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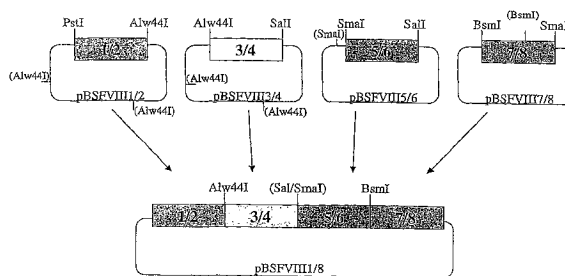
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(54) 发明名称

重组凝血因子在人类细胞系中的生产

(57) 摘要

本发明涉及一种用于生产重组人凝血因子、详细地讲是因子 VIII 和因子 IX 的改良方法,该方法利用稳定表达病毒转录激活蛋白并携带含有与编码凝血因子的 DNA 序列功能性连接的启动子的载体的无限增殖化人类细胞系,条件是所述启动子不是由所述病毒转录激活蛋白刺激的病毒启动子;还涉及携带所述载体的无限增殖化人类细胞系;还涉及特别适用于上面所述生产方法的因子 VIII 突变蛋白;还涉及包含这类因子 VIII 突变蛋白的药用组合物以及这类因子 VIII 突变蛋白在制备用于治疗血友病的药物上的应用。



1. 一种因子 VIII 突变蛋白,所述突变蛋白中在 Arg740 和 Glu1649 位置之间的 B- 结构域被 SEQ ID NO :9 的序列的富含 Arg 的接头肽所取代,其中所述因子 VIII 编号对应于在 SEQ ID NO :2 中显示的成熟野生型因子 VIII 序列。

2. 权利要求 1 所述的因子 VIII 突变蛋白,其中所述因子 VIII 突变蛋白至少具有下列额外突变 (a)、(b) 和 (c) 中之一:

(a) 162 位置上的 Val 由选自 Gly、Ala、Leu、Ile、Met 和 Pro 的一个中性氨基酸残基所取代;

(b) 2011 位置上的 Ser 由选自 Asn、Thr 和 Gln 的一个亲水性氨基酸残基所取代;和

(c) 2223 位置上的 Val 由选自 Glu 和 Asp 的一个酸性氨基酸所取代。

3. 权利要求 2 中所述的因子 VIII 突变蛋白,其中所述因子 VIII 突变蛋白至少具有突变 (a) 和突变 (b) 其中一种。

4. 权利要求 2 中所述的因子 VIII 突变蛋白,其中所述因子 VIII 突变蛋白具有全部三种突变 (a)、突变 (b) 和突变 (c)。

5. 依照权利要求 2-4 中任一项所述的因子 VIII 突变蛋白,其中在突变 (a) 中 162 位置上的 Val 被 Ala 所取代,在突变 (b) 中 2011 位置上的 Ser 被 Asn 所取代,和 / 或在突变 (c) 中 2223 位置上的 Val 被 Glu 所取代。

6. 一种编码权利要求 1-5 中任一项所限定的因子 VIII 突变蛋白的 DNA 序列。

7. 权利要求 6 中所述的 DNA 序列,它相对于在 SEQ ID NO :1 中显示的成熟野生型因子 VIII 的 DNA 序列至少具有 T485C 突变、G6032A 突变和 T6668A 突变中的一种。

8. 权利要求 7 中所述的 DNA 序列,其中所述 DNA 序列包含全部三种所述突变。

9. 一种包含权利要求 6-8 中任一项所限定的 DNA 的载体。

10. 权利要求 9 中所述的载体,它是分别显示于 SEQ ID NO :3、12 和 14 中的 pTGF8-1、pTGF8-2hyg-s 或 pTGF8-3。

11. 权利要求 9 中所述的载体,它是一种基因转移载体。

12. 一种权利要求 9-11 中任一项所限定的载体转化的和 / 或包含权利要求 6-8 中任一项所限定的 DNA 序列的宿主细胞。

13. 用于生产权利要求 1-5 中任一项所述的因子 VIII 突变蛋白的方法,所述方法包括:

(a) 培养权利要求 12 中所限定的转化宿主细胞;并且

(b) 从所述液体培养基中分离所述因子 VIII 突变蛋白。

14. 一种药用组合物,所述药用组合物包含权利要求 1-5 中任一项所限定的因子 VIII 突变蛋白或权利要求 11 所限定的基因转移载体。

15. 权利要求 1-5 中任一项所限定的因子 VIII 突变蛋白或权利要求 11 所限定的基因转移载体在制备用于治疗血友病的药物上的应用。

16. 权利要求 15 的用途,其中所述血友病为 A 型血友病。

17. 权利要求 13 中所述的方法,所述方法包括:

(a) 培养稳定表达猿猴病毒 T 抗原并且携带具有与编码所述因子 VIII 突变蛋白的 DNA 序列功能性连接的 CMV 启动子的载体的无限增殖化人类细胞系。

18. 权利要求 17 所述的方法,其中所述无限增殖化人类细胞系是无限增殖化肾细胞、

膀胱细胞、肝细胞、肺细胞、心肌细胞、平滑肌细胞、卵巢细胞或胃肠细胞。

19. 权利要求 18 所述的方法,其中所述无限增殖化人类细胞系来源于人胚肾细胞。

20. 权利要求 19 所述的方法,其中所述无限增殖化人类细胞系为 293T 细胞系。

21. 依照权利要求 17-20 中任一项所述的方法,其中所述载体还包含一个选择性标记和 / 或调节序列。

22. 依照权利要求 17-20 中任一项所述的方法,其中所述培养是在存在冯·维勒布兰德氏因子(vWF)的情况下进行的。

23. 依照权利要求 13 和 17-22 中任一项所述的方法,所述方法还包括:

(c) 纯化在步骤(b)中分离的凝血因子,和 / 或

(d) 将在步骤(b)中分离的凝血因子或在步骤(c)中纯化的凝血因子进行病毒灭活处理。

24. 一种无限增殖化人类细胞系,所述细胞系稳定表达至少一种病毒转录激活蛋白并携带如权利要求 17-20 中任一项所定义的编码因子 VIII 突变蛋白的载体。

重组凝血因子在人类细胞系中的生产

[0001] 介绍

[0002] 本发明涉及一种用于生产重组人凝血因子,详细地讲是因子 VIII 和因子 IX 的改良方法,该方法利用稳定表达病毒转录激活蛋白并携带含有与编码凝血因子的 DNA 序列功能性连接的启动子的载体的无限增殖化人类细胞系,条件是所述启动子不是由所述病毒转录激活蛋白刺激的病毒启动子;还涉及携带所述载体的无限增殖化人类细胞系;还涉及特别适合于上面所述生产方法的因子 VIII 突变蛋白;还涉及包含这类因子 VIII 突变蛋白的药用组合物以及这类因子 VIII 突变蛋白在制备用于治疗血友病的药物上的应用。

[0003] 相关技术概述

[0004] 血友病患者是由于凝血级联中的蛋白成分的功能受干扰引起的出血性病症而患病的。根据受影响的凝血因子可以区分为两种类型的血友病。它们的可溶性纤维蛋白原向不溶性纤维蛋白凝块的转化都被抑制。它们是主要影响男性人群的隐性 X-染色体连锁遗传疾病。

[0005] A 型血友病在每 10,000 男性中影响 1-2 个个体。它是由于缺少或缺失一个非常大的糖蛋白(分子量大约 330kDa(Furie B., Furie B. C., Cell(1988) 53, 505-518))、在凝血级联中作为一个重要组分的因子 VIII 引起的。所述多肽序列可以细分为 3 个区域,即由所谓的 A1 结构域和 A2 结构域组成的 N-末端区域、中心 B-结构域区域和由 A3 结构域、C1 结构域和 C2 结构域构成的 C-末端区域。在血液凝固中因子 VIII 作为无活性前体存在。它被紧密地而非共价地结合到作为稳定载体蛋白的冯·维勒布兰德因子(vWF)上。因子 VIII 在 3 个特定位置上(740、372、1689)被凝血酶蛋白酶切而导致它脱离 vWF,然后在所述级联中开启前凝血剂功能。因子 VIII 以它的活化形式作为因子 IXa 的辅因子发挥功能,从而将因子 X 的蛋白水解活化加快几个数量级。

[0006] B 型血友病在每 25,000 男性中发生大约 1 例。它的特征在于缺乏丝氨酸蛋白酶因子 IX(克里斯马斯氏因子)。这种 415 个氨基酸的多肽是在肝脏合成为 56kDa 的糖蛋白。为了获得它正确的功能,只在维生素 K 存在下才发生的转译后羧基化是需要的。

[0007] 对于这两种类型出血性疾病的疗法传统上包括输注来源于人血浆的因子 VIII 或因子 IX 蛋白浓缩物。虽然这个方法为血友病患者提供了一个有效的治疗,但它带来了传播各种传染性因子的风险,例如引起肝炎或 AIDS 的病毒,或者血栓栓塞因子。已有描述用于生产凝血因子的几种可替代的重组 DNA 技术。为此,野生型因子 VIII 和野生型因子 IX 的对应 cDNA 已被分离并克隆到合适的表达载体中(EP-A-160457;WO-A-86/01961;美国专利号 4,770,999、5,521,070 和 5,521,070 号)。

[0008] 至于因子 VIII,用于生产显示凝血剂活性的复合体的亚单位的重组表达在本领域是已知的(例如,EP-A-150735、EP-A-232112、EP-A-0500734、WO-91/07490、WO-95/13300、美国专利号:5,045,455 和 5,789,203)。此外,部分或全部缺失编码高糖基化 B-结构域的序列的截短 cDNA 形式的表达已有描述(例如在 WO-86/06101、WO-87/04187、WO-87/07144、WO-88/00381、EP-A-251843、EP-A-253455、EP-A-254076、美国专利号 4,868,112 和 4,980,456、EP-A-294910、EP-A-265778、EP-A-303540 和 WO-91/09122 中)。最近,引入了

各种各样的选定的点突变,以抑制活化C蛋白对因子VIII的蛋白水解失活或者减弱导致治疗患者形成抑制性抗体的免疫原性(例如美国专利5,859,204、5,422,260和5,451,521、WO-97/49725和WO-99/29848)。

[0009] 重组凝血因子通常是从稳定转染的真核生物细胞系、优选哺乳动物细胞系的培养基中分离的。然而,普遍的作法是在上文中提到的参考资料中所公开的生产方法中使用非人类细胞系,来排除共纯化某些可能由人类细胞包含和表达的传染性因子的风险。

[0010] 可是,尤其对于因子VIII,利用非人类细胞系遇到了一些缺陷。例如已有报道已表达蛋白分泌到培养基中的水平不能令人满意。这可能是由于不同类型的哺乳动物细胞在有可能对所述已表达多肽的生物学活性有影响的蛋白翻译和蛋白修饰的细胞内途径方面有细微差别。除开这点,还与从非人类表达系统中纯化得到的治疗性蛋白被能够在患者体内引发抗原反应的细胞成分所污染有关。

[0011] 此外,由非人类表达系统表达的蛋白可能具有在患者体内引发抗原反应的非人类糖基化模式。可是,凝血因子的生物稳定性和效力显著地受它们的N-糖基化模式所影响。特别是外周单糖和末端单糖是重要的,因为它们被来自负责其降解的细胞的特异性受体所探测到。凝血因子带有作为末端单糖的唾液酸残基。例如就所述凝血因子来说,在糖蛋白触角(tentacle)上的唾液酸组成的修饰可以导致异源糖基化模式。因而当修饰发生时,关键性地牵涉到生物稳定性和效力。因此,在生产重组凝血因子中评估相对于人类细胞系的来自非人类生产细胞系的糖基化影响是一个重要的考虑。总的来说,人类细胞系比非人类细胞系更胜任于生产重组凝血因子是似乎有道理的。这个假设的原因是因为在重组因子合成过程中可能没有外来寡糖会掺入到寡糖部分。

[0012] 另一方面,包括表达病毒转录激活蛋白的无限增殖化的稳定转染哺乳动物细胞系、用于所需基因高水平蛋白表达的通用方法在一段时间内已经成为可能(例如美国专利5,712,119)。另外,用一种载体构建物转化这些细胞系,在所述载体构建物中合适的病毒转录启动子与确定兴趣基因的DNA序列有效连接,所述转录激活蛋白激活所述病毒转录启动子从而启动兴趣基因的表达。这又与由这些细胞系表达的所述转录激活蛋白可能在靶治疗蛋白中造成污染是有关的。

[0013] 考虑到上述这些原因,仍然需要一个人凝血因子的有效生产方法。

[0014] 令人惊奇地,已经发现可以用上面提到的无限增殖化人类细胞系获得无污染的凝血因子。详细地讲,所述无限增殖化细胞系-如果携带含有与编码凝血因子的DNA序列功能性连接的启动子的载体,尽管所述启动子不是一个由所述病毒转录激活蛋白刺激的病毒启动子-能够表达所述凝血因子。与合适的蛋白纯化和病毒灭活方案联合,这个方法提供了一个生产可应用于人类治疗的安全和高活性重组凝血因子的有效系统。此外,发现了对蛋白水解失活异常稳定,因而可以承受强力病毒灭活方案的特定因子VIII突变蛋白。

[0015] 发明概述

[0016] 本发明提供:

[0017] (1) 生产重组人凝血因子的方法,所述方法包括:

[0018] (a) 培养稳定表达至少一种病毒转录激活蛋白,并且携带含有与编码所述人凝血因子的DNA序列功能性连接的启动子的载体的无限增殖化人类细胞系,条件是所述启动子不是由所述至少一种病毒转录激活蛋白刺激的病毒启动子,和

- [0019] (b) 从液体培养基中分离所述凝血因子；
- [0020] (2) 在上面 (1) 中限定的所述方法的优选实施方案, 其中所述人凝血因子是因子 VIII 或其突变蛋白；
- [0021] (3) 在上面 (2) 中限定所述方法的优选实施方案, 其中所述因子 VIII 是至少具有下列突变之一的突变蛋白：
- [0022] (a) 162 位置上的 Val 被另外一个中性氨基酸残基所取代，
- [0023] (b) 2011 位置上的 Ser 被另外一个亲水氨基酸残基所取代，
- [0024] (c) 2223 位置上的 Val 被另外一个酸性氨基酸残基所取代，和
- [0025] (d) 在 Arg740 和 Glu1649 之间的 B- 结构域被包含 10 至 25 个、优选为 14 到 20 个氨基酸残基的富含精氨酸的接头肽所取代, 其中所述因子 VIII 编号对应于显示于 SEQ ID NO :2 中的成熟野生型因子 VIII 序列；
- [0026] (4) 在上面 (1) 中限定的所述方法的优选实施方案, 其中所述人凝血因子是因子 IX 或其突变蛋白；
- [0027] (5) 携带编码在上面 (1) 至 (4) 中所限定的人凝血因子的载体的无限增殖化人类细胞系；
- [0028] (6) 在上面 (3) 中所限定的因子 VIII 突变蛋白；
- [0029] (7) 编码在上面 (6) 中限定的所述因子 VIII 突变蛋白的 DNA 序列；
- [0030] (8) 包含上面 (7) 中限定的所述 DNA 的载体；
- [0031] (9) 在上面 (8) 中限定的载体, 它是一种基因转移载体；
- [0032] (10) 用在上面 (8) 中所限定的载体转化的和 / 或包含在上面 (7) 中所限定的 DNA 序列的宿主细胞；
- [0033] (11) 包含在上面 (6) 中限定的所述因子 VIII 突变蛋白或在上面 (9) 中所限定的基因转移载体的药用组合物；
- [0034] (12) 在上面 (6) 中限定的所述因子 VIII 突变蛋白或在上面 (9) 中所限定的基因转移载体在制备用于治疗血友病的药物上的应用；和
- [0035] (13) 治疗血友病的方法, 所述方法包括予人血友病患者在上面 (6) 中限定的所述因子 VIII 突变蛋白或在上面 (9) 中所限定的基因转移载体。
- [0036] 附图详述
- [0037] 图 1 显示用于构建 B- 结构域缺失的因子 VIII 的所述片段 (实施例 1)。
- [0038] 图 2 显示 pTGF8-1 载体, 为 8720bp 环状 DNA, 它的确切 DNA 序列在 SEQ ID NO :3 中给出 (所述 DNA 序列编码的因子 VIII 蛋白的序列参见 SEQ ID NO :4)。
- [0039] 图 3 显示 pTGFG36 载体, 为 5753bp 环状 DNA, 它的确切 DNA 序列在 SEQ ID NO :6 中给出 (SEQ ID NO :6 中的碱基 689-2071 编码因子 IX 蛋白)。
- [0040] 图 4 显示 pTG36hyg 载体, 8124bp 环状 DNA。
- [0041] 图 5A 描述本发明的优选接头序列 (SEQ ID NO :9)。
- [0042] 图 5B 显示在实施例 6 中测定的重组 hFVIII 的凝固时间。
- [0043] 图 6 显示 pTGF8-2hyg-s 和 pTGF8-3 的共同分子结构, 它们均为 10698bp 环状 DNA, 它们的确切 DNA 序列在 SEQ ID NO :12 中和 SEQ ID NO :14 中给出 (所述 DNA 序列编码的因子 VIII 蛋白的序列参见 SEQ ID NO :13 和 SEQ ID NO :15)。

[0044] 图 7A 显示实施例 5 中所描述的 FVIII ELISA 的校准曲线。

[0045] 图 7B 描述在实施例 5 中所述的不同培养滤液中重组 FVIII 浓度的测定结果。

[0046] 图 8 显示在实施例 9 中所描述的因子 VIII 特异性免疫荧光测定结果。上排：pTGF8-3 稳定转染的 293T 细胞，克隆 49/19。下排：阴性对照：未转染的 293T 细胞。A 和 C：白光、无滤光片；B 和 D：因子 VIII 的荧光检测，滤光片 550nm。

[0047] 图 9 显示在实施例 10 中所描述的热处理对培养滤液中 FIX 活性的影响。

[0048] 图 10 显示活性重组因子 IX 的表达对于在培养基中补加维生素 K 的依赖。

[0049] 发明详述

[0050] “功能性连接”是指其中所述启动子以它可以刺激编码人凝血因子的 DNA 序列的转录的方式位于所述载体中的所述载体的配置。“非功能性连接”是指所述启动子远离表达的凝血因子基因序列而不能够刺激它的转录的配置。

[0051] “基因”是指编码多肽、可选地包括前导序列、尾随序列、内含子和外显子的 DNA 序列。

[0052] “载体”是指当与适当的控制元件相连接时能够复制的任何基因构建物，例如质粒、噬菌体、粘粒等。该术语包括克隆载体和表达载体。“携带载体”包括在宿主细胞中稳定掺入和瞬时掺入功能性 DNA 区断。然而，优选稳定掺入。

[0053] 依照本发明的“基因转移载体”包括适用于基因治疗的载体。这种载体包含用于所需目的的本领域已知的功能性序列。

[0054] 术语“成熟”是指给定蛋白刚从细胞分泌出来后的分子结构（即，缺少它的 N- 末端输出信号的多肽）。

[0055] “启动子”是指用于控制 RNA 聚合酶所结合基因的转录的调节 DNA 序列区域。

[0056] 本发明所述药用组合物的“治疗有效剂量”是指对于治疗或预防有效的剂量，例如，产生有效治疗或减轻血友病症状的剂量。治疗有效剂量的确定是在本领域技术人员的技术范围之内。

[0057] “编码”是指核酸序列处于适当的调节序列控制之下时在体外或体内被转录（如果是 DNA）或被翻译（如果是 mRNA）成为多肽的特性。

[0058] 对于本申请的目的而言，“表达”是指编码蛋白的基因的转录和翻译。

[0059] 在上面（1）到（13）中所描述的本发明会在下文中更详细地描述。依照本申请发明的实施方案（1），与编码人凝血因子的 DNA 序列功能性连接的启动子不是由所述无限增殖化人类细胞系表达的至少一种病毒转录激活蛋白刺激的病毒启动子。

[0060] 所述无限增殖化人类细胞系优选是无限增殖化肾细胞、膀胱细胞、肝细胞、肺细胞、心肌细胞、平滑肌细胞、卵巢细胞或胃肠细胞。更优选所述无限增殖化细胞系来源于人胚胎肾细胞，最优选是 293T 细胞系（ECACC：tsa201，ref. 96121229；DSM ACC2494）。

[0061] 所述无限增殖化细胞系表达的至少一种转录激活蛋白包括：猿猴病毒 T 抗原、腺病毒 E1A 蛋白或腺病毒 E1B 蛋白、由牛乳头瘤病毒早期区 DNA 序列编码的蛋白和疱疹病毒 IE 蛋白。优选所述无限增殖化细胞系至少表达两种转录激活蛋白，例如，温度敏感型 SV40T 抗原和腺病毒 E1A 蛋白（例如上面的 293T 细胞系）。

[0062] 与编码人凝血因子的 DNA 序列功能性连接的所述启动子优选包括：

[0063] (i) 不被上面所限定的无限增殖化细胞所表达的激活蛋白刺激的病毒启动子（例

如 SV40 和 CMV) ;

[0064] (ii) 宿主管家启动子 (清蛋白) ;和

[0065] (iii) 组织特异性启动子 (例如对肝脏特异性的 α -抗胰蛋白酶)。依照本发明的最优选的启动子是 CMV 启动子 (由所述无限增殖化细胞表达的转录激活蛋白不刺激所述启动子)。

[0066] 依照本发明,所述载体可以携带另外的由所述病毒转录激活蛋白刺激、但不与凝血因子功能性连接的病毒启动子。这类病毒启动子选自来源于腺病毒、劳斯肉瘤病毒和巨细胞病毒的启动子。所述载体还可以含有一个或多个下列功能性序列:选择标记、调节序列 (例如, PRE) 等。

[0067] 依照本发明实施方案 (1) 的所述人凝血因子包括但不限于因子 IX、因子 VIII、因子 VII、因子 V、冯·维勒布兰德氏因子 (vWF) 以及诸如此类。

[0068] 在本发明的优选实施方案 (2) 中,所述载体包含编码因子 VIII 或其突变蛋白的 DNA 序列。已经设计了多种修饰过的因子 VIII 表达构建物用于重组表达,而重组因子 IX 与从血浆中分离的野生型蛋白在总体结构上相同。考虑到功能性因子 VIII 多肽中与 vWF 相互作用的重要位点的域结构位于 A3 结构域 (氨基酸 1680-1689) 和 C2 结构域 (Kaufman 和 Pipe, Haemophilia(1998)4, 第 370-379 页)。提出在 1689 后切割来从 vWF 释放因子 VIII 并使得因子 VIII 可以与带电荷磷脂相互作用。当缺少 vWF 结合位点的重组因子 VIII 构建物注射入因子 VIII 缺乏的小鼠时,它显示出非常易于被蛋白酶酶切。截短的因子 VIII 构建物在哺乳细胞培养物中的重组表达例证了所述 B 结构域的完全缺失不改变相应的因子 VIII 样蛋白的生物活性 (Eaton 等, Biochemistry(1986)25, 8343-8347)。另外,由于细胞中 mRNA 水平增强了,因此 B 结构域缺失型构建物的可观察表达速度明显高于野生型因子 VIII (Pittman 等, Blood(1993)81, 2925-2935)。目前有四种重组因子 VIII 制品 (Recombinate[®] Baxter HealthCare ;Kogenate[®]和 Kogenate FS[®] Bayer Corporation 以及 Refacto[®] Wyeth, GeneticsInstitute) 上市。

[0069] 在本发明的优选实施方案 (3) 中,所述因子 VIII 突变蛋白至少具有下列 (a) 至 (d) 突变中的一个 :

[0070] (a) 162 位置上的 Val 被另外一个中性氨基酸残基所取代 ;

[0071] (b) 2011 位置上的 Ser 被另外一个亲水性氨基酸残基所取代 ;

[0072] (c) 2223 位置上的 Val 被一个酸性氨基酸残基所取代 ;和

[0073] (d) 在 Arg740 和 Glu1649 之间的 B- 结构域被包含 10 到 25、优选为 14 到 20 个氨基酸残基的富含精氨酸的接头肽所取代,其中所述因子 VIII 编号与显示于 SEQ ID NO :2 中的野生型因子 VIII 的氨基酸序列相对应的 (所述成熟肽的氨基酸序列不包括 19 个氨基酸的信号肽,但包括完整的 B 结构域 (WO 99/29848))。

[0074] 依照本发明的“另外一个中性氨基酸残基”包括甘氨酸、丙氨酸、亮氨酸、异亮氨酸、甲硫氨酸和脯氨酸,优选是丙氨酸。所述“另外一个亲水性氨基酸”包括天冬酰胺、苏氨酸和谷氨酰胺,优选是天冬酰胺。所述酸性氨基酸选自谷氨酸和天冬氨酸,优选是谷氨酸。

[0075] 在实施方案 (3) 的所述因子 VIII 突变蛋白中,优选所述因子 VIII 突变蛋白至少具有 (a)、(b) 和 (c) 突变中的一个,更优选至少具有 (a) 和 (b) 突变中的一个,最优选具有上面所限定的 (a) 至 (c) 全部三个突变。特别优选所述突变蛋白含有全部三个 V162A、

S2011N 和 V2223E 突变。

[0076] 基于同样的考虑,本发明的实施方案(4)中所述载体所包含的 DNA 序列与 SEQ ID NO:1 中显示的成熟野生型因子 VIII DNA 序列相比,具有 T485C、G6032A 和 T6668A 突变。在一个优选实施方案中,所述 DNA 序列也含有 T6816C 平静(即,沉默)突变(所述编号又是与成熟野生型因子 VIII 的 DNA 序列相对应)。

[0077] 在实施方案(3)中的所述因子 VIII 突变蛋白中,另一种优选方式是因子 VIII 突变蛋白具有上面所述(d)突变。

[0078] 本发明的优选表达系统利用独特因子 VIII 突变蛋白,它除了前文所述(a)至(c)点突变之外,还部分或全部缺少其 B 结构域-,优选在 R740 和 E1649 位置间的 B 结构域被上面(d)中所述的特征性富含精氨酸的氨基酸间隔区所取代的突变蛋白。依照本发明的“富含精氨酸的”是指所述间隔区包含至少 3 个、优选至少 4 个精氨酸残基。在一个优选实施方案中,所述间隔区由野生型 B 结构域的 8 个氨基酸、然后是可变结构域的 8 个氨基酸组成(参见图 5a, SEQ ID NO:9)。在这种具有上文中所讨论的 B 结构域修饰的构建物中,提出的 vWF 结合位点保持不变,以阻止细胞培养基中或随后进入到被治疗患者的血液中的分泌型因子 VIII 立即被蛋白酶酶切消化。只有在通过凝血酶酶切特异性活化后,因子 VIII 才会从 vWF 释放。所述优选因子 VIII 的 cDNA 是通过装配 4 个 DNA 片段、例如实施例 1 中所描述的构建的。

[0079] 本发明实施方案(3)中的所述蛋白可以包含另外的 N-末端序列或 C-末端序列,它们包括但不限于天然输出信号肽(对应于 SEQ ID NO:4、13 和 15 中所显示蛋白的氨基酸残基 -19 至 -1)或其片段或类似物、人工肽(例如用于高亲和纯化的寡组氨酸标记物)等等。

[0080] 用于表达因子 VIII 的优选载体是在图 2 中显示的 pTGF8-1 载体。所述载体的 DNA 序列显示于 SEQ ID NO:3 中,而且它包含上文所述的全部 5 个突变(T485C、G6032A、T6668A 和 T6816C(这里:T1217C、G4088A、T4724A 和 T4872C)和编码 SEQ ID NO:9 中的 B 结构域接头的 DNA 序列)并编码在 SEQ ID NO:4 中描述的因子 VIII 突变蛋白。

[0081] 另外的最优选载体是 pTGF8-2hyg-s 和 pTGF8-3,它们共同的分子结构描述于图 6 中。

[0082] 显示于 SEQ ID NO:12 中的 pTGF8-2hyg-s 只包含 T6816C 沉默突变,产生一种由接头肽 SEQ ID NO:9 取代所述 B 结构域的因子 VIII 突变蛋白,但在参比野生型序列 SEQ ID NO:2 时一级蛋白结构上没有进一步的改变。

[0083] 显示于 SEQ ID NO:14 中的 pTGF8-3 含有 T485C、T6668A 和 T6816C 突变,产生一种除了显示出上面所述的 B 结构域取代外,还相对于 SEQ ID NO:2 显示出 V162A 和 V2223E 氨基酸取代的因子 VIII 突变蛋白。

[0084] 在生产因子 VIII 的情况下,所述培养是在冯·维勒布兰德氏因子存在下进行的。所述冯·维勒布兰德氏因子的用量优选为每 mol 因子 VIII 10-100、更优选为 50-60 mol vWF(在液体培养基中和/或纯化过程中在因子 VIII 溶液中)(参见下面)。

[0085] 在本发明的优选实施方案(4)中,所述人凝血因子是因子 IX 或其突变蛋白,优选是显示于 SEQ ID NO:5 中的野生型因子 IX。因子 IX 的合适突变蛋白包括所述因子 IX 的点突变形式和截短形式。用于表达因子 IX 的最优选载体是分别显示于图 3 和图 4 中的

pTGFG36 载体和 pTG36hyg 载体。

[0086] 在生产因子 IX 的情况下,所述培养优选在维生素 K 存在下进行,维生素 K 存在的量可以是 0.1-100 μ g/ml 液体培养基,更优选 1-20 μ g/ml 液体培养基。

[0087] 依照本发明实施方案 (1) 的所述方法还包含以下步骤:

[0088] (c) 纯化在步骤 (b) 中分离的凝血因子和 / 或

[0089] (d) 将在步骤 (b) 中分离的或在步骤 (c) 中纯化的凝血因子进行病毒灭活处理。

[0090] 适当的纯化步骤包括本领域所熟知的最大化地提高纯的、稳定的和高活性制品产量的方法,选自免疫亲和层析、阴离子交换层析、大小排阻层析等和它们联合应用。详细地讲,来自人血浆的凝血因子的详细纯化方法,例如在 W093/15105、EP0813597、W096/40883 和 W096/15140/50 中有公开。它们很容易适合于分离重组因子 VIII 和重组因子 IX 所需要的特殊要求。对于因子 IX 已经采用了一个有效的方案,它包含硫酸铵沉淀步骤,然后是 DEAE 和 HIC 触手层析 (HIC tentacle chromatography) 以及肝素亲和层析 (US5919909)。在纯化过程中和纯化后纯化蛋白的质量和活性可以通过 ELISA 和凝固测定来监测。

[0091] 为了克服在纯化蛋白样品或从含有所选分泌型重组蛋白的细胞培养上清液中直接获得的制品中可能有传染性污染物的问题,所述样品和 / 或所述培养上清液要经过包括热处理 (干燥的或液态,加入或不加入包括蛋白酶抑制剂在内的化学物质) 的病毒灭活程序处理。在病毒灭活后,用于清除所述化学物质的另一纯化步骤可能是必要的。详细地讲,对于从血浆中分离的因子 VIII 来说,通过阴离子交换层析回收高纯度经病毒灭活的蛋白已有描述 (W093/15105)。另外,已报道几种方法用于生产来自血浆或其他生物来源的高纯度、无感染性凝血因子。有脂包膜的病毒通过利用形成一个两相系统的疏水相处理潜在地传染性物质,随后除去水不溶部分而被有效灭活。已经证明,同时或随后利用非离子性生物相容去污剂和磷酸二烷基酯或磷酸三烷基酯的处理补充疏水相处理方法是另一个优点 (W09636369、EP0131740、US6,007,979)。无脂包膜的病毒要求由非离子性去污剂处理然后是数小时加热 (60-65 $^{\circ}$ C) 组成的灭活方案 (W094/17834)。

[0092] 鉴于以上结果,相信基于人类细胞系的有效蛋白表达系统与被批准的用于灭活潜在危险的感染性污染物的方法的结合可作为用于生产重组凝血因子的安全和简单的应用系统。

[0093] 而且,依照本发明的实施方案 (6),提供了一种优良的因子 VIII 突变体。所述因子 VIII 突变体可以作为药用组合物的一部分,可以用于制备治疗血友病的药物以及可以应用于治疗血友病的方法中 (本发明的实施方案 (11) 至实施方案 (13))。上面所述的药用组合物和药物可以包含治疗有效剂量、例如 50-500 μ g (200ng 因子 VIII 相当于一个国际单位 (IU)) 的因子 VIII。根据血友病的类型,患者接受因子 VIII 的年剂量可达到 200,000IU,它通常是以每周一次剂量或每周两次剂量给予。

[0094] 应用于实施方案 (11) 至实施方案 (13) 的治疗血友病方法中的所述药用组合物、药物或制剂含有治疗有效剂量的实施方案 (6) 中所述因子 VIII 突变蛋白或实施方案 (9) 中所述基因转移载体。如果是前者,则它还可以包含药学上可接受的添加剂,包括人血清白蛋白 (HSA; 优选为约 1mg/ml 溶液); 无机盐例如 CaCl_2 (优选为 2-5mM); 氨基酸例如甘氨酸、赖氨酸和组氨酸 (优选为每种氨基酸 0.1-1M); 双糖例如蔗糖和 / 或海藻糖 (优选为 0.4-1M); 有机盐例如柠檬酸钠 (优选为达到 50mM); 等。所述制剂可以是水性的或非水性

的。在后一种情况下,主要成分是甘油和 / 或聚乙二醇 (例如,PEG-300)。所述制剂也可以是干燥形式 (给药前溶解于所需的溶剂中)。

[0095] 如上面所阐述的,依照本发明实施方案 (9) 中的所述基因转移载体也可以作为药用组合物的一部分,可以用于制备治疗血友病的药物以及可以应用于治疗血友病的方法中 (本发明的实施方案 (11) 至实施方案 (13))。所述药用组合物和药物还可以包含适当的基质制剂,例如,在 WO 00/49147 中所论述的脂类或激素 (其公开内容通过引用结合到本文中)。含有所述基因转移载体或本发明的基因转移载体的所述药用组合物或药物可以口服给药、静脉给药、肌内给药、皮下给药、局部给药、通过黏膜 (包括口腔、鼻腔喷雾) 或利用基因枪给药。口服给药 (例如,微粉化激素分散体) 是优选的。

[0096] 本发明实施方案 (6) 中所述因子 VIII 突变蛋白优选如上面实施方案 (3) 所限定的。所述 FVIII 突变蛋白还可以通过标准重组技术来制备,例如包含下面步骤的方法:

[0097] (a) 培养实施方案 (8) 中所述载体转化的和 / 或包含实施方案 (7) 中所述 DNA 的宿主细胞 (也包括培养稳定表达至少一种病毒转录激活蛋白并携带含有与编码人凝血因子的 DNA 序列功能性连接的病毒转录启动子的载体的无限增殖化人类细胞系,其中所述病毒启动子被至少一种所述病毒转录激活蛋白刺激);和

[0098] (b) 从液体培养基中分离所述凝血因子。适当的无限增殖化人类细胞系、转录激活蛋白和病毒启动子是在上文中提到的那些启动子。用于所述方法中的无限增殖化人类细胞系优选表达 2 种病毒转录激活蛋白,最优选表达温度敏感型 SV40T 抗原和腺病毒 E1A 蛋白。所述方法还可以包含上文中所描述的纯化和病毒灭活步骤 (c) 和 (d)。

[0099] 所述市售的 293T 细胞系 (ECACC : tsa201, ref. 96121229) 在 2001 年 2 月 20 日,于 DMSZ (德意志微生物保藏中心 (Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH), Mascheroder Weg 1b, 38124 Braunschweig, Germany) 保藏,保藏号: DSM ACC2494。

[0100] 本发明通过下列实施例进一步举例说明。

[0101] 实施例

[0102] 实施例 1- 因子 VIII 的克隆:

[0103] 所述重组因子 VIII 的序列通过逆转录从完整人肝细胞 RNA 库中获得。然后利用设计的含有限制性位点的引物通过标准 PCR 扩增四个片段 (1/2, 3/4, 5/6, 7/8)。为了将所述 3/4 片段和 5/6 片段安装在一起,将来自 pBSFVIII3/4 质粒的 SmaI/SaII 片段平端插入到 pBSFVIII5/6 的 SaII 位点从而获得 pBSFVIII3/6。然后用 XhoI/BspHI 酶切和用 Alw44I 部分酶切 pBSFVIII3/6, 获得 3/6 片段。这个片段和来自 pBSFVIII1/2 的 PstI/Alw44I 片段一起一步连接到用 PstI 和 XhoI 酶切的 pBSFVIII1/2 的载体骨架中,通过这种方法获得 pBSFVIII1/6。所述 7/8 片段通过用 SmaI 酶切和用 MvaI269I 部分酶切 pBSFVIII7/8 获得的,然后连接到用 XhoI 和 MvaI269I 切割的 pBSFVIII1/6 中,从而得到 pBSFVIII1/8。最后,来自 pBSFVIII1/8 的 SmaI/XhoI 片段平端插入到 Octagene Vector pTGF67 (所述载体的生产在 PCT/EP00/01368 中已经公开) 的 SaII 位点,从而产生人因子 VIII 的真核表达载体 pTGF8-1 (参见图 1 和图 2)。所述产生的载体编码具有 V162A、S201N 和 V2223E 突变的因子 VIII 突变蛋白。

[0104] 实施例 2- 因子 IX 的克隆:

[0105] 载体 pUC19 (MBI Fermentas) 用 XbaI 酶切, 然后用克列诺酶处理并再连接。为了删除 EcoRI 位点, 则这个 XbaI 缺失型载体用 EcoRI 酶切, 然后用克列诺酶处理并再连接。为了将一个 XbaI 位点插入到这个载体的 SacI 位点, 这个载体用 SacI 酶切, 随后用 T4DNA 聚合酶处理, 然后用碱性磷酸酶去磷酸化, 再与 XbaI 接头 CTCTAGAG (Biolabs#1032) 连接。另外一个 XbaI 位点通过用 HindIII 酶切新产生的载体, 用克列诺酶处理, 碱性磷酸酶去磷酸化以及与 XbaI 接头 CTCTAGAG (Biolabs#1032) 连接来插入。这个载体被命名为 pUC19/X。

[0106] 为了破坏存在于载体 pHGFP-S65T (Clontech) 中的 XbaI 位点, 这个载体用 XbaI 酶切, 然后用克列诺酶处理并再连接, 从而产生 pGFP/0 载体。用 MluI 酶切 pGFP/0, 随后用克列诺酶处理, 再用 BamHI 酶切后, 分离到包含 GFP 基因的 2.3kb 片段。这个片段插入到用 SalI 酶切、克列诺酶处理和 BamHI 酶切的 pUC19/X 载体的多克隆位点。产生的载体被命名为 pTGFG1。

[0107] 寡核苷酸 (Metabion) PRE-S(5'-GGG GTA CCA GCT TCG TAGCTA GAA CAT CAT GTT CTG GGA TAT CAG CTT CGT AGC TAG AAC ATCATG TTC TGG TAC CCC-3'; SEQ ID NO:10) 和

[0108] PRE-AS(5'-GGG GTA CCA GAA CAT GAT GTT CTA GCT ACG AAG CTG ATATCC CAG AAC ATG ATG TTC TAG CTA CGA AGC TGG TAC CCC-3'; SEQ IDNO:11) 杂交, 并通过激酶反应磷酸化形成插入片段 PRE(ds)。

[0109] pTGFG1 载体用 Eco0109I 酶切, 用克列诺酶处理然后用碱性磷酸酶去磷酸化。然后与 PRE(ds) 插入片段连接, 形成 pTGFG5 载体。pUC19 载体 (MBI Fermentas) 用 SalI 酶切, 用克列诺酶处理然后用碱性磷酸酶去磷酸化。它与 NotI 接头 GCGGCCGC (Biolabs#1045) 连接, 形成 pUC19/N 载体。

[0110] 利用重叠因子 IX 开放读框的起始密码子和终止密码子的两种引物, 从人肝脏 cDNA (Clontech) 中扩增因子 IX cDNA, 产生包含完整开放读框的 1387bp 片段。EcoRI (上游) 和 BamHI (下游) 的限制性位点被包括在每个引物的末端来促进克隆。用 Pwo DNA 聚合酶 (Boehringer Mannheim) 进行扩增, 以 50 μ l 反应体积 [10mM Tris HCl pH 8.85、25mMKCl、5mM(NH₄)₂SO₄、2mM MgSO₄] 在 96°C 保持 1 分钟、60°C 保持 1 分钟、72°C 保持 2 分钟共 30 个温育循环, 然后是最终的一个延伸步骤, 在 72°C 保持 10 分钟。

[0111] 将反应产物连接到 pUC19 的 EcoRI 位点和 BamHI 位点, 然后转化到大肠杆菌 (E. coli) DH5- α 中。选择阳性克隆。通过用标记引物 (IR-700) 从两端进行循环测序 (Amersham) 和在 LiCor 测序系统 (MWG, Biotech) 中进行自动分析来证实序列。

[0112] 使用下列引物:

[0113] GGAATTCGCAAAGGTTATGCAGCGGTGAACATGATCATGGC (上游; SEQ. ID NO:16)

[0114] CGCGGATCCATTAAGTGAGCTTTGTTTTTTCCTTAATCC (下游; SEQ. ID NO:17)

[0115] 将从人 cDNA 文库中分离的包含人凝血因子 IX 开放读框的 1.4kb 片段插入到上面通过用 PstI 酶切、T4 聚合酶处理和碱性磷酸酶去磷酸化制备的 pUC19/N 载体的 PstI 位点中。通过用 HindIII 和 NotI 双酶切, 从所得的 pUC19/N-FIX 载体切取包含人凝血因子 IX 开放读框的一个 1.4kb 片段。将这个片段连接到 HindIII 和 NotI 双酶切的 pTGFG5 载体的 4.3kb 片段上, 产生显示于图 3 中的 pTGFG36 载体。这个载体是用于将编码因子 IX 的表达盒传递到所述细胞中的优选载体, 它的 DNA 序列在 SEQ ID NO:6 中提供。

[0116] 实施例 3- 用于蛋白表达的人类细胞系

[0117] 一个优选的细胞系是 tsA201 (ECACC Ref. :96121229), 它是稳定表达 SV40 温度敏感 T 抗原的转化的人胚肾细胞系 (293, ECACC 保藏号 85120602) (J. Membrane Biol. 1996 ; 152 :39 ;Gene 1995 ;156 :235 ;PNAS USA 1994 ;91 :12785 ;Pflügers Arch. 1994 ;427 :136 ; J. Gen. Physiol. 1994 ;104 :507 ;BioTechniques 1993 ;15 :906)。这个细胞系的其他名称包括 293tsA1609neo (Mol. Cell. Biol. , 1987, 7 :379) 和 293T。这个上皮样细胞系已经被用于各种功能性表达检测, 而且已有报道可以生产高水平的重组蛋白。它们可以在补充了 2mM 谷氨酰胺和 10% FCS 的 DMEM 中培养。对于因子 IX 的有效生产, 可以通过加入达到 100 μ g/ml 的维生素 K 来改良所述培养基 (US4770999)。

[0118] 为了简化已表达多肽的纯化, 细胞可以培养于含有适当补充成分的无血清培养基或无蛋白培养基中。出于稳定性的原因, 分泌型因子 VIII 要求在培养基中存在 vWF (US5198349)。加入脂蛋白、磷脂、聚乙二醇、痕量金属、肝素、非离子表面活性剂或环糊精也已有报道 (EP0254076、US5679549、US5198349、US5250421、US5576194、EP0872487、W094/11525、US5378612)。

[0119] **实施例 4- 用于瞬时生产因子 VIII 和因子 IX 的 293T 细胞的磷酸钙转染 :** 转染前一天, 融合 293T 细胞以低密度接种到装有 6ml DMEM/10% FCS (对于 FIX 是 10 μ g/ml 维生素 K) 的 10cm 平皿中。转染大致按照 Chen 和 Okayama 的方法 (Mol. Cell Biol. , 7 :2745 (1987)) 进行。对于生产因子 VIII 用 12 μ g pTGF8-1 质粒转染, 对于生产因子 IX 用 12 μ g pTGF36 质粒转染。转染后 6 小时, 培养基用新鲜的培养基更换, 转染后 3 天收获上清液, 然后或者进行进一步的纯化。或者不需要更进一步纯化而通过 ELISA 或凝固实验进行分析 (参见实施例 5 和实施例 6)。

[0120] 实施例 5- 通过 ELISA 对 FIX 和 FVIII 浓度的测定 :

[0121] **因子 IX :** 利用山羊多克隆抗 - 人 FIX (Enzyme Research Laboratories) 作为捕捉抗体, 通过 ELISA 测定在转染 293T 细胞上清液中的人重组因子 IX 水平。所有的温育是在潮湿室中 22°C 下进行 2 小时。用 100 μ l 的 8.8 μ g 抗体 /ml 包被缓冲液包被平板 (Dynex, Immulon-4)。封闭不需要在所描述条件下进行。用 PBS- **Tween**[®] (0.1% v/v) 洗板 4 次 (Encore 2000, Merck) 足以封闭非特异性相互作用。

[0122] 每进行一步, 都需要进行清洗以清除未结合蛋白。在每孔中加入 100 μ l 用 10 μ l 10mM PMSF 和 10 μ l 0.11M 柠檬酸钠处理的上清液。样品和标准品 (人因子 IX, 内标 (house standard), Octapharma) 用稀释缓冲液 (HBS-BSA-EDTA- **Tween**[®]) 稀释, 并以 100 μ l/ 孔进行温育。检测抗体是浓度为 1 μ g 抗体 /ml 稀释缓冲液的过氧化物酶标记的山羊多克隆抗 -FIX (Enzyme Research Laboratories), 并以 100 μ l/ 孔进行温育。在每孔中加入 150 μ l ABTS (Roche) 作为底物, 1-2 小时后在 405nm 检测比色反应。通过标准品浓度对标准品吸光度的线性回归计算结果并总结于下表中 :

[0123]

细胞数量 [/ml]	因子 IX 浓度 [ng/ml]	凝固时间 [s]
2.1×10^5	36	45
8.7×10^5	20	79

[0124] 正常血浆： 37-39s

[0125] 因子 IX 缺乏血浆： 137-140s

[0126] 因子 VIII：利用亲和纯化的多克隆绵羊抗 FVIII :C 制剂 (F8C-EIA-C, Affinity Biologicals) 作为捕捉抗体,通过 ELISA 测定在转染 293T 细胞培养滤液中的人重组因子 VIII 水平。包被在潮湿室中 22°C 下进行 2 小时。用 100 μ l 100 倍稀释到包被缓冲液 (50mM 碳酸钠 pH 9.6) 的抗体包被平板 (Dy nex, Immulon-4)。用 PBS- **Tween**[®] (0.1% v/v) 洗板 4 次 (Encore 2000, Merck) 足以封闭非特异性相互作用。

[0127] 每进行一步,都需要进行清洗以清除未结合蛋白。100 μ l 取自 pTGF8-3 稳定转染的不同 293T 克隆的每种培养滤液样品在温育 48 小时后加入到每孔中。FVIII 标准品 (内标, Octapharma) 用稀释缓冲液 (HBS-BSA-EDTA- **Tween**[®]) 稀释,并以 100 μ l/ 孔进行温育。对于检测来说,过氧化物酶标记的山羊多克隆抗 -F IX (Enzyme Research Laboratories) 的现用现稀释液以 100 μ l/ 孔进行温育 60 分钟。对于比色反应来说,临使用之前将 5mg 的邻苯二胺 (P-6912, Sigma) 片剂溶于 12ml 底物缓冲液中,并补充 12 μ l 30% H₂O₂。在每孔中加入 150 μ l 这种底物溶液,室温下避光温育 10 分钟并通过在每孔中加入 50 μ l 2.5MH₂SO₄ 终止反应后,利用 MRX Reader (Dy nex) 在 490nm 处进行比色纪录。通过标准品浓度对标准品吸光度的线性回归 (图 7A) 计算结果并总结于图 7B 中。

[0128] 实施例 6 :人凝血因子 VIII 和因子 IX 活性的检测

[0129] 在 293T 细胞 (如实施例 4 中所述,通过磷酸钙沉淀用 pTGF8-1 转染的) 的细胞培养物上清液中的人重组因子 VIII 的凝血活性测定如下 :

[0130] 凝血活性的分析基于使用人工凝血仪器 (ML-2, Instrumentation Laboratories) 利用脑磷脂 (磷脂酰乙醇胺) 活化进行的部分凝血致活酶时间检测。对于这个研究来说,来自转染 293T 细胞的 100 μ l 未稀释上清液、100 μ l 缺乏型血浆 (Progen) 和 100 μ l 脑磷脂 (Instrumentation Laboratories) 在 37°C 温育 5 分钟。通过加入 100 μ l CaCl₂ 起始凝固。样品凝固时间与正常血浆进行比较。所述结果总结于图 5B 中。从图 5B 中可以看出,来自 pTGF8-1 转染细胞的细胞上清液显示出与正常血浆相当凝固活性,而未转染细胞与缺乏因子 VIII 血浆的值相等。

[0131] 对于因子 IX 进行相同的检测。所述结果显示于实施例 5 的表中。对于表达对于维生素 K 存在依赖性的参见图 10。

[0132] 实施例 7- 病毒灭活 :

[0133] 病毒灭活是按照美国专利号 6,007,979 的所述方法进行的。也就是,在潜在地感染性蛋白溶液中依次加入下列化合物,并搅拌 :

[0134] 1. 0.2ml **Tween**[®] 80 和 0.06ml TNBP 加入到 19.74ml 的所述溶液中或

[0135] 2. 0.2ml **Triton**[®] X-100 和 0.2ml TNBP 加入到 19.6ml 的所述溶液中。

[0136] 在制剂 1 和制剂 2 中加入 1ml 蓖麻油,然后在室温下剧烈萃取一个小时。

[0137] 一旦分相就进行离心。对于感染性控制,重复地从水相部分每次取走 1ml 样品。

[0138] 实施例 8- 稳定表达因子 VIII 和因子 IX 的细胞系的建立:

[0139] 优选的 pTGF8-1 载体和 pTGFG36 载体分别包含用于在哺乳动物细胞中瞬时表达因子 VIII 和因子 IX 的构建物。为了能够获得稳定转染细胞克隆的选择方法,将潮霉素 B 磷酸转移酶盒(来自 TK-Hyg 的 HindIII-Mva 1260I 片段,Clontech)亚克隆到两个载体中都存在的 SmaI 位点中。这样产生的构建物(pTGF8-1-hyg 和 pTG36hyg)包含带有一个 CMV 启动子和一个 SV40 聚腺苷酸化信号的人因子 VIII 或人因子 IX 的顺式表达盒,以及带有 HSV 胸苷激酶启动子和 HSV 胸苷激酶聚腺苷酸化信号的潮霉素 B 磷酸转移酶表达盒(参见图 4)。

[0140] pTGF8-2hyg-s 载体和 pTGF8-3 载体(图 6, SEQ ID NO:12 和 SEQ ID NO:14)是 pTGF8-1hyg 的衍生物,其中利用 QuikChange[®] 方案(Stratagene)通过依赖于 PCR 的方法,将 V162A、S2011N 和 V2223E(pTGF8-2hyg-s)和 S2011N(pTGF8-3)点突变回复为野生型序列。

[0141] 所述凝血因子的编码序列可以被另外的所选基因序列所取代。这些构建物可供通过磷酸钙转染以及随后的潮霉素抗性选择建立稳定表达的细胞系。此外,所述质粒含有一个孕酮效应元件(PRE)。在用 pTG36hyg 进行的瞬时转染实验中,约 40ng 活性因子 IX/ml 培养基的生产可以通过 ELISA 和凝固检测显示出来(参见实施例 5 和实施例 6)。

[0142] 对于因子 IX 的生产,293T 细胞培养于 10% FCS 和 10 μ g/ml 维生素 K 补充的 DMEM 中(美国专利号:4,770,999;同样参见图 10)。首先,必须建立有效筛选稳定转染 293T 细胞的临界抗生素浓度。出于这个目的,所述细胞以低稀释度铺平板并在存在 10-800 μ g/ml 潮霉素 B 的情况下生长。两周后,在 200 μ g/ml 或更高的浓度下,没有细胞生长,因此选择这个浓度用于筛选稳定转染的细胞。

[0143] 293T 细胞在前一天以 1:15 传代后,在 10cm 的平皿中进行典型的转染。利用磷酸钙沉淀方法(Biotechniques 1998 6:7632-638)每平皿用 12 μ g 质粒转染,两天后,培养基更换为含有 200 μ g/ml 潮霉素 B 的新鲜培养基。选择 2-3 周后,通过 ELISA(参见实施例 5)检测所述培养基中因子 VIII 或因子 IX 的存在。分离阳性克隆并转移到 24 孔板上。经 ELISA 筛选和活性测定后,阳性克隆再进行两个循环的亚克隆,然后扩增并将等分部分冷冻以供进一步的应用和特性鉴定。

[0144] 实施例 9:通过原位免疫荧光检测因子 VIII 表达得到的稳定转染细胞表型一致性的证据:

[0145] 来自 DMEM+9.1% FBS 中贴壁培养物的 pTGF8-3 转染的 5×10^7 293T 细胞(克隆 49/19)和未转染 293T 细胞(阴性对照)全部通过胰酶消化从所述培养平皿中脱离,洗涤多次,然后重新悬浮于 5ml PBS 缓冲液中。

[0146] 2 μ l 的这些细胞悬浮液转移到无菌显微镜载玻片上,在室温下孵育直到所有液体蒸发。将细胞在 70% 的酒精中固定,然后在室温下干燥 5 分钟。通过含有 10% FBS 的 PBS 缓冲液中孵育,封闭玻片以防非特异性检测。第一抗体(羊(sh)抗 F VIII :C F8C-EIA-C, AffinityBiologicals)用含有 10% FBS 和 0.1% 皂苷的 PBS 缓冲液稀释 100 倍,然后在湿润的培养箱中室温孵育 60 分钟。用 PBS 充分洗涤后,制备 100 倍稀释的第二抗体(兔抗羊(rb)抗 sh)CY3 缀合物 313-165-003, Jackson ImmunoResearch)并根据上面所述方法进行

孵育。随后,充分洗涤所述显微镜制备物,然后用一层 50% 甘油和一个盖玻片覆盖。通过白光显微镜和荧光显微镜 (570nm 处发射) 观察细胞。

[0147] 结果描述于图 8 中。

[0148] 实施例 10:对于培养滤液中重组因子 IX 的热稳定性试验:

[0149] 将在 100 μ g/ml 维生素 K 存在下 pTGFG36 瞬时转染 48 小时后从 293T 细胞中收获并在 -80°C 下储存 7 天的培养滤液迅速解冻,分成 7 个 500 μ l 的等分部分,随后用等分部分进行下列的热孵育:

[0150]

样品	温度 ($^{\circ}\text{C}$)	时间 (分钟)
1	0	240
2	20	30
3	20	60
4	20	240
5	37	30
6	37	60
7	37	240

[0151] 将样品于冰上冷却,按照实施例 6 中所标明的测 FIX 活性 (双重测定) 检。结果显示于图 9 中。在达到于 37°C 至多 240 分钟的孵育条件下,活性几乎保持稳定。

序列表

<110> 奥克塔金尼有限责任公司 (Octagene GmbH)

<120> 重组凝血因子在人类细胞系中的生产

<130>010613wo/JH/ml

<140>

<141>

<160>17

<170>PatentIn Ver. 2.1

<210>1

<211>6996

<212>DNA

<213> 人 (Homo sapiens)

<220>

<221>CDS

<222>(1).. (6996)

<400>1

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atg caa agt gat ctc ggt gag ctg cct gtg gac gca aga ttt cct cct   96
Met Gln Ser Asp Leu Gly Glu Leu Pro Val Asp Ala Arg Phe Pro Pro
           20           25           30
aga gtg cca aaa tct ttt cca ttc aac acc tca gtc gtg tac aaa aag  144
Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val Val Tyr Lys Lys
           35           40           45
act ctg ttt gta gaa ttc acg gtt cac ctt ttc aac atc gct aag cca  192
Thr Leu Phe Val Glu Phe Thr Val His Leu Phe Asn Ile Ala Lys Pro
           50           55           60
agg cca ccc tgg atg ggt ctg cta ggt cct acc atc cag gct gag gtt  240
Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile Gln Ala Glu Val

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65	70	75	80	
tat gat aca gtg gtc att aca ctt aag aac atg gct tcc cat cct gtc				288
Tyr Asp Thr Val Val Ile Thr Leu Lys Ash Met Ala Ser His Pro Val				
	85	90	95	
agt ctt cat gct gtt ggt gta tcc tac tgg aaa gct tct gag gga gct				336
Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser Glu Gly Ala				
	100	105	110	
gaa tat gat gat cag acc agt caa agg gag aaa gaa gat gat aaa gtc				384
Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp Asp Lys Val				
	115	120	125	
ttc cct ggt gga agc cat aca tat gtc tgg cag gtc ctg aaa gag aat				432
Phe Pro Gly Gly Ser His Thr Tyr Val Trp Gln Val Leu Lys Glu Asn				
	130	135	140	
ggt cca atg gcc tct gac cca ctg tgc ctt acc tac tca tat ctt tct				480
Gly Pro Met Ala Ser Asp Pro Leu Cys Leu Thr Tyr Ser Tyr Leu Ser				
	145	150	155	160
cat gtg gac ctg gta aaa gac ttg aat tca ggc ctc att gga gcc cta				528
His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu Ile Gly Ala Leu				
	165	170	175	
cta gta tgt aga gaa ggg agt ctg gcc aag gaa aag aca cag acc ttg				576
Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys Thr Gln Thr Leu				
	180	185	190	
cac aaa ttt ata cta ctt ttt gct gta ttt gat gaa ggg aaa agt tgg				624
His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly Lys Ser Trp				
	195	200	205	
cac tca gaa aca aag aac tcc ttg atg cag gat agg gat gct gca tct				672
His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp Ala Ala Ser				
	210	215	220	
gct cgg gcc tgg cct aaa atg cac aca gtc aat ggt tat gta aac agg				720
Ala Arg Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr Val Asn Arg				
	225	230	235	240
tct ctg cca ggt ctg att gga tgc cac agg aaa tca gtc tat tgg cat				768
Ser Leu Pro Gly Leu Ile Gly Cys His Arg Lys Ser Val Tyr Trp His				
	245	250	255	
gtg att gga atg ggc acc act cct gaa gtg cac tca ata ttc ctc gaa				816
Val Ile Gly Met Gly Thr Thr Pro Glu Val His Ser Ile Phe Leu Glu				
	260	265	270	
ggt cac aca ttt ctt gtg agg aac cat cgc cag gcg tcc ttg gaa atc				864
Gly His Thr Phe Leu Val Arg Asn His Arg Gln Ala Ser Leu Glu Ile				

275	280	285	
tcg cca ata act ttc ctt act gct caa aca ctc ttg atg gac ctt gga			912
Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met Asp Leu Gly			
290	295	300	
cag ttt cta ctg ttt tgt cat atc tct tcc cac caa cat gat ggc atg			960
Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His Asp Gly Met			
305	310	315	320
gaa gct tat gtc aaa gta gac agc tgt cca gag gaa ccc caa cta cga			1008
Glu Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro Gln Leu Arg			
	325	330	335
atg aaa aat aat gaa gaa gcg gaa gac tat gat gat gat ctt act gat			1056
Met Lys Asn Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp Leu Thr Asp			
	340	345	350
tct gaa atg gat gtg gtc agg ttt gat gat gac aac tct cct tcc ttt			1104
Ser Glu Met Asp Val Val Arg Phe Asp Asp Asp Asn Ser Pro Ser Phe			
	355	360	365
atc caa att cgc tca gtt gcc aag aag cat cct aaa act tgg gta cat			1152
Ile Gln Ile Arg Ser Val Ala Lys Lys His Pro Lys Thr Trp Val His			
	370	375	380
tac att gct gct gaa gag gag gac tgg gac tat gct ccc tta gtc ctc			1200
Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr Ala Pro Leu Val Leu			
385	390	395	400
gcc ccc gat gac aga agt tat aaa agt caa tat ttg aac aat ggc cct			1248
Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn Asn Gly Pro			
	405	410	415
cag cgg att ggt agg aag tac aaa aaa gtc cga ttt atg gca tac aca			1296
Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met Ala Tyr Thr			
	420	425	430
gat gaa acc ttt aag act cgt gaa gct att cag cat gaa tca gga atc			1344
Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu Ser Gly Ile			
	435	440	445
ttg gga cct tta ctt tat ggg gaa gtt gga gac aca ctg ttg att ata			1392
Leu Gly Pro Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu Leu Ile Ile			
	450	455	460
ttt aag aat caa gca agc aga cca tat aac atc tac cct cac gga atc			1440
Phe Lys Asn Gln Ala Ser Arg Pro Tyr Asn Ile Tyr Pro His Gly Ile			
465	470	475	480
act gat gtc cgt cct ttg tat tca agg aga tta cca aaa ggt gta aaa			1488
Thr Asp Val Arg Pro Leu Tyr Ser Arg Arg Leu Pro Lys Gly Val Lys			

485	490	495	
cat ttg aag gat ttt cca att ctg cca gga gaa ata ttc aaa tat aaa			1536
His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile Phe Lys Tyr Lys			
500	505	510	
tgg aca gtg act gta gaa gat ggg cca act aaa tca gat cct cgg tgc			1584
Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp Pro Arg Cys			
515	520	525	
ctg acc cgc tat tac tct agt ttc gtt aat atg gag aga gat cta gct			1632
Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg Asp Leu Ala			
530	535	540	
tca gga ctc att ggc cct ctc ctc atc tgc tac aaa gaa tct gta gat			1680
Ser Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu Ser Val Asp			
545	550	555	560
caa aga gga aac cag ata atg tca gac aag agg aat gtc atc ctg ttt			1728
Gln Arg Gly Asn Gln Ile Met Ser Asp Lys Arg Asn Val Ile Leu Phe			
565	570	575	
tct gta ttt gat gag aac cga agc tgg tac ctc aca gag aat ata caa			1776
Ser Val Phe Asp Glu Asn Arg Ser Trp Tyr Leu Thr Glu Asn Ile Gln			
580	585	590	
cgc ttt ctc ccc aat cca gct gga gtg cag ctt gag gat cca gag ttc			1824
Arg Phe Leu Pro Asn Pro Ala Gly Val Gln Leu Glu Asp Pro Glu Phe			
595	600	605	
caa gcc tcc aac atc atg cac agc atc aat ggc tat gtt ttt gat agt			1872
Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val Phe Asp Ser			
610	615	620	
ttg cag ttg tca gtt tgt ttg cat gag gtg gca tac tgg tac att cta			1920
Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp Tyr Ile Leu			
625	630	635	640
agc att gga gca cag act gac ttc ctt tct gtc ttc ttc tct gga tat			1968
Ser Ile Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe Ser Gly Tyr			
645	650	655	
acc ttc aaa cac aaa atg gtc tat gaa gac aca ctc acc cta ttc cca			2016
Thr Phe Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr Leu Phe Pro			
660	665	670	
ttc tca gga gaa act gtc ttc atg tcg atg gaa aac cca ggt cta tgg			2064
Phe Ser Gly Glu Thr Val Phe Met Ser Met Glu Asn Pro Gly Leu Trp			
675	680	685	
att ctg ggg tgc cac aac tca gac ttt cgg aac aga ggc atg acc gcc			2112
Ile Leu Gly Cys His Asn Ser Asp Phe Arg Asn Arg Gly Met Thr Ala			

690	695	700	
tta ctg aag gtt tct agt tgt gac aag aac act ggt gat tat tac gag			2160
Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr Gly Asp Tyr Tyr Glu			
705	710	715	720
gac agt tat gaa gat att tca gca tac ttg ctg agt aaa aac aat gec			2208
Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys Asn Asn Ala			
	725	730	735
att gaa cca aga agc ttc tcc cag aat tca aga cac cct agc act agg			2256
Ile Glu Pro Arg Ser Phe Ser Gln Asn Ser Arg His Pro Ser Thr Arg			
	740	745	750
caa aag caa ttt aat gcc acc aca att cca gaa aat gac ata gag aag			2304
Gln Lys Gln Phe Asn Ala Thr Thr Ile Pro Glu Asn Asp Ile Glu Lys			
	755	760	765
act gac cct tgg ttt gca cac aga aca cct atg cct aaa ata caa aat			2352
Thr Asp Pro Trp Phe Ala His Arg Thr Pro Met Pro Lys Ile Gln Asn			
	770	775	780
gtc tcc tct agt gat ttg ttg atg ctc ttg cga cag agt cct act cca			2400
Val Ser Ser Ser Asp Leu Leu Met Leu Leu Arg Gln Ser Pro Thr Pro			
785	790	795	800
cat ggg cta tcc tta tct gat ctc caa gaa gcc aaa tat gag act ttt			2448
His Gly Leu Ser Leu Ser Asp Leu Gln Glu Ala Lys Tyr Glu Thr Phe			
	805	810	815
tct gat gat cca tca cct gga gca ata gac agt aat aac agc ctg tct			2496
Ser Asp Asp Pro Ser Pro Gly Ala Ile Asp Ser Asn Asn Ser Leu Ser			
	820	825	830
gaa atg aca cac ttc agg cca cag ctc cat cac agt ggg gac atg gta			2544
Glu Met Thr His Phe Arg Pro Gln Leu His His Ser Gly Asp Met Val			
	835	840	845
ttt acc cct gag tca ggc ctc caa tta aga tta aat gag aaa ctg ggg			2592
Phe Thr Pro Glu Ser Gly Leu Gln Leu Arg Leu Asn Glu Lys Leu Gly			
	850	855	860
aca act gca gca aca gag ttg aag aaa ctt gat ttc aaa gtt tct agt			2640
Thr Thr Ala Ala Thr Glu Leu Lys Lys Leu Asp Phe Lys Val Ser Ser			
865	870	875	880
aca tca aat aat ctg att tca aca att cca tca gac aat ttg gca gca			2688
Thr Ser Asn Asn Leu Ile Ser Thr Ile Pro Ser Asp Asn Leu Ala Ala			
	885	890	895
ggt act gat aat aca agt tcc tta gga ccc cca agt atg cca gtt cat			2736
Gly Thr Asp Asn Thr Ser Ser Leu Gly Pro Pro Ser Met Pro Val His			

900	905	910	
tat gat agt caa tta gat acc act cta ttt ggc aaa aag tca tct ccc			2784
Tyr Asp Ser Gln Leu Asp Thr Thr Leu Phe Gly Lys Lys Ser Ser Pro			
915	920	925	
ctt act gag tct ggt gga cct ctg agc ttg agt gaa gaa aat aat gat			2832
Leu Thr Glu Ser Gly Gly Pro Leu Ser Leu Ser Glu Glu Asn Asn Asp			
930	935	940	
tca aag ttg tta gaa tca ggt tta atg aat agc caa gaa agt tca tgg			2880
Ser Lys Leu Leu Glu Ser Gly Leu Met Asn Ser Gln Glu Ser Ser Trp			
945	950	955	960
gga aaa aat gta tcg tca aca gag agt ggt agg tta ttt aaa ggg aaa			2928
Gly Lys Asn Val Ser Ser Thr Glu Ser Gly Arg Leu Phe Lys Gly Lys			
965	970	975	
aga gct cat gga cct gct ttg ttg act aaa gat aat gcc tta ttc aaa			2976
Arg Ala His Gly Pro Ala Leu Leu Thr Lys Asp Asn Ala Leu Phe Lys			
980	985	990	
gtt agc atc tct ttg tta aag aca aac aaa act tcc aat aat tca gca			3024
Val Ser Ile Ser Leu Leu Lys Thr Asn Lys Thr Ser Asn Asn Ser Ala			
995	1000	1005	
act aat aga aag act cac att gat ggc cca tca tta tta att gag aat			3072
Thr Asn Arg Lys Thr His Ile Asp Gly Pro Ser Leu Leu Ile Glu Asn			
1010	1015	1020	
agt cca tca gtc tgg caa aat ata tta gaa agt gac act gag ttt aaa			3120
Ser Pro Ser Val Trp Gln Asn Ile Leu Glu Ser Asp Thr Glu Phe Lys			
1025	1030	1035	1040
aaa gtg aca cct ttg att cat gac aga atg ctt atg gac aaa aat gct			3168
Lys Val Thr Pro Leu Ile His Asp Arg Met Leu Met Asp Lys Asn Ala			
1045	1050	1055	
aca gct ttg agg cta aat cat atg tca aat aaa act act tca tca aaa			3216
Thr Ala Leu Arg Leu Asn His Met Ser Asn Lys Thr Thr Ser Ser Lys			
1060	1065	1070	
aac atg gaa atg gtc caa cag aaa aaa gag ggc ccc att cca cca gat			3264
Asn Met Glu Met Val Gln Gln Lys Lys Glu Gly Pro Ile Pro Pro Asp			
1075	1080	1085	
gca caa aat cca gat atg tcg ttc ttt aag atg cta ttc ttg cca gaa			3312
Ala Gln Asn Pro Asp Met Ser Phe Phe Lys Met Leu Phe Leu Pro Glu			
1090	1095	1100	
tca gca agg tgg ata caa agg act cat gga aag aac tct ctg aac tct			3360
Ser Ala Arg Trp Ile Gln Arg Thr His Gly Lys Asn Ser Leu Asn Ser			

1105	1110	1115	1120	
ggg caa ggc ccc agt cca aag caa tta gta tcc tta gga cca gaa aaa				3408
Gly Gln Gly Pro Ser Pro Lys Gln Leu Val Ser Leu Gly Pro Glu Lys				
	1125	1130	1135	
tct gtg gaa ggt cag aat ttc ttg tct gag aaa aac aaa gtg gta gta				3456
Ser Val Glu Gly Gln Asn Phe Leu Ser Glu Lys Asn Lys Val Val Val				
	1140	1145	1150	
gga aag ggt gaa ttt aca aag gac gta gga ctc aaa gag atg gtt ttt				3504
Gly Lys Gly Glu Phe Thr Lys Asp Val Gly Leu Lys Glu Met Val Phe				
	1155	1160	1165	
cca agc agc aga aac cta ttt ctt act aac ttg gat aat tta cat gaa				3552
Pro Ser Ser Arg Asn Leu Phe Leu Thr Asn Leu Asp Asn Leu His Glu				
	11701	175	1180	
aat aat aca cac aat caa gaa aaa aaa att cag gaa gaa ata gaa aag				3600
Asn Asn Thr His Asn Gln Glu Lys Lys Ile Gln Glu Glu Ile Glu Lys				
	1185	1190	1195	1200
aag gaa aca tta atc caa gag aat gta gtt ttg cct cag ata cat aca				3648
Lys Glu Thr Leu Ile Gln Glu Asn Val Val Leu Pro Gln Ile His Thr				
	1205	1210	1215	
gtg act ggc act aag aat ttc atg aag aac ctt ttc tta ctg agc act				3696
Val Thr Gly Thr Lys Asn Phe Met Lys Asn Leu Phe Leu Leu Ser Thr				
	1220	1225	1230	
agg caa aat gta gaa ggt tca tat gag ggg gca tat gct cca gta ctt				3744
Arg Gln Asn Val Glu Gly Ser Tyr Glu Gly Ala Tyr Ala Pro Val Leu				
	1235	1240	1245	
caa gat ttt agg tca tta aat gat tca aca aat aga aca aag aaa cac				3792
Gln Asp Phe Arg Ser Leu Asn Asp Ser Thr Asn Arg Thr Lys Lys His				
	1250	1255	1260	
aca gct cat ttc tca aaa aaa ggg gag gaa gaa aac ttg gaa ggc ttg				3840
Thr Ala His Phe Ser Lys Lys Glu Glu Glu Asn Leu Glu Gly Leu				
	1265	1270	1275	1280
gga aat caa acc aag caa att gta gag aaa tat gca tgc acc aca agg				3888
Gly Asn Gln Thr Lys Gln Ile Val Glu Lys Tyr Ala Cys Thr Thr Arg				
	1285	1290	1295	
ata tct cct aat aca agc cag cag aat ttt gtc acg caa cgt agt aag				3936
Ile Ser Pro Asn Thr Ser Gln Gln Asn Phe Val Thr Gln Arg Ser Lys				
	1300	1305	1310	
aga gct ttg aaa caa ttc aga ctc cca cta gaa gaa aca gaa ctt gaa				3984
Arg Ala Leu Lys Gln Phe Arg Leu Pro Leu Glu Glu Thr Glu Leu Glu				

1315	1320	1325	
aaa agg ata att gtg gat gac acc tca acc cag tgg tcc aaa aac atg			4032
Lys Arg Ile Ile Val Asp Asp Thr Ser Thr Gln Trp Ser Lys Asn Met			
1330	1335	1340	
aaa cat ttg acc ccg agc acc ctc aca cag ata gac tac aat gag aag			4080
Lys His Leu Thr Pro Ser Thr Leu Thr Gln Ile Asp Tyr Asn Glu Lys			
1345	1350	1355	1360
gag aaa ggg gcc att act cag tct ccc tta tca gat tgc ctt acg agg			4128
Glu Lys Gly Ala Ile Thr Gln Ser Pro Leu Ser Asp Cys Leu Thr Arg			
1365	1370	1375	
agt cat agc atc cct caa gca aat aga tct cca tta ccc att gca aag			4176
Ser His Ser Ile Pro Gln Ala Asn Arg Ser Pro Leu Pro Ile Ala Lys			
1380	1385	1390	
gta tca tca ttt cca tct att aga cct ata tat ctg acc agg gtc cta			4224
Val Ser Ser Phe Pro Ser Ile Arg Pro Ile Tyr Leu Thr Arg Val Leu			
1395	1400	1405	
ttc caa gac aac tct tct cat ctt cca gca gca tct tat aga aag aaa			4272
Phe Gln Asp Asn Ser Ser His Leu Pro Ala Ala Ser Tyr Arg Lys Lys			
1410	1415	1420	
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Asp Ser Gly Val Gln Glu Ser Ser His Phe Leu Gln Gly Ala Lys Lys			
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aat aac ctt tct tta gcc att cta acc ttg gag atg act ggt gat caa			4368
Asn Asn Leu Ser Leu Ala Ile Leu Thr Leu Glu Met Thr Gly Asp Gln			
1445	1450	1455	
aga gag gtt ggc tcc ctg ggg aca agt gcc aca aat tca gtc aca tac			4416
Arg Glu Val Gly Ser Leu Gly Thr Ser Ala Thr Asn Ser Val Thr Tyr			
1460	1465	1470	
aag aaa gtt gag aac act gtt ctc ccg aaa cca gac ttg ccc aaa aca			4464
Lys Lys Val Glu Asn Thr Val Leu Pro Lys Pro Asp Leu Pro Lys Thr			
1475	1480	1485	
tct ggc aaa gtt gaa ttg ctt cca aaa gtt cac att tat cag aag gac			4512
Ser Gly Lys Val Glu Leu Leu Pro Lys Val His Ile Tyr Gln Lys Asp			
1490	1495	1500	
cta ttc cct acg gaa act agc aat ggg tct cct ggc cat ctg gat ctc			4560
Leu Phe Pro Thr Glu Thr Ser Asn Gly Ser Pro Gly His Leu Asp Leu			
1505	1510	1515	1520
gtg gaa ggg agc ctt ctt cag gga aca gag gga gcg att aag tgg aat			4608
Val Glu Gly Ser Leu Leu Gln Gly Thr Glu Gly Ala Ile Lys Trp Asn			

1525	1530	1535	
gaa gca aac aga cct gga aaa gtt ccc ttt ctg aga gta gca aca gaa			4656
Glu Ala Asn Arg Pro Gly Lys Val Pro Phe Leu Arg Val Ala Thr Glu			
1540	1545	1550	
agc tct gca aag act ccc tcc aag cta ttg gat cct ctt gct tgg gat			4704
Ser Ser Ala Lys Thr Pro Ser Lys Leu Leu Asp Pro Leu Ala Trp Asp			
1555	1560	1565	
aac cac tat ggt act cag ata cca aaa gaa gag tgg aaa tcc caa gag			4752
Asn His Tyr Gly Thr Gln Ile Pro Lys Glu Glu Trp Lys Ser Gln Glu			
1570	1575	1580	
aag tca cca gaa aaa aca gct ttt aag aaa aag gat acc att ttg tcc			4800
Lys Ser Pro Glu Lys Thr Ala Phe Lys Lys Lys Asp Thr Ile Leu Ser			
1585	1590	1595	1600
ctg aac gct tgt gaa agc aat cat gca ata gca gca ata aat gag gga			4848
Leu Asn Ala Cys Glu Ser Asn His Ala Ile Ala Ala Ile Asn Glu Gly			
1605	1610	1615	
caa aat aag ccc gaa ata gaa gtc acc tgg gca aag caa ggt agg act			4896
Gln Asn Lys Pro Glu Ile Glu Val Thr Trp Ala Lys Gln Gly Arg Thr			
1620	1625	1630	
gaa agg ctg tgc tct caa aac cca cca gtc ttg aaa cgc cat caa cgg			4944
Glu Arg Leu Cys Ser Gln Asn Pro Pro Val Leu Lys Arg His Gln Arg			
1635	1640	1645	
gaa ata act cgt act act ctt cag tca gat caa gag gaa att gac tat			4992
Glu Ile Thr Arg Thr Thr Leu Gln Ser Asp Gln Glu Glu Ile Asp Tyr			
1650	1655	1660	
gat gat acc ata tca gtt gaa atg aag aag gaa gat ttt gac att tat			5040
Asp Asp Thr Ile Ser Val Glu Met Lys Lys Glu Asp Phe Asp Ile Tyr			
1665	1670	1675	1680
gat gag gat gaa aat cag agc ccc cgc agc ttt caa aag aaa aca cga			5088
Asp Glu Asp Glu Asn Gln Ser Pro Arg Ser Phe Gln Lys Lys Thr Arg			
1685	1690	1695	
cac tat ttt att gct gca gtg gag agg ctc tgg gat tat ggg atg agt			5136
His Tyr Phe Ile Ala Ala Val Glu Arg Leu Trp Asp Tyr Gly Met Ser			
1700	1705	1710	
agc tcc cca cat gtt cta aga aac agg gct cag agt ggc agt gtc cct			5184
Ser Ser Pro His Val Leu Arg Asn Arg Ala Gln Ser Gly Ser Val Pro			
1715	1720	1725	
cag ttc aag aaa gtt gtt ttc cag gaa ttt act gat ggc tcc ttt act			5232
Gln Phe Lys Lys Val Val Phe Gln Glu Phe Thr Asp Gly Ser Phe Thr			

1730	1735	1740	
cag ccc tta tac cgt gga gaa cta aat gaa cat ttg gga ctc ctg ggg			5280
Gln Pro Leu Tyr Arg Gly Glu Leu Asn Glu His Leu Gly Leu Leu Gly			
1745	1750	1755	1760
cca tat ata aga gca gaa gtt gaa gat aat atc atg gta act ttc aga			5328
Pro Tyr Ile Arg Ala Glu Val Glu Asp Asn Ile Met Val Thr Phe Arg			
	1765	1770	1775
aat cag gcc tct cgt ccc tat tcc ttc tat tct agc ctt att tct tat			5376
Asn Gln Ala Ser Arg Pro Tyr Ser Phe Tyr Ser Ser Leu Ile Ser Tyr			
	1780	1785	1790
gag gaa gat cag agg caa gga gca gaa cct aga aaa aac ttt gtc aag			5424
Glu Glu Asp Gln Arg Gln Gly Ala Glu Pro Arg Lys Asn Phe Val Lys			
	1795	1800	1805
cct aat gaa acc aaa act tac ttt tgg aaa gtg caa cat cat atg gca			5472
Pro Asn Glu Thr Lys Thr Tyr Phe Trp Lys Val Gln His His Met Ala			
	1810	1815	1820
ccc act aaa gat gag ttt gac tgc aaa gcc tgg gct tat ttc tct gat			5520
Pro Thr Lys Asp Glu Phe Asp Cys Lys Ala Trp Ala Tyr Phe Ser Asp			
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gtt gac ctg gaa aaa gat gtg cac tca ggc ctg att gga ccc ctt ctg			5568
Val Asp Leu Glu Lys Asp Val His Ser Gly Leu Ile Gly Pro Leu Leu			
	1845	1850	1855
gtc tgc cac act aac aca ctg aac cct gct cat ggg aga caa gtg aca			5616
Val Cys His Thr Asn Thr Leu Asn Pro Ala His Gly Arg Gln Val Thr			
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gta cag gaa ttt gct ctg ttt ttc acc atc ttt gat gag acc aaa agc			5664
Val Gln Glu Phe Ala Leu Phe Phe Thr Ile Phe Asp Glu Thr Lys Ser			
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tgg tac ttc act gaa aat atg gaa aga aac tgc agg gct ccc tgc aat			5712
Trp Tyr Phe Thr Glu Asn Met Glu Arg Asn Cys Arg Ala Pro Cys Asn			
	1890	1895	1900
atc cag atg gaa gat ccc act ttt aaa gag aat tat cgc ttc cat gca			5760
Ile Gln Met Glu Asp Pro Thr Phe Lys Glu Asn Tyr Arg Phe His Ala			
	1905	1910	1915
atc aat ggc tac ata atg gat aca cta cct ggc tta gta atg gct cag			5808
Ile Asn Gly Tyr Ile Met Asp Thr Leu Pro Gly Leu Val Met Ala Gln			
	1925	1930	1935
gat caa agg att cga tgg tat ctg ctc agc atg ggc agc aat gaa aac			5856
Asp Gln Arg Ile Arg Trp Tyr Leu Leu Ser Met Gly Ser Asn Glu Asn			

1940	1945	1950	
atc cat tct att cat ttc agt gga cat gtg ttc act gta cga aaa aaa			5904
Ile His Ser Ile His Phe Ser Gly His Val Phe Thr Val Arg Lys Lys			
1955	1960	1965	
gag gag tat aaa atg gca ctg tac aat ctc tat cca ggt gtt ttt gag			5952
Glu Glu Tyr Lys Met Ala Leu Tyr Asn Leu Tyr Pro Gly Val Phe Glu			
1970	1975	1980	
aca gtg gaa atg tta cca tcc aaa gct gga att tgg cgg gtg gaa tgc			6000
Thr Val Glu Met Leu Pro Ser Lys Ala Gly Ile Trp Arg Val Glu Cys			
1985	1990	1995	2000
ctt att ggc gag cat cta cat gct ggg atg agc aca ctt ttt ctg gtg			6048
Leu Ile Gly Glu His Leu His Ala Gly Met Ser Thr Leu Phe Leu Val			
2005	2010	2015	
tac agc aat aag tgt cag act ccc ctg gga atg gct tct gga cac att			6096
Tyr Ser Asn Lys Cys Gln Thr Pro Leu Gly Met Ala Ser Gly His Ile			
2020	2025	2030	
aga gat ttt cag att aca gct tca gga caa tat gga cag tgg gcc cca			6144
Arg Asp Phe Gln Ile Thr Ala Ser Gly Gln Tyr Gly Gln Trp Ala Pro			
2035	2040	2045	
aag ctg gcc aga ctt cat tat tcc gga tca atc aat gcc tgg agc acc			6192
Lys Leu Ala Arg Leu His Tyr Ser Gly Ser Ile Asn Ala Trp Ser Thr			
2050	2055	2060	
aag gag ccc ttt tct tgg atc aag gtg gat ctg ttg gca cca atg att			6240
Lys Glu Pro Phe Ser Trp Ile Lys Val Asp Leu Leu Ala Pro Met Ile			
2065	2070	2075	2080
att cac ggc atc aag acc cag ggt gcc cgt cag aag ttc tcc agc ctc			6288
Ile His Gly Ile Lys Thr Gln Gly Ala Arg Gln Lys Phe Ser Ser Leu			
2085	2090	2095	
tac atc tct cag ttt atc atc atg tat agt ctt gat ggg aag aag tgg			6336
Tyr Ile Ser Gln Phe Ile Ile Met Tyr Ser Leu Asp Gly Lys Lys Trp			
2100	2105	2110	
cag act tat cga gga aat tcc act gga acc tta atg gtc ttc ttt ggc			6384
Gln Thr Tyr Arg Gly Asn Ser Thr Gly Thr Leu Met Val Phe Phe Gly			
2115	2120	2125	
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Asn Val Asp Ser Ser Gly Ile Lys His Asn Ile Phe Asn Pro Pro Ile			
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att gct cga tac atc cgt ttg cac cca act cat tat agc att cgc agc			6480
Ile Ala Arg Tyr Ile Arg Leu His Pro Thr His Tyr Ser Ile Arg Ser			

2145	2150	2155	2160	
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Thr Leu Arg Met Glu Leu Met Gly Cys Asp Leu Asn Ser Cys Ser Met				
	2165	2170	2175	
cca ttg gga atg gag agt aaa gca ata tca gat gca cag att act gct				6576
Pro Leu Gly Met Glu Ser Lys Ala Ile Ser Asp Ala Gln Ile Thr Ala				
	2180	2185	2190	
tca tcc tac ttt acc aat atg ttt gcc acc tgg tct cct tca aaa gct				6624
Ser Ser Tyr Phe Thr Asn Met Phe Ala Thr Trp Ser Pro Ser Lys Ala				
	2195	2200	2205	
cga ctt cac ctc caa ggg agg agt aat gcc tgg aga cct cag gtg aat				6672
Arg Leu His Leu Gln Gly Arg Ser Asn Ala Trp Arg Pro Gln Val Asn				
	2210	2215	2220	
aat cca aaa gag tgg ctg caa gtg gac ttc cag aag aca atg aaa gtc				6720
Asn Pro Lys Glu Trp Leu Gln Val Asp Phe Gln Lys Thr Met Lys Val				
	2225	2230	2235	2240
aca gga gta act act cag gga gta aaa tct ctg ctt acc agc atg tat				6768
Thr Gly Val Thr Thr Gln Gly Val Lys Ser Leu Leu Thr Ser Met Tyr				
	2245	2250	2255	
gtg aag gag ttc ctc atc tcc agc agt caa gat ggc cat cag tgg act				6816
Val Lys Glu Phe Leu Ile Ser Ser Ser Gln Asp Gly His Gln Trp Thr				
	2260	2265	2270	
ctc ttt ttt cag aat ggc aaa gta aag gtt ttt cag gga aat caa gac				6864
Leu Phe Phe Gln Asn Gly Lys Val Lys Val Phe Gln Gly Asn Gln Asp				
	2275	2280	2285	
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Ser Phe Thr Pro Val Val Asn Ser Leu Asp Pro Pro Leu Leu Thr Arg				
	2290	2295	2300	
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Tyr Leu Arg Ile His Pro Gln Ser Trp Val His Gln Ile Ala Leu Arg				
	2305	2310	2315	2320
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Met Glu Val Leu Gly Cys Glu Ala Gln Asp Leu Tyr				
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<212>PRT

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20 25 30
Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val Val Tyr Lys Lys
35 40 45
Thr Leu Phe Val Glu Phe Thr Val His Leu Phe Asn Ile Ala Lys Pro
50 55 60
Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile Gln Ala Glu Val
65 70 75 80
Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser His Pro Val
85 90 95
Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser Glu Gly Ala
100 105 110
Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp Asp Lys Val
115 120 125
Phe Pro Gly Gly Ser His Thr Tyr Val Trp Gln Val Leu Lys Glu Asn
130 135 140
Gly Pro Met Ala Ser Asp Pro Leu Cys Leu Thr Tyr Ser Tyr Leu Ser
145 150 155 160
His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu Ile Gly Ala Leu
165 170 175
Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys Thr Gln Thr Leu
180 185 190
His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly Lys Ser Trp
195 200 205
His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp Ala Ala Ser
210 215 220
Ala Arg Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr Val Asn Arg
225 230 235 240
Ser Leu Pro Gly Leu Ile Gly Cys His Arg Lys Ser Val Tyr Trp His
245 250 255
Val Ile Gly Met Gly Thr Thr Pro Glu Val His Ser Ile Phe Leu Glu
260 265 270
Gly His Thr Phe Leu Val Arg Asn His Arg Gln Ala Ser Leu Glu Ile
275 280 285
Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met Asp Leu Gly
290 295 300

Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His Asp Gly Met																			
305					310					315									320
Glu Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro Gln Leu Arg																			
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Met Lys Asn Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp Leu Thr Asp																			
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Ser Glu Met Asp Val Val Arg Phe Asp Asp Asp Asn Ser Pro Ser Phe																			
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Ile Gln Ile Arg Ser Val Ala Lys Lys His Pro Lys Thr Trp Val His																			
					370					375									380
Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr Ala Pro Leu Val Leu																			
385					390					395									400
Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn Asn Gly Pro																			
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Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met Ala Tyr Thr																			
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Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu Ser Gly Ile																			
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Leu Gly Pro Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu Leu Ile Ile																			
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Phe Lys Asn Gln Ala Ser Arg Pro Tyr Asn Ile Tyr Pro His Gly Ile																			
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Thr Asp Val Arg Pro Leu Tyr Ser Arg Arg Leu Pro Lys Gly Val Lys																			
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His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile Phe Lys Tyr Lys																			
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Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp Pro Arg Cys																			
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Ser Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu Ser Val Asp																			
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Ser Val Phe Asp Glu Asn Arg Ser Trp Tyr Leu Thr Glu Asn Ile Gln																			
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Arg Phe Leu Pro Asn Pro Ala Gly Val Gln Leu Glu Asp Pro Glu Phe																			
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Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val Phe Asp Ser																			

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Ser Ile Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe Ser Gly Tyr		640
	645	650
Thr Phe Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr Leu Phe Pro		655
	660	665
Phe Ser Gly Glu Thr Val Phe Met Ser Met Glu Asn Pro Gly Leu Trp		670
	675	680
Ile Leu Gly Cys His Asn Ser Asp Phe Arg Asn Arg Gly Met Thr Ala		685
690	695	700
Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr Gly Asp Tyr Tyr Glu		
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Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys Asn Asn Ala		720
	725	730
Ile Glu Pro Arg Ser Phe Ser Gln Asn Ser Arg His Pro Ser Thr Arg		735
	740	745
Gln Lys Gln Phe Asn Ala Thr Thr Ile Pro Glu Asn Asp Ile Glu Lys		750
	755	760
Thr Asp Pro Trp Phe Ala His Arg Thr Pro Met Pro Lys Ile Gln Asn		765
	770	775
Val Ser Ser Ser Asp Leu Leu Met Leu Leu Arg Gln Ser Pro Thr Pro		780
785	790	795
His Gly Leu Ser Leu Ser Asp Leu Gln Glu Ala Lys Tyr Glu Thr Phe		800
	805	810
Ser Asp Asp Pro Ser Pro Gly Ala Ile Asp Ser Asn Asn Ser Leu Ser		815
	820	825
Glu Met Thr His Phe Arg Pro Gln Leu His His Ser Gly Asp Met Val		830
	835	840
Phe Thr Pro Glu Ser Gly Leu Gln Leu Arg Leu Asn Glu Lys Leu Gly		845
	850	855
Thr Thr Ala Ala Thr Glu Leu Lys Lys Leu Asp Phe Lys Val Ser Ser		860
865	870	875
Thr Ser Asn Asn Leu Ile Ser Thr Ile Pro Ser Asp Asn Leu Ala Ala		880
	885	890
Gly Thr Asp Asn Thr Ser Ser Leu Gly Pro Pro Ser Met Pro Val His		895
	900	905
Tyr Asp Ser Gln Leu Asp Thr Thr Leu Phe Gly Lys Lys Ser Ser Pro		910
	915	920
		925

Leu Thr Glu Ser Gly Gly Pro Leu Ser Leu Ser Glu Glu Asn Asn Asp
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 Ser Lys Leu Leu Glu Ser Gly Leu Met Asn Ser Gln Glu Ser Ser Trp
 945 950 955 960
 Gly Lys Asn Val Ser Ser Thr Glu Ser Gly Arg Leu Phe Lys Gly Lys
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 Arg Ala His Gly Pro Ala Leu Leu Thr Lys Asp Asn Ala Leu Phe Lys
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 Lys Val Thr Pro Leu Ile His Asp Arg Met Leu Met Asp Lys Asn Ala
 1045 1050 1055
 Thr Ala Leu Arg Leu Asn His Met Ser Asn Lys Thr Thr Ser Ser Lys
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 1140 1145 1150
 Gly Lys Gly Glu Phe Thr Lys Asp Val Gly Leu Lys Glu Met Val Phe
 1155 1160 1165
 Pro Ser Ser Arg Asn Leu Phe Leu Thr Asn Leu Asp Asn Leu His Glu
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 Lys Glu Thr Leu Ile Gln Glu Asn Val Val Leu Pro Gln Ile His Thr
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 Val Thr Gly Thr Lys Asn Phe Met Lys Asn Leu Phe Leu Leu Ser Thr
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265	1270	1275	1280
Gly Asn Gln Thr Lys Gln Ile Val Glu Lys Tyr Ala Cys Thr Thr Arg			
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Ile Ser Pro Asn Thr Ser Gln Gln Asn Phe Val Thr Gln Arg Ser Lys			
1300	1305	1310	
Arg Ala Leu Lys Gln Phe Arg Leu Pro Leu Glu Glu Thr Glu Leu Glu			
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Lys Arg Ile Ile Val Asp Asp Thr Ser Thr Gln Trp Ser Lys Asn Met			
1330	1335	1340	
Lys His Leu Thr Pro Ser Thr Leu Thr Gln Ile Asp Tyr Asn Glu Lys			
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Glu Lys Gly Ala Ile Thr Gln Ser Pro Leu Ser Asp Cys Leu Thr Arg			
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Val Ser Ser Phe Pro Ser Ile Arg Pro Ile Tyr Leu Thr Arg Val Leu			
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Asp Ser Gly Val Gln Glu Ser Ser His Phe Leu Gln Gly Ala Lys Lys			
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1540	1545	1550	

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 His Tyr Phe Ile Ala Ala Val Glu Arg Leu Trp Asp Tyr Gly Met Ser
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 Ser Ser Pro His Val Leu Arg Asn Arg Ala Gln Ser Gly Ser Val Pro
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 Val Cys His Thr Asn Thr Leu Asn Pro Ala His Gly Arg Gln Val Thr

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1890	1895	1900	
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905	1910	1915	1920
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1925	1930	1935	
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1940	1945	1950	
Ile His Ser Ile His Phe Ser Gly His Val Phe Thr Val Arg Lys Lys			
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Gln Thr Tyr Arg Gly Asn Ser Thr Gly Thr Leu Met Val Phe Phe Gly			
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Val Asp Ala Arg Phe Pro Pro Arg Val Pro Lys Ser Phe Pro Phe Asn
          30                      35                      40
acc tca gtc gtg tac aaa aag act ctg ttt gta gaa ttc acg gat cac 903
Thr Ser Val Val Tyr Lys Lys Thr Leu Phe Val Glu Phe Thr Asp His
          45                      50                      55
ctt ttc aac atc gct aag cca agg cca ccc tgg atg ggt ctg cta ggt 951
Leu Phe Asn Ile Ala Lys Pro Arg Pro Pro Trp Met Gly Leu Leu Gly
          60                      65                      70
cct acc atc cag gct gag gtt tat gat aca gtg gtc att aca ctt aag 999
Pro Thr Ile Gln Ala Glu Val Tyr Asp Thr Val Val Ile Thr Leu Lys
          75                      80                      85
aac atg gct tcc cat cct gtc agt ctt cat gct gtt ggt gta tcc tac 1047
Asn Met Ala Ser His Pro Val Ser Leu His Ala Val Gly Val Ser Tyr
  90                      95                      100                      105
tgg aaa gct tct gag gga gct gaa tat gat gat cag acc agt caa agg 1095
Trp Lys Ala Ser Glu Gly Ala Glu Tyr Asp Asp Gln Thr Ser Gln Arg
          110                      115                      120
gag aaa gaa gat gat aaa gtc ttc cct ggt gga agc cat aca tat gtc 1143
Glu Lys Glu Asp Asp Lys Val Phe Pro Gly Gly Ser His Thr Tyr Val

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125	130	135	
tgg cag gtc ctg aaa gag aat ggt cca atg gcc tct gac cca ctg tgc			1191
Trp Gln Val Leu Lys Glu Asn Gly Pro Met Ala Ser Asp Pro Leu Cys			
140	145	150	
ctt acc tac tca tat ctt tct cat gcg gac ctg gta aaa gac ttg aat			1239
Leu Thr Tyr Ser Tyr Leu Ser His Ala Asp Leu Val Lys Asp Leu Asn			
155	160	165	
tca ggc ctc att gga gcc cta cta gta tgt aga gaa ggg agt ctg gcc			1287
Ser Gly Leu Ile Gly Ala Leu Leu Val Cys Arg Glu Gly Ser Leu Ala			
170	175	180	185
aag gaa aag aca cag acc ttg cac aaa ttt ata cta ctt ttt gct gta			1335
Lys Glu Lys Thr Gln Thr Leu His Lys Phe Ile Leu Leu Phe Ala Val			
190	195	200	
ttt gat gaa ggg aaa agt tgg cac tca gaa aca aag aac tcc ttg atg			1383
Phe Asp Glu Gly Lys Ser Trp His Ser Glu Thr Lys Asn Ser Leu Met			
205	210	215	
cag gat agg gat gct gca tct gct cgg gcc tgg cct aaa atg cac aca			1431
Gln Asp Arg Asp Ala Ala Ser Ala Arg Ala Trp Pro Lys Met His Thr			
220	225	230	
gtc aat ggt tat gta aac agg tct ctg cca ggt ctg att gga tgc cac			1479
Val Asn Gly Tyr Val Asn Arg Ser Leu Pro Gly Leu Ile Gly Cys His			
235	240	245	
agg aaa tca gtc tat tgg cat gtg att gga atg ggc acc act cct gaa			1527
Arg Lys Ser Val Tyr Trp His Val Ile Gly Met Gly Thr Thr Pro Glu			
250	255	260	265
gtg cac tca ata ttc ctc gaa ggt cac aca ttt ctt gtg agg aac cat			1575
Val His Ser Ile Phe Leu Glu Gly His Thr Phe Leu Val Arg Asn His			
270	275	280	
cgc cag gcg tcc ttg gaa atc tcg cca ata act ttc ctt act gct caa			1623
Arg Gln Ala Ser Leu Glu Ile Ser Pro Ile Thr Phe Leu Thr Ala Gln			
285	290	295	
aca ctc ttg atg gac ctt gga cag ttt cta ctg ttt tgt cat atc tct			1671
Thr Leu Leu Met Asp Leu Gly Gln Phe Leu Leu Phe Cys His Ile Ser			
300	305	310	
tcc cac caa cat gat ggc atg gaa gct tat gtc aaa gta gac agc tgt			1719
Ser His Gln His Asp Gly Met Glu Ala Tyr Val Lys Val Asp Ser Cys			
315	320	325	
cca gag gaa ccc caa cta cga atg aaa aat aat gaa gaa gcg gaa gac			1767
Pro Glu Glu Pro Gln Leu Arg Met Lys Asn Asn Glu Glu Ala Glu Asp			

330	335	340	345	
tat gat gat gat ctt act gat tct gaa atg gat gtg gtc agg ttt gat				1815
Tyr Asp Asp Asp Leu Thr Asp Ser Glu Met Asp Val Val Arg Phe Asp				
	350	355	360	
gat gac aac tct cct tcc ttt atc caa att cgc tca gtt gcc aag aag				1863
Asp Asp Asn Ser Pro Ser Phe Ile Gln Ile Arg Ser Val Ala Lys Lys				
	365	370	375	
cat cct aaa act tgg gta cat tac att gct gct gaa gag gag gac tgg				1911
His Pro Lys Thr Trp Val His Tyr Ile Ala Ala Glu Glu Glu Asp Trp				
	380	385	390	
gac tat gct ccc tta gtc ctc gcc ccc gat gac aga agt tat aaa agt				1959
Asp Tyr Ala Pro Leu Val Leu Ala Pro Asp Asp Arg Ser Tyr Lys Ser				
	395	400	405	
caa tat ttg aac aat ggc cct cag cgg att ggt agg aag tac aaa aaa				2007
Gln Tyr Leu Asn Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr Lys Lys				
410	415	420	425	
gtc cga ttt atg gca tac aca gat gaa acc ttt aag act cgt gaa gct				2055
Val Arg Phe Met Ala Tyr Thr Asp Glu Thr Phe Lys Thr Arg Glu Ala				
	430	435	440	
att cag cat gaa tca gga atc ttg gga cct tta ctt tat ggg gaa gtt				2103
Ile Gln His Glu Ser Gly Ile Leu Gly Pro Leu Leu Tyr Gly Glu Val				
	445	450	455	
gga gac aca ctg ttg att ata ttt aag aat caa gca agc aga cca tat				2151
Gly Asp Thr Leu Leu Ile Ile Phe Lys Asn Gln Ala Ser Arg Pro Tyr				
	460	465	470	
aac atc tac cct cac gga atc act gat gtc cgt cct ttg tat tca agg				2199
Asn Ile Tyr Pro His Gly Ile Thr Asp Val Arg Pro Leu Tyr Ser Arg				
	475	480	485	
aga tta cca aaa ggt gta aaa cat ttg aag gat ttt cca att ctg cca				2247
Arg Leu Pro Lys Gly Val Lys His Leu Lys Asp Phe Pro Ile Leu Pro				
490	495	500	505	
gga gaa ata ttc aaa tat aaa tgg aca gtg act gta gaa gat ggg cca				2295
Gly Glu Ile Phe Lys Tyr Lys Trp Thr Val Thr Val Glu Asp Gly Pro				
	510	515	520	
act aaa tca gat cct cgg tgc ctg acc cgc tat tac tct agt ttc gtt				2343
Thr Lys Ser Asp Pro Arg Cys Leu Thr Arg Tyr Tyr Ser Ser Phe Val				
	525	530	535	
aat atg gag aga gat cta gct tca gga ctc att ggc cct ctc ctc atc				2391
Asn Met Glu Arg Asp Leu Ala Ser Gly Leu Ile Gly Pro Leu Leu Ile				

540	545	550	
tgc tac aaa gaa tct gta gat caa aga gga aac cag ata atg tca gac			2439
Cys Tyr Lys Glu Ser Val Asp Gln Arg Gly Asn Gln Ile Met Ser Asp			
555	560	565	
aag agg aat gtc atc ctg ttt tct gta ttt gat gag aac cga agc tgg			2487
Lys Arg Asn Val Ile Leu Phe Ser Val Phe Asp Glu Asn Arg Ser Trp			
570	575	580	585
tac ctc aca gag aat ata caa cgc ttt ctc ccc aat cca gct gga gtg			2535
Tyr Leu Thr Glu Asn Ile Gln Arg Phe Leu Pro Asn Pro Ala Gly Val			
	590	595	600
cag ctt gag gat cca gag ttc caa gcc tcc aac atc atg cac agc atc			2583
Gln Leu Glu Asp Pro Glu Phe Gln Ala Ser Asn Ile Met His Ser Ile			
	605	610	615
aat ggc tat gtt ttt gat agt ttg cag ttg tca gtt tgt ttg cat gag			2631
Asn Gly Tyr Val Phe Asp Ser Leu Gln Leu Ser Val Cys Leu His Glu			
	620	625	630
gtg gca tac tgg tac att cta agc att gga gca cag act gac ttc ctt			2679
Val Ala Tyr Trp Tyr Ile Leu Ser Ile Gly Ala Gln Thr Asp Phe Leu			
	635	640	645
tct gtc ttc ttc tct gga tat acc ttc aaa cac aaa atg gtc tat gaa			2727
Ser Val Phe Phe Ser Gly Tyr Thr Phe Lys His Lys Met Val Tyr Glu			
650	655	660	665
gac aca ctc acc cta ttc cca ttc tca gga gaa act gtc ttc atg tcg			2775
Asp Thr Leu Thr Leu Phe Pro Phe Ser Gly Glu Thr Val Phe Met Ser			
	670	675	680
atg gaa aac cca ggt cta tgg att ctg ggg tgc cac aac tca gac ttt			2823
Met Glu Asn Pro Gly Leu Trp Ile Leu Gly Cys His Asn Ser Asp Phe			
	685	690	695
cgg aac aga ggc atg acc gcc tta ctg aag gtt tct agt tgt gac aag			2871
Arg Asn Arg Gly Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asp Lys			
	700	705	710
aac act ggt gat tat tac gag gac agt tat gaa gat att tca gca tac			2919
Asn Thr Gly Asp Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser Ala Tyr			
	715	720	725
ttg ctg agt aaa aac aat gcc att gaa cca aga agc ttc tcc cag aat			2967
Leu Leu Ser Lys Asn Asn Ala Ile Glu Pro Arg Ser Phe Ser Gln Asn			
730	735	740	745
tca aga cat caa gct tat cga tac cgt cga ggg gaa ata act cgt act			3015
Ser Arg His Gln Ala Tyr Arg Tyr Arg Arg Gly Glu Ile Thr Arg Thr			

750	755	760	
act ctt cag tca gat caa gag gaa att gac tat gat gat acc ata tca			3063
Thr Leu Gln Ser Asp Gln Glu Glu Ile Asp Tyr Asp Asp Thr Ile Ser			
765	770	775	
gtt gaa atg aag aag gaa gat ttt gac att tat gat gag gat gaa aat			3111
Val Glu Met Lys Lys Glu Asp Phe Asp Ile Tyr Asp Glu Asp Glu Asn			
780	785	790	
cag agc ccc cgc agc ttt caa aag aaa aca cga cac tat ttt att gct			3159
Gln Ser Pro Arg Ser Phe Gln Lys Lys Thr Arg His Tyr Phe Ile Ala			
795	800	805	
gca gtg gag agg ctc tgg gat tat ggg atg agt agc tcc cca cat gtt			3207
Ala Val Glu Arg Leu Trp Asp Tyr Gly Met Ser Ser Ser Pro His Val			
810	815	820	825
cta aga aac agg gct cag agt ggc agt gtc cct cag ttc aag aaa gtt			3255
Leu Arg Asn Arg Ala Gln Ser Gly Ser Val Pro Gln Phe Lys Lys Val			
830	835	840	
gtt ttc cag gaa ttt act gat ggc tcc ttt act cag ccc tta tac cgt			3303
Val Phe Gln Glu Phe Thr Asp Gly Ser Phe Thr Gln Pro Leu Tyr Arg			
845	850	855	
gga gaa cta aat gaa cat ttg gga ctc ctg ggg cca tat ata aga gca			3351
Gly Glu Leu Asn Glu His Leu Gly Leu Leu Gly Pro Tyr Ile Arg Ala			
860	865	870	
gaa gtt gaa gat aat atc atg gta act ttc aga aat cag gcc tct cgt			3399
Glu Val Glu Asp Asn Ile Met Val Thr Phe Arg Asn Gln Ala Ser Arg			
875	880	885	
ccc tat tcc ttc tat tct agc ctt att tct tat gag gaa gat cag agg			3447
Pro Tyr Ser Phe Tyr Ser Ser Leu Ile Ser Tyr Glu Glu Asp Gln Arg			
890	895	900	905
caa gga gca gaa cct aga aaa aac ttt gtc aag cct aat gaa acc aaa			3495
Gln Gly Ala Glu Pro Arg Lys Asn Phe Val Lys Pro Asn Glu Thr Lys			
910	915	920	
act tac ttt tgg aaa gtg caa cat cat atg gca ccc act aaa gat gag			3543
Thr Tyr Phe Trp Lys Val Gln His His Met Ala Pro Thr Lys Asp Glu			
925	930	935	
ttt gac tgc aaa gcc tgg gct tat ttc tct gat gtt gac ctg gaa aaa			3591
Phe Asp Cys Lys Ala Trp Ala Tyr Phe Ser Asp Val Asp Leu Glu Lys			
940	945	950	
gat gtg cac tca ggc ctg att gga ccc ctt ctg gtc tgc cac act aac			3639
Asp Val His Ser Gly Leu Ile Gly Pro Leu Leu Val Cys His Thr Asn			

955	960	965	
aca ctg aac cct gct cat ggg aga caa gtg aca gta cag gaa ttt gct			3687
Thr Leu Asn Pro Ala His Gly Arg Gln Val Thr Val Gln Glu Phe Ala			
970	975	980	985
ctg ttt ttc acc atc ttt gat gag acc aaa agc tgg tac ttc act gaa			3735
Leu Phe Phe Thr Ile Phe Asp Glu Thr Lys Ser Trp Tyr Phe Thr Glu			
990	995	1000	
aat atg gaa aga aac tgc agg gct ccc tgc aat atc cag atg gaa gat			3783
Asn Met Glu Arg Asn Cys Arg Ala Pro Cys Asn Ile Gln Met Glu Asp			
1005	1010	1015	
ccc act ttt aaa gag aat tat cgc ttc cat gca atc aat ggc tac ata			3831
Pro Thr Phe Lys Glu Asn Tyr Arg Phe His Ala Ile Asn Gly Tyr Ile			
1020	1025	1030	
atg gat aca cta cct ggc tta gta atg gct cag gat caa agg att cga			3879
Met Asp Thr Leu Pro Gly Leu Val Met Ala Gln Asp Gln Arg Ile Arg			
1035	1040	1045	
tgg tat ctg ctc agc atg ggc agc aat gaa aac atc cat tct att cat			3927
Trp Tyr Leu Leu Ser Met Gly Ser Asn Glu Asn Ile His Ser Ile His			
1050	1055	1060	1065
ttc agt gga cat gtg ttc act gta cga aaa aaa gag gag tat aaa atg			3975
Phe Ser Gly His Val Phe Thr Val Arg Lys Lys Glu Glu Tyr Lys Met			
1070	1075	1080	
gca ctg tac aat ctc tat cca ggt gtt ttt gag aca gtg gaa atg tta			4023
Ala Leu Tyr Asn Leu Tyr Pro Gly Val Phe Glu Thr Val Glu Met Leu			
1085	1090	1095	
cca tcc aaa gct gga att tgg cgg gtg gaa tgc ctt att ggc gag cat			4071
Pro Ser Lys Ala Gly Ile Trp Arg Val Glu Cys Leu Ile Gly Glu His			
1100	1105	1110	
cta cat gct ggg atg aac aca ctt ttt ctg gtg tac agc aat aag tgt			4119
Leu His Ala Gly Met Asn Thr Leu Phe Leu Val Tyr Ser Asn Lys Cys			
1115	1120	1125	
cag act ccc ctg gga atg gct tct gga cac att aga gat ttt cag att			4167
Gln Thr Pro Leu Gly Met Ala Ser Gly His Ile Arg Asp Phe Gln Ile			
1130	1135	1140	1145
aca gct tca gga caa tat gga cag tgg gcc cca aag ctg gcc aga ctt			4215
Thr Ala Ser Gly Gln Tyr Gly Gln Trp Ala Pro Lys Leu Ala Arg Leu			
1150	1155	1160	
cat tat tcc gga tca atc aat gcc tgg agc acc aag gag ccc ttt tct			4263
His Tyr Ser Gly Ser Ile Asn Ala Trp Ser Thr Lys Glu Pro Phe Ser			

1165	1170	1175	
tgg atc aag gtg gat ctg ttg gca cca atg att att cac ggc atc aag			4311
Trp Ile Lys Val Asp Leu Leu Ala Pro Met Ile Ile His Gly Ile Lys			
1180	1185	1190	
acc cag ggt gcc cgt cag aag ttc tcc agc ctc tac atc tct cag ttt			4359
Thr Gln Gly Ala Arg Gln Lys Phe Ser Ser Leu Tyr Ile Ser Gln Phe			
1195	1200	1205	
atc atc atg tat agt ctt gat ggg aag aag tgg cag act tat cga gga			4407
Ile Ile Met Tyr Ser Leu Asp Gly Lys Lys Trp Gln Thr Tyr Arg Gly			
1210	1215	1220	1225
aat tcc act gga acc tta atg gtc ttc ttt ggc aat gtg gat tca tct			4455
Asn Ser Thr Gly Thr Leu Met Val Phe Phe Gly Asn Val Asp Ser Ser			
1230	1235	1240	
ggg ata aaa cac aat att ttt aac cct cca att att gct cga tac atc			4503
Gly Ile Lys His Asn Ile Phe Asn Pro Pro Ile Ile Ala Arg Tyr Ile			
1245	1250	1255	
cgt ttg cac cca act cat tat agc att cgc agc act ctt cgc atg gag			4551
Arg Leu His Pro Thr His Tyr Ser Ile Arg Ser Thr Leu Arg Met Glu			
1260	1265	1270	
ttg atg ggc tgt gat tta aat agt tgc agc atg cca ttg gga atg gag			4599
Leu Met Gly Cys Asp Leu Asn Ser Cys Ser Met Pro Leu Gly Met Glu			
1275	1280	1285	
agt aaa gca ata tca gat gca cag att act gct tca tcc tac ttt acc			4647
Ser Lys Ala Ile Ser Asp Ala Gln Ile Thr Ala Ser Ser Tyr Phe Thr			
1290	1295	1300	1305
aat atg ttt gcc acc tgg tct cct tca aaa gct cga ctt cac ctc caa			4695
Asn Met Phe Ala Thr Trp Ser Pro Ser Lys Ala Arg Leu His Leu Gln			
1310	1315	1320	
ggg agg agt aat gcc tgg aga cct cag gag aat aat cca aaa gag tgg			4743
Gly Arg Ser Asn Ala Trp Arg Pro Gln Glu Asn Asn Pro Lys Glu Trp			
1325	1330	1335	
ctg caa gtg gac ttc cag aag aca atg aaa gtc aca gga gta act act			4791
Leu Gln Val Asp Phe Gln Lys Thr Met Lys Val Thr Gly Val Thr Thr			
1340	1345	1350	
cag gga gta aaa tct ctg ctt acc agc atg tat gtg aag gag ttc ctc			4839
Gln Gly Val Lys Ser Leu Leu Thr Ser Met Tyr Val Lys Glu Phe Leu			
1355	1360	1365	
atc tcc agc agt caa gat ggc cat cag tgg acc ctc ttt ttt cag aat			4887
Ile Ser Ser Ser Gln Asp Gly His Gln Trp Thr Leu Phe Phe Gln Asn			

1370	1375	1380	1385	
ggc aaa gta aag gtt ttt cag gga aat caa gac tcc ttc aca cct gtg				4935
Gly Lys Val Lys Val Phe Gln Gly Asn Gln Asp Ser Phe Thr Pro Val				
	1390	1395	1400	
gtg aac tct cta gac cca ccg tta ctg act cgc tac ctt cga att cac				4983
Val Asn Ser Leu Asp Pro Pro Leu Leu Thr Arg Tyr Leu Arg Ile His				
	1405	1410	1415	
ccc cag agt tgg gtg cac cag att gcc ctg agg atg gag gtt ctg ggc				5031
Pro Gln Ser Trp Val His Gln Ile Ala Leu Arg Met Glu Val Leu Gly				
	1420	1425	1430	
tgc gag gca cag gac ctc tac tgagcggccg cgactctact agaggatctt				5082
Cys Glu Ala Gln Asp Leu Tyr				
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<210>4

<211>1459

<212>PRT

<213> 人工序列

<223> 人工序列的描述 :pTGF8-1

<400>4

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

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255	260	265
Phe Leu Glu Gly His Thr	Phe Leu Val Arg Asn His Arg Gln Ala Ser	
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Leu Glu Ile Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met		285
	290	295
Asp Leu Gly Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His		300
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Asp Gly Met Glu Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro		315
	320	325
Gln Leu Arg Met Lys Asn Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp		330
	335	340
Leu Thr Asp Ser Glu Met Asp Val Val Arg Phe Asp Asp Asp Asn Ser		345
350	355	360
Pro Ser Phe Ile Gln Ile Arg Ser Val Ala Lys Lys His Pro Lys Thr		365
	370	375
Trp Val His Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr Ala Pro		380
	385	390
Leu Val Leu Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn		395
	400	405
Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met		410
	415	420
Ala Tyr Thr Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu		425
430	435	440
Ser Gly Ile Leu Gly Pro Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu		445
	450	455
Leu Ile Ile Phe Lys Asn Gln Ala Ser Arg Pro Tyr Asn Ile Tyr Pro		460
	465	470
His Gly Ile Thr Asp Val Arg Pro Leu Tyr Ser Arg Arg Leu Pro Lys		475
	480	485
Gly Val Lys His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile Phe		490
	495	500
Lys Tyr Lys Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp		505
510	515	520
Pro Arg Cys Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg		525
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Asp Leu Ala Ser Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu		540
	545	550
Ser Val Asp Gln Arg Gly Asn Gln Ile Met Ser Asp Lys Arg Asn Val		555
	560	565
		570

Ile	Leu	Phe	Ser	Val	Phe	Asp	Glu	Asn	Arg	Ser	Trp	Tyr	Leu	Thr	Glu
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Asn	Ile	Gln	Arg	Phe	Leu	Pro	Asn	Pro	Ala	Gly	Val	Gln	Leu	Glu	Asp
590					595				600					605	
Pro	Glu	Phe	Gln	Ala	Ser	Asn	Ile	Met	His	Ser	Ile	Asn	Gly	Tyr	Val
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Phe	Asp	Ser	Leu	Gln	Leu	Ser	Val	Cys	Leu	His	Glu	Val	Ala	Tyr	Trp
			625					630						635	
Tyr	Ile	Leu	Ser	Ile	Gly	Ala	Gln	Thr	Asp	Phe	Leu	Ser	Val	Phe	Phe
	640						645						650		
Ser	Gly	Tyr	Thr	Phe	Lys	His	Lys	Met	Val	Tyr	Glu	Asp	Thr	Leu	Thr
	655					660						665			
Leu	Phe	Pro	Phe	Ser	Gly	Glu	Thr	Val	Phe	Met	Ser	Met	Glu	Asn	Pro
670					675					680					685
Gly	Leu	Trp	Ile	Leu	Gly	Cys	His	Asn	Ser	Asp	Phe	Arg	Asn	Arg	Gly
				690						695					700
Met	Thr	Ala	Leu	Leu	Lys	Val	Ser	Ser	Cys	Asp	Lys	Asn	Thr	Gly	Asp
			705						710						715
Tyr	Tyr	Glu	Asp	Ser	Tyr	Glu	Asp	Ile	Ser	Ala	Tyr	Leu	Leu	Ser	Lys
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Asn	Asn	Ala	Ile	Glu	Pro	Arg	Ser	Phe	Ser	Gln	Asn	Ser	Arg	His	Gln
		735					740								745
Ala	Tyr	Arg	Tyr	Arg	Arg	Gly	Glu	Ile	Thr	Arg	Thr	Thr	Leu	Gln	Ser
750					755						760				765
Asp	Gln	Glu	Glu	Ile	Asp	Tyr	Asp	Asp	Thr	Ile	Ser	Val	Glu	Met	Lys
				770						775					780
Lys	Glu	Asp	Phe	Asp	Ile	Tyr	Asp	Glu	Asp	Glu	Asn	Gln	Ser	Pro	Arg
			785						790						795
Ser	Phe	Gln	Lys	Lys	Thr	Arg	His	Tyr	Phe	Ile	Ala	Ala	Val	Glu	Arg
		800						805							810
Leu	Trp	Asp	Tyr	Gly	Met	Ser	Ser	Ser	Pro	His	Val	Leu	Arg	Asn	Arg
	815						820								825
Ala	Gln	Ser	Gly	Ser	Val	Pro	Gln	Phe	Lys	Lys	Val	Val	Phe	Gln	Glu
830						835					840				845
Phe	Thr	Asp	Gly	Ser	Phe	Thr	Gln	Pro	Leu	Tyr	Arg	Gly	Glu	Leu	Asn
				850							855				860
Glu	His	Leu	Gly	Leu	Leu	Gly	Pro	Tyr	Ile	Arg	Ala	Glu	Val	Glu	Asp
			865												870
Asn	Ile	Met	Val	Thr	Phe	Arg	Asn	Gln	Ala	Ser	Arg	Pro	Tyr	Ser	Phe

880	885	890
Tyr Ser Ser Leu Ile Ser Tyr Glu Glu Asp Gln Arg Gln Gly Ala Glu		
895	900	905
Pro Arg Lys Asn Phe Val Lys Pro Asn Glu Thr Lys Thr Tyr Phe Trp		
910	915	920
Lys Val Gln His His Met Ala Pro Thr Lys Asp Glu Phe Asp Cys Lys		
930	935	940
Ala Trp Ala Tyr Phe Ser Asp Val Asp Leu Glu Lys Asp Val His Ser		
945	950	955
Gly Leu Ile Gly Pro Leu Leu Val Cys His Thr Asn Thr Leu Asn Pro		
960	965	970
Ala His Gly Arg Gln Val Thr Val Gln Glu Phe Ala Leu Phe Phe Thr		
975	980	985
Ile Phe Asp Glu Thr Lys Ser Trp Tyr Phe Thr Glu Asn Met Glu Arg		
990	995	1000
Asn Cys Arg Ala Pro Cys Asn Ile Gln Met Glu Asp Pro Thr Phe Lys		
1010	1015	1020
Glu Asn Tyr Arg Phe His Ala Ile Asn Gly Tyr Ile Met Asp Thr Leu		
1025	1030	1035
Pro Gly Leu Val Met Ala Gln Asp Gln Arg Ile Arg Trp Tyr Leu Leu		
1040	1045	1050
Ser Met Gly Ser Asn Glu Asn Ile His Ser Ile His Phe Ser Gly His		
1055	1060	1065
Val Phe Thr Val Arg Lys Lys Glu Glu Tyr Lys Met Ala Leu Tyr Asn		
070	1075	1080
Leu Tyr Pro Gly Val Phe Glu Thr Val Glu Met Leu Pro Ser Lys Ala		
1090	1095	1100
Gly Ile Trp Arg Val Glu Cys Leu Ile Gly Glu His Leu His Ala Gly		
1105	1110	1115
Met Asn Thr Leu Phe Leu Val Tyr Ser Asn Lys Cys Gln Thr Pro Leu		
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Gly Met Ala Ser Gly His Ile Arg Asp Phe Gln Ile Thr Ala Ser Gly		
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Gln Tyr Gly Gln Trp Ala Pro Lys Leu Ala Arg Leu His Tyr Ser Gly		
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Ser Ile Asn Ala Trp Ser Thr Lys Glu Pro Phe Ser Trp Ile Lys Val		
1170	1175	1180
Asp Leu Leu Ala Pro Met Ile Ile His Gly Ile Lys Thr Gln Gly Ala		
1185	1190	1195

Arg Gln Lys Phe Ser Ser Leu Tyr Ile Ser Gln Phe Ile Ile Met Tyr
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 Ser Leu Asp Gly Lys Lys Trp Gln Thr Tyr Arg Gly Asn Ser Thr Gly
 1215 1220 1225
 Thr Leu Met Val Phe Phe Gly Asn Val Asp Ser Ser Gly Ile Lys His
 230 1235 1240 1245
 Asn Ile Phe Asn Pro Pro Ile Ile Ala Arg Tyr Ile Arg Leu His Pro
 1250 1255 1260
 Thr His Tyr Ser Ile Arg Ser Thr Leu Arg Met Glu Leu Met Gly Cys
 1265 1270 1275
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 1280 1285 1290
 Ser Asp Ala Gln Ile Thr Ala Ser Ser Tyr Phe Thr Asn Met Phe Ala
 1295 1300 1305
 Thr Trp Ser Pro Ser Lys Ala Arg Leu His Leu Gln Gly Arg Ser Asn
 310 1315 1320 1325
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 1330 1335 1340
 Phe Gln Lys Thr Met Lys Val Thr Gly Val Thr Thr Gln Gly Val Lys
 1345 1350 1355
 Ser Leu Leu Thr Ser Met Tyr Val Lys Glu Phe Leu Ile Ser Ser Ser
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 1375 1380 1385
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 390 1395 1400 1405
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<211>461

<212>PRT

<213> 人 (Homo sapiens)

<400>5

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	340	345	350
Val Ser Gly Trp Gly Arg Val Phe His Lys Gly Arg Ser Ala Leu Val			
	355	360	365
Leu Gln Tyr Leu Arg Val Pro Leu Val Asp Arg Ala Thr Cys Leu Arg			
	370	375	380
Ser Thr Lys Phe Thr Ile Tyr Asn Asn Met Phe Cys Ala Gly Phe His			
385	390	395	400
Glu Gly Gly Arg Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro His Val			
	405	410	415
Thr Glu Val Glu Gly Thr Ser Phe Leu Thr Gly Ile Ile Ser Trp Gly			
	420	425	430
Glu Glu Cys Ala Met Lys Gly Lys Tyr Gly Ile Tyr Thr Lys Val Ser			
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	450	455	460

<210>6

<211>5753

<212>DNA

<213> 人工序列

<220>

<223> 人工序列的描述 :pTGFG36

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cgcaaatggg cggttagcgt gtacgggtggg aggtctatat aagcagagct ctctggctaa 600

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<211>8

<212>PRT

<213> 人工序列

<220>

<223> 人工序列的描述 :B- 结构域接头肽

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<212>PRT

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<223> 人工序列的描述 :B- 结构域接头肽

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<210>9

<211>16

<212>PRT

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 aagcttgacc tcgag atg caa ata gag etc tcc acc tgc ttc ttt ctg tgc 711
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 -15 -10
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 Leu Leu Arg Phe Cys Phe Ser Ala Thr Arg Arg Tyr Tyr Leu Gly Ala
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 Val Glu Leu Ser Trp Asp Tyr Met Gln Ser Asp Leu Gly Glu Leu Pro
 10 15 20 25
 gtg gac gca aga ttt cct cct aga gtg cca aaa tct ttt cca ttc aac 855
 Val Asp Ala Arg Phe Pro Pro Arg Val Pro Lys Ser Phe Pro Phe Asn
 30 35 40
 acc tca gtc gtg tac aaa aag act ctg ttt gta gaa ttc acg gat cac 903
 Thr Ser Val Val Tyr Lys Lys Thr Leu Phe Val Glu Phe Thr Asp His
 45 50 55
 ctt ttc aac atc gct aag cca agg cca ccc tgg atg ggt ctg cta ggt 951
 Leu Phe Asn Ile Ala Lys Pro Arg Pro Pro Trp Met Gly Leu Leu Gly
 60 65 70
 cct acc atc cag gct gag gtt tat gat aca gtg gtc att aca ctt aag 999
 Pro Thr Ile Gln Ala Glu Val Tyr Asp Thr Val Val Ile Thr Leu Lys
 75 80 85
 aac atg gct tcc cat cct gtc agt ctt cat gct gtt ggt gta tcc tac 1047
 Asn Met Ala Ser His Pro Val Ser Leu His Ala Val Gly Val Ser Tyr
 90 95 100 105
 tgg aaa gct tct gag gga gct gaa tat gat gat cag acc agt caa agg 1095
 Trp Lys Ala Ser Glu Gly Ala Glu Tyr Asp Asp Gln Thr Ser Gln Arg
 110 115 120
 gag aaa gaa gat gat aaa gtc ttc cct ggt gga agc cat aca tat gtc 1143

Glu Lys Glu Asp Asp Lys Val Phe Pro Gly Gly Ser His Thr Tyr Val	
125	130
tgg cag gtc ctg aaa gag aat ggt cca atg gcc tct gac cca ctg tgc	1191
Trp Gln Val Leu Lys Glu Asn Gly Pro Met Ala Ser Asp Pro Leu Cys	
140	145
ctt acc tac tca tat ctt tct cat gtg gac ctg gta aaa gac ttg aat	1239
Leu Thr Tyr Ser Tyr Leu Ser His Val Asp Leu Val Lys Asp Leu Asn	
155	160
tca ggc ctc att gga gcc cta cta gta tgt aga gaa ggg agt ctg gcc	1287
Ser Gly Leu Ile Gly Ala Leu Leu Val Cys Arg Glu Gly Ser Leu Ala	
170	175
aag gaa aag aca cag acc ttg cac aaa ttt ata cta ctt ttt gct gta	1335
Lys Glu Lys Thr Gln Thr Leu His Lys Phe Ile Leu Leu Phe Ala Val	
190	195
ttt gat gaa ggg aaa agt tgg cac tca gaa aca aag aac tcc ttg atg	1383
Phe Asp Glu Gly Lys Ser Trp His Ser Glu Thr Lys Asn Ser Leu Met	
205	210
cag gat agg gat gct gca tct gct cgg gcc tgg cct aaa atg cac aca	1431
Gln Asp Arg Asp Ala Ala Ser Ala Arg Ala Trp Pro Lys Met His Thr	
220	225
gtc aat ggt tat gta aac agg tct ctg cca ggt ctg att gga tgc cac	1479
Val Asn Gly Tyr Val Asn Arg Ser Leu Pro Gly Leu Ile Gly Cys His	
235	240
agg aaa tca gtc tat tgg cat gtg att gga atg ggc acc act cct gaa	1527
Arg Lys Ser Val Tyr Trp His Val Ile Gly Met Gly Thr Thr Pro Glu	
250	255
gtg cac tca ata ttc ctc gaa ggt cac aca ttt ctt gtg agg aac cat	1575
Val His Ser Ile Phe Leu Glu Gly His Thr Phe Leu Val Arg Asn His	
270	275
cgc cag gcg tcc ttg gaa atc tcg cca ata act ttc ctt act gct caa	1623
Arg Gln Ala Ser Leu Glu Ile Ser Pro Ile Thr Phe Leu Thr Ala Gln	
285	290
aca ctc ttg atg gac ctt gga cag ttt cta ctg ttt tgt cat atc tct	1671
Thr Leu Leu Met Asp Leu Gly Gln Phe Leu Leu Phe Cys His Ile Ser	
300	305
tcc cac caa cat gat ggc atg gaa gct tat gtc aaa gta gac age tgt	1719
Ser His Gln His Asp Gly Met Glu Ala Tyr Val Lys Val Asp Ser Cys	
315	320
cca gag gaa ccc caa cta cga atg aaa aat aat gaa gaa gcg gaa gac	1767

Pro Glu Glu Pro Gln Leu Arg Met Lys Asn Asn Glu Glu Ala Glu Asp	
330	335 340 345
tat gat gat gat ctt act gat tct gaa atg gat gtg gtc agg ttt gat	1815
Tyr Asp Asp Asp Leu Thr Asp Ser Glu Met Asp Val Val Arg Phe Asp	
350 355 360	
gat gac aac tct cct tcc ttt atc caa att cgc tca gtt gcc aag aag	1863
Asp Asp Asn Ser Pro Ser Phe Ile Gln Ile Arg Ser Val Ala Lys Lys	
365 370 375	
cat cct aaa act tgg gta cat tac att gct gct gaa gag gag gac tgg	1911
His Pro Lys Thr Trp Val His Tyr Ile Ala Ala Glu Glu Glu Asp Trp	
380 385 390	
gac tat gct ccc tta gtc ctc gcc ccc gat gac aga agt tat aaa agt	1959
Asp Tyr Ala Pro Leu Val Leu Ala Pro Asp Asp Arg Ser Tyr Lys Ser	
395 400 405	
caa tat ttg aac aat ggc cct cag cgg att ggt agg aag tac aaa aaa	2007
Gln Tyr Leu Asn Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr Lys Lys	
410 415 420 425	
gtc cga ttt atg gca tac aca gat gaa acc ttt aag act cgt gaa gct	2055
Val Arg Phe Met Ala Tyr Thr Asp Glu Thr Phe Lys Thr Arg Glu Ala	
430 435 440	
att cag cat gaa tca gga atc ttg gga cct tta ctt tat ggg gaa gtt	2103
Ile Gln His Glu Ser Gly Ile Leu Gly Pro Leu Leu Tyr Gly Glu Val	
445 450 455	
gga gac aca ctg ttg att ata ttt aag aat caa gca agc aga cca tat	2151
Gly Asp Thr Leu Leu Ile Ile Phe Lys Asn Gln Ala Ser Arg Pro Tyr	
460 465 470	
aac atc tac cct cac gga atc act gat gtc cgt cct ttg tat tca agg	2199
Asn Ile Tyr Pro His Gly Ile Thr Asp Val Arg Pro Leu Tyr Ser Arg	
475 480 485	
aga tta cca aaa ggt gta aaa cat ttg aag gat ttt cca att ctg cca	2247
Arg Leu Pro Lys Gly Val Lys His Leu Lys Asp Phe Pro Ile Leu Pro	
490 495 500 505	
gga gaa ata ttc aaa tat aaa tgg aca gtg act gta gaa gat ggg cca	2295
Gly Glu Ile Phe Lys Tyr Lys Trp Thr Val Thr Val Glu Asp Gly Pro	
510 515 520	
act aaa tca gat cct cgg tgc ctg acc cgc tat tac tct agt ttc gtt	2343
Thr Lys Ser Asp Pro Arg Cys Leu Thr Arg Tyr Tyr Ser Ser Phe Val	
525 530 535	
aat atg gag aga gat cta gct tca gga ctc att ggc cct ctc ctc atc	2391

Asn Met Glu Arg Asp Leu Ala Ser Gly Leu Ile Gly Pro Leu Leu Ile	
540	545 550
tgc tac aaa gaa tct gta gat caa aga gga aac cag ata atg tca gac	2439
Cys Tyr Lys Glu Ser Val Asp Gln Arg Gly Asn Gln Ile Met Ser Asp	
555	560 565
aag agg aat gtc atc ctg ttt tct gta ttt gat gag aac cga agc tgg	2487
Lys Arg Asn Val Ile Leu Phe Ser Val Phe Asp Glu Asn Arg Ser Trp	
570	575 580 585
tac ctc aca gag aat ata caa cgc ttt ctc ccc aat cca gct gga gtg	2535
Tyr Leu Thr Glu Asn Ile Gln Arg Phe Leu Pro Asn Pro Ala Gly Val	
590	595 600
cag ctt gag gat cca gag ttc caa gcc tcc aac atc atg cac agc atc	2583
Gln Leu Glu Asp Pro Glu Phe Gln Ala Ser Asn Ile Met His Ser Ile	
605	610 615
aat ggc tat gtt ttt gat agt ttg cag ttg tca gtt tgt ttg cat gag	2631
Asn Gly Tyr Val Phe Asp Ser Leu Gln Leu Ser Val Cys Leu His Glu	
620	625 630
gtg gca tac tgg tac att cta agc att gga gca cag act gac ttc ctt	2679
Val Ala Tyr Trp Tyr Ile Leu Ser Ile Gly Ala Gln Thr Asp Phe Leu	
635	640 645
tct gtc ttc ttc tct gga tat acc ttc aaa cac aaa atg gtc tat gaa	2727
Ser Val Phe Phe Ser Gly Tyr Thr Phe Lys His Lys Met Val Tyr Glu	
650	655 660 665
gac aca ctc acc cta ttc cca ttc tca gga gaa act gtc ttc atg tcg	2775
Asp Thr Leu Thr Leu Phe Pro Phe Ser Gly Glu Thr Val Phe Met Ser	
670	675 680
atg gaa aac cca ggt cta tgg att ctg ggg tgc cac aac tca gac ttt	2823
Met Glu Asn Pro Gly Leu Trp Ile Leu Gly Cys His Asn Ser Asp Phe	
685	690 695
cgg aac aga ggc atg acc gcc tta ctg aag gtt tct agt tgt gac aag	2871
Arg Asn Arg Gly Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asp Lys	
700	705 710
aac act ggt gat tat tac gag gac agt tat gaa gat att tca gca tac	2919
Asn Thr Gly Asp Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser Ala Tyr	
715	720 725
ttg ctg agt aaa aac aat gcc att gaa cca aga agc ttc tcc cag aat	2967
Leu Leu Ser Lys Asn Asn Ala Ile Glu Pro Arg Ser Phe Ser Gln Asn	
730	735 740 745
tca aga cat caa gct tat cga tac cgt cga ggg gaa ata act cgt act	3015

Ser Arg His Gln Ala Tyr Arg Tyr Arg Arg Gly Glu Ile Thr Arg Thr	
750	755
act ctt cag tca gat caa gag gaa att gac tat gat gat acc ata tca	3063
Thr Leu Gln Ser Asp Gln Glu Glu Ile Asp Tyr Asp Asp Thr Ile Ser	
765	770
gtt gaa atg aag aag gaa gat ttt gac att tat gat gag gat gaa aat	3111
Val Glu Met Lys Lys Glu Asp Phe Asp Ile Tyr Asp Glu Asp Glu Asn	
780	785
cag agc ccc cgc agc ttt caa aag aaa aca cga cac tat ttt att gct	3159
Gln Ser Pro Arg Ser Phe Gln Lys Lys Thr Arg His Tyr Phe Ile Ala	
795	800
gca gtg gag agg ctc tgg gat tat ggg atg agt agc tcc cca cat gtt	3207
Ala Val Glu Arg Leu Trp Asp Tyr Gly Met Ser Ser Ser Pro His Val	
810	815
cta aga aac agg gct cag agt ggc agt gtc cct cag ttc aag aaa gtt	3255
Leu Arg Asn Arg Ala Gln Ser Gly Ser Val Pro Gln Phe Lys Lys Val	
830	835
gtt ttc cag gaa ttt act gat ggc tcc ttt act cag ccc tta tac cgt	3303
Val Phe Gln Glu Phe Thr Asp Gly Ser Phe Thr Gln Pro Leu Tyr Arg	
845	850
gga gaa cta aat gaa cat ttg gga ctc ctg ggg cca tat ata aga gca	3351
Gly Glu Leu Asn Glu His Leu Gly Leu Leu Gly Pro Tyr Ile Arg Ala	
860	865
gaa gtt gaa gat aat atc atg gta act ttc aga aat cag gcc tct cgt	3399
Glu Val Glu Asp Asn Ile Met Val Thr Phe Arg Asn Gln Ala Ser Arg	
875	880
ccc tat tcc ttc tat tct agc ctt att tct tat gag gaa gat cag agg	3447
Pro Tyr Ser Phe Tyr Ser Ser Leu Ile Ser Tyr Glu Glu Asp Gln Arg	
890	895
caa gga gca gaa cct aga aaa aac ttt gtc aag cct aat gaa acc aaa	3495
Gln Gly Ala Glu Pro Arg Lys Asn Phe Val Lys Pro Asn Glu Thr Lys	
910	915
act tac ttt tgg aaa gtg caa cat cat atg gca ccc act aaa gat gag	3543
Thr Tyr Phe Trp Lys Val Gln His His Met Ala Pro Thr Lys Asp Glu	
925	930
ttt gac tgc aaa gcc tgg gct tat ttc tct gat gtt gac ctg gaa aaa	3591
Phe Asp Cys Lys Ala Trp Ala Tyr Phe Ser Asp Val Asp Leu Glu Lys	
940	945
gat gtg cac tca ggc ctg att gga ccc ctt ctg gtc tgc cac act aac	3639

Asp Val His Ser Gly Leu Ile Gly Pro Leu Leu Val Cys His Thr Asn 955	960	965	
aca ctg aac cct gct cat ggg aga caa gtg aca gta cag gaa ttt gct Thr Leu Asn Pro Ala His Gly Arg Gln Val Thr Val Gln Glu Phe Ala 970	975	980	3687
ctg ttt ttc acc atc ttt gat gag acc aaa agc tgg tac ttc act gaa Leu Phe Phe Thr Ile Phe Asp Glu Thr Lys Ser Trp Tyr Phe Thr Glu 990	995	1000	3735
aat atg gaa aga aac tgc agg gct ccc tgc aat atc cag atg gaa gat Asn Met Glu Arg Asn Cys Arg Ala Pro Cys Asn Ile Gln Met Glu Asp 1005	1010	1015	3783
ccc act ttt aaa gag aat tat cgc ttc cat gca atc aat ggc tac ata Pro Thr Phe Lys Glu Asn Tyr Arg Phe His Ala Ile Asn Gly Tyr Ile 1020	1025	1030	3831
atg gat aca cta cct ggc tta gta atg gct cag gat caa agg att cga Met Asp Thr Leu Pro Gly Leu Val Met Ala Gln Asp Gln Arg Ile Arg 1035	1040	1045	3879
tgg tat ctg ctc agc atg ggc agc aat gaa aac atc cat tct att cat Trp Tyr Leu Leu Ser Met Gly Ser Asn Glu Asn Ile His Ser Ile His 1050	1055	1060	3927
ttc agt gga cat gtg ttc act gta cga aaa gag gag tat aaa atg Phe Ser Gly His Val Phe Thr Val Arg Lys Lys Glu Glu Tyr Lys Met 1070	1075	1080	3975
gca ctg tac aat ctc tat cca ggt gtt ttt gag aca gtg gaa atg tta Ala Leu Tyr Asn Leu Tyr Pro Gly Val Phe Glu Thr Val Glu Met Leu 1085	1090	1095	4023
cca tcc aaa gct gga att tgg cgg gtg gaa tgc ctt att ggc gag cat Pro Ser Lys Ala Gly Ile Trp Arg Val Glu Cys Leu Ile Gly Glu His 1100	1105	1110	4071
cta cat gct ggg atg agc aca ctt ttt ctg gtg tac agc aat aag tgt Leu His Ala Gly Met Ser Thr Leu Phe Leu Val Tyr Ser Asn Lys Cys 1115	1120	1125	4119
cag act ccc ctg gga atg gct tct gga cac att aga gat ttt cag att Gln Thr Pro Leu Gly Met Ala Ser Gly His Ile Arg Asp Phe Gln Ile 1130	1135	1140	4167
aca gct tca gga caa tat gga cag tgg gcc cca aag ctg gcc aga ctt Thr Ala Ser Gly Gln Tyr Gly Gln Trp Ala Pro Lys Leu Ala Arg Leu 1150	1155	1160	4215
cat tat tcc gga tca atc aat gcc tgg agc acc aag gag ccc ttt tct			4263

His Tyr Ser Gly Ser Ile Asn Ala Trp Ser Thr Lys Glu Pro Phe Ser	
1165	1170
tgg atc aag gtg gat ctg ttg gca cca atg att att cac ggc atc aag	4311
Trp Ile Lys Val Asp Leu Leu Ala Pro Met Ile Ile His Gly Ile Lys	
1180	1185
acc cag ggt gcc cgt cag aag ttc tcc agc ctc tac atc tct cag ttt	4359
Thr Gln Gly Ala Arg Gln Lys Phe Ser Ser Leu Tyr Ile Ser Gln Phe	
1195	1200
atc atc atg tat agt ctt gat ggg aag aag tgg cag act tat cga gga	4407
Ile Ile Met Tyr Ser Leu Asp Gly Lys Lys Trp Gln Thr Tyr Arg Gly	
1210	1215
aat tcc act gga acc tta atg gtc ttc ttt ggc aat gtg gat tca tct	4455
Asn Ser Thr Gly Thr Leu Met Val Phe Phe Gly Asn Val Asp Ser Ser	
1230	1235
ggg ata aaa cac aat att ttt aac cct cca att att gct cga tac atc	4503
Gly Ile Lys His Asn Ile Phe Asn Pro Pro Ile Ile Ala Arg Tyr Ile	
1245	1250
cgt ttg cac cca act cat tat agc att cgc agc act ctt cgc atg gag	4551
Arg Leu His Pro Thr His Tyr Ser Ile Arg Ser Thr Leu Arg Met Glu	
1260	1265
ttg atg ggc tgt gat tta aat agt tgc agc atg cca ttg gga atg gag	4599
Leu Met Gly Cys Asp Leu Asn Ser Cys Ser Met Pro Leu Gly Met Glu	
1275	1280
agt aaa gca ata tca gat gca cag att act gct tca tcc tac ttt acc	4647
Ser Lys Ala Ile Ser Asp Ala Gln Ile Thr Ala Ser Ser Tyr Phe Thr	
1290	1295
aat atg ttt gcc acc tgg tct cct tca aaa gct cga ctt cac ctc caa	4695
Asn Met Phe Ala Thr Trp Ser Pro Ser Lys Ala Arg Leu His Leu Gln	
1310	1315
ggg agg agt aat gcc tgg aga cct cag gtg aat aat cca aaa gag tgg	4743
Gly Arg Ser Asn Ala Trp Arg Pro Gln Val Asn Asn Pro Lys Glu Trp	
1325	1330
ctg caa gtg gac ttc cag aag aca atg aaa gtc aca gga gta act act	4791
Leu Gln Val Asp Phe Gln Lys Thr Met Lys Val Thr Gly Val Thr Thr	
1340	1345
cag gga gta aaa tct ctg ctt acc agc atg tat gtg aag gag ttc ctc	4839
Gln Gly Val Lys Ser Leu Leu Thr Ser Met Tyr Val Lys Glu Phe Leu	
1355	1360
atc tcc agc agt caa gat ggc cat cag tgg acc ctc ttt ttt cag aat	4887

Ile Ser Ser Ser Gln Asp Gly His Gln Trp Thr Leu Phe Phe Gln Asn
 1370 1375 1380 1385
 ggc aaa gta aag gtt ttt cag gga aat caa gac tcc ttc aca cct gtg 4935
 Gly Lys Val Lys Val Phe Gln Gly Asn Gln Asp Ser Phe Thr Pro Val
 1390 1395 1400
 gtg aac tct cta gac cca ccg tta ctg act cgc tac ctt cga att cac 4983
 Val Asn Ser Leu Asp Pro Pro Leu Leu Thr Arg Tyr Leu Arg Ile His
 1405 1410 1415
 ccc cag agt tgg gtg cac cag att gcc ctg agg atg gag gtt ctg ggc 5031
 Pro Gln Ser Trp Val His Gln Ile Ala Leu Arg Met Glu Val Leu Gly
 1420 1425 1430
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 Cys Glu Ala Gln Asp Leu Tyr
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<211>1459

<212>PRT

<213> 人工序列

<223> 人工序列的描述 :pTGF8-2hyg-s

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Trp	Asp	Tyr	Met	Gln	Ser	Asp	Leu	Gly	Glu	Leu	Pro	Val	Asp	Ala	Arg	
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Phe	Pro	Pro	Arg	Val	Pro	Lys	Ser	Phe	Pro	Phe	Asn	Thr	Ser	Val	Val	
	30					35				40					45	
Tyr	Lys	Lys	Thr	Leu	Phe	Val	Glu	Phe	Thr	Asp	His	Leu	Phe	Asn	Ile	
				50					55					60		
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			65					70						75		
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Glu	Gly	Ala	Glu	Tyr	Asp	Asp	Gln	Thr	Ser	Gln	Arg	Glu	Lys	Glu	Asp	
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Lys	Glu	Asn	Gly	Pro	Met	Ala	Ser	Asp	Pro	Leu	Cys	Leu	Thr	Tyr	Ser	
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Tyr	Leu	Ser	His	Val	Asp	Leu	Val	Lys	Asp	Leu	Asn	Ser	Gly	Leu	Ile	
	160							165						170		
Gly	Ala	Leu	Leu	Val	Cys	Arg	Glu	Gly	Ser	Leu	Ala	Lys	Glu	Lys	Thr	
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Gln	Thr	Leu	His	Lys	Phe	Ile	Leu	Leu	Phe	Ala	Val	Phe	Asp	Glu	Gly	
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Ala	Ala	Ser	Ala	Arg	Ala	Trp	Pro	Lys	Met	His	Thr	Val	Asn	Gly	Tyr	
			225						230					235		
Val	Asn	Arg	Ser	Leu	Pro	Gly	Leu	Ile	Gly	Cys	His	Arg	Lys	Ser	Val	
	240						245							250		
Tyr	Trp	His	Val	Ile	Gly	Met	Gly	Thr	Thr	Pro	Glu	Val	His	Ser	Ile	
	255					260								265		
Phe	Leu	Glu	Gly	His	Thr	Phe	Leu	Val	Arg	Asn	His	Arg	Gln	Ala	Ser	
270					275					280					285	
Leu	Glu	Ile	Ser	Pro	Ile	Thr	Phe	Leu	Thr	Ala	Gln	Thr	Leu	Leu	Met	
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 320 325 330
 Gln Leu Arg Met Lys Asn Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp
 335 340 345
 Leu Thr Asp Ser Glu Met Asp Val Val Arg Phe Asp Asp Asp Asn Ser
 350 355 360 365
 Pro Ser Phe Ile Gln Ile Arg Ser Val Ala Lys Lys His Pro Lys Thr
 370 375 380
 Trp Val His Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr Ala Pro
 385 390 395
 Leu Val Leu Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn
 400 405 410
 Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met
 415 420 425
 Ala Tyr Thr Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu
 430 435 440 445
 Ser Gly Ile Leu Gly Pro Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu
 450 455 460
 Leu Ile Ile Phe Lys Asn Gln Ala Ser Arg Pro Tyr Asn Ile Tyr Pro
 465 470 475
 His Gly Ile Thr Asp Val Arg Pro Leu Tyr Ser Arg Arg Leu Pro Lys
 480 485 490
 Gly Val Lys His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile Phe
 495 500 505
 Lys Tyr Lys Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp
 510 515 520 525
 Pro Arg Cys Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg
 530 535 540
 Asp Leu Ala Ser Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu
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 Ser Val Asp Gln Arg Gly Asn Gln Ile Met Ser Asp Lys Arg Asn Val
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 Asn Ile Gln Arg Phe Leu Pro Asn Pro Ala Gly Val Gln Leu Glu Asp
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 Pro Glu Phe Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val

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Phe Asp Ser Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp					
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Tyr Ile Leu Ser Ile Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe					
	640		645		650
Ser Gly Tyr Thr Phe Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr					
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Leu Phe Pro Phe Ser Gly Glu Thr Val Phe Met Ser Met Glu Asn Pro					
670		675		680	685
Gly Leu Trp Ile Leu Gly Cys His Asn Ser Asp Phe Arg Asn Arg Gly					
	690		695		700
Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr Gly Asp					
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Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys					
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Asn Asn Ala Ile Glu Pro Arg Ser Phe Ser Gln Asn Ser Arg His Gln					
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Ala Tyr Arg Tyr Arg Arg Gly Glu Ile Thr Arg Thr Thr Leu Gln Ser					
750		755		760	765
Asp Gln Glu Glu Ile Asp Tyr Asp Asp Thr Ile Ser Val Glu Met Lys					
	770		775		780
Lys Glu Asp Phe Asp Ile Tyr Asp Glu Asp Glu Asn Gln Ser Pro Arg					
	785		790		795
Ser Phe Gln Lys Lys Thr Arg His Tyr Phe Ile Ala Ala Val Glu Arg					
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Leu Trp Asp Tyr Gly Met Ser Ser Ser Pro His Val Leu Arg Asn Arg					
	815		820		825
Ala Gln Ser Gly Ser Val Pro Gln Phe Lys Lys Val Val Phe Gln Glu					
830		835		840	845
Phe Thr Asp Gly Ser Phe Thr Gln Pro Leu Tyr Arg Gly Glu Leu Asn					
	850		855		860
Glu His Leu Gly Leu Leu Gly Pro Tyr Ile Arg Ala Glu Val Glu Asp					
	865		870		875
Asn Ile Met Val Thr Phe Arg Asn Gln Ala Ser Arg Pro Tyr Ser Phe					
	880		885		890
Tyr Ser Ser Leu Ile Ser Tyr Glu Glu Asp Gln Arg Gln Gly Ala Glu					
	895		900		905
Pro Arg Lys Asn Phe Val Lys Pro Asn Glu Thr Lys Thr Tyr Phe Trp					
910		915		920	925

230	1235	1240	1245
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Thr His Tyr Ser Ile Arg Ser Thr Leu Arg Met Glu Leu Met Gly Cys			
	1265	1270	1275
Asp Leu Asn Ser Cys Ser Met Pro Leu Gly Met Glu Ser Lys Ala Ile			
	1280	1285	1290
Ser Asp Ala Gln Ile Thr Ala Ser Ser Tyr Phe Thr Asn Met Phe Ala			
	1295	1300	1305
Thr Trp Ser Pro Ser Lys Ala Arg Leu His Leu Gln Gly Arg Ser Asn			
310	1315	1320	1325
Ala Trp Arg Pro Gln Val Asn Asn Pro Lys Glu Trp Leu Gln Val Asp			
	1330	1335	1340
Phe Gln Lys Thr Met Lys Val Thr Gly Val Thr Thr Gln Gly Val Lys			
	1345	1350	1355
Ser Leu Leu Thr Ser Met Tyr Val Lys Glu Phe Leu Ile Ser Ser Ser			
	1360	1365	1370
Gln Asp Gly His Gln Trp Thr Leu Phe Phe Gln Asn Gly Lys Val Lys			
	1375	1380	1385
Val Phe Gln Gly Asn Gln Asp Ser Phe Thr Pro Val Val Asn Ser Leu			
390	1395	1400	1405
Asp Pro Pro Leu Leu Thr Arg Tyr Leu Arg Ile His Pro Gln Ser Trp			
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<223> 人工序列的描述 :pTGF8-3

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<220>

<221> 成熟肽

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cgcccaacga cccccgcca ttgacgtcaa taatgacgta tgttcccata gtaacgcaa 180
tagggacttt ccattgacgt caatgggtgg agtattttacg gtaaactgcc cacttggcag 240
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ccgcctggca ttatgccag tacatgacct tatgggactt tcctacttgg cagtacatct 360
acgtattagt catcgctatt accatggtga tgcggttttg gcagtacatc aatgggcgtg 420
gatagcggtt tgactcacgg ggatttccaa gtctccaccc cattgacgtc aatgggagtt 480
tgttttggca ccaaaatcaa cgggactttc caaaatgtcg taacaactcc gccccattga 540
cgcaaatggg cggtagcgt gtacgggtggg aggtctatat aagcagagct ctctggctaa 600
ctagagaacc cactgcttac tggcttatcg aaattaatac gactcactat agggagaccc 660
aagcttgacc tegag atg caa ata gag ctc tcc acc tgc ttc ttt ctg tgc 711
          Met Gln Ile Glu Leu Ser Thr Cys Phe Phe Leu Cys
                    -15                               -10
ctt ttg cga ttc tgc ttt agt gcc acc aga aga tac tac ctg ggt gca 759
Leu Leu Arg Phe Cys Phe Ser Ala Thr Arg Arg Tyr Tyr Leu Gly Ala
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gtg gaa ctg tca tgg gac tat atg caa agt gat ctc ggt gag ctg cct 807
Val Glu Leu Ser Trp Asp Tyr Met Gln Ser Asp Leu Gly Glu Leu Pro
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gtg gac gca aga ttt cct cct aga gtg cca aaa tct ttt cca ttc aac 855
Val Asp Ala Arg Phe Pro Pro Arg Val Pro Lys Ser Phe Pro Phe Asn
          30                35                40
acc tca gtc gtg tac aaa aag act ctg ttt gta gaa ttc acg gat cac 903
Thr Ser Val Val Tyr Lys Lys Thr Leu Phe Val Glu Phe Thr Asp His
          45                50                55
ctt ttc aac atc gct aag cca agg cca ccc tgg atg ggt ctg cta ggt 951
Leu Phe Asn Ile Ala Lys Pro Arg Pro Pro Trp Met Gly Leu Leu Gly
          60                65                70
cct acc atc cag gct gag gtt tat gat aca gtg gtc att aca ctt aag 999
Pro Thr Ile Gln Ala Glu Val Tyr Asp Thr Val Val Ile Thr Leu Lys
          75                80                85
aac atg gct tcc cat cct gtc agt ctt cat gct gtt ggt gta tcc tac 1047

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Trp Lys Ala Ser Glu Gly Ala Glu Tyr Asp Asp Gln Thr Ser Gln Arg	
110	120
gag aaa gaa gat gat aaa gtc ttc cct ggt gga agc cat aca tat gtc	1143
Glu Lys Glu Asp Asp Lys Val Phe Pro Gly Gly Ser His Thr Tyr Val	
125	135
tgg cag gtc ctg aaa gag aat ggt cca atg gcc tct gac cca ctg tgc	1191
Trp Gln Val Leu Lys Glu Asn Gly Pro Met Ala Ser Asp Pro Leu Cys	
140	150
ctt acc tac tca tat ctt tct cat gcg gac ctg gta aaa gac ttg aat	1239
Leu Thr Tyr Ser Tyr Leu Ser His Ala Asp Leu Val Lys Asp Leu Asn	
155	165
tca ggc ctc att gga gcc cta cta gta tgt aga gaa ggg agt ctg gcc	1287
Ser Gly Leu Ile Gly Ala Leu Leu Val Cys Arg Glu Gly Ser Leu Ala	
170	185
aag gaa aag aca cag acc ttg cac aaa ttt ata cta ctt ttt gct gta	1335
Lys Glu Lys Thr Gln Thr Leu His Lys Phe Ile Leu Leu Phe Ala Val	
190	200
ttt gat gaa ggg aaa agt tgg cac tca gaa aca aag aac tcc ttg atg	1383
Phe Asp Glu Gly Lys Ser Trp His Ser Glu Thr Lys Asn Ser Leu Met	
205	215
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Gln Asp Arg Asp Ala Ala Ser Ala Arg Ala Trp Pro Lys Met His Thr	
220	230
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Val Asn Gly Tyr Val Asn Arg Ser Leu Pro Gly Leu Ile Gly Cys His	
235	245
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Arg Lys Ser Val Tyr Trp His Val Ile Gly Met Gly Thr Thr Pro Glu	
250	265
gtg cac tca ata ttc ctc gaa ggt cac aca ttt ctt gtg agg aac cat	1575
Val His Ser Ile Phe Leu Glu Gly His Thr Phe Leu Val Arg Asn His	
270	280
cgc cag gcg tcc ttg gaa atc tcg cca ata act ttc ctt act gct caa	1623
Arg Gln Ala Ser Leu Glu Ile Ser Pro Ile Thr Phe Leu Thr Ala Gln	
285	295
aca ctc ttg atg gac ctt gga cag ttt cta ctg ttt tgt cat atc tct	1671

Thr Leu Leu Met Asp Leu Gly Gln Phe Leu Leu Phe Cys His Ile Ser	
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Ser His Gln His Asp Gly Met Glu Ala Tyr Val Lys Val Asp Ser Cys	
315	320 325
cca gag gaa ccc caa cta cga atg aaa aat aat gaa gaa gcg gaa gac	1767
Pro Glu Glu Pro Gln Leu Arg Met Lys Asn Asn Glu Glu Ala Glu Asp	
330	335 340 345
tat gat gat gat ctt act gat tct gaa atg gat gtg gtc agg ttt gat	1815
Tyr Asp Asp Asp Leu Thr Asp Ser Glu Met Asp Val Val Arg Phe Asp	
350	355 360
gat gac aac tct cct tcc ttt atc caa att cgc tca gtt gcc aag aag	1863
Asp Asp Asn Ser Pro Ser Phe Ile Gln Ile Arg Ser Val Ala Lys Lys	
365	370 375
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His Pro Lys Thr Trp Val His Tyr Ile Ala Ala Glu Glu Glu Asp Trp	
380	385 390
gac tat gct ccc tta gtc ctc gcc ccc gat gac aga agt tat aaa agt	1959
Asp Tyr Ala Pro Leu Val Leu Ala Pro Asp Asp Arg Ser Tyr Lys Ser	
395	400 405
caa tat ttg aac aat ggc cct cag cgg att ggt agg aag tac aaa aaa	2007
Gln Tyr Leu Asn Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr Lys Lys	
410	415 420 425
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Val Arg Phe Met Ala Tyr Thr Asp Glu Thr Phe Lys Thr Arg Glu Ala	
430	435 440
att cag cat gaa tca gga atc ttg gga cct tta ctt tat ggg gaa gtt	2103
Ile Gln His Glu Ser Gly Ile Leu Gly Pro Leu Leu Tyr Gly Glu Val	
445	450 455
gga gac aca ctg ttg att ata ttt aag aat caa gca agc aga cca tat	2151
Gly Asp Thr Leu Leu Ile Ile Phe Lys Asn Gln Ala Ser Arg Pro Tyr	
460	465 470
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Asn Ile Tyr Pro His Gly Ile Thr Asp Val Arg Pro Leu Tyr Ser Arg	
475	480 485
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Arg Leu Pro Lys Gly Val Lys His Leu Lys Asp Phe Pro Ile Leu Pro	
490	495 500 505
gga gaa ata ttc aaa tat aaa tgg aca gtg act gta gaa gat ggg cca	2295

Gly Glu Ile Phe Lys Tyr Lys Trp Thr Val Thr Val Glu Asp Gly Pro	
510	515 520
act aaa tca gat cct cgg tgc ctg acc cgc tat tac tct agt ttc gtt	2343
Thr Lys Ser Asp Pro Arg Cys Leu Thr Arg Tyr Tyr Ser Ser Phe Val	
525	530 535
aat atg gag aga gat cta gct tca gga ctc att ggc cct ctc ctc atc	2391
Asn Met Glu Arg Asp Leu Ala Ser Gly Leu Ile Gly Pro Leu Leu Ile	
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tgc tac aaa gaa tct gta gat caa aga gga aac cag ata atg tca gac	2439
Cys Tyr Lys Glu Ser Val Asp Gln Arg Gly Asn Gln Ile Met Ser Asp	
555	560 565
aag agg aat gtc atc ctg ttt tct gta ttt gat gag aac cga agc tgg	2487
Lys Arg Asn Val Ile Leu Phe Ser Val Phe Asp Glu Asn Arg Ser Trp	
570	575 580 585
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Tyr Leu Thr Glu Asn Ile Gln Arg Phe Leu Pro Asn Pro Ala Gly Val	
590	595 600
cag ctt gag gat cca gag ttc caa gcc tcc aac atc atg cac agc atc	2583
Gln Leu Glu Asp Pro Glu Phe Gln Ala Ser Asn Ile Met His Ser Ile	
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aat ggc tat gtt ttt gat agt ttg cag ttg tca gtt tgt ttg cat gag	2631
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Val Ala Tyr Trp Tyr Ile Leu Ser Ile Gly Ala Gln Thr Asp Phe Leu	
635	640 645
tct gtc ttc ttc tct gga tat acc ttc aaa cac aaa atg gtc tat gaa	2727
Ser Val Phe Phe Ser Gly Tyr Thr Phe Lys His Lys Met Val Tyr Glu	
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Asp Thr Leu Thr Leu Phe Pro Phe Ser Gly Glu Thr Val Phe Met Ser	
670	675 680
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Met Glu Asn Pro Gly Leu Trp Ile Leu Gly Cys His Asn Ser Asp Phe	
685	690 695
cgg aac aga ggc atg acc gcc tta ctg aag gtt tct agt tgt gac aag	2871
Arg Asn Arg Gly Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asp Lys	
700	705 710
aac act ggt gat tat tac gag gac agt tat gaa gat att tca gca tac	2919

Asn Thr Gly Asp Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser Ala Tyr	
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730	735 740 745
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Ser Arg His Gln Ala Tyr Arg Tyr Arg Arg Gly Glu Ile Thr Arg Thr	
750	755 760
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Thr Leu Gln Ser Asp Gln Glu Glu Ile Asp Tyr Asp Asp Thr Ile Ser	
765	770 775
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Val Glu Met Lys Lys Glu Asp Phe Asp Ile Tyr Asp Glu Asp Glu Asn	
780	785 790
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Gln Ser Pro Arg Ser Phe Gln Lys Lys Thr Arg His Tyr Phe Ile Ala	
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Leu Arg Asn Arg Ala Gln Ser Gly Ser Val Pro Gln Phe Lys Lys Val	
830	835 840
gtt ttc cag gaa ttt act gat ggc tcc ttt act cag ccc tta tac cgt	3303
Val Phe Gln Glu Phe Thr Asp Gly Ser Phe Thr Gln Pro Leu Tyr Arg	
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Gly Glu Leu Asn Glu His Leu Gly Leu Leu Gly Pro Tyr Ile Arg Ala	
860	865 870
gaa gtt gaa gat aat atc atg gta act ttc aga aat cag gcc tct cgt	3399
Glu Val Glu Asp Asn Ile Met Val Thr Phe Arg Asn Gln Ala Ser Arg	
875	880 885
ccc tat tcc ttc tat tct agc ctt att tct tat gag gaa gat cag agg	3447
Pro Tyr Ser Phe Tyr Ser Ser Leu Ile Ser Tyr Glu Glu Asp Gln Arg	
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Gln Gly Ala Glu Pro Arg Lys Asn Phe Val Lys Pro Asn Glu Thr Lys	
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Thr Tyr Phe Trp Lys Val Gln His His Met Ala Pro Thr Lys Asp Glu	
925	930 935
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Phe Asp Cys Lys Ala Trp Ala Tyr Phe Ser Asp Val Asp Leu Glu Lys	
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Asp Val His Ser Gly Leu Ile Gly Pro Leu Leu Val Cys His Thr Asn	
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Asn Met Glu Arg Asn Cys Arg Ala Pro Cys Asn Ile Gln Met Glu Asp	
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Pro Thr Phe Lys Glu Asn Tyr Arg Phe His Ala Ile Asn Gly Tyr Ile	
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Trp Tyr Leu Leu Ser Met Gly Ser Asn Glu Asn Ile His Ser Ile His	
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Phe Ser Gly His Val Phe Thr Val Arg Lys Lys Glu Glu Tyr Lys Met	
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Gln Thr Pro Leu Gly Met Ala Ser Gly His Ile Arg Asp Phe Gln Ile	
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Arg Leu His Pro Thr His Tyr Ser Ile Arg Ser Thr Leu Arg Met Glu	
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          -1  1                5                10
Trp Asp Tyr Met Gln Ser Asp Leu Gly Glu Leu Pro Val Asp Ala Arg
          15                20                25
Phe Pro Pro Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val Val
          30                35                40                45
Tyr Lys Lys Thr Leu Phe Val Glu Phe Thr Asp His Leu Phe Asn Ile
          50                55                60
Ala Lys Pro Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile Gln
          65                70                75
Ala Glu Val Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser
          80                85                90
His Pro Val Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser
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Lys Glu Asn Gly Pro Met Ala Ser Asp Pro Leu Cys Leu Thr Tyr Ser
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Tyr Leu Ser His Ala Asp Leu Val Lys Asp Leu Asn Ser Gly Leu Ile
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Gly Ala Leu Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys Thr
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Gln Thr Leu His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly
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Lys Ser Trp His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp
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Val Asn Arg Ser Leu Pro Gly Leu Ile Gly Cys His Arg Lys Ser Val
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Ser Gly Tyr Thr Phe Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr		
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Glu His Leu Gly Leu Leu Gly Pro Tyr Ile Arg Ala Glu Val Glu Asp		
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Ser Asp Ala Gln Ile Thr Ala Ser Ser Tyr Phe Thr Asn Met Phe Ala			
1295	1300	1305	
Thr Trp Ser Pro Ser Lys Ala Arg Leu His Leu Gln Gly Arg Ser Asn			
310	1315	1320	1325
Ala Trp Arg Pro Gln Glu Asn Asn Pro Lys Glu Trp Leu Gln Val Asp			
1330	1335	1340	
Phe Gln Lys Thr Met Lys Val Thr Gly Val Thr Thr Gln Gly Val Lys			
1345	1350	1355	
Ser Leu Leu Thr Ser Met Tyr Val Lys Glu Phe Leu Ile Ser Ser Ser			
1360	1365	1370	
Gln Asp Gly His Gln Trp Thr Leu Phe Phe Gln Asn Gly Lys Val Lys			
1375	1380	1385	
Val Phe Gln Gly Asn Gln Asp Ser Phe Thr Pro Val Val Asn Ser Leu			
390	1395	1400	1405
Asp Pro Pro Leu Leu Thr Arg Tyr Leu Arg Ile His Pro Gln Ser Trp			
1410	1415	1420	
Val His Gln Ile Ala Leu Arg Met Glu Val Leu Gly Cys Glu Ala Gln			
1425	1430	1435	
Asp Leu Tyr			
1440			

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<211>43

<212>DNA

<213>人工序列

<220>

<223> 人工序列的描述 :引物

<400>16

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43

<210>17

<211>39

<212>DNA

<213> 人工序列

<220>

<223> 人工序列的描述 :引物

<400>17

cgcgatcca ttaagtgagc ttgtttttt ccttaatcc

39

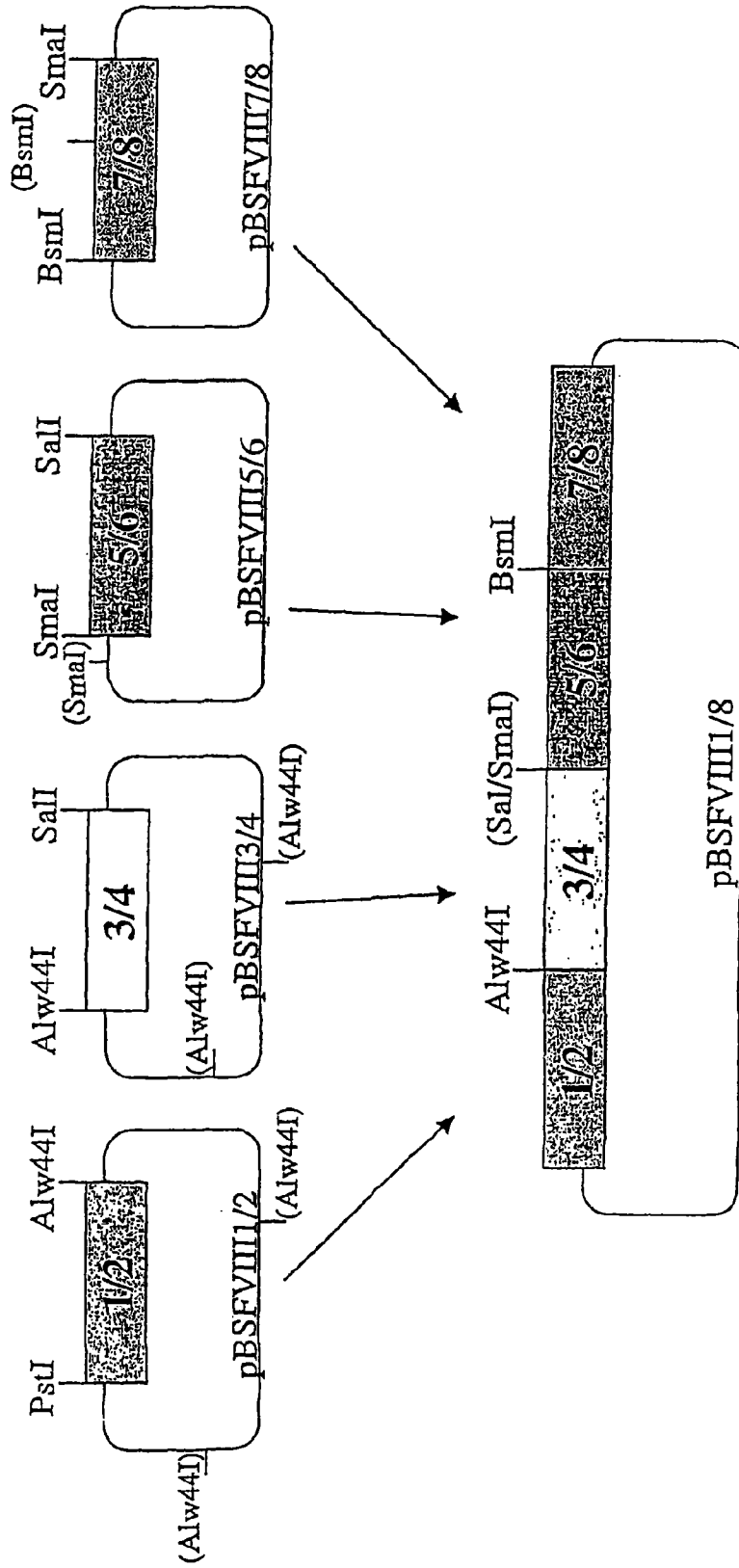


图 1

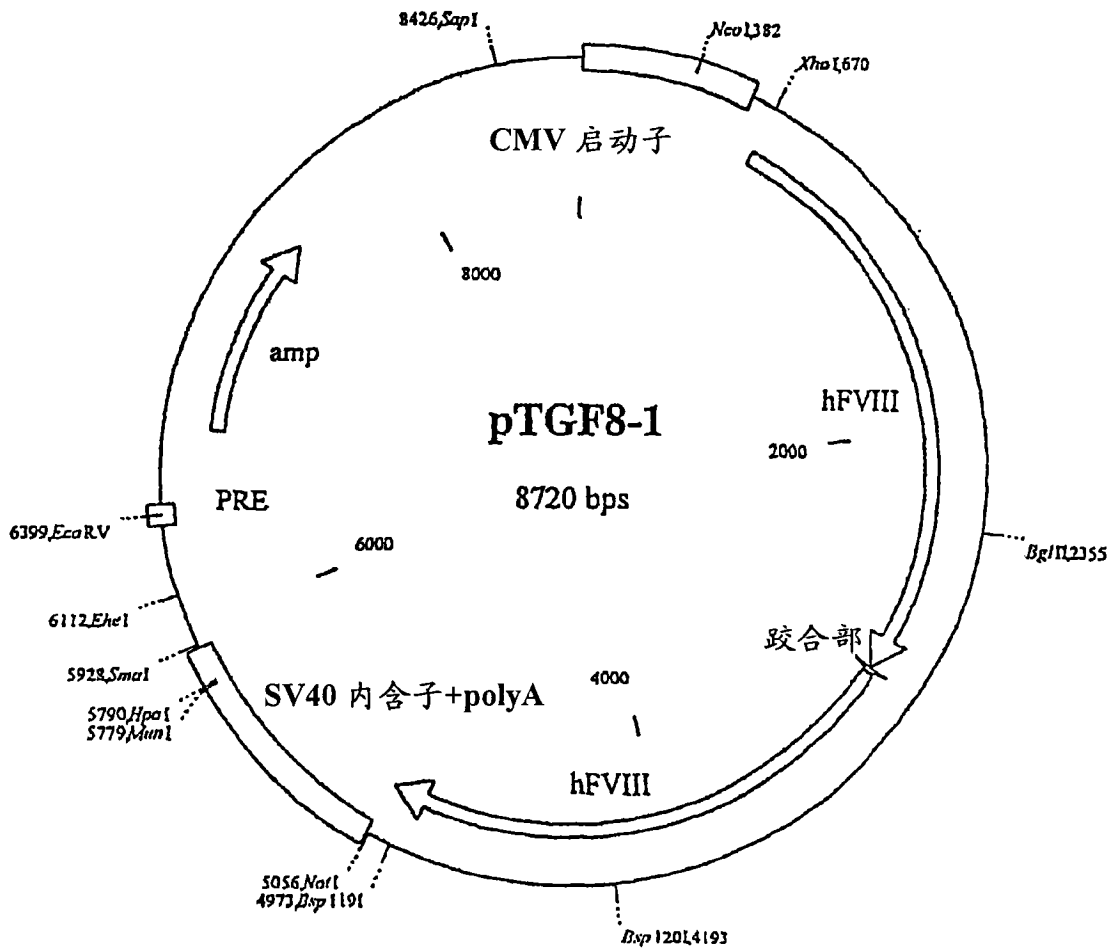


图 2

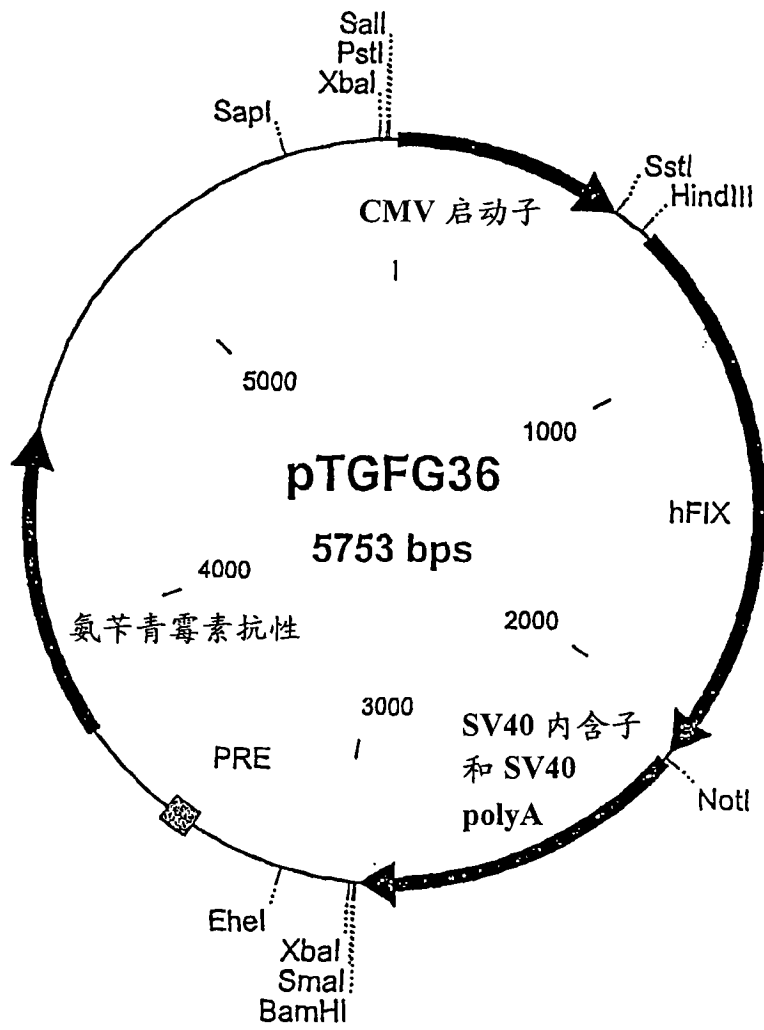


图 3

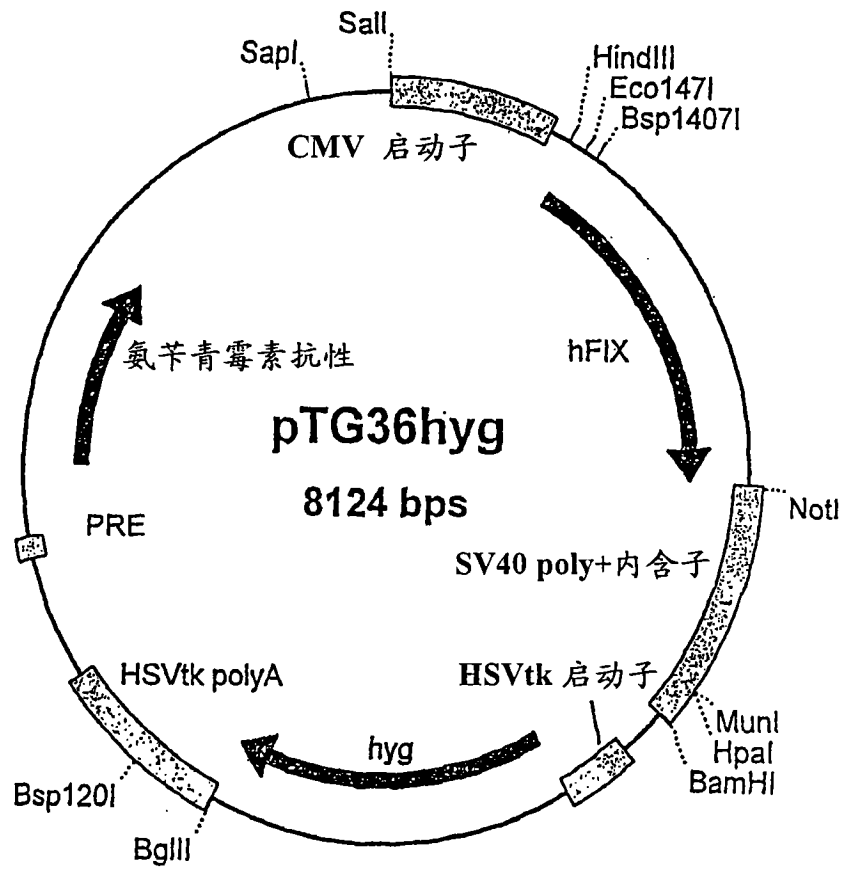


图 4

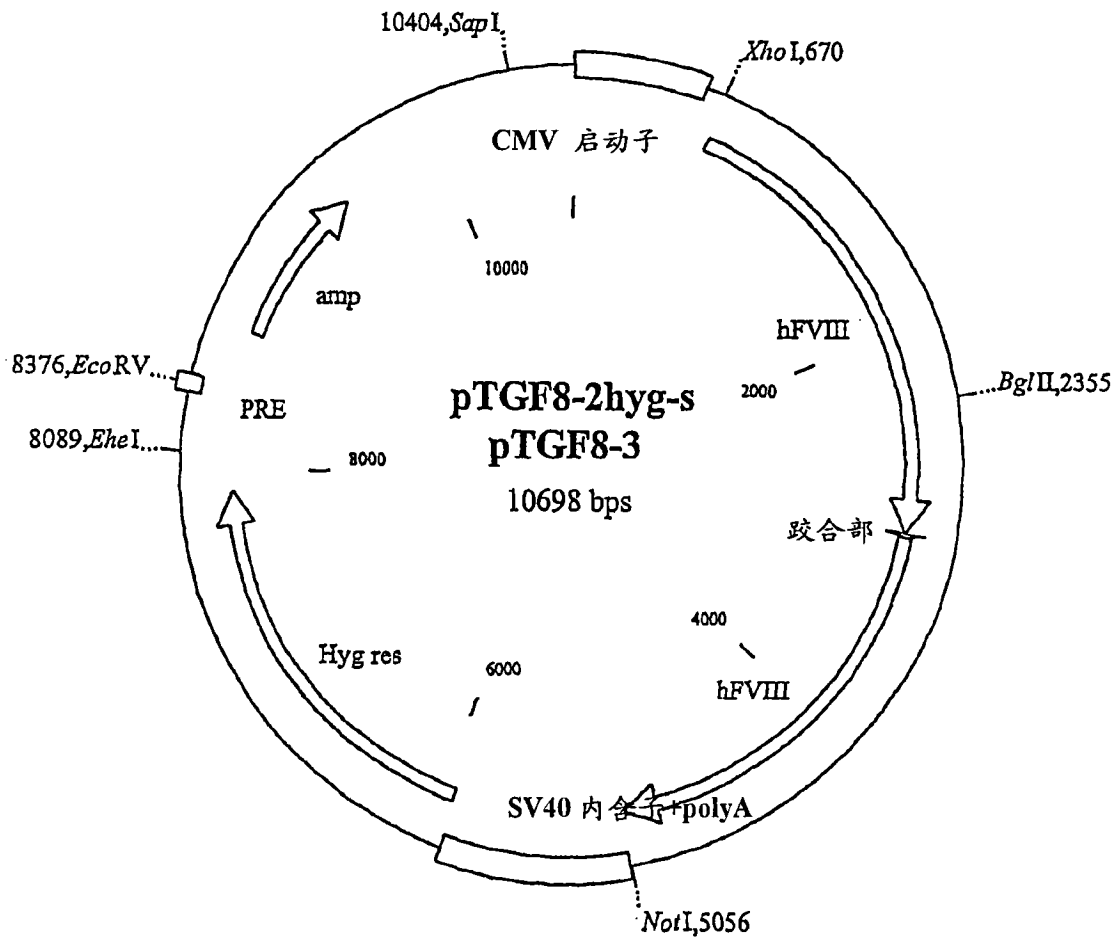


图 6

图 7

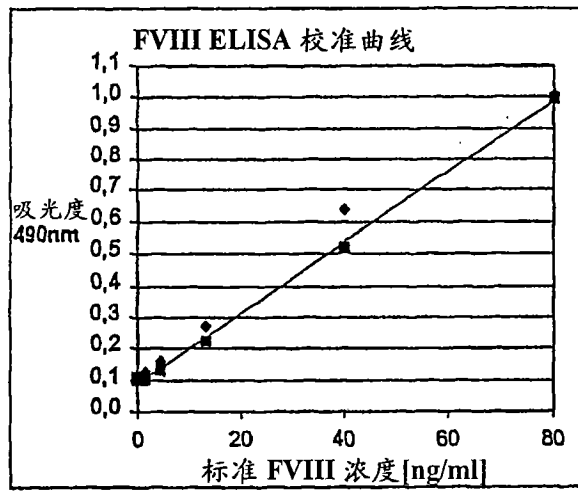


图 7A

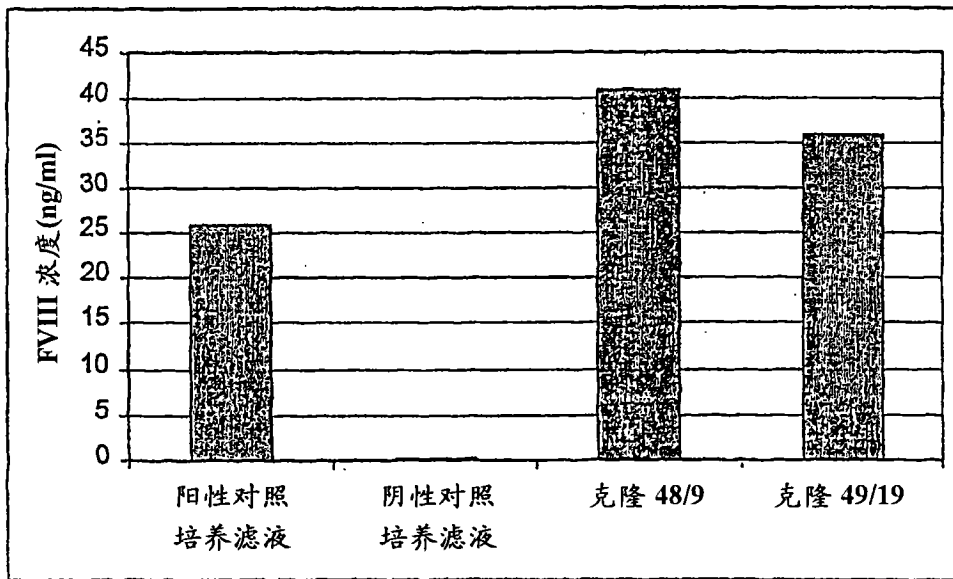


图 7B

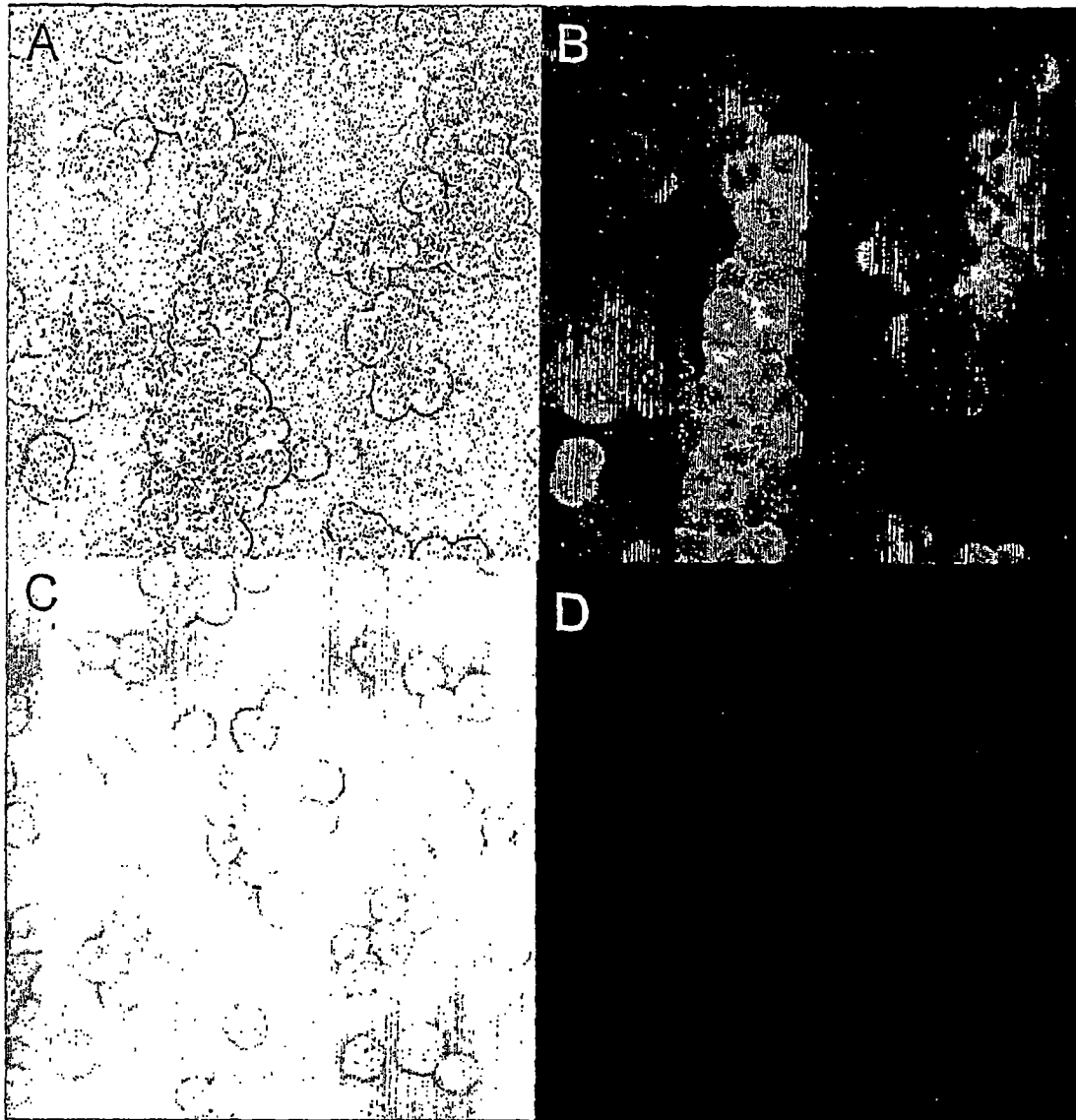


图 8

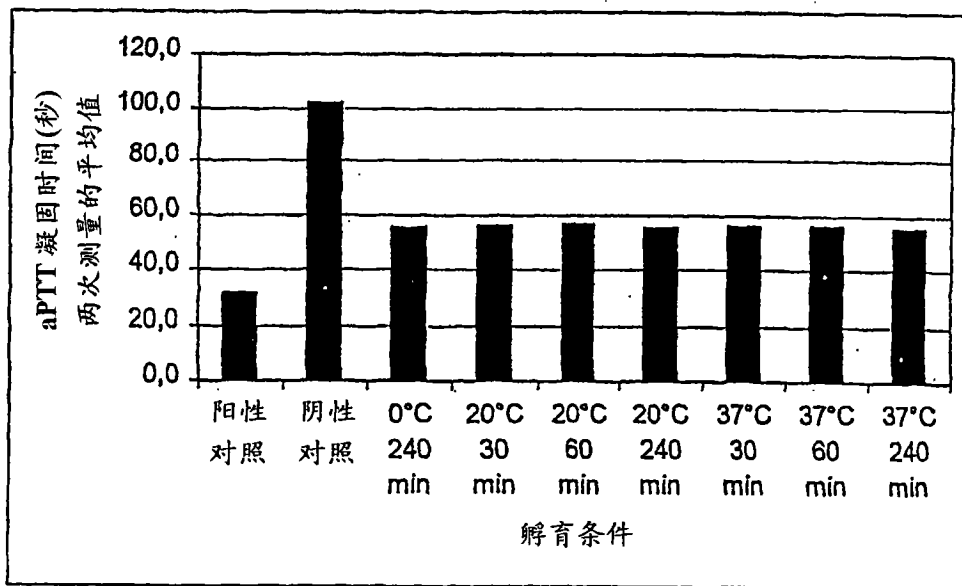


图 9

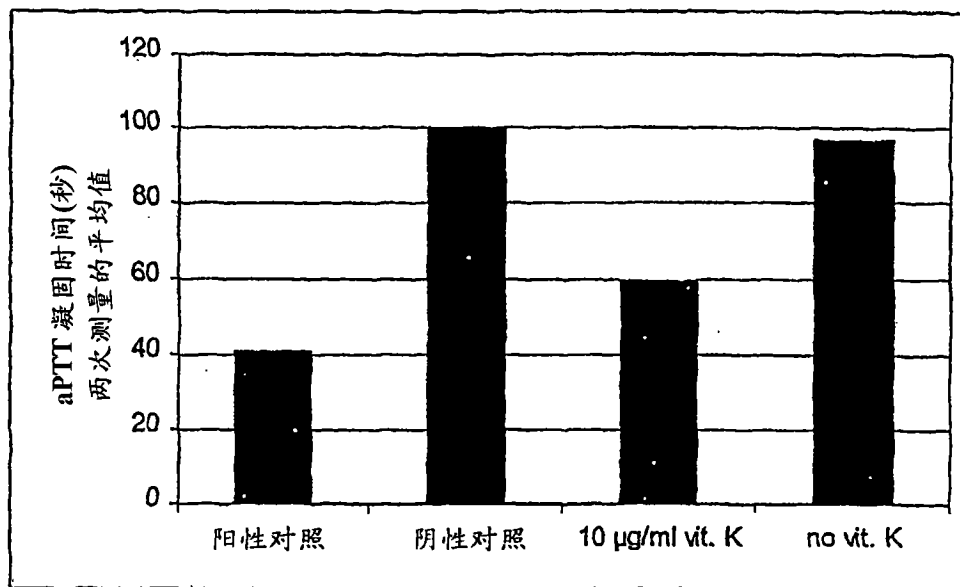


图 10