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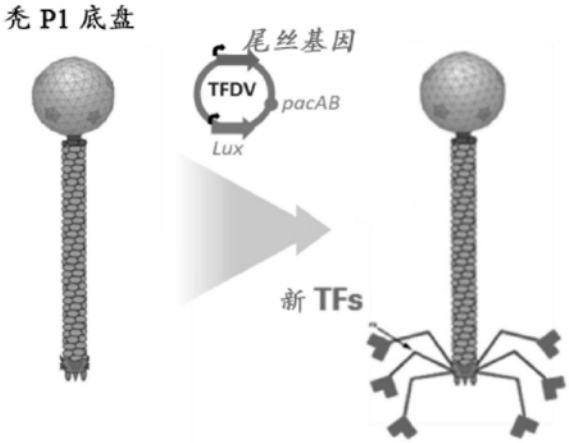
(54)发明名称

具有一个或多个非天然尾丝的非复制转导粒子和基于转导粒子的报告系统

(57)摘要

本发明涉及包含基因工程化的噬菌体、噬菌体样粒子和非复制型转导粒子(NRTP)的组合物和产生所述基因工程化的噬菌体、噬菌体样粒子和非复制型转导粒子(NRTP)的方法，所述基因工程化的噬菌体、噬菌体样粒子和非复制型转导粒子(NRTP)含有显示出改变的宿主特异性和/或反应性的非天然尾丝。本发明还涉及使用这些噬菌体和NRTP开发用于细菌相关疾病的新型诊断、治疗和/或研究试剂的方法。



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1.一种噬菌体尾丝替换平台,所述噬菌体尾丝替换平台包括:

-来自肌尾噬菌体科的噬菌体溶源体(肌尾噬菌体科溶源体),所述噬菌体溶源体含有阻止一种或多种基因或这些基因的任意组合的表达的基因破坏,所述一种或多种基因对产生所述肌尾噬菌体科溶源体天然的尾丝至关重要,其中所述一种或多种基因选自:编码负责结合细菌细胞受体的尾丝结构蛋白的基因、编码折叠尾丝结构蛋白的一个或多个区域所需的分子伴侣蛋白的基因、编码将所述尾丝结构蛋白连接至尾部所需的蛋白的基因;和

-互补核酸分子,所述互补核酸分子包含选自以下的一种或多种基因或这些基因的任意组合:编码负责结合细菌细胞受体的尾丝结构蛋白的基因、编码折叠尾丝结构蛋白的一个或多个区域所需的分子伴侣蛋白的基因、编码将所述尾丝结构蛋白连接至尾部所需的蛋白的基因;其中所述互补核酸对所述肌尾噬菌体科溶源体的所述基因破坏起到补偿作用,由此产生功能性尾丝。

2.根据权利要求1所述的平台,其中所述肌尾噬菌体科溶源体来源于选自以下的属:Bcep781噬菌体属、Bcepmu噬菌体属、FelixO1噬菌体属、Hapuna噬菌体属、I3噬菌体属、Mu噬菌体属、P1噬菌体属、Pbuna噬菌体属、PhiCD119噬菌体属、ΦH噬菌体属、Phikz噬菌体属、Viuna噬菌体属、弯曲噬菌体亚科、Cp220噬菌体属、Cp8una噬菌体属、P2噬菌体亚科、Hpuna噬菌体属、P2噬菌体属、SPO1噬菌体亚科、SPO1噬菌体属、Twort噬菌体属、T4噬菌体亚科、Schizot4噬菌体属或T4噬菌体属。

3.根据权利要求2所述的平台,其中所述肌尾噬菌体科溶源体来源于P1噬菌体属。

4.根据权利要求3所述的平台,其中所述肌尾噬菌体科溶源体是肠杆菌噬菌体P1(P1噬菌体)。

5.根据权利要求1至4中任一项所述的平台,其中所述互补核酸分子上的所述一种或多种基因或所述基因的组合含有不是来源于对所述肌尾噬菌体科溶源体天然的尾丝的产生至关重要的所述一种或多种基因的区域,使得产生的所述功能性尾丝不是天然尾丝。

6.根据权利要求5所述的平台,其中所述一种或多种基因或所述基因的组合含有不是来源于P1噬菌体的区域,使得产生的所述功能性尾丝不是天然P1噬菌体尾丝。

7.根据权利要求1至6中任一项所述的平台,其中所述互补核酸分子是质粒分子;或者

其中所述互补核酸分子整合到所述肌尾噬菌体科溶源体中所述基因破坏的位点处;或者

其中所述互补核酸分子整合到所述肌尾噬菌体科溶源体中不同于所述基因破坏的所述位点的位点处;或者

其中所述互补核酸分子整合到含有所述肌尾噬菌体科溶源体的宿主细菌细胞的基因组中。

8.根据权利要求1至7中任一项所述的平台,其中所述肌尾噬菌体科溶源体含有一种或多种包装基因中的进一步破坏,所述一种或多种包装基因参与包装所述肌尾噬菌体科溶源体的基因组。

9.根据权利要求8所述的平台,其中所述互补核酸分子是质粒分子,并且其中所述质粒分子中含有一种或多种包装基因,所述一种或多种包装基因对所述肌尾噬菌体科溶源体中所述一种或多种包装基因中的所述破坏起到补偿作用;或者

其中所述互补核酸分子是质粒分子,并且其中对所述肌尾噬菌体科溶源体中所述一种

或多种包装基因中的所述破坏起到补偿作用的所述一种或多种包装基因包含在与所述质粒分子分离的报告分子或治疗表达质粒中。

10.一种细菌细胞系,所述细菌细胞系包含P1噬菌体溶源体,所述P1噬菌体溶源体包含SEQ ID NO:97的核酸序列。

11.一种产生具有非天然尾丝的噬菌体粒子的方法,所述方法包括:

-提供含有根据权利要求1至9中任一项所述的噬菌体尾丝替换平台的细菌细胞,其中所述互补核酸分子包含编码尾丝结构蛋白的基因,所述尾丝结构蛋白具有一个或多个区域,所述一个或多个区域不是来源于对所述肌尾噬菌体科溶源体天然的尾丝的产生至关重要的所述一种或多种基因;以及

-向诱导所述肌尾噬菌体科溶源体的裂解期的所述细菌细胞提供条件,以产生具有非天然尾丝的噬菌体粒子。

12.根据权利要求11所述的方法,其中不是来源于所述肌尾噬菌体科溶源体天然的所述一种或多种基因的所述一个或多个区域包含从有尾噬菌体目内的噬菌体获得的所述尾丝结构蛋白的可变区(尾丝可变区)。

13.根据权利要求12所述的方法,其中所述尾丝可变区从肌尾噬菌体科内的噬菌体获得。

14.根据权利要求11至13中任一项所述的方法,其中所述互补核酸分子进一步包含编码分子伴侣蛋白的基因。

15.根据权利要求14所述的方法,其中编码所述分子伴侣蛋白的所述基因从所述有尾噬菌体目内的噬菌体获得。

16.根据权利要求15所述的方法,其中编码所述分子伴侣蛋白的所述基因从所述肌尾噬菌体科内的噬菌体获得。

17.根据权利要求14所述的方法,其中所述分子伴侣蛋白从编码非复制型病毒源结构的细菌基因组获得或从核酸递送粒子获得。

18.根据权利要求11所述的方法,其中不是来源于所述肌尾噬菌体科溶源体天然的所述一种或多种基因的所述一个或多个区域包含从编码噬菌体尾样粒子或结构的细菌基因组获得或从核酸递送粒子获得的所述尾丝结构蛋白的可变区(尾丝可变区)。

19.一种产生具有非天然尾丝的非复制型转导粒子(NRTP)的方法,所述方法包括:

-提供含有根据权利要求1至9中任一项所述的噬菌体尾丝替换平台的细菌细胞,其中所述肌尾噬菌体科溶源体包含参与包装所述肌尾噬菌体科溶源体基因组的一种或多种包装基因中的进一步破坏,并且其中所述互补核酸包含编码所述尾丝结构蛋白的基因,所述尾丝结构蛋白含有一个或多个区域,所述一个或多个区域不是来源于对所述肌尾噬菌体科溶源体天然的尾丝的产生至关重要的一种或多种基因;并且其中所述细菌细胞进一步包含报告质粒,所述报告质粒包含在所述肌尾噬菌体科溶源体中被破坏的所述一种或多种包装基因;以及

-向诱导所述肌尾噬菌体科溶源体的裂解期的所述细菌细胞提供条件,以产生具有非天然尾丝的NRTP。

20.根据权利要求19所述的方法,其中不是来源于所述肌尾噬菌体科溶源体天然的所述一种或多种基因的所述一个或多个区域包含从有尾噬菌体目内的噬菌体获得的所述尾

丝结构蛋白的可变区(尾丝可变区)。

21.根据权利要求20所述的方法,其中所述尾丝可变区从肌尾噬菌体科内的噬菌体获得。

22.根据权利要求19至21中任一项所述的方法,其中所述互补核酸分子进一步包含编码分子伴侣蛋白的基因。

23.根据权利要求22所述的方法,其中编码所述分子伴侣蛋白的所述基因从所述有尾噬菌体目内的噬菌体获得。

24.根据权利要求23所述的方法,其中编码所述分子伴侣蛋白的所述基因从所述肌尾噬菌体科内的噬菌体获得。

25.根据权利要求22所述的方法,其中所述分子伴侣蛋白从编码噬菌体尾样粒子或结构的细菌基因组获得或从核酸递送粒子获得。

26.根据权利要求19所述的方法,其中不是来源于所述肌尾噬菌体科溶源体天然的所述一种或多种基因的所述一个或多个区域包含从编码非复制型病毒源结构的细菌基因组获得或从核酸递送粒子获得的所述尾丝结构蛋白的可变区(尾丝可变区)。

27.一种产生工程化的噬菌体或非复制型转导粒子(NRTP)的方法,所述工程化的噬菌体或非复制型转导粒子(NRTP)显示出不同于天然噬菌体所显示的细菌宿主细胞特异性的细菌宿主细胞特异性,所述方法包括:

-将来自一种尾丝结构蛋白编码基因的第一核苷酸序列与来自不同来源的第二尾丝结构蛋白编码基因的第二核苷酸序列融合,以产生嵌合的尾丝结构蛋白编码基因;以及

-在含有根据权利要求1至9中任一项所述的噬菌体尾丝替换平台的细菌细胞中表达所述嵌合的尾丝结构蛋白基因;以及

-向诱导所述肌尾噬菌体科溶源体的裂解期的所述细菌细胞提供条件,以产生所述工程化的噬菌体或NRTP。

28.根据权利要求27所述的方法,其中所述第一核苷酸序列来源于含有所述基因破坏的所述肌尾噬菌体科溶源体。

29.一种从单一细菌细胞系产生具有多种类型的尾丝的工程化的噬菌体或非复制型转导粒子(NRTP)的方法,其中所述尾丝类型中的至少一种是非天然尾丝,所述方法包括:

-提供包含根据权利要求1至9中任一项所述的噬菌体尾丝替换平台的细菌细胞,其中所述互补核酸分子包含来自尾丝结构蛋白编码基因的至少两个受体结合区,所述至少两个受体结合区与来自尾丝结构蛋白编码基因的一个或多个尾部相互作用区融合,其中所述受体结合区中的至少一个受体结合区来源于与所述尾部相互作用区中的一个尾部相互作用区的来源不同的来源;以及

-向诱导所述噬菌体溶源体的裂解期的所述细菌细胞提供条件,以产生具有多种类型的尾丝的噬菌体或NRTP。

30.根据权利要求29所述的方法,其中所述互补核酸分子整合到所述肌尾噬菌体科溶源体中所述基因破坏的位点处;或者其中所述互补核酸分子整合到所述肌尾噬菌体科溶源体中不同于所述基因破坏的位点的位点处;或者其中所述互补核酸分子整合到所述细菌细胞的基因组中;或者其中所述互补核酸分子整合到质粒分子中。

31.根据权利要求29至30中任一项所述的方法,其中通过cin重组酶并在多个cix重组

位点的存在下将两个或更多个所述受体结合区与所述尾部相互作用区融合;或者

其中通过cin重组酶或所述cin重组酶的同源物、直系同源物或旁系同源物并在多个相关重组位点的存在下将所述两个或更多个受体结合区与所述尾部相互作用区融合。

32.根据权利要求29至31中任一项所述的方法,其中两种或更多种不同的尾丝结构蛋白编码基因在操纵子中表达。

33.根据权利要求29至31中任一项所述的方法,其中所述两种或更多种不同的尾丝结构蛋白编码基因从独立的启动子表达。

34.根据权利要求29至31中任一项所述的方法,其中所述两种或更多种不同的尾丝结构蛋白编码基因从独立的基因组位置表达。

35.一种细菌细胞包装系统,所述细菌细胞包装系统用于将报告分子或治疗性核酸分子包装到非复制型转导粒子(NRTP)中以导入细胞中,所述包装系统包括:

-宿主细菌细胞;

-噬菌体溶源体,所述噬菌体溶源体含有阻止一种或多种基因或这些基因的任何组合的表达的基因破坏,所述一种或多种基因对天然尾丝的产生至关重要的,其中所述一种或多种基因编码负责结合受体的尾丝结构蛋白、折叠尾丝结构蛋白的一个或多个区域所需的分子伴侣蛋白、将所述尾丝结构蛋白连接至尾部结构所需的蛋白;并且所述噬菌体溶源体还包含含有非功能性包装起始位点序列的第一噬菌体基因,其中所述非功能性包装起始位点序列阻止将噬菌体基因组优先包装到所述NRTP中;

-一种或多种互补核酸分子,所述一种或多种互补核酸分子包含:选自以下的一种或多种基因:编码负责结合受体的尾丝结构蛋白的基因、编码折叠尾丝结构蛋白的一个或多个区域所需的分子伴侣蛋白的基因、编码将所述尾丝结构蛋白连接至尾部结构所需的蛋白的基因;或这些基因的任意组合,其对所述噬菌体溶源体的所述基因破坏起到补偿作用从而产生功能性尾丝;和

-报告分子或治疗性核酸分子和第二噬菌体基因,所述第二噬菌体基因含有用于促进将所述报告核酸分子的复制子包装至所述NRTP中的功能性包装起始位点序列,

其中所述报告核酸分子上的所述功能性包装起始位点序列对所述噬菌体溶源体中的非功能性包装起始位点序列起到补偿作用。

36.根据权利要求35所述的细菌细胞包装系统,其中所述报告基因是luxAB,或者其中所述报告基因是荧光报告蛋白。

37.根据权利要求35至36中任一项所述的细菌细胞包装系统,其中所述第一噬菌体基因和所述第二噬菌体基因是pacA末端酶基因。

38.根据权利要求35至36中任一项所述的细菌细胞包装系统,其中所述第一噬菌体基因和所述第二噬菌体基因是terS末端酶基因。

39.一种产生肌尾噬菌体科噬菌体或来源于肌尾噬菌体科的非复制型转导粒子(NRTP)的方法,所述肌尾噬菌体科噬菌体或来源于肌尾噬菌体科的非复制型转导粒子(NRTP)能够识别和转导用于诊断或治疗用途的细菌细胞,所述方法包括:

-提供含有根据权利要求1至9中任一项所述的噬菌体尾丝替换平台的细菌细胞,其中所述互补核酸分子包含非所述肌尾噬菌体科溶源体天然的并且部分地或全部来源于肌尾噬菌体科、长尾噬菌体科或短尾噬菌体科尾丝序列的尾丝基因;以及

-向诱导所述噬菌体溶源体的裂解期的所述细菌细胞提供条件，以产生肌尾噬菌体科噬菌体或来源于肌尾噬菌体科的NRTP，所述肌尾噬菌体科噬菌体或来源于肌尾噬菌体科的NRTP能够识别和转导先前耐天然肌尾噬菌体科噬菌体或来源于肌尾噬菌体科的NRTP粒子的细菌以用于诊断或治疗用途。

具有一个或多个非天然尾丝的非复制转导粒子和基于转导粒子的报告系统

技术领域

[0001] 本发明涉及用于包装和递送源自具有非天然尾丝的噬菌体的非复制性转导颗粒的方法和组合物,所述非天然尾丝含有用于检测靶生物的报告分子。

背景技术

[0002] 转导颗粒是指能够将非病毒核酸递送到细胞中的病毒。基于病毒的报告系统已被用于检测细胞的存在,并依靠病毒的溶源期来允许报告分子从细胞中表达。这些基于病毒的报告系统使用具有复制能力的转导颗粒来表达报告分子,并导致靶细胞发出可检测的信号。

[0003] 然而,病毒的裂解周期已被证明对基于病毒的报告分子测定有害。Carrière,C.et al.,Conditionally replicating luciferase reporter phages:Improved sensitivity for rapid detection and assessment of drug susceptibility of Mycobacterium tuberculosis.Journal of Clinical Microbiology,1997.35(12):p.3232-3239。Carrière等人开发了结核分枝杆菌(M.tuberculosis)/卡介苗(BCG)荧光素酶报告噬菌体,其裂解周期在30℃时被抑制,但在37℃时活跃。使用该系统,Carrière等人已经展示使用具有抑制裂解周期的噬菌体报告分子检测BCG。

[0004] 然而,在基于噬菌体的报告分子测定中抑制但不消除噬菌体的复制功能也存在一些缺点。首先,控制噬菌体的复制功能强加了限制性的测定条件。例如,Carrière等人使用的报告噬菌体phAE40的裂解周期,当噬菌体在30℃的非允许温度下感染细胞时被抑制。此温度要求对报告分子测定强加限制条件,因为靶细菌的最佳温度为37℃。这些限制条件阻碍了最佳测定性能。

[0005] 而且,病毒的复制功能难以控制。在使用转导颗粒作为报告系统的过程中应抑制病毒的复制。例如,Carrière等人报道的报告噬菌体phAE40的裂解活性减少但没有消除,导致测定中荧光素酶信号下降。Carrière等人强调了导致报告信号下降的可能原因,诸如完整的噬菌体表达基因和测定的温度限制,所有这些都源于噬菌体报告分子的裂解周期没有消除这一事实。

[0006] 依赖噬菌体的自然溶源周期的报告分子测定预期会偶尔表现出裂解活性。此外,依赖于噬菌体溶源周期的测定可能容易受到已经用类似噬菌体溶源化的靶细胞的超感染免疫,以及容易受到针对传入病毒核酸的天然宿主限制系统,从而限制这些报告噬菌体的宿主范围。

[0007] 在其他实例中,转导颗粒生产系统被设计成包装外源核酸分子,但转导颗粒通常包含外源核酸分子和天然子代病毒核酸分子的组合。天然病毒会表现出裂解活性,这会阻碍测定性能,并且必须消除病毒的裂解活性以纯化转导颗粒。然而,这种纯化通常是不可能的。在题为“Reporter Plasmid Packaging System for Detection of Bacteria”的U.S.2009/0155768 A中,Scholl等人描述了此类转导颗粒系统的发展。该系统的产物是报

告分子转导颗粒和天然噬菌体的组合(参考文献中的图8)。尽管作者指出转导颗粒和天然噬菌体可以通过超速离心进行分离,但这种分离只有在转导颗粒和天然病毒表现出不同密度的系统中才有可能通过超速离心进行分离。虽然该参考文献中描述的基于噬菌体T7的包装系统表现出这种特征,但这并不是通常适用于其他病毒系统的特征。病毒包装机构通常表现出头部包装,这会导致天然病毒和转导颗粒表现出无法通过超速离心分离的难以区分的密度。病毒包装系统还依赖最少量的包装作为适当病毒结构组装的要求,这导致天然病毒和转导颗粒具有难以区分的密度。

[0008] 最近,在U.S专利No.9,388,453和U.S.专利申请No.2017/0166907中描述了用于将报告核酸分子包装成非复制性转导颗粒(NRTP)(本文也称为Smarticle)的方法和系统,其中由于噬菌体基因组中包装起始位点的破坏,具有复制能力的天然子代病毒核酸分子的产生大大减少。

[0009] 目前,NRTP是由自然界中发现的天然溶源性噬菌体产生的,例如 φ80α 噬菌体或P1噬菌体。寻找、表征新噬菌体并将其修饰为NRTP(其能够以所需的宿主范围特异性转导细胞)是一个耗时的过程。

[0010] 最近的几项研究(Ando et al.,Cell Systems 2015,1:187-196;Yosef et al.,Molecular Cell 2017,66:721-728)已表明T3和T7噬菌体和噬菌体/转导颗粒混合物可以通过交换来自T3/T7噬菌体属来源的尾/尾丝(其能使噬菌体能够识别不同的宿主),从而重新编程以识别所需的宿主。为此,在T3/T7底盘上构建了不同的尾/尾丝,并测试了它们将DNA注入不同宿主的能力。虽然这些实验为生产具有新宿主范围的杂合颗粒铺平了道路,但这些影响仅在T3和T7样噬菌体中发现的噬菌体/尾/尾丝中示出。特别是,这些研究无法建立基于其他噬菌体家族底盘的噬菌体基因组工程化平台,诸如肌尾噬菌体(Myroviridae)科,与T3/T7噬菌体不同,它们具有长而可收缩的尾巴,并且涉及完全不同的尾丝基因。

[0011] 最充分表征的肌尾噬菌体科噬菌体之一是感染大肠杆菌(E.coli)和肠杆菌科其他细菌的P1噬菌体。P1的宿主范围特异性控制在长度约为6kb的尾丝操纵子内(图2),并包括一个可逆的C段区域,其中尾丝基因的两个交替3`末端($s_v$或$s_v$')可以融合到位于可逆区域外的恒定5`末端(s_c)。两个交替基因u和u'位于S基因之外,编码参与尾丝组装的分子伴侣蛋白的交替形式。尾丝操纵子中的另外两种基因是r基因,其基因产物R被认为与尾丝组装有关;基因cin,其编码序列特异性重组酶,该酶可以在Cin重组位点(称为cix位点)之间"翻转"核酸,修饰宿主特异性,描述于Guidolin et al.,1989 Gene,76:239-243,和Sandmeier et al.,1992,Journal of Bacteriology,174(12):3936-3944。

[0012] 因此,本领域需要一种快速、可靠且可扩展的方法来产生源自多种类型噬菌体的尾丝的新NRTP。因此,本发明涉及源自P1噬菌体的尾丝替换平台(或底盘),该平台可以仅在尾丝中进行改变以改变或扩展它们的宿主特异性,并且该平台可以利用来自许多病毒家族的尾丝。此外,本发明涉及提高来自工程化生产线的NRTP的产量的方法,和在单次发酵中生产多种天然或工程化尾丝赋予的NRTP的方法。这种方法可用于其他不同的噬菌体,以开发新的在宿主范围特异性方面具有所需的包容性和排他性特征的NRTP。

发明内容

[0013] 本发明考虑了一种噬菌体溶源体,其被基因破坏以表达对天然尾丝生产至关重要

的一个或多个因子(例如-基因s、u、u'、r和s')。这可以通过本领域技术人员已知的任何诱变方法或通过从天然来源分离尾丝缺陷的噬菌体残余物来实现。这种基因破坏的噬菌体溶源体缺乏表达自身功能性尾丝的能力而没有互补,被称为底盘或"秃"底盘。在一个实施例中,破坏的溶源体在选自以下的一种或多种基因或这些基因的任意组合中具有突变或缺失:编码负责结合细菌细胞受体的尾丝结构蛋白的基因;编码折叠尾丝结构蛋白的一个或多个区域所需的分子伴侣蛋白的基因;编码将尾丝结构蛋白连接到尾部所需的蛋白质的基因。在另一个实施例中,破坏的溶源体含有编码可选择标志物(这会破坏一种或多种基因的表达)的基因。在又一个实施例中,破坏的溶源体包含核苷酸序列SEQ ID NO:97。

[0014] 本发明的另一方面涉及,关于在为天然尾丝表达而被基因破坏的溶源体中表达天然的、新的尾丝基因或杂合尾丝的方法。这可以使用包装质粒、二级表达质粒、基因组表达(噬菌体溶源体或细菌基因组)或本领域技术人员已知的任何其他方法来实现。

[0015] 因此,本发明涉及一种噬菌体尾丝替换平台,其包含来自肌尾噬菌体科的噬菌体溶源体(肌尾噬菌体溶源体)和互补核酸分子,所述噬菌体溶源体含有基因破坏,该基因破坏阻止一种或多种基因表达,这些基因对产生肌尾噬菌体溶源体天然的尾丝至关重要,其中所述一种或多种基因或这些基因的任意组合选自:编码负责结合细菌细胞受体的尾丝结构蛋白的基因、编码折叠尾丝结构蛋白的一个或多个区域所需的分子伴侣蛋白的基因、编码将尾丝结构蛋白连接到尾部所需的蛋白质的基因;所述互补核酸分子包含选自以下的一种或多种基因或这些基因的任意组合:编码负责结合细菌细胞受体的尾丝结构蛋白的基因、编码折叠尾丝结构蛋白的一个或多个区域所需的分子伴侣的基因、编码将尾丝结构蛋白连接到尾部所需的蛋白质的基因,其中所述互补核酸补偿了肌尾噬菌体科溶源体的基因破坏,由此产生功能性尾丝。

[0016] 在一个实施例中,肌尾噬菌体科溶源体来源于选自以下的属:Bcep781噬菌体属、Bcepmu噬菌体属、FelixO1噬菌体属、Hapuna噬菌体属、I3噬菌体属、Mu噬菌体属、P1噬菌体属、Pbuna噬菌体属、PhiCD119噬菌体属、ΦH噬菌体属、Phikz噬菌体属、Viuna噬菌体属、弯曲噬菌体亚科、Cp220噬菌体属、Cp8una噬菌体属、P2噬菌体亚科、Hpuna噬菌体属、P2噬菌体属、SPO1噬菌体亚科、SPO1噬菌体属、Twort噬菌体属、T4噬菌体亚科、Schizot4噬菌体属或T4噬菌体属。在一个实施例中,肌尾噬菌体科溶源体来源于P1噬菌体属。在另一个实施例中,肌尾噬菌体科溶源体是肠杆菌噬菌体P1(P1噬菌体)。

[0017] 在一个实施例中,互补核酸分子上的一种或多种基因或基因的组合含有不是源自对肌尾噬菌体科溶源体天然的尾丝的产生至关重要的一种或多种基因的区域,使得产生的功能性尾丝不是天然尾丝。在此类实施例中,产生的尾丝是非对初始噬菌体溶源体天然的功能性尾丝。在另一个实施例中,一种或多种基因或基因组合包含非源自P1噬菌体的区域,使得产生的功能性尾丝不是天然的P1噬菌体尾丝。

[0018] 在又一个实施例中,对肌尾噬菌体科溶源体的基因破坏包括在一种或多种基因中的任何一种中的一个或多个突变。在一些实施例中,肌尾噬菌体科溶源体可在一种或多种基因之一中包含一个或多个突变。在其他实施例中,肌尾噬菌体科溶源体可在一种或多种基因中的至少两种中包含一个或多个突变。在一个实施例中,该一个或多个突变是在P1噬菌体基因s、s′、u、u′和r中的任何一个中,或在基因s、s′、u、u′和r的任何组合中,或在基因s、s′、u、u′和r的同源物、直系同源物或类似物中。

[0019] 在一个实施例中，对肌尾噬菌体科溶源体的基因破坏包括一种或多种基因中的任何一种中的一个或多个缺失。在一些实施例中，肌尾噬菌体科溶源体可包含一种或多种基因之一中的一个或多个缺失。在其他实施例中，肌尾噬菌体科溶源体可包含一种或多种基因中的至少两种中一个或多个缺失。在某些实施例中，至少一个缺失是一种或多种基因之一的完整编码序列的缺失。在其他实施例中，一个或多个缺失中的任何一个是一种或多种基因之一的完整编码序列的缺失。在一个实施例中，该一个或多个缺失是在P1噬菌体基因s、s′、u、u′和r中的任何一个中，或在基因s、s′、u、u′和r的任何组合中，或在基因s、s′、u、u′和r的同源物、直系同源物或类似物中。在另一个实施例中，对肌尾噬菌体科溶源体的基因破坏还包括插入编码可选择标志物的基因，该可选择标志物破坏P1噬菌体基因中任何一个的表达。在一个实施例中，肌尾噬菌体科溶源体包括核酸序列SEQ ID NO:97。

[0020] 在一个实施例中，互补核酸分子是质粒分子。在另一个实施例中，互补核酸分子在基因破坏位点整合到肌尾噬菌体科溶源体中。在又一个实施例中，互补核酸分子在除基因破坏位点之外的位点整合到肌尾噬菌体科溶源体中。在又一个实施例中，互补核酸分子整合到含有肌尾噬菌体科溶源体的宿主细菌细胞的基因组中。

[0021] 在一个实施例中，肌尾噬菌体科溶源体在一种或多种包装基因中包含进一步的破坏，这些基因参与包装肌尾噬菌体科溶源体的基因组。因此，参与包装肌尾噬菌体科溶源体基因组的一种或多种包装基因变得无功能。在一个实施例中，一种或多种包装基因(其补偿了肌尾噬菌体科溶源体中一种或多种包装基因的破坏)包含在质粒分子中。在另一个实施例中，一种或多种包装基因(其补偿了肌尾噬菌体科溶源体中一种或多种包装基因的破坏)包含在与质粒分子分离的报告分子或治疗性表达质粒中。

[0022] 本发明还涉及包含P1噬菌体溶源体的细菌细胞系，该噬菌体溶源体包含SEQ ID NO:97的核酸序列。

[0023] 本发明进一步涉及用非天然尾丝生产噬菌体颗粒或非复制转导颗粒(NRTP)的方法，包括提供含有本发明的噬菌体尾丝替换平台的细菌细胞，其中互补核酸分子包含编码尾丝结构蛋白的基因，该基因具有一个或多个区域(这些区域不是源自对肌尾噬菌体科溶源体天然的尾丝的产生至关重要的一种或多种基因)，并为细菌细胞提供条件以诱导肌尾噬菌体科溶源体的裂解期，以产生具有非天然尾丝的噬菌体颗粒。

[0024] 在一个实施例中，不是源自于对肌尾噬菌体科溶源体天然的一种或多种基因的一个或多个区域包含从有尾噬菌体目内的噬菌体获得的尾丝结构蛋白的可变区(尾丝可变区)。在一个实施例中，尾丝可变区从肌尾噬菌体科内的噬菌体获得。在另一个实施例中，尾丝可变区从选自以下属内的噬菌体获得:Bcep781噬菌体属、Bcepmu噬菌体属、FelixO1噬菌体属、Hapuna噬菌体属、I3噬菌体属、Mu噬菌体属、P1噬菌体属、Pbuna噬菌体属、PhiCD119噬菌体属、ΦH噬菌体属、Phikz噬菌体属、Viuna噬菌体属、弯曲噬菌体亚科、Cp220噬菌体属、Cp8una噬菌体属、P2噬菌体亚科、Hpuna噬菌体属、P2噬菌体属、SPO1噬菌体亚科、SPO1噬菌体属、Twort噬菌体属、T4噬菌体亚科、Schizot4噬菌体属或T4噬菌体属。在一个实施例中，属是P1噬菌体属。

[0025] 在一个实施例中，互补核酸分子进一步包含编码分子伴侣蛋白的基因。在一个实施例中，编码分子伴侣蛋白的基因获自有尾噬菌体目内的噬菌体。在另一个实施例中，编码分子伴侣蛋白的基因获自肌尾噬菌体科内的噬菌体。在又一个实施例中，编码分子伴侣蛋

白的基因获自选自以下属的噬菌体:Bcep781噬菌体属、Bcepmu噬菌体属、FelixO1噬菌体属、Hapuna噬菌体属、I3噬菌体属、Mu噬菌体属、P1噬菌体属、Pbuna噬菌体属、PhiCD119噬菌体属、ΦH噬菌体属、Phikz噬菌体属、Viuna噬菌体属、弯曲噬菌体亚科、Cp220噬菌体属、Cp8una噬菌体属、P2噬菌体亚科、Hpuna噬菌体属、P2噬菌体属、SPO1噬菌体亚科、SPO1噬菌体属、Twort噬菌体属、T4噬菌体亚科、Schizot4噬菌体属或T4噬菌体属。在一个实施例中,属是P1噬菌体属。在一个实施例中,分子伴侣蛋白获自编码非复制性病毒衍生结构的细菌基因组或获自核酸递送颗粒。在一个实施例中,编码分子伴侣蛋白的基因包含选自由SEQ ID No:67-96和113-117组成的组的氨基酸序列。

[0026] 在一个实施例中,不是源自于对肌尾噬菌体科溶源体天然的一种或多种基因的一个或多个区域包含从编码噬菌体尾样颗粒或结构的细菌基因组获得的,或从核酸递送颗粒获得的尾丝结构蛋白的可变区(尾丝可变区)。在一个实施例中,编码尾丝结构蛋白的基因包含选自由SEQ ID No:35-66和108-112组成的组的氨基酸序列。在另一个实施例中,编码尾丝结构蛋白的基因包含选自由SEQ ID No:1-34、98、100、102、104和106组成的组的核苷酸序列。

[0027] 本发明进一步涉及生产具有非天然尾丝的非复制性转导颗粒(NRTP)的方法,包括:提供含有本发明的噬菌体尾丝替换平台的细菌细胞,其中肌尾噬菌体科溶源体包括涉及包装肌尾噬菌体科溶源基因组的一种或多种包装基因中的进一步破坏,并且其中互补核酸包含编码尾丝结构蛋白的基因,该基因含有一个或多个区域,所述区域不是源自对生产肌尾噬菌体科溶源体天然的尾丝至关重要的一种或多种基因;并且其中所述细菌细胞进一步包含报告质粒,所述报告质粒包含在肌尾噬菌体科溶源体中被破坏的一种或多种包装基因;并为细菌细胞提供条件,诱导肌尾噬菌体科溶源体的裂解期,以产生具有非天然尾丝的NRTP。

[0028] 在一个实施例中,不是源自于对肌尾噬菌体科溶源体天然的一种或多种基因的一个或多个区域包含从有尾噬菌体目内的噬菌体获得的尾丝结构蛋白的可变区(尾丝可变区)。在一个实施例中,尾丝可变区从肌尾噬菌体科内的噬菌体获得。在另一个实施例中,尾丝可变区从选自以下属内的噬菌体获得:Bcep781噬菌体属、Bcepmu噬菌体属、FelixO1噬菌体属、Hapuna噬菌体属、I3噬菌体属、Mu噬菌体属、P1噬菌体属、Pbuna噬菌体属、PhiCD119噬菌体属、ΦH噬菌体属、Phikz噬菌体属、Viuna噬菌体属、弯曲噬菌体亚科、Cp220噬菌体属、Cp8una噬菌体属、P2噬菌体亚科、Hpuna噬菌体属、P2噬菌体属、SPO1噬菌体亚科、SPO1噬菌体属、Twort噬菌体属、T4噬菌体亚科、Schizot4噬菌体属或T4噬菌体属。在一个实施例中,属是P1噬菌体属。

[0029] 在一个实施例中,互补核酸分子进一步包含编码分子伴侣蛋白的基因。在一个实施例中,编码分子伴侣蛋白的基因获自有尾噬菌体目内的噬菌体。在另一个实施例中,编码分子伴侣蛋白的基因获自肌尾噬菌体科内的噬菌体。在又一个实施例中,编码分子伴侣蛋白的基因获自选自以下属的噬菌体:Bcep781噬菌体属、Bcepmu噬菌体属、FelixO1噬菌体属、Hapuna噬菌体属、I3噬菌体属、Mu噬菌体属、P1噬菌体属、Pbuna噬菌体属、PhiCD119噬菌体属、ΦH噬菌体属、Phikz噬菌体属、Viuna噬菌体属、弯曲噬菌体亚科、Cp220噬菌体属、Cp8una噬菌体属、P2噬菌体亚科、Hpuna噬菌体属、P2噬菌体属、SPO1噬菌体亚科、SPO1噬菌体属、Twort噬菌体属、T4噬菌体亚科、Schizot4噬菌体属或T4噬菌体属。在一个实施例中,

属是P1噬菌体属。在一个实施例中，分子伴侣蛋白获自编码非复制性病毒衍生结构的细菌基因组或获自核酸递送颗粒。在一个实施例中，编码分子伴侣蛋白的基因包含选自由SEQ ID No:67-96和113-117组成的组的氨基酸序列。

[0030] 在一个实施例中，不是源自于对肌尾噬菌体科溶源体天然的一种或多种基因的一个或多个区域包含从编码噬菌体尾样颗粒或结构的细菌基因组获得的，或从核酸递送颗粒获得的尾丝结构蛋白的可变区(尾丝可变区)。在一个实施例中，编码尾丝结构蛋白的基因包含选自由SEQ ID No:35-66和108-112组成的组的氨基酸序列。在另一个实施例中，编码尾丝结构蛋白的基因包含选自由SEQ ID No:1-34、98、100、102、104和106组成的组的核苷酸序列。

[0031] 在另一方面，本发明考虑表达嵌合尾丝基因，该基因产生噬菌体和/或NRTP，所述噬菌体和/或NRTP表现出不同于天然噬菌体底盘的宿主范围特异性和/或反应性的宿主范围特异性和/或反应性。因此，本发明涉及一种产生工程化噬菌体或非复制性转导颗粒(NRTP)的方法，其展示的细菌宿主细胞特异性不同于天然噬菌体展示的细菌宿主细胞特异性，包括:将源自一种尾丝结构蛋白编码基因的第一核苷酸序列与源自不同来源的第二种尾丝结构蛋白编码基因的第二核苷酸序列融合，以产生嵌合尾丝结构蛋白编码基因;在含有本发明噬菌体尾丝替换平台的细菌细胞中表达嵌合尾丝结构蛋白基因;并为细菌细胞提供条件，诱导肌尾噬菌体科溶源体的裂解期，以产生工程化噬菌体或NRTP。

[0032] 在一个实施例中，肌尾噬菌体科溶源体来源于选自以下的属:Bcep781噬菌体属、Bcepmu噬菌体属、Felix01噬菌体属、Hapuna噬菌体属、I3噬菌体属、Mu噬菌体属、P1噬菌体属、Pbuna噬菌体属、PhiCD119噬菌体属、ΦH噬菌体属、Phikz噬菌体属、Viuna噬菌体属、弯曲噬菌体亚科、Cp220噬菌体属、Cp8una噬菌体属、P2噬菌体亚科、Hpuna噬菌体属、P2噬菌体属、SPO1噬菌体亚科、SPO1噬菌体属、Twort噬菌体属、T4噬菌体亚科、Schizot4噬菌体属或T4噬菌体属。在一个实施例中，肌尾噬菌体科溶源体来源于P1噬菌体属。在另一个实施例中，肌尾噬菌体科溶源体是肠杆菌噬菌体P1(P1噬菌体)。

[0033] 在一个实施例中，第一核苷酸序列源自含有基因破坏的肌尾噬菌体科溶源体。在另一个实施例中，第一核苷酸序列包含来自P1噬菌体的尾丝基因s的s_c区域。在又一个实施例中，第一核苷酸序列包含与编码SEQ ID NO:53的氨基酸序列1-250的核苷酸序列具有至少90％序列同一性的序列。在又一个实施例中，第一核苷酸序列包含与编码SEQ ID NO:53的氨基酸序列1-500的核苷酸序列具有至少90％序列同一性的序列。在一个实施例中，第一核苷酸序列包含源自质粒p15B(如Ikeda et al.,J.Mol.Biol.,1970,50:457-470中所述)或源自肺炎克雷伯氏菌(Kpn)中的P1样11型噬菌体的s_c区域。

[0034] 在另一方面，本发明涉及一种从单个细菌细胞系产生具有多种类型尾丝的工程化噬菌体或非复制性转导颗粒(NRTP)的方法，其中至少一种尾丝类型是非-天然尾丝，包括:提供含有本发明的噬菌体尾丝替换平台的细菌细胞，其中互补核酸分子包含来自尾丝结构蛋白编码基因的至少两个受体结合区，受体结合区融合到来自尾丝结构蛋白编码基因的一个或多个尾相互作用区，其中至少一个受体结合区源自与尾相互作用区之一的来源不同的来源;并为细菌细胞提供条件，以诱导噬菌体溶源体的裂解期来产生具有多种类型尾丝的噬菌体或NRTP。

[0035] 在一个实施例中，肌尾噬菌体科溶源体来源于选自以下的属:Bcep781噬菌体属、

Bcepmu噬菌体属、FelixO1噬菌体属、Hapuna噬菌体属、I3噬菌体属、Mu噬菌体属、P1噬菌体属、Pbuna噬菌体属、PhiCD119噬菌体属、ΦH噬菌体属、Phikz噬菌体属、Viuna噬菌体属、弯曲噬菌体亚科、Cp220噬菌体属、Cp8una噬菌体属、P2噬菌体亚科、Hpuna噬菌体属、P2噬菌体属、SPO1噬菌体亚科、SPO1噬菌体属、Twort噬菌体属、T4噬菌体亚科、Schizot4噬菌体属或T4噬菌体属。在一个实施例中，肌尾噬菌体科溶源体来源于P1噬菌体属。在另一个实施例中，肌尾噬菌体科溶源体是肠杆菌噬菌体P1(P1噬菌体)。

[0036] 在一个实施例中，互补核酸分子在基因破坏位点整合到肌尾噬菌体科溶源体中。在另一个实施例中，互补核酸分子在除基因破坏位点之外的位点整合到肌尾噬菌体科溶源体中。在又一个实施例中，互补核酸分子整合到细菌细胞的基因组中。在又一个实施例中，互补核酸分子整合到质粒分子中。

[0037] 在一个实施例中，将两个或多个受体结合区与尾相互作用区融合是通过cin重组酶并在多个cix重组位点存在的情况下进行的。在一个实施例中，通过cin重组酶或cin重组酶的同源物、直系同源物或旁系同源物，并在存在多个相关重组位点的情况下，将两个或更多个受体结合区与尾相互作用区融合。在一个实施例中，两个或更多个不同的尾丝结构蛋白编码基因在操纵子中表达。在另一个实施例中，两个或更多个不同的尾丝结构蛋白编码基因由独立的启动子表达。在又一个实施例中，从独立的基因组位置表达两个或更多个不同的尾丝结构蛋白编码基因。

[0038] 在另一方面，本发明涉及一种细菌细胞包装系统，用于将报告分子或治疗性核酸分子包装成非复制性转导颗粒(NRTP)以引入细胞，该包装系统包括：宿主细菌细胞；噬菌体溶源体，其含有阻止对天然尾丝的产生至关重要的一种或多种基因或这些基因的任意组合的表达的基因破坏，其中所述一种或多种基因编码负责结合受体的尾丝结构蛋白、折叠尾丝结构蛋白的一个或多个区域所需的分子伴侣、将尾丝结构蛋白连接至尾结构所需的蛋白；并且还包含含有非功能性包装起始位点序列的第一噬菌体基因，其中该非功能性包装起始位点序列防止噬菌体基因组优先包装到NRTP中；一个或多个互补核酸分子，其包含补偿噬菌体溶源体的基因破坏从而产生功能性尾丝的选自编码以下项的基因的一种或多种基因或这些基因的任意组合：负责结合受体的尾丝结构蛋白、折叠尾丝结构蛋白的一个或多个区域所需的分子伴侣、连接受体将尾丝结构蛋白连接到尾结构所需的蛋白；以及报告分子或治疗性核酸分子和含有功能性包装起始位点序列的第二噬菌体基因，该功能性包装起始位点序列用于促进报告核酸分子的复制子包装到NRTP中，其中报告核酸分子上的功能性包装起始位点序列补偿噬菌体溶源体中的非功能性包装起始位点序列。

[0039] 在一个实施例中，报告基因是luxAB。在另一个实施例中，报告基因是荧光报告蛋白。在一些实施例中，荧光报告蛋白包括但不限于绿色荧光蛋白(GFP)、黄色荧光蛋白(YFP)、青色荧光蛋白(CFP)和红色荧光蛋白(RFP)。在一个实施例中，第一噬菌体基因和第二噬菌体基因是pacA终止酶基因。在另一个实施例中，第一噬菌体基因和第二噬菌体基因是terS终止酶基因。

[0040] 在另一方面，本发明涉及产生能够识别和转导细菌细胞以用于诊断或治疗用途的肌尾噬菌体科噬菌体或肌尾噬菌体科衍生的NRTP的方法，包括：提供含有本发明的的噬菌体尾丝替换平台的细菌细胞，其中互补核酸分子包含对肌尾噬菌体科溶源体非天然的且部分或完全源自肌尾噬菌体科、长尾噬菌体科(如SEQ ID No:5、10、32、33中所示)或短尾噬菌

体科尾丝序列的尾丝基因;并为细菌细胞提供条件,以诱导噬菌体溶源体的裂解期来产生肌尾噬菌体科噬菌体或肌尾噬菌体科衍生的NRTP,其能够识别和转导先前对天然肌尾噬菌体科噬菌体或肌尾噬菌体科衍生的NRTP颗粒难治的细菌,用于诊断或治疗用途。

[0041] 在一个实施例中,肌尾噬菌体科噬菌体或肌尾噬菌体科衍生的NRTP源于选自以下的属:Bcep781噬菌体属、Bcepmu噬菌体属、FelixO1噬菌体属、Hapuna噬菌体属、I3噬菌体属、Mu噬菌体属、P1噬菌体属、Pbuna噬菌体属、PhiCD119噬菌体属、ΦH噬菌体属、Phikz噬菌体属、Viuna噬菌体属、弯曲噬菌体亚科、Cp220噬菌体属、Cp8una噬菌体属、P2噬菌体亚科、Hpuna噬菌体属、P2噬菌体属、SPO1噬菌体亚科、SPO1噬菌体属、Twort噬菌体属、T4噬菌体亚科、Schizot4噬菌体属或T4噬菌体属。在一个实施例中,肌尾噬菌体科噬菌体或肌尾噬菌体科衍生的NRTP源自P1噬菌体属。在另一个实施例中,肌尾噬菌体科噬菌体或肌尾噬菌体科衍生的NRTP是肠杆菌噬菌体P1(P1噬菌体)。

附图说明

[0042] 本发明的这些和其他特征、方面和优点将通过以下描述和附图更好地理解,其中:

[0043] 图1为示出尾丝交换平台的图。

[0044] 图2天然P1尾丝基因组区域的图。基因r编码一种尾丝辅助蛋白,假定其参与将尾丝连接到尾结构。cin基因编码序列特异性重组酶,其在Cin重组位点(称为cix位点)之间翻转DNA,从而能够从单个DNA片段中表达两个不同的尾丝,位点在图中用圆圈表示。基因u和u'编码不同的尾丝辅助蛋白,它们被认为作为分子伴侣分别折叠S和S'尾丝蛋白的结合结构域(结合结构域分别由s_v和s_v'编码序列编码)。S和S′尾丝蛋白两者的保守区由s_c编码序列编码,根据Cin重组酶的活性,该编码序列在转录和翻译上与s_v或s_v'融合。

[0045] 图3尾丝替换平台的图。含有壮观霉素抗性盒代替s和u基因的尾丝缺陷(秃)包装线,被诱导表达重组工程机构(SEQ ID NO:97),并包含操纵子启动子、r基因、壮观霉素抗性启动子、壮观霉素抗性基因、u'基因、sv'编码区、cin基因和cin启动子。然后将带有新尾丝、潮霉素抗性盒和侧翼同源臂的PCR片段转化到诱导的菌株中(在本例中为"三叶草"和"三叶草"u)。重组工程机构将新尾丝操纵子整合取代壮观霉素抗性盒-u'-s_v'区域,以生成能够生产具有尾丝的Smarticle的新染色体包装线。

[0046] 图4尾丝染色体整合后改进的Smarticle性能。图表比较了具有从质粒(TFDV)或染色体表达的尾丝的Smarticle的性能。示出了仅包含S′(左上)、S(右上)或"三叶草"(左下)尾丝的Smarticle对各种大肠杆菌菌株的反应性。右下,与质粒表达的相比,从基因组整合的S尾丝包装线获得的Smarticle产量提高。V3 Smarticle(天然尾丝区域)作为阳性对照提供。

[0047] 图5示出了通过表达天然U蛋白同源物或来自噬菌体基因组的提高的尾丝活性。A)在表达或不表达质粒p15B U蛋白同源物T的包装线中生产的"印度"NRTP的性能;B)从噬菌体基因组或单独的包装质粒产生的"猩红"NRTP的性能。

[0048] 图6在单一生产线A)表达一种、两种、三种或更多种功能性尾丝的单一细菌包装线中生产一种、两种或更多种尾丝。S、S′和三叶草尾丝与抗生素标志物一起添加到包装线。尾丝基因可以与cix交叉位点排列在新的位置。基因的表达也可以布置为不依赖于大或小操纵子的重组。B)从表达单尾丝(表示为S、S′、Smrk)以及工程化双尾丝和三尾丝菌株(表示为

V3、双倍、三倍)的包装生产线产生裂解物。使用对单尾丝具有特异性反应性的大肠杆菌菌株来展示从单个宿主表达多种功能性尾丝。

[0049] 图7双功能Smarticle包装线分析。双功能P1衍生的Smarticle被赋予“Jazzberry”和“三叶草”尾丝两者。A)基因组整合的“ShamJazz”双表达系统的基因排列的卡通描述。B)确认对“Jazzberry”、“三叶草”或“V3”(S和S′)尾丝具有特异性的菌株的双功能活性。C)预测的和/或观察到的选择各个和组合的Smarticle对一组大肠杆菌菌株的活性(EcoAD组合)。百分比覆盖率如下所示,茎须图描绘了组合上的光分布。D)双功能Smarticle的预测活性和观察到的活性(紫色)的比较,它们无法区分。*表示累积预测覆盖率与实际实验观察到的覆盖率。

[0050] 图8功能性尾丝所需元件的建立A)3个不同的尾丝Sc区域(参见天然P1、“Plum”和“橘色”)在P1底盘上功能化,扩展了对功能性尾丝所需决定因素的理解。所有构建体都含有编码R蛋白的P1r基因。每个尾丝可变区(S_v)在与其同源U辅助蛋白表达时功能最强。B)3个功能性S_c区域的蛋白质比对表明N端250个氨基酸很重要。

[0051] 图9显示了从发酵菌株中表达尾丝基因的各种排列。A)示出了来自噬菌体基因组的尾丝和病毒底盘的表达。B)示出从噬菌体基因组表达的病毒底盘和来自包装质粒的尾丝基因。C)示出来自噬菌体基因组的病毒底盘和来自独立质粒的尾丝。D)示出来自噬菌体基因组的病毒底盘和来自细菌基因组的尾丝。E)示出来自噬菌体基因组的病毒底盘和一组尾丝。第二组独特的尾丝由独立的质粒表达。F)示出来自噬菌体基因组的病毒底盘和尾丝。第二组独特的尾丝由包装质粒表达。G)示出来自噬菌体基因组的病毒底盘和两组独特的尾丝。

具体实施方式

[0052] 定义

[0053] 除非另有说明,权利要求和说明书中使用的术语定义如下。

[0054] 如本文所用,“报告核酸分子”是指包含DNA或RNA分子的核苷酸序列。报告核酸分子可以是天然存在的或人工或合成分子。在一些实施例中,报告核酸分子对于宿主细胞是外源的,并且可以作为外源核酸分子诸如质粒或载体的一部分被引入宿主细胞。在某些实施例中,报告核酸分子可以与细胞中的靶基因互补。在其他实施例中,报告核酸分子包含编码报告分子(例如报告酶、蛋白质)的报告基因。在一些实施例中,报告核酸分子被称为“报告构建体”或“核酸报告构建体”。

[0055] 如本文所用,“治疗性核酸分子”是指通过序列特异性识别与疾病相关的靶核酸(例如反义核酸)或通过编码具有治疗活性的基因产物(例如抗菌蛋白)而具有治疗疾病的治疗作用的核苷酸序列。在一些实施例中,治疗性核酸分子可以作为外源核酸分子诸如质粒的一部分被引入宿主细胞。如本文所用,“治疗性表达质粒”是指含有治疗性核酸分子的质粒,所述治疗性核酸分子编码具有治疗活性的基因产物。

[0056] “报告分子(reporter molecule或reporter)”是指赋予生物体可检测或可选择表型的分子(例如,核酸或蛋白质)。例如,可检测的表型可以是比色的、荧光的或发光的。报告分子可以由编码介导发光反应的酶的报告基因(luxA、luxB、luxAB、luc、ruc、nluc)、编码介导比色反应的酶的基因(lacZ、HRP)、编码荧光蛋白的基因(GFP、eGFP、YFP、RFP、CFP、BFP、

mCherry、近红外荧光蛋白)、编码亲和肽的核酸分子(His-tag、3X-FLAG)和编码可选择标志物的基因(ampC、tet(M)、CAT、erm)。报告分子可用作将核酸分子或外源序列(质粒)成功摄取到细胞中的标志物。如本文所述,报告分子还可用于指示靶基因、靶核酸分子、靶细胞内分子或细胞的存在。可替代地,报告分子可以是核酸,诸如适体或核酶。

[0057] 在本发明的一些方面,报告核酸分子与启动子可操作地联接。在本发明的其他方面,基于启动子在特定细胞(例如,特定物种)中而不是在其他细胞中的活性,可以选择或设计启动子以有助于报告系统的反应性和交叉反应性。在某些方面,报告核酸分子包含复制起点。在其他方面,当报告核酸分子在靶细胞内的复制有助于或必需于报告信号产生时,基于复制起点在特定细胞(例如,特定物种)中而不是在其他细胞中的活性,复制起点的选择可类似地有助于报告系统的反应性和交叉反应性。在一些实施例中,报告核酸分子形成能够在病毒复制过程中作为多联体DNA包装到子代病毒中的复制子。

[0058] 如本文所用,“靶转录本”是指由靶细胞自然形成的DNA序列或mRNA分子的核苷酸序列的一部分,包括在靶基因和mRNA的转录过程中形成的,其为初级转录产物的RNA加工产物。靶转录本也可称为细胞转录本或天然存在的转录本。

[0059] 如本文所用,术语“转录本”是指从DNA或RNA模板序列或基因转录的一段核苷酸序列(DNA或RNA)。转录本可以是从RNA模板转录的cDNA序列或从DNA模板转录的mRNA序列。转录本可以是蛋白质编码的或非编码的。转录本也可以从工程化核酸构建体转录。

[0060] 源自报告核酸分子的转录本可称为“报告转录本”。报告转录本可以包括报告序列和顺式抑制序列。报告转录本可以具有形成互补区域的序列,使得转录本包括形成双链体的两个区域(例如,分子间双链体区域)。一个区域可以称为“顺式抑制序列”并且与部分或全部靶转录本和/或报告序列具有互补性。转录本的第二个区域称为“报告序列”,可以与顺式抑制序列互补。互补可以是完全互补或实质互补。顺式抑制序列与报告序列的存在和/或结合可以在报告转录本中形成构象,这可以阻断报告分子的进一步表达。报告转录本可以形成二级结构,诸如发夹结构,使得报告转录本内彼此互补的区域可以彼此杂交。

[0061] 如本领域技术人员所理解的,在提及核酸分子或外源序列(例如,质粒、载体、构建体)时“引入细胞内”是指促进摄取或吸收进入细胞。核酸构建体或转录本的吸收或摄取可通过独立的扩散或活性细胞过程,或通过辅助剂或装置,包括通过使用噬菌体、病毒和转导颗粒而发生。该术语的含义不限于体外细胞;核酸分子也可以“引入细胞内”,其中细胞是活生物体的一部分。在此类情况下,引入细胞内将包括递送至生物体。例如,对于体内递送,本发明的核酸分子、构建体或载体可以注射到组织部位或全身施用。体外引入细胞内包括本领域已知的方法,诸如电穿孔和脂质转染。进一步的方法在本文中描述或在本领域中已知。

[0062] “转导颗粒”是指能够将非病毒核酸分子递送到细胞中的病毒。病毒可以是噬菌体、腺病毒等。

[0063] “噬菌体尾状颗粒”或“噬菌体尾状结构”是指细菌产生的高分子量噬菌体尾状蛋白复合物,其形式类似于噬菌体尾,但不编码或递送复制病毒基因组,因此不是病毒。噬菌体尾状颗粒或结构的非限制性实例包括在多种细菌类型中发现的6型分泌系统(T6SS)和R型尾菌素(也称为脓菌素)。在Williams et al.,Applied and Environmental Microbiology,2008,74:12,3868-3876,and in Scholl et al.,Antimicrobial Agents and Chemotherapy,2009,53:7,3074-3080中可以找到对这些颗粒的进一步描述。虽然这些

实例结构不编码病毒衣壳头部，但它们能够介导结合和尾部注射到靶细胞中，从而杀死靶细胞或递送蛋白效应物。噬菌体尾状颗粒或结构可以包含和利用特异性决定元件，诸如尾丝，因此可以挖掘它们的基因序列以重新靶向细胞结合特异性。SEQ ID NO:11的核苷酸序列示出了源自脓菌素的尾丝的一个实例。

[0064] “非复制性转导颗粒”或“NRTP”是指能够将非病毒核酸分子递送到细胞中但不能将其自身复制的病毒基因组包装到转导颗粒中的病毒。病毒可以是噬菌体、腺病毒等。

[0065] “质粒”是一种小的DNA分子，它与细胞内的染色体DNA物理分离，并且可以独立进行复制。最常见的是细菌中的小环状双链DNA分子，质粒有时存在于古细菌和真核生物中。质粒被认为是复制子，能够在合适的宿主内自主复制。如本文所用，术语“包装质粒”是指编码包装到给定病毒衣壳中所需的元件(即包装基因)和可表达的报告基因两者的质粒。如本文所用，术语“尾丝展示载体”(缩写为“TFDV”)是指编码被包装到给定病毒衣壳中所需的元件、可表达的报告基因、和产生能够附接在给定的衣壳的结合蛋白的尾丝编码序列的质粒。如本文所用，术语“二级尾丝表达质粒”是指编码功能性尾丝的质粒，所述功能性尾丝可附接至给定衣壳，但不一定包含报告分子或包装位点/机构。

[0066] “载体”是一种用作运载器的核酸分子，将外源遗传物质人工携带到另一个细胞中，在那里它可以被复制和/或表达。

[0067] “病毒”是一种小型传染因子，仅在其他生物体的活细胞内复制。病毒颗粒(称为病毒粒)包括两个或三个部分：i)由携带遗传信息的DNA或RNA分子构成的遗传物质；ii)保护这些基因的蛋白质外壳；和在某些情况下，iii)脂质包膜9388

[0068] 如本文所用，术语“补偿物/补偿”是指存在已被破坏的相同序列的非破坏序列，或非破坏序列与破坏序列的关系。在一个实施例中，补偿物包含在细胞中的多核苷酸上编码的基因，该基因是有功能的并且能够表达，并且与噬菌体上的破坏前的破坏基因表达具有相同功能的蛋白质。在一些实施例中，补偿物基因与破坏前的破坏噬菌体基因(即天然噬菌体基因)具有大于80％、85％、90％、91％、92％、93％、94％、95％、96％、97％、98％或99％的序列同一性。在一些实施例中，补偿物基因与破坏前的破坏噬菌体基因，即天然噬菌体基因相同。在一些实施例中，补偿物基因包含噬菌体中已缺失的多核苷酸序列。在一些实施例中，补偿物基因是指编码质粒上噬菌体的包装机构的基因，其中相同的基因已在噬菌体中被破坏。因此，质粒需要存在具有突变的包装机构基因的噬菌体，以提供将多核苷酸包装成转导颗粒所必需的包装机构。

[0069] 如本文所用，术语“包装相关酶活性”是指对于与包装起始位点序列相互作用以将多核苷酸包装成转导颗粒至关重要的一个或多个多肽。在一些实施例中，此类相互作用需要一对终止酶基因，其中每个终止酶编码包装相关酶活性。在一些实施例中，酶活性由来自金黄色葡萄球菌噬菌体φ11或φ80α的terS和/或terL基因、来自粪肠球菌噬菌体φEf11的terA和terB基因、或噬肠杆菌科噬菌体P1的pacA和pacB基因编码。在这些实施例中，这对终止酶基因中的每一个都表达包装相关酶活性，并且包装具有包装起始位点的多核苷酸需要两者的功能版本。在一些实施例中，与包装相关酶活性相关的多种基因中的一种基因的破坏消除了包装相关酶活性。在一些实施例中，在噬菌体上破坏了一对终止酶基因两者，从而破坏了噬菌体上的整套包装相关酶活性编码基因。

[0070] 术语“原位”是指在与活生物体分开生长的活细胞中发生的过程，例如，在组织培

养物中生长。

[0071] 术语“体内”是指在活生物体中发生的过程。

[0072] 如本文所用，术语“哺乳动物”包括人类和非人类两者，并且包括但不限于人类、非人灵长类动物、犬科动物、猫科动物、鼠科动物、牛科动物、马科动物和猪。

[0073] “G”、“C”、“A”和“U”通常分别代表含有鸟嘌呤、胞嘧啶、腺嘌呤和尿嘧啶作为碱基的核苷酸。“T”和“dT”在本文中可互换使用并且指脱氧核糖核苷酸，其中核碱基是胸腺嘧啶，例如脱氧核糖胸腺嘧啶。然而，应当理解，术语“核糖核苷酸”或“核苷酸”或“脱氧核糖核苷酸”也可以指经修饰的核苷酸，如下文进一步详述，或替代替换部分。技术人员非常清楚鸟嘌呤、胞嘧啶、腺嘌呤和尿嘧啶可以被其他部分替换，而不会实质上改变包含带有此类替换部分的核苷酸的寡核苷酸的碱基配对特性。例如但不限于，包含肌苷作为其碱基的核苷酸可以与包含腺嘌呤、胞嘧啶或尿嘧啶的核苷酸碱基配对。因此，含有尿嘧啶、鸟嘌呤或腺嘌呤的核苷酸可以在本发明的核苷酸序列中被含有例如肌苷的核苷酸替换。包含此类替换部分的序列是本发明的实施例。

[0074] 如本文所用，术语“互补”在用于描述与第二核苷酸序列相关的第一核苷酸序列时，是指包含第一核苷酸序列的寡核苷酸或多核苷酸在某些条件下杂交包含第二核苷酸序列的寡核苷酸或多核苷酸并形成双链体结构的能力，如技术人员将理解的。互补序列也被描述为相互结合，并以结合亲和力为特征。

[0075] 例如，当两个序列在严格杂交条件下杂交(例如，退火)时，第一核苷酸序列可以被描述为与第二核苷酸序列互补。杂交条件包括退火和/或洗涤步骤的温度、离子强度、pH和有机溶剂浓度。术语“严格杂交条件”是指第一核苷酸序列将优先与其靶序列例如第二核苷酸序列杂交，并且在较小程度上与其他序列杂交或根本不杂交的条件。严格杂交条件是序列依赖性的，在不同的环境参数下是不同的。通常，严格杂交条件的温度选择可以比核苷酸序列在规定的离子强度和pH下的热熔点(Tm)低约5℃。T_m是50％的第一核苷酸序列与完美匹配的靶序列杂交时的温度(在规定的离子强度和pH值下)。核酸杂交的广泛指南可见于例如Tijssen(1993)Laboratory Techniques in Biochemistry and Molecular Biology--Hybridization with Nucleic Acid Probes part I,chap.2,“Overview of principles of hybridization and the strategy of nucleic acid probe assays,”Elsevier,N.Y.(“Tijssen”)。可以应用其他条件，诸如可能在生物体内遇到的生理相关条件。技术人员将能够根据杂交核苷酸的最终应用确定最适合测试两个序列互补性的条件集。

[0076] 这包括在第一和第二核苷酸序列的整个长度上，将包含第一核苷酸序列的寡核苷酸或多核苷酸与包含第二核苷酸序列的寡核苷酸或多核苷酸碱基配对。此类序列在本文中可被称为彼此“完全互补”。然而，当第一序列相对于本文中的第二序列被称为“基本互补”时，这两个序列可以是完全互补的，或者它们杂交时可以形成一个或多个，但通常不超过4、3或2个错配碱基对，同时保留在与其最终应用最相关的条件下杂交的能力。然而，当两个寡核苷酸被设计为在杂交时形成一个或多个单链突出端时，此类突出端在决定互补性方面不应被视为错配。例如，包含一个长度为21个核苷酸的寡核苷酸和另一个长度为23个核苷酸的寡核苷酸的dsRNA(其中较长的寡核苷酸包含与较短的寡核苷酸完全互补的21个核苷酸的序列)，对于本文描述的目的可以称为“完全互补”。

[0077] 如本文所用，“互补”序列还可以包括或完全由非沃森-克里克碱基对和/或由非天

然和经修饰的核苷酸形成的碱基对，前提是完成上述关于它们的杂交能力的要求。此类非沃森-克里克碱基对包括但不限于G:U Wobble或Hoogstein碱基对。

[0078] 本文中的术语“互补的”、“完全互补的”和“基本互补的”可用于dsRNA的两条链之间的碱基匹配，或dsRNA的反义链和靶序列之间的碱基匹配，单链RNA序列或单链DNA序列的互补链之间的碱基匹配，从它们的使用上下文可以理解。

[0079] 如本文所用，“双链体结构”包含两个反向平行且基本互补的核酸序列。两个转录本之间、转录本内的两个区域之间或转录本与靶序列之间的核酸构建体中互补序列可以形成“双链体结构”。一般而言，每条链的大部分核苷酸是核糖核苷酸，但如本文详细描述的，每条或两条链还可以包括至少一种非核糖核苷酸，例如脱氧核糖核苷酸和/或经修饰的核苷酸。形成双链体结构的两条链可以是一个较大RNA分子的不同部分，或者它们可以是单独的RNA分子。如果两条链是一个较大分子的一部分，因此在一条链的3′-末端和相应的另一条链的5′-末端之间通过不间断的核苷酸链连接，形成双链体结构，则连接RNA链被称为“发夹环”。当两条链通过一条链的3′-末端和形成双链体结构的相应另一条链的5′-末端之间的不间断核苷酸链以外的方式共价连接时，该连接结构称为“连接基”。RNA链可以具有相同或不同数量的核苷酸。碱基对的最大数量是双链体最短链中核苷酸的数量减去双链体中存在的任何突出端。通常，双链体结构的长度为15至30或25至30、或18至25、或19至24、或19至21、或19、20或21个碱基对。在一个实施例中，双链体的长度为19个碱基对。在另一个实施例中，双链体的长度为21个碱基对。当两种不同的siRNA组合使用时，双链体长度可以相同或不同。

[0080] 如本文所用，术语“互补区域”是指反义链上与本文定义的序列例如靶序列基本互补的区域。在互补区域与靶序列不完全互补的情况下，在末端区域最能容忍错配，如果存在，通常在一个或多个末端区域，例如在5′和/或3′末端的6、5、4、3或2个核苷酸内。

[0081] 在两个或多个核酸或多肽序列的上下文中，术语“百分比同一性”是指两个或更多个序列或子序列具有特定百分比的相同核苷酸或氨基酸残基，当进行最大对应性的比较和比对时，如使用下述序列比较算法之一(例如，BLASTP和BLASTN或技术人员可用的其他算法)或通过目视检查来测量的。根据应用，“同一性”百分比可以存在于被比较序列的区域上，例如存在于功能结构域上，可替代地，存在于要比较的两个序列的全长上。

[0082] 对于序列比较，通常以一个序列作为参考序列，用测试序列与其比较。当使用序列比较算法时，将测试和参考序列输入电脑，指定子序列坐标，如有必要，指定序列算法程序参数。然后基于指定的程序参数，序列比较算法计算相对于参考序列的测试序列的序列同一性百分比。

[0083] 用于比较的最佳序列比对可以例如通过Smith&Waterman，Adv.Appl.Math.2:482(1981)的局部同源算法，通过Needleman&Wunsch，J.Mol.Biol.48:443(1970)的同源比对算法，通过Pearson&Lipman，Proc.Nat′l.Acad.Sci.USA 85:2444(1988)的搜索相似性方法，通过计算机实施这些方法(GAP，BESTFIT，FASTA，and TFASTA in the Wisconsin Genetics Software Package，Genetics Computer Group，575 Science Dr.，Madison，Wis.)，或通过目视检查(一般参见Ausubel et al.，infra)。

[0084] 适用于确定百分比序列同一性和序列相似性的算法的一个实例是BLAST算法，描述于Altschul et al.，J.Mol.Biol.215:403-410(1990)。用于执行BLAST分析的软件可通

过国立生物技术信息中心(www.ncbi.nlm.nih.gov/)公开地获得。

[0085] 术语“足够量”是指足以产生所需效果的量,例如足以从细胞产生可检测信号的量。

[0086] 术语“治疗有效量”是有效改善疾病症状的量。治疗有效量可以是“预防有效量”,因为预防可以被认为是治疗。

[0087] 必须注意的是,如在本说明书和所附权利要求中所用,单数形式“一个”、“一种”、“该”和“所述”包括复数指代物,除非上下文另外明确规定。

[0088] 病毒的溶源和裂解周期

[0089] 病毒在宿主细胞中经历溶源和裂解周期。如果采用溶源周期,噬菌体染色体可以整合到细菌染色体中,或者它可以在宿主中建立自己的稳定质粒,在那里它可以长时间保持休眠状态。如果溶源体被诱导,噬菌体基因组从细菌染色体上切除并启动裂解周期,最终导致细胞裂解和噬菌体颗粒的释放。裂解周期导致产生新的噬菌体颗粒,这些颗粒通过宿主裂解而释放。

[0090] 此外,基于病毒的报告分子测定,诸如基于噬菌体的报告分子,由于基于宿主和原噬菌体衍生的噬菌体抗性机制导致噬菌体宿主范围的限制,可能会受到有限的反应性(即分析包容性)的影响。这些抗性机制针对可导致降解或以其他方式抑制噬菌体DNA和功能的天然噬菌体核酸。此类抗性机制包括切割噬菌体DNA的限制系统和抑制噬菌体衍生转录本的CRISPR系统。

[0091] 裂解活性和噬菌体抗性两者都可以抑制基于报告噬菌体的测定。裂解活性可以通过破坏或以其他方式抑制细胞产生可检测信号的能力来抑制信号,从而通过减少可检测信号的量或阻止可检测信号的产生来影响检测限。噬菌体抗性机制可以限制噬菌体的宿主范围并限制基于噬菌体的报告分子的包容性,同样通过减少可检测信号的量或阻止可检测信号的产生来影响检测限。在报告噬菌体中掺入噬菌体DNA引起的裂解活性和噬菌体抗性两者,都会导致在掺入这些噬菌体报告分子的测定中出现假阴性结果。

[0092] III.生产非复制性转导颗粒(NRTP)的方法

[0093] 用于生产非复制性转导颗粒的基于破坏/补偿的方法。

[0094] 本文公开了基于病毒基因组组分的破坏的非复制性转导颗粒包装系统,该组分被病毒包装机制识别为在病毒生产期间启动基因组包装的元件。在某一实施例中,这种破坏破坏了噬菌体的包装起始位点,并且还破坏了终止酶功能。被破坏的元件的实例包括pac型噬菌体的pac位点序列和cos型噬菌体的cos位点序列。当噬菌体内的包装起始位点序列被破坏时,噬菌体不能产生功能性终止酶。在一个实例中,pac位点在pacA基因序列内编码,并且终止酶功能需要功能性PacA和PacB两者。通过补偿所述破坏的终止酶并在质粒DNA上包括可识别的包装起始位点,质粒DNA被包装到噬菌体衣壳中。噬菌体可以是任何噬菌体,诸如肠杆菌科噬菌体P1或φEF11,或金黄色葡萄球菌噬菌体φ80α或噬菌体φ11。

[0095] 包装起始位点通常位于病毒生产所必需的基因编码区内。噬菌体基因组的区域可以通过插入、替换、缺失或破坏包装起始位点的突变来破坏。实现这种破坏的实例包括但不限于等位基因交换事件,该事件将包含包装起始位点序列的噬菌体基因组上的序列替换为另一个序列(诸如抗生素抗性基因的序列),或完全删除小终止酶基因和大终止酶基因。在使用终止酶基因pacA和pacB的实例中,pacA可以以引起极性效应的方式破坏,该极性效应

也破坏pacB表达和/或由PacA和PacB介导的总体终止酶功能。其他实例可以包括终止酶基因，也可以包括来自金黄色葡萄球菌噬菌体Φ11或Φ80α的terS和terL基因，或来自粪肠球菌噬菌体ΦEf11的terS和terL基因

[0096] 在一个实例中，细胞的基因组被病毒基因组溶源化，其中病毒基因组的包装起始位点已被破坏。在一些实施例中，细胞可以是大肠杆菌细胞、金黄色葡萄球菌细胞或粪肠球菌细胞。细胞可以是革兰氏阴性或革兰氏阳性。将补偿质粒(或报告核酸分子)引入细胞中，质粒DNA至少包括在噬菌体中被破坏的基因、以及包装起始位点序列、以及任选地额外的噬菌体基因和报告基因(其可以编码可检测和/或可选择的标志物)。可以使用U.S.专利No.9,388,453和U.S专利申请No.2017/0166907中发现的方法构建质粒。质粒的一种或多种基因可以与启动子可操作地连接，诸如诱导型启动子(当通过诱导噬菌体启动包装时可以诱导启动子)。在一些实施例中，启动子可以是小终止酶基因或大终止酶基因的天然启动子。天然启动子可以被噬菌体控制，因此有效地充当包装过程中诱导的条件启动子。

[0097] 在一些实例中，优选地设计破坏/补偿以使得突变的病毒DNA和补偿性外源DNA之间没有同源性。这是因为突变的病毒DNA和补偿的外源DNA之间缺乏同源性，避免了两个DNA分子之间发生同源重组的可能性，这会导致将包装序列重新引入病毒基因组。为了消除同源性，一种策略是从病毒基因组中删除包含包装起始位点序列的全部基因(或多种基因)，然后用外源DNA分子补偿该基因，外源DNA分子优选不超过从病毒中删除的确切DNA序列。在该策略中，补偿性DNA分子被设计为表达从病毒中删除的基因。此类系统的另一个实例是使用噬菌体 φ80α，一种pac型噬菌体。噬菌体基因组在宿主细菌细胞中溶源化，噬菌体基因组包括小终止酶基因，其中pac型原噬菌体 φ80α 的pac位点已被删除。将包含具有天然pac位点的补偿性小终止酶基因的质粒转化到细胞中。当溶源化原噬菌体的裂解周期被诱导时，噬菌体包装系统将质粒DNA包装成子代噬菌体结构组分，而不是包装天然噬菌体DNA。因此，包装系统产生携带质粒DNA的非复制性转导颗粒。

[0098] 报告基因编码可检测标志物或可选择标志物。在一个实例中，报告基因选自由介导发光反应的酶(luxA、luxB、luxAB、luc、ruc、nluc)、介导比色反应的酶(lacZ、HR)、荧光蛋白(GFP、eGFP、YFP、RFP、CFP、BFP、mCherry、近红外荧光蛋白)、亲和肽(His-tag、3X-FLAG)和可选择标志物(ampC、tet(M)、CAT、erm)组成的组。在某一实施例中，报告基因是luxA。在一些实施例中，抗性标志物包含抗生素抗性基因。在一些实施例中，抗性标志物是卡那霉素抗性基因(kan)。在一些实施例中，组成型启动子包含Pblast。在一些实施例中，噬菌体基因组破坏通过等位基因交换事件完成，该事件替换或破坏噬菌体基因组上包含包装起始位点序列的序列。

[0099] 在一个实例中，噬菌体基因组上的一对终止酶基因，例如pacA和pacB、terA和terB、或terS和terL，可以以引起极性效应的方式被破坏，该极性效应也破坏了一个终止酶基因的表达和/或由终止酶基因介导的总体终止酶功能。破坏的噬菌体可以用包含噬菌体基因组的终止酶基因(例如pacA和pacB、terA和terB、或terS和terL)的质粒来补偿。当突变病毒进行裂解周期时，由噬菌体基因组或(如果被破坏)补偿性质粒产生的病毒包装蛋白会将质粒DNA的复制子包装到包装单元中(因为它包含包装起始位点)，并且产生携带复制质粒DNA的非复制转导颗粒。

[0100] 报告分子

[0101] 在一些实施例中，本发明的NRTP和构建体包含含有报告基因的报告核酸分子。报告基因可以编码报告分子，报告分子可以是可检测或可选择的标志物。在某些实施例中，报告基因编码在细胞中表达时产生可检测信号的报告分子。

[0102] 在某些实施例中，报告分子可以是荧光报告分子，诸如但不限于绿色荧光蛋白(GFP)、增强型GFP、黄色荧光蛋白(YFP)、青色荧光蛋白(CFP)、蓝色荧光蛋白(BFP)、红色荧光蛋白(RFP)或mCherry、以及近红外荧光蛋白。

[0103] 在其他实施例中，报告分子可以是介导发光反应的酶(LuxA、LuxB、LuxAB、Luc、Ruc、nLuc等)。报告分子可以包括细菌萤光素酶、真核萤光素酶、适合比色检测的酶(LacZ、HRP)、适合免疫检测的蛋白质诸如亲和肽(His-tag、3X-FLAG)、用作适体或表现出酶活性的核酸(核酶)、或可选择标志物诸如抗生素抗性基因(ampC、tet(M)、CAT、erm)。本领域已知的其他报告分子可用于产生信号以检测靶核酸或细胞。

[0104] 在其他方面，报告分子包括核酸分子。在一些方面，报告分子是具有特异性结合活性或表现出酶活性的适体(例如，适体酶、DNA酶、核酶)。

[0105] 报告分子和报告分子测定在本文的第V部分中进一步描述。

[0106] V.NRTP和报告分子测定

[0107] 诱导报告分子测定

[0108] 在一些实施例中，本发明包括使用NRTP作为报告分子以与靶向活细胞内的基因启动子的内源性或天然诱导剂一起使用的方法。本发明的NRTP可以使用第III部分和以下实例1-2中描述的方法工程化。

[0109] 在一些实施例中，该方法包括使用NRTP作为报告分子，其中NRTP包含与控制靶细胞内靶基因表达的诱导型启动子可操作联接的报告基因。当包含报告基因的NRTP被引入靶细胞时，通过诱导报告核酸分子中的靶基因启动子，报告基因的表达是可能的。

[0110] 转录本

[0111] 如上所述，转录本是从DNA或RNA模板序列或基因转录的一段核苷酸序列(DNA或RNA)。转录本可以是从RNA模板转录的cDNA序列或从DNA模板转录的mRNA序列。转录本可以从工程化的核酸构建体转录。转录本可以在其自身内具有互补区域，使得转录本包括可以形成分子内双链体的两个区域。一个区域可以称为“顺式抑制序列”，它结合并阻断报告序列的翻译。转录本的第二个区域称为“报告序列”，它编码报告分子，诸如可检测或可选择的标志物。

[0112] 本发明的转录本可以是长度为5个、6个、7个、8个、9个、10个、11个、12个、13个、14个、15个、16个、17个、18个、19个、20个、21个、22个、23个、24个或25个核苷酸的转录本序列。在其他实施例中，转录本的长度可为至少25、30、40、50、60、70、80、90、100、500、1000、1500、2000、3000、4000、5000或更多个核苷酸。顺式抑制序列和报告序列的长度可以相同或不同。

[0113] 在一些实施例中，顺式抑制序列与报告序列隔开1、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、35、40、45、50、55、60或更多个间隔核苷酸。

[0114] 载体

[0115] 在另一方面，本发明的转录本(包括反义和有义序列)由插入到DNA或RNA载体中的

转录单位表达(参见例如,Couture,A,et al.,TIG.(1996),12:5-10;Skillem,A.,et al.,国际PCT公开No.WO 00/22113,Conrad,国际PCT公开No.WO 00/22114,以及Conrad,U.S.专利No.6,054,299)。这些序列可以作为线性构建体、环状质粒或病毒载体引入,包括基于噬菌体的载体,它们可以作为整合到宿主基因组中的转基因来掺入和遗传。还可以构建转录本以允许其作为染色体外质粒遗传(Gassmann,et al.,Proc.Natl.Acad.Sci.USA(1995)92:1292)。

[0116] 转录序列可由位于表达质粒上的启动子转录。在一个实施例中,顺式抑制和报告序列表达为通过连接基多核苷酸序列连接的反向重复序列,使得转录本具有茎和环结构。

[0117] 重组表达载体可用于表达本发明的转录本。重组表达载体一般为DNA质粒或病毒载体。表达转录本的病毒载体的构建可以基于但不限于腺相关病毒(综述参见Muzyczka,et al.,Curr.Topics Micro.Immunol.(1992)158:97-129));腺病毒(参见例如,Berkner,et al.,BioTechniques(1998)6:616),Rosenfeld et al.(1991,Science 252:431-434)和Rosenfeld et al.(1992),Cell 68:143-155));或甲病毒以及本领域已知的其他病毒。逆转录病毒已被用于在体外和/或体内将多种基因引入许多不同的细胞类型,包括上皮细胞(参加例如Eglitis,et al.,Science(1985)230:1395-1398;Danos and Mulligan,Proc.Natl.Acad.Sci.USA(1998)85:6460-6464;Wilson et al.,1988,Proc.Natl.Acad.Sci.USA 85:3014-3018;Armentano et al.,1990,Proc.Natl.Acad.Sci.USA 87:61416145;Huber et al.,1991,Proc.Natl.Acad.Sci.USA 88:8039-8043;Ferry et al.,1991,Proc.Natl.Acad.Sci.USA 88:8377-8381;Chowdhury et al.,1991,Science 254:1802-1805;van Beusechem.et al.,1992,Proc.Natl.Acad.Sci.USA 89:7640-19;KaV et al.,1992,Human Gene Therapy 3:641-647;Dai et al.,1992,Proc.Natl.Acad.Sci.USA 89:10892-10895;Hwu et al.,1993,J.Immunol.150:4104-4115;U.S.专利No.4,868,116;U.S.专利No.4,980,286;PCT申请WO 89/07136;PCT申请WO 89/02468;PCT申请WO 89/05345;和PCT申请WO 92/07573)。能够转导和表达插入细胞基因组的基因的重组逆转录病毒载体可以通过将重组逆转录病毒基因组转染到合适的包装细胞系诸如PA317和Psi-CRIP中来生产(Comette et al.,1991,Human Gene Therapy 2:5-10;Cone et al.,1984,Proc.Natl.Acad.Sci.USA 81:6349)。重组腺病毒载体可用于感染易感宿主(例如,大鼠、仓鼠、狗和黑猩猩)中的多种细胞和组织(Hsu et al.,1992,J.Infectious Disease,166:769),以及具有不需要有丝分裂活性细胞进行感染的优点。

[0118] 可以使用能够接受待表达转录本的编码序列的任何病毒载体,例如,源自腺病毒(AV)、腺相关病毒(AAV)、逆转录病毒(例如,慢病毒(LV)、弹状病毒、鼠白血病病毒)、疱疹病毒等的载体。病毒载体的趋向性可以通过用来自其他病毒的包膜蛋白或其他表面抗原对载体进行假型化,或适当地替换不同的病毒衣壳蛋白来修饰。

[0119] 例如,本发明中的慢病毒载体可以用来自水泡性口炎病毒(VSV)、狂犬病毒、埃博拉病毒、莫科拉病毒等的表面蛋白进行假型化。通过工程化载体以表达不同的衣壳蛋白血清型,可以使本发明中的AAV载体靶向不同的细胞。构建表达不同衣壳蛋白血清型的AAV载体的技术在本领域技术范围内;参见例如Rabinowitz J E et al.(2002),J Virol 76:791-801。

[0120] 适用于本发明的重组病毒载体的选择、将表达转录本的核酸序列插入载体的方法以及将病毒载体递送至目标细胞的方法均在本领域技术范围内。参见例如Dornburg R(1995),Gene Therap.2:301-310;Eglitis M A(1988),Biotechniques 6:608-614;Miller A D(1990),Hum Gene Therap.1:5-14;Anderson W F(1998),Nature 392:25-30;和Rubinson D A et al.,Nat.Genet.33:401-406。

[0121] 病毒载体可以衍生自AV和AAV。用于表达本发明特征转录本的合适AV载体、构建重组AV载体的方法以及将载体递送到靶细胞中的方法描述于Xia H et al.(2002),Nat.Biotech.20:1006-1010。用于表达本发明特征的转录本的合适AAV载体、构建重组AV载体的方法以及将载体递送到靶细胞中的方法描述于Samulski R et al.(1987),J.Virol.61:3096-3101;Fisher K J et al.(1996),J.Virol,70:520-532;Samulski R et al.(1989),J.Virol.63:3822-3826;U.S.专利No.5,252,479;U.S.专利No.5,139,941;国际专利申请No.WO 94/13788;和国际专利申请No.WO 93/24641。

[0122] 驱动本发明表征的DNA质粒或病毒载体中转录本表达的启动子可以是真核RNA聚合酶I(例如核糖体RNA启动子)、RNA聚合酶II(例如CMV早期启动子或肌动蛋白启动子或U1 snRNA启动子)或通常是RNA聚合酶III启动子(例如U6 snRNA或7SK RNA启动子)或原核启动子,例如T7启动子,前提是表达质粒还编码从T7启动子转录所需的T7 RNA聚合酶。启动子还可以将转基因表达引导至胰腺(参见例如,胰腺的胰岛素调节序列(Bucchini et al.,1986,Proc.Natl.Acad.Sci.USA 83:2511-2515))。

[0123] 此外,转录本的表达可以被精确调节,例如,通过使用可诱导的调节序列和表达系统,诸如对某些生理调节剂(例如循环葡萄糖水平或激素)敏感的调节序列(Docherty et al.,1994,FASEB J.8:20-24)。此类适用于控制细胞或哺乳动物中转基因表达的诱导型表达系统包括通过蜕皮激素、雌激素、孕酮、四环素、二聚化化学诱导剂和异丙基-β-D-1-硫代吡喃半乳糖苷(IPTG)进行调节。本领域技术人员将能够基于dsRNA转基因的预期用途选择合适的调节/启动子序列。

[0124] 通常,能够表达转录分子的重组载体如下所述递送,并在靶细胞中持续存在。可替代地,可以使用提供转录分子瞬时表达的病毒载体。此类载体可以根据需要重复施用。一旦表达,转录本就会与靶RNA结合并调节其功能或表达。转录本表达载体的递送可以是全身性的,诸如通过静脉内或肌肉内施用、通过施用至从患者外植的靶细胞然后重新引入患者、或通过允许引入所需靶细胞的任何其他方式。

[0125] 转录表达DNA质粒通常作为与阳离子脂质载体(例如Oligofectamine)或非阳离子脂质载体(例如Transit-TKO^{TM})的复合物转染到靶细胞中。本发明还考虑在一周或更长时间内针对单个PROC基因或多个PROC基因的不同区域的dsRNA介导的敲降的多次脂质转染。可以使用各种已知方法监测载体成功引入宿主细胞。例如,瞬时转染可以用报告分子发出信号,诸如荧光标志物,诸如绿色荧光蛋白(GFP)。可使用标志物确保转染细胞对特定环境因素(例如抗生素和药物)具有抗性,诸如潮霉素B抗性,从而确保离体细胞的稳定转染。

[0126] 包含重组DNA的载体的递送可以通过非生物或生物系统进行。包括但不限于脂质体、病毒样颗粒、源自噬菌体或病毒的转导颗粒以及缀合物。

[0127] 用于转录本测定的报告分子

[0128] 在一些实施例中,核酸构建体包含报告序列(例如,报告基因序列)。报告基因编码

报告分子，当在细胞中表达时产生信号。在一些实施例中，报告分子可以是可检测或可选择的标志物。在某些实施例中，报告分子可以是荧光报告分子，诸如绿色荧光蛋白(GFP)、黄色荧光蛋白(YFP)、青色荧光蛋白(CFP)、蓝色荧光蛋白(BFP)或红色荧光蛋白(RFP)。在其他实施例中，报告分子可以是化学发光蛋白。

[0129] 报告分子可以是细菌萤光素酶、真核萤光素酶、荧光蛋白、适合比色检测的酶、适合免疫检测的蛋白质、适合免疫检测的肽或用作适体或表现出酶活性的核酸。

[0130] 可选择标志物也可用作报告分子。例如，可选择标志物可以是抗生素抗性基因。

[0131] 实例

[0132] 实例1:用于生产具有非天然尾丝的非复制性转导颗粒的基于破坏/补偿的方法。

[0133] 尾丝替换平台的图如图1所示。NTRP与其靶细菌细胞的附接是由噬菌体尾丝介导的。通过去除天然P1 NRTP尾丝基因，创建了一个“秃”底盘来测试异源尾丝的功能。然后使用尾丝展示载体(TFDV)在“秃”背景中表达新的尾丝。使用Murphy et al.(1998)的λ-RED重组工程化方法修饰了基于P1的Smarticle基因组，以在编码S结构尾丝蛋白和U尾丝组装分子伴侣蛋白的基因中创建缺失。这种破坏创造了一个平台来表达任何所需的反式尾丝。细菌菌株在Luria-Bertani(LB)肉汤和LB琼脂上生长，抗生素浓度如下:庆大霉素15μg/mL、卡比西林(Cabinicillin)100μg/mL、壮观霉素50μg/mL、Zeocin 100μg/mL和潮霉素150μg/mL。新英格兰生物实验室(NEB)克隆菌株NEB5a用于繁殖和存档质粒。使用NEB Gibson Assembly Master Mix生产用于质粒的DNA组装以及用于重组工程化的线性DNA产物。EMD Millipore KOD Xtreme热启动聚合酶用于在所有PCR反应中扩增DNA。

[0134] 实例2:构建“秃”P1底盘

[0135] 将λ-RED编码重组工程化质粒pKM208首先转化到细菌菌株BAA-1001(pacAB基因被潮霉素盒替换)以促进重组工程化反应。使该菌株具有电感受态并用1mM IPTG诱导表达重组蛋白。然后将含有抗生素抗性标志物壮观霉素的线性DNA转化到菌株中，该DNA与P1的s和u基因的周围区域具有同源性。30℃恢复后，将转化体接种到含有壮观霉素的LB琼脂上，然后贴片印迹(patched)。使用菌落PCR去除s和u基因，然后进行Sanger测序以确保进行所需的修饰。在构建过程中，u’和s_v’区域保持完整，但由于s_v’不编码完整的结构蛋白，因此无法产生S′尾丝。这种细菌溶源体代表了“秃”P1底盘，它缺乏在没有补偿的情况下表达自身功能性尾丝的能力。所得的包含秃P1底盘的细菌菌株被命名为SEG_170细胞系。底盘的功能测试包括带有和不带有天然S和U蛋白编码序列的包装质粒。从源自包装线的裂解物中看到Smarticle功能的丧失，包装质粒上没有尾丝。从源自包装线的裂解液中回收活性，包装质粒上有尾丝，成功实现反式补偿。

[0136] 实例3:尾丝展示载体(TFDV)的构建

[0137] 尾丝展示载体(TFDV)用于在秃噬菌体P1底盘中表达天然和/或新尾丝。这些展示载体利用庆大霉素或Zeocin抗性盒、pUC/RO1600复制起点和pTac IPTG诱导型启动子控制下的尾丝基因。所有载体还包含pacAB基因/包装位点以及用于转导和光测定的P23-luxAB-TT(荧光素酶)盒。尾丝候选物在IDT处从头合成或从细菌gDNA中PCR扩增，Gibson组装到PCR扩增载体中，转化到NEBa细胞中，贴片印迹，菌落PCR验证和序列验证。将序列验证的质粒转化到充分表征的SEG_170秃包装线(从Lucigen购买的感受态细胞)中。将转化体贴在选择性培养基上，并在小体积裂解物中进行筛选，以确定生产Smarticle的最佳克隆。将顶级克隆

用于大容量裂解物生产、QC和细菌组合上的反应性分析。

[0138] 实例4:尾丝基因组表达的构建

[0139] 为了利用天然和/或新尾丝促进最佳Smarticle生产,将尾丝和分子伴侣基因整合到P1 Smarticle基因组中的s和u基因天然位置。这种来自基因组而不是反式表达的表达确保了基于P1基因组的其余部分的正确表达和时间安排,减少了反式表达的负担。尾丝首先通过PCR扩增,引物含有与尾丝结构基因(s基因)或尾丝分子伴侣基因(u基因)的C端部分上的潮霉素盒同源的引物。PCR也用于扩增潮霉素盒。这两个片段用Gibson Assembly组装,并用含有与P1基因组同源性的引物进一步扩增,其中s先前被发现,并且与刚好位于天然s和u基因下游的重组酶cin具有同源性(见图2)。该重组工程化事件具有在P1基因组上插入尾丝以及破坏负责切换s尾丝基因可变区的cin重组酶的双重功能。这种尾丝和潮霉素盒的线性DNA产物被转化到含有壮观霉素抗性盒的BAA-1001中。在30℃下恢复,并在转化后铺板。将细胞接种到含有潮霉素的LB琼脂上,并针对壮观霉素敏感性进行贴片印迹。用菌落PCR和Sanger测序检查有希望的菌落。

[0140] 然后用包装质粒转化含有非天然尾丝和潮霉素抗性的阳性菌落。细胞在含有抗生素的培养基中生长过夜。使用90分钟42℃热诱导产生裂解物,来灭活P1主阻遏物并促进Smarticle的生产。然后将裂解物离心以沉淀细菌细胞碎片,然后通过2μm过滤器过滤灭菌。类似于上述TFDV包装线的过程,在新宿主上检查裂解物是否具有适当的Smarticle功能。

[0141] 为了构建从单个Smarticle基因组表达两条或更多尾丝的包装生产线,使用了如上所述的类似重组工程化方法。第一条尾丝同样被放置在P1基因组上,但不是将尾丝与潮霉素抗性相联接,而是附接到另一种抗生素上,诸如卡那霉素或庆大霉素。cin重组酶也保持完整以促进多个尾丝的转换。进行第二次重组工程化反应以将附接到潮霉素盒的尾丝的第二个可变部分置于基因组上已经存在的卡那霉素(或庆大霉素)盒的置换处。这可以重复以将三根、四根、五根等尾丝添加到基因组中(参见图6)。

[0142] 实例5:NRTP测定条件

[0143] 该测定包括在测定培养基(10g/L胰蛋白胨+5g/L酵母提取物+5%PEG8000)中以5.0E+05CFU/mL的浓度对细菌细胞进行初始2.5小时的预处理。在预处理步骤之后,将NRTP和转导盐(1M MgCl2+0.5M CaCl2)两者添加到反应中并温育2小时-这允许转导含有荧光素酶基因luxAB的报告分子。使用光度计通过相对光度计单位(RLU)输出测量来自细菌的光产生。

[0144] 实例6:具有工程化尾丝的NRTP的性能。

[0145] 工程化NRTP对各种物种和菌株的反应性提高,见表1。这些数据清楚地表明1)分析的尾丝的多样性,2)不同尾丝蛋白结合结构域观察到的强烈反应性变化,3)一些尾丝对某些物种具有高度特异性,以及4)一些尾丝对许多不同种类的细菌具有高度反应性。序列表中列出了来自这些工程化NRTP(例如“日落”、“印度”、“橘色”等)的尾丝的核苷酸和氨基酸序列两者。

[0146] 表1

[0147]

裂解物*	测试组合										
	Abi (n=73)	Cfl (N=88)	Cko (N=88)	Eae (N=88)	Ecl (N=68)	Eco (N=87)	Kox (N=88)	Kpn (N=89)	Pae (N=87)	Pms (N=88)	Sms (N=88)
5X V3	45.9%***	56.8%*	68.6%*	61.4%*	95.6%*	88.5%*	94.3%*	82%*	23%***	17%*	89.8%*
S	40.3%**	NA	NA	NA	67.6%**	71.3%**	NA	75.3%**	10.3%**	20.5%**	NA
S'	41.6%**	NA	NA	NA	89.7%**	60.9%**	NA	73.0%**	3.4%**	29.5%**	NA
日落 TFDV	0%**	5.7%*	0%*	2.3%*	7.4%**	12.6%**	1.1%*	1.1%**	0%**	0%*	1.1%*
印度 TFDV	1.3%**	10.2%*	0%*	4.5%*	14.7%**	2.3%**	40.9%*	14.6%**	1.1%**	5.7%*	6.8%*
褐色基因组	1.4%***	NA	NA	NA	1.5%*	13.8%*	NA	0%*	9.2%***	NA	NA
褐色 TFDV	NA	3.4%*	0%*	0%*	NA	NA	0%*	NA	NA	0%*	6.8%*
褐红 TFDV	0%**	0%*	0%*	0%*	4.4%**	14.9%**	0%*	0%**	0%**	0%*	4.5%*
猩红基因组	0%**	6.8%*	6.8%*	45.5%*	8.8%**	14.9%**	47.7%*	11.2%**	0%**	6.8%*	11.4%*
葛莱泉基因组	1.4%***	NA	NA	NA	0%*	4.6%*	NA	0%*	0%***	NA	NA
葛莱泉 TFDV	2.7%***	4.5%*	0%*	0%*	0%*	3.4%*	0%*	0%*	0%***	1.1%*	0%*
靛蓝基因组	0%***	NA	NA	NA	16.2%*	1.1%*	NA	0%*	0%***	NA	NA
5x 靛蓝 TFDV	1.4%***	NA	NA	NA	14.7%*	1.1%*	NA	0%*	0%***	NA	NA
牛仔布 TFDV	4.1%***	NA	NA	NA	4.4%*	12.6%*	NA	22.5%*	0%***	NA	NA
铁 TFDV	5.5%***	NA	NA	NA	5.9%*	16.1%*	NA	29.2%*	0%***	NA	NA
松 TFDV	35.1%	23.9%*	68.6%*	47.7%*	88.8%	79.3%**	78.4%*	80.9%**	9.2%**	6.8%*	38.6%*
丛林 TFDV	50.6%**	42%*	12.5%*	48.9%*	88.2%**	65.5%**	90.9%*	79.8%**	1.1%**	26.1%*	97.7%*
三叶草	6.8%***	34.1%*	1.1%*	1.1%*	22.1%*	73.6%*	0%*	0%*	8%***	9.3%*	17.1%*
紫罗兰 TFDV	56.8%***	23.9%*	1.1%*	35.2%*	80.9%*	66.7%*	71.6%*	65.2%*	20.7%***	2.3%*	79.6%*
梅 TFDV	2.7%***	0%*	0%*	0%*	1.5%*	43.7%*	0%*	0%*	8%***	0%*	0%*
三文鱼 TFDV	40.5%***	28.4%*	76.1%*	34.1%*	33.8%*	55.2%*	77.3%*	46.1%*	20.7%***	9.1%*	73.6%*
Jazzberry TFDV	2.7%***	1.1%*	0%*	0%*	1.5%*	42.5%*	0%*	0%*	8%***	0%*	0%*
Razzmatazz TFDV	52.1%***	NA	NA	NA	85.3%*	62.1%*	NA	60.7%*	16.1%***	NA	NA
ShamJazz基因组	4.1%***	NA	NA	NA	14.7%*	72.4%*	NA	0%*	0%***	NA	NA
5x 模糊+分子伴侣 TFDV	0%***	NA	NA	NA	0%*	2.3%*	NA	20.2%*	0%***	NA	NA
香蕉 TFDV	0%***	NA	NA	1.1%*	82.4%*	0%*	NA	1.1%*	0%***	NA	NA
芒果 TFDV	13.7%***	NA	NA	NA	97.1%*	26.4%*	NA	47.2%*	2.3%***	NA	NA
10x 皇后 TFDV (Eco0229)	6.8%***	NA	NA	NA	25%*	80.5%*	NA	0%*	0.0%***	NA	NA
热带 TFDV	0%***	NA	NA	NA	2.9%*	0%*	NA	0%*	0%***	NA	NA
金 TFDV	2.7%**	5.7%**	NA	37.5%**	22.1%**	32.2%**	87.5%**	62.9%**	0%**	22.7%**	68.2%**
Bluetiful TFDV	0%**	1.1%**	NA	22.7%**	NA	0.0%**	30.7%**	NA	0%**	4.5%**	76.1%**
Rio TFDV	0%**	3.4%**	NA	3.4%**	92%**	0%**	84%**	53.9%**	0%**	86.4%**	80.7%*
兰花 TFDV	8.2%**	17.0%**	NA	22.7%**	42.6%**	79.3%**	NA	55.1%**	0%**	5.7%**	53.6%**
柠檬 TFDV	1.4%**	56.8%**	34.1%**	NA	NA	0%**	NA	NA	0%**	NA	NA

*在 1E4 CFU/mL 观察检测
**在 5E5 CFU/mL 观察检测
***在 1E7 CFU/mL 观察检测

粗体表示诊断测定中使用的 1x 裂解物浓度
正常字体表示诊断测定中使用的 5x 浓度
斜体表示诊断测定中使用的 10x 裂解物浓度

鲍曼不动杆菌	Abi
弗氏枸橼酸杆菌	Cfl
克氏枸橼酸杆菌	Cko
产气肠杆菌	Eae
阴沟肠杆菌	Ecl
大肠杆菌	Eco
产酸克雷伯氏菌	Kox
肺炎克雷伯氏菌	Kpn
绿脓杆菌	Pae
奇异变形杆菌	Pms
粘质沙雷氏菌	Sms

[0148] 图3以图形方式描绘了如何改变秃(尾丝缺陷)P1溶源体以表达来自基因组的新尾丝。图4描绘了与来自TFDV的反式表达相比,给定尾丝的基因组整合如何能够提高性能。对于TFDV和基因组表达版本两者的3个指示菌株,示出了3个不同尾丝的光活性。此外,还将TFDV和基因组S尾丝NRTP的转导效率与WT P1 NRTP对照(V3)进行了比较。

[0149] 图5A描绘的图表示出了作为光产生(RLU)的工程化“印度”NRTP的提高的尾丝活性,比较了表达质粒p15B U蛋白“t分子伴侣”的包装线与不表达该蛋白的包装线。图5B描绘的图表示出了与从单独的包装质粒(TFDV)产生的“猩红”NRTP相比,由噬菌体基因组产生的“猩红”NRTP的性能提高。

[0150] 图6A显示了包含0、1、2或3个不同尾丝基因的生产线的基因组排列,并展示了如何工程化溶源体以从单次发酵中产生多个NRTP。尾丝基因可以与cix交叉位点排列在新的位置。基因的表达也可以布置为不依赖于大或小操纵子的重组。图6B描绘了由赋予各个尾丝的给定NRTP特异性检测到的指示菌株(左)。虽然右侧图形示出了表达多个尾丝的包装线可以检测多种指示菌株,但表明可以同时生产具有不同特异性的多种功能性NRTP。

[0151] 图7比较了源自双功能(两个尾丝)表达菌株的NRTP相对于单独生产运行中产生的各个NRTP的性能。顶图示出了来自Jazzberry和三叶草尾丝的双功能尾丝区域的基因组排列。中间左图,比较了对不同尾丝特异性的指示菌株上的单独生产和双功能NRTP。中间右图,示出了除了与其他NRTP(诸如天然P1 NRTP,称为V3)混合到混合物中之外,还如何通过制造双功能生产线来改进一大组的大肠杆菌菌株的检测和光生产。图7的底部直接比较了双功能生产的NRTP的性能与单独生产的各个尾丝的累积性能。

[0152] 图8示出了所进行的实验的结果,该实验识别了在病毒底盘上功能化新尾丝所需

的元件。图形A说明P1r基因是必需的，尾丝可变区(S_v)应与其同源u同源辅助蛋白配对以获得最大活性。此外，图形A示出了3个不同的尾丝保守区域可以允许在新底盘上对非天然尾丝进行功能化。图形B示出了来自P1噬菌体、11型Kpn噬菌体和p15B质粒(与P1相关)的3个S_c区域的氨基酸序列的比对，突出了高度保守的N端150个氨基酸序列基序。

[0153] 图9显示了从发酵菌株中表达尾丝基因的各种排列。A)示出了来自噬菌体基因组的尾丝和病毒底盘的表达。B)示出从噬菌体基因组表达的病毒底盘和来自包装质粒的尾丝基因。C)示出来自噬菌体基因组的病毒底盘和来自独立质粒的尾丝。D)示出来自噬菌体基因组的病毒底盘和来自细菌基因组的尾丝。E)示出来自噬菌体基因组的病毒底盘和一组尾丝。第二组独特的尾丝由独立的质粒表达。F)示出来自噬菌体基因组的病毒底盘和尾丝。第二组独特的尾丝由包装质粒表达。G)示出来自噬菌体基因组的病毒底盘和两组独特的尾丝。

[0154] 虽然已经参考优选实施例和各种替代实施例具体地示出和描述了本公开，但是相关领域的技术人员将理解可以在形式和细节上进行各种修改，而本发明的真实范围阐述于所附权利要求中。

[0155] 序列表中所列序列的描述：

[0156] 在P1底盘上功能性表达的尾丝的核苷酸序列。

芦笋(Asparagus)尾丝核苷酸序列	SEQ ID NO: 1
香蕉(Banana)尾丝核苷酸序列	SEQ ID NO: 2
蜀羊泉(Bittersweet)尾丝核苷酸序列	SEQ ID NO: 3
钴(Cobalt)尾丝核苷酸序列	SEQ ID NO: 4
矢车菊(Cornflower)尾丝核苷酸序列	SEQ ID NO: 5
牛仔布(Denim)尾丝核苷酸序列	SEQ ID NO: 6
茄子(Eggplant)尾丝核苷酸序列	SEQ ID NO: 7
蕨(Fern)尾丝核苷酸序列	SEQ ID NO: 8
樱红(Fuchsia)尾丝核苷酸序列	SEQ ID NO: 9
[0157] 模糊(Fuzzy)尾丝核苷酸序列	SEQ ID NO: 10
尺蠖(Inchworm)尾丝核苷酸序列	SEQ ID NO: 11
印度(Indian)尾丝核苷酸序列	SEQ ID NO: 12
靛蓝(Indigo)尾丝核苷酸序列	SEQ ID NO: 13
Jazzberry 尾丝核苷酸序列	SEQ ID NO: 14
Jazzberry-三叶草(Jazzberry-ShamrocK) 双尾丝核苷酸序列	SEQ ID NO: 15
丛林(Jungle)尾丝核苷酸序列	SEQ ID NO: 16
芒果(Mango)尾丝核苷酸序列	SEQ ID NO: 17
褐红(Maroon)尾丝核苷酸序列	SEQ ID NO: 18
桑葚(Mulberry)尾丝核苷酸序列	SEQ ID NO: 19

	P1_S'基因核苷酸序列	SEQ ID NO: 20
	P1S-P1S'-三叶草（P1S-P1S'-Shamrock）双尾丝核苷酸序列	SEQ ID NO: 21
	松(Pine)尾丝核苷酸序列	SEQ ID NO: 22
	梅(Plum)尾丝核苷酸序列	SEQ ID NO: 23
	皇后(Queen)尾丝核苷酸序列	SEQ ID NO: 24
	Razzmatazz 尾丝核苷酸序列	SEQ ID NO: 25
	三文鱼(Salmon)尾丝核苷酸序列	SEQ ID NO: 26
[0158]	猩红(Scarlet)尾丝核苷酸序列	SEQ ID NO: 27
	三叶草(Shamrock)尾丝核苷酸序列	SEQ ID NO: 28
	日落(Sunset)尾丝核苷酸序列	SEQ ID NO: 29
	橘色(Tangerine)尾丝核苷酸序列	SEQ ID NO: 30
	蓟(Thistle)尾丝核苷酸序列	SEQ ID NO: 31
	热带(Tropical)_pNS88 尾丝核苷酸序列	SEQ ID NO: 32
	热带(Tropical)_pNS92 尾丝核苷酸序列	SEQ ID NO: 33
	紫罗兰(Violet)尾丝核苷酸序列	SEQ ID NO: 34

[0159] 在P1底盘上功能性表达的尾丝的氨基酸序列。

	芦笋_-_P1Sc-(P1Sv-MuS_杂合)_翻译	SEQ ID NO: 35
	香蕉_-_P1Sc(aa1-114)-Ecl112(aa218-末端)_翻译	SEQ ID NO: 36
	蜀羊泉_-_p15b_Sc-p15b_SvQ_翻译	SEQ ID NO: 37
	钴_-_p15bSc-Kpn_SCKP_TF4_翻译	SEQ ID NO: 38
	矢车菊_-_P1Sc(aa1-208)-Kpn478_尾_丝(aa131-499)_翻译	SEQ ID NO: 39
	牛仔布_-_p15bSc-Kpn_SCKP_TF1_翻译	SEQ ID NO: 40
[0160]	茄子_-_D6Sc-D6Sv'_翻译	SEQ ID NO: 41
	蕨_-_P1Sc-(P1Sv-D108S_杂合)_翻译	SEQ ID NO: 42
	樱红_-_P1Sc-D6Sv_翻译	SEQ ID NO: 43
	模糊_-_P1Sc(aa1-208)-Kpn051_TF(aa40-382)_翻译	SEQ ID NO: 44
	尺蠖_-_P1Sc-R2_脓菌素_翻译	SEQ ID NO: 45
	印度_-_p15bSc-p15bSvN_翻译	SEQ ID NO: 46
	靛蓝_-_p15bSc-Kpn_SCKP_TF3_翻译	SEQ ID NO: 47
	Jazzberry_-_P1Sc-KpnSv_翻译	SEQ ID NO: 48

丛林_-_P1Sc-(P1Sv'-MuS'_杂合)_翻译 SEQ ID NO: 49

芒果_-_P1Sc(aa1-214)-Ecl117B(aa214-764)_翻译 SEQ ID NO: 50

褐红_-_p15bSc-p15bSvP_翻译 SEQ ID NO: 51

桑葚_-_D6Sc-D6Sv_翻译 SEQ ID NO: 52

P1_S'_-_P1Sc-P1Sv'_翻译 SEQ ID NO: 53

松_-_P1Sc(nt1-987)-P2H_翻译 SEQ ID NO: 54

梅_-_KpnSc-KpnSv_翻译 SEQ ID NO: 55

皇后_-_S-皇后_Sv_翻译 SEQ ID NO: 56

[0161]

Razzmatazz_-_P1Sc-P7Sv_翻译 SEQ ID NO: 57

三文鱼_-_P1Sc-P7Sv'_翻译 SEQ ID NO: 58

猩红_-_p15bSc-p15bSvI_翻译 SEQ ID NO: 59

三叶草_-_P1Sc-(P1S-SfMuS'_杂合)_翻译 SEQ ID NO: 60

日落_-_p15bSc-p15bSvR_翻译 SEQ ID NO: 61

橘色_-_p15bSc-p15bSv0_翻译 SEQ ID NO: 62

蓟_-_P1Sc-KpnSv_翻译 SEQ ID NO: 63

热带_pNS88_-_P1Sc(aa1-214)-Ecl117A(aa91-437)_翻译 SEQ ID NO: 64

热带_pNS92_-_P1Sc(aa1-214)-Ecl117A(aa96-437)_翻译 SEQ ID NO: 65

紫罗兰_-_RCS47Sc-RCS47Sv_翻译 SEQ ID NO: 66

[0162] 分子伴侣蛋白的氨基酸序列

芦笋_-_MuU_翻译 SEQ ID NO: 67

香蕉_-_Ecl112_U_分子伴侣_翻译 SEQ ID NO: 68

蜀羊泉_-_p15b_T_翻译 SEQ ID NO: 69

钻_-_p15b_T_翻译 SEQ ID NO: 70

牛仔布_-_p15b_T_翻译 SEQ ID NO: 71

茄子_-_P1_U_翻译 SEQ ID NO: 72

蕨_-_D108_U_翻译 SEQ ID NO: 73

樱红_-_P1_U'_翻译 SEQ ID NO: 74

模糊_-_PROKKA_00043_(Kpn478_分子伴侣)_翻译 SEQ ID NO: 75

尺蠖___PA0621_翻译 SEQ ID NO: 76

印度_-_p15b_T_翻译 SEQ ID NO: 77

靛蓝_-_p15b_T_翻译 SEQ ID NO: 78

Jazzberry_-_Kpn_U_翻译 SEQ ID NO: 79

丛林_-_Mu_U'_翻译 SEQ ID NO: 80

芒果_-_Ecl117B_U_分子伴侣_翻译 SEQ ID NO: 81

褐红_-_p15_T_翻译 SEQ ID NO: 82

桑葚_-_P1_U'_翻译 SEQ ID NO: 83

P1_S'_-_P1_U'_翻译 SEQ ID NO: 84

松_-_P2_G_翻译 SEQ ID NO: 85

梅_-_Kpn_U_翻译 SEQ ID NO: 86

[0163] 皇后_-_皇后_U_分子伴侣_翻译 SEQ ID NO: 87

Razzmatazz_-_P7_Ua_翻译 SEQ ID NO: 88

Razzmatazz_-_P7_Ub_翻译 SEQ ID NO: 89

三文鱼_-_P7_U'_translation SEQ ID NO: 90

猩红_-_p15b_T_翻译 SEQ ID NO: 91

三叶草_-_SfMuU'_翻译 SEQ ID NO: 92

日落_-_p15b_T_翻译 SEQ ID NO: 93

橘色_-_p15_T_翻译 SEQ ID NO: 94

蓟_-_KpnU_翻译 SEQ ID NO: 95

紫罗兰_-_RCS47_U_翻译 SEQ ID NO: 96

[0164] 其他序列

秃_底盘_尾_丝_区域_P1_s-u::aadA SEQ ID NO: 97

Rio 尾丝_s_杂合_核苷酸序列 SEQ ID NO: 98

Rio 分子伴侣_u_核苷酸_序列 SEQ ID NO: 99

柠檬(Limon)尾丝_s_杂合_核苷酸序列 SEQ ID NO: 100

柠檬分子伴侣_u_核苷酸_序列 SEQ ID NO: 101

兰花(Orchid)尾丝_s_杂合_核苷酸序列 SEQ ID NO: 102

兰花分子伴侣_u_核苷酸序列 SEQ ID NO: 103

金(Gold)尾丝_s_杂合_核苷酸序列 SEQ ID NO: 104

金分子伴侣_u_核苷酸序列 SEQ ID NO: 105

Bluetiful 尾 丝_s_杂合_核苷酸序列 SEQ ID NO: 106

	Bluetiful 分子伴侣_u_核苷酸序列	**SEQ ID NO: 107**
	Rio 尾丝_S_杂合_氨基酸序列	**SEQ ID NO: 108**
	柠檬尾丝_S_杂合_氨基酸序列	**SEQ ID NO: 109**
	兰花尾丝_S_杂合_氨基酸序列	**SEQ ID NO: 110**
	金尾丝_S_杂种_氨基酸序列	**SEQ ID NO: 111**
[0165]	**Bluetiful** 尾丝_S_杂合_氨基酸序列	**SEQ ID NO: 112**
	Rio 分子伴侣_U_氨基酸序列	**SEQ ID NO: 113**
	柠檬分子伴侣_U_氨基酸序列	**SEQ ID NO: 114**
	兰花分子伴侣_U_氨基酸序列	**SEQ ID NO: 115**
	金分子伴侣_U_氨基酸序列	**SEQ ID NO: 116**
	Bluetiful 分子伴侣_U_氨基酸序列	**SEQ ID NO: 117**

序列表

<110> F. Hoffmann-La Roche AG
罗氏诊断有限公司
罗氏分子系统股份有限公司

<120> 具有一个或多个非天然尾丝的非复制性转导颗粒和基于转导颗粒的报告分子系统

<130> P34922-WO-HS

<150> 62/787,151
<151> 2018-12-31

<150> 62/926,989
<151> 2019-10-28

<160> 117

<170> PatentIn 3.5 版

<210> 1
<211> 3949
<212> DNA
<213> 人工序列

<220>
<223> 芦笋尾丝

<400> 1

[0001]
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cgcgctgaat cgtccattaa caaaggctct cgatttttaa tcagcaaggc cgttttcggt 120

accagttcgc tggttactaa gaaaggagat ggcacttatg agattggaga actgccaaag 180

gctttcgaac tggcagaact gaccagtcaa ttttgcacca tcaacctcgt cccaacctac 240

tcaggcggga taattactgt ccgaatggac cttgatcaaa gccagttgca ggaagggaaa 300

aactacccat tcaacactct ggttgttctg gataacgaga acaagccaat cgccattatt 360

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tccagccgct ggaacgcgct gtcaggctga atatggcaac agacgaggaa cgcacacgac 4440

tggaagcatg ggaacgctac agtgttctgg tcagccgtgt ggatacggca aatcctgaat 4500

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<220>
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gctttcgaac tggcagaact gaccagtcaa ttttgcacca tcaacctcgt cccaacctac 240

tcaggcggga taattactgt ccgaatggac cttgatcaaa gccagttgca ggaagggaaa 300

aactacccat tcaacactct ggttgttctg gataacgaga acaagccaat cgccattatt 360

tgtgtccagg aagactcgct gtatgtgggc aaaacatata ccgcagttat ggccataaac 420

acgactacag cataaggata tgcttgatga atgacgttac agttgttaca tcggttactt 480

acccatcatc cgagtcgttg gctctggtgg ccgatgtgca ataccacgaa ccatatctgt 540

cagccgcgct aaaccgaaaa ttcaggggga ttgttgaccc gggatttat gccggtttct 600

tacctaagcc tggcggtggg atgaacctgt taattacctc agtggatggt gataaaaccg 660

caggcgcggc gtcggtggat attggtgaat tttaccaggt aactattcag caacgtaagg 720

atatttctct tgcacttagt gcaggcaaga aatatgcaat tgtgctgaag ggaagatacc 780

tccttggaga agatacctac caggtgaata ccgcgtcaca tattcatgcg gctgaatttg 840

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aggatgcact catcaaagag tacgacgaga acattggcgc gtgggagacg ttcgccacca 1140

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ttgccgaact caaagcccga tccgcgatat ag 2132

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<212> DNA
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<223> 热带_pNS92 尾丝

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accagttcgc tggttactaa gaaaggagat ggcacttatg agattggaga actgccaaag 180

gctttcgaac tggcagaact gaccagtcaa ttttgcacca tcaacctcgt cccaacctac 240

tcaggcggga taattactgt ccgaatggac cttgatcaaa gccagttgca ggaagggaaa 300

aactacccat tcaacactct ggttgttctg gataacgaga acaagccaat cgccattatt 360

tgtgtccagg aagactcgct gtatgtgggc aaaacatata ccgcagttat ggccataaac 420

acgactacag cataaggata tgcttgatga atgacgttac agttgttaca tcggttactt 480

acccatcatc cgagtcgttg gctctggtgg ccgatgtgca ataccacgaa ccatatctgt 540

cagccgcgct aaaccgaaaa ttcaggggga ttgttgaccc gggattttat gccggtttct 600

tacctaagcc tggcggtggg atgaacctgt taattacctc agtggatggt gataaaaccg 660

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tccttggaga agatacctac caggtgaata ccgcgtcaca tattcatgcg gctgaatttg 840

ttgccagaac ctataccgat tcatatcagt taggagatgg ggagctgctt gtttgtacgg 900

tgaatatccc tgctagtgta tctgccatta cccaggagat gattgataca tccgagcgta 960

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tggaaaaagt gttgcccgtt gctgtaagtt ctggcgggac cggcactaca ccgaccggag 1980

aagagattaa cgatctaaaa accgtggact acagtgcgat gagcgccttg tatgttgagg 2040

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<212> DNA
<213> 人工序列

<220>
<223> 紫罗兰尾丝

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accagttcgc tggttactaa gaaaggagat ggcacttatg agattggaga actgccaaag 180

gctttcgaac tggcagaact gaccagtcaa ttttgcacca tcaacctcgt cccaacctac 240

tcaggcggga taattactgt ccgaatggac cttgatcaaa gccagttgca ggaagggaaa 300

aactacccat tcaacactct ggttgttctg gataacgaga acaagccaat cgccattatt 360

tgtgtccagg aagactcgct gtatgtgggc aaaacatata ccgcagttat ggccataaac 420

[0079] acgactacag cataaggata tgcttgatga atgacgttac agttgtcaca tcggttactt 480

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cagccgcgct aaaccgaaaa ttcaggggga ttgttgaccc gggattttat gccggtttct 600

tacctaagcc tggcggtggg atgaacctgt taatcacctc agtggatggt gataaaaccg 660

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[0081]

ctgaatga 3908

<210> 35
<211> 990
<212> PRT
<213> 人工序列

<220>
<223> 芦笋尾丝

<400> 35

Met Asn Asp Val Thr Val Val Thr Ser Val Thr Tyr Pro Ser Ser Glu
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Ser Leu Ala Leu Val Ala Asp Val Gln Tyr His Glu Pro Tyr Leu Ser
20 25 30

Ala Ala Leu Asn Arg Lys Phe Arg Gly Ile Val Asp Pro Gly Phe Tyr
35 40 45

Ala Gly Phe Leu Pro Lys Pro Gly Gly Gly Met Asn Leu Leu Ile Thr
50 55 60

Ser Val Asp Gly Asp Lys Thr Ala Gly Ala Ala Ser Val Asp Ile Gly
65 70 75 80

Glu Phe Tyr Gln Val Thr Ile Gln Gln Arg Lys Asp Ile Ser Leu Ala
85 90 95

Leu Ser Ala Gly Lys Lys Tyr Ala Ile Val Leu Lys Gly Arg Tyr Leu
100 105 110

Leu Gly Glu Asp Thr Tyr Gln Val Asn Thr Ala Ser His Ile His Ala
115 120 125

Ala Glu Phe Val Ala Arg Thr Tyr Thr Asp Ser Tyr Gln Leu Gly Asp
130 135 140

Gly Glu Leu Leu Val Cys Thr Val Asn Ile Pro Ala Ser Val Ser Ala
145 150 155 160

Ile Thr Gln Glu Met Ile Asp Thr Ser Glu Arg Ile Asn Arg Ser Ile
165 170 175

[0082]

Gly Ile Asp Ile Ser Asp Ser Val Thr Ser Thr Arg Ser Asp Val Ala
180 185 190

Ala Ser Ser Leu Ala Val Lys Lys Ala Tyr Asp Leu Ala Lys Ser Lys
195 200 205

Tyr Thr Ala Gln Asp Ala Ser Thr Thr Gln Lys Gly Leu Val Gln Leu
210 215 220

Ser Ser Ala Thr Asn Ser Asp Ser Glu Thr Met Ala Ala Thr Pro Lys
225 230 235 240

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

Ser Pro Ser Leu Thr Gly Thr Pro Thr Ala Pro Thr Ala Ala Gln Gly
260 265 270

Thr Asn Ser Thr Gln Ile Ala Asn Thr Ala Phe Val Lys Ala Ala Ile
275 280 285

Thr Ala Leu Ile Asn Gly Ala Pro Gly Thr Leu Asp Thr Leu Lys Glu
290 295 300

```
Ile Ala Ala Ala Ile Asn Asn Asp Pro Asn Tyr Ser Thr Thr Ile Asn
305                 310                 315                 320

Asn Ala Leu Ala Leu Lys Ala Pro Leu Ala Ser Pro Ala Leu Thr Gly
                325                 330                 335

Val Pro Thr Ala Pro Thr Ala Ala Gln Gly Thr Asn Asn Thr Gln Ile
            340                 345                 350

Ala Thr Thr Ala Tyr Val Arg Ala Ala Ile Ser Ala Leu Val Gly Ser
        355                 360                 365

Ser Pro Glu Ala Leu Asp Thr Leu Tyr Glu Leu Ala Ala Ala Leu Gly
    370                 375                 380

Asn Asp Pro Asn Phe Ala Thr Thr Met Thr Asn Ala Leu Ala Gly Lys
385                 390                 395                 400

Gln Pro Leu Asp Ala Thr Leu Thr Ala Leu Ala Gly Leu Ala Thr Gly
                405                 410                 415
```

[0083]

```
Ala Asn Lys Leu Pro Tyr Phe Thr Gly Thr Asp Thr Val Ser Gln Thr
            420                 425                 430

Asp Leu Thr Ser Val Gly Arg Asp Ile Leu Ala Lys Thr Ser Ile Leu
        435                 440                 445

Ala Val Ile Gln Tyr Leu Gly Leu Arg Glu Leu Gly Thr Ser Gly Glu
    450                 455                 460

Lys Ile Pro Leu Leu Ser Thr Ala Asn Thr Trp Ser Ala Arg Gln Thr
465                 470                 475                 480

Phe Asn Gly Gly Ile Thr Gly Ala Leu Thr Gly Asn Ala Asp Thr Ala
                485                 490                 495

Thr Lys Leu Lys Thr Ala Arg Asn Ile Asn Gly Val Arg Phe Asp Gly
            500                 505                 510

Ser Gly Asp Ile Asn Ile Asn Thr Leu Val Ser Arg Gly Arg Val Thr
        515                 520                 525
```

```
Ala Leu Glu Ala Asn Ala Gln Gly Thr Ser Gly Ile Gln Leu Tyr Glu
    530                 535                 540

Ala Tyr Asn Asn Gly Tyr Pro Ser Pro Tyr Gly Asn Val Leu His Leu
545                 550                 555                 560

Lys Gly Ala Thr Ala Ala Gly Glu Gly Glu Leu Phe Ile Gly Trp Ser
                565                 570                 575

Gly Thr Ser Gly Ala His Ala Pro Val His Ile Arg Ser Arg Arg Asp
            580                 585                 590

Thr Asp Ser Ala Asn Trp Ser Glu Trp Ala Gln Val Tyr Thr Ser Lys
        595                 600                 605

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

Asn Ala Ala Thr Ala Thr Lys Leu Gln Thr Ala Cys Thr Ile Asn Gly
625                 630                 635                 640
```

[0084]

```
Val Ser Phe Asp Gly Ser Lys Asn Ile Glu Leu Thr Ala Glu Asp Leu
                645                 650                 655

Asn Leu Gln Glu Thr Val Asn Lys Ala Asp Asn Ala Val Gln Lys Thr
            660                 665                 670

Gly Asp Thr Leu Ser Gly Gly Leu Thr Phe Glu Asn Asp Ser Ile Leu
        675                 680                 685

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

Ala Asp Ser Asp Thr Asp Ser Tyr Met Trp Phe Glu Thr Gly Asp Asn
705                 710                 715                 720

Gly Asn Glu Tyr Phe Lys Trp Arg Ser Lys Gln Ser Thr Thr Thr Lys
                725                 730                 735

Asp Leu Met Asn Leu Lys Trp Asp Ala Leu Ser Val Leu Val Asn Ala
            740                 745                 750

Ile Val Asn Gly Glu Val Ile Ser Lys Ser Ala Asn Gly Leu Arg Ile
        755                 760                 765
```

```
Ala Tyr Gly Asn Tyr Gly Phe Phe Ile Arg Asn Asp Gly Ser Asn Thr
    770                 775                 780

Tyr Phe Met Leu Thr Asn Ser Gly Asp Asn Met Gly Thr Tyr Asn Gly
785                 790                 795                 800

Leu Arg Pro Leu Trp Ile Asn Asn Ala Thr Gly Ala Val Ser Met Gly
                805                 810                 815

Arg Gly Leu Asn Val Ser Gly Asp Thr Leu Ser Asp Arg Phe Ala Ile
            820                 825                 830

Asn Ser Ser Asn Gly Met Trp Ile Gln Met Arg Asp Asn Asn Ala Ile
        835                 840                 845

Phe Gly Lys Asn Ile Val Asn Thr Asp Ser Ala Gln Ala Leu Leu Arg
    850                 855                 860

Gln Asn His Ala Asp Arg Lys Phe Met Ile Gly Gly Leu Gly Asn Lys
865                 870                 875                 880
```

[0085]

```
Gln Phe Gly Ile Tyr Met Ile Asn Asn Ser Arg Thr Ala Asn Gly Thr
                885                 890                 895

Asp Gly Gln Ala Tyr Met Asp Asn Asn Gly Asn Trp Leu Cys Gly Ala
            900                 905                 910

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

Asp Val Arg Leu Gly Thr Gln Ser Leu Thr Gly Gly Leu Ser Arg Asp
    930                 935                 940

Tyr Lys Ala Pro Ser Gly His Val Ile Thr Gly Phe His Thr Asn Gly
945                 950                 955                 960

Asp Trp Glu Met Gln Gly Gly Asp Asp Lys Val Tyr Ile Arg Pro Val
                965                 970                 975

Gln Lys Asn Ile Asn Gly Thr Trp Tyr Asn Val Ala Ser Ala
            980                 985                 990
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<210> 36
<211> 763
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<213> 人工序列

<220>
<223> 香蕉尾丝

<400> 36

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Ser Leu Ala Leu Val Ala Asp Val Gln Tyr His Glu Pro Tyr Leu Ser
20 25 30

Ala Ala Leu Asn Arg Lys Phe Arg Gly Ile Val Asp Pro Gly Phe Tyr
35 40 45

Ala Gly Phe Leu Pro Lys Pro Gly Gly Gly Met Asn Leu Leu Ile Thr
50 55 60

Ser Val Asp Gly Asp Lys Thr Ala Gly Ala Ala Ser Val Asp Ile Gly
65 70 75 80

[0086]

Glu Phe Tyr Gln Val Thr Ile Gln Gln Arg Lys Asp Ile Ser Leu Ala
85 90 95

Leu Ser Ala Gly Lys Lys Tyr Ala Ile Val Leu Lys Gly Arg Tyr Leu
100 105 110

Leu Gly Glu Asp Thr Tyr Gln Val Asn Thr Ala Ser His Ile His Ala
115 120 125

Ala Glu Phe Val Ala Arg Thr Tyr Thr Asp Ser Tyr Gln Leu Gly Asp
130 135 140

Gly Glu Leu Leu Val Cys Thr Val Asn Ile Pro Ala Ser Val Ser Ala
145 150 155 160

Ile Thr Gln Glu Met Ile Asp Thr Ser Glu Arg Ile Asn Arg Ser Ile
165 170 175

Gly Ile Asp Ile Ser Asp Ser Val Thr Ser Thr Arg Ser Asp Val Ala
180 185 190

Ala Ser Ser Leu Ala Val Lys Lys Ala Tyr Asp Leu Ala Lys Ser Lys
195 200 205

Tyr Thr Ala Gln Asp Ala Thr Thr Ala Arg Lys Gly Ile Val Gln Leu
210 215 220

Ser Ser Ala Thr Asp Ser Thr Ser Glu Ala Leu Ala Ala Thr Pro Lys
225 230 235 240

Ala Val Lys Ala Val Asn Asp Asn Ala Asn Gly Arg Val Pro Ser Ala
245 250 255

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

Gln Asp Ile Phe Asn Gly Gln Ala Val Ala Ile Gly Asn Ala Ala Asp
275 280 285

Leu Asn Ala Tyr Thr Thr Pro Gly Leu Tyr Tyr Gln Pro Ala Asn Ala
290 295 300

[0087] Gln Ala Gln Thr Gly Arg Asn Tyr Pro Glu Ala Asn Ala Gly Ser Leu
305 310 315 320

Glu Val Tyr Lys His Ala Gly Ile Thr Gln Ile Tyr Arg Ile Tyr Asn
325 330 335

Ser Ser Arg Ser Tyr Ile Arg Thr Leu Tyr Ser Gly Thr Trp Ser Ala
340 345 350

Trp Val Lys Gln Tyr Asp Ala Ala Asn Lys Pro Ser Pro Ala Asp Ile
355 360 365

Asn Ala Val Asn Lys Gly Gly Asp Thr Met Thr Gly Gly Leu Lys Ile
370 375 380

Arg Ala Ala Asp Ala Leu Arg Ile Tyr Asp Ala Ala Tyr Gly Met Ile
385 390 395 400

Phe Arg Arg Ser Glu Asn Asn Phe Tyr Leu Ile Pro Thr Ala Lys Asp
405 410 415

Gln Gly Glu Asp Gly Gly Ile Ser Gly Leu Arg Pro Leu Tyr Ile Asp
420 425 430

```
Leu Thr Asn Gly Arg Val Thr Leu Gly Asn Gly Ala Val Val Asn Gly
        435                 440                 445

Gly Leu Gly Leu Gly Val Val Ser Gly Leu Gly Gly Asn Ser Ile Ala
    450                 455                 460

Leu Gly Asp Asn Asp Thr Gly Phe Lys Gln Asn Gly Asp Gly Val Leu
465                 470                 475                 480

Asp Val Tyr Ala Asn Ser Lys Gln Val Met Arg Phe Leu Asn Ser Gly
                485                 490                 495

Ile Thr Ser Tyr Met Leu Phe Asn Met Asn Ala Gly Ala Ser Val Ser
            500                 505                 510

Ser Thr Leu Thr Phe Lys Asn Gly Ser Gly Ile Thr Ser Glu Lys Thr
        515                 520                 525

Gly Ala Asn Pro Arg Asn Gly Arg Ile Tyr Trp Gly Gly Asp Ala Ser
    530                 535                 540
```

[0088]

```
Arg Gly Asn Arg Ile Glu Phe Ala Asp Asp Ala Gly Trp Lys Ala Tyr
545                 550                 555                 560

Ile Glu Arg His Pro Ser Asn Gly Val Gln Leu Val Val Asn Gly Arg
                565                 570                 575

Ile Asn Gly Ser Ile Val Tyr Ser Ser Gly Glu Val Leu Ala Gly Gly
            580                 585                 590

Gly Ser Ala Arg Phe Ala Ala Asp Gly Asn Ile Phe Gly Ser Lys Trp
        595                 600                 605

Gly Asn Gln Trp Leu Asp Ala Tyr Leu Lys Asn Thr Tyr Gln Pro Lys
    610                 615                 620

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

Gly Arg Phe Gln Pro Lys Gly Ser Tyr Thr Pro Ala Gly Gln Ala Tyr
                645                 650                 655
```

Thr Lys Ala Glu Ser Asp Ala Arg Tyr Asn Leu Lys Asn Thr Ala Thr
660 665 670

Lys Ser Ala Asn Ala Met Thr His Lys Asp Ala Ser Thr Gly Val Met
675 680 685

Glu Val Val Met Ser Asn Ile Asn Val Pro Asn Lys Thr Asn Val Asn
690 695 700

Val Thr Phe Pro Ala Ala Phe Pro Asn Ala Cys Val Gly Val Val Ile
705 710 715 720

Thr Tyr Asn Gly Ala Gly His Gly Ser Gly Asp Asp Ser Ala Ile Tyr
725 730 735

Val Pro Ser Tyr Ser Arg Thr Gly Cys Thr Leu Tyr Ala His Asn Ala
740 745 750

Asp Gly Lys Phe Met Leu Ile Ala Lys Gly Tyr
755 760

[0089]

<210> 37
<211> 748
<212> PRT
<213> 人工序列

<220>
<223> 蜀羊泉尾丝

<400> 37

Met Asn Asp Val Thr Val Val Thr Ser Val Thr Tyr Pro Ser Pro Glu
1 5 10 15

Ser Leu Ala Leu Val Ala Asp Val Gln Tyr His Glu Pro Tyr Leu Ser
20 25 30

Ala Ala Leu Asn Arg Lys Phe Arg Gly Ile Val Asp Pro Gly Phe Tyr
35 40 45

Ala Gly Phe Leu Pro Lys Pro Gly Gly Gly Met Asn Leu Leu Ile Thr
50 55 60

Ser Val Asp Gly Asp Lys Thr Ala Gly Ala Ala Ser Val Asp Ile Gly
65 70 75 80

Glu Phe Tyr Gln Val Thr Ile Gln His Arg Lys Asp Ile Ser Leu Ala
85 90 95

Leu Asn Ala Gly Lys Lys Tyr Ala Ile Val Leu Lys Gly Arg Tyr Leu
100 105 110

Leu Gly Glu Asp Thr Tyr Gln Val Asn Thr Ala Ser His Ile His Ala
115 120 125

Ala Glu Phe Val Ala Arg Thr Tyr Thr Asp Ser Tyr Gln Leu Gly Asp
130 135 140

Gly Glu Leu Leu Val Cys Thr Val Asn Ile Pro Ala Gly Val Ser Thr
145 150 155 160

Ile Thr Gln Glu Met Ile Asp Thr Ser Glu Arg Ile Asn Arg Thr Ile
165 170 175

Gly Ile Asp Ile Ser Asp Ser Val Thr Ser Thr Arg Ser Asp Val Ala
180 185 190

[0090] Ala Ser Ser Leu Ala Val Lys Lys Ala Tyr Asp Leu Ala Lys Ser Lys
195 200 205

Tyr Thr Ala Gln Asp Ala Ser Thr Thr Gln Lys Gly Leu Val Gln Leu
210 215 220

Ser Ser Ala Thr Asn Ser Thr Ser Glu Val Leu Ala Ala Thr Pro Lys
225 230 235 240

Ala Val Lys Ala Ala Tyr Asp Leu Ala Asn Gly Lys Tyr Thr Ala Gln
245 250 255

Asp Ala Thr Thr Thr Gln Lys Gly Ile Val Gln Leu Ser Ser Asp Thr
260 265 270

Asn Ser Thr Ser Glu Thr Leu Ala Ala Thr Pro Lys Ala Val Lys Ala
275 280 285

Ala Tyr Asp Leu Ala Ala Gly Lys Ala Pro Ser Ser His Thr His Pro
290 295 300

Trp Asn Gln Ile Thr Gly Val Pro Thr Ala Ser Leu Thr Ala Lys Gly
305 310 315 320

Ile Thr Gln Leu Ser Ser Ala Thr Asn Ser Thr Ser Glu Val Leu Ala
325 330 335

Ala Thr Pro Lys Ala Val Lys Ala Ala Tyr Asp Leu Ala Asn Gly Lys
340 345 350

Tyr Thr Ala Gln Asp Ala Thr Thr Ala Gln Lys Gly Ile Val Gln Leu
355 360 365

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

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

Asp Ala Thr Thr Thr Gln Lys Gly Ile Val Gln Leu Ser Ser Asp Thr
405 410 415

Asn Ser Thr Ser Glu Thr Leu Ala Ala Thr Pro Lys Ala Val Lys Ala
420 425 430

[0091]

Ala Tyr Asp Leu Ala Ala Gly Lys Ala Pro Ser Ser His Thr His Pro
435 440 445

Trp Asn Gln Ile Thr Val Val Pro Thr Ala Ser Leu Thr Ala Lys Gly
450 455 460

Ile Thr Gln Leu Ser Ser Ala Thr Asn Ser Thr Ser Glu Val Leu Ala
465 470 475 480

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

Tyr Thr Ala Gln Asp Ala Thr Thr Ala Gln Lys Gly Ile Val Gln Leu
500 505 510

Ser Ser Ala Thr Asn Ser Thr Ser Glu Val Leu Ala Ala Thr Pro Lys
515 520 525

Ala Val Lys Ala Ala Tyr Asp Leu Ala Asn Gly Lys Gln Ala Ala Asp
530 535 540

Ala Thr Leu Thr Ala Leu Ala Ala Leu Ala Thr Ala Ala Asp Lys Leu
545 550 555 560

Pro Tyr Phe Thr Gly Val Asp Arg Ala Ala Leu Thr Ala Leu Thr Ser
565 570 575

Val Gly Arg Ala Ile Leu Gly Lys Thr Ser Ile Gln Ser Val Leu Asp
580 585 590

Tyr Leu Gly Leu Gly Glu Gly Ser Ala Leu Pro Val Gly Val Pro Val
595 600 605

Pro Trp Pro Ser Ala Thr Pro Pro Thr Gly Trp Leu Lys Cys Asn Gly
610 615 620

Ala Ala Phe Ser Ser Glu Lys Tyr Pro Asn Leu Ala Lys Ala Tyr Pro
625 630 635 640

Thr Asn Lys Leu Pro Asp Leu Arg Gly Glu Phe Ile Arg Gly Trp Asp
645 650 655

[0092] Asp Gly Arg Gly Val Asp Ala Gly Arg Gln Leu Leu Ser Ser Gln Gly
660 665 670

Asp Ala Ile Arg Asn Ile Glu Gly Phe Ala Asp Gly Gly Ile Gly Met
675 680 685

Ser Phe Asp Ala Ile Arg Gly Ala Phe Tyr Asp Ala Gly Thr Arg Ser
690 695 700

Ala Arg Met Pro Asn Asn Thr Thr Thr Ile Asp Lys Thr Asp Asp Leu
705 710 715 720

Gly Phe Asp Ala Ser Arg Val Val Pro Thr Ala Asn Glu Asn Arg Pro
725 730 735

Arg Asn Ile Ala Phe Asn Tyr Ile Val Arg Ala Ala
740 745

<210> 38
<211> 737
<212> PRT
<213> 人工序列

<220>

<223> 钴尾丝

<400> 38

```
Met Asn Asp Val Thr Val Val Thr Ser Val Thr Tyr Pro Ser Pro Glu
1               5                  10                  15

Ser Leu Ala Leu Val Ala Asp Val Gln Tyr His Glu Pro Tyr Leu Ser
            20                  25                  30

Ala Ala Leu Asn Arg Lys Phe Arg Gly Ile Val Asp Pro Gly Phe Tyr
        35                  40                  45

Ala Gly Phe Leu Pro Lys Pro Gly Gly Gly Met Asn Leu Leu Ile Thr
    50                  55                  60

Ser Val Asp Gly Asp Lys Thr Ala Gly Ala Ala Ser Val Asp Ile Gly
65                  70                  75                  80

Glu Phe Tyr Gln Val Thr Ile Gln His Arg Lys Asp Ile Ser Leu Ala
                85                  90                  95

Leu Asn Ala Gly Lys Lys Tyr Ala Ile Val Leu Lys Gly Arg Tyr Leu
            100                 105                 110

Leu Gly Glu Asp Thr Tyr Gln Val Asn Thr Ala Ser His Ile His Ala
        115                 120                 125

Ala Glu Phe Val Ala Arg Thr Tyr Thr Asp Ser Tyr Gln Leu Gly Asp
    130                 135                 140

Gly Glu Leu Leu Val Cys Thr Val Asn Ile Pro Ala Gly Val Ser Thr
145                 150                 155                 160

Ile Thr Gln Glu Met Ile Asp Thr Ser Glu Arg Ile Asn Arg Thr Ile
                165                 170                 175

Gly Ile Asp Ile Ser Asp Ser Val Thr Ser Thr Arg Ser Asp Val Ala
            180                 185                 190

Ala Ser Ser Leu Ala Val Lys Lys Ala Tyr Asp Leu Ala Lys Ser Lys
        195                 200                 205

Tyr Thr Ala Gln Asp Ala Ser Thr Thr Gln Lys Gly Leu Val Gln Leu
    210                 215                 220
```

[0093]

```
Ser Ser Ala Thr Asn Ser Thr Ser Glu Val Leu Ala Ala Thr Pro Lys
225                 230                 235                 240

Ala Val Lys Ala Ala Tyr Asp Leu Ala Asn Gly Lys Tyr Thr Ala Gln
                245                 250                 255

Asp Ala Thr Thr Thr Gln Lys Gly Ile Val Gln Leu Ser Ser Asp Thr
            260                 265                 270

Asn Ser Thr Ser Glu Thr Leu Ala Ala Thr Pro Lys Ala Val Lys Ala
        275                 280                 285

Ala Tyr Asp Leu Ala Ala Gly Lys Ala Pro Ser Ser His Thr His Pro
    290                 295                 300

Trp Asn Gln Ile Thr Gly Val Pro Thr Ala Ser Leu Thr Ala Lys Gly
305                 310                 315                 320

Ile Thr Gln Leu Ser Ser Ala Thr Asn Ser Thr Ser Glu Val Leu Ala
                325                 330                 335
```

[0094]

```
Ala Thr Pro Lys Ala Val Lys Ala Ala Tyr Asp Leu Ala Asn Gly Lys
            340                 345                 350

Tyr Thr Ala Gln Asp Ala Thr Thr Ala Gln Lys Gly Ile Val Gln Leu
        355                 360                 365

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

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

Asp Ala Thr Thr Thr Gln Lys Gly Ile Val Gln Leu Ser Ser Asp Thr
                405                 410                 415

Asn Ser Thr Ser Glu Thr Leu Ala Ala Thr Pro Lys Ala Val Lys Ala
            420                 425                 430

Ala Tyr Asp Leu Ala Ala Gly Lys Ala Pro Ser Ser His Thr His Pro
        435                 440                 445
```

Trp Asn Gln Ile Thr Val Val Pro Thr Ala Ser Leu Thr Ala Lys Gly
450 455 460

Ile Thr Gln Leu Ser Ser Ala Thr Asn Ser Thr Ser Glu Val Leu Ala
465 470 475 480

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

Tyr Thr Ala Gln Asp Ala Thr Thr Ala Gln Lys Gly Ile Val Gln Leu
500 505 510

Ser Ser Ala Thr Asn Ser Thr Ser Glu Val Leu Ala Ala Thr Pro Lys
515 520 525

Ala Val Lys Ala Ala Tyr Asp Leu Ala Asn Gly Lys Gln Ala Ala Asp
530 535 540

Ala Thr Leu Thr Ala Leu Ala Ala Leu Ala Thr Ala Ala Asp Lys Leu
545 550 555 560

[0095] Pro Tyr Phe Thr Gly Val Asp Arg Ala Ala Leu Thr Ala Leu Thr Ser
565 570 575

Val Gly Arg Ala Ile Leu Gly Lys Thr Ser Ile Gln Ser Val Leu Asp
580 585 590

Tyr Leu Gly Leu Gly Glu Gly Ser Ala Leu Pro Val Gly Val Pro Val
595 600 605

Pro Trp Pro Leu Glu Thr Pro Pro Thr Gly Trp Leu Lys Cys Asn Gly
610 615 620

Ala Ala Phe Ser Ser Glu Met Tyr Pro Lys Leu Ala Lys Ala Tyr Pro
625 630 635 640

Thr Asn Lys Leu Pro Asp Leu Arg Gly Glu Phe Ile Arg Gly Trp Asp
645 650 655

Asp Gly Arg Gly Ile Asp Ala Gly Arg Thr Leu Leu Ser Gly Gln Asp
660 665 670

Gly Thr Ser Phe Ser His Tyr Gly Gly Asn Phe Asp Ile Gly Ser Gly
675 680 685

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

Ser Arg Phe Ser Phe Ala Gly Pro Ser Arg Gly Asp Gly Val Asn Tyr
705 710 715 720

Val Thr Ile Arg Pro Arg Asn Ile Ala Phe Asn Tyr Ile Val Arg Ala
725 730 735

Ala

<210> 39
<211> 578
<212> PRT
<213> 人工序列

<220>
<223> 矢车菊尾丝

<400> 39

[0096]

Met Asn Asp Val Thr Val Val Thr Ser Val Thr Tyr Pro Ser Ser Glu
1 5 10 15

Ser Leu Ala Leu Val Ala Asp Val Gln Tyr His Glu Pro Tyr Leu Ser
20 25 30

Ala Ala Leu Asn Arg Lys Phe Arg Gly Ile Val Asp Pro Gly Phe Tyr
35 40 45

Ala Gly Phe Leu Pro Lys Pro Gly Gly Gly Met Asn Leu Leu Ile Thr
50 55 60

Ser Val Asp Gly Asp Lys Thr Ala Gly Ala Ala Ser Val Asp Ile Gly
65 70 75 80

Glu Phe Tyr Gln Val Thr Ile Gln Gln Arg Lys Asp Ile Ser Leu Ala
85 90 95

Leu Ser Ala Gly Lys Lys Tyr Ala Ile Val Leu Lys Gly Arg Tyr Leu
100 105 110

Leu Gly Glu Asp Thr Tyr Gln Val Asn Thr Ala Ser His Ile His Ala
115 120 125

```
Ala Glu Phe Val Ala Arg Thr Tyr Thr Asp Ser Tyr Gln Leu Gly Asp
    130                 135                 140

Gly Glu Leu Leu Val Cys Thr Val Asn Ile Pro Ala Ser Val Ser Ala
145                 150                 155                 160

Ile Thr Gln Glu Met Ile Asp Thr Ser Glu Arg Ile Asn Arg Ser Ile
                165                 170                 175

Gly Ile Asp Ile Ser Asp Ser Val Thr Ser Thr Arg Ser Asp Val Ala
            180                 185                 190

Ala Ser Ser Leu Ala Val Lys Lys Ala Tyr Asp Leu Ala Lys Ser Lys
        195                 200                 205

Ala Ala Ile Ala Gly Met Ala Lys Ala Ser Asp Leu Asn Ala Leu Ala
    210                 215                 220

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

[0097]

```
Asp Asn Ala Gly Phe Ile Leu Gly Lys Asn Ser Asp Leu Ala Leu Leu
                245                 250                 255

Lys Lys Gln Gly Gln Gly Gly Thr Ile Ala Val Gly Ser Gly Thr Pro
            260                 265                 270

Phe Arg Val Gln Arg Ser Arg Ala Thr Thr Val Ser Pro Ala Asp Thr
        275                 280                 285

Phe Asp Asp Ile Leu Val Ile Asp Ala Asn Asn Arg Thr Thr Leu Pro
    290                 295                 300

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

Leu Tyr Thr Gln Ala Ile Glu Leu Ser Phe Ser Thr Pro Tyr Ile Asp
                325                 330                 335

Phe His Phe Asn Tyr Ser Thr Asp Asp Phe Thr Gly Arg Ile Met Ala
            340                 345                 350
```

Thr Ala Ala Asp Gln Ile Ser Val Gln Gly Ser His Trp Arg Val Asp
355 360 365

Arg Asp Leu Arg Val Gly Gly Met Ala Asp Ile Ala Gly Trp Ala Gln
370 375 380

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

Ile Gly Ser Leu Val Ser Gly Gly Arg Ile Arg Ser Arg Met Leu Gly
405 410 415

Arg Gly Gly Asn Val Asp Pro Ser Gly Ala Trp Gly Gly Phe Tyr Val
420 425 430

Glu Glu His Val Gly Thr Glu His Arg Ile Ile Met Tyr Met Asp Gly
435 440 445

Phe Gly Arg Thr Asp Ala Trp Ser Phe Arg Ala Gly Gly Val Ile Ser
450 455 460

[0098] Thr Pro Lys Gly Asp Val Met Thr Thr Gly Ser Asp Val Arg Leu Lys
465 470 475 480

Thr Asp Phe Thr Gln Ala Pro Gly Asn Ala Ser Glu Arg Ile Glu Arg
485 490 495

Leu Gly Val Cys Glu Tyr Arg Met Lys Gly Glu Thr Arg Arg Arg Arg
500 505 510

Gly Phe Ile Ala Gln Gln Ala Glu Lys Ala Asp Asp Leu Tyr Thr Phe
515 520 525

Leu Gly Ile Glu Gln Glu Ile Asp Gly Glu Lys Phe Lys Val Met Asn
530 535 540

Val Asp Tyr Thr Ala Ile Ile Ala Asp Leu Val Thr Val Ala Gln Gly
545 550 555 560

Leu Leu Val Lys Asn Gln Glu Leu Glu Arg Arg Ile Ser Val Leu Glu
565 570 575

Gly Ile

<210> 40
<211> 737
<212> PRT
<213> 人工序列

<220>
<223> 牛仔布尾丝

<400> 40

Met Asn Asp Val Thr Val Val Thr Ser Val Thr Tyr Pro Ser Pro Glu
1 5 10 15

Ser Leu Ala Leu Val Ala Asp Val Gln Tyr His Glu Pro Tyr Leu Ser
20 25 30

Ala Ala Leu Asn Arg Lys Phe Arg Gly Ile Val Asp Pro Gly Phe Tyr
35 40 45

Ala Gly Phe Leu Pro Lys Pro Gly Gly Gly Met Asn Leu Leu Ile Thr
50 55 60

Ser Val Asp Gly Asp Lys Thr Ala Gly Ala Ala Ser Val Asp Ile Gly
65 70 75 80

[0099]

Glu Phe Tyr Gln Val Thr Ile Gln His Arg Lys Asp Ile Ser Leu Ala
85 90 95

Leu Asn Ala Gly Lys Lys Tyr Ala Ile Val Leu Lys Gly Arg Tyr Leu
100 105 110

Leu Gly Glu Asp Thr Tyr Gln Val Asn Thr Ala Ser His Ile His Ala
115 120 125

Ala Glu Phe Val Ala Arg Thr Tyr Thr Asp Ser Tyr Gln Leu Gly Asp
130 135 140

Gly Glu Leu Leu Val Cys Thr Val Asn Ile Pro Ala Gly Val Ser Thr
145 150 155 160

Ile Thr Gln Glu Met Ile Asp Thr Ser Glu Arg Ile Asn Arg Thr Ile
165 170 175

Gly Ile Asp Ile Ser Asp Ser Val Thr Ser Thr Arg Ser Asp Val Ala
180 185 190

```
Ala Ser Ser Leu Ala Val Lys Lys Ala Tyr Asp Leu Ala Lys Ser Lys
        195                 200                 205

Tyr Thr Ala Gln Asp Ala Ser Thr Thr Gln Lys Gly Leu Val Gln Leu
    210                 215                 220

Ser Ser Ala Thr Asn Ser Thr Ser Glu Val Leu Ala Ala Thr Pro Lys
225                 230                 235                 240

Ala Val Lys Ala Ala Tyr Asp Leu Ala Asn Gly Lys Tyr Thr Ala Gln
                245                 250                 255

Asp Ala Thr Thr Thr Gln Lys Gly Ile Val Gln Leu Ser Ser Asp Thr
            260                 265                 270

Asn Ser Thr Ser Glu Thr Leu Ala Ala Thr Pro Lys Ala Val Lys Ala
        275                 280                 285

Ala Tyr Asp Leu Ala Ala Gly Lys Ala Pro Ser Ser His Thr His Pro
    290                 295                 300
```

[0100]

```
Trp Asn Gln Ile Thr Gly Val Pro Thr Ala Ser Leu Thr Ala Lys Gly
305                 310                 315                 320

Ile Thr Gln Leu Ser Ser Ala Thr Asn Ser Thr Ser Glu Val Leu Ala
                325                 330                 335

Ala Thr Pro Lys Ala Val Lys Ala Ala Tyr Asp Leu Ala Asn Gly Lys
            340                 345                 350

Tyr Thr Ala Gln Asp Ala Thr Thr Ala Gln Lys Gly Ile Val Gln Leu
        355                 360                 365

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

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

Asp Ala Thr Thr Thr Gln Lys Gly Ile Val Gln Leu Ser Ser Asp Thr
                405                 410                 415
```

Asn Ser Thr Ser Glu Thr Leu Ala Ala Thr Pro Lys Ala Val Lys Ala
420 425 430

Ala Tyr Asp Leu Ala Ala Gly Lys Ala Pro Ser Ser His Thr His Pro
435 440 445

Trp Asn Gln Ile Thr Val Val Pro Thr Ala Ser Leu Thr Ala Lys Gly
450 455 460

Ile Thr Gln Leu Ser Ser Ala Thr Asn Ser Thr Ser Glu Val Leu Ala
465 470 475 480

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

Tyr Thr Ala Gln Asp Ala Thr Thr Ala Gln Lys Gly Ile Val Gln Leu
500 505 510

Ser Ser Ala Thr Asn Ser Thr Ser Glu Val Leu Ala Ala Thr Pro Lys
515 520 525

[0101]

Ala Val Lys Ala Ala Tyr Asp Leu Ala Asn Gly Lys Gln Ala Ala Asp
530 535 540

Ala Thr Leu Thr Ala Leu Ala Ala Leu Ala Thr Ala Ala Asp Lys Leu
545 550 555 560

Pro Tyr Phe Thr Gly Val Asp Arg Ala Ala Leu Thr Ala Leu Thr Ser
565 570 575

Val Gly Arg Ala Ile Leu Gly Lys Thr Ser Ile Gln Ser Val Leu Asp
580 585 590

Tyr Leu Gly Leu Gly Glu Gly Ser Ala Leu Pro Val Gly Val Pro Val
595 600 605

Pro Trp Pro Ser Ala Thr Pro Pro Thr Gly Trp Leu Lys Cys Asn Gly
610 615 620

Ala Ala Phe Ser Ser Glu Lys Tyr Pro Asn Leu Ala Lys Val Tyr Pro
625 630 635 640

Thr Asn Lys Leu Pro Asp Leu Arg Gly Glu Phe Ile Arg Gly Trp Asp
645 650 655

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

Ala Thr Asn Phe Ser Gln Arg Ala Gly Asn Ile Gly Asp Gly Ala Gly
675 680 685

His Ala Ile Asn Phe His Asp Gly Ile Val Gly Asn Gln Pro Gly Phe
690 695 700

Ser Arg Phe Asn Phe Thr Ser Asn Ser Val Gly Asp Gly Ile Asn Phe
705 710 715 720

Val Ala Val Arg Pro Arg Asn Ile Ala Phe Asn Tyr Ile Val Arg Ala
725 730 735

Ala

[0102]

<210> 41
<211> 939
<212> PRT
<213> 人工序列

<220>
<223> 茄子尾丝

<400> 41

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

Ser Gln Pro Leu Leu Ala Asp Val Gln Tyr Phe Glu Leu Tyr Ser Ser
20 25 30

Ser Ala Leu Asn Arg Lys Leu Lys Asn Ile Val Leu Pro Gly Phe Tyr
35 40 45

Cys Gly Phe Glu Pro Val Pro Gly Thr Gly Leu Ser Val Arg Ile Thr
50 55 60

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

Val Gln Ile Ser Val Gln Gln Ile Glu Asp Val Thr Val Ser Val Lys
85 90 95

```
Ala Gly Ala Thr Asn Ile Ile Val Leu Glu Ala Asn Phe Glu His Gly
            100                 105                 110

Val Lys Thr Thr Gln Val Asp Ser Ala Ser Ser Val Ser Ala Ala Arg
        115                 120                 125

Ile Tyr Ala Arg Thr Asp Asn Thr Ile Gly Gln Asn Gln Ile Glu Leu
    130                 135                 140

Cys Arg Val Ile Val Pro Asn Gly Ala Thr Ala Val Thr Lys Glu Met
145                 150                 155                 160

Ile Val Leu Lys Tyr Arg Val Asn Arg Ala Val Gly Val Glu Phe Ser
                165                 170                 175

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

Val Lys Thr Leu His Asp Leu Val Asp Thr Lys Ala Pro Leu Asp Ser
        195                 200                 205
```

[0103]

```
Pro His Leu Ser Gly Thr Pro Thr Ser Pro Thr Pro Glu Pro Gly Thr
    210                 215                 220

Asn Asn Thr Gln Ile Ala Asn Ala Ala Phe Val Tyr Ala Ala Ile Asn
225                 230                 235                 240

Ala Leu Ile Asn Gly Ala Pro Gly Thr Met Asp Thr Leu Lys Glu Ile
                245                 250                 255

Ala Ala Ala Ile Asn Asn Asp Pro Asn Phe Ser Thr Thr Ile Asn Asn
            260                 265                 270

Ala Leu Ala Leu Lys Ala Pro Leu Ala Ser Pro Ala Leu Thr Gly Ile
        275                 280                 285

Pro Thr Ala Pro Thr Ala Ala Gln Gly Thr Asn Asn Thr Gln Ile Ala
    290                 295                 300

Thr Thr Ala Tyr Val Arg Ala Ala Ile Ser Ala Leu Val Gly Ser Ser
305                 310                 315                 320
```

```
Pro Glu Ala Leu Asp Thr Leu Asn Glu Leu Ala Ala Ala Leu Gly Asn
                325                 330                 335

Asp Pro Asn Phe Ala Thr Thr Met Thr Asn Ala Leu Ala Gly Lys Gln
            340                 345                 350

Pro Leu Asp Ala Thr Leu Thr Ala Leu Ala Gly Leu Ala Thr Gly Ala
        355                 360                 365

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

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

Val Ile Gln Tyr Leu Gly Leu Arg Glu Leu Gly Thr Ser Gly Glu Lys
                405                 410                 415

Ile Pro Leu Leu Ser Thr Ala Asn Thr Trp Ser Ala Arg Gln Thr Phe
            420                 425                 430
```

[0104]

```
Asn Gly Gly Ile Thr Gly Ala Leu Thr Gly Asn Ala Asp Thr Ala Thr
        435                 440                 445

Lys Leu Lys Thr Ala Ile Asn Ile Asn Gly Val Arg Phe Asp Gly Ser
    450                 455                 460

Thr Asn Ile Ser Ile Pro Thr Ile Thr Ser Arg Gly Arg Val Thr Ala
465                 470                 475                 480

Leu Thr Gly Thr Thr Gln Gly Ala Ala Thr Gly Leu Gln Met Tyr Glu
                485                 490                 495

Ala Tyr Asn Asn Gly Tyr Pro Ser Pro Tyr Gly Asn Val Leu His Leu
            500                 505                 510

Lys Gly Ala Thr Ala Ala Gly Glu Gly Glu Leu Phe Ile Gly Trp Ser
        515                 520                 525

Gly Thr Asn Gly Ala His Ala Pro Ala Phe Ile Arg Ser Lys Arg Asp
    530                 535                 540

Ser Thr Ala Ala Ala Trp Ser Glu Trp Ala Gln Ile Tyr Thr Ser Lys
545                 550                 555                 560
```

```
Asp Ser Val Pro Gly Val Asn Ala Lys Gly Asn Gln Asp Thr Ser Gly
                565                 570                 575

Asn Ala Ala Thr Ala Thr Lys Leu Gln Ile Ala Cys Thr Ile Asn Gly
            580                 585                 590

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

Asn Leu Gln Glu Thr Val Asn Lys Ala Asp Asn Ala Val Gln Lys Thr
    610                 615                 620

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

Ala Trp Ile Arg Asn Thr Asp Trp Ala Lys Ile Gly Phe Lys Asn Asp
                645                 650                 655

Ala Asp Ser Asp Thr Asp Ser Tyr Met Trp Phe Glu Thr Gly Asp Asn
            660                 665                 670
```

[0105]

```
Gly Asn Glu Tyr Phe Lys Trp Arg Ser Lys Gln Ser Thr Thr Thr Lys
        675                 680                 685

Asp Leu Met Asn Leu Lys Trp Asp Ala Leu Tyr Val Leu Val Asn Ala
    690                 695                 700

Ile Val Asn Gly Glu Val Ile Ser Lys Ser Ala Asn Gly Leu Arg Ile
705                 710                 715                 720

Ala Tyr Gly Asn Tyr Gly Phe Phe Ile Arg Asn Asp Gly Ser Asn Thr
                725                 730                 735

Tyr Phe Met Leu Thr Asn Ser Gly Asp Asn Met Gly Thr Tyr Asn Gly
            740                 745                 750

Leu Arg Pro Leu Trp Ile Asn Asn Ala Thr Gly Ala Val Ser Met Gly
        755                 760                 765

Arg Gly Leu Asn Val Ser Gly Glu Thr Leu Ser Asp Arg Phe Ala Ile
    770                 775                 780
```

```
Asn Ser Ser Asn Gly Met Trp Ile Gln Met Arg Asp Asn Asn Ala Ile
785                 790                 795                 800

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

Gln Asn His Ala Asp Arg Lys Phe Met Ile Gly Gly Leu Gly Asn Lys
            820                 825                 830

Gln Phe Gly Ile Tyr Met Ile Asn Asn Ser Arg Thr Ala Asn Gly Thr
        835                 840                 845

Asp Gly Gln Ala Tyr Met Asp Asn Asn Gly Asn Trp Leu Cys Gly Ala
    850                 855                 860

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

Asp Val Arg Leu Gly Thr Arg Val Val Gln Leu Met Ala Arg Gly Gly
                885                 890                 895
```

[0106]

```
Arg Tyr Glu Lys Ala Gly His Ala Ile Thr Gly Leu Arg Ile Ile Gly
            900                 905                 910

Glu Val Asp Gly Asp Asp Glu Ala Ile Phe Arg Pro Ile Gln Lys Tyr
        915                 920                 925

Ile Asn Gly Thr Trp Tyr Asn Val Ala Gln Val
    930                 935
```

<210> 42
<211> 986
<212> PRT
<213> 人工序列

<220>
<223> 蕨尾丝

<400> 42

```
Met Asn Asp Val Thr Val Val Thr Ser Val Thr Tyr Pro Ser Ser Glu
1               5                   10                  15

Ser Leu Ala Leu Val Ala Asp Val Gln Tyr His Glu Pro Tyr Leu Ser
            20                  25                  30
```

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

Ala Gly Phe Leu Pro Lys Pro Gly Gly Gly Met Asn Leu Leu Ile Thr
    50                  55                  60

Ser Val Asp Gly Asp Lys Thr Ala Gly Ala Ala Ser Val Asp Ile Gly
65                  70                  75                  80

Glu Phe Tyr Gln Val Thr Ile Gln Gln Arg Lys Asp Ile Ser Leu Ala
                85                  90                  95

Leu Ser Ala Gly Lys Lys Tyr Ala Ile Val Leu Lys Gly Arg Tyr Leu
            100                 105                 110

Leu Gly Glu Asp Thr Tyr Gln Val Asn Thr Ala Ser His Ile His Ala
        115                 120                 125

Ala Glu Phe Val Ala Arg Thr Tyr Thr Asp Ser Tyr Gln Leu Gly Asp
    130                 135                 140
```

[0107]

```
Gly Glu Leu Leu Val Cys Thr Val Asn Ile Pro Ala Ser Val Ser Ala
145                 150                 155                 160

Ile Thr Gln Glu Met Ile Asp Thr Ser Glu Arg Ile Asn Arg Ser Ile
                165                 170                 175

Gly Ile Asp Ile Ser Asp Ser Val Thr Ser Thr Arg Ser Asp Val Ala
            180                 185                 190

Ala Ser Ser Leu Ala Val Lys Lys Ala Tyr Asp Leu Ala Lys Ser Lys
        195                 200                 205

Tyr Thr Ala Gln Asp Ala Ser Thr Thr Gln Lys Gly Leu Val Gln Leu
    210                 215                 220

Ser Ser Ala Thr Asn Ser Asp Ser Glu Thr Met Ala Ala Thr Pro Lys
225                 230                 235                 240

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

Ser Pro Ser Leu Thr Gly Thr Pro Thr Ala Pro Thr Ala Ala Gln Gly
            260                 265                 270
```

```
Thr Asn Ser Thr Gln Ile Ala Asn Thr Ala Phe Val Lys Ala Ala Ile
        275                 280                 285

Thr Ala Leu Ile Asn Gly Ala Pro Gly Thr Leu Asp Thr Leu Lys Glu
    290                 295                 300

Ile Ala Ala Ala Ile Asn Asn Asp Pro Asn Tyr Ser Thr Thr Ile Asn
305                 310                 315                 320

Asn Ala Leu Ala Leu Lys Ala Pro Leu Ala Ser Pro Ala Leu Thr Gly
                325                 330                 335

Val Pro Thr Ala Pro Thr Ala Ala Gln Gly Thr Asn Asn Thr Gln Ile
            340                 345                 350

Ala Thr Thr Ala Tyr Val Arg Ala Ala Ile Ser Ala Leu Val Gly Ser
        355                 360                 365

Ser Pro Glu Ala Leu Asp Thr Leu Tyr Glu Leu Ala Ala Ala Leu Gly
    370                 375                 380
```

[0108]

```
Asn Asp Pro Asn Phe Ala Thr Thr Met Thr Asn Ala Leu Ala Gly Lys
385                 390                 395                 400

Gln Pro Leu Asp Ala Thr Leu Thr Ala Leu Ala Gly Leu Ala Thr Gly
                405                 410                 415

Ala Asn Lys Leu Pro Tyr Phe Thr Gly Thr Asp Thr Val Ser Gln Thr
            420                 425                 430

Asp Leu Thr Ser Val Gly Arg Asp Ile Leu Ala Lys Thr Ser Ile Leu
        435                 440                 445

Ala Val Ile Gln Tyr Leu Gly Leu Arg Glu Leu Gly Thr Ser Gly Glu
    450                 455                 460

Lys Ile Pro Leu Leu Ser Thr Ala Asn Thr Trp Ser Ala Arg Gln Thr
465                 470                 475                 480

Phe Asn Gly Gly Ile Thr Gly Ala Leu Thr Gly Asn Ala Asp Thr Ala
                485                 490                 495
```

Thr Lys Leu Lys Thr Ala Arg Asn Ile Asn Gly Val Arg Phe Asp Gly
500 505 510

Ser Gly Asp Ile Asn Ile Asn Thr Leu Val Ser Arg Gly Arg Val Thr
515 520 525

Ala Leu Glu Ala Asn Ala Gln Gly Thr Ser Gly Ile Gln Leu Tyr Glu
530 535 540

Ala Tyr Asn Asn Gly Tyr Pro Ser Pro Tyr Gly Asn Val Leu His Leu
545 550 555 560

Lys Gly Ala Thr Ala Ala Gly Glu Gly Glu Leu Phe Ile Gly Trp Ser
565 570 575

Gly Thr Ser Gly Ala His Ala Pro Val His Ile Arg Ser Arg Arg Asp
580 585 590

Thr Asp Ser Ala Asn Trp Ser Glu Trp Ala Gln Val Tyr Thr Ser Lys
595 600 605

[0109]

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

Asn Ala Ala Thr Ala Thr Lys Leu Gln Thr Ala Cys Thr Ile Asn Gly
625 630 635 640

Val Ser Phe Asp Gly Ser Lys Asn Ile Glu Leu Thr Ala Glu Asp Leu
645 650 655

Asn Leu Gln Glu Thr Val Asn Lys Ala Gly Asn Ala Val Gln Lys Thr
660 665 670

Gly Asp Thr Leu Ser Gly Gly Leu Thr Phe Glu Asn Asp Ser Ile Leu
675 680 685

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

Ala Asp Gly Asp Thr Asp Ser Tyr Met Trp Phe Glu Thr Gly Asp Asn
705 710 715 720

Gly Asn Glu Tyr Phe Lys Trp Arg Ser Lys Arg Gly Thr Thr Thr Lys
725 730 735

```
Asp Leu Met Asn Leu Lys Trp Asp Ala Leu Tyr Val Leu Val Asn Ala
            740                 745                 750

Ile Val Asn Gly Glu Val Ile Ser Lys Ser Ala Asn Gly Leu Arg Ile
        755                 760                 765

Ala Tyr Gly Asn Tyr Gly Phe Phe Ile Arg Asn Asp Gly Ser Asn Thr
    770                 775                 780

Tyr Phe Met Leu Thr Asn Ser Gly Asp Asn Met Gly Thr Tyr Asn Gly
785                 790                 795                 800

Leu Arg Pro Leu Trp Ile Asn Asn Ala Thr Gly Ala Val Ser Met Gly
                805                 810                 815

Arg Gly Leu Asn Val Ser Gly Glu Thr Leu Gln Thr Val Cys Tyr Asn
            820                 825                 830

Ser Ser Asn Gly Met Trp Ile Gln Met Arg Asp Asn Asn Ala Ile Phe
        835                 840                 845
```

[0110]

```
Gly Lys Asn Ile Val Asn Thr Asp Ser Ala Gln Ala Leu Leu Arg Gln
    850                 855                 860

Asn His Ala Asp Arg Lys Phe Met Ile Gly Gly Leu Gly Asn Lys Gln
865                 870                 875                 880

Phe Gly Ile Tyr Met Ile Asn Asn Ser Arg Thr Ala Asn Gly Thr Asp
                885                 890                 895

Gly Gln Ala Tyr Met Asp Asn Asn Gly Asn Trp Leu Cys Gly Ala Gln
            900                 905                 910

Ile Ile Pro Gly Asn Tyr Gly Asn Phe Asp Ser Arg Tyr Val Ser Asp
        915                 920                 925

Val Arg Leu Gly Thr Arg Val Val Gln Thr Met Gln Lys Gly Val Met
    930                 935                 940

Tyr Glu Lys Ser Gly His Ala Ile Thr Gly Leu Gly Ile Val Gly Glu
945                 950                 955                 960
```

Val Asp Gly Asp Asp Pro Ala Val Phe Arg Pro Ile Gln Lys Tyr Ile
965 970 975

Asn Gly Thr Trp Tyr Asn Val Ala Gln Val
980 985

<210> 43
<211> 972
<212> PRT
<213> 人工序列

<220>
<223> 樱红尾丝

<400> 43

Met Asn Asp Val Thr Val Val Thr Ser Val Thr Tyr Pro Ser Ser Glu
1 5 10 15

Ser Leu Ala Leu Val Ala Asp Val Gln Tyr His Glu Pro Tyr Leu Ser
20 25 30

Ala Ala Leu Asn Arg Lys Phe Arg Gly Ile Val Asp Pro Gly Phe Tyr
35 40 45

[0111]

Ala Gly Phe Leu Pro Lys Pro Gly Gly Gly Met Asn Leu Leu Ile Thr
50 55 60

Ser Val Asp Gly Asp Lys Thr Ala Gly Ala Ala Ser Val Asp Ile Gly
65 70 75 80

Glu Phe Tyr Gln Val Thr Ile Gln Gln Arg Lys Asp Ile Ser Leu Ala
85 90 95

Leu Ser Ala Gly Lys Lys Tyr Ala Ile Val Leu Lys Gly Arg Tyr Leu
100 105 110

Leu Gly Glu Asp Thr Tyr Gln Val Asn Thr Ala Ser His Ile His Ala
115 120 125

Ala Glu Phe Val Ala Arg Thr Tyr Thr Asp Ser Tyr Gln Leu Gly Asp
130 135 140

Gly Glu Leu Leu Val Cys Thr Val Asn Ile Pro Ala Ser Val Ser Ala
145 150 155 160

```
Ile Thr Gln Glu Met Ile Asp Thr Ser Glu Arg Ile Asn Arg Ser Ile
                165                 170                 175

Gly Ile Asp Ile Ser Asp Ser Val Thr Ser Thr Arg Ser Asp Val Ala
            180                 185                 190

Ala Ser Ser Leu Ala Val Lys Lys Ala Tyr Asp Leu Ala Lys Ser Lys
        195                 200                 205

Tyr Thr Ala Gln Asp Ala Ser Thr Thr Gln Lys Gly Leu Val Gln Leu
    210                 215                 220

Ser Ser Ala Thr Asn Ser Asp Ser Glu Thr Met Ala Ala Thr Pro Lys
225                 230                 235                 240

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

Ser Pro Ser Leu Thr Gly Thr Pro Thr Ala Pro Thr Ala Ala Gln Gly
            260                 265                 270
```

[0112]

```
Thr Asn Ser Thr Gln Ile Ala Asn Thr Ala Phe Val Lys Ala Ala Ile
        275                 280                 285

Thr Ala Leu Ile Asn Gly Ala Pro Gly Thr Leu Asp Thr Leu Lys Glu
    290                 295                 300

Ile Ala Ala Ala Ile Asn Asn Asp Pro Asn Tyr Ser Thr Thr Ile Asn
305                 310                 315                 320

Asn Ala Leu Ala Leu Lys Ala Pro Leu Ala Ser Pro Ala Leu Thr Gly
                325                 330                 335

Val Pro Thr Ala Pro Thr Ala Ala Gln Gly Thr Asn Asn Thr Gln Ile
            340                 345                 350

Ala Thr Thr Ala Tyr Val Arg Ala Ala Ile Ser Ala Leu Val Gly Ser
        355                 360                 365

Ser Pro Glu Ala Leu Asp Thr Leu Tyr Glu Leu Ala Ala Ala Leu Gly
    370                 375                 380

Asn Asp Pro Asn Phe Ala Thr Thr Met Thr Asn Ala Leu Ala Gly Lys
385                 390                 395                 400
```

Gln Pro Leu Asp Ala Thr Leu Thr Ala Leu Ala Gly Leu Ala Thr Gly
405 410 415

Ala Asn Lys Leu Pro Tyr Phe Thr Gly Thr Asp Thr Val Ser Gln Thr
420 425 430

Asp Leu Thr Ser Val Gly Arg Asp Ile Leu Ala Lys Thr Ser Ile Leu
435 440 445

Ala Val Ile His Gly Leu Arg Glu Leu Gly Thr Ser Gly Glu Lys Ile
450 455 460

Pro Leu Leu Ser Thr Ala Asn Thr Trp Ser Ala Arg Gln Thr Phe Asn
465 470 475 480

Gly Gly Ile Thr Gly Ala Leu Ile Gly Asn Ala Asp Thr Ala Thr Lys
485 490 495

Leu Lys Thr Ala Ile Asn Ile Asn Gly Val Arg Phe Asp Gly Ser Ala
500 505 510

[0113]

Asp Ile Asn Ile Asn Thr Leu Val Ser Arg Gly Arg Val Thr Ala Leu
515 520 525

Gly Ala Asn Ala Gln Gly Thr Ser Gly Ile Gln Leu Tyr Glu Ala Tyr
530 535 540

Asn Asn Gly Tyr Pro Ser Pro Tyr Gly Asn Val Leu His Leu Lys Gly
545 550 555 560

Ala Thr Ala Ala Gly Glu Gly Glu Leu Phe Ile Gly Trp Ser Val Ser
565 570 575

Ser Gly Asp His Ala Pro Val His Ile Arg Ser Arg Arg Asp Ile Asp
580 585 590

Ser Ala Asn Trp Ser Glu Trp Ala Gln Val Tyr Thr Ser Lys Asp Ser
595 600 605

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

```
Ala Thr Ala Thr Lys Leu Gln Thr Ala Cys Thr Ile Asn Gly Val Ser
625                 630                 635                 640

Phe Asp Gly Ser Lys Asn Ile Glu Leu Thr Ala Glu Asp Leu Asn Leu
                645                 650                 655

Glu Gln Thr Val Glu Leu Ala Ala Gly Ala Leu Gln Lys Asn Gln Asn
            660                 665                 670

Gly Ala Asp Ile Pro Asn Lys Asp Lys Phe Ile Gln Asn Thr Gly Ala
        675                 680                 685

Cys Arg Ala Phe Ser Gly Gln Thr Asp Ile Asp Gly Ser Gln Gly Glu
    690                 695                 700

Trp Ser Thr Val Ala Phe Ile Ser Trp Leu Glu Asn Asn Gly Ala Phe
705                 710                 715                 720

Arg His Pro Tyr Trp Met Cys Lys Gly Ser Trp Ser Tyr Ala Arg Asn
                725                 730                 735

Arg Val Ile Thr Asp Thr Gly Cys Gly Asn Ile Cys Leu Ala Gly Ala
            740                 745                 750

Val Ile Glu Val Met Gly Thr Arg Gly Ala Met Thr Ile Arg Val Thr
        755                 760                 765

Thr Pro Ser Thr Ser Ser Gly Gly Gly Ile Thr Asn Ala Gln Phe Thr
    770                 775                 780

Tyr Ile Asn His Gly Asp Ala Tyr Ala Pro Gly Trp Arg Arg Asp Tyr
785                 790                 795                 800

Asn Thr Lys Asn Gln Gln Pro Ala Phe Ala Leu Gly Gln Thr Gly Arg
                805                 810                 815

Arg Val Ala Asn Asp Lys Ala Val Gly Trp Asn Trp Asn Ser Gly Val
            820                 825                 830

Tyr Asp Ala Asp Ile Ser Gly Ala Ser Thr Leu Ile Leu His Phe Asn
        835                 840                 845

Met Asn Ala Gly Ser Cys Pro Ala Val Gln Phe Arg Val Asn Tyr Arg
    850                 855                 860
```

[0114]

```
Asn Gly Gly Ile Phe Tyr Arg Ser Ala Arg Asp Gly Tyr Gly Phe Glu
865                 870                 875                 880

Ala Asn Trp Ser Glu Phe Tyr Thr Thr Thr Arg Lys Pro Ser Ala Gly
                885                 890                 895

Asp Val Gly Ala Tyr Thr Gln Ala Glu Cys Asn Ser Arg Phe Ile Thr
            900                 905                 910

Gly Ile Arg Leu Gly Gly Leu Ser Ser Val Gln Thr Trp Asn Gly Pro
        915                 920                 925

Gly Trp Ser Asp Arg Ser Gly Tyr Val Val Thr Gly Ser Val Asn Gly
    930                 935                 940

Asn Arg Asp Glu Leu Ile Asp Thr Thr Gln Ala Arg Pro Ile Gln Tyr
945                 950                 955                 960

Cys Ile Asn Gly Thr Trp Tyr Asn Ala Gly Ser Ile
                965                 970
```

[0115]

<210> 44
<211> 550
<212> PRT
<213> 人工序列

<220>
<223> 模糊尾丝

<400> 44

```
Met Asn Asp Val Thr Val Val Thr Ser Val Thr Tyr Pro Ser Ser Glu
1               5                   10                  15

Ser Leu Ala Leu Val Ala Asp Val Gln Tyr His Glu Pro Tyr Leu Ser
            20                  25                  30

Ala Ala Leu Asn Arg Lys Phe Arg Gly Ile Val Asp Pro Gly Phe Tyr
        35                  40                  45

Ala Gly Phe Leu Pro Lys Pro Gly Gly Gly Met Asn Leu Leu Ile Thr
    50                  55                  60

Ser Val Asp Gly Asp Lys Thr Ala Gly Ala Ala Ser Val Asp Ile Gly
65                  70                  75                  80
```

```
Glu Phe Tyr Gln Val Thr Ile Gln Gln Arg Lys Asp Ile Ser Leu Ala
                85                  90                  95

Leu Ser Ala Gly Lys Lys Tyr Ala Ile Val Leu Lys Gly Arg Tyr Leu
            100                 105                 110

Leu Gly Glu Asp Thr Tyr Gln Val Asn Thr Ala Ser His Ile His Ala
        115                 120                 125

Ala Glu Phe Val Ala Arg Thr Tyr Thr Asp Ser Tyr Gln Leu Gly Asp
    130                 135                 140

Gly Glu Leu Leu Val Cys Thr Val Asn Ile Pro Ala Ser Val Ser Ala
145                 150                 155                 160

Ile Thr Gln Glu Met Ile Asp Thr Ser Glu Arg Ile Asn Arg Ser Ile
                165                 170                 175

Gly Ile Asp Ile Ser Asp Ser Val Thr Ser Thr Arg Ser Asp Val Ala
            180                 185                 190
```

[0116]

```
Ala Ser Ser Leu Ala Val Lys Lys Ala Tyr Asp Leu Ala Lys Ser Lys
        195                 200                 205

Lys Pro Asp Gly Thr Thr Gly Thr Val Lys Ser Trp Ala Gln Phe Leu
    210                 215                 220

Ser Glu Tyr Ser Ser Arg Gln Thr Ala Ile Asp Gly Ala Ile Thr Ala
225                 230                 235                 240

Ala Gly Lys Asn Val Ala Arg Thr Ser Ser Thr Asn Thr Phe Thr Gln
                245                 250                 255

Pro Gln Thr Phe Ser Asn Gly Val Thr Phe Ser Ala Thr Ile Thr Ala
            260                 265                 270

Ala Gly Gln Ile Leu Arg Asn Asn Ser Gly Thr Gln Phe Thr Ala Ile
        275                 280                 285

Asp Ala Gly Ser Leu Glu Ile Ser Ser Asp Thr Thr Pro Tyr Ile Asp
    290                 295                 300
```

Phe His His Lys Gly Ser Val Ala Asp Tyr Thr His Arg Ile Ile Thr
305 310 315 320

Glu Asp Gly Ala Leu Ala Val Tyr Pro Gly Leu Arg Val Arg Gly Gly
325 330 335

Phe Gly Leu Tyr Gly Val Gly Thr Val Tyr Gly Asp Ala Tyr Ser Gln
340 345 350

Gly Phe Ile Ala Arg Leu Asn Asn Asp Pro Asn Ala Ser Ile Gly Asp
355 360 365

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

Asp Ser Asn Val Asp Gly Gly Gln Gly Ala Met Trp Phe Glu Glu Gln
385 390 395 400

Val Gly Thr Asn His Arg Leu Val Leu Met Ala Gly Gly Phe Ser Ala
405 410 415

[0117] Asn Val Gln Tyr Trp Gln Phe Leu Ala Asp Gly Arg Ile Tyr Ser Ser
420 425 430

Gln Asn Gly Asn Val Gln Trp Gln Gly Thr Ser Asp Ala Arg Leu Lys
435 440 445

His Asp Ile Glu Pro Thr Asp Gly Gln Leu Ser Val Glu Arg Ile Arg
450 455 460

Lys Leu Glu Leu Val Thr Phe Val Tyr Asn Asp Asp Glu Gln Asn Arg
465 470 475 480

Thr Arg Arg Gly Ile Ile Ala Gln Gln Ala Gln Lys Val Asp Pro Gln
485 490 495

Tyr Val Lys Gln Val Asn Thr Ser Tyr Met Arg Asn Gly Glu Gln Val
500 505 510

Asn Asp Asp Arg Leu Gln Leu Asp Asn Asn Val Ile Met Met Asp Thr
515 520 525

Leu Ala Ala Val Lys Val Leu Leu Glu Arg Val Asp Glu Leu Glu Glu
530 535 540

Arg Leu Ser Ala His Gly
545 550

<210> 45
<211> 736
<212> PRT
<213> 人工序列

<220>
<223> 尺蠖尾丝

<400> 45

Met Asn Asp Val Thr Val Val Thr Ser Val Thr Tyr Pro Ser Ser Glu
1 5 10 15

Ser Leu Ala Leu Val Ala Asp Val Gln Tyr His Glu Pro Tyr Leu Ser
20 25 30

Ala Ala Leu Asn Arg Lys Phe Arg Gly Ile Val Asp Pro Gly Phe Tyr
35 40 45

Ala Gly Phe Leu Pro Lys Pro Gly Gly Gly Met Asn Leu Leu Ile Thr
50 55 60

[0118]

Ser Val Asp Gly Asp Lys Thr Ala Gly Ala Ala Ser Val Asp Ile Gly
65 70 75 80

Glu Phe Tyr Gln Val Thr Ile Gln Gln Arg Lys Asp Ile Ser Leu Ala
85 90 95

Leu Ser Ala Gly Lys Lys Tyr Ala Ile Val Leu Lys Gly Arg Tyr Leu
100 105 110

Leu Gly Glu Asp Thr Tyr Gln Val Asn Thr Ala Ser His Ile His Ala
115 120 125

Ala Glu Phe Val Ala Arg Thr Tyr Thr Asp Ser Tyr Gln Leu Gly Asp
130 135 140

Gly Glu Leu Leu Val Cys Thr Val Asn Ile Pro Ala Ser Val Ser Ala
145 150 155 160

Ile Thr Gln Glu Met Ile Asp Thr Ser Glu Arg Ile Asn Arg Ser Ile
165 170 175

```
Gly Ile Asp Ile Ser Asp Ser Val Thr Ser Thr Arg Ser Asp Val Ala
            180                 185                 190

Ala Ser Ser Leu Ala Val Lys Lys Ala Tyr Asp Leu Ala Lys Ser Lys
        195                 200                 205

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

Leu Gly Gly Gly Asp Leu Ser Ala Asp Arg Ser Ile Gly Leu Ala Pro
225                 230                 235                 240

Ser Gly Val Thr Ala Gly Ser Tyr Arg Ser Val Thr Val Asn Ala Asn
                245                 250                 255

Gly Val Val Thr Gln Gly Ser Asn Pro Thr Thr Leu Ala Gly Tyr Ala
            260                 265                 270

Ile Gly Asp Ala Tyr Thr Lys Ala Asp Thr Asp Gly Lys Leu Ala Gln
        275                 280                 285
```

[0119]

```
Lys Ala Asn Lys Ala Thr Thr Leu Ala Gly Tyr Gly Ile Thr Asp Ala
    290                 295                 300

Leu Arg Val Asp Gly Asn Ala Val Ser Ser Ser Arg Leu Ala Ala Pro
305                 310                 315                 320

Arg Ser Leu Ala Ala Ser Gly Asp Ala Ser Trp Ser Val Thr Phe Asp
                325                 330                 335

Gly Ser Ala Asn Val Ser Ala Pro Leu Ser Leu Ser Ala Thr Gly Val
            340                 345                 350

Ala Ala Gly Ser Tyr Pro Lys Val Thr Val Asp Thr Lys Gly Arg Val
        355                 360                 365

Thr Ala Gly Met Ala Leu Ala Ala Thr Asp Ile Pro Gly Leu Asp Ala
    370                 375                 380

Ser Lys Leu Val Ser Gly Val Leu Ala Glu Gln Arg Leu Pro Val Phe
385                 390                 395                 400
```

Ala Arg Gly Leu Ala Thr Ala Val Ser Asn Ser Ser Asp Pro Asn Thr
405 410 415

Ala Thr Val Pro Leu Met Leu Thr Asn His Ala Asn Gly Pro Val Ala
420 425 430

Gly Arg Tyr Phe Tyr Ile Gln Ser Met Phe Tyr Pro Asp Gln Asn Gly
435 440 445

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

Val Arg Val Ser Tyr Ala Ala Asn Pro Ser Ile Arg Glu Trp Leu Pro
465 470 475 480

Trp Gln Arg Cys Asp Ile Gly Gly Ser Phe Thr Lys Glu Ala Asp Gly
485 490 495

Glu Leu Pro Gly Gly Val Asn Leu Asp Ser Met Val Thr Ser Gly Trp
500 505 510

[0120] Trp Ser Gln Ser Phe Thr Ala Gln Ala Ala Ser Gly Ala Asn Tyr Pro
515 520 525

Ile Val Arg Ala Gly Leu Leu His Val Tyr Ala Ala Ser Ser Asn Phe
530 535 540

Ile Tyr Gln Thr Tyr Gln Ala Tyr Asp Gly Glu Ser Phe Tyr Phe Arg
545 550 555 560

Cys Arg His Ser Asn Thr Trp Phe Pro Trp Arg Arg Met Trp His Gly
565 570 575

Gly Asp Phe Asn Pro Ser Asp Tyr Leu Leu Lys Ser Gly Phe Tyr Trp
580 585 590

Asn Ala Leu Pro Gly Lys Pro Ala Thr Phe Pro Pro Ser Ala His Asn
595 600 605

His Asp Val Gly Gln Leu Thr Ser Gly Ile Leu Pro Leu Ala Arg Gly
610 615 620

Gly Val Gly Ser Asn Thr Ala Ala Gly Ala Arg Ser Thr Ile Gly Ala
625 630 635 640

Gly Val Pro Ala Thr Ala Ser Leu Gly Ala Ser Gly Trp Trp Arg Asp
645 650 655

Asn Asp Thr Gly Leu Ile Arg Gln Trp Gly Gln Val Thr Cys Pro Ala
660 665 670

Asp Ala Asp Ala Ser Ile Thr Phe Pro Ile Pro Phe Pro Thr Leu Cys
675 680 685

Leu Gly Gly Tyr Ala Asn Gln Thr Ser Ala Phe His Pro Gly Thr Asp
690 695 700

Ala Ser Thr Gly Phe Arg Gly Ala Thr Thr Thr Thr Ala Val Ile Arg
705 710 715 720

Asn Gly Tyr Phe Ala Gln Ala Val Leu Ser Trp Glu Ala Phe Gly Arg
725 730 735

[0121]

<210> 46
<211> 762
<212> PRT
<213> 人工序列

<220>
<223> 印度尾丝

<400> 46

Met Asn Asp Val Thr Val Val Thr Ser Val Thr Tyr Pro Ser Pro Glu
1 5 10 15

Ser Leu Ala Leu Val Ala Asp Val Gln Tyr His Glu Pro Tyr Leu Ser
20 25 30

Ala Ala Leu Asn Arg Lys Phe Arg Gly Ile Val Asp Pro Gly Phe Tyr
35 40 45

Ala Gly Phe Leu Pro Lys Pro Gly Gly Gly Met Asn Leu Leu Ile Thr
50 55 60

Ser Val Asp Gly Asp Lys Thr Ala Gly Ala Ala Ser Val Asp Ile Gly
65 70 75 80

Glu Phe Tyr Gln Val Thr Ile Gln His Arg Lys Asp Ile Ser Leu Ala
85 90 95

```
Leu Asn Ala Gly Lys Lys Tyr Ala Ile Val Leu Lys Gly Arg Tyr Leu
            100                 105                 110

Leu Gly Glu Asp Thr Tyr Gln Val Asn Thr Ala Ser His Ile His Ala
        115                 120                 125

Ala Glu Phe Val Ala Arg Thr Tyr Thr Asp Ser Tyr Gln Leu Gly Asp
    130                 135                 140

Gly Glu Leu Leu Val Cys Thr Val Asn Ile Pro Ala Gly Val Ser Thr
145                 150                 155                 160

Ile Thr Gln Glu Met Ile Asp Thr Ser Glu Arg Ile Asn Arg Thr Ile
                165                 170                 175

Gly Ile Asp Ile Ser Asp Ser Val Thr Ser Thr Arg Ser Asp Val Ala
            180                 185                 190

Ala Ser Ser Leu Ala Val Lys Lys Ala Tyr Asp Leu Ala Lys Ser Lys
        195                 200                 205
```

[0122]

```
Tyr Thr Ala Gln Asp Ala Ser Thr Thr Gln Lys Gly Leu Val Gln Leu
    210                 215                 220

Ser Ser Ala Thr Asn Ser Thr Ser Glu Val Leu Ala Ala Thr Pro Lys
225                 230                 235                 240

Ala Val Lys Ala Ala Tyr Asp Leu Ala Asn Gly Lys Tyr Thr Ala Gln
                245                 250                 255

Asp Ala Thr Thr Thr Gln Lys Gly Ile Val Gln Leu Ser Ser Asp Thr
            260                 265                 270

Asn Ser Thr Ser Glu Thr Leu Ala Ala Thr Pro Lys Ala Val Lys Ala
        275                 280                 285

Ala Tyr Asp Leu Ala Ala Gly Lys Ala Pro Ser Ser His Thr His Pro
    290                 295                 300

Trp Asn Gln Ile Thr Gly Val Pro Thr Ala Ser Leu Thr Ala Lys Gly
305                 310                 315                 320
```

Ile Thr Gln Leu Ser Ser Ala Thr Asn Ser Thr Ser Glu Val Leu Ala
325 330 335

Ala Thr Pro Lys Ala Val Lys Ala Ala Tyr Asp Leu Ala Asn Gly Lys
340 345 350

Tyr Thr Ala Gln Asp Ala Thr Thr Ala Gln Lys Gly Ile Val Gln Leu
355 360 365

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

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

Asp Ala Thr Thr Thr Gln Lys Gly Ile Val Gln Leu Ser Ser Asp Thr
405 410 415

Asn Ser Thr Ser Glu Thr Leu Ala Ala Thr Pro Lys Ala Val Lys Ala
420 425 430

[0123] Ala Tyr Asp Leu Ala Ala Gly Lys Ala Pro Ser Ser His Thr His Pro
435 440 445

Trp Asn Gln Ile Thr Val Val Pro Thr Ala Ser Leu Thr Ala Lys Gly
450 455 460

Ile Thr Gln Leu Ser Ser Ala Thr Asn Ser Thr Ser Glu Val Leu Ala
465 470 475 480

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

Tyr Thr Ala Gln Asp Ala Thr Thr Ala Gln Lys Gly Ile Val Gln Leu
500 505 510

Ser Ser Ala Thr Asn Ser Thr Ser Glu Val Leu Ala Ala Thr Pro Lys
515 520 525

Ala Val Lys Ala Ala Tyr Asp Leu Ala Asn Gly Lys Gln Ala Ala Asp
530 535 540

Ala Thr Leu Thr Ala Leu Ala Ala Leu Ala Thr Ala Ala Asp Lys Leu
545 550 555 560

```
Pro Tyr Phe Thr Gly Val Asp Arg Ala Ala Leu Thr Ala Leu Thr Ser
                565                 570                 575

Val Gly Arg Ala Ile Leu Gly Lys Thr Ser Ile Gln Ser Val Leu Asp
            580                 585                 590

Tyr Leu Gly Leu Gly Glu Gly Ser Ala Leu Pro Val Gly Val Pro Val
        595                 600                 605

Pro Trp Pro Leu Glu Thr Pro Pro Thr Gly Trp Leu Lys Cys Asn Gly
    610                 615                 620

Ala Ala Phe Ser Ser Glu Met Tyr Pro Lys Leu Ala Lys Ala Tyr Pro
625                 630                 635                 640

Thr Asn Lys Leu Pro Asp Leu Arg Gly Glu Phe Ile Arg Gly Trp Asp
                645                 650                 655

Asp Gly Arg Gly Val Asp Ala Gly Arg Ala Leu Leu Asn Trp Gln Pro
            660                 665                 670
```

[0124]

```
His Thr Ile Leu Asp His Ala His Tyr Met Glu Leu Trp Thr Gly Asp
        675                 680                 685

Gly Leu Ala Ala Gly Ser Ala Arg Glu Gly Val Asn Pro Gly Ile Leu
    690                 695                 700

Ala Thr Tyr Gly Asp Gly Gly Ile Val Lys Thr Asp Glu Pro Gly His
705                 710                 715                 720

Lys Val Pro Ser Ser Leu Arg Ala Ile Ser Ser Arg Ser Val Lys Arg
                725                 730                 735

Tyr Gly Glu Ile Ser Gly Asn Val Gly Thr Glu Thr Arg Pro Arg Asn
            740                 745                 750

Val Ala Phe Asn Tyr Ile Val Arg Ala Ala
        755                 760
```

<210> 47
<211> 750
<212> PRT
<213> 人工序列

<220>
<223> 靛蓝尾丝

<400> 47

Met Asn Asp Val Thr Val Val Thr Ser Val Thr Tyr Pro Ser Pro Glu
1 5 10 15

Ser Leu Ala Leu Val Ala Asp Val Gln Tyr His Glu Pro Tyr Leu Ser
20 25 30

Ala Ala Leu Asn Arg Lys Phe Arg Gly Ile Val Asp Pro Gly Phe Tyr
35 40 45

Ala Gly Phe Leu Pro Lys Pro Gly Gly Gly Met Asn Leu Leu Ile Thr
50 55 60

Ser Val Asp Gly Asp Lys Thr Ala Gly Ala Ala Ser Val Asp Ile Gly
65 70 75 80

Glu Phe Tyr Gln Val Thr Ile Gln His Arg Lys Asp Ile Ser Leu Ala
85 90 95

[0125]

Leu Asn Ala Gly Lys Lys Tyr Ala Ile Val Leu Lys Gly Arg Tyr Leu
100 105 110

Leu Gly Glu Asp Thr Tyr Gln Val Asn Thr Ala Ser His Ile His Ala
115 120 125

Ala Glu Phe Val Ala Arg Thr Tyr Thr Asp Ser Tyr Gln Leu Gly Asp
130 135 140

Gly Glu Leu Leu Val Cys Thr Val Asn Ile Pro Ala Gly Val Ser Thr
145 150 155 160

Ile Thr Gln Glu Met Ile Asp Thr Ser Glu Arg Ile Asn Arg Thr Ile
165 170 175

Gly Ile Asp Ile Ser Asp Ser Val Thr Ser Thr Arg Ser Asp Val Ala
180 185 190

Ala Ser Ser Leu Ala Val Lys Lys Ala Tyr Asp Leu Ala Lys Ser Lys
195 200 205

```
Tyr Thr Ala Gln Asp Ala Ser Thr Thr Gln Lys Gly Leu Val Gln Leu
    210                 215                 220

Ser Ser Ala Thr Asn Ser Thr Ser Glu Val Leu Ala Ala Thr Pro Lys
225                 230                 235                 240

Ala Val Lys Ala Ala Tyr Asp Leu Ala Asn Gly Lys Tyr Thr Ala Gln
                245                 250                 255

Asp Ala Thr Thr Thr Gln Lys Gly Ile Val Gln Leu Ser Ser Asp Thr
            260                 265                 270

Asn Ser Thr Ser Glu Thr Leu Ala Ala Thr Pro Lys Ala Val Lys Ala
        275                 280                 285

Ala Tyr Asp Leu Ala Ala Gly Lys Ala Pro Ser Ser His Thr His Pro
    290                 295                 300

Trp Asn Gln Ile Thr Gly Val Pro Thr Ala Ser Leu Thr Ala Lys Gly
305                 310                 315                 320
```

[0126]

```
Ile Thr Gln Leu Ser Ser Ala Thr Asn Ser Thr Ser Glu Val Leu Ala
                325                 330                 335

Ala Thr Pro Lys Ala Val Lys Ala Ala Tyr Asp Leu Ala Asn Gly Lys
            340                 345                 350

Tyr Thr Ala Gln Asp Ala Thr Thr Ala Gln Lys Gly Ile Val Gln Leu
        355                 360                 365

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

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

Asp Ala Thr Thr Thr Gln Lys Gly Ile Val Gln Leu Ser Ser Asp Thr
                405                 410                 415

Asn Ser Thr Ser Glu Thr Leu Ala Ala Thr Pro Lys Ala Val Lys Ala
            420                 425                 430

Ala Tyr Asp Leu Ala Ala Gly Lys Ala Pro Ser Ser His Thr His Pro
        435                 440                 445
```

```
Trp Asn Gln Ile Thr Val Val Pro Thr Ala Ser Leu Thr Ala Lys Gly
    450                 455                 460

Ile Thr Gln Leu Ser Ser Ala Thr Asn Ser Thr Ser Glu Val Leu Ala
465                 470                 475                 480

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

Tyr Thr Ala Gln Asp Ala Thr Thr Ala Gln Lys Gly Ile Val Gln Leu
            500                 505                 510

Ser Ser Ala Thr Asn Ser Thr Ser Glu Val Leu Ala Ala Thr Pro Lys
        515                 520                 525

Ala Val Lys Ala Ala Tyr Asp Leu Ala Asn Gly Lys Gln Ala Ala Asp
    530                 535                 540

Ala Thr Leu Thr Ala Leu Ala Ala Leu Ala Thr Ala Ala Asp Lys Leu
545                 550                 555                 560
```

[0127]

```
Pro Tyr Phe Thr Gly Val Asp Arg Ala Ala Leu Thr Ala Leu Thr Ser
                565                 570                 575

Val Gly Arg Ala Ile Leu Gly Lys Thr Ser Ile Gln Ser Val Leu Asp
            580                 585                 590

Tyr Leu Gly Leu Gly Glu Gly Ser Ala Leu Pro Val Gly Val Pro Val
        595                 600                 605

Pro Trp Pro Leu Glu Thr Pro Pro Thr Gly Trp Leu Lys Cys Asn Gly
    610                 615                 620

Ala Ala Phe Ser Ser Glu Lys Tyr Pro Asn Leu Ala Lys Ala Tyr Pro
625                 630                 635                 640

Thr Asn Lys Leu Pro Asp Leu Arg Gly Glu Phe Ile Arg Gly Trp Asp
                645                 650                 655

Asp Gly Arg Gly Ile Asp Ser Gly Arg Asn Leu Leu Ser Ala Gln Asn
            660                 665                 670
```

Asp Ala Ile Gln Asn Ile Val Gly Ser Phe Gly Arg Thr Gln Leu Phe
675 680 685

Arg Asp Val Leu Ser Ser Gly Pro Phe Ser Gln His Gly Gln Val Leu
690 695 700

Ser Thr Gly Leu Lys Glu Thr Glu Ile Ile Glu Gly Tyr Gly Ser Tyr
705 710 715 720

Asn Trp Thr Phe Asp Ala Ser Arg Ser Val Arg Thr Ala Ser Glu Thr
725 730 735

Arg Pro Arg Asn Ile Ala Phe Asn Tyr Ile Val Arg Ala Ala
740 745 750

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[0128]

<400> 48

Met Asn Asp Val Thr Val Val Thr Ser Val Thr Tyr Pro Ser Ser Glu
1 5 10 15

Ser Leu Ala Leu Val Ala Asp Val Gln Tyr His Glu Pro Tyr Leu Ser
20 25 30

Ala Ala Leu Asn Arg Lys Phe Arg Gly Ile Val Asp Pro Gly Phe Tyr
35 40 45

Ala Gly Phe Leu Pro Lys Pro Gly Gly Gly Met Asn Leu Leu Ile Thr
50 55 60

Ser Val Asp Gly Asp Lys Thr Ala Gly Ala Ala Ser Val Asp Ile Gly
65 70 75 80

Glu Phe Tyr Gln Val Thr Ile Gln Gln Arg Lys Asp Ile Ser Leu Ala
85 90 95

Leu Ser Ala Gly Lys Lys Tyr Ala Ile Val Leu Lys Gly Arg Tyr Leu
100 105 110

Leu Gly Glu Asp Thr Tyr Gln Val Asn Thr Ala Ser His Ile His Ala
115 120 125

Ala Glu Phe Val Ala Arg Thr Tyr Thr Asp Ser Tyr Gln Leu Gly Asp
130 135 140

Gly Glu Leu Leu Val Cys Thr Val Asn Ile Pro Ala Ser Val Ser Ala
145 150 155 160

Ile Thr Gln Glu Met Ile Asp Thr Ser Glu Arg Ile Asn Arg Ser Ile
165 170 175

Gly Ile Asp Ile Ser Asp Ser Val Thr Ser Thr Arg Ser Asp Val Ala
180 185 190

Ala Ser Ser Leu Ala Val Lys Lys Ala Tyr Asp Leu Ala Lys Ser Lys
195 200 205

Tyr Thr Ala Gln Asp Ala Ser Thr Thr Gln Lys Gly Leu Val Gln Leu
210 215 220

[0129] Ser Ser Ala Thr Asn Ser Asp Ser Glu Thr Met Ala Ala Thr Pro Lys
225 230 235 240

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

Ser Pro Ser Leu Thr Gly Thr Pro Thr Ala Pro Thr Ala Ala Gln Gly
260 265 270

Thr Asn Ser Thr Gln Ile Ala Asn Thr Ala Phe Val Lys Ala Ala Ile
275 280 285

Thr Ala Leu Ile Asn Gly Ala Pro Gly Thr Leu Asp Thr Leu Lys Glu
290 295 300

Ile Ala Ala Ala Ile Asn Asn Asp Pro Asn Tyr Ser Thr Thr Ile Asn
305 310 315 320

Asn Ala Leu Ala Leu Lys Ala Pro Leu Ala Ser Pro Ala Leu Thr Gly
325 330 335

Val Pro Thr Ala Pro Thr Ala Ala Gln Gly Thr Asn Asn Thr Gln Ile
340 345 350

```
Ala Thr Thr Ala Tyr Val Arg Ala Ala Ile Ser Ala Leu Val Gly Ser
        355                 360                 365

Ser Pro Glu Ala Leu Asp Thr Leu Tyr Glu Leu Ala Ala Ala Leu Gly
    370                 375                 380

Asn Asp Pro Asn Phe Ala Thr Thr Met Thr Asn Ala Leu Ala Gly Lys
385                 390                 395                 400

Gln Pro Leu Asp Ala Thr Leu Thr Ala Leu Ala Gly Leu Ala Thr Gly
                405                 410                 415

Ala Asn Lys Leu Pro Tyr Phe Thr Gly Thr Asp Thr Val Ser Gln Thr
            420                 425                 430

Asp Leu Thr Ser Val Gly Arg Asp Ile Leu Ala Lys Thr Ser Ile Leu
        435                 440                 445

Ala Val Ile Gln Tyr Leu Gly Leu Arg Glu Leu Gly Thr Ser Gly Glu
    450                 455                 460
```

[0130]

```
Lys Ile Pro Leu Leu Ser Thr Ala Asn Thr Trp Ser Ala Arg Gln Thr
465                 470                 475                 480

Phe Asn Gly Gly Ile Thr Gly Ala Leu Thr Gly Asn Ala Asp Thr Ala
                485                 490                 495

Thr Lys Leu Lys Thr Ala Arg Lys Ile Asn Asn Val Ser Phe Asp Gly
            500                 505                 510

Ser Ala Asp Ile Thr Leu Thr Pro Glu Asn Leu Gly Val Thr Ser Leu
        515                 520                 525

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

Thr Phe Gly Pro Val Glu Ala Tyr Leu Gly Val Trp Ser Lys Ala Thr
545                 550                 555                 560

Ser Thr Asn Ala Thr Leu Glu Lys Asn Phe Pro Glu Asp Asn Ala Val
                565                 570                 575
```

Gly Val Leu Glu Val Phe Ala Ala Gly Asn Phe Ala Gly Thr Gln Arg
580 585 590

Phe Thr Thr Arg Asp Gly Asn Val Tyr Ile Arg Arg Leu Ala Asn Lys
595 600 605

Trp Asn Gly Ser Asp Gly Pro Trp Gly Ile Trp Arg His Thr Gln Ser
610 615 620

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

Ala Glu His Leu Gly Leu Trp Arg Asn Ser Ser Ser Ala Ile Ala Ser
645 650 655

Tyr Glu Arg Asn Tyr Pro Glu Glu Gly Gly Phe Ala Gln Gly Val Leu
660 665 670

Glu Ile Leu Glu Gly Gly Asn Tyr Gly Arg Thr Gln Arg Tyr Thr Thr
675 680 685

[0131]

Arg Arg Gly Asn Met Tyr Val Arg Cys Leu Ala Ala Ser Trp Asp Ala
690 695 700

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

Ser Arg Tyr Tyr Glu Gly Asp Leu Asn Val Leu Thr Asp Pro Gly Ile
725 730 735

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

Gly Ala Thr Leu Leu Gly Ile Leu Glu Val Ile Arg Arg Phe Asp Gly
755 760 765

Val Ser Val Trp Gln Arg Tyr Thr Thr Thr Gly Lys Ser Glu Thr Thr
770 775 780

Gln Gly Arg Thr Phe Glu Arg Val Tyr Ala Gly Ser Lys Trp Thr Glu
785 790 795 800

Trp Arg Glu Val Tyr Asn Ser Phe Ser Leu Pro Leu Asn Leu Gly Ile
805 810 815

```
Gly Gly Ala Val Ala Lys Leu Ser Ser Leu Asp Trp Gln Thr Tyr Asp
            820                 825                 830

Phe Val Pro Gly Ser Leu Ile Thr Val Arg Leu Asp Asn Met Thr Asn
        835                 840                 845

Ile Pro Asp Gly Met Asp Trp Gly Val Ile Asp Gly Asn Leu Ile Asn
    850                 855                 860

Ile Ala Val Gly Pro Ser Asp Asp Ser Gly Thr Gly Arg Ser Met His
865                 870                 875                 880

Val Trp Arg Ser Thr Val Ser Lys Ala Asn Tyr Arg Phe Phe Met Val
                885                 890                 895

Arg Ile Ser Gly Asn Pro Gly Ser Arg Thr Ile Thr Ala Arg Arg Val
            900                 905                 910

Pro Ile Ile Asp Glu Ala Gln Thr Trp Gly Ala Lys Gln Thr Phe Ser
        915                 920                 925
```

[0132]

```
Ala Gly Leu Ser Gly Glu Leu Ser Gly Asn Ala Ala Thr Ala Thr Lys
    930                 935                 940

Leu Lys Thr Ala Arg Lys Ile Asn Asn Val Ser Phe Asp Gly Ser Gly
945                 950                 955                 960

Asp Ile Glu Val Leu Pro Val Gly Val Pro Leu Pro Trp Pro Ser Asp
                965                 970                 975

Thr Val Pro Ser Gly Tyr Ala Leu Met Gln Gly Gln Thr Phe Asp Lys
            980                 985                 990

Ser Ala Tyr Pro Lys Leu Ala Ala  Ala Tyr Pro Ser Gly  Val Ile Pro
        995                 1000                1005

Asp Met  Arg Gly Trp Thr Ile  Lys Gly Lys Pro Ala  Ser Gly Arg
    1010                1015                1020

Asp Val  Leu Ser Leu Glu Gln  Asp Gly Ile Lys Ser  His Thr His
    1025                1030                1035
```

Ser Ala Ser Ala Ser Asn Thr Asp Leu Gly Thr Lys Thr Thr Ser
1040 1045 1050

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

Thr His Asn Val Ser Gly Thr Ala Asn Ser Ala Gly Ala His Thr
1070 1075 1080

His Thr Val Pro Leu Arg Arg Pro Asn Ser Gly Gly Met Asn Phe
1085 1090 1095

Asp Trp Leu Asp Gly Ala Ser Ser Gly Thr Val Val Gly Asn Gly
1100 1105 1110

Thr Val Pro Ser Ser Gly Ala His Thr His Ser Val Ser Gly Thr
1115 1120 1125

Ala Thr Ser Ala Gly Ala His Ala His Thr Val Gly Ile Gly Ala
1130 1135 1140

[0133]

His Thr His Ser Val Ala Ile Gly Ser His Gly His Thr Ile Thr
1145 1150 1155

Val Asn Ala Ala Gly Asn Ala Glu Asn Thr Val Lys Asn Ile Ala
1160 1165 1170

Phe Asn Tyr Ile Val Arg Leu Ala
1175 1180

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<223> 丛林尾丝

<400> 49

Met Asn Asp Val Thr Val Val Thr Ser Val Thr Tyr Pro Ser Ser Glu
1 5 10 15

Ser Leu Ala Leu Val Ala Asp Val Gln Tyr His Glu Pro Tyr Leu Ser
20 25 30

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

Ala Gly Phe Leu Pro Lys Pro Gly Gly Gly Met Asn Leu Leu Ile Thr
    50                  55                  60

Ser Val Asp Gly Asp Lys Thr Ala Gly Ala Ala Ser Val Asp Ile Gly
65                  70                  75                  80

Glu Phe Tyr Gln Val Thr Ile Gln Gln Arg Lys Asp Ile Ser Leu Ala
                85                  90                  95

Leu Ser Ala Gly Lys Lys Tyr Ala Ile Val Leu Lys Gly Arg Tyr Leu
            100                 105                 110

Leu Gly Glu Asp Thr Tyr Gln Val Asn Thr Ala Ser His Ile His Ala
        115                 120                 125

Ala Glu Phe Val Ala Arg Thr Tyr Thr Asp Ser Tyr Gln Leu Gly Asp
    130                 135                 140
```

[0134]

```
Gly Glu Leu Leu Val Cys Thr Val Asn Ile Pro Ala Ser Val Ser Ala
145                 150                 155                 160

Ile Thr Gln Glu Met Ile Asp Thr Ser Glu Arg Ile Asn Arg Ser Ile
                165                 170                 175

Gly Ile Asp Ile Ser Asp Ser Val Thr Ser Thr Arg Ser Asp Val Ala
            180                 185                 190

Ala Ser Ser Leu Ala Val Lys Lys Ala Tyr Asp Leu Ala Lys Ser Lys
        195                 200                 205

Tyr Thr Ala Gln Asp Ala Ser Thr Thr Gln Lys Gly Leu Val Gln Leu
    210                 215                 220

Ser Ser Ala Thr Asn Ser Asp Ser Glu Thr Met Ala Ala Thr Pro Lys
225                 230                 235                 240

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

Ser Pro Ser Leu Thr Gly Thr Pro Thr Ala Pro Thr Ala Ala Gln Gly
            260                 265                 270
```

Thr Asn Ser Thr Gln Ile Ala Asn Thr Ala Phe Val Lys Ala Ala Ile
275 280 285

Thr Ala Leu Ile Asn Gly Ala Pro Gly Thr Leu Asp Thr Leu Lys Glu
290 295 300

Ile Ala Ala Ala Ile Asn Asn Asp Pro Asn Tyr Ser Thr Thr Ile Asn
305 310 315 320

Asn Ala Leu Ala Leu Lys Ala Pro Leu Ala Ser Pro Ala Leu Thr Gly
325 330 335

Val Pro Thr Ala Pro Thr Ala Ala Gln Gly Thr Asn Asn Thr Gln Ile
340 345 350

Ala Thr Thr Ala Tyr Val Arg Ala Ala Ile Ser Ala Leu Val Gly Ser
355 360 365

Ser Pro Glu Ala Leu Asp Thr Leu Tyr Glu Leu Ala Ala Ala Leu Gly
370 375 380

[0135]

Asn Asp Pro Asn Phe Ala Thr Thr Met Thr Asn Ala Leu Ala Gly Lys
385 390 395 400

Gln Pro Leu Asp Ala Thr Leu Thr Ala Leu Ala Gly Leu Ala Thr Gly
405 410 415

Ala Asn Lys Leu Pro Tyr Phe Thr Gly Thr Asp Thr Val Ser Gln Thr
420 425 430

Asp Leu Thr Ser Val Gly Arg Asp Ile Leu Ala Lys Thr Ser Ile Leu
435 440 445

Ala Val Ile Gln Tyr Leu Gly Leu Arg Glu Leu Gly Thr Ser Gly Glu
450 455 460

Lys Ile Pro Leu Leu Ser Thr Ala Asn Thr Trp Ser Ala Arg Gln Thr
465 470 475 480

Phe Asn Gly Gly Ile Thr Gly Ala Leu Thr Gly Asn Ala Asp Thr Ala
485 490 495

Thr Lys Leu Lys Thr Ala Arg Asn Ile Asn Gly Val Arg Phe Asp Gly
500 505 510

Ser Gly Asp Ile Asn Ile Asn Thr Leu Val Ser Arg Gly Arg Val Thr
515 520 525

Ala Leu Glu Ala Asn Ala Gln Gly Thr Ser Gly Ile Gln Leu Tyr Glu
530 535 540

Ala Tyr Asn Asn Gly Tyr Pro Ser Pro Tyr Gly Asn Val Leu His Leu
545 550 555 560

Lys Gly Ala Thr Ala Ala Gly Glu Gly Glu Leu Phe Ile Gly Trp Ser
565 570 575

Gly Thr Ser Gly Ala His Ala Pro Val His Ile Arg Ser Arg Arg Asp
580 585 590

Thr Asp Ser Ala Asn Trp Ser Glu Trp Ala Gln Val Tyr Thr Ser Lys
595 600 605

[0136] Asp Ser Ile Pro Gly Val Asn Ala Lys Gly Asp Gln Asp Thr Ser Gly
610 615 620

Asn Ala Ala Thr Ala Thr Lys Leu Gln Thr Ala Cys Thr Ile Asn Gly
625 630 635 640

Val Ser Phe Asp Gly Ser Lys Asn Ile Glu Leu Thr Ala Glu Asn Leu
645 650 655

Asn Leu Glu Arg Thr Val Glu Leu Ala Ala Gly Ser Leu Gln Lys Asn
660 665 670

Gln Asn Gly Ala Asp Ile Pro Gly Lys Asp Thr Phe Thr Lys Asn Ile
675 680 685

Gly Ala Cys Arg Ala Tyr Ser Ala Trp Leu Asn Ile Gly Gly Asp Ser
690 695 700

Gln Val Trp Thr Thr Ala Gln Phe Ile Ser Trp Leu Glu Ser Gln Gly
705 710 715 720

Ala Phe Asn His Pro Tyr Trp Met Cys Lys Gly Ser Trp Ala Tyr Ala
725 730 735

Asn Asn Lys Val Ile Thr Asp Thr Gly Cys Gly Asn Ile Cys Leu Ala
740 745 750

Gly Ala Val Val Glu Val Ile Gly Thr Arg Gly Ala Met Thr Ile Arg
755 760 765

Val Thr Thr Pro Ser Thr Ser Ser Gly Gly Gly Ile Thr Asn Ala Gln
770 775 780

Phe Thr Tyr Ile Asn His Gly Asp Ala Tyr Ala Pro Gly Trp Arg Arg
785 790 795 800

Asp Tyr Asn Thr Lys Asn Gln Gln Pro Ala Phe Ala Leu Gly Gln Thr
805 810 815

Gly Ser Thr Val Gly Asn Asp Lys Ala Val Gly Trp Asn Trp Asn Ser
820 825 830

Gly Val Tyr Asn Ala Asn Ile Gly Gly Ala Ser Thr Leu Ile Leu His
835 840 845

[0137]

Phe Asn Met Asn Thr Gly Ser Cys Pro Ala Val Gln Phe Arg Val Asn
850 855 860

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

Phe Glu Ala Asp Trp Ser Glu Ile Tyr Thr Thr Thr Arg Lys Pro Ser
885 890 895

Ala Gly Asp Val Gly Ala Tyr Thr Gln Ala Glu Cys Asn Ser Arg Phe
900 905 910

Ile Thr Gly Ile Arg Leu Gly Gly Leu Ser Ser Val Gln Thr Trp Asn
915 920 925

Gly Pro Gly Trp Ser Asp Arg Ser Gly Tyr Val Val Thr Gly Ser Val
930 935 940

Asn Gly Asn Arg Asp Glu Leu Ile Asp Thr Thr Gln Ala Arg Pro Ile
945 950 955 960

Gln Tyr Cys Ile Asn Gly Thr Trp Tyr Asn Ala Gly Ser Ile
965 970

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<223> 芒果尾丝

<400> 50

Met Asn Asp Val Thr Val Val Thr Ser Val Thr Tyr Pro Ser Ser Glu
1 5 10 15

Ser Leu Ala Leu Val Ala Asp Val Gln Tyr His Glu Pro Tyr Leu Ser
20 25 30

Ala Ala Leu Asn Arg Lys Phe Arg Gly Ile Val Asp Pro Gly Phe Tyr
35 40 45

Ala Gly Phe Leu Pro Lys Pro Gly Gly Gly Met Asn Leu Leu Ile Thr
50 55 60

[0138]

Ser Val Asp Gly Asp Lys Thr Ala Gly Ala Ala Ser Val Asp Ile Gly
65 70 75 80

Glu Phe Tyr Gln Val Thr Ile Gln Gln Arg Lys Asp Ile Ser Leu Ala
85 90 95

Leu Ser Ala Gly Lys Lys Tyr Ala Ile Val Leu Lys Gly Arg Tyr Leu
100 105 110

Leu Gly Glu Asp Thr Tyr Gln Val Asn Thr Ala Ser His Ile His Ala
115 120 125

Ala Glu Phe Val Ala Arg Thr Tyr Thr Asp Ser Tyr Gln Leu Gly Asp
130 135 140

Gly Glu Leu Leu Val Cys Thr Val Asn Ile Pro Ala Ser Val Ser Ala
145 150 155 160

Ile Thr Gln Glu Met Ile Asp Thr Ser Glu Arg Ile Asn Arg Ser Ile
165 170 175

Gly Ile Asp Ile Ser Asp Ser Val Thr Ser Thr Arg Ser Asp Val Ala
180 185 190

Ala Ser Ser Leu Ala Val Lys Lys Ala Tyr Asp Leu Ala Lys Ser Lys
195 200 205

Tyr Thr Ala Gln Asp Ala Thr Thr Ala Arg Lys Gly Ile Val Gln Leu
210 215 220

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

Ala Val Lys Thr Ala Tyr Asp Leu Ala Asn Ala Lys Tyr Thr Ala Val
245 250 255

Asp Ala Thr Thr Ala Arg Lys Gly Leu Val Gln Leu Ser Ser Ala Ile
260 265 270

Asp Ser Val Ser Glu Met Leu Ala Ala Thr Pro Lys Ala Val Lys Ser
275 280 285

[0139]

Ala Asn Asp Asn Ala Thr Ala Ala Asn Ile Asn Ala Ser Glu Arg Val
290 295 300

Ser Lys Ala Gly Asp Ser Met Thr Gly Thr Leu Asn Gln Asp Ala Val
305 310 315 320

Ala Gln Ala Thr Tyr Asn Leu Thr Ala Leu Ser Asn Ala Thr Thr Gly
325 330 335

Asn Lys Asn Tyr Leu Arg Lys Met Arg Gly Gly Ala Thr Asp Thr Ile
340 345 350

Trp His Glu Thr Val Gln Gly Gly Glu Tyr Arg Leu Ala Thr Gly Ser
355 360 365

Thr Asp Ser Gln Glu Glu Leu Ala Ile Ser Thr Asn Thr Gly Leu Arg
370 375 380

Val Arg Gly Asn Leu Thr Ser Gln Leu Gly Gly Phe Tyr Ser Gly Asn
385 390 395 400

Thr Lys Lys Phe Ser Phe Tyr Ser Ser Asn Thr Ser Asp Lys Asn Ala
405 410 415

```
Ala Leu Arg Leu Trp Gly Asn Val Asp Arg Pro Ser Val Val Glu Leu
            420                 425                 430

Gly Asp Asp Thr Gly Tyr His Phe Tyr Ser Gln Arg Asn Lys Asp Gly
        435                 440                 445

Ser Leu Leu Leu Gln Ala Asn Gly Ala Gly Gln Phe Ser Gly Tyr Leu
    450                 455                 460

Arg Ser Asn Gly Glu Val Gln Ser Ile Ser Ala Asn Ser Tyr Arg Ile
465                 470                 475                 480

Ala Tyr Gly Asn Tyr Gly Cys Phe Trp Arg Asn Asp Gly Asn Asn Leu
                485                 490                 495

Tyr Leu Met Leu Thr Asn Lys Gly Asp Ala Tyr Gly Asn Tyr Asn Ser
            500                 505                 510

Leu Arg Pro Leu Arg Val Ser Leu Glu Thr Gly Ala Leu Gln Ser Glu
        515                 520                 525
```

[0140]

```
Thr Pro Phe Thr Val Gly Asn Thr Ile Phe Ala Thr Lys Glu Ile Thr
    530                 535                 540

Ala Gly Tyr Ala Gly Ala Leu Ala Trp Ala Glu Gln Tyr Lys Thr Lys
545                 550                 555                 560

Ala Ala Phe Phe Asn Ser Tyr Ser Thr Thr Gly Ala Ser Glu Tyr His
                565                 570                 575

Pro Ala Leu Lys Gln Gln Ala Ser Ile Ala Gly Val Asn Ser Trp Ala
            580                 585                 590

Phe Ser Met Gly Ser Leu Val Ala Asp Thr Ala Leu Ser Trp His Leu
        595                 600                 605

His Met Lys Gly Ser Gly Gly Gln Asp Val Asn Tyr Lys Trp Asp Thr
    610                 615                 620

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

```
Asn Phe Asp Ser Arg Tyr Tyr Thr Lys Gly Gln Ser Asp Ala Gly Tyr
                645                 650                 655

Met Ala Lys Thr Gly Ala Tyr Thr Lys Ala Glu Ser Asp Ala Arg Tyr
            660                 665                 670

Asn Leu Lys Asn Thr Ala Ser Arg Ala Ala Ser Gly Trp Glu Lys Asp
        675                 680                 685

Asn Thr Thr Gly Ile Met Lys Gln Trp Gly Ile Ala Thr Arg Thr Ala
    690                 695                 700

Asp Ser Thr Arg Ile Thr Phe Pro Thr Ala Phe Pro Thr Thr Cys Val
705                 710                 715                 720

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

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

[0141]

```
Ser Gly Glu Val Lys Val Tyr Phe Glu Ala Arg Gly Tyr
        755                 760                 765
```

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<220>
<223> 褐红尾丝

<400> 51

```
Met Asn Asp Val Thr Val Val Thr Ser Val Thr Tyr Pro Ser Pro Glu
1               5                   10                  15

Ser Leu Ala Leu Val Ala Asp Val Gln Tyr His Glu Pro Tyr Leu Ser
            20                  25                  30

Ala Ala Leu Asn Arg Lys Phe Arg Gly Ile Val Asp Pro Gly Phe Tyr
        35                  40                  45

Ala Gly Phe Leu Pro Lys Pro Gly Gly Gly Met Asn Leu Leu Ile Thr
    50                  55                  60
```

```
Ser Val Asp Gly Asp Lys Thr Ala Gly Ala Ala Ser Val Asp Ile Gly
65                  70                  75                  80

Glu Phe Tyr Gln Val Thr Ile Gln His Arg Lys Asp Ile Ser Leu Ala
                85                  90                  95

Leu Asn Ala Gly Lys Lys Tyr Ala Ile Val Leu Lys Gly Arg Tyr Leu
            100                 105                 110

Leu Gly Glu Asp Thr Tyr Gln Val Asn Thr Ala Ser His Ile His Ala
        115                 120                 125

Ala Glu Phe Val Ala Arg Thr Tyr Thr Asp Ser Tyr Gln Leu Gly Asp
    130                 135                 140

Gly Glu Leu Leu Val Cys Thr Val Asn Ile Pro Ala Gly Val Ser Thr
145                 150                 155                 160

Ile Thr Gln Glu Met Ile Asp Thr Ser Glu Arg Ile Asn Arg Thr Ile
                165                 170                 175

Gly Ile Asp Ile Ser Asp Ser Val Thr Ser Thr Arg Ser Asp Val Ala
            180                 185                 190

Ala Ser Ser Leu Ala Val Lys Lys Ala Tyr Asp Leu Ala Lys Ser Lys
        195                 200                 205

Tyr Thr Ala Gln Asp Ala Ser Thr Thr Gln Lys Gly Leu Val Gln Leu
    210                 215                 220

Ser Ser Ala Thr Asn Ser Thr Ser Glu Val Leu Ala Ala Thr Pro Lys
225                 230                 235                 240

Ala Val Lys Ala Ala Tyr Asp Leu Ala Asn Gly Lys Tyr Thr Ala Gln
                245                 250                 255

Asp Ala Thr Thr Thr Gln Lys Gly Ile Val Gln Leu Ser Ser Asp Thr
            260                 265                 270

Asn Ser Thr Ser Glu Thr Leu Ala Ala Thr Pro Lys Ala Val Lys Ala
        275                 280                 285

Ala Tyr Asp Leu Ala Ala Gly Lys Ala Pro Ser Ser His Thr His Pro
    290                 295                 300
```

[0142]

```
Trp Asn Gln Ile Thr Gly Val Pro Thr Ala Ser Leu Thr Ala Lys Gly
305                 310                 315                 320

Ile Thr Gln Leu Ser Ser Ala Thr Asn Ser Thr Ser Glu Val Leu Ala
                325                 330                 335

Ala Thr Pro Lys Ala Val Lys Ala Ala Tyr Asp Leu Ala Asn Gly Lys
            340                 345                 350

Tyr Thr Ala Gln Asp Ala Thr Thr Ala Gln Lys Gly Ile Val Gln Leu
        355                 360                 365

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

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

Asp Ala Thr Thr Thr Gln Lys Gly Ile Val Gln Leu Ser Ser Asp Thr
                405                 410                 415
```

[0143]

```
Asn Ser Thr Ser Glu Thr Leu Ala Ala Thr Pro Lys Ala Val Lys Ala
            420                 425                 430

Ala Tyr Asp Leu Ala Ala Gly Lys Ala Pro Ser Ser His Thr His Pro
        435                 440                 445

Trp Asn Gln Ile Thr Val Val Pro Thr Ala Ser Leu Thr Ala Lys Gly
    450                 455                 460

Ile Thr Gln Leu Ser Ser Ala Thr Asn Ser Thr Ser Glu Val Leu Ala
465                 470                 475                 480

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

Tyr Thr Ala Gln Asp Ala Thr Thr Ala Gln Lys Gly Ile Val Gln Leu
            500                 505                 510

Ser Ser Ala Thr Asn Ser Thr Ser Glu Val Leu Ala Ala Thr Pro Lys
        515                 520                 525
```

Ala Val Lys Ala Ala Tyr Asp Leu Ala Asn Gly Lys Gln Ala Ala Asp
530 535 540

Ala Thr Leu Thr Ala Leu Ala Ala Leu Ala Thr Ala Ala Asp Lys Leu
545 550 555 560

Pro Tyr Phe Thr Gly Val Asp Arg Ala Ala Leu Thr Ala Leu Thr Ser
565 570 575

Val Gly Arg Ala Ile Leu Gly Lys Thr Ser Ile Gln Ser Val Leu Asp
580 585 590

Tyr Leu Gly Leu Gly Glu Gly Ser Ala Leu Pro Val Gly Val Pro Val
595 600 605

Pro Trp Pro Ser Ala Thr Pro Pro Thr Gly Trp Leu Lys Cys Asn Gly
610 615 620

Ala Ala Phe Ser Ser Glu Met Tyr Pro Lys Leu Ala Lys Ala Tyr Pro
625 630 635 640

[0144] Thr Asn Lys Leu Pro Asp Leu Arg Gly Glu Phe Ile Arg Gly Trp Asp
645 650 655

Asp Gly Arg Gly Val Asp Ala Gly Arg Ala Leu Leu Ser Ile Gln Thr
660 665 670

Gly Met Leu Glu Lys His Arg His Ile Val Val Ala Asn Asp Gly Tyr
675 680 685

Asp Thr Lys Asp Glu Trp Glu Leu Ala Thr Ile Phe Lys Lys Thr Tyr
690 695 700

Thr Gln Gly Arg Gly Leu Asp Ala Ser Asn Thr Gly Gly Asn Leu Ile
705 710 715 720

Pro Ser Pro Thr Leu His Ser Arg Gly Ser Ile Gly Asn Thr Gly Gly
725 730 735

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

Ala

<210> 52
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<220>
<223> 桑葚尾丝

<400> 52

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

Ser Gln Pro Leu Leu Ala Asp Val Gln Tyr Phe Glu Leu Tyr Ser Ser
20 25 30

Ser Ala Leu Asn Arg Lys Leu Lys Asn Ile Val Leu Pro Gly Phe Tyr
35 40 45

Cys Gly Phe Glu Pro Val Pro Gly Thr Gly Leu Ser Val Arg Ile Thr
50 55 60

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

[0145]

Val Gln Ile Ser Val Gln Gln Ile Glu Asp Val Thr Val Ser Val Lys
85 90 95

Ala Gly Ala Thr Asn Ile Ile Val Leu Glu Ala Asn Phe Glu His Gly
100 105 110

Val Lys Thr Thr Gln Val Asp Ser Ala Ser Ser Val Ser Ala Ala Arg
115 120 125

Ile Tyr Ala Arg Thr Asp Asn Thr Ile Gly Gln Asn Gln Ile Glu Leu
130 135 140

Cys Arg Val Ile Val Pro Asn Gly Ala Thr Ala Val Thr Lys Glu Met
145 150 155 160

Ile Val Leu Lys Tyr Arg Val Asn Arg Ala Val Gly Val Glu Phe Ser
165 170 175

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

```
Val Lys Thr Leu His Asp Leu Val Asp Thr Lys Ala Pro Leu Asp Ser
        195                 200                 205

Pro His Leu Ser Gly Thr Pro Thr Ser Pro Thr Pro Glu Pro Gly Thr
    210                 215                 220

Asn Asn Thr Gln Ile Ala Asn Ala Ala Phe Val Tyr Ala Ala Ile Asn
225                 230                 235                 240

Ala Leu Ile Asn Gly Ala Pro Gly Thr Met Asp Thr Leu Lys Glu Ile
                245                 250                 255

Ala Ala Ala Ile Asn Asn Asp Pro Asn Phe Ser Thr Thr Ile Asn Asn
            260                 265                 270

Ala Leu Ala Leu Lys Ala Pro Leu Ala Ser Pro Ala Leu Thr Gly Ile
        275                 280                 285

Pro Thr Ala Pro Thr Ala Ala Gln Gly Thr Asn Asn Thr Gln Ile Ala
    290                 295                 300
```

[0146]

```
Thr Thr Ala Tyr Val Arg Ala Ala Ile Ser Ala Leu Val Gly Ser Ser
305                 310                 315                 320

Pro Glu Ala Leu Asp Thr Leu Asn Glu Leu Ala Ala Ala Leu Gly Asn
                325                 330                 335

Asp Pro Asn Phe Ala Thr Thr Met Thr Asn Ala Leu Ala Gly Lys Gln
            340                 345                 350

Pro Leu Asp Ala Thr Leu Thr Ala Leu Ala Gly Leu Ala Thr Gly Ala
        355                 360                 365

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

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

Val Ile Gln Tyr Leu Gly Leu Arg Glu Leu Gly Thr Ser Gly Glu Lys
                405                 410                 415
```

Ile Pro Leu Leu Ser Thr Ala Asn Thr Trp Ser Ala Arg Gln Thr Phe
420 425 430

Asn Gly Gly Ile Thr Gly Ala Leu Ile Gly Asn Ala Asp Thr Ala Thr
435 440 445

Lys Leu Lys Thr Ala Ile Asn Ile Asn Gly Val Arg Phe Asp Gly Ser
450 455 460

Ala Asp Ile Asn Ile Asn Thr Leu Val Ser Arg Gly Arg Val Thr Ala
465 470 475 480

Leu Gly Ala Asn Ala Gln Gly Thr Ser Gly Ile Gln Leu Tyr Glu Ala
485 490 495

Tyr Asn Asn Gly Tyr Pro Ser Pro Tyr Gly Asn Val Leu His Leu Lys
500 505 510

Gly Ala Thr Ala Ala Gly Glu Gly Glu Leu Phe Ile Gly Trp Ser Val
515 520 525

[0147] Ser Ser Gly Asp His Ala Pro Val His Ile Arg Ser Arg Arg Asp Ile
530 535 540

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

Ser Val Pro Gly Val Asn Ala Lys Gly Asn Gln Asp Thr Ser Gly Asn
565 570 575

Ala Ala Thr Ala Thr Lys Leu Gln Thr Ala Cys Thr Ile Asn Gly Val
580 585 590

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

Leu Glu Gln Thr Val Glu Leu Ala Ala Gly Ala Leu Gln Lys Asn Gln
610 615 620

Asn Gly Ala Asp Ile Pro Asn Lys Asp Lys Phe Ile Gln Asn Thr Gly
625 630 635 640

Ala Cys Arg Ala Phe Ser Gly Gln Thr Asp Ile Asp Gly Ser Gln Gly
645 650 655

```
Glu Trp Ser Thr Val Ala Phe Ile Ser Trp Leu Glu Asn Asn Gly Ala
            660                 665                 670

Phe Arg His Pro Tyr Trp Met Cys Lys Gly Ser Trp Ser Tyr Ala Arg
        675                 680                 685

Asn Arg Val Ile Thr Asp Thr Gly Cys Gly Asn Ile Cys Leu Ala Gly
    690                 695                 700

Ala Val Ile Glu Val Met Gly Thr Arg Gly Ala Met Thr Ile Arg Val
705                 710                 715                 720

Thr Thr Pro Ser Thr Ser Ser Gly Gly Gly Ile Thr Asn Ala Gln Phe
                725                 730                 735

Thr Tyr Ile Asn His Gly Asp Ala Tyr Ala Pro Gly Trp Arg Arg Asp
            740                 745                 750

Tyr Asn Thr Lys Asn Gln Gln Pro Ala Phe Ala Leu Gly Gln Thr Gly
        755                 760                 765
```

[0148]

```
Arg Arg Val Ala Asn Asp Lys Ala Val Gly Trp Asn Trp Asn Ser Gly
    770                 775                 780

Val Tyr Asp Ala Asp Ile Ser Gly Ala Ser Thr Leu Ile Leu His Phe
785                 790                 795                 800

Asn Met Asn Ala Gly Ser Cys Pro Ala Val Gln Phe Arg Val Asn Tyr
                805                 810                 815

Arg Asn Gly Gly Ile Phe Tyr Arg Ser Ala Arg Asp Gly Tyr Gly Phe
            820                 825                 830

Glu Ala Asn Trp Ser Glu Phe Tyr Thr Thr Thr Arg Lys Pro Ser Ala
        835                 840                 845

Gly Asp Val Gly Ala Tyr Thr Gln Ala Glu Cys Asn Ser Arg Phe Ile
    850                 855                 860

Thr Gly Ile Arg Leu Gly Gly Leu Ser Ser Val Gln Thr Trp Asn Gly
865                 870                 875                 880
```

Pro Gly Trp Ser Asp Arg Ser Gly Tyr Val Val Thr Gly Ser Val Asn
885 890 895

Gly Asn Arg Asp Glu Leu Ile Asp Thr Thr Gln Ala Arg Pro Ile Gln
900 905 910

Tyr Cys Ile Asn Gly Thr Trp Tyr Asn Ala Gly Ser Ile
915 920 925

<210> 53
<211> 972
<212> PRT
<213> 噬菌体 P1

<220>
<221> 未归类特征
<223> P1-S`尾丝蛋白

<400> 53

Met Asn Asp Val Thr Val Val Thr Ser Val Thr Tyr Pro Ser Ser Glu
1 5 10 15

[0149]

Ser Leu Ala Leu Val Ala Asp Val Gln Tyr His Glu Pro Tyr Leu Ser
20 25 30

Ala Ala Leu Asn Arg Lys Phe Arg Gly Ile Val Asp Pro Gly Phe Tyr
35 40 45

Ala Gly Phe Leu Pro Lys Pro Gly Gly Gly Met Asn Leu Leu Ile Thr
50 55 60

Ser Val Asp Gly Asp Lys Thr Ala Gly Ala Ala Ser Val Asp Ile Gly
65 70 75 80

Glu Phe Tyr Gln Val Thr Ile Gln Gln Arg Lys Asp Ile Ser Leu Ala
85 90 95

Leu Ser Ala Gly Lys Lys Tyr Ala Ile Val Leu Lys Gly Arg Tyr Leu
100 105 110

Leu Gly Glu Asp Thr Tyr Gln Val Asn Thr Ala Ser His Ile His Ala
115 120 125

Ala Glu Phe Val Ala Arg Thr Tyr Thr Asp Ser Tyr Gln Leu Gly Asp
130 135 140

```
Gly Glu Leu Leu Val Cys Thr Val Asn Ile Pro Ala Ser Val Ser Ala
145                 150                 155                 160

Ile Thr Gln Glu Met Ile Asp Thr Ser Glu Arg Ile Asn Arg Ser Ile
                165                 170                 175

Gly Ile Asp Ile Ser Asp Ser Val Thr Ser Thr Arg Ser Asp Val Ala
            180                 185                 190

Ala Ser Ser Leu Ala Val Lys Lys Ala Tyr Asp Leu Ala Lys Ser Lys
        195                 200                 205

Tyr Thr Ala Gln Asp Ala Ser Thr Thr Gln Lys Gly Leu Val Gln Leu
    210                 215                 220

Ser Ser Ala Thr Asn Ser Asp Ser Glu Thr Met Ala Ala Thr Pro Lys
225                 230                 235                 240

Ala Val Lys Ser Ile Lys Asp Leu Ala Asp Thr Lys Ala Pro Ile Glu
                245                 250                 255
```

[0150]

```
Ser Pro Ser Leu Thr Gly Thr Pro Thr Ala Pro Thr Ala Ala Gln Gly
            260                 265                 270

Thr Asn Ser Thr Gln Ile Ala Asn Thr Ala Phe Val Lys Ala Ala Ile
        275                 280                 285

Thr Ala Leu Ile Asn Gly Ala Pro Gly Thr Leu Asp Thr Leu Lys Glu
    290                 295                 300

Ile Ala Ala Ala Ile Asn Asn Asp Pro Asn Tyr Ser Thr Thr Ile Asn
305                 310                 315                 320

Asn Ala Leu Ala Leu Lys Ala Pro Leu Ala Ser Pro Ala Leu Thr Gly
                325                 330                 335

Val Pro Thr Ala Pro Thr Ala Ala Gln Gly Thr Asn Asn Thr Gln Ile
            340                 345                 350

Ala Thr Thr Ala Tyr Val Arg Ala Ala Ile Ser Ala Leu Val Gly Ser
        355                 360                 365
```

```
Ser Pro Glu Ala Leu Asp Thr Leu Tyr Glu Leu Ala Ala Ala Leu Gly
    370                 375                 380

Asn Asp Pro Asn Phe Ala Thr Thr Met Thr Asn Ala Leu Ala Gly Lys
385                 390                 395                 400

Gln Pro Leu Asp Ala Thr Leu Thr Ala Leu Ala Gly Leu Ala Thr Gly
                405                 410                 415

Ala Asn Lys Leu Pro Tyr Phe Thr Gly Thr Asp Thr Val Ser Gln Thr
            420                 425                 430

Asp Leu Thr Ser Val Gly Arg Asp Ile Leu Ala Lys Thr Ser Ile Leu
        435                 440                 445

Ala Val Ile Gln Tyr Leu Gly Leu Arg Glu Leu Gly Thr Ser Gly Glu
    450                 455                 460

Lys Ile Pro Leu Leu Ser Thr Ala Asn Thr Trp Ser Ala Arg Gln Thr
465                 470                 475                 480
```

[0151]

```
Phe Asn Gly Gly Ile Thr Gly Ala Leu Thr Gly Asn Ala Asp Thr Ala
                485                 490                 495

Thr Lys Leu Lys Thr Ala Arg Asn Ile Asn Gly Val Arg Phe Asp Gly
            500                 505                 510

Ser Gly Asp Ile Asn Ile Asn Thr Leu Val Ser Arg Gly Arg Val Thr
        515                 520                 525

Ala Leu Glu Ala Asn Ala Gln Gly Thr Ser Gly Ile Gln Leu Tyr Glu
    530                 535                 540

Ala Tyr Asn Asn Gly Tyr Pro Ser Pro Tyr Gly Asn Val Leu His Leu
545                 550                 555                 560

Lys Gly Ala Thr Ala Ala Gly Glu Gly Glu Leu Phe Ile Gly Trp Ser
                565                 570                 575

Gly Thr Ser Gly Ala His Ala Pro Val His Ile Arg Ser Arg Arg Asp
            580                 585                 590

Thr Asp Ser Ala Asn Trp Ser Glu Trp Ala Gln Val Tyr Thr Ser Lys
        595                 600                 605
```

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

Asn Ala Ala Thr Ala Thr Lys Leu Gln Thr Ala Cys Thr Ile Asn Gly
625                 630                 635                 640

Val Ser Phe Asp Gly Ser Lys Asn Ile Glu Leu Thr Ala Glu Asn Leu
                645                 650                 655

Asn Leu Glu Arg Thr Val Glu Leu Ala Ala Gly Ser Leu Gln Lys Asn
            660                 665                 670

Gln Asn Gly Ala Asp Ile Pro Gly Lys Asp Thr Phe Thr Lys Asn Ile
        675                 680                 685

Gly Ala Cys Arg Ala Phe His Ser Ser Ile Ser Thr Gly Ala Gly Asn
    690                 695                 700

Trp Thr Thr Ala Gln Leu Ile Glu Trp Leu Asp Ser Gln Gly Ala Phe
705                 710                 715                 720
```

[0152]

```
Asn His Pro Tyr Trp Met Cys Lys Cys Ser Trp Ser Tyr Gly Asn Asn
                725                 730                 735

Lys Ile Ile Thr Asp Thr Gly Cys Gly Thr Ile His Leu Ala Gly Cys
            740                 745                 750

Val Ile Glu Val Met Gly Asn Lys Gly Ala Met Thr Ile Arg Val Thr
        755                 760                 765

Thr Pro Ser Thr Ser Ser Gly Gly Gly Ile Thr Asn Ala Gln Phe Thr
    770                 775                 780

Tyr Ile Asn His Gly Asp Ala Tyr Ala Pro Gly Trp Arg Arg Asp Tyr
785                 790                 795                 800

Asn Thr Lys Asn Leu Gln Pro Ala Phe Ala Leu Gly Gln Thr Gly Asn
                805                 810                 815

Arg Val Ala Asn Asp Lys Ala Val Gly Trp Asn Trp Asn Ser Gly Val
            820                 825                 830
```

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

Met Asn Ala Gly Ser Cys Pro Ala Val Gln Leu Arg Val Asn Tyr Lys
850 855 860

Asn Gly Gly Ile Tyr Tyr Arg Ser Ala Arg Asp Gly Tyr Gly Phe Glu
865 870 875 880

Ala Asp Trp Ser Glu Phe Tyr Thr Thr Thr Arg Lys Pro Ser Ala Gly
885 890 895

Asp Val Gly Ala Tyr Thr Gln Ala Glu Cys Asn Ser Arg Phe Ile Thr
900 905 910

Gly Ile Arg Leu Gly Gly Leu Ser Ser Val Gln Thr Trp Asn Gly Pro
915 920 925

Gly Trp Ser Asp Arg Ser Gly Tyr Val Val Thr Gly Ser Val Asn Gly
930 935 940

[0153]

Asn Arg Asp Glu Leu Ile Asp Thr Thr Gln Ala Arg Pro Ile Gln Tyr
945 950 955 960

Cys Ile Asn Gly Thr Trp Tyr Asn Ala Gly Ser Ile
965 970

<210> 54
<211> 744
<212> PRT
<213> 人工序列

<220>
<223> 松尾丝

<400> 54

Met Asn Asp Val Thr Val Val Thr Ser Val Thr Tyr Pro Ser Ser Glu
1 5 10 15

Ser Leu Ala Leu Val Ala Asp Val Gln Tyr His Glu Pro Tyr Leu Ser
20 25 30

Ala Ala Leu Asn Arg Lys Phe Arg Gly Ile Val Asp Pro Gly Phe Tyr
35 40 45

```
Ala Gly Phe Leu Pro Lys Pro Gly Gly Gly Met Asn Leu Leu Ile Thr
    50                  55                  60

Ser Val Asp Gly Asp Lys Thr Ala Gly Ala Ala Ser Val Asp Ile Gly
65                  70                  75                  80

Glu Phe Tyr Gln Val Thr Ile Gln Gln Arg Lys Asp Ile Ser Leu Ala
                85                  90                  95

Leu Ser Ala Gly Lys Lys Tyr Ala Ile Val Leu Lys Gly Arg Tyr Leu
            100                 105                 110

Leu Gly Glu Asp Thr Tyr Gln Val Asn Thr Ala Ser His Ile His Ala
        115                 120                 125

Ala Glu Phe Val Ala Arg Thr Tyr Thr Asp Ser Tyr Gln Leu Gly Asp
    130                 135                 140

Gly Glu Leu Leu Val Cys Thr Val Asn Ile Pro Ala Ser Val Ser Ala
145                 150                 155                 160
```

[0154]

```
Ile Thr Gln Glu Met Ile Asp Thr Ser Glu Arg Ile Asn Arg Ser Ile
                165                 170                 175

Gly Ile Asp Ile Ser Asp Ser Val Thr Ser Thr Arg Ser Asp Val Ala
            180                 185                 190

Ala Ser Ser Leu Ala Val Lys Lys Ala Tyr Asp Leu Ala Lys Ser Lys
        195                 200                 205

Tyr Thr Ala Gln Asp Ala Ser Thr Thr Gln Lys Gly Leu Val Gln Leu
    210                 215                 220

Ser Ser Ala Thr Asn Ser Asp Ser Glu Thr Met Ala Ala Thr Pro Lys
225                 230                 235                 240

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

Ser Pro Ser Leu Thr Gly Thr Pro Thr Ala Pro Thr Ala Ala Gln Gly
            260                 265                 270

Thr Asn Ser Thr Gln Ile Ala Asn Thr Ala Phe Val Lys Ala Ala Ile
        275                 280                 285
```

```
Thr Ala Leu Ile Asn Gly Ala Pro Gly Thr Leu Asp Thr Leu Lys Glu
    290                 295                 300

Ile Ala Ala Ala Ile Asn Asn Asp Pro Asn Tyr Ser Thr Thr Ile Asn
305                 310                 315                 320

Asn Ala Leu Ala Leu Lys Ala Pro Leu Asn Ser Pro Ala Leu Thr Gly
                325                 330                 335

Thr Pro Thr Thr Pro Thr Ala Arg Gln Gly Thr Asn Asn Thr Gln Ile
            340                 345                 350

Ala Asn Thr Ala Phe Val Met Ala Ala Ile Ala Ala Leu Val Asp Ser
        355                 360                 365

Ser Pro Asp Ala Leu Asn Thr Leu Asn Glu Leu Ala Ala Ala Leu Gly
    370                 375                 380

Asn Asp Pro Asn Phe Ala Thr Thr Met Thr Asn Ala Leu Ala Gly Lys
385                 390                 395                 400
```

[0155]

```
Gln Pro Lys Asp Ala Thr Leu Thr Ala Leu Ala Gly Leu Ala Thr Ala
                405                 410                 415

Ala Asp Arg Phe Pro Tyr Phe Thr Gly Asn Asp Val Ala Ser Leu Ala
            420                 425                 430

Thr Leu Thr Lys Val Gly Arg Asp Ile Leu Ala Lys Ser Thr Val Ala
        435                 440                 445

Ala Val Ile Glu Tyr Leu Gly Leu Gln Glu Thr Val Asn Arg Ala Gly
    450                 455                 460

Asn Ala Val Gln Lys Asn Gly Asp Thr Leu Ser Gly Gly Leu Thr Phe
465                 470                 475                 480

Glu Asn Asp Ser Ile Leu Ala Trp Ile Arg Asn Thr Asp Trp Ala Lys
                485                 490                 495

Ile Gly Phe Lys Asn Asp Ala Asp Gly Asp Thr Asp Ser Tyr Met Trp
            500                 505                 510
```

Phe Glu Thr Gly Asp Asn Gly Asn Glu Tyr Phe Lys Trp Arg Ser Arg
515 520 525

Gln Ser Thr Thr Thr Lys Asp Leu Met Thr Leu Lys Trp Asp Ala Leu
530 535 540

Asn Ile Leu Val Asn Ala Val Ile Asn Gly Cys Phe Gly Val Gly Thr
545 550 555 560

Thr Asn Ala Leu Gly Gly Ser Ser Ile Val Leu Gly Asp Asn Asp Thr
565 570 575

Gly Phe Lys Gln Asn Gly Asp Gly Ile Leu Asp Val Tyr Ala Asn Ser
580 585 590

Gln Arg Val Phe Arg Phe Gln Asn Gly Val Ala Ile Ala Phe Lys Asn
595 600 605

Ile Gln Ala Gly Asp Ser Lys Lys Phe Ser Leu Ser Ser Ser Asn Thr
610 615 620

[0156]

Ser Thr Lys Asn Ile Thr Phe Asn Leu Trp Gly Ala Ser Thr Arg Pro
625 630 635 640

Val Val Ala Glu Leu Gly Asp Glu Ala Gly Trp His Phe Tyr Ser Gln
645 650 655

Arg Asn Thr Asp Asn Ser Val Ile Phe Ala Val Asn Gly Gln Met Gln
660 665 670

Pro Ser Asn Trp Gly Asn Phe Asp Ser Arg Tyr Val Lys Asp Val Arg
675 680 685

Leu Gly Thr Arg Val Val Gln Leu Met Ala Arg Gly Gly Arg Tyr Glu
690 695 700

Lys Ala Gly His Thr Ile Thr Gly Leu Arg Ile Ile Gly Glu Val Asp
705 710 715 720

Gly Asp Asp Glu Ala Ile Phe Arg Pro Ile Gln Lys Tyr Ile Asn Gly
725 730 735

Thr Trp Tyr Asn Val Ala Gln Val
740

<210> 55
<211> 1181
<212> PRT
<213> 人工序列

<220>
<223> 梅尾丝

<400> 55

Met Asn Asp Val Thr Val Val Thr Ser Val Thr Tyr Pro Ser Pro Glu
1 5 10 15

Ser Leu Ala Leu Val Ala Asp Val Gln Tyr His Glu Pro Tyr Leu Ser
20 25 30

Ala Ala Leu Asn Arg Lys Phe Arg Gly Ile Val Asp Pro Gly Phe Tyr
35 40 45

Ala Gly Phe Leu Pro Lys Pro Gly Gly Gly Met Asn Leu Leu Ile Thr
50 55 60

Ser Val Asp Gly Asp Lys Thr Ala Gly Ala Ala Ser Val Asp Ile Gly
65 70 75 80

[0157]

Glu Phe Tyr Gln Val Thr Ile Gln His Arg Lys Asp Ile Ser Leu Ala
85 90 95

Leu Ser Ala Gly Lys Lys Tyr Ala Ile Val Leu Lys Gly Arg Tyr Leu
100 105 110

Leu Gly Glu Asp Thr Tyr Gln Val Asn Thr Ala Ser His Ile His Ala
115 120 125

Ala Glu Phe Val Ala Arg Thr Tyr Thr Asp Ser Tyr Gln Leu Gly Asp
130 135 140

Gly Glu Leu Leu Val Cys Thr Val Asn Ile Pro Ala Gly Val Ser Ala
145 150 155 160

Ile Thr Gln Glu Met Ile Asp Thr Ser Glu Arg Ile Asn Arg Thr Ile
165 170 175

Gly Ile Asp Ile Ser Asp Ser Val Thr Ser Ser Arg Ser Asp Val Ala
180 185 190

```
Ala Ser Ser Leu Ala Val Lys Lys Ala Tyr Asp Leu Ala Lys Ser Lys
        195                 200                 205

Tyr Thr Ala Gln Asp Ala Ser Thr Thr Gln Lys Gly Leu Val Gln Leu
    210                 215                 220

Ser Ser Glu Thr Asn Ser Asp Ser Glu Thr Met Ala Ala Thr Pro Lys
225                 230                 235                 240

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

Ser Pro Ser Leu Thr Gly Thr Pro Thr Ala Pro Thr Ala Ala Gln Gly
            260                 265                 270

Thr Asn Ser Thr Gln Ile Ala Asn Thr Ala Phe Val Lys Ala Ala Ile
        275                 280                 285

Thr Ala Leu Ile Asn Gly Ala Pro Gly Thr Leu Asp Thr Leu Lys Glu
    290                 295                 300
```

[0158]

```
Ile Ala Ala Ala Ile Asn Asn Asp Pro Asn Phe Ser Thr Thr Ile Asn
305                 310                 315                 320

Asn Ala Leu Ala Leu Lys Ala Pro Leu Ala Ser Pro Ala Leu Thr Gly
                325                 330                 335

Ile Pro Thr Ala Pro Thr Ala Ala Gln Gly Thr Asn Asn Thr Gln Ile
            340                 345                 350

Ala Thr Thr Ala Tyr Val Arg Ala Ala Ile Ser Ala Leu Val Gly Ser
        355                 360                 365

Ser Pro Glu Ala Leu Asp Thr Leu Asn Glu Leu Ala Ala Ala Leu Gly
    370                 375                 380

Asn Asp Pro Asn Phe Ala Thr Thr Met Thr Asn Ala Leu Ala Gly Lys
385                 390                 395                 400

Gln Pro Leu Asp Ala Thr Leu Thr Ala Leu Ala Gly Leu Ala Thr Gly
                405                 410                 415
```

Ala Asn Lys Leu Pro Tyr Phe Thr Gly Thr Asp Thr Val Ser Gln Thr
420 425 430

Asp Leu Thr Ser Val Gly Arg Asp Ile Leu Ala Lys Thr Ser Val Leu
435 440 445

Ala Val Ile Gln Tyr Leu Gly Leu Arg Glu Leu Gly Thr Ser Gly Glu
450 455 460

Lys Ile Pro Leu Leu Ser Thr Ala Asn Thr Trp Ser Ala Arg Gln Thr
465 470 475 480

Phe Asn Gly Gly Ile Thr Gly Ala Leu Thr Gly Asn Ala Asp Thr Ala
485 490 495

Thr Lys Leu Lys Thr Ala Arg Lys Ile Asn Asn Val Ser Phe Asp Gly
500 505 510

Ser Ala Asp Ile Thr Leu Thr Pro Glu Asn Leu Gly Val Thr Ser Leu
515 520 525

[0159]

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

Thr Phe Gly Pro Val Glu Ala Tyr Leu Gly Val Trp Ser Lys Ala Thr
545 550 555 560

Ser Thr Asn Ala Thr Leu Glu Lys Asn Phe Pro Glu Asp Asn Ala Val
565 570 575

Gly Val Leu Glu Val Phe Ala Ala Gly Asn Phe Ala Gly Thr Gln Arg
580 585 590

Phe Thr Thr Arg Asp Gly Asn Val Tyr Ile Arg Arg Leu Ala Asn Lys
595 600 605

Trp Asn Gly Ser Asp Gly Pro Trp Gly Ile Trp Arg His Thr Gln Ser
610 615 620

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

Ala Glu His Leu Gly Leu Trp Arg Asn Ser Ser Ser Ala Ile Ala Ser
645 650 655

Tyr Glu Arg Asn Tyr Pro Glu Glu Gly Gly Phe Ala Gln Gly Val Leu
660 665 670

Glu Ile Leu Glu Gly Gly Asn Tyr Gly Arg Thr Gln Arg Tyr Thr Thr
675 680 685

Arg Arg Gly Asn Met Tyr Val Arg Cys Leu Ala Ala Ser Trp Asp Ala
690 695 700

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

Ser Arg Tyr Tyr Glu Gly Asp Leu Asn Val Leu Thr Asp Pro Gly Ile
725 730 735

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

Gly Ala Thr Leu Leu Gly Ile Leu Glu Val Ile Arg Arg Phe Asp Gly
755 760 765

[0160]

Val Ser Val Trp Gln Arg Tyr Thr Thr Thr Gly Lys Ser Glu Thr Thr
770 775 780

Gln Gly Arg Thr Phe Glu Arg Val Tyr Ala Gly Ser Lys Trp Thr Glu
785 790 795 800

Trp Arg Glu Val Tyr Asn Ser Phe Ser Leu Pro Leu Asn Leu Gly Ile
805 810 815

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

Phe Val Pro Gly Ser Leu Ile Thr Val Arg Leu Asp Asn Met Thr Asn
835 840 845

Ile Pro Asp Gly Met Asp Trp Gly Val Ile Asp Gly Asn Leu Ile Asn
850 855 860

Ile Ala Val Gly Pro Ser Asp Asp Ser Gly Thr Gly Arg Ser Met His
865 870 875 880

```
Val Trp Arg Ser Thr Val Ser Lys Ala Asn Tyr Arg Phe Phe Met Val
                885                 890                 895

Arg Ile Ser Gly Asn Pro Gly Ser Arg Thr Ile Thr Ala Arg Arg Val
            900                 905                 910

Pro Ile Ile Asp Glu Ala Gln Thr Trp Gly Ala Lys Gln Thr Phe Ser
        915                 920                 925

Ala Gly Leu Ser Gly Glu Leu Ser Gly Asn Ala Ala Thr Ala Thr Lys
    930                 935                 940

Leu Lys Thr Ala Arg Lys Ile Asn Asn Val Ser Phe Asp Gly Ser Gly
945                 950                 955                 960

Asp Ile Glu Val Leu Pro Val Gly Val Pro Leu Pro Trp Pro Ser Asp
                965                 970                 975

Thr Val Pro Ser Gly Tyr Ala Leu Met Gln Gly Gln Thr Phe Asp Lys
            980                 985                 990
```

[0161]

```
Ser Ala Tyr Pro Lys Leu Ala Ala  Ala Tyr Pro Ser Gly  Val Ile Pro
        995                 1000                1005

Asp Met  Arg Gly Trp Thr Ile  Lys Gly Lys Pro Ala  Ser Gly Arg
    1010                1015                1020

Asp Val  Leu Ser Leu Glu Gln  Asp Gly Ile Lys Ser  His Thr His
    1025                1030                1035

Ser Ala  Ser Ala Ser Asn Thr  Asp Leu Gly Thr Lys  Thr Thr Ser
    1040                1045                1050

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

Thr His  Asn Val Ser Gly Thr  Ala Asn Ser Ala Gly  Ala His Thr
    1070                1075                1080

His Thr  Val Pro Leu Arg Arg  Pro Asn Ser Gly Gly  Met Asn Phe
    1085                1090                1095

Asp Trp  Leu Asp Gly Ala Ser  Ser Gly Thr Val Val  Gly Asn Gly
    1100                1105                1110
```

Thr Val Pro Ser Ser Gly Ala His Thr His Ser Val Ser Gly Thr
1115 1120 1125

Ala Thr Ser Ala Gly Ala His Ala His Thr Val Gly Ile Gly Ala
1130 1135 1140

His Thr His Ser Val Ala Ile Gly Ser His Gly His Thr Ile Thr
1145 1150 1155

Val Asn Ala Ala Gly Asn Ala Glu Asn Thr Val Lys Asn Ile Ala
1160 1165 1170

Phe Asn Tyr Ile Val Arg Leu Ala
1175 1180

<210> 56
<211> 1250
<212> PRT
<213> 人工序列

<220>
<223> 皇后尾丝

[0162]

<220>
<221> 未归类特征
<222> (642)..(642)
<223> Xaa 可以是任何天然存在的氨基酸

<220>
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<222> (647)..(647)
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<220>
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<222> (662)..(662)
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<223> Xaa 可以是任何天然存在的氨基酸

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<222> (943)..(943)
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<400> 56

```
Met Asn Asp Val Thr Val Val Thr Ser Val Thr Tyr Pro Ser Ser Glu
1               5                  10                  15

Ser Leu Ala Leu Val Ala Asp Val Gln Tyr His Glu Pro Tyr Leu Ser
            20                  25                  30

Ala Ala Leu Asn Arg Lys Phe Arg Gly Ile Val Asp Pro Gly Phe Tyr
        35                  40                  45

Ala Gly Phe Leu Pro Lys Pro Gly Gly Gly Met Asn Leu Leu Ile Thr
    50                  55                  60

Ser Val Asp Gly Asp Lys Thr Ala Gly Ala Ala Ser Val Asp Ile Gly
65                  70                  75                  80

Glu Phe Tyr Gln Val Thr Ile Gln Gln Arg Lys Asp Ile Ser Leu Ala
                85                  90                  95
```

[0163]

```
Leu Ser Ala Gly Lys Lys Tyr Ala Ile Val Leu Lys Gly Arg Tyr Leu
            100                 105                 110

Leu Gly Glu Asp Thr Tyr Gln Val Asn Thr Ala Ser His Ile His Ala
        115                 120                 125

Ala Glu Phe Val Ala Arg Thr Tyr Thr Asp Ser Tyr Gln Leu Gly Asp
    130                 135                 140

Gly Glu Leu Leu Val Cys Thr Val Asn Ile Pro Ala Ser Val Ser Ala
145                 150                 155                 160

Ile Thr Gln Glu Met Ile Asp Thr Ser Glu Arg Ile Asn Arg Ser Ile
                165                 170                 175

Gly Ile Asp Ile Ser Asp Ser Val Thr Ser Thr Arg Ser Asp Val Ala
            180                 185                 190

Ala Ser Ser Leu Ala Val Lys Lys Ala Tyr Asp Leu Ala Lys Ser Lys
        195                 200                 205

Tyr Thr Ala Gln Asp Ala Ser Thr Thr Gln Lys Gly Leu Val Gln Leu
```

210 215 220

Ser Ser Ala Thr Asn Ser Asp Ser Glu Thr Met Ala Ala Thr Pro Lys
225 230 235 240

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

Ser Pro Ser Leu Thr Gly Thr Pro Thr Ala Pro Thr Ala Ala Gln Gly
260 265 270

Thr Asn Ser Thr Gln Ile Ala Asn Thr Ala Phe Val Lys Ala Ala Ile
275 280 285

Thr Ala Leu Ile Asn Gly Ala Pro Gly Thr Leu Asp Thr Leu Lys Glu
290 295 300

Ile Ala Ala Ala Ile Asn Asn Asp Pro Asn Tyr Ser Thr Thr Ile Asn
305 310 315 320

Asn Ala Leu Ala Leu Lys Ala Pro Leu Ala Ser Pro Ala Leu Thr Gly
[0164] 325 330 335

Val Pro Thr Ala Pro Thr Ala Ala Gln Gly Thr Asn Asn Thr Gln Ile
340 345 350

Ala Thr Thr Ala Tyr Val Arg Ala Ala Ile Ser Ala Leu Val Gly Ser
355 360 365

Ser Pro Glu Ala Leu Asp Thr Leu Tyr Glu Leu Ala Ala Ala Leu Gly
370 375 380

Asn Asp Pro Asn Phe Ala Thr Thr Met Thr Asn Ala Leu Ala Gly Lys
385 390 395 400

Gln Pro Leu Asp Ala Thr Leu Thr Ala Leu Ala Gly Leu Ala Thr Gly
405 410 415

Ala Asn Lys Leu Pro Tyr Phe Thr Gly Thr Asp Thr Val Ser Gln Thr
420 425 430

Asp Leu Thr Ser Val Gly Arg Asp Ile Leu Ala Lys Thr Ser Ile Leu
435 440 445

Ala Val Ile Gln Tyr Leu Gly Leu Arg Glu Leu Gly Thr Ser Gly Glu
450 455 460

Lys Ile Pro Leu Leu Ser Thr Ala Asn Thr Trp Ser Ala Arg Gln Thr
465 470 475 480

Phe Asn Gly Gly Ile Thr Gly Ala Leu Thr Gly Asn Ala Asp Thr Ala
485 490 495

Thr Lys Leu Lys Thr Lys Arg Ser Leu Gln Val Asp Leu Gln Ser Asp
500 505 510

Asn Ala Ile Asp Phe Asp Gly Ser Ser Asn Ala Leu Leu Gly Ile Lys
515 520 525

Gly Ile Leu Pro Ile Thr His Gly Gly Leu Gly Ala Ser Ser Val Ser
530 535 540

Gly Gly Arg Thr Asn Leu Gly Leu Gly Val Ala Asp Ile Pro Gln Phe
545 550 555 560

[0165] Lys Gly Ile Asn Leu Val Asn Ser Thr Asp Ser Asp Leu Ala Ala Ser
565 570 575

Gly Ile Val Ser Gly Tyr Leu Asn Asn Ser Ala Gly Val Gln Arg Ser
580 585 590

Arg Phe Arg Ile Tyr Ser Glu Ile Arg Ser Asp Asn Arg Ser Trp Leu
595 600 605

Thr Leu His Leu Gln Ser Asp Thr Asn Thr Asn Lys Tyr Ala Gly Leu
610 615 620

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

Leu Xaa Pro Thr Asp Val Xaa Leu Thr Arg Lys Asn Ile Asp Val Tyr
645 650 655

Ser Lys Ala Glu Val Xaa Leu Lys Lys Gly Met Lys Phe Thr Arg Val
660 665 670

Asn Ala Pro Ser Gly Ala Glu Glu Gly Lys Phe Tyr Pro Val Val Ile

675 680 685

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

Ser Thr Ala Pro Arg Gln Ala Ala His Arg Met Asn Asn Cys Glu Phe
705 710 715 720

Asn Gly Phe Val Met Pro Ala Gly Trp Ser Asp Arg Gly Arg Tyr Ala
725 730 735

Tyr Gly Met Phe Trp Gln Tyr Gln Asp Ala Glu Arg Ala Ile His Ser
740 745 750

Ile Ala Met Ser Asn Lys Asp Asp Glu Val Ser Ser Val Phe Tyr Ile
755 760 765

Glu Gly Gly Ala Phe Pro Val Cys Val Leu Val Glu Glu Gly Leu Ser
770 775 780

[0166] Val Val Val Pro Thr Thr Asp Tyr Xaa Val Gly Gln Thr Thr Tyr Lys
785 790 795 800

Trp Gly Ala Thr Asn Pro Lys Ala Glu Cys Ile Ala Ala Asp Ile Ile
805 810 815

Ile Asp Phe Ser Asn Gly Arg Gly Phe Tyr Ser Ser Gly Asn Leu Asn
820 825 830

Gly Asn Ala Ala Thr Ala Thr Lys Leu Gln Thr Ala Arg Thr Ile Asn
835 840 845

Gly Val Thr Phe Asp Gly Thr Thr Asp Ile Ser Leu Thr Pro Glu Asn
850 855 860

Ile Gly Ala Leu Ser Leu Ser Gly Gly Thr Leu Leu Gly Gly Leu Thr
865 870 875 880

Ala Pro Leu Leu Thr Thr Lys Ser Asp Leu Ile Phe Ser Ser His Thr
885 890 895

Ser Arg His Ile Arg Phe Thr Tyr Thr Lys Asn Asp Gly Thr Thr Leu
900 905 910

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Thr Asp Gly Tyr Ile Phe Lys Asp Gly Val Asp Asn Pro Asn Arg Arg
        915                 920                 925

Pro Gly Ile Arg Ile Asn Cys Ala Ala Pro Asn Xaa Val Leu Xaa Ser
    930                 935                 940

Val Val Asp Asp Ala Lys Met Tyr Leu Arg Arg Phe Arg Ser Ser Thr
945                 950                 955                 960

Gly Ala Ser Ile Trp His Glu Thr Ile Glu Asn Asn Val Tyr Arg Leu
                965                 970                 975

Cys Thr Gly Thr Thr Asp Ala Gln Glu Glu Leu Val Leu Arg Thr Gly
            980                 985                 990

Ser Tyr Ala Lys Phe Ala Gly Glu  Ile Ile Ser Lys Ser  Ala Asn Gly
        995                 1000                1005

Leu Arg  Ile Ala Tyr Gly Asn  Tyr Gly Phe Phe Ile  Arg Asn Asp
    1010                1015                1020
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[0167]

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Gly Ser  Ser Thr Tyr Phe Met  Leu Thr Ala Ser Gly  Asp Asn Leu
    1025                1030                1035

Gly Thr  Trp Asn Ser Leu Arg  Pro Leu Thr Ile Asn  Asn Ala Asn
    1040                1045                1050

Gly Ala  Val Ser Ile Gly Asn  Gly Leu Asn Val Thr  Gly Asp Ile
    1055                1060                1065

Arg Thr  Asn Ala Trp Val Tyr  Ala Asn Arg Phe Ser  Val Asn Ser
    1070                1075                1080

Ser Ser  Gly Ser Trp Ile Ser  Met Arg Asp Gln Asn  Val Ile Phe
    1085                1090                1095

Gly Leu  Asn Lys Val Ser Thr  Ser Ser Ala Gln Ala  Leu Leu Arg
    1100                1105                1110

Gln Asp  His Ala Asp Arg Lys  Phe Phe Ile Gly Gly  Leu Gly Asn
    1115                1120                1125

Ser Gln  Phe Gly Phe Tyr Met  Ile Asn Asn Ser Arg  Thr Ser Asn
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1130 1135 1140

Gly Thr Asp Gly Gln Ala Phe Leu Asp Ser Ser Gly Asn Phe Gln
1145 1150 1155

Cys Gly Gly Gln Ile Leu Pro Thr Asn Tyr Ser Asn Phe Asp Ser
1160 1165 1170

Arg Tyr Thr Leu Lys Thr Ala Cys Val Thr Ser Val Arg Met Gly
1175 1180 1185

Ser Ala Ala Ser Tyr Lys Pro Ser Ser Asn Gly Val Ser Trp Thr
1190 1195 1200

Gln Asn Leu Gly Ser Gly Leu Val Met Thr Gly Ile Ile Val Gln
1205 1210 1215

Glu Thr Gly Gly Asn Ser Ala Asp Asn Ile Gly Gly Ile Tyr Tyr
1220 1225 1230

Arg Pro Val Gln Tyr Cys Ile Asn Gly Thr Trp Tyr Thr Ala Ala
1235 1240 1245

[0168]

Ser Val
1250

<210> 57
<211> 975
<212> PRT
<213> 人工序列

<220>
<223> Razzmatazz 尾丝

<400> 57

Met Asn Asp Val Thr Val Val Thr Ser Val Thr Tyr Pro Ser Pro Glu
1 5 10 15

Ser Leu Ala Leu Val Ala Asp Val Gln Tyr His Glu Pro Tyr Leu Ser
20 25 30

Ala Ala Leu Asn Arg Lys Phe Arg Gly Ile Val Asp Pro Gly Phe Tyr
35 40 45

Ala Gly Phe Leu Pro Lys Pro Gly Gly Gly Met Asn Leu Leu Ile Thr

50 55 60

Ser Val Asp Gly Asp Lys Thr Ala Gly Ala Ala Ser Val Asp Ile Gly
65 70 75 80

Glu Phe Tyr Gln Val Thr Ile Gln Gln Arg Lys Asp Ile Ser Leu Ala
85 90 95

Leu Ser Ala Gly Lys Lys Tyr Ala Ile Val Leu Lys Gly Arg Tyr Leu
100 105 110

Leu Gly Glu Asp Thr Tyr Gln Val Asn Thr Ala Ser His Ile His Ala
115 120 125

Ala Glu Phe Val Ala Arg Thr Tyr Thr Asp Ser Tyr Gln Leu Gly Asp
130 135 140

Gly Glu Leu Leu Val Cys Thr Val Asn Ile Pro Ala Gly Val Ser Ala
145 150 155 160

Ile Thr Gln Glu Met Ile Asp Thr Ser Glu Arg Ile Asn Arg Thr Ile
[0169] 165 170 175

Gly Ile Asp Ile Ser Asp Ser Val Thr Ser Thr Arg Ser Asp Val Ala
180 185 190

Ala Ser Ser Leu Ala Val Lys Lys Ala Tyr Asp Leu Ala Lys Ser Lys
195 200 205

Tyr Thr Ala Gln Asp Ala Ser Ile Thr Gln Lys Gly Leu Val Gln Leu
210 215 220

Ser Ser Ala Thr Asn Ser Asp Ser Glu Thr Met Ala Ala Thr Pro Lys
225 230 235 240

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

Ser Pro Ser Leu Thr Gly Thr Pro Ser Ala Pro Thr Ala Ala Gln Gly
260 265 270

Thr Asn Ser Thr Gln Ile Ala Asn Thr Ala Phe Val Lys Ala Ala Ile
275 280 285

Thr Ala Leu Ile Asn Gly Ala Pro Gly Thr Leu Asp Thr Leu Lys Glu
290 295 300

Ile Ala Ala Ala Ile Asn Asn Asp Pro Asn Phe Ser Thr Thr Val Asn
305 310 315 320

Asn Ala Leu Ala Leu Lys Ala Pro Leu Ala Ser Pro Ala Leu Thr Gly
325 330 335

Ile Pro Thr Ala Pro Thr Ala Ala Gln Gly Thr Asn Asn Thr Gln Ile
340 345 350

Ala Thr Thr Ala Tyr Val Arg Ala Ala Ile Ser Ala Leu Val Gly Ser
355 360 365

Ser Pro Glu Ala Leu Asp Thr Leu Asn Glu Leu Ala Ala Ala Leu Gly
370 375 380

Asn Asp Pro Asn Phe Ala Thr Thr Met Thr Asn Ala Leu Ala Gly Lys
385 390 395 400

[0170] Gln Pro Leu Asp Ala Thr Leu Thr Ala Leu Ala Gly Leu Ala Thr Asp
405 410 415

Ala Asn Lys Leu Pro Tyr Phe Thr Gly Thr Asp Thr Val Ser Gln Thr
420 425 430

Asp Leu Thr Ser Val Gly Arg Asp Ile Leu Ala Lys Thr Ser Val Leu
435 440 445

Ala Val Ile Gln Tyr Leu Gly Leu Arg Glu Leu Gly Thr Ser Gly Glu
450 455 460

Lys Ile Pro Leu Leu Ser Thr Ala Asn Thr Trp Ser Ala Arg Gln Thr
465 470 475 480

Phe Asn Gly Gly Ile Thr Gly Ala Leu Thr Gly Asn Ala Asp Thr Ala
485 490 495

Thr Lys Leu Lys Thr Ala Ile Asn Ile Asn Gly Val Arg Phe Asp Gly
500 505 510

Ser Thr Asn Ile Ser Ile Pro Thr Ile Thr Ser Arg Gly Arg Val Thr

515 520 525

Ala Leu Thr Gly Thr Thr Gln Gly Ala Ala Thr Gly Leu Gln Met Tyr
530 535 540

Glu Ala Tyr Asn Asn Gly Tyr Pro Thr Thr Tyr Gly Asn Val Leu His
545 550 555 560

Leu Lys Gly Ala Ala Ser Thr Gly Glu Gly Glu Leu Leu Ile Gly Trp
565 570 575

Ser Gly Thr Asn Gly Ala His Ala Pro Ala Phe Ile Arg Ser Lys Arg
580 585 590

Asp Ser Thr Ala Ala Ala Trp Ser Glu Trp Ala Gln Ile Tyr Thr Ser
595 600 605

Lys Asp Ser Val Pro Gly Val Asn Thr Lys Gly Asn Gln Asp Thr Ser
610 615 620

[0171] Gly Asn Ala Ala Thr Ala Thr Lys Leu Gln Thr Ala Cys Thr Ile Asn
625 630 635 640

Gly Val Ser Phe Asp Gly Ser Lys Asn Ile Glu Leu Thr Ala Ala Asp
645 650 655

Leu Asn Leu Glu Gln Thr Val Glu Leu Ala Ala Gly Ala Leu Gln Lys
660 665 670

Asn Gln Asn Gly Ala Asp Ile Pro Gly Lys Asp Thr Phe Thr Lys Asn
675 680 685

Ile Gly Ala Cys Arg Ala Tyr Ser Ala Trp Leu Asn Ile Gly Gly Asp
690 695 700

Ser Gln Val Trp Thr Thr Ala Gln Phe Ile Ser Trp Leu Glu Ser Gln
705 710 715 720

Gly Ala Phe Asn His Pro Tyr Trp Met Cys Lys Gly Ser Trp Ala Tyr
725 730 735

Ala Asn Asn Lys Val Ile Thr Asp Thr Gly Cys Gly Asn Ile Cys Leu
740 745 750

Ala Gly Ala Val Val Glu Val Ile Gly Thr Arg Gly Ala Met Thr Ile
755 760 765

Arg Val Thr Thr Pro Ser Thr Ser Ser Gly Gly Gly Ile Thr Asn Ala
770 775 780

Gln Phe Thr Tyr Ile Asn His Gly Asp Ala Tyr Ala Pro Gly Trp Arg
785 790 795 800

Arg Asp Tyr Asn Thr Lys Asn Gln Gln Pro Ala Phe Ala Leu Gly Gln
805 810 815

Thr Gly Ser Arg Val Ala Asn Asp Lys Ala Val Gly Trp Asn Trp Asn
820 825 830

Ser Gly Val Tyr Asp Ala Asp Ile Ser Gly Ala Ser Thr Leu Ile Leu
835 840 845

His Phe Asn Met Asn Ala Gly Ser Cys Pro Ala Val Gln Phe Arg Val
850 855 860

[0172] Asn Tyr Lys Asn Gly Gly Ile Phe Tyr Arg Ser Ala Arg Asp Gly Tyr
865 870 875 880

Gly Phe Glu Ala Asn Trp Ser Glu Phe Tyr Thr Thr Thr Arg Lys Pro
885 890 895

Ser Ala Gly Asp Val Gly Ala Tyr Thr Gln Ala Glu Cys Asn Ser Arg
900 905 910

Phe Ile Thr Gly Ile Arg Leu Gly Gly Leu Ser Ser Val Gln Thr Trp
915 920 925

Asn Gly Pro Gly Trp Ser Asp Arg Ser Gly Tyr Val Val Thr Gly Ser
930 935 940

Val Asn Gly Asn Arg Asp Glu Leu Ile Asp Thr Thr Gln Ala Arg Pro
945 950 955 960

Ile Gln Tyr Cys Ile Asn Gly Thr Trp Tyr Asn Ala Gly Ser Ile
965 970 975

<210> 58

<211> 901
<212> PRT
<213> 人工序列

<220>
<223> 三文鱼尾丝

<400> 58

Met Asn Asp Val Thr Val Val Thr Ser Val Thr Tyr Pro Ser Ser Glu
1 5 10 15

Ser Leu Ala Leu Val Ala Asp Val Gln Tyr His Glu Pro Tyr Leu Ser
20 25 30

Ala Ala Leu Asn Arg Lys Phe Arg Gly Ile Val Asp Pro Gly Phe Tyr
35 40 45

Ala Gly Phe Leu Pro Lys Pro Gly Gly Gly Met Asn Leu Leu Ile Thr
50 55 60

Ser Val Asp Gly Asp Lys Thr Ala Gly Ala Ala Ser Val Asp Ile Gly
65 70 75 80

[0173]

Glu Phe Tyr Gln Val Thr Ile Gln Gln Arg Lys Asp Ile Ser Leu Ala
85 90 95

Leu Ser Ala Gly Lys Lys Tyr Ala Ile Val Leu Lys Gly Arg Tyr Leu
100 105 110

Leu Gly Glu Asp Thr Tyr Gln Val Asn Thr Ala Ser His Ile His Ala
115 120 125

Ala Glu Phe Val Ala Arg Thr Tyr Thr Asp Ser Tyr Gln Leu Gly Asp
130 135 140

Gly Glu Leu Leu Val Cys Thr Val Asn Ile Pro Ala Ser Val Ser Ala
145 150 155 160

Ile Thr Gln Glu Met Ile Asp Thr Ser Glu Arg Ile Asn Arg Ser Ile
165 170 175

Gly Ile Asp Ile Ser Asp Ser Val Thr Ser Thr Arg Ser Asp Val Ala
180 185 190

Ala Ser Ser Leu Ala Val Lys Lys Ala Tyr Asp Leu Ala Lys Ser Lys

195 200 205

Tyr Thr Ala Gln Asp Ala Ser Thr Thr Gln Lys Gly Leu Val Gln Leu
210 215 220

Ser Ser Ala Thr Asn Ser Asp Ser Glu Thr Met Ala Ala Thr Pro Lys
225 230 235 240

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

Ser Pro Ser Leu Thr Gly Thr Pro Thr Ala Pro Thr Ala Ala Gln Gly
260 265 270

Thr Asn Ser Thr Gln Ile Ala Asn Thr Ala Phe Val Lys Ala Ala Ile
275 280 285

Thr Ala Leu Ile Asn Gly Ala Pro Gly Thr Leu Asp Thr Leu Lys Glu
290 295 300

[0174] Ile Ala Ala Ala Ile Asn Asn Asp Pro Asn Tyr Ser Thr Thr Ile Asn
305 310 315 320

Asn Ala Leu Ala Leu Lys Ala Pro Leu Ala Ser Pro Ala Leu Thr Gly
325 330 335

Val Pro Thr Ala Pro Thr Ala Ala Gln Gly Thr Asn Asn Thr Gln Ile
340 345 350

Ala Thr Thr Ala Tyr Val Arg Ala Ala Ile Ser Ala Leu Val Gly Ser
355 360 365

Ser Pro Glu Ala Leu Asp Thr Leu Tyr Glu Leu Ala Ala Ala Leu Gly
370 375 380

Asn Asp Pro Asn Phe Ala Thr Thr Met Thr Asn Ala Leu Ala Gly Lys
385 390 395 400

Gln Pro Leu Asp Ala Thr Leu Thr Ala Leu Ala Gly Leu Ala Thr Gly
405 410 415

Ala Asn Lys Leu Pro Tyr Phe Thr Gly Thr Asp Thr Val Ser Gln Thr
420 425 430

Asp Leu Thr Ser Val Gly Arg Asp Ile Leu Ala Lys Thr Ser Ile Leu
435 440 445

Ala Val Ile Gln Tyr Leu Gly Leu Arg Glu Leu Gly Thr Ser Gly Glu
450 455 460

Lys Ile Pro Leu Leu Ser Thr Ala Asn Thr Trp Ser Ala Arg Gln Thr
465 470 475 480

Phe Asn Gly Gly Ile Thr Gly Ala Leu Thr Gly Asn Ala Asp Thr Ala
485 490 495

Thr Lys Leu Lys Thr Ala Arg Thr Ile Gly Gly Val Ala Phe Asp Gly
500 505 510

Thr Ala Asn Ile Asn Leu Pro Gly Val Asn Val Ala Gly Asn Gln Asn
515 520 525

Thr Ser Gly Asn Ala Ala Thr Ala Thr Lys Leu Gln Thr Ala Cys Thr
530 535 540

[0175] Ile Asn Gly Val Ser Phe Asp Gly Ser Lys Asn Ile Glu Leu Thr Ala
545 550 555 560

Glu Asp Leu Asn Leu Gln Glu Phe Ile Asn Lys Ala Asn Asn Ala Val
565 570 575

Gln Arg Ser Gly Asp Ile Leu Ser Gly Gly Leu Thr Phe Glu Asn Asp
580 585 590

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

Lys Asn Asp Ala Asp Ser Asp Thr Asp Ser Tyr Met Trp Phe Glu Thr
610 615 620

Gly Asp Asn Gly Asn Glu Tyr Phe Lys Trp Arg Ser Lys Gln Ser Thr
625 630 635 640

Thr Thr Lys Asp Leu Met Asn Leu Lys Trp Asp Ala Leu Ser Val Leu
645 650 655

Val Lys Ala Leu Phe Ser Ser Glu Val Lys Ile Ser Thr Val Asn Ala

660 665 670

Leu Arg Ile Phe Asn Ser Ser Phe Gly Ala Ile Phe Arg Arg Ser Glu
675 680 685

Glu Cys Leu His Ile Ile Pro Thr Arg Glu Asn Glu Gly Glu Asn Gly
690 695 700

Asp Ile Gly Pro Leu Arg Pro Phe Thr Leu Asn Leu Arg Thr Gly Arg
705 710 715 720

Ile Thr Met Gly His Gly Leu Asp Val Thr Gly Asp Ile Thr Thr Asn
725 730 735

Ala Trp Val Tyr Ala Asn Arg Phe Ala Ile Asn Ser Gly Ser Thr Ser
740 745 750

Trp Ile Asp Met Arg Asn Gln Asn Val Ile Phe Gly Arg Asn Ala Val
755 760 765

[0176] Ser Thr Ser Ser Ala Gln Ala Leu Leu Arg Gln Asp His Ala Glu Arg
770 775 780

Lys Phe Phe Val Gly Gly Leu Gly Asn Tyr Gln Phe Gly Phe Tyr Met
785 790 795 800

Ile Asn Asn Ser Arg Thr Ala Asn Gly Thr Asp Gly Gln Ala Tyr Met
805 810 815

Asp Asn Asn Gly Asn Trp Leu Cys Gly Ser Gln Val Ile Pro Gly Asn
820 825 830

Tyr Gly Asn Phe Asp Ser Arg Tyr Val Arg Asp Val Arg Leu Gly Thr
835 840 845

Arg Val Val Gln Leu Met Ala Arg Gly Gly Arg Tyr Glu Lys Ala Gly
850 855 860

His Ala Ile Thr Gly Leu Arg Ile Ile Gly Glu Val Asp Gly Asp Asp
865 870 875 880

Glu Ala Ile Phe Arg Pro Ile Gln Lys Tyr Ile Asn Gly Thr Trp Tyr
885 890 895

Asn Val Ala Gln Val
900

<210> 59
<211> 747
<212> PRT
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<220>
<223> 猩红尾丝

<400> 59

Met Asn Asp Val Thr Val Val Thr Ser Val Thr Tyr Pro Ser Pro Glu
1 5 10 15

Ser Leu Ala Leu Val Ala Asp Val Gln Tyr His Glu Pro Tyr Leu Ser
20 25 30

Ala Ala Leu Asn Arg Lys Phe Arg Gly Ile Val Asp Pro Gly Phe Tyr
35 40 45

Ala Gly Phe Leu Pro Lys Pro Gly Gly Gly Met Asn Leu Leu Ile Thr
50 55 60

[0177]

Ser Val Asp Gly Asp Lys Thr Ala Gly Ala Ala Ser Val Asp Ile Gly
65 70 75 80

Glu Phe Tyr Gln Val Thr Ile Gln His Arg Lys Asp Ile Ser Leu Ala
85 90 95

Leu Asn Ala Gly Lys Lys Tyr Ala Ile Val Leu Lys Gly Arg Tyr Leu
100 105 110

Leu Gly Glu Asp Thr Tyr Gln Val Asn Thr Ala Ser His Ile His Ala
115 120 125

Ala Glu Phe Val Ala Arg Thr Tyr Thr Asp Ser Tyr Gln Leu Gly Asp
130 135 140

Gly Glu Leu Leu Val Cys Thr Val Asn Ile Pro Ala Gly Val Ser Thr
145 150 155 160

Ile Thr Gln Glu Met Ile Asp Thr Ser Glu Arg Ile Asn Arg Thr Ile
165 170 175

Gly Ile Asp Ile Ser Asp Ser Val Thr Ser Thr Arg Ser Asp Val Ala
180 185 190

Ala Ser Ser Leu Ala Val Lys Lys Ala Tyr Asp Leu Ala Lys Ser Lys
195 200 205

Tyr Thr Ala Gln Asp Ala Ser Thr Thr Gln Lys Gly Leu Val Gln Leu
210 215 220

Ser Ser Ala Thr Asn Ser Thr Ser Glu Val Leu Ala Ala Thr Pro Lys
225 230 235 240

Ala Val Lys Ala Ala Tyr Asp Leu Ala Asn Gly Lys Tyr Thr Ala Gln
245 250 255

Asp Ala Thr Thr Thr Gln Lys Gly Ile Val Gln Leu Ser Ser Asp Thr
260 265 270

Asn Ser Thr Ser Glu Thr Leu Ala Ala Thr Pro Lys Ala Val Lys Ala
275 280 285

[0178] Ala Tyr Asp Leu Ala Ala Gly Lys Ala Pro Ser Ser His Thr His Pro
290 295 300

Trp Asn Gln Ile Thr Gly Val Pro Thr Ala Ser Leu Thr Ala Lys Gly
305 310 315 320

Ile Thr Gln Leu Ser Ser Ala Thr Asn Ser Thr Ser Glu Val Leu Ala
325 330 335

Ala Thr Pro Lys Ala Val Lys Ala Ala Tyr Asp Leu Ala Asn Gly Lys
340 345 350

Tyr Thr Ala Gln Asp Ala Thr Thr Ala Gln Lys Gly Ile Val Gln Leu
355 360 365

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

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

Asp Ala Thr Thr Thr Gln Lys Gly Ile Val Gln Leu Ser Ser Asp Thr

405 410 415

Asn Ser Thr Ser Glu Thr Leu Ala Ala Thr Pro Lys Ala Val Lys Ala
420 425 430

Ala Tyr Asp Leu Ala Ala Gly Lys Ala Pro Ser Ser His Thr His Pro
435 440 445

Trp Asn Gln Ile Thr Val Val Pro Thr Ala Ser Leu Thr Ala Lys Gly
450 455 460

Ile Thr Gln Leu Ser Ser Ala Thr Asn Ser Thr Ser Glu Val Leu Ala
465 470 475 480

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

Tyr Thr Ala Gln Asp Ala Thr Thr Ala Gln Lys Gly Ile Val Gln Leu
500 505 510

Ser Ser Ala Thr Asn Ser Thr Ser Glu Val Leu Ala Ala Thr Pro Lys
[0179] 515 520 525

Ala Val Lys Ala Ala Tyr Asp Leu Ala Asn Gly Lys Gln Ala Ala Asp
530 535 540

Ala Thr Leu Thr Ala Leu Ala Ala Leu Ala Thr Ala Ala Asp Lys Leu
545 550 555 560

Pro Tyr Phe Thr Gly Val Asp Arg Ala Ala Leu Thr Ala Leu Thr Ser
565 570 575

Val Gly Arg Ala Ile Leu Gly Lys Thr Ser Ile Gln Ser Val Leu Asp
580 585 590

Tyr Leu Gly Leu Gly Glu Gly Ser Ala Leu Pro Val Gly Val Pro Val
595 600 605

Pro Trp Pro Leu Glu Thr Pro Pro Thr Gly Trp Leu Lys Cys Asn Gly
610 615 620

Ala Ala Phe Ser Ser Glu Met Tyr Pro Lys Leu Ala Lys Ala Tyr Pro
625 630 635 640

Thr Asn Lys Leu Pro Asp Leu Arg Gly Glu Phe Ile Arg Gly Trp Asp
645 650 655

Asp Gly Arg Gly Val Asp Ala Gly Arg Val Ile Leu Ser Ile Gln Gly
660 665 670

Trp Leu Thr Gly Ser His Tyr His Asn Ile Arg Ser Trp Asp Ala Trp
675 680 685

Asp Asn Thr Val Leu Val Pro Asn Asp Arg Gly Gly Asp Ser Leu Leu
690 695 700

Ser Thr Asp Asn Ala Val Arg Gln Gly Ala Ile Asn Gly Lys Phe Thr
705 710 715 720

Ser Gln Tyr Arg Thr Glu Leu Ser Gly Gly Asn Glu Thr Arg Pro Arg
725 730 735

Asn Ile Ala Phe Asn Tyr Ile Val Arg Ala Ala
740 745

[0180]

<210> 60
<211> 996
<212> PRT
<213> 人工序列

<220>
<223> 三叶草尾丝

<400> 60

Met Asn Asp Val Thr Val Val Thr Ser Val Thr Tyr Pro Ser Ser Glu
1 5 10 15

Ser Leu Ala Leu Val Ala Asp Val Gln Tyr His Glu Pro Tyr Leu Ser
20 25 30

Ala Ala Leu Asn Arg Lys Phe Arg Gly Ile Val Asp Pro Gly Phe Tyr
35 40 45

Ala Gly Phe Leu Pro Lys Pro Gly Gly Gly Met Asn Leu Leu Ile Thr
50 55 60

Ser Val Asp Gly Asp Lys Thr Ala Gly Ala Ala Ser Val Asp Ile Gly
65 70 75 80

Glu Phe Tyr Gln Val Thr Ile Gln Gln Arg Lys Asp Ile Ser Leu Ala
85 90 95

Leu Ser Ala Gly Lys Lys Tyr Ala Ile Val Leu Lys Gly Arg Tyr Leu
100 105 110

Leu Gly Glu Asp Thr Tyr Gln Val Asn Thr Ala Ser His Ile His Ala
115 120 125

Ala Glu Phe Val Ala Arg Thr Tyr Thr Asp Ser Tyr Gln Leu Gly Asp
130 135 140

Gly Glu Leu Leu Val Cys Thr Val Asn Ile Pro Ala Ser Val Ser Ala
145 150 155 160

Ile Thr Gln Glu Met Ile Asp Thr Ser Glu Arg Ile Asn Arg Ser Ile
165 170 175

Gly Ile Asp Ile Ser Asp Ser Val Thr Ser Thr Arg Ser Asp Val Ala
180 185 190

[0181] Ala Ser Ser Leu Ala Val Lys Lys Ala Tyr Asp Leu Ala Lys Ser Lys
195 200 205

Tyr Thr Ala Gln Asp Ala Ser Thr Thr Gln Lys Gly Leu Val Gln Leu
210 215 220

Ser Ser Ala Thr Asn Ser Asp Ser Glu Thr Met Ala Ala Thr Pro Lys
225 230 235 240

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

Ser Pro Ser Leu Thr Gly Thr Pro Thr Ala Pro Thr Ala Ala Gln Gly
260 265 270

Thr Asn Ser Thr Gln Ile Ala Asn Thr Ala Phe Val Lys Ala Ala Ile
275 280 285

Thr Ala Leu Ile Asn Gly Ala Pro Gly Thr Leu Asp Thr Leu Lys Glu
290 295 300

Ile Ala Ala Ala Ile Asn Asn Asp Pro Asn Tyr Ser Thr Thr Ile Asn

305 310 315 320

Asn Ala Leu Ala Leu Lys Ala Pro Leu Ala Ser Pro Ala Leu Thr Gly
325 330 335

Val Pro Thr Ala Pro Thr Ala Ala Gln Gly Thr Asn Asn Thr Gln Ile
340 345 350

Ala Thr Thr Ala Tyr Val Arg Ala Ala Ile Ser Ala Leu Val Gly Ser
355 360 365

Ser Pro Glu Ala Leu Asp Thr Leu Tyr Glu Leu Ala Ala Ala Leu Gly
370 375 380

Asn Asp Pro Asn Phe Ala Thr Thr Met Thr Asn Ala Leu Ala Gly Lys
385 390 395 400

Gln Pro Leu Asp Ala Thr Leu Thr Ala Leu Ala Gly Leu Ala Thr Gly
405 410 415

[0182] Ala Asn Lys Leu Pro Tyr Phe Thr Gly Thr Asp Thr Val Ser Gln Thr
420 425 430

Asp Leu Thr Ser Val Gly Arg Asp Ile Leu Ala Lys Thr Ser Ile Leu
435 440 445

Ala Val Ile Gln Tyr Leu Gly Leu Arg Glu Leu Gly Thr Ser Gly Glu
450 455 460

Lys Ile Pro Leu Leu Ser Thr Ala Asn Thr Trp Ser Ala Arg Gln Thr
465 470 475 480

Phe Asn Gly Gly Ile Thr Gly Ala Leu Thr Gly Asn Ala Asp Thr Ala
485 490 495

Thr Lys Leu Lys Thr Ala Arg Asn Ile Asn Gly Val Arg Phe Asp Gly
500 505 510

Ser Gly Asp Ile Asn Ile Asn Thr Leu Val Ser Arg Gly Arg Val Thr
515 520 525

Ala Leu Glu Ala Asn Ala Gln Gly Thr Ser Gly Ile Gln Leu Tyr Glu
530 535 540

Ala Tyr Asn Asn Gly Tyr Pro Ser Pro Tyr Gly Asn Val Leu His Leu
545 550 555 560

Lys Gly Ala Thr Ala Ala Gly Glu Gly Glu Leu Phe Ile Gly Trp Ser
565 570 575

Gly Thr Ser Gly Ala His Ala Pro Val His Ile Arg Ser Arg Arg Asp
580 585 590

Thr Asp Ser Ala Asn Trp Ser Glu Trp Ala Gln Val Tyr Thr Ser Lys
595 600 605

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

Asn Ala Ala Thr Ala Thr Lys Leu Gln Thr Ala Cys Thr Ile Asn Gly
625 630 635 640

Val Ser Phe Asp Gly Ser Lys Asn Ile Glu Leu Thr Ala Glu Asp Leu
645 650 655

[0183] Asn Leu Gln Glu Thr Val Asn Lys Ala Asp Asn Ala Val Gln Lys Thr
660 665 670

Gly Asp Thr Leu Ser Gly Gly Leu Thr Phe Glu Asn Asp Ser Ile Leu
675 680 685

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

Ser Asp Ala Asp Thr Asp Ser Tyr Met Trp Phe Glu Thr Gly Asn Asn
705 710 715 720

Gly Asn Glu Tyr Phe Lys Trp Arg His Arg Ile Ile Gly Thr Arg Pro
725 730 735

Lys Asp Leu Met Asn Leu Lys Trp Asn Ala Leu Ser Val Leu Val Glu
740 745 750

Ala Leu Phe Ser Ser Glu Val Lys Ile Ser Thr Val Asn Ala Leu Arg
755 760 765

Ile Phe Asn Ser Ser Phe Gly Ala Ile Phe Arg Arg Ser Glu Glu Cys

770 775 780

Leu His Ile Ile Pro Thr Arg Glu Asn Glu Gly Glu Asn Gly Asn Ile
785 790 795 800

Gly Pro Leu Arg Pro Phe Thr Leu Asn Leu Arg Thr Gly Arg Ile Ser
805 810 815

Met Gly His Gly Leu Asp Val Thr Gly Asp Ile Phe Ala Asn Arg Phe
820 825 830

Ala Ile Asn Ser Ser Thr Gly Met Trp Ile His Met Arg Asp Gln Asn
835 840 845

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

Leu Arg Gln Asp His Ala Asp Arg Lys Phe Met Ile Gly Gly Leu Gly
865 870 875 880

[0184] Asn Lys Gln Phe Gly Ile Tyr Met Ile Asn Asn Ser Arg Thr Ala Asn
885 890 895

Gly Thr Asp Gly Gln Ala Tyr Met Asp Asn Asn Gly Asn Trp Leu Cys
900 905 910

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

Val Lys Asp Val Arg Leu Gly Ser Gln Gln Tyr Tyr Gly Val Asn Asn
930 935 940

Trp Gln Thr Trp Asn Phe Gln Cys Pro Ser Gly His Val Leu Ser Gly
945 950 955 960

Ile Asn Val Gln Asp Thr Gly Lys Asn Ser Ala Asp Asn Ile Ala Gly
965 970 975

Val Tyr Tyr Arg Pro Val Gln Lys Tyr Ile Asn Gly Thr Trp Tyr Asn
980 985 990

Val Ala Ser Val
995

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<400> 61

Met Asn Asp Val Thr Val Val Thr Ser Val Thr Tyr Pro Ser Pro Glu
1 5 10 15

Ser Leu Ala Leu Val Ala Asp Val Gln Tyr His Glu Pro Tyr Leu Ser
20 25 30

Ala Ala Leu Asn Arg Lys Phe Arg Gly Ile Val Asp Pro Gly Phe Tyr
35 40 45

Ala Gly Phe Leu Pro Lys Pro Gly Gly Gly Met Asn Leu Leu Ile Thr
50 55 60

Ser Val Asp Gly Asp Lys Thr Ala Gly Ala Ala Ser Val Asp Ile Gly
65 70 75 80

[0185]

Glu Phe Tyr Gln Val Thr Ile Gln His Arg Lys Asp Ile Ser Leu Ala
85 90 95

Leu Asn Ala Gly Lys Lys Tyr Ala Ile Val Leu Lys Gly Arg Tyr Leu
100 105 110

Leu Gly Glu Asp Thr Tyr Gln Val Asn Thr Ala Ser His Ile His Ala
115 120 125

Ala Glu Phe Val Ala Arg Thr Tyr Thr Asp Ser Tyr Gln Leu Gly Asp
130 135 140

Gly Glu Leu Leu Val Cys Thr Val Asn Ile Pro Ala Gly Val Ser Thr
145 150 155 160

Ile Thr Gln Glu Met Ile Asp Thr Ser Glu Arg Ile Asn Arg Thr Ile
165 170 175

Gly Ile Asp Ile Ser Asp Ser Val Thr Ser Thr Arg Ser Asp Val Ala
180 185 190

Ala Ser Ser Leu Ala Val Lys Lys Ala Tyr Asp Leu Ala Lys Ser Lys
195 200 205

Tyr Thr Ala Gln Asp Ala Ser Thr Thr Gln Lys Gly Leu Val Gln Leu
210 215 220

Ser Ser Ala Thr Asn Ser Thr Ser Glu Val Leu Ala Ala Thr Pro Lys
225 230 235 240

Ala Val Lys Ala Ala Tyr Asp Leu Ala Asn Gly Lys Tyr Thr Ala Gln
245 250 255

Asp Ala Thr Thr Thr Gln Lys Gly Ile Val Gln Leu Ser Ser Asp Thr
260 265 270

Asn Ser Thr Ser Glu Thr Leu Ala Ala Thr Pro Lys Ala Val Lys Ala
275 280 285

Ala Tyr Asp Leu Ala Ala Gly Lys Ala Pro Ser Ser His Thr His Pro
290 295 300

[0186] Trp Asn Gln Ile Thr Gly Val Pro Thr Ala Ser Leu Thr Ala Lys Gly
305 310 315 320

Ile Thr Gln Leu Ser Ser Ala Thr Asn Ser Thr Ser Glu Val Leu Ala
325 330 335

Ala Thr Pro Lys Ala Val Lys Ala Ala Tyr Asp Leu Ala Asn Gly Lys
340 345 350

Tyr Thr Ala Gln Asp Ala Thr Thr Ala Gln Lys Gly Ile Val Gln Leu
355 360 365

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

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

Asp Ala Thr Thr Thr Gln Lys Gly Ile Val Gln Leu Ser Ser Asp Thr
405 410 415

Asn Ser Thr Ser Glu Thr Leu Ala Ala Thr Pro Lys Ala Val Lys Ala

420 425 430

Ala Tyr Asp Leu Ala Ala Gly Lys Ala Pro Ser Ser His Thr His Pro
435 440 445

Trp Asn Gln Ile Thr Val Val Pro Thr Ala Ser Leu Thr Ala Lys Gly
450 455 460

Ile Thr Gln Leu Ser Ser Ala Thr Asn Ser Thr Ser Glu Val Leu Ala
465 470 475 480

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

Tyr Thr Ala Gln Asp Ala Thr Thr Ala Gln Lys Gly Ile Val Gln Leu
500 505 510

Ser Ser Ala Thr Asn Ser Thr Ser Glu Val Leu Ala Ala Thr Pro Lys
515 520 525

[0187] Ala Val Lys Ala Ala Tyr Asp Leu Ala Asn Gly Lys Gln Ala Ala Asp
530 535 540

Ala Thr Leu Thr Ala Leu Ala Ala Leu Ala Thr Ala Ala Asp Lys Leu
545 550 555 560

Pro Tyr Phe Thr Gly Val Asp Arg Ala Ala Leu Thr Ala Leu Thr Ser
565 570 575

Val Gly Arg Ala Ile Leu Gly Lys Thr Ser Ile Gln Ser Val Leu Asp
580 585 590

Tyr Leu Gly Leu Gly Glu Gly Ser Ala Leu Pro Val Gly Val Pro Val
595 600 605

Pro Trp Pro Ser Ala Thr Pro Pro Thr Gly Trp Leu Lys Cys Asn Gly
610 615 620

Ala Ala Phe Ser Ser Glu Lys Tyr Pro Asn Leu Ala Lys Val Tyr Pro
625 630 635 640

Thr Leu Lys Leu Pro Asp Leu Arg Gly Glu Phe Ile Arg Gly Trp Asp
645 650 655

Asp Gly Arg Gly Ile Asp Ser Gly Arg Ser Ile Leu Ser Glu Gln Gly
660 665 670

Tyr Ala Thr Glu Asp His Ala His Gly Leu Pro Ser Lys Ser Thr Val
675 680 685

Ala Thr Asp Arg Ser Ile Asn Phe Tyr Phe Asp Glu Ala Trp Ala Thr
690 695 700

Ser Gly Asn Thr Gly Val Ile Arg Trp Gly Asn Thr Ser Asp Ala Gly
705 710 715 720

Leu Pro Ala Pro Asn Tyr Gly Thr Phe Lys Thr Tyr Lys Gln Ser Val
725 730 735

Ala Asn Leu Gly Thr Ala Gly Leu Glu Thr Arg Pro Arg Asn Ile Ala
740 745 750

Phe Asn Tyr Ile Val Arg Ala Asp
755 760

[0188]

<210> 62
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<400> 62

Met Asn Asp Val Thr Val Val Thr Ser Val Thr Tyr Pro Ser Pro Glu
1 5 10 15

Ser Leu Ala Leu Val Ala Asp Val Gln Tyr His Glu Pro Tyr Leu Ser
20 25 30

Ala Ala Leu Asn Arg Lys Phe Arg Gly Ile Val Asp Pro Gly Phe Tyr
35 40 45

Ala Gly Phe Leu Pro Lys Pro Gly Gly Gly Met Asn Leu Leu Ile Thr
50 55 60

Ser Val Asp Gly Asp Lys Thr Ala Gly Ala Ala Ser Val Asp Ile Gly
65 70 75 80

Glu Phe Tyr Gln Val Thr Ile Gln His Arg Lys Asp Ile Ser Leu Ala
85 90 95

Leu Asn Ala Gly Lys Lys Tyr Ala Ile Val Leu Lys Gly Arg Tyr Leu
100 105 110

Leu Gly Glu Asp Thr Tyr Gln Val Asn Thr Ala Ser His Ile His Ala
115 120 125

Ala Glu Phe Val Ala Arg Thr Tyr Thr Asp Ser Tyr Gln Leu Gly Asp
130 135 140

Gly Glu Leu Leu Val Cys Thr Val Asn Ile Pro Ala Gly Val Ser Thr
145 150 155 160

Ile Thr Gln Glu Met Ile Asp Thr Ser Glu Arg Ile Asn Arg Thr Ile
165 170 175

Gly Ile Asp Ile Ser Asp Ser Val Thr Ser Thr Arg Ser Asp Val Ala
180 185 190

[0189] Ala Ser Ser Leu Ala Val Lys Lys Ala Tyr Asp Leu Ala Lys Ser Lys
195 200 205

Tyr Thr Ala Gln Asp Ala Ser Thr Thr Gln Lys Gly Leu Val Gln Leu
210 215 220

Ser Ser Ala Thr Asn Ser Thr Ser Glu Val Leu Ala Ala Thr Pro Lys
225 230 235 240

Ala Val Lys Ala Ala Tyr Asp Leu Ala Asn Gly Lys Tyr Thr Ala Gln
245 250 255

Asp Ala Thr Thr Thr Gln Lys Gly Ile Val Gln Leu Ser Ser Asp Thr
260 265 270

Asn Ser Thr Ser Glu Thr Leu Ala Ala Thr Pro Lys Ala Val Lys Ala
275 280 285

Ala Tyr Asp Leu Ala Ala Gly Lys Ala Pro Ser Ser His Thr His Pro
290 295 300

Trp Asn Gln Ile Thr Gly Val Pro Thr Ala Ser Leu Thr Ala Lys Gly

305 310 315 320

Ile Thr Gln Leu Ser Ser Ala Thr Asn Ser Thr Ser Glu Val Leu Ala
325 330 335

Ala Thr Pro Lys Ala Val Lys Ala Ala Tyr Asp Leu Ala Asn Gly Lys
340 345 350

Tyr Thr Ala Gln Asp Ala Thr Thr Ala Gln Lys Gly Ile Val Gln Leu
355 360 365

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

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

Asp Ala Thr Thr Thr Gln Lys Gly Ile Val Gln Leu Ser Ser Asp Thr
405 410 415

Asn Ser Thr Ser Glu Thr Leu Ala Ala Thr Pro Lys Ala Val Lys Ala
[0190] 420 425 430

Ala Tyr Asp Leu Ala Ala Gly Lys Ala Pro Ser Ser His Thr His Pro
435 440 445

Trp Asn Gln Ile Thr Val Val Pro Thr Ala Ser Leu Thr Ala Lys Gly
450 455 460

Ile Thr Gln Leu Ser Ser Ala Thr Asn Ser Thr Ser Glu Val Leu Ala
465 470 475 480

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

Tyr Thr Ala Gln Asp Ala Thr Thr Ala Gln Lys Gly Ile Val Gln Leu
500 505 510

Ser Ser Ala Thr Asn Ser Thr Ser Glu Val Leu Ala Ala Thr Pro Lys
515 520 525

Ala Val Lys Ala Ala Tyr Asp Leu Ala Asn Gly Lys Gln Ala Ala Asp
530 535 540

Ala Thr Leu Thr Ala Leu Ala Ala Leu Ala Thr Ala Ala Asp Lys Leu
545 550 555 560

Pro Tyr Phe Thr Gly Val Asp Arg Ala Ala Leu Thr Ala Leu Thr Ser
565 570 575

Val Gly Arg Ala Ile Leu Gly Lys Thr Ser Ile Gln Ser Val Leu Asp
580 585 590

Tyr Leu Gly Leu Gly Glu Gly Ser Ala Leu Pro Val Gly Val Pro Val
595 600 605

Pro Trp Pro Ser Ala Thr Pro Pro Thr Gly Trp Leu Lys Cys Asn Gly
610 615 620

Ala Ala Phe Ser Ser Glu Lys Tyr Pro Asn Leu Ala Lys Val Tyr Pro
625 630 635 640

Thr Leu Lys Leu Pro Asp Leu Arg Gly Glu Phe Ile Arg Gly Trp Asp
645 650 655

[0191] Asp Ser Arg Gly Ile Asp Thr Gly Arg Ser Leu Leu Ser Gly Gln Thr
660 665 670

Ala Thr Phe Ile Arg Thr Ala Leu Gln Asp Tyr Tyr Gly Val Asp Leu
675 680 685

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

Ile Thr Val Gly Asn Pro Ala Asn Pro Lys Ala Gly Asp Asn Ser Asp
705 710 715 720

Tyr Val Pro Ala Ser Ser Asp Asn Ser Ile Thr Gly Thr Gln Arg Thr
725 730 735

Ala Glu Asp Asn Phe Thr Gly Ala Trp Ile Ser Met Arg Pro Arg Asn
740 745 750

Val Ala Phe Asn Tyr Ile Val Arg Ala Thr
755 760

<210> 63

<211> 1181
<212> PRT
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<220>
<223> 蓟尾丝

<400> 63

Met Asn Asp Val Thr Val Val Thr Ser Val Thr Tyr Pro Ser Ser Glu
1 5 10 15

Ser Leu Ala Leu Val Ala Asp Val Gln Tyr His Glu Pro Tyr Leu Ser
20 25 30

Ala Ala Leu Asn Arg Lys Phe Arg Gly Ile Val Asp Pro Gly Phe Tyr
35 40 45

Ala Gly Phe Leu Pro Lys Pro Gly Gly Gly Met Asn Leu Leu Ile Thr
50 55 60

Ser Val Asp Gly Asp Lys Thr Ala Gly Ala Ala Ser Val Asp Ile Gly
65 70 75 80

[0192]

Glu Phe Tyr Gln Val Thr Ile Gln Gln Arg Lys Asp Ile Ser Leu Ala
85 90 95

Leu Ser Ala Gly Lys Lys Tyr Ala Ile Val Leu Lys Gly Arg Tyr Leu
100 105 110

Leu Gly Glu Asp Thr Tyr Gln Val Asn Thr Ala Ser His Ile His Ala
115 120 125

Ala Glu Phe Val Ala Arg Thr Tyr Thr Asp Ser Tyr Gln Leu Gly Asp
130 135 140

Gly Glu Leu Leu Val Cys Thr Val Asn Ile Pro Ala Ser Val Ser Ala
145 150 155 160

Ile Thr Gln Glu Met Ile Asp Thr Ser Glu Arg Ile Asn Arg Ser Ile
165 170 175

Gly Ile Asp Ile Ser Asp Ser Val Thr Ser Thr Arg Ser Asp Val Ala
180 185 190

Ala Ser Ser Leu Ala Val Lys Lys Ala Tyr Asp Leu Ala Lys Ser Lys

195 200 205

Tyr Thr Ala Gln Asp Ala Ser Thr Thr Gln Lys Gly Leu Val Gln Leu
210 215 220

Ser Ser Ala Thr Asn Ser Asp Ser Glu Thr Met Ala Ala Thr Pro Lys
225 230 235 240

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

Ser Pro Ser Leu Thr Gly Thr Pro Thr Ala Pro Thr Ala Ala Gln Gly
260 265 270

Thr Asn Ser Thr Gln Ile Ala Asn Thr Ala Phe Val Lys Ala Ala Ile
275 280 285

Thr Ala Leu Ile Asn Gly Ala Pro Gly Thr Leu Asp Thr Leu Lys Glu
290 295 300

[0193] Ile Ala Ala Ala Ile Asn Asn Asp Pro Asn Tyr Ser Thr Thr Ile Asn
305 310 315 320

Asn Ala Leu Ala Leu Lys Ala Pro Leu Ala Ser Pro Ala Leu Thr Gly
325 330 335

Val Pro Thr Ala Pro Thr Ala Ala Gln Gly Thr Asn Asn Thr Gln Ile
340 345 350

Ala Thr Thr Ala Tyr Val Arg Ala Ala Ile Ser Ala Leu Val Gly Ser
355 360 365

Ser Pro Glu Ala Leu Asp Thr Leu Tyr Glu Leu Ala Ala Ala Leu Gly
370 375 380

Asn Asp Pro Asn Phe Ala Thr Thr Met Thr Asn Ala Leu Ala Gly Lys
385 390 395 400

Gln Pro Leu Asp Ala Thr Leu Thr Ala Leu Ala Gly Leu Ala Thr Gly
405 410 415

Ala Asn Lys Leu Pro Tyr Phe Thr Gly Thr Asp Thr Val Ser Gln Thr
420 425 430

Asp Leu Thr Ser Val Gly Arg Asp Ile Leu Ala Lys Thr Ser Ile Leu
435 440 445

Ala Val Ile Gln Tyr Leu Gly Leu Arg Glu Leu Gly Thr Ser Gly Glu
450 455 460

Lys Ile Pro Leu Leu Ser Thr Ala Asn Thr Trp Ser Ala Arg Gln Thr
465 470 475 480

Phe Asn Gly Gly Ile Thr Gly Ala Leu Thr Gly Asn Ala Asp Thr Ala
485 490 495

Thr Lys Leu Lys Thr Ala Arg Lys Ile Asn Asn Val Ser Phe Asp Gly
500 505 510

Ser Ala Asp Ile Thr Leu Thr Pro Glu Asn Leu Gly Val Thr Ser Leu
515 520 525

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

[0194] Thr Phe Gly Pro Val Glu Ala Tyr Leu Gly Val Trp Ser Lys Ala Thr
545 550 555 560

Ser Thr Asn Ala Thr Leu Glu Lys Asn Phe Pro Glu Asp Asn Ala Val
565 570 575

Gly Val Leu Glu Val Phe Ala Ala Gly Asn Phe Ala Gly Thr Gln Arg
580 585 590

Phe Thr Thr Arg Asp Gly Asn Val Tyr Ile Arg Arg Leu Ala Asn Lys
595 600 605

Trp Asn Gly Ser Asp Gly Pro Trp Gly Ile Trp Arg His Thr Gln Ser
610 615 620

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

Ala Glu His Leu Gly Leu Trp Arg Asn Ser Ser Ser Ala Ile Ala Ser
645 650 655

Tyr Glu Arg Asn Tyr Pro Glu Glu Gly Gly Phe Ala Gln Gly Val Leu

660 665 670

Glu Ile Leu Glu Gly Gly Asn Tyr Gly Arg Thr Gln Arg Tyr Thr Thr
675 680 685

Arg Arg Gly Asn Met Tyr Val Arg Cys Leu Ala Ala Ser Trp Asp Ala
690 695 700

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

Ser Arg Tyr Tyr Glu Gly Asp Leu Asn Val Leu Thr Asp Pro Gly Ile
725 730 735

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

Gly Ala Thr Leu Leu Gly Ile Leu Glu Val Ile Arg Arg Phe Asp Gly
755 760 765

Val Ser Val Trp Gln Arg Tyr Thr Thr Thr Gly Lys Ser Glu Thr Thr
[0195] 770 775 780

Gln Gly Arg Thr Phe Glu Arg Val Tyr Ala Gly Ser Lys Trp Thr Glu
785 790 795 800

Trp Arg Glu Val Tyr Asn Ser Phe Ser Leu Pro Leu Asn Leu Gly Ile
805 810 815

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

Phe Val Pro Gly Ser Leu Ile Thr Val Arg Leu Asp Asn Met Thr Asn
835 840 845

Ile Pro Asp Gly Met Asp Trp Gly Val Ile Asp Gly Asn Leu Ile Asn
850 855 860

Ile Ala Val Gly Pro Ser Asp Asp Ser Gly Thr Gly Arg Ser Met His
865 870 875 880

Val Trp Arg Ser Thr Val Ser Lys Ala Asn Tyr Arg Phe Phe Met Val
885 890 895

```
Arg Ile Ser Gly Asn Pro Gly Ser Arg Thr Ile Thr Ala Arg Arg Val
            900                 905                 910

Pro Ile Ile Asp Glu Ala Gln Thr Trp Gly Ala Lys Gln Thr Phe Ser
        915                 920                 925

Ala Gly Leu Ser Gly Glu Leu Ser Gly Asn Ala Ala Thr Ala Thr Lys
    930                 935                 940

Leu Lys Thr Ala Arg Lys Ile Asn Asn Val Ser Phe Asp Gly Ser Gly
945                 950                 955                 960

Asp Ile Glu Val Leu Pro Val Gly Val Pro Leu Pro Trp Pro Ser Asp
                965                 970                 975

Thr Val Pro Ser Gly Tyr Ala Leu Met Gln Gly Gln Thr Phe Asp Lys
            980                 985                 990

Ser Ala Tyr Pro Lys Leu Ala Ala  Ala Tyr Pro Ser Gly  Val Ile Pro
        995                 1000                1005
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[0196]

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Asp Met  Arg Gly Trp Thr Ile  Lys Gly Lys Pro Ala  Ser Gly Arg
    1010                1015                1020

Asp Val  Leu Ser Leu Glu Gln  Asp Gly Ile Lys Ser  His Thr His
    1025                1030                1035

Ser Ala  Ser Ala Ser Asn Thr  Asp Leu Gly Thr Lys  Thr Thr Ser
    1040                1045                1050

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

Thr His  Asn Val Ser Gly Thr  Ala Asn Ser Ala Gly  Ala His Thr
    1070                1075                1080

His Thr  Val Pro Leu Arg Arg  Pro Asn Ser Gly Gly  Met Asn Phe
    1085                1090                1095

Asp Trp  Leu Asp Gly Ala Ser  Ser Gly Thr Val Val  Gly Asn Gly
    1100                1105                1110

Thr Val  Pro Ser Ser Gly Ala  His Thr His Ser Val  Ser Gly Thr
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1115 1120 1125

Ala Thr Ser Ala Gly Ala His Ala His Thr Val Gly Ile Gly Ala
1130 1135 1140

His Thr His Ser Val Ala Ile Gly Ser His Gly His Thr Ile Thr
1145 1150 1155

Val Asn Ala Ala Gly Asn Ala Glu Asn Thr Val Lys Asn Ile Ala
1160 1165 1170

Phe Asn Tyr Ile Val Arg Leu Ala
1175 1180

<210> 64
<211> 561
<212> PRT
<213> 人工序列

<220>
<223> 热带_pNS88 尾丝

<400> 64

[0197]

Met Asn Asp Val Thr Val Val Thr Ser Val Thr Tyr Pro Ser Ser Glu
1 5 10 15

Ser Leu Ala Leu Val Ala Asp Val Gln Tyr His Glu Pro Tyr Leu Ser
20 25 30

Ala Ala Leu Asn Arg Lys Phe Arg Gly Ile Val Asp Pro Gly Phe Tyr
35 40 45

Ala Gly Phe Leu Pro Lys Pro Gly Gly Gly Met Asn Leu Leu Ile Thr
50 55 60

Ser Val Asp Gly Asp Lys Thr Ala Gly Ala Ala Ser Val Asp Ile Gly
65 70 75 80

Glu Phe Tyr Gln Val Thr Ile Gln Gln Arg Lys Asp Ile Ser Leu Ala
85 90 95

Leu Ser Ala Gly Lys Lys Tyr Ala Ile Val Leu Lys Gly Arg Tyr Leu
100 105 110

Leu Gly Glu Asp Thr Tyr Gln Val Asn Thr Ala Ser His Ile His Ala

115 120 125

Ala Glu Phe Val Ala Arg Thr Tyr Thr Asp Ser Tyr Gln Leu Gly Asp
130 135 140

Gly Glu Leu Leu Val Cys Thr Val Asn Ile Pro Ala Ser Val Ser Ala
145 150 155 160

Ile Thr Gln Glu Met Ile Asp Thr Ser Glu Arg Ile Asn Arg Ser Ile
165 170 175

Gly Ile Asp Ile Ser Asp Ser Val Thr Ser Thr Arg Ser Asp Val Ala
180 185 190

Ala Ser Ser Leu Ala Val Lys Lys Ala Tyr Asp Leu Ala Lys Ser Lys
195 200 205

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

[0198]
Ala Trp Glu Thr Phe Ala Thr Thr Ser Ala Asn Gln Ser Ile Thr Val
225 230 235 240

Thr Ile Asn Gly Thr Pro Val Thr Ile Pro Gly Ile Gly Lys Leu Ala
245 250 255

Gln Lys Gly Thr Asn Gly Ala Leu Pro Ile Asp Gln Gly Gly Thr Gly
260 265 270

Ala Thr Asn Ala Ala Asp Val Arg Thr Asn Leu Gly Leu Gly Asp Ser
275 280 285

Val Thr Ala Asn Phe Gly Ser Leu Glu Ile Gly Ala Lys Asn Ala Ser
290 295 300

Ser Ala Ser Phe Val Asp Phe His Phe Leu Gly Thr Asn Asp Tyr Asp
305 310 315 320

Ala Arg Ile Leu Cys Gly Gly Asn Ser Asn Gly Gly Met Gly Lys Gly
325 330 335

Asp Phe Thr Phe Tyr Ala Gly Lys Tyr Thr Phe Ile Gly Asp Ser Phe
340 345 350

Glu Phe Arg Asn Pro Ile Thr Cys Gln Asn Ser Ile Thr Ala Ser Gly
355 360 365

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

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

Gly Gly Ile Glu Ser Arg Gly Val Ile Tyr Ala Pro Arg Glu Gly Thr
405 410 415

Ile Arg Leu Arg Pro Asp Asn Asn Asp Asn Gly Gly Ala Asn Gly Tyr
420 425 430

Ser Phe Ser Phe Gly Ala Asp Gly Arg Phe Thr Cys Ile Ser Val Asn
435 440 445

Gln Thr Ser Asp Glu Arg Val Lys Phe Asp Lys Glu Pro Val Ser Asn
450 455 460

[0199] Ala Leu Glu Lys Ile Cys Ser Leu Thr Gly Tyr Thr Phe Gly Ile Gln
465 470 475 480

Leu Thr Glu Ser Glu Ser Val His Ser Ala Gly Ile Ile Ala Gln Asp
485 490 495

Leu Glu Lys Val Leu Pro Val Ala Val Ser Ser Gly Gly Thr Gly Thr
500 505 510

Thr Pro Thr Gly Glu Glu Ile Asn Asp Leu Lys Thr Val Asp Tyr Ser
515 520 525

Ala Met Ser Ala Leu Tyr Val Glu Ala Met Lys Glu Leu Ala Asn Arg
530 535 540

Val Lys Ser Ile Glu Ser Glu Phe Ala Glu Leu Lys Ala Arg Ser Ala
545 550 555 560

Ile

<210> 65

<211> 556
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<213> 人工序列

<220>
<223> 热带_pNS92 尾丝

<400> 65

Met Asn Asp Val Thr Val Val Thr Ser Val Thr Tyr Pro Ser Ser Glu
1 5 10 15

Ser Leu Ala Leu Val Ala Asp Val Gln Tyr His Glu Pro Tyr Leu Ser
20 25 30

Ala Ala Leu Asn Arg Lys Phe Arg Gly Ile Val Asp Pro Gly Phe Tyr
35 40 45

Ala Gly Phe Leu Pro Lys Pro Gly Gly Gly Met Asn Leu Leu Ile Thr
50 55 60

Ser Val Asp Gly Asp Lys Thr Ala Gly Ala Ala Ser Val Asp Ile Gly
65 70 75 80

[0200]

Glu Phe Tyr Gln Val Thr Ile Gln Gln Arg Lys Asp Ile Ser Leu Ala
85 90 95

Leu Ser Ala Gly Lys Lys Tyr Ala Ile Val Leu Lys Gly Arg Tyr Leu
100 105 110

Leu Gly Glu Asp Thr Tyr Gln Val Asn Thr Ala Ser His Ile His Ala
115 120 125

Ala Glu Phe Val Ala Arg Thr Tyr Thr Asp Ser Tyr Gln Leu Gly Asp
130 135 140

Gly Glu Leu Leu Val Cys Thr Val Asn Ile Pro Ala Ser Val Ser Ala
145 150 155 160

Ile Thr Gln Glu Met Ile Asp Thr Ser Glu Arg Ile Asn Arg Ser Ile
165 170 175

Gly Ile Asp Ile Ser Asp Ser Val Thr Ser Thr Arg Ser Asp Val Ala
180 185 190

Ala Ser Ser Leu Ala Val Lys Lys Ala Tyr Asp Leu Ala Lys Ser Lys

195 200 205

Tyr Thr Ala Gln Asp Ala Asp Glu Asn Ile Gly Ala Trp Glu Thr Phe
210 215 220

Ala Thr Thr Ser Ala Asn Gln Ser Ile Thr Val Thr Ile Asn Gly Thr
225 230 235 240

Pro Val Thr Ile Pro Gly Ile Gly Lys Leu Ala Gln Lys Gly Thr Asn
245 250 255

Gly Ala Leu Pro Ile Asp Gln Gly Gly Thr Gly Ala Thr Asn Ala Ala
260 265 270

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

Gly Ser Leu Glu Ile Gly Ala Lys Asn Ala Ser Ser Ala Ser Phe Val
290 295 300

[0201] Asp Phe His Phe Leu Gly Thr Asn Asp Tyr Asp Ala Arg Ile Leu Cys
305 310 315 320

Gly Gly Asn Ser Asn Gly Gly Met Gly Lys Gly Asp Phe Thr Phe Tyr
325 330 335

Ala Gly Lys Tyr Thr Phe Ile Gly Asp Ser Phe Glu Phe Arg Asn Pro
340 345 350

Ile Thr Cys Gln Asn Ser Ile Thr Ala Ser Gly Ser Ile Ser Ala Gly
355 360 365

Gly Ser Leu Arg Ala Val Thr Ser Ser Asn Val Trp Ala Ser Ser Asp
370 375 380

Thr Gln Asn Ala His Val Trp Phe Tyr Gly Ala Gly Gly Ile Glu Ser
385 390 395 400

Arg Gly Val Ile Tyr Ala Pro Arg Glu Gly Thr Ile Arg Leu Arg Pro
405 410 415

Asp Asn Asn Asp Asn Gly Gly Ala Asn Gly Tyr Ser Phe Ser Phe Gly
420 425 430

```
Ala Asp Gly Arg Phe Thr Cys Ile Ser Val Asn Gln Thr Ser Asp Glu
        435                 440                 445

Arg Val Lys Phe Asp Lys Glu Pro Val Ser Asn Ala Leu Glu Lys Ile
    450                 455                 460

Cys Ser Leu Thr Gly Tyr Thr Phe Gly Ile Gln Leu Thr Glu Ser Glu
465                 470                 475                 480

Ser Val His Ser Ala Gly Ile Ile Ala Gln Asp Leu Glu Lys Val Leu
                485                 490                 495

Pro Val Ala Val Ser Ser Gly Gly Thr Gly Thr Thr Pro Thr Gly Glu
            500                 505                 510

Glu Ile Asn Asp Leu Lys Thr Val Asp Tyr Ser Ala Met Ser Ala Leu
        515                 520                 525

Tyr Val Glu Ala Met Lys Glu Leu Ala Asn Arg Val Lys Ser Ile Glu
    530                 535                 540
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[0202]

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Ser Glu Phe Ala Glu Leu Lys Ala Arg Ser Ala Ile
545                 550                 555
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<210> 66
<211> 975
<212> PRT
<213> 人工序列

<220>
<223> 紫罗兰尾丝

<400> 66

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Met Asn Asp Val Thr Val Val Thr Ser Val Thr Tyr Pro Ser Pro Glu
1               5                   10                  15

Ser Leu Ala Leu Val Ala Asp Val Gln Tyr His Glu Pro Tyr Leu Ser
            20                  25                  30

Ala Ala Leu Asn Arg Lys Phe Arg Gly Ile Val Asp Pro Gly Phe Tyr
        35                  40                  45

Ala Gly Phe Leu Pro Lys Pro Gly Gly Gly Met Asn Leu Leu Ile Thr
    50                  55                  60
```

Ser Val Asp Gly Asp Lys Thr Ala Gly Ala Ala Ser Val Asp Ile Gly
65 70 75 80

Glu Phe Tyr Gln Val Thr Ile Gln Gln Arg Lys Asp Ile Ser Leu Ala
85 90 95

Leu Ser Ala Gly Lys Lys Tyr Ala Ile Val Leu Lys Gly Arg Tyr Leu
100 105 110

Leu Gly Glu Asp Thr Tyr Gln Val Asn Thr Ala Ser His Ile His Ala
115 120 125

Ala Glu Phe Val Ala Arg Thr Tyr Thr Asp Ser Tyr Gln Leu Gly Asp
130 135 140

Gly Glu Leu Leu Val Cys Thr Val Asn Ile Pro Ala Gly Val Ser Ala
145 150 155 160

Ile Thr Gln Glu Met Ile Asp Thr Ser Glu Arg Ile Asn Arg Thr Ile
165 170 175

[0203] Gly Ile Asp Ile Ser Asp Ser Val Thr Ser Thr Arg Ser Asp Val Ala
180 185 190

Ala Ser Ser Leu Ala Val Lys Lys Ala Tyr Asp Leu Ala Lys Ser Lys
195 200 205

Tyr Thr Ala Gln Asp Ala Ser Ile Thr Gln Lys Gly Leu Val Gln Leu
210 215 220

Ser Ser Ala Thr Asn Ser Asp Ser Glu Thr Met Ala Ala Thr Pro Lys
225 230 235 240

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

Ser Pro Ser Leu Thr Gly Thr Pro Ser Ala Pro Thr Ala Ala Gln Gly
260 265 270

Thr Asn Ser Thr Gln Ile Ala Asn Thr Ala Phe Val Lys Ala Ala Ile
275 280 285

Thr Ala Leu Ile Asn Gly Ala Pro Gly Thr Leu Asp Thr Leu Lys Glu

290 295 300

Ile Ala Ala Ala Ile Asn Asn Asp Pro Asn Phe Ser Thr Thr Val Asn
305 310 315 320

Asn Ala Leu Ala Leu Lys Ala Pro Leu Ala Ser Pro Ala Leu Thr Gly
325 330 335

Ile Pro Thr Ala Pro Thr Ala Ala Gln Gly Thr Asn Asn Thr Gln Ile
340 345 350

Ala Thr Thr Ala Tyr Val Arg Ala Ala Ile Ser Ala Leu Val Gly Ser
355 360 365

Ser Pro Glu Ala Leu Asp Thr Leu Asn Glu Leu Ala Ala Ala Leu Gly
370 375 380

Asn Asp Pro Asn Phe Ala Thr Thr Met Thr Asn Ala Leu Ala Gly Lys
385 390 395 400

Gln Pro Leu Asp Ala Thr Leu Thr Ala Leu Ala Gly Leu Ala Thr Gly
[0204] 405 410 415

Ala Asn Lys Leu Pro Tyr Phe Thr Gly Lys Asp Thr Val Ala Gln Thr
420 425 430

Asp Leu Thr Ser Val Gly Arg Asp Ile Leu Ala Lys Thr Ser Val Leu
435 440 445

Ala Val Ile Gln Tyr Leu Gly Leu Arg Glu Leu Gly Thr Ser Gly Glu
450 455 460

Lys Ile Pro Leu Leu Ser Thr Ala Asn Thr Trp Ser Ala Arg Gln Thr
465 470 475 480

Phe Asn Gly Gly Ile Thr Gly Ala Leu Thr Gly Asn Ala Asp Thr Ala
485 490 495

Thr Lys Leu Lys Thr Ala Ile Asn Ile Asn Gly Val Arg Phe Asp Gly
500 505 510

Ser Thr Asn Ile Ser Ile Pro Thr Ile Thr Ser Arg Gly Arg Val Thr
515 520 525

Ala Leu Thr Gly Thr Thr Gln Gly Ala Ala Thr Gly Leu Gln Met Tyr
530 535 540

Glu Ala Tyr Asn Asn Gly Tyr Pro Thr Thr Tyr Gly Asn Val Leu His
545 550 555 560

Leu Lys Gly Ala Ala Ser Thr Gly Glu Gly Glu Leu Leu Ile Gly Trp
565 570 575

Ser Gly Thr Asn Gly Ala His Ala Pro Ala Phe Ile Arg Ser Lys Arg
580 585 590

Asp Ile Thr Ala Ala Ala Trp Ser Glu Trp Ala Gln Ile Tyr Thr Ser
595 600 605

Lys Asp Ser Val Pro Gly Val Asn Thr Lys Gly Asn Gln Asp Thr Ser
610 615 620

Gly Asn Ala Ala Thr Ala Thr Lys Leu Gln Thr Ala Cys Thr Ile Asn
625 630 635 640

[0205] Gly Val Ser Phe Asp Gly Ser Lys Asn Ile Glu Leu Thr Ala Ala Asp
645 650 655

Leu Asn Leu Glu Gln Thr Val Glu Leu Ala Ala Gly Ala Leu Gln Lys
660 665 670

Asn Gln Asn Gly Ala Asp Ile Pro Gly Lys Asp Thr Phe Thr Lys Asn
675 680 685

Ile Gly Ala Cys Arg Ala Tyr Ser Ala Trp Leu Asn Ile Gly Gly Asp
690 695 700

Ser Gln Val Trp Thr Thr Ala Gln Phe Ile Ser Trp Leu Glu Ser Gln
705 710 715 720

Gly Ala Phe Asn His Pro Tyr Trp Met Cys Lys Gly Ser Trp Ala Tyr
725 730 735

Ala Asn Asn Lys Val Ile Thr Asp Thr Gly Cys Gly Asn Ile Cys Leu
740 745 750

Ala Gly Ala Val Val Glu Val Ile Gly Thr Arg Gly Ala Met Thr Ile

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          755                 760                 765

Arg Val Thr Thr Pro Ser Thr Ser Ser Gly Gly Gly Ile Thr Asn Ala
    770                 775                 780

Gln Phe Thr Tyr Ile Asn His Gly Asp Ala Tyr Ala Pro Gly Trp Arg
785                 790                 795                 800

Arg Asp Tyr Asn Thr Lys Asn Gln Gln Pro Ala Phe Ala Leu Gly Gln
                805                 810                 815

Thr Gly Ser Arg Val Ala Asn Asp Lys Ala Val Gly Trp Asn Trp Asn
            820                 825                 830

Ser Gly Val Tyr Asp Ala Asp Ile Ser Gly Ala Ser Thr Leu Ile Leu
        835                 840                 845

His Phe Asn Met Asn Ala Gly Ser Cys Pro Ala Val Gln Phe Arg Val
    850                 855                 860

Asn Tyr Lys Asn Gly Gly Ile Phe Tyr Arg Ser Ala Arg Asp Gly Tyr
865                 870                 875                 880

Gly Phe Glu Ala Asn Trp Ser Glu Phe Tyr Thr Thr Thr Arg Lys Pro
                885                 890                 895

Ser Ala Gly Asp Val Gly Ala Tyr Thr Gln Ala Glu Cys Asn Ser Arg
            900                 905                 910

Phe Ile Thr Gly Ile Arg Leu Gly Gly Leu Ser Ser Val Gln Thr Trp
        915                 920                 925

Asn Gly Pro Gly Trp Ser Asp Arg Ser Gly Tyr Val Val Thr Gly Ser
    930                 935                 940

Val Asn Gly Asn Arg Asp Glu Leu Ile Asp Thr Thr Gln Ala Arg Pro
945                 950                 955                 960

Ile Gln Tyr Cys Ile Asn Gly Thr Trp Tyr Asn Ala Gly Ser Ile
                965                 970                 975
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[0206]

<210> 67
<211> 175
<212> PRT

<213> 人工序列

<220>
<223> 芦笋分子伴侣

<400> 67

Met Met His Leu Lys Asn Ile Lys Ser Glu Asn Pro Lys Thr Lys Glu
1 5 10 15

Gln Tyr Gln Leu Thr Lys Asn Phe Asp Val Ile Trp Leu Trp Ser Glu
20 25 30

Asp Gly Lys Asn Trp Tyr Glu Glu Val Asn Asn Phe Gln Asp Asp Thr
35 40 45

Ile Lys Ile Val Tyr Asp Glu Asn Asn Ile Ile Val Ala Ile Thr Lys
50 55 60

Asp Ala Ser Thr Leu Asn Pro Glu Gly Phe Ser Val Val Glu Ile Pro
65 70 75 80

Asp Ile Thr Ala Asn Arg Arg Ala Asp Asp Ser Gly Lys Trp Met Phe
85 90 95

[0207]

Lys Asp Gly Ala Val Val Lys Arg Ile Tyr Thr Ala Asp Glu Gln Gln
100 105 110

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

Val Ile Gln Pro Leu Glu Arg Ala Val Arg Leu Asn Met Ala Thr Asp
130 135 140

Glu Glu Arg Ala Arg Leu Glu Ser Trp Glu Arg Tyr Ser Val Leu Val
145 150 155 160

Ser Arg Val Asp Thr Ala Asn Pro Glu Trp Pro Gln Lys Pro Glu
165 170 175

<210> 68
<211> 140
<212> PRT
<213> 人工序列

<220>
<223> 香蕉分子伴侣

<400> 68

Met Arg Ile Tyr Phe Ser Pro Ser Glu Ile Gly Phe Tyr His Glu Ser
1 5 10 15

Asp Lys Gln Ala Tyr Leu Leu Ala Gly Thr Trp Pro Asn Asp Leu Leu
20 25 30

Glu Ile Ser Glu Lys Trp Phe Leu Tyr Leu Leu Glu Gly Gln Gln Lys
35 40 45

Gly Lys Val Ile Thr Val Asn Asp Tyr Asp Gln Pro Val Leu Val Asp
50 55 60

Pro Pro Thr Ala Thr Lys Glu Gln Leu Leu Ala Glu Ala Asp Ala Gln
65 70 75 80

Lys Glu Ala Leu Met Asn Ser Ala Ser Ala Val Ile Glu Pro Leu Lys
85 90 95

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

[0208]

Leu Ala Trp Gln Gln Tyr Arg Val Leu Leu Met Arg Val Asp Thr Ser
115 120 125

His Ala Pro Asp Ile Glu Trp Pro Val Leu Pro Ala
130 135 140

<210> 69
<211> 203
<212> PRT
<213> 人工序列

<220>
<223> 蜀羊泉陪伴

<400> 69

Met Asp Asn Ala Ile Leu Asn Ser Glu Leu Ile Ala Ile Gln Ala Gly
1 5 10 15

Asn Ile Ile Val Tyr Asn Tyr Asp Gly Gly Asn Arg Glu Tyr Ile Ser
20 25 30

Ala Ser Thr Glu Tyr Leu Ala Val Gly Val Gly Ile Pro Ala Asn Ser

35 40 45

Cys Leu Asp Ala Pro Gly Ser His Lys Ala Gly Tyr Ala Ile Leu Arg
50 55 60

Ser Glu Asp Leu Ser Ser Trp Glu Tyr Val Pro Asp His Arg Gly Glu
65 70 75 80

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

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

Asp Lys Trp Asp Gly Glu Lys Trp Val Val Asp Thr Glu Ala Gln His
115 120 125

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

Thr Ala Met Asp Ser Ile Ser Leu Ile Gln Leu Lys Leu Arg Ala Gly
145 150 155 160

[0209]

Arg Lys Leu Thr Gln Ala Glu Thr Thr Gln Leu Asn Ser Val Leu Asp
165 170 175

Tyr Ile Asp Glu Leu Asn Ala Met Asp Leu Thr Thr Ala Pro Asp Leu
180 185 190

Asn Trp Pro Glu Lys Gln Leu Ser Thr Ala Ser
195 200

<210> 70
<211> 203
<212> PRT
<213> 人工序列

<220>
<223> 钴分子伴侣

<400> 70

Met Asp Asn Ala Ile Leu Asn Ser Glu Leu Ile Ala Ile Gln Ala Gly
1 5 10 15

Asn Ile Ile Val Tyr Asn Tyr Asp Gly Gly Asn Arg Glu Tyr Ile Ser

20 25 30

Ala Ser Thr Glu Tyr Leu Ala Val Gly Val Gly Ile Pro Ala Asn Ser
35 40 45

Cys Leu Asp Ala Pro Gly Ser His Lys Ala Gly Tyr Ala Ile Leu Arg
50 55 60

Ser Glu Asp Leu Ser Ser Trp Glu Tyr Val Pro Asp His Arg Gly Glu
65 70 75 80

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

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

Asp Lys Trp Asp Gly Glu Lys Trp Val Val Asp Thr Glu Ala Gln His
115 120 125

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

[0210]

Thr Ala Met Asp Ser Ile Ser Leu Ile Gln Leu Lys Leu Arg Ala Gly
145 150 155 160

Arg Lys Leu Thr Gln Ala Glu Thr Thr Gln Leu Asn Ser Val Leu Asp
165 170 175

Tyr Ile Asp Glu Leu Asn Ala Met Asp Leu Thr Thr Ala Pro Asp Leu
180 185 190

Asn Trp Pro Glu Lys Gln Leu Ser Thr Ala Ser
195 200

<210> 71
<211> 203
<212> PRT
<213> 人工序列

<220>
<223> 牛仔布分子伴侣

<400> 71

Met Asp Asn Ala Ile Leu Asn Ser Glu Leu Ile Ala Ile Gln Ala Gly

1 5 10 15

Asn Ile Ile Val Tyr Asn Tyr Asp Gly Gly Asn Arg Glu Tyr Ile Ser
20 25 30

Ala Ser Thr Glu Tyr Leu Ala Val Gly Val Gly Ile Pro Ala Asn Ser
35 40 45

Cys Leu Asp Ala Pro Gly Ser His Lys Ala Gly Tyr Ala Ile Leu Arg
50 55 60

Ser Glu Asp Leu Ser Ser Trp Glu Tyr Val Pro Asp His Arg Gly Glu
65 70 75 80

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

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

Asp Lys Trp Asp Gly Glu Lys Trp Val Val Asp Thr Glu Ala Gln His
115 120 125

[0211]

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

Thr Ala Met Asp Ser Ile Ser Leu Ile Gln Leu Lys Leu Arg Ala Gly
145 150 155 160

Arg Lys Leu Thr Gln Ala Glu Thr Thr Gln Leu Asn Ser Val Leu Asp
165 170 175

Tyr Ile Asp Glu Leu Asn Ala Met Asp Leu Thr Thr Ala Pro Asp Leu
180 185 190

Asn Trp Pro Glu Lys Gln Leu Ser Thr Ala Ser
195 200

<210> 72
<211> 175
<212> PRT
<213> 人工序列

<220>
<223> 茄子分子伴侣

<400> 72

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

Gln Tyr Gln Leu Thr Lys Asn Phe Asp Val Ile Trp Leu Trp Ser Glu
20 25 30

Asp Gly Lys Asn Trp Tyr Glu Glu Val Lys Asn Phe Gln Pro Asp Thr
35 40 45

Ile Lys Ile Val Tyr Asp Glu Asn Asn Ile Ile Val Ala Ile Thr Lys
50 55 60

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

Asp Ile Thr Ala Asn Arg Arg Ala Asp Asp Ser Gly Lys Trp Met Phe
85 90 95

Lys Asp Gly Ala Val Val Lys Arg Ile Tyr Thr Ala Asp Glu Gln Gln
100 105 110

[0212]

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

Val Ile Gln Pro Leu Glu Arg Ala Val Arg Leu Asn Met Ala Thr Asp
130 135 140

Glu Glu Arg Thr Arg Leu Glu Ala Trp Glu Arg Tyr Ser Val Leu Val
145 150 155 160

Ser Arg Val Asp Thr Ala Asn Pro Glu Trp Pro Gln Lys Pro Glu
165 170 175

<210> 73
<211> 175
<212> PRT
<213> 人工序列

<220>
<223> 蕨分子伴侣

<400> 73

Met Gln His Leu Lys Asn Ile Lys Ser Gly Asn Pro Lys Thr Lys Glu

1 5 10 15

Gln Tyr Gln Leu Thr Lys Asn Phe Asp Val Ile Trp Leu Trp Ser Glu
20 25 30

Asp Gly Lys Asn Trp Tyr Glu Glu Val Lys Asn Phe Gln Pro Asp Thr
35 40 45

Ile Lys Ile Val Tyr Asp Ala Asn Asn Ile Ile Val Ala Ile Thr Lys
50 55 60

Asp Ala Ser Thr Leu Asn Pro Glu Gly Tyr Ser Val Val Glu Val Pro
65 70 75 80

Asp Ile Thr Ala Asn Arg Arg Ala Asp Asp Ser Gly Lys Trp Met Phe
85 90 95

Lys Asp Gly Ala Val Val Lys Arg Ile Tyr Thr Ala Asp Glu Gln Gln
100 105 110

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

[0213]

Val Ile Gln Pro Leu Glu Arg Ala Val Arg Leu Asn Met Ala Thr Asp
130 135 140

Glu Glu Arg Ala Arg Leu Glu Ser Trp Glu Arg Tyr Ser Val Leu Val
145 150 155 160

Ser Arg Val Asp Thr Ala Asn Pro Glu Trp Pro Gln Lys Pro Glu
165 170 175

<210> 74
<211> 177
<212> PRT
<213> 人工序列

<220>
<223> 樱红分子伴侣

<400> 74

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

Gln Tyr Gln Leu Thr Lys Gln Phe Asn Ile Lys Trp Leu Tyr Thr Glu

20 25 30

Asp Gly Lys Asn Trp Tyr Glu Glu Gln Lys Asn Phe Gln Tyr Asp Thr
35 40 45

Leu Lys Met Ala Tyr Asp His Asn Gly Val Ile Ile Cys Ile Glu Lys
50 55 60

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

Asp Ile Thr Ala Asn Arg Arg Ala Asp Ile Ser Gly Lys Trp Met Phe
85 90 95

Lys Asp Gly Val Val Val Lys Arg Thr Tyr Thr Glu Glu Glu Gln Arg
100 105 110

Gln Gln Ala Glu Asn Glu Lys Gln Ser Leu Leu Gln Leu Val Arg Asp
115 120 125

Lys Thr Gln Leu Trp Asp Ser Gln Leu Arg Leu Gly Ile Ile Ser Ala
130 135 140

[0214]

Glu Asn Lys Gln Lys Leu Thr Glu Trp Met Leu Phe Ala Gln Lys Val
145 150 155 160

Glu Ser Thr Asp Thr Ser Ser Leu Pro Val Thr Phe Pro Glu Gln Pro
165 170 175

Glu

<210> 75
<211> 197
<212> PRT
<213> 人工序列

<220>
<223> 模糊分子伴侣

<400> 75

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

Thr Phe Gly Lys Val His Tyr Arg Leu Ile Lys Asn Ile Asn Glu Ala

20 25 30

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

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

Asn Ile Gly His Asp Asp Leu Gly Phe Pro Val Ser Gly Glu Ile Ile
65 70 75 80

Arg Ile Val Pro Val Ile Ile Gly Ser Lys Lys Ala Gly Ile Leu Gln
85 90 95

Thr Ile Leu Gly Ala Val Ile Val Ala Ala Ser Val Ala Tyr Gly Phe
100 105 110

Phe Thr Glu Asp Trp Ala Asn Ala Ala Tyr Gly Ile Gln Ala Gly Gly
115 120 125

Ala Met Met Leu Gly Gly Val Val Gln Met Leu Ser Pro Gln Pro Ala
130 135 140

[0215]

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

Gly Gly Val Thr Asn Thr Ala Ser Gln Gly Tyr Pro Val Pro Leu Leu
165 170 175

Tyr Gly Lys Arg Arg Ile Gly Gly Ala Ile Ile Ser Ala Gly Ile Tyr
180 185 190

Val Glu Asp Gln Gln
195

<210> 76
<211> 152
<212> PRT
<213> 人工序列

<220>
<223> 尺蠖分子伴侣

<400> 76

Met Lys Gly Glu Tyr Tyr Phe Ser Pro Ser Gln Val Ala Phe Tyr Pro

1 5 10 15

Ala Ser Leu Arg Glu Val Tyr Glu Tyr Ala Gly Cys Trp Pro Val Asp
20 25 30

Gly Glu Trp Val Ser Ala Glu Leu His Glu Gln Leu Met Asn Glu Gln
35 40 45

Ala Ala Gly Arg Ala Ile Ser Ser Asp Val Asn Gly Asn Pro Val Ala
50 55 60

Ile Glu Arg Pro Pro Leu Ser Arg Gln Gln Arg Ser Thr His Glu Arg
65 70 75 80

Arg Trp Arg Asp Ser Gln Leu Leu Ala Thr Asp Gly Leu Val Val Arg
85 90 95

His Arg Asp Gln Leu Glu Thr Gly Lys Glu Thr Thr Leu Leu Pro Val
100 105 110

Gln Tyr His Glu Leu Met Ser Tyr Arg Ala Ser Leu Arg Asp Trp Pro
115 120 125

[0216]

Glu Glu Pro Leu Phe Pro Asp Ser Gly Gly Arg Pro Ser Val Pro Asp
130 135 140

Trp Leu Arg Arg Tyr Val Thr Pro
145 150

<210> 77
<211> 203
<212> PRT
<213> 人工序列

<220>
<223> 印度分子伴侣

<400> 77

Met Asp Asn Ala Ile Leu Asn Ser Glu Leu Ile Ala Ile Gln Ala Gly
1 5 10 15

Asn Ile Ile Val Tyr Asn Tyr Asp Gly Gly Asn Arg Glu Tyr Ile Ser
20 25 30

Ala Ser Thr Glu Tyr Leu Ala Val Gly Val Gly Ile Pro Ala Asn Ser

35 40 45

Cys Leu Asp Ala Pro Gly Ser His Lys Ala Gly Tyr Ala Ile Leu Arg
50 55 60

Ser Glu Asp Leu Ser Ser Trp Glu Tyr Val Pro Asp His Arg Gly Glu
65 70 75 80

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

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

Asp Lys Trp Asp Gly Glu Lys Trp Val Val Asp Thr Glu Ala Gln His
115 120 125

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

Thr Ala Met Asp Ser Ile Ser Leu Ile Gln Leu Lys Leu Arg Ala Gly
145 150 155 160

[0217]

Arg Lys Leu Thr Gln Ala Glu Thr Thr Gln Leu Asn Ser Val Leu Asp
165 170 175

Tyr Ile Asp Glu Leu Asn Ala Met Asp Leu Thr Thr Ala Pro Asp Leu
180 185 190

Asn Trp Pro Glu Lys Gln Leu Ser Thr Ala Ser
195 200

<210> 78
<211> 203
<212> PRT
<213> 人工序列

<220>
<223> 靛蓝分子伴侣

<400> 78

Met Asp Asn Ala Ile Leu Asn Ser Glu Leu Ile Ala Ile Gln Ala Gly
1 5 10 15

Asn Ile Ile Val Tyr Asn Tyr Asp Gly Gly Asn Arg Glu Tyr Ile Ser

20 25 30

Ala Ser Thr Glu Tyr Leu Ala Val Gly Val Gly Ile Pro Ala Asn Ser
35 40 45

Cys Leu Asp Ala Pro Gly Ser His Lys Ala Gly Tyr Ala Ile Leu Arg
50 55 60

Ser Glu Asp Leu Ser Ser Trp Glu Tyr Val Pro Asp His Arg Gly Glu
65 70 75 80

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

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

Asp Lys Trp Asp Gly Glu Lys Trp Val Val Asp Thr Glu Ala Gln His
115 120 125

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

[0218]

Thr Ala Met Asp Ser Ile Ser Leu Ile Gln Leu Lys Leu Arg Ala Gly
145 150 155 160

Arg Lys Leu Thr Gln Ala Glu Thr Thr Gln Leu Asn Ser Val Leu Asp
165 170 175

Tyr Ile Asp Glu Leu Asn Ala Met Asp Leu Thr Thr Ala Pro Asp Leu
180 185 190

Asn Trp Pro Glu Lys Gln Leu Ser Thr Ala Ser
195 200

<210> 79
<211> 205
<212> PRT
<213> 人工序列

<220>
<223> Jazzberry 分子伴侣

<400> 79

Met Ala Phe Arg Met Ser Glu Gln Ser Arg Thr Val Lys Ile Tyr Asn

1 5 10 15

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

Pro Pro His Thr Gly Leu Pro Ala Asn Ser Thr Asp Ile Ala Pro Pro
35 40 45

Glu Ile Pro Ala Gly Phe Val Ala Val Phe Asn Ser Glu Asn Glu Ser
50 55 60

Trp Asn Ile Val Glu Asp His Arg Gly Lys Thr Val Tyr Asp Val Ala
65 70 75 80

Ser Gly Asp Ala Leu Phe Ile Ser Glu Pro Gly Pro Leu Pro Glu Asn
85 90 95

Val Thr Trp Leu Ser Pro Ala Gly Glu Tyr Gln Lys Trp Asp Gly Val
100 105 110

Ser Trp Val Lys Asp Glu Glu Ala Glu Lys Leu Phe Arg Ile Arg Glu
115 120 125

[0219]

Ala Glu Glu Lys Lys Ala Arg Leu Ile Gln Glu Ala Thr Asp Asn Ile
130 135 140

Ala Ile Leu Gln Asp Ala Val Asn Leu Glu Ile Ala Thr Asn Glu Glu
145 150 155 160

Asn Ser Gln Leu Asp Ser Trp Arg Lys Tyr Arg Val Leu Val Ser Arg
165 170 175

Ile Asp Thr Ser Thr Ala Pro Asp Ile Val Trp Pro Glu Leu Met Asn
180 185 190

Gln Gly Tyr Val Arg Glu Asp Glu Gln Ile Thr Ser Asp
195 200 205

<210> 80
<211> 177
<212> PRT
<213> 人工序列

<220>
<223> 丛林分子伴侣

<400> 80

Met Met His Leu Lys Asn Ile Thr Ala Gly Asn Pro Lys Thr Lys Glu
1 5 10 15

Gln Tyr Gln Leu Thr Lys Gln Phe Asn Ile Lys Trp Leu Tyr Thr Glu
20 25 30

Asp Gly Lys Asn Trp Tyr Glu Glu Gln Lys Asn Phe Gln Pro Asp Thr
35 40 45

Leu Lys Met Val Tyr Asp His Asn Gly Val Ile Ile Cys Ile Glu Lys
50 55 60

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

Asp Ile Thr Ala Asn Arg Arg Ala Asp Ile Ser Gly Lys Trp Met Phe
85 90 95

Lys Asp Gly Val Val Ile Lys Arg Thr Tyr Thr Glu Glu Glu Gln Arg
100 105 110

[0220]

Gln Gln Ala Glu Asn Glu Lys Gln Ser Leu Leu Gln Leu Val Arg Asp
115 120 125

Lys Thr Gln Leu Trp Asp Ser Gln Leu Arg Leu Gly Ile Ile Ser Asp
130 135 140

Glu Asn Lys Gln Lys Leu Thr Glu Trp Met Leu Tyr Ala Gln Lys Val
145 150 155 160

Glu Ser Thr Asp Thr Ser Ser Leu Pro Val Thr Phe Pro Glu Gln Pro
165 170 175

Glu

<210> 81
<211> 140
<212> PRT
<213> 人工序列

<220>
<223> 芒果分子伴侣

<400> 81

Met Gly Tyr Val Tyr Cys His Ala Thr Gly Ala Phe Tyr Asn Asp Ala
1 5 10 15

Leu Val Ala Asp Tyr Arg Ser Ala Gly Ser Trp Pro Asp Asn Tyr Val
20 25 30

Thr Val Leu Asp Asp Asp Tyr Glu Ser Leu Met Ala Gly Gln Ala Val
35 40 45

Gly Lys Met Ile Val Ser Asp Asn Asn Gly Tyr Pro Val Leu Thr Glu
50 55 60

Pro Pro Glu Pro Thr His Glu Glu Gln Val Asn Gln Ala Ser Ser Gln
65 70 75 80

Lys Leu Phe Leu Met Lys Thr Ala Asn Glu Ile Ile Thr Pro Leu Glu
85 90 95

Asp Ala Val Glu Leu Gly Ile Ala Thr Asp Glu Glu Ala Ala Thr Leu
100 105 110

[0221]

Leu Leu Trp Lys Arg Tyr Arg Val Leu Leu Asn Arg Leu Asp Leu Ser
115 120 125

Lys Ala Pro Asp Ile Gln Trp Pro Glu Arg Pro Ala
130 135 140

<210> 82
<211> 203
<212> PRT
<213> 人工序列

<220>
<223> 褐红分子伴侣

<400> 82

Met Asp Asn Ala Ile Leu Asn Ser Glu Leu Ile Ala Ile Gln Ala Gly
1 5 10 15

Asn Ile Ile Val Tyr Asn Tyr Asp Gly Gly Asn Arg Glu Tyr Ile Ser
20 25 30

Ala Ser Thr Glu Tyr Leu Ala Val Gly Val Gly Ile Pro Ala Asn Ser

35 40 45

Cys Leu Asp Ala Pro Gly Ser His Lys Ala Gly Tyr Ala Ile Leu Arg
50 55 60

Ser Glu Asp Leu Ser Ser Trp Glu Tyr Val Pro Asp His Arg Gly Glu
65 70 75 80

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

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

Asp Lys Trp Asp Gly Glu Lys Trp Val Val Asp Thr Glu Ala Gln His
115 120 125

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

Thr Ala Met Asp Ser Ile Ser Leu Ile Gln Leu Lys Leu Arg Ala Gly
145 150 155 160

[0222]

Arg Lys Leu Thr Gln Ala Glu Thr Thr Gln Leu Asn Ser Val Leu Asp
165 170 175

Tyr Ile Asp Glu Leu Asn Ala Met Asp Leu Thr Thr Ala Pro Asp Leu
180 185 190

Asn Trp Pro Glu Lys Gln Leu Ser Thr Ala Ser
195 200

<210> 83
<211> 177
<212> PRT
<213> 人工序列

<220>
<223> 桑葚分子伴侣

<400> 83

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

Gln Tyr Gln Leu Thr Lys Gln Phe Asn Ile Lys Trp Leu Tyr Thr Glu

20 25 30

Asp Gly Lys Asn Trp Tyr Glu Glu Gln Lys Asn Phe Gln Tyr Asp Thr
35 40 45

Leu Lys Met Ala Tyr Asp His Asn Gly Val Ile Ile Cys Ile Glu Lys
50 55 60

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

Asp Ile Thr Ala Asn Arg Arg Ala Asp Ile Ser Gly Lys Trp Met Phe
85 90 95

Lys Asp Gly Val Val Val Lys Arg Thr Tyr Thr Glu Glu Glu Gln Arg
100 105 110

Gln Gln Ala Glu Asn Glu Lys Gln Ser Leu Leu Gln Leu Val Arg Asp
115 120 125

Lys Thr Gln Leu Trp Asp Ser Gln Leu Arg Leu Gly Ile Ile Ser Ala
[0223] 130 135 140

Glu Asn Lys Gln Lys Leu Thr Glu Trp Met Leu Phe Ala Gln Lys Val
145 150 155 160

Glu Ser Thr Asp Thr Ser Ser Leu Pro Val Thr Phe Pro Glu Gln Pro
165 170 175

Glu

<210> 84
<211> 177
<212> PRT
<213> 噬菌体 P1

<220>
<221> 未归类特征
<223> P1_U`分子陪伴

<400> 84

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

Gln Tyr Gln Leu Thr Lys Gln Phe Asn Ile Lys Trp Leu Tyr Thr Glu
20 25 30

Asp Gly Lys Asn Trp Tyr Glu Glu Gln Lys Asn Phe Gln Tyr Asp Thr
35 40 45

Leu Lys Met Ala Tyr Asp His Asn Gly Val Ile Ile Cys Ile Glu Lys
50 55 60

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

Asp Ile Thr Ala Asn Arg Arg Ala Asp Ile Ser Gly Lys Trp Met Phe
85 90 95

Lys Asp Gly Val Val Val Lys Arg Thr Tyr Thr Glu Glu Glu Gln Arg
100 105 110

Gln Gln Ala Glu Asn Glu Lys Gln Ser Leu Leu Gln Leu Val Arg Asp
115 120 125

[0224]

Lys Thr Gln Leu Trp Asp Ser Gln Leu Arg Leu Gly Ile Ile Ser Ala
130 135 140

Glu Asn Lys Gln Lys Leu Thr Glu Trp Met Leu Phe Ala Gln Lys Val
145 150 155 160

Glu Ser Thr Asp Thr Ser Ser Leu Pro Val Thr Phe Pro Glu Gln Pro
165 170 175

Glu

<210> 85
<211> 175
<212> PRT
<213> 人工序列

<220>
<223> 松分子伴侣

<400> 85

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

Gln Tyr Gln Leu Thr Lys Asn Phe Asp Val Ile Trp Leu Trp Ser Glu
20 25 30

Asp Gly Lys Asn Trp Tyr Glu Glu Val Lys Asn Phe Gln Pro Asp Thr
35 40 45

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

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

Asp Ile Thr Ser Asn Arg Arg Ala Asp Asp Ser Gly Lys Trp Met Phe
85 90 95

Lys Asp Gly Ala Val Val Lys Arg Ile Tyr Thr Ala Asp Glu Gln Gln
100 105 110

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

[0225]

Val Ile Gln Pro Leu Glu Arg Ala Val Arg Leu Asn Met Ala Thr Asp
130 135 140

Glu Glu Arg Ala Arg Leu Glu Ser Trp Glu Arg Tyr Ser Val Leu Val
145 150 155 160

Ser Arg Val Asp Pro Ala Asn Pro Glu Trp Pro Glu Met Pro Gln
165 170 175

<210> 86
<211> 205
<212> PRT
<213> 人工序列

<220>
<223> 梅分子伴侣

<400> 86

Met Ala Phe Arg Met Ser Glu Gln Ser Arg Thr Val Lys Ile Tyr Asn
1 5 10 15

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

Pro Pro His Thr Gly Leu Pro Ala Asn Ser Thr Asp Ile Ala Pro Pro
35 40 45

Glu Ile Pro Ala Gly Phe Val Ala Val Phe Asn Ser Glu Asn Glu Ser
50 55 60

Trp Asn Ile Val Glu Asp His Arg Gly Lys Thr Val Tyr Asp Val Ala
65 70 75 80

Ser Gly Asp Ala Leu Phe Ile Ser Glu Pro Gly Pro Leu Pro Glu Asn
85 90 95

Val Thr Trp Leu Ser Pro Ala Gly Glu Tyr Gln Lys Trp Asp Gly Val
100 105 110

Ser Trp Val Lys Asp Glu Glu Ala Glu Lys Leu Phe Arg Ile Arg Glu
115 120 125

Ala Glu Glu Lys Lys Ala Arg Leu Ile Gln Glu Ala Thr Asp Asn Ile
130 135 140

[0226]

Ala Ile Leu Gln Asp Ala Val Asn Leu Glu Ile Ala Thr Asn Glu Glu
145 150 155 160

Asn Ser Gln Leu Asp Ser Trp Arg Lys Tyr Arg Val Leu Val Ser Arg
165 170 175

Ile Asp Thr Ser Thr Ala Pro Asp Ile Val Trp Pro Glu Leu Met Asn
180 185 190

Gln Gly Tyr Val Arg Glu Asp Glu Gln Ile Thr Ser Asp
195 200 205

<210> 87
<211> 170
<212> PRT
<213> 人工序列

<220>
<223> 皇后分子伴侣

<400> 87

Met Asn Asn Phe Lys Asn Phe Ala Pro Tyr Thr Pro Gly Glu Asp Lys
1 5 10 15

Arg Glu Leu Val Asp Ala Gly Val Leu Phe Leu Leu Asp Glu Asn Gly
20 25 30

Asn Asp Trp Tyr Glu Cys Gln Lys Leu Phe Ser Glu Cys Thr Lys Val
35 40 45

Ile Ala Tyr Asp Ser Asn Asn Ile Val Val Ser Ile Thr Asp Asp Ala
50 55 60

Ser Thr Leu Trp Pro Ile Gly Leu Ser Val Ala Glu Val Asp Ser Leu
65 70 75 80

Pro Glu Asp Val Asp Ile Asn Gly Gly Trp Val Phe Arg Asp Asn Ser
85 90 95

Val Val Lys Arg Ile Tyr Ser Asp Thr Glu Leu Gln Gln Gln Ala Glu
100 105 110

Ser Lys Lys Ala Ala Leu Leu Ser His Ala Glu Ser Val Ile Val Thr
115 120 125

[0227]

Leu Glu Arg Ala Val Lys Leu Asn Met Ala Thr Asp Glu Glu Arg Ala
130 135 140

Lys Leu Glu Ala Trp Glu Arg Tyr Ser Val Leu Val Tyr Arg Val Asp
145 150 155 160

Thr Ala Lys Pro Glu Trp Pro Glu Glu Pro
165 170

<210> 88
<211> 93
<212> PRT
<213> 人工序列

<220>
<223> Razzmatazz 分子伴侣 A

<400> 88

Met Met His Leu Lys Asn Ile Thr Ala Gly Asn Pro Lys Thr Lys Glu
1 5 10 15

Gln Tyr Gln Leu Thr Lys Gln Phe Asn Ile Lys Trp Leu Tyr Thr Glu
20 25 30

Asp Gly Lys Asn Trp Tyr Glu Glu Gln Lys Asn Phe Gln Pro Asp Thr
35 40 45

Leu Lys Met Val Tyr Asp His Asn Asp Val Ile Ile Cys Ile Glu Lys
50 55 60

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

Asp Ile Thr Ala Asn Arg Arg Ala Asp Ile Ser Gly Lys
85 90

<210> 89
<211> 83
<212> PRT
<213> 人工序列

<220>
<223> Razzmatazz 分子伴侣 B

<400> 89

Met Phe Lys Asp Gly Val Val Ile Lys Arg Thr Tyr Thr Glu Glu Glu
1 5 10 15

[0228]

Gln Arg Gln Gln Ala Glu Asn Glu Lys Gln Ser Leu Leu Gln Leu Val
20 25 30

Arg Asp Lys Thr Gln Leu Trp Asp Ser Gln Leu Arg Leu Gly Ile Ile
35 40 45

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

Lys Val Glu Ser Thr Asp Thr Ser Ser Leu Pro Val Thr Phe Pro Glu
65 70 75 80

Gln Pro Glu

<210> 90
<211> 176
<212> PRT
<213> 人工序列

<220>
<223> 三文鱼分子伴侣

<400> 90

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

Glu Gln Tyr Gln Leu Thr Lys Asn Phe Asp Val Ile Trp Leu Trp Ser
20 25 30

Glu Asp Asp Lys Asn Trp Tyr Glu Glu Val Lys Asn Phe Gln Pro Asp
35 40 45

Thr Ile Lys Ile Val Tyr Asp Ala Asn Asn Ile Ile Val Ala Ile Thr
50 55 60

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

Pro Asp Ile Thr Ala Asn Arg Arg Ala Asp Asp Ser Gly Lys Trp Met
85 90 95

Phe Lys Asp Gly Ala Val Val Lys Arg Ile Tyr Thr Ala Asp Glu Gln
100 105 110

[0229]

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

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

Asp Glu Glu Arg Thr Arg Leu Glu Ala Trp Glu Arg Tyr Ser Val Leu
145 150 155 160

Val Ser Arg Val Asp Thr Ala Asn Pro Glu Trp Pro Gln Lys Pro Glu
165 170 175

<210> 91
<211> 203
<212> PRT
<213> 人工序列

<220>
<223> 猩红分子伴侣

<400> 91

Met Asp Asn Ala Ile Leu Asn Ser Glu Leu Ile Ala Ile Gln Ala Gly

1 5 10 15

Asn Ile Ile Val Tyr Asn Tyr Asp Gly Gly Asn Arg Glu Tyr Ile Ser
20 25 30

Ala Ser Thr Glu Tyr Leu Ala Val Gly Val Gly Ile Pro Ala Asn Ser
35 40 45

Cys Leu Asp Ala Pro Gly Ser His Lys Ala Gly Tyr Ala Ile Leu Arg
50 55 60

Ser Glu Asp Leu Ser Ser Trp Glu Tyr Val Pro Asp His Arg Gly Glu
65 70 75 80

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

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

Asp Lys Trp Asp Gly Glu Lys Trp Val Val Asp Thr Glu Ala Gln His
115 120 125

[0230]

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

Thr Ala Met Asp Ser Ile Ser Leu Ile Gln Leu Lys Leu Arg Ala Gly
145 150 155 160

Arg Lys Leu Thr Gln Ala Glu Thr Thr Gln Leu Asn Ser Val Leu Asp
165 170 175

Tyr Ile Asp Glu Leu Asn Ala Met Asp Leu Thr Thr Ala Pro Asp Leu
180 185 190

Asn Trp Pro Glu Lys Gln Leu Ser Thr Ala Ser
195 200

<210> 92
<211> 175
<212> PRT
<213> 人工序列

<220>
<223> 三叶草分子伴侣

<400> 92

Met Met His Leu Lys Asn Ile Lys Ala Gly Asn Ala Lys Thr Leu Glu
1 5 10 15

Gln Tyr Glu Leu Thr Lys Lys His Gly Val Ile Trp Leu Tyr Ala Glu
20 25 30

Asp Gly Lys Asn Trp Tyr Glu Glu Val Lys Asn Phe Gln Pro Asp Thr
35 40 45

Ile Lys Ile Val Tyr Asp Glu Asn Asn Ile Ile Val Ala Val Thr Lys
50 55 60

Asp Ala Ser Thr Leu Asn Pro Glu Gly Phe Ser Val Val Glu Ile Pro
65 70 75 80

Asp Ile Thr Ala Asn Arg Arg Ala Asp Asp Ser Gly Lys Trp Met Phe
85 90 95

Lys Asp Gly Ala Val Val Arg Arg Thr Tyr Thr Ala Asp Glu Gln Gln
100 105 110

[0231]

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

Val Ile Gln Pro Leu Glu Arg Ala Val Arg Leu Asn Met Ala Thr Asp
130 135 140

Glu Glu His Ala Arg Leu Glu Ser Trp Glu Arg Tyr Ser Val Leu Val
145 150 155 160

Ser Arg Val Asp Thr Ala Asn Pro Glu Trp Pro Gln Lys Pro Glu
165 170 175

<210> 93
<211> 203
<212> PRT
<213> 人工序列

<220>
<223> 日落分子伴侣

<400> 93

Met Asp Asn Ala Ile Leu Asn Ser Glu Leu Ile Ala Ile Gln Ala Gly

1 5 10 15

Asn Ile Ile Val Tyr Asn Tyr Asp Gly Gly Asn Arg Glu Tyr Ile Ser
20 25 30

Ala Ser Thr Glu Tyr Leu Ala Val Gly Val Gly Ile Pro Ala Asn Ser
35 40 45

Cys Leu Asp Ala Pro Gly Ser His Lys Ala Gly Tyr Ala Ile Leu Arg
50 55 60

Ser Glu Asp Leu Ser Ser Trp Glu Tyr Val Pro Asp His Arg Gly Glu
65 70 75 80

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

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

Asp Lys Trp Asp Gly Glu Lys Trp Val Val Asp Thr Glu Ala Gln His
115 120 125

[0232]

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

Thr Ala Met Asp Ser Ile Ser Leu Ile Gln Leu Lys Leu Arg Ala Gly
145 150 155 160

Arg Lys Leu Thr Gln Ala Glu Thr Thr Gln Leu Asn Ser Val Leu Asp
165 170 175

Tyr Ile Asp Glu Leu Asn Ala Met Asp Leu Thr Thr Ala Pro Asp Leu
180 185 190

Asn Trp Pro Glu Lys Gln Leu Ser Thr Ala Ser
195 200

<210> 94
<211> 203
<212> PRT
<213> 人工序列

<220>
<223> 橘色分子伴侣

<400> 94

Met Asp Asn Ala Ile Leu Asn Ser Glu Leu Ile Ala Ile Gln Ala Gly
1 5 10 15

Asn Ile Ile Val Tyr Asn Tyr Asp Gly Gly Asn Arg Glu Tyr Ile Ser
20 25 30

Ala Ser Thr Glu Tyr Leu Ala Val Gly Val Gly Ile Pro Ala Asn Ser
35 40 45

Cys Leu Asp Ala Pro Gly Ser His Lys Ala Gly Tyr Ala Ile Leu Arg
50 55 60

Ser Glu Asp Leu Ser Ser Trp Glu Tyr Val Pro Asp His Arg Gly Glu
65 70 75 80

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

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

[0233]

Asp Lys Trp Asp Gly Glu Lys Trp Val Val Asp Thr Glu Ala Gln His
115 120 125

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

Thr Ala Met Asp Ser Ile Ser Leu Ile Gln Leu Lys Leu Arg Ala Gly
145 150 155 160

Arg Lys Leu Thr Gln Ala Glu Thr Thr Gln Leu Asn Ser Val Leu Asp
165 170 175

Tyr Ile Asp Glu Leu Asn Ala Met Asp Leu Thr Thr Ala Pro Asp Leu
180 185 190

Asn Trp Pro Glu Lys Gln Leu Ser Thr Ala Ser
195 200

<210> 95
<211> 175
<212> PRT

<213> 人工序列

<220>
<223> 蓟分子伴侣

<400> 95

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

Gln Tyr Gln Leu Thr Lys Asn Phe Asp Val Ile Trp Leu Trp Ser Glu
20 25 30

Asp Gly Lys Asn Trp Tyr Glu Glu Val Lys Asn Phe Gln Pro Asp Thr
35 40 45

Ile Lys Ile Val Tyr Asp Glu Asn Asn Ile Ile Val Ala Ile Thr Lys
50 55 60

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

Asp Ile Thr Ala Asn Arg Arg Ala Asp Asp Ser Gly Lys Trp Met Phe
85 90 95

[0234]

Lys Asp Gly Ala Val Val Lys Arg Ile Tyr Thr Ala Asp Glu Gln Gln
100 105 110

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

Val Ile Gln Pro Leu Glu Arg Ala Val Arg Leu Asn Met Ala Thr Asp
130 135 140

Glu Glu Arg Thr Arg Leu Glu Ala Trp Glu Arg Tyr Ser Val Leu Val
145 150 155 160

Ser Arg Val Asp Thr Ala Asn Pro Glu Trp Pro Gln Lys Pro Glu
165 170 175

<210> 96
<211> 177
<212> PRT
<213> 人工序列

<220>
<223> 紫罗兰分子伴侣

<400> 96

Met Met His Leu Lys Asn Ile Thr Ala Gly Asn Pro Lys Thr Lys Glu
1 5 10 15

Gln Tyr Gln Leu Thr Lys Gln Phe Asn Ile Lys Trp Leu Tyr Thr Glu
20 25 30

Asp Gly Lys Asn Trp Tyr Glu Glu Gln Lys Asn Phe Gln Pro Asp Thr
35 40 45

Leu Lys Met Val Tyr Asp His Asn Asp Val Ile Ile Cys Ile Glu Lys
50 55 60

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

Asp Ile Thr Ala Asn Arg Arg Ala Asp Ile Ser Gly Lys Trp Met Phe
85 90 95

Lys Asp Gly Val Val Ile Lys Arg Thr Tyr Thr Glu Glu Glu Gln Arg
100 105 110

[0235]

Gln Gln Ala Glu Asn Glu Lys Gln Ser Leu Leu Gln Leu Val Arg Asp
115 120 125

Lys Thr Gln Leu Trp Asp Ser Gln Leu Arg Leu Gly Ile Ile Ser Asp
130 135 140

Glu Asn Lys Gln Lys Leu Thr Glu Trp Met Leu Tyr Ala Gln Lys Val
145 150 155 160

Glu Ser Thr Asp Thr Ser Ser Leu Pro Val Thr Phe Pro Glu Gln Pro
165 170 175

Glu

<210> 97
<211> 4494
<212> DNA
<213> 人工序列

<220>
<223> P1 秃底盘尾丝区域

<400> 97

[0236]

taatcacccc gtccgcaggg cggggtgaca agttacttat cttacaatga ggcttcacaa 60

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attggagaac tgccaaaggc tttcgaactg gcagaactga ccagtcaatt ttgcaccatc 300

aacctcgtcc caacctactc aggcgggata attactgtcc gaatggacct tgatcaaagc 360

cagttgcagg aagggaaaaa ctacccattc aacactctgg ttgttctgga taacgagaac 420

aagccaatcg ccattatttg tgtccaggaa gactcgctgt atgtgggcaa aacatatacc 480

gcagttatgg ccataaacac gactacagca taaggatatg cttgcggaat ctgtgggtaa 540

ctttgtatgt gtccgcagcg cccgccgcag tctcacgccc ggagcgtagc gaccgagtga 600

gctagctatt tgtttatttt tctaaataca ttcaaatatg tatccgctca tgagacaata 660

accctgataa atgcttcaat aatattgaaa aaggaagagt atgagggaag cggtgatcgc 720

cgaagtatcg actcaactat cagaggtagt tggcgtcatc gagcgccatc tcgaaccgac 780

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gaaatcacaa agtacatacc gtttcccaat gatatttaat tcactattaa ggaaatagtt 4440

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<210> 98
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<220>
<223> Rio 尾丝 S 基因

<400> 98
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aataccgcgt cacatattca tgcggctgaa tttgttgcca gaacctatac cgattcatat 420

cagttaggag atggggagct gcttgtttgt acggtgaata tccctgctag tgtatctgcc 480

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tttacaaagt taaataatca ggtgggtgac agtgaaaata ccgcattaac tccttacggc 720

gctaaaaaag aattagaaaa ctatcaaccc aaaggcaatt atcaacccgc tggtaattat 780

gtcactactg cgacatttaa tttagaaatc aataaaaaaa tagataaagc aagtctctca 840

cagcaacttg gtaatgatgt aaataaagta cctagtttag atttggtgac taaagagcta 900

gggaataaac aacctaaagg tgattatgca ttaaaaacat gggttgataa tatttattat 960

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gttaacgtcg cgctaaaagg ggattgctat acaaaatcag aatctgataa taaatattct 1080

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caggttgccc gcattgcggc ggtggcgcgg catatcgcgc cattacagga tgctgttgat 420

ttggacatgg cgaccgagga agaaaaagcg ctgttggcgg actggaaaaa ataccgtgtg 480

atgctgaatc gtctggatat gtcgtcggcc ccggatattg actggccagt ggcgcccagt 540

gcctaa 546

<210> 108
<211> 649
<212> PRT
<213> 人工序列

<220>
<223> Rio 尾丝 (S)

<400> 108

Met Asn Asp Val Thr Val Val Thr Ser Val Thr Tyr Pro Ser Ser Glu
1 5 10 15

Ser Leu Ala Leu Val Ala Asp Val Gln Tyr His Glu Pro Tyr Leu Ser
20 25 30

Ala Ala Leu Asn Arg Lys Phe Arg Gly Ile Val Asp Pro Gly Phe Tyr
35 40 45

Ala Gly Phe Leu Pro Lys Pro Gly Gly Gly Met Asn Leu Leu Ile Thr
50 55 60

Ser Val Asp Gly Asp Lys Thr Ala Gly Ala Ala Ser Val Asp Ile Gly
65 70 75 80

Glu Phe Tyr Gln Val Thr Ile Gln Gln Arg Lys Asp Ile Ser Leu Ala
85 90 95

Leu Ser Ala Gly Lys Lys Tyr Ala Ile Val Leu Lys Gly Arg Tyr Leu
100 105 110

[0249] Leu Gly Glu Asp Thr Tyr Gln Val Asn Thr Ala Ser His Ile His Ala
115 120 125

Ala Glu Phe Val Ala Arg Thr Tyr Thr Asp Ser Tyr Gln Leu Gly Asp
130 135 140

Gly Glu Leu Leu Val Cys Thr Val Asn Ile Pro Ala Ser Val Ser Ala
145 150 155 160

Ile Thr Gln Glu Met Ile Asp Thr Ser Glu Arg Ile Asn Arg Ser Ile
165 170 175

Gly Ile Asp Ile Ser Asp Ser Val Thr Ser Thr Arg Ser Asp Val Ala
180 185 190

Ala Ser Ser Leu Ala Val Lys Lys Ala Tyr Asp Leu Ala Lys Ser Lys
195 200 205

Tyr Thr Ala Gln Asp Ala Thr Thr Thr Val Lys Gly Phe Thr Lys Leu
210 215 220

Asn Asn Gln Val Gly Asp Ser Glu Asn Thr Ala Leu Thr Pro Tyr Gly

225 230 235 240

Ala Lys Lys Glu Leu Glu Asn Tyr Gln Pro Lys Gly Asn Tyr Gln Pro
245 250 255

Ala Gly Asn Tyr Val Thr Thr Ala Thr Phe Asn Leu Glu Ile Asn Lys
260 265 270

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

Lys Val Pro Ser Leu Asp Leu Val Thr Lys Glu Leu Gly Asn Lys Gln
290 295 300

Pro Lys Gly Asp Tyr Ala Leu Lys Thr Trp Val Asp Asn Ile Tyr Tyr
305 310 315 320

Lys Arg Asp Asp Ser Pro Ser Phe Asn Glu Ile Ser Ala Thr Ala Ile
325 330 335

[0250] Arg Val Asn Ser Val Asn Val Ala Leu Lys Gly Asp Cys Tyr Thr Lys
340 345 350

Ser Glu Ser Asp Asn Lys Tyr Ser Pro Lys Leu Pro Phe Val Tyr Ser
355 360 365

Ser Gly Glu Glu Ser Lys Ile Ile Ser Pro Asn Asn Lys Ile Leu Ile
370 375 380

Phe Val Asn Asp Asn Gly Thr Thr Gly Gly Tyr Asp Arg Asp Thr Gln
385 390 395 400

Ala Thr Val Trp Gly Phe Asp Lys Arg Gly Phe Met Thr Arg Gly Thr
405 410 415

Val His Phe Asp Arg Met Ser Gly Val Tyr Ser Gln Ser Gln Val Asp
420 425 430

Ala Lys Leu Lys Glu Cys Leu Asn Leu Lys Thr Ser Ser Lys Gln Phe
435 440 445

Ile Ala Ser Asp Ile Tyr Ala Pro Thr Phe Ile Thr Gly Ser Gln Tyr
450 455 460

Gly Glu Arg Ser Tyr Leu Glu His Lys Ser Asp Glu Leu Thr Ile Thr
465 470 475 480

His Ile Ser Pro Lys Ser Gly Ala Thr Asn Ile Thr Cys Arg Asn Lys
485 490 495

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

Pro Val Gly Ser Pro Ile Pro Trp Ser Leu Ala Thr Ala Pro Ser Gly
515 520 525

Tyr Leu Ile Cys Asn Gly Gln Thr Phe Asn Lys Ser Thr Tyr Pro Lys
530 535 540

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

Phe Ile Arg Gly Leu Asp Ser Gly Arg Gly Ile Asp Ala Gly Arg Ser
565 570 575

[0251] Val Leu Ser Val Gln Lys Gly Asn Ser Leu Leu Ser Ser Asn Ile Phe
580 585 590

Gly Gly Leu Ser Ser Ser Glu Ser Asn Lys Trp His Lys Ala Ile Asn
595 600 605

Tyr Ile Gly Ile Thr Gly Thr Asp Asn Asp Gly Gly Tyr Gly Val His
610 615 620

Gln Gln Ile Glu Gly Ala Asn Gly Asn Glu Thr Arg Pro Arg Asn Ile
625 630 635 640

Ala Phe Leu Tyr Ile Val Arg Ala Ala
645

<210> 109
<211> 581
<212> PRT
<213> 人工序列

<220>
<223> 柠檬尾丝 (S)

<400> 109

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Met Asn Asp Val Thr Val Val Thr Ser Val Thr Tyr Pro Ser Ser Glu
1               5                  10                  15

Ser Leu Ala Leu Val Ala Asp Val Gln Tyr His Glu Pro Tyr Leu Ser
            20                  25                  30

Ala Ala Leu Asn Arg Lys Phe Arg Gly Ile Val Asp Pro Gly Phe Tyr
        35                  40                  45

Ala Gly Phe Leu Pro Lys Pro Gly Gly Gly Met Asn Leu Leu Ile Thr
    50                  55                  60

Ser Val Asp Gly Asp Lys Thr Ala Gly Ala Ala Ser Val Asp Ile Gly
65                  70                  75                  80

Glu Phe Tyr Gln Val Thr Ile Gln Gln Arg Lys Asp Ile Ser Leu Ala
                85                  90                  95

Leu Ser Ala Gly Lys Lys Tyr Ala Ile Val Leu Lys Gly Arg Tyr Leu
            100                 105                 110
```

[0252]

```
Leu Gly Glu Asp Thr Tyr Gln Val Asn Thr Ala Ser His Ile His Ala
        115                 120                 125

Ala Glu Phe Val Ala Arg Thr Tyr Thr Asp Ser Tyr Gln Leu Gly Asp
    130                 135                 140

Gly Glu Leu Leu Val Cys Thr Val Asn Ile Pro Ala Ser Val Ser Ala
145                 150                 155                 160

Ile Thr Gln Glu Met Ile Asp Thr Ser Glu Arg Ile Asn Arg Ser Ile
                165                 170                 175

Gly Ile Asp Ile Ser Asp Ser Val Thr Ser Thr Arg Ser Asp Val Ala
            180                 185                 190

Ala Ser Ser Leu Ala Val Lys Lys Ala Tyr Asp Leu Ala Lys Ser Lys
        195                 200                 205

Tyr Thr Ala Gln Asp Ala Thr Thr Ala Arg Lys Gly Ile Val Gln Leu
    210                 215                 220

Ser Ser Ala Thr Asp Ser Thr Ser Glu Glu Leu Ala Ala Thr Leu Lys
```

225 230 235 240

Ala Val Lys Ile Ala Met Asp Asn Ala Asn Ala Arg Leu Ala Lys Glu
245 250 255

Arg Asn Gly Gly Asp Val Pro Asn Lys Pro Leu Phe Ile Gln Asn Ile
260 265 270

Gly Leu Gln Glu Thr Val Asn Lys Ala Ala Gly Ala Val Gln Arg Ser
275 280 285

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

Asn Gly Ser Ala Ile Ala Val Arg Gly Ile Arg Ala Ile Asn Gly Gly
305 310 315 320

Gln Val Asp Asp Ala Asn Asn Leu Pro Val Asn Ala Val Ser Phe Val
325 330 335

[0253] Tyr Gly Asp Ala Lys Asn Ser Pro Ser Gly Asn Thr Gly Thr Ile Leu
340 345 350

Asp Val Ser Gly Leu Gly Ser Gly Tyr Ser Ile Gln Leu Phe Ala Asn
355 360 365

Tyr Ser Thr Gly Glu Ile Leu Ala Phe Arg Ala Arg Asn Gly Asp Asn
370 375 380

Arg Thr Trp Asn Lys Trp Asn Tyr Val Phe His Thr Gly Asn Lys Pro
385 390 395 400

Thr Ser Thr Asp Val Gly Ala Leu Pro Ile Thr Gly Gly Asp Leu Lys
405 410 415

Gly Gln Leu Ser Phe Ser Phe Ser Gln Pro Arg Asn Gly Ala Asn His
420 425 430

Leu Ile Tyr Asn Gly Asp Asp Asn Gly Val Leu Ala Cys Gly Tyr Gly
435 440 445

Tyr Tyr Gln Asp Arg Phe Asp Ile His Phe Tyr Asp Ile Lys Gly Ala
450 455 460

```
Trp Glu Ser Asn Pro Leu Thr Ile Gly Arg Asn Gly Asn Thr Thr Val
465                 470                 475                 480

Ser Gly Asn Leu Ser Gly Arg Ala Val Tyr Glu Gly Asn Thr Arg Val
                485                 490                 495

Tyr Ser Pro Asn Asn Pro Gln Pro Val Ser Phe Glu Gly Tyr Ala Thr
            500                 505                 510

Gln Ser Trp Val Leu Gln Asn Phe Val Gln Asn Ile Asp Leu Thr Ala
        515                 520                 525

Pro Ala Glu Val Gly Phe Arg Asp Gly Trp Gly Tyr Pro Arg Gly Thr
    530                 535                 540

Asp Gly Ala Ala Met Tyr Asn Phe Asn Met Val Gly Gly Ser Ser Asn
545                 550                 555                 560

Val Gly Asn Phe Ile Ile Arg Tyr Met Arg Lys Gln Val Asn Asn Thr
                565                 570                 575
```

[0254]

```
Trp Tyr Val Ile Asn
            580
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<210> 110
<211> 1069
<212> PRT
<213> 人工序列

<220>
<223> 兰花尾丝 (S)

<400> 110

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Met Asn Asp Val Thr Val Val Thr Ser Val Thr Tyr Pro Ser Ser Glu
1               5                   10                  15

Ser Leu Ala Leu Val Ala Asp Val Gln Tyr His Glu Pro Tyr Leu Ser
            20                  25                  30

Ala Ala Leu Asn Arg Lys Phe Arg Gly Ile Val Asp Pro Gly Phe Tyr
        35                  40                  45

Ala Gly Phe Leu Pro Lys Pro Gly Gly Gly Met Asn Leu Leu Ile Thr
    50                  55                  60
```

Ser Val Asp Gly Asp Lys Thr Ala Gly Ala Ala Ser Val Asp Ile Gly
65 70 75 80

Glu Phe Tyr Gln Val Thr Ile Gln Gln Arg Lys Asp Ile Ser Leu Ala
85 90 95

Leu Ser Ala Gly Lys Lys Tyr Ala Ile Val Leu Lys Gly Arg Tyr Leu
100 105 110

Leu Gly Glu Asp Thr Tyr Gln Val Asn Thr Ala Ser His Ile His Ala
115 120 125

Ala Glu Phe Val Ala Arg Thr Tyr Thr Asp Ser Tyr Gln Leu Gly Asp
130 135 140

Gly Glu Leu Leu Val Cys Thr Val Asn Ile Pro Ala Ser Val Ser Ala
145 150 155 160

Ile Thr Gln Glu Met Ile Asp Thr Ser Glu Arg Ile Asn Arg Ser Ile
165 170 175

[0255] Gly Ile Asp Ile Ser Asp Ser Val Thr Ser Thr Arg Ser Asp Val Ala
180 185 190

Ala Ser Ser Leu Ala Val Lys Lys Ala Tyr Asp Leu Ala Lys Ser Lys
195 200 205

Tyr Thr Ala Gln Asp Ala Ser Thr Thr Gln Lys Gly Leu Val Gln Leu
210 215 220

Ser Ser Ala Thr Asn Ser Asp Ser Glu Thr Met Ala Ala Thr Pro Lys
225 230 235 240

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

Ser Pro Ser Leu Thr Gly Thr Pro Thr Ala Pro Thr Ala Ala Gln Gly
260 265 270

Thr Asn Ser Thr Gln Ile Ala Asn Thr Ala Phe Val Lys Ala Ala Ile
275 280 285

Thr Ala Leu Ile Asn Gly Ala Pro Gly Thr Leu Asp Thr Leu Lys Glu

290 295 300

Ile Ala Ala Ala Ile Asn Asn Asp Pro Asn Tyr Ser Thr Thr Ile Asn
305 310 315 320

Asn Ala Leu Ala Leu Lys Ala Pro Leu Ala Ser Pro Ala Leu Thr Gly
325 330 335

Val Pro Thr Ala Pro Thr Ala Ala Gln Gly Thr Asn Asn Thr Gln Ile
340 345 350

Ala Thr Thr Ala Tyr Val Arg Ala Ala Ile Ser Ala Leu Val Gly Ser
355 360 365

Ser Pro Glu Ala Leu Asp Thr Leu Tyr Glu Leu Ala Ala Ala Leu Gly
370 375 380

Asn Asp Pro Asn Phe Ala Thr Thr Met Thr Asn Ala Leu Ala Gly Lys
385 390 395 400

Gln Pro Leu Asp Ala Thr Leu Thr Ala Leu Ala Gly Leu Ala Thr Gly
[0256] 405 410 415

Ala Asn Lys Leu Pro Tyr Phe Thr Gly Thr Asp Thr Val Ser Gln Thr
420 425 430

Asp Leu Thr Ser Val Gly Arg Asp Ile Leu Ala Lys Thr Ser Ile Leu
435 440 445

Ala Val Ile Gln Tyr Leu Gly Leu Arg Glu Leu Gly Thr Ser Gly Glu
450 455 460

Lys Ile Pro Leu Leu Ser Thr Ala Asn Thr Trp Ser Ala Arg Gln Thr
465 470 475 480

Phe Asn Gly Gly Ile Thr Gly Ala Leu Thr Gly Asn Ala Asp Thr Ala
485 490 495

Thr Lys Leu Lys Thr Ala Ala Arg Ser Ile Gly Gly Val Ala Phe Asp
500 505 510

Gly Ser Ala Asn Ile Asn Leu Pro Gly Val Asn Thr Thr Gly Asn Gln
515 520 525

Asn Thr Thr Gly Asn Ala Ala Thr Ala Thr Lys Leu Ala Thr Ala Arg
530 535 540

Asn Ile Asn Gly Val Lys Phe Asp Gly Ser Val Asp Ile Ser Ile Pro
545 550 555 560

Thr Ile Thr Ser Arg Gly Arg Val Thr Ala Leu Thr Gly Thr Thr Gln
565 570 575

Gly Ala Ala Thr Gly Leu Gln Met Tyr Glu Ala Tyr Asn Asn Gly Tyr
580 585 590

Pro Ser Ala Tyr Gly Asn Val Leu His Leu Lys Gly Ala Thr Ala Val
595 600 605

Gly Glu Gly Glu Leu Phe Ile Gly Trp Ser Gly Thr Ser Gly Ala His
610 615 620

Ala Pro Val His Val Arg Ser Arg Arg Asp Thr Asp Thr Ala Ser Trp
625 630 635 640

[0257] Ser Glu Trp Ala Gln Val Tyr Thr Ser Lys Asp Ser Ile Pro Gly Val
645 650 655

Asn Thr Thr Gly Asn Gln Asn Thr Thr Gly Asn Ala Ala Ser Ala Thr
660 665 670

Lys Leu Gln Thr Ala Arg Thr Ile Gly Gly Val Ser Phe Asn Gly Thr
675 680 685

Ala Asn Ile Asp Leu Pro Gly Val Asn Lys Thr Gly Asn Gln Asn Thr
690 695 700

Thr Gly Asn Ala Ala Thr Ala Thr Lys Leu Gln Thr Ala Arg Thr Ile
705 710 715 720

Asn Gly Val Ser Phe Asp Gly Ser Lys Asn Ile Glu Leu Thr Ala Glu
725 730 735

Asp Leu Asn Leu Gln Glu Phe Ile Asn Lys Ala Asn Asn Ala Val Gln
740 745 750

Arg Ser Gly Asp Thr Leu Ser Gly Gly Leu Thr Phe Lys Asn Asp Ser

755 760 765

Ile Leu Ala Trp Ile Arg Asn Thr Asp Trp Ala Lys Ile Gly Phe Lys
770 775 780

Asn Asp Ala Asp Gly Asp Thr Asp Ser Tyr Met Trp Phe Glu Thr Gly
785 790 795 800

Asp Asn Gly Asn Glu Tyr Phe Lys Trp Arg Ser Lys Gln Ser Thr Thr
805 810 815

Thr Lys Asp Leu Met Asn Leu Lys Trp Asp Ala Leu Tyr Val Leu Val
820 825 830

Asn Ala Ile Val Asn Gly Glu Val Ile Ser Lys Ser Ala Asn Gly Leu
835 840 845

Arg Ile Ala Tyr Gly Asn Tyr Gly Phe Phe Ile Arg Asn Asp Gly Ser
850 855 860

[0258] Asp Thr Tyr Phe Met Leu Thr Asn Ser Gly Asp Asn Met Gly Thr Tyr
865 870 875 880

Asn Gly Leu Arg Pro Leu Trp Ile Asn Asn Ala Thr Gly Ala Val Ser
885 890 895

Met Gly Arg Gly Leu Asn Val Ser Gly Glu Thr Leu Ser Asp Arg Phe
900 905 910

Ala Ile Asn Ser Ser Thr Gly Met Trp Ile Asn Met Arg Asp Gln Asn
915 920 925

Val Ile Met Gly Arg Asn Ala Val Ser Thr Asp Gly Ala Gln Ala Leu
930 935 940

Leu Arg Gln Asp His Ala Asp Arg Lys Phe Met Ile Gly Gly Leu Gly
945 950 955 960

Asn Lys Gln Phe Gly Ile Tyr Met Ile Asn Asn Ser Arg Thr Ala Asn
965 970 975

Gly Thr Asp Gly Gln Ala Tyr Met Asp Asn Asn Gly Asn Trp Leu Cys
980 985 990

Gly Ala Gln Ile Ile Pro Gly Asn Tyr Gly Asn Phe Asp Ser Arg Tyr
995 1000 1005

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

Arg Gly Gly Arg Tyr Glu Lys Ala Gly His Ala Ile Thr Gly Leu
1025 1030 1035

Arg Ile Ile Gly Glu Val Asp Gly Asp Asp Glu Ala Ile Phe Arg
1040 1045 1050

Pro Ile Gln Lys Tyr Ile Asn Gly Thr Trp Tyr Asn Val Ala Gln
1055 1060 1065

Val

[0259]

<210> 111
<211> 671
<212> PRT
<213> 人工序列

<220>
<223> 金尾丝 (S)

<400> 111

Met Asn Asp Val Thr Val Val Thr Ser Val Thr Tyr Pro Ser Ser Glu
1 5 10 15

Ser Leu Ala Leu Val Ala Asp Val Gln Tyr His Glu Pro Tyr Leu Ser
20 25 30

Ala Ala Leu Asn Arg Lys Phe Arg Gly Ile Val Asp Pro Gly Phe Tyr
35 40 45

Ala Gly Phe Leu Pro Lys Pro Gly Gly Gly Met Asn Leu Leu Ile Thr
50 55 60

Ser Val Asp Gly Asp Lys Thr Ala Gly Ala Ala Ser Val Asp Ile Gly
65 70 75 80

Glu Phe Tyr Gln Val Thr Ile Gln Gln Arg Lys Asp Ile Ser Leu Ala
85 90 95

Leu Ser Ala Gly Lys Lys Tyr Ala Ile Val Leu Lys Gly Arg Tyr Leu
100 105 110

Leu Gly Glu Asp Thr Tyr Gln Val Asn Thr Ala Ser His Ile His Ala
115 120 125

Ala Glu Phe Val Ala Arg Thr Tyr Thr Asp Ser Tyr Gln Leu Gly Asp
130 135 140

Gly Glu Leu Leu Val Cys Thr Val Asn Ile Pro Ala Ser Val Ser Ala
145 150 155 160

Ile Thr Gln Glu Met Ile Asp Thr Ser Glu Arg Ile Asn Arg Ser Ile
165 170 175

Gly Ile Asp Ile Ser Asp Ser Val Thr Ser Thr Arg Ser Asp Val Ala
180 185 190

Ala Ser Ser Leu Ala Val Lys Lys Ala Tyr Asp Leu Ala Lys Ser Lys
195 200 205

[0260] Tyr Thr Ala Gln Asp Ala Thr Leu Leu Ala Lys Gly Phe Thr Gln Leu
210 215 220

Ser Asn Asp Ser Asn Ser Gly Ser Glu Thr Leu Ala Ala Thr Pro Lys
225 230 235 240

Ala Val Lys Ala Val Asn Asp Ala Ser Leu Lys Ile Ala Ala Asn Leu
245 250 255

Lys Asp Leu Pro Asn Lys Ser Val Ala Arg Gly Asn Leu Glu Leu Gly
260 265 270

Thr Ala Ala Thr Arg Asn Val Gly Ala Gln Lys Thr Asn Leu Met Glu
275 280 285

Val Gly Ala Phe Gly Leu Gly Gly Gly Pro Ile His Arg Glu Asp Ala
290 295 300

Leu Ser Asn Arg Gly Glu Ile Tyr Arg Val Thr Gly Ala Ser Lys Asn
305 310 315 320

Ala Pro Gly Gly Gly Val Tyr Gly Val Leu Asn Leu Pro Cys Asp Gly

325 330 335

Gly Pro Ser Ser Gly Tyr Leu Ala Ile Gln Pro Asn Gly Ser Ser Tyr
340 345 350

Ile Gly Thr Ser Thr Thr Pro Asp Lys Pro Leu Asn Trp Tyr Arg Ile
355 360 365

Tyr Thr Thr Gly Phe Lys Pro Thr Ala Thr Asp Val Asp Ala Tyr Ser
370 375 380

Lys Ala Glu Ala Asp Gly Lys Phe Val Lys Gln Ser Gly Asp Thr Ile
385 390 395 400

Thr Gly Ala Leu Thr Val Asn Gly Ala Ile Glu Ser Lys Ser Gly Leu
405 410 415

Thr Thr Pro Ser Leu Ala Val Asn Gly Ser Val Thr Ile Ala Gly Ala
420 425 430

[0261] Leu Thr Thr Lys Ala Gly Val Glu Leu Phe Gly Thr Thr Pro Tyr Leu
435 440 445

Asp Phe His Tyr Gly Asn Ser Asn Gly Asp Phe Asp Val Arg Leu Ile
450 455 460

Asn Asp Asn Lys Gly Thr Leu Ala Phe His Gly Asn Glu Tyr Tyr Val
465 470 475 480

Asn Gly Lys Leu Ser Ala Thr Gly Asp Ala Trp Ile Gly Gly Lys Ala
485 490 495

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

Gln Gly Asn Leu Thr His Pro Asp Gly Asn Arg Gln Thr Asn Gly Met
515 520 525

Arg Leu Gln Gly Gln Gly Asn Leu Leu Val Asp Leu Tyr His Tyr Glu
530 535 540

Lys Val Gly Ser His His Glu Phe Gly Ile His Val Ala Asn Gly Gly
545 550 555 560

Ala Asp Gly Trp Phe Ser Phe Arg Asn Asn Gly Glu Leu Arg Ala Asn
565 570 575

Gly Thr Leu Phe Ala Ala Gly Ala Ala Tyr Gln Thr Asp Gly Asn Ile
580 585 590

Asn Gly Gly Ile Trp Gly Gly Tyr Leu Ser Asn Tyr Leu Asn His Asn
595 600 605

Phe Val Arg Asp Val Arg Leu Gly Asn Val Glu Ser Ile Ala Thr Trp
610 615 620

Arg Gly Pro Gly Tyr Ser Asp Ser Ala Gly Tyr Val Leu Thr Gly Ala
625 630 635 640

Ala Asn Asn Asn Val Asp Glu Tyr Ile Asp Val Ile Phe Arg Arg Pro
645 650 655

Leu Gln Lys His Ile Gly Gly Asn Trp Val Thr Val Trp Ser Val
660 665 670

[0262]

<210> 112
<211> 919
<212> PRT
<213> 人工序列

<220>
<223> Bluetiful 尾丝 (S)

<400> 112

Met Asn Asp Val Thr Val Val Thr Ser Val Thr Tyr Pro Ser Ser Glu
1 5 10 15

Ser Leu Ala Leu Val Ala Asp Val Gln Tyr His Glu Pro Tyr Leu Ser
20 25 30

Ala Ala Leu Asn Arg Lys Phe Arg Gly Ile Val Asp Pro Gly Phe Tyr
35 40 45

Ala Gly Phe Leu Pro Lys Pro Gly Gly Gly Met Asn Leu Leu Ile Thr
50 55 60

Ser Val Asp Gly Asp Lys Thr Ala Gly Ala Ala Ser Val Asp Ile Gly
65 70 75 80

Glu Phe Tyr Gln Val Thr Ile Gln Gln Arg Lys Asp Ile Ser Leu Ala
85 90 95

Leu Ser Ala Gly Lys Lys Tyr Ala Ile Val Leu Lys Gly Arg Tyr Leu
100 105 110

Leu Gly Glu Asp Thr Tyr Gln Val Asn Thr Ala Ser His Ile His Ala
115 120 125

Ala Glu Phe Val Ala Arg Thr Tyr Thr Asp Ser Tyr Gln Leu Gly Asp
130 135 140

Gly Glu Leu Leu Val Cys Thr Val Asn Ile Pro Ala Ser Val Ser Ala
145 150 155 160

Ile Thr Gln Glu Met Ile Asp Thr Ser Glu Arg Ile Asn Arg Ser Ile
165 170 175

Gly Ile Asp Ile Ser Asp Ser Val Thr Ser Thr Arg Ser Asp Val Ala
180 185 190

[0263] Ala Ser Ser Leu Ala Val Lys Lys Ala Tyr Asp Leu Ala Lys Ser Lys
195 200 205

Tyr Thr Ala Gln Asp Ala Ser Thr Thr Ala Lys Gly Leu Val Gln Leu
210 215 220

Ser Ser Ala Thr Thr Ser Thr Asp Glu Thr Lys Ala Ser Thr Pro Lys
225 230 235 240

Ala Leu Lys Thr Val Ser Asp Ala Ser Met Lys Lys Ala Ala Asn Leu
245 250 255

Ser Asp Val Ala Asp Lys Ala Ala Ala Arg Gly Asn Leu Ala Leu Gly
260 265 270

Thr Ala Ala Thr Lys Asn Val Gly Val Asp Gly Gly Gln Leu Met Glu
275 280 285

Val Gly Ala Phe Gly Leu Gly Ser Gly Ser Arg His Arg Glu Asp Ala
290 295 300

Tyr Cys Asn Gln Gly Glu Ile Tyr Arg Val Asn Gly Ser Ser Lys Asn

305 310 315 320

Ala Pro Gly Gly Asp Val Tyr Gly Val Leu Ser Leu Pro Cys Asp Gly
325 330 335

Gly Pro Ser Gly Ala Tyr Leu Ala Val Gln Asn Ser Gly Asn Ala Phe
340 345 350

Phe Gly Arg Ser Asn Ile Ala Glu Asn Gly Val Thr Trp Phe Gln Ala
355 360 365

Tyr Thr Thr Lys Phe Lys Pro Thr Ala Ala Asp Val Gly Ala Trp Ser
370 375 380

Lys Ala Glu Ala Asp Gly Arg Phe Leu Met Leu Ser Gly Gly Thr Val
385 390 395 400

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

Leu Asn Ile Glu Gly Asn Gln His Thr Pro Leu Val Met Ser Arg Leu
[0264] 420 425 430

Ser Ala Gln Gly Asn Leu Ser Ile Gly Phe Gln Val Ala Gly Lys Ala
435 440 445

Leu Met Arg Leu Gly Phe Gly Ala Asp Asp Glu Leu His Trp Gly Thr
450 455 460

Glu Ala Asn Gln Ala Ser Asn Pro Arg Ile Tyr Thr Thr Ala Lys Pro
465 470 475 480

Pro Thr Ala Gln Glu Thr Gly Ala Leu Thr Asp Ala Gln Ala Val Lys
485 490 495

Lys Tyr Ala Leu Arg Ser Ile Lys Val Asn Gly Lys Pro Leu Ser Gly
500 505 510

Asp Val Asn Leu Leu Ala Gly Asp Val Asn Ala Trp Asn Lys Thr Glu
515 520 525

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

Leu Thr Leu Pro Arg Ile Val Phe Pro Asn Glu Asn Thr Ala Asn Ala
545 550 555 560

Asp Asp Asp Leu Asn Arg Glu Asn Gly Phe Thr Val Glu Ser Leu Val
565 570 575

Ala Thr Thr Asn Lys Gly Tyr Pro Val Pro Gly Gly Met Gly Val Leu
580 585 590

Phe Thr Gly Lys Val Asn Glu Phe Arg Asn Val Gln Phe Ala Val Gly
595 600 605

Ser Gly Asp Met Ala Phe Tyr Leu Arg Ser Met Arg Lys Asp Asn Ser
610 615 620

Ala Ser Leu Arg Trp Ala Arg Val Tyr Thr Thr Asp Tyr Lys Pro Thr
625 630 635 640

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

[0265] Ala Leu Arg Ser Ile Lys Val Asn Gly Lys Pro Leu Ser Ala Asp Val
660 665 670

Asn Leu Leu Ala Gly Asp Val Asn Ala Trp Asn Lys Thr Glu Ala Asp
675 680 685

Gly Arg Tyr Leu Ala Lys Thr Gly Gly Asn Ile Thr Gly Gly Val Ser
690 695 700

Ser Ser Ser Trp Val Ser Ala Ala Ala Leu Thr Ser Asp Tyr His Gly
705 710 715 720

Thr Gly Asp Asn Thr Asn Lys Ala Pro Glu Gly Ala Gly Ala Tyr Ser
725 730 735

Asn Gln Leu Ala Thr Arg Ala Pro Phe Tyr Gln Thr Asp Phe Gln Trp
740 745 750

Glu Ala Asn Ser Gly Ala Ile Tyr Val Pro Leu Val Lys Gly Lys Ser
755 760 765

Thr Arg Lys Gly Lys Gly Trp Pro Thr Ala Val Ser Tyr Gly Tyr Leu

770 775 780

Met Pro Gly Glu Asn Met His Ala His Pro Val Ile His Ala Leu Gly
785 790 795 800

Asp Gly Val Glu Ser Ile Trp Gln Phe Asn Thr Gln Thr Gly Gly Ile
805 810 815

Ile Ser Gly Lys Met Gly Glu Phe Ala Ser Gln Ala Trp Val Asn Asn
820 825 830

Gly Leu Asn Gly Arg Val Asp Trp Pro Ser Phe Asn Gln His Val Gly
835 840 845

Ala Arg Ala Thr Ile Asp Trp Val Asn Gln Asn Phe Ile Gln Asn Val
850 855 860

Arg Tyr Ser Ala Glu Met His Val Gly Ala Thr Gly Ile Tyr Thr Tyr
865 870 875 880

His Asp Asn Thr Val Leu Thr Gly Phe Asn Asn Lys Asp Gly Asp Tyr
885 890 895

[0266]

Ser Ala Glu Glu Leu Phe Trp Ser Tyr Ile Gln Ile Tyr Lys Asn Gly
900 905 910

Gln Trp Ile Thr Val Gly Arg
915

<210> 113
<211> 206
<212> PRT
<213> 人工序列

<220>
<223> Rio 分子伴侣 (U)

<400> 113

Met Ser Lys Tyr Ser Leu Asp Ile Gln Lys Gly Lys Ile Gly Asp Asn
1 5 10 15

Gly Leu Ala Glu Ile Ala Gly Trp Val Lys Cys Tyr Leu Ala His Pro
20 25 30

Ile Thr His Glu Tyr Met Gly Ala Thr Met Glu Asn Val Met Phe Asp

35 40 45

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

Lys Glu Asn Gln Ala Val Arg Arg Arg Glu Asp Gly Ser Ala Trp Glu
65 70 75 80

Ile Val Asp Asp Cys Arg Gly Leu Thr Ala Tyr Asn Thr Gln Thr Lys
85 90 95

Gln Pro Ile Ile Ile Asp Phe Met Gly Pro Leu Pro Glu Ser Leu Thr
100 105 110

Leu Leu Lys Pro Asn Ser Glu Phe Asp Lys Trp Asp Gly Lys Asn Trp
115 120 125

Ile Val Asp Thr Glu Ala Gln Lys Ala Ala Leu Ile Thr Gln Ile Lys
130 135 140

Gln Glu Lys Ser Arg Arg Leu Asp Glu Ala Asp Asn Ile Ile Thr Tyr
145 150 155 160

[0267]

Leu Gln Glu Ala Val Asp Val Asp Leu Ala Thr Glu Glu Glu Ala Thr
165 170 175

Ala Leu Gln Lys Trp Lys Lys Tyr Arg Val Leu Leu Asn Arg Val Asp
180 185 190

Ile Ser Thr Ala Pro Asp Ile Glu Trp Pro Glu Lys Pro Gln
195 200 205

<210> 114
<211> 177
<212> PRT
<213> 人工序列

<220>
<223> 柠檬分子伴侣 (U)

<400> 114

Met Gln Arg Phe Gly Lys Phe Thr Pro Tyr Thr Pro Asp Thr Thr Asp
1 5 10 15

Arg Pro Arg Ile Ile Asp Gly Gln Asn Val Met Phe Leu Gln Asp Asp

20 25 30

Lys Gly Asn Asp Trp Tyr Asp Val Ile Glu Leu Phe Asp Glu Ser Lys
35 40 45

Thr Leu Lys Ile Gly Tyr Asp Asp Asp Gly Arg Val Arg Thr Phe Thr
50 55 60

Thr Asn Ile His Ala Leu Phe Pro Val Asn Leu Ser Val Val Glu Leu
65 70 75 80

Pro Ala Thr Lys Ala Asn Leu Arg Val Thr Leu Gly Asp Asp Trp Phe
85 90 95

Tyr Lys Asp Gly Lys Leu Gln Gln Ile Arg Asn Tyr Leu Ala Asp Ala
100 105 110

Glu Ala Glu Arg Gly Asn Arg Met Ala Glu Val Thr Thr Arg Ile Asp
115 120 125

Trp Leu Glu Asp Ala Gln Lys Asp Gly Asp Ile Ser Ser Tyr Glu Glu
130 135 140

[0268]

Thr Glu Leu Ala Thr Leu Arg Ala Tyr Arg Thr Ala Leu Arg Arg Leu
145 150 155 160

Asp Leu Ser Thr Ala Pro Asp Ile Asn Trp Pro Glu Val Pro Asp Val
165 170 175

Ala

<210> 115
<211> 175
<212> PRT
<213> 人工序列

<220>
<223> 兰花分子伴侣 (U)

<400> 115

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

Gln Tyr Gln Leu Thr Lys Asn Phe Asp Val Ile Trp Leu Trp Ser Glu

20 25 30

Asp Gly Lys Asn Trp Tyr Glu Glu Val Asn Asn Phe Gln Asp Asp Thr
35 40 45

Ile Lys Ile Val Tyr Asp Glu Asn Asn Ile Ile Val Ala Ile Thr Lys
50 55 60

Asp Ala Ser Thr Leu Asn Pro Glu Gly Phe Ser Val Val Glu Ile Pro
65 70 75 80

Asp Ile Thr Ala Asn Arg Arg Ala Asp Asp Ser Gly Lys Trp Met Phe
85 90 95

Lys Asp Gly Ser Val Val Lys Arg Ile Tyr Thr Ala Asp Glu Gln Gln
100 105 110

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

Val Ile Gln Pro Leu Glu Arg Ala Val Arg Leu Asn Met Ala Thr Asp
130 135 140

[0269]

Glu Glu Arg Thr Arg Leu Glu Ala Trp Glu Arg Tyr Ser Val Leu Val
145 150 155 160

Ser Arg Val Asp Thr Ala Asn Pro Glu Trp Pro Gln Lys Pro Glu
165 170 175

<210> 116
<211> 185
<212> PRT
<213> 人工序列

<220>
<223> 金分子伴侣 (U)

<400> 116

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

Glu Gln Lys Gln Leu Ala Ala Ser His Gly Val Leu Phe Leu Lys Ser
20 25 30

Asp Ala Gly Glu Asp Trp Tyr Glu Cys Gln Lys Ser Phe Arg Pro Glu

35 40 45

Thr Val Lys Leu Met Tyr Asp Lys Asp Gly Ile Ile Arg Ser Ile Thr
50 55 60

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

Glu Asn Met Ser Val Ala Glu Val Glu Asn Leu Pro Glu Gly Ala Asp
85 90 95

Ile Asn Gly Arg Trp Ile Phe Asp Gly Glu Asn Ile Ile Pro Arg Ser
100 105 110

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

Leu Ile Lys Gln Ser Ser Leu Gln Ile Glu Thr Leu Asn Asp Ala Thr
130 135 140

Asp Leu Gly Met Ala Ser Glu Glu Glu Leu Arg Leu Leu Thr Arg Trp
145 150 155 160

[0270]

Lys Thr Tyr Arg Val Leu Leu Asn Arg Val Asp Pro Glu Ala Ala Pro
165 170 175

Asp Ile Asp Trp Pro Gln Pro Pro Gln
180 185

<210> 117
<211> 181
<212> PRT
<213> 人工序列

<220>
<223> Bluetiful 分子伴侣 (U)

<400> 117

Val Lys Asn Ile Lys Asn Phe Gln Leu Gly Glu Pro Lys Thr Pro Glu
1 5 10 15

Gln Leu Lys Leu Arg Asn Gln His Asn Ala Met Phe Leu Phe Ser Asp
20 25 30

Asp Gly Lys Glu Trp Tyr His Cys Gln Lys Asp Phe Ala Ala Asp Thr

35 40 45

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

Asn Asn Asp Ile Ser Thr Leu Trp Pro Val Gly Leu Ser Val Ala Glu
65 70 75 80

Val Ala Asn Thr Thr Ala Asn Arg Arg Ala Asp Ile Ser Gly Gly Trp
85 90 95

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

[0271]

Tyr Gln Glu Gln Ala Lys Lys Glu Gln Val Ala Arg Ile Ala Ala Val
115 120 125

Ala Arg His Ile Ala Pro Leu Gln Asp Ala Val Asp Leu Asp Met Ala
130 135 140

Thr Glu Glu Glu Lys Ala Leu Leu Ala Asp Trp Lys Lys Tyr Arg Val
145 150 155 160

Met Leu Asn Arg Leu Asp Met Ser Ser Ala Pro Asp Ile Asp Trp Pro
165 170 175

Val Ala Pro Ser Ala
180

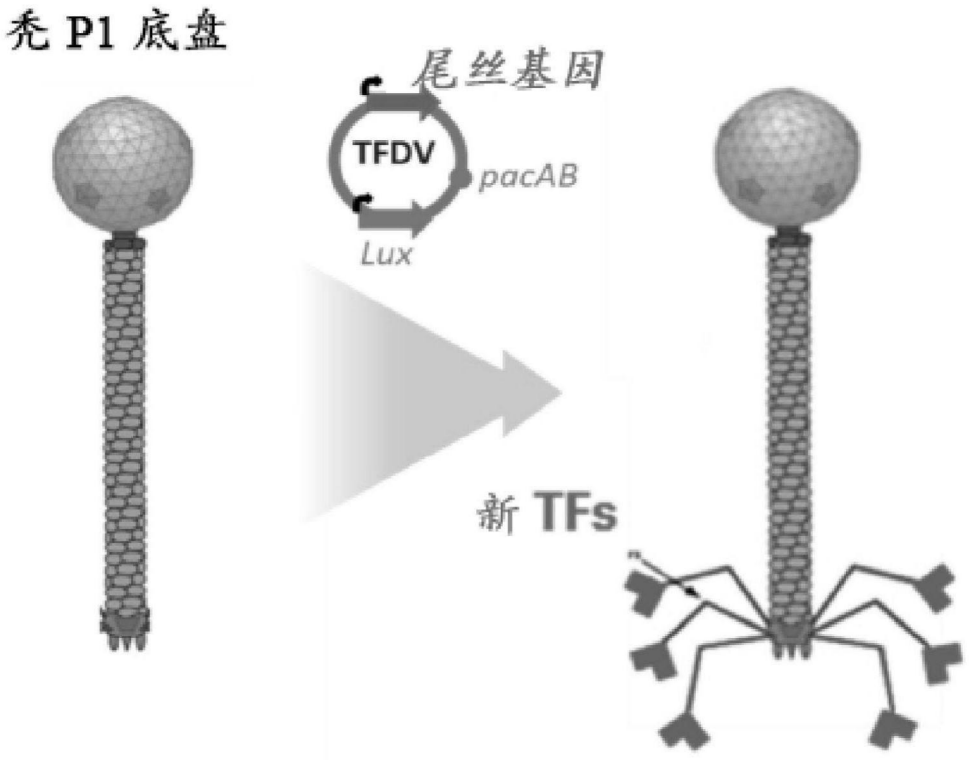

图1

图2

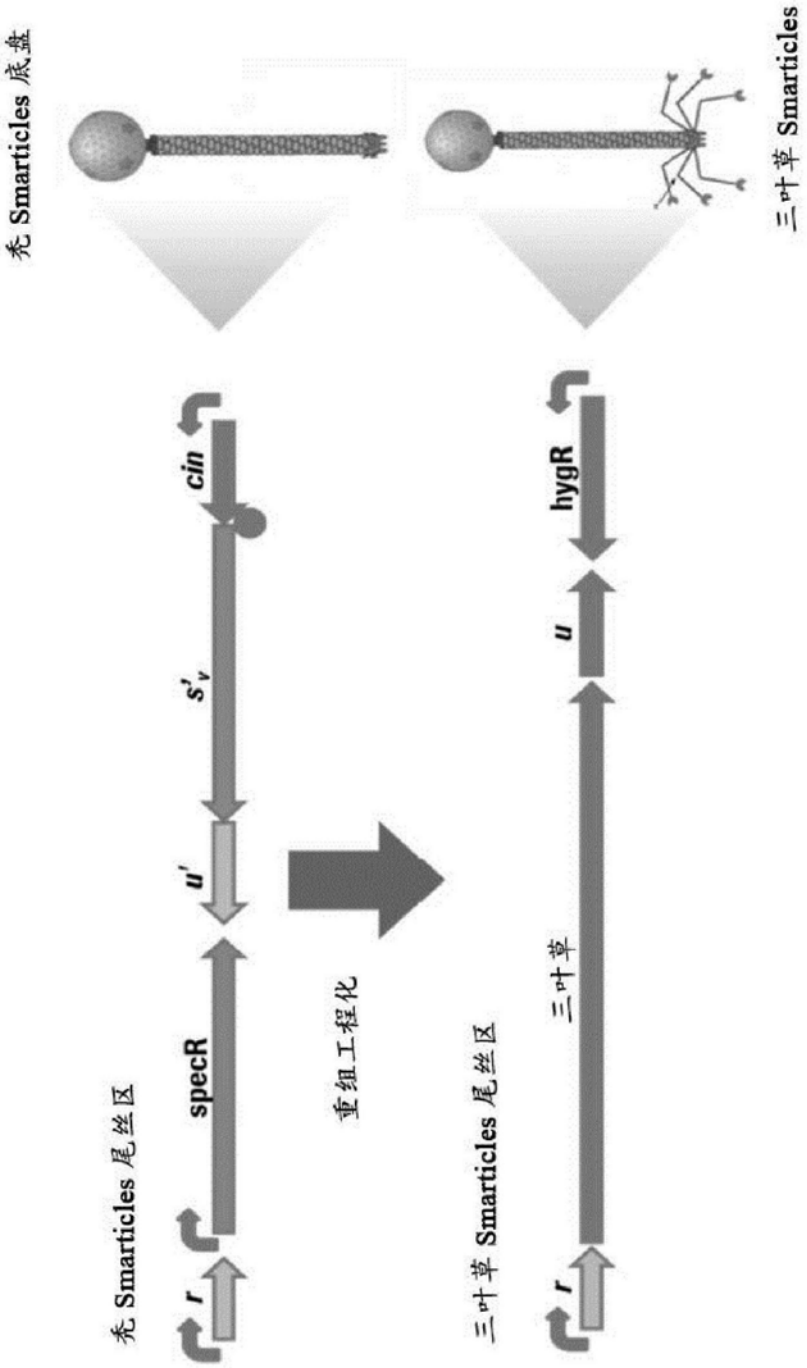
秃 Smarticles 底盘
三叶草 Smarticles
cin
u'
s'_v
specR
r
秃 Smarticles 尾丝区
重组工程化
三叶草 Smarticles 尾丝区
三叶草
u
hygR
r

图3

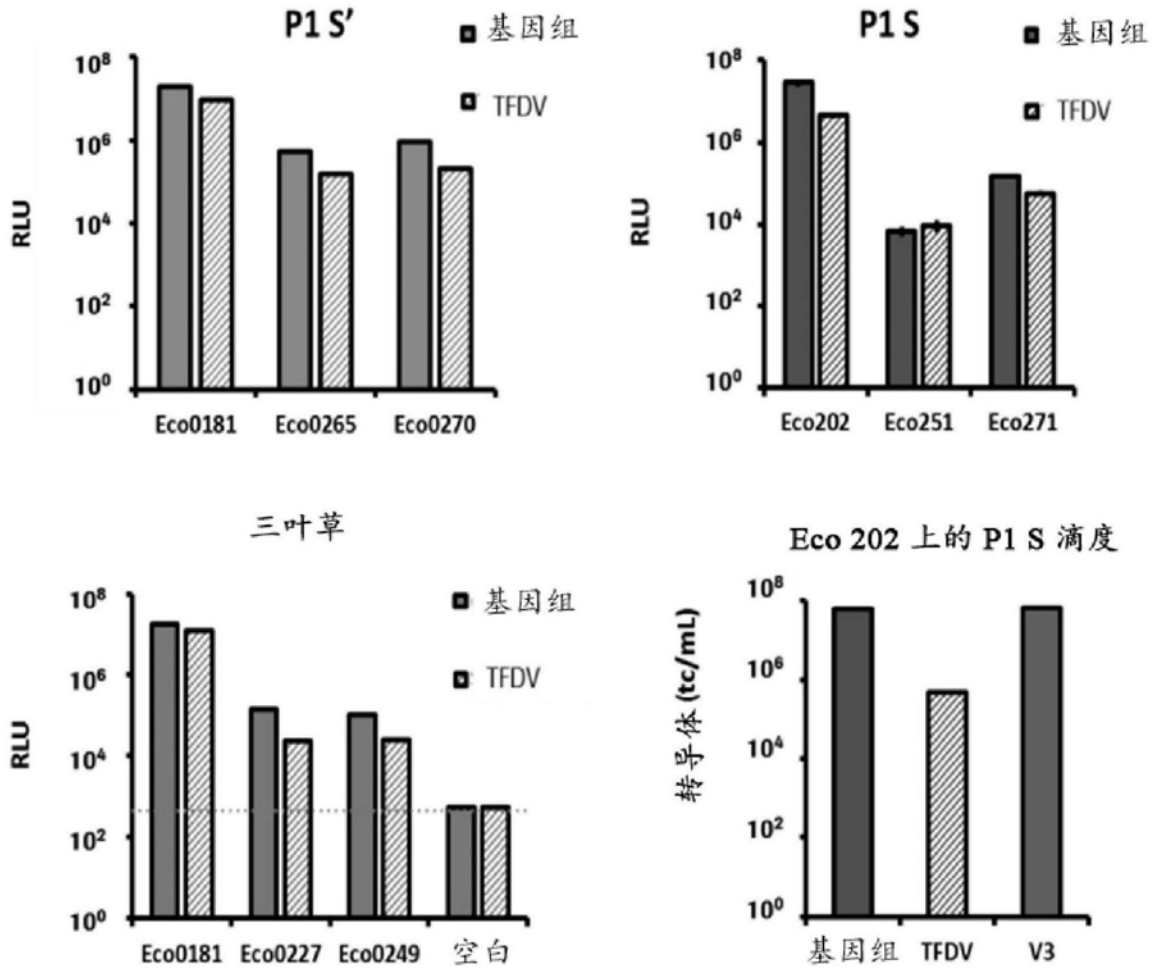
P1 S'
基因组
TFDV
RLU
10^8
10^6
10^4
10^2
10^0
Eco0181
Eco0265
Eco0270
P1 S
基因组
TFDV
RLU
10^8
10^6
10^4
10^2
10^0
Eco202
Eco251
Eco271
三叶草
基因组
TFDV
RLU
10^8
10^6
10^4
10^2
10^0
Eco0181
Eco0227
Eco0249
空白
Eco 202 上的 P1 S 滴度
转导体 (tc/mL)
10^8
10^6
10^4
10^2
10^0
基因组
TFDV
V3

图4

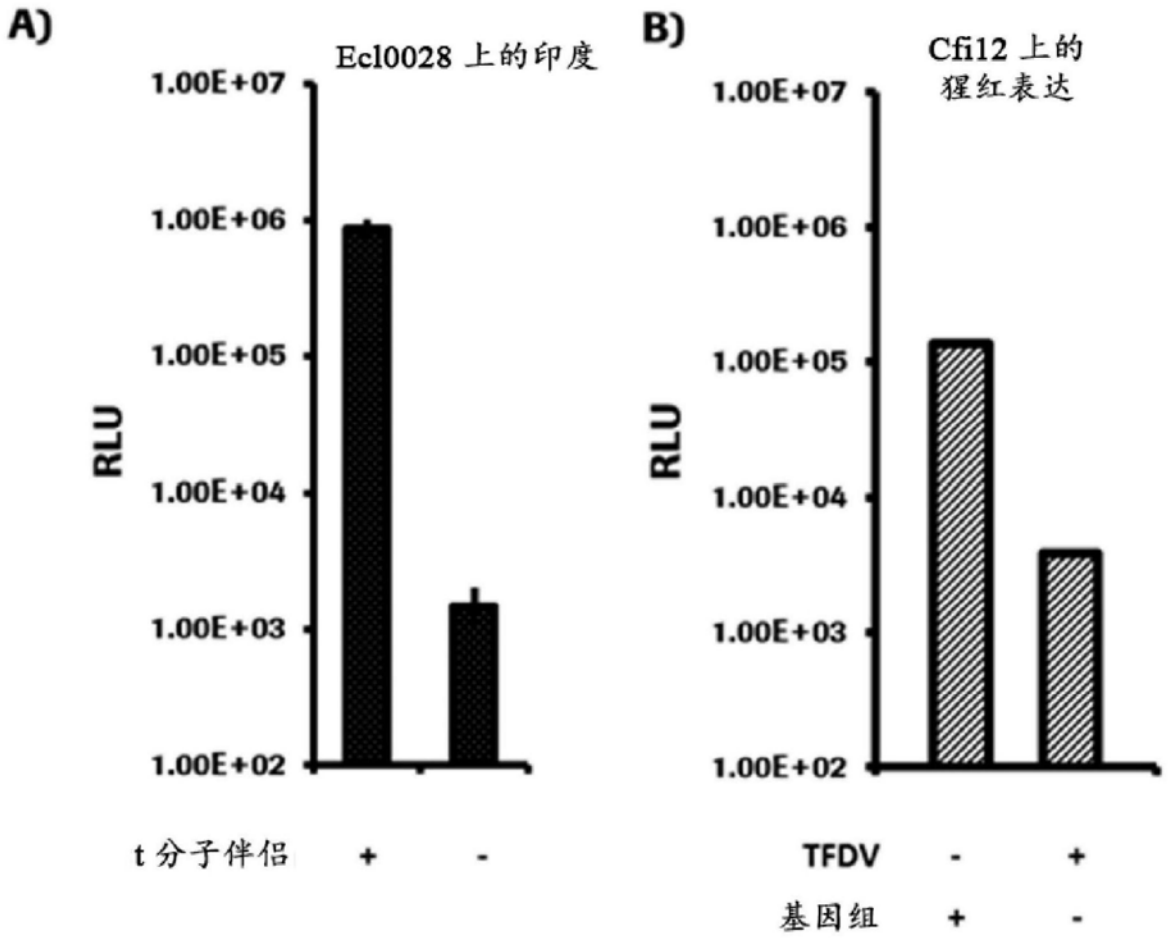
A)
Ecl0028 上的印度
1.00E+07
1.00E+06
1.00E+05
1.00E+04
1.00E+03
1.00E+02
RLU
t 分子伴侣 + -
B)
Cfi12 上的
猩红表达
1.00E+07
1.00E+06
1.00E+05
1.00E+04
1.00E+03
1.00E+02
RLU
TFDV - +
基因组 + -

图5

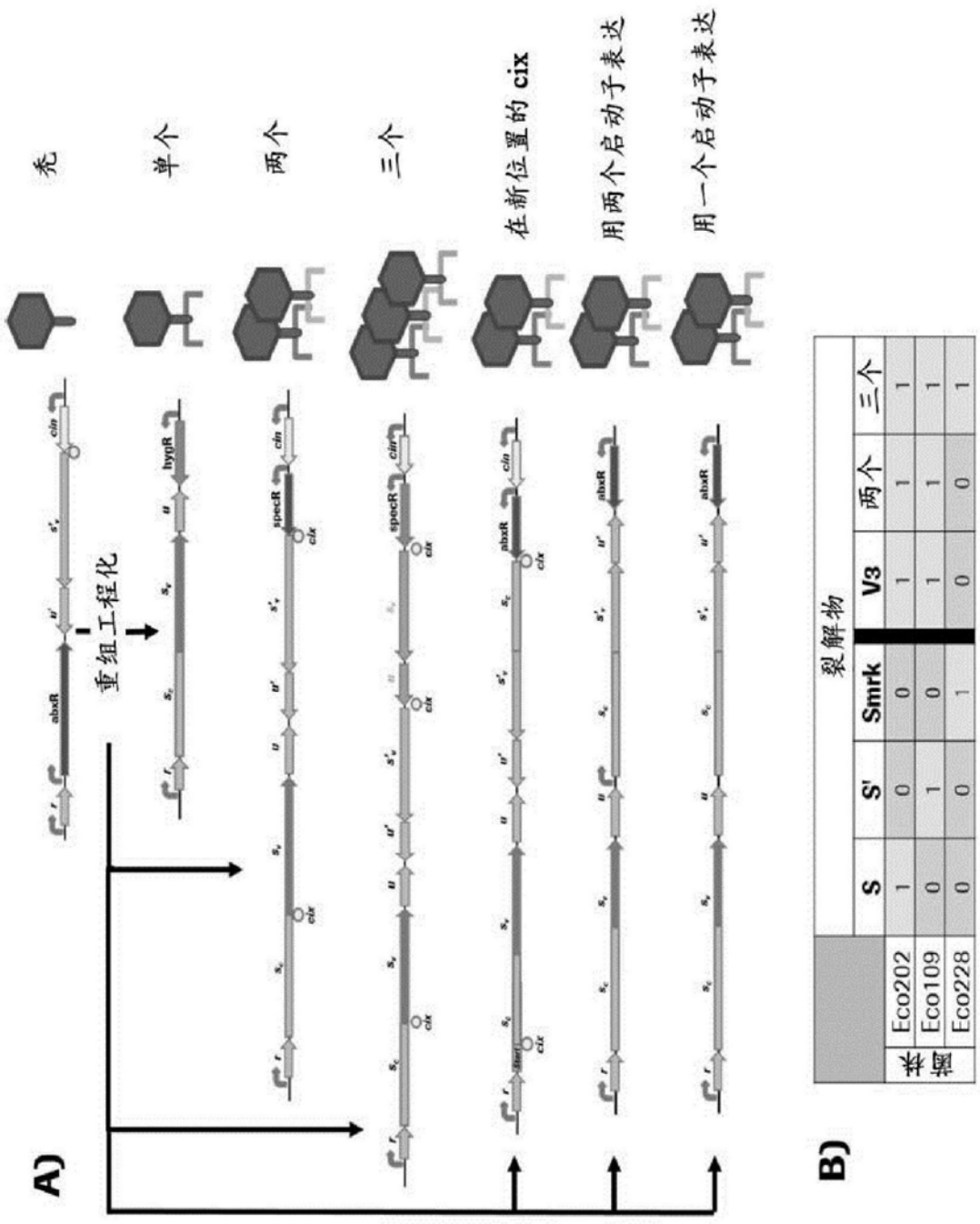
A)
无
单个
两个
三个
在新位置的 cixP
用两个启动子表达
用一个启动子表达
重组工程化
abxR
hygR
specR
cixP
cixB
cixD
B)
裂解物
S
S'
Smrk
V3
两个
三个
基因组
Eco202
Eco109
Eco228

图6

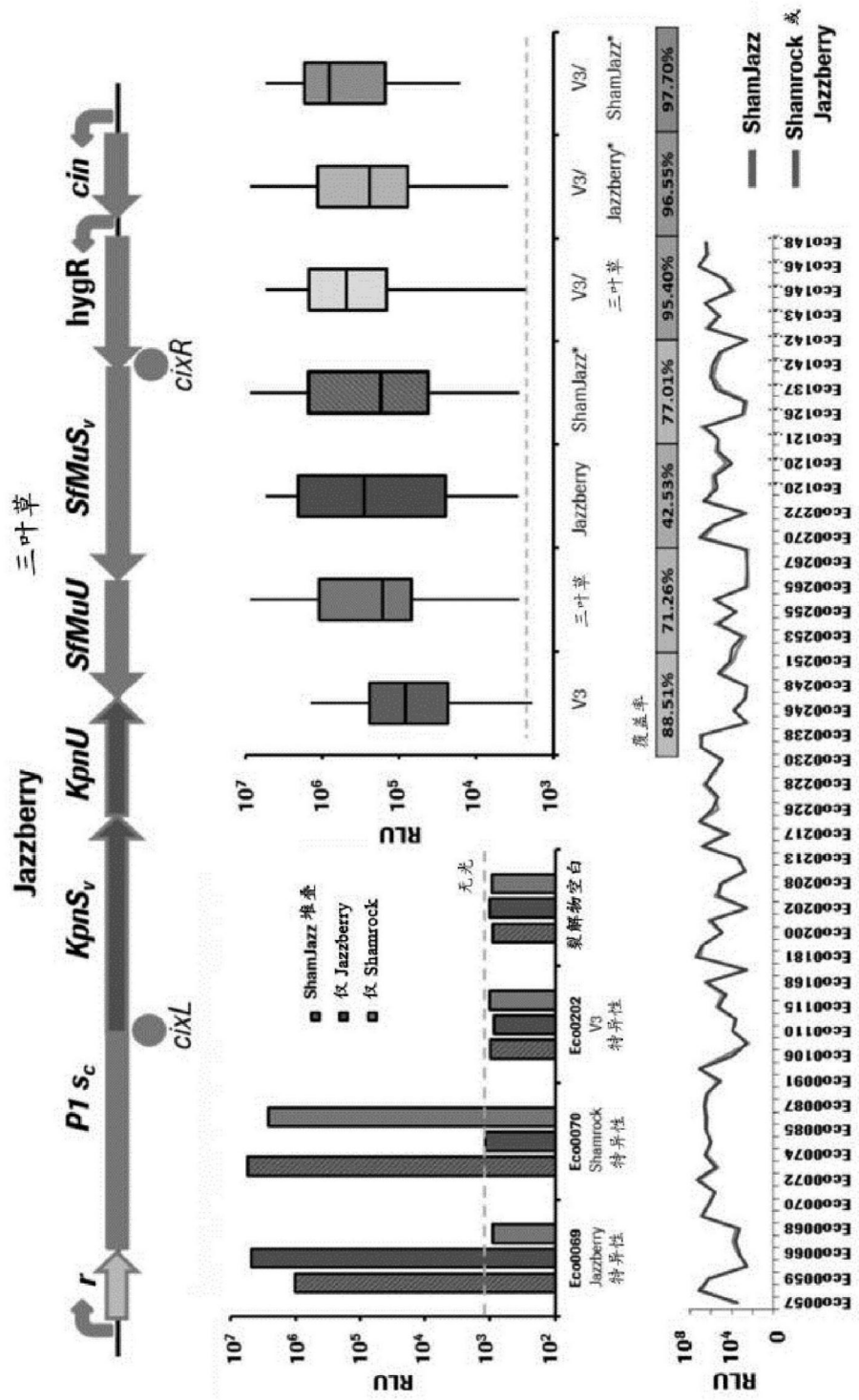
三叶草
Jazzberry
r
P1 sc
KpnSv
cixL
KpnU
SfMuU
SfMuSv
cixR
hygR
cin
RLU
ShamJazz 堆叠
仅 Jazzberry
仅 Shamrock
无光
Eco0069 Jazzberry 特异性
Eco0070 Shamrock 特异性
Eco0202 V3 特异性
裂解物空白
V3
三叶草
Jazzberry
ShamJazz*
V3/三叶草
V3/Jazzberry*
V3/ShamJazz*
覆盖率
88.51%
71.26%
42.53%
77.01%
95.40%
96.55%
97.70%
ShamJazz
Shamrock 或 Jazzberry

图7

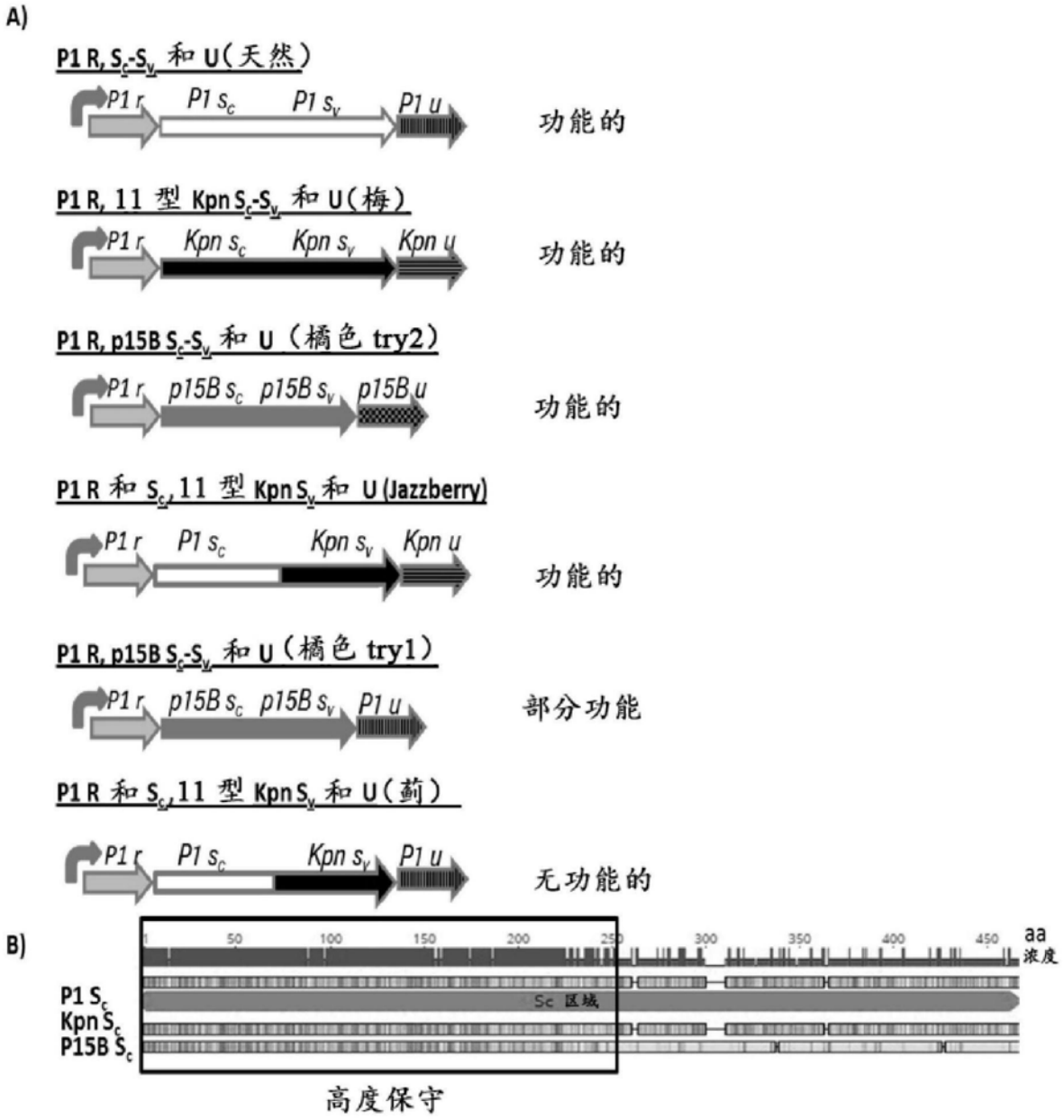
A)
P1 R, Sc-Sv 和 U(天然)
P1 r
P1 sc
P1 sv
P1 u
功能的
P1 R, 11 型 Kpn Sc-Sv 和 U(梅)
Kpn sc
Kpn sv
Kpn u
功能的
P1 R, p15B Sc-Sv 和 U (橘色 try2)
p15B sc
p15B sv
p15B u
功能的
P1 R 和 Sc, 11 型 Kpn Sv 和 U (Jazzberry)
功能的
P1 R, p15B Sc-Sv 和 U (橘色 try1)
部分功能
P1 R 和 Sc, 11 型 Kpn Sv 和 U(蓟)
无功能的
B)
aa
浓度
Sc 区域
P1 Sc
Kpn Sc
P15B Sc
高度保守

图8

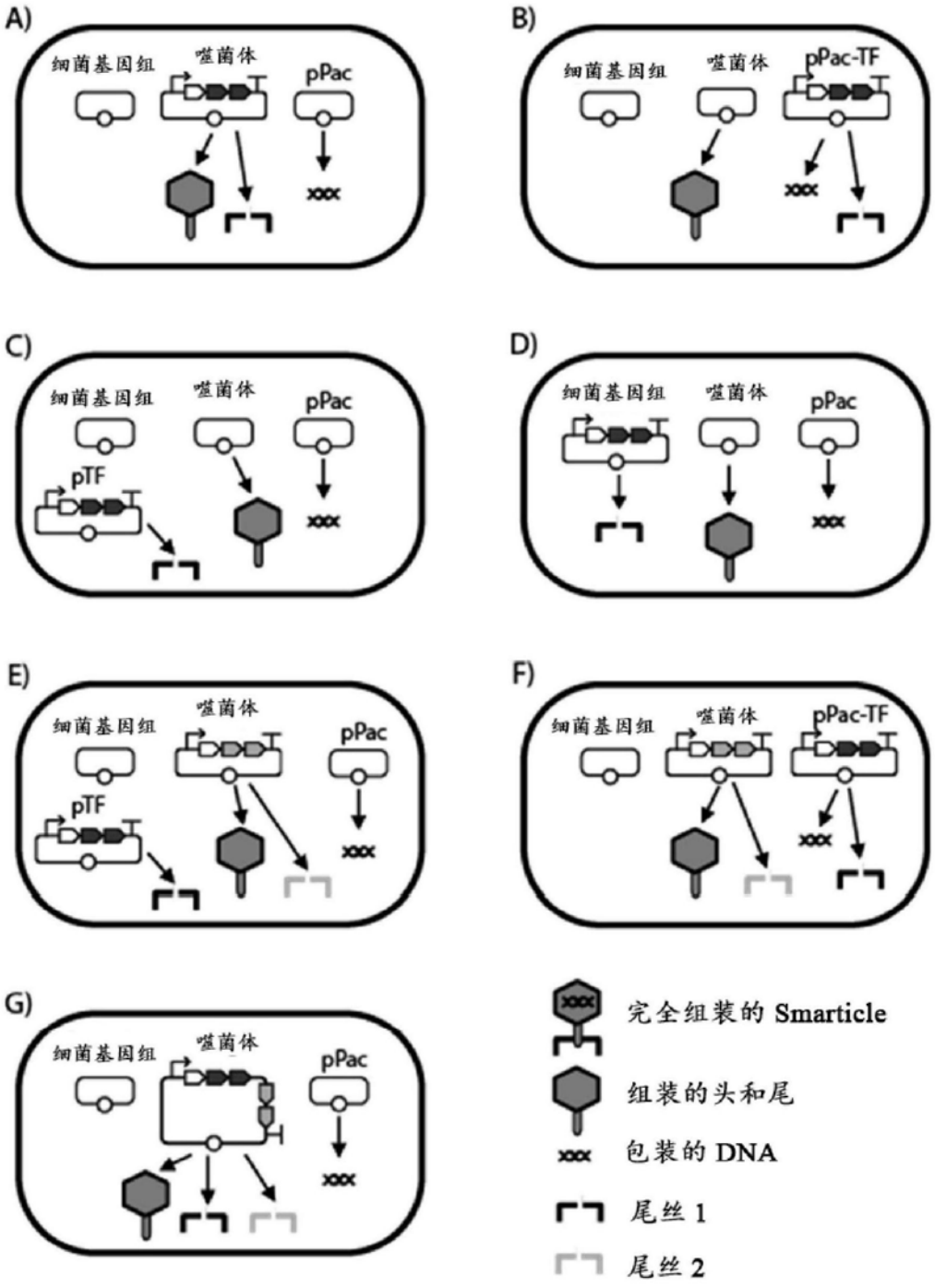
A)
细菌基因组
噬菌体
pPac
xxx
B)
细菌基因组
噬菌体
pPac-TF
xxx
C)
细菌基因组
噬菌体
pPac
pTF
xxx
D)
细菌基因组
噬菌体
pPac
xxx
E)
细菌基因组
噬菌体
pPac
pTF
xxx
F)
细菌基因组
噬菌体
pPac-TF
xxx
G)
细菌基因组
噬菌体
pPac
xxx
完全组装的 Smarticle
组装的头和尾
包装的 DNA
尾丝 1
尾丝 2

图9