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(54)发明名称

海藻糖磷酸化酶

(57)摘要

本发明涉及一种包含氨基酸序列的海藻糖磷酸化酶,其中该海藻糖磷酸化酶的氨基酸序列与SEQ ID NO:1的氨基酸序列具有至少80%同一性和/或至少80%同源性,其中该海藻糖磷酸化酶的氨基酸序列在一个或更多个氨基酸位置处包含氨基酸取代,其中该一个或更多个氨基酸位置选自由下列氨基酸位置组成的组:SEQ ID NO:1的位置712、383、10、114、118、192、197、220、225、304、306、318、323、339、349、357、459、476、481、484、487、488、506、511、526、530、532、533、537、550、556、564、590、649、667、703以及705。

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1.一种海藻糖磷酸化酶,其中所述海藻糖磷酸化酶的氨基酸序列由下列任一种氨基酸序列组成:SEQ ID NO:2、3、4、5、6、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、47、48、49、50、51、52、53、54、55、56、57、58、59、60、61、62、63、64、65、66、67、68、69、70、71、72、73、74、75、76、77、78、79、84、85、86、87、88、89、90、91、92、93、94、95、96、97、98、99、100、101、102、103、104、105、106、107、108、109、110、111、112、113、114、115、116、117、118、119、120、121、122、123、124、125、126、127、128、129、130、131、132、133、134、135、136、137、138、139、140、141、142、143、144、145、146、147、148、149、150、151、152、153、154、155、156、157、158、159,或190。

2.一种使葡糖基单醣与α-D-葡萄糖-1磷酸盐反应的方法,

其中所述方法包括使葡糖基单醣和α-D-葡萄糖-1磷酸盐与如权利要求1所定义的海藻糖磷酸化酶反应。

3.一种制备海藻糖的方法,包括在海藻糖磷酸化酶存在下,在至少40℃的温度使葡萄糖与α-D-葡萄糖-1磷酸盐反应,其中所述海藻糖磷酸化酶

(i)在含有1M蔗糖的缓冲液中于52℃温育15分钟后,与没有热处理的其活性相比,保留其活性的至少30%;或

(ii)在含有1M蔗糖的缓冲液中于52℃温育15分钟后,与没有热处理的其活性相比,保留其活性的至少50%;或

(iii)在100mM葡萄糖下的活性与在500mM葡萄糖下的活性的比至少为0.65,

其中所述海藻糖磷酸化酶是权利要求1所定义的海藻糖磷酸化酶。

4.根据权利要求1所述的海藻糖磷酸化酶用于生产海藻糖的用途。

海藻糖磷酸化酶

技术领域

[0001] 本发明涉及磷酸化酶,使葡糖基单醣与α-D-葡萄糖1-磷酸盐(alpha-D-glucose 1-phosphate)反应的方法,将葡萄糖与α-D-葡萄糖1-磷酸盐转化为海藻糖与无机磷酸盐的方法以及该磷酸化酶用于生产海藻糖的用途。

背景技术

[0002] 磷酸化酶是催化将来自无机磷酸盐的磷酸基团添加至受体分子的酶。催化海藻糖的可逆磷酸化裂解(phosphorolytic cleavage)的磷酸化酶在本领域中是已知的,并被称为海藻糖磷酸化酶。海藻糖磷酸化酶可基于其所催化的反应的机制来加以区分。

[0003] 第一组海藻糖磷酸化酶使用无机磷酸盐作为进入葡萄糖与α-D-葡萄糖1-磷酸(aG1P)的葡糖基受体,以催化具有变旋异构组态净保留的海藻糖的磷酸化裂解,因此被归类为保留磷酸化酶。这种第一组海藻糖磷酸化酶已被国际生物化学暨分子生物学联盟(International Union of Biochemistry and Molecular Biology)指定为EC号为EC 2.4.1.231,并已经从各种真核生物真菌中进行功能鉴定。

[0004] 第二组海藻糖磷酸化酶为将EC号为EC 2.4.1.64的海藻糖磷酸化酶翻转并催化海藻糖的磷酸化裂解,并将构型转化为葡萄糖与β-D-葡萄糖-1磷酸盐。因此这些磷酸化酶具有不同于EC 2.4.1.231的海藻糖磷酸化酶的反应机制。

[0005] 具体地,本发明涉及EC号为EC 2.4.1.231的某些磷酸化酶,其能够在其它反应中将葡萄糖与α-D-葡萄糖-1磷酸(“aG1P”)转化为海藻糖,或能够在无机磷酸盐的存在下将海藻糖磷酸化裂解为葡萄糖与aG1P。

[0006] 海藻糖磷酸化酶的工业用途源于这样的事实,亦即其生物化学特征的反应,即催化海藻糖的磷酸化裂解,是可逆的。因此,海藻糖磷酸化酶特别适用于催化葡萄糖与aG1P将其转化为海藻糖与无机磷酸盐。

[0007] 由海藻糖磷酸化酶催化的反应是可逆的(平衡反应),且可能经历基质或产物抑制,取决于该反应的具体方向。为了获得一所需产物工业上相关的量,需要海藻糖磷酸化酶催化具有高比活性的基质的转化。此外,海藻糖磷酸化酶的其它动力学因子,例如基质选择性与KM可能对产品收获率具有重要作用。其它相关方面可以包括但不限于区域选择性,由其它因素(例如,粗提取物组成分、基质污染物或副产物)造成的抑制以及在合适宿主中的重组可溶性表现。

[0008] 野生型海藻糖磷酸化酶的主要缺点为,即使在25℃至40℃之间的中等温度下溶液中的酶活性也会迅速丧失,这明显限制了它们的应用。对于工业应用而言,在高于30℃的温度下几天之内的高稳定性,或者甚至高于40℃的高温稳定性都是需要的。对于热不稳定的酶来说,反应时间长,在整个加工过程中需要更大量的酶,通常通过重复添加酶来进行。例如,来自秀珍菇(Pleurotus ostreatus)的海藻糖磷酸化酶在25℃显示约1.3小时的半衰期以及在约41℃3分钟的半衰期(Schwarz等人,J Biotechnol 129,140-150(2007),Han等人,Protein Expression and Purification 30,194-202(2003))。来自裂褶菌

(Schizophyllum commune)以及千佛菌(Grifola frondosa)的海藻糖磷酸化酶则稍微稳定些,分别在30℃的半衰期为4.8小时,在37℃的半衰期为1小时(Schwarz等人,J Biotechnol 129,140-150(2007))。

[0009] 本领域应用了各种策略来解决这些缺点。例如,添加海藻糖、甘油以及聚乙二醇(polyethylene glycol,PEG)显示增加海藻糖磷酸化酶的稳定性(Klimacek等人,Biotechnology Techniques 13:243-248,1999,Eis等人,Biochem J 341,385-393(1999),Schwarz等人,J Biotechnol 129,140-150(2007))。通过添加20%的PEG4000达到了最佳稳定化,这导致来自裂褶菌的海藻糖磷酸化酶在30℃、40℃以及50℃的半衰期分别为4.5天、2.2小时以及6分钟(Klimacek等人,Biotechnology Techniques 13:243-248,1999,Eis等人,Biochem J 341,385-393(1999))。虽然添加PEG 4000改善了酶的稳定性,但是在40℃或40℃以上的应用仍然不足,且需要数小时至数天的处理时间进行这样的改进。PEG 4000的存在可能进一步干扰通过酶促反应获得的产物的工业规模成本结构以及下游加工要求。

[0010] 来自裂褶菌的海藻糖磷酸化酶的半衰期也可通过分别在30℃、40℃以及50℃固定化22天、3.3天以及2小时来改善(Klimacek等人,Biotechnology Techniques 13:243-248,1999)。然而,由于昂贵的载体及制造成本,固定化会导致较高的酶生产成本,且只有当酶可以回收并重新使用多个循环时,在工业应用方面才是有效的。此外,固定化限制了酶促反应产物的过程及下游加工的选择。

[0011] 因此,在25℃至35℃的温度进行以海藻糖磷酸化酶的合成反应并不令人惊讶(Schwarz等人,J of Biotechnology 129 140-150(2007),Saito等人,Appl Microbiol Biotechnol 50:193-198(1998),Saito等人,Appl Microbiol Biotechnol 64:4340-4345(1998))。

[0012] 改进酶的性能及其在工业过程中的适用性的另一种方法为酶工程。该技术涉及开发具有改进性能的起始酶的变体(回顾文献请参见,例如S.Lutz,U.T.Bornscheuer,Protein Engineering Handbook,Wiley VCH,Weinheim,2009)。其中磷酸化酶通过酶工程改善。例如,美国专利申请公开号US 2013-0029384揭露了具有改善的热稳定性的属于糖基水解酶家族13的蔗糖磷酸化酶的变体。EC号为EC 2.4.1.231的海藻糖磷酸化酶的变体迄今仅限于用于阐明所述的海藻糖磷酸化酶的反应机理的变体。基于这样的变体,Goedl等人(Biochem J 397;491-500;2006)发现在来自裂褶菌(Shizophyllum commune)的海藻糖磷酸化酶的氨基酸位置D379、H403、R507以及K512的取代导致活性降低。具有以下单一突变D379N、H403A、R507A以及K512A中的的变体显示出海藻糖磷酸分解活性降低。Goedl等人(FEBS J 275;903-913,2008)更具体地发现来自裂褶菌(Shizophyllum commune)的海藻糖磷酸化酶突变R507A以及K512A对野生型海藻糖磷酸化酶的催化效率(kcat/KM)有影响。

[0013] 由于现有技术中可获得的野生型海藻糖磷酸化酶在各方面都令人不满意,且试图有效地提高海藻糖磷酸化酶的工业应用性,如本领域所描述的那样不成功,因此需要与野生型海藻糖磷酸化酶相比具有优势的海藻糖磷酸化酶,特别是在工业生产海藻糖的高温工艺稳定性方面有优势者。

[0014] 因此,本发明的基础问题为提供适用于工业生产海藻糖的海藻糖磷酸化酶。

[0015] 本发明的另一问题为提供热稳定的海藻糖磷酸化酶,且于52℃温育15分钟后显示出30%至90%或55%至100%的残余活性,而不需要酶的固定化或添加除了蔗糖以外的任

何稳定剂(例如,PEG或甘油)。

[0016] 本发明的另一问题为提供一种热稳定的海藻糖磷酸化酶,并且于45℃显示3小时至9天或更长的半衰期,而不需要酶的固定化或添加除了蔗糖以外的任何稳定剂(例如,PEG或甘油)。

[0017] 本发明的另一问题为提供具有介于0.65和1.0之间的100/500-比的海藻糖磷酸化酶。

[0018] 另一问题为提供允许将葡萄糖与α-D-葡萄糖-1磷酸盐转化为海藻糖与无机磷酸盐的方法。

发明内容

[0019] 所附的独立权利要求解决了这些和其它的问题。优选的实施方式可以由所附的从属权利要求获得。

[0020] 更具体地,在第一方面,其也是第一方面的第一实施方式,中的这些及其它问题通过包含氨基酸序列的多肽解决,该多肽优选海藻糖磷酸化酶,其中该海藻糖磷酸化酶的氨基酸序列与SEQ ID NO:1的氨基酸序列具有至少80%同一性和/或至少80%同源性,其中该海藻糖磷酸化酶的氨基酸序列包含在一个或更多个氨基酸位置处的氨基酸取代,其中该一个或更多个氨基酸位置选自由下列SEQ ID NO:1的氨基酸位置组成的组:712、383、10、114、118、192、197、220、225、304、306、318、323、339、349、357、459、476、481、484、487、488、506、511、526、530、532、533、537、550、556、564、590、649、667、703以及705。优选地,该一个或更多个氨基酸位置是各自并独立地选自由下列SEQ ID NO:1的氨基酸位置组成的组:712、383、10、114、118、192、197、220、225、304、306、318、323、339、349、357、459、476、481、484、487、488、506、511、526、530、532、533、537、550、556、564、590、649、667、703以及705。甚至更优选,该一个或更多个氨基酸位置是各自并独立地选自由下列SEQ ID NO:1的氨基酸位置组成的组:712、383、114、118、192、197、220、225、304、306、318、323、339、349、357、459、476、481、484、487、488、506、511、526、530、532、533、537、550、556、564、590、667、703以及705。如在本发明的上下文中令人惊讶地发现的,一个或更多个这些位置的突变导致与SEQ ID NO:1的野生型序列相比的改善特征,例如,该酶的热稳定性提高导致于52℃温育15分钟后的残余活性为至少22%,这是与由SEQ ID NO:1的野生型氨基酸序列编码的海藻糖磷酸化酶的19%相比。

[0021] 在第一方面的第二实施方式中,其也是该第一方面的第一实施方式的一实施方式,该一个或更多个氨基酸位置选自由下列SEQ ID NO:1的氨基酸位置组成的组:L712、P383、V10、L114、I118、S192、S197、Y220、N225、A304、D306、P318、T323、L339、F349、G357、A459、Q476、E481、A484、Q487、K488、A506、A511、R526、E530、G532、D533、D537、V550、S556、T564、D590、A649、R667、A703以及K705。

[0022] 在第一方面的第三实施方式中,其也是该第一方面的第一和第二实施方式的一实施方式,该一个或更多个氨基酸位置选自由下列SEQ ID NO:1的氨基酸位置组成的组:712、383、10、114、118、220、225、304、318、323、349、357、481、487、488、506、511、550、556、564、590、649、703以及705。

[0023] 在第一方面的第四实施方式中,其也是该第一方面的第一、第二及第三实施方式

的一实施方式,该一个或更多个氨基酸位置选自由下列SEQ ID NO:1的氨基酸位置组成的组:L712、P383、V10、L114、I118、Y220、N225、A304、P318、T323、F349、G357、E481、Q487、K488、A506、A511、V550、S556、T564、D590、A649、A703以及K705。

[0024] 在第一方面的第五实施方式中,其也是该第一方面的第一、第二、第三及第四实施方式的一实施方式,该一个或更多个氨基酸位置选自由下列SEQ ID NO:1的氨基酸位置组成的组:712、383、114、118、225、304、323、349、357、487、550、556、564、590以及649。

[0025] 在第一方面的第六实施方式中,其也是该第一方面的第一、第二、第三、第四及第五实施方式的一实施方式,优选第一方面的第五实施方式,该一个或更多个氨基酸位置选自由下列SEQ ID NO:1的氨基酸位置组成的组:L712、P383、L114、I118、N225、A304、T323、F349、G357、Q487、V550、S556、T564、D590以及A649。

[0026] 在第一方面的另一优选实施方式中,其也是该第一方面的前述任一实施方式的一实施方式,该一个或更多个氨基酸位置选自由下列SEQ ID NO:1的氨基酸位置组成的组:383、225、304、323、487、550、556、564、590以及705。

[0027] 在第一方面的另一实施方式中,其也是该第一方面的前述任一实施方式的一实施方式,该一个或更多个氨基酸位置选自由下列SEQ ID NO:1的氨基酸位置组成的组:383、225、304、487、556、590以及705。

[0028] 在第一方面的另一实施方式中,其也是该第一方面的前述任一实施方式的一实施方式,该一个或更多个氨基酸位置选自由下列SEQ ID NO:1的氨基酸位置组成的组:383、225、304、487、556以及590。

[0029] 在第一方面的另一实施方式中,其也是该第一方面的前述任一实施方式的一实施方式,该一个或更多个氨基酸位置选自由下列SEQ ID NO:1的氨基酸位置组成的组:383、556以及590。

[0030] 在第一方面的另一实施方式中,其也是该第一方面的前述任一实施方式的一实施方式,该一个或更多个氨基酸位置选自由SEQ ID NO:1的氨基酸位置383与590组成的组。

[0031] 在第一方面的另一实施方式中,其也是该第一方面的前述任一实施方式的一实施方式,该一个或更多个氨基酸位置是为SEQ ID NO:1的氨基酸位置383。

[0032] 在第一方面的另一实施方式中,其也是该第一方面的前述任一实施方式的一实施方式,该一个或更多个氨基酸位置选自由下列SEQ ID NO:1的氨基酸位置组成的组:P383、N225、A304、T323、Q487、V550、S556、T564、D590以及N705。

[0033] 在第一方面的另一实施方式中,其也是该第一方面的前述任一实施方式的一实施方式,该海藻糖磷酸化酶的氨基酸序列包含根据SEQ ID NO:2、84、85、86、87、88、89、90、91、92、93、94、95、96、97、98、99、100、101、102、103、104、105、106、107、108、109,优选根据SEQ ID NO:2、84、85、87、88、89、91、92、93、94、95、97、98、99、100、101、102、103、104、105、106、107、109的任何中的,更优选根据SEQ ID NO:84、85、87、88、89、91、92、93、94、95、97、98、99、100、101、102、103、104、105、106、107、109的任何中的,同等优选根据SEQ ID NO:87、89、91、97、98、99、100、101、102、103、104、109的任何中的,甚至更优选根据SEQ ID NO:87、91、97、98、99、100、101、102、103、104、109的任何中的以及最优选根据SEQ ID NO:87、97、98、99、100、101、102、103、104的任何中的的氨基酸序列。

[0034] 在第一方面的第七实施方式中,其也是该第一方面的第一、第二、第三、第四、第五

及第六实施方式或前述的任何其它的一实施方式，该一个或更多个氨基酸位置为两个或更多个氨基酸位置。

[0035] 在第一方面的第八实施方式中，其也是该第一方面的第一、第二、第三、第四、第五、第六及第七实施方式或前述的任何其它的一实施方式，优选第一方面的第七实施例，该一个或更多个氨基酸位置为三个或更多个氨基酸位置。

[0036] 在第一方面的第九实施方式中，其也是该第一方面的第一、第二、第三、第四、第五、第六、第七及第八实施方式或前述的任何其它的一实施方式，优选第一方面的第八实施例，该一个或更多个氨基酸位置为四个或更多个氨基酸位置。

[0037] 在第一方面的第十实施方式中，其也是该第一方面的第一、第二、第三、第四、第五、第六、第七、第八及第九实施方式或前述的任何其它的一实施方式，优选第一方面的第九实施例，该一个或更多个氨基酸位置为五个或更多个氨基酸位置。

[0038] 在第一方面的第十一实施方式中，其也是该第一方面的第一、第二、第三、第四、第五、第六、第七、第八、第九及第十实施方式或前述的任何其它的一实施方式，优选第一方面的第十实施例，该一个或更多个氨基酸位置为六个或更多个氨基酸位置。

[0039] 在第一方面的第十二实施方式中，其也是该第一方面的第一、第二、第三、第四、第五、第六、第七、第八、第九、第十及第十一实施方式或前述的任何其它的一实施方式，优选第一方面的第十一实施例，该一个或更多个氨基酸位置为七个或更多个氨基酸位置。

[0040] 在第一方面的第十三实施方式中，其也是该第一方面的第一、第二、第三、第四、第五、第六、第七、第八、第九、第十、第十一及第十二实施方式或前述的任何其它的一实施方式，优选第一方面的第十二实施例，该一个或更多个氨基酸位置为八个或更多个氨基酸位置。

[0041] 在第一方面的第十四实施方式中，其也是该第一方面的第一、第二、第三、第四、第五、第六、第七、第八、第九、第十、第十一、第十二及第十三实施方式或前述的任何其它的一实施方式，优选第一方面的第十三实施例，该一个或更多个氨基酸位置为九个或更多个氨基酸位置。

[0042] 在第一方面的第十五实施方式中，其也是该第一方面的第一、第二、第三、第四、第五、第六、第七、第八、第九、第十、第十一、第十二、第十三及第十四实施方式或前述的任何其它的一实施方式，优选第一方面的第十四实施例，该一个或更多个氨基酸位置为十个或更多个氨基酸位置。

[0043] 在第一方面的第十六实施方式中，其也是该第一方面的第一、第二、第三、第四、第五、第六、第七、第八、第九、第十、第十一、第十二、第十三、第十四及第十五实施方式或前述的任何其它的一实施方式，优选第一方面的第十五实施例，该一个或更多个氨基酸位置为十一个或更多个氨基酸位置。

[0044] 在第一方面的第十七实施方式中，其也是该第一方面的第一、第二、第三、第四、第五、第六、第七、第八、第九、第十、第十一、第十二、第十三、第十四、第十五及第十六实施方式或前述的任何其它的一实施方式，优选第一方面的第十六实施例，该一个或更多个氨基酸位置为十两个或更多个氨基酸位置。

[0045] 在第一方面的第十八实施方式中，其也是该第一方面的第一、第二、第三、第四、第五、第六、第七、第八、第九、第十、第十一、第十二、第十三、第十四、第十五、第十六及第十七

实施方式或前述的任何其它的一实施方式,优选第一方面的第十七实施例,该一个或更多个氨基酸位置为十三个或更多个氨基酸位置。

[0046] 在第一方面的第十九实施方式中,其也是该第一方面的第一、第二、第三、第四、第五、第六、第七、第八、第九、第十、第十一、第十二、第十三、第十四、第十五、第十六、第十七及第十八实施方式或前述的任何其它的一实施方式,优选第一方面的第十八实施例,该一个或更多个氨基酸位置为十四个或更多个氨基酸位置。

[0047] 在第一方面的第二十实施方式中,其也是该第一方面的第一、第二、第三、第四、第五、第六、第七、第八、第九、第十、第十一、第十二、第十三、第十四、第十五、第十六、第十七、第十八及第十九实施方式或前述的任何其它的一实施方式,优选第一方面的第七、第八、第九、第十、第十一、第十二、第十三、第十四、第十五、第十六、第十七、第十八及第十九实施例,每个及任何该氨基酸位置选自由下列SEQ ID NO:1的氨基酸位置组成的组:712、383、10、114、118、192、197、220、225、304、306、318、323、339、349、357、459、476、481、484、487、488、506、511、526、530、532、533、537、550、556、564、590、649、667、703以及705,优选地每个及任何该氨基酸位置是独立并各别地选自由下列SEQ ID NO:1的氨基酸位置组成的组:712、383、10、114、118、192、197、220、225、304、306、318、323、339、349、357、459、476、481、484、487、488、506、511、526、530、532、533、537、550、556、564、590、649、667、703以及705。

[0048] 在第一方面的第二十一实施方式中,其也是该第一方面的第二十实施例的一实施例,每个及任何该氨基酸位置选自由下列SEQ ID NO:1的氨基酸位置组成的组:L712、P383、V10、L114、I118、S192、S197、Y220、N225、A304、D306、P318、T323、L339、F349、G357、A459、Q476、E481、A484、Q487、K488、A506、A511、R526、E530、G532、D533、D537、V550、S556、T564、D590、A649、R667、A703以及K705,优选地每个及任何氨基酸位置是各自且独立地选自由下列SEQ ID NO:1的氨基酸位置组成的组:L712、P383、V10、L114、I118、S192、S197、Y220、N225、A304、D306、P318、T323、L339、F349、G357、A459、Q476、E481、A484、Q487、K488、A506、A511、R526、E530、G532、D533、D537、V550、S556、T564、D590、A649、R667、A703以及K705。

[0049] 在第一方面的第二十二实施方式中,其也是该第一方面的第二十实施例的一实施例,每个及任何该氨基酸位置选自由下列SEQ ID NO:1的氨基酸位置组成的组:712、383、10、114、118、220、225、304、318、323、349、357、481、487、488、506、511、550、556、564、590、649、703以及705,优选地每个及任何氨基酸位置是各自且独立地选自由下列SEQ ID NO:1的氨基酸位置组成的组:712、383、10、114、118、220、225、304、318、323、349、357、481、487、488、506、511、550、556、564、590、649、703以及705。

[0050] 在第一方面的第二十三实施方式中,其也是该第一方面的第二十二实施例的一实施例,每个及任何该氨基酸位置选自由下列SEQ ID NO:1的氨基酸位置组成的组:L712、P383、V10、L114、I118、Y220、N225、A304、P318、T323、F349、G357、E481、Q487、K488、A506、A511、V550、S556、T564、D590、A649、A703以及K705,优选地每个及任何氨基酸位置是各自且独立地选自由下列SEQ ID NO:1的氨基酸位置组成的组:L712、P383、V10、L114、I118、Y220、N225、A304、P318、T323、F349、G357、E481、Q487、K488、A506、A511、V550、S556、T564、D590、A649、A703以及K705。

[0051] 在第一方面的第二十四实施方式中,其也是该第一方面的第二十二实施例的一实施例,每个及任何该氨基酸位置选自由下列SEQ ID NO:1的氨基酸位置组成的组:712、383、

114、118、225、304、323、349、357、487、550、556、564、590以及649,优选地每个及任何氨基酸位置是各自且独立地选自由下列SEQ ID NO:1的氨基酸位置组成的组:712、383、114、118、225、304、323、349、357、487、550、556、564、590以及649。

[0052] 在第一方面的第二十五实施方式中,其也是该第一方面的第二十四实施例的一实施例,每个及任何该氨基酸位置选自由下列SEQ ID NO:1的氨基酸位置组成的组:L712、P383、L114、I118、N225、A304、T323、F349、G357、Q487、V550、S556、T564、D590以及A649,优选地每个及任何氨基酸位置是各自且独立地选自由下列SEQ ID NO:1的氨基酸位置组成的组:L712、P383、L114、I118、N225、A304、T323、F349、G357、Q487、V550、S556、T564、D590以及A649。

[0053] 在第一方面的第二十六实施方式中,其也是该第一方面的第七、第八、第九、第十、第十一、第十二、第十三、第十四、第十五、第十六、第十七、第十八、第十九、第二十、第二十一、第二十二、第二十三、第二十四及第二十五实施方式的一实施方式,该两个或更多个氨基酸位置包含一对两个氨基酸位置,其中该对两个氨基酸位置选自由下列组成的组:10与114、10与118、10与220、10与225、10与304、10与323、10与349、10与357、10与383、10与487、10与506、10与550、10与556、10与564、10与590、10与649、10与705、10与712、114与118、114与220、114与225、114与304、114与323、114与349、114与357、114与383、114与487、114与506、114与550、114与556、114与564、114与590、114与649、114与705、114与712、118与220、118与225、118与304、118与323、118与349、118与357、118与383、118与487、118与506、118与550、118与556、118与564、118与590、118与649、L118与705、118与712、220与225、220与304、220与323、220与349、220与357、220与383、220与487、220与506、220与550、220与556、220与564、220与590、220与649、220与705、220与712、225与304、225与323、225与349、225与357、225与383、225与487、225与506、225与550、225与556、225与564、225与590、225与649、225与705、225与712、304与323、304与349、304与357、304与383、304与487、304与506、304与550、304与556、304与564、304与590、304与649、304与705、304与712、323与349、323与357、323与383、323与487、323与506、323与550、323与556、323与564、323与590、323与649、323与705、323与712、349与357、349与383、349与487、349与506、349与550、349与556、349与564、349与590、349与649、349与705、349与712、357与383、357与487、357与506、357与550、357与556、357与564、357与590、357与649、357与705、357与712、383与487、383与506、383与550、383与556、383与564、383与590、383与649、383与705、383与712、487与506、487与550、487与556、487与564、487与590、487与649、487与705、487与712、506与550、506与556、506与564、506与590、506与649、506与705、506与712、550与556、550与564、550与590、550与649、550与705、550与712、556与564、556与590、556与649、556与705、556与712、564与590、564与649、564与705、564与712、590与649、590与705、590与712、649与712、649与705以及705与712,优选地,该对两个氨基酸位置选自由下列组成的组:V10与L114、V10与I118、V10与Y220、V10与N225、V10与A304、V10与T323、V10与F349、V10与G357、V10与P383、V10与Q487、V10与A506、V10与V550、V10与S556、V10与T564、V10与D590、V10与A649、V10与K705、V10与L712、L114与I118、L114与Y220、L114与N225、L114与A304、L114与T323、V10与F349、L114与G357、L114与P383、L114与Q487、L114与A506、L114与V550、L114与S556、L114与T564、L114与D590、L114与A649、L114与K705、L114与L712、I118与Y220、I118与N225、I118与A304、I118与T323、I118与F349、

I118与G357、I118与P383、I118与Q487、I118与A506、I118与V550、I118与S556、I118与T564、I118与D590、118与A649、L118与K705、I118与L712、Y220与N225、Y220与A304、Y220与T323、Y220与F349、Y220与G357、Y220与P383、Y220与Q487、Y220与A506、Y220与V550、Y220与S556、Y220与T564、Y220与D590、Y220与A649、Y220与K705、Y220与L712、N225与A304、N225与T323、N225与F349、N225与G357、N225与P383、N225与Q487、N225与A506、N225与V550、N225与S556、N225与T564、N225与D590、N225与A649、N225与K705、N225与L712、A304与T323、A304与F349、A304与G357、A304与P383、A304与Q487、A304与A506、A304与V550、A304与S556、A304与T564、A304与D590、A304与A649、A304与K705、A304与L712、T323与F349、T323与G357、T323与P383、T323与Q487、T323与A506、T323与V550、T323与S556、T323与T564、T323与D590、T323与A649、T323与K705、T323与L712、F349与G357、F349与P383、F349与Q487、F349与A506、F349与V550、F349与S556、F349与T564、F349与D590、F349与A649、F349与K705、F349与L712、G357与P383、G357与Q487、G357与A506、G357与V550、G357与S556、G357与T564、G357与D590、G357与A649、G357与K705、G357与L712、P383与Q487、P383与A506、P383与V550、P383与S556、P383与T564、P383与D590、P383与A649、P383与K705、P383与L712、Q487与A506、Q487与V550、Q487与S556、Q487与T564、Q487与D590、Q487与A649、Q487与K705、Q487与L712、A506与V550、A506与S556、A506与T564、A506与D590、A506与A649、A506与K705、A506与L712、V550与S556、V550与T564、V550与D590、V550与A649、V550与K705、V550与L712、S556与T564、S556与D590、S556与A649、S556与K705、S556与L712、T564与D590、T564与A649、T564与K705、T564与L712、D590与A649、D590与K705、D590与L712、A649与L712、A649与K705以及K705与L712。

[0054] 在第一方面的第二十七实施方式中,其也是该第一方面的第二十六实施方式的一实施方式,该对两个氨基酸位置选自由下列组成的组:10与114、10与220、10与383、10与506、10与705、10与712、114与118、114与220、114与225、114与304、114与225、114与349、114与357、114与383、114与487、114与506、114与550、114与556、114与564、114与590、114与649、114与705、114与712、118与225、118与304、118与323、118与349、118与357、118与383、118与487、118与550、118与556、118与564、118与590、118与649、118与712、220与383、220与506、220与705、220与712、225与304、225与323、225与349、225与357、225与383、225与487、225与550、225与556、225与564、225与590、225与649、225与712、304与323、304与349、304与357、304与383、304与487、304与550、304与556、304与564、304与590、304与649、304与712、323与349、323与357、323与383、323与487、323与550、323与556、323与564、323与590、323与649、323与712、349与357、349与383、349与487、349与550、349与556、349与564、349与590、349与649、349与712、357与383、357与487、357与550、357与556、357与564、357与590、357与649、357与705、357与712、383与487、383与506、383与550、383与556、383与564、383与590、383与649、383与705、383与712、487与550、487与556、487与564、487与590、487与649、487与712、506与705、506与712、550与556、550与564、550与590、550与649、550与712、556与564、556与590、556与649、556与712、564与590、564与649、564与712、590与649、590与712、649与712、705与712,且优选地该对两个氨基酸位置选自由下列组成的组:V10与L114、V10与Y220、V10与P383、V10与A506、V10与K705、V10与L712、L114与I118、L114与Y220、L114与N225、L114与A304、L114与T323、L114与F349、L114与G357、L114与P383、L114与Q487、L114与A506、L114与V550、L114与S556、L114与T564、L114与D590、L114与A649、L114与K705、L114与

L712、I118与N225、I118与A304、I118与T323、I118与F349、I118与G357、I118与P383、I118与Q487、I118与V550、I118与S556、I118与T564、I118与D590、118与A649、I118与L712、Y220与P383、Y220与A506、Y220与K705、Y220与L712、N225与A304、N225与T323、N225与F349、N225与G357、N225与P383、N225与Q487、N225与V550、N225与S556、N225与T564、N225与D590、N225与A649、N225与L712、A304与T323、A304与F349、A304与G357、A304与P383、A304与Q487、A304与V550、A304与S556、A304与T564、A304与D590、A304与A649、A304与L712、T323与F349、T323与G357、T323与P383、T323与Q487、T323与V550、T323与S556、T323与T564、T323与D590、T323与A649、T323与L712、F349与G357、F349与P383、F349与Q487、F349与V550、F349与S556、F349与T564、F349与D590、F349与A649、F349与L712、G357与P383、G357与Q487、G357与V550、G357与S556、G357与T564、G357与D590、G357与A649、G357与K705、G357与L712、P383与Q487、P383与A506、P383与V550、P383与S556、P383与T564、P383与D590、P383与A649、P383与K705、P383与L712、Q487与V550、Q487与S556、Q487与T564、Q487与D590、Q487与A649、Q487与L712、A506与K705、A506与L712、V550与S556、V550与T564、V550与D590、V550与A649、V550与L712、S556与T564、S556与D590、S556与A649、S556与L712、T564与D590、T564与A649、T564与L712、D590与A649、D590与L712、A649与L712、K705与L712。

[0055] 在第一方面的第二十八实施方式中,其也是该第一方面的第二十七实施方式的一实施方式,该对两个氨基酸位置选自由下列组成的组:10与114、10与712、114与118、114与304、114与357、114与383、114与590、114与712、118与304、118与357、118与383、118与556、118与564、118与590、118与712、225与304、225与383、225与487、225与550、225与556、225与590、304与323、304与357、304与383、304与487、304与556、304与564、304与590、304与712、323与357、323与487、323与556、323与564、323与590、323与649、349与383、349与590、357与383、357与590、357与705、357与712、383与487、383与550、383与556、383与564、383与590、383与649、383与712、487与564、487与590、487与649、550与590、556与564、556与590、556与649、564与590、564与712、590与649、590与712、以及649与712,且优选地该对两个氨基酸位置选自由下列组成的组:V10与L114、V10与L712、L114与I118、L114与A304、L114与G357、L114与P383、L114与D590、L114与L712、I118与A304、I118与G357、I118与P383、I118与S556、I118与T564、I118与D590、I118与L712、N225与A304、N225与P383、N225与Q487、N225与V550、N225与S556、N225与D590、A304与T323、A304与G357、A304与P383、A304与Q487、A304与S556、A304与T564、A304与D590、A304与L712、T323与G357、T323与Q487、T323与S556、T323与T564、T323与D590、T323与A649、F349与P383、F349与D590、G357与P383、G357与D590、G357与K705、G357与L712、P383与Q487、P383与V550、P383与S556、P383与T564、P383与D590、P383与A649、P383与L712、Q487与T564、Q487与D590、Q487与A649、V550与D590、S556与T564、S556与D590、S556与A649、T564与D590、T564与L712、D590与A649、D590与L712以及A649与L712。

[0056] 在第一方面的第二十九实施方式中,其也是该第一方面的第二十八实施方式的一实施方式,该对两个氨基酸位置选自由下列组成的组:114与118、114与304、114与357、114与383、114与590、114与712、118与304、118与357、118与383、118与556、118与564、118与590、118与712、225与304、225与383、225与487、225与550、225与556、225与590、304与323、304与357、304与383、304与487、304与556、304与564、304与590、304与712、323与357、323与487、323与556、323与564、323与590、323与649、349与383、349与590、357与383、357与590、

357与705、357与712、383与487、383与550、383与556、383与564、383与590、383与649、383与712、487与564、487与590、487与649、550与590、556与564、556与590、556与649、564与590、564与712、590与649、590与712以及649与712,且优选地该对两个氨基酸位置选自由下列组成的组:L114与I118、L114与A304、L114与G357、L114与P383、L114与D590、L114与L712、I118与A304、I118与G357、I118与P383、I118与S556、I118与T564、I118与D590、I118与L712、N225与A304、N225与P383、N225与Q487、N225与V550、N225与S556、N225与D590、A304与T323、A304与G357、A304与P383、A304与Q487、A304与S556、A304与T564、A304与D590、A304与L712、T323与G357、T323与Q487、T323与S556、T323与T564、T323与D590、T323与A649、F349与P383、F349与D590、G357与P383、G357与D590、G357与K705、G357与L712、P383与Q487、P383与V550、P383与S556、P383与T564、P383与D590、P383与A649、P383与L712、Q487与T564、Q487与D590、Q487与A649、V550与D590、S556与T564、S556与D590、S556与A649、T564与D590、T564与L712、D590与A649、D590与L712以及A649与L712。

[0057] 在第一方面的另一优选实施方式中,其也是该第一方面的任何其它的前述实施方式的一实施方式,该对两个氨基酸位置选自由下列组成的组:114与118、114与304、114与357、114与383、114与590、114与712、118与304、118与357、118与383、118与556、118与564、118与590、118与712、225与304、225与383、225与487、225与550、225与556、225与590、304与323、304与357、304与383、304与487、304与556、304与564、304与590、304与712、323与357、323与487、323与556、323与564、323与590、349与383、349与590、357与383、357与590、357与705、357与712、383与487、383与550、383与556、383与564、383与590、383与712、487与564、487与590、550与590、556与564、556与590、564与590、564与712以及590与712,且优选地该对两个氨基酸位置选自由下列组成的组:L114与I118、L114与A304、L114与G357、L114与P383、L114与D590、L114与L712、I118与A304、I118与G357、I118与P383、I118与S556、I118与T564、I118与D590、I118与L712、N225与A304、N225与P383、N225与Q487、N225与V550、N225与S556、N225与D590、A304与T323、A304与G357、A304与P383、A304与Q487、A304与S556、A304与T564、A304与D590、A304与L712、T323与G357、T323与Q487、T323与S556、T323与T564、T323与D590、F349与P383、F349与D590、G357与P383、G357与D590、G357与K705、G357与L712、P383与Q487、P383与V550、P383与S556、P383与T564、P383与D590、P383与L712、Q487与T564、Q487与D590、V550与D590、S556与T564、S556与D590、T564与D590、T564与L712以及D590与L712。

[0058] 在第一方面的第三十实施方式中,其也是该第一方面的第二十九实施方式的一实施方式,该对两个氨基酸位置选自由下列组成的组:118与383、118与556、118与564、118与590、225与304、225与383、225与487、225与550、225与556、225与590、304与323、304与383、304与487、304与556、304与564、304与590、323与357、323与487、323与556、323与564、323与590、323与649、349与383、349与590、357与383、357与590、383与487、383与550、383与556、383与564、383与590、383与649、383与712、487与564、487与590、487与649、550与590、556与564、556与590、556与649、564与590、564与712、590与649、590与712、649与712以及705与712,且优选地该对两个氨基酸位置选自由下列组成的组:I118与P383、I118与S556、I118与T564、I118与D590、N225与A304、N225与P383、N225与Q487、N225与V550、N225与S556、N225与D590、A304与T323、A304与P383、A304与Q487、A304与S556、A304与T564、A304与D590、T323与G357、T323与Q487、T323与S556、T323与T564、T323与D590、T323与A649、F349与P383、F349与

D590、G357与P383、G357与D590、P383与Q487、P383与V550、P383与S556、P383与T564、P383与D590、P383与A649、P383与L712、Q487与T564、Q487与D590、Q487与A649、V550与D590、S556与T564、S556与D590、S556与A649、T564与D590、T564与L712、D590与A649、D590与L712、A649与L712以及K705与L712。

[0059] 在第一方面的另一优选实施方式中,其也是该第一方面的任何其它的前述实施方式的一实施方式,该对两个氨基酸位置选自由下列组成的组:118与383、118与556、118与564、118与590、225与304、225与383、225与487、225与550、225与556、225与590、304与323、304与383、304与487、304与556、304与564、304与590、323与357、323与487、323与556、323与564、323与590、349与383、349与590、357与383、357与590、383与487、383与550、383与556、383与564、383与590、383与712、487与564、487与590、550与590、556与564、556与590、564与590、564与712、590与712以及705与712且优选地该对两个氨基酸位置选自由下列组成的组:I118与P383、I118与S556、I118与T564、I118与D590、N225与A304、N225与P383、N225与Q487、N225与V550、N225与S556、N225与D590、A304与T323、A304与P383、A304与Q487、A304与S556、A304与T564、A304与D590、T323与G357、T323与Q487、T323与S556、T323与T564、T323与D590、F349与P383、F349与D590、G357与P383、G357与D590、P383与Q487、P383与V550、P383与S556、P383与T564、P383与D590、P383与L712、Q487与T564、Q487与D590、V550与D590、S556与T564、S556与D590、T564与D590、T564与L712、D590与L712以及K705与L712。

[0060] 在第一方面的第三十一实施方式中,其也是该第一方面的第二十九实施方式的一实施方式,该对两个氨基酸位置选自由下列组成的组:114与118、114与383、114与712、118与383、118与556、118与590、118与712、225与304、225与383、225与550、225与590、304与383、304与556、304与590、323与556、323与590、323与649、349与383、349与590、357与383、357与590、383与487、383与550、383与556、383与564、383与590、383与649、383与712、556与564、556与590、564与590、564与712、590与649以及590与712,且优选地该对两个氨基酸位置选自由下列组成的组:L114与I118、L114与P383、L114与L712、I118与P383、I118与S556、I118与D590、I118与L712、N225与A304、N225与P383、N225与V550、N225与D590、A304与P383、A304与S556、A304与D590、T323与S556、T323与D590、T323与A649、F349与P383、F349与D590、G357与P383、G357与D590、P383与Q487、P383与V550、P383与S556、P383与T564、P383与D590、P383与A649、P383与L712、S556与T564、S556与D590、T564与D590、T564与L712、D590与A649以及D590与L712。

[0061] 在第一方面的另一优选实施方式中,其也是该第一方面的任何其它的前述实施方式的一实施方式,该对两个氨基酸位置选自由下列组成的组:114与118、114与383、114与712、118与383、118与556、118与590、118与712、225与304、225与383、225与550、225与590、304与383、304与556、304与590、323与556、323与590、349与383、349与590、357与383、357与590、383与487、383与550、383与556、383与564、383与590、383与712、556与564、556与590、564与590、564与712以及590与712且优选地该对两个氨基酸位置选自由下列组成的组:L114与I118、L114与P383、L114与L712、I118与P383、I118与S556、I118与D590、I118与L712、N225与A304、N225与P383、N225与V550、N225与D590、A304与P383、A304与S556、A304与D590、T323与S556、T323与D590、F349与P383、F349与D590、G357与P383、G357与D590、P383与Q487、P383与V550、P383与S556、P383与T564、P383与D590、P383与L712、S556与T564、S556与D590、

T564与D590、T564与L712以及D590与L712。

[0062] 在第一方面的第三十二实施方式中,其也是该第一方面的第二十九实施方式的一实施方式,该对两个氨基酸位置选自由下列组成的组:114与118、114与304、114与357、114与383、114与590、114与712、118与304、118与357、118与383、118与556、118与590、118与712、225与383、304与357、304与383、304与590、304与712、323与590、349与383、349与590、357与383、357与590、357与705、357与712、383与487、383与550、383与556、383与564、383与590、383与649、383与712、556与590、564与590、590与649以及590与712,且优选地该对两个氨基酸位置选自由下列组成的组:L114与I118、L114与A304、L114与G357、L114与P383、L114与D590、L114与L712、I118与A304、I118与G357、I118与P383、I118与S556、I118与D590、I118与L712、N225与P383、A304与G357、A304与P383、A304与D590、A304与L712、T323与D590、F349与P383、F349与D590、G357与P383、G357与D590、G357与K705、G357与L712、P383与Q487、P383与V550、P383与S556、P383与T564、P383与D590、P383与A649、P383与L712、S556与D590、T564与D590、D590与A649以及D590与L712。

[0063] 在第一方面的另一优选实施方式中,其也是该第一方面的任何其它的前述实施方式的一实施方式,该对两个氨基酸位置选自由下列组成的组:114与118、114与304、114与357、114与383、114与590、114与712、118与304、118与357、118与383、118与556、118与590、118与712、225与383、304与357、304与383、304与590、304与712、323与590、349与383、349与590、357与383、357与590、357与705、357与712、383与487、383与550、383与556、383与564、383与590、383与712、556与590、564与590以及590与712,且优选地该对两个氨基酸位置选自由下列组成的组:L114与I118、L114与A304、L114与G357、L114与P383、L114与D590、L114与L712、I118与A304、I118与G357、I118与P383、I118与S556、I118与D590、I118与L712、N225与P383、A304与G357、A304与P383、A304与D590、A304与L712、T323与D590、F349与P383、F349与D590、G357与P383、G357与D590、G357与K705、G357与L712、P383与Q487、P383与V550、P383与S556、P383与T564、P383与D590、P383与L712、S556与D590、T564与D590以及D590与L712。

[0064] 在第一方面的另一优选实施方式中,其也是该第一方面的任何其它的前述实施方式的一实施方式,该对两个氨基酸位置选自由下列组成的组:118与383、118与590、225与383、225与590、304与383、304与590、323与590、349与383、349与590、357与383、357与590、383与487、383与550、383与556、383与564、383与590、383与649、383与712、487与590、550与590、556与590、564与590、590与649、590与712,且优选地该对两个氨基酸位置选自由下列组成的组:I118与P383、I118与D590、N225与P383、N225与D590、A304与P383、A304与D590、T323与D590、F349与P383、F349与D590、G357与P383、G357与D590、P383与Q487、P383与V550、P383与S556、P383与T564、P383与D590、P383与A649、P383与L712、Q487与D590、V550与D590、S556与D590、T564与D590、D590与A649、D590与L712。

[0065] 在第一方面的第三十三实施方式中,其也是该第一方面的第七、第八、第九、第十、第十一、第十二、第十三、第十四、第十五、第十六、第十七、第十八、第十九、第二十、第二十一、第二十二、第二十三、第二十四、第二十五、第二十六、第二十七、第二十八、第二十九、第三十、第三十一及第三十二实施方式或前述的任何其它的一实施方式,优选第一方面的第二十六、第二十七、第二十八、第二十九、第三十、第三十一及第三十二实施例或前述的任何其它的实施方式,该海藻糖磷酸化酶的氨基酸序列在至少一个或更多个另外的氨基酸位置

处包含氨基酸取代,其中该一个或更多个另外的氨基酸位置选自由下列SEQ ID NO:1的氨基酸位置组成的组:712、383、10、114、118、192、197、220、225、304、306、318、323、339、349、357、459、476、481、484、487、488、506、511、526、530、532、533、537、550、556、564、590、649、667、703以及705,优选地,除了在两个氨基酸位置处的取代之外,该海藻糖磷酸化酶的氨基酸序列在至少一个或更多个另外的氨基酸位置处包含氨基酸取代,其中该一个或更多个另外的氨基酸位置是独立且各别选自氨基酸位置选自由下列SEQ ID NO:1的氨基酸位置组成的组712、383、10、114、118、192、197、220、225、304、306、318、323、339、349、357、459、476、481、484、487、488、506、511、526、530、532、533、537、550、556、564、590、649、667、703以及705。

[0066] 在第一方面的第三十四实施方式中,其也是该第一方面的第三十三实施方式的一实施方式,该一个或更多个另外的氨基酸位置选自由下列SEQ ID NO:1的氨基酸位置组成的组:L712、P383、V10、L114、I118、S192、S197、Y220、N225、A304、D306、P318、T323、L339、F349、G357、A459、Q476、E481、A484、Q487、K488、A506、A511、R526、E530、G532、D533、D537、V550、S556、T564、D590、A649、R667、A703与K705,优选地该一个或更多个另外的氨基酸位置是独立并各别地选自由下列SEQ ID NO:1的氨基酸位置组成的组:L712、P383、V10、L114、I118、S192、S197、Y220、N225、A304、D306、P318、T323、L339、F349、G357、A459、Q476、E481、A484、Q487、K488、A506、A511、R526、E530、G532、D533、D537、V550、S556、T564、D590、A649、R667、A703以及K705。

[0067] 在第一方面的第三十五实施方式中,其也是该第一方面的第三十三实施方式的一实施方式,该一个或更多个另外的氨基酸位置选自由下列SEQ ID NO:1的氨基酸位置组成的组:712、383、10、114、118、220、225、304、318、323、349、357、481、487、488、506、511、550、556、564、590、649、703以及705,优选地该一个或更多个另外的氨基酸位置是独立并各别地选自由下列SEQ ID NO:1的氨基酸位置组成的组:712、383、10、114、118、220、225、304、318、323、349、357、481、487、488、506、511、550、556、564、590、649、703以及705。

[0068] 在第一方面的第三十六实施方式中,其也是该第一方面的第三十五实施方式的一实施方式,该一个或更多个另外的氨基酸位置选自由下列SEQ ID NO:1的氨基酸位置组成的组:L712、P383、V10、L114、I118、Y220、N225、A304、P318、T323、F349、G357、E481、Q487、K488、A506、A511、V550、S556、T564、D590、A649、A703以及K705,优选地该一个或更多个另外的氨基酸位置是独立并各别地选自由下列SEQ ID NO:1的氨基酸位置组成的组:L712、P383、V10、L114、I118、Y220、N225、A304、P318、T323、F349、G357、E481、Q487、K488、A506、A511、V550、S556、T564、D590、A649、A703以及K705。

[0069] 在第一方面的第三十七实施方式中,其也是该第一方面的第三十三实施方式的一实施方式,该一个或更多个另外的氨基酸位置选自由下列SEQ ID NO:1的氨基酸位置组成的组:712、383、10、114、118、225、304、323、349、357、487、550、556、564、590以及649,优选地该一个或更多个另外的氨基酸位置是独立并各别地选自由下列SEQ ID NO:1的氨基酸位置组成的组:712、383、10、114、118、225、304、323、349、357、487、550、556、564、590以及649。

[0070] 在第一方面的第三十八实施方式中,其也是该第一方面的第三十七实施方式的一实施方式,该一个或更多个另外的氨基酸位置选自由下列SEQ ID NO:1的氨基酸位置组成的组:L712、P383、V10、L114、I118、N225、A304、T323、F349、G357、Q487、V550、S556、T564、

D590以及A649,优选地该一个或更多个另外的氨基酸位置是独立并各别地选自由下列SEQ ID NO:1的氨基酸位置组成的组:L712、P383、V10、L114、I118、N225、A304、T323、F349、G357、Q487、V550、S556、T564、D590以及A649。

[0071] 在第一方面的第三十九实施方式中,其也是该第一方面的第三十三实施方式的一实施方式,该一个或更多个另外的氨基酸位置选自由下列SEQ ID NO:1的氨基酸位置组成的组:712、383、114、118、225、304、323、349、357、487、550、556、564、590以及649,优选地该一个或更多个另外的氨基酸位置是独立并各别地选自由下列SEQ ID NO:1的氨基酸位置组成的组:712、383、114、118、225、304、323、349、357、487、550、556、564、590以及649。

[0072] 在第一方面的第四十实施方式中,其也是该第一方面的第三十九实施方式的一实施方式,该一个或更多个另外的氨基酸位置选自由下列SEQ ID NO:1的氨基酸位置组成的组:L712、P383、L114、I118、N225、A304、T323、F349、G357、Q487、V550、S556、T564、D590以及A649,优选地该一个或更多个另外的氨基酸位置是独立并各别地选自由下列SEQ ID NO:1的氨基酸位置组成的组:L712、P383、L114、I118、N225、A304、T323、F349、G357、Q487、V550、S556、T564、D590以及A649。

[0073] 在第一方面的第四十一实施方式中,其也是该第一方面的第三十三实施方式的一实施方式,该一个或更多个另外的氨基酸位置选自由下列SEQ ID NO:1的氨基酸位置组成的组:712、383、114、118、225、304、357、487、556以及590,优选地该一个或更多个另外的氨基酸位置是独立并各别地选自由下列SEQ ID NO:1的氨基酸位置组成的组:712、383、114、118、225、304、357、487、556以及590。

[0074] 在第一方面的第四十二实施方式中,其也是该第一方面的第四十一实施方式的一实施方式,该一个或更多个另外的氨基酸位置选自由下列SEQ ID NO:1的氨基酸位置组成的组:L712、P383、L114、I118、N225、A304、G357、Q487、S556以及D590,优选地该一个或更多个另外的氨基酸位置是独立并各别地选自由下列SEQ ID NO:1的氨基酸位置组成的组:L712、P383、L114、I118、N225、A304、G357、Q487、S556以及D590。

[0075] 在第一方面的另一优选实施方式中,其也是第一方面的任何其它前述实施方式中的实施方式,该海藻糖磷酸化酶的氨基酸序列包含在SEQ ID NO:1的氨基酸位置383以及590处的氨基酸取代,优选在SEQ ID NO:1的氨基酸位置P383以及D590处,且其中该海藻糖磷酸化酶的氨基酸序列在下列SEQ ID NO:1的氨基酸位置处包含进一步的氨基酸取代

[0076] (i)114、118、304、357以及712、优选L114、I118、A304、G357以及L712,或

[0077] (ii)114、118、304、357、550、556以及712、优选L114、I118、A304、G357、V550、S556以及L712,或

[0078] (iii)114、118、225、304、357、487、564以及712、优选L114、I118、N225、A304、G357、Q487、T564以及L712,或

[0079] (iv)114、118、304、323、357、550、564以及712、优选L114、I118、A304、T323、G357、V550、T564以及L712,或

[0080] (v)114、118、225、304、323、357、487以及712、优选L114、I118、N225、A304、T323、G357、Q487以及L712,或

[0081] (vi)114、118、225、304、357、487、550、556以及712、优选L114、I118、N225、A304、G357、Q487、V550、S556以及L712,或

[0082] (vii)114、118、225、304、357、487、550、564以及712、优选L114、I118、N225、A304、G357、Q487、V550、T564以及L712,或

[0083] (viii)114、118、225、304、357、550、556、564以及712、优选L114、I118、N225、A304、G357、V550、S556、T564以及L712,或

[0084] (ix)114、118、225、304、357、550、564以及712、优选L114、I118、N225、A304、G357、V550、T564以及L712,或

[0085] (x)114、118、304、323、357、550、556、564以及712、优选L114、I118、A304、T323、G357、V550、S556、T564以及L712,或

[0086] (xi)114、118、304、323、357、487、550、649以及712、优选L114、I118、A304、T323、G357、Q487、V550、A649以及L712,或

[0087] (xii)114、118、225、304、357、487、550、556、564以及712、优选L114、I118、N225、A304、G357、Q487、V550、S556、T564以及L712,或

[0088] (xiii)114、118、225、304、357、550、556、564、649以及712、优选L114、I118、N225、A304、G357、V550、S556、T564、A649以及L712,或

[0089] (xiv)114、118、225、304、323、357、487、550、564以及712、优选L114、I118、N225、A304、T323、G357、Q487、V550、T564以及L712,或

[0090] (xv)114、118、225、304、323、357、487、550、649以及712、优选L114、I118、N225、A304、T323、G357、Q487、V550、A649以及L712,或

[0091] (xvi)114、118、225、304、323、357、487、550、556以及712、优选L114、I118、N225、A304、T323、G357、Q487、V550、S556以及L712,或

[0092] (xvii)114、118、225、304、323、357、550、556、564以及712、优选L114、I118、N225、A304、T323、G357、V550、S556、T564以及L712,或

[0093] (xviii)114、118、304、323、349、357、487、550、649以及712、优选L114、I118、A304、T323、F349、G357、Q487、V550、A649以及L712,或

[0094] (xix)114、118、304、323、357、487、550、556、564以及712、优选L114、I118、A304、T323、G357、Q487、V550、S556、T564以及L712,或

[0095] (xx)114、118、304、357、487、550、556、564、649以及712、优选L114、I118、A304、G357、Q487、V550、S556、T564、A649以及L712,或

[0096] (xxi)114、118、225、304、323、349、357、550、556、649以及712、优选L114、I118、N225、A304、T323、F349、G357、V550、S556、A649以及L712,或

[0097] (xxii)114、118、225、304、323、357、487、550、556、649以及712、优选L114、I118、N225、A304、T323、G357、Q487、V550、S556、A649以及L712,或

[0098] (xxiii)114、118、225、304、349、357、487、550、556、564以及712、优选L114、I118、N225、A304、F349、G357、Q487、V550、S556、T564以及L712,或

[0099] (xxiv)114、118、225、304、349、357、487、550、564、649以及712、优选L114、I118、N225、A304、F349、G357、Q487、V550、T564、A649以及L712,或

[0100] (xxv)114、118、225、304、323、349、357、487、550、556、564、649以及712、优选L114、I118、N225、A304、T323、F349、G357、Q487、V550、S556、T564、A649以及L712,或

[0101] (xxvi)114、118、225、304、357、487、550、556、564、649以及712、优选L114、I118、

N225、A304、G357、Q487、V550、S556、T564、A649以及L712,或

[0102] (xxvii)114、118、304、323、357、487、550、556、564、649以及712、优选L114、I118、A304、T323、G357、Q487、V550、S556、T564、A649以及L712,或

[0103] (xxviii)114、118、225、304、323、357、487、550、556、564、649以及712、优选L114、I118、N225、A304、T323、G357、Q487、V550、S556、T564、A649以及L712,或

[0104] (xxix)114、118、225、304、323、349、357、487、550、556、564、649以及712、优选L114、I118、N225、A304、T323、F349、G357、Q487、V550、S556、T564、A649以及L712,或

[0105] (xxx)114、225、304、323、357、487、550、556、564、649以及712、优选L114、N225、A304、T323、G357、Q487、V550、S556、T564、A649以及L712,或

[0106] (xxxi)114、118、225、323、357、487、550、556、564、649以及712、优选L114、I118、N225、T323、G357、Q487、V550、S556、T564、A649以及L712,或

[0107] (xxxii)114、118、225、304、323、349、487、550、556、564、649以及712、优选L114、I118、N225、A304、T323、F349、Q487、V550、S556、T564、A649以及L712,或

[0108] (xxxiii)114、118、225、304、323、349、357、487、550、556、564以及649、优选L114、I118、N225、A304、T323、F349、G357、Q487、V550、S556、T564以及A649.

[0109] 在第一方面的另一优选实施方式,其也是第一方面的任何其它前述实施方式中的实施方式,该海藻糖磷酸化酶的氨基酸序列在选自由下列SEQ ID NO:1的氨基酸位置组成的组处包含一个或更多个另外的氨基酸取代:712、10、114、118、192、197、220、225、304、306、318、323、339、349、357、459、476、481、484、487、488、506、511、526、530、532、533、537、550、556、564、649、667、703以及705,优选选自由下列SEQ ID NO:1的位置组成的组:L712、V10、L114、I118、S192、S197、Y220、N225、A304、D306、P318、T323、L339、F349、G357、A459、Q476、E481、A484、Q487、K488、A506、A511、R526、E530、G532、D533、D537、V550、S556、T564、A649、R667、A703以及K705。

[0110] 在第一方面的另一优选实施方式,其也是第一方面的任何其它前述实施方式中的实施方式,该海藻糖磷酸化酶的氨基酸序列在SEQ ID NO:1的三个氨基酸位置处包含氨基酸取代,优选在SEQ ID NO:1的四个氨基酸位置处,更佳在SEQ ID NO:1的五个氨基酸位置处,且最佳在SEQ ID NO:1的六个氨基酸位置处,其中SEQ ID NO:1的每个及任何氨基酸位置选自由712、383、114、118、225、304、357、487、556以及590组成的组。

[0111] 在第一方面的另一优选实施方式,其也是第一方面的任何其它前述实施方式中的实施方式,该海藻糖磷酸化酶的氨基酸序列在SEQ ID NO:1的三个氨基酸位置处包含氨基酸取代,优选在SEQ ID NO:1的四个氨基酸位置处,更佳在SEQ ID NO:1的五个氨基酸位置处,且最佳在SEQ ID NO:1的六个氨基酸位置处,其中SEQ ID NO:1的每个及任何氨基酸位置选自由L712、P383、L114、I118、N225、A304、G357、Q487、S556以及D590组成的组。

[0112] 在第一方面的第四十三实施方式中,其也是该第一方面的第一、第二、第三、第四、第五、第六、第七、第八、第九、第十、第十一、第十二、第十三、第十四、第十五、第十六、第十七、第十八、第十九、第二十、第二十一、第二十二、第二十三、第二十四、第二十五、第二十六、第二十七、第二十八、第二十九、第三十、第三十一、第三十二、第三十三、第三十四、第三十五、第三十六、第三十七、第三十八、第三十九、第四十、第四十一及第四十二实施方式或前述的任何其它的一实施方式,优选第一方面的第二十六、第二十七、第二十八、第二十九、

第三十、第三十一、第三十二、第三十三、第三十四、第三十五、第三十六、第三十七、第三十八、第三十九、第四十、第四十一及第四十二实施例或前述的任何其它的实施方式，更优选第一方面的第二十九、第三十、第三十一、第三十二、第三十三、第三十四、第三十五、第三十六、第三十七、第三十八、第三十九、第四十、第四十一及第四十二实施例或前述的任何其它的实施方式，该海藻糖磷酸化酶的氨基酸序列在SEQ ID NO:1的三个氨基酸位置处包含氨基酸取代，优选在SEQ ID NO:1的四个氨基酸位置处，更佳在SEQ ID NO:1的五个氨基酸位置处，且最佳在SEQ ID NO:1的六个氨基酸位置处，其中SEQ ID NO:1的每个及任何氨基酸位置选自由712、383、114、118、304以及357组成的组。

[0113] 在第一方面的第四十四实施方式中，其也是该第一方面的第四十三实施方式中的实施方式，该海藻糖磷酸化酶的氨基酸序列在SEQ ID NO:1的三个氨基酸位置处包含氨基酸取代，优选在SEQ ID NO:1的四个氨基酸位置处，更佳在SEQ ID NO:1的五个氨基酸位置处，且最佳在SEQ ID NO:1的六个氨基酸位置处，其中SEQ ID NO:1的每个及任何氨基酸位置选自由L712、P383、L114、I118、A304以及G357组成的组。

[0114] 在第一方面的第四十五实施方式中，其也是该第一方面的第四十三及第四十四实施方式中的实施方式，该海藻糖磷酸化酶的氨基酸序列在SEQ ID NO:1的四个氨基酸位置处包含氨基酸取代，其中SEQ ID NO:1的每个及任何氨基酸位置选自由712、383、114、118、304以及357组成的组。

[0115] 在第一方面的第四十六实施方式中，其也是该第一方面的第四十三及第四十四实施方式中的实施方式，该海藻糖磷酸化酶的氨基酸序列在SEQ ID NO:1的四个氨基酸位置处包含氨基酸取代，其中SEQ ID NO:1的每个及任何氨基酸位置选自由L712、P383、L114、I118、A304以及G357组成的组。

[0116] 在第一方面的第四十七实施方式中，其也是该第一方面的第四十三、第四十四、第四十五及第四十六实施方式中的实施方式，该海藻糖磷酸化酶的氨基酸序列在SEQ ID NO:1的五个氨基酸位置处包含氨基酸取代，其中SEQ ID NO:1的每个及任何氨基酸位置选自由712、383、114、118、304以及357组成的组。

[0117] 在第一方面的第四十八实施方式中，其也是该第一方面的第四十三、第四十四、第四十五及第四十六实施方式中的实施方式，该海藻糖磷酸化酶的氨基酸序列在SEQ ID NO:1的五个氨基酸位置处包含氨基酸取代，其中SEQ ID NO:1的每个及任何氨基酸位置选自由L712、P383、L114、I118、A304以及G357组成的组。

[0118] 在第一方面的第四十九实施方式中，其也是该第一方面的第四十三、第四十四、第四十五、第四十六、第四十七及第四十八实施方式中的实施方式，该海藻糖磷酸化酶的氨基酸序列在SEQ ID NO:1的六个氨基酸位置处包含氨基酸取代，其中SEQ ID NO:1的每个及任何氨基酸位置选自由712、383、114、118、304以及357组成的组。

[0119] 在第一方面的第五十实施方式中，其也是该第一方面的第四十三、第四十四、第四十五、第四十六、第四十七及第四十八实施方式中的实施方式，该海藻糖磷酸化酶的氨基酸序列在SEQ ID NO:1的六个氨基酸位置处包含氨基酸取代，其中SEQ ID NO:1的每个及任何氨基酸位置选自由L712、P383、L114、I118、A304以及G357组成的组。

[0120] 在第一方面的另一优选实施方式，其也是第一方面的任何其它前述实施方式中的实施方式，该海藻糖磷酸化酶的氨基酸序列在SEQ ID NO:1的三个氨基酸位置处包含氨基

酸取代,优选在SEQ ID NO:1的四个氨基酸位置处,更佳在SEQ ID NO:1的五个氨基酸位置处,且最佳在SEQ ID NO:1的六个氨基酸位置处,其中SEQ ID NO:1的每个及任何氨基酸位置选自由712、383、118、225、304、349、357、487、556、564以及590组成的组。

[0121] 在第一方面的另一优选实施方式,其也是第一方面的任何其它前述实施方式中的实施方式,该海藻糖磷酸化酶的氨基酸序列在SEQ ID NO:1的三个氨基酸位置处包含氨基酸取代,优选在SEQ ID NO:1的四个氨基酸位置处,更佳在SEQ ID NO:1的五个氨基酸位置处,且最佳在SEQ ID NO:1的六个氨基酸位置处,其中SEQ ID NO:1的每个及任何氨基酸位置选自由712、383、225、304、349、556以及590组成的组。

[0122] 在第一方面的另一优选实施方式,其也是第一方面的任何其它前述实施方式中的实施方式,该海藻糖磷酸化酶的氨基酸序列在SEQ ID NO:1的三个氨基酸位置处包含氨基酸取代,优选在SEQ ID NO:1的四个氨基酸位置处,更佳在SEQ ID NO:1的五个氨基酸位置处,其中SEQ ID NO:1的每个及任何氨基酸位置选自由383、225、304、556以及590组成的组。

[0123] 在第一方面的另一优选实施方式,其也是第一方面的任何其它前述实施方式中的实施方式,该海藻糖磷酸化酶的氨基酸序列在SEQ ID NO:1的三个氨基酸位置处包含氨基酸取代,其中SEQ ID NO:1的每个及任何氨基酸位置选自由383、556以及590组成的组。

[0124] 在第一方面的另一优选实施方式,其也是第一方面的任何其它前述实施方式中的实施方式,该海藻糖磷酸化酶的氨基酸序列在SEQ ID NO:1的三个氨基酸位置处包含氨基酸取代,优选在SEQ ID NO:1的四个氨基酸位置处,更佳在SEQ ID NO:1的五个氨基酸位置处,且最佳在SEQ ID NO:1的六个氨基酸位置处,其中SEQ ID NO:1的每个及任何氨基酸位置选自由L712、P383、I118、N225、A304、F349、G357、Q487、S556、T564以及D590组成的组。

[0125] 在第一方面的第五十一实施方式中,其也是该第一方面的第三十三、第三十四、第三十五、第三十六、第三十七、第三十八、第三十九、第四十、第四十一、第四十二、第四十三、第四十四、第四十五、第四十六、第四十七、第四十八、第四十九、第五十实施方式或前述的任何其它的一实施方式,该海藻糖磷酸化酶的氨基酸序列包含

[0126] (a)氨基酸取代,在SEQ ID NO:1的四个氨基酸位置712、383、114与118,和/或SEQ ID NO:1的位置383、487、556以及590,和/或SEQ ID NO:1的位置383、225、556以及590;或

[0127] (b)氨基酸取代,在SEQ ID NO:1的五个氨基酸位置712、383、114、118与304,和/或SEQ ID NO:1的位置712、383、114、118与357,和/或SEQ ID NO:1的位置383、225、304、556以及590,和/或SEQ ID NO:1的位置383、225、487、556以及590;或

[0128] (c)氨基酸取代,在SEQ ID NO:1的六个氨基酸位置712、383、114、118、304与357,和/或SEQ ID NO:1的位置383、225、304、487、556以及590;或

[0129] (d)氨基酸取代,在SEQ ID NO:1的三个氨基酸位置383、556以及590。

[0130] 在第一方面的第五十二实施方式中,其也是该第一方面的第三十三、第三十四、第三十五、第三十六、第三十七、第三十八、第三十九、第四十、第四十一、第四十二、第四十三、第四十四、第四十五、第四十六、第四十七、第四十八、第四十九、第五十实施方式或前述的任何其它的一实施方式,该海藻糖磷酸化酶的氨基酸序列包含

[0131] (a)氨基酸取代,在SEQ ID NO:1的四个氨基酸位置712、383、114与118,和/或SEQ ID NO:1的位置383、487、556以及590,和/或SEQ ID NO:1的位置383、225、556以及590,且优选在SEQ ID NO:1的四个氨基酸位置L712、P383、L114与I118,和/或SEQ ID NO:1的位置

P383、Q487、S556以及D590,和/或SEQ ID NO:1的位置P383、N225、S556以及D590;或

[0132] (b)氨基酸取代,在SEQ ID NO:1的五个氨基酸位置712、383、114、I118与304,和/或SEQ ID NO:1的位置712、383、114、118与357,和/或SEQ ID NO:1的位置383、225、304、556以及590,和/或SEQ ID NO:1的位置383、225、487、556以及590,且优选在SEQ ID NO:1的五个氨基酸位置L712、P383、L114、I118与A304,和/或SEQ ID NO:1的位置L712、P383、L114、I118与G357,和/或SEQ ID NO:1的位置P383、N225、A304、S556以及D590,和/或SEQ ID NO:1的位置P383、N225、Q487、S556以及D590;或

[0133] (c)氨基酸取代,在SEQ ID NO:1的六个氨基酸位置712、383、114、118、304与357,和/或SEQ ID NO:1的位置383、225、304、487、556以及590,且优选在SEQ ID NO:1的六个氨基酸位置L712、P383、L114、I118、A304与G357,和/或SEQ ID NO:1的位置P383、N225、A304、Q487、S556以及D590;或

[0134] (d)氨基酸取代,在SEQ ID NO:1的三个氨基酸位置383、556以及590,且优选在SEQ ID NO:1的三个氨基酸位置P383、S556以及D590。

[0135] 在第一方面的第五十三实施方式中,其也是该第一方面的第四十三、第四十四、第四十五、第四十六、第四十七、第四十八、第四十九、第五十、第五十一及第五十二实施方式或前述的任何其它的一实施方式,该海藻糖磷酸化酶的氨基酸序列包含如SEQ ID NO:14所示的氨基酸序列。

[0136] 在第一方面的第五十四实施方式中,其也是该第一方面的第四十三、第四十四、第四十五、第四十六、第四十七、第四十八、第四十九、第五十、第五十一及第五十二实施方式或前述的任何其它的一实施方式,该海藻糖磷酸化酶的氨基酸序列由如SEQ ID NO:14所示的氨基酸序列组成。

[0137] 在第一方面的另一优选实施方式中,其也是第一方面的任何其它前述实施方式中的实施方式,该海藻糖磷酸化酶的氨基酸序列在一个或更多个另外的氨基酸位置处包含氨基酸取代,其中该一个或更多个另外的氨基酸位置是独立且各别地选自由下列SEQ ID NO:1的氨基酸位置组成的组:10、114、118、192、197、220、225、304、306、318、323、339、349、357、383、459、476、481、484、487、488、506、511、526、530、532、533、537、550、556、564、590、649、667、703、705以及712。

[0138] 在第一方面的另一优选实施方式中,其也是第一方面的任何其它前述实施方式中的实施方式,该海藻糖磷酸化酶的氨基酸序列在一个或更多个另外的氨基酸位置处包含氨基酸取代,其中该一个或更多个另外的氨基酸位置是独立且各别地选自由下列SEQ ID NO:1的氨基酸位置组成的组:V10、L114、I118、S192、S197、Y220、N225、A304、D306、P318、T323、L339、F349、G357、A459、Q476、E481、A484、Q487、K488、A506、A511、R526、E530、G532、D533、D537、V550、S556、T564、D590、A649、R667、A703、K705以及L712。

[0139] 在第一方面的第五十五实施方式中,其也是该第一方面的第四十三、第四十四、第四十五、第四十六、第四十七、第四十八、第四十九、第五十、第五十一、第五十二、第五十三及第五十四实施方式或前述的任何其它的一实施方式,该海藻糖磷酸化酶的氨基酸序列在一个或更多个另外的氨基酸位置处包含氨基酸取代,其中该一个或更多个另外的氨基酸位置选自由下列SEQ ID NO:1的氨基酸位置组成的组:10、192、197、220、225、304、306、318、323、339、349、357、459、476、481、484、487、488、506、511、526、530、532、533、537、550、556、

564、590、649、667、703以及705,优选地该一个或更多个另外的氨基酸位置是独立且各别地选自由下列SEQ ID NO:1的氨基酸位置组成的组:10、192、197、220、225、304、306、318、323、339、349、357、459、476、481、484、487、488、506、511、526、530、532、533、537、550、556、564、590、649、667、703以及705。

[0140] 在第一方面的第五十六实施方式中,其也是该第一方面的第五十五实施方式中的实施方式,该一个或更多个另外的氨基酸位置选自由下列SEQ ID NO:1的氨基酸位置组成的组:V10、S192、S197、Y220、N225、A304、D306、P318、T323、L339、F349、G357、A459、Q476、E481、A484、Q487、K488、A506、A511、R526、E530、G532、D533、D537、V550、S556、T564、D590、A649、R667、A703以及K705,优选地该一个或更多个另外的氨基酸位置是独立且各别地选自由下列SEQ ID NO:1的氨基酸位置组成的组:V10、S192、S197、Y220、N225、A304、D306、P318、T323、L339、F349、G357、A459、Q476、E481、A484、Q487、K488、A506、A511、R526、E530、G532、D533、D537、V550、S556、T564、D590、A649、R667、A703以及K705。

[0141] 在第一方面的第五十七实施方式中,其也是该第一方面的第五十五实施方式中的实施方式,该一个或更多个另外的氨基酸位置选自由下列SEQ ID NO:1的氨基酸位置组成的组:10、220、225、304、318、323、349、357、481、487、488、506、511、550、556、564、590、649、703以及705,优选地该一个或更多个另外的氨基酸位置是独立且各别地选自由下列SEQ ID NO:1的氨基酸位置组成的组:10、220、225、304、318、323、349、357、481、487、488、506、511、550、556、564、590、649、703以及705。

[0142] 在第一方面的第五十八实施方式中,其也是该第一方面的第五十七实施方式中的实施方式,该一个或更多个另外的氨基酸位置选自由下列SEQ ID NO:1的氨基酸位置组成的组:V10、Y220、N225、A304、P318、T323、F349、G357、E481、Q487、K488、A506、A511、V550、S556、T564、D590、A649、A703以及K705,优选地该一个或更多个另外的氨基酸位置是独立且各别地选自由下列SEQ ID NO:1的氨基酸位置组成的组:V10、Y220、N225、A304、P318、T323、F349、G357、E481、Q487、K488、A506、A511、V550、S556、T564、D590、A649、A703以及K705。

[0143] 在第一方面的第五十九实施方式中,其也是该第一方面的第五十五实施方式中的实施方式,该一个或更多个另外的氨基酸位置选自由下列SEQ ID NO:1的氨基酸位置组成的组:10、225、304、323、349、357、487、550、556、564、590以及649,优选地该一个或更多个另外的氨基酸位置是独立且各别地选自由下列SEQ ID NO:1的氨基酸位置组成的组:10、225、304、323、349、357、487、550、556、564、590以及649。

[0144] 在第一方面的第六十实施方式中,其也是该第一方面的第五十九实施方式中的实施方式,该一个或更多个另外的氨基酸位置选自由下列SEQ ID NO:1的氨基酸位置组成的组:V10、N225、A304、T323、F349、G357、Q487、V550、S556、T564、D590以及A649,优选地该一个或更多个另外的氨基酸位置是独立且各别地选自由下列SEQ ID NO:1的氨基酸位置组成的组:V10、N225、A304、T323、F349、G357、Q487、V550、S556、T564、D590以及A649。

[0145] 在第一方面的第六十一实施方式中,其也是该第一方面的第五十五实施方式中的实施方式,该一个或更多个另外的氨基酸位置选自由下列SEQ ID NO:1的氨基酸位置组成的组:225、304、323、349、357、487、550、556、564、590以及649,优选地该一个或更多个另外的氨基酸位置是独立且各别地选自由下列SEQ ID NO:1的氨基酸位置组成的组:225、304、323、349、357、487、550、556、564、590以及649。

[0146] 在第一方面的第六十二实施方式中,其也是该第一方面的第六十一实施方式中的实施方式,该一个或更多个另外的氨基酸位置选自由下列SEQ ID NO:1的氨基酸位置组成的组:N225、A304、T323、F349、G357、Q487、V550、S556、T564、D590以及A649,优选地该一个或更多个另外的氨基酸位置是独立且各别地选自由下列SEQ ID NO:1的氨基酸位置组成的组:N225、A304、T323、F349、G357、Q487、V550、S556、T564、D590以及A649。

[0147] 在第一方面的第六十三实施方式中,其也是该第一方面的第五十五实施方式中的实施方式,该一个或更多个另外的氨基酸位置选自由下列SEQ ID NO:1的氨基酸位置组成的组:304、357以及590,优选地该一个或更多个另外的氨基酸位置是独立且各别地选自由下列SEQ ID NO:1的氨基酸位置组成的组:304、357以及590。

[0148] 在第一方面的第六十四实施方式中,其也是该第一方面的第六十三实施方式中的实施方式,该一个或更多个另外的氨基酸位置选自由下列SEQ ID NO:1的氨基酸位置组成的组:A304、G357以及D590,优选地该一个或更多个另外的氨基酸位置是独立且各别地选自由下列SEQ ID NO:1的氨基酸位置组成的组:A304、G357以及D590。

[0149] 在第一方面的第六十五实施方式中,其也是该第一方面的第五十五、第五十六、第五十七、第五十八、第五十九、第六十、第六十一、第六十二、第六十三及第六十四实施方式或前述的任何其它的一实施方式,该海藻糖磷酸化酶的氨基酸序列包含如SEQ ID NO:44所示的氨基酸序列。

[0150] 在第一方面的第六十六实施方式中,其也是该第一方面的第六十五实施方式中的实施方式,该海藻糖磷酸化酶的氨基酸序列是由如SEQ ID NO:44所示的氨基酸序列组成。

[0151] 在第一方面的另一优选实施方式中,其也是第一方面的任何其它前述实施方式中的实施方式,该海藻糖磷酸化酶的氨基酸序列在一个或更多个另外的氨基酸位置处包含氨基酸取代,其中该一个或更多个另外的氨基酸位置是各别并独立地选自由下列SEQ ID NO:1的氨基酸位置组成的组:10、114、118、192、197、220、225、304、306、318、323、339、349、357、383、459、476、481、484、487、488、506、511、526、530、532、533、537、550、556、564、590、649、667、703、705以及712。

[0152] 在第一方面的另一优选实施方式中,其也是第一方面的任何其它前述实施方式中的实施方式,该海藻糖磷酸化酶的氨基酸序列在一个或更多个另外的氨基酸位置处包含氨基酸取代,其中该一个或更多个另外的氨基酸位置是各别并独立地选自由下列SEQ ID NO:1的氨基酸位置组成的组:V10、L114、I118、S192、S197、Y220、N225、A304、D306、P318、T323、L339、F349、G357、A459、Q476、E481、A484、Q487、K488、A506、A511、R526、E530、G532、D533、D537、V550、S556、T564、D590、A649、R667、A703、K705以及L712。

[0153] 在第一方面的第六十五实施方式中,其也是该第一方面的第五十五、第五十六、第五十七、第五十八、第五十九、第六十、第六十一、第六十二、第六十三及第六十四实施方式或前述的任何其它的一实施方式,该海藻糖磷酸化酶的氨基酸序列在一个或更多个另外的氨基酸位置处包含氨基酸取代,其中该一个或更多个另外的氨基酸位置是各别并独立地选自由下列SEQ ID NO:1的氨基酸位置组成的组:10、192、197、220、225、306、318、323、339、349、459、476、481、484、487、488、506、511、526、530、532、533、537、550、556、564、649、667、703以及705,优选地该海藻糖磷酸化酶的氨基酸序列在一个或更多个更进一步的氨基酸位置处包含氨基酸取代,其中该一个或更多个更进一步的氨基酸位置是各别并独立地选自由

下列SEQ ID NO:1的氨基酸位置组成的组:10、192、197、220、225、306、318、323、339、349、459、476、481、484、487、488、506、511、526、530、532、533、537、550、556、564、649、667、703以及705。

[0154] 在第一方面的第六十八实施方式中,其也是该第一方面的第六十七实施方式中的实施方式,该一个或更多个更进一步的氨基酸位置选自由下列SEQ ID NO:1的氨基酸位置组成的组:V10、S192、S197、Y220、N225、D306、P318、T323、L339、F349、A459、Q476、E481、A484、Q487、K488、A506、A511、R526、E530、G532、D533、D537、V550、S556、T564、A649、R667、A703以及K705,优选地该一个或更多个更进一步的氨基酸位置是各别并独立地选自由下列SEQ ID NO:1的氨基酸位置组成的组:V10、S192、S197、Y220、N225、D306、P318、T323、L339、F349、A459、Q476、E481、A484、Q487、K488、A506、A511、R526、E530、G532、D533、D537、V550、S556、T564、A649、R667、A703以及K705。

[0155] 在第一方面的第六十九实施方式中,其也是该第一方面的第六十七实施方式中的实施方式,该一个或更多个更进一步的氨基酸位置选自由下列SEQ ID NO:1的氨基酸位置组成的组:10、220、225、318、323、349、481、487、488、506、511、550、556、564、649、703以及705,优选地该一个或更多个更进一步的氨基酸位置是各别并独立地选自由下列SEQ ID NO:1的氨基酸位置组成的组:10、220、225、318、323、349、481、487、488、506、511、550、556、564、649、703以及705。

[0156] 在第一方面的第七十实施方式中,其也是该第一方面的第六十九实施方式中的实施方式,该一个或更多个更进一步的氨基酸位置选自由下列SEQ ID NO:1的氨基酸位置组成的组:V10、Y220、N225、P318、T323、F349、E481、Q487、K488、A506、A511、V550、S556、T564、A649、A703以及K705,优选地该一个或更多个更进一步的氨基酸位置是各别并独立地选自由下列SEQ ID NO:1的氨基酸位置组成的组:V10、Y220、N225、P318、T323、F349、E481、Q487、K488、A506、A511、V550、S556、T564、A649、A703以及K705。

[0157] 在第一方面的第七十一实施方式中,其也是该第一方面的第六十七实施方式中的实施方式,该一个或更多个更进一步的氨基酸位置选自由下列SEQ ID NO:1的氨基酸位置组成的组:10、225、323、349、487、550、556、564以及649,优选地该一个或更多个更进一步的氨基酸位置是各别并独立地选自由下列SEQ ID NO:1的氨基酸位置组成的组:10、225、323、349、487、550、556、564以及649。

[0158] 在第一方面的第七十二实施方式中,其也是该第一方面的第七十一实施方式中的实施方式,该一个或更多个更进一步的氨基酸位置选自由下列SEQ ID NO:1的氨基酸位置组成的组:V10、N225、T323、F349、Q487、V550、S556、T564以及A649,优选地该一个或更多个更进一步的氨基酸位置是各别并独立地选自由下列SEQ ID NO:1的氨基酸位置组成的组:V10、N225、T323、F349、Q487、V550、S556、T564以及A649。

[0159] 在第一方面的第七十三实施方式中,其也是该第一方面的第六十七实施方式中的实施方式,该一个或更多个更进一步的氨基酸位置选自由下列SEQ ID NO:1的氨基酸位置组成的组:225、323、349、487、550、556、564以及649,优选地该一个或更多个更进一步的氨基酸位置是各别并独立地选自由下列SEQ ID NO:1的氨基酸位置组成的组:225、323、349、487、550、556、564以及649。

[0160] 在第一方面的第七十四实施方式中,其也是该第一方面的第七十三实施方式中的

实施方式,该一个或更多个更进一步的氨基酸位置选自由下列SEQ ID NO:1的氨基酸位置组成的组:N225、T323、F349、Q487、V550、S556、T564以及A649,优选地该一个或更多个更进一步的氨基酸位置是各别并独立地选自由下列SEQ ID NO:1的氨基酸位置组成的组:N225、T323、F349、Q487、V550、S556、T564以及A649。

[0161] 在第一方面的第七十五实施方式中,其也是该第一方面的第六十七、第六十八、第六十九、第七十、第七十一、第七十二、第七十三及第七十四实施方式或前述的任何其它的一实施方式,该海藻糖磷酸化酶的氨基酸序列在SEQ ID NO:1的氨基酸位置处包含氨基酸取代,优选在SEQ ID NO:1的氨基酸位置处,且该海藻糖磷酸化酶的氨基酸序列在下列SEQ ID NO:1的氨基酸位置处包含另外的氨基酸取代:

[0162] (i)550与556、优选V550与S556,或

[0163] (ii)225、487与564、优选N225、Q487与T564,或

[0164] (iii)323、550与564、优选T323、V550与T564,或

[0165] (iv)225、323与487、优选N225、T323与Q487,或

[0166] (v)225、487、550与556、优选N225、Q487、V550与S556,或

[0167] (vi)225、487、550与564、优选N225、Q487、V550与T564,或

[0168] (vii)225、550、556与564、优选N225、V550、S556与T564,或

[0169] (viii)225、550、564与649、优选N225、V550、T564、A649,或

[0170] (ix)323、550、556与564、优选T323、V550、S556、T564,或

[0171] (x)323、487、550与649、优选T323、Q487、V550与A649,或

[0172] (xii)225、487、550、556与564、优选N225、Q487、V550、S556与T564,或

[0173] (xiii)225、550、556、564与649、优选N225、V550、S556、T564与A649,或

[0174] (xiv)225、323、487、550与564、优选N225、T323、Q487、V550、T564,或

[0175] (xv)225、323、487、550与649、优选N225、T323、Q487、V550与A649,或

[0176] (xvi)225、323、487、550与556、优选N225、T323、Q487、V550与S556,或

[0177] (xvii)225、323、550、556、564、优选N225、T323、V550、S556、T564,或

[0178] (xviii)323、349、487、550与649、优选T323、F349、Q487、V550与A649,或

[0179] (ixx)323、487、550、556与564、优选T323、Q487、V550、S556与T564,或

[0180] (xx)487、550、556、564与649、优选Q487、V550、S556、T564与A649,或

[0181] (xxi)225、323、349、550、556与649、优选N225、T323、F349、V550、S556与A649,或

[0182] (xxii)225、323、487、550、556、649、优选N225、T323、Q487、V550、S556与A649,或

[0183] (xxiiii)225、349、487、550、556与564、优选N225、F349、Q487、V550、S556与T564、和/或

[0184] (xxiv)225、349、487、550、564与649、优选N225、F349、Q487、V550、T564、A649,或

[0185] (xxv)225、487、550、556、564与649、优选N225、Q487、V550、S556、T564与A649,或

[0186] (xxvi)323、487、550、556、564与649、优选T323、Q487、V550、S556、T564与A649,或

[0187] (xxvii)225、323、487、550、556、564与649、优选N225、T323、Q487、V550、S556、T564与A649。

[0188] 在第一方面的第七十六实施方式中,其也是该第一方面的第一、第二、第三、第四、第五、第六、第七、第八、第九、第十、第十一、第十二、第十三、第十四、第十五、第十六、第十

七、第十八、第十九、第二十、第二十一、第二十二、第二十三、第二十四、第二十五、第二十六、第二十七、第二十八、第二十九、第三十、第三十一、第三十二、第三十三、第三十四、第三十五、第三十六、第三十七、第三十八、第三十九、第四十、第四十一、第四十二、第四十三、第四十四、第四十五、第四十六、第四十七、第四十八、第四十九、第五十、第五十一、第五十二、第五十三、第五十四、第五十五、第五十六、第五十七、第五十八、第五十九、第六十、第六十一、第六十二、第六十三、第六十四、第六十五、第六十六、第六十七、第六十八、第六十九、第七十、第七十一、第七十二、第七十三、第七十四及第七十五实施方式或前述的任何其它的一实施方式,在该任何氨基酸位置的取代选自由氨基酸A、R、N、D、C、Q、E、G、H、I、L、K、M、F、P、S、T、W、Y以及V组成的组,优选地在该任何氨基酸位置的取代是各别且独立地选自由氨基酸A、R、N、D、C、Q、E、G、H、I、L、K、M、F、P、S、T、W、Y以及V组成的组。

[0189] 在第一方面的第七十七实施方式中,其也是该第一方面的第七十六实施方式中的实施方式,该取代是位于任何下列SEQ ID NO:1的氨基酸位置:712、383、10、114、118、192、197、220、225、304、306、318、323、339、349、357、459、476、481、484、487、488、506、511、526、530、532、533、537、550、556、564、590、649、667、703与705。

[0190] 在第一方面的第七十八实施方式中,其也是该第一方面的第七十七实施方式中的实施方式,该取代是位于任何下列SEQ ID NO:1的氨基酸位置:L712、P383、V10、L114、I118、S192、S197、Y220、N225、A304、D306、P318、T323、L339、F349、G357、A459、Q476、E481、A484、Q487、K488、A506、A511、R526、E530、G532、D533、D537、V550、S556、T564、D590、A649、R667、A703与K705。

[0191] 在第一方面的第七十九实施方式中,其也是该第一方面的第一、第二、第三、第四、第五、第六、第七、第八、第九、第十、第十一、第十二、第十三、第十四、第十五、第十六、第十七、第十八、第十九、第二十、第二十一、第二十二、第二十三、第二十四、第二十五、第二十六、第二十七、第二十八、第二十九、第三十、第三十一、第三十二、第三十三、第三十四、第三十五、第三十六、第三十七、第三十八、第三十九、第四十、第四十一、第四十二、第四十三、第四十四、第四十五、第四十六、第四十七、第四十八、第四十九、第五十、第五十一、第五十二、第五十三、第五十四、第五十五、第五十六、第五十七、第五十八、第五十九、第六十、第六十一、第六十二、第六十三、第六十四、第六十五、第六十六、第六十七、第六十八、第六十九、第七十、第七十一、第七十二、第七十三、第七十四、第七十五、第七十六、第七十七及第七十八实施方式或前述的任何其它的一实施方式,优选该第一方面的第七十六、第七十七及第七十八实施方式,该海藻糖磷酸化酶的氨基酸序列包含一个或更多个取代,其中该取代选自由下列组成的组:

[0192] 在SEQ ID NO:1的V10位置处的氨基酸取代,其中该取代为V10R、V10H或V10K,优选V10R;

[0193] 在SEQ ID NO:1的L114位置处的氨基酸取代,其中该取代为L114A、L114G、L114I、L114M、L114P或L114V,优选L114I;

[0194] 在SEQ ID NO:1的I118位置处的氨基酸取代,其中该取代为I118A、I118G、I118L、I118M、I118P或I118V,优选I118V;

[0195] 在SEQ ID NO:1的S192位置处的氨基酸取代,其中该取代为S192A、S192G、S192I、S192L、S192M、S192P或S192V,优选S192V;

[0196] 在SEQ ID NO:1的S197位置处的氨基酸取代,其中该取代为S197A、S197G、S197I、S197L、S197M、S197P或S197V,优选S197G;

[0197] 在SEQ ID NO:1的Y220位置处的氨基酸取代,其中该取代为Y220F或Y220W,优选Y220F;

[0198] 在SEQ ID NO:1的N225位置处的氨基酸取代,其中该取代为N225A、N225G、N225I、N225L、N225M、N225P或N225V,优选N225I、N225L、N225M或N225V以及更优选N225V;

[0199] 在SEQ ID NO:1的A304位置处的氨基酸取代,其中该取代为A304G、A304I、A304L、A304M、A304P或A304V,优选A304I或A304L以及更优选A304I;

[0200] 在SEQ ID NO:1的D306位置处的氨基酸取代,其中该取代为D306R、D306H或D306K,优选D306H;

[0201] 在SEQ ID NO:1的P318位置处的氨基酸取代,其中该取代为P318R、P318H或P318K,优选P318H;

[0202] 在SEQ ID NO:1的T323位置处的氨基酸取代,其中该取代为T323A、T323G、T323I、T323L、T323M、T323P,或T323V,优选T323I或T323V以及更优选T323I;

[0203] 在SEQ ID NO:1的L339位置处的氨基酸取代,其中该取代为L339A、L339G、L339I、L339L、L339M、L339P或L339V,优选L339I;

[0204] 在SEQ ID NO:1的F349位置处的氨基酸取代,其中该取代为F349W或F349Y,优选F349Y;

[0205] 在SEQ ID NO:1的G357位置处的氨基酸取代,其中该取代为G357A、G357I、G357L、G357M、G357P或G357V,优选G357A;

[0206] 在SEQ ID NO:1的P383位置处的氨基酸取代,其中该取代为P383A、P383G、P383I、P383L、P383M、P383V、P383N、P383C、P383Q、P383S或P383T,优选P383A、P383G、P383M、P383V、P383N、P383C、P383Q、P383S或P383T,更优选P383G、P383V、P383C或P383S,或P383T,甚至更优选P383V或P383T以及最优选P383V;

[0207] 在SEQ ID NO:1的A459位置处的氨基酸取代,其中该取代为A459N、A459C、A459Q或A459S、A459T,优选A459S;

[0208] 在SEQ ID NO:1的Q476位置处的氨基酸取代,其中该取代为Q476A、Q476G、Q476I、Q476L、Q476M、Q476P或Q476V,优选Q476G;

[0209] 在SEQ ID NO:1的E481位置处的氨基酸取代,其中该取代为E481A、E481G、E481I、E481L、E481M、E481P或E481V,优选E481I;

[0210] 在SEQ ID NO:1的A484位置处的氨基酸取代,其中该取代为A484N、A484C、A484Q、A484S或A484T,优选A484S;

[0211] 在SEQ ID NO:1的Q487位置处的氨基酸取代,其中该取代为Q487A、Q487G、Q487I、Q487L、Q487M、Q487P或Q487V,优选Q487A、Q487G、Q487L、Q487M或Q487V,更优选Q487A;

[0212] 在SEQ ID NO:1的K488位置处的氨基酸取代,其中该取代为K488A、K488G、K488I、K488L、K488M、K488P或K488V,优选K488A;

[0213] 在SEQ ID NO:1的A506位置处的氨基酸取代,其中该取代为A506N、A506C、A506Q、A506S或A506T,优选A506S;

[0214] 在SEQ ID NO:1的A511位置处的氨基酸取代,其中该取代为A511N、A511C、A511Q、

A511S或A511T,优选A511S;

[0215] 在SEQ ID NO:1的R526位置处的氨基酸取代,其中该取代为R526D或R526E优选R526E;

[0216] 在SEQ ID NO:1的E530位置处的氨基酸取代,其中该取代为E530A、E530G、E530I、E530L、E530M、E530P、E530V,优选E530V;

[0217] 在SEQ ID NO:1的G532位置处的氨基酸取代,其中该取代为G532R、G532H或G532K,优选G532R;

[0218] 在SEQ ID NO:1的D533位置处的氨基酸取代,其中该取代为D533A、D533G、D533I、D533L、D533M、D533P或D533V,优选D533G;

[0219] 在SEQ ID NO:1的D537位置处的氨基酸取代,其中该取代为D537A、D537G、D537I、D537L、D537M、D537P或D537V,优选D537M;

[0220] 在SEQ ID NO:1的V550位置处的氨基酸取代,其中该取代为V550A、V550G、V550I、V550L、V550M或V550P,优选V550I或V550P以及更优选V550I;

[0221] 在SEQ ID NO:1的S556位置处的氨基酸取代,其中该取代为S556N、S556C、S556Q或S556T,优选S556T;

[0222] 在SEQ ID NO:1的T564位置处的氨基酸取代,其中该取代为T564D或T564E,优选T564E;

[0223] 在SEQ ID NO:1的D590位置处的氨基酸取代,其中该取代为D590N、D590C、D590Q、D590S、D590T、D590A、D590G、D590I、D590L、D590M、D590P或D590V,优选D590N、D590G或D590A以及更优选D590N;

[0224] 在SEQ ID NO:1的A649位置处的氨基酸取代,其中该取代为A649D或A649E,优选A649E;

[0225] 在SEQ ID NO:1的R667位置处的氨基酸取代,其中该取代为R667D、R667E、R667R、R667H或R667K,优选R667E或R667K、更优选R667E;

[0226] 在SEQ ID NO:1的A703位置处的氨基酸取代,其中该取代为A703D或A703E,优选A703E;以及

[0227] 在SEQ ID NO:1的K705位置处的氨基酸取代,其中该取代为K705N、K705C、K705Q、K705S或K705T,优选K705N;

[0228] 在SEQ ID NO:1的L712位置处的氨基酸取代,其中该取代为L712A、L712G、L712I、L712M、L712P或L712V,优选L712M。

[0229] 在第一方面的另一优选实施方式中,其也是第一方面的任何其它前述实施方式中的实施方式,该海藻糖磷酸化酶包含一个或更多个取代,其中该取代选自由下列SEQ ID NO:1的氨基酸位置组成的组:L712M、P383G、P383V、P383C、P383S、P383T、V10R、L114I、I118V、S192V、S197G、Y220F、N225I、N225L、N225M、N225V、A304L、A304I、D306H、P318H、T323I、T323V、L339I、F349Y、G357A、A459S、Q476G、E481I、A484S、487A、Q487G、Q487L、Q487M、Q487V、K488A、A506S、A511S、R526E、E530V、G532R、D533G、D537M、V550I、V550P、S556T、T564E、D590N、D590G、D590A、A649E、R667E、R667K、A703E以及K705N,优选地选自由下列SEQ ID NO:1的氨基酸位置组成的组:P383G、P383V、P383C、P383S、P383T、V10R、L114I、S192V、S197G、N225I、N225L、N225M、N225V、A304L、A304I、D306H、P318H、T323I、T323V、L339I、

F349Y、G357A、A459S、Q476G、E481I、A484SQ487G、Q487L、Q487M、Q487V、K488A、A506S、A511S、R526E、E530V、G532R、D533G、D537M、V550I、V550P、S556T、T564E、D590G、D590A、A649E、R667E、R667K、A703E以及K705N。

[0230] 在第一方面的第八十实施方式中,其也是该第一方面的第一、第二、第三、第四、第五、第六、第七、第八、第九、第十、第十一、第十二、第十三、第十四、第十五、第十六、第十七、第十八、第十九、第二十、第二十一、第二十二、第二十三、第二十四、第二十五、第二十六、第二十七、第二十八、第二十九、第三十、第三十一、第三十二、第三十三、第三十四、第三十五、第三十六、第三十七、第三十八、第三十九、第四十、第四十一、第四十二、第四十三、第四十四、第四十五、第四十六、第四十七、第四十八、第四十九、第五十、第五十一、第五十二、第五十三、第五十四、第五十五、第五十六、第五十七、第五十八、第五十九、第六十、第六十一、第六十二、第六十三、第六十四、第六十五、第六十六、第六十七、第六十八、第六十九、第七十、第七十一、第七十二、第七十三、第七十四、第七十五、第七十六、第七十七、第七十八及第七十九实施方式或前述的任何其它的一实施方式,该海藻糖磷酸化酶的氨基酸序列与SEQ ID NO:1的氨基酸序列具至少81%、或至少82%、或至少83%、或至少84%、或至少85%、仍然更优选至少86%、或至少87%、或至少88%、或至少89%、或至少90%、甚至更优选至少91%、或至少92%、或至少93%、或至少94%、或至少95%、以及最优选至少96%、或至少97%、或至少98%、或至少99%、至少99.1%、或至少99.2%、或至少99.3%、或至少99.4%、或至少99.5%、或至少99.6%、或至少99.7%、或至少99.8%、以及尤其是至少99.9%,或100%的同一性。

[0231] 在第一方面的第八十一实施方式中,其也是该第一方面的第一、第二、第三、第四、第五、第六、第七、第八、第九、第十、第十一、第十二、第十三、第十四、第十五、第十六、第十七、第十八、第十九、第二十、第二十一、第二十二、第二十三、第二十四、第二十五、第二十六、第二十七、第二十八、第二十九、第三十、第三十一、第三十二、第三十三、第三十四、第三十五、第三十六、第三十七、第三十八、第三十九、第四十、第四十一、第四十二、第四十三、第四十四、第四十五、第四十六、第四十七、第四十八、第四十九、第五十、第五十一、第五十二、第五十三、第五十四、第五十五、第五十六、第五十七、第五十八、第五十九、第六十、第六十一、第六十二、第六十三、第六十四、第六十五、第六十六、第六十七、第六十八、第六十九、第七十、第七十一、第七十二、第七十三、第七十四、第七十五、第七十六、第七十七、第七十八、第七十九及第八十实施方式或前述的任何其它的一实施方式,该海藻糖磷酸化酶的氨基酸序列与SEQ ID NO:2、3、4、5、6、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、47、48、49、50、51、52、53、54、55、56、57、58、59、60、61、62、63、64、65、66、67、68、69、70、71、72、73、74、75、76、77、78、79、84、85、86、87、88、89、90、91、92、93、94、95、96、97、98、99、100、101、102、103、104、105、106、107、108、109、110、111、112、113、114、115、116、117、118、119、120、121、122、123、124、125、126、127、128、129、130、131、132、133、134、135、136、137、138、139、140、141、142、143、144、145、146、147、148、149、150、151、152、153、154、155、156、157、158、159,或190的氨基酸序列具有至少85%的同一性。

[0232] 在第一方面的第八十二实施方式中,其也是该第一方面的第八十一实施方式的一实施方式,该海藻糖磷酸化酶的氨基酸序列与SEQ ID NO:2、3、4、5、6、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、47、48、49、50、51、52、53、54、55、56、57、58、59、60、61、62、63、64、65、66、67、68、69、70、71、72、73、74、75、76、77、78、79、87、88、89、91、93、94、95、97、98、101、103、104、105、107、109、110、111、113、114、115、117、119、121、123、125、128、130、131、132、133、134、135、136、137、138、139、140、141、146、147、149、150、151、152、154、155、156、157、158、159,或190的氨基酸序列具有至少85%的同一性。

[0233] 在第一方面的另一优选实施方式中,其也是第一方面的任何其它前述实施方式中的实施方式,该海藻糖磷酸化酶的氨基酸序列与SEQ ID NO: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、47、48、49、50、51、52、53、54、55、56、57、58、59、60、61、62、63、64、65、66、67、68、69、70、71、72、73、74、75、76、77、78、79、155、156、157,或190的氨基酸序列具有至少85%的同一性。

[0234] 在第一方面的第八十三实施方式中,其也是该第一方面的第八十二实施方式的一实施方式,该海藻糖磷酸化酶的氨基酸序列与SEQ ID NO:3、7、9、10、12、13、15、20、29、44、45、50、51、52、53、54、55、56、57、58、59、60、61、62、63、64、65、66、67、68、69、70、71、72、73、74、75、76、77、78、79、98、104、110、113、115、121、125、132、133、134、135、136、137、138、139、140、141、147、152、154、155、156、157、158、159,或190的氨基酸序列具有至少85%的同一性。

[0235] 在第一方面的另一优选实施方式中,其也是第一方面的任何其它前述实施方式中的实施方式,该海藻糖磷酸化酶的氨基酸序列与SEQ ID NO:44、45、50、51、52、53、54、55、56、57、58、59、60、61、62、63、64、65、66、67、68、69、70、71、72、73、74、75、76、77、78、79,或190的氨基酸序列具有至少85%的同一性。

[0236] 在第一方面的第八十四实施方式中,其也是该第一方面的第一、第二、第三、第四、第五、第六、第七、第八、第九、第十、第十一、第十二、第十三、第十四、第十五、第十六、第十七、第十八、第十九、第二十、第二十一、第二十二、第二十三、第二十四、第二十五、第二十六、第二十七、第二十八、第二十九、第三十、第三十一、第三十二、第三十三、第三十四、第三十五、第三十六、第三十七、第三十八、第三十九、第四十、第四十一、第四十二、第四十三、第四十四、第四十五、第四十六、第四十七、第四十八、第四十九、第五十、第五十一、第五十二、第五十三、第五十四、第五十五、第五十六、第五十七、第五十八、第五十九、第六十、第六十一、第六十二、第六十三、第六十四、第六十五、第六十六、第六十七、第六十八、第六十九、第七十、第七十一、第七十二、第七十三、第七十四、第七十五、第七十六、第七十七、第七十八、第七十九、第八十、第八十一、第八十二及第八十三实施方式或前述的任何其它的一实施方式,该海藻糖磷酸化酶的氨基酸序列与SEQ ID NO:2、3、4、5、6、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、47、48、49、50、51、52、53、54、55、56、57、58、59、60、61、62、63、64、65、66、67、68、69、70、71、72、73、74、75、76、77、78 79、84、85、86、87、88、89、90、91、92、93、94、95、96、97、98、99、100、101、102、103、104、105、106、107、108、109、110、111、112、113、114、115、116、117、118、119、120、121、122、123、124、125、126、127、128、129、130、131、132、133、134、135、136、137、138、139、140、141、142、143、144、145、146、147、148、149、150、151、152、

153、154、155、156、157、158、159,或190的两个或更多个氨基酸序列具有至少85%的同一性。

[0237] 在第一方面的第八十五实施方式中,其也是该第一方面的第八十四实施方式的一实施方式,该海藻糖磷酸化酶的氨基酸序列与SEQ ID NO:2、3、4、5、6、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、47、48、49、50、51、52、53、54、55、56、57、58、59、60、61、62、63、64、65、66、67、68、69、70、71、72、73、74、75、76、77、78、79、87、88、89、91、93、94、95、97、98、101、103、104、105、107、109、110、111、113、114、115、117、119、121、123、125、128、130、131、132、133、134、135、136、137、138、139、140、141、146、147、149、150、151、152、154、155、156、157、158、159,或190的两个或更多个氨基酸序列具有至少85%的同一性。

[0238] 在第一方面的另一优选实施方式中,其也是第一方面的任何其它前述实施方式的一实施方式,该海藻糖磷酸化酶的氨基酸序列与SEQ ID NO: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、47、48、49、50、51、52、53、54、55、56、57、58、59、60、61、62、63、64、65、66、67、68、69、70、71、72、73、74、75、76、77、78、79、155、156、157,或190的两个或更多个氨基酸序列具有至少85%的同一性。

[0239] 在第一方面的第八十六实施方式中,其也是该第一方面的第八十五实施方式的一实施方式,该海藻糖磷酸化酶的氨基酸序列与SEQ ID NO:3、7、9、10、12、13、15、20、29、44、45、50、51、52、53、54、55、56、57、58、59、60、61、62、63、64、65、66、67、68、69、70、71、72、73、74、75、76、77、78、79、98、104、110、113、115、121、125、132、133、134、135、136、137、138、139、140、141、147、152、154、155、156、157、158、159,或190的两个或更多个氨基酸序列具有至少85%的同一性。

[0240] 在第一方面的另一优选实施方式中,其也是第一方面的任何其它前述实施方式中的实施方式,该海藻糖磷酸化酶的氨基酸序列与SEQ ID NO:44、45、50、51、52、53、54、55、56、57、58、59、60、61、62、63、64、65、66、67、68、69、70、71、72、73、74、75、76、77、78、79,或190的两个或更多个氨基酸序列具有至少85%的同一性。

[0241] 在第一方面的第八十七实施方式中,其也是该第一方面的第八十、第八十一、第八十二、第八十三、第八十四、第八十五及第八十六实施方式或前述的任何其它的一实施方式,该氨基酸序列的同一性为至少86%、或至少87%、或至少88%、或至少89%、或至少90%、更优选至少91%、或至少92%、或至少93%、或至少94%、或至少95%、以及最优选至少96%、或至少97%、或至少98%、或至少99%、至少99.1%、或至少99.2%、或至少99.3%、或至少99.4%、或至少99.5%、或至少99.6%、或至少99.7%、或至少99.8%、以及尤其至少99.9%,或100%。

[0242] 在第一方面的第八十八实施方式中,其也是该第一方面的第一、第二、第三、第四、第五、第六、第七、第八、第九、第十、第十一、第十二、第十三、第十四、第十五、第十六、第十七、第十八、第十九、第二十、第二十一、第二十二、第二十三、第二十四、第二十五、第二十六、第二十七、第二十八、第二十九、第三十、第三十一、第三十二、第三十三、第三十四、第三十五、第三十六、第三十七、第三十八、第三十九、第四十、第四十一、第四十二、第四十三、第四十四、第四十五、第四十六、第四十七、第四十八、第四十九、第五十、第五十一、第五十二、

第五十三、第五十四、第五十五、第五十六、第五十七、第五十八、第五十九、第六十、第六十一、第六十二、第六十三、第六十四、第六十五、第六十六、第六十七、第六十八、第六十九、第七十、第七十一、第七十二、第七十三、第七十四、第七十五、第七十六、第七十七、第七十八、第七十九、第八十、第八十一、第八十二、第八十三、第八十四、第八十五、第八十六及第八十七实施方式或前述的任何其它的一实施方式,优选该第一方面的第一、第二、第三、第四、第五、第六、第七、第八、第九、第十、第十一、第十二、第十三、第十四、第十五、第十六、第十七、第十八、第十九、第二十、第二十一、第二十二、第二十三、第二十四、第二十五、第二十六、第二十七、第二十八、第二十九、第三十、第三十一、第三十二、第三十三、第三十四、第三十五、第三十六、第三十七、第三十八、第三十九、第四十、第四十一、第四十二、第四十三、第四十四、第四十五、第四十六、第四十七、第四十八、第四十九、第五十、第五十一、第五十二、第五十三、第五十四、第五十五、第五十六、第五十七、第五十八、第五十九、第六十、第六十一、第六十二、第六十三、第六十四、第六十五、第六十六、第六十七、第六十八、第六十九、第七十、第七十一、第七十二、第七十三、第七十四、第七十五、第七十六、第七十七、第七十八及第七十九实施方式或前述的任何其它的一实施方式,该海藻糖磷酸化酶的氨基酸序列与SEQ ID NO:1的氨基酸序列具有至少81%、或至少82%、或至少83%、或至少84%、或至少85%、仍然更优选至少86%、或至少87%、或至少88%、或至少89%、或至少90%、更优选至少91%、或至少92%、或至少93%、或至少94%、或至少95%、以及最优选至少96%、或至少97%、或至少98%、或至少99%、至少99.1%、或至少99.2%、或至少99.3%、或至少99.4%、或至少99.5%、或至少99.6%、或至少99.7%、或至少99.8%、以及尤其至少99.9%,或100%的同源性。

[0243] 在第一方面的第八十九实施方式中,其也是该第一方面的第一、第二、第三、第四、第五、第六、第七、第八、第九、第十、第十一、第十二、第十三、第十四、第十五、第十六、第十七、第十八、第十九、第二十、第二十一、第二十二、第二十三、第二十四、第二十五、第二十六、第二十七、第二十八、第二十九、第三十、第三十一、第三十二、第三十三、第三十四、第三十五、第三十六、第三十七、第三十八、第三十九、第四十、第四十一、第四十二、第四十三、第四十四、第四十五、第四十六、第四十七、第四十八、第四十九、第五十、第五十一、第五十二、第五十三、第五十四、第五十五、第五十六、第五十七、第五十八、第五十九、第六十、第六十一、第六十二、第六十三、第六十四、第六十五、第六十六、第六十七、第六十八、第六十九、第七十、第七十一、第七十二、第七十三、第七十四、第七十五、第七十六、第七十七、第七十八、第七十九、第八十、第八十一、第八十二、第八十三、第八十四、第八十五、第八十六、第八十七及第八十八实施方式或前述的任何其它的一实施方式,该海藻糖磷酸化酶的氨基酸序列与SEQ ID NO:2、3、4、5、6、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、47、48、49、50、51、52、53、54、55、56、57、58、59、60、61、62、63、64、65、66、67、68、69、70、71、72、73、74、75、76、77、78、79、84、85、86、87、88、89、90、91、92、93、94、95、96、97、98、99、100、101、102、103、104、105、106、107、108、109、110、111、112、113、114、115、116、117、118、119、120、121、122、123、124、125、126、127、128、129、130、131、132、133、134、135、136、137、138、139、140、141、142、143、144、145、146、147、148、149、150、151、152、153、154、155、156、157、158,或159的氨基酸序列具有至少85%的同源性。

[0244] 在第一方面的第九十实施方式中,其也是该第一方面的第八十九实施方式的一实施方式,该海藻糖磷酸化酶的氨基酸序列与SEQ ID NO:2、3、4、5、6、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、47、48、49、50、51、52、53、54、55、56、57、58、59、60、61、62、63、64、65、66、67、68、69、70、71、72、73、74、75、76、77、78、79、87、88、89、91、93、94、95、97、98、101、103、104、105、107、109、110、111、113、114、115、117、119、121、123、125、128、130、131、132、133、134、135、136、137、138、139、140、141、146、147、149、150、151、152、154、155、156、157、158、159,或190的氨基酸序列具有至少85%的同源性。

[0245] 在第一方面的另一优选实施方式中,其也是第一方面的任何其它前述实施方式中的实施方式,该海藻糖磷酸化酶的氨基酸序列与SEQ ID NO: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、47、48、49、50、51、52、53、54、55、56、57、58、59、60、61、62、63、64、65、66、67、68、69、70、71、72、73、74、75、76、77、78、79、155、156、157,或190的氨基酸序列具有至少85%的同源性。

[0246] 在第一方面的第九十一实施方式中,其也是该第一方面的第九十实施方式的一实施方式,该海藻糖磷酸化酶的氨基酸序列与SEQ ID NO:3、7、9、10、12、13、15、20、29、44、45、50、51、52、53、54、55、56、57、58、59、60、61、62、63、64、65、66、67、68、69、70、71、72、73、74、75、76、77、78、79、98、104、110、113、115、121、125、132、133、134、135、136、137、138、139、140、141、147、152、154、155、156、157、158、159,或190的氨基酸序列具有至少85%的同源性。

[0247] 在第一方面的另一优选实施方式中,其也是第一方面的任何其它前述实施方式中的实施方式,该海藻糖磷酸化酶的氨基酸序列与SEQ ID NO:44、45、50、51、52、53、54、55、56、57、58、59、60、61、62、63、64、65、66、67、68、69、70、71、72、73、74、75、76、77、78、79,或190的氨基酸序列具有至少85%的同源性。

[0248] 在第一方面的第九十二实施方式中,其也是该第一方面的第一、第二、第三、第四、第五、第六、第七、第八、第九、第十、第十一、第十二、第十三、第十四、第十五、第十六、第十七、第十八、第十九、第二十、第二十一、第二十二、第二十三、第二十四、第二十五、第二十六、第二十七、第二十八、第二十九、第三十、第三十一、第三十二、第三十三、第三十四、第三十五、第三十六、第三十七、第三十八、第三十九、第四十、第四十一、第四十二、第四十三、第四十四、第四十五、第四十六、第四十七、第四十八、第四十九、第五十、第五十一、第五十二、第五十三、第五十四、第五十五、第五十六、第五十七、第五十八、第五十九、第六十、第六十一、第六十二、第六十三、第六十四、第六十五、第六十六、第六十七、第六十八、第六十九、第七十、第七十一、第七十二、第七十三、第七十四、第七十五、第七十六、第七十七、第七十八、第七十九、第八十、第八十一、第八十二、第八十三、第八十四、第八十五、第八十六、第八十七、第八十八、第八十九、第九十及第九十一实施方式或前述的任何其它的一实施方式,该海藻糖磷酸化酶的氨基酸序列与SEQ ID NO:2、3、4、5、6、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、47、48、49、50、51、52、53、54、55、56、57、58、59、60、61、62、63、64、65、66、67、68、69、70、71、72、73、74、75、76、77、78 79、84、85、86、87、88、89、90、91、92、93、94、95、

96、97、98、99、100、101、102、103、104、105、106、107、108、109、110、111、112、113、114、115、116、117、118、119、120、121、122、123、124、125、126、127、128、129、130、131、132、133、134、135、136、137、138、139、140、141、142、143、144、145、146、147、148、149、150、151、152、153、154、155、156、157、158、159,或190的两个或更多个氨基酸序列具有至少85%的同源性。

[0249] 在第一方面的第九十三实施方式中,其也是该第一方面的第九十二实施方式的一实施方式,该海藻糖磷酸化酶的氨基酸序列与SEQ ID NO:2、3、4、5、6、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、47、48、49、50、51、52、53、54、55、56、57、58、59、60、61、62、63、64、65、66、67、68、69、70、71、72、73、74、75、76、77、78、79、87、88、89、91、93、94、95、97、98、101、103、104、105、107、109、110、111、113、114、115、117、119、121、123、125、128、130、131、132、133、134、135、136、137、138、139、140、141、146、147、149、150、151、152、154、155、156、157、158、159,或190的两个或更多个氨基酸序列具有至少85%的同源性。

[0250] 在第一方面的另一优选实施方式中,其也是第一方面的任何其它前述实施方式中的实施方式,该海藻糖磷酸化酶的氨基酸序列与SEQ ID NO: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、47、48、49、50、51、52、53、54、55、56、57、58、59、60、61、62、63、64、65、66、67、68、69、70、71、72、73、74、75、76、77、78、79、155、156、157,或190的两个或更多个氨基酸序列具有至少85%的同源性。

[0251] 在第一方面的第九十四实施方式中,其也是该第一方面的第九十三实施方式的一实施方式,该海藻糖磷酸化酶的氨基酸序列与SEQ ID NO:3、7、9、10、12、13、15、20、29、44、45、50、51、52、53、54、55、56、57、58、59、60、61、62、63、64、65、66、67、68、69、70、71、72、73、74、75、76、77、78、79、98、104、110、113、115、121、125、132、133、134、135、136、137、138、139、140、141、147、152、154、155、156、157、158、159,或190的两个或更多个氨基酸序列具有至少85%的同一性。

[0252] 在第一方面的另一优选实施方式中,其也是第一方面的任何其它前述实施方式中的实施方式,该海藻糖磷酸化酶的氨基酸序列与SEQ ID NO:44、45、50、51、52、53、54、55、56、57、58、59、60、61、62、63、64、65、66、67、68、69、70、71、72、73、74、75、76、77、78、79,或190的两个或更多个氨基酸序列具有至少85%的同一性。

[0253] 在第一方面的第九十五实施方式中,其也是该第一方面的第八十八、第八十九、第九十、第九十一、第九十二、第九十三及第九十四实施方式或前述的任何其它的一实施方式,该氨基酸序列的同源性为至少86%、或至少87%、或至少88%、或至少89%、或至少90%、更佳至少91%、或至少92%、或至少93%、或至少94%、或至少95%、最佳至少96%、或至少97%、或至少98%、或至少99%、至少99.1%或至少99.2%或者至少99.3%、或者至少99.4%、或者至少99.5%、或者至少99.6%、或者至少99.7%、或者至少99.8%,并且尤其是至少99.9%或者100%。

[0254] 在第一方面的第九十六实施方式中,其也是该第一方面的第一、第二、第三、第四、第五、第六、第七、第八、第九、第十、第十一、第十二、第十三、第十四、第十五、第十六、第十七、第十八、第十九、第二十、第二十一、第二十二、第二十三、第二十四、第二十五、第二十六、第二十七、第二十八、第二十九、第三十、第三十一、第三十二、第三十三、第三十四、第三

十五、第三十六、第三十七、第三十八、第三十九、第四十、第四十一、第四十二、第四十三、第四十四、第四十五、第四十六、第四十七、第四十八、第四十九、第五十、第五十一、第五十二、第五十三、第五十四、第五十五、第五十六、第五十七、第五十八、第五十九、第六十、第六十一、第六十二、第六十三、第六十四、第六十五、第六十六、第六十七、第六十八、第六十九、第七十、第七十一、第七十二、第七十三、第七十四、第七十五、第七十六、第七十七、第七十八、第七十九、第八十、第八十一、第八十二、第八十三、第八十四、第八十五、第八十六、第八十七、第八十八、第八十九、第九十、第九十一、第九十二、第九十三、第九十四及第九十五实施方式或前述的任何其它的一实施方式，本发明的基础问题通过多肽，优选多肽，来解决，其中该多肽包含如SEQ ID NO:2、3、4、5、6、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、47、48、49、50、51、52、53、54、55、56、57、58、59、60、61、62、63、64、65、66、67、68、69、70、71、72、73、74、75、76、77、78、79、84、85、86、87、88、89、90、91、92、93、94、95、96、97、98、99、100、101、102、103、104、105、106、107、108、109、110、111、112、113、114、115、116、117、118、119、120、121、122、123、124、125、126、127、128、129、130、131、132、133、134、135、136、137、138、139、140、141、142、143、144、145、146、147、148、149、150、151、152、153、154、155、156、157、158、159，或190所示的氨基酸序列。在一个优选实施方式中，该多肽为海藻糖磷酸化酶。无论何时在本公开中，其指该第一方面及其任何实施方式的多肽及海藻糖磷酸化酶，这样的第一方面包括其任何的子方面，包括其任何实施方式。

[0255] 在第一方面的第九十七实施方式中，其也是该第一方面的第九十六实施方式的一实施方式，该多肽包含或由如下列所示的氨基酸序列组成:2、3、4、5、6、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、47、48、49、50、51、52、53、54、55、56、57、58、59、60、61、62、63、64、65、66、67、68、69、70、71、72、73、74、75、76、77、78、79、87、88、89、91、93、94、95、97、98、101、103、104、105、107、109、110、111、113、114、115、117、119、121、123、125、128、130、131、132、133、134、135、136、137、138、139、140、141、146、147、149、150、151、152、154、155、156、157、158、159，或190。

[0256] 在第一方面的第九十八实施方式中，其也是该第一方面的第九十七实施方式的一实施方式，该多肽，优选该海藻糖磷酸化酶，包含或由如下列所示的氨基酸序列组成:3、7、9、10、12、13、15、20、29、44、45、50、51、52、53、54、55、56、57、58、59、60、61、62、63、64、65、66、67、68、69、70、71、72、73、74、75、76、77、78、79、98、104、110、113、115、121、125、132、133、134、135、136、137、138、139、140、141、147、152、154、155、156、157、158、159，或190。

[0257] 在第一方面的第九十九实施方式中，其也是该第一方面的第一、第二、第三、第四、第五、第六、第七、第八、第九、第十、第十一、第十二、第十三、第十四、第十五、第十六、第十七、第十八、第十九、第二十、第二十一、第二十二、第二十三、第二十四、第二十五、第二十六、第二十七、第二十八、第二十九、第三十、第三十一、第三十二、第三十三、第三十四、第三十五、第三十六、第三十七、第三十八、第三十九、第四十、第四十一、第四十二、第四十三、第四十四、第四十五、第四十六、第四十七、第四十八、第四十九、第五十、第五十一、第五十二、第五十三、第五十四、第五十五、第五十六、第五十七、第五十八、第五十九、第六十、第六十一、第六十二、第六十三、第六十四、第六十五、第六十六、第六十七、第六十八、第六十九、第

七十、第七十一、第七十二、第七十三、第七十四、第七十五、第七十六、第七十七、第七十八、第七十九、第八十、第八十一、第八十二、第八十三、第八十四、第八十五、第八十六、第八十七、第八十八、第八十九、第九十、第九十一、第九十二、第九十三、第九十四、第九十五、第九十六、第九十七及第九十八实施方式或前述的任何其它的一实施方式，该多肽，优选该海藻糖磷酸化酶，能够催化糖基单醣与α-D-葡萄糖-1磷酸盐的反应。

[0258] 在第一方面的第一百实施方式中，其也是该第一方面的第九十九实施方式的一实施方式，该多肽，优选该海藻糖磷酸化酶，能够催化

[0259] 葡萄糖与α-D-葡萄糖-1磷酸盐转化为海藻糖与无机磷酸盐

[0260] 和/或

[0261] 海藻糖与无机磷酸盐转化为葡萄糖与α-D-葡萄糖-1磷酸盐。

[0262] 在第一方面的第一百零一实施方式中，其也是该第一方面的第九十九及第一百实施方式的一实施方式，该转化为一可逆的转化。

[0263] 在第一方面的第一百零二实施方式中，其也是该第一方面的第一、第二、第三、第四、第五、第六、第七、第八、第九、第十、第十一、第十二、第十三、第十四、第十五、第十六、第十七、第十八、第十九、第二十、第二十一、第二十二、第二十三、第二十四、第二十五、第二十六、第二十七、第二十八、第二十九、第三十、第三十一、第三十二、第三十三、第三十四、第三十五、第三十六、第三十七、第三十八、第三十九、第四十、第四十一、第四十二、第四十三、第四十四、第四十五、第四十六、第四十七、第四十八、第四十九、第五十、第五十一、第五十二、第五十三、第五十四、第五十五、第五十六、第五十七、第五十八、第五十九、第六十、第六十一、第六十二、第六十三、第六十四、第六十五、第六十六、第六十七、第六十八、第六十九、第七十、第七十一、第七十二、第七十三、第七十四、第七十五、第七十六、第七十七、第七十八、第七十九、第八十、第八十一、第八十二、第八十三、第八十四、第八十五、第八十六、第八十七、第八十八、第八十九、第九十、第九十一、第九十二、第九十三、第九十四、第九十五、第九十六、第九十七、第九十八、第九十九、第一百及第一百零一实施方式或前述的任何其它的一实施方式，该多肽，优选该海藻糖磷酸化酶，是为如EC号为EC 2.4.1.231所示的海藻糖磷酸化酶。

[0264] 在第一方面的第一百零三实施方式中，其也是该第一方面的第一、第二、第三、第四、第五、第六、第七、第八、第九、第十、第十一、第十二、第十三、第十四、第十五、第十六、第十七、第十八、第十九、第二十、第二十一、第二十二、第二十三、第二十四、第二十五、第二十六、第二十七、第二十八、第二十九、第三十、第三十一、第三十二、第三十三、第三十四、第三十五、第三十六、第三十七、第三十八、第三十九、第四十、第四十一、第四十二、第四十三、第四十四、第四十五、第四十六、第四十七、第四十八、第四十九、第五十、第五十一、第五十二、第五十三、第五十四、第五十五、第五十六、第五十七、第五十八、第五十九、第六十、第六十一、第六十二、第六十三、第六十四、第六十五、第六十六、第六十七、第六十八、第六十九、第七十、第七十一、第七十二、第七十三、第七十四、第七十五、第七十六、第七十七、第七十八、第七十九、第八十、第八十一、第八十二、第八十三、第八十四、第八十五、第八十六、第八十七、第八十八、第八十九、第九十、第九十一、第九十二、第九十三、第九十四、第九十五、第九十六、第九十七、第九十八、第九十九、第一百、第一百零一及第一百零二实施方式或前述的任何其它的一实施方式，该多肽，优选该海藻糖磷酸化酶，具有特征(A)、(B)、(C)、(D)与(E)

中的至少一个,或其任何组合,

[0265] 其中特征(A)为于52℃温育15分钟后的热稳定性,由一具有以下百分比的残余活性所定义:

[0266] i)30%至90%,优选39%至90%,更优选42%至90%,更优选54%至90%,更优选55%至90%,甚至更优选63%至90%,甚至更优选64%至90%,甚至更优选68%至90%,最优选64%至86%,和/或,

[0267] ii)30%至90%,优选31%至90%,优选32%至90%,优选33%至90%,优选34%至90%,优选35%至90%,优选36%至90%,优选37%至90%,优选38%至90%,优选39%至90%,更优选40%至90%,更优选41%至90%,优选42%至90%,更优选43%至90%,更优选44%至90%,更优选45%至90%,更优选46%至90%,更优选47%至90%,更优选48%至90%,更优选49%至90%,进一步优选50%至90%,进一步优选51%至90%,进一步优选52%至90%,甚至更优选53%至90%,甚至更优选54%至90%,甚至更优选55%至90%,甚至更优选60%至90%,甚至更优选61%至90%,甚至更优选65%至90%,甚至更优选70%至90%,甚至更优选75%至90%,且最优选72%至81%,和/或

[0268] iii)55%至100%,优选60%至100%,优选70%至100%,优选75%至100%,优选76%至100%,优选77%至100%,优选78%至100%,优选79%至100%,更优选80%至100%,更优选81%至100%,更优选82%至100%,更优选83%至100%,更优选84%至100%,更优选85%至100%,更优选86%至100%,更优选87%至100%,更优选88%至100%,更优选89至100%,进一步优选90%至100%,进一步优选91%至100%,进一步优选92%至100%,进一步优选93%至100%,进一步优选94%至100%,进一步优选95%至100%,进一步优选96%至100%,进一步优选97%至100%,进一步优选98%至100%,特别优选99%至100%,且最优选100%

[0269] 以及

[0270] 其中特征(B)为于52℃温育15分钟后的热稳定性,其特征在于

[0271] i)至少52℃的Tm30值,和/或

[0272] ii)至少52℃的Tm50值;

[0273] 以及

[0274] 其中特征(C)为以以下为特征的热稳定性

[0275] i)一介于以下温度之间的Tm30值:52℃至90℃,优选52℃至80℃,优选52.5℃至80℃,优选53℃至80℃,优选53.5℃至80℃,更优选54℃至80℃,优选54.5℃至80℃,甚至更优选55℃至80℃,优选55.5℃ 80℃,优选56℃至80℃,优选56.5℃至80℃,优选57℃至80℃,优选57.5℃至80℃,优选58℃至80℃,优选58.5℃至80℃,甚至更优选52℃至70℃,甚至更优选52.5℃至70℃,甚至更优选53℃至70℃,甚至更优选53.5℃至70℃,甚至更优选54℃至70℃,甚至更优选54.5℃至70℃,甚至更优选55℃至70℃,甚至更优选55.5℃至70℃,甚至更优选56℃至70℃,更优选56.5℃至70℃,甚至更优选57℃至70℃,甚至更优选57.5℃至70℃,甚至更优选58℃至70℃,甚至更优选58.5℃至70℃,甚至更优选52℃至65℃,甚至更优选52.5℃至65℃,甚至更优选53℃至65℃,甚至更优选53.5℃至65℃,甚至更优选54℃至65℃,甚至更优选54.5℃,甚至更优选55℃至65℃,甚至更优选55.5℃至65℃,甚至更优选56℃至65℃,甚至更优选56.5℃至65℃,甚至更优选57℃至65℃,甚至更优选57.5℃至65℃,

甚至更优选58℃至65℃,甚至更优选58.5℃至65℃,甚至更优选52℃至60℃,甚至更优选52.5℃至60℃,甚至更优选53℃至60℃,甚至更优选53.5℃至60℃,甚至更优选54℃至60℃,甚至更优选54.5℃至60℃,甚至更优选55℃至60℃,甚至更优选55.5℃至60℃,甚至更优选56℃至60℃,甚至更优选56.5℃至60℃,甚至更优选57℃至60℃,甚至更优选57.5℃至60℃,甚至更优选58℃至60℃,甚至更优选58.5℃至60℃,最优选53.5℃至58.5℃,和/或

[0276] ii)一介于以下温度之间的Tm50值:52℃至90℃,优选52℃至80℃,优选52.5℃至80℃,优选53℃至80℃,优选53.5℃至80℃,更优选54℃至80℃,优选54.5℃至80℃,甚至更优选55℃至80℃,优选55.5℃至80℃,优选56℃至80℃,优选56.5℃至80℃,优选57℃至80℃,优选57.5℃至80℃,甚至更优选52℃至70℃,甚至更优选52.5℃至70℃,甚至更优选53℃至70℃,甚至更优选53.5℃至70℃,甚至更优选54℃至70℃,甚至更优选54.5℃至70℃,甚至更优选55℃至70℃,甚至更优选55.5℃至70℃,甚至更优选56℃至70℃,甚至更优选56.5℃至70℃,更优选57℃至70℃,甚至更优选57.5℃至70℃,甚至更优选52℃至65℃,甚至更优选52.5℃至70℃,更优选53℃至65℃,甚至更优选53.5℃至65℃,甚至更优选54℃至65℃,甚至更优选54.5℃至65℃,甚至更优选55℃至65℃,甚至更优选55.5℃至65℃,甚至更优选56℃至65℃,甚至更佳56.5℃至65℃,甚至更佳57℃至65℃,甚至更佳57.5℃至65℃,甚至更佳52℃至60℃,甚至更优选52.5℃至60℃,甚至更优选53℃至60℃,甚至更优选53.5℃至60℃,甚至更优选54℃至60℃,甚至更优选54.5℃至60℃,甚至更优选55℃至60℃,甚至更优选55.5℃至60℃,甚至更优选56℃至60℃,甚至更优选56.5℃至60℃,甚至更优选57℃至60℃,甚至更优选57.5℃至60℃,最优选52℃至57.5℃

[0277] 以及

[0278] 其中特征(D)为以以下为特征的热稳定性

[0279] i)一工艺稳定性,其特征在于45℃的半衰期为3小时至9天或更多,优选24小时至9天或更多,优选39小时至9天或更多,优选2天至9天或更多,更优选4天至9天或更多,更优选5.5天至9天或更多,更优选至少7天至9天或更多,更优选至少9天或更多,且最优选9天;

[0280] ii)一工艺稳定性,其特征在于45℃半衰期为24小时至9天或更多,更优选39小时至9天或更多,更优选2天至9天或更多,更优选4天至9天或更多,更优选5.5天至9天或更多,更优选7天至9天或更多,甚至更优选至少9天或更多,且最优选9天;

[0281] iii)一工艺稳定性,其特征在于45℃半衰期为4天至9天或更多,优选5.5天至9天或更多,更优选7天至9天或更多,甚至更优选至少9天或更多,且最优选9天;

[0282] 以及

[0283] 其中特征(E)为以介于下列范围的100/500-比表示的相对活性

[0284] i)0.65至1.0,优选0.7至1.0,优选0.75至1.0,优选0.8至1.0,优选0.85至1.0,优选0.9至1.0,优选0.95至1.0以及更优选至少0.7至1.0;

[0285] ii)0.65至1.0之间,优选0.7至1.0之间,优选0.75至1.0之间,优选0.8至1.0之间,优选0.85至1.0之间,优选0.9至1.0之间,优选0.95至1.0之间;且更优选0.8至1.0之间;

[0286] 其中该100/500-比被定义为

[0287] [100mM葡萄糖与100mMα-葡萄糖-1磷酸盐的海藻糖活性]/

[0288] [500mM葡萄糖与100mMα-葡萄糖-1磷酸盐的海藻糖活性]的比。

[0289] 在第一方面的第一百零四实施方式中,其也是该第一方面的第一百零三实施方式

的一实施方式,该多肽,优选该海藻糖磷酸化酶,于52℃温育15分钟后具有热稳定性,该热稳定性由具有介于以下之间的百分比的残余活性所定义

[0290] 30％至90％,优选39％至90％,更优选42％至90％,更优选54％至90％,更优选55％至90％,且甚至更优选63％至90％,甚至更优选64％～90％,甚至更优选68％至90％,且最优选64％至86％;和/或

[0291] 30％至90％,优选31％至90％,优选32％至90％,优选33％至90％,优选34％至90％,优选35％至90％,优选36％至90％,优选37％至90％,优选38％至90％,优选39％至90％,更优选40％至90％,更优选41％至90％,更优选42％至90％,更优选43％至90％,更优选44％至90％,更优选45％至90％,更优选46％至90％,更优选47％至90％,更优选48％至90％,更优选49％至90％,甚至更优选50％至90％,甚至更优选51％至90％,甚至更优选52％至90％,甚至更优选53％至90％,甚至更优选54％至90％,甚至更优选55％至90％,甚至更优选60％至90％,甚至更优选61％至90％,甚至更优选65％至90％,甚至更优选70％至90％,甚至更优选75％至90％,且最优选72％至81％,和/或

[0292] 55％至100％,优选60％至100％,优选70％至100％,优选75％至100％,优选76％至100％,优选77％至100％,优选78至100％,更优选79至100％,更优选80至100％,更优选81至100％,更优选82至100％,更优选83至100％,优选84％至100％,更优选85％至100％,更优选86％至100％,更优选87％至100％,更优选88％至100％,更优选89％至100％,甚至更优选90％至100％,甚至更优选91％至100％,甚至更优选92％至100％,甚至更优选93％至100％,甚至更优选94％至100％,甚至更优选95％至100％,甚至更优选96％至100％,甚至更优选97％至100％,甚至更优选98％至100％,甚至更优选99％至100％,且最优选100％。

[0293] 在第一方面的第一百零五实施方式中,其也是该第一方面的第一百零三及第一百零四实施方式的一实施方式,该多肽,优选该海藻糖磷酸化酶,具有由至少52℃的Tm30-值所定义的热稳定性。

[0294] 在第一方面的第一百零六实施方式中,其也是该第一方面的第一百零三、第一百零四及第一百零五实施方式的一实施方式,该多肽,优选该海藻糖磷酸化酶,于45℃的半衰期为3小时至9天或更多,优选24小时至9天或更多,优选39小时至9天或更多,优选2天至9天或更多,更优选4天至9天或更多,更优选5.5天至9天或更多,更优选7天至9天或更多,甚至更优选至少9天或更多,最优选9天。

[0295] 在第一方面的第一百零七实施方式中,其也是该第一方面的第一百零三、第一百零四、第一百零五及第一百零六实施方式的一实施方式,该多肽,优选该海藻糖磷酸化酶,具有相对活性,其表现为100/500比在0.65至1.0之间,优选0.7至1.0之间,优选0.75至1.0之间,优选0.8至1.0之间,优选0.85至1.0之间,优选0.9至1.0之间,优选0.95至1.0之间,且更优选0.7至1.0之间。

[0296] 在第一方面的第一百零八实施方式中,其也是该第一方面的第一百零三、第一百零四、第一百零五、第一百零六及第一百零七实施方式的一实施方式,其中该多肽为该第一方面的第二十六、第二十七、第二十八、第二十九、第三十、第三十三、第三十四、第四十一、第四十二、第四十三、第四十四、第四十五、第四十六、第五十五、第六十七、第六十八、第七十五、第七十六、第七十七、第七十八、第七十九、第八十、第八十一、第八十四、第八十八、第

八十九、第九十二、第九十九、第一百及第一百零二实施方式或前述的任何其它的一实施方式的任何一个，优选该第一方面的第二十六、第二十七、第二十八、第二十九、第三十、第三十三、第五十五、第六十七、第六十八、第七十五、第七十六、第七十七、第七十八、第七十九、第八十、第八十一、第八十四、第八十八、第八十九、第九十二、第九十九、第一百及第一百零二实施方式的任何一个。

[0297] 在第一方面的第一百零九实施方式中，其也是该第一方面的第一百零三实施方式的一实施方式，该多肽，优选该海藻糖磷酸化酶，于52℃温育15分钟后具有热稳定性，该热稳定性是由介于以下范围之间的残余活性所定义：

[0298] 30％至90％，优选31％至90％，优选32％至90％，优选33％至90％，优选34％至90％，优选35％至90％，优选36％至90％，优选37％至90％，优选38％至90％，优选39％至90％，更优选40％至90％，更优选41％至90％，更优选42％至90％，更优选43％至90％，更优选44％至90％，更优选45％至90％，更优选46％至90％，更优选47％至90％，更优选48％至90％，更优选49％至90％，甚至更优选50％至90％，甚至更优选51％至90％，甚至更优选52％至90％，甚至更优选更优选53％至90％，甚至更优选54％至90％，甚至更优选55％至90％，甚至更优选60％～90％，甚至更优选61％至90％，更优选65％至90％，甚至更优选70％至90％，甚至更优选75％至90％，最优选72％至81％，和/或

[0299] 55％至100％，优选60％至100％，优选70％至100％，优选75％至100％，优选76％至100％，优选77％至100％，优选78％至100％，更优选79至100％，更优选80％至100％，更优选81％至100％，更优选82％至100％，更优选83％至100％，优选84％至100％，更优选85％至100％，更优选86％至100％，更优选87％至100％，更优选88％至100％，更优选89％至100％，甚至更优选90％％至100％，甚至更优选91％至100％，甚至更优选92％至100％，甚至更优选93％至100％，甚至更优选94％至100％，甚至更优选95％至100％，甚至更优选96％至100％，甚至更优选97％至100％，甚至更优选98％至100％，甚至更优选99％至100％，且最优选100％。

[0300] 在第一方面的第一百一十实施方式中，其也是该第一方面的第一百零三、第一百零四、第一百零五、第一百零六、第一百零七、第一百零八及第一百零九实施方式的一实施方式，该多肽，优选该海藻糖磷酸化酶，具有热稳定性，该热稳定性的特征在于至少52℃的Tm30值和/或至少52℃的Tm50值。

[0301] 在第一方面的第一百一十一实施方式中，其也是该第一方面的第一百零三、第一百零四、第一百零五、第一百零六、第一百零七、第一百零八、第一百零九及第一百一十实施方式的一实施方式，该多肽，优选该海藻糖磷酸化酶，具有于45℃的半衰期1天至9天，更优选2天至9天，更优选4天至9天，更优选5.5天至9天，更优选7天至9天，最优选9天。

[0302] 在第一方面的第一百一十二实施方式中，其也是该第一方面的第一百零三、第一百零四、第一百零五、第一百零六、第一百零七、第一百零八、第一百零九、第一百一十及第一百一十一实施方式的一实施方式，该多肽，优选该海藻糖磷酸化酶，具有相对活性表示为介于0.65至1.0，优选0.7至1.0，优选0.75至1.0，优选0.8至1.0，优选0.85至1.0，优选0.9至1.0，优选0.95至1.0之间，更优选0.7至1.0之间的100/500比。

[0303] 在第一方面的第一百一十三实施方式中，其也是该第一方面的第一百零九、第一百一十、第一百一十一及第一百一十二实施方式的一实施方式，该多肽，优选该海藻糖磷酸

化酶,是为该第一方面的第二十七、第二十八、第二十九、第三十一、第三十五、第三十六、第四十一、第四十二、第四十三、第四十四、第四十五、第四十六、第五十七、第六十九、第七十、第七十五、第七十六、第七十七、第七十八、第七十九、第八十、第八十二、第八十四、第八十八、第九十、第九十三、第九十九、第一百及第一百零二实施方式或前述的任何其它的一实施方式的任何一个,优选该第一方面的第二十七、第二十八、第二十九、第三十一、第三十五、第三十六、第五十七、第六十九、第七十、第七十五、第七十六、第七十七、第七十八、第七十九、第八十、第八十二、第八十四、第八十八、第九十、第九十三、第九十九、第一百及第一百零二实施方式的任何一个。

[0304] 在第一方面的第一百一十四实施方式中,其也是该第一方面的第一百一十三实施方式的一实施方式,该多肽,优选该海藻糖磷酸化酶,于52℃温育15分钟后具有热稳定性,该热稳定性由介于以下百分比之间的残余活性所定义:55%至100%,优选60%至100%,优选70%至100%,优选75%至100%,优选76%至100%,优选77%至100%,优选78%至100%,优选79%至100%,更优选80%至100%,更优选81%至100%,更优选82%至100%,更优选83%至100%,更优选84%至100%,更优选85%至100%,更优选86%至100%,更优选87%至100%,更优选88%至100%,甚至更优选89%至100%,甚至更优选90%至100%,甚至更优选91%至100%,甚至更优选92%至100%,甚至更优选93%至100%,甚至更优选94%至100%,甚至更优选95%至100%,甚至更优选96%至100%,甚至更优选97%至100%,甚至更优选98%至100%,甚至更优选99%至100%,最优选100%。

[0305] 在第一方面的第一百一十五实施方式中,其也是该第一方面的第一百零三、第一百零四、第一百零五、第一百零六、第一百零七、第一百零八、第一百零九、第一百一十、第一百一十一、第一百一十二、第一百一十三及第一百一十四实施方式的一实施方式,该多肽,优选该海藻糖磷酸化酶,具有热稳定性,该热稳定性的特征在于至少52℃的Tm30值和/或至少52℃的Tm50值,且其优选的特征在于至少52℃的Tm30值及至少52℃的Tm50值。

[0306] 在第一方面的第一百一十六实施方式中,其也是该第一方面的第一百零三、第一百零四、第一百零五、第一百零六、第一百零七、第一百零八、第一百零九、第一百一十、第一百一十一、第一百一十二、第一百一十三、第一百一十四及第一百一十五实施方式的一实施方式,该多肽,优选该海藻糖磷酸化酶,具有热稳定性,该热稳定性的特征在于:

[0307] i)介于以下温度之间的的Tm30值:52℃至90℃,优选52℃至80℃,优选52.5℃至80℃,优选53℃至80℃,优选53.5℃至80℃,更优选54℃至80℃,优选54.5℃至80℃,甚至更优选55℃至80℃,优选55.5℃至80℃,优选56℃至80℃,优选56.5℃至80℃,优选57℃至80℃,优选57.5℃至80℃,优选58℃至80℃,优选58.5℃至80℃,甚至更优选52℃至70℃,甚至更优选52.5℃至70℃,甚至更优选53℃至70℃,甚至更优选53.5℃至70℃,更优选54℃至70℃,甚至更优选54.5℃至70℃,甚至更优选55℃至70℃,甚至更优选55.5℃至70℃,甚至更优选56.5℃至70℃,甚至更优选57℃至70℃,甚至更优选57.5℃至70℃,甚至更优选57.5℃至70℃,甚至更优选58℃至70℃,甚至更优选58.5℃至70℃,甚至更优选52℃至65℃,更优选52.5℃至65℃,甚至更优选53℃至65℃,甚至更优选53.5℃至65℃,甚至更优选54℃至65℃,甚至更优选54.5℃至65℃,甚至更优选55℃至65℃,更优选55.5℃至65℃,甚至更优选56℃至65℃,甚至更优选56.5℃至65℃,甚至更优选57℃至65℃,甚至更优选57.5℃至65℃,甚至更优选58℃至65℃,甚至更优选58.5℃至65℃,甚至更优选52℃至65℃,甚至更优

选52.5℃至60℃,甚至更优选53℃至60℃,甚至更优选53.5℃至60℃,甚至更优选54℃至60℃,甚至更优选54.5℃至60℃,甚至更优选55℃至60℃,甚至更优选55.5℃至60℃,甚至更优选56℃至60℃,更优选56.5℃至60℃,甚至更优选57℃至60℃,甚至更优选57.5℃至60℃,甚至更优选58℃至60℃,甚至更优选58.5℃至60℃,最优选53.5℃至58.5℃,和/或

[0308] ii)介于以下温度之间的的Tm50值:52℃至90℃,优选52℃至80℃,优选52.5℃至80℃,优选53℃至80℃,优选53.5℃至80℃,更优选54℃至80℃,优选54.5℃至80℃,甚至更优选55℃至80℃,优选55.5℃至80℃,优选56℃至80℃,优选56.5℃至80℃,优选57℃至80℃,优选57.5℃至80℃,甚至更优选52℃至70℃,甚至更优选52.5℃至70℃,甚至更优选53℃至70℃,甚至更优选53.5℃至70℃,甚至更优选54℃至70℃,甚至更优选54.5℃至70℃,甚至更优选55℃至70℃,甚至更优选55.5℃至70℃,甚至更优选56℃至70℃,甚至更优选56.5℃至70℃,甚至更优选57℃至70℃,甚至更优选57.5℃至70℃,甚至更优选52℃至65℃,甚至更优选52.5℃至70℃,更优选53℃至65℃,甚至更优选53.5℃至65℃,甚至更优选54℃至65℃,甚至更优选55℃至65℃,甚至更优选55.5℃至65℃,甚至更优选56℃至65℃,甚至更优选56.5℃至65℃,甚至更优选57℃至65℃,甚至更优选57.5℃至65℃,甚至更优选52℃至60℃,甚至更优选52.5℃至60℃,甚至更优选53℃至60℃,甚至更优选53.5℃至60℃,甚至更优选54℃之间至60℃,甚至更优选54.5℃至60℃,甚至更优选55℃至60℃,甚至更优选55.5℃至60℃,甚至更优选56℃至60℃,甚至更优选56.5℃至60℃,甚至更优选57℃至60℃,甚至更优选57.5℃至60℃,且最优选52℃至57.5℃。

[0309] 在第一方面的第一百一十七实施方式中,其也是该第一方面的第一百零三、第一百零四、第一百零五、第一百零六、第一百零七、第一百零八、第一百零九、第一百一十、第一百一十一、第一百一十二、第一百一十三、第一百一十四、第一百一十五及第一百一十六实施方式的一实施方式,其中该多肽,优选该海藻糖磷酸化酶,于45℃的半衰期为4天至9天或更多,优选5.5天至9天或更多,更优选7天至9天或更多,甚至更优选至少9天或更多,最优选9天。

[0310] 在第一方面的第一百一十八实施方式中,其也是该第一方面的第一百零三、第一百零四、第一百零五、第一百零六、第一百零七、第一百零八、第一百零九、第一百一十、第一百一十一、第一百一十二、第一百一十三、第一百一十四、第一百一十五、第一百一十六及第一百一十七实施方式的一实施方式,该多肽,优选该海藻糖磷酸化酶,具有一相对活性,该相对活性表示为介于0.65-1.0之间的100/500比,优选0.7至1.0,优选0.75至1.0,优选0.8至1.0,优选0.85至1.0,优选0.9至1.0,优选0.95至1.0,更优选0.8至1.0。

[0311] 在第一方面的第一百一十九实施方式中,其也是该第一方面的第一百零四、第一百零五、第一百零六、第一百零七实施方式的一实施方式,其中该多肽,优选该海藻糖磷酸化酶,是为该第一方面的第二十八、第二十九、第三十二、第三十七、第三十八、第三十九、第四十、第四十一、第四十二、第四十三、第四十四、第四十五、第四十六、第五十九、第六十、第六十一、第六十二、第七十一、第七十二、第七十三、第七十四、第七十五、第七十六、第七十七、第七十八、第七十九、第八十、第八十二、第八十四、第八十八、第九十一、第九十四、第九十九、第一百及第一百零二实施方式或前述的任何其它的一实施方式的任何一个,优选该第一方面的第二十八、第二十九、第三十二、第三十七、第三十八、第三十九、第四十、第五十九、第六十、第六十一、第六十二、第七十一、第七十二、第七十三、第七十四、第七十五、第七

十六、第七十七、第七十八、第七十九、第八十、第八十二、第八十四、第八十八、第九十一、第九十四、第九十九、第一百及第一百零二实施方式的任何一个。

[0312] 在第一方面的第一百二十实施方式中,其也是该第一方面的第一、第二、第三、第四、第五、第六、第七、第八、第九、第十、第十一、第十二、第十三、第十四、第十五、第十六、第十七、第十八、第十九、第二十、第二十一、第二十二、第二十三、第二十四、第二十五、第二十六、第二十七、第二十八、第二十九、第三十、第三十一、第三十二、第三十三、第三十四、第三十五、第三十六、第三十七、第三十八、第三十九、第四十、第四十一、第四十二、第四十三、第四十四、第四十五、第四十六、第四十七、第四十八、第四十九、第五十、第五十一、第五十二、第五十三、第五十四、第五十五、第五十六、第五十七、第五十八、第五十九、第六十、第六十一、第六十二、第六十三、第六十四、第六十五、第六十六、第六十七、第六十八、第六十九、第七十、第七十一、第七十二、第七十三、第七十四、第七十五、第七十六、第七十七、第七十八、第七十九、第八十、第八十一、第八十二、第八十三、第八十四、第八十五、第八十六、第八十七、第八十八、第八十九、第九十、第九十一、第九十二、第九十三、第九十四、第九十五、第九十六、第九十七、第九十八、第九十九、第一百、第一百零一、第一百零二、第一百零三、第一百零四、第一百零五、第一百零六、第一百零七、第一百零八、第一百零九、第一百一十、第一百一十一、第一百一十二、第一百一十三、第一百一十四、第一百一十五、第一百一十六、第一百一十七、第一百一十八及第一百一十九实施方式或前述的任何其它的一实施方式,优选该第一方面的第二十八、第二十九、第三十二、第三十七、第三十八、第三十九、第四十、第四十一、第四十二、第四十三、第四十四、第四十五、第四十六、第五十九、第六十、第六十一、第六十二、第七十一、第七十二、第七十三、第七十四、第七十五、第七十六、第七十七、第七十八、第七十九、第八十、第八十二、第八十四、第八十八、第九十一、第九十四、第九十九、第一百及第一百零二实施方式,更优选该第一方面的第二十九、第三十二、第三十七、第三十八、第三十九、第四十、第五十九、第六十、第六十一、第六十二、第七十一、第七十二、第七十三、第七十四、第七十五、第七十六、第七十七、第七十八、第七十九、第八十、第八十二、第八十四、第八十八、第九十一、第九十四、第九十九、第一百及第一百零二实施方式,其中该多肽,优选该海藻糖磷酸化酶,相较于SEQ ID NO:1的海藻糖磷酸化酶,其特征在于热稳定性的提高,由此该热稳定性的提高为

[0313] i)将Tm30值增加至少2℃至40.5℃,优选2℃至30.5℃,优选至少2.5℃至30.5℃,优选至少3℃至30.5℃,优选至少3.5℃至30.5℃,优选至少4℃至30.5℃,优选至少4.5℃至30.5℃,优选至少5℃至30.5℃,优选至少5.5℃至30.5℃,优选至少6℃至30.5℃,优选至少6.5℃至30.5℃,优选至少7℃至30.5℃,优选至少7.5℃至30.5℃,优选至少8℃至30.5℃,优选至少8.5℃至30.5℃,优选至少9℃至30.5℃,更优选2℃至20.5℃,更优选至少2.5℃至20.5℃,更优选至少3℃至20.5℃,更优选至少3.5℃至20.5℃,更优选至少4℃至20.5℃,更优选至少4.5℃至20.5℃,更优选至少5℃至20.5℃,更优选至少5.5℃至20.5℃,更优选至少6℃至20.5℃,更优选至少6.5℃至20.5℃,更优选至少7℃至20.5℃,更优选至少7.5℃至20.5℃,更优选至少8℃至20.5℃,更优选至少8.5℃至20.5℃,更优选至少9℃至20.5℃,甚至更优选2℃至15.5℃,甚至更优选至少2.5℃至15.5℃,甚至更优选至少3℃至15.5℃,甚至更优选至少3.5℃至15.5℃,甚至更优选至少4℃至15.5℃,甚至更优选至少4.5℃至15.5℃,甚至更优选至少5℃至15.5℃,甚至更优选至少5.5℃至15.5℃,甚至更优选至少6℃至

15.5℃,甚至更优选至少6.5℃至15.5℃,甚至更优选至少7℃至15.5℃,甚至更优选至少7.5℃至15.5℃,甚至更优选至少8℃至15.5℃,甚至更优选至少8.5℃至15.5℃,甚至更优选至少9℃至15.5℃,甚至更优选2℃至10.5℃,甚至更优选至少2.5℃至10.5℃,甚至更优选至少3℃至10.5℃,甚至更优选至少3.5℃至10.5℃,甚至更优选至少4℃至10.5℃,甚至更优选至少4.5℃至10.5℃,甚至更优选至少5℃至10.5℃,甚至更优选至少5.5℃至10.5℃,甚至更优选至少6℃至10.5℃,甚至更优选至少6.5℃至10.5℃,甚至更优选至少7℃至10.5℃,甚至更优选至少7.5℃至10.5℃,甚至更优选至少8℃至10.5℃,甚至更优选至少8.5℃至10.5℃,甚至更优选至少9℃至10.5℃,最优选至少4℃至9℃;和/或

[0314] ii)将Tm50值增加至少2℃至42.5℃,优选2℃至32.5℃,优选至少2.5℃至32.5℃,优选至少3℃至32.5℃,优选至少3.5℃至32.5℃,优选至少4℃至32.5℃,优选至少4.5℃至32.5℃,优选至少5℃至32.5℃,优选至少5.5℃至32.5℃,优选至少6℃至32.5℃,优选至少6.5℃至32.5℃,优选至少7℃至32.5℃,优选至少7.5℃至32.5℃,优选至少8℃至32.5℃,优选至少8.5℃至32.5℃,优选至少9℃至32.5℃,优选至少9.5℃至32.5℃,优选至少10℃至32.5℃,更优选2℃至22.5℃,更优选至少2.5℃至22.5℃,更优选至少3℃至22.5℃,更优选至少3.5℃至22.5℃,更优选至少4℃至22.5℃,更优选至少4.5℃至22.5℃,更优选至少5℃至22.5℃,更优选至少5.5℃至22.5℃,更优选至少6℃至22.5℃,更优选至少6.5℃至22.5℃,更优选至少7℃至22.5℃,更优选至少7.5℃至22.5℃,更优选至少8℃至22.5℃,更优选至少8.5℃至22.5℃,更优选至少9℃至22.5℃,更优选至少9.5℃至22.5℃,更优选至少10℃至22.5℃,甚至更优选2℃至17.5℃,甚至更优选至少2.5℃至17.5℃,甚至更优选至少3℃至17.5℃,甚至更优选至少3.5℃至17.5℃,甚至更优选至少4℃至17.5℃,甚至更优选至少4.5℃至17.5℃,甚至更优选至少5℃至17.5℃,甚至更优选至少5.5℃至17.5℃,甚至更优选至少6℃至17.5℃,甚至更优选至少6.5℃至17.5℃,甚至更优选至少7℃至17.5℃,甚至更优选至少7.5℃至17.5℃,甚至更优选至少8℃至17.5℃,甚至更优选至少8.5℃至17.5℃,甚至更优选至少9℃至17.5℃,甚至更优选至少9.5℃至17.5℃,甚至更优选至少10℃至17.5℃,更优选2℃至12.5℃,甚至更优选至少2.5℃至12.5℃,甚至更优选至少3℃至12.5℃,甚至更优选至少3.5℃至12.5℃,甚至更优选至少4℃至12.5℃,甚至更优选至少4.5℃至12.5℃,甚至更优选至少5℃至12.5℃,甚至更优选至少5.5℃至12.5℃,甚至更优选至少6℃至12.5℃,甚至更优选至少6.5℃至12.5℃,甚至更优选至少7℃至12.5℃,甚至更优选至少7.5℃至12.5℃,甚至更优选至少8℃至12.5℃,甚至更优选至少8.5℃至12.5℃,甚至更优选至少9℃至12.5℃,甚至更优选至少9.5℃至12.5℃,甚至更优选至少10℃至12.5℃,且最优选至少4℃至9℃;和/或

[0315] iii)改进的工艺稳定性,其特征在于45℃半衰期延长

[0316] i)至少3倍至216倍或更多,优选至少24倍至216倍或更多,优选至少39倍至216倍或更多,优选至少48倍至216倍或更多,优选至少96倍至216倍或更多,优选至少132倍至216倍或更多,更优选至少216倍或更多倍,最优选216倍;

[0317] ii)至少24倍至216倍或更多,优选至少39倍至216倍或更多,优选至少48倍至216倍或更多,优选至少96倍至216倍或更多,优选至少132倍至216倍或更多,更优选至少216倍或更多,最优选216倍;

[0318] iii)至少96倍至216倍或更多,优选至少132倍至216倍或更多,更优选至少216倍

或更多,最优选216倍。

[0319] 更具体地,在第二方面,其也是第二方面的第一个体实施例,通过包含氨基酸序列的多肽,优选海藻糖磷酸化酶,解决了这些及其它问题,其中该多肽,优选海藻糖磷酸化酶,的该氨基酸序列与SEQ ID NO:1的氨基酸序列具有至少80%同一性和/或至少80%同源性,其中该多肽,优选海藻糖磷酸化酶,具有特征(A)、(B)、(C)、(D)与(E)中的至少一个或其任何组合,

[0320] 其中特征(A)为于52℃温育15分钟后的热稳定性,其由一介于以下范围之间的残留活性所定义

[0321] i)30%至90%,优选39%至90%,更优选42%至90%,更优选54%至90%,更优选55%至90%,甚至更优选63%%至90%,甚至更优选64%至90%,甚至更优选68%至90%,最优选64%至86%,和/或

[0322] ii)30%至90%,优选31%至90%,优选32%至90%,优选33%至90%,优选34%至90%,优选35%至90%,优选36%至90%,优选37%至90%,优选38%至90%,优选39%至90%,更优选40%至90%,更优选41%至90%,优选42%至90%,更优选43%至90%,更优选44%至90%,更优选45%至90%,更优选46%至90%,更优选47%至90%,更优选48%至90%,更优选49%至90%,甚至更优选50%至90%,甚至更优选51%至90%,甚至更优选52%至90%,甚至更优选53%至90%,甚至更优选54%至90%,甚至更优选55%至90%,甚至更优选60%至90%,甚至更优选61%至90%,甚至更优选65%至90%,甚至更优选70%至90%,甚至更优选75%至90%,最优选72%至81%,和/或

[0323] iii)55%至100%,优选60%至100%,优选70%至100%,优选75%至100%,优选76%至100%,优选77%至100%,优选78%至100%,优选79%至100%,更优选80%至100%,更优选81%至100%,更优选82%至100%,更优选83%至100%,更优选84%至100%,更优选85%至100%,更优选86%至100%,更优选87%至100%,更优选88%至100%,更优选89%至100%,甚至更优选90%至100%,甚至更优选91%至100%,甚至更优选92%至100%,甚至更优选93%至100%,甚至更优选94%至100%,甚至更优选95%至100%,甚至更优选96%至100%,甚至更优选97%至100%,甚至更优选98%至100%,尤其优选99%至100%,最优选100%以及

[0324] 其中特征(B)为于52℃温育15分钟后的热稳定性,其特征在于

[0325] i)至少52℃的Tm30值,和/或

[0326] ii)至少52℃的Tm50值,

[0327] 以及

[0328] 特征(C)为以以下为特征的热稳定性

[0329] i)介于以下温度之间的Tm30值:52℃至90℃,优选52℃至80℃,优选52.5℃至80℃,优选53℃至80℃,优选53.5℃至80℃,更优选54℃至80℃,优选54.5℃至80℃,甚至更优选55℃至80℃,优选55.5℃ 80℃,优选56℃至80℃,优选56.5℃至80℃,优选57℃至80℃,优选57.5℃至80℃,优选58℃至80℃,优选58.5℃至80℃,甚至更优选52℃至70℃,甚至更优选52.5℃至70℃,甚至更优选53℃至70℃,甚至更优选53.5℃至70℃,甚至更优选54℃至70℃,甚至更优选54.5℃至70℃,甚至更优选55℃至70℃,甚至更优选55.5℃至70℃,甚至更优选56℃至70℃,更优选56.5℃至70℃,甚至更优选57℃至70℃,甚至更优选57.5℃至70

℃,甚至更优选58℃至70℃,甚至更优选58.5℃至70℃,甚至更优选52℃至65℃,甚至更优选52.5℃至65℃,甚至更优选53℃至65℃,甚至更优选53.5℃至65℃,甚至更优选54℃至65℃,甚至更优选54.5℃至65℃,甚至更优选55℃至65℃,甚至更优选55.5℃至65℃,甚至更优选56℃至65℃,甚至更优选56℃至65℃,甚至更优选5℃至65℃,甚至更优选57℃至65℃,甚至更优选57.5℃至65℃,甚至更优选58℃至65℃,甚至更优选58.5℃至65℃,甚至更优选52℃至65℃,甚至更优选52.5℃至60℃,甚至更优选53℃至60℃,甚至更优选53.5℃至60℃,甚至更优选54℃至60℃,甚至更优选54.5℃至60℃,甚至更加为55℃至60℃,甚至更优选55.5℃至60℃,甚至更优选56℃至60℃,甚至更优选56.5℃至60℃,甚至更优选57℃至60℃,甚至更优选57.5℃至60℃之间,甚至更优选58℃至60℃,甚至更优选58.5℃至60℃,最优选53.5℃至58.5℃,和/或

[0330] i)介于以下温度之间的Tm50值:52℃至90℃,优选52℃至80℃,优选52.5℃至80℃,优选53℃至80℃,优选53.5℃至80℃,更优选在54℃至80℃,优选54.5℃至80℃,甚至更优选55℃至80℃,优选55.5℃至80℃,优选56℃至80℃,优选56.5℃至80℃,优选57℃至80℃,优选57.5℃至80℃,甚至更优选52℃至70℃,甚至更优选52.5℃至70℃,甚至更优选53℃至70℃,甚至更优选53.5℃至70℃,更优选54℃至70℃,甚至更优选54.5℃至70℃,甚至更加更优选55℃至70℃,甚至更优选55.5℃至70℃,甚至更优选56℃至70℃,甚至更优选56.5℃至70℃,更优选57℃至70℃,甚至更优选57.5℃至70℃,甚至更优选52℃至65℃,甚至更优选60℃至70℃,优选52.5℃至65℃,甚至更优选53℃至55℃,甚至更优选53.5℃至65℃,更加优选54℃至65℃,甚至更优选在54.5℃至65℃,甚至更优选55℃至65℃,甚至更优选55.5℃至65℃,甚至更优选56℃至65℃,甚至更优选56.5℃至65℃,甚至更优选57℃至65℃,甚至更优选57.5℃至65℃,甚至更优选52℃至65℃,更优选52.5℃至60℃,甚至更优选53℃至60℃,甚至更优选53.5℃至60℃,甚至更优选54℃至60℃,甚至更优选54.5℃至60℃,甚至更优选55℃至60℃,甚至更优选55.5℃至60℃,甚至更优选56℃至60℃,甚至更优选56.5℃至60℃,甚至更优选57℃至60℃,甚至更优选57.5℃至60℃,最优选52℃至57.5℃;

[0331] 以及

[0332] 特征(D)为以以下为特征的热稳定性

[0333] i)一工艺稳定性,其特征在于45℃的半衰期为3小时至9天或更多,优选24小时至9天或更多,优选39小时至9天或更多,优选2天至9天或更多,更优选4天至9天或更多,更优选5.5天至9天或更多,更优选至少7天至9天或更多,再更优选至少9天或更多,且最优选9天;

[0334] ii)一工艺稳定性,其特征在于45℃的半衰期为24小时至9天或更多,更优选39小时至9天或更多,更优选2天至9天或更多,更优选4天至9天或更多,更优选5.5天至9天或更多,更优选7天至9天或更多,甚至更优选至少9天或更多,且最优选9天;

[0335] iii)一工艺稳定性,其特征在于45℃的半衰期为4天至9天或更多,优选5.5天至9天或更多,更优选7天至9天或更多,甚至更优选至少9天或更多,且最优选9天;

[0336] 以及

[0337] 其中特征(E)为表示为100/500-比的介于以下数值之间的相对活性,

[0338] (i)0.65至1.0,优选0.7至1.0,优选0.75至1.0,优选0.8至1.0,优选0.85至1.0,优选0.9至1.0,优选0.95至1.0,且更优选至少0.7至1.0;

[0339] (ii)0.65至1.0,优选0.7至1.0,优选0.75至1.0,优选0.8至1.0,优选0.85至1.0,优选0.9至1.0,优选0.95至1.0,更优选0.8至1.0之间;其中100/500比被定义为

[0340] [100mM葡萄糖与100mMα-葡萄糖-1磷酸盐的海藻糖活性]/

[0341] [500mM葡萄糖与100mMα-葡萄糖-1磷酸盐的海藻糖活性]的比。

[0342] 在第二方面的第二实施方式中,其也是该第二方面的第一实施方式的一实施方式,该多肽,优选海藻糖磷酸化酶,于52℃温育15分钟后具有热稳定性,该热稳定性是由一介于以下百分比之间的残余活性所定义:

[0343] 为30%至90%,优选39%至90%,更优选42%至90%,更优选54%至90%,更优选55%至90%,且甚至更优选63%至90%,甚至优选64%至90%,甚至优选68%至90%,最优选64%至86%,和/或

[0344] 30%至90%,优选31%至90%,优选32%至90%,优选33%至90%,优选34%至90%,优选35%至90%,优选36%至90%,优选37%至90%,优选38%至90%,优选39%至90%,更优选40%至90%,更优选41%至90%,更优选42%至90%,更优选43%至90%,更优选44%至90%,更优选45%至90%,更优选46%至90%,更优选47%至90%,更优选48%至90%,更优选49%至90%,甚至更优选50%至90%,甚至更优选51%至90%,甚至更优选52%至90%,甚至更优选更优选53%至90%,甚至优选54%至90%,甚至优选55%至90%,甚至优选60%至90%,甚至优选61%至90%,更优选65%至90%,甚至更优选70%至90%,甚至更优选75%至90%,最优选72%至81%,和/或

[0345] 55%至100%,优选60%至100%,优选70%至100%,优选75%至100%,优选76%至100%,优选77%至100%,优选78%至100%,优选80%至100%,更优选79%至100%,更优选80%至100%,更优选81%至100%,更优选82%至100%,更优选83%至100%,优选84%至100%,更优选85%至100%,更优选86%至100%,更优选87%至100%,更优选88%至100%,更优选89%至100%,甚至优选90%至100%,甚至优选91%至100%,甚至优选92%至100%,甚至优选93%至100%,甚至优选94%至100%,甚至优选95%至100%,甚至优选96%至100%,甚至优选97%至100%,甚至优选98%至100%,甚至优选99%至100%,最优选100%。

[0346] 在第二方面的第三实施方式中,其也是第二个方面的第一及第二实施方式一的实施方式,其中该多肽,优选海藻糖磷酸化酶,具有热稳定性,其特征在于至少52℃的Tm30值。

[0347] 在第二方面的第四实施方式中,其也是第二个方面的第一、第二及第三实施方式中的实施方式,其中该多肽,优选海藻糖磷酸化酶,于45℃的半衰期为3小时至9天或更多,优选24小时至9天或更多,优选39小时至9天或更多,优选2天至9天或更多,更优选4天至9天或更多,更优选5.5天至9天或更多,更优选7天至9天或更多,甚至更优选至少9天或更多,最优选9天。

[0348] 在第二方面的第五实施方式中,其也是第二个方面的第一、第二、第三及第四实施方式中的实施方式,其中该多肽,优选海藻糖磷酸化酶,具有以100/500-比表示的相对活性,该100/500-比介于0.65至1.0之间,优选0.7至1.0,优选0.75至1.0,优选0.8至1.0,优选0.85至1.0,优选0.9至1.0,优选0.95至1.0,更优选0.7至1.0。

[0349] 在第二方面的第六实施方式中,其也是第二个方面的第一、第二、第三、第四及第五实施方式中的实施方式,其中该多肽,优选海藻糖磷酸化酶,是定义如在该第一方面的第

二十六、第二十七、第二十八、第二十九、第三十、第三十三、第三十四、第四十一、第四十二、第四十三、第四十四、第四十五、第四十六、第五十五、第六十七、第六十八、第七十五、第七十六、第七十七、第七十八、第七十九、第八十、第八十一、第八十四、第八十八、第八十九、第九十二、第九十九、第一百及第一百零二实施方式中的任何一个所述，优选定义如在该第一方面的第二十六、第二十七、第二十八、第二十九、第三十、第三十三、第三十四、第五十五、第六十七、第六十八、第七十五、第七十六、第七十七、第七十八、第七十九、第八十、第八十一、第八十四、第八十八、第八十九、第九十二、第九十九、第一百及第一百零二实施方式中的任何一个所述。

[0350] 在第二方面的第七实施方式中，其也是第二个方面的第一、第二、第三、第四、第五及第六实施方式中的实施方式，其中该多肽，优选海藻糖磷酸化酶，于52℃温育15分钟后具有以残余活性所定义的热稳定性，该残余活性为

[0351] 30％至90％，优选31％至90％，优选32％至90％，优选33％至90％，优选34％至90％，优选35％至90％，优选36％至90％，优选37％至90％，优选38％至90％，优选39％至90％，更优选40％至90％，更优选41％至90％，更优选42％至90％，更优选43％至90％，更优选44％至90％，更优选45％至90％，更优选46％至90％，更优选47％至90％，更优选48％至90％，更优选49％至90％，甚至更优选50％至90％，甚至更优选51％至90％，甚至更优选52％至90％，甚至更优选更优选53％至90％，甚至更优选54％至90％，甚至更优选55％至90％，甚至更优选60％至90％，甚至更优选61％至90％，更优选65％至90％，甚至更优选70％至90％，甚至更优选75％至90％，最优选72％至81％；和/或

[0352] 55％至100％，优选60％至100％，优选70％至100％，优选75％至100％，优选76％至100％，优选77％至100％，优选78％至100％，更优选79％至100％，更优选80％至100％，更优选81％至100％，更优选82％至100％，更优选83％至100％，优选84％至100％，更优选85％至100％，更优选86％至100％，更优选87％至100％，更优选88％至100％，更优选89％至100％，甚至更优选90％至100％，甚至更优选91％至100％，甚至更优选92％至100％，甚至更优选93％至100％，甚至更优选94％至100％，甚至更优选95％至100％，甚至更优选96％至100％，甚至更优选97％至100％，甚至更优选98％至100％，甚至更优选99％至100％，最优选100％；

[0353] 且其中该海藻糖磷酸化酶是定义如在该第一方面的第一至第一百二十实施方式或其任何其它实施方式的任何一个所述，优选如该第一方面的第二十七、第二十八、第二十九、第三十一、第三十五、第三十六、第四十一、第四十二、第四十三、第四十四、第四十五、第四十六、第五十七、第六十九、第七十、第七十五、第七十六、第七十七、第七十八、第七十九、第八十、第八十二、第八十四、第八十八、第九十、第九十三、第九十九、第一百及第一百零二实施方式中的任何一个所述，更佳定义如在该第一方面的第二十七、第二十八、第二十九、第三十一、第三十五、第三十六、第五十七、第六十九、第七十、第七十五、第七十六、第七十七、第七十八、第七十九、第八十、第八十二、第八十四、第八十八、第九十、第九十三、第九十九、第一百及第一百零二实施方式中的任何一个所述。

[0354] 在第二方面的第八实施方式中，其也是第二个方面的第一、第二、第三、第四、第五、第六及第七实施方式中的实施方式，其中该多肽，优选海藻糖磷酸化酶，具有以至少为52℃的Tm30值和/或至少为52℃的Tm50值为特征的热稳定性；且其中该海藻糖磷酸化酶是

定义如在该第一方面的第一至第一百二十实施方式或其任何其它实施方式的任何一个所述,优选如该第一方面的第二十七、第二十八、第二十九、第三十一、第三十五、第三十六、第四十一、第四十二、第四十三、第四十四、第四十五、第四十六、第五十七、第六十九、第七十、第七十五、第七十六、第七十七、第七十八、第七十九、第八十、第八十二、第八十四、第八十八、第九十、第九十三、第九十九、第一百及第一百零二实施方式中的任何一个所述,更佳定义如在该第一方面的第二十七、第二十八、第二十九、第三十一、第三十五、第三十六、第五十七、第六十九、第七十、第七十五、第七十六、第七十七、第七十八、第七十九、第八十、第八十二、第八十四、第八十八、第九十、第九十三、第九十九、第一百及第一百零二实施方式中的任何一个所述。

[0355] 在第二方面的第九实施方式中,其也是第二个方面的第一、第二、第三、第四、第五、第六、第七及第八实施方式中的实施方式,其中该多肽,优选海藻糖磷酸化酶,具有于45℃的半衰期1天至9天或更多,更优选2天至9天或更多,更优选4天至9天或更多,更优选5.5天至9天或更多,更优选7天至9天或更多,甚至更优选9天或更多,最优选9天;且其中该多肽,优选海藻糖磷酸化酶,是定义如在该第一方面的第一至第一百二十实施方式或其任何其它实施方式的任何一个所述,优选如该第一方面的第二十七、第二十八、第二十九、第三十一、第三十五、第三十六、第四十一、第四十二、第四十三、第四十四、第四十五、第四十六、第五十七、第六十九、第七十、第七十五、第七十六、第七十七、第七十八、第七十九、第八十、第八十二、第八十四、第八十八、第九十、第九十三、第九十九、第一百及第一百零二实施方式中的任何一个所述,更佳定义如在该第一方面的第二十七、第二十八、第二十九、第三十一、第三十五、第三十六、第五十七、第六十九、第七十、第七十五、第七十六、第七十七、第七十八、第七十九、第八十、第八十二、第八十四、第八十八、第九十、第九十三、第九十九、第一百及第一百零二实施方式中的任何一个所述。

[0356] 在第二方面的第十实施方式中,其也是第二个方面的第一、第二、第三、第四、第五、第六、第七、第八及第九实施方式中的实施方式,其中该多肽,优选海藻糖磷酸化酶,具有以100/500-比表示的相对活性,该100/500-比介于0.65至1.0之间,优选0.7至1.0,优选0.75至1.0,优选0.8至1.0,优选0.85至1.0,优选0.9至1.0,优选0.95至1.0,更优选0.7至1.0,且其中该海藻糖磷酸化酶,是定义如在该第一方面的第一至第一百二十实施方式或其任何其它实施方式的任何一个所述,优选如该第一方面的第二十七、第二十八、第二十九、第三十一、第三十五、第三十六、第四十一、第四十二、第四十三、第四十四、第四十五、第四十六、第五十七、第六十九、第七十、第七十五、第七十六、第七十七、第七十八、第七十九、第八十、第八十二、第八十四、第八十八、第九十、第九十三、第九十九、第一百及第一百零二实施方式中的任何一个所述,更佳定义如在该第一方面的第二十七、第二十八、第二十九、第三十一、第三十五、第三十六、第五十七、第六十九、第七十、第七十五、第七十六、第七十七、第七十八、第七十九、第八十、第八十二、第八十四、第八十八、第九十、第九十三、第九十九、第一百及第一百零二实施方式中的任何一个所述。

[0357] 在第二方面的第十一实施方式中,其也是第二个方面的第一、第二、第三、第四、第五、第六、第七、第八、第九及第十实施方式中的实施方式,其中该多肽,优选海藻糖磷酸化酶,于52℃温育15分钟后具有以一残余活性定义的热稳定性,该残余活性为55%至100%,优选60%至100%,优选70%至100%,优选75%至100%,优选76%至100%,优选77%至

100％,优选78％至100％,优选79％至100％,更优选80％至100％,更优选81％至100％,更优选82％至100％,优选83％至100％,更优选84％至100％,更优选85％至100％,更优选86％至100％,更优选87％至100％,更优选88％至100％,更优选89％至100％,甚至更优选90％至100％,甚至更优选91％至100％,甚至更优选92％至100％,更优选93％至100％,甚至更优选94％至100％,甚至更优选95％至100％,甚至更优选96％至100％,甚至更优选97％至100％,更优选98％至100％,甚至更优选99％至100％,最优选100％;且其中该海藻糖磷酸化酶,是定义如在该第一方面的第一至第一百二十实施方式或其任何其它实施方式的任何一个所述,优选如该第一方面的第二十八、第二十九、第三十二、第三十七、第三十八、第三十九、第四十、第四十一、第四十二、第四十三、第四十四、第四十五、第四十六、第五十九、第六十、第六十一、第六十二、第七十一、第七十二、第七十三、第七十四、第七十五、第七十六、第七十七、第七十八、第七十九、第八十、第八十二、第八十四、第八十八、第九十一、第九十四、第九十九、第一百及第一百零二实施方式中的任何一个所述,更佳定义如在该第一方面的第二十八、第二十九、第三十二、第三十七、第三十八、第三十九、第四十、第五十九、第六十、第六十一、第六十二、第七十一、第七十二、第七十三、第七十四、第七十五、第七十六、第七十七、第七十八、第七十九、第八十、第八十二、第八十四、第八十八、第九十一、第九十四、第九十九、第一百及第一百零二实施方式中的任何一个所述。

[0358] 在第二方面的第十二实施方式中,其也是第二个方面的第一、第二、第三、第四、第五、第六、第七、第八、第九、第十及第十一实施方式中的实施方式,其中该多肽,优选海藻糖磷酸化酶,具有以至少为52℃的Tm30值和/或至少为52℃的Tm50值为特征的热稳定性,且其优选特征在于至少52℃的Tm30值与至少52℃的Tm50值;且其中该海藻糖磷酸化酶,是定义如在该第一方面的第一至第一百二十实施方式或其任何其它实施方式的任何一个所述,优选如该第一方面的第二十八、第二十九、第三十二、第三十七、第三十八、第三十九、第四十、第四十一、第四十二、第四十三、第四十四、第四十五、第四十六、第五十九、第六十、第六十一、第六十二、第七十一、第七十二、第七十三、第七十四、第七十五、第七十六、第七十七、第七十八、第七十九、第八十、第八十二、第八十四、第八十八、第九十一、第九十四、第九十九、第一百及第一百零二实施方式中的任何一个所述,更佳定义如在该第一方面的第二十八、第二十九、第三十二、第三十七、第三十八、第三十九、第四十、第五十九、第六十、第六十一、第六十二、第七十一、第七十二、第七十三、第七十四、第七十五、第七十六、第七十七、第七十八、第七十九、第八十、第八十二、第八十四、第八十八、第九十一、第九十四、第九十九、第一百及第一百零二实施方式中的任何一个所述。

[0359] 在第二方面的第十三实施方式中,其也是第二个方面的第一、第二、第三、第四、第五、第六、第七、第八、第九、第十、第十一及第十二实施方式中的实施方式,其中该多肽,优选海藻糖磷酸化酶,具有热稳定性,其特征在于

[0360] i)一Tm30值,介于52℃至90℃之间,优选52℃至80℃,优选52.5℃至80℃,优选53℃至80℃,优选53.5℃至80℃,更优选54℃至80℃,优选54.5℃至80℃,甚至更优选55℃至80℃,优选55.5℃至80℃,优选56℃至80℃,优选56.5℃至80℃,优选57℃至80℃,优选57.5℃至80℃,优选58℃至80℃,优选58.5℃至80℃,甚至更优选52℃至70℃,甚至更优选52.5℃至70℃,甚至更优选53℃至70℃,甚至更优选53.5℃至70℃,更优选54℃至70℃,甚至更优选54.5℃至70℃,甚至更优选55℃至70℃,甚至更优选55.5℃至70℃,甚至更优选56.5℃

至70℃,甚至更优选57℃至70℃,甚至更优选57.5℃至70℃,甚至更优选57.5℃至70℃,甚至更优选58℃至70℃,甚至更优选58.5℃至70℃,甚至更优选52℃至65℃,更优选52.5℃至65℃,甚至更优选53℃至65℃,甚至更优选53.5℃至65℃,甚至更优选54℃至65℃,甚至更优选54.5℃至65℃,甚至更优选55℃至65℃,更优选55.5℃至65℃,甚至更优选56℃至65℃,甚至更优选56.5℃至65℃,甚至更优选57℃至65℃,甚至更优选57.5℃至65℃,甚至更优选58℃至65℃,甚至更优选58.5℃至65℃,甚至更优选52℃至65℃,甚至更优选52.5℃至60℃,甚至更优选53℃至60℃,甚至更优选53.5℃至60℃,甚至更优选54℃至60℃,甚至更优选54.5℃至60℃,甚至更优选55℃至60℃,甚至更优选55.5℃至60℃,甚至更优选56℃至65℃,更优选56.5℃至60℃,甚至更优选57℃至60℃,甚至更优选57.5℃至60℃,甚至更优选58℃至60℃,甚至更优选58.5℃至60℃,最优选53.5℃至58.5℃,和/或

[0361] ii)一Tm50值,介于52℃至90℃之间,优选52℃至80℃,优选52.5℃至80℃,优选53℃至80℃,优选53.5℃至80℃,更优选54℃至80℃,优选54.5℃至80℃,甚至更优选55℃至80℃,优选55.5℃至80℃,优选56℃至80℃,优选56.5℃至80℃,优选57℃至80℃,优选57.5℃至80℃,甚至更优选52℃至70℃,甚至更优选52.5℃至70℃,甚至更优选53℃至70℃,甚至更优选53.5℃至70℃,甚至更优选54℃至70℃,甚至更优选54.5℃至70℃,甚至更优选55℃至70℃,甚至更优选55.5℃至70℃,甚至更优选56℃至70℃,甚至更优选56.5℃至70℃,甚至更优选57℃至70℃,甚至更优选57.5℃至70℃,甚至更优选52℃至65℃,甚至更优选52.5℃至65℃,更优选53℃至65℃,甚至更优选53.5℃至65℃,甚至更优选54℃至65℃,甚至更优选55℃至65℃,甚至更优选55.5℃至65℃,甚至更优选56℃至65℃,甚至更优选56.5℃至65℃,甚至更优选57℃至65℃,甚至更优选57.5℃至65℃,甚至更优选52℃至60℃,甚至更优选52.5℃至60℃,甚至更优选53℃至60℃,甚至更优选53.5℃至60℃,甚至更优选54℃至60℃,甚至更优选54.5℃至60℃,甚至更优选55℃至60℃,甚至更优选55.5℃至60℃,甚至更优选56℃至60℃,甚至更优选56.5℃至60℃,更优选57℃至60℃,甚至更优选57.5℃至60℃,且最优选52℃至57.5℃;且其中该海藻糖磷酸化酶,是定义如在该第一方面的第一至第一百二十实施方式或其任何其它实施方式的任何一个所述,优选如该第一方面的第二十八、第二十九、第三十二、第三十七、第三十八、第三十九、第四十、第四十一、第四十二、第四十三、第四十四、第四十五、第四十六、第五十九、第六十、第六十一、第六十二、第七十一、第七十二、第七十三、第七十四、第七十五、第七十六、第七十七、第七十八、第七十九、第八十、第八十二、第八十四、第八十八、第九十一、第九十四、第九十九、第一百及第一百零二实施方式中的任何一个所述,更佳定义如在该第一方面的第二十八、第二十九、第三十二、第三十七、第三十八、第三十九、第四十、第五十九、第六十、第六十一、第六十二、第七十一、第七十二、第七十三、第七十四、第七十五、第七十六、第七十七、第七十八、第七十九、第八十、第八十二、第八十四、第八十八、第九十一、第九十四、第九十九、第一百及第一百零二实施方式中的任何一个所述。

[0362] 在第二方面的第十四实施方式中,其也是第二个方面的第一、第二、第三、第四、第五、第六、第七、第八、第九、第十、第十一、第十二及第十三实施方式中的实施方式,其中该多肽,优选海藻糖磷酸化酶,具有于45℃半衰期为4天至9天或更多,优选5.5天至9天或更多,更优选7天至9天或更多,甚至更优选9天或更多,且最优选9天;且其中该多肽,优选海藻糖磷酸化酶,是定义如在该第一方面的第一至第一百二十实施方式或其任何其它实施方式

的任何一个所述,优选如该第一方面的第二十八、第二十九、第三十二、第三十七、第三十八、第三十九、第四十、第四十一、第四十二、第四十三、第四十四、第四十五、第四十六、第五十九、第六十、第六十一、第六十二、第七十一、第七十二、第七十三、第七十四、第七十五、第七十六、第七十七、第七十八、第七十九、第八十、第八十二、第八十四、第八十八、第九十一、第九十四、第九十九、第一百及第一百零二实施方式中的任何一个所述,更佳定义如在该第一方面的第二十八、第二十九、第三十二、第三十七、第三十八、第三十九、第四十、第五十九、第六十、第六十一、第六十二、第七十一、第七十二、第七十三、第七十四、第七十五、第七十六、第七十七、第七十八、第七十九、第八十、第八十二、第八十四、第八十八、第九十一、第九十四、第九十九、第一百及第一百零二实施方式中的任何一个所述。

[0363] 在第二方面的第十五实施方式中,其也是第二个方面的第一、第二、第三、第四、第五、第六、第七、第八、第九、第十、第十一、第十二、第十三及第十四实施方式中的实施方式,其中该多肽,优选海藻糖磷酸化酶,具有以100/500-比表示的相对活性,该100/500-比介于0.65至1.0之间,优选0.7至1.0,优选0.75至1.0,优选0.8至1.0,优选0.85至1.0,优选0.9至1.0,优选0.95至1.0,更优选0.8至1.0;且其中该海藻糖磷酸化酶,是定义如在该第一方面的第一至第一百二十实施方式或其任何其它实施方式的任何一个所述,优选如该第一方面的第二十八、第二十九、第三十二、第三十七、第三十八、第三十九、第四十、第四十一、第四十二、第四十三、第四十四、第四十五、第四十六、第五十九、第六十、第六十一、第六十二、第七十一、第七十二、第七十三、第七十四、第七十五、第七十六、第七十七、第七十八、第七十九、第八十、第八十二、第八十四、第八十八、第九十一、第九十四、第九十九、第一百及第一百零二实施方式中的任何一个所述,更佳定义如在该第一方面的第二十八、第二十九、第三十二、第三十七、第三十八、第三十九、第四十、第五十九、第六十、第六十一、第六十二、第七十一、第七十二、第七十三、第七十四、第七十五、第七十六、第七十七、第七十八、第七十九、第八十、第八十二、第八十四、第八十八、第九十一、第九十四、第九十九、第一百及第一百零二实施方式中的任何一个所述。

[0364] 在第二方面的第十六实施方式中,其也是第二个方面的第一、第二、第三、第四、第五及第六实施方式中的实施方式,其中该多肽,优选海藻糖磷酸化酶,相较于SEQ ID NO:1的海藻糖磷酸化酶,其热稳定性增加,由此热稳定性增加为

[0365] i)该Tm30值增加至少2℃至40.5℃,优选2℃至30.5℃,优选至少2.5℃至30.5℃,优选至少3℃至30.5℃,优选至少3.5℃至30.5℃,优选至少4℃至30.5℃,优选至少4.5℃至30.5℃,优选至少5℃至30.5℃,优选至少5.5℃至30.5℃,优选至少6℃至30.5℃,优选至少6.5℃至30.5℃,优选至少7℃至30.5℃,优选至少7.5℃至30.5℃,优选至少8℃至30.5℃,优选至少8.5℃至30.5℃,优选至少9℃至30.5℃,更优选2℃至20.5℃,更优选至少2.5℃至20.5℃,更优选至少3℃至20.5℃,更优选至少3.5℃至20.5℃,更优选至少4℃至20.5℃,更优选至少4.5℃至20.5℃,更优选至少5℃至20.5℃,更优选至少5.5℃至20.5℃,更优选至少6℃至20.5℃,更优选至少6.5℃至20.5℃,更优选至少7℃至20.5℃,更优选至少7.5℃至20.5℃,更优选至少8℃至20.5℃,更优选至少8.5℃至20.5℃,更优选至少9℃至20.5℃,甚至更优选2℃至15.5℃,甚至更优选至少2.5℃至15.5℃,甚至更优选至少3℃至15.5℃,甚至更优选至少3.5℃至15.5℃,甚至更优选至少4℃至15.5℃,甚至更优选至少4.5℃至15.5℃,甚至更优选至少5℃至15.5℃,甚至更优选至少5.5℃至15.5℃,甚至更优选至少5℃至

15.5℃,优选至少6℃至15.5℃,甚至更优选至少6.5℃至15.5℃,甚至更优选至少7℃至15.5℃,甚至更优选至少7.5℃至15.5℃,甚至更优选至少8℃至15.5℃,甚至更优选至少8.5℃至15.5℃,甚至更优选至少9℃至15.5℃,甚至更优选2℃至10.5℃,甚至更优选至少2.5℃至10.5℃,甚至更优选至少3℃至10.5℃,甚至更优选至少3.5℃至10.5℃,甚至更优选至少4℃至10.5℃,甚至更优选至少4.5℃至10.5℃,甚至更优选至少5℃至10.5℃,甚至更优选至少5.5℃至10.5℃,甚至更优选至少6℃至10.5℃,甚至更优选至少6.5℃至10.5℃,甚至更优选至少7℃至10.5℃,甚至更优选至少7.5℃至10.5℃,甚至更优选至少7.5℃至最高10.5℃,更优选至少8℃至10.5℃,甚至更优选至少8.5℃至10.5℃,甚至更优选至少9℃至10.5℃,最优选至少4℃至9℃;

[0366] ii)该Tm50值增加至少2℃至42.5℃,优选2℃至32.5℃,优选至少2.5℃至32.5℃,优选至少3℃至32.5℃,优选至少3.5℃至32.5℃,优选至少4℃至32.5℃,优选至少4.5℃至32.5℃,优选至少5℃至32.5℃,优选至少5.5℃至32.5℃,优选至少6℃至32.5℃,优选至少6.5℃至32.5℃,优选至少7℃至32.5℃,优选至少7.5℃至32.5℃,优选至少8℃至32.5℃,优选至少8.5℃至32.5℃,优选至少9℃至32.5℃,优选至少9.5℃至32.5℃,优选至少10℃至32.5℃,更优选2℃至22.5℃,更优选至少2.5℃至22.5℃,更优选至少3℃至22.5℃,更优选至少3.5℃至22.5℃,更优选至少4℃至22.5℃,更优选至少4.5℃至22.5℃,更优选至少5℃至22.5℃,更优选至少5.5℃至22.5℃,更优选至少6℃至22.5℃,更优选至少6.5℃至22.5℃,更优选至少7℃至22.5℃,更优选至少7.5℃至22.5℃,更优选至少8℃至22.5℃,更优选至少8.5℃至22.5℃,更优选至少9℃至22.5℃,更优选至少9.5℃至22.5℃,更优选至少10℃至22.5℃,甚至更优选2℃至17.5℃,甚至更优选至少2.5℃至17.5℃,甚至更优选至少3℃至17.5℃,甚至更优选至少3.5℃至17.5℃,甚至更优选至少4℃至17.5℃,甚至更优选至少4.5℃至17.5℃,甚至更优选至少5℃至17.5℃,甚至更优选5.5℃至17.5℃,甚至更优选6℃至17.5℃,甚至更优选6.5℃至17.5℃,甚至更优选至少7℃至17.5℃,甚至更优选至少7.5℃至17.5℃,甚至更优选至少8℃至17.5℃,甚至更优选至少8.5℃至17.5℃,甚至更优选至少9℃至17.5℃,甚至更优选至少9.5℃至17.5℃,甚至更优选至少10℃至17.5℃,甚至更优选2℃至12.5℃,甚至更优选2.5℃至12.5℃,甚至更优选3℃至12.5℃,甚至更优选至少3.5℃至12.5℃,甚至更优选至少4℃至12.5℃,甚至更优选至少4.5℃至12.5℃,甚至更优选至少5℃至12.5℃,甚至更优选至少5.5℃至12.5℃,甚至更优选至少6℃至12.5℃,甚至更优选至少6.5℃至12.5℃,甚至更优选至少7℃至12.5℃,甚至更优选至少7.5℃至12.5℃,甚至更优选至少8℃至12.5℃,甚至更优选至少8.5℃至12.5℃,甚至更优选至少9℃至12.5℃,甚至更优选至少9.5℃至12.5℃,甚至更优选至少10℃至12.5℃,最优选至少4℃至9℃;

[0367] iii)改进的工艺稳定性,其特征在于45℃半衰期延长

[0368] i)至少3倍至216倍或更多,优选至少24倍至216倍或更多,优选至少39倍至216倍或更多,优选至少48倍至216倍或更多,优选至少96倍至216倍或更多,优选至少132倍至216倍或更多,甚至更优选至少216倍或更多,最优选216倍;

[0369] ii)至少24倍至216倍或更多,优选至少39倍至216倍或更多,优选至少48倍至216倍或更多,优选至少96迭至216倍或更多,优选至少132倍至216倍或更多,甚至更优选至少216倍或更多,最优选216倍;

[0370] iii)至少96倍至216倍或更多,优选至少132倍至216倍或更多,甚至更优选至少216倍或更多,最优选216倍。

[0371] 在第二方面的第十七实施方式中,其也是第二个方面的第十六实施方式中的实施方式,该多肽,优选该海藻糖磷酸化酶,是为多肽,优选海藻糖磷酸化酶,是定义如在该第一方面的第一至第一百二十实施方式或其任何其它实施方式的任何一个所述,优选如该第一方面的第二十七、第二十八、第二十九、第三十一、第三十五、第三十六、第四十一、第四十二、第四十三、第四十四、第四十五、第四十六、第五十七、第六十九、第七十、第七十五、第七十六、第七十七、第七十八、第七十九、第八十、第八十二、第八十四、第八十八、第九十、第九十三、第九十九、第一百及第一百零二实施方式中的任何一个所述,更佳定义如在该第一方面的第二十七、第二十八、第二十九、第三十一、第三十五、第三十六、第五十七、第六十九、第七十、第七十五、第七十六、第七十七、第七十八、第七十九、第八十、第八十二、第八十四、第八十八、第九十、第九十三、第九十九、第一百及第一百零二实施方式中的任何一个所述。

[0372] 在第二方面的第十八实施方式中,其也是第二个方面的第十六实施方式中的实施方式,其中该多肽,优选海藻糖磷酸化酶,是为多肽,优选海藻糖磷酸化酶,是定义如在该第一方面的第一至第一百二十实施方式或其任何其它实施方式的任何一个所述,优选如该第一方面的第二十八、第二十九、第三十二、第三十七、第三十八、第三十九、第四十、第四十一、第四十二、第四十三、第四十四、第四十五、第四十六、第五十九、第六十、第六十一、第六十二、第七十一、第七十二、第七十三、第七十四、第七十五、第七十六、第七十七、第七十八、第七十九、第八十、第八十二、第八十四、第八十八、第九十一、第九十四、第九十九、第一百及第一百零二实施方式中的任何一个所述,更佳定义如在该第一方面的第二十八、第二十九、第三十二、第三十七、第三十八、第三十九、第四十、第五十九、第六十、第六十一、第六十二、第七十一、第七十二、第七十三、第七十四、第七十五、第七十六、第七十七、第七十八、第七十九、第八十、第八十二、第八十四、第八十八、第九十一、第九十四、第九十九、第一百及第一百零二实施方式中的任何一个所述。

[0373] 在第二方面的第十九实施方式中,其也是第二个方面的第一、第二、第三、第四、第五、第六、第七、第八、第九、第十、第十一、第十二、第十三、第十四、第十五、第十六、第十七及第十八实施方式中的实施方式,其中该多肽,优选海藻糖磷酸化酶,是为多肽,优选海藻糖磷酸化酶,是定义如在该第一方面的第一至第一百二十实施方式或其任何其它实施方式的任何一个所述,优选如该第一方面的第二十八、第二十九、第三十二、第三十七、第三十八、第三十九、第四十、第四十一、第四十二、第四十三、第四十四、第四十五、第四十六、第五十九、第六十、第六十一、第六十二、第七十一、第七十二、第七十三、第七十四、第七十五、第七十六、第七十七、第七十八、第七十九、第八十、第八十二、第八十四、第八十八、第九十一、第九十四、第九十九、第一百及第一百零二实施方式中的任何一个所述,更佳定义如在该第一方面的第二十八、第二十九、第三十二、第三十七、第三十八、第三十九、第四十、第五十九、第六十、第六十一、第六十二、第七十一、第七十二、第七十三、第七十四、第七十五、第七十六、第七十七、第七十八、第七十九、第八十、第八十二、第八十四、第八十八、第九十一、第九十四、第九十九、第一百及第一百零二实施方式中的任何一个所述,其中该多肽,优选该海藻糖磷酸化酶,能够催化葡糖基单醣与α-D-葡萄糖-1磷酸盐的反应。

[0374] 在第二方面的第二十实施方式中,其也是第二个方面的第十九实施方式中的实施

方式,其中该多肽,优选海藻糖磷酸化酶,能够催化

[0375] 葡萄糖与α-D-葡萄糖-1磷酸盐转化为海藻糖与无机磷酸盐

[0376] 和/或

[0377] 海藻糖与无机磷酸盐转化为葡萄糖与α-D-葡萄糖-1磷酸盐。

[0378] 在第二方面的第二十一实施方式中,其也是第二个方面的第十九及第二十实施方式中的实施方式,该转化为可逆的转化。

[0379] 在第二方面的第二十二实施方式中,其也是第二个方面的第一、第二、第三、第四、第五、第六、第七、第八、第九、第十、第十一、第十二、第十三、第十四、第十五、第十六、第十七、第十八、第十九、第二十及第二十一实施方式中的实施方式,该多肽,优选海藻糖磷酸化酶,是根据EC号为EC 2.4.1.231的海藻糖磷酸化酶。

[0380] 更具体地,在第三方面,其也是第三方面的第一实施方式,通过一热稳定的海藻糖磷酸化酶变体解决了这些与其它问题,其中该变体在含有1M蔗糖的缓冲液中于52℃温育15分钟后保留其初始活性的至少30%,且该初始活性在室温温育15分钟后所测定。

[0381] 在第三方面的第二实施方式中,其也是第三个方面的第一实施方式中的实施方式,该变体在含有1M蔗糖的缓冲液中于52℃温育15分钟后保留其初始活性的至少50%,且该初始活性在室温温育15分钟后测定。

[0382] 更具体地,在第四方面,其也是第四方面的第一实施方式,通过热稳定的海藻糖磷酸化酶的变体来解决这些及其它问题,该变体是衍生自属于担子菌门(Basidomycota)的一生物体,优选来自属于伞菌纲(Agaricomycetes)的一生物体,且更佳来自属于由裂折菌属(Schizophyllum)、侧耳属(Pleurotus)、奇果菌属(Grifola)、蘑菇属(Agaricus)、栓菌属(Trametes)、革盖菌属(Coriolus)、栓菌属(Trametes)、附毛菌属(Trichaptum)以及折孔菌属(Lenzites)组成的组的属的一生物体,且最佳来自裂折菌(Schizophyllum commune),或来自千佛菌(Grifola frondosa)的一生物体,其中该变体于52℃温育15分钟后具有至少30%的残余活性,且其初始活性在室温温育15分钟后测定。

[0383] 在本发明第四方面的第一实施方式中的优选实施方式中,该热稳定的海藻糖磷酸化酶的变体于52℃温育15分钟后具有至少30%的残余活性,其中初始活性在室温温育15分钟后测定,且其中该海藻糖磷酸化酶是为来自裂褶菌的海藻糖磷酸化酶的变体。

[0384] 在本发明第四方面的第一实施方式的另一优选实施方式中,该热稳定的海藻糖磷酸化酶的变体于52℃温育15分钟后具有至少30%的残余活性,且其中该初始活性在室温温育15分钟后测定,且其中该海藻糖磷酸化酶是为来自千佛菌的海藻糖磷酸化酶的变体。

[0385] 更具体而言,在第十四方面,其也是该第十四个方面的第一实施方式,通过包含氨基酸序列的多肽来解决这些及其它问题,该多肽优选海藻糖磷酸化酶,其中该海藻糖磷酸化酶的氨基酸序列与SEQ ID NO:81或SEQ ID NO:160,优选SEQ ID NO:160,的氨基酸序列具有至少85%同一性和/或至少86%同源性,其中该海藻糖磷酸化酶的氨基酸序列在一个或更多个氨基酸位置处包含氨基酸取代,其中该一个或更多个氨基酸位置选自由下列SEQ ID NO:81或SEQID NO:160,优选SEQ ID NO:160,的氨基酸位置组成的组:108、112、221、300、319、345、379、483、544、550、558、584、643以及707,且其优选选自由下列SEQ ID NO:81或SEQ ID NO:160,优选SEQ ID NO:160,的氨基酸位置组成的组:108、112、221、300、319、379、483、544、550以及558,且其更佳选自由下列SEQ ID NO:81或SEQ ID NO:160,优选SEQ

ID NO:160,的氨基酸位置组成的组:108、221、319、379、483、550以及558。

[0386] 在该第十四方面的第二实施方式,其也是该第十四个方面的第一实施方式中的实施方式,该一个或更多个氨基酸位置选自由下列SEQ ID NO:160的氨基酸位置组成的组:L108、V112、N221、A300、T319、F345、P379、V483、V544、S550、Q558、N584、A643以及L707,其优选选自由下列SEQ ID NO:160的氨基酸位置组成的组:L108、V112、N221、A300、T319、P379、V483、V544、S550以及Q558,且其更加选自由下列SEQ ID NO:160的氨基酸位置组成的组:L108、V221、T319、P379、V483、S550以及Q558。

[0387] 在该第十四方面的第三实施方式,其也是该第十四个方面的第一实施方式中的实施方式,该一个或更多个氨基酸位置选自由下列SEQ ID NO:81的氨基酸位置组成的组:L108、V112、N221、A300、T319、F345、P379、I483、V544、S550、Q558、N584、A643以及L707,其优选选自由下列SEQ ID NO:81的氨基酸位置组成的组:L108、V112、N221、A300、T319、P379、I483、V544、S550以及Q558,且其更加选自由下列SEQ ID NO:81的氨基酸位置组成的组:L108、V221、T319、P379、I483、S550以及558。

[0388] 在该第十四方面的第四实施方式,其也是该第十四个方面的任何其它实施方式中的实施方式,该海藻糖磷酸化酶的氨基酸序列在一个或更多个氨基酸位置处包含氨基酸取代,其中该一个或更多个氨基酸位置选自由下列SEQ ID NO:81或SEQ ID NO:160,优选SEQ ID NO:160,的氨基酸位置组成的组:108、112、221、300、319、345、379、483、544、550、558、584、643以及707。如在本发明的上下文中令人惊讶地发现的,一个或更多个这些位置的突变增加了该酶的热稳定性,导致于52.5℃温育15分钟后的残余活性至少为12%,与由SEQ ID NO:160的野生型氨基酸序列编码的海藻糖磷酸化酶的9%残余活性相比。

[0389] 在该第十四方面的第五实施方式,其也是该第十四个方面的任何其它实施方式中的实施方式,该海藻糖磷酸化酶的氨基酸序列在一个或更多个氨基酸位置处包含氨基酸取代,其中该一个或更多个氨基酸位置选自由下列SEQ ID NO:81或SEQ ID NO:160,优选SEQ ID NO:160,的氨基酸位置组成的组:108、112、221、300、319、379、483、544、550以及558。如在本发明的上下文中令人惊讶地发现的,一个或更多个这些位置的突变增加了该酶的热稳定性,导致于52.5℃温育15分钟后的残余活性至少为30%,与由SEQ ID NO:160的野生型氨基酸序列编码的海藻糖磷酸化酶的9%残余活性相比。

[0390] 在该第十四方面的第六实施方式,其也是该第十四个方面的第一实施方式中的实施方式,该海藻糖磷酸化酶的氨基酸序列在一个或更多个氨基酸位置处包含氨基酸取代,其中该一个或更多个氨基酸位置选自由下列SEQ ID NO:81或SEQ ID NO:160,优选SEQ ID NO:160,的氨基酸位置组成的组:108、221、319、379、483、550以及558。如在本发明的上下文中令人惊讶地发现的,一个或更多个这些位置的突变增加了该酶的热稳定性,导致于52.5℃温育15分钟后的残余活性至少为50%,与由SEQ ID NO:160的野生型氨基酸序列编码的海藻糖磷酸化酶的9%残余活性相比。

[0391] 在该第十四方面的第七实施方式,其也是该第十四个方面的前述任何实施方式中的实施方式,该海藻糖磷酸化酶的氨基酸序列包含氨基酸序列,其是根据SEQ ID NO:161、162、163、164、165、166、167、168、169、170、171、172、173、174、175、176、177、178、179、180、181、182、183、184、185、186、187、188以及189的任一个,优选根据SEQ ID NO:163、165、166、168、171、173、176、177、178、179、180、184、185、186、187、188以及189的任一个,更优选根据

SEQ ID NO:176、178、180、185以及188的任一个。

[0392] 在该第十四方面的第八实施方式,其也是该第十四个方面的前述任何实施方式中的实施方式,该海藻糖磷酸化酶的氨基酸序列是由氨基酸序列组成,其是根据SEQ ID NO:161、162、163、164、165、166、167、168、169、170、171、172、173、174、175、176、177、178、179、180、181、182、183、184、185、186、187、188以及189的任一个,优选根据SEQ ID NO:163、165、166、168、171、173、176、177、178、179、180、184、185、186、187、188以及189的任一个,更优选根据SEQ ID NO:176、178、180、185以及188的任一个。

[0393] 该第十四方面的第九实施方式,其也是该第十四个方面的前述任何实施方式中的实施方式,该一个或更多个氨基酸位置为两个或更多个氨基酸位置。

[0394] 在该第十四方面的第十实施方式,其也是该第十四个方面的前述任何实施方式中的实施方式,该一个或更多个氨基酸位置为三个或更多个氨基酸位置。

[0395] 在该第十四方面的第十一实施方式,其也是该第十四个方面的前述任何实施方式中的实施方式,该一个或更多个氨基酸位置为四个或更多个氨基酸位置。

[0396] 在该第十四方面的第十二实施方式,其也是该第十四个方面的前述任何实施方式中的实施方式,该两个或更多个氨基酸位置包含一两个氨基酸对位置,其中该两个氨基酸对位置选自由下列SEQ ID NO:81或SEQ ID NO:160,优选SEQ ID NO:160,的氨基酸位置组成的组:108与112、108与221、108与300、108与319、108与345、108与379、108与483、108与544、108与550、108与558、108与584、108与643、108与707、112与221、112与300、112与319、112与345、112与379、112与483、112与544、112与550、112与558、112与584、112与643、112与707、221与300、221与319、221与345、221与379、221与483、221与544、221与550、221与558、221与584、221与643、221与707、300与319、300与345、300与379、300与483、300与544、300与550、300与558、300与584、300与643、300与707、319与345、319与379、319与483、319与544、319与550、319与558、319与584、319与643、319与707、345与379、345与483、345与544、345与550、345与558、345与584、345与643、345与707、379与483、379与544、379与550、379与558、379与584、379与643、379与707、483与544、483与550、483与558、483与584、483与643、483与707、544与550、544与558、544与584、544与643、544与707、550与558、550与584、550与643、550与707、558与584、558与643、558与707、584与643、584与707以及643与707,优选选自由下列氨基酸位置组成的组:L108与V112、L108与N221、L108与A300、L108与T319、L108与F345、L108与P379、L108与分别为SEQ ID NO:160的V483或SEQ ID NO:81的I483、L108与V544、L108与S550、L108与Q558、L108与N584、L108与A643、L108与L707、V112与N221、V112与A300、V112与T319、V112与F345、V112与P379、V112与分别为SEQ ID NO:160的V483或SEQ ID NO:81的I483、V112与V544、V112与S550、V112与Q558、V112与N584、V112与A643、V112与L707、N221与A300、N221与T319、N221与F345、N221与P379、N221与分别为SEQ ID NO:160的V483或SEQ ID NO:81的I483、N221与V544、N221与S550、N221与Q558、N221与N584、N221与A643、N221与L707、A300与T319、A300与F345、A300与P379、A300与分别为SEQ ID NO:160的V483或SEQ ID NO:81的I483、A300与V544、A300与S550、A300与Q558、A300与N584、A300与A643、A300与L707、T319与F345、T319与P379、T319与SEQ ID NO:160的V483或SEQ ID NO:81的I483、T319与V544、T319与S550、T319与Q558、T319与N584、T319与A643、T319与L707、F345与P379、F345与分别为SEQ ID NO:160的V483或SEQ ID NO:81的I483、F345与V544、F345与

S550、F345与Q558、F345与N584、F345与A643、F345与L707、P379与分别为SEQ ID NO:160的V483或SEQ ID NO:81的I483、P379与V544、P379与S550、P379与Q558、P379与N584、P379与A643、P379与L707、分别为SEQ ID NO:160的V483或SEQ ID NO:81的I483与V544、分别为SEQ ID NO:160的V483或SEQ ID NO:81的I483与S550、分别为SEQ ID NO:160的V483或SEQ ID NO:81的I483与Q558、分别为SEQ ID NO:160的V483或SEQ ID NO:81的I483与N584、分别为SEQ ID NO:160的V483或SEQ ID NO:81的I483与A643、分别为SEQ ID NO:160的V483或SEQ ID NO:81的I483与L707、V544与S550、V544与Q558、V544与N584、V544与A643、V544与L707、S550与Q558、S550与N584、S550与A643、S550与L707、Q558与N584、Q558与A643、Q558与L707、N584与A643、N584与L707以及A643与L707。

[0397] 在该第十四方面的第十三实施方式,其也是该第十四个方面的前述任何实施方式中的实施方式,该两个氨基酸对位置选自由下列氨基酸位置组成的组:L108与V112、L108与N221、L108与A300、L108与T319、L108与P379、L108与分别为SEQ ID NO:160的V483或SEQ ID NO:81的I483、L108与V544、L108与S550、L108与Q558、V112与N221、V112与A300、V112与T319、V112与P379、V112与分别为SEQ ID NO:160的V483或SEQ ID NO:81的I483、V112与V544、V112与S550、V112与Q558、N221与A300、N221与T319、N221与P379、N221与分别为SEQ ID NO:160的V483或SEQ ID NO:81的I483、N221与V544、N221与S550、N221与Q558、A300与T319、A300与P379、A300与分别为SEQ ID NO:160的V483或SEQ ID NO:81的I483、A300与V544、A300与S550、A300与Q558、T319与P379、T319与分别为SEQ ID NO:160的V483或SEQ ID NO:81的I483、T319与V544、T319与S550、T319与Q558、P379与分别为SEQ ID NO:160的V483或SEQ ID NO:81的I483、P379与V544、P379与S550、P379与Q558、分别为SEQ ID NO:160的V483或SEQ ID NO:81的I483与V544、分别为SEQ ID NO:160的V483或SEQ ID NO:81的I483与S550、分别为SEQ ID NO:160的V483或SEQ ID NO:81的I483与Q558、V544与S550、V544与Q558以及S550与Q558。

[0398] 在该第十四方面的第十四实施方式,其也是该第十四个方面的前述任何实施方式中的实施方式,该两个氨基酸对位置选自由下列氨基酸位置组成的组:L108与T319、L108与P379、L108与分别为SEQ ID NO:160的V483或SEQ ID NO:81的I483、L108与S550、L108与Q558、N221与T319、N221与P379、N221与分别为SEQ ID NO:160的V483或SEQ ID NO:81的I483、N221与V544、N221与S550、N221与Q558、T319与P379、T319与分别为SEQ ID NO:160的V483或SEQ ID NO:81的I483、T319与V544、T319与S550、T319与Q558、P379与分别为SEQ ID NO:160的V483或SEQ ID NO:81的I483、P379与V544、P379与S550、P379与Q558、分别为SEQ ID NO:160的V483或SEQ ID NO:81的I483与V544、分别为SEQ ID NO:160的V483或SEQ ID NO:81的I483与S550、分别为SEQ ID NO:160的V483或SEQ ID NO:81的I483与Q558以及S550与Q558。

[0399] 在该第十四方面的第十五实施方式,其也是该第十四个方面的前述任何实施方式中的实施方式,除了在该两个氨基酸位置处的取代之外,该海藻糖磷酸化酶的氨基酸序列包含在至少一个或更多个另外的氨基酸位置处的氨基酸取代,其中该一个或更多个另外的氨基酸位置选自由下列SEQ ID NO:81或SEQ ID NO:160,优选SEQ ID NO:160,的氨基酸位置组成的组:108、112、221、300、319、345、379、483、544、550、558、584、643以及707,优选除了在该两个氨基酸位置处的取代之外,该海藻糖磷酸化酶的氨基酸序列包含在至少一个或

更多个另外的氨基酸位置处的氨基酸取代,其中该一个或更多个另外的氨基酸位置选自由下列SEQ ID NO:81或SEQ ID NO:160,优选SEQ ID NO:160,的氨基酸位置组成的组:108、112、221、300、319、379、483、544、550以及558,更优选除了在该两个氨基酸位置处的取代之外,该海藻糖磷酸化酶的氨基酸序列包含在至少一个或更多个另外的氨基酸位置处的氨基酸取代,其中该一个或更多个另外的氨基酸位置选自由下列SEQ ID NO:81或SEQ ID NO:160,优选SEQ ID NO:160,的氨基酸位置组成的组:108、221、319、379、483、550以及558。

[0400] 在该第十四方面的第十六实施方式,其也是该第十四个方面的另一实施方式中的实施方式,该一个或更多个另外的氨基酸位置选自由下列SEQ ID NO:81或SEQ ID NO:160,优选SEQ ID NO:160,的氨基酸位置组成的组:L108、V112、N221、A300、T319、F345、P379,分别为SEQ ID NO:160的V483或SEQ ID NO:81的I483、V544、S550、Q558、N584、A643以及L707,优选除了在该两个氨基酸位置处的取代之外,该海藻糖磷酸化酶的氨基酸序列包含在至少一个或更多个另外的氨基酸位置处的氨基酸取代,其中该一个或更多个另外的氨基酸位置选自由下列SEQ ID NO:81或SEQ ID NO:160,优选SEQ ID NO:160,的氨基酸位置组成的组:L108、V112、N221、A300、T319、P379,分别为SEQ ID NO:160的V483或SEQ ID NO:81的I483、V544、S550以及Q558,更优选除了在该两个氨基酸位置处的取代之外,该海藻糖磷酸化酶的氨基酸序列包含在至少一个或更多个另外的氨基酸位置处的氨基酸取代,其中该一个或更多个另外的氨基酸位置选自由下列SEQ ID NO:81或SEQ ID NO:160,优选SEQ ID NO:160,的氨基酸位置组成的组:L108、V221、T319、P379,分别为SEQ ID NO:160的V483或SEQ ID NO:81的I483、S550以及Q558。

[0401] 在该第十四方面的第十七实施方式,其也是该第十四个方面的前述任何实施方式中的实施方式,在该氨基酸位置处的任何取代选自由A、R、N、D、C、Q、E、G、H、I、L、K、M、F、P、S、T、W、Y以及V组成的组,优选在该氨基酸位置处的任何取代是各别且独立地选自由A、R、N、D、C、Q、E、G、H、I、L、K、M、F、P、S、T、W、Y以及V组成的组。

[0402] 在该第十四方面的第十八实施方式,其也是该第十四个方面的第十二实施方式或该第十四方面的前述实施方式的任何其它中的实施方式,该取代是位于SEQ ID NO:81或SEQ ID NO:160,优选SEQ ID NO:160,的以下任何氨基酸位置:160 108、112、221、300、319、345、379、483、544、550、558、584、643以及707。

[0403] 在该第十四方面的第十九实施方式,其也是该第十四个方面的第十三实施方式或该第十四方面的前述实施方式的任何其它中的实施方式,该取代是位于SEQ ID NO:81或SEQ ID NO:160,优选SEQ ID NO:160,的以下任何氨基酸位置:L108、V112、N221、A300、T319、F345、P379、V483、V544、S550、Q558、N584、A643以及L707。

[0404] 在该第十四方面的第二十实施方式,其也是该第十四个方面的前述实施方式的任何其它中的实施方式,该海藻糖磷酸化酶的氨基酸序列包含一个或更多个取代,其中该取代选自由下列组成的组:

[0405] 在SEQ ID NO:81或SEQ ID NO:160,优选SEQ ID NO:160,的位置L108处的氨基酸取代,其中该取代为L108A、L108G、L108I、L108M、L108P或L108V,优选L108I;

[0406] 在SEQ ID NO:81或SEQ ID NO:160,优选SEQ ID NO:160,的位置V112处的氨基酸取代,其中该取代为V112A、V112G、V112L、V112M、V112P或V112I,优选V112I;

[0407] 在SEQ ID NO:81或SEQ ID NO:160,优选SEQ ID NO:160,的位置N221处的氨基酸

取代,其中该取代为N221A、N221G、N221I、N221L、N221M、N221P或N221V,优选N221I、N221L、N221M或N221V以及更优选N221V;

[0408] 在SEQ ID NO:81或SEQ ID NO:160,优选SEQ ID NO:160,的位置A300处的氨基酸取代,其中该取代为A300G、A300I、A300L、A300M、A300P或A300V,优选A300I或A300L以及更优选A300I;

[0409] 在SEQ ID NO:81或SEQ ID NO:160,优选SEQ ID NO:160,的位置T319处的氨基酸取代,其中该取代为T319A、T319G、T319I、T319L、T319M、T319P,或T319V,优选T319I或T319V以及更优选T319I;

[0410] 在SEQ ID NO:81或SEQ ID NO:160,优选SEQ ID NO:160,的位置P379处的氨基酸取代,其中该取代为P379A、P379G、P379I、P379L、P379M、P379V、P379N、P379C、P379Q、P379S或P379T,优选P379A、P379G、P379M、P379V、P379N、P379C、P379Q、P379S或P379T、更优选P379G、P379V、P379C或P379S,或P379T、even更优选P379V或P379T以及最优选P379V;

[0411] 在SEQ ID NO:81或SEQ ID NO:160,优选SEQ ID NO:160,的位置I483处的氨基酸取代,其中该取代为I483A、I483G、I483I、I483L、I483M、I483P或I483V,优选I483A、I483G、I483L、I483M或I483V、更优选I483A;

[0412] 在SEQ ID NO:81或SEQ ID NO:160,优选SEQ ID NO:160,的位置Q483处的氨基酸取代,其中该取代为Q483A、Q483G、Q483I、Q483L、Q483M、Q483P或Q483V,优选Q483A、Q483G、Q483L、Q483M或Q483V、更优选Q483A;

[0413] 在SEQ ID NO:81或SEQ ID NO:160,优选SEQ ID NO:160,的位置V544处的氨基酸取代,其中该取代为V544A、V544G、V544I、V544L、V544M或V544P,优选V544I或V544P以及更优选V544I;

[0414] 在SEQ ID NO:81或SEQ ID NO:160,优选SEQ ID NO:160,的位置S550处的氨基酸取代,其中该取代为S550N、S550C、S550Q或S550T,优选S550T;

[0415] 在SEQ ID NO:81或SEQ ID NO:160,优选SEQ ID NO:160,的位置Q558处的氨基酸取代,其中该取代为Q558D或Q558E,优选Q558E;

[0416] 在SEQ ID NO:81或SEQ ID NO:160,优选SEQ ID NO:160,的位置D558处的氨基酸取代,其中该取代为D558N、D558C、D558Q、D558S、D558T、D558A、D558G、D558I、D558L、D558M、D558P或D558V,优选D558N、D558G或D558A以及更优选D558N;

[0417] 在SEQ ID NO:81或SEQ ID NO:160,优选SEQ ID NO:160,的位置A643处的氨基酸取代,其中该取代为A643D或A643E,优选A643E;

[0418] 在SEQ ID NO:81或SEQ ID NO:160,优选SEQ ID NO:160,的位置L707处的氨基酸取代,其中该取代为L707A、L707G、L707I、L707M、L707P或L707V,优选L707M。

[0419] 在该第十四方面的第二十一实施方式,其也是该第十四个方面的前述实施方式的任何其它中的实施方式,该海藻糖磷酸化酶的氨基酸序列与SEQ ID NO:81或SEQ ID NO:160,优选SEQ ID NO:160,的氨基酸序列具有以下同一性:至少85%,还更优选至少86%,或至少87%,或至少88%,或至少89%,或至少90%、甚至更优选至少91%,或至少92%,或至少93%,或至少94%,或至少95%以及最优选至少96%,或至少97%,或至少98%,或至少99%、至少99.1%,或至少99.2%,或至少99.3%,或至少99.4%,或至少99.5%,或至少99.6%,或至少99.7%,或至少99.8%以及尤其至少99.9%,或100%。

[0420] 在该第十四方面的第二十二实施方式,其也是该第十四个方面的前述实施方式的任何其它中的实施方式,该海藻糖磷酸化酶的氨基酸序列与下列氨基酸序列具有至少85%同一性:SEQ ID NO:161、162、163、164、165、166、167、168、169、170、171、172、173、174、175、176、177、178、179、180、181、182、183、184、185、186、187、188、189,优选根据SEQ ID NO:163、165、166、168、171、173、176、177、178、179、180、184、185、186、187、188、189、2、84、85、87、88、89、91、92、93、94、95、97、98、99、100、101、102、103、104、105、106、107、109的任何中的,更优选根据SEQ ID NO:176、178、180、185、188的任何中的。

[0421] 在该第十四方面的第二十三实施方式,其也是该第十四个方面的第十七实施方式或该第十四方面的前述实施方式的任何其它中的实施方式,该氨基酸序列的同一性为至少86%,或至少87%,或至少88%,或至少89%,或至少90%、更优选至少91%,或至少92%,或至少93%,或至少94%,或至少95%以及最优选至少96%,或至少97%,或至少98%,或至少99%、至少99.1%,或至少99.2%,或至少99.3%,或至少99.4%,或至少99.5%,或至少99.6%,或至少99.7%,或至少99.8%以及尤其是至少99.9%,或100%。

[0422] 在该第十四方面的第二十四实施方式,其也是该第十四个方面的前述实施方式的任何其它中的实施方式,该多肽,优选海藻糖磷酸化酶,能够催化一糖基单醣与α-D葡萄糖-1磷酸盐的反应。

[0423] 在该第十四方面的第二十五实施方式,其也是该第十四个方面的第十九实施方式中的实施方式,该多肽,优选海藻糖磷酸化酶能够催化

[0424] 葡萄糖与α-D-葡萄糖-1磷酸盐转化为海藻糖与无机磷酸盐

[0425] 和/或

[0426] 将海藻糖与无机磷酸盐转化为葡萄糖与α-D-葡萄糖-1磷酸盐。

[0427] 在该第十四方面的第二十六实施方式,其也是该第十四个方面的第十九及第二十实施方式中的实施方式,该转化为一可逆的转化。

[0428] 在该第十四方面的第二十七实施方式,其也是该第十四个方面的前述实施方式的任何其它中的实施方式,该多肽,优选海藻糖磷酸化酶,是一根据EC号为EC 2.4.1.231的海藻糖磷酸化酶。

[0429] 在该第十四方面的第二十八实施方式,其也是该第十四个方面的前述实施方式的任何其它中的实施方式,该多肽,优选海藻糖磷酸化酶,其特征在于于52.5℃温育15分钟后的热稳定性,其是由一残余活性所定义,该残余活性为15%至100%,优选30%至100%,更优选50%至100%,最优选70%至100%。

[0430] 更具体而言,在第十五方面,其也是该第十五个方面的第一实施方式,通过包含氨基酸序列的多肽,优选海藻糖磷酸化酶,解决了这些及其它问题,其中该多肽,优选海藻糖磷酸化酶,的氨基酸序列与SEQ ID NO:81或SEQ ID NO:160,优选SEQ ID NO:160,的氨基酸序列具有至少85%同一性和/或至少85%同源性,其中该多肽,优选海藻糖磷酸化酶,其特征在于于52.5℃温育15分钟后的热稳定性,其是由一残余活性所定义,该残余活性为15%至100%,优选30%至100%,更优选50%至100%,最优选70%至100%。

[0431] 在该第十五方面的第二实施方式,其也是该第十五个方面的第一实施方式中的实施方式,该多肽,优选海藻糖磷酸化酶,是如该第十四方面的任一实施方式所定义。

[0432] 在该第十五方面的第二实施方式的一优选实施方式,该多肽,优选海藻糖磷酸化

酶,是如该第十四方面的任一实施方式,优选第十四方面的第五个实施方式所定义。

[0433] 在该第十五方面的第二实施方式的一优选实施方式,该多肽,优选海藻糖磷酸化酶,是如该第十四方面的任一实施方式,优选第十四方面的第六个实施方式所定义。

[0434] 在该第十五方面的第三个实施方式,其也是第十四及第十五个方面的任何其它实施方式中的实施方式,该多肽,优选海藻糖磷酸化酶,的特征在于于52.5℃温育15分钟后的热稳定性,其是由一残余活性所定义,该残余活性为30%至100%,优选50%至100%,最优选70%至100%。

[0435] 在该第十五方面的第三实施方式的一优选实施方式,该多肽,优选海藻糖磷酸化酶,是如该第十四方面的任一实施方式,优选第十四方面的第五个实施方式所定义。

[0436] 在该第十五方面的第三实施方式的一优选实施方式,该多肽,优选海藻糖磷酸化酶,是如该第十四方面的任一实施方式,优选第十四方面的第六个实施方式所定义。

[0437] 在该第十五方面的第四实施方式,其也是该第十四及第十五方面的任何其它的实施方式中的实施方式,其中该多肽,优选海藻糖磷酸化酶,其中该多肽,优选海藻糖磷酸化酶,能够催化一葡糖基单醣与α-D-葡萄糖-1磷酸盐的反应。

[0438] 在该第十五方面的第五实施方式,其也是该第十四及第十五方面的任何的实施方式中的实施方式,该多肽,优选海藻糖磷酸化酶,能够催化

[0439] 葡萄糖与α-D-葡萄糖-1磷酸盐转化为海藻糖与无机磷酸盐

[0440] 和/或

[0441] 将海藻糖与无机磷酸盐转化为葡萄糖与α-D-葡萄糖-1磷酸盐。

[0442] 在该第十五方面的第六实施方式,其也是该第十五方面的第四及第六实施方式或该第十四及第十五方面的任何的实施方式中的实施方式,该转化为一可逆的转化。

[0443] 在该第十五方面的第七实施方式,其也是该第十四及第十五方面的任何的实施方式中的实施方式,该多肽,优选海藻糖磷酸化酶,为一根据EC号为EC2.4.1.231的海藻糖磷酸化酶。

[0444] 更具体而言,在第五方面,其也是该第五方面的第一实施方式,通过包含SEQ ID NO:1,或SEQ ID NO:160或SEQ ID NO:81的氨基酸序列的热稳定的海藻糖磷酸化酶的变体,解决了这些和其它问题,其中该变体于52℃温育15分钟后具有至少30%的残余活性,且初始活性在室温温育15分钟后测定。

[0445] 在本发明的第五方面的第一实施方式中的优选实施方式,该热稳定的海藻糖磷酸化酶的变体包含SEQ ID NO:1的氨基酸序列,其中该变体于52℃温育15分钟后具有至少30%的残余活性,且初始活性在室温温育15分钟后测定。

[0446] 在本发明的第五方面的第一实施方式的另一优选实施方式,该热稳定的海藻糖磷酸化酶的变体包含SEQ ID NO:160的氨基酸序列,其中该变体于52℃温育15分钟后具有至少30%的残余活性,且初始活性在室温温育15分钟后测定。

[0447] 在本发明的第五方面的第一实施方式中的优选实施方式,该热稳定的海藻糖磷酸化酶的变体包含SEQ ID NO:81的氨基酸序列,其中该变体于52℃温育15分钟后具有至少30%的残余活性,且初始活性在室温温育15分钟后测定。

[0448] 在第四方面及第五方面的第二实施方式,其也是该第四方面的第一实施方式的实施方式以及该第五方面的第一实施方式以及也是该第四方面及该第五方面的前述实施方

式的任何其它中的实施方式,该变体在含有1M蔗糖的缓冲液中于52℃温育15分钟后具有至少50%的残余活性,且初始活性在室温温育15分钟后测定。

[0449] 在该第二方面的第二十三实施方式,其也是该第三方面中的第三实施方式,该第四方面中的第三实施方式以及该第五方面中的第三实施方式以及该第十五方面的另一实施方式,或该第二、第三、第四、第五或第十五方面的前述任一实施方式,该多肽,优选海藻糖磷酸化酶,包含

[0450] (i)如该第一方面的第一至一百二十实施方式或任何其它实施方式中任一个所定义的氨基酸序列,优选如本发明第一方面的第一至九十八实施方式的任一项所定义

[0451] 和/或

[0452] (ii)如本发明第十四方面的任一个实施方式中所定义的氨基酸序列

[0453] 和/或

[0454] (iii)如本发明第十三方面的任一实施方式中所定义的氨基酸序列。

[0455] 更具体而言,在第十六方面,该方面也是该第十六方面的第一实施方式,且其也是本发明的所有方面中的优选实施方式以及本发明的所有方面的任何所有的实施方式,且特别是如本文所述的本发明的第一、第二、第三、第四、第五、第十三、第十四,及第十五方面的任何实施方式中,这些和其它问题是由该多肽解决,其中该多肽,优选海藻糖磷酸化酶,是为该多肽的酶促活性片段,优选本发明的海藻糖磷酸化酶的酶促活性片段,如在任何方面或在本文所述和/或如上所述的方面的任何优选实施方式中所定义。

[0456] 在该第十六方面中的优选实施方式,其也是该第十六方面的前述实施方式的任何一实施方式,该海藻糖磷酸化酶是为该多肽的酶促活性片段,优选本发明的海藻糖磷酸化酶的酶促活性片段,具有一至少400个至750个氨基酸,或至少450个至750个氨基酸,或至少500个至750个氨基酸,或至少550个至750个氨基酸,或至少600个至750个氨基酸,或至少650个至750个氨基酸,或至少700个至750个氨基酸,或至少700个至730个氨基酸的长度。

[0457] 在该第十六方面中的优选实施方式,其也是该第十六方面的前述实施方式的任何一实施方式,该多肽是为该多肽的酶促活性片段,优选本发明的海藻糖磷酸化酶的酶促活性片段,其中该海藻糖磷酸化酶为

[0458] (i)在其N-端截短至少1至37个氨基酸,至少1至87个氨基酸,至少1至137个氨基酸,至少1至187个氨基酸,至少1至237个氨基酸,至少1至287个氨基酸,至少1至337个氨基酸;和/或

[0459] (ii)在其C-端截短至少1至˘37个氨基酸,至少1至87个氨基酸,至少1至137个氨基酸,至少1至187个氨基酸酸,至少1至237个氨基酸,至少1至287个氨基酸,至少1至337个氨基酸;和/或

[0460] (iii)在一个或更多个内部位置截短,其中每个或多个内部位置携带删除1、2、3、4、5、6、7、8、9、10,或至少10至15、至少15至20、至少20至25、至少25至30、至少30至35、至少35至40、至少40至45,或至少45至50个氨基酸。

[0461] 在该第十六方面中的优选实施方式,其也是该第十六方面的前述实施方式的任何一实施方式,该多肽,优选本发明的海藻糖磷酸化酶,为该多肽,优选本发明的海藻糖磷酸化酶,的酶促活性片段,根据本文和/或上下文定义的任何实施方式,其保留海藻糖磷酸化酶活性。

[0462] 更具体而言,在第六方面,其也是该第六方面的第一实施方式,这些及其它问题通过一种用于以下的反应的方法解决:

[0463] 葡糖基单醣与α-D-葡萄糖-1磷酸盐的反应方法

[0464] 其中该方法包括

[0465] 以本文公开的本发明的第一、第二、第三、第四、第五、第十三、第十四、第十五及第十六方面的任何实施方式中所定义的海藻糖磷酸化酶

[0466] 使葡糖基单醣与α-D-葡萄糖-1磷酸盐反应。

[0467] 更具体而言,在第七方面,其也是该第七方面的第一实施方式,通过一种方法解决这些及其它问题,该方法是用于将葡萄糖与α-D-葡萄糖-1磷酸盐转化为海藻糖与无机磷酸盐,其中该方法包括以如本文所揭露的本发明的第一、第二、第三、第四、第五、第十三、第十四、第十五及第十六方面的任何实施方式中所定义的海藻糖磷酸化酶,使葡萄糖与α-D-葡萄糖-1磷酸盐产生反应。

[0468] 更具体而言,在第八方面,其也是该第八方面的第一实施方式,通过一种方法解决这些及其它问题,该方法是用于将海藻糖与无机磷酸盐转化为葡萄糖与α-D-葡萄糖-1磷酸盐,其中该方法包括以如本文所揭露的本发明的第一、第二、第三、第四、第五、第十三、第十四、第十五及第十六方面的任何实施方式中所定义的海藻糖磷酸化酶,使海藻糖与无机磷酸盐反应为葡萄糖与α-D-葡萄糖-1磷酸盐。

[0469] 在该第六方面中的第二实施方式以及该第七方面中的第二实施方式以及在该第八方面的第二方面,其也是该第六方面的第一实施方式以及该第七方面的第一实施方式以及该第八方面的第一实施方式的实施方式,该转化为一可逆的转化。

[0470] 更具体而言,在第九方面,其也是该第九方面的第一实施方式,通过一种用于制备海藻糖的方法解决这些及其它问题,该方法包括使葡萄糖与α-D-葡萄糖-1磷酸盐在海藻糖磷酸化酶存在下于至少40℃的温度进行反应,其中该海藻糖磷酸化酶

[0471] (i)与未经热处理的海藻糖磷酸化酶的活性相比,在含有1M蔗糖的缓冲液中于52℃温育15分钟后保留其活性的至少30%,和/或

[0472] (ii)与未经热处理的海藻糖磷酸化酶的活性相比,在含有1M蔗糖的缓冲液中于52℃温育15分钟后保留其活性的至少50%,和/或

[0473] (iii)在100mM葡萄糖下的活性与在500mM葡萄糖下的活性的比至少为0.65。

[0474] 在该第九方面中的第二实施方式,其也是该第九方面的第一实施方式中的实施方式,该反应是于40至55℃进行。

[0475] 在该第九方面中的第三实施方式,其也是该第九方面的第一实施方式中的实施方式,该反应是于45至55℃进行。

[0476] 在该第九方面中的第四实施方式,其也是该第九方面的第一、第二及第三实施方式中的实施方式,该海藻糖磷酸化酶为一热稳定的海藻糖磷酸化酶。

[0477] 在该第九方面中的第五实施方式,其也是该第九方面的第一、第二、第三及第四实施方式中的实施方式,该海藻糖磷酸化酶为一突变的海藻糖磷酸化酶。

[0478] 在该第九方面中的第六实施方式,其也是该第九方面的第一、第二、第三、第四及第五实施方式中的实施方式,该海藻糖磷酸化酶为一重组的海藻糖磷酸化酶。

[0479] 在该第九方面中的第七实施方式,其也是该第九方面的第一、第二、第三、第四、第

五及第六实施方式中的实施方式,该活性是以如本文所述,更具体而言是如第[0371]及[0372]段所述者决定。

[0480] 在该第六方面的另一实施方式,其也是该第六方面的每个及任一个实施方式中的实施方式,在该第七方面的另一实施方式,其也是该第七方面的每个及任一个实施方式中的实施方式,在该第八方面的另一实施方式,其也是该第八方面的每个及任一个实施方式中的实施方式以及在该第九方面的另一实施方式,其也是该第九方面的每个及任一个实施方式中的实施方式,其中在该反应中唯一含有的稳定剂为蔗糖。

[0481] 在该第六方面的另一实施方式,其也是该第六方面的每个及任一个实施方式中的实施方式,在该第七方面的另一实施方式,其也是该第七方面的每个及任一个实施方式中的实施方式,在该第八方面的另一实施方式,其也是该第八方面的每个及任一个实施方式中的实施方式以及在该第九方面的另一实施方式,其也是该第九方面的每个及任一个实施方式中的实施方式,该海藻糖磷酸化酶以非-固定化形式存在。

[0482] 在该第六方面的另一实施方式,其也是该第六方面的每个及任一个实施方式中的实施方式,在该第七方面的另一实施方式,其也是该第七方面的每个及任一个实施方式中的实施方式,在该第八方面的另一实施方式,其也是该第八方面的每个及任一个实施方式中的实施方式以及在该第九方面的另一实施方式,其也是该第九方面的每个及任一个实施方式中的实施方式,该海藻糖磷酸化酶为一在如本文所述的该第一、第二、第三、第四、第五、第十三、第十四第十五,及第十六方面的任何实施方式中的,包括其任何的实施方式,所定义的海藻糖磷酸化酶。

[0483] 更具体而言,在第十方面,其也是该第十方面的第一实施方式,通过使用如本文所述的该第一、第二、第三、第四、第五、第十三、第十四、第十五及第十六个方面的任何实施方式中的的用于生产海藻糖的海藻糖磷酸化酶解决了这些及其它问题。

[0484] 更具体而言,在第十一方面,其也是该第十一方面的第一实施方式,通过一方法解决了这些及其它问题,该方法是用于提高海藻糖磷酸化酶的热稳定性,其中该方法包括:

[0485] -比对第一海藻糖磷酸化酶的氨基酸序列与第二海藻糖磷酸化酶的氨基酸序列,

[0486] -鉴定对应在该第一海藻糖磷酸化酶的该氨基酸序列的一个或更多个氨基酸位置的该第二海藻糖磷酸化酶的该氨基酸序列的一个或更多个氨基酸位置,其中在该第一海藻糖磷酸化酶的该氨基酸序列的一个或更多个氨基酸位置的氨基酸残基的取代提高了该第一海藻糖磷酸化酶的热稳定性,

[0487] -取代对应在该第一海藻糖磷酸化酶的该氨基酸序列的一个或更多个氨基酸位置的在该第二海藻糖磷酸化酶的一个或更多个氨基酸位置处的氨基酸残基,其中在该第一海藻糖磷酸化酶的该氨基酸序列的一个或更多个氨基酸位置的氨基酸残基的取代提高了该第一海藻糖磷酸化酶的热稳定性,

[0488] 其中该第一海藻糖磷酸化酶为包含根据SEQ ID NO:1或根据SEQ ID NO:160的氨基酸序列,优选根据SEQ ID NO:1的氨基酸序列的海藻糖磷酸化酶。

[0489] 在该第十一方面的第二实施方式,其也是该第十一方面的第一实施方式中的实施方式,该方法还包括

[0490] -测试该第二海藻糖磷酸化酶的该一个或更多个氨基酸位置处的取代的氨基酸残基是否对应在该第一海藻糖磷酸化酶的氨基酸序列的一个或更多个氨基酸位置,导致与该

第一海藻糖磷酸化酶的热稳定性相比,该第二海藻糖磷酸化酶的热稳定性增加,优选热稳定性是以如本文描述中所定义的方式确定。

[0491] 在该第十一方面的第三实施方式,其也是该第十一方面的第一及第二实施方式中的实施方式,对应在该第一海藻糖磷酸化酶的氨基酸序列的一个或更多个氨基酸位置的该第二海藻糖磷酸化酶的一个或更多个氨基酸位置处的氨基酸残基被取代,使得取代的氨基酸残基导致该第二海藻糖磷酸化酶的热稳定性增加。

[0492] 在该第十一方面的第四实施方式,其也是该第十一方面的第一、第二及第三实施方式中的实施方式,该第一海藻糖磷酸化酶的氨基酸序列与该第二海藻糖磷酸化酶的氨基酸序列的同源性为至少50%。

[0493] 在该第十一方面的第五实施方式,其也是该第十一方面的第四实施方式中的实施方式,该同源性为至少51%、52%、53%、54%、55%、56%、57%、58%、59%、60%、61%、62%、63%、64%、65%、66%、67%、68%、69%、70、%、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%,优选该同源性为至少55%、60%、63%、65%、68%、70%、75%、77%或80%。

[0494] 在该第十一方面的第六实施方式,其也是该第十一方面的第一、第二及第三实施方式中的实施方式,该第一海藻糖磷酸化酶的氨基酸序列与该第二海藻糖磷酸化酶的氨基酸序列的同一性为至少50%。

[0495] 在该第十一方面的第七实施方式,其也是该第十一方面的第六实施方式中的实施方式,该同一性为至少51%、52%、53%、54%、55%、56%、57%、58%、59%、60%、61%、62%、63%、64%、65%、66%、67%、68%、69%、70、%、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%,优选至少55%、60%、63%、65%、68%、70%、75%、77%或80%,更优选至少68%、73%、75%、76%、77%或78%。

[0496] 在该第十一方面的第八实施方式,其也是该第十一方面的第一、第二、第三、第四、第五、第六及第七实施方式中的实施方式,该第一海藻糖磷酸化酶的氨基酸序列的一个或更多个氨基酸位置为:

[0497] (A)选自由下列SEQ ID NO:1的氨基酸位置组成的组:712、383、10、114、118、192、197、220、225、304、306、318、323、339、349、357、459、476、481、484、487、488、506、511、526、530、532、533、537、550、556、564、590、649、667、703与705,优选该第一海藻糖磷酸化酶的氨基酸序列的一个或更多个氨基酸位置是各别且独立地选自由下列SEQ ID NO:1的氨基酸位置组成的组:712、383、10、114、118、192、197、220、225、304、306、318、323、339、349、357、459、476、481、484、487、488、506、511、526、530、532、533、537、550、556、564、590、649、667、703与705,优选选自由下列氨基酸位置组成的组:712、383、114、118、225、304、323、349、357、487、550、556、564、590与649,更优选选自由下列SEQ ID NO:1的氨基酸位置组成的组:712、383、114、118、225、304、323、349、487、550、556、564、590以及649,甚至更优选选自由下列SEQ ID NO:1的氨基酸位置组成的组:383、114、118、225、304、323、487、550、556以及564以及甚至更优选选自由下列SEQ ID NO:1的氨基酸位置组成的组:383、114、225、323、487、556以及564,或

[0498] (B)选自由下列SEQ ID NO:81或SEQ ID NO:160,优选SEQ ID NO:160,的氨基酸位置组成的组:108、112、221、300、319、345、379、483、544、550、558、584、643以及707,优选该第一海藻糖磷酸化酶的氨基酸序列的一个或更多个氨基酸位置是各别且独立地选自由下列SEQ ID NO:81或SEQ ID NO:160,优选SEQ ID NO:160,的氨基酸位置组成的组:108、112、221、300、319、345、379、483、544、550、558、584、643以及707,更优选选自由下列SEQ ID NO:81或SEQ ID NO:160,优选SEQ ID NO:160,的氨基酸位置组成的组:108、221、319、379、483、550以及558。

[0499] 在该第十一方面的第九实施方式,其也是该第十一方面的第八实施方式中的实施方式,该第一海藻糖磷酸化酶的氨基酸序列的一个或更多个氨基酸位置为:

[0500] (A)选自由下列SEQ ID NO:1的氨基酸位置组成的组:L712、P383、V10、L114、I118、S192、S197、Y220、N225、A304、D306、P318、T323、L339、F349、G357、A459、Q476、E481、A484、Q487、K488、A506、A511、R526、E530、G532、D533、D537、V550、S556、T564、D590、A649、R667、A703与K705,优选该第一海藻糖磷酸化酶的氨基酸序列的一个或更多个氨基酸位置是各别且独立地选自由下列SEQ ID NO:1的氨基酸位置组成的组:L712、P383、V10、L114、I118、S192、S197、Y220、N225、A304、D306、P318、T323、L339、F349、G357、A459、Q476、E481、A484、Q487、K488、A506、A511、R526、E530、G532、D533、D537、V550、S556、T564、D590、A649、R667、A703与K705,优选选自由下列SEQ ID NO:1的氨基酸位置组成的组:L712、P383、L114、I118、N225、A304、T323、F349、Q487、V550、S556、T564、D590以及A649,更优选选自由下列SEQ ID NO:1的氨基酸位置组成的组:P383、L114、I118、N225、A304、T323、Q487、V550、S556以及T564,且甚至更优选选自由下列SEQ ID NO:1的氨基酸位置组成的组:P383、L114、N225、A323、Q487、S556以及T564。

[0501] (B)选自由下列SEQ ID NO:160的氨基酸位置组成的组:L108、V112、N221、A300、T319、F345、P379、V483、V544、S550、Q558、N584、A643以及L707,优选该第一海藻糖磷酸化酶的氨基酸序列的一个或更多个氨基酸位置是各别且独立地选自由下列SEQ ID NO:160的氨基酸位置组成的组:L108、V112、N221、A300、T319、F345、P379、V483、V544、S550、Q558、N584、A643以及L707,优选选自由下列SEQ ID NO:160的氨基酸位置组成的组:L108、V112、N221、A300、T319、P379、V483、V544、S550以及Q558,更优选选自由下列SEQ ID NO:160的氨基酸位置组成的组:L108、V221、T319、P379、V483、S550以及Q558。

[0502] (C)选自由下列SEQ ID NO:81的氨基酸位置组成的组:L108、V112、N221、A300、T319、F345、P379、I483、V544、S550、Q558、N584、A643以及L707,优选该第一海藻糖磷酸化酶的氨基酸序列的一个或更多个氨基酸位置是各别且独立地选自由下列SEQ ID NO:81的氨基酸位置组成的组:L108、V112、N221、A300、T319、F345、P379、I483、V544、S550、Q558、N584、A643以及L707,优选选自由下列SEQ ID NO:81的氨基酸位置组成的组:L108、V112、N221、A300、T319、P379、I483、V544、S550以及Q558,更优选选自由下列SEQ ID NO:81的氨基酸位置组成的组:L108、V221、T319、P379、I483、S550以及Q558。

[0503] 在该第十一方面的第十实施方式,其也是该第十一方面的第一、第二、第三、第四、第五、第六、第七、第八及第九实施方式中的实施方式,该取代的氨基酸残基为

[0504] (A)针对SEQ ID NO:1:

[0505] A、G、I、M、P、V,优选M,代表对应在该第一海藻糖磷酸化酶的SEQ ID NO:1的氨基酸

位置712的第二海藻糖磷酸化酶的氨基酸位置;

[0506] A、G、I、L、M、V、N、C、Q、S、T,优选A、G、M、V、N、C、Q、S、T、更优选G、V、S或T,甚至更优选V或T以及最优选V,代表对应在该第一海藻糖磷酸酶的SEQ ID NO:1的氨基酸位置383的第二海藻糖磷酸酶的氨基酸位置;

[0507] R、H或K,优选R,代表对应在该第一海藻糖磷酸酶的SEQ ID NO:1的氨基酸位置10的第二海藻糖磷酸酶的氨基酸位置;

[0508] A、G、I、M、P、V,优选I,代表对应在第一海藻糖磷酸化酶的SEQ ID NO:1的氨基酸位置114的第二海藻糖磷酸化酶的氨基酸位置;

[0509] A、G、I、L、M、P、V,优选V,代表对应在第一海藻糖磷酸化酶的SEQ ID NO:1的氨基酸位置118的第二海藻糖磷酸化酶的氨基酸位置;

[0510] A、G、I、L、M、P、V,优选V,代表对应在第一海藻糖磷酸化酶的SEQ ID NO:1的氨基酸位置192的第二海藻糖磷酸化酶的氨基酸位置;

[0511] A、G、I、L、M、P、V,优选G,代表与第一海藻糖磷酸化酶的SEQ ID NO:1的氨基酸位置197对应的第二海藻糖磷酸化酶的氨基酸位置;

[0512] F、W,优选F,代表对应在第一海藻糖磷酸酶的SEQ ID NO:1的氨基酸位置220的第二海藻糖磷酸化酶的氨基酸位置;

[0513] A、G、I、L、M、P、V,优选I、L、M或V以及最优选V,代表对应于SEQ ID NO:1的氨基酸位置225的第二海藻糖磷酸化酶的氨基酸位置第一个海藻糖磷酸化酶;

[0514] G、I、L、M、P、V,优选I或L以及更优选I,代表对应在第一海藻糖磷酸酶的SEQ ID NO:1的氨基酸位置304的第二海藻糖磷酸化酶的氨基酸位置;

[0515] R、H、K,优选H,代表对应在第一海藻糖磷酸酶的SEQ ID NO:1的氨基酸位置306的第二海藻糖磷酸化酶的氨基酸位置;

[0516] R、H、K,优选H,代表对应在第一海藻糖磷酸酶的SEQ ID NO:1的氨基酸位置318的第二海藻糖磷酸化酶的氨基酸位置;

[0517] A、G、I、L、M、P、V,优选I或V、更优选I,代表对应在第一海藻糖磷酸酶的SEQ ID NO:1的氨基酸位置323的第二海藻糖磷酸化酶的氨基酸位置;

[0518] A、G、I、L、M、P、V,优选I,代表对应在第一海藻糖磷酸化酶的SEQ ID NO:1的氨基酸位置339的第二海藻糖磷酸化酶的氨基酸位置;

[0519] W或Y,优选Y,代表对应在第一海藻糖磷酸酶的SEQ ID NO:1的氨基酸位置349的第二海藻糖磷酸化酶的氨基酸位置;

[0520] A、I、L、M、P、V,优选A,代表对应在第一海藻糖磷酸化酶的SEQ ID NO:1的氨基酸位置357的第二海藻糖磷酸化酶的氨基酸位置;

[0521] N、C、Q、S、T,优选S,代表对应在第一海藻糖磷酸酶的SEQ ID NO:1的氨基酸位置459的第二海藻糖磷酸化酶的氨基酸位置;

[0522] A、G、I、L、M、P、V,优选G,代表对应在第一海藻糖磷酸化酶的SEQ ID NO:1的氨基酸位置476的第二海藻糖磷酸化酶的氨基酸位置;

[0523] A、G、I、L、M、P、V,优选I,代表对应在第一海藻糖磷酸化酶的SEQ ID NO:1的氨基酸位置481的第二海藻糖磷酸化酶的氨基酸位置;

[0524] N、C、Q、S、T,优选S,代表对应在第一海藻糖磷酸化酶的SEQ ID NO:1的氨基酸位置

484的第二海藻糖磷酸化酶的氨基酸位置;

[0525] A、G、I、L、M、P、V,优选A、M、G、V或L、更优选A,代表对应在第一海藻糖磷酸化酶的SEQ ID NO:1的氨基酸位置487的第二海藻糖磷酸化酶的氨基酸位置;

[0526] A、G、I、L、M、P、V,优选A,代表对应在第一海藻糖磷酸化酶的SEQ ID NO:1的氨基酸位置488的第二海藻糖磷酸化酶的氨基酸位置;

[0527] N、C、Q、S、T,优选S,代表对应在第一海藻糖磷酸化酶的SEQ ID NO:1的氨基酸位置506的第二海藻糖磷酸化酶的氨基酸位置;

[0528] N、C、Q、S、T,优选S,代表对应在第一海藻糖磷酸酶的SEQ ID NO:1的氨基酸位置511的第二海藻糖磷酸化酶的氨基酸位置;

[0529] D或E,优选E,代表对应在第一海藻糖磷酸化酶的SEQ ID NO:1的氨基酸位置526所对应的第二海藻糖磷酸化酶的氨基酸位置;

[0530] A、G、I、L、M、P、V,优选V,代表对应在第一海藻糖磷酸化酶的SEQ ID NO:1的氨基酸位置530的第二海藻糖磷酸化酶的氨基酸位置;

[0531] R、H、K,优选R,代表对应在第一海藻糖磷酸化酶的SEQ ID NO:1的氨基酸位置532对应的第二海藻糖磷酸化酶的氨基酸位置;

[0532] A、G、I、L、M、P、V,优选G,代表对应在第一海藻糖磷酸化酶的SEQ ID NO:1的氨基酸位置533对应的第二海藻糖磷酸化酶的氨基酸位置;

[0533] A、G、I、L、M、P、V,优选M,代表对应在第一海藻糖磷酸化酶的SEQ ID NO:1的氨基酸位置537的第二海藻糖磷酸化酶的氨基酸位置;

[0534] A、G、I、L、M、P,优选I或P、更优选I,代表对应在第一海藻糖磷酸化酶的SEQ ID NO:1的氨基酸位置550的第二海藻糖磷酸化酶的氨基酸位置;

[0535] N、C、Q、T,优选T,代表对应在第一海藻糖磷酸化酶的SEQ ID NO:1的氨基酸位置556的第二海藻糖磷酸化酶的氨基酸位置;

[0536] D,E,优选E,代表对应在第一海藻糖磷酸酶的SEQ ID NO:1的氨基酸位置564的第二海藻糖磷酸化酶的氨基酸位置;

[0537] N、C、Q、S、T、A、G、I、L、M、P、V,优选N或A、更优选N,代表对应在第一海藻糖磷酸酶的SEQ ID NO:1的氨基酸位置590的第二海藻糖磷酸化酶的氨基酸位置;

[0538] D、E,优选E,代表对应在第一海藻糖磷酸化酶的SEQ ID NO:1的氨基酸位置649的第二海藻糖磷酸化酶的氨基酸位置;

[0539] D、E、R、H、K,优选E或K、更优选E,代表对应在第一海藻糖磷酸酶的SEQ ID NO:1的氨基酸位置667的第二海藻糖磷酸化酶的氨基酸位置;

[0540] D、E,优选E,代表对应在第一海藻糖磷酸化酶的SEQ ID NO:1的氨基酸位置703的第二海藻糖磷酸化酶的氨基酸位置;以及

[0541] N、C、Q、S、T,优选N,代表对应在第一海藻糖磷酸化酶的SEQ ID NO:1的氨基酸位置705的第二海藻糖磷酸化酶的氨基酸位置;或者

[0542] (B)针对SEQ ID NO:81与SEQ ID NO:160:

[0543] 在SEQ ID NO:81或SEQ ID NO:160,优选SEQ ID NO:160,的位置L108处的氨基酸取代,其中该取代为L108A、L108G、L108I、L108M、L108P或L108V,优选L108I;

[0544] 在SEQ ID NO:81或SEQ ID NO:160,优选SEQ ID NO:160,的位置V112处的氨基酸

取代,其中该取代为V112A、V112G、V112L、V112M、V112P或V112I,优选V112I;

[0545] 在SEQ ID NO:81或SEQ ID NO:160,优选SEQ ID NO:160,的位置N221处的氨基酸取代,其中该取代为N221A、N221G、N221I、N221L、N221M、N221P或N221V,优选N221I、N221L、N221M或N221V以及更优选N221V;

[0546] 在SEQ ID NO:81或SEQ ID NO:160,优选SEQ ID NO:160,的位置A300处的氨基酸取代,其中该取代为A300G、A300I、A300L、A300M、A300P或A300V,优选A300I或A300L以及更优选A300I

[0547] 在SEQ ID NO:81或SEQ ID NO:160,优选SEQ ID NO:160,的位置T319处的氨基酸取代,其中该取代为T319A、T319G、T319I、T319L、T319M、T319P,或T319V,优选T319I或T319V以及更优选T319I;

[0548] 在SEQ ID NO:81或SEQ ID NO:160,优选SEQ ID NO:160,的位置P379处的氨基酸取代,其中该取代为P379A、P379G、P379I、P379L、P379M、P379V、P379N、P379C、P379Q、P379S或P379T,优选P379A、P379G、P379M、P379V、P379N、P379C、P379Q、P379S或P379T、更优选P379G、P379V、P379C或P379S,或P379T,甚至更优选P379V或P379T以及最优选P379V;

[0549] 在SEQ ID NO:81或SEQ ID NO:160,优选SEQ ID NO:160,的位置I483处的氨基酸取代,其中该取代为I483A、I483G、I483I、I483L、I483M、I483P或I483V,优选I483A、I483G、I483L、I483M或I483V,更优选I483A;

[0550] 在SEQ ID NO:81或SEQ ID NO:160,优选SEQ ID NO:160,的位置Q483处的氨基酸取代,其中该取代为Q483A、Q483G、Q483I、Q483L、Q483M、Q483P或Q483V,优选Q483A、Q483G、Q483L、Q483M或Q483V、更优选Q483A;

[0551] 在SEQ ID NO:81或SEQ ID NO:160,优选SEQ ID NO:160,的位置V544处的氨基酸取代,其中该取代为V544A、V544G、V544I、V544L、V544M或V544P,优选V544I或V544P以及更优选V544I;

[0552] 在SEQ ID NO:81或SEQ ID NO:160,优选SEQ ID NO:160,的位置S550处的氨基酸取代,其中该取代为S550N、S550C、S550Q或S550T,优选S550T;

[0553] 在SEQ ID NO:81或SEQ ID NO:160,优选SEQ ID NO:160,的位置Q558处的氨基酸取代,其中该取代为Q558D或Q558E,优选Q558E;

[0554] 在SEQ ID NO:81或SEQ ID NO:160,优选SEQ ID NO:160,的位置D558处的氨基酸取代,其中该取代为D558N、D558C、D558Q、D558S、D558T、D558A、D558G、D558I、D558L、D558M、D558P或D558V,优选D558N、D558G或D558A以及更优选D558N;

[0555] 在SEQ ID NO:81或SEQ ID NO:160,优选SEQ ID NO:160,的位置A643处的氨基酸取代,其中该取代为A643D或A643E,优选A643E;

[0556] 在SEQ ID NO:81或SEQ ID NO:160,优选SEQ ID NO:160,的位置L707处的氨基酸取代,其中该取代为L707A、L707G、L707I、L707M、L707P或L707V,优选L707M。

[0557] 在第十一方面的第十一实施方式中,其也是第十一方面的第一、第二、第三、第四、第五、第六、第七、第八、第九及第十实施方式的一实施方式,若该对应在该第一海藻糖磷酸化酶氨基酸序列的一个或更多个氨基酸位置的该第二海藻糖磷酸化酶的氨基酸残基与该第一海藻糖磷酸化酶的取代的氨基酸残基相同,则该第二海藻糖磷酸化酶的氨基酸残基未被取代。

[0558] 在第十一方面的第十二实施方式中,其也是第十一方面的第一、第二、第三、第四、第五、第六、第七、第八、第九、第十及第十一实施方式的一实施方式,热稳定性是表示为Tm30值或Tm50值,如在说明书中所定义的,更具体地如第[0367]与[0368]段中所公开的。

[0559] 更具体而言,在第十二方面,其也是该第十二方面的第一实施方式,通过用于增加海藻糖磷酸化酶的表现为100/500比的相对活性的方法解决了这些及其它问题,其中该方法包括:

[0560] -比对第一海藻糖磷酸化酶的氨基酸序列与第二海藻糖磷酸化酶的氨基酸序列,

[0561] -鉴定对应在该第一海藻糖磷酸化酶的该氨基酸序列的一个或更多个氨基酸位置的该第二海藻糖磷酸化酶的该氨基酸序列的一个或更多个氨基酸位置,其中在该第一海藻糖磷酸化酶的该氨基酸序列的一个或更多个氨基酸位置的氨基酸残基的取代增加该第一海藻糖磷酸化酶的100/500比,

[0562] -取代对应在该第一海藻糖磷酸化酶的该氨基酸序列的一个或更多个氨基酸位置的在该第二海藻糖磷酸化酶的一个或更多个氨基酸位置处的氨基酸残基,其中在该第一海藻糖磷酸化酶的该氨基酸序列的一个或更多个氨基酸位置的氨基酸残基的取代增加该第一海藻糖磷酸化酶的100/500比活性;

[0563] 其中该第一海藻糖磷酸化酶为包含根据SEQ ID NO:1的氨基酸序列的海藻糖磷酸化酶。

[0564] 在第十二方面的第二实施方式中,其也是第十二方面的第一实施方式的一实施方式,该方法包括

[0565] -检测对应在该第一海藻糖磷酸化酶的氨基酸序列的一个或更多个氨基酸位置的该第二海藻糖磷酸化酶的一个或更多个氨基酸位置处的取代的氨基酸残基是否导致,相较在该第一海藻糖磷酸化酶的活性,该第二海藻糖磷酸化酶的活性增加。

[0566] 在第十二方面的第三实施方式中,其也是第十二方面的第一及第二实施方式的一实施方式,对应在该第一海藻糖磷酸化酶的氨基酸序列的一个或更多个氨基酸位置的该第二海藻糖磷酸化酶的一个或更多个氨基酸位置处的氨基酸残基被取代,使得该取代的氨基酸残基导致该第二海藻糖磷酸化酶的活性增加。

[0567] 在第十二方面的第四实施方式中,其也是第十二方面的第一、第二及第三实施方式的一实施方式,该第一海藻糖磷酸化酶的氨基酸序列与该第二海藻糖磷酸化酶的氨基酸序列的同源性为至少50%。

[0568] 在第十二方面的第五实施方式中,其也是第十二方面的第四实施方式的一实施方式,该同源性为至少55%、56%、57%、58%、59%、60%、61%、62%、63%、64%、65%、66%、67%、68%、69%、70、%、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%,优选该同源性为至少55%、60%、65%、70%、75%或80%。

[0569] 在第十二方面的第六实施方式中,其也是第十二方面的第一、第二及第三实施方式的一实施方式,该第一海藻糖磷酸化酶的氨基酸序列与该第二海藻糖磷酸化酶的氨基酸序列的同一性为至少50%。

[0570] 在第十二方面的第七实施方式中,其也是第十二方面的第六实施方式的一实施方式,该同一性为至少55%、56%、57%、58%、59%、60%、61%、62%、63%、64%、65%、66%、

67％、68％、69％、70、％、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％,优选该同一性为至少55％、60％、65％、70％、75％或80％以及更优选该同一性为至少73％、75％、76％,或78％.。

[0571] 在第十二方面的第八实施方式中,其也是第十二方面的第一、第二、第三、第四、第五、第六及第七实施方式的一实施方式,该第一海藻糖磷酸化酶的氨基酸序列的一个或更多个氨基酸位置选自由下列SEQ ID NO:1的氨基酸位置组成的组:712、383、10、114、118、192、197、220、225、304、306、318、323、339、349、357、459、476、481、484、487、488、506、511、526、530、532、533、537、550、556、564、590、649、667、703与705,优选该第一海藻糖磷酸化酶的氨基酸序列的一个或更多个氨基酸位置是各别且独立地选自由下列SEQ ID NO:1的氨基酸位置组成的组:712、383、10、114、118、192、197、220、225、304、306、318、323、339、349、357、459、476、481、484、487、488、506、511、526、530、532、533、537、550、556、564、590、649、667、703与705,且甚至更优选选自由下列SEQ ID NO:1的氨基酸位置组成的组:712、383、114、118、225、304、323、349、357、487、550、556、564、590与649。

[0572] 在第十二方面的第九实施方式中,其也是第十二方面的第八实施方式的一实施方式,该第一海藻糖磷酸化酶的氨基酸序列的一个或更多个氨基酸位置选自由下列SEQ ID NO:1的氨基酸位置组成的组:L712、P383、V10、L114、I118、S192、S197、Y220、N225、A304、D306、P318、T323、L339、F349、G357、A459、Q476、E481、A484、Q487、K488、A506、A511、R526、E530、G532、D533、D537、V550、S556、T564、D590、A649、R667、A703与K705,优选该第一海藻糖磷酸化酶的氨基酸序列的一个或更多个氨基酸位置是各别且独立地选自由下列SEQ ID NO:1的氨基酸位置组成的组:L712、P383、V10、L114、I118、S192、S197、Y220、N225、A304、D306、P318、T323、L339、F349、G357、A459、Q476、E481、A484、Q487、K488、A506、A511、R526、E530、G532、D533、D537、V550、S556、T564、D590、A649、R667、A703与K705。

[0573] 在第十二方面的第十实施方式中,其也是第十二方面的第一、第二、第三、第四、第五、第六、第七、第八及第九实施方式的一实施方式,该取代的氨基酸残基为

[0574] A、G、I、M、P、V,优选M,代表对应在该第一海藻糖磷酸化酶的SEQ ID NO:1的氨基酸位置712的第二海藻糖磷酸化酶的氨基酸位置;

[0575] A、G、I、L、M、V、N、C、Q、S、T,优选A、G、M、V、N、C、Q、S、T、更优选G、V、C、S或T,甚至更优选V或T以及最优选V,代表对应在该第一海藻糖磷酸酶的SEQ ID NO:1的氨基酸位置383的第二海藻糖磷酸酶的氨基酸位置;

[0576] R、H或K,优选R,代表对应在该第一海藻糖磷酸酶的SEQ ID NO:1的氨基酸位置10的第二海藻糖磷酸酶的氨基酸位置;

[0577] A、G、I、M、P、V,优选I,代表对应在第一海藻糖磷酸化酶的SEQ ID NO:1的氨基酸位置114的第二海藻糖磷酸化酶的氨基酸位置;

[0578] A、G、I、L、M、P、V,优选V,代表对应在第一海藻糖磷酸化酶的SEQ ID NO:1的氨基酸位置118的第二海藻糖磷酸化酶的氨基酸位置;

[0579] A、G、I、L、M、P、V,优选V,代表对应在第一海藻糖磷酸化酶的SEQ ID NO:1的氨基酸位置192的第二海藻糖磷酸化酶的氨基酸位置;

[0580] A、G、I、L、M、P、V,优选G,代表与第一海藻糖磷酸化酶的SEQ ID NO:1的氨基酸位置

197对应的第二海藻糖磷酸化酶的氨基酸位置;

[0581] F、W,优选F,代表对应在第一海藻糖磷酸酶的SEQ ID NO:1的氨基酸位置220的第二海藻糖磷酸化酶的氨基酸位置;

[0582] A、G、I、L、M、P、V,优选I、L、M或V以及最优选V,代表对应于SEQ ID NO:1的氨基酸位置225的第二海藻糖磷酸化酶的氨基酸位置第一个海藻糖磷酸化酶;

[0583] G、I、L、M、P、V,优选I或L以及更优选I,代表对应在第一海藻糖磷酸酶的SEQ ID NO:1的氨基酸位置304的第二海藻糖磷酸化酶的氨基酸位置;

[0584] R、H、K,优选H,代表对应在第一海藻糖磷酸酶的SEQ ID NO:1的氨基酸位置306的第二海藻糖磷酸化酶的氨基酸位置;

[0585] R、H、K,优选H,代表对应在第一海藻糖磷酸酶的SEQ ID NO:1的氨基酸位置318的第二海藻糖磷酸化酶的氨基酸位置;

[0586] A、G、I、L、M、P、V,优选I或V、更优选I,代表对应在第一海藻糖磷酸酶的SEQ ID NO:1的氨基酸位置323的第二海藻糖磷酸化酶的氨基酸位置;

[0587] A、G、I、L、M、P、V,优选I,代表对应在第一海藻糖磷酸化酶的SEQ ID NO:1的氨基酸位置339的第二海藻糖磷酸化酶的氨基酸位置;

[0588] W或Y,优选Y,代表对应在第一海藻糖磷酸酶的SEQ ID NO:1的氨基酸位置349的第二海藻糖磷酸化酶的氨基酸位置;

[0589] A、I、L、M、P、V,优选A,代表对应在第一海藻糖磷酸化酶的SEQ ID NO:1的氨基酸位置357的第二海藻糖磷酸化酶的氨基酸位置;

[0590] N、C、Q、S、T,优选S,代表对应在第一海藻糖磷酸酶的SEQ ID NO:1的氨基酸位置459的第二海藻糖磷酸化酶的氨基酸位置;

[0591] A、G、I、L、M、P、V,优选G,代表对应在第一海藻糖磷酸化酶的SEQ ID NO:1的氨基酸位置476的第二海藻糖磷酸化酶的氨基酸位置;

[0592] A、G、I、L、M、P、V,优选I,代表对应在第一海藻糖磷酸化酶的SEQ ID NO:1的氨基酸位置481的第二海藻糖磷酸化酶的氨基酸位置;

[0593] N、C、Q、S、T,优选S,代表对应在第一海藻糖磷酸化酶的SEQ ID NO:1的氨基酸位置484的第二海藻糖磷酸化酶的氨基酸位置;

[0594] A、G、I、L、M、P、V,优选A、G、V或L、更优选A,代表对应在第一海藻糖磷酸化酶的SEQ ID NO:1的氨基酸位置487的第二海藻糖磷酸化酶的氨基酸位置;

[0595] A、G、I、L、M、P、V,优选A,代表对应在第一海藻糖磷酸化酶的SEQ ID NO:1的氨基酸位置488的第二海藻糖磷酸化酶的氨基酸位置;

[0596] N、C、Q、S、T,优选S,代表对应在第一海藻糖磷酸化酶的SEQ ID NO:1的氨基酸位置506的第二海藻糖磷酸化酶的氨基酸位置;

[0597] N、C、Q、S、T,优选S,代表对应在第一海藻糖磷酸酶的SEQ ID NO:1的氨基酸位置511的第二海藻糖磷酸化酶的氨基酸位置;

[0598] D或E,优选E,代表对应在第一海藻糖磷酸化酶的SEQ ID NO:1的氨基酸位置526所对应的第二海藻糖磷酸化酶的氨基酸位置;

[0599] A、G、I、L、M、P、V,优选V,代表对应在第一海藻糖磷酸化酶的SEQ ID NO:1的氨基酸位置530的第二海藻糖磷酸化酶的氨基酸位置;

[0600] R、H、K,优选R,代表对应在第一海藻糖磷酸化酶的SEQ ID NO:1的氨基酸位置532对应的第二海藻糖磷酸化酶的氨基酸位置;

[0601] A、G、I、L、M、P、V,优选G,代表对应在第一海藻糖磷酸化酶的SEQ ID NO:1的氨基酸位置533对应的第二海藻糖磷酸化酶的氨基酸位置;

[0602] A、G、I、L、M、P、V,优选M,代表对应在第一海藻糖磷酸化酶的SEQ ID NO:1的氨基酸位置537的第二海藻糖磷酸化酶的氨基酸位置;

[0603] A、G、I、L、M、P,优选I或P、更优选I,代表对应在第一海藻糖磷酸化酶的SEQ ID NO:1的氨基酸位置550的第二海藻糖磷酸化酶的氨基酸位置;

[0604] N、C、Q、T,优选T,代表对应在第一海藻糖磷酸化酶的SEQ ID NO:1的氨基酸位置556的第二海藻糖磷酸化酶的氨基酸位置;

[0605] D,E,优选E,代表对应在第一海藻糖磷酸酶的SEQ ID NO:1的氨基酸位置564的第二海藻糖磷酸化酶的氨基酸位置;

[0606] N、C、Q、S、T、A、G、I、L、M、P、V,优选N、G或A、更优选N,代表对应在第一海藻糖磷酸酶的SEQ ID NO:1的氨基酸位置590的第二海藻糖磷酸化酶的氨基酸位置;

[0607] D、E,优选E,代表对应在第一海藻糖磷酸化酶的SEQ ID NO:1的氨基酸位置649的第二海藻糖磷酸化酶的氨基酸位置;

[0608] D、E、R、H、K,优选E或K、更优选E,代表对应在第一海藻糖磷酸酶的SEQ ID NO:1的氨基酸位置667的第二海藻糖磷酸化酶的氨基酸位置;

[0609] D、E,优选E,代表对应在第一海藻糖磷酸化酶的SEQ ID NO:1的氨基酸位置703的第二海藻糖磷酸化酶的氨基酸位置;以及

[0610] N、C、Q、S、T,优选N,代表对应在第一海藻糖磷酸化酶的SEQ ID NO:1的氨基酸位置705的第二海藻糖磷酸化酶的氨基酸位置。

[0611] 在第十二方面的第十一实施方式中,其也是第十二方面的第一、第二、第三、第四、第五、第六、第七、第八、第九及第十实施方式的一实施方式,若对应在该第一海藻糖磷酸化酶氨基酸序列的一个或更多个氨基酸位置的该第二海藻糖磷酸化酶的氨基酸残基与该第一海藻糖磷酸化酶的取代的氨基酸残基相同,则该第二海藻糖磷酸化酶的氨基酸残基不被取代。

[0612] 在第十二方面的第十二实施方式中,其也是第十二方面的第一、第二、第三、第四、第五、第六、第七、第八、第九、第十及第十一实施方式的一实施方式,海藻糖磷酸化酶的活性为如本说明书中所定义的磷酸解活性与合成活性。

[0613] 更具体而言,在第十三方面,也是该第十三方面的第一实施方式,通过具有海藻糖磷酸化酶活性的多肽解决了这些及其它问题,其中该多肽包含氨基酸序列,其中该氨基酸序列与SEQ ID NO:1的氨基酸序列具有至少20%同源性,其中该多肽在选自由氨基酸位置712、383、114、118、225、304、323、349、357、487、550、556、564、590与649组成的组中的两个或更多个位置包含有氨基酸取代,其中

[0614] 在氨基酸位置712处的氨基酸取代选自由下列取代组成的组:712A、712G、712I、712M、712P或712V,优选712M,

[0615] 在氨基酸位置383处的氨基酸取代选自由下列取代组成的组:383A、383G、383I、383L、383M、383V、383N、383C、383Q、383S或383T,优选383A、383G、383M、383V、383N、383C、

383Q、383S或383T,更优选383G、383V、383C、383S或383T,甚至更优选383V或383T以及最优选383V,

[0616] 在氨基酸位置114处的氨基酸取代选自由下列取代组成的组:114A、114G、114I、114M、114P或114V,优选114I,

[0617] 在氨基酸位置118处的氨基酸取代选自由下列取代组成的组:118A、118G、118I、118L、118M、118P或118V,优选118V,

[0618] 在氨基酸位置225处的氨基酸取代选自由下列取代组成的组:225A、225G、225I、225L、225M、225P或225V,优选225I、225L、225M或225V以及更优选225V,

[0619] 在氨基酸位置304处的氨基酸取代选自由下列取代组成的组:304G、304I、304L、304M、304P或304V,优选304I或304L以及更优选304I,

[0620] 在氨基酸位置323处的氨基酸取代选自由下列取代组成的组:323A、323G、323I、323L、323M、323P,或323V,优选323I或323V以及更优选323I,

[0621] 在氨基酸位置349处的氨基酸取代选自由下列取代组成的组:349W或349Y,优选349Y,

[0622] 在氨基酸位置357处的氨基酸取代选自由下列取代组成的组:357A、357I、357L、357M、357P或357V,优选357A,

[0623] 在氨基酸位置487处的氨基酸取代选自由下列取代组成的组:487A、487G、487I、487L、487M、487P或487V,优选487A、487M、487G、487L或487V、更优选487A,

[0624] 在氨基酸位置550处的氨基酸取代选自由下列取代组成的组:550A、550G、550I、550L、550M或550P,优选550I或550P以及更优选550I,

[0625] 在氨基酸位置556处的氨基酸取代选自由下列取代组成的组:556N、556C、556Q或S556T,优选556T,

[0626] 在氨基酸位置564处的氨基酸取代选自由下列取代组成的组:564D或564E,优选564E,

[0627] 在氨基酸位置590处的氨基酸取代选自由下列取代组成的组:590N、590C、590Q、590S、590T、590A、590G、590I、590L、590M、590P或590V,优选590N、590G或590A,更优选590N以及

[0628] 在氨基酸位置649处的氨基酸取代选自由下列取代组成的组:649D或649E,优选649E;

[0629] 其中该氨基酸编号指SEQ ID NO:1中的比对位置。

[0630] 在本发明的第十三方面的一优选实施方式中,其也是该第十三方面的任何其它前述实施方式中的实施方式,该多肽为一具有海藻糖磷酸化酶活性的多肽,其中该多肽包含氨基酸序列,其是与SEQ ID NO:1的氨基酸序列具有至少77%同源性,其中该多肽在选自由氨基酸位置383、114、225、304、323、349、357、550、556、564与649处所组合的组的两个或更多个包含氨基酸取代,其中,

[0631] 在氨基酸位置383处的氨基酸取代选自由下列取代组成的组:383A、383G、383I、383L、383M、383V、383N、383C、383Q、383S或383T,优选383A、383G、383M、383V、383N、383C、383Q、383S或383T、更优选383G、383V、383C、383S或383T,甚至更优选383V或383T以及最优选383V,

[0632] 在氨基酸位置114处的氨基酸取代选自由下列取代组成的组:114A、114G、114I、114M、114P或114V,优选114I,

[0633] 在氨基酸位置225处的氨基酸取代选自由下列取代组成的组:225A、225G、225I、225L、225M、225P或225V,优选225I、225L、225M或225V以及更优选225V,

[0634] 在氨基酸位置304处的氨基酸取代选自由下列取代组成的组:304G、304I、304L、304M、304P或304V,优选304I或304L以及更优选304I,

[0635] 在氨基酸位置323处的氨基酸取代选自由下列取代组成的组:323A、323G、323I、323L、323M、323P,或323V,优选323I或323V以及更优选323I,

[0636] 在氨基酸位置349处的氨基酸取代选自由下列取代组成的组:349W或349Y,优选349Y,

[0637] 在氨基酸位置357处的氨基酸取代选自由下列取代组成的组:357A、357I、357L、357M、357P或357V,优选357A,

[0638] 在氨基酸位置550处的氨基酸取代选自由下列取代组成的组:550A、550G、550I、550L、550M或550P,优选550I或550P以及更优选550I,

[0639] 在氨基酸位置556处的氨基酸取代选自由下列取代组成的组:556N、556C、556Q或S556T,优选556T,

[0640] 在氨基酸位置564处的氨基酸取代选自由下列取代组成的组:564D或564E,优选564E以及

[0641] 在氨基酸位置649处的氨基酸取代选自由下列取代组成的组:649D或649E,优选649E,

[0642] 其中该氨基酸编号指SEQ ID NO:1中的比对位置。

[0643] 在本发明的第十三方面的另一优选实施方式中,其也是该第十三方面的任何其它前述实施方式中的实施方式,该多肽在选自氨基酸位置712、118、487与590处包含至少一个另外的氨基酸取代,其中:

[0644] 在氨基酸位置712处的氨基酸取代选自由下列取代组成的组:712A、712G、712I、712M、712P或712V,优选712M,

[0645] 在氨基酸位置118处的氨基酸取代选自由下列取代组成的组:118A、118G、118I、118L、118M、118P或118V,优选118V,

[0646] 在氨基酸位置487处的氨基酸取代选自由下列取代组成的组:487A、487G、487I、487L、487M、487P或487V,优选487A、487G、487L、487M或487V,更优选487A以及

[0647] 在氨基酸位置590处的氨基酸取代选自由下列取代组成的组:590N、590C、590Q、590S、590T、590A、590G、590I、590L、590M、590P或590V,优选590N、590G或590A,更优选590N,

[0648] 其中该氨基酸编号指SEQ ID NO:1中的比对位置。

[0649] 在本发明的第十三方面的另一优选实施方式中,其也是该第十三方面的任何其它前述实施方式中的实施方式,该多肽为一具有海藻糖磷酸化酶活性的多肽,其中该多肽包含氨基酸序列,其是与SEQ ID NO:1的氨基酸序列具有至少68%同源性,其中该多肽在选自由氨基酸位置383、114、225、304、323、349、357、550、556与564处所组合的组的两个或更多个包含氨基酸取代,其中,

[0650] 在氨基酸位置383处的氨基酸取代选自由下列取代组成的组:383A、383G、383I、

383L、383M、383V、383N、383C、383Q、383S或383T,优选383A、383G、383M、383V、383N、383C、383Q、383S或383T,更优选383G、383V、383C、383S或383T,甚至更优选383V或383T以及最优选383V,

[0651] 在氨基酸位置114处的氨基酸取代选自由下列取代组成的组:114A、114G、114I、114M、114P或114V,优选114I,

[0652] 在氨基酸位置225处的氨基酸取代选自由下列取代组成的组:225A、225G、225I、225L、225M、225P或225V,优选225I、225L、225M或225V以及更优选225V,

[0653] 在氨基酸位置304处的氨基酸取代为304I,

[0654] 在氨基酸位置323处的氨基酸取代选自由下列取代组成的组:323A、323G、323I、323L、323M、323P,或323V,优选323I或323V以及更优选323I,

[0655] 在氨基酸位置349处的氨基酸取代选自由下列取代组成的组:349W或349Y,优选349Y,

[0656] 在氨基酸位置357处的氨基酸取代选自由下列取代组成的组:357A、357I、357L、357M、357P或357V,优选357A,

[0657] 在氨基酸位置550处的氨基酸取代选自由下列取代组成的组:550A、550G、550I、550L、550M或550P,优选550I或550P以及更优选550I,

[0658] 在氨基酸位置556处的氨基酸取代选自由下列取代组成的组:556N、556C、556Q或S556T,优选556T以及

[0659] 在氨基酸位置564处的氨基酸取代选自由下列取代组成的组:564D或564E,优选564E,

[0660] 其中该氨基酸编号指SEQ ID NO:1中的比对位置。

[0661] 在本发明的第十三方面的另一优选实施方式中,其也是该第十三方面的任何其它前述实施方式中的实施方式,本发明的多肽在选自由氨基酸位置712、118、487、590与649处组成的组中的至少一个包含至少一个另外的氨基酸取代,其中

[0662] 在氨基酸位置712处的氨基酸取代选自由下列取代组成的组:712A、712G、712I、712M、712P或712V,优选712M,

[0663] 在氨基酸位置118处的氨基酸取代选自由下列取代组成的组:118A、118G、118I、118L、118M、118P或118V,优选118V,

[0664] 在氨基酸位置487处的氨基酸取代选自由下列取代组成的组:487A、487G、487I、487L、487M、487P或487V,优选487A、487G、487L、487M或487V,更优选487A,

[0665] 在氨基酸位置590处的氨基酸取代选自由下列取代组成的组:590N、590C、590Q、590S、590T、590A、590G、590I、590L、590M、590P或590V,优选590N、590G或590A,更优选590N以及

[0666] 在氨基酸位置649处的氨基酸取代选自由下列取代组成的组:649D或649E,优选649E,

[0667] 其中该氨基酸编号指SEQ ID NO:1中的比对位置。

[0668] 在本发明的第十三方面的另一优选实施方式中,其也是该第十三方面的任何其它前述实施方式中的实施方式,该多肽为一具有海藻糖磷酸化酶活性的多肽,其中该多肽包含氨基酸序列,其是与SEQ ID NO:1的氨基酸序列具有至少63%同源性,其中该多肽在选自

由氨基酸位置383、114、225、304、323、349、357、556与564处所组合的组的两个或更多个包含氨基酸取代,其中,

[0669] 在氨基酸位置383处的氨基酸取代选自由下列取代组成的组:383A、383G、383I、383L、383M、383V、383N、383C、383Q、383S或383T,优选383A、383G、383M、383V、383N、383C、383Q、383S或383T、更优选383G、383V、383C、383S或383T,甚至更优选383V或383T以及最优选383V,

[0670] 在氨基酸位置114处的氨基酸取代选自由下列取代组成的组:114A、114G、114I、114M、114P或114V,优选114I,

[0671] 在氨基酸位置225处的氨基酸取代选自由下列取代组成的组:225A、225G、225I、225L、225M、225P或225V,优选225I、225L、225M或225V以及更优选225V,

[0672] 在氨基酸位置304处的氨基酸取代为304I,

[0673] 在氨基酸位置323处的氨基酸取代选自由下列取代组成的组:323A、323G、323I、323L、323M、323P,或323V,优选323I或323V以及更优选323I,

[0674] 在氨基酸位置349处的氨基酸取代选自由下列取代组成的组:349W或349Y,优选349Y,

[0675] 在氨基酸位置357处的氨基酸取代选自由下列取代组成的组:357A、357I、357L、357M、357P或357V,优选357A,

[0676] 在氨基酸位置556处的氨基酸取代选自由下列取代组成的组:556N、556C、556Q或S556T,优选556T以及

[0677] 在氨基酸位置564处的氨基酸取代选自由下列取代组成的组:564D或564E,优选564E,

[0678] 其中该氨基酸编号指SEQ ID NO:1中的比对位置。

[0679] 在本发明的第十三方面的另一优选实施方式中,其也是该第十三方面的任何其它前述实施方式中的实施方式,本发明的多肽在选自由氨基酸位置712、118、487、550、590与649处组成的组中的至少一个包含至少一个另外的氨基酸取代,其中

[0680] 在氨基酸位置712处的氨基酸取代选自由下列取代组成的组:712A、712G、712I、712M、712P或712V,优选712M,

[0681] 在氨基酸位置118处的氨基酸取代选自由下列取代组成的组:118A、118G、118I、118L、118M、118P或118V,优选118V,

[0682] 在氨基酸位置487处的氨基酸取代选自由下列取代组成的组:487A、487G、487I、487L、487M、487P或487V,优选487A、487G、487L、487M或487V,更优选487A,

[0683] 在氨基酸位置550处的氨基酸取代选自由下列取代组成的组:550A、550G、550I、550L、550M或550P,优选550I或550P以及更优选550I,

[0684] 在氨基酸位置590处的氨基酸取代选自由下列取代组成的组:590N、590C、590Q、590S、590T、590A、590G、590I、590L、590M、590P或590V,优选590N、590G或590A,更优选590N以及

[0685] 在氨基酸位置649处的氨基酸取代选自由下列取代组成的组:649D或649E,优选649E,

[0686] 其中该氨基酸编号指SEQ ID NO:1中的比对位置。

[0687] 在第十三方面的第二实施方式中,其也是第十三方面的第一实施方式或第十三个方面的任何其它实施方式的的一实施方式,该氨基酸序列与SEQ ID NO:1的氨基酸序列具有至少50%同源性。

[0688] 在第十三方面的第三实施方式中,其也是第十三方面的第二实施方式或第十三个方面的任何其它实施方式的的一实施方式,该氨基酸序列与SEQ ID NO:1的氨基酸序列具有至少51%、52%、53%、54%、55%、56%、57%、58%、59%、60%、61%、62%、63%、64%、65%、66%、67%、68%、69%、70%、71%、72%、73%、74%、75%、76%、77%、78%、79%或80%的同源性。

[0689] 在第十三方面的第四实施方式中,其也是第十三方面的第一、第二及第三实施方式或第十三个方面的任何其它实施方式的的一实施方式,该氨基酸序列在选自由氨基酸位置712、383、114、118、225、304、323、349、357、487、550、556、564、590与649组成的组的二、三、四、五、六、七、八、九、十、十一、十二、十三、十四或十五个处包含氨基酸取代。

[0690] 在第十三方面的另一优选实施方式中,其也是第十三方面的第一、第二、第三及第四实施方式或第十三个方面的任何其它实施方式的的一实施方式,该具有海藻糖磷酸化酶活性的多肽为一野生型海藻糖磷酸化酶和/或来自一野生型海藻糖磷酸化酶的变异体,该变体是衍生自属于担子菌门(Basidomycota)的一生物体,优选来自属于伞菌纲(Agaricomycetes)的一生物体,且更佳来自属于由裂折菌属(Schizophyllum)、侧耳属(Pleurotus)、奇果菌属(Grifola)、蘑菇属(Agaricus)、栓菌属(Trametes)、革盖菌属(Coriolus)、栓菌属(Trametes)、附毛菌属(Trichaptum)以及折孔菌属(Lenzites)组成的组的属的一生物体。在第十三方面的另一优选实施方式中,其也是第十三方面的第一、第二、第三及第四实施方式或第十三个方面的任何其它实施方式的的一实施方式,该海藻糖磷酸化酶活性以如本文所公开,更具体地如在第[0371]与[0372]段中所公开的方法测定。

[0691] 应该理解的是,在本文各个方面及实施方式中所述的海藻糖磷酸化酶也可以称为本发明的海藻糖磷酸化酶。

[0692] 本发明基于令人惊讶的发现,即EC编号为EC 2.4.1.231的海藻糖磷酸化酶,其也被称为“TP”,可通过酶工程改进。作为这种酶工程的起点,使用具有根据如SEQ ID NO:1所示的氨基酸序列的海藻糖磷酸化酶。该具有根据SEQ ID NO:1的氨基酸序列的海藻糖磷酸化酶可由Eis等人描述的从裂折菌(Shizophyllum commune)制备(FEBS Letters 440,440-443(1998))。UniProt:D8PWQ7(GenBank:EFJ00254.1)公开了一各别的裂折菌(Shizophyllumcommune)分离株H4-8的野生型蛋白质序列(99.1%同一性)。该序列在SEQ ID NO:1的7个位置上与SEQ ID NO:1不同,其中该分离物H4-8在与SEQ ID NO:1的位置10同源的位置上带有赖氨酸(lysine)氨基酸残基,在与SEQ ID NO:1的位置32同源的位置上带有丝氨酸(serine)氨基酸残基,在与SEQ ID NO:1的位置374同源的位置上带有缬氨酸(valine)氨基酸残基,在与SEQ ID NO:1的位置535同源的位置上带有麸氨酸(glutamic acid)氨基酸残基,在与SEQ ID NO:1的位置536同源的位置上带有脯氨酸(proline)氨基酸残基,在与SEQ ID NO:1的位置616同源的位置上带有异白氨酸(isoleucine)氨基酸残基以及在与SEQ ID NO:1的位置649同源的位置上带有缬氨酸(valine)氨基酸残基。UniProt:A0A151VW19(GenBank:KYQ39707.1)公开了来自生物体鸿禧菇(Hypsizygus marmoreus)的海藻糖磷酸化酶的野生型蛋白质序列,其与SEQ ID NO:1具有77.9%的同一性。除了裂折菌

(Shizophyllum commune)TP之外,其它源于真菌的TP已被描述,例如环柄香菇(Lentinus sajor-caju)(73.2%同源性)、秀珍菇(Pleurotus ostreatus)(75.8%同源性),或千佛菌(Grifola frondosa)(76.7%同源性)。针对千佛菌(Grifola frondosa),已经描述了源自不同分离株的蛋白质序列,其中包括序列SEQ ID NO:160(UniProtKB/Swiss-Prot:登录号:O75003.1)以及SEQ ID NO:81(Genbank登录号:ADM15725.1)。

[0693] 本案发明人已惊讶地发现,在SEQ ID NO:1的氨基酸序列的一个或几个下列氨基酸位置替换氨基酸残基,适合于改进SEQ ID NO:1的海藻糖磷酸化酶的反应特征:712、383、10、114、118、192、197、220、225、304、306、318、323、339、349、357、459、476、481、484、487、488、506、511、526、530、532、533、537、550、556、564、590、649、667、703与705。于这些SEQ ID NO:1的氨基酸位置中,氨基酸位置712、383、10、114、118、220、225、304、318、323、349、357、481、487、488、506、511、550、556、564、590、649、703与705为特别合适的,且SEQ ID NO:1中的氨基酸位置712、383、114、118、225、304、323、349、357、487、550、556、564、590与649中的每一个甚至更为合适。

[0694] 因此,本发明在第一方面涉及包含氨基酸序列的多肽,其中该海藻糖磷酸酶的氨基酸序列与SEQ ID NO:1的氨基酸序列具有至少80%同一性和/或至少80%同源性,其中该海藻糖磷酸化酶的氨基酸序列包含在一个或更多个氨基酸位置处的氨基酸取代,其中该一个或更多个氨基酸位置是各自且独立地选自由下列SEQ ID NO:1的氨基酸位置组成的组:712、383、10、114、118、192、197、220、225、304、306、318、323、339、349、357、459、476、481、484、487、488、506、511、526、530、532、533、537、550、556、564、590、649、667、703与705。

[0695] 在一优选实施方式中,SEQ ID NO:1的氨基酸序列为多肽的氨基酸序列,其中优选地该多肽为海藻糖磷酸化酶。

[0696] 因此,本发明在第一方面同样涉及包含氨基酸序列的海藻糖磷酸化酶,其中该海藻糖磷酸化酶的氨基酸序列与SEQ ID NO:1的氨基酸序列具有至少80%同一性和/或至少80%同源性,其中该海藻糖磷酸化酶的氨基酸序列包含在一个或更多个氨基酸位置处的氨基酸取代,其中该一个或更多个氨基酸位置选自由以下氨基酸位置组成的组:712、383、10、114、118、192、197、220、225、304、306、318、323、339、349、357、459、476、481、484、487、488、506、511、526、530、532、533、537、550、556、564、590、649、667、703与705。

[0697] 在一实施方式中,该第一方面的多肽为海藻糖磷酸化酶,优选一具有本文所公开中的个或多个特征的海藻糖磷酸化酶。因此,本发明的海藻糖磷酸化酶的公开内容,特别是根据每一个及任何方面,同样适用在本发明的多肽,反之亦然。此外,在一实施方式中,本发明的多肽为具有海藻糖磷酸化酶活性的多肽。优选地,海藻糖活性为本文定义的活性。

[0698] 包含氨基酸序列的海藻糖磷酸化酶的措辞,其中该海藻糖磷酸化酶的氨基酸序列与SEQ ID NO:1的氨基酸序列具有至少80%同一性和/或至少80%同源性,其中该海藻糖磷酸化酶的氨基酸序列包含在一个或更多个氨基酸位置处的氨基酸取代,其中该一个或更多个氨基酸位置选自由以下氨基酸位置组成的组:712、383、10、114、118、192、197、220、225、304、306、318、323、339、349、357、459、476、481、484、487、488、506、511、526、530、532、533、537、550、556、564、590、649、667、703与705以及,在一实施方式中,与该措辞海藻糖磷酸化酶与SEQ ID NO:1具有至少80%同源性具有相同含义,其中该海藻糖磷酸化酶在选自以下一个或更多个位置处具有一取代:712、383、10、114、118、192、197、220、225、304、306、318、

323、339、349、357、459、476、481、484、487、488、506、511、526、530、532、533、537、550、556、564、590、649、667、703与705,其中每个位置对应SEQ ID NO:1的氨基酸序列的一个位置。

[0699] 迄今为止,本发明的海藻糖磷酸化酶,优选包括本发明的任何方面,为一突变的海藻糖磷酸化酶,更具体为具有SEQ ID NO:1的氨基酸序列的海藻糖磷酸化酶的突变的海藻糖磷酸化酶。在一实施方式中,本发明的海藻糖磷酸化酶为一具有与SEQ ID NO:1的氨基酸序列不同的氨基酸序列的海藻糖磷酸化酶。在另一个实施方式中,本发明的海藻糖磷酸化酶为海藻糖磷酸化酶,其不同于由SEQ ID NO:1的氨基酸序列组成的海藻糖磷酸化酶。

[0700] 根据本发明的第一方面,本发明的海藻糖磷酸化酶在SEQ ID NO:1的至少一个氨基酸位置处包含至少一个氨基酸取代。值得注意的是,原则上,这种取代的氨基酸位置及取代的氨基酸的种类都是重要的。因此,在本发明的海藻糖磷酸化酶的一个实施方式中,该氨基酸取代在SEQ ID NO:1的特定的指定氨基酸位置中的处进行,其中,任选地,存在于SEQ ID NO:1的这种位置上的氨基酸残基对本发明的海藻糖磷酸化酶中存在的取代氨基酸残基的种类没有任何影响;或者,任选地,存在于SEQ ID NO:1的这种位置上的非常氨基酸残基与存在在本发明的海藻糖磷酸化酶中的取代的氨基酸残基的种类有关。替代可能是非保守或保守的。为了本发明的目的,保守意指将氨基酸G换为A;A换为G、S;V换为I、L、A、T、S;I换为V、L、M;L换为I、M、V;M换为L、I、V;P换为A、S、N;F换为Y、W、H;Y换为F、W、H;W换为Y、F、H;R换为K、E、D;K换为R、E、D;H换为Q、N、S;D换为N、E、K、R、Q;E换为Q、D、K、R、N;S换为T、A;T换为S、V、A;C换为S、T、A;N换为D、Q、H、S;Q换为E、N、H、K、R。

[0701] 还因此,在本发明的海藻糖磷酸化酶的一个实施方式中,该氨基酸取代为其中SEQ ID NO:1的任何所示氨基酸位置的非常氨基酸残基被取代的氨基酸取代,任选地,取代的氨基酸残基的氨基酸位置不完全如参照SEQ ID NO:1所示的那样;相反地,在一实施方式中,取代的氨基酸残基的氨基酸位置与SEQ ID NO:1的相应位置不同,优选1至5个,优选1至3个,更优选1至2个,最优选1个氨基酸位置。

[0702] 就本发明的海藻糖磷酸化酶的特征在于包含在一个或更多个特定氨基酸位置处的氨基酸取代而言,应当理解的是,本发明的海藻糖磷酸化酶是为在一个所示的氨基酸位置中的具有单一取代的海藻糖磷酸化酶;然而,也应该理解的是,如此描述的本发明的海藻糖磷酸化酶也包括其中多于一个氨基酸残基被取代的那些海藻糖磷酸化酶,例如两个、三个等氨基酸残基。在后一种情况下,被取代的氨基酸残基的数目为介于1及指定及定义为被取代的氨基酸残基数目之间的任何整数。因此,本发明的海藻糖磷酸化酶为任何具有或实现氨基酸取代,或具有或实现指定及定义为被取代的氨基酸残基的任何组合,实际上为每个及任何的排列,的海藻糖磷酸化酶。

[0703] 因此,该海藻糖磷酸化酶可以包含氨基酸取代,所述氨基酸取代分别在氨基酸位置712、383、10、114、118、192、197、220、225、304、306、318、323、339、349、357、459、476、481、484、487、488、506、511、526、530、532、533、537、550、556、564、590、649、667、703与705的一个或任何组合处。因此,在一实施方式中,本发明的海藻糖磷酸化酶在SEQ ID NO:1的该氨基酸位置的一个上包含至少一个氨基酸取代,在SEQ ID NO:1的该氨基酸位置的至少两个上包含至少一个氨基酸取代,在SEQ ID NO:1的该氨基酸位置的至少三个上包含至少一个氨基酸取代,在SEQ ID NO:1的该氨基酸位置的至少四个上包含至少一个氨基酸取代,在SEQ ID NO:1的该氨基酸位置的至少五个上包含至少一个氨基酸取代,在SEQ ID NO:1的该

氨基酸位置的至少六个上包含至少一个氨基酸取代,在SEQ ID NO:1的该氨基酸位置的至少七个上包含至少一个氨基酸取代,在SEQ ID NO:1的该氨基酸位置的至少八个上包含至少一个氨基酸取代,在SEQ ID NO:1的该氨基酸位置的至少九个上包含至少一个氨基酸取代,在SEQ ID NO:1的该氨基酸位置的至少十个上包含至少一个氨基酸取代,在SEQ ID NO:1的该氨基酸位置的至少十一个上包含至少一个氨基酸取代,在SEQ ID NO:1的该氨基酸位置的至少十二个上包含至少一个氨基酸取代,在SEQ ID NO:1的该氨基酸位置的至少十三个上包含至少一个氨基酸取代,在SEQ ID NO:1的该氨基酸位置的至少十四个上包含至少一个氨基酸取代。

[0704] 然而,也在本发明的范围内的是本发明的海藻糖磷酸化酶在SEQ ID NO:1所示的氨基酸位置处包含甚至多于上述取代,优选在该海藻糖磷酸化酶的氨基酸序列符合本发明的海藻糖磷酸化酶的最小结构特征和/或最小功能特征中的至少一个的条件下。这样的最小结构特征为该海藻糖磷酸化酶包含氨基酸序列,其中该海藻糖磷酸化酶的氨基酸序列与SEQ ID NO:1的氨基酸序具有列至少80%同一性和/或至少80%同源性,其中该海藻糖磷酸化酶的氨基酸序列包含在一个或更多个氨基酸位置处的氨基酸取代,其中该一个或更多个氨基酸位置各自且独立地选自由下列SEQ ID NO:1的氨基酸位置组成的组:712、383、10、114、118、192、197、220、225、304、306、318、323、339、349、357、459、476、481、484、487、488、506、511、526、530、532、533、537、550、556、564、590、649、667、703与705。这样的最小功能特征为包括本文公开的任何其它的说明书的特征(A)、(B)、(C)、(D)与(E)中的至少一个或其任何组合,其中特征(A)为于52℃温育15分钟后的热稳定性,其由(i)至少30%至90%;或(ii)至少55%至100%的剩余活性定义,特征(B)为于52℃温育15分钟后的热稳定性,其特征在于(i)Tm30值至少为52℃和/或Tm50值至少为52℃,特征(C)为以52℃至90℃之间的Tm30值和/或52℃至90℃之间的Tm50值为特征的热稳定性,特征(D)为以以下为特征的热稳定性:(i)于45℃半衰期为至少3小时至9天的工艺稳定性,(ii)于45℃半衰期为24小时至9天的工艺稳定性,和/或于45℃半衰期为4天至9天的工艺稳定性以及特征(E)为表示为100/500-比的介于0.65和1.0之间的相对活性,其中该100/500-比被定义为[100mM葡萄糖与100mMα-葡萄糖-1磷酸盐的海藻糖活性]/[500mM葡萄糖与100mMα-葡萄糖-1磷酸盐的海藻糖活性]的比。在本发明中,本发明的海藻糖磷酸化酶展现特征(A)、特征(B)、特征(C)、特征(D)、特征(E)、特征(A)及(B)、特征(A)及(C)、特征(A)及(D)、特征(A)及(E)、特征(B)及(C)、特征(B)及(D)、特征(B)及(E)、特征(C)及(D)、特征(C)及(E)、特征(D)及(E)、特征(A)、(B)及(C)、特征(A)、(B)及(D)、特征(A)、(B)及(E)、特征(B)、(C)及(D)、特征(B)、(C)及(E)、特征(C)、(D)及(E)、特征(A)、(B)、(C)及(D)、特征(A)、(B)、(C)及(E)、特征(B)、(C)、(D)及(E)、特征(A)、(C)、(D)及(E),或特征(A)、(B)、(C)、(D)及(E)。

[0705] 在本发明的海藻糖磷酸化酶的一实施方式中,该海藻糖磷酸化酶的氨基酸序列在SEQ ID NO:1的氨基酸序列的至少两个氨基酸位置处包含氨基酸取代。这些至少两个氨基酸位置在本文中也称为两个氨基酸对位置。在本发明的海藻糖磷酸化酶的一实施方式中,该两个氨基酸对位置选自由下列组成的组:V10与L114、V10与I118、V10与Y220、V10与N225、V10与A304、V10与T323、V10与F349、V10与G357、V10与P383、V10与Q487、V10与A506、V10与V550、V10与S556、V10与T564、V10与D590、V10与A649、V10与K705、V10与L712、L114与I118、L114与Y220、L114与N225、L114与A304、L114与T323、V10与F349、L114与G357、L114与P383、

L114与Q487、L114与A506、L114与V550、L114与S556、L114与T564、L114与D590、L114与A649、L114与K705、L114与L712、I118an Y220、I118与N225、I118与A304、I118与T323、V10与F349、I118与G357、I118与P383、I118与Q487、I118与A506、I118与V550、I118与S556、I118与T564、I118与D590、118与A649、L118与K705、I118与L712、Y220与N225、Y220与A304、Y220与T323、V10与F349、Y220与G357、Y220与P383、Y220与Q487、Y220与A506、Y220与V550、Y220与S556、Y220与T564、Y220与D590、Y220与A649、Y220与K705、Y220与L712、N225与A304、N225与T323、V10与F349、N225与G357、N225与P383、N225与Q487、N225与A506、N225与V550、N225与S556、N225与T564、N225与D590、N225与A649、N225与K705、N225与L712、A304与T323、V10与F349、A304与G357、A304与P383、A304与Q487、A304与A506、A304与V550、A304与S556、A304与T564、A304与D590、A304与A649、A304与K705、A304与L712、T323与F349、T323与G357、T323与P383、T323与Q487、T323与A506、T323与V550、T323与S556、T323与T564、T323与D590、T323与A649、T323与K705、T323与L712、F349与G357、F349与P383、F349与Q487、F349与A506、F349与V550、F349与S556、F349与T564、F349与D590、F349与A649、F349与K705、F349与L712、G357与P383、G357与Q487、G357与A506、G357与V550、G357与S556、G357与T564、G357与D590、G357与A649、G357与K705、G357与L712、P383与Q487、P383与A506、P383与V550、P383与S556、P383与T564、P383与D590、P383与A649、P383与K705、P383与L712、Q487与A506、Q487与V550、Q487与S556、Q487与T564、Q487与D590、Q487与A649、Q487与K705、Q487与L712、A506与V550、A506与S556、A506与T564、A506与D590、A506与A649、A506与K705、A506与L712、V550与S556、V550与T564、V550与D590、V550与A649、V550与K705、V550与L712、S556与T564、S556与D590、S556与A649、S556与K705、S556与L712、T564与D590、T564与A649、T564与K705、T564与L712、D590与A649、D590与K705、D590与L712、A649与L712、A649与K705以及K705与L712。本发明的海藻糖磷酸化酶的另外的实施方式为其中该两个氨基酸对位置选自更有限的群组,包括本文具体公开的两个氨基酸对位置的更有限群组的那些。在本发明的范围内,海藻糖磷酸化酶在SEQ ID NO:1的这二对氨基酸对位置中的处包含氨基酸取代。

[0706] 如本文所公开的,在另一个实施方式中,该海藻糖磷酸化酶除了在SEQ ID NO:1的两个氨基酸对位置处的氨基酸取代之外,还包含在SEQ ID NO:1的至少一个或更多个另外的氨基酸位置处的氨基酸取代。SEQ ID NO:1的这样的一个或更多个另外的氨基酸位置是各别且独立地选自以下SEQ ID NO:1的每个氨基酸位置组成的组:712、383、10、114、118、192、197、220、225、304、306、318、323、339、349、357、459、476、481、484、487、488、506、511、526、530、532、533、537、550、556、564、590、649、667、703与705。本发明的海藻糖磷酸化酶的其它实施方式为其中一个或更多个另外的氨基酸位置,选自于一更受限制的群组的那些,包括那些如本文具体公开的另外的氨基酸位置的更有限的群组。在本发明的范围内,海藻糖磷酸化酶在SEQ ID NO:1的两个氨基酸对位置的这些对中的处以及在该另外的氨基酸序列中的处包含氨基酸取代。因此,本发明的海藻糖磷酸化酶各别在一实施方式中为,在至少三个氨基酸位置,亦即在SEQ ID NO:1的该两个氨基酸对位置与一个该另外的氨基酸位置处,具有氨基酸取代的海藻糖磷酸化酶,在至少四个氨基酸位置,亦即在SEQ ID NO:1的该两个氨基酸对位置与两个该另外的氨基酸位置处,具有氨基酸取代的海藻糖磷酸化酶,在至少五个氨基酸位置,亦即在SEQ ID NO:1的该两个氨基酸对位置与三个该另外的氨基酸位置处,具有氨基酸取代的海藻糖磷酸化酶,或在至少六个氨基酸位置,亦即在SEQ ID NO:

1的该两个氨基酸对位置与四个该另外的氨基酸位置处,具有氨基酸取代的海藻糖磷酸化酶。本发明的海藻糖磷酸的一实施方式,其中该海藻糖磷酸化酶在至少四个氨基酸位置处包含氨基酸取代,为在SEQ ID NO:1的每个氨基酸位置712、383、114及118处包含氨基酸取代的海藻糖磷酸化酶。本发明的海藻糖磷酸的一实施方式,其中该海藻糖磷酸化酶在至少五个氨基酸位置处包含氨基酸取代,为在SEQ ID NO:1的每个氨基酸位置712、383、114、118与304处,和/或在SEQ ID NO:1的每个氨基酸位置712、383、114、118与357处包含氨基酸取代的海藻糖磷酸化酶。本发明的海藻糖磷酸的一实施方式,其中该海藻糖磷酸化酶在至少六个氨基酸位置处包含氨基酸取代,为在SEQ ID NO:1的每个氨基酸位置712、383、114、118、304与357处包含氨基酸取代的海藻糖磷酸化酶。

[0707] 在又一个实施方式中,该海藻糖磷酸化酶除了包含在SEQ ID NO:1的两个氨基酸对位置上的该氨基酸取代以及在SEQ ID NO:1的至少另外一个氨基酸位置处的该氨基酸取代,并带有SEQ ID NO:1的一个或更多个另外的氨基酸位置,优选本文公开的SEQ ID NO:1的一个、两个、三个或四个氨基酸位置之外,仍可包含在SEQ ID NO:1的更进一步的一个或更多个氨基酸位置处的氨基酸取代。SEQ ID NO:1的这种一个或更多个更进一步的氨基酸位置是各别并独立地选自由下列SEQ IS NO:1的每个氨基酸位置组成的组:10、192、197、220、225、306、318、323、339、349、459、476、481、484、487、488、506、511、526、530、532、533、537、550、556、564、649、667、703与705。本发明的海藻糖磷酸化酶的另外的实施方式为该一个或更多个更进一步的氨基酸位置选自一更有限的群组的那些,包括本文中具体公开的另外的氨基酸位置的更有限的群组。

[0708] 关于本文公开的具体取代,应该注意的是,根据氨基酸取代领域中的常规做法,取代指进行取代的氨基酸位置的编号,其中左侧的数字在两侧由氨基酸残基指示,其左侧的氨基酸残基是存在于未取代的氨基酸序列中的氨基酸残基,而右侧的氨基酸残基是存在于取代的氨基酸序列中的氨基酸残基。因此,仅为了说明的目的,取代V10R表示在氨基酸位置10,缬氨酸残基被精氨酸所取代。

[0709] 在本发明的范围内,如本文所公开的SEQ ID NO:1的氨基酸位置处的任何突变是以单独或以任何组合的形式,产生仍为海藻糖磷酸化酶活性的蛋白质,更具体而言,是以根据EC 2.4.1.213的海藻糖磷酸化酶。优选地,在EC号为EC 2.4.1.213的海藻糖磷酸化酶中的任何该突变结果,不论是单独或任何组合,如本文所公开,具有特征(A)、(B)、(C)、(D)与(E)中的至少一个,或这样的特征的任何组合。

[0710] 应当理解的是,除了本文具体公开的取代之外,本发明的海藻糖磷酸化酶优选如本文所公开的SEQ ID NO:1的氨基酸位置处的该取代,进一步和/或不同的取代是可以被制造的。优选地,这样的进一步取代在与SEQ ID NO:1的氨基酸位置D379、H403、R507与K512不同的位置处进行,该位置被描述为正确的反应催化所必需的。

[0711] 已知如何分别确定氨基酸残基的聚合物的同一性及同源性。同源性优选是使用BLASTP(参见,例如,Stephen F.Altschul,Thomas L.Madden,Alejandro A.Schäffer,Jinghui Zhang,Zheng Zhang,Webb Miller以及David J.Lipman(1997年)"Gapped BLAST and PSI-BLAST:a new generation of protein database search programs",Nucleic Acids Res.25:3389-3402;或Stephen F.Altschul,John C.Wootton,E.Michael Gertz,Richa Agarwala,Aleksandr Morgulis,Alejandro A.Schäffer以及Yi-Kuo Yu(2005年)

“Protein database searches using compositionally adjusted substitution matrices.”FEBS J.272:5101-5109)。

[0712] 在一实施方式中,本发明的海藻糖为一分类为EC2.4.1.231的磷酸化酶,其催化海藻糖的磷酸化裂解,并使用无机磷酸盐作为葡糖基受体,将端基异构构象净保留在葡萄糖与α-D-葡萄糖-1磷酸盐(aG1P)。这样的反应是可逆的,因此,本发明的海藻糖磷酸化酶将葡萄糖与α-D-葡萄糖-1磷酸盐(aG1P)转化为海藻糖与无机磷酸盐。海藻糖为二糖α-D-吡喃葡萄糖基α-D-吡喃葡萄糖苷(α,α-海藻糖),其特征在于具有如IUPAC定义的分子结构为任何物理形式的(2R,3S,4S,5R,6R)-2-(羟甲基)-6-[(2R,3R,4S,5S,6R)-3,4,5-三羟基-6-(羟基甲基)氧杂环戊烷-2-基]氧基恶唑-3,4,5-三醇。

[0713] 在又一个实施方式中,基于氨基酸序列的相似性,本发明的海藻糖磷酸化酶在碳水化合物-活性酶数据库中被归类为糖基转移酶家族GT4的成员(CAZy,Lombard等人(2014年)Nucleic Acids Res 42:D490-D495,http://www.cazy.org/)。

[0714] 在一实施方式中,本发明的海藻糖磷酸化酶与葡糖基单醣及α-D-葡萄糖-1磷酸盐反应。于一优选实施方式中,该葡糖基单醣为葡萄糖,其中反应产物优选海藻糖。

[0715] 在又一个实施方式中,本发明的海藻糖磷酸化酶与不同于葡萄糖的单醣反应。这种不同于葡萄糖的单醣优选选自D-甘露糖、2-脱氧D-葡萄糖、2-氟D-葡萄糖2-脱氧-2-氟-D-葡萄糖、5-硫代-D-葡萄糖与2-酮-D-葡萄糖,其是被描述为适合用于被分类为EP 2.4.1.231的磷酸化酶的单醣,参阅,例如,(Schwarz等人,J Biotechnol 129,140-150(2007年),Nidetzky 2001等人,Biochem J(2001年)360,727-736)。

[0716] 在又一个实施方式中,本发明的海藻糖磷酸化酶不与β-D-葡萄糖-1磷酸盐、α-D-半乳糖1-磷酸盐、α-D-甘露糖1-磷酸盐,或α-木糖1-磷酸盐反应而作为取代αG1P的替代糖基供体(Schwarz等人,J Biotechnol 129,140-150(2007年),Saito等人,Appl Microbiol Biotechnol 64:4340-4345(1998年))。

[0717] 根据另一实施方式,本发明的海藻糖磷酸化酶优选分类为EC 2.4.1.231的磷酸化酶,不磷酸化裂解其它二糖,例如α,β-海藻糖、β,β-海藻糖、蔗糖、纤维二糖、乳糖、麦芽糖、异麦芽酮糖、异麦芽糖、乳果糖或蜜二糖(参见,例如,Schwarz等人,J Biotechnol 129,140-150(2007年),Eis等人,FEBS Letters 440(1998年)440-443,Saito等人,Appl Microbiol Biotechnol 64:4340-4345(1998年))。

[0718] 在第二方面,本发明涉及一具有某些功能特征的多肽。优选地,该多肽为具有海藻糖磷酸化酶活性的多肽。更佳地,该多肽为海藻糖磷酸化酶。

[0719] 在第二方面中的优选实施方式中,其也是第二方面的任何先前实施方式的一实施方式,并且也是本发明的另一方面,该多肽包含氨基酸序列,其中该氨基酸序列的多肽,优选海藻糖磷酸化酶的多肽,是与SEQ ID NO:1的氨基酸序列具有至少80%同一性和/或至少80%同源性,其中该多肽,优选海藻糖磷酸化酶,具有特征(A)、(B)、(C)、(D)与(E)中的至少一个或其任何组合,特征(A)为于52℃温育15分钟后的热稳定性,其是由一残余活性所定义,特征(B)为于52℃温育15分钟后的热稳定性,由此这种热稳定性由最小Tm30值和/或最小Tm50值所定义,其中Tm30值与Tm50值如本文所定义,特征(C)为由一特定温度范围内的Tm30值和/或Tm50值所定义的热稳定性,特征(D)为热稳定性,其中热稳定性由工艺稳定性定义,工艺稳定性定义为半衰期,优选海藻糖磷酸化酶活性于45℃一段时间的半衰期,特征

(E)为表示为100/500比的相对活性。

[0720] 在第二方面的另一优选实施方式中,其也是第二方面的任何前述实施方式的一实施方式,并且也是本发明的另一方面,本发明涉及一热稳定的海藻糖磷酸化酶变体,其中在含有1M蔗糖的缓冲液中于52℃温育15分钟后保留其初始活性的至少30%,且在室温温育15分钟后测定其初始活性。优选地,这样的海藻糖变体为一热稳定的海藻糖磷酸化酶变体,更优选根据本发明的第一方面的海藻糖磷酸化酶。

[0721] 在第二方面的另一优选实施方式中,其也是第二方面的任何前述实施方式的一实施方式,并且也是本发明的另一方面,本发明涉及来自裂褶菌(Schizophyllum commune)的热稳定的海藻糖磷酸化酶的变体,其中该变体于52℃温育15分钟后具有至少30%的残余活性。优选地,这样的海藻糖变体为一热稳定的海藻糖磷酸化酶变体,更优选根据本发明的第一方面的海藻糖磷酸化酶。

[0722] 在第二方面的另一优选实施方式中,其也是第二方面的任何前述实施方式的一实施方式,并且也是本发明的另一方面,本发明涉及包含SEQ ID NO:1氨基酸序列的海藻糖磷酸化酶的变体,其中该变体于52℃温育15分钟后具有至少30%的残余活性。优选地,这样的海藻糖变体为一热稳定的海藻糖磷酸化酶变体,更优选根据本发明的第一方面的海藻糖磷酸化酶。

[0723] 在第二方面的另一优选实施方式中,其也是第二方面的任何前述实施方式的一实施方式,并且也是本发明的另一方面,本发明涉及来自千佛菌(Grifola frondosa)的热稳定的海藻糖磷酸化酶的变体,其中该变体于52℃温育15分钟后具有至少30%的残余活性。优选地,这样的海藻糖变体为一热稳定的海藻糖磷酸化酶变体,更优选根据本发明的第十四方面的海藻糖磷酸化酶。

[0724] 在第二方面的另一优选实施方式中,其也是第二方面的任何先前实施方式的一实施方式,并且也是本发明的另一方面,本发明涉及多肽,优选海藻糖酸化酶的多肽,其为如本文所述的任何方面或任何优选实施方式中所定的多肽的酶促活性片段,优选海藻糖磷酸化酶的片段,更优选根据本发明的第一、第三、第四、第五,或第十四方面的海藻糖磷酸化酶。

[0725] 在第二方面的另一优选实施方式中,其也是第二方面的任何前述实施方式的一实施方式,并且也是本发明的另一方面,本发明涉及一具有海藻糖磷酸化酶活性的多肽,其中该多肽包含氨基酸序列,其中该氨基酸序列与SEQ ID NO:1的氨基酸序列具有至少20%的同源性,其中该多肽包含选自下列氨基酸位置的两个或更多个:712A、712G、712I、712M、712P或712V、优选712M、383A、383G、383I、383L、383M、383V、383N、383C、383Q、383S或383T、优选383V或383S、最优选383V、114A、114G、114I、114M、114P或114V、优选114I、118A、118G、118I、118L、118M、118P或118V、优选118V、225A、225G、225I、225L、225M、225P或225V、优选225V、304G、304I、304L、304M、304P或304V、优选304I 323A、323G、323I、323L、323M、323P、或323V、优选323I、349W或349Y、优选349Y、357A、357I、357L、357M、357P或357V、优选357A、487A、487G、487I、487L、487M、487P或487V、优选487A、487G、487L或487V、更优选487A、550A、550G、550I、550L、550M或550P、优选550I、556N、556C、556Q或S556T、优选556T、564D或564E、优选564E、590N、590C、590Q、590S、590T、590A、590G、590I、590L、590M、590P或590V、优选590N或590A、更优选590N、以及649D或649E、优选649E,编号指SEQ ID NO:1中的比对位置。

[0726] 本领域技术人员将理解如何鉴定对应于SEQ ID NO:1中的上述位置的任何海藻糖磷酸酶的野生型序列的氨基酸位置。为了澄清,且不限制ㄋ本发明的公开内容,图3显示了SEQ ID NO:1与本领域已知的几种野生型海藻糖磷酸化酶的完全比对。此外,表5显示了另外的野生型海藻糖磷酸化酶的序列位置中的编号及氨基酸,其对应于SEQ ID NO:1的位置114、118、225、304、323、349、383、487、550、556、564、590、649以及712。

[0727] 在另一个优选实施方式中,其也是该第二方面的任何先前实施方式的一实施方式,本发明涉及根据下表的多肽A1-A10至N1-N10(具有表示位置数目的列与代表同源性百分比的排),其中具有根据本发明的具有与SEQ ID NO:1不同的同源性的具有海藻糖磷酸化酶活性的多肽包含选自以下氨基酸位置的不同数目的组合:712A、712G、712I、712M、712P或712V、优选712M、383A、383G、383I、383L、383M、383V、383N、383C、383Q、383S或383T、优选383V或383S、最优选383V、114A、114G、114I、114M、114P或114V、优选114I、118A、118G、118I、118L、118M、118P或118V、优选118V、225A、225G、225I、225L、225M、225P或225V、优选225V、304G、304I、304L、304M、304P或304V、优选304I 323A、323G、323I、323L、323M、323P、或323V、优选323I、349W或349Y、优选349Y、357A、357I、357L、357M、357P或357V、优选357A、487A、487G、487I、487L、487M、487P或487V、优选487A、487G、487L或487V、更优选487A、550A、550G、550I、550L、550M或550P、优选550I、556N、556C、556Q或S556T、优选556T、564D或564E、优选564E、590N、590C、590Q、590S、590T、590A、590G、590I、590L、590M、590P或590V、优选590N或590A、更优选590N、以及649D或649E、优选649E,编号指SEQ ID NO:1中的比对位置。例如位置712M/118V的组合描述了在与SEQ ID NO:1的位置712比对的位置具有甲硫氨酸以及在与SEQ ID NO:1的位置118比对的位置处具有缬氨酸的多肽。

[0728] 表1

[0729]

编号	与 SEQ ID NO: 1 的同源性	结合的取代位置的数目													
		A	B	C	D	E	F	G	H	I	J	K	L	M	N
1	≥20%<30%	2	3	4	5	6	7	8	9	10	11	12	13	14	15
2	≥30%<40%	2	3	4	5	6	7	8	9	10	11	12	13	14	15
3	≥40%<50%	2	3	4	5	6	7	8	9	10	11	12	13	14	15
4	≥50%<55%	2	3	4	5	6	7	8	9	10	11	12	13	14	15
5	≥55%<60%	2	3	4	5	6	7	8	9	10	11	12	13	14	15
6	≥60%<65%	2	3	4	5	6	7	8	9	10	11	12	13	14	15
7	≥65%<70%	2	3	4	5	6	7	8	9	10	11	12	13	14	15
8	≥70%<75%	2	3	4	5	6	7	8	9	10	11	12	13	14	15
9	≥75%<80%	2	3	4	5	6	7	8	9	10	11	12	13	14	15
10	≥80%	2	3	4	5	6	7	8	9	10	11	12	13	14	15

[0730] 例如,D_4指多肽与SEQ ID NO:1具有至少50%的同源性,并且在选自712A、712G、712I、712M、712P或712V、优选712M、383A、383G、383I、383L、383M、383V、383N、383C、383Q、383S或383T、优选383V或383S、最优选383V、114A、114G、114I、114M、114P或114V、优选114I、

118A、118G、118I、118L、118M、118P或118V、优选118V、225A、225G、225I、225L、225M、225P或225V、优选225V、304G、304I、304L、304M、304P或304V、优选304I 323A、323G、323I、323L、323M、323P、或323V、优选323I、349W或349Y、优选349Y、357A、357I、357L、357M、357P或357V、优选357A、487A、487G、487I、487L、487M、487P或487V、优选487A、487G、487L或487V、更优选487A、550A、550G、550I、550L、550M或550P、优选550I、556N、556C、556Q或S556T、优选556T、564D或564E、优选564E、590N、590C、590Q、590S、590T、590A、590G、590I、590L、590M、590P或590V、优选590N或590A、更优选590N、以及649D或649E、优选649E的5个位置包含取代。

[0731] 在另一个优选实施方式中,其也是该第二方面的任何先前实施方式的一实施方式,本发明涉及具有海藻糖磷酸化酶活性的多肽,其中该多肽包含氨基酸序列,其中该氨基酸序列与SEQ ID NO:1的氨基酸序列具有至少77%的同源性,其中该多肽在选自氨基酸位置383、114、225、304、323、349、357、550、556、564以及649的两个或更多个处包含氨基酸取代,其中该氨基酸编号指SEQ ID NO:1中的比对位置。

[0732] 在另一个优选实施方式中,其也是该第二方面的任何先前实施方式的一实施方式,本发明涉及具有海藻糖磷酸化酶活性的多肽,其中该氨基酸序列与SEQ ID NO:1的氨基酸序列具有至少68%的同源性,其中该多肽在选自氨基酸位置383、114、225、304、323、349、357、550、556以及564的两个或更多个处包含氨基酸取代,其中该氨基酸编号指SEQ ID NO:1中的比对位置。

[0733] 在另一个优选实施方式中,其也是该第二方面的任何先前实施方式的一实施方式,本发明涉及具有海藻糖磷酸化酶活性的多肽,其中该多肽包含氨基酸序列,其中该氨基酸序列与SEQ ID NO:1的氨基酸序列具有至少63%的同源性,其中该多肽在选自氨基酸位置383、114、225、304、323、349、357、556以及564的两个或更多个处包含氨基酸取代,其中该氨基酸编号指SEQ ID NO:1中的比对位置。

[0734] 在另一个优选实施方式中,其也是该第二方面的任何先前实施方式的一实施方式,本发明涉及具有海藻糖磷酸化酶活性的多肽,其中氨基酸序列与SEQ ID NO:1的氨基酸序列至少具有50%同源性。

[0735] 在另一个优选实施方式中,本发明涉及具有海藻糖磷酸化酶活性的多肽,其中氨基酸序列与SEQ ID NO:1的氨基酸序列具有至少51%、52%、53%、54%、55%、56%、57%、58%、59%、60%、61%、62%、63%、64%、65%、66%、67%、68%、69%、70%、71%、72%、73%、74%、75%、76%、77%、78%、79%或80%的同源性。

[0736] 还将理解的是,该多肽且优选该第一方面的海藻糖磷酸化酶以及其任何实施方式的多肽可为该第二方面中的实施方式以及其任何实施方式的多肽。还应理解的是,该多肽且优选该第二方面的海藻糖磷酸化酶以及其任何实施方式的多肽可为该第一方面中的实施方式以及其任何实施方式的多肽。

[0737] 在第六方面,本发明涉及一种使葡糖基单醣与α-D-葡萄糖-1磷酸盐反应的方法,其中该方法包括使葡糖基单醣和α-D-葡萄糖-1磷酸盐与本发明的海藻糖磷酸化酶反应,优选根据第一和/或第二方面的海藻糖磷酸化酶。

[0738] 在第七方面,本发明涉及将葡萄糖与α-D-葡萄糖-1磷酸转化为海藻糖与无机磷酸盐的方法,其中该方法包括以本发明的海藻糖磷酸化酶,优选根据第一和/或第二方面的海藻糖磷酸化酶,使葡萄糖与α-D-葡萄糖-1-磷酸海藻糖反应为海藻糖及无机磷酸盐。

[0739] 在第八方面,本发明涉及将海藻糖与无机磷酸盐转化为葡萄糖与α-D-葡萄糖-1-磷酸的方法,且其中该方法包括以本发明的海藻糖磷酸化酶,优选根据第一和/或第二方面的海藻糖磷酸化酶,使海藻糖及无机磷酸盐反应为葡萄糖与α-D-葡萄糖-1磷酸盐。

[0740] 在第九方面,本发明涉及根据第一和/或第二方面的海藻糖磷酸化酶用于生产海藻糖的用途。

[0741] 在第十方面,本发明涉及一种制备海藻糖的方法,包括在海藻糖磷酸化酶存在下,在至少40℃的温度使葡萄糖与α-D-葡萄糖-1磷酸盐反应,其中该海藻糖磷酸化酶

[0742] (i)在含有1M蔗糖的缓冲液中于52℃温育15分钟,与没有热处理的活性相比,保留至少30％的活性;和/或(ii)在100mM葡萄糖下的活性与在500mM葡萄糖下的活性的比至少为0.65。

[0743] 在一实施方式中,该海藻糖磷酸化酶为根据第一和/或第二方面的海藻糖磷酸化酶。

[0744] 在第十一方面,本发明涉及一种提高海藻糖磷酸化酶的热稳定性的方法,其中该方法包括:

[0745] -比对第一海藻糖磷酸化酶的氨基酸序列与第二海藻糖磷酸化酶的氨基酸序列,

[0746] -鉴定对应在该第一海藻糖磷酸化酶的该氨基酸序列的一个或更多个氨基酸位置的该第二海藻糖磷酸化酶的该氨基酸序列的一个或更多个氨基酸位置,其中在该第一海藻糖磷酸化酶的该氨基酸序列的一个或更多个氨基酸位置的氨基酸残基的取代提高了该第一海藻糖磷酸化酶的热稳定性,

[0747] -取代对应在该第一海藻糖磷酸化酶的该氨基酸序列的一个或更多个氨基酸位置的在该第二海藻糖磷酸化酶的一个或更多个氨基酸位置处的氨基酸残基,其中在该第一海藻糖磷酸化酶的该氨基酸序列的一个或更多个氨基酸位置的氨基酸残基的取代提高了该第一海藻糖磷酸化酶的热稳定性,

[0748] 其中该第一海藻糖磷酸化酶为包含根据SEQ ID NO:1的氨基酸序列的海藻糖磷酸化酶。

[0749] 在本发明范围内,本发明的海藻糖磷酸化酶是以全长酶的形式存在。本发明的海藻糖磷酸化酶作为片段存在也在本发明的范围内。优选地,所述片段保留海藻糖磷酸化酶活性,优选如本文分别对本发明的海藻糖磷酸化酶所定义及分别公开的海藻糖磷酸化酶活性。

[0750] 在另一方面,本发明涉及编码本发明的海藻糖磷酸化酶的核酸分子。通常已知基于本文公开的氨基酸序列衍生此类核酸分子。优选地,核酸序列取决于用于表达本发明的海藻糖磷酸化酶的表达系统。用于表达本发明的海藻糖磷酸化酶的优选表达系统为大肠杆菌(E.coli)、芽孢杆菌(Bacillus sp)、巴斯德毕赤酵母菌(P.pastoris)及真菌表达系统如曲菌属(Aspergillus sp.)。

[0751] 在另一方面,本发明涉及含有编码本发明的海藻糖磷酸化酶的核酸分子的载体。优选地,该载体是表达载体。适用于表达酶的合适载体已经在现有技术中被描述。

[0752] 在另一方面,本发明涉及含有本发明载体的宿主生物体。已经描述了含有用于表达酶的载体的合适宿主,且优选地,该宿主生物体为大肠杆菌(E.coli)、芽孢杆菌(Bacillus sp)、巴斯德毕赤酵母菌(P.pastoris)或真菌表达系统如曲菌属(Aspergillus

sp.),优选大肠杆菌及巴斯德毕赤酵母菌。将这种载体整合到该宿主生物体中的方法也是已知的。

[0753] 在另一方面,本发明涉及用于表达海藻糖磷酸化酶的方法。所述方法包括培养如该说明书中所揭露的宿主生物体,其中该宿主生物体包含一表达载体,其中该表达载体包含一编码根据本发明的海藻糖磷酸化酶的核酸分子,在允许所述核酸分子表达的条件下进行培养,并收获该海藻糖磷酸化酶。

[0754] 在本发明的每个及任何方面,包括其任何实施方式,的实施方式中,使用如本文所公开的测定I测定Tm30值。

[0755] 在本发明的每个及任何方面,包括其任何实施方式,的实施方式中,使用如本文所公开的测定II测定Tm30值。

[0756] 在本发明的每个及任何方面,包括其任何实施方式,的实施方式中,使用如本文所公开的测定I测定Tm50值。

[0757] 在本发明的每个及任何方面,包括其任何实施方式,的实施方式中,使用如本文所公开的测定II测定Tm50值。

[0758] 在本发明的范围内,本发明的每个及任何方面,包括其任何实施方式,的海藻糖磷酸化酶以下列形式中的存在:液体溶液、干燥粉末、冷冻干燥的粉末、以固定的形式。

[0759] 在本发明的每个及任何方面,包括其任何实施例,的实施例中,适用以下定义。

[0760] 定义热稳定性:热稳定性为酶在给定的时间段内暴露于特定的高温后抵抗不可逆失活的能力。计算在升高的温度温育一定时间的酶的残余活性作为酶活性与未在高温下温育的酶样品的相对关是。原则上可以使用任何活性测定来确定酶活性。为了本发明的目的,如下所述测定1或测定2已经按照实施例中的规定使用。

[0761] 测量与描述热稳定性有许多方法。为了本发明的目的,通过测量及描述一个或更多个以下特征来确定热稳定性:

[0762] Tm30值:就本发明的目的而言,Tm30值是在含有1M蔗糖的缓冲液中在该温度温育15分钟后,酶具有其初始活性的30%的温度。初始活性为没有温度处理的各种酶的活性,即在室温温育15分钟。原则上可以使用任何活性测定来确定酶活性;为了本发明的目的,已经使用如下所述测定1或测定2,如实施例中所指定的。

[0763] Tm50值:对在本发明的目的而言,Tm50值为在含有1M蔗糖的缓冲液中在该温度温育15分钟后酶具有其初始活性的50%时的温度。初始活性为没有温度处理的各种酶的活性,即在室温温育15分钟。原则上可以使用任何活性测定来确定酶活性;为了本发明的目的,已经使用如下所述测定1或测定2,如实施例中所指定的。

[0764] 工艺稳定性/半衰期:对在本发明的目的而言,如实施例中所示,分别在40或45℃,在具有1M蔗糖的50mM磷酸钾缓冲液pH 7中测定长期稳定性。半衰期定义为在t=0分钟时酶具有50%活性的期间。原则上可以使用任何活性测定来确定酶活性;为了本发明的目的,已经使用如下所述测定1或测定2,如实施例中所指定的。

[0765] 磷酸解活性与合成活性的定义:由于TP催化海藻糖的可逆磷酸化裂解,因此可以在海藻糖磷酸解或合成的方向上测定活性。为了本发明的目的,将磷酸解活性定义为在如下所述测定1的条件下,在无机磷酸盐存在下将海藻糖裂解成αG1P与葡萄糖的活性。合成活性定义为在如下所述分析2的条件下由αG1P与葡萄糖合成海藻糖的活性。在本发明内,任何

活性与该海藻糖磷酸化酶的任何活性在一实施方式中为催化活性。

[0766] 测定I:使用连续偶联测定于30℃常规测定磷酸解活性,其中由海藻糖产生的aG1P通过磷酸葡萄糖变位酶转化为葡萄糖-6-磷酸盐。通过葡萄糖-6-磷酸脱氢酶将葡萄糖-6-磷酸盐与NADP转化为6-磷酸葡萄糖酸与NADPH。检测是基于在340nm处测量NADPH的吸光度。测定溶液含有:75mM的磷酸钾缓冲液pH 7、2.5mM的NADP、10μM葡萄糖-1,6-二磷酸盐、10mM MgCl2、225mM海藻糖、3U/mL的磷酸葡萄糖变位酶与3.4U/mL葡萄糖-6-磷酸脱氢酶。

[0767] 测定II:使用以下条件于40℃常规测定合成活性:50mM钠MES缓冲液pH 7、100mM aG1P与100或500mM葡萄糖浓度,如给出的。反应进程通过基于在酸性条件下与钼酸盐的络合物形成的测定来测量释放的磷酸盐而不连续地测定。钼酸盐络合物被硫酸亚铁还原并产生蓝色,在750nm处以光度法分析。为了分析,将250μL样品与250μL0.5M HCl与500μL钼酸盐试剂(73.2g/L Fe(II)SO_4*7$H_2$0及10g/L钼酸铵*4H20于3.5%硫酸中)。在室温温育15-30分钟后,在750nm处测量吸光度。样品中无机磷酸盐的量以外标量化。

[0768] 定义S/P比:就本发明而言,S/P比定义为如实施例中所述,使用500mM葡萄糖分别以测定1与测定2测量的磷酸解活性与合成活性之间的比。

[0769] 定义100/500比:就本发明而言,根据测定2,100/500比是为使用100mM葡萄糖的TP变体的活性与使用500mM葡萄糖与100mM aG1P的TP变体的活性之间的比。与野生型酶相比,酶变体的100/500比的增加表示葡萄糖的KM值降低。

[0770] 在一实施方式中,若无相反的说明,通过该多肽被展示或将被展示的,且优选任何海藻糖磷酸化酶的,本发明的酶活性、磷酸解活性以及合成活性由本文所述的方法及分析所各别定义及各别确定。

[0771] 表2:序列编号的概述:野生型海藻糖磷酸化酶

[0772]

序列编号 (SEQ ID)	来源
SEQ ID NO: 1	野生型，裂褶菌(*S. commune*)
SEQ ID NO: 80	野生型，簇生垂幕菇(*Hypholoma sublateritium*) FD-334 SS-4, Genbank: KJA27491.1
SEQ ID NO: 81	野生型，千佛菌(*Grifola frondosa*), Genbank: ADM15725
SEQ ID NO: 82	野生型，秀珍菇(*Pleurotus ostreatus*), Genbank: KDQ33172.1
SEQ ID NO: 83	野生型，环柄香菇(*Lentinus sajor-caju*), UniProtKB/Swiss-Prot: Q9UV63.1
SEQ ID NO: 160	野生型，千佛菌(*Grifola frondosa*), UniProtKB/Swiss-Prot: O75003.1
SEQ ID NO: 191	裂褶菌(*Schizophyllum commune*) H4-8, NCBI 参考序列: XP_003035156.1
SEQ ID NO: 192	朱红菌(*Trametes cinnabarina*), Genbank: CDO74881.1
SEQ ID NO: 193	鸿禧菇(*Hypsizygus marmoreus*), Genbank: KYQ39707.1
SEQ ID NO: 194	彩绒栓菌(*Trametes versicolor*) FP-101664 SS1, NCBI 参考序列: XP_008036133.1
SEQ ID NO: 195	肺形侧耳(*Pleurotus pulmonarius*), UniProtKB/Swiss-Prot: A6YRN9.1

	SEQ ID NO: 196	双孢蘑菇变种蘑菇(*Agaricus bisporus* var. bisporus) H97, NCBI 参考序列: XP_006458503.1
	SEQ ID NO: 197	双孢蘑菇(*Agaricus bisporus*)变种贝纳特(burnettii) JB137-S8, NCBI 参考序列: XP_007326883.1
[0773]	SEQ ID NO: 198	硫磺菌(*Laetiporus sulphureus*) 93-53, Genbank: KZT11205.1
	SEQ ID NO: 199	密褐褶菌(*Gloeophyllum trabeum*) ATCC 11539, NCBI 参考序列: XP_007863746.1
	SEQ ID NO: 200	千佛菌(*Grifola frondosa*), Genbank: OBZ75413.1
	SEQ ID NO: 201	绒毛栓菌(*Trametes pubescens*), Genbank: OJT04097.1

[0774] 表3:序列编号的概述:SEQ ID NO:1的海藻糖磷酸化酶的变体

序列编号(SEQ ID)	来源	在变体中的突变数	对 SEQ ID NO: 1 的突变
SEQ ID NO: 2	SEQ ID NO: 1 的变体	1	K705N
SEQ ID NO: 3	SEQ ID NO: 1 的变体	2	P383S、L712M
SEQ ID NO: 4	SEQ ID NO: 1 的变体	2	K705N、L712M
SEQ ID NO: 5	SEQ ID NO: 1 的变体	3	V10R、A506S、L712M
SEQ ID NO: 6	SEQ ID NO: 1 的变体	4	V10R、Y220F、A506S、L712M
SEQ ID NO: 7	SEQ ID NO: 1 的变体	4	V10R、L114I、Y220F、L712M
SEQ ID NO: 8	SEQ ID NO: 1 的变体	4	Y220F、A506S、K705N、L712M
SEQ ID NO: 9	SEQ ID NO: 1 的变体	6	V10R、L114I、Y220F、A506S、K705N、L712M
[0775] SEQ ID NO: 10	SEQ ID NO: 1 的变体	2	P383V、L712M
SEQ ID NO: 11	SEQ ID NO: 1 的变体	8	L114I、I118V、P383V、Q476G、K488A、A506S、A511S、L712M
SEQ ID NO: 12	SEQ ID NO: 1 的变体	9	L114I、I118V、A304I、F349Y、G357A、P383V、A506S、A511S、L712M
SEQ ID NO: 13	SEQ ID NO: 1 的变体	7	L114I、I118V、A304I、F349Y、P383V、E481I、L712M
SEQ ID NO: 14	SEQ ID NO: 1 的变体	6	L114I、I118V、A304I、G357A、P383V、L712M
SEQ ID NO: 15	SEQ ID NO: 1 的变体	8	L114I、I118V、F349Y、G357A、P383V、E481I、K488A、L712M
SEQ ID NO: 16	SEQ ID NO: 1 的变体	8	L114I、I118V、A304I、P383V、E481I、A506S、A511S、L712M
SEQ ID NO: 17	SEQ ID NO: 1 的变体	7	L114I、I118V、P383V、K488A、A506S、A511S、L712M
SEQ ID NO: 18	SEQ ID NO: 1 的变体	9	L114I、I118V、A304I、G357A、P383V、K488A、A506S、A511S、L712M
SEQ ID NO: 19	SEQ ID NO: 1 的变体	5	L114I、I118V、P383V、E481I、L712M

[0776]

SEQ ID NO: 20	SEQ ID NO: 1 的变体	7	L114I、I118V、A304I、F349Y、P383V、K488A、L712M
SEQ ID NO: 21	SEQ ID NO: 1 的变体	7	L114I、I118V、P383V、E481I、A506S、A511S、L712M
SEQ ID NO: 22	SEQ ID NO: 1 的变体	7	L114I、I118V、S192V、A304I、G357A、P383V、L712M
SEQ ID NO: 23	SEQ ID NO: 1 的变体	7	L114I、I118V、S197G、A304I、G357A、P383V、L712M
SEQ ID NO: 24	SEQ ID NO: 1 的变体	7	L114I、I118V、N225V、A304I、G357A、P383V、L712M
SEQ ID NO: 25	SEQ ID NO: 1 的变体	7	L114I、I118V、A304I、D306H、G357A、P383V、L712M
SEQ ID NO: 26	SEQ ID NO: 1 的变体	7	L114I、I118V、A304I、P318H、G357A、P383V、L712M
SEQ ID NO: 27	SEQ ID NO: 1 的变体	7	L114I、I118V、A304I、T323I、G357A、P383V、L712M
SEQ ID NO: 28	SEQ ID NO: 1 的变体	7	L114I、I118V、A304I、L339I、G357A、P383V、L712M
SEQ ID NO: 29	SEQ ID NO: 1 的变体	7	L114I、I118V、A304I、F349Y、G357A、P383V、L712M
SEQ ID NO: 30	SEQ ID NO: 1 的变体	7	L114I、I118V、A304I、G357A、P383V、A459S、L712M
SEQ ID NO: 31	SEQ ID NO: 1 的变体	7	L114I、I118V、A304I、G357A、P383V、E481I、L712M
SEQ ID NO: 32	SEQ ID NO: 1 的变体	7	L114I、I118V、A304I、G357A、P383V、A484S、L712M
SEQ ID NO: 33	SEQ ID NO: 1 的变体	7	L114I、I118V、A304I、G357A、P383V、Q487V、L712M
SEQ ID NO: 34	SEQ ID NO: 1 的变体	7	L114I、I118V、A304I、G357A、P383V、Q487A、L712M
SEQ ID NO: 35	SEQ ID NO: 1 的变体	7	L114I、I118V、A304I、G357A、P383V、Q487L、L712M
SEQ ID NO: 36	SEQ ID NO: 1 的变体	7	L114I、I118V、A304I、G357A、P383V、R526E、L712M
SEQ ID NO: 37	SEQ ID NO: 1 的变体	7	L114I、I118V、A304I、G357A、P383V、E530V、L712M
SEQ ID NO: 38	SEQ ID NO: 1 的变体	7	L114I、I118V、A304I、G357A、P383V、G532R、L712M
SEQ ID NO: 39	SEQ ID NO: 1 的变体	7	L114I、I118V、A304I、G357A、P383V、D533G、L712M
SEQ ID NO: 40	SEQ ID NO: 1 的变体	7	L114I、I118V、A304I、G357A、P383V、D537M、L712M
SEQ ID NO: 41	SEQ ID NO: 1 的变体	7	L114I、I118V、A304I、G357A、P383V、V550I、L712M
SEQ ID NO: 42	SEQ ID NO: 1 的变体	7	L114I、I118V、A304I、G357A、P383V、S556T、L712M
SEQ ID NO: 43	SEQ ID NO: 1 的变体	7	L114I、I118V、A304I、G357A、P383V、T564E、L712M
SEQ ID NO: 44	SEQ ID NO: 1 的变体	7	L114I、I118V、A304I、G357A、P383V、D590N、L712M

[0777]

SEQ ID NO: 45	SEQ ID NO: 1 的变体	7	L114I、I118V、A304I、G357A、P383V、D590A、L712M
SEQ ID NO: 46	SEQ ID NO: 1 的变体	7	L114I、I118V、A304I、G357A、P383V、A649E、L712M
SEQ ID NO: 47	SEQ ID NO: 1 的变体	7	L114I、I118V、A304I、G357A、P383V、R667E、L712M
SEQ ID NO: 48	SEQ ID NO: 1 的变体	7	L114I、I118V、A304I、G357A、P383V、R667K、L712M
SEQ ID NO: 49	SEQ ID NO: 1 的变体	7	L114I、I118V、A304I、G357A、P383V、A703E、L712M
SEQ ID NO: 50	SEQ ID NO: 1 的变体	9	L114I、118V、A304I、G357A、P383V、V550I、S556T、D590N、L712M
SEQ ID NO: 51	SEQ ID NO: 1 的变体	10	L114I、118V、N225V、A304I、G357A、P383V、Q487L、T564E、D590N、L712M
SEQ ID NO: 52	SEQ ID NO: 1 的变体	10	L114I、118V、A304I、T323I、G357A、P383V、V550I、T564E、D590N、L712M
SEQ ID NO: 53	SEQ ID NO: 1 的变体	10	L114I、118V、N225V、A304I、T323I、G357A、P383V、Q487L、D590N、L712M
SEQ ID NO: 54	SEQ ID NO: 1 的变体	11	L114I、118V、N225V、A304I、G357A、P383V、Q487L、V550I、S556T、D590N、L712M
SEQ ID NO: 55	SEQ ID NO: 1 的变体	11	L114I、118V、N225V、A304I、G357A、P383V、Q487L、V550I、T564E、D590N、L712M
SEQ ID NO: 56	SEQ ID NO: 1 的变体	11	L114I、118V、N225V、A304I、G357A、P383V、V550I、S556T、T564E、D590N、L712M
SEQ ID NO: 57	SEQ ID NO: 1 的变体	11	L114I、118V、N225V、A304I、G357A、P383V、V550I、T564E、D590N、A649E、L712M
SEQ ID NO: 58	SEQ ID NO: 1 的变体	11	L114I、118V、A304I、T323I、G357A、P383V、V550I、S556T、T564E、D590N、L712M
SEQ ID NO: 59	SEQ ID NO: 1 的变体	11	L114I、118V、A304I、T323I、G357A、P383V、Q487L、V550I、D590N、A649E、L712M
SEQ ID NO: 60	SEQ ID NO: 1 的变体	12	L114I、118V、N225V、A304I、G357A、P383V、Q487A、V550I、S556T、T564E、D590N、L712M
SEQ ID NO: 61	SEQ ID NO: 1 的变体	12	L114I、118V、N225V、A304I、G357A、P383V、V550I、S556T、T564E、D590N、A649E、L712M
SEQ ID NO: 62	SEQ ID NO: 1 的变体	12	L114I、118V、N225V、A304I、T323I、G357A、P383V、Q487L、V550I、T564E、D590N、L712M
SEQ ID NO: 63	SEQ ID NO: 1 的变体	12	L114I、118V、N225V、A304I、T323I、G357A、P383V、Q487L、V550I、D590N、A649E、L712M
SEQ ID NO: 64	SEQ ID NO: 1 的变体	12	L114I、118V、N225V、A304I、T323I、G357A、P383V、Q487A、V550I、S556T、D590N、L712M

[0778]

SEQ ID NO: 65	SEQ ID NO: 1 的变体	12	L114I、118V、N225V、A304I、T323I、G357A、P383V、V550I、S556T、T564E、D590N、L712M
SEQ ID NO: 66	SEQ ID NO: 1 的变体	12	L114I、118V、A304I、T323I、F349Y、G357A、P383V、Q487L、V550I、D590N、A649E、L712M
SEQ ID NO: 67	SEQ ID NO: 1 的变体	12	L114I、118V、A304I、T323I、G357A、P383V、Q487A、V550I、S556T、T564E、D590N、L712M
SEQ ID NO: 68	SEQ ID NO: 1 的变体	12	L114I、118V、A304I、G357A、P383V、Q487A、V550I、S556T、T564E、D590N、A649E、L712M
SEQ ID NO: 69	SEQ ID NO: 1 的变体	12	L114I、118V、A304I、G357A、P383V、Q487L、V550I、S556T、T564E、D590N、A649E、L712M
SEQ ID NO: 70	SEQ ID NO: 1 的变体	13	L114I、118V、N225V、A304I、T323I、F349Y、G357A、P383V、V550I、S556T、D590N、A649E、L712M
SEQ ID NO: 71	SEQ ID NO: 1 的变体	13	L114I、118V、N225V、A304I、T323I、G357A、P383V、Q487L、V550I、S556T、D590N、A649E、L712M
SEQ ID NO: 72	SEQ ID NO: 1 的变体	13	L114I、118V、N225V、A304I、F349Y、G357A、P383V、Q487A、V550I、S556T、T564E、D590N、L712M
SEQ ID NO: 73	SEQ ID NO: 1 的变体	13	L114I、118V、N225V、A304I、F349Y、G357A、P383V、Q487L、V550I、T564E、D590N、A649E、L712M
SEQ ID NO: 74	SEQ ID NO: 1 的变体	13	L114I、118V、N225V、A304I、G357A、P383V、Q487L、V550I、S556T、T564E、D590N、A649E、L712M
SEQ ID NO: 75	SEQ ID NO: 1 的变体	13	L114I、118V、N225V、A304I、G357A、P383V、Q487A、V550I、S556T、T564E、D590N、A649E、L712M
SEQ ID NO: 76	SEQ ID NO: 1 的变体	13	L114I、118V、A304I、T323I、G357A、P383V、Q487L、V550I、S556T、T564E、D590N、A649E、L712M
SEQ ID NO: 77	SEQ ID NO: 1 的变体	13	L114I、118V、A304I、T323I、G357A、P383V、Q487L、V550I、S556T、T564E、D590N、A649E、L712M
SEQ ID NO: 78	SEQ ID NO: 1 的变体	14	L114I、118V、N225V、A304I、T323I、G357A、P383V、Q487A、V550I、S556T、T564E、D590N、A649E、L712M
SEQ ID NO: 79	SEQ ID NO: 1 的变体	14	L114I、118V、N225V、A304I、T323I、G357A、P383V、Q487G、V550I、S556T、T564E、D590N、A649E、L712M
SEQ ID NO: 84	SEQ ID NO: 1 的变体	1	N225V
SEQ ID NO: 85	SEQ ID NO: 1 的变体	1	A304I

[0779]

SEQ ID NO: 86	SEQ ID NO: 1 的变体	1	T323I
SEQ ID NO: 87	SEQ ID NO: 1 的变体	1	P383V
SEQ ID NO: 88	SEQ ID NO: 1 的变体	1	Q487A
SEQ ID NO: 89	SEQ ID NO: 1 的变体	1	S556T
SEQ ID NO: 90	SEQ ID NO: 1 的变体	1	T564E
SEQ ID NO: 91	SEQ ID NO: 1 的变体	1	D590N
SEQ ID NO: 92	SEQ ID NO: 1 的变体	1	N225I
SEQ ID NO: 93	SEQ ID NO: 1 的变体	1	N225L
SEQ ID NO: 94	SEQ ID NO: 1 的变体	1	N225M
SEQ ID NO: 95	SEQ ID NO: 1 的变体	1	A304L
SEQ ID NO: 96	SEQ ID NO: 1 的变体	1	T323V
SEQ ID NO: 97	SEQ ID NO: 1 的变体	1	P383A
SEQ ID NO: 98	SEQ ID NO: 1 的变体	1	P383G
SEQ ID NO: 99	SEQ ID NO: 1 的变体	1	P383M
SEQ ID NO: 100	SEQ ID NO: 1 的变体	1	P383N
SEQ ID NO: 101	SEQ ID NO: 1 的变体	1	P383C
SEQ ID NO: 102	SEQ ID NO: 1 的变体	1	P383Q
SEQ ID NO: 103	SEQ ID NO: 1 的变体	1	P383S
SEQ ID NO: 104	SEQ ID NO: 1 的变体	1	P383T
SEQ ID NO: 105	SEQ ID NO: 1 的变体	1	Q487G
SEQ ID NO: 106	SEQ ID NO: 1 的变体	1	Q487L
SEQ ID NO: 107	SEQ ID NO: 1 的变体	1	Q487M
SEQ ID NO: 108	SEQ ID NO: 1 的变体	1	V550P
SEQ ID NO: 109	SEQ ID NO: 1 的变体	1	D590G
SEQ ID NO: 110	SEQ ID NO: 1 的变体	2	I118V、P383V

[0780]

SEQ ID NO: 111	SEQ ID NO: 1 的变体	2	I118V、S556T
SEQ ID NO: 112	SEQ ID NO: 1 的变体	2	I118V、T564E
SEQ ID NO: 113	SEQ ID NO: 1 的变体	2	I118V、D590N
SEQ ID NO: 114	SEQ ID NO: 1 的变体	2	N225V、A304I
SEQ ID NO: 115	SEQ ID NO: 1 的变体	2	N225V、P383V
SEQ ID NO: 116	SEQ ID NO: 1 的变体	2	N225V、Q487A
SEQ ID NO: 117	SEQ ID NO: 1 的变体	2	N225V、V550I
SEQ ID NO: 118	SEQ ID NO: 1 的变体	2	N225V、S556T
SEQ ID NO: 119	SEQ ID NO: 1 的变体	2	N225V、D590N
SEQ ID NO: 120	SEQ ID NO: 1 的变体	2	A304I、T323I
SEQ ID NO: 121	SEQ ID NO: 1 的变体	2	A304I、P383V
SEQ ID NO: 122	SEQ ID NO: 1 的变体	2	A304I、Q487A
SEQ ID NO: 123	SEQ ID NO: 1 的变体	2	A304I、S556T
SEQ ID NO: 124	SEQ ID NO: 1 的变体	2	A304I、T564E
SEQ ID NO: 125	SEQ ID NO: 1 的变体	2	A304I、D590N
SEQ ID NO: 126	SEQ ID NO: 1 的变体	2	T323I、G357A
SEQ ID NO: 127	SEQ ID NO: 1 的变体	2	T323I、Q487A
SEQ ID NO: 128	SEQ ID NO: 1 的变体	2	T323I、S556T
SEQ ID NO: 129	SEQ ID NO: 1 的变体	2	T323I、T564E
SEQ ID NO: 130	SEQ ID NO: 1 的变体	2	T323I、D590N
SEQ ID NO: 131	SEQ ID NO: 1 的变体	2	T323I、A649E
SEQ ID NO: 132	SEQ ID NO: 1 的变体	2	F349Y、P383V
SEQ ID NO: 133	SEQ ID NO: 1 的变体	2	F349Y、D590N
SEQ ID NO: 134	SEQ ID NO: 1 的变体	2	G357A、P383V
SEQ ID NO: 135	SEQ ID NO: 1 的变体	2	G357A、D590N

[0781]

SEQ ID NO: 136	SEQ ID NO: 1 的变体	2	P383V、Q487A
SEQ ID NO: 137	SEQ ID NO: 1 的变体	2	P383V、V550I
SEQ ID NO: 138	SEQ ID NO: 1 的变体	2	P383V、S556T
SEQ ID NO: 139	SEQ ID NO: 1 的变体	2	P383V、T564E
SEQ ID NO: 140	SEQ ID NO: 1 的变体	2	P383V、D590N
SEQ ID NO: 141	SEQ ID NO: 1 的变体	2	P383V、A649E
SEQ ID NO: 142	SEQ ID NO: 1 的变体	2	Q487A、T564E
SEQ ID NO: 143	SEQ ID NO: 1 的变体	2	Q487A、D590N
SEQ ID NO: 144	SEQ ID NO: 1 的变体	2	Q487A、A649E
SEQ ID NO: 145	SEQ ID NO: 1 的变体	2	V550I、D590N
SEQ ID NO: 146	SEQ ID NO: 1 的变体	2	S556T、T564E
SEQ ID NO: 147	SEQ ID NO: 1 的变体	2	S556T、D590N
SEQ ID NO: 148	SEQ ID NO: 1 的变体	2	S556T、A649E
SEQ ID NO: 149	SEQ ID NO: 1 的变体	2	T564E、D590N
SEQ ID NO: 150	SEQ ID NO: 1 的变体	2	T564E、L712M
SEQ ID NO: 151	SEQ ID NO: 1 的变体	2	D590N、A649E
SEQ ID NO: 152	SEQ ID NO: 1 的变体	2	D590N、L712M
SEQ ID NO: 153	SEQ ID NO: 1 的变体	2	A649E、L712M
SEQ ID NO: 154	SEQ ID NO: 1 的变体	13	L114I、N225V、A304I、T323I、 G357A、P383V、Q487A、V550I、S556T、T564E、D590N、A649E、 L712M
SEQ ID NO: 155	SEQ ID NO: 1 的变体	13	L114I、118V、N225V、T323I、 G357A、P383V、Q487A、V550I、S556T、T564E、D590N、A649E、 L712M
SEQ ID NO: 156	SEQ ID NO: 1 的变体	13	L114I、118V、N225V、A304I、T323I、P383V、Q487A、V550I、S556T、T564E、D590N、A649E、 L712M
SEQ ID NO: 157	SEQ ID NO: 1 的变体	13	L114I、118V、N225V、A304I、T323I、G357A、Q487A、V550I、S556T、T564E、D590N、A649E、 L712M
SEQ ID NO: 158	SEQ ID NO: 1 的变体	13	L114I、118V、N225V、A304I、T323I、G357A、P383V、Q487A、V550I、S556T、T564E、

			A649E、 L712M
SEQ ID NO: 159	SEQ ID NO: 1 的变体	13	L114I、118V、N225V、A304I、T323I、 G357A、P383V、 Q487A、 V550I、 S556T、 T564E、D590N、 A649E
SEQ ID NO: 190	SEQ ID NO: 1 的变体	14	L114I、118V、N225V、A304I、T323I、 G357A、P383V、 Q487L、 V550I、 S556T、 T564E、D590N、 A649E、 L712M

[0782]

[0783] 表4序列编号的概述:SEQ ID NO:160的变体海藻糖磷酸化酶

[0784]

序列编号(SEQ ID)	来源	在变体中的突变数	对 SEQ ID NO: 160 的突变
SEQ ID NO: 161	SEQ ID NO: 160 的变体	1	L108I
SEQ ID NO: 162	SEQ ID NO: 160 的变体	1	V112I
SEQ ID NO: 163	SEQ ID NO: 160 的变体	1	N221V
SEQ ID NO: 164	SEQ ID NO: 160 的变体	1	A300I
SEQ ID NO: 165	SEQ ID NO: 160 的变体	1	T319I
SEQ ID NO: 166	SEQ ID NO: 160 的变体	1	P379V
SEQ ID NO: 167	SEQ ID NO: 160 的变体	1	S550T
SEQ ID NO: 168	SEQ ID NO: 160 的变体	1	Q558E
SEQ ID NO: 169	SEQ ID NO: 160 的变体	1	A643E
SEQ ID NO: 170	SEQ ID NO: 160 的变体	1	L707M
SEQ ID NO: 171	SEQ ID NO: 160 的变体	2	L108I、N221V
SEQ ID NO: 172	SEQ ID NO: 160 的变体	2	L108I、A300I
SEQ ID NO: 173	SEQ ID NO: 160 的变体	2	L108I、T319I
SEQ ID NO: 174	SEQ ID NO: 160 的变体	2	L108I、V483A
SEQ ID NO: 175	SEQ ID NO: 160 的变体	2	L108I、S550T
SEQ ID NO: 176	SEQ ID NO: 160 的变体	2	P379V、L108I
SEQ ID NO: 177	SEQ ID NO: 160 的变体	2	P379V、V112I
SEQ ID NO: 178	SEQ ID NO: 160 的变体	2	P379V、N221V
SEQ ID NO: 179	SEQ ID NO: 160 的变体	2	P379V、A300I

[0785]

SEQ ID NO: 180	SEQ ID NO: 160 的变体	2	P379V、T319I
SEQ ID NO: 181	SEQ ID NO: 160 的变体	2	P379V、F345Y
SEQ ID NO: 182	SEQ ID NO: 160 的变体	2	P379V、V483A
SEQ ID NO: 183	SEQ ID NO: 160 的变体	2	P379V、V544I
SEQ ID NO: 184	SEQ ID NO: 160 的变体	2	P379V、S550T
SEQ ID NO: 185	SEQ ID NO: 160 的变体	3	P379V、V483A、Q558E
SEQ ID NO: 186	SEQ ID NO: 160 的变体	3	P379V、V544I、S550T
SEQ ID NO: 187	SEQ ID NO: 160 的变体	3	P379V、V544I、Q558E
SEQ ID NO: 188	SEQ ID NO: 160 的变体	3	P379V、S550T、Q558E
SEQ ID NO: 189	SEQ ID NO: 160 的变体	4	P379V、V483A、V544I、Q558E

[0786] 表5在与不同野生型TP的SEQ ID NO:1比对后,在SEQ ID NO:1的位置114、118、225、304、323、349、383、487、550、556、564、590、649、712处的氨基酸及对应位置(该比对是以Clustal omega(Goujon M,McWilliam H,Li W,Valentin F,Squizzato S,Paern J,Lopez R Nucleic acids research 2010 7月,38增刊:W695-9)进行)。

[0787]

序列编号(SEQ ID)	来源	Genbank/Uniprot															
SEQ ID NO: 1	裂褶菌(*Schizophyllum commune*)	ABC84380.1	位置	114	118	225	304	323	349	383	487	550	556	564	590	649	712
			氨基酸	L	I	N	A	T	F	P	Q	V	S	T	D	A	L
SEQ ID NO: 191	裂褶菌(*Schizophyllum commune*) H4-8	XP_003035156.1	位置	114	118	225	304	323	349	383	487	550	556	564	590	649	712
			氨基酸	L	I	N	A	T	F	P	Q	V	S	T	D	V	L
SEQ ID NO: 80	裂褶菌(*Schizophyllum commune*) FD-334 SS-4	KJA27491.1	位置	70	74	183	262	281	307	341	445	509	515	523	550	609	672
			氨基酸	L	V	N	A	T	F	P	T	V	S	Q	N	A	M
SEQ ID NO: 192	朱红菌(*Trametes cinnabarina*)	CDO74881.1	位置	108	112	221	300	319	345	379	483	546	552	560	587	646	709
			氨基酸	L	V	N	A	T	F	P	A	V	S	Q	N	A	M
SEQ ID NO: 193	鸿禧菇(*Hypsizygus marmoreus*)	KYQ39707.1	位置	2	6	115	194	213	239	273	377	438	444	452	478	537	601
			氨基酸	P	S	N	L	T	F	P	V	V	S	Q	N	A	L
SEQ ID NO: 160	千佛菌(*Grifola frondosa*)	O75003.1	位置	108	112	221	300	319	345	379	483	544	550	558	584	643	707
			氨基酸	L	V	N	A	T	F	P	V	V	S	Q	N	A	L
SEQ ID NO: 81	千佛菌	ADM15725.1	位置	108	112	221	300	319	345	379	483	544	550	558	584	643	707

[0788]

	(*Grifola frondosa*)		氨基酸	L	V	N	A	T	F	P	I	V	S	Q	N	A	L
SEQ ID NO: 194	彩绒栓菌(*Trametes versicolor*) FP-101664 SS1	XP_008036133.1	位置	110	114	223	302	321	347	381	485	549	555	563	590	649	712
			氨基酸	L	I	N	A	T	F	P	A	V	S	A	N	D	L
SEQ ID NO: 82	秀珍菇(*Pleurotus ostreatus*) PC15	KDQ33172.1	位置	112	116	225	304	323	349	383	487	551	557	565	592	651	714
			氨基酸	L	I	N	A	T	F	P	A	V	S	A	N	D	L
SEQ ID NO: 195	肺形侧耳(*Pleurotus pulmonarius*)	A6YRN9.1	位置	111	115	224	303	322	348	382	486	547	553	561	587	646	710
			氨基酸	L	V	N	L	T	F	P	V	V	S	Q	N	A	L
SEQ ID NO: 196	双孢蘑菇(*Agaricus bisporus*) var. bisporus H97	XP_006458503.1	位置	110	114	223	302	321	347	381	485	549	555	563	590	649	712
			氨基酸	L	V	N	A	T	F	P	A	V	S	Q	N	E	L
SEQ ID NO: 197	双孢蘑菇(*Agaricus bisporus*) var. burnettii JB137-S8	XP_007326883.1	位置	110	114	223	302	321	347	381	485	549	555	563	590	649	712
			氨基酸	L	V	N	A	T	F	P	A	V	S	Q	N	E	L
SEQ ID NO: 198	硫磺菌(*Laetiporus sulphureus*) 93-53	KZT11205.1	位置	108	112	221	300	319	345	380	484	545	551	559	585	644	708
			氨基酸	L	V	N	A	T	F	P	A	V	S	A	N	E	M
SEQ ID NO: 83	环柄香菇(*Lentinus sajor-caju*) 凤尾菇(*Pleurotus sajor-caju*)	Q9UV63.1	位置	112	116	225	304	323	349	383	499	563	569	577	604	663	726
			氨基酸	L	I	N	A	T	F	P	A	V	S	A	N	D	F
SEQ ID NO: 199	密褐褶菌(*Gloeophyllum trabeum*) ATCC 11539	XP_007863746.1	位置	106	110	227	306	325	351	385	489	552	558	566	592	651	715
			氨基酸	L	V	N	L	T	F	P	V	V	S	G	N	E	L
SEQ ID NO: 200	千佛菌(*Grifola frondosa*)	OBZ75413.1	位置	108	112	221	300	319	345	379	483	505	511	519	545	604	668
			氨基酸	L	V	N	V	T	F	P	S	V	S	Q	N	A	L
SEQ ID NO: 201	绒毛栓菌(*Trametes pubescens*)	OJT04097.1	位置	70	74	183			263	297	401	462	468	476	502	561	625
			氨基酸	L	V	N	-	-	F	P	V	V	S	Q	N	A	L

附图说明

[0789] 本发明进一步通过附图、实施例以及序列表说明,来自其中的进一步特征、实施方式及优点可以被撷取,其中

[0790] 图1为显示在含有与没有加入的1M蔗糖稳定剂的情况下,对于SEQ ID NO:1的野生型海藻糖磷酸化酶,随温度变化的残余活性百分比的图;以及

[0791] 图2为显示对于SEQ ID NO:1的野生型海藻糖磷酸化酶与本发明的各种海藻糖磷酸化酶,随时间变化的残余活性百分比的图;以及

[0792] 图3所示为来自千佛菌(Grifola frondosa)的野生型TPs(UniProtKB/Swiss-Prot:登录号:O75003.1以及Genebank登录号:ADM15725.1),来自秀珍菇(Pleurotus ostreatus)的野生型TPs(Genurbank登录号:KDQ33172.1),来自环柄香菇(Lentinus

sajor-caju)(别名:凤尾菇(Pleurotus sajor-caju))的野生型TPs(Genebank登录号:Q9UV63.1)。使用Clustal omega (Goujon M,McWilliam H,Li W,Valentin F,Squizzato S,Paern J,Lopez R Nucleic acids research 2010 7月,38增刊:W695-9)进行序列比对。

[0793] 在说明书、申请专利范围、序列表和/或附图中公开的本发明的特征可为单独地并且以其任何组合用于以其各种形式实现本发明的材料。

具体实施方式

[0794] 实施例:

[0795] 实施例1:一般方法

[0796] 野生型TP的克隆:来自裂褶菌(S.commune)的海藻糖磷酸化酶基因进行密码子优化用于在大肠杆菌中表达,并由Eurofins MWG操纵子合成。将该基因克隆至表达载体pLE1A17(pRSF-1b,Novagen公司,的衍生物)中。所得的质体用于大肠杆菌BL21(DE3)细胞的转化(transformation)。

[0797] 分子生物学方法:通过本领域已知的标准定点突变技术(site-directed mutagenesis technology)产生TP酶的突变体。

[0798] 重组TP的表达:通过用新鲜的过夜培养物接种培养基I(4.6g/L酵母提取物、9.3g/L蛋白胨、25mM Na_2HPO_4*12H_2O、25mM KH_2PO_4、50mM NH_4Cl_2、Na_2SO_4、5g/L甘油、0.5g/L葡萄糖*1H_2O、2mM $MgSO_4$、50μg/mL卡那霉素)常规表达重组TP。培养物在37℃生长直至在600nm处的光密度为0.6-0.8。以终浓度为0.1mM的IPTG诱导培养物。表达在24-25℃过夜进行。

[0799] TP酶制剂的制备:使用其它地方所述公知的方法制备无细胞提取物。细胞通过离心收获并悬浮于含有50mM磷酸钾的缓冲液中-缓冲液pH 7、2mM $MgCl_2$、0.5mg/mL溶菌酶与20U/mL核酸酶。有时加入1M蔗糖作为稳定剂。通过超声处理或反复冷冻/解冻循环达到细胞破碎。含有可溶性酶的无细胞提取物通过离心与碎片分离。

[0800] 活性测量:如测定I与测定II中所述,可以在海藻糖裂解(磷酸解活性)与合成(合成的活性)的指导下测定海藻糖磷酸化酶的活性:

[0801] 测定I:使用连续偶联分析于30℃常规测定磷酸解活性,其中由海藻糖产生的aG1P通过磷酸葡萄糖变位酶转化为葡萄糖-6-磷酸盐。通过葡萄糖-6-磷酸脱氢酶将葡萄糖-6-磷酸盐与NADP转化为6-磷酸葡萄糖酸与NADPH。检测是基于在340nm波长处测量NADPH的吸光度。测定溶液含有:75mM的磷酸钾缓冲液pH 7、2.5mM的NADP、10μM葡萄糖1,6-二磷酸盐、10mM MgCl2、225mM海藻糖、3U/mL的磷酸葡萄糖变位酶与3.4U/mL葡萄糖-6-磷酸脱氢酶。

[0802] 测定II:使用以下条件于40℃常规测定合成活性:50mM钠MES缓冲液pH 7、100mM aG1P与100或500mM葡萄糖浓度,如给出的。反应进程通过基于在酸性条件下与钼酸盐的络合物形成的测定来测量释放的磷酸盐而不连续地测定。钼酸盐络合物被硫酸亚铁还原并产生蓝色,在750nm处以光度法分析。为了分析,将250μL样品与250μL0.5M HCl与500μL钼酸盐试剂(73.2g/L Fe(II)SO4*7H2O及10g/L钼酸铵*4H_2O于3.5%硫酸中)。在室温温育15-30分钟后,在750nm处测量吸光度。样品中无机磷酸盐的量以外标量化。

[0803] 实施例2:蔗糖对热稳定性的影响

[0804] 重组TP的表达:通过用新鲜的过夜培养物接种培养基I(4.6g/L酵母提取物、9.3g/L蛋白胨、25mM Na_2HPO_4*12H_2O、25mM KH_2PO_4、50mM NH_4Cl_2、Na_2SO_4、5g/L甘油、0.5g/L葡萄糖*

1H_2O、2mM $MgSO_4$、50μg/mL卡那霉素)在摇瓶中表达野生型酶SEQ ID NO:1。培养物在对数期以0.1mM IPTG诱导,并在24-25℃表达过夜。

[0805] TP酶制剂的制备:为了制备不含蔗糖的细胞提取物,细胞通过离心收获并悬浮于含有50mM磷酸钾的缓冲液中-缓冲液pH 7、2mM $MgCl_2$、0.5mg/mL溶菌酶以及20U/mL核酸酶。通过超声破碎细胞。含有可溶性酶的无细胞提取物通过离心与碎片分离。为了制备以蔗糖作为稳定剂的细胞提取物,细胞通过离心收集并悬浮于含有100mM磷酸钾的缓冲液中-缓冲液pH 7、2mM MgC12、0.5mg/mL溶菌酶以及20U/mL核酸酶。以超声破碎细胞。含有可溶性酶的无细胞提取物通过离心与碎片分离,并以2M蔗糖溶液以1:2稀释。

[0806] 变性图谱的测定:将50μL具有及不具有1M蔗糖的酶制剂的等分试样于36至53.7℃的温度范围下温育15分钟。通过离心分离变性的蛋白质。所得的上清液以及未经热失活步骤的细胞提取物的活性以测定I确定。图1为具有及不具有1M蔗糖作为稳定剂的SEQ ID NO:1的变性图谱,显示与未经热失活的酶制剂相比的所获得的残余活性。添加1M蔗糖导致Tm50从大约40℃增加至47.5℃。因此选择1M蔗糖作为TP的稳定剂。

[0807] 实施例3:于52℃温育15分钟后TP变体的残余活性

[0808] 重组TP的表达:通过接种培养基I(4.6g/L酵母提取物、9.3g/L蛋白胨、25mM Na_2HPO_4*12H_2O、25mM KH_2PO_4、50mM NH_4Cl_2、Na_2SO_4、5g/L甘油、0.5g/L葡萄糖*1H_2O、2mM $MgSO_4$、50μg/mL卡那霉素)与新鲜的过夜培养物,在深孔盘中表达重组TP。培养物于37℃生长至在600nm下的光密度为0.6-0.8。以终浓度为0.1mM IPTG诱导培养物。于24-25℃表达过夜。

[0809] TP酶制剂的制备:通过离心收获细胞并悬浮于100mM磷酸钾缓冲液pH7、2mM $MgCl_2$、0.5mg/mL溶菌酶与20U/mL核酸酶中。细胞通过反复的冷冻/解冻循环被破坏。含有可溶性酶的无细胞提取物通过离心与碎片分离。用2M蔗糖溶液以1:2稀释无细胞提取物。

[0810] 热失活与活性测量:将50μL的每种TP的等分试样于52℃温育15分钟。通过离心分离变性的蛋白质。使用以500mM葡萄糖的测定II测定上清液的活性。使用以500mM葡萄糖的测定II直接测定每个TP的另一等分试样的活性而没有热失活。所得残余活性列于表6中。所有变体显示比野生型酶具有更高的残余活性,这表示与野生型相比,它们具有改善的热稳定性。

[0811] 表6:于52℃温育15分钟后TP变体的残余活性

[0812]

序列编号(SEQ ID)	于 52°C 温育 15 分钟后 TP 变体的残余活性百分数[%]
SEQ ID NO: 1	19
SEQ ID NO: 2	30
SEQ ID NO: 3	64
SEQ ID NO: 4	30
SEQ ID NO: 5	39
SEQ ID NO: 6	54
SEQ ID NO: 7	55
SEQ ID NO: 8	42
SEQ ID NO: 9	63
SEQ ID NO: 10	68
SEQ ID NO: 11	39
SEQ ID NO: 12	55
SEQ ID NO: 13	61
SEQ ID NO: 14	30
SEQ ID NO: 15	75
SEQ ID NO: 16	43
SEQ ID NO: 17	50
SEQ ID NO: 18	41
SEQ ID NO: 19	48
SEQ ID NO: 20	75
SEQ ID NO: 21	52
SEQ ID NO: 22	37
SEQ ID NO: 23	36
SEQ ID NO: 24	47
SEQ ID NO: 25	41
SEQ ID NO: 26	45
SEQ ID NO: 27	42
SEQ ID NO: 28	31
SEQ ID NO: 29	55
SEQ ID NO: 30	38
SEQ ID NO: 31	33

[0813]

SEQ ID NO: 32	39
SEQ ID NO: 33	31
SEQ ID NO: 34	53
SEQ ID NO: 35	51
SEQ ID NO: 36	34
SEQ ID NO: 37	37
SEQ ID NO: 38	39
SEQ ID NO: 39	35
SEQ ID NO: 40	46
SEQ ID NO: 41	51
SEQ ID NO: 42	43
SEQ ID NO: 43	42
SEQ ID NO: 44	55
SEQ ID NO: 45	32
SEQ ID NO: 46	43
SEQ ID NO: 47	41
SEQ ID NO: 48	35
SEQ ID NO: 49	53
SEQ ID NO: 50	96
SEQ ID NO: 51	106
SEQ ID NO: 52	99
SEQ ID NO: 53	105
SEQ ID NO: 54	105
SEQ ID NO: 55	77
SEQ ID NO: 56	106
SEQ ID NO: 57	84
SEQ ID NO: 58	88
SEQ ID NO: 59	86
SEQ ID NO: 60	113
SEQ ID NO: 61	117
SEQ ID NO: 62	101
SEQ ID NO: 63	79
SEQ ID NO: 64	101
SEQ ID NO: 65	99
SEQ ID NO: 66	105
SEQ ID NO: 67	99
SEQ ID NO: 68	92
SEQ ID NO: 69	104
SEQ ID NO: 70	76
SEQ ID NO: 71	97
SEQ ID NO: 72	90
SEQ ID NO: 73	105
SEQ ID NO: 74	108
SEQ ID NO: 75	107
SEQ ID NO: 76	97
SEQ ID NO: 78	109
SEQ ID NO: 79	97
SEQ ID NO: 84	29
SEQ ID NO: 85	23
SEQ ID NO: 86	28
SEQ ID NO: 87	38
SEQ ID NO: 88	38
SEQ ID NO: 89	42
SEQ ID NO: 90	28
SEQ ID NO: 91	40

[0814]

SEQ ID NO: 92	25
SEQ ID NO: 93	35
SEQ ID NO: 94	31
SEQ ID NO: 95	35
SEQ ID NO: 96	29
SEQ ID NO: 97	38
SEQ ID NO: 98	64
SEQ ID NO: 99	22
SEQ ID NO: 100	22
SEQ ID NO: 101	54
SEQ ID NO: 102	26
SEQ ID NO: 103	41
SEQ ID NO: 104	78
SEQ ID NO: 105	33
SEQ ID NO: 106	29
SEQ ID NO: 107	30
SEQ ID NO: 108	26
SEQ ID NO: 109	33
SEQ ID NO: 110	56
SEQ ID NO: 111	43
SEQ ID NO: 112	25
SEQ ID NO: 113	63
SEQ ID NO: 114	32
SEQ ID NO: 115	72
SEQ ID NO: 116	24
SEQ ID NO: 117	37
SEQ ID NO: 118	25
SEQ ID NO: 119	32
SEQ ID NO: 120	29
SEQ ID NO: 121	72
SEQ ID NO: 122	27
SEQ ID NO: 123	32
SEQ ID NO: 124	27
SEQ ID NO: 125	55
SEQ ID NO: 126	25
SEQ ID NO: 127	23
SEQ ID NO: 128	30
SEQ ID NO: 129	23
SEQ ID NO: 130	51
SEQ ID NO: 131	31
SEQ ID NO: 132	64
SEQ ID NO: 133	67
SEQ ID NO: 134	61
SEQ ID NO: 135	59
SEQ ID NO: 136	63
SEQ ID NO: 137	56
SEQ ID NO: 138	70
SEQ ID NO: 139	62
SEQ ID NO: 140	69
SEQ ID NO: 141	62
SEQ ID NO: 142	26
SEQ ID NO: 143	28
SEQ ID NO: 144	23
SEQ ID NO: 145	29
SEQ ID NO: 146	34

[0815]

SEQ ID NO: 147	55
SEQ ID NO: 148	26
SEQ ID NO: 149	43
SEQ ID NO: 150	34
SEQ ID NO: 151	40
SEQ ID NO: 152	56
SEQ ID NO: 153	26
SEQ ID NO: 154	81
SEQ ID NO: 155	68
SEQ ID NO: 156	94
SEQ ID NO: 157	69
SEQ ID NO: 158	74
SEQ ID NO: 159	87
SEQ ID NO: 190	100

[0816] 实施例4:TP变体的100/500比

[0817] 如实施例2所述制备TP-变体的细胞提取物。分别使用以500mM葡萄糖的测定II以及以100mM葡萄糖的测定II来测定活性,并计算每个变体的100/500比。表7中列出了所得到的100/500比。可以看出,除了改善的热稳定性之外,一些变体显示出与野生型相比还具有更高的100/500比。这是改善的葡萄糖Km值的指标。

[0818] 表7:TP变体的100/500比

[0819]

序列编号(SEQ ID)	100/500 比
SEQ ID NO: 1	0.6
SEQ ID NO: 5	0.7
SEQ ID NO: 6	0.8
SEQ ID NO: 8	0.7
SEQ ID NO: 22	0.7
SEQ ID NO: 24	0.8
SEQ ID NO: 26	0.7
SEQ ID NO: 27	0.9
SEQ ID NO: 29	0.7
SEQ ID NO: 34	0.7
SEQ ID NO: 36	0.7
SEQ ID NO: 37	0.9
SEQ ID NO: 38	0.8
SEQ ID NO: 41	1.0
SEQ ID NO: 42	0.8
SEQ ID NO: 52	0.8
SEQ ID NO: 53	0.9
SEQ ID NO: 56	0.7
SEQ ID NO: 57	0.9

[0820]

SEQ ID NO: 60	1.0
SEQ ID NO: 61	1.0
SEQ ID NO: 62	0.8
SEQ ID NO: 63	0.9
SEQ ID NO: 64	0.8
SEQ ID NO: 65	0.8
SEQ ID NO: 66	0.9
SEQ ID NO: 68	0.7
SEQ ID NO: 69	0.7
SEQ ID NO: 75	0.9
SEQ ID NO: 76	0.7
SEQ ID NO: 190	0.9

[0821] 实施例5:TP变体的变性图谱

[0822] 选择在实施例3中显示出高度热稳定性改进的14种TP变体以用于测定其Tm30-与Tm50-值。如实施例2中所述,在含有1M蔗糖的50mM磷酸钾缓冲液pH7中测定变性图谱。从变性图谱外推以下Tm30-与Tm-50-值:

[0823] 表8:在含有1M蔗糖的50mM磷酸钾缓冲液pH 7中的TP-变体的Tm30-与Tm50-值

[0824]

序列编号(SEQ ID)	Tm30值	Tm50值
SEQ ID NO:1	49.5	47.5
SEQ ID NO:44	53.5	52
SEQ ID NO:50	54.5	53.5
SEQ ID NO:54	55.5	54.5
SEQ ID NO:57	55.5	54.5
SEQ ID NO:58	56	54.5
SEQ ID NO:62	57.5	56
SEQ ID NO:64	57.5	56
SEQ ID NO:65	57.5	56
SEQ ID NO:71	57	56
SEQ ID NO:72	58	56.5
SEQ ID NO:73	58.5	57.5
SEQ ID NO:74	57.5	56
SEQ ID NO:78	58	56
SEQ ID NO:79	57.5	56

[0825] 实施例6:S/P比

[0826] 选择野生型酶与23个TP-变体以用于测定S/P比。如实施例2中所述制备细胞提取物。以海藻糖磷酸解(测定I)与海藻糖合成(测定II,500mM葡萄糖)的方向测定活性。野生型酶的合成与磷酸解活性之间的比(S/P比)为0.3,表示该酶在海藻糖裂解(cleavage)的方向上显示出较高的反应速率。测试的TP变体都显现出S/P比高于0.3。与野生型酶相比,SEQ ID NO:42与SEQ ID NO:53显现出最高的改善,其S/P比高3倍以上。

[0827] 表9:S/P比

[0828]

序列编号(SEQ ID)	S/P-比
SEQ ID NO:1	0.3
SEQ ID NO:14	0.5
SEQ ID NO:24	0.4
SEQ ID NO:27	0.5
SEQ ID NO:29	0.7
SEQ ID NO:34	0.6
SEQ ID NO:41	0.5
SEQ ID NO:42	0.9
SEQ ID NO:43	0.9
SEQ ID NO:44	0.5
SEQ ID NO:46	0.8
SEQ ID NO:50	0.6
SEQ ID NO:54	0.5
SEQ ID NO:57	0.4
SEQ ID NO:58	0.5
SEQ ID NO:62	0.5
SEQ ID NO:64	0.5
SEQ ID NO:65	0.5
SEQ ID NO:71	0.5
SEQ ID NO:72	0.5
SEQ ID NO:73	0.6
SEQ ID NO:74	0.5
SEQ ID NO:78	0.5
SEQ ID NO:79	0.5

[0829] 实施例7:于45℃的工艺稳定性

[0830] 野生型酶与TP变体SEQ ID NO:14、SEQ ID NO:44、SEQ ID NO:62、SEQID NO:64、SEQ ID NO:65以及SEQ ID NO:78的工艺稳定性于45℃,在含有1M蔗糖的50mM磷酸钾缓冲液pH 7中测定。如实施例2中所述制备细胞提取物。将样品于45℃温育16天。随时间采集样品,并使用测定I测量活性。结果显示在图2中。SEQ ID NO:1在前3个小时内显现出快速的活性丧失,且其半衰期约1小时。正如从Tm50值预期的那样,新的变体显现出极大改进的工艺稳定性。SEQ ID NO:62、SEQ ID NO:65以及SEQ ID NO:78的半衰期显现出最高的改善,具有约8.8天的半衰期。与野生型酶相比,这构成了超过200倍的改善。

[0831] 实施例8:替代的TP酶

[0832] 鉴定具有海藻糖磷酸化酶活性的替代野生型酶的可能性是将已知的海藻糖磷酸化酶与保藏在序列数据库如GenBank中的序列进行比较。为了鉴定替代的TP酶,将SEQ ID NO:1针对GenBank(NCBI)的不含重复性的信息的数据库进行了序列比对(blast)。替代的海藻糖磷酸化酶可以选自与SEQ ID:1具有高度序列相似性的数据库序列,例如来自簇生垂幕

菇(Hypholoma sublateritium)FD-334SS-4(GenBank登录号:KJA27491.1)的推定的海藻糖磷酸化酶或以功能性为特征的海藻糖磷酸化酶,例如,来自环柄香菇(Lentinus sajor-caju)的酶(Genbank登录号:Q9UV63.1)、千佛菌(Grifola frondosa)的酶(Genbank登录号:O75003.1或ADM15725.1)或秀珍菇的酶(Genbank登录号:KDQ33172.1)。这四种酶的序列与图3中的SEQ ID NO:1进行比对。

[0833] 使用实施例1中描述的方法创造替代的野生型海藻糖磷酸化酶的变体。该变体在对应于SEQ ID NO:1中的L114、I118、G357、P383、N225、A304、T323、S556、T564、A649以及L712的位置处含有一个或更多个突变。如实施例3所述测试变体的改善的热稳定性。热失活步骤在相应的野生型温育15分钟后保留约20%残余活性的温度进行。预期新的变体将显现出与实施例3中的变体相似的改进。可添加对应于SEQ ID NO:1中的位置L114、I118、G357、P383、N225、A304、T323、F349、Q487、V550、S556、T564、A649以及L712的更多的突变。预期加入这些突变中的一个或更多个将导致热稳定性的进一步改善。

[0834] 表10:于52.5℃温育15分钟后的残余活性

[0835]

序列编号(SEQ ID)	于52.5℃温育15分钟后的残余活性百分数[%]
SEQ ID NO:160	9
SEQ ID NO:161	14
SEQ ID NO:162	22
SEQ ID NO:163	33
SEQ ID NO:164	26
SEQ ID NO:165	37
SEQ ID NO:166	37
SEQ ID NO:167	20
SEQ ID NO:168	34
SEQ ID NO:169	12
SEQ ID NO:170	15
SEQ ID NO:171	37
SEQ ID NO:172	29
SEQ ID NO:173	42
SEQ ID NO:174	12
SEQ ID NO:175	25
SEQ ID NO:176	57
SEQ ID NO:177	42
SEQ ID NO:178	56
SEQ ID NO:179	38
SEQ ID NO:180	74
SEQ ID NO:181	16
SEQ ID NO:182	28
SEQ ID NO:183	21
SEQ ID NO:184	43

SEQ ID NO:185	58
SEQ ID NO:186	42
SEQ ID NO:187	49
SEQ ID NO:188	70
SEQ ID NO:189	41

<110> 希-莱科塔有限公司 新马特霍恩公司

<120> 海藻糖磷酸化酶

<130> C71105PC

<160> 201

<170> BiSSAP 1.3.6

<210> 1
<211> 737
<212> PRT
<213> 裂褶菌(Schizophyllum commune)

<220>
<223> >SEQ ID NO:1

<400> 1

[0001]

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

290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
[0002] Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 2
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:2

<400> 2

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Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1               5                  10                  15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
            20                  25                  30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
        35                  40                  45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
    50                  55                  60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65                  70                  75                  80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
                85                  90                  95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
            100                 105                 110
Phe Leu Gly Ala Gly Ile Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
        115                 120                 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
    130                 135                 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145                 150                 155                 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
                165                 170                 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
            180                 185                 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
        195                 200                 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
    210                 215                 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225                 230                 235                 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
                245                 250                 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
            260                 265                 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
        275                 280                 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ala
    290                 295                 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305                 310                 315                 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
                325                 330                 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
            340                 345                 350
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[0003]

Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
[0004] 565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Asn Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 3
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:3

<400> 3
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Leu Gly Ala Gly Ile Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
[0005] 180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ala
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Ser Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser

405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
[0006] Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 4
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:4

<400> 4
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15

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

[0007]

Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ala
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460

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

[0008]

Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Asn Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 5
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:5

<400> 5
Met Ser Pro Pro His Gly Phe Ser Ser Arg Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile

[0009]

```
65                  70                  75                  80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
                85                  90                  95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
            100                 105                 110
Phe Leu Gly Ala Gly Ile Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
        115                 120                 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
    130                 135                 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145                 150                 155                 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
                165                 170                 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
            180                 185                 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
        195                 200                 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
    210                 215                 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225                 230                 235                 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
                245                 250                 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
            260                 265                 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
        275                 280                 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ala
    290                 295                 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305                 310                 315                 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
                325                 330                 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
            340                 345                 350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
        355                 360                 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly
    370                 375                 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385                 390                 395                 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
                405                 410                 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
            420                 425                 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
        435                 440                 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
    450                 455                 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465                 470                 475                 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
                485                 490                 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ser Arg Phe Asp Pro Ala Lys
            500                 505                 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
```

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

[0010]

<210> 6
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:6

<400> 6
Met Ser Pro Pro His Gly Phe Ser Ser Arg Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Leu Gly Ala Gly Ile Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125

Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Phe Gly Pro Asn Asn
210 215 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ala
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350

[0011]

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

Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 7
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

[0012]

<220>
<223> >SEQ ID NO:7

<400> 7
Met Ser Pro Pro His Gly Phe Ser Ser Arg Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Ile Gly Ala Gly Ile Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser

180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Phe Gly Pro Asn Asn
210 215 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ala
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
[0013] Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly

625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 8
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:8

<400> 8
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
[0014] Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Leu Gly Ala Gly Ile Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Phe Gly Pro Asn Asn
210 215 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240

Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ala
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460

[0015]

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

Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Asn Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 9
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:9

<400> 9
Met Ser Pro Pro His Gly Phe Ser Ser Arg Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
[0016] Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Ile Gly Ala Gly Ile Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Phe Gly Pro Asn Asn
210 215 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ala

290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ser Arg Phe Asp Pro Ala Lys
500 505 510
[0017] Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Asn Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 10
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:10

<400> 10

[0018]

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

Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
[0019] 565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 11
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:11

<400> 11

[0020]

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

405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gly Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Ala Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ser Arg Phe Asp Pro Ser Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
[0021] Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 12
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:12

<400> 12
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15

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

[0022]

Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Tyr Asp Ala Trp
340 345 350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460

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

[0023]

Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 13
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:13

<400> 13
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile

[0024]

```
65                  70                  75                  80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
                85                  90                  95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
            100                 105                 110
Phe Ile Gly Ala Gly Val Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
        115                 120                 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
    130                 135                 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145                 150                 155                 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
                165                 170                 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
            180                 185                 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
        195                 200                 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
    210                 215                 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225                 230                 235                 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
                245                 250                 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
            260                 265                 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
        275                 280                 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
    290                 295                 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305                 310                 315                 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
                325                 330                 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Tyr Asp Ala Trp
            340                 345                 350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
        355                 360                 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
    370                 375                 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385                 390                 395                 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
                405                 410                 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
            420                 425                 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
        435                 440                 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
    450                 455                 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465                 470                 475                 480
Ile Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
                485                 490                 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
            500                 505                 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
```

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

[0025]

<210> 14
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:14

<400> 14
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Ile Gly Ala Gly Val Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125

Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350

[0026]

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

Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 15
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

[0027]

<220>
<223> >SEQ ID NO:15

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

[0028]

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                180                 185                 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
        195                 200                 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
    210                 215                 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225                 230                 235                 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
                245                 250                 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
            260                 265                 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
        275                 280                 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ala
    290                 295                 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305                 310                 315                 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
                325                 330                 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Tyr Asp Ala Trp
            340                 345                 350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
        355                 360                 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
    370                 375                 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385                 390                 395                 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
                405                 410                 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
            420                 425                 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
        435                 440                 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
    450                 455                 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465                 470                 475                 480
Ile Phe Arg Ala Leu Cys Gln Ala Asp Lys Met Asn Thr Leu Asp Trp
                485                 490                 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
            500                 505                 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
        515                 520                 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
    530                 535                 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545                 550                 555                 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
                565                 570                 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
            580                 585                 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
        595                 600                 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
    610                 615                 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
```

625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 16
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:16

<400> 16
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
[0029] Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Ile Gly Ala Gly Val Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240

Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460

[0030]

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

Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 17
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:17

<400> 17
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
[0031] Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Ile Gly Ala Gly Val Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ala

290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Ala Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ser Arg Phe Asp Pro Ser Lys
500 505 510
[0032] Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 18
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:18

<400> 18

[0033]

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

Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Ala Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ser Arg Phe Asp Pro Ser Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
[0034] 565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 19
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:19

<400> 19

[0035]

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

405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Ile Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
[0036] Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 20
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:20

<400> 20
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15

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

[0037]

Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Tyr Asp Ala Trp
340 345 350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460

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

[0038]

Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 21
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:21

<400> 21
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile

65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Ile Gly Ala Gly Val Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
[0039] Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ala
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Ile Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ser Arg Phe Asp Pro Ser Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu

```
        515                 520                 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
    530                 535                 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545                 550                 555                 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
                565                 570                 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
            580                 585                 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
        595                 600                 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
    610                 615                 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625                 630                 635                 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
                645                 650                 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
            660                 665                 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
        675                 680                 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
    690                 695                 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705                 710                 715                 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
                725                 730                 735
```

[0040] Asp

<210> 22
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:22

<400> 22

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

[0041]

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

Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 23
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

[0042]

<220>
<223> >SEQ ID NO:23

<400> 23
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Ile Gly Ala Gly Val Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser

[0043]

```
                180                 185                 190
Ala Gly Thr Ala Gly Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
            195                 200                 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
        210                 215                 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225                 230                 235                 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
                245                 250                 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
            260                 265                 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
        275                 280                 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
    290                 295                 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305                 310                 315                 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
                325                 330                 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
            340                 345                 350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
        355                 360                 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
    370                 375                 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385                 390                 395                 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
                405                 410                 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
            420                 425                 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
        435                 440                 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
    450                 455                 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465                 470                 475                 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
                485                 490                 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
            500                 505                 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
        515                 520                 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
    530                 535                 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545                 550                 555                 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
                565                 570                 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
            580                 585                 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
        595                 600                 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
    610                 615                 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
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625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 24
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:24

<400> 24
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
[0044] Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Ile Gly Ala Gly Val Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Val Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240

Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460

[0045]

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

Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 25
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:25

<400> 25
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
[0046] Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Ile Gly Ala Gly Val Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile

290 295 300
Leu His Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
[0047] Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 26
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:26

<400> 26

[0048]

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

Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
[0049] 565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 27
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:27

<400> 27

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

[0050]

405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
[0051] Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 28
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:28

<400> 28
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15

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

[0052]

Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Ile Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460

Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
[0053] Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 29
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:29

<400> 29
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile

65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Ile Gly Ala Gly Val Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
[0054] Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Tyr Asp Ala Trp
340 345 350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu

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

[0055] Asp

<210> 30
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:30

<400> 30
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Ile Gly Ala Gly Val Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125

Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
[0056] Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ser Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575

Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 31
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

[0057]

<220>
<223> >SEQ ID NO:31

<400> 31
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Ile Gly Ala Gly Val Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser

180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
[0058] Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Ile Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly

625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 32
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:32

<400> 32
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
[0059] Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Ile Gly Ala Gly Val Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240

Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460

[0060]

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

Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 33
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:33

<400> 33

[0061]

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

[0062]

```
    290                 295                 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305                 310                 315                 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
                325                 330                 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
            340                 345                 350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
        355                 360                 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
    370                 375                 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385                 390                 395                 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
                405                 410                 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
            420                 425                 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
        435                 440                 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
    450                 455                 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465                 470                 475                 480
Glu Phe Arg Ala Leu Cys Val Lys Asp Lys Met Asn Thr Leu Asp Trp
                485                 490                 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
            500                 505                 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
        515                 520                 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
    530                 535                 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545                 550                 555                 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
                565                 570                 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
            580                 585                 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
        595                 600                 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
    610                 615                 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625                 630                 635                 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
                645                 650                 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
            660                 665                 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
        675                 680                 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
    690                 695                 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705                 710                 715                 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
                725                 730                 735
Asp
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<210> 34
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:34

<400> 34

[0063]

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

Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Ala Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
[0064] 565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 35
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:35

<400> 35
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Ile Gly Ala Gly Val Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
[0065] 180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser

405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Leu Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
[0066] Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 36
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:36

<400> 36
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15

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

[0067]

Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460

Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Glu Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
[0068] Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 37
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:37

<400> 37
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile

65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Ile Gly Ala Gly Val Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
[0069] Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu

```
        515                 520                 525
Asn Val Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
    530                 535                 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545                 550                 555                 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
                565                 570                 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
            580                 585                 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
        595                 600                 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
    610                 615                 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625                 630                 635                 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
                645                 650                 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
            660                 665                 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
        675                 680                 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
    690                 695                 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705                 710                 715                 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
                725                 730                 735
Asp
```

[0070]

<210> 38
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:38

<400> 38

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

Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350

[0071]

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

Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 39
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

[0072]

<220>
<223> >SEQ ID NO:39

<400> 39
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Ile Gly Ala Gly Val Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser

180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
[0073] Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Gly Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly

625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 40
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:40

<400> 40
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
[0074] Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Ile Gly Ala Gly Val Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240

Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460

[0075]

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

Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 41
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:41

<400> 41

[0076]

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

290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
[0077] Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Ile Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 42
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:42

<400> 42

[0078]

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Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1               5                  10                  15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
            20                  25                  30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
        35                  40                  45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
    50                  55                  60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65                  70                  75                  80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
                85                  90                  95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
            100                 105                 110
Phe Ile Gly Ala Gly Val Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
        115                 120                 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
    130                 135                 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145                 150                 155                 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
                165                 170                 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
            180                 185                 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
        195                 200                 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
    210                 215                 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225                 230                 235                 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
                245                 250                 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
            260                 265                 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
        275                 280                 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
    290                 295                 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305                 310                 315                 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
                325                 330                 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
            340                 345                 350
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Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Thr Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
[0079] 565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 43
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:43

<400> 43
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Ile Gly Ala Gly Val Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
[0080] 180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser

405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Glu Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
[0081] Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 44
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:44

<400> 44
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15

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

[0082]

Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460

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

[0083]

Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 45
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:45

<400> 45
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile

[0084]

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65                  70                  75                  80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
                85                  90                  95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
            100                 105                 110
Phe Ile Gly Ala Gly Val Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
        115                 120                 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
    130                 135                 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145                 150                 155                 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
                165                 170                 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
            180                 185                 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
        195                 200                 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
    210                 215                 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225                 230                 235                 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
                245                 250                 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
            260                 265                 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
        275                 280                 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
    290                 295                 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305                 310                 315                 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
                325                 330                 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
            340                 345                 350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
        355                 360                 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
    370                 375                 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385                 390                 395                 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
                405                 410                 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
            420                 425                 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
        435                 440                 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
    450                 455                 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465                 470                 475                 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
                485                 490                 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
            500                 505                 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
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        515                 520                 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
    530                 535                 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545                 550                 555                 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
                565                 570                 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Ala Cys Leu
            580                 585                 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
        595                 600                 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
    610                 615                 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625                 630                 635                 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
                645                 650                 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
            660                 665                 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
        675                 680                 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
    690                 695                 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705                 710                 715                 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
                725                 730                 735
Asp
```

[0085]

<210> 46
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:46

<400> 46

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

[0086]

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

Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Glu Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 47
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

[0087]

<220>
<223> >SEQ ID NO:47

<400> 47
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Ile Gly Ala Gly Val Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser

[0088]

180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly

625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Glu Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 48
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:48

<400> 48
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
[0089] Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Ile Gly Ala Gly Val Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240

Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460

[0090]

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

Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 49
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:49

<400> 49
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
[0091] Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Ile Gly Ala Gly Val Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile

290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510

[0092]

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

<210> 50
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:50

<400> 50

[0093]

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

Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Ile Asp Asp Pro Asp Ala Thr Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
[0094] 565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 51
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:51

<400> 51
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Ile Gly Ala Gly Val Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
[0095] 180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Val Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser

405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Leu Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Glu Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
[0096] Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 52
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:52

<400> 52
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15

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

[0097]

Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Ile Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460

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

[0098]

Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 53
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:53

<400> 53
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile

65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Ile Gly Ala Gly Val Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Val Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
[0099] Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Ile Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Leu Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu

```
        515                 520                 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
    530                 535                 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545                 550                 555                 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
                565                 570                 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
            580                 585                 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
        595                 600                 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
    610                 615                 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625                 630                 635                 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
                645                 650                 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
            660                 665                 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
        675                 680                 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
    690                 695                 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705                 710                 715                 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
                725                 730                 735
Asp
```

[0100]

<210> 54
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:54

<400> 54

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

Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Val Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
[0101] Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Leu Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Ile Asp Asp Pro Asp Ala Thr Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575

Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 55
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

[0102]

<220>
<223> >SEQ ID NO:55

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

180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Val Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
[0103] Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Leu Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Ile Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Glu Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly

625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 56
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:56

<400> 56
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
[0104] Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Ile Gly Ala Gly Val Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Val Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240

Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460

[0105]

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

Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 57
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:57

<400> 57
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
[0106] Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Ile Gly Ala Gly Val Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Val Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile

290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510

[0107]

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

<210> 58
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:58

<400> 58

[0108]

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

Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Ile Asp Asp Pro Asp Ala Thr Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Glu Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
[0109] 565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 59
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:59

<400> 59

[0110]

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

405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Leu Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Ile Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
[0111] Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Glu Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 60
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:60

<400> 60
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15

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

[0112]

Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460

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

[0113]

Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 61
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:61

<400> 61
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile

[0114]

```
65                  70                  75                  80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
                85                  90                  95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
            100                 105                 110
Phe Ile Gly Ala Gly Val Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
        115                 120                 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
    130                 135                 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145                 150                 155                 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
                165                 170                 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
            180                 185                 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
        195                 200                 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
    210                 215                 220
Val Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225                 230                 235                 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
                245                 250                 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
            260                 265                 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
        275                 280                 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
    290                 295                 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305                 310                 315                 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
                325                 330                 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
            340                 345                 350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
        355                 360                 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
    370                 375                 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385                 390                 395                 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
                405                 410                 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
            420                 425                 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
        435                 440                 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
    450                 455                 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465                 470                 475                 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
                485                 490                 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
            500                 505                 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
```

```
          515                 520                 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
      530                 535                 540
Cys Gly His Gly Ala Ile Asp Asp Pro Asp Ala Thr Ile Ile Tyr Asp
545                 550                 555                 560
Gln Val Leu Glu Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
                  565                 570                 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
              580                 585                 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
          595                 600                 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
      610                 615                 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625                 630                 635                 640
Phe Leu Thr Glu Pro Gly Asp Asn Glu Gln Val Ala Arg His Met Tyr
                  645                 650                 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
              660                 665                 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
          675                 680                 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
      690                 695                 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705                 710                 715                 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
                  725                 730                 735
Asp
```

[0115]

<210> 62
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:62

<400> 62

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

Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Val Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Ile Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350

[0116]

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

```
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
            580                 585                 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
        595                 600                 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
    610                 615                 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625                 630                 635                 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
                645                 650                 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
            660                 665                 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
        675                 680                 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
    690                 695                 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705                 710                 715                 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
                725                 730                 735
Asp
```

<210> 63
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

[0117]

<220>
<223> >SEQ ID NO:63

<400> 63

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

180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Val Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Ile Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
[0118] Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Leu Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Ile Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly

625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Glu Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 64
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:64

<400> 64
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
[0119] Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Ile Gly Ala Gly Val Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Val Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240

Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Ile Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460

[0120]

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

Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 65
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:65

<400> 65

[0121]

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

290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Ile Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510

[0122] Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Ile Asp Asp Pro Asp Ala Thr Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Glu Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 66
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:66

<400> 66

[0123]

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

Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Leu Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Ile Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
[0124] 565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Glu Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 67
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:67

<400> 67

Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Ile Gly Ala Gly Val Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
[0125] 180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Ile Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser

405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Ala Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Ile Asp Asp Pro Asp Ala Thr Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Glu Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
[0126] Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 68
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:68

<400> 68
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15

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

[0127]

Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460

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

[0128]

Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 69
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:69

<400> 69
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile

65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Ile Gly Ala Gly Val Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
[0129] Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Leu Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu

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

[0130]

<210> 70
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:70

<400> 70
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Ile Gly Ala Gly Val Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125

Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Val Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Ile Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Tyr Asp Ala Trp
340 345 350

[0131]

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

```
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
            580                 585                 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
        595                 600                 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
    610                 615                 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625                 630                 635                 640
Phe Leu Thr Glu Pro Gly Asp Asn Glu Gln Val Ala Arg His Met Tyr
                645                 650                 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
            660                 665                 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
        675                 680                 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
    690                 695                 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705                 710                 715                 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
                725                 730                 735
Asp
```

<210> 71
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

[0132]

<220>
<223> >SEQ ID NO:71

<400> 71

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

[0133]

```
                180                 185                 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
        195                 200                 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
    210                 215                 220
Val Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225                 230                 235                 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
                245                 250                 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
            260                 265                 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
        275                 280                 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
    290                 295                 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305                 310                 315                 320
Phe Arg Ile Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
                325                 330                 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
            340                 345                 350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
        355                 360                 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
    370                 375                 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385                 390                 395                 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
                405                 410                 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
            420                 425                 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
        435                 440                 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
    450                 455                 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465                 470                 475                 480
Glu Phe Arg Ala Leu Cys Leu Lys Asp Lys Met Asn Thr Leu Asp Trp
                485                 490                 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
            500                 505                 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
        515                 520                 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
    530                 535                 540
Cys Gly His Gly Ala Ile Asp Asp Pro Asp Ala Thr Ile Ile Tyr Asp
545                 550                 555                 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
                565                 570                 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
            580                 585                 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
        595                 600                 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
    610                 615                 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
```

625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Glu Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 72
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:72

<400> 72
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
[0134] Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Ile Gly Ala Gly Val Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Val Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240

Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Tyr Asp Ala Trp
340 345 350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460

[0135]

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

Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 73
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:73

<400> 73

[0136]

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

[0137]

```
290                 295                 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305                 310                 315                 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
                325                 330                 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Tyr Asp Ala Trp
            340                 345                 350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
        355                 360                 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
    370                 375                 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385                 390                 395                 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
                405                 410                 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
            420                 425                 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
        435                 440                 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
    450                 455                 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465                 470                 475                 480
Glu Phe Arg Ala Leu Cys Leu Lys Asp Lys Met Asn Thr Leu Asp Trp
                485                 490                 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
            500                 505                 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
        515                 520                 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
    530                 535                 540
Cys Gly His Gly Ala Ile Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545                 550                 555                 560
Gln Val Leu Glu Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
                565                 570                 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
            580                 585                 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
        595                 600                 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
    610                 615                 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625                 630                 635                 640
Phe Leu Thr Glu Pro Gly Asp Asn Glu Gln Val Ala Arg His Met Tyr
                645                 650                 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
            660                 665                 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
        675                 680                 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
    690                 695                 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705                 710                 715                 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
                725                 730                 735
Asp
```

<210> 74
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:74

<400> 74

[0138]

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

Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Leu Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Ile Asp Asp Pro Asp Ala Thr Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Glu Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
[0139] 565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Glu Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 75
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:75

<400> 75

[0140]

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

405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Ala Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Ile Asp Asp Pro Asp Ala Thr Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Glu Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
[0141] Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Glu Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 76
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:76

<400> 76
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15

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

[0142]

Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Ile Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460

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

[0143]

Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 77
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:77

<400> 77
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile

[0144]

```
65                  70                  75                  80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
                85                  90                  95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
            100                 105                 110
Phe Ile Gly Ala Gly Val Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
        115                 120                 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
    130                 135                 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145                 150                 155                 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
                165                 170                 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
            180                 185                 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
        195                 200                 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
    210                 215                 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225                 230                 235                 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
                245                 250                 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
            260                 265                 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
        275                 280                 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
    290                 295                 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305                 310                 315                 320
Phe Arg Ile Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
                325                 330                 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
            340                 345                 350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
        355                 360                 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
    370                 375                 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385                 390                 395                 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
                405                 410                 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
            420                 425                 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
        435                 440                 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
    450                 455                 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465                 470                 475                 480
Glu Phe Arg Ala Leu Cys Leu Lys Asp Lys Met Asn Thr Leu Asp Trp
                485                 490                 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
            500                 505                 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
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```
        515                 520                 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
    530                 535                 540
Cys Gly His Gly Ala Ile Asp Asp Pro Asp Ala Thr Ile Ile Tyr Asp
545                 550                 555                 560
Gln Val Leu Glu Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
                565                 570                 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
            580                 585                 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
        595                 600                 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
    610                 615                 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625                 630                 635                 640
Phe Leu Thr Glu Pro Gly Asp Asn Glu Gln Val Ala Arg His Met Tyr
                645                 650                 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
            660                 665                 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
        675                 680                 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
    690                 695                 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705                 710                 715                 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
                725                 730                 735
Asp
```

[0145]

<210> 78
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:78

<400> 78

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

Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Val Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Ile Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350

[0146]

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

Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Glu Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 79
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

[0147]

<220>
<223> >SEQ ID NO:79

<400> 79
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Ile Gly Ala Gly Val Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser

[0148]

```
                180                 185                 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
        195                 200                 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
    210                 215                 220
Val Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225                 230                 235                 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
                245                 250                 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
            260                 265                 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
        275                 280                 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
    290                 295                 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305                 310                 315                 320
Phe Arg Ile Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
                325                 330                 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
            340                 345                 350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
        355                 360                 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
    370                 375                 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385                 390                 395                 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
                405                 410                 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
            420                 425                 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
        435                 440                 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
    450                 455                 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465                 470                 475                 480
Glu Phe Arg Ala Leu Cys Gly Lys Asp Lys Met Asn Thr Leu Asp Trp
                485                 490                 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
            500                 505                 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
        515                 520                 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
    530                 535                 540
Cys Gly His Gly Ala Ile Asp Asp Pro Asp Ala Thr Ile Ile Tyr Asp
545                 550                 555                 560
Gln Val Leu Glu Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
                565                 570                 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
            580                 585                 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
        595                 600                 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
    610                 615                 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
```

625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Glu Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 80
<211> 696
<212> PRT
<213> Hypholoma sublateritium FD-334 SS-4

<220>
<223> >KJA27491.1

<400> 80
Met Trp Ala Ala Val Ala Gly Ala Val Ile Asn Asn Asn Thr Gln Tyr
1 5 10 15
[0149] Glu Ile Ala Val Ser Ile His Asp Ser Val Tyr Ser Thr Asp Phe Ala
20 25 30
Ser Ser Val Leu Ser Phe Asn Pro Asn Asn Pro Asp Lys Asn Ala Lys
35 40 45
Glu Ile Glu Gln Tyr Val Leu Gln Thr Leu Arg Met Phe Ser Val Gly
50 55 60
His Leu Cys Lys Phe Leu Gly Ala Gly Val Thr Leu Leu Leu Leu Lys
65 70 75 80
Glu Ser Pro Asn Leu Cys Thr Arg Leu Trp Leu Asp Met Asp Ile Val
85 90 95
Pro Phe Val Phe Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg
100 105 110
Pro Asn Ile Lys His Arg Ile Ser Ser Thr Thr Gly Ser Tyr Val Pro
115 120 125
Ser Gly Ala Asp Thr Pro Thr Val Tyr Val Asp Ser Ala His Leu Thr
130 135 140
Ala Met Ser Gly Leu Gln Thr Gly Val Ser Gly Arg Leu Pro Ile Pro
145 150 155 160
Arg Thr Leu Asp Glu Gln Ala Asp Ser Ala Ala Arg Lys Cys Leu Met
165 170 175
Tyr Phe Gly Pro Gly Asn Asn Pro Arg Leu Ser Ile Gly Pro Arg Asn
180 185 190
Gln Val Thr Val Asp Ser Ala Gly Lys Ala His Leu Ile Asp Asp Ile
195 200 205
Asp Glu Tyr Lys Ala Thr Val Gly Pro Arg Thr Trp Asn Ala Val Val
210 215 220
Lys Leu Ala Asp Glu Leu Arg Glu Lys Lys Val Lys Ile Gly Phe Phe
225 230 235 240

Ser Ser Thr Pro Gln Gly Gly Gly Val Ala Leu Met Arg His Ala Leu
245 250 255
Ile Arg Phe Leu Thr Ala Leu Asp Val Asp Ala Ala Trp Tyr Val Pro
260 265 270
Asn Pro Ser Pro Ser Val Phe Arg Thr Thr Lys Asn Asn His Asn Ile
275 280 285
Leu Gln Gly Val Ala Ala Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys
290 295 300
Asp Asn Phe Asp Ala Trp Ile Leu Lys Asn Gly Leu Arg Trp Thr Ala
305 310 315 320
Glu Gly Gly Pro Leu Ala Pro Gly Gly Val Asp Ile Ala Phe Ile Asp
325 330 335
Asp Pro Gln Met Pro Gly Leu Ile Pro Leu Ile Lys Lys Ile Arg Pro
340 345 350
Asp Leu Pro Ile Val Tyr Arg Ser His Ile Glu Ile Arg Ser Asp Leu
355 360 365
Val His Val Pro Gly Ser Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp
370 375 380
Asn Asn Ile Gln Leu Ala Asp Leu Phe Ile Ser His Pro Val Asn Lys
385 390 395 400
Phe Val Pro Ser Asp Val Pro Ile Glu Lys Leu Ala Leu Leu Gly Ala
405 410 415
Ala Thr Asp Trp Leu Asp Gly Leu Asn Lys Glu Leu Asp Pro Trp Asp
420 425 430
Ser Gln Tyr Tyr Met Gly Glu Phe Arg Asn Leu Cys Thr Lys Glu Lys
435 440 445
Met His Thr Leu Asn Trp Pro Glu Arg Asp Tyr Val Val Gln Ile Ala
450 455 460

[0150]

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

Pro Arg Gly Gly Leu Thr Met Gln
690 695

<210> 81
<211> 732
<212> PRT
<213> 千佛菌(Grifola frondosa)

<220>
<223> ADM15725.1 海藻糖合成酶

<400> 81
Met Ala Pro Pro His Gln Phe Gln Ser Lys Pro Ser Asp Val Ile Arg
1 5 10 15
Arg Arg Leu Ser Ser Ala Val Ser Ser Lys Arg Pro Asn Val Pro Gly
20 25 30
Tyr Thr Ser Leu Thr Pro Met Trp Ala Gly Ile Ala Gly Ala Val Val
35 40 45
Asn Asn Asn Ser Gln Phe Glu Val Ala Ile Ser Ile His Asp Ser Val
50 55 60
Tyr Asn Thr Asp Phe Ala Ser Ser Ile Val Pro Tyr Ser Pro Asn Glu
65 70 75 80
Pro Glu Ala Gln Ala Gly Ile Ile Glu Lys His Val Leu Glu Thr Leu
85 90 95
Arg Lys Phe Ser Thr Glu His Met Cys Lys Phe Leu Gly Ala Gly Val
100 105 110
[0151] Thr Val Ile Leu Leu Arg Glu Ala Pro Asn Leu Cys Thr Arg Leu Trp
115 120 125
Leu Asp Met Asp Ile Val Pro Ile Val Phe Asn Ile Lys Pro Phe His
130 135 140
Thr Asp Ser Ile Thr Arg Pro Asn Val Arg His Arg Ile Ser Ser Thr
145 150 155 160
Thr Gly Ser Tyr Val Pro Ser Gly Ala Glu Thr Pro Thr Val Tyr Tyr
165 170 175
Asp Pro Ala Gln Leu Gln Asp Pro Asn Lys Leu Ser Ala Asn Val Gln
180 185 190
Thr Arg Leu Pro Ile Pro Arg Thr Val Asp Glu Gln Ala Asp Ser Ala
195 200 205
Ala Arg Lys Cys Ile Met Tyr Phe Gly Pro Gly Asn Asn Pro Arg Leu
210 215 220
Gln Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala Gly Gly Lys Ile
225 230 235 240
His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr Val Gly Lys Gly
245 250 255
Thr Trp Asn Ser Val Ile Lys Leu Ala Asp Glu Leu Arg Glu Lys Lys
260 265 270
Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly Gly Gly Val Ala
275 280 285
Leu Met Arg His Ala Ile Ile Arg Phe Phe Thr Ala Leu Asp Val Asp
290 295 300
Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val Phe Arg Thr Thr
305 310 315 320
Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Asp Pro Ser Leu Arg
325 330 335
Leu Thr Lys Glu Ala Ala Asp Asn Phe Asp Ser Trp Ile Leu Lys Asn

340 345 350
Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala Pro Gly Gly Val
355 360 365
Asp Ile Ala Phe Ile Asp Asp Pro Gln Val Pro Gly Leu Ile Pro Leu
370 375 380
Ile Lys Arg Ile Arg Pro Asp Leu Pro Ile Ile Tyr Arg Ser His Ile
385 390 395 400
Glu Ile Arg Ser Asp Leu Val His Val Lys Gly Ser Pro Gln Glu Glu
405 410 415
Val Trp Asn Tyr Leu Trp Asn Asn Ile Gln His Ser Asp Leu Phe Ile
420 425 430
Ser His Pro Val Asn Lys Phe Val Pro Ser Asp Val Pro Leu Glu Lys
435 440 445
Leu Ala Leu Leu Gly Ala Ala Thr Asp Trp Leu Asp Gly Leu Ser Lys
450 455 460
His Leu Asp Ala Trp Asp Ala Gln Tyr Tyr Met Gly Glu Phe Arg Asn
465 470 475 480
Leu Cys Ile Lys Glu Lys Met Asn Glu Leu Gly Trp Pro Ala Arg Asp
485 490 495
Tyr Ile Val Gln Ile Ala Arg Phe Asp Pro Ser Lys Gly Ile Pro Asn
500 505 510
Val Ile Asp Ser Tyr Ala Arg Phe Arg Lys Leu Cys Val Asp Lys Val
515 520 525
Met Glu Asp Asp Ile Pro Gln Leu Leu Leu Cys Gly His Gly Ala Val
530 535 540
Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp Gln Val Leu Gln Leu Ile
545 550 555 560

[0152]

His Ala Lys Tyr Lys Glu Tyr Ala Pro Asp Ile Val Val Met Arg Cys
565 570 575
Pro Pro Ser Asp Gln Leu Leu Asn Thr Leu Met Ala Asn Ala Lys Phe
580 585 590
Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe Glu Val Lys Val Ser Glu
595 600 605
Ala Leu His Ala Gly Lys Pro Val Ile Ala Cys Arg Thr Gly Gly Ile
610 615 620
Pro Leu Gln Ile Glu His Gly Lys Ser Gly Tyr Leu Cys Glu Pro Gly
625 630 635 640
Asp Asn Ala Ala Val Ala Gln His Met Leu Asp Leu Tyr Thr Asp Glu
645 650 655
Asp Leu Tyr Asp Thr Met Ser Glu Tyr Ala Arg Thr His Val Ser Asp
660 665 670
Glu Val Gly Thr Val Gly Asn Ala Ala Ala Trp Met Tyr Leu Ala Val
675 680 685
Met Tyr Val Ser Arg Gly Val Lys Leu Arg Pro His Gly Ala Trp Ile
690 695 700
Asn Asp Leu Met Arg Thr Glu Met Gly Glu Pro Tyr Arg Ala Gly Glu
705 710 715 720
Pro Arg Leu Pro Arg Gly Glu Leu His Val Gln Gly
725 730

<210> 82
<211> 737
<212> PRT
<213> 秀珍菇(Pleurotus ostreatus)

<220>
<223> KDQ33172.1

<400> 82
Met Ser Thr His His Gln Phe Glu Ser Lys Pro Ser Thr Ala Ile Arg
1 5 10 15
Arg Arg Leu Ser Ser Ser Val Ser Ser Lys Gln Arg Pro Asn Met Thr
20 25 30
Thr Thr Phe Ala Ser Leu Thr Pro Met Trp Ala Gly Val Ala Gly Thr
35 40 45
Leu Val Asn Asn Asn Thr Gln Tyr Glu Ile Ala Val Thr Val His Asp
50 55 60
Gly Val Tyr Ser Thr Asp Phe Ala Ser Val Ile Ile Pro Val Thr Pro
65 70 75 80
Gly Asp Thr Ala Lys Asn Ser Lys Asp Ile Glu Ala Gln Val Leu Asn
85 90 95
Leu Ile Arg Lys Phe Ser Ala Glu His Leu Cys Lys Phe Leu Gly Ala
100 105 110
Gly Ile Thr Leu Ala Leu Leu Lys Glu Cys Pro Asn Leu Cys Thr Arg
115 120 125
Leu Trp Leu Asp Met Asp Ile Val Pro Ile Val Phe Asn Ile Lys Pro
130 135 140
Phe His Thr Asp Ser Val Thr Arg Pro Asn Ile Lys His Arg Ile Ser
145 150 155 160
Ser Thr Thr Gly Ser Tyr Val Pro Ser Gly Ser Glu Thr Pro Thr Val
165 170 175
Tyr Val Glu Ala Ala His Leu Gly Asp Pro Ser His Leu Ser Pro Asn
180 185 190
[0153] Ala Ala Gln Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln Ser Asp
195 200 205
Ser Ala Ala Arg Lys Cys Leu Met Tyr Phe Gly Pro Asn Asn Asn Pro
210 215 220
Arg Leu Ser Ile Gly Ala Arg Asn Gln Val Thr Val Asp Ala Gly Gly
225 230 235 240
Lys Ile His Leu Ile Asp Asp Leu Glu Glu Tyr Arg Lys Thr Val Gly
245 250 255
Thr Gly Thr Trp Asn Ala Val Ile Lys Leu Ala Asp Glu Leu Arg Glu
260 265 270
Lys Lys Val Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly Gly Gly
275 280 285
Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Leu Thr Ala Leu Asp
290 295 300
Val Asp Val Ala Trp Tyr Val Pro Asn Pro Ser Pro Gln Val Phe Arg
305 310 315 320
Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ala Pro Asp
325 330 335
Leu Arg Leu Thr Gln Asp Ala Lys Asp Ala Phe Asp Ala Trp Ile Leu
340 345 350
Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala Pro Gly
355 360 365
Gly Val Asp Val Val Phe Ile Asp Asp Pro Gln Met Pro Gly Leu Ile
370 375 380
Pro Leu Ile Lys Lys Val Arg Pro Glu Val Pro Ile Val Tyr Arg Ser
385 390 395 400
His Ile Glu Ile Arg Ser Asp Leu Val His Val Ala Gly Ser Pro Gln
405 410 415

Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala Asp Leu
420 425 430
Phe Ile Ser His Pro Val Ser Lys Phe Val Pro Ser Asp Val Pro Ile
435 440 445
Glu Lys Leu Ala Leu Leu Gly Ala Ala Thr Asp Trp Leu Asp Gly Leu
450 455 460
Asn Lys Asp Leu Asp Pro Trp Asp Ser Gln Phe Tyr Met Gly Glu Phe
465 470 475 480
Arg Ser Leu Cys Ala Lys Glu Lys Met Val Glu Leu Asp Trp Pro Thr
485 490 495
Arg Asp Tyr Ile Val Gln Val Ala Arg Phe Asp Pro Ser Lys Gly Ile
500 505 510
Pro Asn Val Val Asp Ser Tyr Tyr Lys Phe Arg Asn Leu Leu Arg Thr
515 520 525
Arg Ser Pro Glu Met Glu Leu Ser Asp His Pro Gln Leu Leu Ile Cys
530 535 540
Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp Gln
545 550 555 560
Ile Met Ala Leu Val Asn Ser Asp Pro Tyr Lys Glu Tyr Ala His Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Glu Leu Leu Asn Ala Met
580 585 590
Met Ala Asn Ser Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Leu His Thr Gly Lys Pro Val Ile Ala
610 615 620
Cys Arg Thr Gly Gly Ile Pro Leu Gln Ile Gln His Gly Lys Ser Gly
625 630 635 640

[0154]

Tyr Leu Thr Thr Pro Gly Asp Asn Asp Ala Val Ala Gly Tyr Leu Tyr
645 650 655
Asp Leu Tyr Thr Asp Glu Ala Leu Tyr Arg Arg Met Ser Asp Phe Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Val Met Tyr Ser Arg Gly Glu Lys Ile Lys Pro
690 695 700
Asn Gly Ala Trp Ile Asn Asp Leu Leu Arg Glu Glu Thr Gly Glu Pro
705 710 715 720
Tyr Lys Glu Gly Glu Thr Lys Leu Pro Arg Thr Lys Leu Asp Met Gln
725 730 735
Gly

<210> 83
<211> 751
<212> PRT
<213> 环柄香菇(Lentinus sajor-caju)

<220>
<223> Q9UV63.1

<400> 83
Met Ser Thr Pro His His Gln Phe Glu Ser Lys Ser Ser Thr Ala Ile
1 5 10 15
Arg Arg Arg Leu Ser Ser Ser Val Ser Ser Lys Gln Arg Pro Asn Ile

[0155]

```
                20                  25                  30
Met Thr Thr Thr Phe Ala Ser Leu Thr Pro Met Trp Ala Gly Val Ala
            35                  40                  45
Gly Thr Leu Val Asn Asn Asn Thr Gln Tyr Glu Ile Ala Val Thr Val
        50                  55                  60
His Asp Gly Val Tyr Ser Thr Asp Phe Ala Ser Val Ile Ile Pro Val
65                  70                  75                  80
Thr Pro Gly Asp Thr Val Lys Asn Ser Lys Asp Ile Glu Ala Gln Val
                85                  90                  95
Leu Asn Leu Ile Arg Lys Phe Ser Ala Glu His Leu Cys Lys Phe Leu
            100                 105                 110
Gly Ala Gly Ile Thr Leu Ala Leu Leu Lys Glu Cys Pro Asn Leu Cys
        115                 120                 125
Thr Arg Leu Trp Leu Asp Met Asp Ile Val Pro Ile Val Phe Asn Ile
    130                 135                 140
Lys Pro Phe His Thr Asp Ser Val Thr Arg Pro Asn Ile Lys His Arg
145                 150                 155                 160
Ile Ser Ser Thr Thr Gly Ser Tyr Val Pro Ser Gly Ser Glu Thr Pro
                165                 170                 175
Thr Val Tyr Val Glu Ala Ser His Leu Gly Asp Pro Ser His Leu Ser
            180                 185                 190
Pro Asn Ala Ala Gln Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
        195                 200                 205
Ser Asp Ser Ala Ala Arg Lys Cys Leu Met Tyr Phe Gly Pro Asn Asn
    210                 215                 220
Asn Pro Arg Leu Ser Ile Gly Ala Arg Asn Pro Val Thr Val Asp Ala
225                 230                 235                 240
Gly Gly Lys Ile His Leu Ile Asp Asp Leu Glu Glu Tyr Arg Met Thr
                245                 250                 255
Val Gly Ala Gly Thr Trp Asn Ala Val Ile Lys Leu Ala Asp Glu Leu
            260                 265                 270
Arg Glu Lys Lys Val Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
        275                 280                 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Leu Thr Ala
    290                 295                 300
Leu Asp Val Asp Val Ala Trp Tyr Val Pro Asn Pro Ser Pro Gln Val
305                 310                 315                 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ala
                325                 330                 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Ala Phe Asp Ala Trp
            340                 345                 350
Ile Leu Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
        355                 360                 365
Pro Gly Gly Val Asp Val Val Phe Ile Asp Asp Pro Gln Met Pro Gly
    370                 375                 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Val Pro Ile Val Tyr
385                 390                 395                 400
Arg Ser His Ile Glu Ile Arg Asn Asp Leu Val His Val Ala Trp Ser
                405                 410                 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
            420                 425                 430
Asp Leu Phe Ile Ser His Pro Val Ser Lys Phe Val Pro Ser Asp Val
        435                 440                 445
Pro Thr Glu Lys Leu Ala Leu Leu Gly Ala Ala Thr Asp Trp Leu Asp
    450                 455                 460
Gly Leu Asn Lys Asp Leu Asp Pro Trp Asp Ser Pro Phe Tyr Met Gly
```

465 470 475 480
Glu Phe Arg Pro Arg Gly Ser His Leu Asn Arg Gly Glu Phe Arg Ser
485 490 495
Leu Cys Ala Lys Glu Lys Met His Glu Leu Asn Trp Pro Ala Arg Asp
500 505 510
Tyr Ile Val Gln Val Ala Arg Phe Asp Pro Ser Lys Gly Ile Pro Asn
515 520 525
Val Val Asp Ser Tyr Tyr Lys Phe Arg Asn Leu Leu Arg Thr Arg Ser
530 535 540
Pro Asp Met Asp Glu Ser Glu His Pro Gln Leu Leu Ile Cys Gly His
545 550 555 560
Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp Gln Ile Met
565 570 575
Ala Leu Val Asn Ser Asp Pro Tyr Lys Glu Tyr Ala His Asp Ile Val
580 585 590
Val Met Arg Leu Pro Pro Ser Asp Glu Leu Leu Asn Ala Met Met Ala
595 600 605
Asn Ser Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe Glu Val
610 615 620
Lys Val Ser Glu Ala Leu His Thr Gly Lys Pro Val Ile Ala Cys Arg
625 630 635 640
Thr Gly Gly Ile Pro Leu Gln Ile Gln His Gly Lys Ser Gly Tyr Leu
645 650 655
Thr Thr Pro Gly Glu Lys Asp Ala Val Ala Gly His Phe Tyr Asp Phe
660 665 670
Tyr Thr Asp Glu Ala Leu Tyr Arg Lys Met Ser Asp Phe Ala Arg Thr
675 680 685
[0156] His Val Ser Asn Glu Val Gly Thr Val Gly Asn Ala Ala Ala Trp Leu
690 695 700
Tyr Leu Ala Val Met Tyr Ser Arg Gly Glu Lys Ile Lys Pro Asn Gly
705 710 715 720
Ala Trp Ile Asn Asp Phe Phe Arg Glu Glu Thr Gly Glu Pro Tyr Lys
725 730 735
Glu Gly Glu Thr Lys Leu Pro Arg Thr Lys Leu Asp Met Gln Gly
740 745 750

<210> 84
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 84

<400> 84
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80

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

[0157]

Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525

Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

[0158]

<210> 85
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 85

<400> 85
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Leu Gly Ala Gly Ile Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe

130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
[0159] Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu

580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 86
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

[0160]
<220>
<223> SEQ ID NO: 86

<400> 86
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Leu Gly Ala Gly Ile Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190

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

[0161]

Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640

Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 87
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 87

<400> 87
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
[0162] Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Leu Gly Ala Gly Ile Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr

245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ala
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
[0163] Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro

690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 88
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 88

<400> 88
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
[0164] Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Leu Gly Ala Gly Ile Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ala
290 295 300

Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Ala Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
[0165] 515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 89
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 89

<400> 89

```
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1               5                  10                  15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
            20                  25                  30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
        35                  40                  45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
    50                  55                  60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65                  70                  75                  80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
                85                  90                  95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
            100                 105                 110
Phe Leu Gly Ala Gly Ile Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
        115                 120                 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
    130                 135                 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145                 150                 155                 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
                165                 170                 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
            180                 185                 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
        195                 200                 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
    210                 215                 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225                 230                 235                 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
                245                 250                 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
            260                 265                 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
        275                 280                 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ala
    290                 295                 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305                 310                 315                 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
                325                 330                 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
            340                 345                 350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
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[0166]

355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Thr Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
[0167] Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 90
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 90

<400> 90

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

[0168]

Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Glu Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
[0169] Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 91
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 91

<400> 91
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr

[0170]

```
                20                  25                  30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
            35                  40                  45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
        50                  55                  60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65                  70                  75                  80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
                85                  90                  95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
            100                 105                 110
Phe Leu Gly Ala Gly Ile Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
        115                 120                 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
    130                 135                 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145                 150                 155                 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
                165                 170                 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
            180                 185                 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
        195                 200                 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
    210                 215                 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225                 230                 235                 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
                245                 250                 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
            260                 265                 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
        275                 280                 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ala
    290                 295                 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305                 310                 315                 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
                325                 330                 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
            340                 345                 350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
        355                 360                 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly
    370                 375                 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385                 390                 395                 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
                405                 410                 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
            420                 425                 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
        435                 440                 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
    450                 455                 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
```

465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
[0171] Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 92
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 92

<400> 92
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80

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

[0172]

Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525

Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

[0173]

<210> 93
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 93

<400> 93
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Leu Gly Ala Gly Ile Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe

[0174]

130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Leu Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ala
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu

580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 94
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

[0175]
<220>
<223> SEQ ID NO: 94

<400> 94
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Leu Gly Ala Gly Ile Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190

Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Met Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ala
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
[0176] Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640

Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 95
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 95

<400> 95
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
[0177] Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Leu Gly Ala Gly Ile Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr

245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Leu
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
[0178] Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro

690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 96
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 96

<400> 96
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
[0179] Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Leu Gly Ala Gly Ile Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ala
290 295 300

Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Val Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
[0180] 515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 97
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 97

<400> 97

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

[0181]

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

[0182]

Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 98
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 98

<400> 98

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

[0183]

Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640

[0184]

Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 99
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 99

<400> 99
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr

[0185]

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                20                  25                  30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
            35                  40                  45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
        50                  55                  60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65                  70                  75                  80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
                85                  90                  95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
            100                 105                 110
Phe Leu Gly Ala Gly Ile Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
        115                 120                 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
    130                 135                 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145                 150                 155                 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
                165                 170                 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
            180                 185                 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
        195                 200                 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
    210                 215                 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225                 230                 235                 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
                245                 250                 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
            260                 265                 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
        275                 280                 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ala
    290                 295                 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305                 310                 315                 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
                325                 330                 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
            340                 345                 350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
        355                 360                 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Met Gly
    370                 375                 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385                 390                 395                 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
                405                 410                 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
            420                 425                 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
        435                 440                 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
    450                 455                 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
```

465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
[0186] Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 100
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 100

<400> 100
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80

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

[0187]

Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Asn Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525

Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

[0188]

<210> 101
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 101

<400> 101
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Leu Gly Ala Gly Ile Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe

130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ala
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
[0189] Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Cys Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu

580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 102
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

[0190]

<220>
<223> SEQ ID NO: 102

<400> 102
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Leu Gly Ala Gly Ile Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190

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

[0191]

Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640

Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 103
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 103

<400> 103
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
[0192] Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Leu Gly Ala Gly Ile Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr

245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ala
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Ser Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
[0193] Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro

690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 104
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 104

<400> 104
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
[0194] Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Leu Gly Ala Gly Ile Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ala
290 295 300

Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Thr Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
[0195] 515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 105
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 105

<400> 105

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

[0196]

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

[0197]

Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 106
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 106

<400> 106

[0198]

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

Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Leu Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640

[0199]

Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 107
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 107

<400> 107
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr

[0200]

```
                20                  25                  30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
            35                  40                  45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
        50                  55                  60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65                  70                  75                  80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
                85                  90                  95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
            100                 105                 110
Phe Leu Gly Ala Gly Ile Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
        115                 120                 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
    130                 135                 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145                 150                 155                 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
                165                 170                 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
            180                 185                 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
        195                 200                 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
    210                 215                 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225                 230                 235                 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
                245                 250                 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
            260                 265                 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
        275                 280                 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ala
    290                 295                 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305                 310                 315                 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
                325                 330                 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
            340                 345                 350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
        355                 360                 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly
    370                 375                 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385                 390                 395                 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
                405                 410                 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
            420                 425                 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
        435                 440                 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
    450                 455                 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
```

465 470 475 480
Glu Phe Arg Ala Leu Cys Met Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
[0201] Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 108
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 108

<400> 108
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80

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

[0202]

Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525

Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Pro Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

[0203]

<210> 109
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 109

<400> 109
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Leu Gly Ala Gly Ile Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe

130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ala
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
[0204] Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Gly Cys Leu

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            580                 585                 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
        595                 600                 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
    610                 615                 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625                 630                 635                 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
                645                 650                 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
            660                 665                 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
        675                 680                 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
    690                 695                 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705                 710                 715                 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
                725                 730                 735
Asp
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<210> 110
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

[0205]

<220>
<223> SEQ ID NO: 110

<400> 110

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

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

[0206]

Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640

Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 111
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 111

<400> 111
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
[0207] Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Leu Gly Ala Gly Val Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr

245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ala
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
[0208] Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Thr Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro

690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 112
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 112

<400> 112
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
[0209] Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Leu Gly Ala Gly Val Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ala
290 295 300

Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
[0210] 515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Glu Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 113
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 113

<400> 113

[0211]

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

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

[0212]

Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 114
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 114

<400> 114

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

[0213]

Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
[0214] Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 115
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 115

<400> 115
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr

20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Leu Gly Ala Gly Ile Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Val Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240
[0215] Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ala
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly

465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
[0216] Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 116
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 116

<400> 116
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80

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

[0217]

Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Ala Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525

Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

[0218]

<210> 117
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 117

<400> 117
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Leu Gly Ala Gly Ile Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe

130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Val Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ala
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
[0219] Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Ile Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu

```
                580                 585                 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
            595                 600                 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
        610                 615                 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625                 630                 635                 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
                645                 650                 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
            660                 665                 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
        675                 680                 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
    690                 695                 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705                 710                 715                 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
                725                 730                 735
Asp
```

<210> 118
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

[0220]

<220>
<223> SEQ ID NO: 118

<400> 118

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

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

[0221]

Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Thr Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640

Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 119
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 119

<400> 119
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
[0222] Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Leu Gly Ala Gly Ile Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Val Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr

245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ala
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
[0223] Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro

690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 120
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 120

<400> 120
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
[0224] Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Leu Gly Ala Gly Ile Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
290 295 300

Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Ile Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
[0225] 515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 121
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 121

<400> 121

[0226]

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

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

[0227]

Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 122
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 122

<400> 122

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

[0228]

Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Ala Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640

[0229]

Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 123
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 123

<400> 123
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr

[0230]

```
                20                  25                  30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
            35                  40                  45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
        50                  55                  60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65                  70                  75                  80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
                85                  90                  95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
            100                 105                 110
Phe Leu Gly Ala Gly Ile Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
        115                 120                 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
    130                 135                 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145                 150                 155                 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
                165                 170                 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
            180                 185                 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
        195                 200                 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
    210                 215                 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225                 230                 235                 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
                245                 250                 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
            260                 265                 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
        275                 280                 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
    290                 295                 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305                 310                 315                 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
                325                 330                 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
            340                 345                 350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
        355                 360                 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly
    370                 375                 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385                 390                 395                 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
                405                 410                 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
            420                 425                 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
        435                 440                 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
    450                 455                 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
```

465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Thr Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
[0231] Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 124
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 124

<400> 124
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80

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

[0232]

Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525

Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Glu Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

[0233]

<210> 125
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 125

<400> 125
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Leu Gly Ala Gly Ile Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe

130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
[0234] Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu

580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 126
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

[0235]

<220>
<223> SEQ ID NO: 126

<400> 126
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Leu Gly Ala Gly Ile Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190

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

[0236]

Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640

Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 127
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 127

<400> 127
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
[0237] Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Leu Gly Ala Gly Ile Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr

245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ala
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Ile Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
[0238] Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Ala Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro

690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 128
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 128

<400> 128
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
[0239] Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Leu Gly Ala Gly Ile Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ala
290 295 300

Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Ile Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
[0240] Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Thr Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 129
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 129

<400> 129

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

[0241]

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

[0242]

Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 130
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 130

<400> 130

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

[0243]

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

Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640

[0244]

Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 131
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 131

<400> 131
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr

[0245]

```
                20                  25                  30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
            35                  40                  45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
        50                  55                  60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65                  70                  75                  80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
                85                  90                  95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
            100                 105                 110
Phe Leu Gly Ala Gly Ile Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
        115                 120                 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
    130                 135                 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145                 150                 155                 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
                165                 170                 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
            180                 185                 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
        195                 200                 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
    210                 215                 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225                 230                 235                 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
                245                 250                 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
            260                 265                 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
        275                 280                 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ala
    290                 295                 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305                 310                 315                 320
Phe Arg Ile Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
                325                 330                 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
            340                 345                 350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
        355                 360                 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly
    370                 375                 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385                 390                 395                 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
                405                 410                 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
            420                 425                 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
        435                 440                 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
    450                 455                 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
```

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

[0246] Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 132
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 132

<400> 132
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80

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

[0247]

Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Tyr Asp Ala Trp
340 345 350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525

Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

[0248]

<210> 133
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 133

<400> 133
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Leu Gly Ala Gly Ile Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe

[0249]

```
    130                 135                 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145                 150                 155                 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
                165                 170                 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
            180                 185                 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
        195                 200                 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
    210                 215                 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225                 230                 235                 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
                245                 250                 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
            260                 265                 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
        275                 280                 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ala
    290                 295                 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305                 310                 315                 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
                325                 330                 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Tyr Asp Ala Trp
            340                 345                 350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
        355                 360                 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly
    370                 375                 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385                 390                 395                 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
                405                 410                 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
            420                 425                 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
        435                 440                 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
    450                 455                 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465                 470                 475                 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
                485                 490                 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
            500                 505                 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
        515                 520                 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
    530                 535                 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545                 550                 555                 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
                565                 570                 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
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580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 134
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

[0250]

<220>
<223> SEQ ID NO: 134

<400> 134
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Leu Gly Ala Gly Ile Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190

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

[0251]

Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640

Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 135
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 135

<400> 135
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
[0252] Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Leu Gly Ala Gly Ile Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr

245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ala
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
[0253] Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro

690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 136
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 136

<400> 136
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
[0254] Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Leu Gly Ala Gly Ile Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ala
290 295 300

Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Ala Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
[0255] 515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 137
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 137

<400> 137

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

[0256]

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

[0257]

Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 138
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 138

<400> 138

[0258]

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

Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Thr Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640

[0259]

Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 139
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 139

<400> 139
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr

[0260]

```
                20                  25                  30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
            35                  40                  45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
        50                  55                  60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65                  70                  75                  80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
                85                  90                  95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
            100                 105                 110
Phe Leu Gly Ala Gly Ile Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
        115                 120                 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
    130                 135                 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145                 150                 155                 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
                165                 170                 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
            180                 185                 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
        195                 200                 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
    210                 215                 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225                 230                 235                 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
                245                 250                 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
            260                 265                 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
        275                 280                 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ala
    290                 295                 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305                 310                 315                 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
                325                 330                 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
            340                 345                 350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
        355                 360                 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
    370                 375                 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385                 390                 395                 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
                405                 410                 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
            420                 425                 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
        435                 440                 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
    450                 455                 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
```

465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Glu Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
[0261] Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 140
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 140

<400> 140
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80

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

[0262]

Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525

```
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
    530                 535                 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545                 550                 555                 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
                565                 570                 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
            580                 585                 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
        595                 600                 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
    610                 615                 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625                 630                 635                 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
                645                 650                 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
            660                 665                 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
        675                 680                 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
    690                 695                 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705                 710                 715                 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
                725                 730                 735
Asp
```

[0263]

<210> 141
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 141

<400> 141

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

130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ala
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
[0264] Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu

580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Glu Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 142
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

[0265]

<220>
<223> SEQ ID NO: 142

<400> 142
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Leu Gly Ala Gly Ile Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190

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

[0266]

Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Ala Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Glu Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640

Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 143
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 143

<400> 143
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
[0267] Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Leu Gly Ala Gly Ile Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr

[0268]

```
                245                 250                 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
            260                 265                 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
        275                 280                 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ala
    290                 295                 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305                 310                 315                 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
                325                 330                 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
            340                 345                 350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
        355                 360                 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly
    370                 375                 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385                 390                 395                 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
                405                 410                 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
            420                 425                 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
        435                 440                 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
    450                 455                 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465                 470                 475                 480
Glu Phe Arg Ala Leu Cys Ala Lys Asp Lys Met Asn Thr Leu Asp Trp
                485                 490                 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
            500                 505                 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
        515                 520                 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
    530                 535                 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545                 550                 555                 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
                565                 570                 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
            580                 585                 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
        595                 600                 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
    610                 615                 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625                 630                 635                 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
                645                 650                 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
            660                 665                 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
        675                 680                 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
```

690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 144
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 144

<400> 144
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
[0269] Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Leu Gly Ala Gly Ile Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ala
290 295 300

Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Ala Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
[0270] 515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Glu Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 145
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 145

<400> 145

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

[0271]

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

[0272]

Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 146
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 146

<400> 146

Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Leu Gly Ala Gly Ile Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190
[0273] Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ala
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415

Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Thr Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Glu Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640

[0274]

Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 147
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 147

<400> 147
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr

[0275]

```
                20                  25                  30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
            35                  40                  45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
        50                  55                  60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65                  70                  75                  80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
                85                  90                  95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
            100                 105                 110
Phe Leu Gly Ala Gly Ile Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
        115                 120                 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
    130                 135                 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145                 150                 155                 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
                165                 170                 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
            180                 185                 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
        195                 200                 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
    210                 215                 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225                 230                 235                 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
                245                 250                 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
            260                 265                 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
        275                 280                 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ala
    290                 295                 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305                 310                 315                 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
                325                 330                 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
            340                 345                 350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
        355                 360                 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly
    370                 375                 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385                 390                 395                 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
                405                 410                 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
            420                 425                 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
        435                 440                 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
    450                 455                 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
```

465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Thr Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
[0276] Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 148
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 148

<400> 148
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80

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

[0277]

Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525

```
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
    530                 535                 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Thr Ile Ile Tyr Asp
545                 550                 555                 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
                565                 570                 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
            580                 585                 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
        595                 600                 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
    610                 615                 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625                 630                 635                 640
Phe Leu Thr Glu Pro Gly Asp Asn Glu Gln Val Ala Arg His Met Tyr
                645                 650                 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
            660                 665                 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
        675                 680                 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
    690                 695                 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705                 710                 715                 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
                725                 730                 735
Asp
```

[0278]

<210> 149
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 149

<400> 149

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

[0279]

```
    130                 135                 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145                 150                 155                 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
                165                 170                 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
            180                 185                 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
        195                 200                 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
    210                 215                 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225                 230                 235                 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
                245                 250                 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
            260                 265                 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
        275                 280                 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ala
    290                 295                 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305                 310                 315                 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
                325                 330                 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
            340                 345                 350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
        355                 360                 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly
    370                 375                 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385                 390                 395                 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
                405                 410                 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
            420                 425                 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
        435                 440                 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
    450                 455                 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465                 470                 475                 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
                485                 490                 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
            500                 505                 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
        515                 520                 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
    530                 535                 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545                 550                 555                 560
Gln Val Leu Glu Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
                565                 570                 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
```

580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 150
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

[0280]
<220>
<223> SEQ ID NO: 150

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

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

[0281]

Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Glu Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640

Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 151
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 151

<400> 151
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
[0282] Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Leu Gly Ala Gly Ile Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr

245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ala
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
[0283] Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Glu Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro

690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 152
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 152

<400> 152
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
[0284] Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Leu Gly Ala Gly Ile Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ala
290 295 300

Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
[0285] 515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 153
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 153

<400> 153

[0286]

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

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

[0287]

Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Glu Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 154
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQIDNO:154

<400> 154

[0288]

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

Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Ala Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Ile Asp Asp Pro Asp Ala Thr Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Glu Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
[0289] Phe Leu Thr Glu Pro Gly Asp Asn Glu Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 155
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQIDNO:155

<400> 155
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr

[0290]

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                20                  25                  30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
            35                  40                  45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
        50                  55                  60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65                  70                  75                  80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
                85                  90                  95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
            100                 105                 110
Phe Ile Gly Ala Gly Val Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
        115                 120                 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
    130                 135                 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145                 150                 155                 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
                165                 170                 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
            180                 185                 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
        195                 200                 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
    210                 215                 220
Val Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225                 230                 235                 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
                245                 250                 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
            260                 265                 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
        275                 280                 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ala
    290                 295                 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305                 310                 315                 320
Phe Arg Ile Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
                325                 330                 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
            340                 345                 350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
        355                 360                 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
    370                 375                 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385                 390                 395                 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
                405                 410                 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
            420                 425                 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
        435                 440                 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
    450                 455                 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
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465 470 475 480
Glu Phe Arg Ala Leu Cys Ala Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Ile Asp Asp Pro Asp Ala Thr Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Glu Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Glu Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
[0291] Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 156
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQIDNO:156

<400> 156
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80

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

[0292]

Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Ile Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Ala Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525

Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Ile Asp Asp Pro Asp Ala Thr Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Glu Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Glu Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

[0293]

<210> 157
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQIDNO:157

<400> 157
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Ile Gly Ala Gly Val Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe

130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Val Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Ile Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
[0294] Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Ala Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Ile Asp Asp Pro Asp Ala Thr Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Glu Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu

580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Glu Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 158
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

[0295]

<220>
<223> SEQIDNO:158

<400> 158
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Ile Gly Ala Gly Val Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190

Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Val Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Ile Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
[0296] Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Ala Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Ile Asp Asp Pro Asp Ala Thr Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Glu Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640

Phe Leu Thr Glu Pro Gly Asp Asn Glu Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 159
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQIDNO:159

<400> 159

[0297]

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

245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Ile Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
[0298] Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Ala Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Ile Asp Asp Pro Asp Ala Thr Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Glu Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Glu Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro

690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 160
<211> 732
<212> PRT
<213> 千佛菌(Grifola frondosa)

<220>
<223> SEQ ID NO: 160

<400> 160
Met Ala Pro Pro His Gln Phe Gln Ser Lys Pro Ser Asp Val Ile Arg
1 5 10 15
Arg Arg Leu Ser Ser Ala Val Ser Ser Lys Arg Pro Asn Ile Pro Gly
20 25 30
Tyr Thr Ser Leu Thr Pro Met Trp Ala Gly Ile Ala Gly Ala Val Val
35 40 45
Asn Asn Asn Thr Gln Phe Glu Val Ala Ile Ser Ile His Asp Ser Val
50 55 60
Tyr Asn Thr Asp Phe Ala Ser Ser Val Val Pro Tyr Ser Pro Asn Glu
65 70 75 80
[0299] Pro Glu Ala Gln Ala Gly Ile Ile Glu Lys His Val Leu Glu Thr Leu
85 90 95
Arg Lys Phe Ser Thr Glu His Met Cys Lys Phe Leu Gly Ala Gly Val
100 105 110
Thr Val Ile Leu Leu Arg Glu Ala Pro Asn Leu Cys Thr Arg Leu Trp
115 120 125
Leu Asp Met Asp Ile Val Pro Ile Val Phe Asn Ile Lys Pro Phe His
130 135 140
Thr Asp Ser Ile Thr Arg Pro Asn Val Arg His Arg Ile Ser Ser Thr
145 150 155 160
Thr Gly Ser Tyr Val Pro Ser Gly Ala Glu Thr Pro Thr Val Tyr Tyr
165 170 175
Asp Pro Ala Gln Leu Gln Asp Pro Asn Lys Leu Ser Ala Asn Val Gln
180 185 190
Thr Arg Leu Pro Ile Pro Arg Thr Val Asp Glu Gln Ala Asp Ser Ala
195 200 205
Ala Arg Lys Cys Ile Met Tyr Phe Gly Pro Gly Asn Asn Pro Arg Leu
210 215 220
Gln Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala Gly Gly Lys Ile
225 230 235 240
His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr Val Gly Lys Gly
245 250 255
Thr Trp Asn Ser Val Ile Lys Leu Ala Asp Glu Leu Arg Glu Lys Lys
260 265 270
Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly Gly Gly Val Ala
275 280 285
Leu Met Arg His Ala Ile Ile Arg Phe Phe Thr Ala Leu Asp Val Asp
290 295 300

Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val Phe Arg Thr Thr
305 310 315 320
Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Asp Pro Ser Leu Arg
325 330 335
Leu Thr Lys Glu Ala Ala Asp Asn Phe Asp Ser Trp Ile Leu Lys Asn
340 345 350
Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala Pro Gly Gly Val
355 360 365
Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly Leu Ile Pro Leu
370 375 380
Ile Lys Arg Ile Arg Pro Asp Leu Pro Ile Ile Tyr Arg Ser His Ile
385 390 395 400
Glu Ile Arg Ser Asp Leu Val His Val Lys Gly Ser Pro Gln Glu Glu
405 410 415
Val Trp Asn Tyr Leu Trp Asn Asn Ile Gln His Ser Asp Leu Phe Ile
420 425 430
Ser His Pro Val Asn Lys Phe Val Pro Ser Asp Val Pro Leu Glu Lys
435 440 445
Leu Ala Leu Leu Gly Ala Ala Thr Asp Trp Leu Asp Gly Leu Ser Lys
450 455 460
His Leu Asp Ala Trp Asp Ser Gln Tyr Tyr Met Gly Glu Phe Arg Asn
465 470 475 480
Leu Cys Val Lys Glu Lys Met Asn Glu Leu Gly Trp Pro Ala Arg Glu
485 490 495
Tyr Ile Val Gln Ile Ala Arg Phe Asp Pro Ser Lys Gly Ile Pro Asn
500 505 510
Val Ile Asp Ser Tyr Ala Arg Phe Arg Lys Leu Cys Val Asp Lys Val
515 520 525

[0300]

Met Glu Asp Asp Ile Pro Gln Leu Leu Leu Cys Gly His Gly Ala Val
530 535 540
Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp Gln Val Leu Gln Leu Ile
545 550 555 560
His Ala Lys Tyr Lys Glu Tyr Ala Pro Asp Ile Val Val Met Arg Cys
565 570 575
Pro Pro Ser Asp Gln Leu Leu Asn Thr Leu Met Ala Asn Ala Lys Phe
580 585 590
Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe Glu Val Lys Val Ser Glu
595 600 605
Ala Leu His Ala Gly Lys Pro Val Ile Ala Cys Arg Thr Gly Gly Ile
610 615 620
Pro Leu Gln Ile Glu His Gly Lys Ser Gly Tyr Leu Cys Glu Pro Gly
625 630 635 640
Asp Asn Ala Ala Val Ala Gln His Met Leu Asp Leu Tyr Thr Asp Glu
645 650 655
Asp Leu Tyr Asp Thr Met Ser Glu Tyr Ala Arg Thr His Val Ser Asp
660 665 670
Glu Val Gly Thr Val Gly Asn Ala Ala Ala Trp Met Tyr Leu Ala Val
675 680 685
Met Tyr Val Ser Arg Gly Val Lys Leu Arg Pro His Gly Ala Trp Ile
690 695 700
Asn Asp Leu Met Arg Thr Glu Met Gly Glu Pro Tyr Arg Pro Gly Glu
705 710 715 720
Pro Arg Leu Pro Arg Gly Glu Leu His Val Gln Gly
725 730

<210> 161

<211> 732
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 161

<400> 161

[0301]

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

370 375 380
Ile Lys Arg Ile Arg Pro Asp Leu Pro Ile Ile Tyr Arg Ser His Ile
385 390 395 400
Glu Ile Arg Ser Asp Leu Val His Val Lys Gly Ser Pro Gln Glu Glu
405 410 415
Val Trp Asn Tyr Leu Trp Asn Asn Ile Gln His Ser Asp Leu Phe Ile
420 425 430
Ser His Pro Val Asn Lys Phe Val Pro Ser Asp Val Pro Leu Glu Lys
435 440 445
Leu Ala Leu Leu Gly Ala Ala Thr Asp Trp Leu Asp Gly Leu Ser Lys
450 455 460
His Leu Asp Ala Trp Asp Ser Gln Tyr Tyr Met Gly Glu Phe Arg Asn
465 470 475 480
Leu Cys Val Lys Glu Lys Met Asn Glu Leu Gly Trp Pro Ala Arg Glu
485 490 495
Tyr Ile Val Gln Ile Ala Arg Phe Asp Pro Ser Lys Gly Ile Pro Asn
500 505 510
Val Ile Asp Ser Tyr Ala Arg Phe Arg Lys Leu Cys Val Asp Lys Val
515 520 525
Met Glu Asp Asp Ile Pro Gln Leu Leu Leu Cys Gly His Gly Ala Val
530 535 540
Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp Gln Val Leu Gln Leu Ile
545 550 555 560
His Ala Lys Tyr Lys Glu Tyr Ala Pro Asp Ile Val Val Met Arg Cys
565 570 575
Pro Pro Ser Asp Gln Leu Leu Asn Thr Leu Met Ala Asn Ala Lys Phe
580 585 590
[0302] Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe Glu Val Lys Val Ser Glu
595 600 605
Ala Leu His Ala Gly Lys Pro Val Ile Ala Cys Arg Thr Gly Gly Ile
610 615 620
Pro Leu Gln Ile Glu His Gly Lys Ser Gly Tyr Leu Cys Glu Pro Gly
625 630 635 640
Asp Asn Ala Ala Val Ala Gln His Met Leu Asp Leu Tyr Thr Asp Glu
645 650 655
Asp Leu Tyr Asp Thr Met Ser Glu Tyr Ala Arg Thr His Val Ser Asp
660 665 670
Glu Val Gly Thr Val Gly Asn Ala Ala Ala Trp Met Tyr Leu Ala Val
675 680 685
Met Tyr Val Ser Arg Gly Val Lys Leu Arg Pro His Gly Ala Trp Ile
690 695 700
Asn Asp Leu Met Arg Thr Glu Met Gly Glu Pro Tyr Arg Pro Gly Glu
705 710 715 720
Pro Arg Leu Pro Arg Gly Glu Leu His Val Gln Gly
725 730

<210> 162
<211> 732
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 162

<400> 162

Met Ala Pro Pro His Gln Phe Gln Ser Lys Pro Ser Asp Val Ile Arg
1 5 10 15
Arg Arg Leu Ser Ser Ala Val Ser Ser Lys Arg Pro Asn Ile Pro Gly
20 25 30
Tyr Thr Ser Leu Thr Pro Met Trp Ala Gly Ile Ala Gly Ala Val Val
35 40 45
Asn Asn Asn Thr Gln Phe Glu Val Ala Ile Ser Ile His Asp Ser Val
50 55 60
Tyr Asn Thr Asp Phe Ala Ser Ser Val Val Pro Tyr Ser Pro Asn Glu
65 70 75 80
Pro Glu Ala Gln Ala Gly Ile Ile Glu Lys His Val Leu Glu Thr Leu
85 90 95
Arg Lys Phe Ser Thr Glu His Met Cys Lys Phe Leu Gly Ala Gly Ile
100 105 110
Thr Val Ile Leu Leu Arg Glu Ala Pro Asn Leu Cys Thr Arg Leu Trp
115 120 125
Leu Asp Met Asp Ile Val Pro Ile Val Phe Asn Ile Lys Pro Phe His
130 135 140
Thr Asp Ser Ile Thr Arg Pro Asn Val Arg His Arg Ile Ser Ser Thr
145 150 155 160
Thr Gly Ser Tyr Val Pro Ser Gly Ala Glu Thr Pro Thr Val Tyr Tyr
165 170 175
Asp Pro Ala Gln Leu Gln Asp Pro Asn Lys Leu Ser Ala Asn Val Gln
180 185 190
Thr Arg Leu Pro Ile Pro Arg Thr Val Asp Glu Gln Ala Asp Ser Ala
195 200 205
Ala Arg Lys Cys Ile Met Tyr Phe Gly Pro Gly Asn Asn Pro Arg Leu
210 215 220
[0303] Gln Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala Gly Gly Lys Ile
225 230 235 240
His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr Val Gly Lys Gly
245 250 255
Thr Trp Asn Ser Val Ile Lys Leu Ala Asp Glu Leu Arg Glu Lys Lys
260 265 270
Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly Gly Gly Val Ala
275 280 285
Leu Met Arg His Ala Ile Ile Arg Phe Phe Thr Ala Leu Asp Val Asp
290 295 300
Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val Phe Arg Thr Thr
305 310 315 320
Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Asp Pro Ser Leu Arg
325 330 335
Leu Thr Lys Glu Ala Ala Asp Asn Phe Asp Ser Trp Ile Leu Lys Asn
340 345 350
Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala Pro Gly Gly Val
355 360 365
Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly Leu Ile Pro Leu
370 375 380
Ile Lys Arg Ile Arg Pro Asp Leu Pro Ile Ile Tyr Arg Ser His Ile
385 390 395 400
Glu Ile Arg Ser Asp Leu Val His Val Lys Gly Ser Pro Gln Glu Glu
405 410 415
Val Trp Asn Tyr Leu Trp Asn Asn Ile Gln His Ser Asp Leu Phe Ile
420 425 430
Ser His Pro Val Asn Lys Phe Val Pro Ser Asp Val Pro Leu Glu Lys
435 440 445

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

[0304]

Glu Val Gly Thr Val Gly Asn Ala Ala Ala Trp Met Tyr Leu Ala Val
675 680 685
Met Tyr Val Ser Arg Gly Val Lys Leu Arg Pro His Gly Ala Trp Ile
690 695 700
Asn Asp Leu Met Arg Thr Glu Met Gly Glu Pro Tyr Arg Pro Gly Glu
705 710 715 720
Pro Arg Leu Pro Arg Gly Glu Leu His Val Gln Gly
725 730

<210> 163
<211> 732
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 163

<400> 163
Met Ala Pro Pro His Gln Phe Gln Ser Lys Pro Ser Asp Val Ile Arg
1 5 10 15
Arg Arg Leu Ser Ser Ala Val Ser Ser Lys Arg Pro Asn Ile Pro Gly
20 25 30
Tyr Thr Ser Leu Thr Pro Met Trp Ala Gly Ile Ala Gly Ala Val Val
35 40 45
Asn Asn Asn Thr Gln Phe Glu Val Ala Ile Ser Ile His Asp Ser Val
50 55 60
Tyr Asn Thr Asp Phe Ala Ser Ser Val Val Pro Tyr Ser Pro Asn Glu

65 70 75 80
Pro Glu Ala Gln Ala Gly Ile Ile Glu Lys His Val Leu Glu Thr Leu
85 90 95
Arg Lys Phe Ser Thr Glu His Met Cys Lys Phe Leu Gly Ala Gly Val
100 105 110
Thr Val Ile Leu Leu Arg Glu Ala Pro Asn Leu Cys Thr Arg Leu Trp
115 120 125
Leu Asp Met Asp Ile Val Pro Ile Val Phe Asn Ile Lys Pro Phe His
130 135 140
Thr Asp Ser Ile Thr Arg Pro Asn Val Arg His Arg Ile Ser Ser Thr
145 150 155 160
Thr Gly Ser Tyr Val Pro Ser Gly Ala Glu Thr Pro Thr Val Tyr Tyr
165 170 175
Asp Pro Ala Gln Leu Gln Asp Pro Asn Lys Leu Ser Ala Asn Val Gln
180 185 190
Thr Arg Leu Pro Ile Pro Arg Thr Val Asp Glu Gln Ala Asp Ser Ala
195 200 205
Ala Arg Lys Cys Ile Met Tyr Phe Gly Pro Gly Asn Val Pro Arg Leu
210 215 220
Gln Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala Gly Gly Lys Ile
225 230 235 240
His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr Val Gly Lys Gly
245 250 255
Thr Trp Asn Ser Val Ile Lys Leu Ala Asp Glu Leu Arg Glu Lys Lys
260 265 270
Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly Gly Gly Val Ala
275 280 285
[0305] Leu Met Arg His Ala Ile Ile Arg Phe Phe Thr Ala Leu Asp Val Asp
290 295 300
Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val Phe Arg Thr Thr
305 310 315 320
Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Asp Pro Ser Leu Arg
325 330 335
Leu Thr Lys Glu Ala Ala Asp Asn Phe Asp Ser Trp Ile Leu Lys Asn
340 345 350
Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala Pro Gly Gly Val
355 360 365
Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly Leu Ile Pro Leu
370 375 380
Ile Lys Arg Ile Arg Pro Asp Leu Pro Ile Ile Tyr Arg Ser His Ile
385 390 395 400
Glu Ile Arg Ser Asp Leu Val His Val Lys Gly Ser Pro Gln Glu Glu
405 410 415
Val Trp Asn Tyr Leu Trp Asn Asn Ile Gln His Ser Asp Leu Phe Ile
420 425 430
Ser His Pro Val Asn Lys Phe Val Pro Ser Asp Val Pro Leu Glu Lys
435 440 445
Leu Ala Leu Leu Gly Ala Ala Thr Asp Trp Leu Asp Gly Leu Ser Lys
450 455 460
His Leu Asp Ala Trp Asp Ser Gln Tyr Tyr Met Gly Glu Phe Arg Asn
465 470 475 480
Leu Cys Val Lys Glu Lys Met Asn Glu Leu Gly Trp Pro Ala Arg Glu
485 490 495
Tyr Ile Val Gln Ile Ala Arg Phe Asp Pro Ser Lys Gly Ile Pro Asn
500 505 510
Val Ile Asp Ser Tyr Ala Arg Phe Arg Lys Leu Cys Val Asp Lys Val

515 520 525
Met Glu Asp Asp Ile Pro Gln Leu Leu Leu Cys Gly His Gly Ala Val
530 535 540
Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp Gln Val Leu Gln Leu Ile
545 550 555 560
His Ala Lys Tyr Lys Glu Tyr Ala Pro Asp Ile Val Val Met Arg Cys
565 570 575
Pro Pro Ser Asp Gln Leu Leu Asn Thr Leu Met Ala Asn Ala Lys Phe
580 585 590
Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe Glu Val Lys Val Ser Glu
595 600 605
Ala Leu His Ala Gly Lys Pro Val Ile Ala Cys Arg Thr Gly Gly Ile
610 615 620
Pro Leu Gln Ile Glu His Gly Lys Ser Gly Tyr Leu Cys Glu Pro Gly
625 630 635 640
Asp Asn Ala Ala Val Ala Gln His Met Leu Asp Leu Tyr Thr Asp Glu
645 650 655
Asp Leu Tyr Asp Thr Met Ser Glu Tyr Ala Arg Thr His Val Ser Asp
660 665 670
Glu Val Gly Thr Val Gly Asn Ala Ala Ala Trp Met Tyr Leu Ala Val
675 680 685
Met Tyr Val Ser Arg Gly Val Lys Leu Arg Pro His Gly Ala Trp Ile
690 695 700
Asn Asp Leu Met Arg Thr Glu Met Gly Glu Pro Tyr Arg Pro Gly Glu
705 710 715 720
Pro Arg Leu Pro Arg Gly Glu Leu His Val Gln Gly
725 730

[0306]

<210> 164
<211> 732
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 164

<400> 164
Met Ala Pro Pro His Gln Phe Gln Ser Lys Pro Ser Asp Val Ile Arg
1 5 10 15
Arg Arg Leu Ser Ser Ala Val Ser Ser Lys Arg Pro Asn Ile Pro Gly
20 25 30
Tyr Thr Ser Leu Thr Pro Met Trp Ala Gly Ile Ala Gly Ala Val Val
35 40 45
Asn Asn Asn Thr Gln Phe Glu Val Ala Ile Ser Ile His Asp Ser Val
50 55 60
Tyr Asn Thr Asp Phe Ala Ser Ser Val Val Pro Tyr Ser Pro Asn Glu
65 70 75 80
Pro Glu Ala Gln Ala Gly Ile Ile Glu Lys His Val Leu Glu Thr Leu
85 90 95
Arg Lys Phe Ser Thr Glu His Met Cys Lys Phe Leu Gly Ala Gly Val
100 105 110
Thr Val Ile Leu Leu Arg Glu Ala Pro Asn Leu Cys Thr Arg Leu Trp
115 120 125
Leu Asp Met Asp Ile Val Pro Ile Val Phe Asn Ile Lys Pro Phe His
130 135 140

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

[0307]

Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly Leu Ile Pro Leu
370 375 380
Ile Lys Arg Ile Arg Pro Asp Leu Pro Ile Ile Tyr Arg Ser His Ile
385 390 395 400
Glu Ile Arg Ser Asp Leu Val His Val Lys Gly Ser Pro Gln Glu Glu
405 410 415
Val Trp Asn Tyr Leu Trp Asn Asn Ile Gln His Ser Asp Leu Phe Ile
420 425 430
Ser His Pro Val Asn Lys Phe Val Pro Ser Asp Val Pro Leu Glu Lys
435 440 445
Leu Ala Leu Leu Gly Ala Ala Thr Asp Trp Leu Asp Gly Leu Ser Lys
450 455 460
His Leu Asp Ala Trp Asp Ser Gln Tyr Tyr Met Gly Glu Phe Arg Asn
465 470 475 480
Leu Cys Val Lys Glu Lys Met Asn Glu Leu Gly Trp Pro Ala Arg Glu
485 490 495
Tyr Ile Val Gln Ile Ala Arg Phe Asp Pro Ser Lys Gly Ile Pro Asn
500 505 510
Val Ile Asp Ser Tyr Ala Arg Phe Arg Lys Leu Cys Val Asp Lys Val
515 520 525
Met Glu Asp Asp Ile Pro Gln Leu Leu Leu Cys Gly His Gly Ala Val
530 535 540
Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp Gln Val Leu Gln Leu Ile
545 550 555 560
His Ala Lys Tyr Lys Glu Tyr Ala Pro Asp Ile Val Val Met Arg Cys
565 570 575
Pro Pro Ser Asp Gln Leu Leu Asn Thr Leu Met Ala Asn Ala Lys Phe
580 585 590

Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe Glu Val Lys Val Ser Glu
595 600 605
Ala Leu His Ala Gly Lys Pro Val Ile Ala Cys Arg Thr Gly Gly Ile
610 615 620
Pro Leu Gln Ile Glu His Gly Lys Ser Gly Tyr Leu Cys Glu Pro Gly
625 630 635 640
Asp Asn Ala Ala Val Ala Gln His Met Leu Asp Leu Tyr Thr Asp Glu
645 650 655
Asp Leu Tyr Asp Thr Met Ser Glu Tyr Ala Arg Thr His Val Ser Asp
660 665 670
Glu Val Gly Thr Val Gly Asn Ala Ala Ala Trp Met Tyr Leu Ala Val
675 680 685
Met Tyr Val Ser Arg Gly Val Lys Leu Arg Pro His Gly Ala Trp Ile
690 695 700
Asn Asp Leu Met Arg Thr Glu Met Gly Glu Pro Tyr Arg Pro Gly Glu
705 710 715 720
Pro Arg Leu Pro Arg Gly Glu Leu His Val Gln Gly
725 730

<210> 165
<211> 732
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 165

[0308] <400> 165
Met Ala Pro Pro His Gln Phe Gln Ser Lys Pro Ser Asp Val Ile Arg
1 5 10 15
Arg Arg Leu Ser Ser Ala Val Ser Ser Lys Arg Pro Asn Ile Pro Gly
20 25 30
Tyr Thr Ser Leu Thr Pro Met Trp Ala Gly Ile Ala Gly Ala Val Val
35 40 45
Asn Asn Asn Thr Gln Phe Glu Val Ala Ile Ser Ile His Asp Ser Val
50 55 60
Tyr Asn Thr Asp Phe Ala Ser Ser Val Val Pro Tyr Ser Pro Asn Glu
65 70 75 80
Pro Glu Ala Gln Ala Gly Ile Ile Glu Lys His Val Leu Glu Thr Leu
85 90 95
Arg Lys Phe Ser Thr Glu His Met Cys Lys Phe Leu Gly Ala Gly Val
100 105 110
Thr Val Ile Leu Leu Arg Glu Ala Pro Asn Leu Cys Thr Arg Leu Trp
115 120 125
Leu Asp Met Asp Ile Val Pro Ile Val Phe Asn Ile Lys Pro Phe His
130 135 140
Thr Asp Ser Ile Thr Arg Pro Asn Val Arg His Arg Ile Ser Ser Thr
145 150 155 160
Thr Gly Ser Tyr Val Pro Ser Gly Ala Glu Thr Pro Thr Val Tyr Tyr
165 170 175
Asp Pro Ala Gln Leu Gln Asp Pro Asn Lys Leu Ser Ala Asn Val Gln
180 185 190
Thr Arg Leu Pro Ile Pro Arg Thr Val Asp Glu Gln Ala Asp Ser Ala
195 200 205
Ala Arg Lys Cys Ile Met Tyr Phe Gly Pro Gly Asn Asn Pro Arg Leu

210 215 220
Gln Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala Gly Gly Lys Ile
225 230 235 240
His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr Val Gly Lys Gly
245 250 255
Thr Trp Asn Ser Val Ile Lys Leu Ala Asp Glu Leu Arg Glu Lys Lys
260 265 270
Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly Gly Gly Val Ala
275 280 285
Leu Met Arg His Ala Ile Ile Arg Phe Phe Thr Ala Leu Asp Val Asp
290 295 300
Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val Phe Arg Ile Thr
305 310 315 320
Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Asp Pro Ser Leu Arg
325 330 335
Leu Thr Lys Glu Ala Ala Asp Asn Phe Asp Ser Trp Ile Leu Lys Asn
340 345 350
Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala Pro Gly Gly Val
355 360 365
Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly Leu Ile Pro Leu
370 375 380
Ile Lys Arg Ile Arg Pro Asp Leu Pro Ile Ile Tyr Arg Ser His Ile
385 390 395 400
Glu Ile Arg Ser Asp Leu Val His Val Lys Gly Ser Pro Gln Glu Glu
405 410 415
Val Trp Asn Tyr Leu Trp Asn Asn Ile Gln His Ser Asp Leu Phe Ile
420 425 430
[0309] Ser His Pro Val Asn Lys Phe Val Pro Ser Asp Val Pro Leu Glu Lys
435 440 445
Leu Ala Leu Leu Gly Ala Ala Thr Asp Trp Leu Asp Gly Leu Ser Lys
450 455 460
His Leu Asp Ala Trp Asp Ser Gln Tyr Tyr Met Gly Glu Phe Arg Asn
465 470 475 480
Leu Cys Val Lys Glu Lys Met Asn Glu Leu Gly Trp Pro Ala Arg Glu
485 490 495
Tyr Ile Val Gln Ile Ala Arg Phe Asp Pro Ser Lys Gly Ile Pro Asn
500 505 510
Val Ile Asp Ser Tyr Ala Arg Phe Arg Lys Leu Cys Val Asp Lys Val
515 520 525
Met Glu Asp Asp Ile Pro Gln Leu Leu Leu Cys Gly His Gly Ala Val
530 535 540
Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp Gln Val Leu Gln Leu Ile
545 550 555 560
His Ala Lys Tyr Lys Glu Tyr Ala Pro Asp Ile Val Val Met Arg Cys
565 570 575
Pro Pro Ser Asp Gln Leu Leu Asn Thr Leu Met Ala Asn Ala Lys Phe
580 585 590
Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe Glu Val Lys Val Ser Glu
595 600 605
Ala Leu His Ala Gly Lys Pro Val Ile Ala Cys Arg Thr Gly Gly Ile
610 615 620
Pro Leu Gln Ile Glu His Gly Lys Ser Gly Tyr Leu Cys Glu Pro Gly
625 630 635 640
Asp Asn Ala Ala Val Ala Gln His Met Leu Asp Leu Tyr Thr Asp Glu
645 650 655
Asp Leu Tyr Asp Thr Met Ser Glu Tyr Ala Arg Thr His Val Ser Asp

660 665 670
Glu Val Gly Thr Val Gly Asn Ala Ala Ala Trp Met Tyr Leu Ala Val
675 680 685
Met Tyr Val Ser Arg Gly Val Lys Leu Arg Pro His Gly Ala Trp Ile
690 695 700
Asn Asp Leu Met Arg Thr Glu Met Gly Glu Pro Tyr Arg Pro Gly Glu
705 710 715 720
Pro Arg Leu Pro Arg Gly Glu Leu His Val Gln Gly
725 730

<210> 166
<211> 732
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 166

<400> 166
Met Ala Pro Pro His Gln Phe Gln Ser Lys Pro Ser Asp Val Ile Arg
1 5 10 15
Arg Arg Leu Ser Ser Ala Val Ser Ser Lys Arg Pro Asn Ile Pro Gly
20 25 30
Tyr Thr Ser Leu Thr Pro Met Trp Ala Gly Ile Ala Gly Ala Val Val
35 40 45
Asn Asn Asn Thr Gln Phe Glu Val Ala Ile Ser Ile His Asp Ser Val
50 55 60
[0310] Tyr Asn Thr Asp Phe Ala Ser Ser Val Val Pro Tyr Ser Pro Asn Glu
65 70 75 80
Pro Glu Ala Gln Ala Gly Ile Ile Glu Lys His Val Leu Glu Thr Leu
85 90 95
Arg Lys Phe Ser Thr Glu His Met Cys Lys Phe Leu Gly Ala Gly Val
100 105 110
Thr Val Ile Leu Leu Arg Glu Ala Pro Asn Leu Cys Thr Arg Leu Trp
115 120 125
Leu Asp Met Asp Ile Val Pro Ile Val Phe Asn Ile Lys Pro Phe His
130 135 140
Thr Asp Ser Ile Thr Arg Pro Asn Val Arg His Arg Ile Ser Ser Thr
145 150 155 160
Thr Gly Ser Tyr Val Pro Ser Gly Ala Glu Thr Pro Thr Val Tyr Tyr
165 170 175
Asp Pro Ala Gln Leu Gln Asp Pro Asn Lys Leu Ser Ala Asn Val Gln
180 185 190
Thr Arg Leu Pro Ile Pro Arg Thr Val Asp Glu Gln Ala Asp Ser Ala
195 200 205
Ala Arg Lys Cys Ile Met Tyr Phe Gly Pro Gly Asn Asn Pro Arg Leu
210 215 220
Gln Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala Gly Gly Lys Ile
225 230 235 240
His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr Val Gly Lys Gly
245 250 255
Thr Trp Asn Ser Val Ile Lys Leu Ala Asp Glu Leu Arg Glu Lys Lys
260 265 270
Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly Gly Gly Val Ala
275 280 285

Leu Met Arg His Ala Ile Ile Arg Phe Phe Thr Ala Leu Asp Val Asp
290 295 300
Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val Phe Arg Thr Thr
305 310 315 320
Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Asp Pro Ser Leu Arg
325 330 335
Leu Thr Lys Glu Ala Ala Asp Asn Phe Asp Ser Trp Ile Leu Lys Asn
340 345 350
Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala Pro Gly Gly Val
355 360 365
Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly Leu Ile Pro Leu
370 375 380
Ile Lys Arg Ile Arg Pro Asp Leu Pro Ile Ile Tyr Arg Ser His Ile
385 390 395 400
Glu Ile Arg Ser Asp Leu Val His Val Lys Gly Ser Pro Gln Glu Glu
405 410 415
Val Trp Asn Tyr Leu Trp Asn Asn Ile Gln His Ser Asp Leu Phe Ile
420 425 430
Ser His Pro Val Asn Lys Phe Val Pro Ser Asp Val Pro Leu Glu Lys
435 440 445
Leu Ala Leu Leu Gly Ala Ala Thr Asp Trp Leu Asp Gly Leu Ser Lys
450 455 460
His Leu Asp Ala Trp Asp Ser Gln Tyr Tyr Met Gly Glu Phe Arg Asn
465 470 475 480
Leu Cys Val Lys Glu Lys Met Asn Glu Leu Gly Trp Pro Ala Arg Glu
485 490 495
Tyr Ile Val Gln Ile Ala Arg Phe Asp Pro Ser Lys Gly Ile Pro Asn
500 505 510

[0311]

Val Ile Asp Ser Tyr Ala Arg Phe Arg Lys Leu Cys Val Asp Lys Val
515 520 525
Met Glu Asp Asp Ile Pro Gln Leu Leu Leu Cys Gly His Gly Ala Val
530 535 540
Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp Gln Val Leu Gln Leu Ile
545 550 555 560
His Ala Lys Tyr Lys Glu Tyr Ala Pro Asp Ile Val Val Met Arg Cys
565 570 575
Pro Pro Ser Asp Gln Leu Leu Asn Thr Leu Met Ala Asn Ala Lys Phe
580 585 590
Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe Glu Val Lys Val Ser Glu
595 600 605
Ala Leu His Ala Gly Lys Pro Val Ile Ala Cys Arg Thr Gly Gly Ile
610 615 620
Pro Leu Gln Ile Glu His Gly Lys Ser Gly Tyr Leu Cys Glu Pro Gly
625 630 635 640
Asp Asn Ala Ala Val Ala Gln His Met Leu Asp Leu Tyr Thr Asp Glu
645 650 655
Asp Leu Tyr Asp Thr Met Ser Glu Tyr Ala Arg Thr His Val Ser Asp
660 665 670
Glu Val Gly Thr Val Gly Asn Ala Ala Ala Trp Met Tyr Leu Ala Val
675 680 685
Met Tyr Val Ser Arg Gly Val Lys Leu Arg Pro His Gly Ala Trp Ile
690 695 700
Asn Asp Leu Met Arg Thr Glu Met Gly Glu Pro Tyr Arg Pro Gly Glu
705 710 715 720
Pro Arg Leu Pro Arg Gly Glu Leu His Val Gln Gly
725 730

<210> 167
<211> 732
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 167

<400> 167

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Met Ala Pro Pro His Gln Phe Gln Ser Lys Pro Ser Asp Val Ile Arg
1               5                  10                  15
Arg Arg Leu Ser Ser Ala Val Ser Ser Lys Arg Pro Asn Ile Pro Gly
            20                  25                  30
Tyr Thr Ser Leu Thr Pro Met Trp Ala Gly Ile Ala Gly Ala Val Val
        35                  40                  45
Asn Asn Asn Thr Gln Phe Glu Val Ala Ile Ser Ile His Asp Ser Val
    50                  55                  60
Tyr Asn Thr Asp Phe Ala Ser Ser Val Val Pro Tyr Ser Pro Asn Glu
65                  70                  75                  80
Pro Glu Ala Gln Ala Gly Ile Ile Glu Lys His Val Leu Glu Thr Leu
                85                  90                  95
Arg Lys Phe Ser Thr Glu His Met Cys Lys Phe Leu Gly Ala Gly Val
            100                 105                 110
Thr Val Ile Leu Leu Arg Glu Ala Pro Asn Leu Cys Thr Arg Leu Trp
        115                 120                 125
Leu Asp Met Asp Ile Val Pro Ile Val Phe Asn Ile Lys Pro Phe His
    130                 135                 140
Thr Asp Ser Ile Thr Arg Pro Asn Val Arg His Arg Ile Ser Ser Thr
145                 150                 155                 160
Thr Gly Ser Tyr Val Pro Ser Gly Ala Glu Thr Pro Thr Val Tyr Tyr
                165                 170                 175
Asp Pro Ala Gln Leu Gln Asp Pro Asn Lys Leu Ser Ala Asn Val Gln
            180                 185                 190
Thr Arg Leu Pro Ile Pro Arg Thr Val Asp Glu Gln Ala Asp Ser Ala
        195                 200                 205
Ala Arg Lys Cys Ile Met Tyr Phe Gly Pro Gly Asn Asn Pro Arg Leu
    210                 215                 220
Gln Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala Gly Gly Lys Ile
225                 230                 235                 240
His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr Val Gly Lys Gly
                245                 250                 255
Thr Trp Asn Ser Val Ile Lys Leu Ala Asp Glu Leu Arg Glu Lys Lys
            260                 265                 270
Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly Gly Gly Val Ala
        275                 280                 285
Leu Met Arg His Ala Ile Ile Arg Phe Phe Thr Ala Leu Asp Val Asp
    290                 295                 300
Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val Phe Arg Thr Thr
305                 310                 315                 320
Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Asp Pro Ser Leu Arg
                325                 330                 335
Leu Thr Lys Glu Ala Ala Asp Asn Phe Asp Ser Trp Ile Leu Lys Asn
            340                 345                 350
Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala Pro Gly Gly Val
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[0312]

355 360 365
Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly Leu Ile Pro Leu
370 375 380
Ile Lys Arg Ile Arg Pro Asp Leu Pro Ile Ile Tyr Arg Ser His Ile
385 390 395 400
Glu Ile Arg Ser Asp Leu Val His Val Lys Gly Ser Pro Gln Glu Glu
405 410 415
Val Trp Asn Tyr Leu Trp Asn Asn Ile Gln His Ser Asp Leu Phe Ile
420 425 430
Ser His Pro Val Asn Lys Phe Val Pro Ser Asp Val Pro Leu Glu Lys
435 440 445
Leu Ala Leu Leu Gly Ala Ala Thr Asp Trp Leu Asp Gly Leu Ser Lys
450 455 460
His Leu Asp Ala Trp Asp Ser Gln Tyr Tyr Met Gly Glu Phe Arg Asn
465 470 475 480
Leu Cys Val Lys Glu Lys Met Asn Glu Leu Gly Trp Pro Ala Arg Glu
485 490 495
Tyr Ile Val Gln Ile Ala Arg Phe Asp Pro Ser Lys Gly Ile Pro Asn
500 505 510
Val Ile Asp Ser Tyr Ala Arg Phe Arg Lys Leu Cys Val Asp Lys Val
515 520 525
Met Glu Asp Asp Ile Pro Gln Leu Leu Leu Cys Gly His Gly Ala Val
530 535 540
Asp Asp Pro Asp Ala Thr Ile Ile Tyr Asp Gln Val Leu Gln Leu Ile
545 550 555 560
His Ala Lys Tyr Lys Glu Tyr Ala Pro Asp Ile Val Val Met Arg Cys
565 570 575
[0313] Pro Pro Ser Asp Gln Leu Leu Asn Thr Leu Met Ala Asn Ala Lys Phe
580 585 590
Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe Glu Val Lys Val Ser Glu
595 600 605
Ala Leu His Ala Gly Lys Pro Val Ile Ala Cys Arg Thr Gly Gly Ile
610 615 620
Pro Leu Gln Ile Glu His Gly Lys Ser Gly Tyr Leu Cys Glu Pro Gly
625 630 635 640
Asp Asn Ala Ala Val Ala Gln His Met Leu Asp Leu Tyr Thr Asp Glu
645 650 655
Asp Leu Tyr Asp Thr Met Ser Glu Tyr Ala Arg Thr His Val Ser Asp
660 665 670
Glu Val Gly Thr Val Gly Asn Ala Ala Ala Trp Met Tyr Leu Ala Val
675 680 685
Met Tyr Val Ser Arg Gly Val Lys Leu Arg Pro His Gly Ala Trp Ile
690 695 700
Asn Asp Leu Met Arg Thr Glu Met Gly Glu Pro Tyr Arg Pro Gly Glu
705 710 715 720
Pro Arg Leu Pro Arg Gly Glu Leu His Val Gln Gly
725 730

<210> 168
<211> 732
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 168

<400> 168

Met Ala Pro Pro His Gln Phe Gln Ser Lys Pro Ser Asp Val Ile Arg
1 5 10 15
Arg Arg Leu Ser Ser Ala Val Ser Ser Lys Arg Pro Asn Ile Pro Gly
20 25 30
Tyr Thr Ser Leu Thr Pro Met Trp Ala Gly Ile Ala Gly Ala Val Val
35 40 45
Asn Asn Asn Thr Gln Phe Glu Val Ala Ile Ser Ile His Asp Ser Val
50 55 60
Tyr Asn Thr Asp Phe Ala Ser Ser Val Val Pro Tyr Ser Pro Asn Glu
65 70 75 80
Pro Glu Ala Gln Ala Gly Ile Ile Glu Lys His Val Leu Glu Thr Leu
85 90 95
Arg Lys Phe Ser Thr Glu His Met Cys Lys Phe Leu Gly Ala Gly Val
100 105 110
Thr Val Ile Leu Leu Arg Glu Ala Pro Asn Leu Cys Thr Arg Leu Trp
115 120 125
Leu Asp Met Asp Ile Val Pro Ile Val Phe Asn Ile Lys Pro Phe His
130 135 140
Thr Asp Ser Ile Thr Arg Pro Asn Val Arg His Arg Ile Ser Ser Thr
145 150 155 160
Thr Gly Ser Tyr Val Pro Ser Gly Ala Glu Thr Pro Thr Val Tyr Tyr
165 170 175
Asp Pro Ala Gln Leu Gln Asp Pro Asn Lys Leu Ser Ala Asn Val Gln
180 185 190
Thr Arg Leu Pro Ile Pro Arg Thr Val Asp Glu Gln Ala Asp Ser Ala
195 200 205
[0314] Ala Arg Lys Cys Ile Met Tyr Phe Gly Pro Gly Asn Asn Pro Arg Leu
210 215 220
Gln Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala Gly Gly Lys Ile
225 230 235 240
His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr Val Gly Lys Gly
245 250 255
Thr Trp Asn Ser Val Ile Lys Leu Ala Asp Glu Leu Arg Glu Lys Lys
260 265 270
Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly Gly Gly Val Ala
275 280 285
Leu Met Arg His Ala Ile Ile Arg Phe Phe Thr Ala Leu Asp Val Asp
290 295 300
Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val Phe Arg Thr Thr
305 310 315 320
Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Asp Pro Ser Leu Arg
325 330 335
Leu Thr Lys Glu Ala Ala Asp Asn Phe Asp Ser Trp Ile Leu Lys Asn
340 345 350
Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala Pro Gly Gly Val
355 360 365
Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly Leu Ile Pro Leu
370 375 380
Ile Lys Arg Ile Arg Pro Asp Leu Pro Ile Ile Tyr Arg Ser His Ile
385 390 395 400
Glu Ile Arg Ser Asp Leu Val His Val Lys Gly Ser Pro Gln Glu Glu
405 410 415
Val Trp Asn Tyr Leu Trp Asn Asn Ile Gln His Ser Asp Leu Phe Ile
420 425 430

Ser His Pro Val Asn Lys Phe Val Pro Ser Asp Val Pro Leu Glu Lys
435 440 445
Leu Ala Leu Leu Gly Ala Ala Thr Asp Trp Leu Asp Gly Leu Ser Lys
450 455 460
His Leu Asp Ala Trp Asp Ser Gln Tyr Tyr Met Gly Glu Phe Arg Asn
465 470 475 480
Leu Cys Val Lys Glu Lys Met Asn Glu Leu Gly Trp Pro Ala Arg Glu
485 490 495
Tyr Ile Val Gln Ile Ala Arg Phe Asp Pro Ser Lys Gly Ile Pro Asn
500 505 510
Val Ile Asp Ser Tyr Ala Arg Phe Arg Lys Leu Cys Val Asp Lys Val
515 520 525
Met Glu Asp Asp Ile Pro Gln Leu Leu Leu Cys Gly His Gly Ala Val
530 535 540
Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp Gln Val Leu Glu Leu Ile
545 550 555 560
His Ala Lys Tyr Lys Glu Tyr Ala Pro Asp Ile Val Val Met Arg Cys
565 570 575
Pro Pro Ser Asp Gln Leu Leu Asn Thr Leu Met Ala Asn Ala Lys Phe
580 585 590
Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe Glu Val Lys Val Ser Glu
595 600 605
Ala Leu His Ala Gly Lys Pro Val Ile Ala Cys Arg Thr Gly Gly Ile
610 615 620
Pro Leu Gln Ile Glu His Gly Lys Ser Gly Tyr Leu Cys Glu Pro Gly
625 630 635 640
Asp Asn Ala Ala Val Ala Gln His Met Leu Asp Leu Tyr Thr Asp Glu
645 650 655

[0315]

Asp Leu Tyr Asp Thr Met Ser Glu Tyr Ala Arg Thr His Val Ser Asp
660 665 670
Glu Val Gly Thr Val Gly Asn Ala Ala Ala Trp Met Tyr Leu Ala Val
675 680 685
Met Tyr Val Ser Arg Gly Val Lys Leu Arg Pro His Gly Ala Trp Ile
690 695 700
Asn Asp Leu Met Arg Thr Glu Met Gly Glu Pro Tyr Arg Pro Gly Glu
705 710 715 720
Pro Arg Leu Pro Arg Gly Glu Leu His Val Gln Gly
725 730

<210> 169
<211> 732
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 169

<400> 169
Met Ala Pro Pro His Gln Phe Gln Ser Lys Pro Ser Asp Val Ile Arg
1 5 10 15
Arg Arg Leu Ser Ser Ala Val Ser Ser Lys Arg Pro Asn Ile Pro Gly
20 25 30
Tyr Thr Ser Leu Thr Pro Met Trp Ala Gly Ile Ala Gly Ala Val Val
35 40 45
Asn Asn Asn Thr Gln Phe Glu Val Ala Ile Ser Ile His Asp Ser Val

50 55 60
Tyr Asn Thr Asp Phe Ala Ser Ser Val Val Pro Tyr Ser Pro Asn Glu
65 70 75 80
Pro Glu Ala Gln Ala Gly Ile Ile Glu Lys His Val Leu Glu Thr Leu
85 90 95
Arg Lys Phe Ser Thr Glu His Met Cys Lys Phe Leu Gly Ala Gly Val
100 105 110
Thr Val Ile Leu Leu Arg Glu Ala Pro Asn Leu Cys Thr Arg Leu Trp
115 120 125
Leu Asp Met Asp Ile Val Pro Ile Val Phe Asn Ile Lys Pro Phe His
130 135 140
Thr Asp Ser Ile Thr Arg Pro Asn Val Arg His Arg Ile Ser Ser Thr
145 150 155 160
Thr Gly Ser Tyr Val Pro Ser Gly Ala Glu Thr Pro Thr Val Tyr Tyr
165 170 175
Asp Pro Ala Gln Leu Gln Asp Pro Asn Lys Leu Ser Ala Asn Val Gln
180 185 190
Thr Arg Leu Pro Ile Pro Arg Thr Val Asp Glu Gln Ala Asp Ser Ala
195 200 205
Ala Arg Lys Cys Ile Met Tyr Phe Gly Pro Gly Asn Asn Pro Arg Leu
210 215 220
Gln Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala Gly Gly Lys Ile
225 230 235 240
His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr Val Gly Lys Gly
245 250 255
Thr Trp Asn Ser Val Ile Lys Leu Ala Asp Glu Leu Arg Glu Lys Lys
260 265 270
[0316] Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly Gly Gly Val Ala
275 280 285
Leu Met Arg His Ala Ile Ile Arg Phe Phe Thr Ala Leu Asp Val Asp
290 295 300
Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val Phe Arg Thr Thr
305 310 315 320
Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Asp Pro Ser Leu Arg
325 330 335
Leu Thr Lys Glu Ala Ala Asp Asn Phe Asp Ser Trp Ile Leu Lys Asn
340 345 350
Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala Pro Gly Gly Val
355 360 365
Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly Leu Ile Pro Leu
370 375 380
Ile Lys Arg Ile Arg Pro Asp Leu Pro Ile Ile Tyr Arg Ser His Ile
385 390 395 400
Glu Ile Arg Ser Asp Leu Val His Val Lys Gly Ser Pro Gln Glu Glu
405 410 415
Val Trp Asn Tyr Leu Trp Asn Asn Ile Gln His Ser Asp Leu Phe Ile
420 425 430
Ser His Pro Val Asn Lys Phe Val Pro Ser Asp Val Pro Leu Glu Lys
435 440 445
Leu Ala Leu Leu Gly Ala Ala Thr Asp Trp Leu Asp Gly Leu Ser Lys
450 455 460
His Leu Asp Ala Trp Asp Ser Gln Tyr Tyr Met Gly Glu Phe Arg Asn
465 470 475 480
Leu Cys Val Lys Glu Lys Met Asn Glu Leu Gly Trp Pro Ala Arg Glu
485 490 495
Tyr Ile Val Gln Ile Ala Arg Phe Asp Pro Ser Lys Gly Ile Pro Asn

500 505 510
Val Ile Asp Ser Tyr Ala Arg Phe Arg Lys Leu Cys Val Asp Lys Val
515 520 525
Met Glu Asp Asp Ile Pro Gln Leu Leu Leu Cys Gly His Gly Ala Val
530 535 540
Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp Gln Val Leu Gln Leu Ile
545 550 555 560
His Ala Lys Tyr Lys Glu Tyr Ala Pro Asp Ile Val Val Met Arg Cys
565 570 575
Pro Pro Ser Asp Gln Leu Leu Asn Thr Leu Met Ala Asn Ala Lys Phe
580 585 590
Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe Glu Val Lys Val Ser Glu
595 600 605
Ala Leu His Ala Gly Lys Pro Val Ile Ala Cys Arg Thr Gly Gly Ile
610 615 620
Pro Leu Gln Ile Glu His Gly Lys Ser Gly Tyr Leu Cys Glu Pro Gly
625 630 635 640
Asp Asn Glu Ala Val Ala Gln His Met Leu Asp Leu Tyr Thr Asp Glu
645 650 655
Asp Leu Tyr Asp Thr Met Ser Glu Tyr Ala Arg Thr His Val Ser Asp
660 665 670
Glu Val Gly Thr Val Gly Asn Ala Ala Ala Trp Met Tyr Leu Ala Val
675 680 685
Met Tyr Val Ser Arg Gly Val Lys Leu Arg Pro His Gly Ala Trp Ile
690 695 700
Asn Asp Leu Met Arg Thr Glu Met Gly Glu Pro Tyr Arg Pro Gly Glu
705 710 715 720
[0317] Pro Arg Leu Pro Arg Gly Glu Leu His Val Gln Gly
725 730

<210> 170
<211> 732
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 170

<400> 170
Met Ala Pro Pro His Gln Phe Gln Ser Lys Pro Ser Asp Val Ile Arg
1 5 10 15
Arg Arg Leu Ser Ser Ala Val Ser Ser Lys Arg Pro Asn Ile Pro Gly
20 25 30
Tyr Thr Ser Leu Thr Pro Met Trp Ala Gly Ile Ala Gly Ala Val Val
35 40 45
Asn Asn Asn Thr Gln Phe Glu Val Ala Ile Ser Ile His Asp Ser Val
50 55 60
Tyr Asn Thr Asp Phe Ala Ser Ser Val Val Pro Tyr Ser Pro Asn Glu
65 70 75 80
Pro Glu Ala Gln Ala Gly Ile Ile Glu Lys His Val Leu Glu Thr Leu
85 90 95
Arg Lys Phe Ser Thr Glu His Met Cys Lys Phe Leu Gly Ala Gly Val
100 105 110
Thr Val Ile Leu Leu Arg Glu Ala Pro Asn Leu Cys Thr Arg Leu Trp
115 120 125

Leu Asp Met Asp Ile Val Pro Ile Val Phe Asn Ile Lys Pro Phe His
130 135 140
Thr Asp Ser Ile Thr Arg Pro Asn Val Arg His Arg Ile Ser Ser Thr
145 150 155 160
Thr Gly Ser Tyr Val Pro Ser Gly Ala Glu Thr Pro Thr Val Tyr Tyr
165 170 175
Asp Pro Ala Gln Leu Gln Asp Pro Asn Lys Leu Ser Ala Asn Val Gln
180 185 190
Thr Arg Leu Pro Ile Pro Arg Thr Val Asp Glu Gln Ala Asp Ser Ala
195 200 205
Ala Arg Lys Cys Ile Met Tyr Phe Gly Pro Gly Asn Asn Pro Arg Leu
210 215 220
Gln Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala Gly Gly Lys Ile
225 230 235 240
His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr Val Gly Lys Gly
245 250 255
Thr Trp Asn Ser Val Ile Lys Leu Ala Asp Glu Leu Arg Glu Lys Lys
260 265 270
Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly Gly Gly Val Ala
275 280 285
Leu Met Arg His Ala Ile Ile Arg Phe Phe Thr Ala Leu Asp Val Asp
290 295 300
Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val Phe Arg Thr Thr
305 310 315 320
Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Asp Pro Ser Leu Arg
325 330 335
Leu Thr Lys Glu Ala Ala Asp Asn Phe Asp Ser Trp Ile Leu Lys Asn
340 345 350

[0318]

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

Pro Pro Ser Asp Gln Leu Leu Asn Thr Leu Met Ala Asn Ala Lys Phe
580 585 590
Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe Glu Val Lys Val Ser Glu
595 600 605
Ala Leu His Ala Gly Lys Pro Val Ile Ala Cys Arg Thr Gly Gly Ile
610 615 620
Pro Leu Gln Ile Glu His Gly Lys Ser Gly Tyr Leu Cys Glu Pro Gly
625 630 635 640
Asp Asn Ala Ala Val Ala Gln His Met Leu Asp Leu Tyr Thr Asp Glu
645 650 655
Asp Leu Tyr Asp Thr Met Ser Glu Tyr Ala Arg Thr His Val Ser Asp
660 665 670
Glu Val Gly Thr Val Gly Asn Ala Ala Ala Trp Met Tyr Leu Ala Val
675 680 685
Met Tyr Val Ser Arg Gly Val Lys Leu Arg Pro His Gly Ala Trp Ile
690 695 700
Asn Asp Met Met Arg Thr Glu Met Gly Glu Pro Tyr Arg Pro Gly Glu
705 710 715 720
Pro Arg Leu Pro Arg Gly Glu Leu His Val Gln Gly
725 730

<210> 171
<211> 732
<212> PRT
<213> 人工序列(Artificial Sequence)

[0319] <220>
<223> SEQ ID NO: 171

<400> 171
Met Ala Pro Pro His Gln Phe Gln Ser Lys Pro Ser Asp Val Ile Arg
1 5 10 15
Arg Arg Leu Ser Ser Ala Val Ser Ser Lys Arg Pro Asn Ile Pro Gly
20 25 30
Tyr Thr Ser Leu Thr Pro Met Trp Ala Gly Ile Ala Gly Ala Val Val
35 40 45
Asn Asn Asn Thr Gln Phe Glu Val Ala Ile Ser Ile His Asp Ser Val
50 55 60
Tyr Asn Thr Asp Phe Ala Ser Ser Val Val Pro Tyr Ser Pro Asn Glu
65 70 75 80
Pro Glu Ala Gln Ala Gly Ile Ile Glu Lys His Val Leu Glu Thr Leu
85 90 95
Arg Lys Phe Ser Thr Glu His Met Cys Lys Phe Ile Gly Ala Gly Val
100 105 110
Thr Val Ile Leu Leu Arg Glu Ala Pro Asn Leu Cys Thr Arg Leu Trp
115 120 125
Leu Asp Met Asp Ile Val Pro Ile Val Phe Asn Ile Lys Pro Phe His
130 135 140
Thr Asp Ser Ile Thr Arg Pro Asn Val Arg His Arg Ile Ser Ser Thr
145 150 155 160
Thr Gly Ser Tyr Val Pro Ser Gly Ala Glu Thr Pro Thr Val Tyr Tyr
165 170 175
Asp Pro Ala Gln Leu Gln Asp Pro Asn Lys Leu Ser Ala Asn Val Gln
180 185 190
Thr Arg Leu Pro Ile Pro Arg Thr Val Asp Glu Gln Ala Asp Ser Ala

[0320]

```
          195                 200                 205
Ala Arg Lys Cys Ile Met Tyr Phe Gly Pro Gly Asn Val Pro Arg Leu
    210                 215                 220
Gln Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala Gly Gly Lys Ile
225                 230                 235                 240
His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr Val Gly Lys Gly
                245                 250                 255
Thr Trp Asn Ser Val Ile Lys Leu Ala Asp Glu Leu Arg Glu Lys Lys
            260                 265                 270
Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly Gly Gly Val Ala
        275                 280                 285
Leu Met Arg His Ala Ile Ile Arg Phe Phe Thr Ala Leu Asp Val Asp
    290                 295                 300
Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val Phe Arg Thr Thr
305                 310                 315                 320
Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Asp Pro Ser Leu Arg
                325                 330                 335
Leu Thr Lys Glu Ala Ala Asp Asn Phe Asp Ser Trp Ile Leu Lys Asn
            340                 345                 350
Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala Pro Gly Gly Val
        355                 360                 365
Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly Leu Ile Pro Leu
    370                 375                 380
Ile Lys Arg Ile Arg Pro Asp Leu Pro Ile Ile Tyr Arg Ser His Ile
385                 390                 395                 400
Glu Ile Arg Ser Asp Leu Val His Val Lys Gly Ser Pro Gln Glu Glu
                405                 410                 415
Val Trp Asn Tyr Leu Trp Asn Asn Ile Gln His Ser Asp Leu Phe Ile
            420                 425                 430
Ser His Pro Val Asn Lys Phe Val Pro Ser Asp Val Pro Leu Glu Lys
        435                 440                 445
Leu Ala Leu Leu Gly Ala Ala Thr Asp Trp Leu Asp Gly Leu Ser Lys
    450                 455                 460
His Leu Asp Ala Trp Asp Ser Gln Tyr Tyr Met Gly Glu Phe Arg Asn
465                 470                 475                 480
Leu Cys Val Lys Glu Lys Met Asn Glu Leu Gly Trp Pro Ala Arg Glu
                485                 490                 495
Tyr Ile Val Gln Ile Ala Arg Phe Asp Pro Ser Lys Gly Ile Pro Asn
            500                 505                 510
Val Ile Asp Ser Tyr Ala Arg Phe Arg Lys Leu Cys Val Asp Lys Val
        515                 520                 525
Met Glu Asp Asp Ile Pro Gln Leu Leu Leu Cys Gly His Gly Ala Val
    530                 535                 540
Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp Gln Val Leu Gln Leu Ile
545                 550                 555                 560
His Ala Lys Tyr Lys Glu Tyr Ala Pro Asp Ile Val Val Met Arg Cys
                565                 570                 575
Pro Pro Ser Asp Gln Leu Leu Asn Thr Leu Met Ala Asn Ala Lys Phe
            580                 585                 590
Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe Glu Val Lys Val Ser Glu
        595                 600                 605
Ala Leu His Ala Gly Lys Pro Val Ile Ala Cys Arg Thr Gly Gly Ile
    610                 615                 620
Pro Leu Gln Ile Glu His Gly Lys Ser Gly Tyr Leu Cys Glu Pro Gly
625                 630                 635                 640
Asp Asn Ala Ala Val Ala Gln His Met Leu Asp Leu Tyr Thr Asp Glu
```

645 650 655
Asp Leu Tyr Asp Thr Met Ser Glu Tyr Ala Arg Thr His Val Ser Asp
660 665 670
Glu Val Gly Thr Val Gly Asn Ala Ala Ala Trp Met Tyr Leu Ala Val
675 680 685
Met Tyr Val Ser Arg Gly Val Lys Leu Arg Pro His Gly Ala Trp Ile
690 695 700
Asn Asp Leu Met Arg Thr Glu Met Gly Glu Pro Tyr Arg Pro Gly Glu
705 710 715 720
Pro Arg Leu Pro Arg Gly Glu Leu His Val Gln Gly
725 730

<210> 172
<211> 732
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 172

<400> 172
Met Ala Pro Pro His Gln Phe Gln Ser Lys Pro Ser Asp Val Ile Arg
1 5 10 15
Arg Arg Leu Ser Ser Ala Val Ser Ser Lys Arg Pro Asn Ile Pro Gly
20 25 30
Tyr Thr Ser Leu Thr Pro Met Trp Ala Gly Ile Ala Gly Ala Val Val
35 40 45
[0321] Asn Asn Asn Thr Gln Phe Glu Val Ala Ile Ser Ile His Asp Ser Val
50 55 60
Tyr Asn Thr Asp Phe Ala Ser Ser Val Val Pro Tyr Ser Pro Asn Glu
65 70 75 80
Pro Glu Ala Gln Ala Gly Ile Ile Glu Lys His Val Leu Glu Thr Leu
85 90 95
Arg Lys Phe Ser Thr Glu His Met Cys Lys Phe Ile Gly Ala Gly Val
100 105 110
Thr Val Ile Leu Leu Arg Glu Ala Pro Asn Leu Cys Thr Arg Leu Trp
115 120 125
Leu Asp Met Asp Ile Val Pro Ile Val Phe Asn Ile Lys Pro Phe His
130 135 140
Thr Asp Ser Ile Thr Arg Pro Asn Val Arg His Arg Ile Ser Ser Thr
145 150 155 160
Thr Gly Ser Tyr Val Pro Ser Gly Ala Glu Thr Pro Thr Val Tyr Tyr
165 170 175
Asp Pro Ala Gln Leu Gln Asp Pro Asn Lys Leu Ser Ala Asn Val Gln
180 185 190
Thr Arg Leu Pro Ile Pro Arg Thr Val Asp Glu Gln Ala Asp Ser Ala
195 200 205
Ala Arg Lys Cys Ile Met Tyr Phe Gly Pro Gly Asn Asn Pro Arg Leu
210 215 220
Gln Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala Gly Gly Lys Ile
225 230 235 240
His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr Val Gly Lys Gly
245 250 255
Thr Trp Asn Ser Val Ile Lys Leu Ala Asp Glu Leu Arg Glu Lys Lys
260 265 270

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

[0322]

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

Pro Arg Leu Pro Arg Gly Glu Leu His Val Gln Gly
725 730

<210> 173
<211> 732
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 173

<400> 173
Met Ala Pro Pro His Gln Phe Gln Ser Lys Pro Ser Asp Val Ile Arg
1 5 10 15
Arg Arg Leu Ser Ser Ala Val Ser Ser Lys Arg Pro Asn Ile Pro Gly
20 25 30
Tyr Thr Ser Leu Thr Pro Met Trp Ala Gly Ile Ala Gly Ala Val Val
35 40 45
Asn Asn Asn Thr Gln Phe Glu Val Ala Ile Ser Ile His Asp Ser Val
50 55 60
Tyr Asn Thr Asp Phe Ala Ser Ser Val Val Pro Tyr Ser Pro Asn Glu
65 70 75 80
Pro Glu Ala Gln Ala Gly Ile Ile Glu Lys His Val Leu Glu Thr Leu
85 90 95
Arg Lys Phe Ser Thr Glu His Met Cys Lys Phe Ile Gly Ala Gly Val
100 105 110
[0323] Thr Val Ile Leu Leu Arg Glu Ala Pro Asn Leu Cys Thr Arg Leu Trp
115 120 125
Leu Asp Met Asp Ile Val Pro Ile Val Phe Asn Ile Lys Pro Phe His
130 135 140
Thr Asp Ser Ile Thr Arg Pro Asn Val Arg His Arg Ile Ser Ser Thr
145 150 155 160
Thr Gly Ser Tyr Val Pro Ser Gly Ala Glu Thr Pro Thr Val Tyr Tyr
165 170 175
Asp Pro Ala Gln Leu Gln Asp Pro Asn Lys Leu Ser Ala Asn Val Gln
180 185 190
Thr Arg Leu Pro Ile Pro Arg Thr Val Asp Glu Gln Ala Asp Ser Ala
195 200 205
Ala Arg Lys Cys Ile Met Tyr Phe Gly Pro Gly Asn Asn Pro Arg Leu
210 215 220
Gln Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala Gly Gly Lys Ile
225 230 235 240
His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr Val Gly Lys Gly
245 250 255
Thr Trp Asn Ser Val Ile Lys Leu Ala Asp Glu Leu Arg Glu Lys Lys
260 265 270
Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly Gly Gly Val Ala
275 280 285
Leu Met Arg His Ala Ile Ile Arg Phe Phe Thr Ala Leu Asp Val Asp
290 295 300
Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val Phe Arg Ile Thr
305 310 315 320
Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Asp Pro Ser Leu Arg
325 330 335
Leu Thr Lys Glu Ala Ala Asp Asn Phe Asp Ser Trp Ile Leu Lys Asn

340 345 350
Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala Pro Gly Gly Val
355 360 365
Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly Leu Ile Pro Leu
370 375 380
Ile Lys Arg Ile Arg Pro Asp Leu Pro Ile Ile Tyr Arg Ser His Ile
385 390 395 400
Glu Ile Arg Ser Asp Leu Val His Val Lys Gly Ser Pro Gln Glu Glu
405 410 415
Val Trp Asn Tyr Leu Trp Asn Asn Ile Gln His Ser Asp Leu Phe Ile
420 425 430
Ser His Pro Val Asn Lys Phe Val Pro Ser Asp Val Pro Leu Glu Lys
435 440 445
Leu Ala Leu Leu Gly Ala Ala Thr Asp Trp Leu Asp Gly Leu Ser Lys
450 455 460
His Leu Asp Ala Trp Asp Ser Gln Tyr Tyr Met Gly Glu Phe Arg Asn
465 470 475 480
Leu Cys Val Lys Glu Lys Met Asn Glu Leu Gly Trp Pro Ala Arg Glu
485 490 495
Tyr Ile Val Gln Ile Ala Arg Phe Asp Pro Ser Lys Gly Ile Pro Asn
500 505 510
Val Ile Asp Ser Tyr Ala Arg Phe Arg Lys Leu Cys Val Asp Lys Val
515 520 525
Met Glu Asp Asp Ile Pro Gln Leu Leu Leu Cys Gly His Gly Ala Val
530 535 540
Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp Gln Val Leu Gln Leu Ile
545 550 555 560
[0324] His Ala Lys Tyr Lys Glu Tyr Ala Pro Asp Ile Val Val Met Arg Cys
565 570 575
Pro Pro Ser Asp Gln Leu Leu Asn Thr Leu Met Ala Asn Ala Lys Phe
580 585 590
Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe Glu Val Lys Val Ser Glu
595 600 605
Ala Leu His Ala Gly Lys Pro Val Ile Ala Cys Arg Thr Gly Gly Ile
610 615 620
Pro Leu Gln Ile Glu His Gly Lys Ser Gly Tyr Leu Cys Glu Pro Gly
625 630 635 640
Asp Asn Ala Ala Val Ala Gln His Met Leu Asp Leu Tyr Thr Asp Glu
645 650 655
Asp Leu Tyr Asp Thr Met Ser Glu Tyr Ala Arg Thr His Val Ser Asp
660 665 670
Glu Val Gly Thr Val Gly Asn Ala Ala Ala Trp Met Tyr Leu Ala Val
675 680 685
Met Tyr Val Ser Arg Gly Val Lys Leu Arg Pro His Gly Ala Trp Ile
690 695 700
Asn Asp Leu Met Arg Thr Glu Met Gly Glu Pro Tyr Arg Pro Gly Glu
705 710 715 720
Pro Arg Leu Pro Arg Gly Glu Leu His Val Gln Gly
725 730

<210> 174
<211> 732
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 174

<400> 174

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

[0325]

Val Trp Asn Tyr Leu Trp Asn Asn Ile Gln His Ser Asp Leu Phe Ile
420 425 430
Ser His Pro Val Asn Lys Phe Val Pro Ser Asp Val Pro Leu Glu Lys
435 440 445
Leu Ala Leu Leu Gly Ala Ala Thr Asp Trp Leu Asp Gly Leu Ser Lys
450 455 460
His Leu Asp Ala Trp Asp Ser Gln Tyr Tyr Met Gly Glu Phe Arg Asn
465 470 475 480
Leu Cys Ala Lys Glu Lys Met Asn Glu Leu Gly Trp Pro Ala Arg Glu
485 490 495
Tyr Ile Val Gln Ile Ala Arg Phe Asp Pro Ser Lys Gly Ile Pro Asn
500 505 510
Val Ile Asp Ser Tyr Ala Arg Phe Arg Lys Leu Cys Val Asp Lys Val
515 520 525
Met Glu Asp Asp Ile Pro Gln Leu Leu Leu Cys Gly His Gly Ala Val
530 535 540
Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp Gln Val Leu Gln Leu Ile
545 550 555 560
His Ala Lys Tyr Lys Glu Tyr Ala Pro Asp Ile Val Val Met Arg Cys
565 570 575
Pro Pro Ser Asp Gln Leu Leu Asn Thr Leu Met Ala Asn Ala Lys Phe
580 585 590
Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe Glu Val Lys Val Ser Glu
595 600 605
Ala Leu His Ala Gly Lys Pro Val Ile Ala Cys Arg Thr Gly Gly Ile
610 615 620
Pro Leu Gln Ile Glu His Gly Lys Ser Gly Tyr Leu Cys Glu Pro Gly
625 630 635 640

[0326]

Asp Asn Ala Ala Val Ala Gln His Met Leu Asp Leu Tyr Thr Asp Glu
645 650 655
Asp Leu Tyr Asp Thr Met Ser Glu Tyr Ala Arg Thr His Val Ser Asp
660 665 670
Glu Val Gly Thr Val Gly Asn Ala Ala Ala Trp Met Tyr Leu Ala Val
675 680 685
Met Tyr Val Ser Arg Gly Val Lys Leu Arg Pro His Gly Ala Trp Ile
690 695 700
Asn Asp Leu Met Arg Thr Glu Met Gly Glu Pro Tyr Arg Pro Gly Glu
705 710 715 720
Pro Arg Leu Pro Arg Gly Glu Leu His Val Gln Gly
725 730

<210> 175
<211> 732
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 175

<400> 175
Met Ala Pro Pro His Gln Phe Gln Ser Lys Pro Ser Asp Val Ile Arg
1 5 10 15
Arg Arg Leu Ser Ser Ala Val Ser Ser Lys Arg Pro Asn Ile Pro Gly
20 25 30
Tyr Thr Ser Leu Thr Pro Met Trp Ala Gly Ile Ala Gly Ala Val Val

[0327]

```
          35                  40                  45
Asn Asn Asn Thr Gln Phe Glu Val Ala Ile Ser Ile His Asp Ser Val
      50                  55                  60
Tyr Asn Thr Asp Phe Ala Ser Ser Val Val Pro Tyr Ser Pro Asn Glu
65                  70                  75                  80
Pro Glu Ala Gln Ala Gly Ile Ile Glu Lys His Val Leu Glu Thr Leu
                  85                  90                  95
Arg Lys Phe Ser Thr Glu His Met Cys Lys Phe Ile Gly Ala Gly Val
             100                 105                 110
Thr Val Ile Leu Leu Arg Glu Ala Pro Asn Leu Cys Thr Arg Leu Trp
         115                 120                 125
Leu Asp Met Asp Ile Val Pro Ile Val Phe Asn Ile Lys Pro Phe His
     130                 135                 140
Thr Asp Ser Ile Thr Arg Pro Asn Val Arg His Arg Ile Ser Ser Thr
145                 150                 155                 160
Thr Gly Ser Tyr Val Pro Ser Gly Ala Glu Thr Pro Thr Val Tyr Tyr
                 165                 170                 175
Asp Pro Ala Gln Leu Gln Asp Pro Asn Lys Leu Ser Ala Asn Val Gln
             180                 185                 190
Thr Arg Leu Pro Ile Pro Arg Thr Val Asp Glu Gln Ala Asp Ser Ala
         195                 200                 205
Ala Arg Lys Cys Ile Met Tyr Phe Gly Pro Gly Asn Asn Pro Arg Leu
     210                 215                 220
Gln Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala Gly Gly Lys Ile
225                 230                 235                 240
His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr Val Gly Lys Gly
                 245                 250                 255
Thr Trp Asn Ser Val Ile Lys Leu Ala Asp Glu Leu Arg Glu Lys Lys
             260                 265                 270
Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly Gly Gly Val Ala
         275                 280                 285
Leu Met Arg His Ala Ile Ile Arg Phe Phe Thr Ala Leu Asp Val Asp
     290                 295                 300
Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val Phe Arg Thr Thr
305                 310                 315                 320
Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Asp Pro Ser Leu Arg
                 325                 330                 335
Leu Thr Lys Glu Ala Ala Asp Asn Phe Asp Ser Trp Ile Leu Lys Asn
             340                 345                 350
Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala Pro Gly Gly Val
         355                 360                 365
Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly Leu Ile Pro Leu
     370                 375                 380
Ile Lys Arg Ile Arg Pro Asp Leu Pro Ile Ile Tyr Arg Ser His Ile
385                 390                 395                 400
Glu Ile Arg Ser Asp Leu Val His Val Lys Gly Ser Pro Gln Glu Glu
                 405                 410                 415
Val Trp Asn Tyr Leu Trp Asn Asn Ile Gln His Ser Asp Leu Phe Ile
             420                 425                 430
Ser His Pro Val Asn Lys Phe Val Pro Ser Asp Val Pro Leu Glu Lys
         435                 440                 445
Leu Ala Leu Leu Gly Ala Ala Thr Asp Trp Leu Asp Gly Leu Ser Lys
     450                 455                 460
His Leu Asp Ala Trp Asp Ser Gln Tyr Tyr Met Gly Glu Phe Arg Asn
465                 470                 475                 480
Leu Cys Val Lys Glu Lys Met Asn Glu Leu Gly Trp Pro Ala Arg Glu
```

485 490 495
Tyr Ile Val Gln Ile Ala Arg Phe Asp Pro Ser Lys Gly Ile Pro Asn
500 505 510
Val Ile Asp Ser Tyr Ala Arg Phe Arg Lys Leu Cys Val Asp Lys Val
515 520 525
Met Glu Asp Asp Ile Pro Gln Leu Leu Leu Cys Gly His Gly Ala Val
530 535 540
Asp Asp Pro Asp Ala Thr Ile Ile Tyr Asp Gln Val Leu Gln Leu Ile
545 550 555 560
His Ala Lys Tyr Lys Glu Tyr Ala Pro Asp Ile Val Val Met Arg Cys
565 570 575
Pro Pro Ser Asp Gln Leu Leu Asn Thr Leu Met Ala Asn Ala Lys Phe
580 585 590
Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe Glu Val Lys Val Ser Glu
595 600 605
Ala Leu His Ala Gly Lys Pro Val Ile Ala Cys Arg Thr Gly Gly Ile
610 615 620
Pro Leu Gln Ile Glu His Gly Lys Ser Gly Tyr Leu Cys Glu Pro Gly
625 630 635 640
Asp Asn Ala Ala Val Ala Gln His Met Leu Asp Leu Tyr Thr Asp Glu
645 650 655
Asp Leu Tyr Asp Thr Met Ser Glu Tyr Ala Arg Thr His Val Ser Asp
660 665 670
Glu Val Gly Thr Val Gly Asn Ala Ala Ala Trp Met Tyr Leu Ala Val
675 680 685
Met Tyr Val Ser Arg Gly Val Lys Leu Arg Pro His Gly Ala Trp Ile
690 695 700
[0328] Asn Asp Leu Met Arg Thr Glu Met Gly Glu Pro Tyr Arg Pro Gly Glu
705 710 715 720
Pro Arg Leu Pro Arg Gly Glu Leu His Val Gln Gly
725 730

<210> 176
<211> 732
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 176

<400> 176
Met Ala Pro Pro His Gln Phe Gln Ser Lys Pro Ser Asp Val Ile Arg
1 5 10 15
Arg Arg Leu Ser Ser Ala Val Ser Ser Lys Arg Pro Asn Ile Pro Gly
20 25 30
Tyr Thr Ser Leu Thr Pro Met Trp Ala Gly Ile Ala Gly Ala Val Val
35 40 45
Asn Asn Asn Thr Gln Phe Glu Val Ala Ile Ser Ile His Asp Ser Val
50 55 60
Tyr Asn Thr Asp Phe Ala Ser Ser Val Val Pro Tyr Ser Pro Asn Glu
65 70 75 80
Pro Glu Ala Gln Ala Gly Ile Ile Glu Lys His Val Leu Glu Thr Leu
85 90 95
Arg Lys Phe Ser Thr Glu His Met Cys Lys Phe Ile Gly Ala Gly Val
100 105 110

```
Thr Val Ile Leu Leu Arg Glu Ala Pro Asn Leu Cys Thr Arg Leu Trp
        115                 120                 125
Leu Asp Met Asp Ile Val Pro Ile Val Phe Asn Ile Lys Pro Phe His
    130                 135                 140
Thr Asp Ser Ile Thr Arg Pro Asn Val Arg His Arg Ile Ser Ser Thr
145                 150                 155                 160
Thr Gly Ser Tyr Val Pro Ser Gly Ala Glu Thr Pro Thr Val Tyr Tyr
                165                 170                 175
Asp Pro Ala Gln Leu Gln Asp Pro Asn Lys Leu Ser Ala Asn Val Gln
            180                 185                 190
Thr Arg Leu Pro Ile Pro Arg Thr Val Asp Glu Gln Ala Asp Ser Ala
        195                 200                 205
Ala Arg Lys Cys Ile Met Tyr Phe Gly Pro Gly Asn Asn Pro Arg Leu
    210                 215                 220
Gln Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala Gly Gly Lys Ile
225                 230                 235                 240
His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr Val Gly Lys Gly
                245                 250                 255
Thr Trp Asn Ser Val Ile Lys Leu Ala Asp Glu Leu Arg Glu Lys Lys
            260                 265                 270
Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly Gly Gly Val Ala
        275                 280                 285
Leu Met Arg His Ala Ile Ile Arg Phe Phe Thr Ala Leu Asp Val Asp
    290                 295                 300
Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val Phe Arg Thr Thr
305                 310                 315                 320
Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Asp Pro Ser Leu Arg
                325                 330                 335
```

[0329]

```
Leu Thr Lys Glu Ala Ala Asp Asn Phe Asp Ser Trp Ile Leu Lys Asn
            340                 345                 350
Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala Pro Gly Gly Val
        355                 360                 365
Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly Leu Ile Pro Leu
    370                 375                 380
Ile Lys Arg Ile Arg Pro Asp Leu Pro Ile Ile Tyr Arg Ser His Ile
385                 390                 395                 400
Glu Ile Arg Ser Asp Leu Val His Val Lys Gly Ser Pro Gln Glu Glu
                405                 410                 415
Val Trp Asn Tyr Leu Trp Asn Asn Ile Gln His Ser Asp Leu Phe Ile
            420                 425                 430
Ser His Pro Val Asn Lys Phe Val Pro Ser Asp Val Pro Leu Glu Lys
        435                 440                 445
Leu Ala Leu Leu Gly Ala Ala Thr Asp Trp Leu Asp Gly Leu Ser Lys
    450                 455                 460
His Leu Asp Ala Trp Asp Ser Gln Tyr Tyr Met Gly Glu Phe Arg Asn
465                 470                 475                 480
Leu Cys Val Lys Glu Lys Met Asn Glu Leu Gly Trp Pro Ala Arg Glu
                485                 490                 495
Tyr Ile Val Gln Ile Ala Arg Phe Asp Pro Ser Lys Gly Ile Pro Asn
            500                 505                 510
Val Ile Asp Ser Tyr Ala Arg Phe Arg Lys Leu Cys Val Asp Lys Val
        515                 520                 525
Met Glu Asp Asp Ile Pro Gln Leu Leu Leu Cys Gly His Gly Ala Val
    530                 535                 540
Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp Gln Val Leu Gln Leu Ile
545                 550                 555                 560
```

His Ala Lys Tyr Lys Glu Tyr Ala Pro Asp Ile Val Val Met Arg Cys
565 570 575
Pro Pro Ser Asp Gln Leu Leu Asn Thr Leu Met Ala Asn Ala Lys Phe
580 585 590
Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe Glu Val Lys Val Ser Glu
595 600 605
Ala Leu His Ala Gly Lys Pro Val Ile Ala Cys Arg Thr Gly Gly Ile
610 615 620
Pro Leu Gln Ile Glu His Gly Lys Ser Gly Tyr Leu Cys Glu Pro Gly
625 630 635 640
Asp Asn Ala Ala Val Ala Gln His Met Leu Asp Leu Tyr Thr Asp Glu
645 650 655
Asp Leu Tyr Asp Thr Met Ser Glu Tyr Ala Arg Thr His Val Ser Asp
660 665 670
Glu Val Gly Thr Val Gly Asn Ala Ala Ala Trp Met Tyr Leu Ala Val
675 680 685
Met Tyr Val Ser Arg Gly Val Lys Leu Arg Pro His Gly Ala Trp Ile
690 695 700
Asn Asp Leu Met Arg Thr Glu Met Gly Glu Pro Tyr Arg Pro Gly Glu
705 710 715 720
Pro Arg Leu Pro Arg Gly Glu Leu His Val Gln Gly
725 730

<210> 177
<211> 732
<212> PRT
<213> 人工序列(Artificial Sequence)

[0330]

<220>
<223> SEQ ID NO: 177

<400> 177
Met Ala Pro Pro His Gln Phe Gln Ser Lys Pro Ser Asp Val Ile Arg
1 5 10 15
Arg Arg Leu Ser Ser Ala Val Ser Ser Lys Arg Pro Asn Ile Pro Gly
20 25 30
Tyr Thr Ser Leu Thr Pro Met Trp Ala Gly Ile Ala Gly Ala Val Val
35 40 45
Asn Asn Asn Thr Gln Phe Glu Val Ala Ile Ser Ile His Asp Ser Val
50 55 60
Tyr Asn Thr Asp Phe Ala Ser Ser Val Val Pro Tyr Ser Pro Asn Glu
65 70 75 80
Pro Glu Ala Gln Ala Gly Ile Ile Glu Lys His Val Leu Glu Thr Leu
85 90 95
Arg Lys Phe Ser Thr Glu His Met Cys Lys Phe Leu Gly Ala Gly Ile
100 105 110
Thr Val Ile Leu Leu Arg Glu Ala Pro Asn Leu Cys Thr Arg Leu Trp
115 120 125
Leu Asp Met Asp Ile Val Pro Ile Val Phe Asn Ile Lys Pro Phe His
130 135 140
Thr Asp Ser Ile Thr Arg Pro Asn Val Arg His Arg Ile Ser Ser Thr
145 150 155 160
Thr Gly Ser Tyr Val Pro Ser Gly Ala Glu Thr Pro Thr Val Tyr Tyr
165 170 175
Asp Pro Ala Gln Leu Gln Asp Pro Asn Lys Leu Ser Ala Asn Val Gln

[0331]

```
                180                 185                 190
Thr Arg Leu Pro Ile Pro Arg Thr Val Asp Glu Gln Ala Asp Ser Ala
        195                 200                 205
Ala Arg Lys Cys Ile Met Tyr Phe Gly Pro Gly Asn Asn Pro Arg Leu
    210                 215                 220
Gln Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala Gly Gly Lys Ile
225                 230                 235                 240
His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr Val Gly Lys Gly
                245                 250                 255
Thr Trp Asn Ser Val Ile Lys Leu Ala Asp Glu Leu Arg Glu Lys Lys
            260                 265                 270
Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly Gly Gly Val Ala
        275                 280                 285
Leu Met Arg His Ala Ile Ile Arg Phe Phe Thr Ala Leu Asp Val Asp
    290                 295                 300
Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val Phe Arg Thr Thr
305                 310                 315                 320
Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Asp Pro Ser Leu Arg
                325                 330                 335
Leu Thr Lys Glu Ala Ala Asp Asn Phe Asp Ser Trp Ile Leu Lys Asn
            340                 345                 350
Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala Pro Gly Gly Val
        355                 360                 365
Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly Leu Ile Pro Leu
    370                 375                 380
Ile Lys Arg Ile Arg Pro Asp Leu Pro Ile Ile Tyr Arg Ser His Ile
385                 390                 395                 400
Glu Ile Arg Ser Asp Leu Val His Val Lys Gly Ser Pro Gln Glu Glu
                405                 410                 415
Val Trp Asn Tyr Leu Trp Asn Asn Ile Gln His Ser Asp Leu Phe Ile
            420                 425                 430
Ser His Pro Val Asn Lys Phe Val Pro Ser Asp Val Pro Leu Glu Lys
        435                 440                 445
Leu Ala Leu Leu Gly Ala Ala Thr Asp Trp Leu Asp Gly Leu Ser Lys
    450                 455                 460
His Leu Asp Ala Trp Asp Ser Gln Tyr Tyr Met Gly Glu Phe Arg Asn
465                 470                 475                 480
Leu Cys Val Lys Glu Lys Met Asn Glu Leu Gly Trp Pro Ala Arg Glu
                485                 490                 495
Tyr Ile Val Gln Ile Ala Arg Phe Asp Pro Ser Lys Gly Ile Pro Asn
            500                 505                 510
Val Ile Asp Ser Tyr Ala Arg Phe Arg Lys Leu Cys Val Asp Lys Val
        515                 520                 525
Met Glu Asp Asp Ile Pro Gln Leu Leu Leu Cys Gly His Gly Ala Val
    530                 535                 540
Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp Gln Val Leu Gln Leu Ile
545                 550                 555                 560
His Ala Lys Tyr Lys Glu Tyr Ala Pro Asp Ile Val Val Met Arg Cys
                565                 570                 575
Pro Pro Ser Asp Gln Leu Leu Asn Thr Leu Met Ala Asn Ala Lys Phe
            580                 585                 590
Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe Glu Val Lys Val Ser Glu
        595                 600                 605
Ala Leu His Ala Gly Lys Pro Val Ile Ala Cys Arg Thr Gly Gly Ile
    610                 615                 620
Pro Leu Gln Ile Glu His Gly Lys Ser Gly Tyr Leu Cys Glu Pro Gly
```

625 630 635 640
Asp Asn Ala Ala Val Ala Gln His Met Leu Asp Leu Tyr Thr Asp Glu
645 650 655
Asp Leu Tyr Asp Thr Met Ser Glu Tyr Ala Arg Thr His Val Ser Asp
660 665 670
Glu Val Gly Thr Val Gly Asn Ala Ala Ala Trp Met Tyr Leu Ala Val
675 680 685
Met Tyr Val Ser Arg Gly Val Lys Leu Arg Pro His Gly Ala Trp Ile
690 695 700
Asn Asp Leu Met Arg Thr Glu Met Gly Glu Pro Tyr Arg Pro Gly Glu
705 710 715 720
Pro Arg Leu Pro Arg Gly Glu Leu His Val Gln Gly
725 730

<210> 178
<211> 732
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 178

<400> 178
Met Ala Pro Pro His Gln Phe Gln Ser Lys Pro Ser Asp Val Ile Arg
1 5 10 15
Arg Arg Leu Ser Ser Ala Val Ser Ser Lys Arg Pro Asn Ile Pro Gly
20 25 30
[0332] Tyr Thr Ser Leu Thr Pro Met Trp Ala Gly Ile Ala Gly Ala Val Val
35 40 45
Asn Asn Asn Thr Gln Phe Glu Val Ala Ile Ser Ile His Asp Ser Val
50 55 60
Tyr Asn Thr Asp Phe Ala Ser Ser Val Val Pro Tyr Ser Pro Asn Glu
65 70 75 80
Pro Glu Ala Gln Ala Gly Ile Ile Glu Lys His Val Leu Glu Thr Leu
85 90 95
Arg Lys Phe Ser Thr Glu His Met Cys Lys Phe Leu Gly Ala Gly Val
100 105 110
Thr Val Ile Leu Leu Arg Glu Ala Pro Asn Leu Cys Thr Arg Leu Trp
115 120 125
Leu Asp Met Asp Ile Val Pro Ile Val Phe Asn Ile Lys Pro Phe His
130 135 140
Thr Asp Ser Ile Thr Arg Pro Asn Val Arg His Arg Ile Ser Ser Thr
145 150 155 160
Thr Gly Ser Tyr Val Pro Ser Gly Ala Glu Thr Pro Thr Val Tyr Tyr
165 170 175
Asp Pro Ala Gln Leu Gln Asp Pro Asn Lys Leu Ser Ala Asn Val Gln
180 185 190
Thr Arg Leu Pro Ile Pro Arg Thr Val Asp Glu Gln Ala Asp Ser Ala
195 200 205
Ala Arg Lys Cys Ile Met Tyr Phe Gly Pro Gly Asn Val Pro Arg Leu
210 215 220
Gln Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala Gly Gly Lys Ile
225 230 235 240
His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr Val Gly Lys Gly
245 250 255

Thr Trp Asn Ser Val Ile Lys Leu Ala Asp Glu Leu Arg Glu Lys Lys
260 265 270
Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly Gly Gly Val Ala
275 280 285
Leu Met Arg His Ala Ile Ile Arg Phe Phe Thr Ala Leu Asp Val Asp
290 295 300
Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val Phe Arg Thr Thr
305 310 315 320
Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Asp Pro Ser Leu Arg
325 330 335
Leu Thr Lys Glu Ala Ala Asp Asn Phe Asp Ser Trp Ile Leu Lys Asn
340 345 350
Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala Pro Gly Gly Val
355 360 365
Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly Leu Ile Pro Leu
370 375 380
Ile Lys Arg Ile Arg Pro Asp Leu Pro Ile Ile Tyr Arg Ser His Ile
385 390 395 400
Glu Ile Arg Ser Asp Leu Val His Val Lys Gly Ser Pro Gln Glu Glu
405 410 415
Val Trp Asn Tyr Leu Trp Asn Asn Ile Gln His Ser Asp Leu Phe Ile
420 425 430
Ser His Pro Val Asn Lys Phe Val Pro Ser Asp Val Pro Leu Glu Lys
435 440 445
Leu Ala Leu Leu Gly Ala Ala Thr Asp Trp Leu Asp Gly Leu Ser Lys
450 455 460
His Leu Asp Ala Trp Asp Ser Gln Tyr Tyr Met Gly Glu Phe Arg Asn
465 470 475 480

[0333]

Leu Cys Val Lys Glu Lys Met Asn Glu Leu Gly Trp Pro Ala Arg Glu
485 490 495
Tyr Ile Val Gln Ile Ala Arg Phe Asp Pro Ser Lys Gly Ile Pro Asn
500 505 510
Val Ile Asp Ser Tyr Ala Arg Phe Arg Lys Leu Cys Val Asp Lys Val
515 520 525
Met Glu Asp Asp Ile Pro Gln Leu Leu Leu Cys Gly His Gly Ala Val
530 535 540
Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp Gln Val Leu Gln Leu Ile
545 550 555 560
His Ala Lys Tyr Lys Glu Tyr Ala Pro Asp Ile Val Val Met Arg Cys
565 570 575
Pro Pro Ser Asp Gln Leu Leu Asn Thr Leu Met Ala Asn Ala Lys Phe
580 585 590
Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe Glu Val Lys Val Ser Glu
595 600 605
Ala Leu His Ala Gly Lys Pro Val Ile Ala Cys Arg Thr Gly Gly Ile
610 615 620
Pro Leu Gln Ile Glu His Gly Lys Ser Gly Tyr Leu Cys Glu Pro Gly
625 630 635 640
Asp Asn Ala Ala Val Ala Gln His Met Leu Asp Leu Tyr Thr Asp Glu
645 650 655
Asp Leu Tyr Asp Thr Met Ser Glu Tyr Ala Arg Thr His Val Ser Asp
660 665 670
Glu Val Gly Thr Val Gly Asn Ala Ala Ala Trp Met Tyr Leu Ala Val
675 680 685
Met Tyr Val Ser Arg Gly Val Lys Leu Arg Pro His Gly Ala Trp Ile
690 695 700

Asn Asp Leu Met Arg Thr Glu Met Gly Glu Pro Tyr Arg Pro Gly Glu
705 710 715 720
Pro Arg Leu Pro Arg Gly Glu Leu His Val Gln Gly
725 730

<210> 179
<211> 732
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 179

<400> 179
Met Ala Pro Pro His Gln Phe Gln Ser Lys Pro Ser Asp Val Ile Arg
1 5 10 15
Arg Arg Leu Ser Ser Ala Val Ser Ser Lys Arg Pro Asn Ile Pro Gly
20 25 30
Tyr Thr Ser Leu Thr Pro Met Trp Ala Gly Ile Ala Gly Ala Val Val
35 40 45
Asn Asn Asn Thr Gln Phe Glu Val Ala Ile Ser Ile His Asp Ser Val
50 55 60
Tyr Asn Thr Asp Phe Ala Ser Ser Val Val Pro Tyr Ser Pro Asn Glu
65 70 75 80
Pro Glu Ala Gln Ala Gly Ile Ile Glu Lys His Val Leu Glu Thr Leu
85 90 95
[0334] Arg Lys Phe Ser Thr Glu His Met Cys Lys Phe Leu Gly Ala Gly Val
100 105 110
Thr Val Ile Leu Leu Arg Glu Ala Pro Asn Leu Cys Thr Arg Leu Trp
115 120 125
Leu Asp Met Asp Ile Val Pro Ile Val Phe Asn Ile Lys Pro Phe His
130 135 140
Thr Asp Ser Ile Thr Arg Pro Asn Val Arg His Arg Ile Ser Ser Thr
145 150 155 160
Thr Gly Ser Tyr Val Pro Ser Gly Ala Glu Thr Pro Thr Val Tyr Tyr
165 170 175
Asp Pro Ala Gln Leu Gln Asp Pro Asn Lys Leu Ser Ala Asn Val Gln
180 185 190
Thr Arg Leu Pro Ile Pro Arg Thr Val Asp Glu Gln Ala Asp Ser Ala
195 200 205
Ala Arg Lys Cys Ile Met Tyr Phe Gly Pro Gly Asn Asn Pro Arg Leu
210 215 220
Gln Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala Gly Gly Lys Ile
225 230 235 240
His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr Val Gly Lys Gly
245 250 255
Thr Trp Asn Ser Val Ile Lys Leu Ala Asp Glu Leu Arg Glu Lys Lys
260 265 270
Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly Gly Gly Val Ala
275 280 285
Leu Met Arg His Ala Ile Ile Arg Phe Phe Thr Ile Leu Asp Val Asp
290 295 300
Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val Phe Arg Thr Thr
305 310 315 320
Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Asp Pro Ser Leu Arg

325 330 335
Leu Thr Lys Glu Ala Ala Asp Asn Phe Asp Ser Trp Ile Leu Lys Asn
340 345 350
Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala Pro Gly Gly Val
355 360 365
Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly Leu Ile Pro Leu
370 375 380
Ile Lys Arg Ile Arg Pro Asp Leu Pro Ile Ile Tyr Arg Ser His Ile
385 390 395 400
Glu Ile Arg Ser Asp Leu Val His Val Lys Gly Ser Pro Gln Glu Glu
405 410 415
Val Trp Asn Tyr Leu Trp Asn Asn Ile Gln His Ser Asp Leu Phe Ile
420 425 430
Ser His Pro Val Asn Lys Phe Val Pro Ser Asp Val Pro Leu Glu Lys
435 440 445
Leu Ala Leu Leu Gly Ala Ala Thr Asp Trp Leu Asp Gly Leu Ser Lys
450 455 460
His Leu Asp Ala Trp Asp Ser Gln Tyr Tyr Met Gly Glu Phe Arg Asn
465 470 475 480
Leu Cys Val Lys Glu Lys Met Asn Glu Leu Gly Trp Pro Ala Arg Glu
485 490 495
Tyr Ile Val Gln Ile Ala Arg Phe Asp Pro Ser Lys Gly Ile Pro Asn
500 505 510
Val Ile Asp Ser Tyr Ala Arg Phe Arg Lys Leu Cys Val Asp Lys Val
515 520 525
Met Glu Asp Asp Ile Pro Gln Leu Leu Leu Cys Gly His Gly Ala Val
530 535 540
[0335] Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp Gln Val Leu Gln Leu Ile
545 550 555 560
His Ala Lys Tyr Lys Glu Tyr Ala Pro Asp Ile Val Val Met Arg Cys
565 570 575
Pro Pro Ser Asp Gln Leu Leu Asn Thr Leu Met Ala Asn Ala Lys Phe
580 585 590
Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe Glu Val Lys Val Ser Glu
595 600 605
Ala Leu His Ala Gly Lys Pro Val Ile Ala Cys Arg Thr Gly Gly Ile
610 615 620
Pro Leu Gln Ile Glu His Gly Lys Ser Gly Tyr Leu Cys Glu Pro Gly
625 630 635 640
Asp Asn Ala Ala Val Ala Gln His Met Leu Asp Leu Tyr Thr Asp Glu
645 650 655
Asp Leu Tyr Asp Thr Met Ser Glu Tyr Ala Arg Thr His Val Ser Asp
660 665 670
Glu Val Gly Thr Val Gly Asn Ala Ala Ala Trp Met Tyr Leu Ala Val
675 680 685
Met Tyr Val Ser Arg Gly Val Lys Leu Arg Pro His Gly Ala Trp Ile
690 695 700
Asn Asp Leu Met Arg Thr Glu Met Gly Glu Pro Tyr Arg Pro Gly Glu
705 710 715 720
Pro Arg Leu Pro Arg Gly Glu Leu His Val Gln Gly
725 730

<210> 180
<211> 732
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 180

<400> 180

[0336]

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

Glu Ile Arg Ser Asp Leu Val His Val Lys Gly Ser Pro Gln Glu Glu
405 410 415
Val Trp Asn Tyr Leu Trp Asn Asn Ile Gln His Ser Asp Leu Phe Ile
420 425 430
Ser His Pro Val Asn Lys Phe Val Pro Ser Asp Val Pro Leu Glu Lys
435 440 445
Leu Ala Leu Leu Gly Ala Ala Thr Asp Trp Leu Asp Gly Leu Ser Lys
450 455 460
His Leu Asp Ala Trp Asp Ser Gln Tyr Tyr Met Gly Glu Phe Arg Asn
465 470 475 480
Leu Cys Val Lys Glu Lys Met Asn Glu Leu Gly Trp Pro Ala Arg Glu
485 490 495
Tyr Ile Val Gln Ile Ala Arg Phe Asp Pro Ser Lys Gly Ile Pro Asn
500 505 510
Val Ile Asp Ser Tyr Ala Arg Phe Arg Lys Leu Cys Val Asp Lys Val
515 520 525
Met Glu Asp Asp Ile Pro Gln Leu Leu Leu Cys Gly His Gly Ala Val
530 535 540
Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp Gln Val Leu Gln Leu Ile
545 550 555 560
His Ala Lys Tyr Lys Glu Tyr Ala Pro Asp Ile Val Val Met Arg Cys
565 570 575
Pro Pro Ser Asp Gln Leu Leu Asn Thr Leu Met Ala Asn Ala Lys Phe
580 585 590
Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe Glu Val Lys Val Ser Glu
595 600 605
Ala Leu His Ala Gly Lys Pro Val Ile Ala Cys Arg Thr Gly Gly Ile
610 615 620

[0337]

Pro Leu Gln Ile Glu His Gly Lys Ser Gly Tyr Leu Cys Glu Pro Gly
625 630 635 640
Asp Asn Ala Ala Val Ala Gln His Met Leu Asp Leu Tyr Thr Asp Glu
645 650 655
Asp Leu Tyr Asp Thr Met Ser Glu Tyr Ala Arg Thr His Val Ser Asp
660 665 670
Glu Val Gly Thr Val Gly Asn Ala Ala Ala Trp Met Tyr Leu Ala Val
675 680 685
Met Tyr Val Ser Arg Gly Val Lys Leu Arg Pro His Gly Ala Trp Ile
690 695 700
Asn Asp Leu Met Arg Thr Glu Met Gly Glu Pro Tyr Arg Pro Gly Glu
705 710 715 720
Pro Arg Leu Pro Arg Gly Glu Leu His Val Gln Gly
725 730

<210> 181
<211> 732
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 181

<400> 181
Met Ala Pro Pro His Gln Phe Gln Ser Lys Pro Ser Asp Val Ile Arg
1 5 10 15
Arg Arg Leu Ser Ser Ala Val Ser Ser Lys Arg Pro Asn Ile Pro Gly

[0338]

```
                20                  25                  30
Tyr Thr Ser Leu Thr Pro Met Trp Ala Gly Ile Ala Gly Ala Val Val
            35                  40                  45
Asn Asn Asn Thr Gln Phe Glu Val Ala Ile Ser Ile His Asp Ser Val
        50                  55                  60
Tyr Asn Thr Asp Phe Ala Ser Ser Val Val Pro Tyr Ser Pro Asn Glu
65                  70                  75                  80
Pro Glu Ala Gln Ala Gly Ile Ile Glu Lys His Val Leu Glu Thr Leu
                85                  90                  95
Arg Lys Phe Ser Thr Glu His Met Cys Lys Phe Leu Gly Ala Gly Val
            100                 105                 110
Thr Val Ile Leu Leu Arg Glu Ala Pro Asn Leu Cys Thr Arg Leu Trp
        115                 120                 125
Leu Asp Met Asp Ile Val Pro Ile Val Phe Asn Ile Lys Pro Phe His
    130                 135                 140
Thr Asp Ser Ile Thr Arg Pro Asn Val Arg His Arg Ile Ser Ser Thr
145                 150                 155                 160
Thr Gly Ser Tyr Val Pro Ser Gly Ala Glu Thr Pro Thr Val Tyr Tyr
                165                 170                 175
Asp Pro Ala Gln Leu Gln Asp Pro Asn Lys Leu Ser Ala Asn Val Gln
            180                 185                 190
Thr Arg Leu Pro Ile Pro Arg Thr Val Asp Glu Gln Ala Asp Ser Ala
        195                 200                 205
Ala Arg Lys Cys Ile Met Tyr Phe Gly Pro Gly Asn Asn Pro Arg Leu
    210                 215                 220
Gln Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala Gly Gly Lys Ile
225                 230                 235                 240
His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr Val Gly Lys Gly
                245                 250                 255
Thr Trp Asn Ser Val Ile Lys Leu Ala Asp Glu Leu Arg Glu Lys Lys
            260                 265                 270
Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly Gly Gly Val Ala
        275                 280                 285
Leu Met Arg His Ala Ile Ile Arg Phe Phe Thr Ala Leu Asp Val Asp
    290                 295                 300
Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val Phe Arg Thr Thr
305                 310                 315                 320
Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Asp Pro Ser Leu Arg
                325                 330                 335
Leu Thr Lys Glu Ala Ala Asp Asn Tyr Asp Ser Trp Ile Leu Lys Asn
            340                 345                 350
Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala Pro Gly Gly Val
        355                 360                 365
Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly Leu Ile Pro Leu
    370                 375                 380
Ile Lys Arg Ile Arg Pro Asp Leu Pro Ile Ile Tyr Arg Ser His Ile
385                 390                 395                 400
Glu Ile Arg Ser Asp Leu Val His Val Lys Gly Ser Pro Gln Glu Glu
                405                 410                 415
Val Trp Asn Tyr Leu Trp Asn Asn Ile Gln His Ser Asp Leu Phe Ile
            420                 425                 430
Ser His Pro Val Asn Lys Phe Val Pro Ser Asp Val Pro Leu Glu Lys
        435                 440                 445
Leu Ala Leu Leu Gly Ala Ala Thr Asp Trp Leu Asp Gly Leu Ser Lys
    450                 455                 460
His Leu Asp Ala Trp Asp Ser Gln Tyr Tyr Met Gly Glu Phe Arg Asn
```

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

[0339]

<210> 182
<211> 732
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 182

<400> 182

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

Arg Lys Phe Ser Thr Glu His Met Cys Lys Phe Leu Gly Ala Gly Val
100 105 110
Thr Val Ile Leu Leu Arg Glu Ala Pro Asn Leu Cys Thr Arg Leu Trp
115 120 125
Leu Asp Met Asp Ile Val Pro Ile Val Phe Asn Ile Lys Pro Phe His
130 135 140
Thr Asp Ser Ile Thr Arg Pro Asn Val Arg His Arg Ile Ser Ser Thr
145 150 155 160
Thr Gly Ser Tyr Val Pro Ser Gly Ala Glu Thr Pro Thr Val Tyr Tyr
165 170 175
Asp Pro Ala Gln Leu Gln Asp Pro Asn Lys Leu Ser Ala Asn Val Gln
180 185 190
Thr Arg Leu Pro Ile Pro Arg Thr Val Asp Glu Gln Ala Asp Ser Ala
195 200 205
Ala Arg Lys Cys Ile Met Tyr Phe Gly Pro Gly Asn Asn Pro Arg Leu
210 215 220
Gln Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala Gly Gly Lys Ile
225 230 235 240
His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr Val Gly Lys Gly
245 250 255
Thr Trp Asn Ser Val Ile Lys Leu Ala Asp Glu Leu Arg Glu Lys Lys
260 265 270
Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly Gly Gly Val Ala
275 280 285
Leu Met Arg His Ala Ile Ile Arg Phe Phe Thr Ala Leu Asp Val Asp
290 295 300
Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val Phe Arg Thr Thr
305 310 315 320
[0340] Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Asp Pro Ser Leu Arg
325 330 335
Leu Thr Lys Glu Ala Ala Asp Asn Phe Asp Ser Trp Ile Leu Lys Asn
340 345 350
Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala Pro Gly Gly Val
355 360 365
Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly Leu Ile Pro Leu
370 375 380
Ile Lys Arg Ile Arg Pro Asp Leu Pro Ile Ile Tyr Arg Ser His Ile
385 390 395 400
Glu Ile Arg Ser Asp Leu Val His Val Lys Gly Ser Pro Gln Glu Glu
405 410 415
Val Trp Asn Tyr Leu Trp Asn Asn Ile Gln His Ser Asp Leu Phe Ile
420 425 430
Ser His Pro Val Asn Lys Phe Val Pro Ser Asp Val Pro Leu Glu Lys
435 440 445
Leu Ala Leu Leu Gly Ala Ala Thr Asp Trp Leu Asp Gly Leu Ser Lys
450 455 460
His Leu Asp Ala Trp Asp Ser Gln Tyr Tyr Met Gly Glu Phe Arg Asn
465 470 475 480
Leu Cys Ala Lys Glu Lys Met Asn Glu Leu Gly Trp Pro Ala Arg Glu
485 490 495
Tyr Ile Val Gln Ile Ala Arg Phe Asp Pro Ser Lys Gly Ile Pro Asn
500 505 510
Val Ile Asp Ser Tyr Ala Arg Phe Arg Lys Leu Cys Val Asp Lys Val
515 520 525
Met Glu Asp Asp Ile Pro Gln Leu Leu Leu Cys Gly His Gly Ala Val
530 535 540

Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp Gln Val Leu Gln Leu Ile
545 550 555 560
His Ala Lys Tyr Lys Glu Tyr Ala Pro Asp Ile Val Val Met Arg Cys
565 570 575
Pro Pro Ser Asp Gln Leu Leu Asn Thr Leu Met Ala Asn Ala Lys Phe
580 585 590
Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe Glu Val Lys Val Ser Glu
595 600 605
Ala Leu His Ala Gly Lys Pro Val Ile Ala Cys Arg Thr Gly Gly Ile
610 615 620
Pro Leu Gln Ile Glu His Gly Lys Ser Gly Tyr Leu Cys Glu Pro Gly
625 630 635 640
Asp Asn Ala Ala Val Ala Gln His Met Leu Asp Leu Tyr Thr Asp Glu
645 650 655
Asp Leu Tyr Asp Thr Met Ser Glu Tyr Ala Arg Thr His Val Ser Asp
660 665 670
Glu Val Gly Thr Val Gly Asn Ala Ala Ala Trp Met Tyr Leu Ala Val
675 680 685
Met Tyr Val Ser Arg Gly Val Lys Leu Arg Pro His Gly Ala Trp Ile
690 695 700
Asn Asp Leu Met Arg Thr Glu Met Gly Glu Pro Tyr Arg Pro Gly Glu
705 710 715 720
Pro Arg Leu Pro Arg Gly Glu Leu His Val Gln Gly
725 730

<210> 183
<211> 732
<212> PRT
[0341] <213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 183

<400> 183
Met Ala Pro Pro His Gln Phe Gln Ser Lys Pro Ser Asp Val Ile Arg
1 5 10 15
Arg Arg Leu Ser Ser Ala Val Ser Ser Lys Arg Pro Asn Ile Pro Gly
20 25 30
Tyr Thr Ser Leu Thr Pro Met Trp Ala Gly Ile Ala Gly Ala Val Val
35 40 45
Asn Asn Asn Thr Gln Phe Glu Val Ala Ile Ser Ile His Asp Ser Val
50 55 60
Tyr Asn Thr Asp Phe Ala Ser Ser Val Val Pro Tyr Ser Pro Asn Glu
65 70 75 80
Pro Glu Ala Gln Ala Gly Ile Ile Glu Lys His Val Leu Glu Thr Leu
85 90 95
Arg Lys Phe Ser Thr Glu His Met Cys Lys Phe Leu Gly Ala Gly Val
100 105 110
Thr Val Ile Leu Leu Arg Glu Ala Pro Asn Leu Cys Thr Arg Leu Trp
115 120 125
Leu Asp Met Asp Ile Val Pro Ile Val Phe Asn Ile Lys Pro Phe His
130 135 140
Thr Asp Ser Ile Thr Arg Pro Asn Val Arg His Arg Ile Ser Ser Thr
145 150 155 160
Thr Gly Ser Tyr Val Pro Ser Gly Ala Glu Thr Pro Thr Val Tyr Tyr

[0342]

```
                    165                 170                 175
Asp Pro Ala Gln Leu Gln Asp Pro Asn Lys Leu Ser Ala Asn Val Gln
                180                 185                 190
Thr Arg Leu Pro Ile Pro Arg Thr Val Asp Glu Gln Ala Asp Ser Ala
            195                 200                 205
Ala Arg Lys Cys Ile Met Tyr Phe Gly Pro Gly Asn Asn Pro Arg Leu
        210                 215                 220
Gln Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala Gly Gly Lys Ile
225                 230                 235                 240
His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr Val Gly Lys Gly
                245                 250                 255
Thr Trp Asn Ser Val Ile Lys Leu Ala Asp Glu Leu Arg Glu Lys Lys
            260                 265                 270
Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly Gly Gly Val Ala
        275                 280                 285
Leu Met Arg His Ala Ile Ile Arg Phe Phe Thr Ala Leu Asp Val Asp
    290                 295                 300
Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val Phe Arg Thr Thr
305                 310                 315                 320
Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Asp Pro Ser Leu Arg
                325                 330                 335
Leu Thr Lys Glu Ala Ala Asp Asn Phe Asp Ser Trp Ile Leu Lys Asn
            340                 345                 350
Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala Pro Gly Gly Val
        355                 360                 365
Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly Leu Ile Pro Leu
    370                 375                 380
Ile Lys Arg Ile Arg Pro Asp Leu Pro Ile Ile Tyr Arg Ser His Ile
385                 390                 395                 400
Glu Ile Arg Ser Asp Leu Val His Val Lys Gly Ser Pro Gln Glu Glu
                405                 410                 415
Val Trp Asn Tyr Leu Trp Asn Asn Ile Gln His Ser Asp Leu Phe Ile
            420                 425                 430
Ser His Pro Val Asn Lys Phe Val Pro Ser Asp Val Pro Leu Glu Lys
        435                 440                 445
Leu Ala Leu Leu Gly Ala Ala Thr Asp Trp Leu Asp Gly Leu Ser Lys
    450                 455                 460
His Leu Asp Ala Trp Asp Ser Gln Tyr Tyr Met Gly Glu Phe Arg Asn
465                 470                 475                 480
Leu Cys Val Lys Glu Lys Met Asn Glu Leu Gly Trp Pro Ala Arg Glu
                485                 490                 495
Tyr Ile Val Gln Ile Ala Arg Phe Asp Pro Ser Lys Gly Ile Pro Asn
            500                 505                 510
Val Ile Asp Ser Tyr Ala Arg Phe Arg Lys Leu Cys Val Asp Lys Val
        515                 520                 525
Met Glu Asp Asp Ile Pro Gln Leu Leu Leu Cys Gly His Gly Ala Ile
    530                 535                 540
Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp Gln Val Leu Gln Leu Ile
545                 550                 555                 560
His Ala Lys Tyr Lys Glu Tyr Ala Pro Asp Ile Val Val Met Arg Cys
                565                 570                 575
Pro Pro Ser Asp Gln Leu Leu Asn Thr Leu Met Ala Asn Ala Lys Phe
            580                 585                 590
Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe Glu Val Lys Val Ser Glu
        595                 600                 605
Ala Leu His Ala Gly Lys Pro Val Ile Ala Cys Arg Thr Gly Gly Ile
```

610 615 620
Pro Leu Gln Ile Glu His Gly Lys Ser Gly Tyr Leu Cys Glu Pro Gly
625 630 635 640
Asp Asn Ala Ala Val Ala Gln His Met Leu Asp Leu Tyr Thr Asp Glu
645 650 655
Asp Leu Tyr Asp Thr Met Ser Glu Tyr Ala Arg Thr His Val Ser Asp
660 665 670
Glu Val Gly Thr Val Gly Asn Ala Ala Ala Trp Met Tyr Leu Ala Val
675 680 685
Met Tyr Val Ser Arg Gly Val Lys Leu Arg Pro His Gly Ala Trp Ile
690 695 700
Asn Asp Leu Met Arg Thr Glu Met Gly Glu Pro Tyr Arg Pro Gly Glu
705 710 715 720
Pro Arg Leu Pro Arg Gly Glu Leu His Val Gln Gly
725 730

<210> 184
<211> 732
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 184

<400> 184
Met Ala Pro Pro His Gln Phe Gln Ser Lys Pro Ser Asp Val Ile Arg
1 5 10 15
[0343] Arg Arg Leu Ser Ser Ala Val Ser Ser Lys Arg Pro Asn Ile Pro Gly
20 25 30
Tyr Thr Ser Leu Thr Pro Met Trp Ala Gly Ile Ala Gly Ala Val Val
35 40 45
Asn Asn Asn Thr Gln Phe Glu Val Ala Ile Ser Ile His Asp Ser Val
50 55 60
Tyr Asn Thr Asp Phe Ala Ser Ser Val Val Pro Tyr Ser Pro Asn Glu
65 70 75 80
Pro Glu Ala Gln Ala Gly Ile Ile Glu Lys His Val Leu Glu Thr Leu
85 90 95
Arg Lys Phe Ser Thr Glu His Met Cys Lys Phe Leu Gly Ala Gly Val
100 105 110
Thr Val Ile Leu Leu Arg Glu Ala Pro Asn Leu Cys Thr Arg Leu Trp
115 120 125
Leu Asp Met Asp Ile Val Pro Ile Val Phe Asn Ile Lys Pro Phe His
130 135 140
Thr Asp Ser Ile Thr Arg Pro Asn Val Arg His Arg Ile Ser Ser Thr
145 150 155 160
Thr Gly Ser Tyr Val Pro Ser Gly Ala Glu Thr Pro Thr Val Tyr Tyr
165 170 175
Asp Pro Ala Gln Leu Gln Asp Pro Asn Lys Leu Ser Ala Asn Val Gln
180 185 190
Thr Arg Leu Pro Ile Pro Arg Thr Val Asp Glu Gln Ala Asp Ser Ala
195 200 205
Ala Arg Lys Cys Ile Met Tyr Phe Gly Pro Gly Asn Asn Pro Arg Leu
210 215 220
Gln Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala Gly Gly Lys Ile
225 230 235 240

His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr Val Gly Lys Gly
245 250 255
Thr Trp Asn Ser Val Ile Lys Leu Ala Asp Glu Leu Arg Glu Lys Lys
260 265 270
Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly Gly Gly Val Ala
275 280 285
Leu Met Arg His Ala Ile Ile Arg Phe Phe Thr Ala Leu Asp Val Asp
290 295 300
Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val Phe Arg Thr Thr
305 310 315 320
Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Asp Pro Ser Leu Arg
325 330 335
Leu Thr Lys Glu Ala Ala Asp Asn Phe Asp Ser Trp Ile Leu Lys Asn
340 345 350
Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala Pro Gly Gly Val
355 360 365
Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly Leu Ile Pro Leu
370 375 380
Ile Lys Arg Ile Arg Pro Asp Leu Pro Ile Ile Tyr Arg Ser His Ile
385 390 395 400
Glu Ile Arg Ser Asp Leu Val His Val Lys Gly Ser Pro Gln Glu Glu
405 410 415
Val Trp Asn Tyr Leu Trp Asn Asn Ile Gln His Ser Asp Leu Phe Ile
420 425 430
Ser His Pro Val Asn Lys Phe Val Pro Ser Asp Val Pro Leu Glu Lys
435 440 445
Leu Ala Leu Leu Gly Ala Ala Thr Asp Trp Leu Asp Gly Leu Ser Lys
450 455 460

[0344]

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

Met Tyr Val Ser Arg Gly Val Lys Leu Arg Pro His Gly Ala Trp Ile
690 695 700
Asn Asp Leu Met Arg Thr Glu Met Gly Glu Pro Tyr Arg Pro Gly Glu
705 710 715 720
Pro Arg Leu Pro Arg Gly Glu Leu His Val Gln Gly
725 730

<210> 185
<211> 732
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 185

<400> 185
Met Ala Pro Pro His Gln Phe Gln Ser Lys Pro Ser Asp Val Ile Arg
1 5 10 15
Arg Arg Leu Ser Ser Ala Val Ser Ser Lys Arg Pro Asn Ile Pro Gly
20 25 30
Tyr Thr Ser Leu Thr Pro Met Trp Ala Gly Ile Ala Gly Ala Val Val
35 40 45
Asn Asn Asn Thr Gln Phe Glu Val Ala Ile Ser Ile His Asp Ser Val
50 55 60
Tyr Asn Thr Asp Phe Ala Ser Ser Val Val Pro Tyr Ser Pro Asn Glu
65 70 75 80
[0345] Pro Glu Ala Gln Ala Gly Ile Ile Glu Lys His Val Leu Glu Thr Leu
85 90 95
Arg Lys Phe Ser Thr Glu His Met Cys Lys Phe Leu Gly Ala Gly Val
100 105 110
Thr Val Ile Leu Leu Arg Glu Ala Pro Asn Leu Cys Thr Arg Leu Trp
115 120 125
Leu Asp Met Asp Ile Val Pro Ile Val Phe Asn Ile Lys Pro Phe His
130 135 140
Thr Asp Ser Ile Thr Arg Pro Asn Val Arg His Arg Ile Ser Ser Thr
145 150 155 160
Thr Gly Ser Tyr Val Pro Ser Gly Ala Glu Thr Pro Thr Val Tyr Tyr
165 170 175
Asp Pro Ala Gln Leu Gln Asp Pro Asn Lys Leu Ser Ala Asn Val Gln
180 185 190
Thr Arg Leu Pro Ile Pro Arg Thr Val Asp Glu Gln Ala Asp Ser Ala
195 200 205
Ala Arg Lys Cys Ile Met Tyr Phe Gly Pro Gly Asn Asn Pro Arg Leu
210 215 220
Gln Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala Gly Gly Lys Ile
225 230 235 240
His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr Val Gly Lys Gly
245 250 255
Thr Trp Asn Ser Val Ile Lys Leu Ala Asp Glu Leu Arg Glu Lys Lys
260 265 270
Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly Gly Gly Val Ala
275 280 285
Leu Met Arg His Ala Ile Ile Arg Phe Phe Thr Ala Leu Asp Val Asp
290 295 300
Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val Phe Arg Thr Thr

305 310 315 320
Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Asp Pro Ser Leu Arg
325 330 335
Leu Thr Lys Glu Ala Ala Asp Asn Phe Asp Ser Trp Ile Leu Lys Asn
340 345 350
Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala Pro Gly Gly Val
355 360 365
Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly Leu Ile Pro Leu
370 375 380
Ile Lys Arg Ile Arg Pro Asp Leu Pro Ile Ile Tyr Arg Ser His Ile
385 390 395 400
Glu Ile Arg Ser Asp Leu Val His Val Lys Gly Ser Pro Gln Glu Glu
405 410 415
Val Trp Asn Tyr Leu Trp Asn Asn Ile Gln His Ser Asp Leu Phe Ile
420 425 430
Ser His Pro Val Asn Lys Phe Val Pro Ser Asp Val Pro Leu Glu Lys
435 440 445
Leu Ala Leu Leu Gly Ala Ala Thr Asp Trp Leu Asp Gly Leu Ser Lys
450 455 460
His Leu Asp Ala Trp Asp Ser Gln Tyr Tyr Met Gly Glu Phe Arg Asn
465 470 475 480
Leu Cys Ala Lys Glu Lys Met Asn Glu Leu Gly Trp Pro Ala Arg Glu
485 490 495
Tyr Ile Val Gln Ile Ala Arg Phe Asp Pro Ser Lys Gly Ile Pro Asn
500 505 510
Val Ile Asp Ser Tyr Ala Arg Phe Arg Lys Leu Cys Val Asp Lys Val
515 520 525

[0346]

Met Glu Asp Asp Ile Pro Gln Leu Leu Leu Cys Gly His Gly Ala Val
530 535 540
Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp Gln Val Leu Glu Leu Ile
545 550 555 560
His Ala Lys Tyr Lys Glu Tyr Ala Pro Asp Ile Val Val Met Arg Cys
565 570 575
Pro Pro Ser Asp Gln Leu Leu Asn Thr Leu Met Ala Asn Ala Lys Phe
580 585 590
Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe Glu Val Lys Val Ser Glu
595 600 605
Ala Leu His Ala Gly Lys Pro Val Ile Ala Cys Arg Thr Gly Gly Ile
610 615 620
Pro Leu Gln Ile Glu His Gly Lys Ser Gly Tyr Leu Cys Glu Pro Gly
625 630 635 640
Asp Asn Ala Ala Val Ala Gln His Met Leu Asp Leu Tyr Thr Asp Glu
645 650 655
Asp Leu Tyr Asp Thr Met Ser Glu Tyr Ala Arg Thr His Val Ser Asp
660 665 670
Glu Val Gly Thr Val Gly Asn Ala Ala Ala Trp Met Tyr Leu Ala Val
675 680 685
Met Tyr Val Ser Arg Gly Val Lys Leu Arg Pro His Gly Ala Trp Ile
690 695 700
Asn Asp Leu Met Arg Thr Glu Met Gly Glu Pro Tyr Arg Pro Gly Glu
705 710 715 720
Pro Arg Leu Pro Arg Gly Glu Leu His Val Gln Gly
725 730

<210> 186
<211> 732

<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 186

<400> 186

[0347]

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

Ile Lys Arg Ile Arg Pro Asp Leu Pro Ile Ile Tyr Arg Ser His Ile
385 390 395 400
Glu Ile Arg Ser Asp Leu Val His Val Lys Gly Ser Pro Gln Glu Glu
405 410 415
Val Trp Asn Tyr Leu Trp Asn Asn Ile Gln His Ser Asp Leu Phe Ile
420 425 430
Ser His Pro Val Asn Lys Phe Val Pro Ser Asp Val Pro Leu Glu Lys
435 440 445
Leu Ala Leu Leu Gly Ala Ala Thr Asp Trp Leu Asp Gly Leu Ser Lys
450 455 460
His Leu Asp Ala Trp Asp Ser Gln Tyr Tyr Met Gly Glu Phe Arg Asn
465 470 475 480
Leu Cys Val Lys Glu Lys Met Asn Glu Leu Gly Trp Pro Ala Arg Glu
485 490 495
Tyr Ile Val Gln Ile Ala Arg Phe Asp Pro Ser Lys Gly Ile Pro Asn
500 505 510
Val Ile Asp Ser Tyr Ala Arg Phe Arg Lys Leu Cys Val Asp Lys Val
515 520 525
Met Glu Asp Asp Ile Pro Gln Leu Leu Leu Cys Gly His Gly Ala Ile
530 535 540
Asp Asp Pro Asp Ala Thr Ile Ile Tyr Asp Gln Val Leu Gln Leu Ile
545 550 555 560
His Ala Lys Tyr Lys Glu Tyr Ala Pro Asp Ile Val Val Met Arg Cys
565 570 575
Pro Pro Ser Asp Gln Leu Leu Asn Thr Leu Met Ala Asn Ala Lys Phe
580 585 590
Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe Glu Val Lys Val Ser Glu
595 600 605

[0348]

Ala Leu His Ala Gly Lys Pro Val Ile Ala Cys Arg Thr Gly Gly Ile
610 615 620
Pro Leu Gln Ile Glu His Gly Lys Ser Gly Tyr Leu Cys Glu Pro Gly
625 630 635 640
Asp Asn Ala Ala Val Ala Gln His Met Leu Asp Leu Tyr Thr Asp Glu
645 650 655
Asp Leu Tyr Asp Thr Met Ser Glu Tyr Ala Arg Thr His Val Ser Asp
660 665 670
Glu Val Gly Thr Val Gly Asn Ala Ala Ala Trp Met Tyr Leu Ala Val
675 680 685
Met Tyr Val Ser Arg Gly Val Lys Leu Arg Pro His Gly Ala Trp Ile
690 695 700
Asn Asp Leu Met Arg Thr Glu Met Gly Glu Pro Tyr Arg Pro Gly Glu
705 710 715 720
Pro Arg Leu Pro Arg Gly Glu Leu His Val Gln Gly
725 730

<210> 187
<211> 732
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 187

<400> 187
Met Ala Pro Pro His Gln Phe Gln Ser Lys Pro Ser Asp Val Ile Arg

[0349]

```
1               5                   10                  15
Arg Arg Leu Ser Ser Ala Val Ser Ser Lys Arg Pro Asn Ile Pro Gly
            20                  25                  30
Tyr Thr Ser Leu Thr Pro Met Trp Ala Gly Ile Ala Gly Ala Val Val
        35                  40                  45
Asn Asn Asn Thr Gln Phe Glu Val Ala Ile Ser Ile His Asp Ser Val
    50                  55                  60
Tyr Asn Thr Asp Phe Ala Ser Ser Val Val Pro Tyr Ser Pro Asn Glu
65                  70                  75                  80
Pro Glu Ala Gln Ala Gly Ile Ile Glu Lys His Val Leu Glu Thr Leu
                85                  90                  95
Arg Lys Phe Ser Thr Glu His Met Cys Lys Phe Leu Gly Ala Gly Val
            100                 105                 110
Thr Val Ile Leu Leu Arg Glu Ala Pro Asn Leu Cys Thr Arg Leu Trp
        115                 120                 125
Leu Asp Met Asp Ile Val Pro Ile Val Phe Asn Ile Lys Pro Phe His
    130                 135                 140
Thr Asp Ser Ile Thr Arg Pro Asn Val Arg His Arg Ile Ser Ser Thr
145                 150                 155                 160
Thr Gly Ser Tyr Val Pro Ser Gly Ala Glu Thr Pro Thr Val Tyr Tyr
                165                 170                 175
Asp Pro Ala Gln Leu Gln Asp Pro Asn Lys Leu Ser Ala Asn Val Gln
            180                 185                 190
Thr Arg Leu Pro Ile Pro Arg Thr Val Asp Glu Gln Ala Asp Ser Ala
        195                 200                 205
Ala Arg Lys Cys Ile Met Tyr Phe Gly Pro Gly Asn Asn Pro Arg Leu
    210                 215                 220
Gln Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala Gly Gly Lys Ile
225                 230                 235                 240
His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr Val Gly Lys Gly
                245                 250                 255
Thr Trp Asn Ser Val Ile Lys Leu Ala Asp Glu Leu Arg Glu Lys Lys
            260                 265                 270
Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly Gly Gly Val Ala
        275                 280                 285
Leu Met Arg His Ala Ile Ile Arg Phe Phe Thr Ala Leu Asp Val Asp
    290                 295                 300
Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val Phe Arg Thr Thr
305                 310                 315                 320
Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Asp Pro Ser Leu Arg
                325                 330                 335
Leu Thr Lys Glu Ala Ala Asp Asn Phe Asp Ser Trp Ile Leu Lys Asn
            340                 345                 350
Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala Pro Gly Gly Val
        355                 360                 365
Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly Leu Ile Pro Leu
    370                 375                 380
Ile Lys Arg Ile Arg Pro Asp Leu Pro Ile Ile Tyr Arg Ser His Ile
385                 390                 395                 400
Glu Ile Arg Ser Asp Leu Val His Val Lys Gly Ser Pro Gln Glu Glu
                405                 410                 415
Val Trp Asn Tyr Leu Trp Asn Asn Ile Gln His Ser Asp Leu Phe Ile
            420                 425                 430
Ser His Pro Val Asn Lys Phe Val Pro Ser Asp Val Pro Leu Glu Lys
        435                 440                 445
Leu Ala Leu Leu Gly Ala Ala Thr Asp Trp Leu Asp Gly Leu Ser Lys
```

[0350]

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

<210> 188
<211> 732
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 188

<400> 188

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

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

[0351]

Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val Phe Arg Thr Thr
305 310 315 320
Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Asp Pro Ser Leu Arg
325 330 335
Leu Thr Lys Glu Ala Ala Asp Asn Phe Asp Ser Trp Ile Leu Lys Asn
340 345 350
Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala Pro Gly Gly Val
355 360 365
Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly Leu Ile Pro Leu
370 375 380
Ile Lys Arg Ile Arg Pro Asp Leu Pro Ile Ile Tyr Arg Ser His Ile
385 390 395 400
Glu Ile Arg Ser Asp Leu Val His Val Lys Gly Ser Pro Gln Glu Glu
405 410 415
Val Trp Asn Tyr Leu Trp Asn Asn Ile Gln His Ser Asp Leu Phe Ile
420 425 430
Ser His Pro Val Asn Lys Phe Val Pro Ser Asp Val Pro Leu Glu Lys
435 440 445
Leu Ala Leu Leu Gly Ala Ala Thr Asp Trp Leu Asp Gly Leu Ser Lys
450 455 460
His Leu Asp Ala Trp Asp Ser Gln Tyr Tyr Met Gly Glu Phe Arg Asn
465 470 475 480
Leu Cys Val Lys Glu Lys Met Asn Glu Leu Gly Trp Pro Ala Arg Glu
485 490 495
Tyr Ile Val Gln Ile Ala Arg Phe Asp Pro Ser Lys Gly Ile Pro Asn
500 505 510
Val Ile Asp Ser Tyr Ala Arg Phe Arg Lys Leu Cys Val Asp Lys Val
515 520 525

Met Glu Asp Asp Ile Pro Gln Leu Leu Leu Cys Gly His Gly Ala Val
530 535 540
Asp Asp Pro Asp Ala Thr Ile Ile Tyr Asp Gln Val Leu Glu Leu Ile
545 550 555 560
His Ala Lys Tyr Lys Glu Tyr Ala Pro Asp Ile Val Val Met Arg Cys
565 570 575
Pro Pro Ser Asp Gln Leu Leu Asn Thr Leu Met Ala Asn Ala Lys Phe
580 585 590
Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe Glu Val Lys Val Ser Glu
595 600 605
Ala Leu His Ala Gly Lys Pro Val Ile Ala Cys Arg Thr Gly Gly Ile
610 615 620
Pro Leu Gln Ile Glu His Gly Lys Ser Gly Tyr Leu Cys Glu Pro Gly
625 630 635 640
Asp Asn Ala Ala Val Ala Gln His Met Leu Asp Leu Tyr Thr Asp Glu
645 650 655
Asp Leu Tyr Asp Thr Met Ser Glu Tyr Ala Arg Thr His Val Ser Asp
660 665 670
Glu Val Gly Thr Val Gly Asn Ala Ala Ala Trp Met Tyr Leu Ala Val
675 680 685
Met Tyr Val Ser Arg Gly Val Lys Leu Arg Pro His Gly Ala Trp Ile
690 695 700
Asn Asp Leu Met Arg Thr Glu Met Gly Glu Pro Tyr Arg Pro Gly Glu
705 710 715 720
Pro Arg Leu Pro Arg Gly Glu Leu His Val Gln Gly
725 730

[0352] <210> 189
<211> 732
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> SEQ ID NO: 189

<400> 189
Met Ala Pro Pro His Gln Phe Gln Ser Lys Pro Ser Asp Val Ile Arg
1 5 10 15
Arg Arg Leu Ser Ser Ala Val Ser Ser Lys Arg Pro Asn Ile Pro Gly
20 25 30
Tyr Thr Ser Leu Thr Pro Met Trp Ala Gly Ile Ala Gly Ala Val Val
35 40 45
Asn Asn Asn Thr Gln Phe Glu Val Ala Ile Ser Ile His Asp Ser Val
50 55 60
Tyr Asn Thr Asp Phe Ala Ser Ser Val Val Pro Tyr Ser Pro Asn Glu
65 70 75 80
Pro Glu Ala Gln Ala Gly Ile Ile Glu Lys His Val Leu Glu Thr Leu
85 90 95
Arg Lys Phe Ser Thr Glu His Met Cys Lys Phe Leu Gly Ala Gly Val
100 105 110
Thr Val Ile Leu Leu Arg Glu Ala Pro Asn Leu Cys Thr Arg Leu Trp
115 120 125
Leu Asp Met Asp Ile Val Pro Ile Val Phe Asn Ile Lys Pro Phe His
130 135 140
Thr Asp Ser Ile Thr Arg Pro Asn Val Arg His Arg Ile Ser Ser Thr

145 150 155 160
Thr Gly Ser Tyr Val Pro Ser Gly Ala Glu Thr Pro Thr Val Tyr Tyr
165 170 175
Asp Pro Ala Gln Leu Gln Asp Pro Asn Lys Leu Ser Ala Asn Val Gln
180 185 190
Thr Arg Leu Pro Ile Pro Arg Thr Val Asp Glu Gln Ala Asp Ser Ala
195 200 205
Ala Arg Lys Cys Ile Met Tyr Phe Gly Pro Gly Asn Asn Pro Arg Leu
210 215 220
Gln Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala Gly Gly Lys Ile
225 230 235 240
His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr Val Gly Lys Gly
245 250 255
Thr Trp Asn Ser Val Ile Lys Leu Ala Asp Glu Leu Arg Glu Lys Lys
260 265 270
Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly Gly Gly Val Ala
275 280 285
Leu Met Arg His Ala Ile Ile Arg Phe Phe Thr Ala Leu Asp Val Asp
290 295 300
Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val Phe Arg Thr Thr
305 310 315 320
Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Asp Pro Ser Leu Arg
325 330 335
Leu Thr Lys Glu Ala Ala Asp Asn Phe Asp Ser Trp Ile Leu Lys Asn
340 345 350
Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala Pro Gly Gly Val
355 360 365
[0353] Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly Leu Ile Pro Leu
370 375 380
Ile Lys Arg Ile Arg Pro Asp Leu Pro Ile Ile Tyr Arg Ser His Ile
385 390 395 400
Glu Ile Arg Ser Asp Leu Val His Val Lys Gly Ser Pro Gln Glu Glu
405 410 415
Val Trp Asn Tyr Leu Trp Asn Asn Ile Gln His Ser Asp Leu Phe Ile
420 425 430
Ser His Pro Val Asn Lys Phe Val Pro Ser Asp Val Pro Leu Glu Lys
435 440 445
Leu Ala Leu Leu Gly Ala Ala Thr Asp Trp Leu Asp Gly Leu Ser Lys
450 455 460
His Leu Asp Ala Trp Asp Ser Gln Tyr Tyr Met Gly Glu Phe Arg Asn
465 470 475 480
Leu Cys Ala Lys Glu Lys Met Asn Glu Leu Gly Trp Pro Ala Arg Glu
485 490 495
Tyr Ile Val Gln Ile Ala Arg Phe Asp Pro Ser Lys Gly Ile Pro Asn
500 505 510
Val Ile Asp Ser Tyr Ala Arg Phe Arg Lys Leu Cys Val Asp Lys Val
515 520 525
Met Glu Asp Asp Ile Pro Gln Leu Leu Leu Cys Gly His Gly Ala Ile
530 535 540
Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp Gln Val Leu Glu Leu Ile
545 550 555 560
His Ala Lys Tyr Lys Glu Tyr Ala Pro Asp Ile Val Val Met Arg Cys
565 570 575
Pro Pro Ser Asp Gln Leu Leu Asn Thr Leu Met Ala Asn Ala Lys Phe
580 585 590
Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe Glu Val Lys Val Ser Glu

595 600 605
Ala Leu His Ala Gly Lys Pro Val Ile Ala Cys Arg Thr Gly Gly Ile
610 615 620
Pro Leu Gln Ile Glu His Gly Lys Ser Gly Tyr Leu Cys Glu Pro Gly
625 630 635 640
Asp Asn Ala Ala Val Ala Gln His Met Leu Asp Leu Tyr Thr Asp Glu
645 650 655
Asp Leu Tyr Asp Thr Met Ser Glu Tyr Ala Arg Thr His Val Ser Asp
660 665 670
Glu Val Gly Thr Val Gly Asn Ala Ala Ala Trp Met Tyr Leu Ala Val
675 680 685
Met Tyr Val Ser Arg Gly Val Lys Leu Arg Pro His Gly Ala Trp Ile
690 695 700
Asn Asp Leu Met Arg Thr Glu Met Gly Glu Pro Tyr Arg Pro Gly Glu
705 710 715 720
Pro Arg Leu Pro Arg Gly Glu Leu His Val Gln Gly
725 730

<210> 190
<211> 737
<212> PRT
<213> 人工序列(Artificial Sequence)

<220>
<223> >SEQ ID NO:190

[0354] <400> 190
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Ile Gly Ala Gly Val Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220

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

[0355]

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

Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 191
<211> 737
<212> PRT
<213> 裂褶菌(Schizophyllum commune) H4-8

<220>
<223> >XP_003035156.1 糖基转移酶家族 4 蛋白质 [裂褶菌 H4-8] >EFJ00254.1 糖基转移酶家族 4 蛋白质 [裂褶菌 H4-8]

<400> 191
Met Ser Pro Pro His Gly Phe Ser Ser Lys Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Ser
20 25 30
[0356] Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Leu Gly Ala Gly Ile Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu

[0357]

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                260                 265                 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
        275                 280                 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ala
    290                 295                 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305                 310                 315                 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
                325                 330                 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
            340                 345                 350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
        355                 360                 365
Pro Gly Gly Val Asp Val Ala Phe Ile Asp Asp Pro Gln Met Pro Gly
    370                 375                 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385                 390                 395                 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
                405                 410                 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
            420                 425                 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
        435                 440                 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
    450                 455                 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465                 470                 475                 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
                485                 490                 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
            500                 505                 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
        515                 520                 525
Asn Glu Ala Gly Asp Val Glu Pro Asp Asp Gln Pro Gln Leu Leu Ile
    530                 535                 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545                 550                 555                 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
                565                 570                 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
            580                 585                 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
        595                 600                 605
Glu Val Lys Val Ser Glu Ala Ile His Ala Gly Lys Pro Ile Ile Ala
    610                 615                 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625                 630                 635                 640
Phe Leu Thr Glu Pro Gly Asp Asn Val Gln Val Ala Arg His Met Tyr
                645                 650                 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
            660                 665                 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
        675                 680                 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
    690                 695                 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
```

705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 192
<211> 626
<212> PRT
<213> 朱红菌(Trametes cinnabarina)

<220>
<223> >CDO74881.1 糖基转移酶家族 4 蛋白质 [朱红菌]

<400> 192
Met Pro Ala Ile Gly Ser Arg Gln Ala Asn Leu Ala Gln Ala Pro Asn
1 5 10 15
Leu Cys Thr Arg Leu Trp Leu Glu Leu Asp Ile Val Pro Ile Val Phe
20 25 30
Asn Ile Lys Pro Tyr His Thr Asp Ser Ile Thr Arg Pro Asn Ile Arg
35 40 45
His Arg Ile Ser Ser Thr Thr Gly Ser Tyr Val Pro Ser Gly Ala Glu
50 55 60
Thr Pro Thr Val Tyr Tyr Asp Pro Ser Gln Leu Pro Gly Ala Gln Ala
65 70 75 80
Asn Leu Thr Ala Thr Gln Asn Lys Leu Pro Ile Pro Arg Thr Val Asp
85 90 95
[0358] Glu Gln Ala Asp Ser Ala Ala Arg Lys Cys Ile Met Tyr Phe Gly Pro
100 105 110
Ser Asn Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val
115 120 125
Asp Ala Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg
130 135 140
Lys Gly Val Gly Lys Gly Thr Trp Asn Cys Val Asn Lys Leu Ala Asp
145 150 155 160
Glu Leu Arg Glu Lys Lys Ile Lys Met Ala Phe Phe Ser Ser Thr Pro
165 170 175
Gln Gly Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Leu
180 185 190
Asn Leu Leu Asp Val Asp Cys Ala Trp Tyr Val Pro Asn Pro Ser Pro
195 200 205
Thr Val Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val
210 215 220
Ala Asp Pro Asn Leu Arg Leu Thr Lys Glu Ala Lys Asp Asn Phe Asp
225 230 235 240
Ala Trp Ile Leu Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro
245 250 255
Leu Ala Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met
260 265 270
Pro Gly Leu Ile Pro Leu Ile Arg Arg Val Arg Pro Asp Leu Pro Ile
275 280 285
Ile Tyr Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Val Ala
290 295 300
Gly Ser Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln
305 310 315 320

His Ala Asp Met Phe Ile Ser His Pro Val Asn Lys Phe Val Pro Ser
325 330 335
Asp Val Pro Thr Asp Lys Leu Ala Leu Leu Gly Ala Ala Thr Asp Trp
340 345 350
Leu Asp Gly Leu Asn Lys Pro Leu Asp Gln Trp Asp Leu Gln Tyr Tyr
355 360 365
Met Gly Glu Phe Arg Ser Leu Cys Val Lys Glu Lys Met Thr Glu Leu
370 375 380
Gly Trp Pro Ala Arg Glu Tyr Ile Val Gln Ile Ala Arg Phe Asp Pro
385 390 395 400
Ser Lys Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Lys
405 410 415
Leu Leu Ala Glu Lys Glu Pro Asp Ile Glu Pro Pro Gln Met Leu Ile
420 425 430
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
435 440 445
Gln Thr Met Gln Leu Ile His Asn Lys Tyr Ala Gln Tyr Ala Gly Asp
450 455 460
Phe Val Val Met Arg Cys Pro Pro Ser Asp Gln Leu Leu Asn Ala Leu
465 470 475 480
Met Glu Asn Ser Lys Phe Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
485 490 495
Glu Val Lys Val Ser Glu Ala Leu His Ala Gly Lys Pro Val Ile Ala
500 505 510
Ser Arg Thr Gly Gly Ile Pro Leu Gln Ile Glu His Gly Lys Ser Gly
515 520 525
Tyr Leu Cys Glu Pro Gly Asp Asn Ala Ala Val Ala Gln His Met Phe
530 535 540

[0359]

Asp Leu Tyr Thr Asp Asp Asp Leu Phe Asp Gln Met Ser Glu Tyr Ala
545 550 555 560
Arg Thr His Val Ser Asp Glu Val Ser Thr Val Gly Asn Ala Thr Ala
565 570 575
Trp Met Tyr Leu Ala Val Met Tyr Cys Ser Arg Gly Val Arg Leu Gln
580 585 590
Pro Asn Gly Ala Trp Leu Asn Asp Leu Met Arg Thr Glu Cys Gly Glu
595 600 605
Pro Tyr Gln Pro Gly Glu Pro Arg Leu Pro Arg Gly Gly Leu Asn Val
610 615 620
Gln Gly
625

<210> 193
<211> 735
<212> PRT
<213> 鸿禧菇(Hypsizygus marmoreus)

<220>
<223> >KYQ39707.1 海藻糖磷酸化酶 [鸿禧菇]

<400> 193
Met Ala Pro Tyr His Gln Phe Glu Ser Lys Pro Ser Leu Ala Met Arg
1 5 10 15
Arg Arg Leu Ser Ser Ser Val Ser Thr Arg Pro Glu Val Thr Ala Thr
20 25 30
Phe Ala Ser Leu Thr Pro Met Trp Ala Gly Ile Ala Gly Asn Pro Ile

[0360]

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          35                  40                  45
Ser Asn Asn Thr His Tyr Glu Ile Ala Ile Ser Ile His Asp Ser Val
    50                  55                  60
Tyr Ser Thr Asp Phe Ser Ser Thr Val Ile Ser Tyr Phe Pro Asp Glu
65                  70                  75                  80
Pro Glu Lys Thr Ala Lys Ser Ile Gln Ala His Val Leu Glu Thr Leu
                85                  90                  95
Arg Lys Phe Ser Lys Glu His Leu Cys Lys Phe Leu Gly Ala Gly Val
            100                 105                 110
Thr Leu Ser Leu Leu Arg Glu Ala Pro Asn Leu Cys Thr Arg Leu Trp
        115                 120                 125
Leu Asp Met Asp Ile Val Pro Ile Val Phe Asn Ile Lys Pro Tyr His
    130                 135                 140
Thr Asp Ser Ile Thr Arg Pro Asn Ile Lys His Arg Ile Ser Ser Thr
145                 150                 155                 160
Thr Gly Ser Tyr Val Pro Ser Gly Ala Glu Thr Pro Thr Val Tyr Ile
                165                 170                 175
Asp Ser Ala Gln Leu Thr Ala Ala Gly Leu Leu Pro Thr Gly Leu Ser
            180                 185                 190
Asp Arg Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln Ala Asp Ser Ala
        195                 200                 205
Ala Arg Lys Cys Ile Met Tyr Phe Gly Pro Asn Asn Asn Pro Arg Leu
    210                 215                 220
Ser Ile Gly Pro Arg Asn Gln Val Thr Val Asp Ala Ala Gly Lys Ile
225                 230                 235                 240
His Leu Ile Asp Asp Leu Asp Glu Tyr Lys Lys Thr Val Gly Pro Gly
                245                 250                 255
Thr Trp Asn Ala Val Val Lys Leu Ala Asp Glu Leu Arg Glu Lys Lys
            260                 265                 270
Val Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly Gly Gly Val Ala
        275                 280                 285
Leu Met Arg His Ala Leu Ile Arg Phe Leu Thr Ala Leu Asp Val Asp
    290                 295                 300
Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val Phe Arg Thr Thr
305                 310                 315                 320
Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Pro Pro Asp Leu Arg
                325                 330                 335
Leu Thr Lys Glu Ala Lys Glu Asn Phe Asp Ala Trp Ile Leu Lys Asn
            340                 345                 350
Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala Pro Gly Gly Val
        355                 360                 365
Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly Leu Ile Pro Leu
    370                 375                 380
Ile Lys Arg Val Arg Pro Gly Met Pro Ile Val Tyr Arg Ser His Ile
385                 390                 395                 400
Glu Ile Arg Ser Asp Leu Val His Val Pro Gly Ser Pro Gln Glu Glu
                405                 410                 415
Val Trp Lys Tyr Leu Trp Asn Asn Ile Lys Leu Ala Asp Leu Phe Ile
            420                 425                 430
Ser His Pro Val Ser Lys Phe Val Pro Ser Asp Val Pro Glu Ala Lys
        435                 440                 445
Leu Ala Leu Leu Gly Ala Ala Thr Asp Trp Leu Asp Gly Leu Asn Lys
    450                 455                 460
His Leu Asp Pro Trp Asp Ala Gln Phe Tyr Met Gly Glu Phe Arg Ser
465                 470                 475                 480
Leu Cys Ala Lys Glu Lys Met Asn Glu Leu Gln Trp Pro Gln Arg Asp
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485 490 495
Tyr Val Ile Gln Val Ala Arg Phe Asp Pro Ala Lys Gly Ile Pro Asn
500 505 510
Val Ile Asp Ser Tyr Cys Lys Phe Arg His Leu Leu Thr Gln Pro Pro
515 520 525
Val Leu Thr Ser Asp Glu Tyr Pro Gln Leu Leu Ile Cys Gly His Gly
530 535 540
Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp Gln Val Met Gln
545 550 555 560
Leu Ile Asn Ser Glu Lys Tyr Ala Glu Tyr Ala Gln Asp Ile Val Val
565 570 575
Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Ala Leu Met Ala Asn
580 585 590
Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe Glu Val Lys
595 600 605
Val Ser Glu Ala Val His Ala Gly Ile Pro Val Ile Ala Ser Gln Thr
610 615 620
Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly Tyr Leu Thr
625 630 635 640
Ala Pro Gly Asp Asn Ala Ala Val Ala Gln His Leu Tyr Glu Leu Tyr
645 650 655
Thr Asp Glu Gly Leu Tyr Arg Arg Ile Ser Ala Tyr Ala Lys Thr His
660 665 670
Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala Trp Leu Tyr
675 680 685
Leu Ala Val Met Tyr His Arg Gly Val Lys Ile Arg Pro Gln Gly Ala
690 695 700
[0361] Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Glu Ala Tyr Val Glu
705 710 715 720
Gly Glu Pro Arg Leu Pro Arg Gly Gly Leu Val Val Gln Gly Asn
725 730 735

<210> 194
<211> 735
<212> PRT
<213> 彩绒栓菌(Trametes versicolor)

<220>
<223> >XP_008036133.1 海藻糖合成酶 [彩绒栓菌 FP-101664 SS1] >EIW60750.1 海藻糖合成酶 [彩绒栓菌 FP-101664 SS1]

<400> 194
Met Ala Pro Ser Ser Pro His His Gln Phe Gln Ser Lys Thr Ser Asp
1 5 10 15
Ala Ile Arg Arg Arg Leu Ser Ser Val Val Ser Ser Lys Arg Pro Asn
20 25 30
Val Gln Ala Tyr Ser Ser Leu Thr Pro Met Trp Ala Gly Ile Ala Gly
35 40 45
Thr Val Ile Asn Asn Asn Thr Ala Leu Glu Leu Ala Ile Ser Ile His
50 55 60
Asp Ser Val Tyr Asn Thr Asp Phe Ala Ser Ser Thr Val Pro Tyr Asn
65 70 75 80
Pro Asn Asn Pro Glu Glu Gln Ala Ser Asn Val Glu Lys His Val Leu
85 90 95

[0362]

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Glu Leu Leu Arg Lys Phe Ala Thr Glu His Met Cys Lys Phe Leu Gly
                100                 105                 110
Ala Gly Val Thr Val Ser Leu Leu Arg Glu Ala Pro Asn Leu Cys Thr
            115                 120                 125
Arg Leu Trp Phe Asp Leu Asp Ile Val Pro Ile Val Phe Asn Ile Lys
    130                 135                 140
Pro Phe His Thr Asp Ser Val Thr Arg Pro Asn Ile Lys His Arg Ile
145                 150                 155                 160
Ser Ser Thr Thr Gly Ser Tyr Val Pro Ser Gly Ala Glu Thr Pro Thr
                165                 170                 175
Val Tyr Tyr Asp Pro Ala Gln Leu Pro Ala Gly Gln Ala Asn Val Thr
            180                 185                 190
Ala Thr Gln Asn Lys Leu Pro Ile Pro Arg Thr Val Asp Glu Gln Ala
        195                 200                 205
Asp Ser Ala Ala Arg Lys Cys Ile Met Tyr Phe Gly Pro Gly Asn Asn
    210                 215                 220
Pro Arg Leu Ser Ile Gly Ala Arg Asn Gln Val Thr Val Asp Ala Gly
225                 230                 235                 240
Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Gly Asn
                245                 250                 255
Ser Lys Gly Thr Trp Asn Ser Val Ile Lys Leu Ala Asp Glu Leu Arg
            260                 265                 270
Glu Lys Lys Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly Gly
        275                 280                 285
Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Leu Asn Leu Leu
    290                 295                 300
Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val Phe
305                 310                 315                 320
Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Asp Pro
                325                 330                 335
Asn Leu Arg Leu Ser Lys Glu Ala Lys Asp Asn Phe Asp Ala Trp Ile
            340                 345                 350
Leu Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala Pro
        355                 360                 365
Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly Leu
    370                 375                 380
Ile Pro Leu Ile Lys Arg Val Arg Pro Asp Leu Pro Ile Ile Tyr Arg
385                 390                 395                 400
Ser His Ile Glu Ile Arg Ser Asp Leu Val His Val Ala Gly Ser Pro
                405                 410                 415
Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln His Ala Asp
            420                 425                 430
Leu Phe Ile Ser His Pro Val Asn Lys Phe Val Pro Ser Asp Val Pro
        435                 440                 445
Pro Glu Lys Leu Thr Leu Leu Gly Ala Ala Thr Asp Trp Leu Asp Gly
    450                 455                 460
Leu Asn Lys Pro Leu Gly Asp Trp Asp Leu Gln Tyr Tyr Met Gly Glu
465                 470                 475                 480
Phe Arg Gln Leu Cys Val Lys Glu Lys Met Asn Glu Leu Gly Trp Pro
                485                 490                 495
Leu Arg Asp Tyr Ile Val Gln Ile Ala Arg Phe Asp Pro Ser Lys Gly
            500                 505                 510
Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Lys Leu Leu Ala
        515                 520                 525
Glu Lys Glu Pro Ala Thr Glu Pro Pro Gln Met Leu Ile Cys Gly His
    530                 535                 540
```

Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp Glu Thr Met
545 550 555 560
Gln Leu Ile His Thr Lys Tyr Ala Glu Tyr Ala Lys Asp Phe Val Val
565 570 575
Met Arg Cys Pro Pro Ser Asp Gln Leu Leu Asn Ala Leu Met Glu Asn
580 585 590
Ser Lys Phe Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe Glu Val Lys
595 600 605
Val Ser Glu Ala Leu His Ala Gly Lys Pro Val Ile Ala Ser Arg Thr
610 615 620
Gly Gly Ile Pro Leu Gln Ile Glu His Gly Lys Ser Gly Tyr Leu Cys
625 630 635 640
Glu Pro Gly Asp Asn Ala Ala Val Ala Ser His Met Phe Asp Leu Tyr
645 650 655
Thr Asp Asp Asp Leu Phe Asp Thr Met Ser Glu Tyr Ala Arg Thr His
660 665 670
Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala Trp Met Tyr
675 680 685
Leu Ala Val Met Tyr Cys Ser Arg Gly Val Arg Leu Gln Pro Lys Gly
690 695 700
Ala Trp Leu Asn Asp Leu Met Arg Thr Glu Cys Gly Glu Pro Tyr Ala
705 710 715 720
Pro Asn Glu Pro Arg Leu Pro Arg Ala Gly Leu Asn Val Gln Gly
725 730 735

<210> 195
<211> 739
<212> PRT
[0363] <213> 肺形侧耳(Pleurotus pulmonarius)

<220>
<223> >A6YRN9.1 原名：全长=海藻糖磷酸化酶；替换名：
全长=海藻糖合成酶；缩短=TSase；标志：前体
>ABR88135.1 海藻糖磷酸化酶 [肺形侧耳]

<400> 195
Met Ser Thr Pro His His Gln Phe Glu Ser Lys Ser Ser Thr Ala Ile
1 5 10 15
Arg Arg Arg Leu Ser Ser Ser Val Ser Ser Lys Gln Arg Pro Asn Ile
20 25 30
Met Thr Thr Thr Phe Ala Ser Leu Thr Pro Met Trp Ala Gly Val Ala
35 40 45
Gly Thr Leu Val Asn Asn Asn Thr Gln Tyr Glu Ile Ala Val Thr Val
50 55 60
His Asp Gly Val Tyr Ser Thr Asp Phe Ala Ser Val Ile Ile Pro Val
65 70 75 80
Thr Pro Gly Asp Thr Val Lys Asn Ser Lys Asp Ile Glu Ala Gln Val
85 90 95
Leu Asn Leu Ile Arg Lys Phe Ser Ala Glu His Leu Cys Lys Phe Leu
100 105 110
Gly Ala Gly Ile Thr Leu Ala Leu Leu Lys Glu Cys Pro Asn Leu Cys
115 120 125
Thr Arg Leu Trp Leu Asp Met Asp Ile Val Pro Ile Val Phe Asn Ile
130 135 140
Lys Pro Phe His Thr Asp Ser Val Thr Arg Pro Asn Ile Lys His Arg

[0364]

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145                 150                 155                 160
Ile Ser Ser Thr Thr Gly Ser Tyr Val Pro Ser Gly Ser Glu Thr Pro
                165                 170                 175
Thr Val Tyr Val Glu Ala Ser His Leu Asp Asp Pro Ser His Leu Ser
            180                 185                 190
Pro Asn Ala Ala Gln Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
        195                 200                 205
Ser Asp Ser Ala Ala Arg Lys Cys Leu Met Tyr Phe Gly Pro Asn Asn
    210                 215                 220
Asn Pro Arg Leu Ser Ile Gly Ala Arg Asn Gln Val Thr Val Asp Ala
225                 230                 235                 240
Gly Gly Lys Ile His Leu Ile Asp Asp Leu Glu Glu Tyr Arg Glu Thr
                245                 250                 255
Val Gly Ala Gly Thr Trp Asn Ala Val Ile Lys Leu Ala Asp Glu Leu
            260                 265                 270
Arg Glu Lys Lys Val Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
        275                 280                 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Leu Thr Ala
    290                 295                 300
Leu Asp Val Asp Val Ala Trp Tyr Val Pro Asn Pro Ser Pro Gln Val
305                 310                 315                 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ala
                325                 330                 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Ala Phe Asp Ala Trp
            340                 345                 350
Ile Leu Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
        355                 360                 365
Pro Gly Gly Val Asp Val Val Phe Ile Asp Asp Pro Gln Met Pro Gly
    370                 375                 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Val Pro Ile Val Tyr
385                 390                 395                 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Val Ala Gly Ser
                405                 410                 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
            420                 425                 430
Asp Leu Phe Ile Ser His Pro Val Ser Lys Phe Val Pro Ser Asp Val
        435                 440                 445
Pro Thr Glu Lys Leu Ala Leu Leu Gly Ala Ala Thr Asp Trp Leu Asp
    450                 455                 460
Gly Leu Asn Lys Asp Leu Asp Pro Trp Asp Ser Gln Phe Tyr Met Gly
465                 470                 475                 480
Glu Phe Arg Ser Pro Cys Ala Lys Glu Lys Met His Glu Leu Asn Trp
                485                 490                 495
Pro Ala Arg Asp Tyr Ile Val Gln Val Ala Arg Phe Asp Pro Ser Lys
            500                 505                 510
Gly Ile Pro Asn Val Val Asp Ser Tyr Tyr Lys Phe Arg Asn Leu Leu
        515                 520                 525
Arg Thr Arg Ser Pro Asp Met Asp Glu Ser Glu His Pro Gln Leu Leu
    530                 535                 540
Ile Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr
545                 550                 555                 560
Asp Gln Ile Met Ala Leu Val Asn Ser Asp Pro Tyr Lys Glu Tyr Ala
                565                 570                 575
His Asp Ile Val Val Met Arg Leu Pro Pro Ser Asp Glu Leu Leu Asn
            580                 585                 590
Ala Met Met Ala Asn Ser Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu
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595 600 605
Gly Phe Glu Val Lys Val Ser Glu Ala Leu His Thr Gly Lys Pro Val
610 615 620
Ile Ala Cys Arg Thr Gly Gly Ile Pro Leu Gln Ile Gln His Gly Lys
625 630 635 640
Ser Gly Tyr Leu Thr Thr Pro Gly Asp Asn Asp Ala Val Ala Gly His
645 650 655
Leu Tyr Asp Leu Tyr Thr Asp Glu Ala Leu Tyr Arg Lys Met Ser Asp
660 665 670
Phe Ala Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala
675 680 685
Ala Ala Trp Leu Tyr Leu Ala Val Met Tyr Ser Arg Gly Glu Lys Ile
690 695 700
Lys Pro Asn Gly Ala Trp Ile Asn Asp Leu Leu Arg Glu Glu Thr Gly
705 710 715 720
Glu Pro Tyr Lys Glu Gly Glu Thr Lys Leu Pro Arg Thr Lys Leu Asp
725 730 735
Met Gln Gly

<210> 196
<211> 737
<212> PRT
<213> 双孢蘑菇(Agaricus bisporus)

<220>
[0365] <223> >XP_006458503.1 假定蛋白 AGABI2DRAFT_190782 [双孢蘑菇变种蘑菇 H97] >EKV50461.1 假定蛋白 AGABI2DRAFT_190782 [双孢蘑菇变种蘑菇 H97]

<400> 196
Met Ala His Thr Ala His Pro Phe Ser Ser Val Pro Ser Ala Ala Val
1 5 10 15
Arg Arg Arg Leu Ser Ser Ser Val Ser Ala Lys Lys Pro Leu Val Thr
20 25 30
Ala Thr Phe Ser Ser Leu Thr Pro Met Trp Ala Gly Val Ala Gly Val
35 40 45
Ile Ile Asn Asn Asn Thr Glu Phe Glu Val Ala Val Ser Val His Asp
50 55 60
Ser Val Tyr Ser Thr Asp Phe Ala Ser Val Val Leu Pro Tyr Asp Pro
65 70 75 80
Asn Asp Pro Glu Lys Asn Ala Lys Thr Ile Glu Gln Tyr Ile Leu Gln
85 90 95
Val Leu Arg Arg Phe Ser Val Glu His Leu Cys Lys Phe Leu Gly Ala
100 105 110
Gly Val Thr Leu Thr Leu Leu Arg Glu Val Pro Asn Val Cys Thr Arg
115 120 125
Leu Trp Leu Asp Leu Asp Ile Val Pro Phe Val Phe Asn Ile Lys Gln
130 135 140
Tyr His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys His Arg Ile Ser
145 150 155 160
Ser Thr Thr Gly Ser Tyr Val Pro Ser Gly Ala Glu Thr Pro Thr Val
165 170 175
Tyr Val Asp Ser Ala His Leu Lys Ala Met Ser Gly Leu Gln Thr Gly
180 185 190

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

[0366]

Glu Glu Val Trp Lys Tyr Leu Trp Lys Asn Ile Gln Leu Ala Asp Leu
420 425 430
Phe Ile Ser His Pro Val Ser Lys Phe Val Pro Gln Asp Val Pro Leu
435 440 445
Glu Lys Val Ala Leu Leu Gly Ala Ala Thr Asp Trp Leu Asp Gly Leu
450 455 460
Asn Lys Asp Leu Asp Pro Trp Asp Ser Gln Tyr Tyr Met Gly Glu Phe
465 470 475 480
Arg Ala Leu Cys Ala Arg Glu Arg Met Leu Glu Leu Arg Trp Pro Gln
485 490 495
Arg Asp Tyr Ile Ile Gln Val Ala Arg Phe Asp Pro Ser Lys Gly Ile
500 505 510
Pro Asn Val Ile Asp Ser Tyr Val Lys Phe Arg Glu Leu Leu Lys Leu
515 520 525
Lys Ser Pro Glu Leu Asp Asp Glu Asp His Pro Gln Leu Leu Val Cys
530 535 540
Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp Gln
545 550 555 560
Ile Met Gln Ile Ile Asn Ser Glu Gln Tyr Glu Ala Tyr Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Ser Leu
580 585 590
Met Ser Asn Ala Lys Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Leu His Thr Gly Lys Pro Val Ile Ala
610 615 620
Ser Arg Thr Gly Gly Ile Pro Leu Gln Ile Glu His Gly Lys Ser Gly
625 630 635 640

Tyr Leu Cys Thr Pro Gly Asp Asn Glu Ala Val Ala Gly His Leu Tyr
645 650 655
Asp Leu Tyr Thr Asp Glu Ile Leu Tyr Lys Thr Met Ser Asp Tyr Ala
660 665 670
Lys Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Thr Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Val Met Tyr Asn Arg Gly Ile Lys Ile Lys Pro
690 695 700
Asn Gly Ala Trp Leu Asn Asp Leu Leu Arg Thr Glu Thr Gly Glu Asp
705 710 715 720
Tyr Glu Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Leu Lys Met Gln
725 730 735
Gly

<210> 197
<211> 737
<212> PRT
<213> 双孢蘑菇(Agaricus bisporus)

<220>
<223> >XP_007326883.1 假定蛋白 AGABI1DRAFT_111552 [双孢蘑菇变种贝纳特 JB137-S8] >EKM83027.1 假定蛋白 AGABI1DRAFT_111552 [双孢蘑菇变种贝纳特 JB137-S8]

<400> 197

[0367]

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

225 230 235 240
Arg Val His Leu Leu Asp Asp Leu Asp Glu Tyr Arg Asn Thr Val Gly
245 250 255
Pro Arg Thr Trp Asn Ala Val Ile Lys Leu Ala Asp Glu Leu Arg Glu
260 265 270
Lys Lys Val Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly Gly Gly
275 280 285
Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Leu Thr Ala Leu Asp
290 295 300
Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ala Val Phe Arg
305 310 315 320
Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ala Pro Asp
325 330 335
Leu Arg Leu Thr Glu Glu Ala Arg Asp Ala Phe Asp Ala Trp Ile Leu
340 345 350
Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala Arg Gly
355 360 365
Gly Val Asp Val Ala Phe Ile Asp Asp Pro Gln Met Pro Gly Leu Ile
370 375 380
Pro Leu Ile Lys Lys Ile Arg Pro Glu Leu Pro Ile Val Tyr Arg Ser
385 390 395 400
His Ile Glu Ile Arg Ser Asp Leu Val His Val Pro Gly Ser Pro Gln
405 410 415
Glu Glu Val Trp Lys Tyr Leu Trp Lys Asn Ile Gln Leu Ala Asp Leu
420 425 430
Phe Ile Ser His Pro Val Ser Lys Phe Val Pro Gln Asp Val Pro Leu
435 440 445
[0368] Glu Lys Val Ala Leu Leu Gly Ala Ala Thr Asp Trp Leu Asp Gly Leu
450 455 460
Asn Lys Asp Leu Asp Pro Trp Asp Ser Gln Tyr Tyr Met Gly Glu Phe
465 470 475 480
Arg Ala Leu Cys Ala Arg Glu Arg Met Leu Glu Leu Arg Trp Pro Gln
485 490 495
Arg Asp Tyr Ile Ile Gln Val Ala Arg Phe Asp Pro Ser Lys Gly Ile
500 505 510
Pro Asn Val Ile Asp Ser Tyr Val Lys Phe Arg Glu Leu Leu Lys Leu
515 520 525
Lys Ser Pro Glu Leu Glu Asp Glu Asp His Pro Gln Leu Leu Val Cys
530 535 540
Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp Gln
545 550 555 560
Ile Met Gln Ile Val Asn Ser Glu Pro Tyr Glu Ala Tyr Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Ser Leu
580 585 590
Met Ser Asn Ala Lys Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Leu His Thr Gly Lys Pro Val Ile Ala
610 615 620
Ser Arg Thr Gly Gly Ile Pro Leu Gln Ile Glu His Gly Lys Ser Gly
625 630 635 640
Tyr Leu Cys Thr Pro Gly Asp Asn Glu Ala Val Ala Gly His Leu Tyr
645 650 655
Asp Leu Tyr Thr Asp Glu Ile Leu Tyr Lys Thr Met Ser Asp Tyr Ala
660 665 670
Lys Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Thr Ala Ala

675 680 685
Trp Leu Tyr Leu Ala Val Met Tyr Asn Arg Gly Ile Lys Ile Lys Pro
690 695 700
Asn Gly Ala Trp Leu Asn Asp Leu Leu Arg Thr Glu Thr Gly Glu Asp
705 710 715 720
Tyr Glu Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Leu Lys Met Gln
725 730 735
Gly

<210> 198
<211> 733
<212> PRT
<213> 硫磺菌(Laetiporus sulphureus)

<220>
<223> >KZT11205.1 糖基转移酶家族 4 蛋白质 [硫磺菌 93-53]

<400> 198
Met Ala Pro Pro His Ser Phe Thr Ser Lys Pro Ser Val Ala Thr Arg
1 5 10 15
Arg Arg Leu Ser Ser Val Val Thr Pro Asn Arg Pro Asn Val Pro Gly
20 25 30
Phe Thr Ser Leu Thr Pro Met Trp Ala Gly Ile Ala Gly Thr Ile Ile
35 40 45
Asn Asp Asn Thr Ala Phe Glu Val Ala Ile Ser Ile His Asp Ser Val
50 55 60
[0369] Tyr Cys Thr Asp Phe Ala Ser Ser Val Val Pro Tyr Asp Ala Thr Asp
65 70 75 80
Pro Glu Lys Gln Ser Val Ala Ile Glu Lys His Val Leu Asp Thr Leu
85 90 95
Arg Lys Phe Ser Asn Glu His Leu Cys Lys Phe Leu Gly Ala Gly Val
100 105 110
Thr Leu Ser Leu Leu Arg Glu Ala Pro Asn Leu Cys Thr Arg Leu Trp
115 120 125
Leu Glu Met Asp Ile Val Pro Ile Val Phe Asn Ile Lys Pro Tyr His
130 135 140
Thr Asp Ser Ile Thr Arg Pro Asn Val Lys His Arg Ile Ser Ser Thr
145 150 155 160
Thr Gly Ser Tyr Val Pro Ser Gly Ala Glu Thr Pro Thr Val Tyr Val
165 170 175
Asp Ala Ser Gln Leu Gln Asp Gln Ser Lys Leu Thr Thr Gly Ala Gln
180 185 190
Gln Arg Leu Pro Ile Pro Arg Thr Val Asp Glu Gln Ala Asp Ser Ala
195 200 205
Ala Arg Lys Cys Ile Met Tyr Phe Gly Pro Gly Asn Asn Pro Arg Leu
210 215 220
Ser Ile Ala Pro Arg Asn Gln Val Ala Val Asp Ser Gly Gly Lys Ile
225 230 235 240
His Leu Ile Asp Asp Leu Asp Glu Tyr Arg Lys Thr Val His Lys Gly
245 250 255
Thr Trp Asn Ala Val Ile Lys Leu Ala Asp Glu Leu Arg Glu Lys Lys
260 265 270
Ile Arg Phe Ala Phe Phe Ser Ser Thr Pro Gln Gly Gly Gly Val Ala
275 280 285

Leu Met Arg His Ala Leu Ile Arg Phe Phe Gln Ala Leu Asp Val Asp
290 295 300
Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val Phe Arg Thr Thr
305 310 315 320
Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Asp Pro Ser Leu Arg
325 330 335
Leu Thr Gln Asp Gln Lys Glu Asn Phe Asp Ala Trp Ile Leu Lys Asn
340 345 350
Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala Lys Gly Gly Val
355 360 365
Asp Ile Ala Phe Ile Val Asp Asp Pro Gln Met Pro Gly Leu Ile Pro
370 375 380
Leu Ile Lys Arg Val Arg Pro Asp Met Pro Ile Val Tyr Arg Ser His
385 390 395 400
Ile Glu Ile Arg Ser Asp Leu Val Ser Val Ala Gly Ser Pro Gln Glu
405 410 415
Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Tyr Ala Asp Met Phe
420 425 430
Ile Ser His Pro Val Asn Lys Phe Val Pro Thr Asp Val Pro Leu Glu
435 440 445
Lys Leu Ala Leu Leu Gly Ala Ala Thr Asp Trp Leu Asp Gly Leu Asn
450 455 460
Lys His Leu His Pro Trp Asp Thr Gln Tyr Tyr Met Gly Glu Phe Arg
465 470 475 480
Gln Leu Cys Ala Arg Glu Lys Met His Glu Leu Leu Trp Pro Val Arg
485 490 495
Asp Tyr Val Val Gln Ile Ala Arg Phe Asp Pro Ser Lys Gly Ile Pro
500 505 510

[0370]

Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Met Met Lys Ser Asn
515 520 525
Ala Pro Asn Glu Asp Pro Pro Gln Leu Leu Val Cys Gly His Gly Ala
530 535 540
Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp Gln Ile Ile Ala Leu
545 550 555 560
Val Thr Gly Pro Tyr Lys Glu Tyr Glu Gln Asp Met Ile Val Met Arg
565 570 575
Cys Pro Pro Ser Asp Gln Leu Leu Asn Val Leu Met Ala Asn Ser Arg
580 585 590
Val Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe Glu Val Lys Val Ser
595 600 605
Glu Ala Leu His Ala Gly Lys Pro Val Ile Ala Ser Arg Thr Gly Gly
610 615 620
Ile Pro Leu Gln Ile Glu His Gly Lys Ser Gly Phe Leu Cys Asp Ala
625 630 635 640
Gly Asp Asn Glu Ala Val Ala Lys His Met Phe Asp Leu Ile Thr Asn
645 650 655
Glu Asp Leu Tyr Glu Glu Met Ser Glu Tyr Ala Arg Thr His Val Ser
660 665 670
Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala Trp Met Tyr Leu Ala
675 680 685
Val Met Tyr Cys Ser Arg Gly Val Lys Leu Gln Pro Lys Gly Ala Trp
690 695 700
Val Asn Asp Met Met Arg Glu Glu Thr Gly Glu Pro Tyr Glu Pro Gly
705 710 715 720
Glu Pro Arg Leu Pro Arg Gly His Ile His Val Gln Gly
725 730

<210> 199
<211> 736
<212> PRT
<213> 密褐褶菌(Gloeophyllum trabeum)

<220>
<223> >XP_007863746.1 海藻糖合成酶 [密褐褶菌 ATCC 11539] >EPQ58616.1 海藻糖合成酶 [密褐褶菌 ATCC 11539]

<400> 199

Met Ser Pro Thr Gln His Phe Gln Ser Lys Pro Pro Asp Ser Tyr Arg
1 5 10 15
Arg Arg Leu Ser Ser Val Ile Ser Arg Arg Arg Pro Asn Val Pro Gln
20 25 30
Phe Ser Ser Leu Gln Ala Met Trp Ala Gly Ile Ala Gly Gly Val Val
35 40 45
Asn Asn Asn Thr Gln Phe Glu Ile Ala Ile Ser Ile His Asp Ser Val
50 55 60
Tyr Ala Thr Asp Tyr Ala Ser Met Gln Ile Pro Tyr Ser Pro Asn Gly
65 70 75 80
Asp Asn Gly Asp Lys Ile Glu Gln Gln Ile Leu Ser Thr Leu Arg Lys
85 90 95
Phe Ser Ala Asp His Leu Cys Lys Phe Leu Gly Ala Gly Val Thr Leu
100 105 110
Ser Leu Leu Lys Glu Ala Pro Asn Leu Cys Thr Arg Leu Trp Leu Thr
[0371] 115 120 125
Leu Asp Ile Val Pro Ile Val Phe Asn Ile Lys Pro Tyr His Thr Asp
130 135 140
Ser Val Thr Arg Pro Asn Ile Lys His Arg Leu Tyr Ser Gln Thr Gly
145 150 155 160
Ser Phe Ala Pro Ser Gly Ala Asp Thr Pro Thr Val Tyr Val Asp Pro
165 170 175
Thr Pro Leu Ala Lys Asn Asn Val Leu Ala Pro Gly Thr Ala Ala Asn
180 185 190
Leu Gly Thr Pro Thr Thr Lys Gly Leu Pro Ile Pro Arg Thr Met Asp
195 200 205
Glu Gln Ala Asp Ser Ala Ala Arg Lys Cys Ile Met Tyr Phe Gly Pro
210 215 220
Gly Asn Asn Pro Arg Leu Ser Ile Gly Pro Arg Asn Gln Val Leu Val
225 230 235 240
Asp Ser Ala Gly Lys Ile His Leu Ile Asp Asp Leu Asp Glu Tyr Arg
245 250 255
Lys Thr Val Ser Ser Gly Thr Trp Asn Ala Val Asn Lys Leu Ala Asp
260 265 270
Glu Leu Arg Glu Lys Lys Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro
275 280 285
Gln Gly Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Leu
290 295 300
Thr Leu Leu Asp Val Asp Ala Ser Trp Tyr Val Pro Asn Pro Ser Pro
305 310 315 320
Ser Val Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val
325 330 335
Ala Ala Pro Ser Leu Arg Leu Thr Gln Asp Gln Lys Asp Asn Phe Asp

[0372]

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                340                 345                 350
Ala Trp Ile Gln Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro
            355                 360                 365
Leu Ala Gln Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met
    370                 375                 380
Pro Gly Leu Ile Pro Leu Ile Lys Gln Val Arg Pro Asp Met Pro Ile
385                 390                 395                 400
Ile Tyr Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Val Lys
                405                 410                 415
Gly Ser Pro Gln Glu Glu Val Trp Asn Tyr Leu Trp Lys Asn Ile Gln
            420                 425                 430
Leu Ala Asp Met Phe Ile Ser His Pro Val Lys Lys Phe Val Pro Ser
        435                 440                 445
Asp Val Pro Thr Glu Lys Leu Ala Phe Leu Gly Ala Ala Thr Asp Trp
    450                 455                 460
Leu Asp Gly Leu Asn Lys Pro Leu Asp Thr Trp Asp Ser Gln Tyr Tyr
465                 470                 475                 480
Met Gly Glu Phe Arg Ser Leu Cys Val Arg Glu Lys Met His Glu Leu
                485                 490                 495
Lys Trp Pro Ala Arg Glu Tyr Val Val Gln Ile Ala Arg Phe Asp Pro
            500                 505                 510
Ser Lys Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Lys Phe Arg Lys
        515                 520                 525
Met Leu Ala Glu Lys Thr Glu Leu Glu Glu Asp Ile Met Pro Gln Leu
    530                 535                 540
Leu Ile Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile
545                 550                 555                 560
Tyr Asp Gln Val Thr Gly Leu Ile His Ser Gln Tyr Ser Gln Tyr Ser
                565                 570                 575
Asn Asp Ile Ile Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn
            580                 585                 590
Ala Leu Met Asp Asn Ala Lys Ile Ala Leu Gln Leu Ser Thr Arg Glu
        595                 600                 605
Gly Phe Glu Val Lys Val Ser Glu Ala Leu His Thr Gly Lys Pro Val
    610                 615                 620
Val Ala Ser Arg Thr Gly Gly Ile Pro Leu Gln Ile Glu His Gly Lys
625                 630                 635                 640
Ser Gly Tyr Leu Val Glu Val Gly Asp Asn Glu Thr Val Ala Lys His
                645                 650                 655
Leu Phe Asp Leu Tyr Thr Asp Glu Lys Leu Tyr Asp Thr Met Ser Glu
            660                 665                 670
Tyr Ala Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala
        675                 680                 685
Ala Ala Trp Leu Tyr Leu Ala Met Met Tyr Cys Ser Arg Gly Glu Lys
    690                 695                 700
Val Lys Pro Asn Gly Ala Trp Leu Asn Asp Leu Met Arg Glu Val Thr
705                 710                 715                 720
Gly Glu Pro Tyr Ala Pro Asp Glu Pro Lys Leu Pro Arg Val Val Asn
                725                 730                 735
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<210> 200
<211> 693
<212> PRT
<213> 千佛菌(Grifola frondosa)

<220>
<223> >OBZ75413.1 海藻糖磷酸化酶 [千佛菌]

<400> 200
Met Ala Pro Pro His Gln Phe Gln Ser Lys Pro Ser Asp Val Ile Arg
1 5 10 15
Arg Arg Leu Ser Ser Ala Val Ser Ser Lys Arg Pro Asn Ile Pro Gly
20 25 30
Tyr Thr Ser Leu Thr Pro Met Trp Ala Gly Ile Ala Gly Ala Val Val
35 40 45
Asn Asn Asn Thr Gln Phe Glu Val Ala Ile Ser Ile His Asp Ser Val
50 55 60
Tyr Asn Thr Asp Phe Ala Ser Ser Val Val Pro Tyr Ser Pro Asn Glu
65 70 75 80
Pro Glu Ala Gln Ala Gly Ile Ile Glu Lys His Val Leu Glu Thr Leu
85 90 95
Arg Lys Phe Ser Thr Glu His Met Cys Lys Phe Leu Gly Ala Gly Val
100 105 110
Thr Val Ile Leu Leu Arg Glu Ala Pro Asn Leu Cys Thr Arg Leu Trp
115 120 125
Leu Asp Met Asp Ile Val Pro Ile Val Phe Asn Ile Lys Pro Phe His
130 135 140
Thr Asp Ser Ile Thr Arg Pro Asn Val Arg His Arg Ile Ser Ser Thr
145 150 155 160
Thr Gly Ser Tyr Val Pro Ser Gly Ala Glu Thr Pro Thr Val Tyr Tyr
165 170 175
[0373] Asp Pro Ala Gln Leu Gln Asp Pro Asn Lys Leu Ser Ala Asn Val Gln
180 185 190
Thr Arg Leu Pro Ile Pro Arg Thr Val Asp Glu Gln Ala Asp Ser Ala
195 200 205
Ala Arg Lys Cys Ile Met Tyr Phe Gly Pro Gly Asn Asn Pro Arg Leu
210 215 220
Gln Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala Gly Gly Lys Ile
225 230 235 240
His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr Val Gly Lys Gly
245 250 255
Thr Trp Asn Ser Val Ile Lys Leu Ala Asp Glu Leu Arg Glu Lys Lys
260 265 270
Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly Gly Gly Val Ala
275 280 285
Leu Met Arg His Ala Ile Ile Arg Phe Phe Thr Val Leu Asp Val Asp
290 295 300
Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val Phe Arg Thr Thr
305 310 315 320
Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Asp Pro Ser Leu Arg
325 330 335
Leu Thr Lys Glu Ala Ala Asp Asn Phe Asp Ser Trp Ile Leu Lys Asn
340 345 350
Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala Pro Gly Gly Val
355 360 365
Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly Leu Ile Pro Leu
370 375 380
Ile Lys Arg Ile Arg Pro Asp Leu Pro Ile Ile Tyr Arg Ser His Ile
385 390 395 400

Glu Ile Arg Ser Asp Leu Val His Val Lys Gly Ser Pro Gln Glu Glu
405 410 415
Val Trp Asn Tyr Leu Trp Asn Asn Ile Gln His Ser Asp Leu Phe Ile
420 425 430
Ser His Pro Val Asn Lys Phe Val Pro Ser Asp Val Pro Leu Glu Lys
435 440 445
Leu Ala Leu Leu Gly Ala Ala Thr Asp Trp Leu Asp Gly Leu Ser Lys
450 455 460
His Leu Asp Ala Trp Asp Ala Gln Tyr Tyr Met Gly Ser Ser Ala Thr
465 470 475 480
Tyr Arg Ser Leu Arg Pro Val Gln Gly Tyr Pro Glu Arg Asp Arg Leu
485 490 495
Leu Leu Leu Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile
500 505 510
Ile Tyr Asp Gln Val Leu Gln Leu Ile His Ala Lys Tyr Lys Glu Tyr
515 520 525
Ala Pro Asp Ile Val Val Met Arg Cys Pro Pro Ser Asp Gln Leu Leu
530 535 540
Asn Thr Leu Met Ala Asn Ala Lys Phe Ala Leu Gln Leu Ser Thr Arg
545 550 555 560
Glu Gly Phe Glu Val Lys Val Ser Glu Ala Leu His Ala Gly Lys Pro
565 570 575
Val Ile Ala Cys Arg Thr Gly Gly Ile Pro Leu Gln Ile Glu His Gly
580 585 590
Lys Ser Gly Tyr Leu Cys Glu Pro Gly Asp Asn Ala Ala Val Ala Gln
595 600 605
His Met Leu Asp Leu Tyr Thr Asp Glu Asp Leu Tyr Asp Thr Met Ser
610 615 620

[0374]

Glu Tyr Ala Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn
625 630 635 640
Ala Ala Ala Trp Met Tyr Leu Ala Val Met Tyr Val Ser Arg Gly Val
645 650 655
Lys Leu Arg Pro His Gly Ala Trp Ile Asn Asp Leu Met Arg Thr Glu
660 665 670
Met Gly Glu Pro Tyr Arg Ala Gly Glu Pro Arg Leu Pro Arg Gly Glu
675 680 685
Leu His Val Gln Gly
690

<210> 201
<211> 650
<212> PRT
<213> 绒毛栓菌(Trametes pubescens)

<220>
<223> >OJT04097.1 海藻糖磷酸化酶 [绒毛栓菌]

<400> 201
Met Trp Ala Gly Ile Ala Gly Thr Val Ile Asn Asn Asn Thr Ala Leu
1 5 10 15
Glu Leu Ala Ile Ser Ile His Asp Ser Val Tyr Asn Thr Asp Phe Ala
20 25 30
Ser Ser Thr Val Pro Tyr Asn Pro Asn Asn Pro Glu Glu Gln Ala Ser
35 40 45
Asn Val Glu Lys His Val Leu Glu Leu Leu Arg Lys Phe Ala Thr Glu

[0375]

```
     50                  55                  60
His Met Cys Lys Phe Leu Gly Ala Gly Val Thr Val Ser Leu Leu Arg
65                  70                  75                  80
Glu Ala Pro Asn Leu Cys Thr Arg Leu Trp Phe Asp Leu Asp Ile Val
                85                  90                  95
Pro Ile Val Phe Asn Ile Lys Pro Phe His Thr Asp Ser Val Thr Arg
            100                 105                 110
Pro Asn Ile Lys His Arg Ile Ser Ser Thr Thr Gly Ser Tyr Val Pro
        115                 120                 125
Ser Gly Ala Glu Thr Pro Thr Val Tyr Tyr Asp Pro Ala Gln Leu Pro
    130                 135                 140
Ala Gly Gln Ala Asn Val Ala Ala Thr Gln Asn Lys Leu Pro Ile Pro
145                 150                 155                 160
Arg Thr Val Asp Glu Gln Ala Asp Ser Ala Ala Arg Lys Cys Ile Met
                165                 170                 175
Tyr Phe Gly Pro Gly Asn Asn Pro Arg Leu Ser Ile Gly Ala Arg Asn
            180                 185                 190
Gln Val Thr Val Asp Ala Gly Gly Lys Ile His Leu Ile Asp Asp Ile
        195                 200                 205
Asp Glu Tyr Arg Lys Gly Asn Ser Lys Gly Thr Trp Asn Ser Val Ile
    210                 215                 220
Lys Leu Ala Asp Glu Leu Arg Glu Lys Lys Ile Lys Ile Gly Phe Phe
225                 230                 235                 240
Ser Ser Thr Pro Gln Gly Gly Val Ala Asp Pro Asn Leu Arg Leu Ser
                245                 250                 255
Lys Glu Ala Lys Asp Asn Phe Asp Ala Trp Ile Leu Lys Asn Gly Leu
            260                 265                 270
Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala Pro Gly Gly Val Asp Ile
        275                 280                 285
Ala Phe Ile Asp Asp Pro Gln Met Pro Gly Leu Ile Pro Leu Ile Lys
    290                 295                 300
Arg Val Arg Pro Asp Leu Pro Ile Ile Tyr Arg Ser His Ile Glu Ile
305                 310                 315                 320
Arg Ser Asp Leu Val His Val Ala Gly Ser Pro Gln Glu Glu Val Trp
                325                 330                 335
Lys Tyr Leu Trp Asn Asn Ile Gln His Ala Asp Leu Phe Ile Ser His
            340                 345                 350
Pro Val Asn Lys Phe Val Pro Ser Asp Val Pro Pro Glu Lys Leu Thr
        355                 360                 365
Leu Leu Gly Ala Ala Thr Asp Trp Leu Asp Gly Leu Asn Lys Pro Leu
    370                 375                 380
Gly Asp Trp Asp Leu Gln Tyr Tyr Met Gly Glu Phe Arg Gln Leu Cys
385                 390                 395                 400
Val Lys Glu Lys Met Thr Glu Leu Gly Trp Pro Leu Arg Asp Tyr Ile
                405                 410                 415
Val Gln Ile Ala Arg Phe Asp Pro Ser Lys Gly Ile Pro Asn Val Ile
            420                 425                 430
Asp Ser Tyr Ala Arg Phe Arg Lys Leu Leu Ala Glu Lys Glu Pro Gly
        435                 440                 445
Thr Glu Pro Pro Gln Met Leu Ile Cys Gly His Gly Ala Val Asp Asp
    450                 455                 460
Pro Asp Ala Ser Ile Ile Tyr Asp Glu Thr Met Gln Leu Ile His Thr
465                 470                 475                 480
Lys Tyr Ala Glu Tyr Ala Lys Asp Phe Val Val Met Arg Cys Pro Pro
                485                 490                 495
Ser Asp Gln Leu Leu Asn Ala Leu Met Glu Asn Ser Lys Phe Ala Leu
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500 505 510

Gln Leu Ser Thr Arg Glu Gly Phe Glu Val Lys Val Ser Glu Ala Leu
515 520 525

His Ala Gly Lys Pro Val Ile Ala Ser Arg Thr Gly Gly Ile Pro Leu
530 535 540

Gln Ile Glu His Gly Lys Ser Gly Tyr Leu Cys Glu Pro Gly Asp Asn
545 550 555 560

Ala Ala Val Ala Ser His Met Phe Asp Leu Tyr Thr Asp Asp Asp Leu
565 570 575

[0376] Phe Asp Thr Met Ser Glu Tyr Ala Arg Thr His Val Ser Asp Glu Val
580 585 590

Gly Thr Val Gly Asn Ala Ala Ala Trp Met Tyr Leu Ala Val Met Tyr
595 600 605

Val Ser Arg Gly Val Arg Leu Gln Pro Lys Gly Ala Trp Leu Asn Asp
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Leu Met Arg Thr Glu Cys Gly Glu Pro Tyr Ala Pro Asn Glu Pro Arg
625 630 635 640

Leu Pro Arg Ala Gly Leu Asn Val Gln Gly
645 650

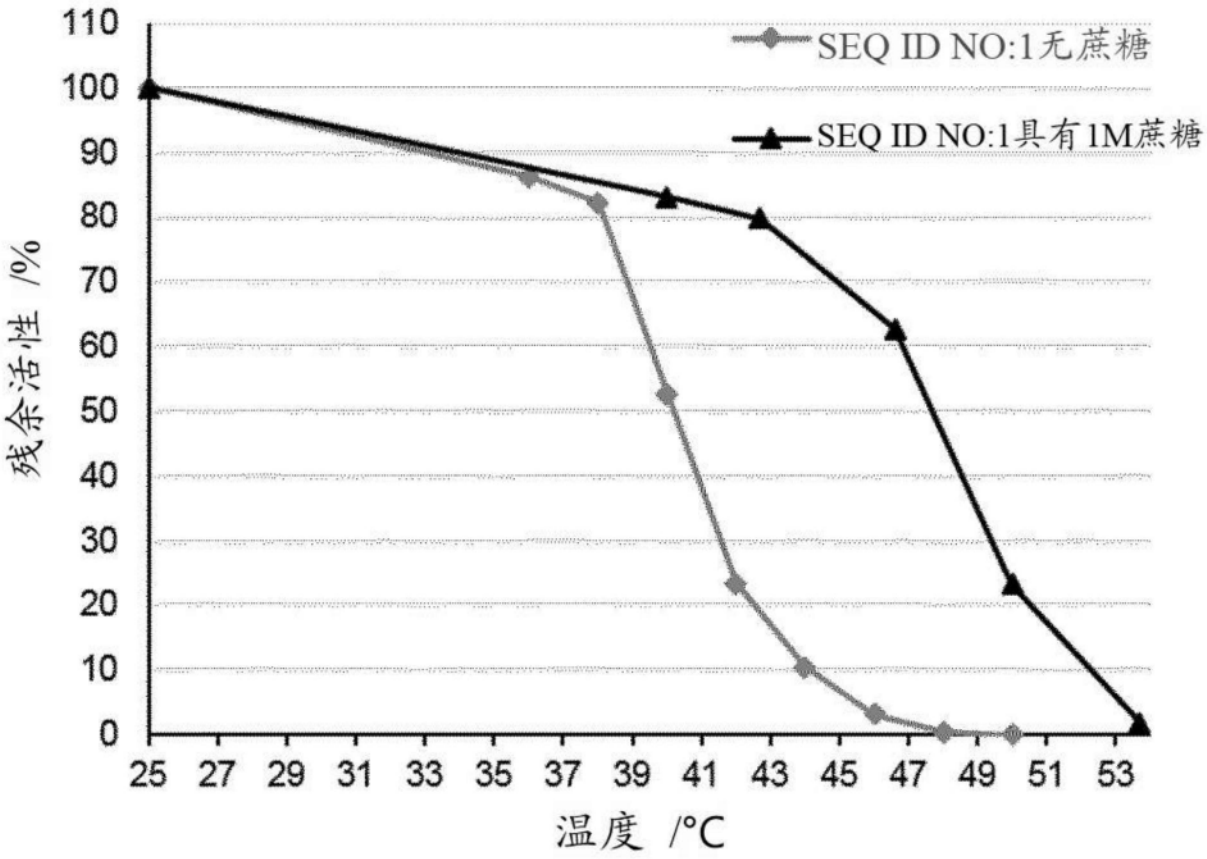

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SEQ ID NO:1具有1M蔗糖
残余活性 /%
温度 /°C
110
100
90
80
70
60
50
40
30
20
10
0
25 27 29 31 33 35 37 39 41 43 45 47 49 51 53

图1

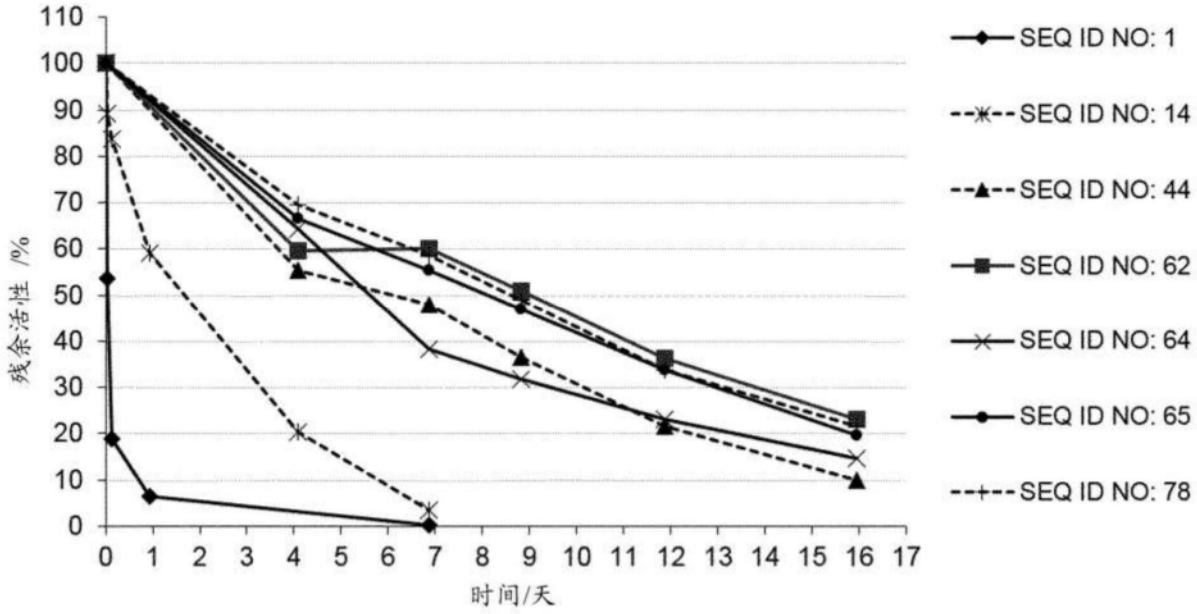

SEQ ID NO: 1
SEQ ID NO: 14
SEQ ID NO: 44
SEQ ID NO: 62
SEQ ID NO: 64
SEQ ID NO: 65
SEQ ID NO: 78
残余活性 /%
时间/天
110
100
90
80
70
60
50
40
30
20
10
0
0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17

图2

```
SEQ_ID_NO:1          -MSPPHGFSSVPSTAARRLSSKASLTNRPTFTKITTQTYASLTPMWAGIAGAPINNGSQ 59
KJA27491.1_簇生垂幕菇 ----------------------------------------MWAAVAGAVINNNTQ 15
ADM15725.1_千佛菌     -MAPPHQFQSKPSDVIRRRLSSAVSSKR-PN-----VPGYTSLTPMWAGIAGAVVNNNSQ 53
KDQ33172.1_秀珍菇     -MSTHHQFESKPSTAIRRRLSSSVSSKQRPN---M-TTTFASLTPMWAGVAGTLVNNNTQ 55
Q9UV63.1_环柄香菇     MSTPHHQFESKSSTAIRRRLSSSVSSKQRPN---IMTTTFASLTPMWAGVAGTLVNNNTQ 57
                                                        ***.:**:: :**.:*

SEQ_ID_NO:1          FELAISVHDSVYSTDFASFVIDHTPLDPEKAAKEIEKHVLDALRKFSQEHLCKFLGAGIT 119
KJA27491.1_簇生垂幕菇 YEIAVSIHDSVYSTDFASSVLSFNPNNPDKNAKEIEQYVLQTLRMFSVGHLCKFLGAGVT 75
ADM15725.1_千佛菌     FEVAISIHDSVYNTDFASSIVPYSPNEPEAQAGIIEKHVLETLRKFSTEHMCKFLGAGVT 113
KDQ33172.1_秀珍菇     YEIAVTVHDGVYSTDFASVIIPVTPGDTAKNSKDIEAQVLNLIRKFSAEHLCKFLGAGIT 115
Q9UV63.1_环柄香菇     YEIAVTVHDGVYSTDFASVIIPVTPGDTVKNSKDIEAQVLNLIRKFSAEHLCKFLGAGIT 117
                      :*:*:::**.**.***** ::  .* :   :  **  **: :* **  *:*******:*

SEQ_ID_NO:1          LALLRESPNICTRLWLDLDIVPIVFNIKPFHTDSLTRPNIKHRISSTSGSYVPSGAETPT 179
KJA27491.1_簇生垂幕菇 LLLLKESPNLCTRLWLDMDIVPFVFNIKPFHTDSLTRPNIKHRISSTTGSYVPSGADTPT 135
ADM15725.1_千佛菌     VILLREAPNLCTRLWLDMDIVPIVFNIKPFHTDSITRPNVRHRISSTTGSYVPSGAETPT 173
KDQ33172.1_秀珍菇     LALLKECPNLCTRLWLDMDIVPIVFNIKPFHTDSVTRPNIKHRISSTTGSYVPSGSETPT 175
Q9UV63.1_环柄香菇     LALLKECPNLCTRLWLDMDIVPIVFNIKPFHTDSVTRPNIKHRISSTTGSYVPSGSETPT 177
                      : **:*.**:********:****:**********:****::*******:********::***

SEQ_ID_NO:1          VYVEASHLGN--NLSAGTASKLPIPRTLDEQADSAARKAIMYYGPNNNPRLTIGPRNQVA 237
KJA27491.1_簇生垂幕菇 VYVDSAHLTAMSGLQTGVSGRLPIPRTLDEQADSAARKCLMYFGPGNNPRLSIGPRNQVT 195
ADM15725.1_千佛菌     VYYDPAQLQDPNKLSANVQTRLPIPRTVDEQADSAARKCIMYFGPGNNPRLQIGPRNQVA 233
KDQ33172.1_秀珍菇     VYVEAAHLGDPSHLSPNAAQKLPIPRTLDEQSDSAARKCLMYFGPNNNPRLSIGARNQVT 235
Q9UV63.1_环柄香菇     VYVEASHLGDPSHLSPNAAQKLPIPRTLDEQSDSAARKCLMYFGPNNNPRLSIGARNPVT 237
                      ** : ::*    *. ..  :*******:***:******.:**:**.***** ** ** *:
```

图3

```
SEQ_ID_NO:1          VDAGGKIHLIDDIDEYRKTVGPSTWTAVNKLADELRERQIKIGFFSSTPQGGGVALMRHA 297
KJA27491.1_簇生垂幕菇 VDSAGKAHLIDDIDEYKATVGPRTWNAVVKLADELREKKVKIGFFSSTPQGGGVALMRHA 255
ADM15725.1_千佛菌     VDAGGKIHLIDDIDEYRKTVGKGTWNSVIKLADELREKKIKIGFFSSTPQGGGVALMRHA 293
KDQ33172.1_秀珍菇     VDAGGKIHLIDDLEEYRKTVGTGTWNAVIKLADELREKKVKIGFFSSTPQGGGVALMRHA 295
Q9UV63.1_环柄香菇     VDAGGKIHLIDDLEEYRMTVGAGTWNAVIKLADELREKKVKIGFFSSTPQGGGVALMRHA 297
                      **:.** ******::**:  ***  **.:* ***********::*********************

SEQ_ID_NO:1          LIRFFSALDVDAAWYVPNPSPSVFRTTKNNHNILQGVASPDLRLTQEAKDNFDAWITKNG 357
KJA27491.1_簇生垂幕菇 LIRFLTALDVDAAWYVPNPSPSVFRTTKNNHNILQGVAAPDLRLTQEAKDNFDAWILKNG 315
ADM15725.1_千佛菌     IIRFFTALDVDAAWYVPNPSPSVFRTTKNNHNILQGVADPSLRLTKEAADNFDSWILKNG 353
KDQ33172.1_秀珍菇     LIRFLTALDVDVAWYVPNPSPQVFRTTKNNHNILQGVAAPDLRLTQDAKDAFDAWILKNG 355
Q9UV63.1_环柄香菇     LIRFLTALDVDVAWYVPNPSPQVFRTTKNNHNILQGVAAPDLRLTQEAKDAFDAWILKNG 357
                      :***::******.**********.**********************  *.****::* * **:** ***

SEQ_ID_NO:1          LRWTAEGGPLAPGGVDIAFIDDPQMPGLIPLIKKVRPELPIIYRSHIEIRSDLVHIAGSP 417
KJA27491.1_簇生垂幕菇 LRWTAEGGPLAPGGVDIAFIDDPQMPGLIPLIKKIRPDLPIVYRSHIEIRSDLVHVPGSP 375
ADM15725.1_千佛菌     LRWTAEGGPLAPGGVDIAFIDDPQVPGLIPLIKRIRPDLPIIYRSHIEIRSDLVHVKGSP 413
KDQ33172.1_秀珍菇     LRWTAEGGPLAPGGVDVVFIDDPQMPGLIPLIKKVRPEVPIVYRSHIEIRSDLVHVAGSP 415
Q9UV63.1_环柄香菇     LRWTAEGGPLAPGGVDVVFIDDPQMPGLIPLIKKVRPEVPIVYRSHIEIRNDLVHVAWSP 417
                      ********************:.*******:*********::**::**:*********.*****:  **

SEQ_ID_NO:1          QEEVWKYLWNNIQLADLFISHPVKAFVPEDVPIERVALLPAATDWLDGLNKELSDWDRQY 477
KJA27491.1_簇生垂幕菇 QEEVWKYLWNNIQLADLFISHPVNKFVPSDVPIEKLALLGAATDWLDGLNKELDPWDSQY 435
ADM15725.1_千佛菌     QEEVWNYLWNNIQHSDLFISHPVNKFVPSDVPLEKLALLGAATDWLDGLSKHLDAWDAQY 473
KDQ33172.1_秀珍菇     QEEVWKYLWNNIQLADLFISHPVSKFVPSDVPIEKLALLGAATDWLDGLNKDLDPWDSQF 475
Q9UV63.1_环柄香菇     QEEVWKYLWNNIQLADLFISHPVSKFVPSDVPTEKLALLGAATDWLDGLNKDLDPWDSPF 477
                      *****:********* :********** ***.*** *::*** ********** *.*. **  :
```

图3继续

```
SEQ_ID_NO:1          YMGE----------FRALCQKDKMNTLDWPNREYCIQIARFDPAKGIPNVIDSYARFR 525
KJA27491.1_簇生垂幕菇 YMGE----------FRNLCTKEKMHTLNWPERDYVVQIARFDPAKGINNVIDSYYKFR 483
ADM15725.1_千佛菌     YMGE----------FRNLCIKEKMNELGWPARDYIVQIARFDPSKGIPNVIDSYARFR 521
KDQ33172.1_秀珍菇     YMGE----------FRSLCAKEKMVELDWPTRDYIVQVARFDPSKGIPNVVDSYYKFR 523
Q9UV63.1_环柄香菇     YMGEFRPRGSHLNRGEFRSLCAKEKMHELNWPARDYIVQVARFDPSKGIPNVVDSYYKFR 537
                      **** **  *:**  *.** *:* :*:*****:*** **:*** :**

SEQ_ID_NO:1          RLLNE-AGDVDADDQPQLLICGHGAVDDPDASIIYDQVLTLIH-EKYAEFAKDIVVMRLP 583
KJA27491.1_簇生垂幕菇 NMLKEKSPDLTEEEHPQLLLCGHGAVDDPDASIIYDQVLQLVESEPYKTYAKDIVVMRLP 543
ADM15725.1_千佛菌     KLCVDK---VMEDDIPQLLLCGHGAVDDPDASIIYDQVLQLIH-AKYKEYAPDIVVMRCP 577
KDQ33172.1_秀珍菇     NLLRTRSPEMELSDHPQLLICGHGAVDDPDASIIYDQIMALVNSDPYKEYAHDIVVMRLP 583
Q9UV63.1_环柄香菇     NLLRTRSPDMDESEHPQLLICGHGAVDDPDASIIYDQIMALVNSDPYKEYAHDIVVMRLP 597
                      .:      :  .: ****:**********************:: *:.   *  :* ****** *

SEQ_ID_NO:1          PSDQLLDCLMANARIALQLSTREGFEVKVSEAVHAGKPIIAATTGGIPLQVEHGKSGFLT 643
KJA27491.1_簇生垂幕菇 PSDQLLNALMANSRIALQLSTREGFEVKVSEALHAGKPVIASRTGGIPLQIEHGKSGYLT 603
ADM15725.1_千佛菌     PSDQLLNTLMANAKFALQLSTREGFEVKVSEALHAGKPVIACRTGGIPLQIEHGKSGYLC 637
KDQ33172.1_秀珍菇     PSDELLNAMMANSRIALQLSTREGFEVKVSEALHTGKPVIACRTGGIPLQIQHGKSGYLT 643
Q9UV63.1_环柄香菇     PSDELLNAMMANSRIALQLSTREGFEVKVSEALHTGKPVIACRTGGIPLQIQHGKSGYLT 657
                      ***:**: :***:::**********************:*:***:**. ********::******:*

SEQ_ID_NO:1          EPGDNAQVARHMYDLYTDVALYDRMSQYARTHVSDEVGTVGNAAAWLYLAAVY-TRGQKL 702
KJA27491.1_簇生垂幕菇 TAGDNAAVANHLYELYTDEALYRKMSQYAKTHVSDEVGTVGNAASWLYLAVMY-HRGIKI 662
ADM15725.1_千佛菌     EPGDNAAVAQHMLDLYTDEDLYDTMSEYARTHVSDEVGTVGNAAAWMYLAVMYVSRGVKL 697
KDQ33172.1_秀珍菇     TPGDNDAVAGYLYDLYTDEALYRRMSDFARTHVSDEVGTVGNAAAWLYLAVMY-SRGEKI 702
Q9UV63.1_环柄香菇     TPGEKDAVAGHFYDFYTDEALYRKMSDFARTHVSNEVGTVGNAAAWLYLAVMY-SRGEKI 716
                        *::  ** :: ::***  **  **::*:*****:**********:*:***.:*  ** *:
```

图3继续

```
SEQ_ID_NO:1                APKGAWLNDLLREETGTPYVEGEPRLPRGGIKVQD   737
KJA27491.1_簇生垂幕菇      KPNGAWLNDMLREETGEEYVEGEPRLPRGGLTMQ-   696
ADM15725.1_千佛菌          RPHGAWINDLMRTEMGEPYRAGEPRLPRGELHVQG   732
KDQ33172.1_秀珍菇          KPNGAWINDLLREETGEPYKEGETKLPRTKLDMQG   737
Q9UV63.1_环柄香菇          KPNGAWINDFFREETGEPYKEGETKLPRTKLDMQG   751
                             *:***:**::* * *  *  ** :***  : :*
```

图3继续