thr Lys Arg Thr Asp
595 600 605

Glu Asn Gly Tyr Leu Tyr Phe Leu Asn Asp Asp Leu Lys Gly Val Ala
610 615 620

Asn Pro Gln Ile Ser Gly Phe Leu Gln Val Trp Val Pro Val Gly Ala
625 630 635 640

Pro Ala Asp Gln Asp Ile Arg Val Ala Ala Thr Asn Ala Ala Ser Thr
645 650 655

Asp Gly Lys Ser Leu His Gln Asp Ala Ala Met Asp Ser Arg Val Met
660 665 670

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

Tyr Ala Asn Val Val Ile Ala Lys Asn Val Asp Lys Phe Val Ser Trp
690 695 700

Gly Ile Thr Asp Phe Glu Met Ala Pro Gln Tyr Thr Ser Ser Asp Asp
705 710 715 720

[0078] Gly Gln Phe Leu Asp Ser Val Ile Gln Asn Gly Tyr Ala Phe Thr Asp
725 730 735

Arg Tyr Asp Leu Gly Met Ser Lys Ala Asn Lys Tyr Gly Thr Ala Glu
740 745 750

His Leu Val Lys Ala Ile Lys Ala Leu His Lys Ala Gly Leu Lys Val
755 760 765

Met Ala Asp Trp Val Pro Asp Gln Met Tyr Thr Phe Pro Lys Lys Glu
770 775 780

Val Val Thr Val Thr Arg Thr Asp Lys Phe Gly Lys Pro Val Ala Gly
785 790 795 800

Ser Gln Ile Asn His Thr Leu Tyr Val Thr Asp Thr Lys Gly Ser Gly
805 810 815

Asp Asp Tyr Gln Ala Lys Tyr Gly Gly Ala Phe Leu Asp Glu Leu Lys
820 825 830

Glu Lys Tyr Pro Glu Leu Phe Thr Lys Lys Gln Ile Ser Thr Gly Gln
835 840 845

Ala Ile Asp Pro Ser Val Lys Ile Lys Gln Trp Ser Ala Lys Tyr Phe
850 855 860

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

Gln Ala Ser Asn Lys Tyr Phe Asn Val Ala Glu Gly Lys Val Phe Leu
885 890 895

Pro Gly Ala Met Leu Gly Lys Val Val Glu Ser Gly Ile Arg Phe Asp
900 905 910

Gly Lys Gly Tyr Ile Tyr Asn Ser Ser Thr Thr Gly Glu Gln Val Lys
915 920 925

Asp Ser Phe Ile Thr Glu Ala Gly Asn Leu Tyr Tyr Phe Gly Lys Asp
930 935 940

Gly Tyr Met Val Met Gly Ala Gln Asn Ile Gln Gly Ala Asn Tyr Tyr
945 950 955 960

Phe Leu Ala Asn Gly Ala Ala Leu Arg Asn Ser Ile Leu Thr Asp Gln
965 970 975

Asp Gly Lys Ser His Tyr Tyr Ala Asn Asp Gly Lys Arg Tyr Glu Asn
980 985 990

Gly Tyr Tyr Gln Phe Gly Asn Asp Ser Trp Arg Tyr Phe Glu Asn Gly
995 1000 1005

Val Met Ala Val Gly Val Thr Arg Val Ala Gly His Asp Gln Tyr
1010 1015 1020

[0079] Phe Asp Lys Asp Gly Ile Gln Ala Lys Asn Lys Ile Ile Val Thr
1025 1030 1035

Arg Asp Gly Lys Val Arg Tyr Phe Asp Glu His Asn Gly Asn Ala
1040 1045 1050

Val Thr Asn Thr Phe Ile Ser Asp Gln Ala Gly His Trp Tyr Tyr
1055 1060 1065

Leu Gly Lys Asp Gly Val Ala Val Thr Gly Ala Gln Thr Val Gly
1070 1075 1080

Lys Gln His Leu Tyr Phe Glu Ala Asn Gly Gln Gln Val Lys Gly
1085 1090 1095

Asp Phe Val Thr Ala Lys Asp Gly Lys Leu Tyr Phe Phe Asp Gly
1100 1105 1110

Asp Ser Gly Asp Met Trp Thr Asp Thr Phe Val Gln Asp Lys Thr
1115 1120 1125

Gly His Trp Phe Tyr Leu Gly Lys Asp Gly Ala Ala Val Thr Gly
1130 1135 1140

Ala Gln Thr Val Arg Gly Gln Lys Leu Tyr Phe Lys Ala Asn Gly
1145 1150 1155

Gln Gln Val Lys Gly Asp Ile Val Lys Gly Ala Asp Gly Lys Ile
1160 1165 1170

Arg Tyr Tyr Asp Ala Asn Ser Gly Asp Gln Val Tyr Asn Arg Thr
1175 1180 1185

Val Lys Gly Ser Asp Gly Lys Thr Tyr Ile Ile Gly Lys Asp Gly
1190 1195 1200

Val Ala Ile Thr Gln Thr Ile Ala Lys Gly Gln Thr Ile Lys Asp
1205 1210 1215

Gly Ser Val Leu Arg Phe Tyr Ser Met Glu Gly Gln Leu Val Thr
1220 1225 1230

Gly Ser Gly Trp Tyr Ser Asn Ala Lys Gly Gln Trp Leu Tyr Val
1235 1240 1245

Lys Asn Gly Gln Val Leu Thr Gly Leu Gln Thr Val Gly Ser Gln
1250 1255 1260

Arg Val Tyr Phe Asp Ala Asn Gly Ile Gln Ala Lys Gly Lys Ala
1265 1270 1275

Val Arg Thr Ser Asp Gly Lys Leu Arg Tyr Phe Asp Ala Asn Ser
1280 1285 1290

Gly Ser Met Ile Thr Asn Gln Trp Lys Glu Val Asn Gly Gln Tyr
1295 1300 1305

[0080] Tyr Tyr Phe Asp Asn Asn Gly Val Ala Ile Tyr Arg Gly Trp Asn
1310 1315 1320

<210> 25
<211> 4308
<212> DNA
<213> 远缘链球菌（Streptococcus sobrinus）

<400> 25
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gttagcgttg gtgacaagat ctactacttt gacgagactg gtgcctacaa agacacctct 120

aaagtggacg cggacaagtc tagcagcgcc gttagccaaa atgcgacgat ctttgcggct 180

aacaatcgtg cgtatagcac ctctgctgag aactttgagg ccgttgataa ctatctgacg 240

gcagatagct ggtatcgtcc taaatctatt ctgaaagatg gcaagacgtg gaccgagtcg 300

ggtaaggacg acttccgtcc gctgctgatg gcgtggtggc cggacacgga gactaaacgc 360

aattacgtga attacatgaa cctggttgtc ggcatcgaca agacgtacac cgcggaaacc 420

tctcaagcag atttgaccgc agcggcggag ctggtccagg cgcgtattga acagaaaatc 480

accacggaac agaatacgaa atggctgcgc gaggcgatct ctgctttcgt caagacccag 540

ccgcagtgga atggtgaaag cgagaagccg tatgacgacc acctgcaaaa cggtgctctg 600

aaattcgata atcagagcga cctgaccccg gacacccaga gcaactatcg cctgctgaat 660

cgcaccccga ctaaccagac tggcagcctg gacagccgtt tcacctataa tgcgaacgat 720

ccgttgggtg gctacgaatt tctgctggct aacgacgtgg ataatagcaa ccctgtggtg 780

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ctgttgcaga ttagcagcga ttacctgaag gcagcctatg gcattgacaa gaacaataag 960

aacgcgaaca accatgttag cattgttgag gcttggagcg ataacgatac gccgtacctg 1020

cacgatgacg gtgataacct gatgaacatg gacaataagt tccgcttgag catgctgtgg 1080

agcctggcca agccgctgga caagcgcagc ggtctgaatc ctctgattca taacagcctg 1140

gtggaccgtg aggttgatga ccgtgaagtg gaaacggttc cgagctactc ttttgcgcgt 1200

gcgcatgatt ccgaggtcca agacattatc cgcgacatta tcaaggccga aatcaacccg 1260

aatagctttg gttatagctt cacccaagaa gagattgacc aggcgtttaa gatctataat 1320

gaagatctga agaaaaccga caagaaatac acccactata atgtcccgtt gagctatact 1380

ttgctgctga cgaataaagg ttcgattccg cgtgtgtatt acggtgatat gttcaccgat 1440

gatggtcaat acatggcgaa caaaacggtt aactatgatg ccattgagtc gctgctgaaa 1500

gcgcgcatga agtacgttag cggcggtcaa gcgatgcaaa actatcaaat cggcaatggt 1560

gagattctga ccagcgttcg ttatggtaag ggtgcattga agcaatccga caagggtgac 1620

gcgaccacgc gtacgtccgg tgtgggcgtc gtgatgggca accagccgaa ctttagcctg 1680

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aagggtgtgg caaacccaca agtcagcggt ttcttgcagg tgtgggtccc agtgggtgcg 1920

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[0081] ctgcatcaag atgcggcaat ggatagccgt gttatgtttg agggttttag caacttccag 2040

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ttcgttagct ggggtattac cgactttgag atggcaccgc aatatgtcag ctccaccgat 2160

ggccagtttc tggatagcgt tatccagaat ggttacgcgt tcaccgaccg ttatgatctg 2220

ggtatgagca aagccaacaa atacggtacc gcggatcagc tggttaaagc aatcaaagcg 2280

ttgcacgcga agggtctgaa ggtgatggcg gactgggttc cagaccagat gtacacgttt 2340

ccgaagcagg aagttgtcac tgtcacgcgc accgacaaat ttggtaagcc gattgcgggc 2400

agccaaatca atcacagcct gtacgtgacg gacaccaaat ccagcggtga tgattaccag 2460

gccaaatatg gtggtgcgtt cctggatgag ctgaaagaga aatacccgga gctgttcacc 2520

aaaaagcaga tctcgaccgg tcaggcgatc gacccgagcg tgaagattaa gcagtggagc 2580

gcgaaatact ttaatggtag caacattctg ggtcgtggtg ccgactacgt cctgtccgat 2640

caagttagca acaagtattt caatgtggcc agcgacacgc tgtttctgcc gtctagcctg 2700

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tggcgttact tcaaagatgg taacatggcc gtcggtctga ccacggtgga tggtaacgtt 3060

cagtatttcg acaaggacgg tgtccaagct aaagacaaga ttattgtgac ccgcgatggt 3120

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aaggtgcgct actttgatca acacaatggc aacgcggtca cgaatacctt tatcgccgac     3180
aagaccggtc actggtacta cctgggcaaa gatggcgtcg cggtcaccgg cgctcaaacc     3240
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agcggtgcac agaccattcg cggtcaaaag ctgtacttca aggcgtacgg tcaacaggtc     3480
aaaggtgaca tcgttaaagg caccgacggc aagatccgtt actacgatgc gaaatccggc     3540
gagcaggttt tcaataagac ggtcaaagcc gctgatggca aaacctatgt gatcggcaac     3600
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ggtaacccga aaggccaaat cttcaaggac ggcagcgttc tgcgtttcta tagcatggaa     4020
ggccagctgg taattggcag cggctggtat tccaacgcgc aaggccaatg gctgtatgtg     4080
aagaatggta aagtgttgac cggtttgcag accgtcggtt cccagcgcgt gtactttgat     4140
gagaatggca ttcaagcaaa aggcaaagcg gttcgcacga gcgacggcaa aattcgctac     4200
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[0082]

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ttcgacgaga acagcggtag catgatcacc aatcaatgga agtttgttta cggtcaatac     4260
tattactttg gtaatgacgg tgcggcaatc taccgtggtt ggaattaa                  4308
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<210> 26
<211> 1435
<212> PRT
<213> 远缘链球菌（Streptococcus sobrinus）

<400> 26

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Met Val Asp Gly Lys Tyr Tyr Tyr Tyr Asp Gln Asp Gly Asn Val Lys
1               5                   10                  15

Lys Asn Phe Ala Val Ser Val Gly Asp Lys Ile Tyr Tyr Phe Asp Glu
            20                  25                  30

Thr Gly Ala Tyr Lys Asp Thr Ser Lys Val Asp Ala Asp Lys Ser Ser
        35                  40                  45

Ser Ala Val Ser Gln Asn Ala Thr Ile Phe Ala Ala Asn Asn Arg Ala
    50                  55                  60

Tyr Ser Thr Ser Ala Glu Asn Phe Glu Ala Val Asp Asn Tyr Leu Thr
65                  70                  75                  80

Ala Asp Ser Trp Tyr Arg Pro Lys Ser Ile Leu Lys Asp Gly Lys Thr
                85                  90                  95

Trp Thr Glu Ser Gly Lys Asp Asp Phe Arg Pro Leu Leu Met Ala Trp
            100                 105                 110
```

```
Trp Pro Asp Thr Glu Thr Lys Arg Asn Tyr Val Asn Tyr Met Asn Leu
        115                 120                 125

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

Leu Thr Ala Ala Ala Glu Leu Val Gln Ala Arg Ile Glu Gln Lys Ile
145                 150                 155                 160

Thr Thr Glu Gln Asn Thr Lys Trp Leu Arg Glu Ala Ile Ser Ala Phe
                165                 170                 175

Val Lys Thr Gln Pro Gln Trp Asn Gly Glu Ser Glu Lys Pro Tyr Asp
            180                 185                 190

Asp His Leu Gln Asn Gly Ala Leu Lys Phe Asp Asn Gln Ser Asp Leu
        195                 200                 205

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

Asn Gln Thr Gly Ser Leu Asp Ser Arg Phe Thr Tyr Asn Ala Asn Asp
225                 230                 235                 240

Pro Leu Gly Gly Tyr Glu Phe Leu Leu Ala Asn Asp Val Asp Asn Ser
                245                 250                 255
```

[0083]

```
Asn Pro Val Val Gln Ala Glu Gln Leu Asn Trp Leu His Tyr Leu Leu
            260                 265                 270

Asn Phe Gly Ser Ile Tyr Ala Lys Asp Ala Asp Ala Asn Phe Asp Ser
        275                 280                 285

Ile Arg Val Asp Ala Val Asp Asn Val Asp Ala Asp Leu Leu Gln Ile
    290                 295                 300

Ser Ser Asp Tyr Leu Lys Ala Ala Tyr Gly Ile Asp Lys Asn Asn Lys
305                 310                 315                 320

Asn Ala Asn Asn His Val Ser Ile Val Glu Ala Trp Ser Asp Asn Asp
                325                 330                 335

Thr Pro Tyr Leu His Asp Asp Gly Asp Asn Leu Met Asn Met Asp Asn
            340                 345                 350

Lys Phe Arg Leu Ser Met Leu Trp Ser Leu Ala Lys Pro Leu Asp Lys
        355                 360                 365

Arg Ser Gly Leu Asn Pro Leu Ile His Asn Ser Leu Val Asp Arg Glu
    370                 375                 380

Val Asp Asp Arg Glu Val Glu Thr Val Pro Ser Tyr Ser Phe Ala Arg
385                 390                 395                 400

Ala His Asp Ser Glu Val Gln Asp Ile Ile Arg Asp Ile Ile Lys Ala
                405                 410                 415
```

Glu Ile Asn Pro Asn Ser Phe Gly Tyr Ser Phe Thr Gln Glu Glu Ile
420 425 430

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

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

Asn Lys Gly Ser Ile Pro Arg Val Tyr Tyr Gly Asp Met Phe Thr Asp
465 470 475 480

Asp Gly Gln Tyr Met Ala Asn Lys Thr Val Asn Tyr Asp Ala Ile Glu
485 490 495

Ser Leu Leu Lys Ala Arg Met Lys Tyr Val Ser Gly Gly Gln Ala Met
500 505 510

Gln Asn Tyr Gln Ile Gly Asn Gly Glu Ile Leu Thr Ser Val Arg Tyr
515 520 525

Gly Lys Gly Ala Leu Lys Gln Ser Asp Lys Gly Asp Ala Thr Thr Arg
530 535 540

Thr Ser Gly Val Gly Val Val Met Gly Asn Gln Pro Asn Phe Ser Leu
545 550 555 560

[0084] Asp Gly Lys Val Val Ala Leu Asn Met Gly Ala Ala His Ala Asn Gln
565 570 575

Glu Tyr Arg Ala Leu Met Val Ser Thr Lys Asp Gly Val Ala Thr Tyr
580 585 590

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

Glu Asn Gly Tyr Leu Tyr Phe Leu Asn Asp Asp Leu Lys Gly Val Ala
610 615 620

Asn Pro Gln Val Ser Gly Phe Leu Gln Val Trp Val Pro Val Gly Ala
625 630 635 640

Ala Asp Asp Gln Asp Ile Arg Val Ala Ala Ser Asp Thr Ala Ser Thr
645 650 655

Asp Gly Lys Ser Leu His Gln Asp Ala Ala Met Asp Ser Arg Val Met
660 665 670

Phe Glu Gly Phe Ser Asn Phe Gln Ser Phe Ala Thr Lys Glu Glu Glu
675 680 685

Tyr Thr Asn Val Val Ile Ala Asn Asn Val Asp Lys Phe Val Ser Trp
690 695 700

Gly Ile Thr Asp Phe Glu Met Ala Pro Gln Tyr Val Ser Ser Thr Asp
705 710 715 720

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

Arg Tyr Asp Leu Gly Met Ser Lys Ala Asn Lys Tyr Gly Thr Ala Asp
740 745 750

Gln Leu Val Lys Ala Ile Lys Ala Leu His Ala Lys Gly Leu Lys Val
755 760 765

Met Ala Asp Trp Val Pro Asp Gln Met Tyr Thr Phe Pro Lys Gln Glu
770 775 780

Val Val Thr Val Thr Arg Thr Asp Lys Phe Gly Lys Pro Ile Ala Gly
785 790 795 800

Ser Gln Ile Asn His Ser Leu Tyr Val Thr Asp Thr Lys Ser Ser Gly
805 810 815

Asp Asp Tyr Gln Ala Lys Tyr Gly Gly Ala Phe Leu Asp Glu Leu Lys
820 825 830

Glu Lys Tyr Pro Glu Leu Phe Thr Lys Lys Gln Ile Ser Thr Gly Gln
835 840 845

Ala Ile Asp Pro Ser Val Lys Ile Lys Gln Trp Ser Ala Lys Tyr Phe
850 855 860

[0085] Asn Gly Ser Asn Ile Leu Gly Arg Gly Ala Asp Tyr Val Leu Ser Asp
865 870 875 880

Gln Val Ser Asn Lys Tyr Phe Asn Val Ala Ser Asp Thr Leu Phe Leu
885 890 895

Pro Ser Ser Leu Leu Gly Lys Val Val Glu Ser Gly Ile Arg Tyr Asp
900 905 910

Gly Lys Gly Tyr Ile Tyr Asn Ser Ser Ala Thr Gly Asp Gln Val Lys
915 920 925

Ala Ser Phe Ile Thr Glu Ala Gly Asn Leu Tyr Tyr Phe Gly Lys Asp
930 935 940

Gly Tyr Met Val Thr Gly Ala Gln Thr Ile Asn Gly Ala Asn Tyr Phe
945 950 955 960

Phe Leu Glu Asn Gly Thr Ala Leu Arg Asn Thr Ile Tyr Thr Asp Ala
965 970 975

Gln Gly Asn Ser His Tyr Tyr Ala Asn Asp Gly Lys Arg Tyr Glu Asn
980 985 990

Gly Tyr Gln Gln Phe Gly Asn Asp Trp Arg Tyr Phe Lys Asp Gly Asn
995 1000 1005

Met Ala Val Gly Leu Thr Thr Val Asp Gly Asn Val Gln Tyr Phe
1010 1015 1020

Asp Lys Asp Gly Val Gln Ala Lys Asp Lys Ile Ile Val Thr Arg
1025 1030 1035

Asp Gly Lys Val Arg Tyr Phe Asp Gln His Asn Gly Asn Ala Val
1040 1045 1050

Thr Asn Thr Phe Ile Ala Asp Lys Thr Gly His Trp Tyr Tyr Leu
1055 1060 1065

Gly Lys Asp Gly Val Ala Val Thr Gly Ala Gln Thr Val Gly Lys
1070 1075 1080

Gln Lys Leu Tyr Phe Glu Ala Asn Gly Glu Gln Val Lys Gly Asp
1085 1090 1095

Phe Val Thr Ser His Glu Gly Lys Leu Tyr Phe Tyr Asp Val Asp
1100 1105 1110

Ser Gly Asp Met Trp Thr Asp Thr Phe Ile Glu Asp Lys Ala Gly
1115 1120 1125

Asn Trp Phe Tyr Leu Gly Lys Asp Gly Ala Ala Val Ser Gly Ala
1130 1135 1140

Gln Thr Ile Arg Gly Gln Lys Leu Tyr Phe Lys Ala Tyr Gly Gln
1145 1150 1155

[0086] Gln Val Lys Gly Asp Ile Val Lys Gly Thr Asp Gly Lys Ile Arg
1160 1165 1170

Tyr Tyr Asp Ala Lys Ser Gly Glu Gln Val Phe Asn Lys Thr Val
1175 1180 1185

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

Ala Val Asp Pro Ser Val Val Lys Gly Gln Thr Phe Lys Asp Ala
1205 1210 1215

Ser Gly Ala Leu Arg Phe Tyr Asn Leu Lys Gly Gln Leu Val Thr
1220 1225 1230

Gly Ser Gly Trp Tyr Glu Thr Ala Asn His Asp Trp Val Tyr Ile
1235 1240 1245

Gln Ser Gly Lys Ala Leu Thr Gly Glu Gln Thr Ile Asn Gly Gln
1250 1255 1260

His Leu Tyr Phe Lys Glu Asp Gly His Gln Val Lys Gly Gln Leu
1265 1270 1275

Val Thr Arg Thr Asp Gly Lys Val Arg Tyr Tyr Asp Ala Asn Ser
1280 1285 1290

Gly Asp Gln Ala Phe Asn Lys Ser Val Thr Val Asn Gly Lys Thr
1295 1300 1305

Tyr Tyr Phe Gly Asn Asp Gly Thr Ala Gln Thr Ala Gly Asn Pro
1310 1315 1320

Lys Gly Gln Ile Phe Lys Asp Gly Ser Val Leu Arg Phe Tyr Ser
1325 1330 1335

Met Glu Gly Gln Leu Val Ile Gly Ser Gly Trp Tyr Ser Asn Ala
1340 1345 1350

Gln Gly Gln Trp Leu Tyr Val Lys Asn Gly Lys Val Leu Thr Gly
1355 1360 1365

Leu Gln Thr Val Gly Ser Gln Arg Val Tyr Phe Asp Glu Asn Gly
1370 1375 1380

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

Arg Tyr Phe Asp Glu Asn Ser Gly Ser Met Ile Thr Asn Gln Trp
1400 1405 1410

Lys Phe Val Tyr Gly Gln Tyr Tyr Tyr Phe Gly Asn Asp Gly Ala
1415 1420 1425

Ala Ile Tyr Arg Gly Trp Asn
1430 1435

<210> 27
[0087] <211> 4023
<212> DNA
<213> 唾液链球菌（Streptococcus salivarius）

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acctacagct ttacgcaggg caccaccaac atcgttgatg gctttagcaa aaacaaccgt 180

gcgtacgatt ccagcgaggc gagctttgaa ctgatcgacg gttatctgac cgcggactcc 240

tggtatcgtc cggtgagcat tatcaaggac ggcgttacgt ggcaagccag caccaaagag 300

gactttcgcc cgctgctgat ggcctggtgg ccgaatgttg acacccaggt caactacctg 360

aattacatgt cgaaggtgtt taacctggac gcgaagtata cgagcaccga caaacaggtt 420

gacctgaatc gcgcagccaa ggacattcag gttaagattg agcaaaagat tcaggccgag 480

aagagcactc aatggctgcg tgaagcgatt tcggccttcg tcaaaaccca gccgcagtgg 540

aataaagaaa cggagaactt ctccaagggt ggtggtgagg atcatctgca aggtggtgca 600

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taa                                                                  4023
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<212> PRT
<213> 唾液链球菌（Streptococcus salivarius）

<400> 28

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            20                  25                  30

Asp Gly Ala Leu Thr Ser Ser Ser Thr Tyr Ser Phe Thr Gln Gly Thr
        35                  40                  45

Thr Asn Ile Val Asp Gly Phe Ser Lys Asn Asn Arg Ala Tyr Asp Ser
    50                  55                  60

Ser Glu Ala Ser Phe Glu Leu Ile Asp Gly Tyr Leu Thr Ala Asp Ser
65                  70                  75                  80

Trp Tyr Arg Pro Val Ser Ile Ile Lys Asp Gly Val Thr Trp Gln Ala
                85                  90                  95

Ser Thr Lys Glu Asp Phe Arg Pro Leu Leu Met Ala Trp Trp Pro Asn
            100                 105                 110

Val Asp Thr Gln Val Asn Tyr Leu Asn Tyr Met Ser Lys Val Phe Asn
        115                 120                 125

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

Ala Ala Lys Asp Ile Gln Val Lys Ile Glu Gln Lys Ile Gln Ala Glu
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Lys Ser Thr Gln Trp Leu Arg Glu Ala Ile Ser Ala Phe Val Lys Thr
                165                 170                 175
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Gln Pro Gln Trp Asn Lys Glu Thr Glu Asn Phe Ser Lys Gly Gly Gly
            180                 185                 190

Glu Asp His Leu Gln Gly Gly Ala Leu Leu Tyr Val Asn Asp Pro Arg
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Thr Pro Trp Ala Asn Ser Asn Tyr Arg Leu Leu Asn Arg Thr Ala Thr
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Asn Gln Thr Gly Thr Ile Asp Lys Ser Val Leu Asp Glu Gln Ser Asp
225                 230                 235                 240

Pro Asn His Met Gly Gly Phe Asp Phe Leu Leu Ala Asn Asp Val Asp
                245                 250                 255

Thr Ser Asn Pro Val Val Gln Ala Glu Gln Leu Asn Gln Ile His Tyr
            260                 265                 270

Leu Met Asn Trp Gly Ser Ile Val Met Gly Asp Lys Asp Ala Asn Phe
        275                 280                 285

Asp Gly Ile Arg Val Asp Ala Val Asp Asn Val Asp Ala Asp Met Leu
    290                 295                 300

Gln Leu Tyr Thr Asn Tyr Phe Arg Glu Tyr Tyr Gly Val Asn Lys Ser
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[0090]

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Glu Ala Asn Ala Leu Ala His Ile Ser Val Leu Glu Ala Trp Ser Leu
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Asn Asp Asn His Tyr Asn Asp Lys Thr Asp Gly Ala Ala Leu Ala Met
            340                 345                 350

Glu Asn Lys Gln Arg Leu Ala Leu Leu Phe Ser Leu Ala Lys Pro Ile
        355                 360                 365

Lys Glu Arg Thr Pro Ala Val Ser Pro Leu Tyr Asn Asn Thr Phe Asn
    370                 375                 380

Thr Thr Gln Arg Asp Glu Lys Thr Asp Trp Ile Asn Lys Asp Gly Ser
385                 390                 395                 400

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

Tyr Asn Glu Lys Tyr Gly Asp Ala Ser Gly Asn Tyr Val Phe Ile Arg
            420                 425                 430

Ala His Asp Asn Asn Val Gln Asp Ile Ile Ala Glu Ile Ile Lys Lys
        435                 440                 445

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

Lys Lys Ala Phe Glu Ile Tyr Asn Lys Asp Met Leu Ser Ser Asp Lys
465                 470                 475                 480
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Lys Tyr Thr Leu Asn Asn Ile Pro Ala Ala Tyr Ala Val Met Leu Gln
485 490 495

Asn Met Glu Thr Ile Thr Arg Val Tyr Tyr Gly Asp Leu Tyr Thr Asp
500 505 510

Asp Gly His Tyr Met Glu Thr Lys Ser Pro Tyr Tyr Asp Thr Ile Val
515 520 525

Asn Leu Met Lys Asn Arg Ile Lys Tyr Val Ser Gly Gly Gln Ala Gln
530 535 540

Arg Ser Tyr Trp Leu Pro Thr Asp Gly Lys Met Asp Lys Ser Asp Val
545 550 555 560

Glu Leu Tyr Arg Thr Asn Glu Val Tyr Thr Ser Val Arg Tyr Gly Lys
565 570 575

Asp Ile Met Thr Ala Asp Asp Thr Gln Gly Ser Lys Tyr Ser Arg Thr
580 585 590

Ser Gly Gln Val Thr Leu Val Val Asn Asn Pro Lys Leu Ser Leu Asp
595 600 605

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

[0091] Lys Tyr Arg Ala Leu Ile Val Gly Thr Pro Asn Gly Ile Lys Asn Phe
625 630 635 640

Thr Ser Asp Ala Glu Ala Ile Ala Ala Gly Tyr Val Lys Glu Thr Asp
645 650 655

Gly Asn Gly Val Leu Thr Phe Gly Ala Asn Asp Ile Lys Gly Tyr Glu
660 665 670

Thr Phe Asp Met Ser Gly Phe Val Ala Val Trp Val Pro Val Gly Ala
675 680 685

Ser Asp Asp Gln Asp Ile Arg Val Ala Ala Ser Thr Ala Ala Lys Lys
690 695 700

Glu Gly Glu Leu Thr Leu Lys Ala Thr Glu Ala Tyr Asp Ser Gln Leu
705 710 715 720

Ile Tyr Glu Gly Phe Ser Asn Phe Gln Thr Ile Pro Asp Gly Ser Asp
725 730 735

Pro Ser Val Tyr Thr Asn Arg Lys Ile Ala Glu Asn Val Asp Leu Phe
740 745 750

Lys Ser Trp Gly Val Thr Ser Phe Glu Met Ala Pro Gln Phe Val Ser
755 760 765

Ala Asp Asp Gly Thr Phe Leu Asp Ser Val Ile Gln Asn Gly Tyr Ala
770 775 780

Phe Ala Asp Arg Tyr Asp Leu Ala Met Ser Lys Asn Asn Lys Tyr Gly
785 790 795 800

Ser Lys Glu Asp Leu Arg Asn Ala Leu Lys Ala Leu His Lys Ala Gly
805 810 815

Ile Gln Ala Ile Ala Asp Trp Val Pro Asp Gln Ile Tyr Gln Leu Pro
820 825 830

Gly Lys Glu Val Val Thr Ala Thr Arg Thr Asp Gly Ala Gly Arg Lys
835 840 845

Ile Ser Asp Ala Ile Ile Asp His Ser Leu Tyr Val Ala Asn Ser Lys
850 855 860

Ser Ser Gly Lys Asp Tyr Gln Ala Lys Tyr Gly Gly Glu Phe Leu Ala
865 870 875 880

Glu Leu Lys Ala Lys Tyr Pro Glu Met Phe Lys Val Asn Met Ile Ser
885 890 895

Thr Gly Lys Pro Ile Asp Asp Ser Val Lys Leu Lys Gln Trp Lys Ala
900 905 910

Glu Tyr Phe Asn Gly Thr Asn Val Leu Asp Arg Gly Val Gly Tyr Val
915 920 925

[0092] Leu Ser Asp Glu Ala Thr Gly Lys Tyr Phe Thr Val Thr Lys Glu Gly
930 935 940

Asn Phe Ile Pro Leu Gln Leu Lys Gly Asn Glu Lys Val Ile Thr Gly
945 950 955 960

Phe Ser Ser Asp Gly Lys Gly Ile Thr Tyr Phe Gly Thr Ser Gly Asn
965 970 975

Gln Ala Lys Ser Ala Phe Val Thr Phe Asn Gly Asn Thr Tyr Tyr Phe
980 985 990

Asp Ala Arg Gly His Met Val Thr Asn Gly Glu Tyr Ser Pro Asn Gly
995 1000 1005

Lys Asp Val Tyr Arg Phe Leu Pro Asn Gly Ile Met Leu Ser Asn
1010 1015 1020

Ala Phe Tyr Val Asp Gly Asn Gly Asn Thr Tyr Leu Tyr Asn Ser
1025 1030 1035

Lys Gly Gln Met Tyr Lys Gly Gly Tyr Ser Lys Phe Asp Val Thr
1040 1045 1050

Glu Thr Lys Asp Gly Lys Glu Ser Lys Val Val Lys Phe Arg Tyr
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Phe Thr Asn Glu Gly Val Met Ala Lys Gly Val Thr Val Val Asp
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Gly Phe Thr Gln Tyr Phe Asn Glu Asp Gly Ile Gln Ser Lys Asp
1085 1090 1095

Glu Leu Val Thr Tyr Asn Gly Lys Thr Tyr Tyr Phe Glu Ala His
1100 1105 1110

Thr Gly Asn Ala Ile Lys Asn Thr Trp Arg Asn Ile Lys Gly Lys
1115 1120 1125

Trp Tyr His Phe Asp Ala Asn Gly Val Ala Ala Thr Gly Ala Gln
1130 1135 1140

Val Ile Asn Gly Gln His Leu Tyr Phe Asn Glu Asp Gly Ser Gln
1145 1150 1155

Val Lys Gly Gly Val Val Lys Asn Ala Asp Gly Thr Phe Ser Lys
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Tyr Lys Asp Gly Ser Gly Asp Leu Val Val Asn Glu Phe Phe Thr
1175 1180 1185

Thr Gly Asp Asn Val Trp Tyr Tyr Ala Gly Ala Asn Gly Lys Thr
1190 1195 1200

Val Thr Gly Ala Gln Val Ile Asn Gly Gln His Leu Phe Phe Lys
1205 1210 1215

[0093] Glu Asp Gly Ser Gln Val Lys Gly Asp Phe Val Lys Asn Ser Asp
1220 1225 1230

Gly Thr Tyr Ser Lys Tyr Asp Ala Ala Ser Gly Glu Arg Leu Thr
1235 1240 1245

Asn Glu Phe Phe Thr Thr Gly Asp Asn His Trp Tyr Tyr Ile Gly
1250 1255 1260

Ala Asn Gly Lys Thr Val Thr Gly Glu Val Lys Ile Gly Asp Asp
1265 1270 1275

Thr Tyr Phe Phe Ala Lys Asp Gly Lys Gln Leu Lys Gly Gln Ile
1280 1285 1290

Val Thr Thr Arg Ser Gly Arg Ile Ser Tyr Tyr Phe Gly Asp Ser
1295 1300 1305

Gly Lys Lys Ala Ile Ser Thr Trp Val Glu Ile Gln Pro Gly Val
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Phe Val Phe Phe Asp Lys Asn Gly Leu Ala Tyr Pro Pro Glu Asn
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caaccgggta tctatgtcta ttttgataag acgggcatcg cgtacccacc gcgtgtgctg 4020

aattaa 4026

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<212> PRT
<213> 唾液链球菌（Streptococcus salivarius）

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

Ser Glu Ala Ser Phe Glu Leu Ile Asn Gly Tyr Leu Thr Ala Asp Ser
65 70 75 80

Trp Tyr Arg Pro Val Ser Ile Ile Lys Asp Gly Val Thr Trp Gln Ala
85 90 95

Ser Thr Ala Glu Asp Phe Arg Pro Leu Leu Met Ala Trp Trp Pro Asn
100 105 110

Val Asp Thr Gln Val Asn Tyr Leu Asn Tyr Met Ser Lys Val Phe Asn
115 120 125

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

Ala Ala Lys Asp Ile Gln Val Lys Ile Glu Gln Lys Ile Gln Ala Glu
145 150 155 160

[0096] Lys Ser Thr Gln Trp Leu Arg Glu Thr Ile Ser Ala Phe Val Lys Thr
165 170 175

Gln Pro Gln Trp Asn Lys Glu Thr Glu Asn Tyr Ser Lys Gly Gly Gly
180 185 190

Glu Asp His Leu Gln Gly Gly Ala Leu Leu Tyr Val Asn Asp Ser Arg
195 200 205

Thr Pro Trp Ala Asn Ser Asn Tyr Arg Leu Leu Asn Arg Thr Ala Thr
210 215 220

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

Pro Asn His Met Gly Gly Phe Asp Phe Leu Leu Ala Asn Asp Val Asp
245 250 255

Leu Ser Asn Pro Val Val Gln Ala Glu Gln Leu Asn Gln Ile His Tyr
260 265 270

Leu Met Asn Trp Gly Ser Ile Val Met Gly Asp Lys Asp Ala Asn Phe
275 280 285

Asp Gly Ile Arg Val Asp Ala Val Asp Asn Val Asn Ala Asp Met Leu
290 295 300

Gln Leu Tyr Thr Asn Tyr Phe Arg Glu Tyr Tyr Gly Val Asn Lys Ser
305 310 315 320

Glu Ala Gln Ala Leu Ala His Ile Ser Val Leu Glu Ala Trp Ser Leu
325 330 335

Asn Asp Asn His Tyr Asn Asp Lys Thr Asp Gly Ala Ala Leu Ala Met
340 345 350

Glu Asn Lys Gln Arg Leu Ala Leu Leu Phe Ser Leu Ala Lys Pro Ile
355 360 365

Lys Asp Arg Thr Pro Ala Val Ser Pro Leu Tyr Asn Asn Thr Phe Asn
370 375 380

Thr Thr Gln Arg Asp Phe Lys Thr Asp Trp Ile Asn Lys Asp Gly Ser
385 390 395 400

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

Tyr Asn Glu Lys Tyr Gly Asp Ala Ser Gly Asn Tyr Val Phe Ile Arg
420 425 430

Ala His Asp Asn Asn Val Gln Asp Ile Ile Ala Glu Ile Ile Lys Lys
435 440 445

Glu Ile Asn Lys Lys Ser Asp Gly Phe Thr Ile Ser Asp Ser Glu Met
450 455 460

[0097] Lys Gln Ala Phe Glu Ile Tyr Asn Lys Asp Met Leu Ser Ser Asn Lys
465 470 475 480

Lys Tyr Thr Leu Asn Asn Ile Pro Ala Ala Tyr Ala Val Met Leu Gln
485 490 495

Asn Met Glu Thr Ile Thr Arg Val Tyr Tyr Gly Asp Leu Tyr Thr Asp
500 505 510

Asp Gly His Tyr Met Glu Thr Lys Ser Pro Tyr His Asp Thr Ile Val
515 520 525

Asn Leu Met Lys Asn Arg Ile Lys Tyr Val Ser Gly Gly Gln Ala Gln
530 535 540

Arg Ser Tyr Trp Leu Pro Thr Asp Gly Lys Met Asp Asn Ser Asp Val
545 550 555 560

Glu Leu Tyr Arg Thr Ser Glu Val Tyr Thr Ser Val Arg Tyr Gly Lys
565 570 575

Asp Ile Met Thr Ala Asp Asp Thr Glu Gly Ser Lys Tyr Ser Arg Thr
580 585 590

Ser Gly Gln Val Thr Leu Val Val Asn Asn Pro Lys Leu Thr Leu His
595 600 605

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

Lys Tyr Arg Ala Leu Ile Val Gly Thr Ala Asp Gly Ile Lys Asn Phe
625 630 635 640

Thr Ser Asp Ala Glu Ala Ile Ala Ala Gly Tyr Val Lys Glu Thr Asp
645 650 655

Ser Asn Gly Val Leu Thr Phe Gly Ala Asn Asp Ile Lys Gly Tyr Glu
660 665 670

Thr Phe Asp Met Ser Gly Phe Val Ala Val Trp Val Pro Val Gly Ala
675 680 685

Ser Asp Asp Gln Asp Ile Arg Val Ala Pro Ser Thr Glu Ala Lys Lys
690 695 700

Glu Gly Glu Leu Thr Leu Lys Ala Thr Glu Ala Tyr Asp Ser Gln Leu
705 710 715 720

Ile Tyr Glu Gly Phe Ser Asn Phe Gln Thr Ile Pro Asp Gly Ser Asp
725 730 735

Pro Ser Val Tyr Thr Asn Arg Lys Ile Ala Glu Asn Val Asp Leu Phe
740 745 750

Lys Ser Trp Gly Val Thr Ser Phe Glu Met Ala Pro Gln Phe Val Ser
755 760 765

[0098] Ala Asp Asp Gly Thr Phe Leu Asp Ser Val Ile Gln Asn Gly Tyr Ala
770 775 780

Phe Ala Asp Arg Tyr Asp Leu Ala Met Ser Lys Asn Asn Lys Tyr Gly
785 790 795 800

Ser Lys Glu Asp Leu Arg Asp Ala Leu Lys Ala Leu His Lys Ala Gly
805 810 815

Ile Gln Ala Ile Ala Asp Trp Val Pro Asp Gln Ile Tyr Gln Leu Pro
820 825 830

Gly Lys Glu Val Val Thr Ala Thr Arg Thr Asp Gly Ala Gly Arg Lys
835 840 845

Ile Ala Asp Ala Ile Ile Asp His Ser Leu Tyr Val Ala Asn Ser Lys
850 855 860

Ser Ser Gly Arg Asp Tyr Gln Ala Gln Tyr Gly Gly Glu Phe Leu Ala
865 870 875 880

Glu Leu Lys Ala Lys Tyr Pro Lys Met Phe Thr Glu Asn Met Ile Ser
885 890 895

Thr Gly Lys Pro Ile Asp Asp Ser Val Lys Leu Lys Gln Trp Lys Ala
900 905 910

Lys Tyr Phe Asn Gly Thr Asn Val Leu Asp Arg Gly Val Gly Tyr Val
915 920 925

Leu Ser Asp Glu Ala Thr Gly Lys Tyr Phe Thr Val Thr Lys Glu Gly
930 935 940

Asn Phe Ile Pro Leu Gln Leu Thr Gly Asn Glu Lys Ala Val Thr Gly
945 950 955 960

Phe Ser Asn Asp Gly Lys Gly Ile Thr Tyr Phe Gly Thr Ser Gly Asn
965 970 975

Gln Ala Lys Ser Ala Phe Val Thr Phe Asn Gly Asn Thr Tyr Tyr Phe
980 985 990

Asp Ala Arg Gly His Met Val Thr Asn Gly Glu Tyr Ser Pro Asn Gly
995 1000 1005

Lys Asp Val Tyr Arg Phe Leu Pro Asn Gly Ile Met Leu Ser Asn
1010 1015 1020

Ala Phe Tyr Val Asp Ala Asn Gly Asn Thr Tyr Leu Tyr Asn Tyr
1025 1030 1035

Lys Gly Gln Met Tyr Lys Gly Gly Tyr Thr Lys Phe Asp Val Thr
1040 1045 1050

Glu Thr Asp Lys Asp Gly Asn Glu Ser Lys Val Val Lys Phe Arg
1055 1060 1065

[0099] Tyr Phe Thr Asn Glu Gly Val Met Ala Lys Gly Leu Thr Val Ile
1070 1075 1080

Asp Gly Ser Thr Gln Tyr Phe Gly Glu Asp Gly Phe Gln Thr Lys
1085 1090 1095

Asp Lys Leu Ala Thr Tyr Lys Gly Lys Thr Tyr Tyr Phe Glu Ala
1100 1105 1110

His Thr Gly Asn Ala Ile Lys Asn Thr Trp Arg Asn Ile Asp Gly
1115 1120 1125

Lys Trp Tyr His Phe Asp Glu Asn Gly Val Ala Ala Thr Gly Ala
1130 1135 1140

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

Gln Val Lys Gly Gly Val Val Lys Asn Ala Asp Gly Thr Tyr Ser
1160 1165 1170

Lys Tyr Lys Glu Gly Ser Gly Glu Leu Val Thr Asn Glu Phe Phe
1175 1180 1185

Thr Thr Asp Gly Asn Val Trp Tyr Tyr Ala Gly Ala Asp Gly Lys
1190 1195 1200

Thr Val Thr Gly Ala Gln Val Ile Asn Gly Gln His Leu Tyr Phe
1205 1210 1215

Lys Glu Asp Gly Ser Gln Val Lys Gly Gly Val Val Lys Asn Ala
1220 1225 1230

Asp Gly Thr Tyr Ser Lys Tyr Asp Ala Ala Thr Gly Glu Arg Leu
1235 1240 1245

Thr Asn Glu Phe Phe Thr Thr Gly Asp Asn Asn Trp Tyr Tyr Ile
1250 1255 1260

Gly Ser Asn Gly Lys Thr Val Thr Gly Glu Val Lys Ile Gly Ala
1265 1270 1275

Asp Thr Tyr Tyr Phe Ala Lys Asp Gly Lys Gln Val Lys Gly Gln
1280 1285 1290

Thr Val Thr Ala Gly Asn Gly Arg Ile Ser Tyr Tyr Tyr Gly Asp
1295 1300 1305

Ser Gly Lys Lys Ala Ile Ser Thr Trp Ile Glu Ile Gln Pro Gly
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Ile Tyr Val Tyr Phe Asp Lys Thr Gly Ile Ala Tyr Pro Pro Arg
1325 1330 1335

Val Leu Asn
1340

[0100]

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<211> 3918
<212> DNA
<213> 唾液链球菌（Streptococcus salivarius）

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ccgttgtatc gtgcggacgc gattccgaac aactctatct acgccgtgta caaccaagcg 180

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tatatgtctc aacagggttt tggtaacaaa acgtacacca cggatatgat gagctacgac 420

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tttctgaaca atagcgcaac gagccacgcg aatagcgact ttcgtctgat gaaccgtacc 660

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tggctgcact acattatgaa tattggcagc atcttgggta atgacccgag cgcgaatttt 840

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agcattctgg aagcgtggag ctataatgat catcagtaca acaaggacac gaagggcgca 1020

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[0101]

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<210> 32
<211> 1305
<212> PRT
<213> 唾液链球菌（Streptococcus salivarius）

<400> 32

Met Ile Asp Gly Lys Gln Tyr Tyr Val Glu Asn Gly Val Val Lys Lys
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Asn Ala Ala Ile Glu Leu Asp Gly Arg Leu Tyr Tyr Phe Asp Glu Thr
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[0102] Gly Ala Met Val Asp Gln Ser Lys Pro Leu Tyr Arg Ala Asp Ala Ile
35 40 45

Pro Asn Asn Ser Ile Tyr Ala Val Tyr Asn Gln Ala Tyr Asp Thr Ser
50 55 60

Ser Lys Ser Phe Glu His Leu Asp Asn Phe Leu Thr Ala Asp Ser Trp
65 70 75 80

Tyr Arg Pro Lys Gln Ile Leu Lys Asp Gly Lys Asn Trp Thr Ala Ser
85 90 95

Thr Glu Lys Asp Tyr Arg Pro Leu Leu Met Thr Trp Trp Pro Asp Lys
100 105 110

Val Thr Gln Val Asn Tyr Leu Asn Tyr Met Ser Gln Gln Gly Phe Gly
115 120 125

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

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

Asn Thr Thr Trp Leu Arg Gln Leu Met Ser Asp Phe Ile Lys Thr Gln
165 170 175

Pro Gly Trp Asn Ser Glu Ser Glu Asp Asn Leu Leu Val Gly Lys Asp
180 185 190

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His Leu Gln Gly Gly Ala Leu Thr Phe Leu Asn Asn Ser Ala Thr Ser
        195                 200                 205

His Ala Asn Ser Asp Phe Arg Leu Met Asn Arg Thr Pro Thr Asn Gln
    210                 215                 220

Thr Gly Thr Arg Lys Tyr His Ile Asp Arg Ser Asn Gly Gly Tyr Glu
225                 230                 235                 240

Leu Leu Leu Ala Asn Asp Ile Asp Asn Ser Asn Pro Ala Val Gln Ala
                245                 250                 255

Glu Gln Leu Asn Trp Leu His Tyr Ile Met Asn Ile Gly Ser Ile Leu
            260                 265                 270

Gly Asn Asp Pro Ser Ala Asn Phe Asp Gly Val Arg Ile Asp Ala Val
        275                 280                 285

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

Glu Lys Tyr Arg Val Ala Asp Asn Glu Ala Asn Ala Ile Ala His Leu
305                 310                 315                 320

Ser Ile Leu Glu Ala Trp Ser Tyr Asn Asp His Gln Tyr Asn Lys Asp
                325                 330                 335
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[0103]

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Thr Lys Gly Ala Gln Leu Ser Ile Asp Asn Pro Leu Arg Glu Thr Leu
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Leu Thr Thr Phe Leu Arg Lys Ser Asn Tyr Arg Gly Ser Leu Glu Arg
        355                 360                 365

Val Ile Thr Asn Ser Leu Asn Asn Arg Ser Ser Glu Gln Lys His Thr
    370                 375                 380

Pro Arg Asp Ala Asn Tyr Ile Phe Val Arg Ala His Asp Ser Glu Val
385                 390                 395                 400

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

Asp Gly Phe Thr Phe Thr Met Asp Glu Leu Lys Gln Ala Phe Glu Ile
            420                 425                 430

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

Ile Pro Ala Ala Tyr Ala Thr Met Leu Thr Asn Lys Asp Ser Ile Thr
    450                 455                 460

Arg Val Tyr Tyr Gly Asp Leu Phe Thr Asp Asp Gly Gln Tyr Met Ala
465                 470                 475                 480

Glu Lys Ser Pro Tyr Tyr Asn Ala Ile Asp Ala Leu Leu Arg Ala Arg
                485                 490                 495
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Ile Lys Tyr Val Ala Gly Gly Gln Asp Met Lys Val Thr Lys Leu Asn
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Gly Tyr Glu Ile Met Ser Ser Val Arg Tyr Gly Lys Gly Ala Glu Glu
515 520 525

Ala Asn Gln Leu Gly Thr Ala Glu Thr Arg Asn Gln Gly Met Leu Val
530 535 540

Leu Thr Ala Asn Arg Pro Asp Met Lys Leu Gly Ala Asn Asp Arg Leu
545 550 555 560

Val Val Asn Met Gly Ala Ala His Lys Asn Gln Ala Tyr Arg Pro Leu
565 570 575

Leu Leu Ser Lys Ser Thr Gly Leu Ala Thr Tyr Leu Lys Asp Ser Asp
580 585 590

Val Pro Ala Gly Leu Val Arg Tyr Thr Asp Asn Gln Gly Asn Leu Thr
595 600 605

Phe Thr Ala Asp Asp Ile Ala Gly His Ser Thr Val Glu Val Ser Gly
610 615 620

Tyr Leu Ala Val Trp Val Pro Val Gly Ala Ser Glu Asn Gln Asp Ala
625 630 635 640

[0104] Arg Thr Lys Ala Ser Ser Thr Lys Lys Gly Glu Gln Val Phe Glu Ser
645 650 655

Ser Ala Ala Leu Asp Ser Gln Val Ile Tyr Glu Gly Phe Ser Asn Phe
660 665 670

Gln Asp Phe Val Lys Thr Pro Ser Gln Tyr Thr Asn Arg Val Ile Ala
675 680 685

Gln Asn Ala Lys Leu Phe Lys Glu Trp Gly Ile Thr Ser Phe Glu Phe
690 695 700

Ala Pro Gln Tyr Val Ser Ser Gln Asp Gly Thr Phe Leu Asp Ser Ile
705 710 715 720

Ile Glu Asn Gly Tyr Ala Phe Glu Asp Arg Tyr Asp Ile Ala Met Ser
725 730 735

Lys Asn Asn Lys Tyr Gly Ser Leu Lys Asp Leu Met Asp Ala Leu Arg
740 745 750

Ala Leu His Ala Glu Gly Ile Ser Ala Ile Ala Asp Trp Val Pro Asp
755 760 765

Gln Ile Tyr Asn Leu Pro Gly Lys Glu Val Val Thr Ala Ser Arg Thr
770 775 780

Asn Ser Tyr Gly Thr Pro Arg Pro Asn Ala Glu Ile Tyr Asn Ser Leu
785 790 795 800

Tyr Ala Ala Lys Thr Arg Thr Phe Gly Asn Asp Phe Gln Gly Lys Tyr
805 810 815

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

Glu Arg Val Gln Ile Ser Asn Gly Arg Lys Leu Thr Thr Asn Glu Lys
835 840 845

Ile Thr Gln Trp Ser Ala Lys Tyr Phe Asn Gly Ser Asn Ile Gln Gly
850 855 860

Thr Gly Ala Arg Tyr Val Leu Gln Asp Asn Ala Thr Asn Gln Tyr Phe
865 870 875 880

Ser Val Lys Ala Gly Gln Thr Phe Leu Pro Lys Gln Met Thr Glu Ile
885 890 895

Thr Gly Ser Gly Phe Arg Arg Val Gly Asp Asp Val Gln Tyr Leu Ser
900 905 910

Ile Gly Gly Tyr Leu Ala Lys Asn Thr Phe Ile Gln Val Gly Ala Asn
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Gln Trp Tyr Tyr Phe Asp Lys Asn Gly Asn Met Val Thr Gly Glu Gln
930 935 940

[0105] Val Ile Asp Gly Lys Lys Tyr Phe Phe Leu Asp Asn Gly Leu Gln Leu
945 950 955 960

Arg His Val Leu Arg Gln Gly Ser Asp Gly His Val Tyr Tyr Tyr Asp
965 970 975

Pro Lys Gly Val Gln Ala Phe Asn Gly Phe Tyr Asp Phe Ala Gly Pro
980 985 990

Arg Gln Asp Val Arg Tyr Phe Asp Gly Asn Gly Gln Met Tyr Arg Gly
995 1000 1005

Leu His Asp Met Tyr Gly Thr Thr Phe Tyr Phe Asp Glu Lys Thr
1010 1015 1020

Gly Ile Gln Ala Lys Asp Lys Phe Ile Arg Phe Ala Asp Gly Arg
1025 1030 1035

Thr Arg Tyr Phe Ile Pro Asp Thr Gly Asn Leu Ala Val Asn Arg
1040 1045 1050

Phe Ala Gln Asn Pro Glu Asn Lys Ala Trp Tyr Tyr Leu Asp Ser
1055 1060 1065

Asn Gly Tyr Ala Val Thr Gly Leu Gln Thr Ile Asn Gly Lys Gln
1070 1075 1080

Tyr Tyr Phe Asp Asn Glu Gly Arg Gln Val Lys Gly His Phe Val
1085 1090 1095

Thr Ile Asn Asn Gln Arg Tyr Phe Leu Asp Gly Asp Ser Gly Glu
1100 1105 1110

Ile Ala Pro Ser Arg Phe Val Thr Glu Asn Asn Lys Trp Tyr Tyr
1115 1120 1125

Val Asp Gly Asn Gly Lys Leu Val Lys Gly Ala Gln Val Ile Asn
1130 1135 1140

Gly Asn His Tyr Tyr Phe Asn Asn Asp Tyr Ser Gln Val Lys Gly
1145 1150 1155

Ala Trp Ala Asn Gly Arg Tyr Tyr Asp Gly Asp Ser Gly Gln Ala
1160 1165 1170

Val Ser Asn Gln Phe Ile Gln Ile Ala Ala Asn Gln Trp Ala Tyr
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Leu Asn Gln Asp Gly His Lys Val Thr Gly Leu Gln Asn Ile Asn
1190 1195 1200

Asn Lys Val Tyr Tyr Phe Gly Ser Asn Gly Ala Gln Val Lys Gly
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Lys Leu Leu Thr Val Gln Gly Lys Lys Cys Tyr Phe Asp Ala His
1220 1225 1230

[0106] Thr Gly Glu Gln Val Val Asn Arg Phe Val Glu Ala Ala Arg Gly
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Cys Trp Tyr Tyr Phe Asn Ser Ala Gly Gln Ala Val Thr Gly Gln
1250 1255 1260

Gln Val Ile Asn Gly Lys Gln Leu Tyr Phe Asp Gly Ser Gly Arg
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Gln Val Lys Gly Arg Tyr Val Tyr Val Gly Gly Lys Arg Leu Phe
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Cys Asp Ala Lys Thr Gly Glu Leu Arg Gln Arg Arg
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<210> 33
<211> 4026
<212> DNA
<213> 唾液链球菌（Streptococcus salivarius）

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cgcatcagct actattacgg tgactctggt aaacgtgcgg ttagcacgtg ggttgaaatt 3960

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aattaa 4026

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<213> 唾液链球菌（Streptococcus salivarius）

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35 40 45

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

Ser Glu Ala Ser Phe Glu Leu Ile Asp Gly Tyr Leu Thr Ala Asp Ser
65 70 75 80

Trp Tyr Arg Pro Ala Ser Ile Ile Lys Asp Gly Val Thr Trp Gln Ala
85 90 95

Ser Thr Ala Glu Asp Phe Arg Pro Leu Leu Met Ala Trp Trp Pro Asn
100 105 110

Val Asp Thr Gln Val Asn Tyr Leu Asn Tyr Met Ser Lys Val Phe Asn
115 120 125

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

Ala Ala Lys Asp Ile Gln Val Lys Ile Glu Gln Lys Ile Gln Ala Glu
145 150 155 160

Lys Ser Thr Gln Trp Leu Arg Glu Thr Ile Ser Ala Phe Val Lys Thr
165 170 175

Gln Pro Gln Trp Asn Lys Glu Thr Glu Asn Tyr Ser Lys Gly Gly Gly
180 185 190

Glu Asp His Leu Gln Gly Gly Ala Leu Leu Tyr Val Asn Asp Ser Arg
195 200 205

Thr Pro Trp Ala Asn Ser Asn Tyr Arg Leu Leu Asn His Thr Ala Thr
210 215 220

[0109] Asn Gln Lys Gly Thr Ile Asp Lys Ser Val Leu Asp Glu Gln Ser Asp
225 230 235 240

Pro Asn His Met Gly Gly Phe Asp Phe Leu Leu Ala Asn Asp Val Asp
245 250 255

Leu Ser Asn Pro Val Val Gln Ala Glu Gln Leu Asn Gln Ile His Tyr
260 265 270

Leu Met Asn Trp Gly Ser Ile Val Met Gly Asp Lys Asp Ala Asn Phe
275 280 285

Asp Gly Ile Arg Val Asp Ala Val Asp Asn Val Asp Ala Asp Met Leu
290 295 300

Gln Leu Tyr Thr Asn Tyr Phe Arg Glu Tyr Tyr Gly Val Asn Lys Ser
305 310 315 320

Glu Ala Asn Ala Leu Ala His Ile Ser Val Leu Glu Ala Trp Ser Leu
325 330 335

Asn Asp Asn His Tyr Asn Asp Lys Thr Asp Gly Ala Ala Leu Ala Met
340 345 350

Glu Asn Lys Gln Arg Leu Ala Leu Leu Phe Ser Leu Ala Lys Pro Ile
355 360 365

Lys Glu Arg Thr Pro Ala Val Ser Pro Leu Tyr Asn Asn Thr Phe Asn
370 375 380

Thr Thr Gln Arg Asp Glu Lys Thr Asp Trp Ile Asn Lys Asp Gly Ser
385 390 395 400

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

Tyr Asn Glu Lys Tyr Gly Asp Ala Ser Gly Asn Tyr Val Phe Ile Arg
420 425 430

Ala His Asp Asn Asn Val Gln Asp Ile Ile Ala Glu Ile Ile Lys Lys
435 440 445

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

Lys Lys Ala Phe Glu Ile Tyr Asn Lys Asp Met Leu Ser Ser Asp Lys
465 470 475 480

Lys Tyr Thr Leu Asn Asn Ile Pro Ala Ala Tyr Ala Val Met Leu Gln
485 490 495

Asn Met Glu Thr Ile Thr Arg Val Tyr Tyr Gly Asp Leu Tyr Thr Asp
500 505 510

Asn Gly Asn Tyr Met Glu Thr Lys Ser Pro Tyr Tyr Asp Thr Ile Val
515 520 525

[0110] Asn Leu Met Lys Asn Arg Ile Lys Tyr Val Ser Gly Gly Gln Ala Gln
530 535 540

Arg Ser Tyr Trp Leu Pro Thr Asp Gly Lys Met Asp Asn Ser Asp Val
545 550 555 560

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

Asp Ile Met Thr Ala Asp Asp Thr Glu Gly Ser Lys Tyr Ser Arg Thr
580 585 590

Ser Gly Gln Val Thr Leu Val Ala Asn Asn Pro Lys Leu Thr Leu Asp
595 600 605

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

Lys Tyr Arg Ala Leu Ile Val Gly Thr Ala Asp Gly Ile Lys Asn Phe
625 630 635 640

Thr Ser Asp Ala Asp Ala Ile Ala Ala Gly Tyr Val Lys Glu Thr Asp
645 650 655

Ser Asn Gly Val Leu Thr Phe Gly Ala Asn Asp Ile Lys Gly Tyr Glu
660 665 670

Thr Phe Asp Met Ser Gly Phe Val Ala Val Trp Val Pro Val Gly Ala
675 680 685

Ser Asp Asp Gln Asp Ile Arg Val Ala Pro Ser Thr Glu Ala Lys Lys
690 695 700

Glu Gly Glu Leu Thr Leu Lys Ala Thr Glu Ala Tyr Asp Ser Gln Leu
705 710 715 720

Ile Tyr Glu Gly Phe Ser Asn Phe Gln Thr Ile Pro Asp Gly Ser Asp
725 730 735

Pro Ser Val Tyr Thr Asn Arg Lys Ile Ala Glu Asn Val Asp Leu Phe
740 745 750

Lys Ser Trp Gly Val Thr Ser Phe Glu Met Ala Pro Gln Phe Val Ser
755 760 765

Ala Asp Asp Gly Thr Phe Leu Asp Ser Val Ile Gln Asn Gly Tyr Ala
770 775 780

Phe Ala Asp Arg Tyr Asp Leu Ala Met Ser Lys Asn Asn Lys Tyr Gly
785 790 795 800

Ser Lys Glu Asp Leu Arg Asp Ala Leu Lys Ala Leu His Lys Ala Gly
805 810 815

Ile Gln Ala Ile Ala Asp Trp Val Pro Asp Gln Ile Tyr Gln Leu Pro
820 825 830

[0111] Gly Lys Glu Val Val Thr Ala Thr Arg Thr Asp Gly Ala Gly Arg Lys
835 840 845

Ile Ala Asp Ala Ile Ile Asp His Ser Leu Tyr Val Ala Asn Thr Lys
850 855 860

Ser Ser Gly Lys Asp Tyr Gln Ala Lys Tyr Gly Gly Glu Phe Leu Ala
865 870 875 880

Glu Leu Lys Ala Lys Tyr Pro Glu Met Phe Lys Val Asn Met Ile Ser
885 890 895

Thr Gly Lys Pro Ile Asp Asp Ser Val Lys Leu Lys Gln Trp Lys Ala
900 905 910

Glu Tyr Phe Asn Gly Thr Asn Val Leu Glu Arg Gly Val Gly Tyr Val
915 920 925

Leu Ser Asp Glu Ala Thr Gly Lys Tyr Phe Thr Val Thr Lys Asp Gly
930 935 940

Asn Phe Ile Pro Leu Gln Leu Thr Gly Asn Glu Lys Val Val Thr Gly
945 950 955 960

Phe Ser Asn Asp Gly Lys Gly Ile Thr Tyr Phe Gly Thr Ser Gly Thr
965 970 975

Gln Ala Lys Ser Ala Phe Val Thr Phe Asn Gly Asn Thr Tyr Tyr Phe
980 985 990

Asp Ala Arg Gly His Met Val Thr Asn Gly Glu Tyr Ser Pro Asn Gly
995 1000 1005

Lys Asp Val Tyr Arg Phe Leu Pro Asn Gly Ile Met Leu Ser Asn
1010 1015 1020

Ala Phe Tyr Val Asp Ala Asn Gly Asn Thr Tyr Leu Tyr Asn Ser
1025 1030 1035

Lys Gly Gln Met Tyr Lys Gly Gly Tyr Thr Lys Phe Asp Val Thr
1040 1045 1050

Glu Thr Asp Lys Asp Gly Lys Glu Ser Lys Val Val Lys Phe Arg
1055 1060 1065

Tyr Phe Thr Asn Glu Gly Val Met Ala Lys Gly Val Thr Val Ile
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Asp Gly Phe Thr Gln Tyr Phe Gly Glu Asp Gly Phe Gln Ala Lys
1085 1090 1095

Asp Lys Leu Val Thr Phe Lys Gly Lys Thr Tyr Tyr Phe Asp Ala
1100 1105 1110

His Thr Gly Asn Ala Ile Lys Asn Thr Trp Arg Asn Ile Asp Gly
1115 1120 1125

[0112] Lys Trp Tyr His Phe Asp Ala Asn Gly Val Ala Ala Thr Gly Ala
1130 1135 1140

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

Gln Val Lys Gly Gly Val Val Lys Asn Ala Asp Gly Thr Tyr Ser
1160 1165 1170

Lys Tyr Lys Glu Gly Ser Gly Glu Leu Val Thr Asn Glu Phe Phe
1175 1180 1185

Thr Thr Asp Gly Asn Val Trp Tyr Tyr Ala Gly Ala Asn Gly Lys
1190 1195 1200

Thr Val Thr Gly Ala Gln Val Ile Asn Gly Gln His Leu Tyr Phe
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Asn Ala Asp Gly Ser Gln Val Lys Gly Gly Val Val Lys Asn Ala
1220 1225 1230

Asp Gly Thr Tyr Ser Lys Tyr Asp Ala Ala Thr Gly Glu Arg Leu
1235 1240 1245

Thr Asn Glu Phe Phe Thr Thr Gly Asp Asn Asn Trp Tyr Tyr Ile
1250 1255 1260

Gly Ala Asn Gly Lys Thr Val Thr Gly Glu Val Lys Ile Gly Asp
1265 1270 1275

Asp Thr Tyr Tyr Phe Ala Lys Asp Gly Lys Gln Val Lys Gly Gln
1280 1285 1290

Thr Val Ser Ala Gly Asn Gly Arg Ile Ser Tyr Tyr Tyr Gly Asp
1295 1300 1305

Ser Gly Lys Arg Ala Val Ser Thr Trp Val Glu Ile Gln Pro Gly
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Val Tyr Val Tyr Phe Asp Lys Asn Gly Leu Ala Tyr Pro Pro Arg
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Val Leu Asn
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<213> 唾液链球菌（Streptococcus salivarius）

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gtgctgggtg agcgtgtcac caacacctgg atcaccttcc aagacggcaa aaccgtgttc      3960

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<212>  PRT
<213>  唾液链球菌（Streptococcus salivarius）

<400>  36

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


Asp Gly Ala Leu Thr Ser Thr Ser Thr His Ser Phe Thr Pro Gly Thr
        35                  40                  45


Thr Asn Leu Val Asp Ala Phe Ser Ser His Asn Arg Ala Tyr Asp Ser
    50                  55                  60


Lys Lys Glu Ser Phe Glu Leu Val Asp Gly Tyr Leu Thr Pro Asn Ser
65                  70                  75                  80


[0115] Trp Tyr Arg Pro Val Thr Ile Leu Glu Asn Gly Glu Lys Trp Arg Val
                       85                  90                  95


Ser Thr Glu Lys Asp Phe Arg Pro Leu Leu Met Ala Trp Trp Pro Asp
            100                 105                 110


Val Asp Thr Gln Val Ala Tyr Leu Asn Thr Phe Ser Lys His Phe Asn
        115                 120                 125


Leu Asn Ala Thr Tyr Ser Thr Ser Gln Ser Gln Ser Glu Leu Asn Ala
    130                 135                 140


Ala Ala Lys Thr Ile Gln Ile Lys Ile Glu Gln Glu Ile Ser Ala Lys
145                 150                 155                 160


Lys Ser Thr Glu Trp Leu Arg Gln Ala Ile Glu Ser Phe Val Lys Glu
                165                 170                 175


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


Leu Gln Gly Gly Ala Leu Leu Tyr Val Asn Asn Asp Lys Thr Pro Trp
        195                 200                 205


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


Gly Ser Leu Asn Gly Thr Gly Arg Tyr Leu Gly Gly Tyr Glu Phe Leu
225                 230                 235                 240
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Leu Ala Asn Asp Val Asp Asn Ser Asn Pro Val Val Gln Ala Glu Gln
245 250 255

Leu Asn Gln Ile His Tyr Leu Val Asn Trp Gly Ser Ile Val Met Gly
260 265 270

Asp Lys Asp Ala Asn Phe Asp Gly Ile Arg Val Asp Ala Val Asp Asn
275 280 285

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

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

Leu Glu Ala Trp Asp Leu Asn Asp Asn Ala Tyr Asn Gln Lys His Asp
325 330 335

Gly Ala Ala Leu Ala Met Asp Asn Asn Leu Arg Tyr Ala Ile Met Gly
340 345 350

Ala Leu Tyr Gly Ser Gly Ser Ser Leu Lys Asp Leu Ile Thr Ser Ser
355 360 365

Leu Thr Asp Arg Thr Asn Asn Ser Lys Tyr Gly Asp Thr Gln Ala Asn
370 375 380

[0116] Tyr Ile Phe Ala Arg Ala His Asp Asn Leu Val Gln Asp Ile Ile Arg
385 390 395 400

Asp Ile Val Gln Lys Glu Ile Asn Pro Lys Ser Asp Gly Tyr Thr Met
405 410 415

Thr Asp Ala Glu Leu Lys Arg Ala Phe Glu Ile Tyr Asn Glu Asp Met
420 425 430

Lys Lys Ala Glu Lys Arg Tyr Thr Ile Asn Asn Ile Pro Ala Ala Tyr
435 440 445

Ala Leu Ile Leu Gln Asn Met Glu Gln Val Thr Arg Val Tyr Tyr Gly
450 455 460

Asp Leu Tyr Thr Asp Asn Gly Gln Tyr Met Ala Thr Lys Ser Pro Tyr
465 470 475 480

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

Gly Gly Gln Ser Met Lys Val Asp Thr Phe Asn Gly Lys Glu Ile Leu
500 505 510

Ser Ser Val Arg Tyr Gly Lys Asp Ile Met Thr Ala Asp Gln Thr Thr
515 520 525

Gly Val Ala Glu Thr Ser Lys His Ser Gly Met Leu Thr Leu Ile Ala
530 535 540

Asn Asn Gln Asp Phe Ser Leu Gly Asp Gly Thr Leu Lys Val Asn Met
545   550   555   560

Gly Lys Leu His Ala Asn Gln Ala Tyr Arg Pro Leu Leu Leu Gly Thr
                565   570   575

Asp Lys Gly Ile Val Thr Tyr Glu Asn Asp Ala Ala Ala Ala Gly Lys
            580   585   590

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

Ile Lys Gly Tyr Arg Thr Val Asp Met Arg Gly Tyr Leu Gly Val Trp
    610   615   620

Val Pro Val Gly Ala Pro Asp Asn Gln Asp Ile Arg Val Lys Gly Ser
625   630   635   640

Asp Lys Lys Leu Asp Lys Thr Phe Ser Ala Thr Glu Ala Leu Asp Ser
                645   650   655

Gln Val Ile Tyr Glu Gly Phe Ser Asn Phe Gln Asp Phe Val Glu Lys
            660   665   670

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

[0117] Lys Ser Trp Gly Ile Thr Ser Phe Glu Met Ala Pro Gln Phe Val Ser
    690   695   700

Ala Asp Asp Arg Thr Phe Leu Asp Ser Val Ile Gln Asn Gly Tyr Ala
705   710   715   720

Phe Thr Asp Arg Tyr Asp Leu Ala Met Ser Lys Asn Asn Lys Tyr Gly
                725   730   735

Ser Lys Glu Asp Leu Arg Asp Ala Leu Lys Ala Leu His Lys Gln Gly
            740   745   750

Ile Gln Ala Ile Ala Asp Trp Val Pro Asp Gln Leu Tyr Gln Leu Pro
        755   760   765

Gly Gln Glu Val Val Thr Ala Thr Arg Ala Asn Ser Tyr Gly Thr Pro
    770   775   780

Lys Ala Asn Ala Tyr Ile Asn Asn Thr Leu Tyr Val Ala Asn Ser Lys
785   790   795   800

Ser Ser Gly Lys Asp Phe Gln Ala Gln Tyr Gly Gly Glu Phe Leu Asp
                805   810   815

Glu Leu Gln Lys Lys Tyr Pro Gln Leu Phe Glu Asp Val Met Ile Ser
            820   825   830

Thr Gly Lys Lys Ile Asp Pro Ser Val Lys Ile Lys Gln Trp Ser Ala
        835   840   845

Lys Tyr Met Asn Gly Thr Asn Ile Leu Gly Arg Gly Asn Arg Tyr Val
850 855 860

Leu Ser Asn Asp Ala Thr Gly Arg Tyr Tyr Gln Val Thr Asp Asn Gly
865 870 875 880

Ile Phe Leu Pro Lys Pro Leu Thr Asp Gln Gly Gly Lys Thr Gly Phe
885 890 895

Tyr Tyr Asp Gly Lys Gly Met Ala Tyr Phe Asp Asn Ser Gly Phe Gln
900 905 910

Ala Lys Asn Ala Phe Ile Lys Tyr Ala Gly Asn Tyr Tyr Tyr Phe Asp
915 920 925

Lys Glu Gly Tyr Met Leu Thr Gly Arg Gln Asp Ile Asp Ser Lys Thr
930 935 940

Tyr Phe Phe Leu Pro Asn Gly Ile Gln Leu Arg Asp Ser Ile Tyr Gln
945 950 955 960

Gln Asp Gly Lys Tyr Tyr Tyr Phe Gly Ser Phe Gly Glu Gln Tyr Lys
965 970 975

Asp Gly Tyr Phe Val Phe Asp Val Pro Lys Glu Gly Thr Ser Glu Thr
980 985 990

[0118] Glu Ala Lys Phe Arg Tyr Phe Ser Pro Thr Gly Glu Met Ala Val Gly
995 1000 1005

Leu Thr Tyr Ala Gly Gly Gly Leu Gln Tyr Phe Asp Glu Asn Gly
1010 1015 1020

Phe Gln Ala Lys Gly Thr Lys Tyr Val Thr Pro Asp Gly Lys Leu
1025 1030 1035

Tyr Phe Phe Asp Lys Asn Ser Gly Asn Ala Tyr Thr Asn Arg Trp
1040 1045 1050

Ala Glu Ile Asp Gly Ile Trp Tyr Glu Phe Asn Asp Gln Gly Tyr
1055 1060 1065

Ala Gln Ala Lys Lys Gly Glu Phe Tyr Thr Thr Asp Gly Ser Thr
1070 1075 1080

Trp Phe Tyr Arg Asp Ala Ala Gly Lys Asn Val Thr Gly Ala Leu
1085 1090 1095

Thr Leu Asp Gly His Glu Tyr Tyr Phe Arg Ala Asn Gly Ala Gln
1100 1105 1110

Val Lys Gly Glu Phe Val Thr Glu Asn Gly Lys Ile Ser Tyr Tyr
1115 1120 1125

Thr Val Asp Asn Gly Tyr Lys Val Lys Asp Lys Phe Phe Glu Val
1130 1135 1140

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       Asn Gly  Lys Trp Tyr His Ala  Asp Lys Asp Gly Asn  Leu Ala Thr
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       Gly Arg  Gln Thr Ile Asp His  Leu Asn Tyr Tyr Phe  Asn Ala Asp
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       Gly Ser  Gln Val Lys Ser Asp  Phe Phe Thr Leu Asp  Gly Gly Lys
           1175                 1180                 1185

       Thr Trp  Tyr Tyr Ala Lys Asp  Asn Gly Glu Ile Val  Thr Gly Ala
           1190                 1195                 1200

       Tyr Ser  Val Arg Gly Lys Asn  Tyr Tyr Phe Lys Glu  Asp Gly Ser
           1205                 1210                 1215

       Gln Val  Lys Gly Asp Phe Val  Lys Asn Ala Asp Gly  Ser Leu Ser
           1220                 1225                 1230

       Tyr Tyr  Asp Lys Asp Ser Gly  Glu Arg Leu Asn Asn  Arg Phe Leu
           1235                 1240                 1245

       Thr Thr  Gly Asn Asn Val Trp  Tyr Tyr Phe Lys Asp  Gly Lys Ala
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       Val Thr  Gly Arg Gln Asn Ile  Asp Gly Lys Glu Tyr  Tyr Phe Asp
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       His Leu  Gly Arg Gln Val Lys  Gly Ser Pro Ile Ser  Thr Pro Lys
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       Gly Val  Glu Tyr Tyr Glu Ser  Val Leu Gly Glu Arg  Val Thr Asn
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       Thr Trp  Ile Thr Phe Gln Asp  Gly Lys Thr Val Phe  Phe Asp Glu
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       <212>  DNA
       <213>  唾液链球菌（Streptococcus salivarius）

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       ccgctgtatc gcgcggatgc aatcccgaac aactctatct acgcagttta caaccaggct     180

       tacgacacca gcagcaagag ctttgaacac ctggacaact ttctgacggc cgatagctgg     240

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       ctggcggcag cggcggaaac ggttcagcgt ggcatcgaag agcgtattgg tcgtgagggt     480

       aatacgacgt ggctgcgtca gttgatgagc gacttcatca aaacccagcc gggctggaat     540
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[0121]

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<211> 1305
<212> PRT
<213> 唾液链球菌（Streptococcus salivarius）

<400> 38

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Gly Ala Met Val Asp Gln Ser Lys Pro Leu Tyr Arg Ala Asp Ala Ile
        35                  40                  45

Pro Asn Asn Ser Ile Tyr Ala Val Tyr Asn Gln Ala Tyr Asp Thr Ser
    50                  55                  60

Ser Lys Ser Phe Glu His Leu Asp Asn Phe Leu Thr Ala Asp Ser Trp
65                  70                  75                  80

Tyr Arg Pro Lys Gln Ile Leu Lys Asp Gly Lys Asn Trp Thr Ala Ser
                85                  90                  95

Thr Glu Lys Asp Tyr Arg Pro Leu Leu Met Thr Trp Trp Pro Asp Lys
            100                 105                 110

Val Thr Gln Val Asn Tyr Leu Asn Tyr Met Ser Gln Gln Gly Phe Gly
        115                 120                 125
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Asn Lys Thr Tyr Thr Thr Asp Met Met Ser Tyr Asp Leu Ala Ala Ala
130 135 140

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

Asn Thr Thr Trp Leu Arg Gln Leu Met Ser Asp Phe Ile Lys Thr Gln
165 170 175

Pro Gly Trp Asn Ser Glu Ser Glu Asp Asn Leu Leu Val Gly Lys Asp
180 185 190

His Leu Gln Gly Gly Ala Leu Thr Phe Leu Asn Asn Ser Thr Thr Ser
195 200 205

His Ala Asn Ser Asp Phe Arg Leu Met Asn Arg Thr Pro Thr Asn Gln
210 215 220

Thr Gly Thr Arg Lys Tyr His Ile Asp Arg Ser Asn Gly Gly Tyr Glu
225 230 235 240

Leu Leu Leu Ala Asn Asp Ile Asp Asn Ser Asn Pro Ala Val Gln Ala
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Glu Gln Leu Asn Trp Leu His Tyr Ile Met Asn Ile Gly Ser Ile Leu
260 265 270

[0122] Gly Asn Asp Pro Ser Ala Asn Phe Asp Gly Val Arg Ile Asp Ala Val
275 280 285

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

Glu Lys Tyr Arg Val Ala Asp Asn Glu Ala Asn Ala Ile Ala His Leu
305 310 315 320

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

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

Leu Thr Thr Phe Leu Arg Lys Ser Asn Tyr Arg Gly Ser Leu Glu Arg
355 360 365

Val Ile Thr Asn Ser Leu Asn Asn Arg Ser Ser Glu Gln Lys His Thr
370 375 380

Pro Arg Asp Ala Asn Tyr Ile Phe Val Arg Ala His Asp Ser Glu Val
385 390 395 400

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

Asp Gly Phe Thr Phe Thr Met Asp Glu Leu Lys Gln Ala Phe Glu Ile
420 425 430

```
Tyr Asn Ala Asp Met Arg Lys Ala Asp Lys Lys Tyr Thr Gln Tyr Asn
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Ile Pro Ala Ala Tyr Ala Thr Met Leu Thr Asn Lys Asp Ser Ile Thr
    450                 455                 460

Arg Val Tyr Tyr Gly Asp Leu Phe Thr Asp Asp Gly Gln Tyr Met Ala
465                 470                 475                 480

Glu Lys Ser Pro Tyr Tyr Asn Ala Ile Asp Ala Leu Leu Arg Ala Arg
                485                 490                 495

Ile Lys Tyr Val Ala Gly Gly Gln Asp Met Lys Val Thr Lys Leu Asn
            500                 505                 510

Gly Tyr Glu Ile Met Ser Ser Val Arg Tyr Gly Lys Gly Ala Glu Glu
        515                 520                 525

Ala Asn Gln Leu Gly Thr Ala Glu Thr Arg Asn Gln Gly Met Leu Val
    530                 535                 540

Leu Thr Ala Asn Arg Pro Asp Met Lys Leu Gly Thr Asn Asp Arg Leu
545                 550                 555                 560

Val Val Asn Met Gly Ala Ala His Lys Asn Gln Ala Tyr Arg Pro Leu
                565                 570                 575
```

[0123]

```
Leu Leu Ser Lys Ser Thr Gly Leu Ala Thr Tyr Leu Lys Asp Ser Asp
            580                 585                 590

Val Pro Ala Gly Leu Val Arg Tyr Thr Asp Asn Gln Gly Asn Leu Thr
        595                 600                 605

Phe Thr Ala Asp Asp Ile Thr Gly His Ser Thr Val Glu Val Ser Gly
    610                 615                 620

Tyr Leu Ala Val Trp Val Pro Val Gly Ala Ser Glu Asn Gln Asp Ala
625                 630                 635                 640

Arg Thr Lys Ala Ser Thr Thr Lys Lys Gly Glu Gln Val Phe Glu Ser
                645                 650                 655

Ser Ala Ala Leu Asp Ser Gln Val Ile Tyr Glu Gly Phe Ser Asn Phe
            660                 665                 670

Gln Asp Phe Val Lys Thr Pro Ser Gln Tyr Thr Asn Arg Val Ile Ala
        675                 680                 685

Gln Asn Ala Lys Arg Phe Lys Glu Trp Gly Ile Thr Ser Phe Glu Phe
    690                 695                 700

Ala Pro Gln Tyr Val Ser Ser Gln Asp Gly Thr Phe Leu Asp Ser Ile
705                 710                 715                 720

Ile Glu Asn Gly Tyr Ala Phe Glu Asp Arg Tyr Asp Ile Ala Met Ser
                725                 730                 735
```

```
Lys Asn Asn Lys Tyr Gly Ser Leu Lys Asp Leu Met Asp Ala Leu Arg
            740                 745                 750

Ala Leu His Ala Glu Gly Ile Ser Ala Ile Ala Asp Trp Val Pro Asp
        755                 760                 765

Gln Ile Tyr Asn Leu Pro Gly Lys Glu Val Val Thr Ala Ser Arg Thr
    770                 775                 780

Asn Ser Tyr Gly Thr Pro Arg Pro Asn Ala Glu Ile Tyr Asn Ser Leu
785                 790                 795                 800

Tyr Ala Ala Lys Thr Arg Thr Phe Gly Asn Asp Phe Gln Gly Lys Tyr
                805                 810                 815

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

Glu Arg Val Gln Ile Ser Asn Gly Arg Lys Leu Thr Thr Asn Glu Lys
        835                 840                 845

Ile Thr Gln Trp Ser Ala Lys Tyr Phe Asn Gly Ser Asn Ile Gln Gly
    850                 855                 860

Thr Gly Ala Arg Tyr Val Leu Gln Asp Asn Ala Thr Asn Gln Tyr Phe
865                 870                 875                 880
```

[0124]

```
Asn Leu Lys Ala Gly Gln Thr Phe Leu Pro Lys Gln Met Thr Glu Ile
                885                 890                 895

Thr Ala Thr Gly Phe Arg Arg Val Gly Asp Lys Val Gln Tyr Leu Ser
            900                 905                 910

Thr Ser Gly Tyr Leu Ala Lys Asn Thr Phe Ile Gln Ile Gly Ala Asn
        915                 920                 925

Gln Trp Tyr Tyr Phe Asp Lys Asn Gly Asn Met Val Thr Gly Glu Gln
    930                 935                 940

Val Ile Asp Gly Lys Lys Tyr Phe Phe Leu Asp Asn Gly Leu Gln Leu
945                 950                 955                 960

Arg His Val Leu Arg Gln Gly Ser Asp Gly His Val Tyr Tyr Tyr Asp
                965                 970                 975

Pro Lys Gly Val Gln Ala Phe Asn Gly Phe Tyr Asp Phe Ala Gly Pro
            980                 985                 990

Arg Gln Asp Val Arg Tyr Phe Asp  Gly Asn Gly Gln Met  Tyr Arg Gly
        995                 1000                 1005

Leu His  Asp Met Tyr Gly Thr  Thr Phe Tyr Phe Asp  Glu Lys Thr
    1010                 1015                 1020

Gly Ile  Gln Ala Lys Asp Lys  Phe Ile Arg Phe Ala  Asp Gly Arg
    1025                 1030                 1035
```

Thr Arg Tyr Phe Ile Pro Asp Thr Gly Asn Leu Ala Val Asn Arg
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Phe Ala Gln Asn Pro Glu Asn Lys Ala Trp Tyr Tyr Leu Asp Ser
1055 1060 1065

Asn Gly Tyr Ala Val Thr Gly Leu Gln Thr Ile Asn Gly Lys Gln
1070 1075 1080

Tyr Tyr Phe Asp Asn Glu Gly Arg Gln Val Lys Gly His Phe Val
1085 1090 1095

Thr Ile Asn Asn Gln Arg Tyr Phe Leu Asp Gly Asp Ser Gly Glu
1100 1105 1110

Ile Ala Arg Ser Arg Phe Val Thr Glu Asn Asn Lys Trp Tyr Tyr
1115 1120 1125

Val Asp Gly Asn Gly Lys Leu Val Lys Gly Ala Gln Val Ile Asn
1130 1135 1140

Gly Asn His Tyr Tyr Phe Asn Asn Asp Tyr Ser Gln Val Lys Gly
1145 1150 1155

Ala Trp Ala Asn Gly Arg Tyr Tyr Asp Gly Asp Ser Gly Gln Ala
1160 1165 1170

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1175 1180 1185

Leu Asn Gln Asn Gly Gln Lys Val Val Gly Leu Gln His Ile Asn
1190 1195 1200

Gly Lys Leu Tyr Tyr Phe Glu Gly Asn Gly Val Gln Ala Lys Gly
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Lys Leu Leu Thr Tyr Lys Gly Lys Lys Tyr Tyr Phe Asp Ala Asn
1220 1225 1230

Ser Gly Glu Ala Val Thr Asn Arg Phe Ile Gln Ile Ser Arg Gly
1235 1240 1245

Val Trp Tyr Tyr Phe Asn Ala Ser Gly Gln Ala Val Thr Gly Glu
1250 1255 1260

Gln Val Ile Asn Gly Gln His Leu Tyr Phe Asp Ala Ser Gly Arg
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Gln Val Lys Gly Arg Tyr Val Trp Ile Lys Gly Gln Arg Arg Tyr
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Tyr Asp Ala Asn Thr Gly Ala Trp Val Arg Asn Arg
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<211> 3933

<212> DNA
<213> 解没食子酸链球菌（Streptococcus gallolyticus）

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<213> 解没食子酸链球菌（Streptococcus gallolyticus）

<400> 40

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


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

```
Glu Thr Gly Ala Leu Thr Ser Thr Ser Thr Tyr Ser Phe Thr Glu Gly
        35                  40                  45

Leu Thr Asn Leu Val Asp Asn Phe Ser Lys Asn Asn Gln Ala Tyr Asp
    50                  55                  60

Ser Thr Glu Lys Ser Phe Glu Leu Val Asp Gly Tyr Leu Thr Ala Asn
65                  70                  75                  80

Ser Trp Tyr Arg Pro Thr Lys Val Leu Glu Asn Gly Glu Thr Trp Val
                85                  90                  95

Asp Ser Thr Glu Glu Ser Phe Arg Pro Leu Val Met Ala Trp Trp Pro
            100                 105                 110

Asp Val Asp Thr Gln Ile Asn Tyr Leu Asn Ser Met Ser Glu Tyr Phe
        115                 120                 125

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

Val Ala Ala Glu Ala Ile Gln Val Lys Ile Glu Gln Glu Ile Ala Arg
145                 150                 155                 160

Arg Gly Ser Thr Glu Trp Leu Arg Glu Val Ile Ser Ser Phe Val Thr
                165                 170                 175
```

[0128]

```
Thr Gln Asp Lys Trp Asn Met Asn Ser Glu Asp Arg Asp Thr Asp His
            180                 185                 190

Leu Gln Gly Gly Ala Leu Leu Tyr Val Asn Ser Asp Leu Thr Glu Trp
        195                 200                 205

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

Gly Glu Thr Lys Tyr His Lys Ala Asp Arg Thr Gly Gly Tyr Asp Phe
225                 230                 235                 240

Leu Leu Ala Asn Asp Val Asp Asn Ser Asn Pro Val Val Gln Ala Glu
                245                 250                 255

Gln Leu Asn Gln Leu Tyr Tyr Leu Met Asn Trp Gly Lys Ile Val Phe
            260                 265                 270

Gly Asp Ala Asp Ala Asn Phe Asp Gly Val Arg Val Asp Ala Val Asp
        275                 280                 285

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

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

Ile Leu Glu Ala Trp Ser Phe Asn Asp Pro Asp Tyr Asn His Asp Thr
                325                 330                 335
```

Asn Gly Ala Ala Leu Ala Ile Asp Asn Gly Leu Arg Met Ala Phe Leu
340 345 350

Asp Ala Leu Thr Arg Pro Leu Asp Ser Arg Thr Asn Leu Glu Ser Leu
355 360 365

Ile His Asn Asp Leu Gly Met Thr Asp Arg Thr Val Asp Ser Ala Tyr
370 375 380

Gly Asp Ala Met Pro Ser Tyr Ala Phe Val Arg Ala His Asp Ser Glu
385 390 395 400

Val Gln Gly Ile Ile Ala Ser Ile Ile Ala Gly Gln Ile Asn Pro Lys
405 410 415

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

Ile Tyr Asn Ala Asp Met Asn Ser Val His Lys Lys Tyr Thr His Phe
435 440 445

Asn Ile Pro Ala Ala Tyr Ala Leu Leu Leu Thr Asn Met Glu Ser Val
450 455 460

Pro Arg Val Tyr Tyr Gly Asp Leu Phe Thr Asp Asn Gly Gln Tyr Met
465 470 475 480

[0129] Ala Val Lys Ser Pro Tyr Tyr Asp Gln Ile Thr Ala Leu Leu Lys Ser
485 490 495

Arg Ile Lys Tyr Ala Ala Gly Gly Gln Ala Met Asn Val Gln Tyr Pro
500 505 510

Asp Gly Ala Gly Ala Gly Ile Leu Thr Ser Val Arg Phe Gly Tyr Gly
515 520 525

Ile Met Thr Ala Asp Gln Lys Ala Thr Asp Asp Ser Val Thr Thr Ser
530 535 540

Gly Ile Val Thr Ile Val Ser Asn Asn Pro Asn Leu Lys Leu Asn Ser
545 550 555 560

Ser Asp Lys Ile Ala Val Gln Val Gly Leu Ala His Ala Gly Gln Tyr
565 570 575

Tyr Arg Pro Leu Leu Ser Pro Thr Glu Asn Gly Leu Gln Val Phe Leu
580 585 590

Asn Asp Ser Asp Thr Asp Ile Thr Lys Leu Val Asp Asp Asn Gly Tyr
595 600 605

Ile Tyr Phe Thr Gly Asp Glu Ile Lys Gly Phe Glu Thr Val Asp Met
610 615 620

Asn Gly Phe Leu Thr Val Trp Val Pro Val Gly Ala Ala Ala Asp Gln
625 630 635 640

Asp Ile Arg Val Lys Ala Ser Thr Glu Ala Lys Lys Asp Gly Glu Leu
645 650 655

Thr Tyr Glu Thr Ser Ala Ala Leu Asp Ser Gln Val Ile Phe Glu Gly
660 665 670

Phe Ser Asn Phe Gln Asp Phe Val Gln Asp Pro Ser Gln Tyr Thr Asn
675 680 685

Lys Val Ile Ala Glu Asn Ala Asp Leu Phe Ala Ser Trp Gly Ile Thr
690 695 700

Ser Phe Glu Leu Ala Pro Gln Tyr Val Ser Ser Thr Asp Gly Thr Phe
705 710 715 720

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

Leu Ala Met Ser Lys Asn Asn Lys Tyr Gly Ser Ala Glu Asp Leu Arg
740 745 750

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

Trp Val Pro Asp Gln Ile Tyr Ala Leu Pro Gly Glu Glu Ile Val Thr
770 775 780

[0130] Ala Thr Arg Val Asn Asp Tyr Gly Glu Glu Arg Glu Gly Ala Gln Ile
785 790 795 800

Lys Asn Lys Pro Tyr Ala Ala Asn Thr Lys Ser Ser Gly Glu Asp Tyr
805 810 815

Gln Ala Gln Tyr Gly Gly Glu Phe Leu Glu Tyr Leu Gln Glu Asn Tyr
820 825 830

Pro Glu Leu Phe Glu Lys Val Met Ile Ser Thr Gly Lys Thr Ile Asp
835 840 845

Pro Ser Thr Lys Ile Lys Val Trp Lys Ala Glu Tyr Phe Asn Gly Thr
850 855 860

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

Gly Thr Tyr Phe Thr Val Thr Glu Asn Gly Ala Phe Leu Pro Lys Gln
885 890 895

Met Thr Ser Asp Thr Ala Gln Thr Gly Phe Tyr Tyr Asp Gly Thr Gly
900 905 910

Met Thr Tyr Tyr Ser Thr Ser Gly Tyr Gln Ala Lys Ser Ser Phe Val
915 920 925

Leu Tyr Asn Gly Asn Arg Tyr Tyr Phe Asp Glu Asn Gly His Met Val
930 935 940

Thr Gly Met Arg Asp Ile Asp Gly Gln Thr Tyr Tyr Phe Leu Pro Asn
945 950 955 960

Gly Ile Glu Leu Arg Asp Ala Ile Tyr Glu Asp Ala Asn Gly Asn Gln
965 970 975

Tyr Tyr Phe Gly Lys Ser Gly Asn Arg Tyr Ala Gly His Tyr Tyr Ala
980 985 990

Phe Glu Thr Thr Ser Thr Val Asp Gly Val Thr Lys Thr Thr Thr Asn
995 1000 1005

Trp Arg Tyr Phe Asp Glu Asn Gly Val Met Ala Arg Gly Leu Val
1010 1015 1020

Lys Ile Gly Asn Asp Tyr Gln Tyr Tyr Asp Asp Asn Gly Asn Gln
1025 1030 1035

Ile Lys Gly Gln Leu Val Thr Asp Lys Asp Gly Asn Thr Arg Tyr
1040 1045 1050

Phe Lys Ala Asp Ser Gly Ala Met Val Thr Gly Glu Phe Ala Leu
1055 1060 1065

Val Asn Gly Gly Trp Tyr Tyr Phe Asp Asp Asn Gly Val Ala Val
1070 1075 1080

[0131] Lys Gly Ala Gln Thr Ile Asn Gly Gln Gln Leu Tyr Phe Asp Glu
1085 1090 1095

Asn Gly Val Gln Ala Lys Gly Val Phe Val Thr Asn Glu Asp Gly
1100 1105 1110

Thr Arg Ser Tyr Tyr Asp Ala Lys Ser Gly Glu Lys Phe Val Gly
1115 1120 1125

Asp Phe Phe Thr Thr Gly Asp Asn His Trp Tyr Tyr Ala Asp Glu
1130 1135 1140

Asn Gly Asn Leu Ala Thr Gly Ser Gln Val Ile Arg Gly Gln Lys
1145 1150 1155

Leu Tyr Phe Ala Ala Asp Gly Leu Gln Ala Lys Gly Ile Phe Thr
1160 1165 1170

Thr Asp Ala Glu Gly Asn Arg His Phe Tyr Asp Pro Asp Ser Gly
1175 1180 1185

Asp Leu Ala Glu Asn Lys Phe Ile Ala Asp Gly Asp Asp Trp Tyr
1190 1195 1200

Tyr Phe Asp Glu Thr Gly His Val Val Thr Gly Glu Gln Val Ile
1205 1210 1215

Asn Gly Gln Gln Leu Tyr Phe Asp Glu Asn Gly Val Gln Ala Lys
1220 1225 1230

Gly Val Phe Val Thr Asp Asp Asn Gly Asn Lys Arg Tyr Tyr Asp
1235 1240 1245

Ala Gln Thr Gly Glu Met Val Val Asn Gln Thr Leu Thr Val Asp
1250 1255 1260

Gly Val Glu Tyr Thr Phe Gly Ala Asp Gly Val Ala Val Val Asn
1265 1270 1275

Ala Gln Asp Ser Asp Glu Gln Ser Glu Ser Thr Asp Glu Thr Gln
1280 1285 1290

Val Thr Ser Asp Asp Ala Thr Val Ala Lys Thr Glu Thr Ser Ser
1295 1300 1305

Ala Glu
1310

<210> 41
<211> 3804
<212> DNA
<213> 变异链球菌(Streptococcus mutans)

<400> 41
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ctgaacatta acggcaagac ctttttcttt gacgagactg gcgccctgag caataacacc 120

ctgccgagca agaaaggtaa catcaccaat aacgacaata ccaatagctt cgcgcaatac 180

[0132] aatcaggtgt attcgacgga tgcagcgaac ttcgaacatg tcgatcacta cctgacggcg 240

gagtcctggt atcgcccgaa gtatattctg aaagatggca agacgtggac tcagtccacg 300

gagaaagatt ttcgcccgtt gttgatgacc tggtggccgg atcaggaaac ccagcgtcag 360

tatgtaaact atatgaatgc ccagctgggt attcaccaga cctacaacac ggcgaccagc 420

ccgttgcaac tgaatctggc ggcacagacg atccagacca agattgaaga gaagatcacg 480

gcggagaaga acactaattg gctgcgtcaa acgatttcgg cctttgtcaa aacccagagc 540

gcgtggaact cggacagcga aaaaccgttt gacgatcatc tgcaaaaggg tgcactgctg 600

tactctaaca atagcaagtt gacctctcaa gctaatagca actaccgtat tctgaaccgt 660

accccaacca accaaaccgg caagaaagat ccgcgttata ccgctgaccg taccatcggt 720

ggttatgagt tcttgctggc gaacgatgtg gataatagca atcctgttgt tcaagcggaa 780

cagctgaact ggctgcactt cctgatgaac tttggcaata tctatgcaaa cgaccctgac 840

gccaactttg acagcatccg tgtagacgcc gtggacaacg tggatgcaga tttgttgcaa 900

atcgctggtg actatctgaa ggctgcaaag ggcatccata agaacgacaa agcagcgaac 960

gaccacctgt cgatcctgga agcatggagc tataatgaca ccccgtatct gcacgacgac 1020

ggtgacaaca tgatcaatat ggacaaccgt ctgcgtctga gcctgctgta tagcctggcg 1080

aagccgttga accagcgttc gggcatgaac ccgctgatca cgaacagcct ggttaaccgt 1140

accgatgaca acgcagaaac cgcagcggtc ccgagctaca gctttatccg tgcacacgat 1200

agcgaggttc aagacctgat tcgtaacatt attcgtgctg agattaatcc gaacgtcgtc 1260

ggttatagct tcacgatgga agagatcaag aaggcctttg agatttacaa caaggatctg 1320

ctggcgacgg aaaagaaata cacccactat aacaccgcgc tgagctacgc gctgctgctg 1380

[0133]

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tacatggcac ataaaacgat caactacgag gctatcgaaa cgctgttgaa ggcgcgcatt      1500
aagtacgtgt ctggtggcca agcgatgcgt aatcaacagg tgggtaatag cgaaatcatt      1560
acgagcgtcc gctatggcaa gggcgcactg aaagcgacgg ataccggcga tcgtaccacg      1620
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gaccgcgtcg ttgttaacat gggtgcagca cacaagaacc aggcatatcg tccgctgttg      1740
ctgaccactg ataatggcat caaagcgtat cacagcgatc aggaagctgc gggcctggtg      1800
cgctatacca atgatcgtgg tgaattgatc ttcacggcag ctgacattaa aggttatgca      1860
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gacgtgcgtg tggccgcgag caccgcgcca tcgaccgacg gtaaaagcgt gcaccagaat      1980
gcggcgctgg acagccgtgt catgtttgag ggttttagca actttcaagc ctttgcaacg      2040
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ggcgttaccg atttcgaaat ggcaccgcag tatgtgtcta gcaccgatgg ctcgtttctg      2160
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tggcgctact ttcaaaatgg tattatggcc gtcggtctga cccgtgtcca cggtgcggtg      3060
cagtattttg acgccagcgg cttccaagcc aagggccagt tcatcaccac tgcggacggt      3120
aaactgcgtt actttgaccg tgacagcggc aaccaaatca gcaatcgttt tgttcgtaac      3180
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ttcaatggtc aacgtctgta ctttaagccg aacggtgttc aggcaaaggg tgagttcatt      3300
cgcgacgcgg atggtcactt gcgttactac gaccctaatt ccggtaatga ggttcgtaac      3360
cgtttcgtcc gcaactctaa gggcgaatgg ttcctgtttg accacaatgg catcgcagtc      3420
accggcgctc gtgtggtcaa cggccaacgc ttgtacttca aaagcaatgg cgtccaagct      3480
aagggtgagc tgattaccga acgtaagggc cgtattaagt attatgatcc taacagcggt      3540
aacgaagtgc gtaaccgcta cgtccgcacc agcagcggta attggtacta ttttggtaac      3600
gatggttacg cgctgatcgg ctggcatgtt gttgagggtc gtcgtgtgta ctttgatgag      3660
```

aacggtgtct atcgttacgc gagccacgac cagcgtaatc attggaacta cgactatcgt 3720

cgcgatttcg gtcgtggtag cagctccgct atccgttttc gccatagccg taacggcttt 3780

ttcgacaact tcttccgctt ctaa 3804

<210> 42
<211> 1267
<212> PRT
<213> 变异链球菌(Streptococcus mutans)

<400> 42

Met Val Asn Gly Lys Tyr Tyr Tyr Tyr Lys Glu Asp Gly Thr Leu Gln
1 5 10 15

Lys Asn Tyr Ala Leu Asn Ile Asn Gly Lys Thr Phe Phe Phe Asp Glu
20 25 30

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

Thr Asn Asn Asp Asn Thr Asn Ser Phe Ala Gln Tyr Asn Gln Val Tyr
50 55 60

Ser Thr Asp Ala Ala Asn Phe Glu His Val Asp His Tyr Leu Thr Ala
65 70 75 80

Glu Ser Trp Tyr Arg Pro Lys Tyr Ile Leu Lys Asp Gly Lys Thr Trp
85 90 95

[0134] Thr Gln Ser Thr Glu Lys Asp Phe Arg Pro Leu Leu Met Thr Trp Trp
100 105 110

Pro Asp Gln Glu Thr Gln Arg Gln Tyr Val Asn Tyr Met Asn Ala Gln
115 120 125

Leu Gly Ile His Gln Thr Tyr Asn Thr Ala Thr Ser Pro Leu Gln Leu
130 135 140

Asn Leu Ala Ala Gln Thr Ile Gln Thr Lys Ile Glu Glu Lys Ile Thr
145 150 155 160

Ala Glu Lys Asn Thr Asn Trp Leu Arg Gln Thr Ile Ser Ala Phe Val
165 170 175

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

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

Ser Gln Ala Asn Ser Asn Tyr Arg Ile Leu Asn Arg Thr Pro Thr Asn
210 215 220

Gln Thr Gly Lys Lys Asp Pro Arg Tyr Thr Ala Asp Arg Thr Ile Gly
225 230 235 240

Gly Tyr Glu Phe Leu Leu Ala Asn Asp Val Asp Asn Ser Asn Pro Val
245 250 255

```
Val Gln Ala Glu Gln Leu Asn Trp Leu His Phe Leu Met Asn Phe Gly
            260                 265                 270

Asn Ile Tyr Ala Asn Asp Pro Asp Ala Asn Phe Asp Ser Ile Arg Val
        275                 280                 285

Asp Ala Val Asp Asn Val Asp Ala Asp Leu Leu Gln Ile Ala Gly Asp
    290                 295                 300

Tyr Leu Lys Ala Ala Lys Gly Ile His Lys Asn Asp Lys Ala Ala Asn
305                 310                 315                 320

Asp His Leu Ser Ile Leu Glu Ala Trp Ser Tyr Asn Asp Thr Pro Tyr
                325                 330                 335

Leu His Asp Asp Gly Asp Asn Met Ile Asn Met Asp Asn Arg Leu Arg
            340                 345                 350

Leu Ser Leu Leu Tyr Ser Leu Ala Lys Pro Leu Asn Gln Arg Ser Gly
        355                 360                 365

Met Asn Pro Leu Ile Thr Asn Ser Leu Val Asn Arg Thr Asp Asp Asn
    370                 375                 380

Ala Glu Thr Ala Ala Val Pro Ser Tyr Ser Phe Ile Arg Ala His Asp
385                 390                 395                 400
```

[0135]

```
Ser Glu Val Gln Asp Leu Ile Arg Asn Ile Ile Arg Ala Glu Ile Asn
                405                 410                 415

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

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

His Tyr Asn Thr Ala Leu Ser Tyr Ala Leu Leu Leu Thr Asn Lys Ser
    450                 455                 460

Ser Val Pro Arg Val Tyr Tyr Gly Asp Met Phe Thr Asp Asp Gly Gln
465                 470                 475                 480

Tyr Met Ala His Lys Thr Ile Asn Tyr Glu Ala Ile Glu Thr Leu Leu
                485                 490                 495

Lys Ala Arg Ile Lys Tyr Val Ser Gly Gly Gln Ala Met Arg Asn Gln
            500                 505                 510

Gln Val Gly Asn Ser Glu Ile Ile Thr Ser Val Arg Tyr Gly Lys Gly
        515                 520                 525

Ala Leu Lys Ala Thr Asp Thr Gly Asp Arg Thr Thr Arg Thr Ser Gly
    530                 535                 540

Val Ala Val Ile Glu Gly Asn Asn Pro Ser Leu Arg Leu Lys Ala Ser
545                 550                 555                 560
```

Asp Arg Val Val Val Asn Met Gly Ala Ala His Lys Asn Gln Ala Tyr
565 570 575

Arg Pro Leu Leu Leu Thr Thr Asp Asn Gly Ile Lys Ala Tyr His Ser
580 585 590

Asp Gln Glu Ala Ala Gly Leu Val Arg Tyr Thr Asn Asp Arg Gly Glu
595 600 605

Leu Ile Phe Thr Ala Ala Asp Ile Lys Gly Tyr Ala Asn Pro Gln Val
610 615 620

Ser Gly Tyr Leu Gly Val Trp Val Pro Val Gly Ala Ala Ala Asp Gln
625 630 635 640

Asp Val Arg Val Ala Ala Ser Thr Ala Pro Ser Thr Asp Gly Lys Ser
645 650 655

Val His Gln Asn Ala Ala Leu Asp Ser Arg Val Met Phe Glu Gly Phe
660 665 670

Ser Asn Phe Gln Ala Phe Ala Thr Lys Lys Glu Glu Tyr Thr Asn Val
675 680 685

Val Ile Ala Lys Asn Val Asp Lys Phe Ala Glu Trp Gly Val Thr Asp
690 695 700

[0136] Phe Glu Met Ala Pro Gln Tyr Val Ser Ser Thr Asp Gly Ser Phe Leu
705 710 715 720

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

Gly Ile Ser Lys Pro Asn Lys Tyr Gly Thr Ala Asp Asp Leu Val Lys
740 745 750

Ala Ile Lys Ala Leu His Ser Lys Gly Ile Lys Val Met Ala Asp Trp
755 760 765

Val Pro Asp Gln Met Tyr Ala Phe Pro Glu Lys Glu Val Val Thr Ala
770 775 780

Thr Arg Val Asp Lys Tyr Gly Thr Pro Val Ala Gly Ser Gln Ile Lys
785 790 795 800

Asn Thr Leu Tyr Val Val Asp Gly Lys Ser Ser Gly Lys Asp Gln Gln
805 810 815

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

Glu Leu Phe Ala Arg Lys Gln Ile Ser Thr Gly Val Pro Met Asp Pro
835 840 845

Ser Val Lys Ile Lys Gln Trp Ser Ala Lys Tyr Phe Asn Gly Thr Asn
850 855 860

Ile Leu Gly Arg Gly Ala Gly Tyr Val Leu Lys Asp Gln Ala Thr Asn
865 870 875 880

Thr Tyr Phe Ser Leu Val Ser Asp Asn Thr Phe Leu Pro Lys Ser Leu
885 890 895

Val Asn Pro Asn His Gly Thr Ser Ser Ser Val Thr Gly Leu Val Phe
900 905 910

Asp Gly Lys Gly Tyr Val Tyr Tyr Ser Thr Ser Gly Tyr Gln Ala Lys
915 920 925

Asn Thr Phe Ile Ser Leu Gly Asn Asn Trp Tyr Tyr Phe Asp Asn Asn
930 935 940

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

Phe Leu Ser Asn Gly Ile Gln Leu Arg Asn Ala Ile Tyr Asp Asn Gly
965 970 975

Asn Lys Val Leu Ser Tyr Tyr Gly Asn Asp Gly Arg Arg Tyr Glu Asn
980 985 990

Gly Tyr Tyr Leu Phe Gly Gln Gln Trp Arg Tyr Phe Gln Asn Gly Ile
995 1000 1005

[0137] Met Ala Val Gly Leu Thr Arg Val His Gly Ala Val Gln Tyr Phe
1010 1015 1020

Asp Ala Ser Gly Phe Gln Ala Lys Gly Gln Phe Ile Thr Thr Ala
1025 1030 1035

Asp Gly Lys Leu Arg Tyr Phe Asp Arg Asp Ser Gly Asn Gln Ile
1040 1045 1050

Ser Asn Arg Phe Val Arg Asn Ser Lys Gly Glu Trp Phe Leu Phe
1055 1060 1065

Asp His Asn Gly Val Ala Val Thr Gly Thr Val Thr Phe Asn Gly
1070 1075 1080

Gln Arg Leu Tyr Phe Lys Pro Asn Gly Val Gln Ala Lys Gly Glu
1085 1090 1095

Phe Ile Arg Asp Ala Asp Gly His Leu Arg Tyr Tyr Asp Pro Asn
1100 1105 1110

Ser Gly Asn Glu Val Arg Asn Arg Phe Val Arg Asn Ser Lys Gly
1115 1120 1125

Glu Trp Phe Leu Phe Asp His Asn Gly Ile Ala Val Thr Gly Ala
1130 1135 1140

Arg Val Val Asn Gly Gln Arg Leu Tyr Phe Lys Ser Asn Gly Val
1145 1150 1155

```
Gln Ala  Lys Gly Glu Leu Ile  Thr Glu Arg Lys Gly  Arg Ile Lys
    1160                 1165                 1170

Tyr Tyr  Asp Pro Asn Ser Gly  Asn Glu Val Arg Asn  Arg Tyr Val
    1175                 1180                 1185

Arg Thr  Ser Ser Gly Asn Trp  Tyr Tyr Phe Gly Asn  Asp Gly Tyr
    1190                 1195                 1200

Ala Leu  Ile Gly Trp His Val  Val Glu Gly Arg Arg  Val Tyr Phe
    1205                 1210                 1215

Asp Glu  Asn Gly Val Tyr Arg  Tyr Ala Ser His Asp  Gln Arg Asn
    1220                 1225                 1230

His Trp  Asn Tyr Asp Tyr Arg  Arg Asp Phe Gly Arg  Gly Ser Ser
    1235                 1240                 1245

Ser Ala  Ile Arg Phe Arg His  Ser Arg Asn Gly Phe  Phe Asp Asn
    1250                 1255                 1260

Phe Phe  Arg Phe
    1265
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[0138]

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<210>  43
<211>  3864
<212>  DNA
<213>  变异链球菌(Streptococcus mutans)

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ttgacggtta acaataaagt cctgtatttt gacaagaaca cgggtgcgct gaccgacacc     120

agccaatatc agttcaaaca aggtctgacg aagctgaaca acgactacac ccctcacaat     180

cagattgtca actttgaaaa tactagcctg gaaactattg ataactatgt tactgccgac     240

tcttggtatc gtccgaaaga cattctgaag aacggtaaga cgtggaccgc gtcctctgag     300

agcgatctgc gtccgctgct gatgtcctgg tggcctgata agcagaccca gatcgcatac     360

ctgaactaca tgaaccaaca aggcttgggc actggcgaga actataccgc tgatagctct     420

caagagagcc tgaacctggc ggcacaaacc gttcaagtca aaatcgaaac caagatcagc     480

caaacgcaac agactcagtg gctgcgtgac atcattaact ctttcgttaa gacgcaaccg     540

aactggaata gccaaaccga gtctgacacg agcgctggtg aaaaagatca tttgcagggc     600

ggtgccctgc tgtatagcaa ttcggacaaa accgcatacg caaatagcga ctatcgtctg     660

ctgaaccgta ccccgaccag ccagactggt aagccgaaat acttcgagga caatagcagc     720

ggtggttacg acttcctgtt ggcaaacgat attgataatt ccaatccggt ggtgcaggct     780

gagcagctga attggctgca ttacctgatg aattacggta gcattgtcgc aaatgacccg     840

gaagcgaatt tcgatggtgt ccgtgttgac gcggtggata acgtgaacgc agacctgttg     900

cagatcgcaa gcgattatct gaaagcccat tatggtgttg ataagagcga gaagaatgcg     960

atcaaccacc tgagcatcct ggaagcgtgg tctgacaacg acccacagta taacaaagac    1020

accaaaggtg cccagctgcc gatcgacaac aaactgcgtc tgtcgttgct gtacgcactg    1080
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gttattacca attccctgaa taatcgttcc gctgagggca agaactctga acgcatggcg 1200

aattacatct tcatccgtgc tcacgattct gaagttcaaa cggtgatcgc aaagatcatc 1260

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gcgttcaaaa tctataacga ggatatgcgc caggcgaaga agaagtatac ccagagcaat 1380

atcccgacgg catacgccct gatgctgagc aataaggact ccatcacgcg cctgtattac 1440

ggtgatatgt acagcgatga tggccaatac atggcgacca aatccccgta ctacgatgcg 1500

attgacaccc tgctgaaggc gcgcattaag tatgccgctg gcggtcagga tatgaagatc 1560

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gttcgctacg gcacgggcgc aaacgaagcg accgaccagg gcagcgaagc taccaagacg 1680

caaggtatgg ccgtcatcac ttctaacaac ccgtccctga agctgaatca gaacgacaag 1740

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acgaacgata agggcgagtt ggtgttcgat gcaagcgaca ttcagggcta tctgaatccg 1920

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cgtgtcgcgg ccagcaataa agccaatgcg accggccaag tctatgaaag cagcagcgca 2040

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atggtttacg gtctgcaaca tctgaacggc gaggtgcaat acttcctgag caatggcgtg 2940

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ggcaaccgtt atagcaatgg ttactacagc ttcgataatg atagcaaatg gcgctatttc 3060

gatgcgagcg gtgttatggc agtgggtctg aaaactatta acggtaacac ccagtatttc 3120

gatcaagacg gctaccaagt gaagggtgca tggattaccg gcagcgatgg taagaagcgt 3180

tacttcgacg acggtagcgg caatatggca gttaatcgct ttgctaacga caagaatggc 3240

gattggtatt acctgaatag cgacggtatt gcactggtgg gtgttcagac catcaacggc 3300

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gacagccaga acaactggta ttacttcggc tcggatggtg ttgcggttac gggttcgcag 3480

acgattgcgg gtaaaaagtt gtactttgcg tccgacggta aacaggtgaa gggtagcttt 3540

gttacttaca atggtaaagt gcactattac catgcggaca gcggcgaact gcaagtcaac 3600

cgtttcgagg cggataaaga cggtaattgg tactatctgg acagcaacgg tgaggcactg 3660

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aagggtgatg tcgcgtatga tgaacgcggc ttgctgcgct attacgacaa aaacagcggt 3780

aatatggtgt acaacaaggt ggtcacgctg gcgaacggtc gtcgtattgg tattgaccgc 3840

tggggtattg ctcgctatta ctaa 3864

<210> 44
<211> 1287
<212> PRT
<213> 变异链球菌(Streptococcus mutans)

<400> 44

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1 5 10 15

Lys Asn Phe Ala Leu Thr Val Asn Asn Lys Val Leu Tyr Phe Asp Lys
20 25 30

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

[0140] Leu Thr Lys Leu Asn Asn Asp Tyr Thr Pro His Asn Gln Ile Val Asn
50 55 60

Phe Glu Asn Thr Ser Leu Glu Thr Ile Asp Asn Tyr Val Thr Ala Asp
65 70 75 80

Ser Trp Tyr Arg Pro Lys Asp Ile Leu Lys Asn Gly Lys Thr Trp Thr
85 90 95

Ala Ser Ser Glu Ser Asp Leu Arg Pro Leu Leu Met Ser Trp Trp Pro
100 105 110

Asp Lys Gln Thr Gln Ile Ala Tyr Leu Asn Tyr Met Asn Gln Gln Gly
115 120 125

Leu Gly Thr Gly Glu Asn Tyr Thr Ala Asp Ser Ser Gln Glu Ser Leu
130 135 140

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

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

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

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

Asp Lys Thr Ala Tyr Ala Asn Ser Asp Tyr Arg Leu Leu Asn Arg Thr
210 215 220

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

Gly Gly Tyr Asp Phe Leu Leu Ala Asn Asp Ile Asp Asn Ser Asn Pro
245 250 255

Val Val Gln Ala Glu Gln Leu Asn Trp Leu His Tyr Leu Met Asn Tyr
260 265 270

Gly Ser Ile Val Ala Asn Asp Pro Glu Ala Asn Phe Asp Gly Val Arg
275 280 285

Val Asp Ala Val Asp Asn Val Asn Ala Asp Leu Leu Gln Ile Ala Ser
290 295 300

Asp Tyr Leu Lys Ala His Tyr Gly Val Asp Lys Ser Glu Lys Asn Ala
305 310 315 320

Ile Asn His Leu Ser Ile Leu Glu Ala Trp Ser Asp Asn Asp Pro Gln
325 330 335

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

[0141] Arg Leu Ser Leu Leu Tyr Ala Leu Thr Arg Pro Leu Glu Lys Asp Ala
355 360 365

Ser Asn Lys Asn Glu Ile Arg Ser Gly Leu Glu Pro Val Ile Thr Asn
370 375 380

Ser Leu Asn Asn Arg Ser Ala Glu Gly Lys Asn Ser Glu Arg Met Ala
385 390 395 400

Asn Tyr Ile Phe Ile Arg Ala His Asp Ser Glu Val Gln Thr Val Ile
405 410 415

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

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

Met Arg Gln Ala Lys Lys Lys Tyr Thr Gln Ser Asn Ile Pro Thr Ala
450 455 460

Tyr Ala Leu Met Leu Ser Asn Lys Asp Ser Ile Thr Arg Leu Tyr Tyr
465 470 475 480

Gly Asp Met Tyr Ser Asp Asp Gly Gln Tyr Met Ala Thr Lys Ser Pro
485 490 495

Tyr Tyr Asp Ala Ile Asp Thr Leu Leu Lys Ala Arg Ile Lys Tyr Ala
500 505 510

Ala Gly Gly Gln Asp Met Lys Ile Thr Tyr Val Glu Gly Asp Lys Ser
515 520 525

His Met Asp Trp Asp Tyr Thr Gly Val Leu Thr Ser Val Arg Tyr Gly
530 535 540

Thr Gly Ala Asn Glu Ala Thr Asp Gln Gly Ser Glu Ala Thr Lys Thr
545 550 555 560

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

Gln Asn Asp Lys Val Ile Val Asn Met Gly Thr Ala His Lys Asn Gln
580 585 590

Glu Tyr Arg Pro Leu Leu Leu Thr Thr Lys Asp Gly Leu Thr Ser Tyr
595 600 605

Thr Ser Asp Ala Ala Ala Lys Ser Leu Tyr Arg Lys Thr Asn Asp Lys
610 615 620

Gly Glu Leu Val Phe Asp Ala Ser Asp Ile Gln Gly Tyr Leu Asn Pro
625 630 635 640

Gln Val Ser Gly Tyr Leu Ala Val Trp Val Pro Val Gly Ala Ser Asp
645 650 655

[0142] Asn Gln Asp Val Arg Val Ala Ala Ser Asn Lys Ala Asn Ala Thr Gly
660 665 670

Gln Val Tyr Glu Ser Ser Ser Ala Leu Asp Ser Gln Leu Ile Tyr Glu
675 680 685

Gly Phe Ser Asn Phe Gln Asp Phe Val Thr Lys Asp Ser Asp Tyr Thr
690 695 700

Asn Lys Lys Ile Ala Gln Asn Val Gln Leu Phe Lys Ser Trp Gly Val
705 710 715 720

Thr Ser Phe Glu Met Ala Pro Gln Tyr Val Ser Ser Glu Asp Gly Ser
725 730 735

Phe Leu Asp Ser Ile Ile Gln Asn Gly Tyr Ala Phe Glu Asp Arg Tyr
740 745 750

Asp Leu Ala Met Ser Lys Asn Asn Lys Tyr Gly Ser Gln Gln Asp Met
755 760 765

Ile Asn Ala Val Lys Ala Leu His Lys Ser Gly Ile Gln Val Ile Ala
770 775 780

Asp Trp Val Pro Asp Gln Ile Tyr Asn Leu Pro Gly Lys Glu Val Val
785 790 795 800

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

Ile Lys Asn Thr Leu Tyr Ala Ala Asn Thr Lys Ser Asn Gly Lys Asp
820 825 830

Tyr Gln Ala Lys Tyr Gly Gly Ala Phe Leu Ser Glu Leu Ala Ala Lys
835 840 845

Tyr Pro Ser Ile Phe Asn Arg Thr Gln Ile Ser Asn Gly Lys Lys Ile
850 855 860

Asp Pro Ser Glu Lys Ile Thr Ala Trp Lys Ala Lys Tyr Phe Asn Gly
865 870 875 880

Thr Asn Ile Leu Gly Arg Gly Val Gly Tyr Val Leu Lys Asp Asn Ala
885 890 895

Ser Asp Lys Tyr Phe Glu Leu Lys Gly Asn Gln Thr Tyr Leu Pro Lys
900 905 910

Gln Met Thr Asn Lys Glu Ala Ser Thr Gly Phe Val Asn Asp Gly Asn
915 920 925

Gly Met Thr Phe Tyr Ser Thr Ser Gly Tyr Gln Ala Lys Asn Ser Phe
930 935 940

Val Gln Asp Ala Lys Gly Asn Trp Tyr Tyr Phe Asp Asn Asn Gly His
945 950 955 960

[0143] Met Val Tyr Gly Leu Gln His Leu Asn Gly Glu Val Gln Tyr Phe Leu
965 970 975

Ser Asn Gly Val Gln Leu Arg Glu Ser Phe Leu Glu Asn Ala Asp Gly
980 985 990

Ser Lys Asn Tyr Phe Gly His Leu Gly Asn Arg Tyr Ser Asn Gly Tyr
995 1000 1005

Tyr Ser Phe Asp Asn Asp Ser Lys Trp Arg Tyr Phe Asp Ala Ser
1010 1015 1020

Gly Val Met Ala Val Gly Leu Lys Thr Ile Asn Gly Asn Thr Gln
1025 1030 1035

Tyr Phe Asp Gln Asp Gly Tyr Gln Val Lys Gly Ala Trp Ile Thr
1040 1045 1050

Gly Ser Asp Gly Lys Lys Arg Tyr Phe Asp Asp Gly Ser Gly Asn
1055 1060 1065

Met Ala Val Asn Arg Phe Ala Asn Asp Lys Asn Gly Asp Trp Tyr
1070 1075 1080

Tyr Leu Asn Ser Asp Gly Ile Ala Leu Val Gly Val Gln Thr Ile
1085 1090 1095

Asn Gly Lys Thr Tyr Tyr Phe Gly Gln Asp Gly Lys Gln Ile Lys
1100 1105 1110

```
Gly Lys  Ile Ile Thr Asp Asn  Gly Lys Leu Lys Tyr  Phe Leu Ala
    1115                 1120                 1125

Asn Ser  Gly Glu Leu Ala Arg  Asn Ile Phe Ala Thr  Asp Ser Gln
    1130                 1135                 1140

Asn Asn  Trp Tyr Tyr Phe Gly  Ser Asp Gly Val Ala  Val Thr Gly
    1145                 1150                 1155

Ser Gln  Thr Ile Ala Gly Lys  Lys Leu Tyr Phe Ala  Ser Asp Gly
    1160                 1165                 1170

Lys Gln  Val Lys Gly Ser Phe  Val Thr Tyr Asn Gly  Lys Val His
    1175                 1180                 1185

Tyr Tyr  His Ala Asp Ser Gly  Glu Leu Gln Val Asn  Arg Phe Glu
    1190                 1195                 1200

Ala Asp  Lys Asp Gly Asn Trp  Tyr Tyr Leu Asp Ser  Asn Gly Glu
    1205                 1210                 1215

Ala Leu  Thr Gly Ser Gln Arg  Ile Asn Gly Gln Arg  Val Phe Phe
    1220                 1225                 1230

Thr Arg  Glu Gly Lys Gln Val  Lys Gly Asp Val Ala  Tyr Asp Glu
    1235                 1240                 1245
```

[0144]

```
Arg Gly  Leu Leu Arg Tyr Tyr  Asp Lys Asn Ser Gly  Asn Met Val
    1250                 1255                 1260

Tyr Asn  Lys Val Val Thr Leu  Ala Asn Gly Arg Arg  Ile Gly Ile
    1265                 1270                 1275

Asp Arg  Trp Gly Ile Ala Arg  Tyr Tyr
    1280                 1285
```

<210> 45
<211> 4068
<212> DNA
<213> 解没食子酸链球菌（Streptococcus gallolyticus）

<400> 45

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tccacctata gcttctccga gggcctgact aatctggtcg ataacttcag cattaacaac       180

cagtcctacg acagcaccga agagtcgttt gagctgatcg acggttacct gaccgtcaat       240

acttggtacc gtccgaccaa aattctggaa aacggtgaaa cctgggtcga tagcaccgaa       300

acggatttcc gtccgctgct gatggcctgg tggccggatg ttgacaccca aattgactac       360

ttgaactaca tgagcgatta cttcgatctg ggtacgacct atagcgctga cgattcccaa       420

gcgagcctga atctggcagc tgaggcggtt caggtgaaaa ttgaacaaga aattacccgt       480

caagagaaca ccgcctggct gcgcgagatc atctctagct ttgttaccac ccaggataaa       540

tggaatatca ataccgagaa tgagggcacc gaccatctgc aaggtggtgc cctgctgtac       600
```

gttaacagcg acttgactcc gtgggcaaac agcgattatc gcctgctgaa ccgcaccccg 660

acgtaccaga cgggtgagac taattacttt aaagcagatc gtactggtgg ctacgaattt 720

ctgctggcaa atgacgtgga taattctaac ccggtcgttc aagccgaaca gttgaaccag 780

ctgtactact tgatgaattg gggctctatt gtattcggtg atgacgacgc caattttgat 840

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aacaactatt acagctttga cgttgaagag gtggtggacg gtgtaacgac tacggtaacg      3060

aagtggcgtc attttgacga gaacggcgtg atggcgcgtg gtttggtcga gattgatggt      3120

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caaaccattg ccggccagaa cttgtatttc gatgacaacg gtgtgcaggc gaaaggtgcc      3360

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tacgatgcag attccggcga aatggcagtt aacacctttg tggagattga cggtgtttgg      3840

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ttgtacttta acgcagacgg tagccaagtc aagggtgacg ttgtccgtat caacggtttg      3960

[0146] cgttactact acgacgctaa tagcggcgaa caggtgcgca atcagtgggt cacgctgccg      4020

gatggtactg ttgttttctt taatgcgcgt ggctatactt ggggctaa                   4068
```

<210> 46
<211> 1355
<212> PRT
<213> 解没食子酸链球菌（Streptococcus gallolyticus）

<400> 46

```
Met Ile Asp Gly Lys Tyr Tyr Tyr Ile Asp Glu Asp Gly Asn Val Lys
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Lys Asn Phe Ala Ile Thr Val Asp Gly Gln Leu Leu Tyr Phe Asp Ala
            20                  25                  30

Glu Thr Gly Ala Leu Thr Ser Thr Ser Thr Tyr Ser Phe Ser Glu Gly
        35                  40                  45

Leu Thr Asn Leu Val Asp Asn Phe Ser Ile Asn Asn Gln Ser Tyr Asp
    50                  55                  60

Ser Thr Glu Glu Ser Phe Glu Leu Ile Asp Gly Tyr Leu Thr Val Asn
65                  70                  75                  80

Thr Trp Tyr Arg Pro Thr Lys Ile Leu Glu Asn Gly Glu Thr Trp Val
                85                  90                  95

Asp Ser Thr Glu Thr Asp Phe Arg Pro Leu Leu Met Ala Trp Trp Pro
            100                 105                 110
```

```
Asp Val Asp Thr Gln Ile Asp Tyr Leu Asn Tyr Met Ser Asp Tyr Phe
        115                 120                 125

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

Leu Ala Ala Glu Ala Val Gln Val Lys Ile Glu Gln Glu Ile Thr Arg
145                 150                 155                 160

Gln Glu Asn Thr Ala Trp Leu Arg Glu Ile Ile Ser Ser Phe Val Thr
                165                 170                 175

Thr Gln Asp Lys Trp Asn Ile Asn Thr Glu Asn Glu Gly Thr Asp His
            180                 185                 190

Leu Gln Gly Gly Ala Leu Leu Tyr Val Asn Ser Asp Leu Thr Pro Trp
        195                 200                 205

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

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

Leu Leu Ala Asn Asp Val Asp Asn Ser Asn Pro Val Val Gln Ala Glu
                245                 250                 255
```

[0147]

```
Gln Leu Asn Gln Leu Tyr Tyr Leu Met Asn Trp Gly Ser Ile Val Phe
            260                 265                 270

Gly Asp Asp Asp Ala Asn Phe Asp Gly Val Arg Val Asp Ala Val Asp
        275                 280                 285

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

Ala Tyr Gly Val Asn Glu Ser Glu Ala Gln Ala Leu Ala His Ile Ser
305                 310                 315                 320

Ile Leu Glu Ala Trp Ser Tyr Asn Asp Pro Asp Tyr Asn His Asp Thr
                325                 330                 335

Asn Gly Ala Ala Leu Ala Ile Asp Asn Gly Leu Arg Leu Ser Phe Leu
            340                 345                 350

Tyr Ser Leu Thr Arg Pro Thr Asp Glu Arg Ser Gly Leu Glu Pro Leu
        355                 360                 365

Ile Thr Ser Glu Ile Gly Leu Thr Asp Arg Ser Glu Asp Ser Ala Tyr
    370                 375                 380

Gly Asp Thr Met Pro Ser Tyr Val Phe Val Arg Ala His Asp Ser Glu
385                 390                 395                 400

Val Gln Thr Ile Ile Ala Ser Ile Ile Ala Glu Gln Ile Asn Pro Glu
                405                 410                 415
```

```
Thr Asp Gly Tyr Thr Phe Thr Leu Asp Glu Leu Asn Gln Ala Phe Glu
            420                 425                 430

Ile Tyr Asn Ala Asp Met Asn Ser Val Asp Lys Glu Tyr Thr His Tyr
        435                 440                 445

Asn Ile Pro Ala Ala Tyr Ser Leu Leu Leu Thr Asn Met Glu Ser Val
    450                 455                 460

Pro Arg Val Tyr Tyr Gly Asp Leu Tyr Thr Asp Asn Gly Gln Tyr Met
465                 470                 475                 480

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

Arg Ile Arg Tyr Ala Ala Gly Gly Gln Ser Met Ala Val Thr Tyr Tyr
            500                 505                 510

Thr Pro Ala Ser Ser Met Ser Thr Asp Asn Ala Asp Ser Val Leu Asn
        515                 520                 525

Glu Thr Gly Val Leu Thr Ser Val Arg Tyr Gly Tyr Gly Ile Met Thr
    530                 535                 540

Ala Asp Gln Glu Ala Thr Asp Asp Ser Val Leu Thr Ser Gly Ile Val
545                 550                 555                 560
```

[0148]

```
Thr Ile Ile Ser Asn Asn Pro Asn Leu Gln Leu Asp Asp Ser Glu Val
                565                 570                 575

Ile Ala Val Gln Val Gly Val Ala His Ala Gly Gln Tyr Tyr Arg Pro
            580                 585                 590

Leu Leu Tyr Pro Thr Ala Asp Gly Leu Gln Ser Tyr Leu Asn Asp Ser
        595                 600                 605

Asp Thr Asp Ile Thr Lys Leu Val Asp Asp Asn Gly Tyr Ile Tyr Phe
    610                 615                 620

Thr Ala Asp Glu Ile Lys Gly Tyr Glu Thr Val Asp Met Asn Gly Tyr
625                 630                 635                 640

Leu Ser Val Trp Val Pro Val Gly Ala Asp Glu Asn Gln Asp Ile Arg
                645                 650                 655

Val Ser Ala Asp Thr Ser Ala Tyr Thr Glu Gly Glu Leu Ile Tyr Gln
            660                 665                 670

Ala Thr Ala Ala Leu Asp Ser Gln Val Ile Tyr Glu Gly Phe Ser Asn
        675                 680                 685

Phe Gln Asp Phe Val Thr Ser Asn Ser Glu Tyr Thr Asn Lys Leu Ile
    690                 695                 700

Ala Glu Asn Val Asp Leu Phe Thr Ser Trp Gly Ile Thr Ser Phe Glu
705                 710                 715                 720
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Met Ala Pro Gln Tyr Val Ser Thr Asp Asp Gly Thr Phe Leu Asp Ser
725 730 735

Ile Ile Gln Asn Gly Tyr Ala Phe Asp Asp Arg Tyr Asp Leu Ala Met
740 745 750

Ser Gln Asn Asn Lys Tyr Gly Ser Ala Glu Asp Leu Arg Asn Ala Ile
755 760 765

Lys Ala Leu His Ala Ala Gly Ile Gln Val Ile Ala Asp Trp Val Pro
770 775 780

Asp Gln Ile Tyr Ser Leu Pro Gly Glu Glu Val Val Thr Ala Thr Arg
785 790 795 800

Val Asn Asp Tyr Gly Glu Glu Thr Glu Gly Ala Tyr Ile Asn Asn Thr
805 810 815

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

Tyr Gly Gly Glu Phe Leu Asp Tyr Leu Gln Glu Thr Tyr Pro Glu Met
835 840 845

Phe Glu Val Ala Met Ile Ser Thr Gly Glu Pro Ile Asp Pro Ser Thr
850 855 860

[0149] Lys Ile Lys Ile Trp Lys Ala Glu Tyr Phe Asn Gly Thr Asn Ile Leu
865 870 875 880

Gly Lys Gly Ala Gly Tyr Val Leu Ser Asp Ala Ala Thr Gly Thr Tyr
885 890 895

Phe Thr Val Thr Glu Asn Gly Thr Phe Leu Pro Lys Gln Leu Thr Thr
900 905 910

Asp Ser Ala Ile Thr Gly Phe Tyr Tyr Asp Gly Thr Gly Met Ser Tyr
915 920 925

Phe Ser Thr Ser Gly Tyr Arg Ala Lys Ala Ser Phe Ile Val Tyr Asn
930 935 940

Gly Tyr Tyr Tyr Tyr Phe Asp Asp Asn Gly Tyr Met Val Thr Gly Thr
945 950 955 960

Val Glu Ile Asn Gly Lys Thr Tyr Tyr Phe Leu Pro Asn Gly Ile Gln
965 970 975

Leu Arg Asp Ala Ile Tyr Glu Asp Glu Asn Gly Asn Gln Tyr Tyr Phe
980 985 990

Gly Pro Leu Gly Asn Gln Tyr Phe Asn Asn Tyr Tyr Ser Phe Asp Val
995 1000 1005

Glu Glu Val Val Asp Gly Val Thr Thr Thr Val Thr Lys Trp Arg
1010 1015 1020

His Phe Asp Glu Asn Gly Val Met Ala Arg Gly Leu Val Glu Ile
1025 1030 1035

Asp Gly Val Tyr Gln Tyr Tyr Asp Glu Asn Gly Tyr Gln Val Lys
1040 1045 1050

Gly Glu Leu Ile Thr Asp Ala Asp Gly Asn Leu Arg Tyr Phe Lys
1055 1060 1065

Glu Asp Ser Gly Glu Met Val Val Ser Asp Phe Val Lys Ile Gly
1070 1075 1080

Asp Asn Asn Trp Tyr Tyr Phe Asp Glu Asn Gly Ile Ala Val Thr
1085 1090 1095

Gly Ala Gln Thr Ile Ala Gly Gln Asn Leu Tyr Phe Asp Asp Asn
1100 1105 1110

Gly Val Gln Ala Lys Gly Ala Phe Val Thr Asn Ala Asp Gly Thr
1115 1120 1125

Arg Ser Tyr Tyr Asp Ala Asp Ser Gly Glu Lys Ile Val Ala Asp
1130 1135 1140

Phe Phe Thr Thr Gly Asp Asn Asp Trp Tyr Tyr Ala Asp Glu Asn
1145 1150 1155

[0150] Gly Asn Leu Val Thr Gly Ser Gln Thr Ile Asn Gly Gln Asn Leu
1160 1165 1170

Tyr Phe Ala Glu Asp Gly Leu Gln Ala Lys Gly Val Phe Val Thr
1175 1180 1185

Asp Thr Ala Gly Asn Ile His Tyr Tyr Asp Ala Asn Ser Gly Glu
1190 1195 1200

Leu Ala Val Asn Thr Phe Val Gly Asp Gly Asp Asp Trp Tyr Tyr
1205 1210 1215

Phe Asp Glu Asn Gly Ile Ala Val Thr Gly Ala Gln Val Ile Asn
1220 1225 1230

Gly Gln His Leu Tyr Phe Ala Asp Asn Gly Ile Gln Val Lys Gly
1235 1240 1245

Glu Ile Val Thr Asp Ala Asn Gly Asn Arg Tyr Tyr Tyr Asp Ala
1250 1255 1260

Asp Ser Gly Glu Met Ala Val Asn Thr Phe Val Glu Ile Asp Gly
1265 1270 1275

Val Trp Tyr Tyr Phe Gly Ala Asp Gly Ile Ala Val Thr Gly Ala
1280 1285 1290

Gln Val Ile Asp Gly Gln Asn Leu Tyr Phe Asn Ala Asp Gly Ser
1295 1300 1305

Gln Val Lys Gly Asp Val Val Arg Ile Asn Gly Leu Arg Tyr Tyr
1310 1315 1320

Tyr Asp Ala Asn Ser Gly Glu Gln Val Arg Asn Gln Trp Val Thr
1325 1330 1335

Leu Pro Asp Gly Thr Val Val Phe Phe Asn Ala Arg Gly Tyr Thr
1340 1345 1350

Trp Gly
1355

<210> 47
<211> 4047
<212> DNA
<213> 血链球菌（Streptococcus sanguinis）

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gcggagtacc agtttcaaca gggtacgagc tccctgaata acgagttcag ccgcatgaat 180

gcgttccatg gcacgacgga gaaagatatt gaaaccgtcg atggctatct gaccgcagat 240

acgtggtacc gcccgaaggc catcctgaaa gatggcaaaa cctggactca gagcaccgaa 300

accgatctgc gtccgctgct gatggcatgg tggccggaca aacaaacgca ggtaagctac 360

ttgaactata tgaaccagca gggtctgggt gcgggtgcgt ttgagaacaa agttgagcag 420

gcaatcttga cgggcgcaag ccagcaggtg cagcgcaaga tcgaagaacg tattggcaaa 480

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gcgctgctgt acaccaactc tgaaaagacg agccacgcga acagcaaata ccgtattctg 660

aatcgtaccc cgaccaatca gaccggtacg ccgaagtatt tcatcgacaa atcgaatggt 720

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gcaaacttcg atggcgtgcg tgtggatgcg gtggacaatg ttaatgccga tttgctgcaa 900

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aagtacgttg cgggtggcca ggacatgaaa gttacctaca tgggtgtgcc gcgtgaaacc 1560

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ttcgacatga acgatatcgc aggttacagc aatgtccaag tatctggcta cttggctgtg 1920

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aacgccagcg gtcaggtgta tgagtccagc gctgcactgg acagccaact gatttatgaa 2040

ggcttctcta acttccaaga cttcgcgacc cgcgacgatc aatacaccaa caaagttatt 2100

gccaaaaatg ttaatctgtt taaagagtgg ggtgtgacca gctttgagct gccacctcag 2160

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gaagatcgtt atgacatggc gatgagcaaa aacaataagt acggtagcct ggacgacctg 2280

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tactacgtgc tgaaagattg ggccagcaat gagtatctga acaataagaa tggtgagatg 2700

[0152] gtgttgccga agcaactggt taacaaaaac gcgtacaccg gctttgttaa ggacaccacc 2760

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aacggtaatt ggtactactt tgacaaacgt ggttacctgg cgactggtgc acacgaaatc 2880

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gcggcgaatc gctttgcaca gggcgataat ccgagcgatt ggtattactt tggtgccgat 3240

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aagaatgagt ggtactactt tgaccaggcg ggcaaggcgg tgaccggctt gcagaaaatt 3660

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cgtggtcgtc gtttcggctg gaattaa 4047

<210> 48
<211> 1348
<212> PRT
<213> 血链球菌（Streptococcus sanguinis）

<400> 48

Met Ile Asp Gly Lys Lys Tyr Tyr Val Gln Asp Asp Gly Thr Val Lys
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Lys Asn Phe Ala Val Glu Leu Asn Gly Lys Val Leu Tyr Phe Asp Ala
20 25 30

Glu Thr Gly Ala Leu Val Asp Ser Ala Glu Tyr Gln Phe Gln Gln Gly
35 40 45

Thr Ser Ser Leu Asn Asn Glu Phe Ser Arg Met Asn Ala Phe His Gly
50 55 60

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

Thr Trp Tyr Arg Pro Lys Ala Ile Leu Lys Asp Gly Lys Thr Trp Thr
85 90 95

[0153] Gln Ser Thr Glu Thr Asp Leu Arg Pro Leu Leu Met Ala Trp Trp Pro
100 105 110

Asp Lys Gln Thr Gln Val Ser Tyr Leu Asn Tyr Met Asn Gln Gln Gly
115 120 125

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

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

Asp Gly Asp Thr Lys Trp Leu Arg Thr Leu Met Gly Ala Phe Val Lys
165 170 175

Thr Gln Pro Asn Trp Asn Ile Lys Thr Glu Ser Glu Thr Thr Gly Thr
180 185 190

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

Lys Thr Ser His Ala Asn Ser Lys Tyr Arg Ile Leu Asn Arg Thr Pro
210 215 220

Thr Asn Gln Thr Gly Thr Pro Lys Tyr Phe Ile Asp Lys Ser Asn Gly
225 230 235 240

Gly Tyr Glu Phe Leu Leu Ala Asn Asp Phe Asp Asn Ser Asn Pro Ala
245 250 255

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Val Gln Ala Glu Gln Leu Asn Trp Leu His Phe Met Met Asn Phe Gly
            260                 265                 270

Ser Ile Val Ala Asn Asp Pro Thr Ala Asn Phe Asp Gly Val Arg Val
        275                 280                 285

Asp Ala Val Asp Asn Val Asn Ala Asp Leu Leu Gln Ile Ala Ser Asp
    290                 295                 300

Tyr Phe Lys Ser Arg Tyr Lys Val Gly Glu Ser Glu Glu Gln Ala Ile
305                 310                 315                 320

Lys His Leu Ser Ile Leu Glu Ala Trp Ser Asp Asn Asp Pro Asp Tyr
                325                 330                 335

Asn Lys Asp Thr Lys Gly Ala Gln Leu Pro Ile Asp Asn Lys Leu Arg
            340                 345                 350

Leu Ser Leu Leu Tyr Ser Phe Met Arg Lys Leu Ser Ile Arg Ser Gly
        355                 360                 365

Val Glu Pro Thr Ile Thr Asn Ser Leu Asn Asp Arg Ser Ala Glu Lys
    370                 375                 380

Lys Asn Gly Glu Arg Met Ala Asn Tyr Ile Phe Val Arg Ala His Asp
385                 390                 395                 400
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[0154]

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Ser Glu Val Gln Thr Val Ile Ala Asp Ile Ile Arg Glu Asn Ile Asn
                405                 410                 415

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

Phe Lys Ile Tyr Asn Glu Asp Met Arg Lys Ala Asp Lys Lys Tyr Thr
        435                 440                 445

Gln Phe Asn Ile Pro Thr Ala His Ala Leu Met Leu Ser Asn Lys Asp
    450                 455                 460

Ser Ile Thr Arg Val Tyr Tyr Gly Asp Leu Tyr Thr Asp Asp Gly Gln
465                 470                 475                 480

Tyr Met Glu Lys Lys Ser Pro Tyr Tyr Asp Ala Ile Asp Ala Leu Leu
                485                 490                 495

Arg Ala Arg Ile Lys Tyr Val Ala Gly Gly Gln Asp Met Lys Val Thr
            500                 505                 510

Tyr Met Gly Val Pro Arg Glu Thr Asp Lys Trp Ser Tyr Asn Gly Ile
        515                 520                 525

Leu Thr Ser Val Arg Tyr Gly Thr Gly Ala Asn Glu Ala Thr Asp Glu
    530                 535                 540

Gly Thr Ala Glu Thr Arg Thr Gln Gly Met Ala Val Ile Ala Ser Asn
545                 550                 555                 560
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Asn Pro Asn Leu Lys Leu Asn Glu Trp Asp Lys Leu Gln Val Asn Met
565 570 575

Gly Ala Ala His Lys Asn Gln Tyr Tyr Arg Pro Val Leu Leu Thr Thr
580 585 590

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

Leu Trp Lys Lys Thr Asp Ala Asn Gly Ile Leu Thr Phe Asp Met Asn
610 615 620

Asp Ile Ala Gly Tyr Ser Asn Val Gln Val Ser Gly Tyr Leu Ala Val
625 630 635 640

Trp Val Pro Val Gly Ala Lys Ala Asp Gln Asp Ala Arg Val Thr Ala
645 650 655

Ser Lys Lys Lys Asn Ala Ser Gly Gln Val Tyr Glu Ser Ser Ala Ala
660 665 670

Leu Asp Ser Gln Leu Ile Tyr Glu Gly Phe Ser Asn Phe Gln Asp Phe
675 680 685

Ala Thr Arg Asp Asp Gln Tyr Thr Asn Lys Val Ile Ala Lys Asn Val
690 695 700

[0155] Asn Leu Phe Lys Glu Trp Gly Val Thr Ser Phe Glu Leu Pro Pro Gln
705 710 715 720

Tyr Val Ser Ser Gln Asp Gly Thr Phe Leu Asp Ser Ile Ile Gln Asn
725 730 735

Gly Tyr Ala Phe Glu Asp Arg Tyr Asp Met Ala Met Ser Lys Asn Asn
740 745 750

Lys Tyr Gly Ser Leu Asp Asp Leu Leu Asn Ala Leu Arg Ala Leu His
755 760 765

Ser Val Asn Ile Gln Ala Ile Ala Asp Trp Val Pro Asp Gln Ile Tyr
770 775 780

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

Gly Thr Tyr Arg Glu Gly Ala Glu Ile Lys Glu Asn Leu Tyr Val Ala
805 810 815

Asn Thr Lys Thr Asn Gly Thr Asp Tyr Gln Gly Lys Tyr Gly Gly Ala
820 825 830

Phe Leu Asp Glu Leu Lys Ala Lys Tyr Pro Glu Ile Phe Glu Arg Val
835 840 845

Gln Ile Ser Asn Gly Gln Lys Met Thr Thr Asp Glu Lys Ile Thr Lys
850 855 860

Trp Ser Ala Lys His Phe Asn Gly Thr Asn Ile Leu Gly Arg Gly Ala
865 870 875 880

Tyr Tyr Val Leu Lys Asp Trp Ala Ser Asn Glu Tyr Leu Asn Asn Lys
885 890 895

Asn Gly Glu Met Val Leu Pro Lys Gln Leu Val Asn Lys Asn Ala Tyr
900 905 910

Thr Gly Phe Val Lys Asp Thr Thr Gly Phe Lys Tyr Tyr Ser Thr Ser
915 920 925

Gly Tyr Gln Ala Arg Asn Ser Phe Ile Gln Asp Glu Asn Gly Asn Trp
930 935 940

Tyr Tyr Phe Asp Lys Arg Gly Tyr Leu Ala Thr Gly Ala His Glu Ile
945 950 955 960

Asp Gly Lys Gln Val Tyr Phe Leu Lys Asn Gly Ile Gln Leu Arg Asp
965 970 975

Ser Leu Arg Glu Asp Glu Asn Gly Asn Gln Tyr Tyr Tyr Asp Lys Thr
980 985 990

Gly Ala Gln Val Leu Asn Arg Tyr Tyr Thr Thr Asp Gly Gln Asn Trp
995 1000 1005

[0156] Arg Tyr Phe Asp Ala Lys Gly Val Met Ala Arg Gly Leu Val Thr
1010 1015 1020

Met Gly Gly Asn Gln Gln Phe Phe Asp Gln Asn Gly Tyr Gln Val
1025 1030 1035

Lys Gly Lys Ile Ala Arg Ala Lys Asp Gly Lys Leu Arg Tyr Phe
1040 1045 1050

Asp Lys Asp Ser Gly Asn Ala Ala Ala Asn Arg Phe Ala Gln Gly
1055 1060 1065

Asp Asn Pro Ser Asp Trp Tyr Tyr Phe Gly Ala Asp Gly Val Ala
1070 1075 1080

Val Thr Gly Leu Gln Lys Leu Gly Gln Gln Thr Leu Tyr Phe Asp
1085 1090 1095

Gln Glu Gly Lys Gln Val Lys Gly Lys Ile Val Thr Leu Ala Asp
1100 1105 1110

Lys Ser Ile Arg Tyr Phe Asp Ala Asn Ser Gly Glu Met Ala Val
1115 1120 1125

Gly Lys Phe Ala Glu Gly Ser Lys Asn Glu Trp Tyr Tyr Phe Asp
1130 1135 1140

Gln Thr Gly Lys Ala Val Thr Gly Leu Gln Lys Ile Gly Gln Gln
1145 1150 1155

Thr Leu Tyr Phe Asp Gln Asp Gly Lys Gln Val Lys Gly Lys Val
1160 1165 1170

Val Thr Leu Ala Asp Lys Ser Ile Arg Tyr Phe Asp Ala Asn Ser
1175 1180 1185

Gly Glu Met Ala Val Gly Lys Phe Ala Glu Gly Ala Lys Asn Glu
1190 1195 1200

Trp Tyr Tyr Phe Asp Gln Ala Gly Lys Ala Val Thr Gly Leu Gln
1205 1210 1215

Lys Ile Gly Gln Gln Thr Leu Tyr Phe Asp Gln Asp Gly Lys Gln
1220 1225 1230

Val Lys Gly Gln Leu Val Thr Leu Ala Asp Lys Ser Ile Arg Tyr
1235 1240 1245

Phe Asp Ala Asn Ser Gly Glu Met Ala Ser Asn Lys Phe Val Glu
1250 1255 1260

Gly Ala Lys Asn Glu Trp Tyr Tyr Phe Asp Gln Ala Gly Lys Ala
1265 1270 1275

Val Thr Gly Leu Gln Gln Ile Gly Gln Gln Thr Leu Tyr Phe Asp
1280 1285 1290

[0157] Gln Asn Gly Lys Gln Val Lys Gly Lys Ile Val Tyr Val Asn Gly
1295 1300 1305

Ala Asn Arg Tyr Phe Asp Ala Asn Ser Gly Glu Met Ala Arg Asn
1310 1315 1320

Lys Trp Ile Gln Leu Glu Asp Gly Ser Trp Met Tyr Phe Asp Arg
1325 1330 1335

Asn Gly Arg Gly Arg Arg Phe Gly Trp Asn
1340 1345

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<211> 4284
<212> DNA
<213> 唾液链球菌（Streptococcus salivarius）

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acgtacagct tcacgcagga aaccaccaat ctggttacgg actttacgaa gaataatgcg 180

gcgtatgact ccacgaaagc gtctttcgaa ttggtggacg gctatctgac cgcagacagc 240

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aattacatga cgaaagcact gtcgaacggc gaagaaacca aggatgtctt tacgatcgaa 420

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caagataagt ggaatatcaa tagcgaaagc cctggcaaag agcatttcca gaagggtgcg 600

ctgctgtttg ttaatagcga cagcaccaag tgggcgaact ccgattatcg taaactgaat 660

cagaccgcga cgtcttacat caagaatcat aagatcgtga acggtagcga tggtggttac 720

gagttcttgc tgagcaacga catcgacaac agcaacccgg tggtccaggc agagatgctg 780

aatcaactgt actactttat gaactggggt cagattgtgt tcggcgataa agataaagac 840

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atccacaacc tggcaggcga tggtgtcagc tcggccaaag ataacaaaga ggttctggtt 1620

[0158]

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

Thr Asn Leu Val Thr Asp Phe Thr Lys Asn Asn Ala Ala Tyr Asp Ser
50 55 60

Thr Lys Ala Ser Phe Glu Leu Val Asp Gly Tyr Leu Thr Ala Asp Ser
65 70 75 80

Trp Tyr Arg Pro Lys Glu Ile Leu Glu Ala Gly Thr Thr Trp Lys Ala
85 90 95

Ser Thr Glu Lys Asp Phe Arg Pro Leu Leu Met Ser Trp Trp Pro Asp
100 105 110

Lys Asp Thr Gln Val Ala Tyr Leu Asn Tyr Met Thr Lys Ala Leu Ser
115 120 125

Asn Gly Glu Glu Thr Lys Asp Val Phe Thr Ile Glu Asn Ser Gln Ala
130 135 140

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

Ile Ala Ala Asn Lys Ser Thr Asp Trp Leu Arg Gln Ser Ile Glu Ala
165 170 175

Phe Val Lys Asp Gln Asp Lys Trp Asn Ile Asn Ser Glu Ser Pro Gly
180 185 190

Lys Glu His Phe Gln Lys Gly Ala Leu Leu Phe Val Asn Ser Asp Ser
195 200 205

[0160] Thr Lys Trp Ala Asn Ser Asp Tyr Arg Lys Leu Asn Gln Thr Ala Thr
210 215 220

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

Glu Phe Leu Leu Ser Asn Asp Ile Asp Asn Ser Asn Pro Val Val Gln
245 250 255

Ala Glu Met Leu Asn Gln Leu Tyr Tyr Phe Met Asn Trp Gly Gln Ile
260 265 270

Val Phe Gly Asp Lys Asp Lys Asp Ala His Phe Asp Gly Ile Arg Val
275 280 285

Asp Ala Val Asp Asn Val Ser Val Asp Met Leu Gln Leu Val Ser Ser
290 295 300

Tyr Met Lys Ala Ala Tyr Lys Val Asn Glu Ser Glu Ala Arg Ala Leu
305 310 315 320

Ala Asn Ile Ser Ile Leu Glu Ala Trp Ser His Asn Asp Pro Tyr Tyr
325 330 335

Val Asn Glu His Asn Thr Ala Ala Leu Ser Met Asp Asn Gly Leu Arg
340 345 350

Leu Ser Ile Val His Gly Leu Thr Arg Pro Val Thr Asn Lys Gly Thr
355 360 365

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Gly Ala Arg Asn Ala Ser Met Lys Asp Leu Ile Asn Gly Gly Tyr Phe
    370                 375                 380

Gly Leu Ser Asn Arg Ala Glu Val Thr Ser Tyr Asp Gln Leu Gly Phe
385                 390                 395                 400

Ala Thr Tyr Leu Phe Val Arg Ala His Asp Ser Glu Val Gln Thr Val
                405                 410                 415

Ile Ala Asp Ile Ile Ser Lys Lys Ile Asp Pro Thr Thr Asp Gly Phe
            420                 425                 430

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

Asp Met Leu Lys Val Asp Lys Glu Tyr Thr His Ser Asn Ile Pro Ala
    450                 455                 460

Ala Tyr Ala Leu Met Leu Gln Thr Met Gly Ala Ala Thr Arg Val Tyr
465                 470                 475                 480

Tyr Gly Asp Leu Tyr Thr Asp Asn Gly Gln Tyr Met Ala Lys Lys Ser
                485                 490                 495

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

[0161]
Val Ala Gly Gly Gln Thr Ser Tyr Ile His Asn Leu Ala Gly Asp Gly
        515                 520                 525

Val Ser Ser Ala Lys Asp Asn Lys Glu Val Leu Val Ser Val Arg Tyr
    530                 535                 540

Gly Gln Asp Leu Met Ser Lys Thr Asp Thr Glu Gly Gly Lys Tyr Gly
545                 550                 555                 560

Arg Asn Ser Gly Met Leu Thr Leu Ile Ala Asn Asn Pro Asp Leu Lys
                565                 570                 575

Leu Ala Asp Gly Glu Thr Ile Thr Val Asn Met Gly Ala Ala His Lys
            580                 585                 590

Asn Gln Ala Tyr Arg Pro Leu Leu Leu Gly Thr Glu Lys Gly Ile Val
        595                 600                 605

Ser Ser Leu Asn Asp Ser Asp Thr Lys Ile Val Lys Tyr Thr Asp Ala
    610                 615                 620

Gln Gly Asn Leu Val Phe Thr Ala Asp Glu Ile Lys Gly Phe Lys Thr
625                 630                 635                 640

Val Asp Met Ser Gly Tyr Leu Ser Val Trp Val Pro Val Gly Ala Thr
                645                 650                 655

Asp Asp Gln Asn Val Leu Ala Lys Pro Ser Thr Lys Ala Tyr Lys Glu
            660                 665                 670
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Gly Asp Lys Val Tyr Ser Ser Ser Ala Ala Leu Glu Ala Gln Val Ile
675 680 685

Tyr Glu Gly Phe Ser Asn Phe Gln Asp Phe Val Lys Glu Asp Ser Gln
690 695 700

Tyr Thr Asn Lys Leu Ile Ala Ala Asn Ala Asp Leu Phe Lys Ser Trp
705 710 715 720

Gly Ile Thr Ser Phe Glu Ile Ala Pro Gln Tyr Val Ser Ser Lys Asp
725 730 735

Gly Thr Phe Leu Asp Ser Ile Ile Glu Asn Gly Tyr Ala Phe Thr Asp
740 745 750

Arg Tyr Asp Phe Ala Met Ser Lys Asn Asn Lys Tyr Gly Ser Lys Glu
755 760 765

Asp Leu Arg Asp Ala Leu Lys Ala Leu His Lys Gln Gly Ile Gln Val
770 775 780

Ile Ala Asp Trp Val Pro Asp Gln Leu Tyr Thr Leu Pro Gly Lys Glu
785 790 795 800

Val Val Thr Ala Thr Arg Thr Asp Thr His Gly Lys Val Leu Asp Asp
805 810 815

[0162] Thr Ser Leu Val Asn Lys Leu Tyr Val Thr Asn Thr Lys Ser Ser Gly
820 825 830

Asn Asp Phe Gln Ala Gln Tyr Gly Gly Ala Phe Leu Asp Lys Leu Gln
835 840 845

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

Thr Ile Asp Pro Ser Val Lys Ile Lys Gln Trp Glu Ala Lys Tyr Phe
865 870 875 880

Asn Gly Thr Asn Ile Gln Lys Arg Gly Ser Asp Tyr Val Leu Ser Asp
885 890 895

Gly Lys Leu Tyr Phe Thr Val Asn Asp Lys Gly Thr Phe Leu Pro Ala
900 905 910

Ala Leu Thr Gly Asp Thr Lys Ala Lys Thr Gly Phe Ala Tyr Asp Gly
915 920 925

Thr Gly Val Thr Tyr Tyr Thr Thr Ser Gly Thr Gln Ala Lys Ser Gln
930 935 940

Phe Val Thr Tyr Asn Gly Lys Gln Tyr Tyr Phe Asn Asp Lys Gly Tyr
945 950 955 960

Leu Val Thr Gly Glu Gln Thr Ile Asp Gly Ser Asn Tyr Phe Phe Leu
965 970 975

Pro Asn Gly Val Met Phe Thr Asp Gly Val Arg Lys Asn Ala Lys Gly
980 985 990

Gln Ser Leu Val Tyr Gly Lys Ser Gly Lys Leu Thr Thr Gln Thr Gly
995 1000 1005

Trp Lys Glu Val Thr Val Lys Asp Asp Ser Gly Lys Glu Glu Lys
1010 1015 1020

Phe Tyr Gln Tyr Phe Phe Lys Gly Gly Ile Met Ala Thr Gly Leu
1025 1030 1035

Thr Glu Val Glu Gly Lys Glu Lys Tyr Phe Tyr Asp Asn Gly Tyr
1040 1045 1050

Gln Ala Lys Gly Val Phe Val Pro Thr Lys Asp Gly His Leu Met
1055 1060 1065

Phe Phe Cys Gly Asp Ser Gly Glu Arg Lys Tyr Ser Gly Phe Phe
1070 1075 1080

Glu Gln Asp Gly Asn Trp Tyr Tyr Ala Asn Asp Lys Gly Tyr Val
1085 1090 1095

Ala Thr Gly Phe Thr Lys Val Gly Lys Gln Asn Leu Tyr Phe Asn
1100 1105 1110

[0163] Glu Lys Gly Val Gln Val Lys Asn Arg Phe Phe Gln Val Gly Asp
1115 1120 1125

Ala Thr Tyr Tyr Ala Asn Asn Glu Gly Asp Val Leu Arg Gly Ala
1130 1135 1140

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

Gln Val Lys Gly Glu Phe Val Asn Asn Pro Asp Gly Thr Thr Ser
1160 1165 1170

Tyr Tyr Asp Ala Ile Thr Gly Val Lys Leu Val Asp Thr Ser Leu
1175 1180 1185

Val Val Asp Gly Gln Thr Phe Asn Val Asp Ala Lys Gly Val Val
1190 1195 1200

Thr Lys Ala His Thr Pro Gly Phe Tyr Thr Thr Gly Asp Asn Asn
1205 1210 1215

Trp Phe Tyr Ala Asp Ser Tyr Gly Arg Asn Val Thr Gly Ala Gln
1220 1225 1230

Val Ile Asn Gly Gln His Leu Tyr Phe Asp Ala Asn Gly Arg Gln
1235 1240 1245

Val Lys Gly Gly Phe Val Thr Asn Thr Asp Gly Ser Arg Ser Phe
1250 1255 1260

Tyr His Trp Asn Thr Gly Asp Lys Leu Val Ser Thr Phe Phe Ala
1265 1270 1275

Thr Gly His Asp Arg Trp Tyr Tyr Ala Asp Asp Arg Gly Asn Val
1280 1285 1290

Val Thr Gly Ala Gln Val Ile Asn Gly Gln Lys Leu Phe Phe Asp
1295 1300 1305

Thr Asp Gly Lys Gln Val Lys Gly Ala Phe Ala Thr Asn Ala Asn
1310 1315 1320

Gly Ser Arg Ser Tyr Tyr His Trp Asn Thr Gly Asn Lys Leu Val
1325 1330 1335

Ser Thr Phe Phe Thr Ser Gly Asp Asn Asn Trp Tyr Tyr Ala Asp
1340 1345 1350

Ala Lys Gly Glu Val Val Val Gly Glu Gln Thr Ile Asn Gly Gln
1355 1360 1365

His Leu Tyr Phe Asp Gln Thr Gly Lys Gln Val Lys Gly Ala Thr
1370 1375 1380

Ala Thr Asn Pro Asp Gly Ser Ile Ser Tyr Tyr Asp Val His Thr
1385 1390 1395

Gly Glu Lys Ala Ile Asn Arg Trp Val Lys Ile Pro Ser Gly Gln
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Trp Val Tyr Phe Asn Ala Gln Gly Lys Gly Tyr Val Ser Asn
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gcatggtacc gccctaagtc tattctgaag gatggcaaaa cctggaccgc gtctaccgaa 300

gctgataagc gtccgttgct gatggtgtgg tggccggaca agtccaccca agttaactac 360

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gaatccctga atctggctgc gaaagcagtt cagaccaaga tcgaagaacg catcgcacgt 480

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<220>
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Lys Asn Phe Val Phe Glu Gln Asp Gly Lys Ser Tyr Tyr Phe Asp Ala
            20   25   30

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

Pro Ile Lys Ala Ala Val Asp Phe Ser Ser Gly Asn Gln Leu Tyr Lys
    50   55   60

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

Ala Trp Tyr Arg Pro Lys Ser Ile Leu Lys Asp Gly Lys Thr Trp Thr
                85   90   95

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Ala Ser Thr Glu Ala Asp Lys Arg Pro Leu Leu Met Val Trp Trp Pro
            100                 105                 110

Asp Lys Ser Thr Gln Val Asn Tyr Leu Asn Tyr Met Gln Asn Gln Gly
        115                 120                 125

Leu Gly Ala Gly Ser Phe Ser Thr Asn Ser Ser Gln Glu Ser Leu Asn
    130                 135                 140

Leu Ala Ala Lys Ala Val Gln Thr Lys Ile Glu Glu Arg Ile Ala Arg
145                 150                 155                 160

Glu Gly Asn Thr Asn Trp Leu Arg Thr Ser Ile Asp Gln Phe Ile Lys
                165                 170                 175

Thr Gln Pro Gly Trp Asn Ser Ser Thr Glu Asn Ser Ser Tyr Asp His
            180                 185                 190

Leu Gln Gly Gly Gln Leu Leu Phe Asn Asn Ser Lys Gly Asp Thr Gly
        195                 200                 205

Asn Arg Thr Ser Tyr Ala Asn Ser Asp Tyr Arg Leu Leu Asn Arg Thr
    210                 215                 220

Pro Thr Asn Gln Ser Gly Thr Arg Lys Tyr Phe Lys Asp Asn Ser Ile
225                 230                 235                 240
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[0167]

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Gly Gly Leu Glu Phe Leu Leu Ala Asn Asp Ile Asp Asn Ser Asn Pro
                245                 250                 255

Ala Val Gln Ala Glu Gln Leu Asn Trp Leu His Phe Met Met Asn Ile
            260                 265                 270

Gly Ser Ile Met Ala Asn Asp Pro Thr Ala Asn Phe Asp Gly Leu Arg
        275                 280                 285

Val Asp Ala Leu Asp Asn Val Asp Ala Asp Leu Leu Gln Ile Ala Ser
    290                 295                 300

Asp Tyr Phe Lys Ala Val Tyr Gly Val Asp Lys Ser Glu Ala Asn Ala
305                 310                 315                 320

Ile Lys His Leu Ser Tyr Leu Glu Ala Trp Ser Ala Asn Asp Pro Tyr
                325                 330                 335

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

Arg Asn Ala Leu Thr Asn Leu Leu Met Arg Asp Lys Asn Thr Arg Met
        355                 360                 365

Gln Leu Gly Asp Met Thr Ala Phe Met Asn Ser Ser Leu Asn Pro Arg
    370                 375                 380

Gly Ala Asn Asp Lys Asn Gly Glu Arg Met Ala Asn Tyr Ile Phe Thr
385                 390                 395                 400
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Arg Ala His Asp Thr Glu Ala Gln Thr Ile Ile Gln Arg Ile Ile Arg
405 410 415

Asp Arg Ile Asn Pro Asn Leu Phe Gly Tyr Asn Phe Thr Arg Asp Glu
420 425 430

Ile Lys Lys Ala Phe Glu Ile Tyr Asn Ala Asp Ile Asn Thr Ala His
435 440 445

Lys Thr Tyr Ala Ser Tyr Asn Leu Pro Ser Val Tyr Ala Leu Met Leu
450 455 460

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

Glu Asp Gly His Tyr Met Ala Lys Lys Thr Pro Tyr Phe Asp Ala Ile
485 490 495

Asp Thr Leu Leu Arg Ala Arg Ile Lys Tyr Val Ala Gly Gly Gln Asp
500 505 510

Met Glu Val Lys Lys Val Gly Asn Asp Gly Leu Leu Thr Ser Val Arg
515 520 525

Tyr Gly Lys Gly Ala Asn Asn Ser Thr Asp Trp Gly Thr Thr Glu Thr
530 535 540

[0168] Arg Thr Gln Gly Met Gly Val Ile Leu Thr Asn Asn Tyr Asp Phe Arg
545 550 555 560

Leu Gly Ser Asn Glu Thr Val Thr Met Asn Met Gly Arg Ala His Arg
565 570 575

Asn Gln Leu Tyr Arg Pro Leu Leu Leu Thr Thr Lys Asp Gly Leu Ala
580 585 590

Thr Tyr Leu Asn Asp Ser Asp Val Pro Ser Asn Leu Leu Lys Arg Thr
595 600 605

Asp Trp Asn Gly Asn Leu Thr Phe Asn Ala Asn Asp Val Phe Gly Val
610 615 620

Glu Asn Val Gln Val Ser Gly Tyr Leu Gly Val Trp Val Pro Val Gly
625 630 635 640

Ala Lys Ala Asn Gln Asp Ala Arg Thr Gln Pro Ser Asn Arg Ala Asn
645 650 655

Ser Asp Gly Gln Val Tyr Lys Ser Ser Ala Ala Leu Asp Ser Gln Val
660 665 670

Met Tyr Glu Ala Phe Ser Asn Phe Gln Ala Phe Ala Asp Asp Gln Pro
675 680 685

Glu Leu Tyr Met Asn Arg Val Leu Ala Lys Asn Thr Asp Leu Leu Lys
690 695 700

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Ala Trp Gly Val Thr Ser Val Gly Leu Pro Pro Gln Tyr Val Ser Ser
705                 710                 715                 720

Lys Asp Gly Thr Phe Leu Asp Ser Thr Ile Asp Asn Gly Tyr Ala Phe
                725                 730                 735

Asp Asp Arg Tyr Asp Met Ala Leu Ser Gln Asn Asn Lys Tyr Gly Ser
            740                 745                 750

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

Gln Ala Ile Ala Asp Trp Val Pro Asp Gln Ile Tyr Asn Leu Pro Gly
    770                 775                 780

Lys Glu Val Val Asn Ala Thr Arg Val Asn Gly Tyr Gly Tyr His Gln
785                 790                 795                 800

Gln Gly Tyr Gln Ile Val Asp Gln Ala Tyr Val Ala Asn Thr Arg Thr
                805                 810                 815

Asp Gly Thr Asp Tyr Gln Gly Arg Tyr Gly Gly Ala Phe Leu Asp Glu
            820                 825                 830

Leu Lys Ala Lys Tyr Pro Ser Ile Phe Asn Arg Val Gln Ile Ser Asn
        835                 840                 845
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[0169]

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Gly Lys Gln Leu Pro Thr Asn Glu Lys Ile Thr Lys Trp Ser Ala Lys
    850                 855                 860

Tyr Phe Asn Gly Thr Asn Ile Leu Gly Arg Gly Ile Asn Tyr Val Leu
865                 870                 875                 880

Arg Asp Asp Lys Thr Asn Gln Tyr Phe Asn Thr Ser Ala Asn Gly Gln
                885                 890                 895

Leu Leu Pro Thr Pro Leu Arg Asp Thr Gly Ala Ile Thr Ser Thr Gln
            900                 905                 910

Val Phe Gln Arg Arg Gly Gln Asp Val Tyr Phe Leu Arg Asp Asn Gln
        915                 920                 925

Val Ile Lys Asn Glu Phe Val Gln Asp Gly Asn Gly Asn Trp Tyr Tyr
    930                 935                 940

Phe Gly Ala Asp Gly Lys Met Thr Lys Gly Ala Gln Asn Ile Asn Ser
945                 950                 955                 960

Lys Asp Tyr Tyr Phe Phe Asp Asn Gly Val Gln Leu Arg Asn Ala Leu
                965                 970                 975

Arg Arg Ala Ser Asn Gly Tyr Thr Tyr Tyr Tyr Gly Leu Asp Gly Ala
            980                 985                 990

Met Ile Lys Asn Ala Phe Val Asp  Phe Asp Asp Lys His  Gln Gln Val
        995                 1000                 1005
```

Arg Ala Phe Thr Thr Gln Gly Thr Met Val Val Gly Asn Leu His
1010 1015 1020

Trp Ser Gly His His Phe Tyr Phe Asp Arg Glu Thr Gly Ile Gln
1025 1030 1035

Ala Lys Asp Arg Ile Val Arg Thr Asp Asp Gly Lys Leu His Tyr
1040 1045 1050

Tyr Val Ala Gln Thr Gly Asp Met Gly Arg Asn Val Phe Ala Thr
1055 1060 1065

Asp Ser Arg Thr Gly Lys Arg Tyr Tyr Phe Asp Ala Asp Gly Asn
1070 1075 1080

Thr Val Thr Gly Ser Arg Val Ile Asp Gly Lys Thr Tyr Tyr Phe
1085 1090 1095

Asn Gln Asp Gly Ser Val Gly Thr Ala Tyr Ser Asn Arg Ala Asp
1100 1105 1110

Ser Ile Ile Phe Glu Asn Gly Lys Ala Arg Tyr Ile Thr Pro Ala
1115 1120 1125

Gly Glu Ile Gly Arg Ser Ile Phe Val Tyr Asn Pro Ala Thr Lys
1130 1135 1140

[0170] Ala Trp Asn Tyr Phe Asp Lys Glu Gly Asn Arg Val Thr Gly Arg
1145 1150 1155

Gln Tyr Ile Asp Gly Asn Leu Tyr Tyr Phe Lys Glu Asp Gly Ser
1160 1165 1170

Gln Val Lys Gly Ala Ile Val Glu Glu Asn Gly Ile Lys Tyr Tyr
1175 1180 1185

Tyr Glu Pro Gly Ser Gly Ile Leu Ala Ser Gly Arg Tyr Leu Gln
1190 1195 1200

Val Gly Asp Asp Gln Trp Ile Tyr Phe Lys His Asp Gly Ser Leu
1205 1210 1215

Ala Ile Gly Gln Val Arg Ala Asp Gly Gly Tyr Leu Lys Tyr Phe
1220 1225 1230

Asp Lys Asn Gly Ile Gln Val Lys Gly Gln Thr Ile Val Glu Asp
1235 1240 1245

Gly His Thr Tyr Tyr Tyr Asp Ala Asp Ser Gly Ala Leu Val Thr
1250 1255 1260

Ser Ser Phe Ala Glu Ile Ala Pro Asn Gln Trp Ala Tyr Phe Asn
1265 1270 1275

Thr Glu Gly Gln Ala Leu Lys Gly Lys Trp Thr Ile Asn Gly Lys
1280 1285 1290

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Glu Tyr  Tyr Phe Asp Gln Asn  Gly Ile Gln Tyr Lys  Gly Lys Ala
    1295                 1300                 1305

Val Lys  Val Gly Ser Arg Tyr  Lys Tyr Tyr Asp Glu  Asn Asp Gly
    1310                 1315                 1320

Gln Pro  Val Thr Asn Arg Phe  Ala Gln Ile Glu Pro  Asn Val Trp
    1325                 1330                 1335

Ala Tyr  Phe Gly Ala Asp Gly  Tyr Ala Val Thr Gly  Glu Gln Val
    1340                 1345                 1350

Ile Asn  Gly Gln His Leu Tyr  Phe Asp Gln Ser Gly  Arg Gln Val
    1355                 1360                 1365

Lys Gly  Ala Tyr Val Thr Val  Asn Gly Gln Arg Arg  Tyr Tyr Asp
    1370                 1375                 1380

Ala Asn  Thr Gly Glu Tyr Ile  Pro Gly Arg
    1385                 1390
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<213>  柠檬明串珠菌（Leuconostoc citreum）

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[0171]

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accgacagcc aaatcaaaga gggcttgacg agccaaacga ccgactacac cgcccataac       180

gcggtccaca gcacggactc cgcagatttt gacaacttca atggttacct gaccgcgagc       240

agctggtatc gtcctaagga cgttctgcgt aacggccaac attgggaagc caccaccgcg       300

aatgacttcc gtcctatcgt cagcgtgtgg tggccgagca agcaaacgca ggtcaactac       360

ctgaactata tgagccagat gggtttgatc gataaccgtc aaatgttctc gttgaaagat       420

aaccaagcga tgctgaacat cgcgtgcacg accgtgcaac aagcaatcga aactaaaatc       480

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ccgcagtgga acatgagcag cgaagatccg aagaatgacc atctgcaaaa tggcgccctg       600

acgtttgtta acagcccgct gaccccggat acgaatagca atttccgcct gctgaatcgt       660

accccgacca atcaaaccgg tgttccgaaa tacaccatcg accaaagcaa aggtggtttt       720

gaactgctgc tggcgaatga cgtggataat tcgaacccgg ttgtgcaggc cgagcagttg       780

aactggctgc actacctgat gaactttggt agcattactg cgaatgacag cgcagcaaac       840

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gcagattact tcaaagcagc atacggtgtg gacaagaacg acgcaacggc aaatcagcat       960

ctgtcgatcc tggaagattg gagccacaac gacccggagt acgttaaaga cttcggcaat      1020

aaccaactga ccatggacga ttacatgcac acgcagctga tctggagcct gacgaaagac      1080

atgcgtatgc gtggtacgat gcagcgcttt atggactact atctggttaa ccgcaatcac      1140

gacagcaccg agaatactgc cattccgaat tacagctttg tccgtgccca tgacagcgaa      1200

gttcaaacgg ttattgcgca gatcatttct gagctgcatc cagacgtgaa gaatagcctg      1260
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aaagataccg ttccgcgtgt ttactacggt gacctgtata ccgatgacgg tcagtatatg 1440

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tacaccaacc cgctgacggg tgccatcacg accggcatgc aacagatcgg cgacaaaatc 3360

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cagtggctgc acctgagcac ccagggtcca gcagatacgg gtctggtcaa tatcaatggt 3480

aatctgaagt attttcaggc aaatggtcgt caggtgaaag gccaattcgt caccgacccg 3540 attaccaacg tcagctacta catgaacgcg acggacggta gcgcagtgtt caatgactat 3600

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aaagtggtga acaacaaact gcaacatttc gatgaaatca ccggtgtgca aaccaagagc 3720

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gtggcataa 3789

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<212> PRT
<213> 柠檬明串珠菌（Leuconostoc citreum）

<400> 54

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Lys Gly Phe Thr Gly Val Ile Asp Gly Gln Val Arg Tyr Phe Asp Gln
20 25 30

Glu Ser Gly Gln Glu Val Ser Thr Thr Asp Ser Gln Ile Lys Glu Gly
35 40 45

Leu Thr Ser Gln Thr Thr Asp Tyr Thr Ala His Asn Ala Val His Ser
50 55 60

Thr Asp Ser Ala Asp Phe Asp Asn Phe Asn Gly Tyr Leu Thr Ala Ser
65 70 75 80

[0173] Ser Trp Tyr Arg Pro Lys Asp Val Leu Arg Asn Gly Gln His Trp Glu
85 90 95

Ala Thr Thr Ala Asn Asp Phe Arg Pro Ile Val Ser Val Trp Trp Pro
100 105 110

Ser Lys Gln Thr Gln Val Asn Tyr Leu Asn Tyr Met Ser Gln Met Gly
115 120 125

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

Leu Asn Ile Ala Cys Thr Thr Val Gln Gln Ala Ile Glu Thr Lys Ile
145 150 155 160

Gly Val Ala Asn Ser Thr Ala Trp Leu Lys Thr Ala Ile Asp Asp Phe
165 170 175

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

Asp His Leu Gln Asn Gly Ala Leu Thr Phe Val Asn Ser Pro Leu Thr
195 200 205

Pro Asp Thr Asn Ser Asn Phe Arg Leu Leu Asn Arg Thr Pro Thr Asn
210 215 220

Gln Thr Gly Val Pro Lys Tyr Thr Ile Asp Gln Ser Lys Gly Gly Phe
225 230 235 240

Glu Leu Leu Leu Ala Asn Asp Val Asp Asn Ser Asn Pro Val Val Gln
245 250 255

Ala Glu Gln Leu Asn Trp Leu His Tyr Leu Met Asn Phe Gly Ser Ile
260 265 270

Thr Ala Asn Asp Ser Ala Ala Asn Phe Asp Gly Ile Arg Val Asp Ala
275 280 285

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

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

Leu Ser Ile Leu Glu Asp Trp Ser His Asn Asp Pro Glu Tyr Val Lys
325 330 335

Asp Phe Gly Asn Asn Gln Leu Thr Met Asp Asp Tyr Met His Thr Gln
340 345 350

Leu Ile Trp Ser Leu Thr Lys Asp Met Arg Met Arg Gly Thr Met Gln
355 360 365

Arg Phe Met Asp Tyr Tyr Leu Val Asn Arg Asn His Asp Ser Thr Glu
370 375 380

[0174] Asn Thr Ala Ile Pro Asn Tyr Ser Phe Val Arg Ala His Asp Ser Glu
385 390 395 400

Val Gln Thr Val Ile Ala Gln Ile Ile Ser Glu Leu His Pro Asp Val
405 410 415

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

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

Asn Met Pro Ser Ala Tyr Ala Met Leu Leu Thr Asn Lys Asp Thr Val
450 455 460

Pro Arg Val Tyr Tyr Gly Asp Leu Tyr Thr Asp Asp Gly Gln Tyr Met
465 470 475 480

Ala Asn Lys Ser Pro Tyr Phe Asp Ala Ile Asn Gly Leu Leu Lys Ser
485 490 495

Arg Ile Lys Tyr Val Ala Gly Gly Gln Ser Met Ala Val Asp Gln Asn
500 505 510

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

Asp Ser Gly Asn Ala Asp Thr Arg Thr Gln Gly Ile Gly Val Ile Val
530 535 540

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

His Met Gly Ala Ala His Lys Asn Gln Ala Phe Arg Leu Leu Leu Gly
565 570 575

Thr Thr Ala Asp Asn Leu Ser Tyr Tyr Asp Asn Asp Asn Ala Pro Val
580 585 590

Lys Tyr Thr Asn Asp Gln Gly Asp Leu Ile Phe Asp Asn Thr Glu Ile
595 600 605

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

Pro Val Gly Ala Asp Ser His Gln Asp Ala Arg Thr Leu Ser Asp Asp
625 630 635 640

Thr Ala His His Asp Gly Lys Thr Phe His Ser Asn Ala Ala Leu Asp
645 650 655

Ser Gln Val Ile Tyr Glu Gly Phe Ser Asn Phe Gln Ala Phe Ala Thr
660 665 670

Asn Thr Glu Asp Tyr Thr Asn Ala Val Ile Ala Lys Asn Gly Gln Leu
675 680 685

[0175] Phe Lys Asp Trp Gly Ile Thr Ser Phe Gln Leu Ala Pro Gln Tyr Arg
690 695 700

Ser Ser Thr Asp Thr Ser Phe Leu Asp Ser Ile Ile Gln Asn Gly Tyr
705 710 715 720

Ala Phe Thr Asp Arg Tyr Asp Leu Gly Tyr Gly Thr Pro Thr Lys Tyr
725 730 735

Gly Thr Val Asp Gln Leu Arg Asp Ala Ile Lys Ala Leu His Ala Asn
740 745 750

Gly Ile Gln Ala Ile Ala Asp Trp Val Pro Asp Gln Ile Tyr Asn Leu
755 760 765

Pro Gly Gln Glu Leu Ala Thr Val Thr Arg Thr Asn Ser Tyr Gly Asp
770 775 780

Lys Asp Thr Asn Ser Asp Ile Asp Gln Ser Leu Tyr Val Ile Gln Ser
785 790 795 800

Arg Gly Gly Gly Lys Tyr Gln Ala Gln Tyr Gly Gly Ala Phe Leu Ser
805 810 815

Asp Ile Gln Lys Lys Tyr Pro Ala Leu Phe Glu Thr Lys Gln Ile Ser
820 825 830

Thr Gly Leu Pro Met Asp Pro Ser Gln Lys Ile Thr Glu Trp Ser Gly
835 840 845

Lys Tyr Phe Asn Gly Ser Asn Ile Gln Gly Lys Gly Ala Gly Tyr Val
850 855 860

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

Asn Asn Arg Asp Phe Leu Pro Lys Gln Leu Thr Asp Asp Leu Ser Glu
885 890 895

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

Gly Tyr Leu Ala Arg Asn Thr Phe Ile Gln Asp Asp Asn Gly Asn Tyr
915 920 925

Tyr Tyr Phe Asp Ser Thr Gly His Leu Val Thr Gly Phe Gln Asn Ile
930 935 940

Asn Asn His His Tyr Phe Phe Leu Pro Asn Gly Ile Glu Leu Val Gln
945 950 955 960

Ser Phe Leu Gln Asn Ala Asp Gly Ser Thr Ile Tyr Phe Asp Gln Lys
965 970 975

Gly Arg Gln Val Phe Asn Gln Tyr Ile Thr Asp Gln Thr Gly Thr Ala
980 985 990

[0176] Tyr Tyr Phe Gln Asn Asp Gly Thr Met Val Thr Ser Gly Phe Thr Glu
995 1000 1005

Ile Asp Gly His Lys Gln Tyr Phe Tyr Lys Asn Gly Thr Gln Val
1010 1015 1020

Lys Gly Gln Phe Val Ser Asp Thr Asp Gly His Val Phe Tyr Leu
1025 1030 1035

Glu Ala Gly Asn Gly Asn Val Ala Thr Gln Arg Phe Ala Gln Asn
1040 1045 1050

Ser Gln Gly Gln Trp Phe Tyr Leu Gly Asn Asp Gly Ile Ala Leu
1055 1060 1065

Thr Gly Leu Gln Thr Ile Asn Gly Val Gln Asn Tyr Phe Tyr Ala
1070 1075 1080

Asp Gly His Gln Ser Lys Gly Asp Phe Ile Thr Ile Gln Asn His
1085 1090 1095

Val Leu Tyr Thr Asn Pro Leu Thr Gly Ala Ile Thr Thr Gly Met
1100 1105 1110

Gln Gln Ile Gly Asp Lys Ile Phe Val Phe Asp Asn Thr Gly Asn
1115 1120 1125

Met Leu Thr Asn Gln Tyr Tyr Gln Thr Leu Asp Gly Gln Trp Leu
1130 1135 1140

```
His Leu  Ser Thr Gln Gly Pro  Ala Asp Thr Gly Leu  Val Asn Ile
    1145                 1150                 1155

Asn Gly  Asn Leu Lys Tyr Phe  Gln Ala Asn Gly Arg  Gln Val Lys
    1160                 1165                 1170

Gly Gln  Phe Val Thr Asp Pro  Ile Thr Asn Val Ser  Tyr Tyr Met
    1175                 1180                 1185

Asn Ala  Thr Asp Gly Ser Ala  Val Phe Asn Asp Tyr  Phe Thr Tyr
    1190                 1195                 1200

Gln Gly  Gln Trp Tyr Leu Thr  Asp Ser Asn Tyr Gln  Leu Val Lys
    1205                 1210                 1215

Gly Phe  Lys Val Val Asn Asn  Lys Leu Gln His Phe  Asp Glu Ile
    1220                 1225                 1230

Thr Gly  Val Gln Thr Lys Ser  Ala His Ile Ile Val  Asn Asn Arg
    1235                 1240                 1245

Thr Tyr  Ile Phe Asp Asp Gln  Gly Tyr Phe Val Ser  Val Ala
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[0177]

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caagacaagt ggaatatcaa ttcggagagc ccgggtaaag agcatttcca aaaaggtgct       600

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gagtttttgc tgtcctctga cattgataac agcaacccga ttgttcaggc ggagatgctg       780

aaccaactgt actatttcat gaactggggt cagattgtgt ttggcgacaa agataaggat       840

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ttcacggtaa acgacaaagg taccttcttg ccggcagctc tgaccggtga cacgaaggca 2760

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gttgaaggta aagagaaata cttttatgat aatggttatc aggctaaagg tattttcatc 3180

cctaccaaag acggccatct gatgtttttc tgcggtgata gcggtgagcg taaatacagc 3240

ggtttcttcg aacaagacgg taactggtat tacgcaaacg ataaaggtta cgtcgcgacc 3300

ggttttacca aagtgggtaa gcagaacttg tactttaacg agaaaggtgt gcaggtcaag 3360

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aaaggtgaat ttgtgaataa cccggacggt accacgagct attatgacgc aattaccggt        3540

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ggcgttgtca ccaaggcgca cacgccgggt ttctatacca ctggcgacaa caattggttt        3660

tatgcagata gccacggtcg caatgtcact ggcgcacaga tcattaacgg ccaacacctg        3720

tatttcgatg cgaatggccg tcaggtgaag ggcggctttg ttatgaacac tgatggttct        3780

cgttcgttct atcattggaa taccggtgat aaactggtga gcacgttctt tacgaccggc        3840

cacgatcgtt ggtactacgc cgacgacaaa ggtaacgtgg tgaccggcgc acaagtcatc        3900

aacggtcaga aattgttctt cgcgaccgac ggtaaacaag ttaagggcga tttcgcgacc        3960

aacgcaaatg gttcccgttc ttactatcac ggtgccacgg gtaataagct ggtcagcacc        4020

ttctttacca cgggcgataa caactggtac tatgcagacg cgaagggcga ggttgtcgtt        4080

ggtgaacaaa cgattaacgg tcaaaatctg tattttgatc agaccggtaa gcaagtgaaa        4140

ggtgcgaccg cgaccaatcc agatggcagc atttcttatt acgatgttca cacgggcgag        4200

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```

[0179]

<210> 56
<211> 1427
<212> PRT
<213> 唾液链球菌（Streptococcus salivarius）

<400> 56

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

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

Thr Asn Leu Val Thr Asp Phe Thr Lys Asn Asn Ala Ala Tyr Asp Ser
    50                  55                  60

Thr Lys Ala Ser Phe Glu Leu Val Asp Gly Tyr Leu Thr Ala Asp Ser
65                  70                  75                  80

Trp Tyr Arg Pro Lys Glu Ile Leu Glu Ala Gly Thr Thr Trp Lys Ala
                85                  90                  95

Ser Thr Glu Lys Asp Phe Arg Pro Leu Leu Met Ser Trp Trp Pro Asp
            100                 105                 110

Lys Asp Thr Gln Val Ala Tyr Leu Asn Tyr Met Thr Lys Ala Leu Ser
        115                 120                 125

Asn Gly Glu Glu Thr Lys Asp Val Phe Thr Ile Glu Asn Ser Gln Ala
    130                 135                 140
```

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

Ile Ala Ala Asn Lys Ser Thr Asp Trp Leu Arg Gln Ser Ile Glu Ala
165 170 175

Phe Val Lys Asp Gln Asp Lys Trp Asn Ile Asn Ser Glu Ser Pro Gly
180 185 190

Lys Glu His Phe Gln Lys Gly Ala Leu Leu Phe Val Asn Ser Asp Leu
195 200 205

Thr Lys Trp Ala Asn Ser Asp Tyr Arg Lys Leu Asp Gln Thr Ala Thr
210 215 220

Ser Arg Leu Pro Lys Asp Lys Ile Lys Ser Gly Ser Asp Ala Gly Tyr
225 230 235 240

Glu Phe Leu Leu Ser Ser Asp Ile Asp Asn Ser Asn Pro Ile Val Gln
245 250 255

Ala Glu Met Leu Asn Gln Leu Tyr Tyr Phe Met Asn Trp Gly Gln Ile
260 265 270

Val Phe Gly Asp Lys Asp Lys Asp Ala His Phe Asp Gly Ile Arg Val
275 280 285

[0180] Asp Ala Val Asp Asn Val Ser Ile Asp Met Leu Gln Leu Val Ser Ser
290 295 300

Tyr Met Lys Ala Ala Tyr Lys Val Asn Glu Ser Glu Ala Arg Ala Leu
305 310 315 320

Ala Asn Ile Ser Ile Leu Glu Ala Trp Ser Gln Asn Asp Pro Tyr Tyr
325 330 335

Val Asp Glu His Asn Thr Ala Ala Leu Ser Met Asp Asn Gly Leu Arg
340 345 350

Leu Ser Ile Val His Gly Leu Thr Arg Pro Val Thr Asn Lys Gly Thr
355 360 365

Gly Ala Arg Asn Ala Ser Met Lys Asp Leu Ile Asn Gly Gly Tyr Phe
370 375 380

Gly Leu Ser Asn Arg Ala Glu Val Thr Ser Tyr Asp Gln Leu Gly Phe
385 390 395 400

Ala Thr Tyr Leu Phe Val Arg Ala His Asp Ser Glu Val Gln Thr Val
405 410 415

Ile Ala Asp Ile Ile Ser Lys Lys Ile Asp Pro Thr Thr Asp Gly Phe
420 425 430

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

Asp Met Leu Lys Val Asp Lys Glu Tyr Thr His Ser Asn Ile Pro Ala
450 455 460

Ala Tyr Ala Leu Met Leu Gln Thr Met Gly Ala Ala Thr Arg Val Tyr
465 470 475 480

Tyr Gly Asp Leu Tyr Thr Asp Asn Gly Gln Tyr Met Ala Lys Lys Ser
485 490 495

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

Val Ala Gly Gly Gln Thr Ser Tyr Ile His Asn Leu Ala Gly Asp Gly
515 520 525

Val Ser Ser Ala Lys Asp Asn Lys Glu Val Leu Val Ser Val Arg Tyr
530 535 540

Gly Gln Asp Leu Met Ser Lys Thr Asp Thr Glu Gly Gly Lys Tyr Gly
545 550 555 560

Arg Asn Ser Gly Met Leu Thr Leu Ile Ala Asn Asn Pro Asp Leu Lys
565 570 575

Leu Ala Asp Gly Glu Thr Ile Thr Val Asn Met Gly Ala Ala His Lys
580 585 590

[0181] Asn Gln Ala Tyr Arg Pro Leu Leu Leu Gly Thr Glu Lys Gly Ile Val
595 600 605

Ser Ser Leu Asn Asp Ser Asp Thr Lys Ile Val Lys Tyr Thr Asp Ala
610 615 620

Gln Gly Asn Leu Val Phe Thr Ala Asp Glu Ile Lys Gly Phe Lys Thr
625 630 635 640

Val Asp Met Ser Gly Tyr Leu Ser Val Trp Val Pro Val Gly Ala Thr
645 650 655

Glu Asp Gln Asn Val Leu Ala Lys Pro Ser Thr Lys Val Tyr Lys Glu
660 665 670

Gly Asp Lys Val Tyr Ser Ser Ser Ala Ala Leu Glu Ala Gln Val Ile
675 680 685

Tyr Glu Gly Phe Ser Asn Phe Gln Asp Phe Val Lys Glu Asp Ser Gln
690 695 700

Tyr Thr Asn Lys Leu Ile Ala Ala Asn Ala Asp Leu Phe Lys Ser Trp
705 710 715 720

Gly Ile Thr Ser Phe Glu Ile Ala Pro Gln Tyr Val Ser Ser Lys Asp
725 730 735

Gly Thr Phe Leu Asp Ser Ile Ile Glu Asn Gly Tyr Ala Phe Thr Asp
740 745 750

Arg Tyr Asp Phe Ala Met Ser Lys Asn Asn Lys Tyr Gly Ser Lys Glu
755 760 765

Asp Leu Arg Asp Ala Leu Lys Ala Leu His Lys Gln Gly Ile Gln Val
770 775 780

Ile Ala Asp Trp Val Pro Asp Gln Leu Tyr Thr Leu Pro Gly Lys Glu
785 790 795 800

Val Val Thr Ala Thr Arg Thr Asp Thr His Gly Lys Val Leu Asp Asp
805 810 815

Thr Ser Leu Val Asn Lys Leu Tyr Val Thr Asn Thr Lys Ser Ser Gly
820 825 830

Asn Asp Phe Gln Ala Gln Tyr Gly Gly Ala Phe Leu Asp Lys Leu Gln
835 840 845

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

Thr Ile Asp Pro Ser Val Lys Ile Lys Gln Trp Glu Ala Lys Tyr Phe
865 870 875 880

Asn Gly Thr Asn Ile Gln Lys Arg Gly Ser Asp Tyr Val Leu Ser Asp
885 890 895

[0182] Gly Lys Leu Tyr Phe Thr Val Asn Asp Lys Gly Thr Phe Leu Pro Ala
900 905 910

Ala Leu Thr Gly Asp Thr Lys Ala Lys Thr Gly Phe Ala Tyr Asp Gly
915 920 925

Thr Gly Val Thr Tyr Tyr Thr Thr Ser Gly Thr Gln Ala Lys Ser Gln
930 935 940

Phe Val Thr Tyr Asn Gly Lys Gln Tyr Tyr Phe Asn Asp Lys Gly Tyr
945 950 955 960

Leu Val Thr Gly Glu Gln Ala Ile Asp Gly Ser Asn Tyr Phe Phe Leu
965 970 975

Pro Asn Gly Val Met Phe Thr Asp Gly Val Ile Lys Asn Ala Lys Gly
980 985 990

Gln Ser Leu Val Tyr Gly Lys Ser Gly Lys Leu Thr Thr Gln Thr Gly
995 1000 1005

Trp Lys Glu Val Thr Val Lys Asp Asp Ser Gly Lys Glu Glu Lys
1010 1015 1020

Phe Tyr Gln Tyr Phe Phe Lys Gly Gly Ile Met Ala Thr Gly Leu
1025 1030 1035

Thr Glu Val Glu Gly Lys Glu Lys Tyr Phe Tyr Asp Asn Gly Tyr
1040 1045 1050

Gln Ala Lys Gly Ile Phe Ile Pro Thr Lys Asp Gly His Leu Met
1055 1060 1065

Phe Phe Cys Gly Asp Ser Gly Glu Arg Lys Tyr Ser Gly Phe Phe
1070 1075 1080

Glu Gln Asp Gly Asn Trp Tyr Tyr Ala Asn Asp Lys Gly Tyr Val
1085 1090 1095

Ala Thr Gly Phe Thr Lys Val Gly Lys Gln Asn Leu Tyr Phe Asn
1100 1105 1110

Glu Lys Gly Val Gln Val Lys Asn Arg Phe Phe Gln Val Gly Asp
1115 1120 1125

Ala Thr Tyr Tyr Ala Asn Asn Glu Gly Asp Val Leu Arg Gly Ala
1130 1135 1140

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

Gln Val Lys Gly Glu Phe Val Asn Asn Pro Asp Gly Thr Thr Ser
1160 1165 1170

Tyr Tyr Asp Ala Ile Thr Gly Val Lys Leu Val Asp Thr Ser Leu
1175 1180 1185

[0183] Val Val Asn Gly Gln Thr Phe Asn Ile Asp Ala Lys Gly Val Val
1190 1195 1200

Thr Lys Ala His Thr Pro Gly Phe Tyr Thr Thr Gly Asp Asn Asn
1205 1210 1215

Trp Phe Tyr Ala Asp Ser His Gly Arg Asn Val Thr Gly Ala Gln
1220 1225 1230

Ile Ile Asn Gly Gln His Leu Tyr Phe Asp Ala Asn Gly Arg Gln
1235 1240 1245

Val Lys Gly Gly Phe Val Met Asn Thr Asp Gly Ser Arg Ser Phe
1250 1255 1260

Tyr His Trp Asn Thr Gly Asp Lys Leu Val Ser Thr Phe Phe Thr
1265 1270 1275

Thr Gly His Asp Arg Trp Tyr Tyr Ala Asp Asp Lys Gly Asn Val
1280 1285 1290

Val Thr Gly Ala Gln Val Ile Asn Gly Gln Lys Leu Phe Phe Ala
1295 1300 1305

Thr Asp Gly Lys Gln Val Lys Gly Asp Phe Ala Thr Asn Ala Asn
1310 1315 1320

Gly Ser Arg Ser Tyr Tyr His Gly Ala Thr Gly Asn Lys Leu Val
1325 1330 1335

Ser Thr Phe Phe Thr Thr Gly Asp Asn Asn Trp Tyr Tyr Ala Asp
1340 1345 1350

Ala Lys Gly Glu Val Val Val Gly Glu Gln Thr Ile Asn Gly Gln
1355 1360 1365

Asn Leu Tyr Phe Asp Gln Thr Gly Lys Gln Val Lys Gly Ala Thr
1370 1375 1380

Ala Thr Asn Pro Asp Gly Ser Ile Ser Tyr Tyr Asp Val His Thr
1385 1390 1395

Gly Glu Lys Val Ile Asn Arg Trp Val Lys Ile Pro Ser Gly Gln
1400 1405 1410

Trp Val Tyr Phe Asn Ala Gln Gly Lys Gly Tyr Val Ser Asn
1415 1420 1425

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<211> 5208
<212> DNA
<213> 罗伊氏乳杆菌（Lactobacillus reuteri）

<400> 57
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aatcaggtcg cgaatgatac caccaccaac caaagcaaga cggacagcac cagcacgacg 180

[0184] gttaagaatc cgacgtttat tcctgttagc actttgtcca gctccgataa cgaaaagcag 240

agccagaatt acaataaacc agataacggt aattacggta atgttgatgc ggcctacttc 300

aataacaatc agctgcacat tagcggttgg cacgcaacca acgcgagcca gggtacggat 360

agccgccaag taatcgtacg cgacattacc accaagaccg agctgggtcg tactaatgtg 420

accaacaatg ttctgcgtcc ggacgtgaaa aatgttcaca acgtctacaa cgctgacaac 480

agcggctttg atgtgaatat caatattgat ttcagcaaga tgaaagacta tcgtgacagc 540

atcgagatcg tttctcgtta tagcggcaac ggcaagagcg ttgactggtg gtcgcagccg 600

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gacgttacgt ttaacattgg tgatttggac tacacccatc agtaccagat cctgtctcgt 900

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ggcaatatgg ttgcaaacca aagcccggtt gaaatcagca gcaacggtgc gagcggcacc 4980

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<210> 58
<211> 1735
<212> PRT
<213> 罗伊氏乳杆菌（Lactobacillus reuteri）

<400> 58

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

Gln Pro Ala Gln Thr Thr Asp Lys Asn Gln Val Ala Asn Asp Thr Thr
        35                  40                  45

Thr Asn Gln Ser Lys Thr Asp Ser Thr Ser Thr Thr Val Lys Asn Pro
    50                  55                  60
```

```
Thr Phe Ile Pro Val Ser Thr Leu Ser Ser Ser Asp Asn Glu Lys Gln
65                  70                  75                  80

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

Ala Ala Tyr Phe Asn Asn Asn Gln Leu His Ile Ser Gly Trp His Ala
            100                 105                 110

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

Ile Thr Thr Lys Thr Glu Leu Gly Arg Thr Asn Val Thr Asn Asn Val
    130                 135                 140

Leu Arg Pro Asp Val Lys Asn Val His Asn Val Tyr Asn Ala Asp Asn
145                 150                 155                 160

Ser Gly Phe Asp Val Asn Ile Asn Ile Asp Phe Ser Lys Met Lys Asp
                165                 170                 175

Tyr Arg Asp Ser Ile Glu Ile Val Ser Arg Tyr Ser Gly Asn Gly Lys
            180                 185                 190

Ser Val Asp Trp Trp Ser Gln Pro Ile Thr Phe Asp Lys Asn Asn Tyr
        195                 200                 205
```

[0187]

```
Ala Tyr Leu Asp Thr Phe Glu Val Lys Asn Gly Glu Leu His Ala Thr
    210                 215                 220

Gly Trp Asn Ala Thr Asn Lys Ala Ile Asn Tyr Asn His His Phe Val
225                 230                 235                 240

Ile Leu Phe Asp Arg Thr Asn Gly Lys Glu Val Thr Arg Gln Glu Val
                245                 250                 255

Arg Asp Gly Gln Ser Arg Pro Asp Val Ala Lys Val Tyr Pro Gln Val
            260                 265                 270

Val Gly Ala Asn Asn Ser Gly Phe Asp Val Thr Phe Asn Ile Gly Asp
        275                 280                 285

Leu Asp Tyr Thr His Gln Tyr Gln Ile Leu Ser Arg Tyr Ser Asn Ala
    290                 295                 300

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

Ile Ala Pro Ala Asn Gln Ser Asn Gln Gly Tyr Leu Asp Ser Phe Asp
                325                 330                 335

Ile Ser Lys Asn Gly Glu Val Thr Val Thr Gly Trp Asn Ala Thr Asp
            340                 345                 350

Leu Ser Glu Leu Gln Thr Asn His Tyr Val Ile Leu Phe Asp Gln Thr
        355                 360                 365
```

```
Ala Gly Gln Gln Val Ala Ser Ala Lys Val Asp Leu Ile Ser Arg Pro
    370                 375                 380

Asp Val Ala Lys Ala Tyr Pro Thr Val Lys Thr Ala Glu Thr Ser Gly
385                 390                 395                 400

Phe Lys Val Thr Phe Lys Val Ser Asn Leu Gln Pro Gly His Gln Tyr
                405                 410                 415

Ser Val Val Ser Arg Phe Ser Ala Asp Glu Asn Gly Asn Gly Asn Asp
            420                 425                 430

Lys Arg His Thr Asp Tyr Trp Tyr Ser Pro Val Thr Leu Asn Gln Thr
        435                 440                 445

Ala Ser Asn Ile Asp Thr Ile Thr Met Thr Ser Asn Gly Leu His Ile
    450                 455                 460

Thr Gly Trp Met Ala Ser Asp Asn Ser Ile Asn Glu Ala Thr Pro Tyr
465                 470                 475                 480

Ala Ile Ile Leu Asn Asn Gly Arg Glu Val Thr Arg Gln Lys Leu Thr
                485                 490                 495

Leu Ile Ala Arg Pro Asp Val Ala Ala Val Tyr Pro Ser Leu Tyr Asn
            500                 505                 510
```

[0188]

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

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

Ala Val Asp Gly Asn Pro Asn Gly Thr Asn Thr Val Thr Asp Gln Phe
545                 550                 555                 560

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

Asn Gly Asn Gln Ile Glu Phe Ser Gly Trp His Ala Thr Asn Gln Ser
            580                 585                 590

Asn Asp Lys Asn Ser Gln Trp Ile Ile Val Leu Val Asn Gly Lys Glu
        595                 600                 605

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

Asn Arg Asn Asp Val Tyr Lys Val Asn Pro Ala Ile Glu Asn Ser Ile
625                 630                 635                 640

Met Ser Gly Phe Gln Gly Ile Ile Thr Leu Pro Val Thr Val Lys Asp
                645                 650                 655

Glu Asn Val Gln Leu Val His Arg Phe Ser Asn Asp Ala Lys Thr Gly
            660                 665                 670
```

```
Glu Gly Asn Tyr Val Asp Phe Trp Ser Glu Val Met Ser Val Lys Asp
        675                 680                 685

Ser Phe Gln Lys Gly Asn Gly Pro Leu Asn Gln Phe Gly Leu Gln Thr
    690                 695                 700

Ile Asn Gly Gln Gln Tyr Tyr Ile Asp Pro Thr Thr Gly Gln Pro Arg
705                 710                 715                 720

Lys Asn Phe Leu Leu Gln Asn Gly Asn Asp Trp Ile Tyr Phe Asp Lys
                725                 730                 735

Asp Thr Gly Ala Gly Thr Asn Ala Leu Lys Leu Gln Phe Asp Lys Gly
            740                 745                 750

Thr Ile Ser Ala Asp Glu Gln Tyr Arg Arg Gly Asn Glu Ala Tyr Ser
        755                 760                 765

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

Thr Trp Tyr Arg Pro Lys Gln Ile Leu Lys Asp Gly Thr Thr Trp Thr
785                 790                 795                 800

Asp Ser Lys Glu Thr Asp Met Arg Pro Ile Leu Met Val Trp Trp Pro
                805                 810                 815
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[0189]

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Asn Thr Val Thr Gln Ala Tyr Tyr Leu Asn Tyr Met Lys Gln Tyr Gly
            820                 825                 830

Asn Leu Leu Pro Ala Ser Leu Pro Ser Phe Ser Thr Asp Ala Asp Ser
        835                 840                 845

Ala Glu Leu Asn His Tyr Ser Glu Leu Val Gln Gln Asn Ile Glu Lys
    850                 855                 860

Arg Ile Ser Glu Thr Gly Ser Thr Asp Trp Leu Arg Thr Leu Met His
865                 870                 875                 880

Glu Phe Val Thr Lys Asn Ser Met Trp Asn Lys Asp Ser Glu Asn Val
                885                 890                 895

Asp Tyr Gly Gly Leu Gln Leu Gln Gly Gly Phe Leu Lys Tyr Val Asn
            900                 905                 910

Ser Asp Leu Thr Lys Tyr Ala Asn Ser Asp Trp Arg Leu Met Asn Arg
        915                 920                 925

Thr Ala Thr Asn Ile Asp Gly Lys Asn Tyr Gly Gly Ala Glu Phe Leu
    930                 935                 940

Leu Ala Asn Asp Ile Asp Asn Ser Asn Pro Val Val Gln Ala Glu Glu
945                 950                 955                 960

Leu Asn Trp Leu Tyr Tyr Leu Met Asn Phe Gly Thr Ile Thr Gly Asn
                965                 970                 975
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Asn Pro Glu Ala Asn Phe Asp Gly Ile Arg Val Asp Ala Val Asp Asn
            980                 985                 990

Val Asp Val Asp Leu Leu Ser Ile  Ala Arg Asp Tyr Phe  Asn Ala Ala
        995                 1000                 1005

Tyr Asn  Met Glu Gln Ser Asp  Ala Ser Ala Asn Lys  His Ile Asn
    1010                 1015                 1020

Ile Leu  Glu Asp Trp Gly Trp  Asp Asp Pro Ala Tyr  Val Asn Lys
    1025                 1030                 1035

Ile Gly  Asn Pro Gln Leu Thr  Met Asp Asp Arg Leu  Arg Asn Ala
    1040                 1045                 1050

Ile Met  Asp Thr Leu Ser Gly  Ala Pro Asp Lys Asn  Gln Ala Leu
    1055                 1060                 1065

Asn Lys  Leu Ile Thr Gln Ser  Leu Val Asn Arg Ala  Asn Asp Asn
    1070                 1075                 1080

Thr Glu  Asn Ala Val Ile Pro  Ser Tyr Asn Phe Val  Arg Ala His
    1085                 1090                 1095

Asp Ser  Asn Ala Gln Asp Gln  Ile Arg Gln Ala Ile  Gln Ala Ala
    1100                 1105                 1110

[0190]
Thr Gly  Lys Pro Tyr Gly Glu  Phe Asn Leu Asp Asp  Glu Lys Lys
    1115                 1120                 1125

Gly Met  Glu Ala Tyr Ile Asn  Asp Gln Asn Ser Thr  Asn Lys Lys
    1130                 1135                 1140

Trp Asn  Leu Tyr Asn Met Pro  Ser Ala Tyr Thr Ile  Leu Leu Thr
    1145                 1150                 1155

Asn Lys  Asp Ser Val Pro Arg  Val Tyr Tyr Gly Asp  Leu Tyr Gln
    1160                 1165                 1170

Asp Gly  Gly Gln Tyr Met Glu  His Lys Thr Arg Tyr  Phe Asp Thr
    1175                 1180                 1185

Ile Thr  Asn Leu Leu Lys Thr  Arg Val Lys Tyr Val  Ala Gly Gly
    1190                 1195                 1200

Gln Thr  Met Ser Val Asp Lys  Asn Gly Ile Leu Thr  Asn Val Arg
    1205                 1210                 1215

Phe Gly  Lys Gly Ala Met Asn  Ala Thr Asp Thr Gly  Thr Asp Glu
    1220                 1225                 1230

Thr Arg  Thr Glu Gly Ile Gly  Val Val Ile Ser Asn  Asn Thr Asn
    1235                 1240                 1245

Leu Lys  Leu Asn Asp Gly Glu  Ser Val Val Leu His  Met Gly Ala
    1250                 1255                 1260
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Ala His Lys Asn Gln Lys Tyr Arg Ala Val Ile Leu Thr Thr Glu
1265 1270 1275

Asp Gly Val Lys Asn Tyr Thr Asn Asp Thr Asp Ala Pro Val Ala
1280 1285 1290

Tyr Thr Asp Ala Asn Gly Asp Leu His Phe Thr Asn Thr Asn Leu
1295 1300 1305

Asp Gly Gln Gln Tyr Thr Ala Val Arg Gly Tyr Ala Asn Pro Asp
1310 1315 1320

Val Thr Gly Tyr Leu Ala Val Trp Val Pro Ala Gly Ala Ala Asp
1325 1330 1335

Asp Gln Asp Ala Arg Thr Ala Pro Ser Asp Glu Ala His Thr Thr
1340 1345 1350

Lys Thr Ala Tyr Arg Ser Asn Ala Ala Leu Asp Ser Asn Val Ile
1355 1360 1365

Tyr Glu Gly Phe Ser Asn Phe Ile Tyr Trp Pro Thr Thr Glu Ser
1370 1375 1380

Glu Arg Thr Asn Val Arg Ile Ala Gln Asn Ala Asp Leu Phe Lys
1385 1390 1395

[0191] Ser Trp Gly Ile Thr Thr Phe Glu Leu Ala Pro Gln Tyr Asn Ser
1400 1405 1410

Ser Lys Asp Gly Thr Phe Leu Asp Ser Ile Ile Asp Asn Gly Tyr
1415 1420 1425

Ala Phe Thr Asp Arg Tyr Asp Leu Gly Met Ser Thr Pro Asn Lys
1430 1435 1440

Tyr Gly Ser Asp Glu Asp Leu Arg Asn Ala Leu Gln Ala Leu His
1445 1450 1455

Lys Ala Gly Leu Gln Ala Ile Ala Asp Trp Val Pro Asp Gln Ile
1460 1465 1470

Tyr Asn Leu Pro Gly Lys Glu Ala Val Thr Val Thr Arg Ser Asp
1475 1480 1485

Asp His Gly Thr Thr Trp Glu Val Ser Pro Ile Lys Asn Val Val
1490 1495 1500

Tyr Ile Thr Asn Thr Ile Gly Gly Gly Glu Tyr Gln Lys Lys Tyr
1505 1510 1515

Gly Gly Glu Phe Leu Asp Thr Leu Gln Lys Glu Tyr Pro Gln Leu
1520 1525 1530

Phe Ser Gln Val Tyr Pro Val Thr Gln Thr Thr Ile Asp Pro Ser
1535 1540 1545

Val Lys Ile Lys Glu Trp Ser Ala Lys Tyr Phe Asn Gly Thr Asn
1550 1555 1560

Ile Leu His Arg Gly Ala Gly Tyr Val Leu Arg Ser Asn Asp Gly
1565 1570 1575

Lys Tyr Tyr Asn Leu Gly Thr Ser Thr Gln Gln Phe Leu Pro Ser
1580 1585 1590

Gln Leu Ser Val Gln Asp Asn Glu Gly Tyr Gly Phe Val Lys Glu
1595 1600 1605

Gly Asn Asn Tyr His Tyr Tyr Asp Glu Asn Lys Gln Met Val Lys
1610 1615 1620

Asp Ala Phe Ile Gln Asp Ser Val Gly Asn Trp Tyr Tyr Phe Asp
1625 1630 1635

Lys Asn Gly Asn Met Val Ala Asn Gln Ser Pro Val Glu Ile Ser
1640 1645 1650

Ser Asn Gly Ala Ser Gly Thr Tyr Leu Phe Leu Asn Asn Gly Thr
1655 1660 1665

Ser Phe Arg Ser Gly Leu Val Lys Thr Asp Ala Gly Thr Tyr Tyr
1670 1675 1680

[0192] Tyr Asp Gly Asp Gly Arg Met Val Arg Asn Gln Thr Val Ser Asp
1685 1690 1695

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

Glu Ser Phe Asp Ser Ser Ala Thr Glu Ala His Pro Leu Lys Pro
1715 1720 1725

Gly Asp Leu Asn Gly Gln Lys
1730 1735

<210> 59
<211> 1242
<212> PRT
<213> 未知

<220>
<223> 未知链球菌菌种

<400> 59

Met Ile Asn Gly Lys Glu Tyr Tyr Val Glu Asp Asp Gly Thr Val Arg
1 5 10 15

Lys Asn Tyr Val Leu Glu Arg Asn Gly Gly Ser Gln Tyr Phe Asn Ala
20 25 30

Glu Thr Gly Glu Leu Ser Asn Gln Lys Asp Tyr Arg Phe Asp Lys Asn
35 40 45

Gly Gly Thr Gly Ser Ala Ala Asp Ser Thr Thr Asn Thr Asn Val Thr
50 55 60

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

Glu Leu Val Asp Gly Tyr Phe Thr Ala Asn Thr Trp Tyr Arg Pro Lys
                85   90   95

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

Lys Arg Pro Leu Leu Thr Val Trp Trp Pro Ser Lys Ala Ile Gln Ala
        115   120   125

Ser Tyr Leu Asn Tyr Met Arg Glu Glu Gly Leu Gly Thr Asn Gln Thr
    130   135   140

Phe Thr Ser Tyr Ser Ser Gln Thr Gln Met Asp Gln Ala Ala Leu Glu
145   150   155   160

Val Gln Lys Arg Ile Glu Glu Arg Ile Ala Arg Glu Gly Asn Thr Asp
                165   170   175

Trp Leu Arg Thr Thr Ile Lys Asn Phe Val Lys Thr Gln Pro Gly Trp
            180   185   190

Asn Ser Thr Ser Glu Asn Leu Asp Asn Ser Asp His Leu Gln Gly Gly
        195   200   205

[0193] Ala Leu Leu Tyr Asn Asn Ser Asn Arg Thr Ser Tyr Ala Asn Ser Asp
    210   215   220

Tyr Arg Leu Leu Asn Arg Thr Pro Thr Gln Gln Asp Gly Thr Arg Arg
225   230   235   240

Tyr Phe Lys Asp Asn Ser Ser Gly Gly Phe Glu Phe Leu Leu Ala Asn
                245   250   255

Asp Ile Asp Asn Ser Asn Pro Ala Val Gln Ala Glu Gln Leu Asn Trp
            260   265   270

Leu His Tyr Ile Met Asn Ile Gly Ser Leu Thr Gly Gly Ser Glu Asp
        275   280   285

Glu Asn Phe Asp Gly Val Arg Val Asp Ala Val Asp Asn Val Asn Ala
    290   295   300

Asp Leu Leu Gln Ile Ala Ser Asp Tyr Phe Lys Ala Lys Tyr Gly Val
305   310   315   320

Glu Lys Ser Glu Glu Glu Ala Ile Lys His Leu Ser Ile Leu Glu Ala
                325   330   335

Trp Ser His Asn Asp Ala Tyr Tyr Asn Glu Asp Thr Lys Gly Ala Gln
            340   345   350

Leu Pro Met Asp Asp Pro Leu Arg Leu Ala Met Val Phe Ser Phe Leu
        355   360   365

Arg Pro Ile Gly Asn Arg Ser Gly Leu Glu Pro Leu Ile Thr Asn Ser
370 375 380

Leu Asn Asp Arg Ser Glu Ser Lys Lys Asn Thr Lys Arg Met Ala Asn
385 390 395 400

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

Gln Ile Ile Lys Asn Glu Ile Asn Pro Gln Ser Thr Gly Asn Thr Phe
420 425 430

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

Arg Ser Ala Asn Lys Arg Tyr Thr Gln Tyr Asn Ile Pro Ser Ala Tyr
450 455 460

Ala Phe Met Leu Thr Asn Lys Asp Thr Val Pro Arg Val Tyr Tyr Gly
465 470 475 480

Asp Leu Tyr Thr Asp Asp Gly Gln Tyr Met Ala Gln Lys Ser Pro Tyr
485 490 495

His Asp Ala Ile Ser Thr Leu Leu Gln Ala Arg Ile Arg Tyr Ala Ala
500 505 510

[0194] Gly Gly Gln Asp Met Lys Met Ser Tyr Val Gly Ser Gly Asn Thr Asn
515 520 525

Gly Trp Asp Ala Ser Gly Val Leu Thr Ser Val Arg Tyr Gly Lys Gly
530 535 540

Ala Asn Asn Ala Ser Asp Ala Gly Thr Ala Glu Thr Arg Asn Gln Gly
545 550 555 560

Met Ala Val Ile Leu Ser Asn Gln Pro Ala Leu Arg Leu Asn Ser Asn
565 570 575

Leu Thr Ile Asn Met Gly Ala Ala His Arg Asn Gln Ala Tyr Arg Pro
580 585 590

Leu Leu Leu Thr Thr Ser Asn Gly Val Ala Ser Tyr Leu Asn Asp Gly
595 600 605

Asp Ala Asn Gly Ile Val Lys Tyr Thr Asp Ala Asn Gly Tyr Leu Thr
610 615 620

Phe Asn Pro Gly Glu Ile Ser Gly Val Arg Asn Ala Gln Val Asp Gly
625 630 635 640

Tyr Leu Ala Val Trp Val Pro Leu Gly Ala Ser Glu Asn Gln Asp Val
645 650 655

Arg Val Ala Ala Ser Lys Ser Lys Asn Ser Ser Gly Leu Val Tyr Asp
660 665 670

Ser Ser Ala Ala Leu Asp Ser Gln Val Ile Tyr Glu Gly Phe Ser Asn
675 680 685

Phe Gln Asp Phe Val Gln Asp Pro Ser Gln Tyr Thr Asn Lys Lys Ile
690 695 700

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

Phe Ala Pro Gln Tyr Val Ser Ser Asp Asp Gly Thr Phe Leu Asp Ser
725 730 735

Val Ile Gln Asn Gly Tyr Ala Phe Ser Asp Arg Tyr Asp Ile Gly Met
740 745 750

Ser Lys Asp Asn Lys Tyr Gly Ser Leu Ala Asp Leu Lys Ala Ala Leu
755 760 765

Lys Ser Leu His Ala Val Gly Ile Ser Ala Ile Ala Asp Trp Val Pro
770 775 780

Asp Gln Ile Tyr Asn Leu Pro Gly Asp Glu Val Val Thr Ala Thr Arg
785 790 795 800

Val Asn Asn Tyr Gly Glu Thr Lys Asp Gly Ala Ile Ile Asp His Ser
805 810 815

[0195] Leu Tyr Val Ala Lys Thr Arg Thr Phe Gly Asn Asp Tyr Gln Gly Lys
820 825 830

Tyr Gly Gly Ala Tyr Leu Asp Glu Leu Lys Arg Leu Tyr Pro Gln Phe
835 840 845

Phe Asp Arg Val Gln Ile Ser Thr Gly Lys Arg Leu Thr Thr Asp Glu
850 855 860

Lys Ile Thr Lys Trp Ser Ala Lys Tyr Met Asn Gly Thr Asn Ile Leu
865 870 875 880

Asp Arg Gly Ser Glu Tyr Val Leu Lys Asn Gly Leu Ser Gly Tyr Tyr
885 890 895

Gly Thr Asn Gly Gly Lys Val Ser Leu Pro Lys Val Val Gly Ser Asn
900 905 910

Gln Ser Thr Asn Asn Asn Asn Gln Asn Gly Asp Gly Ser Gly Arg Phe
915 920 925

Glu Lys Ser Trp Gly Ser Val Tyr Tyr Arg Tyr Asn Asp Gly Gln Arg
930 935 940

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

Asp Asn Thr Gly Arg Met Ala Ile Gly Glu Lys Thr Ile Asp Gly Lys
965 970 975

Gln Tyr Phe Phe Leu Ala Asn Gly Val Gln Leu Arg Asp Gly Tyr Arg
980 985 990

Gln Asn Arg Arg Gly Gln Val Phe Tyr Tyr Asp Glu Asn Gly Ile Met
995 1000 1005

Ser Gln Thr Gly Lys Pro Ser Pro Lys Pro Glu Pro Lys Pro Asp
1010 1015 1020

Asn Asn Thr Phe Ser Arg Asn Gln Phe Ile Gln Ile Gly Asn Asn
1025 1030 1035

Val Trp Ala Tyr Tyr Asp Gly Asn Gly Lys Arg Val Ile Gly Arg
1040 1045 1050

Gln Asn Ile Asn Gly Gln Glu Leu Phe Phe Asp Asn Asn Gly Val
1055 1060 1065

Gln Val Lys Gly Arg Thr Ala Gln Val Asp Gly Val Thr Arg Tyr
1070 1075 1080

Phe Asp Ala Asn Ser Gly Glu Met Ala Arg Asn Arg Phe Ala Glu
1085 1090 1095

Val Glu Pro Gly Val Trp Ala Tyr Phe Asn Asn Asp Gly Ala Ala
1100 1105 1110

[0196] Val Thr Gly Ser Gln Asn Ile Asn Gly Gln Thr Leu Tyr Phe Asp
1115 1120 1125

Gln Asn Gly His Gln Val Lys Gly Ala Leu Val Thr Val Asp Gly
1130 1135 1140

Asn Leu Arg Tyr Tyr Asp Ala Asn Ser Gly Asp Leu Tyr Arg Asn
1145 1150 1155

Arg Phe Gln Glu Val Asn Gly Ser Trp Tyr Tyr Phe Asp Gly Asn
1160 1165 1170

Gly Asn Ala Val Lys Gly Met Val Asn Ile Asn Gly Gln Asn Leu
1175 1180 1185

Leu Phe Asp Asn Asp Gly Lys Gln Val Lys Gly His Leu Val Arg
1190 1195 1200

Val Asn Gly Val Ile Arg Tyr Tyr Asp Pro Asn Ser Gly Glu Met
1205 1210 1215

Ala Val Asn Arg Trp Val Glu Ile Ser Ser Gly Trp Trp Val Tyr
1220 1225 1230

Phe Asp Gly Glu Gly Arg Gly Gln Ile
1235 1240

<210> 60
<211> 1518

<212> PRT
<213> 唾液链球菌（Streptococcus salivarius）

<400> 60

[0197]

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Met Glu Asn Lys Ile His Tyr Lys Leu His Lys Val Lys Lys Gln Trp
1               5                   10                  15

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

Leu Ser Val Thr Thr Ser Ser Val Ser Ala Asp Glu Thr Gln Asp Lys
        35                  40                  45

Thr Val Thr Gln Ser Asn Ser Gly Thr Thr Ala Ser Leu Val Thr Ser
    50                  55                  60

Pro Glu Ala Thr Lys Glu Ala Asp Lys Arg Thr Asn Thr Lys Glu Ala
65                  70                  75                  80

Asp Val Leu Thr Pro Ala Lys Glu Thr Asn Ala Val Glu Thr Ala Thr
                85                  90                  95

Thr Thr Asn Thr Gln Ala Thr Ala Glu Ala Ala Thr Thr Ala Thr Thr
            100                 105                 110

Ala Asp Val Ala Val Ala Ala Val Pro Asn Lys Glu Ala Val Val Thr
        115                 120                 125

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

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

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

Lys Asn Ile Asp Gly Lys Tyr Tyr Tyr Val Asn Glu Asp Gly Ser His
            180                 185                 190

Lys Glu Asn Phe Ala Ile Thr Val Asn Gly Gln Leu Leu Tyr Phe Gly
        195                 200                 205

Lys Asp Gly Ala Leu Thr Ser Ser Ser Thr Tyr Ser Phe Thr Pro Gly
    210                 215                 220

Thr Thr Asn Ile Val Asp Gly Phe Ser Ile Asn Asn Arg Ala Tyr Asp
225                 230                 235                 240

Ser Ser Glu Ala Ser Phe Glu Leu Ile Asp Gly Tyr Leu Thr Ala Asp
                245                 250                 255

Ser Trp Tyr Arg Pro Ala Ser Ile Ile Lys Asp Gly Val Thr Trp Gln
            260                 265                 270

Ala Ser Thr Ala Glu Asp Phe Arg Pro Leu Leu Met Ala Trp Trp Pro
        275                 280                 285
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Asn Val Asp Thr Gln Val Asn Tyr Leu Asn Tyr Met Ser Lys Val Phe
290 295 300

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

Val Ala Ala Lys Asp Ile Gln Ile Lys Ile Glu Gln Lys Ile Gln Ala
325 330 335

Glu Lys Ser Thr Gln Trp Leu Arg Glu Thr Ile Ser Ala Phe Val Lys
340 345 350

Thr Gln Pro Gln Trp Asn Lys Glu Thr Glu Asn Tyr Ser Lys Gly Gly
355 360 365

Gly Glu Asp His Leu Gln Gly Gly Ala Leu Leu Tyr Val Asn Asp Ser
370 375 380

Arg Thr Pro Trp Ala Asn Ser Asp Tyr Arg Arg Leu Asn Arg Thr Ala
385 390 395 400

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

Asp Pro Asn His Met Gly Gly Phe Asp Phe Leu Leu Ala Asn Asp Val
420 425 430

[0198] Asp Leu Ser Asn Pro Val Val Gln Ala Glu Gln Leu Asn Gln Ile His
435 440 445

Tyr Leu Met Asn Trp Gly Ser Ile Val Met Gly Asp Lys Asp Ala Asn
450 455 460

Phe Asp Gly Ile Arg Val Asp Ala Val Asp Asn Val Asp Ala Asp Met
465 470 475 480

Leu Gln Leu Tyr Thr Asn Tyr Phe Arg Glu Tyr Tyr Gly Val Asn Lys
485 490 495

Ser Glu Ala Asn Ala Leu Ala His Ile Ser Val Leu Glu Ala Trp Ser
500 505 510

Leu Asn Asp Asn His Tyr Asn Asp Lys Thr Asp Gly Ala Ala Leu Ala
515 520 525

Met Glu Asn Lys Gln Arg Leu Ala Leu Leu Phe Ser Leu Ala Lys Pro
530 535 540

Ile Lys Glu Arg Thr Pro Ala Val Ser Pro Leu Tyr Asn Asn Thr Phe
545 550 555 560

Asn Thr Thr Gln Arg Asp Glu Lys Thr Asp Trp Ile Asn Lys Asp Gly
565 570 575

Ser Lys Ala Tyr Asn Glu Asp Gly Thr Val Lys Gln Ser Thr Ile Gly
580 585 590

Lys Tyr Asn Glu Lys Tyr Gly Asp Ala Ser Gly Asn Tyr Val Phe Ile
595 600 605

Arg Ala His Asp Asn Asn Val Gln Asp Ile Ile Ala Glu Ile Ile Lys
610 615 620

Lys Glu Ile Asn Pro Lys Ser Asp Gly Phe Thr Ile Thr Asp Ala Glu
625 630 635 640

Met Lys Gln Ala Phe Glu Ile Tyr Asn Lys Asp Met Leu Ser Ser Asp
645 650 655

Lys Lys Tyr Thr Leu Asn Asn Ile Pro Ala Ala Tyr Ala Val Met Leu
660 665 670

Gln Asn Met Glu Thr Ile Thr Arg Val Tyr Tyr Gly Asp Leu Tyr Thr
675 680 685

Asp Asp Gly His Tyr Met Glu Thr Lys Ser Pro Tyr Tyr Asp Thr Ile
690 695 700

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

Gln Arg Ser Tyr Trp Leu Pro Thr Asp Gly Lys Met Asp Asn Ser Asp
725 730 735

[0199] Val Glu Leu Tyr Arg Thr Asn Glu Val Tyr Thr Ser Val Arg Tyr Gly
740 745 750

Lys Asp Ile Met Thr Ala Asn Asp Thr Glu Gly Ser Lys Tyr Ser Arg
755 760 765

Thr Ser Gly Gln Val Thr Leu Val Ala Asn Asn Pro Lys Leu Asn Leu
770 775 780

Asp Gln Ser Ala Lys Leu Asn Val Glu Met Gly Lys Ile His Ala Asn
785 790 795 800

Gln Lys Tyr Arg Ala Leu Ile Val Gly Thr Ala Asp Gly Ile Lys Asn
805 810 815

Phe Thr Ser Asp Ala Asp Ala Ile Ala Ala Gly Tyr Val Lys Glu Thr
820 825 830

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

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

Ala Ser Asp Asn Gln Asp Ile Arg Val Ala Pro Ser Thr Glu Ala Lys
865 870 875 880

Lys Glu Gly Glu Leu Thr Leu Lys Ala Thr Glu Ala Tyr Asp Ser Gln
885 890 895

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

Asp Pro Ser Val Tyr Thr Asn Arg Lys Ile Ala Glu Asn Val Asp Leu
915 920 925

Phe Lys Ser Trp Gly Val Thr Ser Phe Glu Met Ala Pro Gln Phe Val
930 935 940

Ser Ala Asp Asp Gly Thr Phe Leu Asp Ser Val Ile Gln Asn Gly Tyr
945 950 955 960

Ala Phe Ala Asp Arg Tyr Asp Leu Ala Met Ser Lys Asn Asn Lys Tyr
965 970 975

Gly Ser Lys Glu Asp Leu Arg Asp Ala Leu Lys Ala Leu His Lys Ala
980 985 990

Gly Ile Gln Ala Ile Ala Asp Trp Val Pro Asp Gln Ile Tyr Gln Leu
995 1000 1005

Pro Gly Lys Glu Val Val Thr Ala Thr Arg Thr Asp Gly Ala Gly
1010 1015 1020

Arg Lys Ile Ala Asp Ala Ile Ile Asp His Ser Leu Tyr Val Ala
1025 1030 1035

[0200] Asn Ser Lys Ser Ser Gly Lys Asp Tyr Gln Ala Lys Tyr Gly Gly
1040 1045 1050

Glu Phe Leu Ala Glu Leu Lys Ala Lys Tyr Pro Glu Met Phe Lys
1055 1060 1065

Val Asn Met Ile Ser Thr Gly Lys Pro Ile Asp Asp Ser Val Lys
1070 1075 1080

Leu Lys Gln Trp Lys Ala Glu Tyr Phe Asn Gly Thr Asn Val Leu
1085 1090 1095

Glu Arg Gly Val Gly Tyr Val Leu Ser Asp Glu Ala Thr Gly Lys
1100 1105 1110

Tyr Phe Thr Val Thr Lys Glu Gly Asn Phe Ile Pro Leu Gln Leu
1115 1120 1125

Thr Gly Lys Glu Lys Val Ile Thr Gly Phe Ser Ser Asp Gly Lys
1130 1135 1140

Gly Ile Thr Tyr Phe Gly Thr Ser Gly Thr Gln Ala Lys Ser Ala
1145 1150 1155

Phe Val Thr Phe Asn Gly Asn Thr Tyr Tyr Phe Asp Ala Arg Gly
1160 1165 1170

His Met Val Thr Asn Ser Glu Tyr Ser Pro Asn Gly Lys Asp Val
1175 1180 1185

Tyr Arg Phe Leu Pro Asn Gly Ile Met Leu Ser Asn Ala Phe Tyr
1190 1195 1200

Ile Asp Ala Asn Gly Asn Thr Tyr Leu Tyr Asn Ser Lys Gly Gln
1205 1210 1215

Met Tyr Lys Gly Gly Tyr Thr Lys Phe Asp Val Ser Glu Thr Asp
1220 1225 1230

Lys Asp Gly Lys Glu Ser Lys Val Val Lys Phe Arg Tyr Phe Thr
1235 1240 1245

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

Thr Gln Tyr Phe Gly Glu Asp Gly Phe Gln Ala Lys Asp Lys Leu
1265 1270 1275

Val Thr Phe Lys Gly Lys Thr Tyr Tyr Phe Asp Ala His Thr Gly
1280 1285 1290

Asn Gly Ile Lys Asp Thr Trp Arg Asn Ile Asn Gly Lys Trp Tyr
1295 1300 1305

Tyr Phe Asp Ala Asn Gly Val Ala Ala Thr Gly Ala Gln Val Ile
1310 1315 1320

[0201] Asn Gly Gln Lys Leu Tyr Phe Asn Glu Asp Gly Ser Gln Val Lys
1325 1330 1335

Gly Gly Val Val Lys Asn Ala Asp Gly Thr Tyr Ser Lys Tyr Lys
1340 1345 1350

Glu Gly Phe Gly Glu Leu Val Thr Asn Glu Phe Phe Thr Thr Asp
1355 1360 1365

Gly Asn Val Trp Tyr Tyr Ala Gly Ala Asn Gly Lys Thr Val Thr
1370 1375 1380

Gly Ala Gln Val Ile Asn Gly Gln His Leu Tyr Phe Asn Ala Asp
1385 1390 1395

Gly Ser Gln Val Lys Gly Gly Val Val Lys Asn Ala Asp Gly Thr
1400 1405 1410

Tyr Ser Lys Tyr Asn Ala Ser Thr Gly Glu Arg Leu Thr Asn Glu
1415 1420 1425

Phe Phe Thr Thr Gly Asp Asn Asn Trp Tyr Tyr Ile Gly Ala Asn
1430 1435 1440

Gly Lys Ser Val Thr Gly Glu Val Lys Ile Gly Asp Asp Thr Tyr
1445 1450 1455

Phe Phe Ala Lys Asp Gly Lys Gln Val Lys Gly Gln Thr Val Ser
1460 1465 1470

Ala Gly Asn Gly Arg Ile Ser Tyr Tyr Tyr Gly Asp Ser Gly Lys
1475 1480 1485

Arg Ala Val Ser Thr Trp Ile Glu Ile Gln Pro Gly Val Tyr Val
1490 1495 1500

Tyr Phe Asp Lys Asn Gly Leu Ala Tyr Pro Pro Arg Val Leu Asn
1505 1510 1515

<210> 61
<211> 1528
<212> PRT
<213> 唾液链球菌（Streptococcus salivarius）

<400> 61

Met Thr Asn Lys Ile Thr Gly Lys Ile Ile Met Glu Asn Lys Val His
1 5 10 15

Tyr Lys Leu His Lys Val Lys Lys Gln Trp Val Thr Ile Ala Val Ala
20 25 30

Ser Ala Ala Leu Ala Thr Val Val Gly Gly Leu Ser Ala Thr Thr Ser
35 40 45

Ser Val Ser Ala Asp Glu Thr Gln Asp Lys Ile Val Thr Gln Pro Asn
50 55 60

[0202] Leu Asp Thr Thr Ala Asp Leu Val Thr Ser Thr Glu Ala Thr Lys Glu
65 70 75 80

Val Asp Lys Arg Thr Asn Thr Lys Glu Ala Asp Val Leu Thr Pro Ala
85 90 95

Lys Glu Thr Asn Ala Val Glu Thr Ala Thr Thr Thr Asn Thr Gln Ala
100 105 110

Thr Ala Glu Ala Ala Thr Thr Ala Thr Thr Ser Asp Val Ala Val Ala
115 120 125

Ala Val Pro Asn Lys Glu Ala Val Val Thr Thr Asp Ala Pro Ala Val
130 135 140

Thr Thr Glu Lys Ala Glu Glu Gln Pro Ala Thr Val Lys Ala Glu Val
145 150 155 160

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

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

Tyr Tyr Tyr Val Asn Glu Asp Gly Ser His Lys Glu Asn Phe Ala Ile
195 200 205

Thr Val Asn Gly Gln Leu Leu Tyr Phe Gly Lys Asp Gly Ala Leu Thr
210 215 220

Ser Ser Ser Thr His Ser Phe Thr Pro Gly Thr Thr Asn Ile Val Asp
225 230 235 240

Gly Phe Ser Ile Asn Asn Arg Ala Tyr Asp Ser Ser Glu Ala Ser Phe
245 250 255

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

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

Phe Arg Pro Leu Leu Met Ala Trp Trp Pro Asn Val Asp Thr Gln Val
290 295 300

Asn Tyr Leu Asn Tyr Met Ser Lys Val Phe Asn Leu Glu Ala Lys Tyr
305 310 315 320

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

Gln Val Lys Ile Glu Gln Lys Ile Gln Ala Glu Lys Ser Thr Gln Trp
340 345 350

Leu Arg Glu Thr Ile Ser Ala Phe Val Lys Thr Gln Pro Gln Trp Asn
355 360 365

[0203] Lys Glu Thr Glu Asn Tyr Ser Lys Gly Gly Gly Glu Asp His Leu Gln
370 375 380

Gly Gly Ala Leu Leu Tyr Val Asn Asp Ser Arg Thr Pro Trp Ala Asn
385 390 395 400

Ser Asn Tyr Arg Leu Leu Asn Arg Thr Ala Thr Asn Gln Thr Gly Thr
405 410 415

Ile Asn Lys Ser Val Leu Asp Glu Gln Ser Asp Pro Asn His Met Gly
420 425 430

Gly Phe Asp Phe Leu Leu Ala Asn Asp Val Asp Leu Ser Asn Pro Val
435 440 445

Val Gln Ala Glu Gln Leu Asn Gln Ile His Tyr Leu Met Asn Trp Gly
450 455 460

Ser Ile Val Met Gly Asp Lys Asp Ala Asn Phe Asp Gly Ile Arg Val
465 470 475 480

Asp Ala Val Asp Asn Val Asn Ala Asp Met Leu Gln Leu Tyr Thr Asn
485 490 495

Tyr Phe Arg Glu Tyr Tyr Gly Val Asn Lys Ser Glu Ala Gln Ala Leu
500 505 510

Ala His Ile Ser Val Leu Glu Ala Trp Ser Leu Asn Asp Asn His Tyr
515 520 525

Asn Asp Lys Thr Asp Gly Ala Ala Leu Ala Met Glu Asn Lys Gln Arg
530 535 540

Leu Ala Leu Leu Phe Ser Leu Ala Lys Pro Ile Lys Asp Arg Thr Pro
545 550 555 560

Ala Val Ser Pro Leu Tyr Asn Asn Thr Phe Asn Thr Thr Gln Arg Asp
565 570 575

Phe Lys Thr Asp Trp Ile Asn Lys Asp Gly Ser Thr Ala Tyr Asn Glu
580 585 590

Asp Gly Thr Ala Lys Gln Ser Thr Ile Gly Lys Tyr Asn Glu Lys Tyr
595 600 605

Gly Asp Ala Ser Gly Asn Tyr Val Phe Ile Arg Ala His Asp Asn Asn
610 615 620

Val Gln Asp Ile Ile Ala Glu Ile Ile Lys Lys Glu Ile Asn Lys Lys
625 630 635 640

Ser Asp Gly Phe Thr Ile Ser Asp Ser Glu Met Lys Gln Ala Phe Glu
645 650 655

Ile Tyr Asn Lys Asp Met Leu Ser Ser Asn Lys Lys Tyr Thr Leu Asn
660 665 670

[0204] Asn Ile Pro Ala Ala Tyr Ala Val Met Leu Gln Asn Met Glu Thr Ile
675 680 685

Thr Arg Val Tyr Tyr Gly Asp Leu Tyr Thr Asp Asp Gly His Tyr Met
690 695 700

Glu Thr Lys Ser Pro Tyr His Asp Thr Ile Val Asn Leu Met Lys Asn
705 710 715 720

Arg Ile Lys Tyr Val Ser Gly Gly Gln Ala Gln Arg Ser Tyr Trp Leu
725 730 735

Pro Thr Asp Gly Lys Met Asp Asn Ser Asp Val Glu Leu Tyr Arg Thr
740 745 750

Ser Glu Val Tyr Thr Ser Val Arg Tyr Gly Lys Asp Ile Met Thr Ala
755 760 765

Asp Asp Thr Glu Gly Ser Lys Tyr Ser Arg Thr Ser Gly Gln Val Thr
770 775 780

Leu Val Val Asn Asn Pro Lys Leu Thr Leu His Glu Ser Ala Lys Leu
785 790 795 800

Asn Val Glu Met Gly Lys Ile His Ala Asn Gln Lys Tyr Arg Ala Leu
805 810 815

Ile Val Gly Thr Ala Asp Gly Ile Lys Asn Phe Thr Ser Asp Ala Glu
820 825 830

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

Thr Phe Gly Ala Asn Asp Ile Lys Gly Tyr Glu Thr Phe Asp Met Ser
    850                 855                 860

Gly Phe Val Ala Val Trp Val Pro Val Gly Ala Ser Asp Asp Gln Asp
865                 870                 875                 880

Ile Arg Val Ala Pro Ser Thr Glu Ala Lys Lys Glu Gly Glu Leu Thr
                885                 890                 895

Leu Lys Ala Thr Glu Ala Tyr Asp Ser Gln Leu Ile Tyr Glu Gly Phe
            900                 905                 910

Ser Asn Phe Gln Thr Ile Pro Asp Gly Ser Asp Pro Ser Val Tyr Thr
        915                 920                 925

Asn Arg Lys Ile Ala Glu Asn Val Asp Leu Phe Lys Ser Trp Gly Val
    930                 935                 940

Thr Ser Phe Glu Met Ala Pro Gln Phe Val Ser Ala Asp Asp Gly Thr
945                 950                 955                 960

Phe Leu Asp Ser Val Ile Gln Asn Gly Tyr Ala Phe Ala Asp Arg Tyr
                965                 970                 975
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[0205]

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Asp Leu Ala Met Ser Lys Asn Asn Lys Tyr Gly Ser Lys Glu Asp Leu
            980                 985                 990

Arg Asp Ala Leu Lys Ala Leu His  Lys Ala Gly Ile Gln  Ala Ile Ala
        995                 1000                 1005

Asp Trp  Val Pro Asp Gln Ile  Tyr Gln Leu Pro Gly  Lys Glu Val
    1010                 1015                 1020

Val Thr  Ala Thr Arg Thr Asp  Gly Ala Gly Arg Lys  Ile Ala Asp
    1025                 1030                 1035

Ala Ile  Ile Asp His Ser Leu  Tyr Val Ala Asn Ser  Lys Ser Ser
    1040                 1045                 1050

Gly Arg  Asp Tyr Gln Ala Gln  Tyr Gly Gly Glu Phe  Leu Ala Glu
    1055                 1060                 1065

Leu Lys  Ala Lys Tyr Pro Lys  Met Phe Thr Glu Asn  Met Ile Ser
    1070                 1075                 1080

Thr Gly  Lys Pro Ile Asp Asp  Ser Val Lys Leu Lys  Gln Trp Lys
    1085                 1090                 1095

Ala Lys  Tyr Phe Asn Gly Thr  Asn Val Leu Asp Arg  Gly Val Gly
    1100                 1105                 1110

Tyr Val  Leu Ser Asp Glu Ala  Thr Gly Lys Tyr Phe  Thr Val Thr
    1115                 1120                 1125
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Lys Glu Gly Asn Phe Ile Pro Leu Gln Leu Thr Gly Asn Glu Lys
1130 1135 1140

Ala Val Thr Gly Phe Ser Asn Asp Gly Lys Gly Ile Thr Tyr Phe
1145 1150 1155

Gly Thr Ser Gly Asn Gln Ala Lys Ser Ala Phe Val Thr Phe Asn
1160 1165 1170

Gly Asn Thr Tyr Tyr Phe Asp Ala Arg Gly His Met Val Thr Asn
1175 1180 1185

Gly Glu Tyr Ser Pro Asn Gly Lys Asp Val Tyr Arg Phe Leu Pro
1190 1195 1200

Asn Gly Ile Met Leu Ser Asn Ala Phe Tyr Val Asp Ala Asn Gly
1205 1210 1215

Asn Thr Tyr Leu Tyr Asn Tyr Lys Gly Gln Met Tyr Lys Gly Gly
1220 1225 1230

Tyr Thr Lys Phe Asp Val Thr Glu Thr Asp Lys Asp Gly Asn Glu
1235 1240 1245

Ser Lys Val Val Lys Phe Arg Tyr Phe Thr Asn Glu Gly Val Met
1250 1255 1260

[0206] Ala Lys Gly Leu Thr Val Ile Asp Gly Ser Thr Gln Tyr Phe Gly
1265 1270 1275

Glu Asp Gly Phe Gln Thr Lys Asp Lys Leu Ala Thr Tyr Lys Gly
1280 1285 1290

Lys Thr Tyr Tyr Phe Glu Ala His Thr Gly Asn Ala Ile Lys Asn
1295 1300 1305

Thr Trp Arg Asn Ile Asp Gly Lys Trp Tyr His Phe Asp Glu Asn
1310 1315 1320

Gly Val Ala Ala Thr Gly Ala Gln Val Ile Asn Gly Gln Lys Leu
1325 1330 1335

Tyr Phe Asn Glu Asp Gly Ser Gln Val Lys Gly Gly Val Val Lys
1340 1345 1350

Asn Ala Asp Gly Thr Tyr Ser Lys Tyr Lys Glu Gly Ser Gly Glu
1355 1360 1365

Leu Val Thr Asn Glu Phe Phe Thr Thr Asp Gly Asn Val Trp Tyr
1370 1375 1380

Tyr Ala Gly Ala Asp Gly Lys Thr Val Thr Gly Ala Gln Val Ile
1385 1390 1395

Asn Gly Gln His Leu Tyr Phe Lys Glu Asp Gly Ser Gln Val Lys
1400 1405 1410

Gly Gly Val Val Lys Asn Ala Asp Gly Thr Tyr Ser Lys Tyr Asp
1415 1420 1425

Ala Ala Thr Gly Glu Arg Leu Thr Asn Glu Phe Phe Thr Thr Gly
1430 1435 1440

Asp Asn Asn Trp Tyr Tyr Ile Gly Ser Asn Gly Lys Thr Val Thr
1445 1450 1455

Gly Glu Val Lys Ile Gly Ala Asp Thr Tyr Tyr Phe Ala Lys Asp
1460 1465 1470

Gly Lys Gln Val Lys Gly Gln Thr Val Thr Ala Gly Asn Gly Arg
1475 1480 1485

Ile Ser Tyr Tyr Tyr Gly Asp Ser Gly Lys Lys Ala Ile Ser Thr
1490 1495 1500

Trp Ile Glu Ile Gln Pro Gly Ile Tyr Val Tyr Phe Asp Lys Thr
1505 1510 1515

Gly Ile Ala Tyr Pro Pro Arg Val Leu Asn
1520 1525

<210> 62
<211> 1518
<212> PRT
<213> 唾液链球菌（Streptococcus salivarius）

[0207] <400> 62

Met Glu Asn Lys Ile His Tyr Lys Leu His Lys Val Lys Lys Gln Trp
1 5 10 15

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

Leu Ser Val Thr Thr Ser Ser Val Ser Ala Asp Glu Thr Gln Asp Lys
35 40 45

Thr Val Thr Gln Ser Asn Ser Gly Thr Thr Ala Ser Leu Val Thr Ser
50 55 60

Pro Glu Ala Thr Lys Glu Ala Asp Lys Arg Thr Asn Thr Lys Glu Ala
65 70 75 80

Asp Val Leu Thr Pro Ala Lys Glu Thr Asn Ala Val Glu Thr Ala Thr
85 90 95

Thr Thr Asn Thr Gln Ala Thr Ala Glu Ala Ala Thr Thr Ala Thr Thr
100 105 110

Ala Asp Val Ala Val Ala Ala Val Pro Asn Lys Glu Ala Val Val Thr
115 120 125

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

Thr Val Lys Ala Glu Val Val Asn Thr Glu Val Lys Ala Pro Glu Ala

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145                 150                 155                 160

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

Lys Asn Ile Asp Gly Lys Tyr Tyr Tyr Val Asn Glu Asp Gly Ser His
            180                 185                 190

Lys Glu Asn Phe Ala Ile Thr Val Asn Gly Gln Leu Leu Tyr Phe Gly
        195                 200                 205

Lys Asp Gly Ala Leu Thr Ser Ser Ser Thr Tyr Ser Phe Thr Pro Gly
    210                 215                 220

Thr Thr Asn Ile Val Asp Gly Phe Ser Ile Asn Asn Arg Ala Tyr Asp
225                 230                 235                 240

Ser Ser Glu Ala Ser Phe Glu Leu Ile Asp Gly Tyr Leu Thr Ala Asp
                245                 250                 255

Ser Trp Tyr Arg Pro Ala Ser Ile Ile Lys Asp Gly Val Thr Trp Gln
            260                 265                 270

Ala Ser Thr Ala Glu Asp Phe Arg Pro Leu Leu Met Ala Trp Trp Pro
        275                 280                 285

Asn Val Asp Thr Gln Val Asn Tyr Leu Asn Tyr Met Ser Lys Val Phe
    290                 295                 300
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[0208]

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

Val Ala Ala Lys Asp Ile Gln Ile Lys Ile Glu Gln Lys Ile Gln Ala
                325                 330                 335

Glu Lys Ser Thr Gln Trp Leu Arg Glu Thr Ile Ser Ala Phe Val Lys
            340                 345                 350

Thr Gln Pro Gln Trp Asn Lys Glu Thr Glu Asn Tyr Ser Lys Gly Gly
        355                 360                 365

Gly Glu Asp His Leu Gln Gly Gly Ala Leu Leu Tyr Val Asn Asp Ser
    370                 375                 380

Arg Thr Pro Trp Ala Asn Ser Asp Tyr Arg Arg Leu Asn Arg Thr Ala
385                 390                 395                 400

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

Asp Pro Asn His Met Gly Gly Phe Asp Phe Leu Leu Ala Asn Asp Val
            420                 425                 430

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

Tyr Leu Met Asn Trp Gly Ser Ile Val Met Gly Asp Lys Asp Ala Asn
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450 455 460

Phe Asp Gly Ile Arg Val Asp Ala Val Asp Asn Val Asp Ala Asp Met
465 470 475 480

Leu Gln Leu Tyr Thr Asn Tyr Phe Arg Glu Tyr Tyr Gly Val Asn Lys
485 490 495

Ser Glu Ala Asn Ala Leu Ala His Ile Ser Val Leu Glu Ala Trp Ser
500 505 510

Leu Asn Asp Asn His Tyr Asn Asp Lys Thr Asp Gly Ala Ala Leu Ala
515 520 525

Met Glu Asn Lys Gln Arg Leu Ala Leu Leu Phe Ser Leu Ala Lys Pro
530 535 540

Ile Lys Glu Arg Thr Pro Ala Val Ser Pro Leu Tyr Asn Asn Thr Phe
545 550 555 560

Asn Thr Thr Gln Arg Asp Glu Lys Thr Asp Trp Ile Asn Lys Asp Gly
565 570 575

Ser Lys Ala Tyr Asn Glu Asp Gly Thr Val Lys Gln Ser Thr Ile Gly
580 585 590

Lys Tyr Asn Glu Lys Tyr Gly Asp Ala Ser Gly Asn Tyr Val Phe Ile
595 600 605

[0209]

Arg Ala His Asp Asn Asn Val Gln Asp Ile Ile Ala Glu Ile Ile Lys
610 615 620

Lys Glu Ile Asn Pro Lys Ser Asp Gly Phe Thr Ile Thr Asp Ala Glu
625 630 635 640

Met Lys Gln Ala Phe Glu Ile Tyr Asn Lys Asp Met Leu Ser Ser Asp
645 650 655

Lys Lys Tyr Thr Leu Asn Asn Ile Pro Ala Ala Tyr Ala Val Met Leu
660 665 670

Gln Asn Met Glu Thr Ile Thr Arg Val Tyr Tyr Gly Asp Leu Tyr Thr
675 680 685

Asp Asp Gly His Tyr Met Glu Thr Lys Ser Pro Tyr Tyr Asp Thr Ile
690 695 700

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

Gln Arg Ser Tyr Trp Leu Pro Thr Asp Gly Lys Met Asp Asn Ser Asp
725 730 735

Val Glu Leu Tyr Arg Thr Asn Glu Val Tyr Thr Ser Val Arg Tyr Gly
740 745 750

Lys Asp Ile Met Thr Ala Asn Asp Thr Glu Gly Ser Lys Tyr Ser Arg

755 760 765

Thr Ser Gly Gln Val Thr Leu Val Ala Asn Asn Pro Lys Leu Thr Leu
770 775 780

Asp Gln Ser Ala Lys Leu Asn Val Glu Met Gly Lys Ile His Ala Asn
785 790 795 800

Gln Lys Tyr Arg Ala Leu Ile Val Gly Thr Ala Asp Gly Ile Lys Asn
805 810 815

Phe Thr Ser Asp Ala Asp Ala Ile Ala Ala Gly Tyr Val Lys Glu Thr
820 825 830

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

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

Ala Ser Asp Asp Gln Asp Ile Arg Val Ala Pro Ser Thr Glu Ala Lys
865 870 875 880

Lys Glu Gly Glu Leu Thr Leu Lys Ala Thr Glu Ala Tyr Asp Ser Gln
885 890 895

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

[0210]

Asp Pro Ser Val Tyr Thr Asn Arg Lys Ile Ala Glu Asn Val Asp Leu
915 920 925

Phe Lys Ser Trp Gly Val Thr Ser Phe Glu Met Ala Pro Gln Phe Val
930 935 940

Ser Ala Asp Asp Gly Thr Phe Leu Asp Ser Val Ile Gln Asn Gly Tyr
945 950 955 960

Ala Phe Ala Asp Arg Tyr Asp Leu Ala Met Ser Lys Asn Asn Lys Tyr
965 970 975

Gly Ser Lys Glu Asp Leu Arg Asp Ala Leu Lys Ala Leu His Lys Ala
980 985 990

Gly Ile Gln Ala Ile Ala Asp Trp Val Pro Asp Gln Ile Tyr Gln Leu
995 1000 1005

Pro Gly Lys Glu Val Val Thr Ala Thr Arg Thr Asp Gly Ala Gly
1010 1015 1020

Arg Lys Ile Ala Asp Ala Ile Ile Asp His Ser Leu Tyr Val Ala
1025 1030 1035

Asn Thr Lys Ser Ser Gly Lys Asp Tyr Gln Ala Lys Tyr Gly Gly
1040 1045 1050

Glu Phe Leu Ala Glu Leu Lys Ala Lys Tyr Pro Glu Met Phe Lys

1055 1060 1065

Val Asn Met Ile Ser Thr Gly Lys Pro Ile Asp Asp Ser Val Lys
1070 1075 1080

Leu Lys Gln Trp Lys Ala Glu Tyr Phe Asn Gly Thr Asn Val Leu
1085 1090 1095

Glu Arg Gly Val Gly Tyr Val Leu Ser Asp Glu Ala Thr Gly Lys
1100 1105 1110

Tyr Phe Thr Val Thr Lys Asp Gly Asn Phe Ile Pro Leu Gln Leu
1115 1120 1125

Thr Gly Asn Glu Lys Val Val Thr Gly Phe Ser Asn Asp Gly Lys
1130 1135 1140

Gly Ile Thr Tyr Phe Gly Thr Ser Gly Thr Gln Ala Lys Ser Ala
1145 1150 1155

Phe Val Thr Phe Asn Gly Asn Thr Tyr Tyr Phe Asp Ala Arg Gly
1160 1165 1170

His Met Val Thr Asn Gly Glu Tyr Ser Pro Asn Gly Lys Asp Val
1175 1180 1185

Tyr Arg Phe Leu Pro Asn Gly Ile Met Leu Ser Asn Ala Phe Tyr
1190 1195 1200

[0211]

Val Asp Ala Asn Gly Asn Thr Tyr Leu Tyr Asn Ser Lys Gly Gln
1205 1210 1215

Met Tyr Lys Gly Gly Tyr Thr Lys Phe Asp Val Thr Glu Thr Asp
1220 1225 1230

Lys Asp Gly Lys Glu Ser Lys Val Val Lys Phe Arg Tyr Phe Thr
1235 1240 1245

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

Thr Gln Tyr Phe Gly Glu Asp Gly Phe Gln Ala Lys Asp Lys Leu
1265 1270 1275

Val Thr Phe Lys Gly Lys Thr Tyr Tyr Phe Asp Ala His Thr Gly
1280 1285 1290

Asn Ala Ile Lys Asp Thr Trp Arg Asn Ile Asn Gly Lys Trp Tyr
1295 1300 1305

His Phe Asp Ala Asn Gly Val Ala Ala Thr Gly Ala Gln Val Ile
1310 1315 1320

Asn Gly Gln Lys Leu Tyr Phe Asn Glu Asp Gly Ser Gln Val Lys
1325 1330 1335

Gly Gly Val Val Lys Asn Ala Asp Gly Thr Tyr Ser Lys Tyr Lys

1340 1345 1350

Glu Gly Ser Gly Glu Leu Val Thr Asn Glu Phe Phe Thr Thr Asp
1355 1360 1365

Gly Asn Val Trp Tyr Tyr Ala Gly Ala Asn Gly Lys Thr Val Thr
1370 1375 1380

Gly Ala Gln Val Ile Asn Gly Gln His Leu Tyr Phe Asn Ala Asp
1385 1390 1395

Gly Ser Gln Val Lys Gly Gly Val Val Lys Asn Ala Asp Gly Thr
1400 1405 1410

Tyr Ser Lys Tyr Asp Ala Ser Thr Gly Glu Arg Leu Thr Asn Glu
1415 1420 1425

Phe Phe Thr Thr Gly Asp Asn Asn Trp Tyr Tyr Ile Gly Ala Asn
1430 1435 1440

Gly Lys Ser Val Thr Gly Glu Val Lys Ile Gly Asp Asp Thr Tyr
1445 1450 1455

Phe Phe Ala Lys Asp Gly Lys Gln Val Lys Gly Gln Thr Val Ser
1460 1465 1470

Ala Gly Asn Gly Arg Ile Ser Tyr Tyr Tyr Gly Asp Ser Gly Lys
1475 1480 1485

[0212]

Arg Ala Val Ser Thr Trp Ile Glu Ile Gln Pro Gly Val Tyr Val
1490 1495 1500

Tyr Phe Asp Lys Asn Gly Ile Ala Tyr Pro Pro Arg Val Leu Asn
1505 1510 1515

<210> 63
<211> 1431
<212> PRT
<213> 唾液链球菌（Streptococcus salivarius）

<400> 63

Met Thr Lys Glu Thr Asn Thr Val Asp Ala Ala Thr Thr Thr Asn Thr
1 5 10 15

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

Ala Leu Pro Asn Lys Glu Ala Val Val Thr Thr Asp Ala Pro Ala Val
35 40 45

Thr Thr Glu Lys Ala Ala Glu Gln Pro Ala Thr Val Lys Ser Glu Val
50 55 60

Val Asn Thr Glu Val Lys Ala Pro Glu Ala Ala Leu Lys Asp Ser Glu
65 70 75 80

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

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

Thr Val Asn Gly Gln Leu Leu Tyr Phe Gly Lys Asp Gly Ala Leu Thr
115 120 125

Ser Ser Ser Thr Tyr Ser Phe Thr Gln Gly Thr Thr Asn Ile Val Asp
130 135 140

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

Glu Leu Ile Asp Gly Tyr Leu Thr Ala Asp Ser Trp Tyr Arg Pro Val
165 170 175

Ser Ile Ile Lys Asp Gly Val Thr Trp Gln Ala Ser Thr Lys Glu Asp
180 185 190

Phe Arg Pro Leu Leu Met Ala Trp Trp Pro Asn Val Asp Thr Gln Val
195 200 205

Asn Tyr Leu Asn Tyr Met Ser Lys Val Phe Asn Leu Asp Ala Lys Tyr
210 215 220

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

[0213] Gln Val Lys Ile Glu Gln Lys Ile Gln Ala Glu Lys Ser Thr Gln Trp
245 250 255

Leu Arg Glu Ala Ile Ser Ala Phe Val Lys Thr Gln Pro Gln Trp Asn
260 265 270

Lys Glu Thr Glu Asn Phe Ser Lys Gly Gly Gly Glu Asp His Leu Gln
275 280 285

Gly Gly Ala Leu Leu Tyr Val Asn Asp Pro Arg Thr Pro Trp Ala Asn
290 295 300

Ser Asn Tyr Arg Leu Leu Asn Arg Thr Ala Thr Asn Gln Thr Gly Thr
305 310 315 320

Ile Asp Lys Ser Val Leu Asp Glu Gln Ser Asp Pro Asn His Met Gly
325 330 335

Gly Phe Asp Phe Leu Leu Ala Asn Asp Val Asp Thr Ser Asn Pro Val
340 345 350

Val Gln Ala Glu Gln Leu Asn Gln Ile His Tyr Leu Met Asn Trp Gly
355 360 365

Ser Ile Val Met Gly Asp Lys Asp Ala Asn Phe Asp Gly Ile Arg Val
370 375 380

Asp Ala Val Asp Asn Val Asp Ala Asp Met Leu Gln Leu Tyr Thr Asn
385 390 395 400

Tyr Phe Arg Glu Tyr Tyr Gly Val Asn Lys Ser Glu Ala Asn Ala Leu
                405   410   415

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

Asn Asp Lys Thr Asp Gly Ala Ala Leu Ala Met Glu Asn Lys Gln Arg
        435   440   445

Leu Ala Leu Leu Phe Ser Leu Ala Lys Pro Ile Lys Glu Arg Thr Pro
    450   455   460

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

Glu Lys Thr Asp Trp Ile Asn Lys Asp Gly Ser Lys Ala Tyr Asn Glu
                485   490   495

Asp Gly Thr Val Lys Gln Ser Thr Ile Gly Lys Tyr Asn Glu Lys Tyr
            500   505   510

Gly Asp Ala Ser Gly Asn Tyr Val Phe Ile Arg Ala His Asp Asn Asn
        515   520   525

Val Gln Asp Ile Ile Ala Glu Ile Ile Lys Lys Glu Ile Asn Pro Lys
    530   535   540

[0214] Ser Asp Gly Phe Thr Ile Thr Asp Ala Glu Met Lys Lys Ala Phe Glu
545   550   555   560

Ile Tyr Asn Lys Asp Met Leu Ser Ser Asp Lys Lys Tyr Thr Leu Asn
                565   570   575

Asn Ile Pro Ala Ala Tyr Ala Val Met Leu Gln Asn Met Glu Thr Ile
            580   585   590

Thr Arg Val Tyr Tyr Gly Asp Leu Tyr Thr Asp Asp Gly His Tyr Met
        595   600   605

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

Arg Ile Lys Tyr Val Ser Gly Gly Gln Ala Gln Arg Ser Tyr Trp Leu
625   630   635   640

Pro Thr Asp Gly Lys Met Asp Lys Ser Asp Val Glu Leu Tyr Arg Thr
                645   650   655

Asn Glu Val Tyr Thr Ser Val Arg Tyr Gly Lys Asp Ile Met Thr Ala
            660   665   670

Asp Asp Thr Gln Gly Ser Lys Tyr Ser Arg Thr Ser Gly Gln Val Thr
        675   680   685

Leu Val Val Asn Asn Pro Lys Leu Ser Leu Asp Lys Ser Ala Lys Leu
    690   695   700

Asp Val Glu Met Gly Lys Ile His Ala Asn Gln Lys Tyr Arg Ala Leu
705 710 715 720

Ile Val Gly Thr Pro Asn Gly Ile Lys Asn Phe Thr Ser Asp Ala Glu
725 730 735

Ala Ile Ala Ala Gly Tyr Val Lys Glu Thr Asp Gly Asn Gly Val Leu
740 745 750

Thr Phe Gly Ala Asn Asp Ile Lys Gly Tyr Glu Thr Phe Asp Met Ser
755 760 765

Gly Phe Val Ala Val Trp Val Pro Val Gly Ala Ser Asp Asp Gln Asp
770 775 780

Ile Arg Val Ala Ala Ser Thr Ala Ala Lys Lys Glu Gly Glu Leu Thr
785 790 795 800

Leu Lys Ala Thr Glu Ala Tyr Asp Ser Gln Leu Ile Tyr Glu Gly Phe
805 810 815

Ser Asn Phe Gln Thr Ile Pro Asp Gly Ser Asp Pro Ser Val Tyr Thr
820 825 830

Asn Arg Lys Ile Ala Glu Asn Val Asp Leu Phe Lys Ser Trp Gly Val
835 840 845

[0215] Thr Ser Phe Glu Met Ala Pro Gln Phe Val Ser Ala Asp Asp Gly Thr
850 855 860

Phe Leu Asp Ser Val Ile Gln Asn Gly Tyr Ala Phe Ala Asp Arg Tyr
865 870 875 880

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

Arg Asn Ala Leu Lys Ala Leu His Lys Ala Gly Ile Gln Ala Ile Ala
900 905 910

Asp Trp Val Pro Asp Gln Ile Tyr Gln Leu Pro Gly Lys Glu Val Val
915 920 925

Thr Ala Thr Arg Thr Asp Gly Ala Gly Arg Lys Ile Ser Asp Ala Ile
930 935 940

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

Tyr Gln Ala Lys Tyr Gly Gly Glu Phe Leu Ala Glu Leu Lys Ala Lys
965 970 975

Tyr Pro Glu Met Phe Lys Val Asn Met Ile Ser Thr Gly Lys Pro Ile
980 985 990

Asp Asp Ser Val Lys Leu Lys Gln Trp Lys Ala Glu Tyr Phe Asn Gly
995 1000 1005

Thr Asn Val Leu Asp Arg Gly Val Gly Tyr Val Leu Ser Asp Glu
1010 1015 1020

Ala Thr Gly Lys Tyr Phe Thr Val Thr Lys Glu Gly Asn Phe Ile
1025 1030 1035

Pro Leu Gln Leu Lys Gly Asn Glu Lys Val Ile Thr Gly Phe Ser
1040 1045 1050

Ser Asp Gly Lys Gly Ile Thr Tyr Phe Gly Thr Ser Gly Asn Gln
1055 1060 1065

Ala Lys Ser Ala Phe Val Thr Phe Asn Gly Asn Thr Tyr Tyr Phe
1070 1075 1080

Asp Ala Arg Gly His Met Val Thr Asn Gly Glu Tyr Ser Pro Asn
1085 1090 1095

Gly Lys Asp Val Tyr Arg Phe Leu Pro Asn Gly Ile Met Leu Ser
1100 1105 1110

Asn Ala Phe Tyr Val Asp Gly Asn Gly Asn Thr Tyr Leu Tyr Asn
1115 1120 1125

Ser Lys Gly Gln Met Tyr Lys Gly Gly Tyr Ser Lys Phe Asp Val
1130 1135 1140

[0216] Thr Glu Thr Lys Asp Gly Lys Glu Ser Lys Val Val Lys Phe Arg
1145 1150 1155

Tyr Phe Thr Asn Glu Gly Val Met Ala Lys Gly Val Thr Val Val
1160 1165 1170

Asp Gly Phe Thr Gln Tyr Phe Asn Glu Asp Gly Ile Gln Ser Lys
1175 1180 1185

Asp Glu Leu Val Thr Tyr Asn Gly Lys Thr Tyr Tyr Phe Glu Ala
1190 1195 1200

His Thr Gly Asn Ala Ile Lys Asn Thr Trp Arg Asn Ile Lys Gly
1205 1210 1215

Lys Trp Tyr His Phe Asp Ala Asn Gly Val Ala Ala Thr Gly Ala
1220 1225 1230

Gln Val Ile Asn Gly Gln His Leu Tyr Phe Asn Glu Asp Gly Ser
1235 1240 1245

Gln Val Lys Gly Gly Val Val Lys Asn Ala Asp Gly Thr Phe Ser
1250 1255 1260

Lys Tyr Lys Asp Gly Ser Gly Asp Leu Val Val Asn Glu Phe Phe
1265 1270 1275

Thr Thr Gly Asp Asn Val Trp Tyr Tyr Ala Gly Ala Asn Gly Lys
1280 1285 1290

Thr Val Thr Gly Ala Gln Val Ile Asn Gly Gln His Leu Phe Phe
1295 1300 1305

Lys Glu Asp Gly Ser Gln Val Lys Gly Asp Phe Val Lys Asn Ser
1310 1315 1320

Asp Gly Thr Tyr Ser Lys Tyr Asp Ala Ala Ser Gly Glu Arg Leu
1325 1330 1335

Thr Asn Glu Phe Phe Thr Thr Gly Asp Asn His Trp Tyr Tyr Ile
1340 1345 1350

Gly Ala Asn Gly Lys Thr Val Thr Gly Glu Val Lys Ile Gly Asp
1355 1360 1365

Asp Thr Tyr Phe Phe Ala Lys Asp Gly Lys Gln Leu Lys Gly Gln
1370 1375 1380

Ile Val Thr Thr Arg Ser Gly Arg Ile Ser Tyr Tyr Phe Gly Asp
1385 1390 1395

Ser Gly Lys Lys Ala Ile Ser Thr Trp Val Glu Ile Gln Pro Gly
1400 1405 1410

Val Phe Val Phe Phe Asp Lys Asn Gly Leu Ala Tyr Pro Pro Glu
1415 1420 1425

[0217] Asn Met Asn
1430

<210> 64
<211> 1532
<212> PRT
<213> 未知

<220>
<223> 未知链球菌菌种

<400> 64

Met Glu Asn Lys Val His Tyr Lys Leu His Lys Val Lys Lys Gln Trp
1 5 10 15

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

Leu Ser Ala Thr Thr Ser Ser Val Ser Ala Asp Glu Thr Gln Asp Lys
35 40 45

Thr Val Thr Gln Pro Asn Ser Asp Thr Thr Ala Asp Leu Val Thr Ser
50 55 60

Thr Glu Ala Thr Lys Glu Val Asp Lys Arg Thr Asn Thr Lys Glu Ala
65 70 75 80

Asp Val Leu Thr Pro Ala Lys Glu Thr Asn Thr Val Glu Thr Ala Ala
85 90 95

Thr Thr Asn Thr Gln Ala Thr Ala Glu Ala Ala Lys Thr Ala Thr Thr
100 105 110

Thr Asn Thr Gln Ala Thr Ala Glu Val Ala Lys Thr Ala Thr Thr Ala
115 120 125

Asp Val Ala Val Ala Ala Val Pro Asn Lys Glu Ala Val Val Thr Thr
130 135 140

Asp Ala Pro Ala Val Thr Thr Glu Lys Ala Glu Glu Gln Pro Ala Thr
145 150 155 160

Val Lys Ala Glu Val Val Asn Thr Glu Val Lys Ala Pro Glu Ala Ala
165 170 175

Leu Lys Asp Ser Glu Val Glu Ala Ala Leu Ser Leu Lys Asn Ile Lys
180 185 190

Asn Ile Asp Gly Lys Tyr Tyr Tyr Val Asn Glu Asp Gly Ser His Lys
195 200 205

Glu Asn Phe Ala Ile Thr Val Asn Gly Gln Leu Leu Tyr Phe Gly Lys
210 215 220

Asp Gly Ala Leu Thr Ser Ser Ser Thr Tyr Ser Phe Thr Gln Gly Thr
225 230 235 240

[0218] Thr Asn Ile Val Asp Gly Phe Ser Ile Asn Asn Arg Ala Tyr Asp Ser
245 250 255

Ser Glu Ala Ser Phe Glu Leu Ile Asp Gly Tyr Leu Thr Ala Asp Ser
260 265 270

Trp Tyr Arg Pro Ala Ser Ile Ile Lys Asp Gly Val Thr Trp Gln Ala
275 280 285

Ser Thr Ala Glu Asp Phe Arg Pro Leu Leu Met Ala Trp Trp Pro Asn
290 295 300

Val Asp Thr Gln Val Asn Tyr Leu Asn Tyr Met Ser Lys Val Phe Asn
305 310 315 320

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

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

Lys Ser Thr Gln Trp Leu Arg Glu Thr Ile Ser Ala Phe Val Lys Thr
355 360 365

Gln Pro Gln Trp Asn Lys Glu Thr Glu Asn Tyr Ser Lys Gly Gly Gly
370 375 380

Glu Asp His Leu Gln Gly Gly Ala Leu Leu Tyr Val Asn Asp Ser Arg
385 390 395 400

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Thr Pro Trp Ala Asn Ser Asn Tyr Arg Leu Leu Asn Arg Thr Ala Thr
                405                 410                 415

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

Pro Asn His Met Gly Gly Phe Asp Phe Leu Leu Ala Asn Asp Val Asp
        435                 440                 445

Leu Ser Asn Pro Val Val Gln Ala Glu Gln Leu Asn Gln Ile His Tyr
    450                 455                 460

Leu Met Asn Trp Gly Ser Ile Val Met Gly Asp Lys Asp Ala Asn Phe
465                 470                 475                 480

Asp Gly Ile Arg Val Asp Ala Val Asp Asn Val Asp Ala Asp Met Leu
                485                 490                 495

Gln Leu Tyr Thr Asn Tyr Phe Arg Glu Tyr Tyr Gly Val Asn Lys Ser
            500                 505                 510

Glu Ala Asn Ala Leu Ala His Ile Ser Val Leu Glu Ala Trp Ser Leu
        515                 520                 525

Asn Asp Asn His Tyr Asn Asp Lys Thr Asp Val Ala Ala Leu Ala Met
    530                 535                 540
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[0219]

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Glu Asn Lys Gln Arg Leu Ala Leu Leu Phe Ser Leu Ala Lys Pro Ile
545                 550                 555                 560

Lys Glu Arg Thr Pro Ala Val Ser Pro Leu Tyr Asn Asn Thr Phe Asn
                565                 570                 575

Thr Thr Gln Arg Asp Glu Lys Thr Asp Trp Ile Asn Lys Asp Gly Ser
            580                 585                 590

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

Tyr Asn Glu Lys Tyr Gly Asp Ala Ser Gly Asn Tyr Val Phe Ile Arg
    610                 615                 620

Ala His Asp Asn Asn Val Gln Asp Ile Ile Ala Glu Ile Ile Lys Lys
625                 630                 635                 640

Glu Ile Asn Glu Lys Ser Asp Gly Phe Thr Ile Thr Asp Ser Glu Met
                645                 650                 655

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

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

Asn Met Glu Thr Ile Thr Arg Val Tyr Tyr Gly Asp Leu Tyr Thr Asp
    690                 695                 700
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Asp Gly Asn Tyr Met Glu Ala Lys Ser Pro Tyr Tyr Asp Thr Ile Val
705 710 715 720

Asn Leu Met Lys Ser Arg Ile Lys Tyr Val Ser Gly Gly Gln Ala Gln
725 730 735

Arg Ser Tyr Trp Leu Pro Thr Asp Gly Lys Met Asp Lys Ser Asp Val
740 745 750

Glu Leu Tyr Arg Thr Asn Glu Val Tyr Thr Ser Val Arg Tyr Gly Lys
755 760 765

Asp Ile Met Thr Ala Asp Asp Thr Gln Gly Ser Lys Tyr Ser Arg Thr
770 775 780

Ser Gly Gln Val Thr Leu Val Val Asn Asn Pro Lys Leu Thr Leu Asp
785 790 795 800

Gln Ser Ala Lys Leu Asn Val Val Met Gly Lys Ile His Ala Asn Gln
805 810 815

Lys Tyr Arg Ala Leu Ile Val Gly Thr Pro Asn Gly Ile Lys Asn Phe
820 825 830

Thr Ser Asp Ala Glu Ala Ile Ala Ala Gly Tyr Val Lys Glu Thr Asp
835 840 845

[0220] Gly Asn Gly Val Leu Thr Phe Gly Ala Asn Asp Ile Lys Gly Tyr Glu
850 855 860

Thr Phe Asp Met Ser Gly Phe Val Ala Val Trp Val Pro Val Gly Ala
865 870 875 880

Ser Asp Asp Gln Asp Ile Arg Val Ala Ala Ser Thr Ala Ala Lys Lys
885 890 895

Glu Gly Glu Leu Thr Leu Lys Ala Thr Glu Ala Tyr Asp Ser Gln Leu
900 905 910

Ile Tyr Glu Gly Phe Ser Asn Phe Gln Thr Ile Pro Asp Gly Ser Asp
915 920 925

Pro Ser Val Tyr Thr Asn Arg Lys Ile Ala Glu Asn Val Asp Leu Phe
930 935 940

Lys Ser Trp Gly Val Thr Ser Phe Glu Met Ala Pro Gln Phe Val Ser
945 950 955 960

Ala Asp Asp Gly Thr Phe Leu Asp Ser Val Ile Gln Asn Gly Tyr Ala
965 970 975

Phe Ala Asp Arg Tyr Asp Leu Ala Met Ser Lys Asn Asn Lys Tyr Gly
980 985 990

Ser Lys Glu Asp Leu Arg Asn Ala Leu Lys Ala Leu His Lys Ala Gly
995 1000 1005

Ile Gln Ala Ile Ala Asp Trp Val Pro Asp Gln Ile Tyr Gln Leu
1010 1015 1020

Pro Gly Lys Glu Val Val Thr Ala Thr Arg Thr Asp Gly Ala Gly
1025 1030 1035

Arg Lys Ile Ser Asp Ala Ile Ile Asp His Ser Leu Tyr Val Ala
1040 1045 1050

Asn Ser Lys Ser Ser Gly Lys Asp Tyr Gln Ala Lys Tyr Gly Gly
1055 1060 1065

Glu Phe Leu Ala Glu Leu Lys Ala Lys Tyr Pro Glu Met Phe Lys
1070 1075 1080

Val Asn Met Ile Ser Thr Gly Lys Pro Ile Asp Asp Ser Val Lys
1085 1090 1095

Leu Lys Gln Trp Lys Ala Glu Tyr Phe Asn Gly Thr Asn Val Leu
1100 1105 1110

Asp Arg Gly Val Gly Tyr Val Leu Ser Asp Glu Ala Thr Gly Lys
1115 1120 1125

Tyr Phe Thr Val Thr Lys Glu Gly Asn Phe Ile Pro Leu Gln Leu
1130 1135 1140

[0221] Lys Gly Asn Lys Lys Val Ile Thr Gly Phe Ser Ser Asp Gly Lys
1145 1150 1155

Gly Ile Thr Tyr Phe Gly Thr Ser Gly Asn Gln Ala Lys Ser Ala
1160 1165 1170

Phe Val Thr Phe Asn Gly Asn Thr Tyr Tyr Phe Asp Ala Arg Gly
1175 1180 1185

His Met Val Thr Asn Gly Glu Tyr Ser Pro Asn Gly Lys Asp Val
1190 1195 1200

Tyr Arg Phe Leu Pro Asn Gly Ile Met Leu Ser Asn Ala Phe Tyr
1205 1210 1215

Val Asp Gly Asn Gly Asn Thr Tyr Leu Tyr Asn Ser Lys Gly Gln
1220 1225 1230

Met Tyr Lys Gly Gly Tyr Ser Lys Phe Asp Val Thr Glu Thr Lys
1235 1240 1245

Asp Gly Lys Glu Ser Lys Val Val Lys Phe Arg Tyr Phe Thr Asn
1250 1255 1260

Glu Gly Val Met Ala Lys Gly Val Thr Val Val Asp Gly Phe Thr
1265 1270 1275

Gln Tyr Phe Asn Glu Asp Gly Ile Gln Ser Lys Asp Glu Leu Val
1280 1285 1290

Thr Tyr Asn Gly Lys Thr Tyr Tyr Phe Glu Ala His Thr Gly Asn
1295 1300 1305

Ala Ile Lys Asn Thr Trp Arg Asn Ile Lys Gly Lys Trp Tyr His
1310 1315 1320

Phe Asp Ala Asn Gly Val Ala Ala Thr Gly Ala Gln Val Ile Asn
1325 1330 1335

Gly Gln His Leu Tyr Phe Asn Glu Asp Gly Ser Gln Val Lys Gly
1340 1345 1350

Ser Ile Val Lys Asn Ala Asp Gly Thr Phe Ser Lys Tyr Lys Asp
1355 1360 1365

Ser Ser Gly Asp Leu Val Val Asn Glu Phe Phe Thr Thr Gly Asp
1370 1375 1380

Asn Val Trp Tyr Tyr Ala Gly Ala Asn Gly Lys Thr Val Thr Gly
1385 1390 1395

Ala Gln Val Ile Asn Gly Gln His Leu Phe Phe Lys Glu Asp Gly
1400 1405 1410

[0222]

Ser Gln Val Lys Gly Asp Phe Val Lys Asn Ser Asp Gly Thr Tyr
1415 1420 1425

Ser Lys Tyr Asp Ala Ala Ser Gly Glu Arg Leu Thr Asn Glu Phe
1430 1435 1440

Phe Thr Thr Gly Asp Asn His Trp Tyr Tyr Ile Gly Ala Asn Gly
1445 1450 1455

Lys Thr Val Thr Gly Glu Val Lys Ile Gly Asp Asp Thr Tyr Phe
1460 1465 1470

Phe Ala Lys Asp Gly Lys Gln Leu Lys Gly Gln Ile Val Thr Thr
1475 1480 1485

Arg Ser Gly Arg Ile Ser Tyr Tyr Phe Gly Asp Ser Gly Lys Lys
1490 1495 1500

Ala Ile Ser Thr Trp Val Glu Ile Gln Pro Gly Val Phe Val Phe
1505 1510 1515

Phe Asp Lys Asn Gly Leu Ala Tyr Pro Pro Glu Asn Met Asn
1520 1525 1530