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(71) 申请人 国立大学法人广岛大学

地址 日本广岛县

申请人 住友化学株式会社

(72) 发明人 佐久间哲史 山本卓 西堀奈穗子

吉间忠彦 堀込一彦

(74) 专利代理机构 中科专利商标代理有限责任

公司 11021

专利代理师 张国梁 张莹

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(54) 发明名称

目标DNA的编辑方法、编辑了目标DNA的细胞的制备方法以及用于它们的DNA编辑系统

(57) 摘要

一种编辑目标DNA的方法,其包括:使(1)含有TALE和核碱基转化酶的融合蛋白、以及(2)含有部分或全部丧失核酸酶活性的Cas9蛋白及其向导RNA的CRISPR-Cas9系统与目标DNA接触,通过所述融合蛋白的核碱基转化酶活性,编辑所述目标DNA的目标位点的碱基的工序,所述融合蛋白中的TALE所识别的TALE识别序列或其互补序列经由7~31bp的链长的间隔区1存在于所述目标位点的5'侧,并且所述CRISPR-Cas9系统中的向导RNA所识别的向导RNA目标序列以含有所述目标位点的互补碱基的方式存在。

1. 一种编辑目标DNA的方法,其包括:

使(1)含有TALE和核碱基转化酶的融合蛋白、以及

(2)含有部分或全部丧失核酸酶活性的Cas9蛋白及其向导RNA的CRISPR-Cas9系统与目标DNA接触,通过所述融合蛋白的核碱基转化酶活性,编辑所述目标DNA的目标位点的碱基的工序,

所述融合蛋白中的TALE所识别的TALE识别序列或其互补序列经由7~31bp的链长的间隔区1存在于所述目标位点的5'侧,并且

所述CRISPR-Cas9系统中的向导RNA所识别的向导RNA目标序列以含有所述目标位点的互补碱基的方式存在。

2. 一种制备编辑了目标DNA的细胞的方法,其包括:

使(1)含有TALE和核碱基转化酶的融合蛋白、以及

(2)含有部分或全部丧失核酸酶活性的Cas9蛋白及其向导RNA的CRISPR-Cas9系统导入细胞或在细胞内表达而与目标DNA接触,通过所述融合蛋白的核碱基转化酶活性,编辑所述目标DNA的目标位点的碱基的工序,

所述融合蛋白中的TALE所识别的TALE识别序列或其互补序列经由7~31bp的链长的间隔区1存在于所述目标位点的5'侧,并且

所述CRISPR-Cas9系统中的向导RNA所识别的向导RNA目标序列以含有所述目标位点的互补碱基的方式存在。

3. 根据权利要求1或2所述的方法,其中,所述融合蛋白进一步含有将TALE与所述核碱基转化酶结合的接头1。

4. 根据权利要求1~3中任一项所述的方法,其中,所述融合蛋白进一步含有经由接头2结合到C末端侧的碱基去除修复抑制剂。

5. 根据权利要求1~4中任一项所述的方法,其中,所述融合蛋白中的核碱基转化酶为脱氨酶。

6. 根据权利要求5所述的方法,其中,所述脱氨酶为选自由APOBEC、PmCDA1、Anc689和TadA组成的组中的至少一种。

7. 一种DNA编辑系统,其用于权利要求1~6中任一项所述的方法中,所述DNA编辑系统包含:

(1)含有TALE和核碱基转化酶的融合蛋白、以及

(2)含有部分或全部丧失核酸酶活性的Cas9蛋白及其向导RNA的CRISPR-Cas9系统。

8. 根据权利要求7所述DNA编辑系统,其中,所述融合蛋白进一步含有将TALE与所述核碱基转化酶结合的接头1。

9. 根据权利要求7或8所述的DNA编辑系统,其中,所述融合蛋白进一步含有经由接头2结合到C末端侧的碱基去除修复抑制剂。

10. 根据权利要求7~9中任一项所述的方法,其中,所述融合蛋白中的核碱基转化酶为脱氨酶。

11. 根据权利要求10所述的DNA编辑系统,其中,所述脱氨酶为选自由APOBEC、PmCDA1、Anc689和TadA组成的组中的至少一种。

目标DNA的编辑方法、编辑了目标DNA的细胞的制备方法及用于它们的DNA编辑系统

技术领域

[0001] 本发明涉及目标DNA的编辑方法、编辑了目标DNA的细胞的制备方法以及用于它们的DNA编辑系统,更详细地,涉及编辑目标DNA的方法、制备使用该方法编辑了基因组的细胞的方法、以及用于它们的组合。

背景技术

[0002] 组合了CRISPR-dCas9/nCas9和脱氨酶等核碱基转化酶的碱基编辑方法,于2016年首次报道(Komor,A.et al.,Nature 533,420-424(2016),DOI:10.1038/nature17946(非专利文献1)之后,由于其高的编辑效率以及不需要供体DNA的简便,利用迅速扩大,报道了各种生物或细胞中的实施例,还开发了许多改良系统(Rees,H.A.和Liu,D.R.,Nat Rev Genet 19,770-788(2018),DOI:10.1038/s41576-018-0059-1(非专利文献2)等)。

[0003] 例如,在从碱基C向T的碱基编辑(C→T(G→A))中,广泛使用利用大鼠APOBEC1(rAPOBEC1)的系统(从上述初次出现的论文中的BE3,改良到现在被称为AncBE4max的系统;Koblan,L.et al.,Nat Biotechnol 36,843-846(2018),DOI:10.1038/nbt.4172(非专利文献3))和利用七鳃鳗的CDA1(PmCDA1)的系统(Target-AID;Nishida,K.et al.,Science 353,aaf8729(2016),DOI:10.1126/science.aaf8729(非专利文献4)),此外还报道了可利用APOBEC3A或APOBEC3B等(Gehrke,J.et al.,Nat Biotechnol 36,977-982(2018),DOI:10.1038/nbt.4199(非专利文献5);Martin,A.S.et al.,SCiRep 9,497(2019),DOI:10.1038/s41598-018-36739-9非专利文献6))。另外,例如,作为从碱基A向G的碱基编辑(A→G(T→C))系统,还报道了对来自大肠杆菌的TadA蛋白进行工程化而构建的腺嘌呤碱基编辑器(AdenineBase Editor:ABE)系统(Gaudelli,N.et al.,Nature 551,464-471(2017),DOI:10.1038/nature24644(非专利文献7))。

[0004] 然而,在所有这些系统中,靶基因组区域的特异性仅依赖于作为CRISPR-dCas9/nCas9的组成部分的向导RNA和dCas9/nCas9所识别的PAM序列。另一方面,还报道了在锌指(ZF)或TAL效应物(TALE)中融合脱氨酶的系统(Yang,L.et al.,Nat Commun 7,13330(2016),DOI:10.1038/ncomms13330(非专利文献8)),然而,ZF或TALE等DNA结合蛋白与CRISPR-dCas9/nCas9不同,不具有使双链DNA分离为单链的性质,因此利用以单链DNA为底物的脱氨酶进行碱基编辑的效率极低。

[0005] 在这种情况下,报道了通过将脱氨酶分割(split)为N末端结构域和C末端结构域,并分别与ZF和nCas9融合,从而当ZF和nCas9这两者的目标序列存在于附近时,首次进行碱基编辑的系统(国际公开第2018/218166号)。如果使用这样的系统,则可以认为与现有的CRISPR-dCas9/nCas9依赖性系统相比,ZF的识别序列增加,能够提高特异性。

[0006] 现有技术文献

[0007] 专利文献

[0008] 专利文献1:国际公开第2018/218166号

- [0009] 非专利文献
- [0010] 非专利文献1:Komor,A.et al.,Nature 533,420-424(2016)
- [0011] 非专利文献2:Rees,H.A.和Liu,D.R.,Nat Rev Genet19,770-788(2018)
- [0012] 非专利文献3:Koblan,L.et al.,Nat Biotechnol36,843-846(2018)
- [0013] 非专利文献4:Nishida,K.et al.,Science 353,aaf8729(2016)
- [0014] 非专利文献5:Gehrke,J.et al.,Nat Biotechnol 36,977-982(2018)
- [0015] 非专利文献6:Martin,A.S.et al.,SCi Rep 9,497(2019)
- [0016] 非专利文献7:Gaudelli,N.et al.,Nature 551,464-471(2017)
- [0017] 非专利文献8:Yang,L.et al.,Nat Commun 7,13330(2016)

发明内容

[0018] 发明要解决的课题

[0019] 然而,利用专利文献1所述的系统的碱基编辑的效率即使是最高,也就是现有的碱基编辑系统BE3(非专利文献1)的1/3程度,认为这是进行分割(split)引起活性降低所导致的。

[0020] 本发明是鉴于上述现有技术所具有的课题而完成的,其目的在于提供一种能够特异性且有效率地进行利用核碱基转化酶的目标DNA的编辑的方法、制备使用该方法编辑了基因组的细胞的方法、以及用于它们的DNA编辑系统。

[0021] 用于解决课题的手段

[0022] 本发明人等为了实现上述目的反复进行了深入研究,结果开发了如下系统,即,在不使核碱基转化酶分割的情况下,将其与TALE融合,并使该TALE-核碱基转化酶融合蛋白(优选TALE-脱氨酶-UGI融合蛋白)和dCas9/向导RNA复合体或nCas9/向导RNA复合体这两者结合到目标DNA的目标位点附近。不使核碱基转化酶分割的结构,例如在脱氨酶的情况下,依据已报道的高活性系统AncBE4max,但并不是通过将其直接与dCas9或nCas9连接,而是通过使其与TALE连接,即使只有TALE-核碱基转化酶(脱氨酶)融合蛋白与目标DNA结合,由于作为底物的单链DNA不露出,因此也几乎不会发生碱基编辑。另外,即使只有dCas9/向导RNA复合体或只有nCas9/向导RNA复合体与目标DNA结合,由于不存在所述核碱基转化酶,因此也不会发生碱基编辑。由此,本发明人等发现了:在TALE-核碱基转化酶融合蛋白和dCas9/向导RNA复合体或nCas9/向导RNA复合体以目标位点为中心隔着特定距离分别与目标DNA结合时,首次发生碱基编辑,确保高特异性,以及通过不使所述核碱基转化酶分割,可以实现高编辑效率。

[0023] 另外,本发明人等在上述CRISPR-dCas9或nCas9与TALE-核碱基转化酶融合蛋白的组合中,通过研究目标DNA上的TALE识别序列(或其互补序列)~目标位点间的间隔区1及目标DNA上的RNA目标序列的位置,已经证实可以实现与现有的AncBE4max系统同等的碱基编辑效率(基于报告基因测定的最大活性),从而完成了本发明。通过这样的见解得到的本发明的实施方式如下。

[0024] [1]一种编辑目标DNA的方法,其包括:

[0025] 使(1)含有TALE和核碱基转化酶的融合蛋白、以及

[0026] (2)含有部分或全部丧失核酸酶活性的Cas9蛋白及其向导RNA的CRISPR-Cas9系统

与目标DNA接触,通过所述融合蛋白的核碱基转化酶活性,编辑所述目标DNA的目标位点的碱基的工序,

[0027] 所述融合蛋白中的TALE所识别的TALE识别序列或其互补序列经由7~31bp的链长的间隔区1存在于所述目标位点的5'侧,并且

[0028] 所述CRISPR-Cas9系统中的向导RNA所识别的向导RNA目标序列以含有所述目标位点的互补碱基的方式存在。

[0029] [2]一种制备编辑了目标DNA的细胞的方法,其包括:

[0030] 使(1)含有TALE和核碱基转化酶的融合蛋白、以及

[0031] (2)含有部分或全部丧失核酸酶活性的Cas9蛋白及其向导RNA的CRISPR-Cas9系统导入细胞或在细胞内表达而与目标DNA接触,通过所述融合蛋白的核碱基转化酶活性,编辑所述目标DNA的目标位点的碱基的工序,

[0032] 所述融合蛋白中的TALE所识别的TALE识别序列或其互补序列经由7~31bp的链长的间隔区1存在于所述目标位点的5'侧,并且

[0033] 所述CRISPR-Cas9系统中的向导RNA所识别的向导RNA目标序列以含有所述目标位点的互补碱基的方式存在。

[0034] [3]根据[1]或[2]所述的方法,其中,所述融合蛋白进一步含有将TALE与核碱基转化酶结合的接头1。

[0035] [4]根据[1]~[3]中任一项所述的方法,其中,所述融合蛋白进一步含有经由接头2结合到C末端侧的碱基去除修复抑制剂。

[0036] [5]根据[1]~[4]中任一项所述的方法,其中,所述融合蛋白中的核碱基转化酶为脱氨酶。

[0037] [6]根据[5]所述的方法,其中,所述脱氨酶为选自由APOBEC、PmCDA1、Anc689和TadA组成的组中的至少一种。

[0038] [7]一种DNA编辑系统,其用于[1]~[6]中任一项所述的方法中,包含:

[0039] (1)含有TALE和核碱基转化酶的融合蛋白、以及

[0040] (2)含有部分或全部丧失核酸酶活性的Cas9蛋白及其向导RNA的CRISPR-Cas9系统。

[0041] [8]根据[7]所述DNA编辑系统,其中,所述融合蛋白进一步含有将TALE与核碱基转化酶结合的接头1。

[0042] [9]根据[7]或[8]所述的DNA编辑系统,其中,所述融合蛋白进一步含有经由接头2结合到C末端侧的碱基去除修复抑制剂。

[0043] [10]根据[7]~[9]中任一项所述的方法,其中,所述融合蛋白中的核碱基转化酶为脱氨酶。

[0044] [11]根据[10]所述的DNA编辑系统,其中,所述脱氨酶为选自由APOBEC、PmCDA1、Anc689和TadA组成的组中的至少一种。

[0045] 发明效果

[0046] 根据本发明,可以提供一种能够特异性且有效率地进行利用核碱基转化酶的目标DNA的编辑的方法、制备使用该方法编辑了基因组的细胞的方法、以及用于它们的DNA编辑系统。

[0047] 附图简单说明

[0048] [图1]是示出报告质粒结构的概念图。

[0049] [图2]是示出报告质粒中的从NheI识别位点到XhoI识别位点的序列的结构的概念图。

[0050] [图3]是NanoLuc表达报告基因的结构和利用TALE-脱氨酶的碱基编辑的一个实施方式的示意图。

[0051] [图4]是示出TALE-脱氨酶结构的一个实施方式的概念图。

[0052] [图5]是示出在试验1中得到的AncBE4max活性值的图。

[0053] [图6]是示出在试验2中得到的TALE-脱氨酶活性值(相对于AncBE4max活性值的比例)的图((A)WT-104-BE4、(B)47-104-BE4)。

[0054] [图7]是示出在试验2中得到的TALE-脱氨酶活性值(相对于AncBE4max活性值的比例)的图((A)WT-104-AID、(B)63-104-AID、(c)47-104-AID、(d)WT-12-AID、(E)63-12-AID、(f)47-12-AID)。

[0055] [图8]是示出在试验3中得到的TALE-脱氨酶活性值(相对于AncBE4max活性值的比例)的图((A)WT-104-AID、(B)63-104-AID、(c)47-104-AID、(d)WT-12-AID、(E)63-12-AID、(f)47-12-AID)。

[0056] [图9]是示出在试验4中得到的TALE-脱氨酶活性值(相对于AncBE4max活性值的比例)与接头1的长度的关系的图。

[0057] [图10]是NanoLuc表达报告基因的结构和利用TALE-脱氨酶的碱基编辑的一个实施方式的示意图。

[0058] [图11]是分别示出TALE-脱氨酶结构的一个实施方式(A、B)的概念图。

[0059] [图12A]是示出在试验5中得到的TALE-脱氨酶活性值(相对于AncBE4max活性值的比例)的图((A)BE4-TALE-WT:BE4-32-WT、BE4-135-WT、BE4-234-WT、(B)BE4-TALE-63:BE4-32-63、BE4-135-63、BE4-234-63)。

[0060] [图12B]是示出在试验5中得到的TALE-脱氨酶活性值(相对于AncBE4max活性值或ABE8e活性值的比例)的图((C)BE4-TALE-47:BE4-32-47、BE4-135-47、BE4-234-47、(D)ABE8e-TALE-47:ABE8e-32-47、ABE8e-135-47、ABE8e-234-47)。

[0061] [图13A]是分别示出内源性DNA(CCR5、HBB)上的目标区域(AS3(a)、AS14(b)、S2(c))、TALE识别序列的位置、向导RNA的目标序列的互补序列的位置的概念图。

[0062] [图13B]是分别示出内源性DNA(CCR5、HBB)上的目标区域(AS5(d)、AS14(e)、AS6(f)、AS7(g))、TALE识别序列及其互补序列的位置、向导RNA的目标序列的互补序列的位置的概念图。

[0063] [图14]是示出使用在试验6中得到的TALE-AID时的、目标AS3上的、向导RNA(sgRNA-AS3)的目标序列的互补序列的第1碱基(A)、第10碱基(B)、第11碱基(C)中的T的比例的图。

[0064] [图15]是示出使用在试验6中得到的TALE-AID时的、目标AS14上的、向导RNA(sgRNA-AS14)的目标序列的互补序列的第1碱基(A)、第5碱基(B)、第6碱基(C)中的T的比例的图。

[0065] [图16]是示出使用在试验6中得到的TALE-AID时的、目标S2上的、向导RNA(sgRNA-

S2)的目标序列的互补序列的第1碱基(A)、第8碱基(B)、第9碱基(C)中的T的比例的图。

[0066] [图17]是示出使用在试验6中得到的BE4-TALE时的、目标AS5上的、向导RNA(sgRNA-AS5)的目标序列的互补序列的第7碱基(A)、第8碱基(B)中的T的比例的图。

[0067] [图18]是示出使用在试验6中得到的BE4-TALE时的、目标AS14上的、向导RNA(sgRNA-AS14)的目标序列的互补序列的第1碱基(A)、第5碱基(B)、第6碱基(C)中的T的比例的图。

[0068] [图19]是示出使用在试验6中得到的BE4-TALE时的、目标AS6上的、向导RNA(sgRNA-AS6)的目标序列的互补序列的第5碱基(A)、第6碱基(B)中的T的比例的图。

[0069] [图20]是示出使用在试验6中得到的BE4-TALE时的、目标AS7上的、向导RNA(sgRNA-AS7)的目标序列的互补序列的第6碱基(A)、第7碱基(B)中的T的比例的图。

[0070] [图21]是示出使用在试验6中得到的ABE8e-TALE时的、目标AS5上的、向导RNA(sgRNA-AS5)的目标序列的互补序列的第3碱基(A)、第4碱基(B)中的G的比例的图。

[0071] [图22]是示出使用在试验6中得到的ABE8e-TALE时的、目标AS6上的、向导RNA(sgRNA-AS6)的目标序列的互补序列的第4碱基(A)、第7碱基(B)中的G的比例的图。

[0072] [图23]是示出使用在试验6中得到的ABE8e-TALE时的、目标AS7上的、向导RNA(sgRNA-AS7)的目标序列的互补序列的第4碱基(A)、第8碱基(B)中的G的比例的图。

[0073] 发明的具体实施方式

[0074] 以下,通过举例具体说明本发明的优选实施方式,但本发明并不限于这些。

[0075] <目标DNA编辑方法>

[0076] 本发明的目标DNA编辑方法,是编辑目标DNA的方式,其包括:

[0077] 一种编辑目标DNA的方法,其包括:

[0078] 使(1)含有TALE和核碱基转化酶的融合蛋白、以及

[0079] (2)含有部分或全部丧失核酸酶活性的Cas9蛋白及其向导RNA的CRISPR-Cas9系统与目标DNA接触,通过所述融合蛋白的核碱基转化酶活性,编辑所述目标DNA的目标位点的碱基的工序,

[0080] 所述融合蛋白中的TALE所识别的TALE识别序列或其互补序列经由7~31bp的链长的间隔区1存在于所述目标位点的5'侧,并且

[0081] 所述CRISPR-Cas9系统中的向导RNA所识别的向导RNA目标序列以含有所述目标位点的互补碱基的方式存在。

[0082] (融合蛋白)

[0083] 本发明涉及的融合蛋白是含有TALE和核碱基转化酶的融合蛋白。在本说明书中,将本发明涉及的融合蛋白根据情况称为“TALE-核碱基转化酶融合蛋白”或“TALE-核碱基转化酶”。作为所述融合蛋白,可以从N末端依次结合TALE、核碱基转化酶,也可以依次结合核碱基转化酶、TALE。另外,作为本发明涉及的融合蛋白,可以含有2种以上(优选2种)的核碱基转化酶,作为此时的核碱基转化酶,可以仅是1种,也可以是2种以上的组合。例如,在本发明涉及的融合蛋白含有2种核碱基转化酶(第1核碱基转化酶、第2核碱基转化酶)的情况下,它们可以依次结合第1核碱基转化酶、TALE、第2核碱基转化酶。其中,作为本发明涉及的融合蛋白,优选从N末端依次结合TALE、核碱基转化酶,或者从N末端依次结合核碱基转化酶、TALE。

[0084] [TALE]

[0085] TALE (Transcription Activator-Like Effector: 转录激活因子样效应物) 是由黄单胞菌属 (*Xanthomonas*) 物种原生菌分泌并激活宿主植物的基因转录的蛋白。本发明涉及的“TALE”至少含有N末端结构域和TALE重复结构域,进一步可以含有C末端结构域。

[0086] TALE重复结构域由形成右旋超螺旋的TALE序列的多个(例如10~30个,优选13~25个,更优选15~20个)串联重复(TALE重复)构成。典型的TALE重复1个单位(一个TALE序列)由33~35个氨基酸组成,通过由其第12个和第13个的2个氨基酸残基组成的可变残基(Repeat variable diresidue: RVD),识别DNA的特定碱基。作为特异性识别碱基的RVD的例子,可举出识别C的HD、识别T的NG、识别A的NI、识别G或A的NN、以及识别A、C、G或T的NS等。基于该TALE重复结构域的DNA识别机制,通过人工连接识别特定碱基的TALE序列,能够制成可识别并结合DNA上的所希望的碱基序列(TALE识别序列)的TALE。

[0087] 只要TALE重复结构域能够识别并结合TALE识别序列,本发明涉及的TALE的所述TALE序列也可以是对天然型的氨基酸序列进行适当改变的序列。例如,在所述TALE序列中,即使分别独立地改变RVD位置,也可以取代、插入和/或缺失1个或多个(例如,10个以下、9个以下、8个以下、7个以下、6个以下、优选5个以下或4个以下、进一步优选3个以下或2个以下)RVD以外的氨基酸残基,另外,RVD的第12个和第13个的2个氨基酸残基为了增强对A、T、C和G的特异性,可以被其他氨基酸残基取代。

[0088] 另外,本发明TALE的TALE重复结构域,以识别在目标DNA的目标位点的5'侧经由7~31bp的链长的间隔区1而存在的碱基序列或其互补序列的方式,即以TALE识别的TALE识别序列或其互补序列成为在所述目标位点的5'侧经由7~31bp的链长的间隔区1而存在的碱基序列的方式被设计。设计、制作这种所希望的TALE的技术是公知的(例如,Miller et al., Nat. Biotechnol., 29, 143—148 (2011); Sakuma et al., Sci. Rep., 3: 3379 (2013)), 例如,通过Sakuma et al. (2013) 中记载的Platinum Gate系统,可制作对所述碱基序列具有高结合活性的TALE。

[0089] 作为本发明涉及的TALE的N末端结构域,可以使用天然型的氨基酸序列(例如,Addgene的pTALETF_v2 (ID: 32185~32188) 中所含的N末端结构域的氨基酸序列),但只要不对本发明涉及的融合蛋白的功能(对TALE识别序列的结合能力、在目标位点的编辑能力等)产生负面影响,也可以是对所述天然型的氨基酸序列进行适当改变的序列。例如,可以取代、插入和/或缺失一个或多个(例如,50个以下、30个以下、20个以下、10个以下、9个以下、8个以下、7个以下、6个以下、优选5个以下或4个以下、更优选3个以下或2个以下)氨基酸残基。另外,也可以含有用于纯化或检测的标记标签、用于将TALE-核碱基转化酶转移到细胞核的核定位信号(NLS)等。

[0090] 作为这种N末端结构域,N末端结构域的链长优选为49~287个氨基酸残基,更优选为80~200个氨基酸残基,进一步优选为120~180个氨基酸残基。所述N末端结构域的链长小于所述下限时,有不能与目标DNA结合的倾向,另一方面,超过所述上限时,在使融合蛋白表达的情况下,有其表达效率降低的倾向。

[0091] 作为本发明涉及的TALE的N末端结构域的具体例,例如可举出Addgene的ptCMV-136/63-VR-HD (ID: 50699) 中所含的N末端结构域的氨基酸序列或Addgene的ptCMV-153/47-VR-HD (ID: 50703) 中所含的N末端结构域的氨基酸序列,但并不限于此。

[0092] 在本发明涉及的TALE进一步含有C末端结构域的情况下,作为该TALE的C末端结构域,也可以使用天然型的氨基酸序列(例如,Addgene的pTALETF_v2(ID:32185~32188)中所含的C末端结构域的氨基酸序列),但只要不对本发明涉及的融合蛋白的功能(对TALE识别序列的结合能力、在目标位点的编辑能力等)产生负面影响,也可以是对所述天然型的氨基酸序列进行适当改变的序列。例如,可以取代、插入和/或缺失一个或多个(例如,50个以下、30个以下、20个以下、10个以下、9个以下、8个以下、7个以下、6个以下、优选5个以下或4个以下、更优选3个以下或2个以下)氨基酸残基。

[0093] 在本发明涉及的TALE进一步含有C末端结构域时,作为所述TALE的C末端结构域,可以在天然型的氨基酸序列中去除C末端侧的部分氨基酸序列的序列。作为这种C末端结构域,C末端结构域的链长优选为1~180个氨基酸残基,更优选为20~100个氨基酸残基,进一步优选为40~70个氨基酸残基。所述C末端结构域的链长超过所述上限时,在使融合蛋白表达的情况下,有其表达效率降低的倾向。

[0094] 作为所述C末端结构域的具体例,例如可举出Addgene的pTALETF_v2(ID:32185~32188)中所含的C末端结构域的氨基酸序列(WT:氨基酸数量=180)、Addgene的pTALEN_v2(ID:32189~32192)中所含的C末端结构域的氨基酸序列(氨基酸数量=63)、Addgene的ptCMV-153/47-VR-NG(ID:50704)中所含的C末端结构域的氨基酸序列(氨基酸数量=47),但并不限于此。

[0095] [核碱基转化酶]

[0096] 在本发明中,核碱基转化酶是指,通过催化将DNA碱基的嘌呤或嘧啶环上的取代基转变或脱落为其他基团或原子的反应,从而在不切割DNA链的情况下可以将目标核苷酸转变或脱落为其他核苷酸的酶。

[0097] 作为这种核碱基转化酶,只要可以催化上述反应,就没有特别限制,例如可举出脱氨酶、糖苷酶,可以是其中的1种,也可以是2种以上的组合。其中,作为本发明涉及的核碱基转化酶,优选脱氨酶。

[0098] (脱氨酶)

[0099] 所述脱氨酶是催化将碱基的氨基转变为羰基的脱氨基化反应的酶,属于核酸/核苷酸脱氨酶超级家族。作为这种脱氨酶,可举出可以将胞嘧啶或5-甲基胞嘧啶分别转变为尿嘧啶或胸腺嘧啶的胞苷脱氨酶、可以将腺嘌呤转变为次黄嘌呤的腺苷脱氨酶、可以将鸟嘌呤转变为黄嘌呤的鸟苷脱氨酶,根据目的碱基取代,可以分开使用。

[0100] 作为所述脱氨酶的来源,没有特别限制,例如可举出七鳃鳗;人、猴子、猪、牛、马、大鼠、小鼠等哺乳动物。

[0101] 作为这种脱氨酶,作为胞苷脱氨酶,例如可举出APOBEC(来自大鼠的rAPOBEC1、来自人的hAPOBEC1、hAPOBEC2、hAPOBEC3(hAPOBEC3A、3B、3C、3D(3E)、3F、3G、3H)、hAPOBEC4等);APOBEC的祖先氨基酸序列Anc689;来自哺乳动物(例如人、猪、牛、马、猴子等)的AID(Activation-induced cytidine deaminase(AICDA));是AID的家族,并来自七鳃鳗的PmCDA1(Petromyzon marinus cytosine deaminase1)。另外,作为腺苷脱氨酶,例如可举出来自大肠杆菌的TadA。上述的各脱氨酶分别含有其突变体(例如TadA-8e、TadA7.10、以及它们的突变体等)。其中,作为所述脱氨酶,优选为选自由APOBEC、PmCDA1、Anc689和TadA(分别包括其突变体)组成的组中的至少一种。

[0102] 另外,在本发明涉及的融合蛋白含有2种以上脱氨酶的情况下,它们的组合可以根据目标碱基取代适当选择,例如,相同或不同的胞苷脱氨酶的组合、相同或不同的腺苷脱氨酶的组合、相同或不同的鸟苷脱氨酶的组合、胞苷脱氨酶与腺苷脱氨酶的组合、胞苷脱氨酶与鸟苷脱氨酶的组合、腺苷脱氨酶与鸟苷脱氨酶的组合。其中,作为脱氨酶的组合,优选TadA与PmCDA1的组合。此外,这些脱氨酶的碱基序列和氨基酸序列是公知的,可以从公共数据库(Genbank等)取得。

[0103] 另外,作为所述脱氨酶,只要具有脱氨基化活性(脱氨酶活性),也可以是基于这些公知的脱氨酶的碱基序列和氨基酸序列进行了改变(例如,氨基酸残基的取代、插入和/或缺失的导入)的脱氨酶。脱氨酶活性的有无可以适当使用公知的方法进行确认。例如,在胞苷脱氨酶中,以胞苷为底物进行酶反应,通过检测、定量,可以确认作为胞苷的代谢产物的尿苷。

[0104] [接头1]

[0105] 作为本发明涉及的融合蛋白,优选进一步含有接头1。在该情况下,在本发明涉及的融合蛋白中,TALE和所述核碱基转化酶通过接头1连接。另外,在本发明涉及的融合蛋白含有多个所述核碱基转化酶的情况下,与此相对应,接头1优选为多个。在本发明涉及的融合蛋白含有多个接头1的情况下,它们可以仅是1种,也可以是2种以上的组合。

[0106] 在本发明涉及的融合蛋白进一步含有接头1的情况下,作为接头1的链长,没有特别限制,优选为1~450个氨基酸残基,更优选为5~250个氨基酸残基,更优选为5~200个氨基酸残基,更优选为12~150个氨基酸残基,进一步优选为12~104个氨基酸残基。所述接头1的链长超过所述上限时,在使融合蛋白表达的情况下,有其表达效率降低的倾向。

[0107] 作为本发明涉及的接头1,例如,可举出YangL et al.,Nat Commun 713330(2016)中记载的12个氨基酸及Nishida,K.et al.,Science353,aaf8729(2016)中记载的104个氨基酸、Koblan,L.etal.,NatBiotechnol36,p.843-846(2018)中记载的32个氨基酸、Sun,N.和Zhao,H.,MolBioSyst10,p.446-453(2014),Doi:10.1039/c3mb70412b)中记载的HTS95氨基酸序列(95个氨基酸)及其重复,但并不限于此。

[0108] 另外,作为本发明的融合蛋白,在所述核碱基转化酶位于TALE的C末端侧的情况下,优选TALE重复结构域与所述核碱基转化酶之间隔着1~630个氨基酸残基。因此,作为本发明涉及的融合蛋白,优选含有所述TALE的C末端结构域和接头1中的至少一种。作为此时的TALE重复结构域与所述核碱基转化酶之间的链长(将与TALE重复结构域的C末端的C末端侧相邻的氨基酸残基作为第1残基,到与核碱基转化酶的N末端的N末端侧相邻的残基为止的氨基酸残基的数量),更优选为25~300个氨基酸残基,进一步优选为52~174个氨基酸残基。所述链长小于所述下限时,有碱基编辑的效率降低的倾向,另一方面,超过所述上限时,在使融合蛋白表达的情况下,有其表达效率降低的倾向。

[0109] 此外,此时的所述TALE重复结构域的C末端的残基可以设成位于截断LHR(truncated last half-repeat)之前(N末端侧)的TALE序列(优选1个单位:33~35个氨基酸)的C末端的残基(在不存在LHR的情况下,构成所述TALE重复结构域的最后的TALE序列(优选1个单位:33~35个氨基酸)的C末端的残基),所述截断LHR位于所述TALE重复结构域的C末端侧。另外,所述核碱基转化酶的N末端的残基可以设成通过使用公知的方法(例如,BLAST(NCBI))的同一性检索,与可从公知的数据库(例如,NCBI)取得的典型的核碱基转化

酶的氨基酸序列的同一性为85%以上(优选90%以上)的氨基酸序列的起始残基(通常为甲硫氨酸)。

[0110] [碱基去除修复抑制剂、接头2]

[0111] 作为本发明涉及的融合蛋白,优选进一步含有在C末端侧,即,在所述核碱基转化酶的C末端(所述核碱基转化酶位于TALE的C末端侧的情况)或TALE的C末端(所述核碱基转化酶仅位于TALE的N末端侧的情况)经由接头2结合的碱基去除修复抑制剂。在进一步含有碱基去除修复抑制剂的情况下,该碱基去除修复抑制剂在每个所述融合蛋白中可以为一个,也可以进一步经由接头2而为2个以上(优选2个)。另外,在为多个的情况下,可以仅是1种,也可以是2种以上的组合,但优选是1种。

[0112] 作为本发明涉及的碱基去除修复抑制剂,只要是阻碍碱基去除修复的抑制剂就没有特别限制,优选DNA糖基化酶抑制剂。作为所述DNA糖基化酶抑制剂,可举出胸腺嘧啶DNA糖基化酶抑制剂、尿嘧啶DNA糖基化酶抑制剂、氧代鸟嘌呤DNA糖基化酶抑制剂、烷基鸟嘌呤DNA糖基化酶抑制剂。例如,在使用脱氨酶即胞苷脱氨酶作为所述核碱基转化酶的情况下,为了阻碍由突变产生的DNA的U:G或G:U错配的修复,适合使用尿嘧啶DNA糖基化酶抑制剂(UGI)。在这种情况下,脱氨酶和UGI存在于一个多肽上,由此进一步提高碱基编辑的效率。

[0113] 作为这种尿嘧啶DNA糖基化酶抑制剂,例如可举出来自枯草芽孢杆菌(*Bacillus subtilis*)噬菌体PBS1的尿嘧啶DNA糖基化酶抑制剂(UGI)或来自枯草芽孢杆菌噬菌体PBS2的尿嘧啶DNA糖基化酶抑制剂(UGI),但并不限于此。这些碱基序列和氨基酸序列是公知的,可以从公共数据库(Genbank等)取得。另外,作为本发明涉及的碱基去除修复抑制剂,只要具有上述DNA的错配的修复阻碍活性,也可以是基于公知的碱基去除修复抑制剂的碱基序列和氨基酸序列进行了改变(例如,氨基酸残基的取代、插入和/或缺失的导入)的抑制剂。

[0114] 在本发明涉及的融合蛋白进一步含有所述碱基去除修复抑制剂的情况下,并且在所述碱基去除修复抑制剂为多个的情况下,能够以融合蛋白-接头2-第1碱基去除修复抑制剂-接头2-第2碱基去除修复抑制剂-……的方式经由接头2连接。作为此时的多个接头2,可以仅是1种,也可以是2种以上的组合,但优选是1种。

[0115] 作为这种接头2,没有特别限制,链长优选为1~50个氨基酸残基,更优选为5~30个氨基酸残基,进一步优选为8~15个氨基酸残基。所述接头2的链长小于所述下限时,有所述碱基去除修复抑制剂的功能性降低的倾向,另一方面,超过所述上限时,在使融合蛋白表达的情况下,有其表达效率降低的倾向。

[0116] 作为本发明涉及的接头2,例如可举出Addgene的pCMV_AncBE4max_P2A_GFP(ID:12100)中记载的10个氨基酸,但并不限于此。

[0117] [其他]

[0118] 作为本发明涉及的融合蛋白,还可以在N末端和/或C末端含有用于纯化或检测的标记标签、用于将TALE-核碱基转化酶转移到细胞核的核定位信号(NLS)等,它们可以含在如上所述TALE的N末端结构域中,也可以附加在融合蛋白的N末端和/或C末端。

[0119] 本发明涉及的融合蛋白例如可以通过以下方式得到,即,使编码上述TALE和核碱基转化酶以及根据需要的接头1、所述碱基去除修复抑制剂、接头2和其他氨基酸的基因作为一体进行转录和表达。另外,本发明涉及的融合蛋白可以通过适当采用、改良现有公知的

方法进行生产,例如,如在基于该氨基酸序列通过市售的合成机化学合成的方法、编辑了下述目标DNA的细胞的制备方法中所述,可以通过将编码融合蛋白的多核苷酸或表达该融合蛋白的载体导入所述细胞并使其表达的方法来得到。

[0120] (CRISPR-Cas9系统)

[0121] 本发明涉及的CRISPR-Cas9系统包含含有部分或全部丧失核酸酶活性的Cas9蛋白及其向导RNA。

[0122] [Cas9蛋白]

[0123] 在本发明涉及的CRISPR-Cas9系统中,作为Cas9蛋白,必需是丧失部分核酸酶活性的Cas9蛋白(在本说明书中,称为“nCas9”)或丧失全部核酸酶活性的Cas9蛋白(在本说明书中,称为“dCas9”)。即,Cas9蛋白典型地含有参与靶链切割的结构域(RuvC结构域)和参与非靶链切割的结构域(HNH结构域),但作为本发明涉及的Cas9蛋白,通过导入突变等,至少一者结构域的核酸酶活性需要丧失。

[0124] 作为这种突变,在SpCas9蛋白(来自化脓性链球菌(*S. pyogenes*)的Cas9蛋白)的情况下,例如,从N末端起第10个氨基酸(天冬氨酸)向丙氨酸的突变(D10A:RuvC结构域内的突变)、从N末端起第840个氨基酸(组氨酸)向丙氨酸的突变(H840A:HNH结构域内的突变)、从N末端起第863个氨基酸(天冬酰胺)向丙氨酸的突变(N863A:HNH结构域内的突变)、从N末端起第762个氨基酸(谷氨酸)向丙氨酸的突变(E762A:RuvCII结构域内的突变)、从N末端起第986个氨基酸(天冬氨酸)向丙氨酸的突变(D986A:RuvCIII结构域内的突变)。除此之外,各种来源的Cas9蛋白是公知的(例如W02014/131833),可以利用它们的nCas9或dCas9,但并不限于此。

[0125] 此外,Cas9蛋白的氨基酸序列和碱基序列被登录在公开的数据库中,例如Genbank(<http://www.ncbi.nlm.nih.gov>) (例如,检索号:KX151730.1等),在本发明中可以利用它们。另外,所述Cas9蛋白中,可以导入进一步的突变,例如用于改变PAM序列的识别的突变(Benjamin, Pet al., Nature 523, 481-485 (2015); Hirano, S. et al., Molecular Cell 61, 886-894 (2016)),还可以附加用于向细胞核转移的核定位信号(NLS)等。另外,作为这种Cas9蛋白,可以是市售的可获得的质粒内所含的序列所编码的蛋白。

[0126] 对于所述CRISPR-Cas9系统中的Cas9蛋白,以向导RNA目标序列包含所述目标DNA的目标位点的互补碱基的方式,设计下述向导RNA。另外,在本发明中,所述目标DNA的目标位点的互补碱基表示所述目标位点存在的链的互补链上的所述目标位点1个碱基的互补碱基。由此,在作为双链的目标DNA中,通过使单链DNA露出的螺旋酶活性而使目标位点特异性露出,提高利用所述核碱基转化酶的编辑效率。

[0127] [向导RNA]

[0128] 在本发明涉及的CRISPR-Cas9系统中,向导RNA是含有与目标DNA上的序列(向导RNA目标序列)互补的碱基序列(以下,根据情况称为“目标化碱基序列”)的crRNA(CRISPR RNA)和tracrRNA(trans-activating crRNA)的组合。所述crRNA进一步在3'侧含有可与tracrRNA相互作用(杂交)的碱基序列。另一方面,tracrRNA在5'侧含有可与crRNA的部分碱基序列相互作用(杂交)的碱基序列,由此,所述向导RNA通过这些碱基序列的相互作用,形成与Cas9蛋白相互作用的双链RNA。因此,所述向导RNA识别并结合所述目标DNA的向导RNA目标序列,将与该向导RNA形成复合体的Cas9蛋白诱导至该目标DNA,被诱导的Cas9蛋白通

过其螺旋酶活性在该目标DNA的目标位点露出单链DNA。

[0129] 作为本发明涉及的CRISPR-Cas9系统的向导RNA,可以是含有crRNA和tracrRNA的单分子向导RNA(sgRNA),也可以是含有crRNA片段和tracrRNA片段的双分子向导RNA。

[0130] 在所述目标DNA中,目标位点碱基的编辑发生在由所述向导RNA的目标化碱基序列与向导RNA目标序列之间的碱基配对形成的互补性和存在于向导RNA目标序列的互补链的3'侧的PAM序列这两者确定的位置。本发明涉及的CRISPR-Cas9系统的向导RNA以该向导RNA目标序列成为含有所述目标位点的互补碱基的序列、Cas9蛋白可以识别该目标位点的3'侧的PAM序列的方式被设计。由此,在作为双链的目标DNA中,通过使单链DNA露出的螺旋酶活性而使目标位点特异性露出,提高利用所述核碱基转化酶的编辑效率。

[0131] 作为设计这种Cas9蛋白的PAM序列和向导RNA目标序列的方法,已知各种方法,例如可以利用E-CRISP(<http://www.e-crisp.org/E-CRISP/>)、Zifit Targeter(<http://zifit.partners.org/ZiFiT/>) (Zing Finger财团)、CRISPRdirect(<http://crispr.dbcls.jp/>) (东京大学)、CRISPR-P(<http://cbi.hzau.edu.cn/crispr/>) (华中农业大学)、Guide RNA Target DesignTool. (<https://www.blueheronbio.com/external/tools/gRNASrc.jsp>) (Blue Heron Biotech)等进行确定。

[0132] 本发明涉及的CRISPR-Cas9系统例如可以通过以下方式得到,即,如下述编辑了目标DNA的细胞的制备方法中所述,使编码上述Cas9蛋白和向导RNA的基因分别同时转录和表达。本发明涉及的Cas9蛋白和向导RNA可以通过适当采用、改良现有公知的方法进行生产,例如可以通过将编码它们的多核苷酸或含有该多核苷酸的表达载体导入所述细胞并使其表达的方法来得到。

[0133] (目标DNA)

[0134] 在本发明中,将含有成为作为目标的DNA编辑的对象的目标位点的DNA称为“目标DNA”。本发明涉及的目标DNA是双链DNA,为了显示与上述融合蛋白和CRISPR-Cas9系统的对应,并且为了方便,设成至少一个链从5'侧依次含有TALE识别序列或其互补序列、间隔区1、所述目标位点、PAM序列的结构。在5'侧含有TALE识别序列的互补序列表示该链的互补链含有TALE识别序列。即,TALE识别序列可以设定在与所述目标位点相同的链上,也可以设定在其互补链上。另外,以该链的互补链含有所述目标位点的互补碱基的方式,含有向导RNA目标序列。将本发明涉及的目标DNA的结构的一例示于下述图2,但并不限于此。

[0135] 本发明涉及的目标位点表示成为利用所述核碱基转化酶的编辑(优选利用脱氨酶的脱氨基化)的靶点的1个碱基。但是,并不否定该1个碱基的两侧附近的碱基(特别是,存在成为利用脱氨酶的脱氨基化的靶点的碱基的情况。优选5'侧和3'侧的各1~10个碱基,更优选1~5个碱基,进一步优选1~2个碱基)被进一步编辑(在脱氨酶的情况下脱氨基化)。

[0136] TALE识别序列是所述TALE识别的序列。作为TALE识别序列的碱基数量,是10~30个碱基,优选是13~25个碱基,更优选是15~20个碱基。所述TALE识别序列以在所述目标位点的5'侧经由7~31bp的链长的间隔区1而存在的方式被选择。通过间隔区1的链长在该范围内,可以特异性且高效率地使所述目标位点的1个碱基脱氨基化。所述间隔区1的链长是将与目标位点的碱基的5'侧邻接的碱基作为第1碱基、从其到与所述TALE识别序列的3'侧邻接的碱基的长度。作为这种间隔区1的链长,更优选为10~31bp,进一步优选为10~28bp,进一步更优选为13~25bp。

[0137] PAM序列是所述Cas9蛋白识别的序列。PAM序列根据所利用的Cas9蛋白的种类而不同。作为典型的PAM序列,例如,与来自化脓性链球菌(*S.pyogenes*)的Cas9蛋白(II型)对应的PAM序列为5'-NGG,与来自硫磺矿硫化叶菌(*S.solfataricus*)的Cas9蛋白(I-A1型)对应的PAM序列为5'-CCN,与来自硫磺矿硫化叶菌(*S.solfataricus*)的Cas9蛋白(I-A2型)对应的PAM序列为5'-TCN,与来自*H.walsbyi*的Cas9蛋白(I-B型)对应的PAM序列为5'-TTC,与来自大肠杆菌(*E.coli*)的Cas9蛋白(I-E型)对应的PAM序列为5'-AWG,与来自大肠杆菌(*E.coli*)的Cas9蛋白(I-F型)对应的PAM序列为5'-CC,与来自绿脓杆菌(*P.aeruginosa*)的Cas9蛋白(I-F型)对应的PAM序列为5'-CC,与来自嗜热链球菌(*S.Thermophilus*)的Cas9蛋白(II-A型)对应的PAM序列为5'-NNAGAA,与来自无乳链球菌(*S.agalactiae*)的Cas9蛋白(II-A型)对应的PAM序列为5'-NGG,与来自金黄色葡萄球菌(*S.aureus*)的Cas9蛋白对应的PAM序列为5'-NGRRT或5'-NGRRN,与来自脑膜炎奈瑟氏菌(*N.meningitidis*)的Cas9蛋白对应的PAM序列为5'-NNNGATT,与来自齿垢密螺旋体(*T.denticola*)的Cas9蛋白对应的PAM序列为5'-NAAAC。此外,如上所述,通过改性Cas9蛋白(例如,导入突变),也可以改变PAM识别。由此,可以扩大目标位点的选择。

[0138] 在本发明中,所述PAM序列存在于所述目标位点的3'侧,所述向导RNA识别的向导RNA目标序列根据所述PAM序列的位置来确定。在本发明中,所述目标位点的互补碱基在所述向导RNA目标序列内的位置没有特别限定,例如优选在第1位~第50位之间,更优选在第1位~第30位之间,进一步优选在第1位~第25位之间。此外,所述向导RNA目标序列内的碱基的位置是将所述向导RNA目标序列的3'末端的碱作为第1位、从其到与所述PAM序列的5'侧邻接的碱基的互补碱基的位置。所述碱基位置的上限和下限依赖于所述向导RNA目标序列的长度,可通过调节所述向导RNA的长度来调节。

[0139] 所述向导RNA识别的向导RNA目标序列以成为含有所述目标位点的互补碱基的序列的方式被选择。通过这样选择向导RNA目标序列的位置,可以特异性且高效率地编辑所述目标位点的1个碱基。作为本发明涉及的向导RNA目标序列的碱基数量,优选为12~50个碱基,更优选为17~30个碱基,进一步优选为17~25个碱基。

[0140] 作为这种目标DNA的碱基序列,没有特别限制,以TALE识别序列或其互补序列、间隔区1、向导RNA目标序列的互补序列、所述互补序列中所含的目标位点及PAM序列满足上述条件的方式,设计TALE及向导RNA的目标化碱基序列,以及根据需要改变PAM的识别特异性,由此可以作为本发明的DNA编辑方法的靶点。

[0141] 进而,作为本发明涉及的目标DNA,根据目的,可以设成存在于细胞内的DNA(内源性DNA)或存在于细胞外的DNA。作为存在于细胞内的DNA,可以是内源性DNA,也可以是外源性DNA。作为内源性DNA,可举出基因组DNA,作为外源性DNA,例如可举出导入细胞内的DNA。作为存在于细胞外的DNA,可以是来自细胞的DNA,也可以是在细胞外扩增、合成的DNA。

[0142] (目标DNA编辑方法)

[0143] 在本发明的目标DNA编辑方法中,使所述融合蛋白和所述CRISPR-Cas9系统与所述目标DNA接触,通过所述融合蛋白的核碱基转化酶活性,编辑所述目标DNA的目标位点的碱基。

[0144] 使融合蛋白和CRISPR-Cas9系统与目标DNA接触时,融合蛋白的TALE识别并结合目标DNA上的TALE识别序列,并将连接到TALE的核碱基转化酶诱导至该目标DNA。另一方面,

CRISPR-Cas9系统的向导RNA识别并结合目标DNA上的向导RNA目标序列,将与该向导RNA形成复合体的Cas9蛋白诱导至该目标DNA。由此,在目标位点中,Cas9蛋白通过螺旋酶活性而露出单链DNA,因此,通过所述核碱基转化酶,可以有效发生目标碱基的取代(例如,碱基的脱氨基化)。由此,在目标位点发生1个碱基的取代(例如,C→U),另外,例如在细胞内,由于双链DNA的不匹配,发生取代的链的相反链的碱基被修复成与取代碱基形成配对(例如,G→A)、修复时被其他核苷酸取代(例如,U→A、G)、或产生1个碱基或多个碱基的缺失或插入,由此可以导入各种突变。

[0145] 因此,本发明涉及的DNA编辑包括在通过所述核碱基转化酶转变的目标位点及含有其的附近中的,一个以上核苷酸的缺失、被另一个以上核苷酸取代,或者一个以上核苷酸的插入或它们的突变组合。

[0146] 本发明的目标DNA编辑方法可以在细胞内进行,也可以在无细胞系统中进行。作为本发明的目标DNA编辑方法的场所“细胞内”,可以是真核细胞内,也可以是原核细胞内,优选是真核细胞内。作为所述真核细胞,例如可举出动物细胞(哺乳类、鱼类、鸟类、爬行动物类、两栖类、昆虫类的细胞等)、植物细胞、藻细胞、酵母,作为所述原核细胞,例如可举出大肠杆菌、沙门氏菌、枯草菌、乳酸菌、高度嗜热菌。

[0147] “动物细胞”中,例如包括构成动物个体的细胞、构成从动物摘除的器官、组织的细胞、来自动物组织的培养细胞等。具体而言,例如可举出卵母细胞或精子等生殖细胞;各阶段胚胎的胚胎细胞(例如,1细胞期胚胎、2细胞期胚胎、4细胞期胚胎、8细胞期胚胎、16细胞期胚胎、桑椹期胚胎等);诱导多能干(iPS)细胞或胚胎干(ES)细胞等干细胞;成纤维细胞、造血细胞、神经元、肌细胞、骨细胞、肝细胞、胰腺细胞、脑细胞、肾细胞等体细胞等。作为用于制作基因组编辑动物的卵母细胞,可以利用受精前和受精后的卵母细胞,优选为受精后的卵母细胞,即受精卵。特别优选地,受精卵为前核期胚胎。卵母细胞可以将冷冻保存的细胞解冻使用。

[0148] “植物细胞”中,例如包括构成植物个体的细胞、构成从植物分离的器官或组织的细胞、来自植物组织的培养细胞等。作为植物的器官或组织,例如可举出叶、茎、茎顶(生长点)、根、块茎、愈伤组织等。

[0149] 另外,作为本发明的目标DNA编辑方法的场所“无细胞系统”表示没有活细胞(所述真核细胞、原核细胞)的系统。作为本发明涉及的无细胞系统,只要是所述融合蛋白及所述CRISPR-Cas9系统与所述目标DNA可以接触的系统,就没有特别限制,例如可举出在缓冲液内、所述真核细胞或原核细胞的细胞破碎液内、细胞提取液内等。

[0150] 作为使所述融合蛋白和所述CRISPR-Cas9系统与所述目标DNA接触的方法,没有特别限制。可举出在细胞内,如下述编辑了目标DNA的细胞的制备方法所述,将所述融合蛋白和所述CRISPR-Cas9系统导入含有所述目标DNA的细胞中或将编码它们的载体等导入细胞中而使其表达的方法。在无细胞系统中,例如将目标DNA的溶液与所述融合蛋白和所述CRISPR-Cas9系统的溶液混合即可。作为这些溶液的溶剂,没有特别限制,例如优选磷酸缓冲液、Tris缓冲液、Good's缓冲液、硼酸缓冲液等缓冲液。

[0151] <编辑了目标DNA的细胞的制备方法>

[0152] 本发明的编辑了目标DNA的细胞的制备方法,

[0153] 一种制备编辑了目标DNA的细胞的方法,其包括:

[0154] 使(1)含有TALE和核碱基转化酶的融合蛋白、以及

[0155] (2)含有部分或全部丧失核酸酶活性的Cas9蛋白及其向导RNA的CRISPR-Cas9系统导入细胞或在细胞内表达而与目标DNA接触,通过所述融合蛋白的核碱基转化酶活性,编辑所述目标DNA的目标位点的碱基的工序,

[0156] 所述融合蛋白中的TALE所识别的TALE识别序列或其互补序列经由7~31bp的链长的间隔区1存在于所述目标位点的5'侧,并且

[0157] 所述CRISPR-Cas9系统中的向导RNA所识别的向导RNA目标序列以含有所述目标位点的互补碱基的方式存在。

[0158] 在本发明的编辑了目标DNA的细胞的制备方法(以下,根据情况简称为“制备方法”)中,所述融合蛋白、CRISPR-Cas9系统以及目标DNA如上述本发明的目标DNA编辑方法中所示。作为本发明的制备方法中的目标DNA,是基因组DNA,根据该基因组DNA的编辑目的,可以设计所述融合蛋白及CRISPR-Cas9系统。

[0159] 另外,在本发明的制备方法中,融合蛋白及CRISPR-Cas9系统与细胞内的目标DNA的接触通过以下方式进行,即,所述融合蛋白及CRISPR-Cas9系统以蛋白形态导入细胞、以多核苷酸形态导入细胞和/或通过以多核苷酸形态导入细胞或导入表达载体而使其在细胞内表达。因此,作为所述融合蛋白及CRISPR-Cas9系统,可以将所述融合蛋白及Cas9蛋白分别独立地以蛋白形态导入细胞,也可以以编码该蛋白的RNA或DNA(多核苷酸)形态导入细胞并使其在细胞内表达,也可以以表达该蛋白的载体(表达载体)形态导入细胞并使其在细胞内表达。另外,与此独立,可以将所述向导RNA以RNA形态导入细胞,也可以以编码该RNA的DNA(多核苷酸)的形态导入细胞并使其在细胞内表达,也可以以表达该RNA的载体(表达载体)的形态导入细胞并使其在细胞内表达。

[0160] 在将所述融合蛋白及CRISPR-Cas9系统以表达载体形态导入细胞并使其在细胞内表达的情况下,例如可以将表达所述融合蛋白的载体、表达所述Cas9蛋白的载体以及表达所述向导RNA的载体分别导入细胞内,另外也可以将组合这些中的2种以上并表达的载体导入细胞内。

[0161] 另外,在将所述融合蛋白及CRISPR-Cas9系统以表达载体形态导入细胞并使其在细胞内表达的情况下,作为编码所述融合蛋白及所述Cas9蛋白的多核苷酸,也可以是分别独立地根据导入的细胞适当进行密码子最佳化的多核苷酸。另外,作为该表达载体,优选含有可操作地与要表达的多核苷酸连接的启动子和/或其他控制序列。进而,作为该表达载体,优选是在不整合到宿主基因组的情况下能够稳定表达编码的蛋白的载体。这种表达载体可以适当地按照现有公知的方法制作。

[0162] 作为将所述融合蛋白及所述CRISPR-Cas9系统的蛋白、编码该蛋白的多核苷酸、表达该蛋白的载体导入细胞的方法,可以将用于向细胞导入蛋白或DNA、RNA片段的公知方法根据细胞的种类适当采用,作为这种方法,例如可举出电穿孔法(electroporation法)、微注入法、粒子枪法、磷酸钙法、聚乙烯亚胺(PEI)法、脂质体法(脂转染法)、DEAE-葡萄糖聚糖法、阳离子性脂质介导的转染、病毒(腺病毒、慢病毒、腺伴随病毒、杆状病毒等)、农杆菌法、醋酸锂法、原生质球法、热冲击法(氯化钙法、氯化铷法)等。这种方法记载于“Leonard G. Davis et al., Basic methods in molecular biology, New York: Elsevier, 1986”等许多标准研究室手册中。

[0163] 所述融合蛋白及所述CRISPR-Cas9系统导入细胞或在细胞内表达时,所述融合蛋白及所述CRISPR-Cas9系统与细胞内的目标DNA接触,通过上述本发明的目标DNA编辑方法所述的目标DNA编辑,在目标位点发生目标碱基的取代,其结果可以得到编辑了目标DNA的细胞。

[0164] 本发明还提供一种非人个体的制作方法,所述非人个体含有编辑了所述目标DNA的细胞。该方法包括由通过上述制备方法得到的细胞制作非人个体的工序。作为非人个体,例如可举出非人动物和植物。作为非人动物,可举出哺乳类(小鼠、大鼠、豚鼠、仓鼠、兔子、猴子、猪、牛、山羊、绵羊等)、鱼类、鸟类、爬行动物类、两栖类、昆虫类。在制作模型动物时,哺乳动物优选是小鼠、大鼠、豚鼠、仓鼠等啮齿类,特别优选是小鼠。作为所述植物,例如可举出谷物类、油料作物、饲料作物、水果、野菜类。作为具体的作物,例如可例示水稻、玉米、香蕉、花生、向日葵、西红柿、油菜、烟草、小麦、大麦、马铃薯、大豆、棉花、康乃馨。

[0165] 作为由编辑了所述目标DNA的细胞制作非人个体的方法,可以利用公知的方法。在动物中由细胞制作非人个体的情况下,通常利用生殖细胞或多能干细胞。例如,可以将所述融合蛋白和所述CRISPR-Cas9系统微注入到卵母细胞中,将得到的卵母细胞移植到处于假妊娠状态的雌性非人哺乳动物的子宫中,然后得到产仔。另外,在植物中,自古以来已知其体细胞具有分化全能性,例如,可以通过将所述融合蛋白及所述CRISPR-Cas9系统微注入到植物细胞中,从得到的植物细胞再生植物体,从而得到编辑了所希望的DNA的植物体。另外,也可以从得到的非人个体中得到编辑了所希望的DNA的子孙或克隆。

[0166] 有无目标DNA编辑的确认以及基因型的确定可以基于现有公知的方法进行,例如可以利用PCR法、序列确定法、Southern印迹法等。

[0167] <DNA编辑系统>

[0168] 另外,本发明提供DNA编辑系统,其用于上述本发明的目标DNA编辑方法、本发明的编辑了目标DNA的细胞的制备方法、或上述本发明的非人个体的制作方法中,包含:

[0169] (1) 含有TALE和核碱基转化酶的融合蛋白、以及

[0170] (2) 含有部分或全部丧失核酸酶活性的Cas9蛋白及其向导RNA的CRISPR-Cas9系统。

[0171] 所述融合蛋白和CRISPR-Cas9系统如上述本发明的目标DNA编辑方法和制作方法中所示。它们分别独立地可以是蛋白或RNA的形态,也可以是编码蛋白或RNA的多核苷酸的形态,也可以是表达蛋白或RNA的载体(表达载体)的形态。

[0172] 另外,在为载体形态的情况下,本发明提供包含以下载体的DNA编辑系统,其根据目标DNA的目标位点,用户可以设计所述融合蛋白及CRISPR-Cas9系统:

[0173] (a) 含有编码TALE的多核苷酸的插入位点和编码所述融合蛋白的TALE以外的多核苷酸的载体,以及

[0174] (b) 编码部分或全部丧失核酸酶活性的Cas9蛋白的多核苷酸、或含有该多核苷酸的载体,

[0175] (c) 编码所述Cas9蛋白质的向导RNA的多核苷酸、或含有该多核苷酸的载体或含有该多核苷酸的插入位点的载体。

[0176] 此外,(a)~(c)的各载体分别含有可以表达各多核苷酸的表达单元。

[0177] 本发明的DNA编辑系统分别可以是由包含所述融合蛋白和所述CRISPR-Cas9系统

的组合组成的组合物,也可以是包含所述组合的试剂盒。在为试剂盒的情况下,该试剂盒可以进一步含有一种或多种附加试剂。作为这种附加试剂,例如可举出稀释缓冲液、重构溶液、洗涤缓冲液、核酸导入试剂、蛋白导入试剂、对照试剂(例如,对照脱氨酶),但并不限于此。另外,该试剂盒可以进一步包含用于实施本发明的方法的使用说明书。

[0178] 所述试剂盒中所包含的各元件可以分别收容在单独的容器中,也可以收容在同一容器中。各元件可以以每次使用量收容在容器中,也可以以多次量收容在一个容器中。各元件可以以干燥形态收容在容器中,也可以以溶解在适当溶剂(包括缓冲液、稳定剂、保存剂、防腐剂等的溶剂)中的形态收容在容器中。

实施例

[0179] 以下,基于实施例对本发明进行更具体说明,但本发明并不限于以下实施例。

[0180] 1. 报告质粒的制作

[0181] 作为报告基因,设成pNLF-M/A,其是使用pNLF1-C[CMV Hygro](PROMEGA公司制, WI, USA),通过位点特异性突变导入法,将第71个和第107个甲硫氨酸密码子(ATG)变更为丙氨酸密码子(ATA)而得。接着,在pNLF-M/A中,首先插入下述表1所示的序列(BEtag)。BEtag序列含有TALE识别序列(表1中的下划线(*1):5'-tACAGAAGCGGCAAAGG-3';小写字母表示TALE的N末端结构域所识别的胸腺嘧啶)、目标密码子(表1中的下划线(*2):5'-ACG-3')及它们之间的间隔区1序列,间隔区1序列的长度包括位于目标密码子5'的碱基(A),为7bp、13bp、19bp、25bp或31bp。在各BEtag序列(BEtag-7~31bp:序列号1~5)中,将设计成可在两端附加NheI识别位点及SbfI识别位点的寡核苷酸退火,插入到用NheI及SbfI处理过的pNLF-M/A中,得到pNLF-BEtag(pNLF-BEtag-7bp~31bp)。

[0182] 此外,所述TALE识别序列是对于已确认到细胞内活性的人腺瘤样结肠息肉(adenomatous polyposis coli)基因的TALEN的Right TALE序列(Sakuma et al., "Repeating pattern of non-RVD variations in DNA-binding modules enhances TALEN activity.", Sci.Rep., 3:3379(2013))。

[0183] 进而,为了在pNLF-BEtag中插入PAM序列(5'-NGG-3'),将下述表1所示的含有PAM部的序列(PAM:序列号6)的寡核苷酸和在该反义序列的5'末端附加5'-TCGA-3'的寡核苷酸退火,插入到用EcoRV及XhoI处理过的各pNLF-BEtag中,制作报告质粒(pNLF-BEtag-7bp-PAM、pNLF-BEtag-13bp-PAM、pNLF-BEtag-19bp-PAM、pNLF-BEtag-25bp-PAM、pNLF-BEtag-31bp-PAM)。

[0184] 由于PAM部(表1中的下划线(*3))含有9个连续的"G",所以通过以位于PAM部的5'侧的向导RNA目标序列的互补序列每1个碱基向3'侧偏移的方式设计向导RNA,可以使PAM序列的位置每1个碱基向下游偏移,由此可以设定8处的PAM序列(下述表7的PAM1~8)。在下述表1中,示出插入pNLF-M/A质粒中的各序列。

[0185] [表1]

[0186]

产物	序列 (5'-3')	序列号
BEtag-7bp	CATAAAATACAGAAGCGGGCAAAGG ^{*1} GGGAAGACG ^{*2} GATATCTCC	1
BEtag-13bp	CATAAAATACAGAAGCGGGCAAAGG ^{*1} CTATTTGGGAAGACG ^{*2} GATATCTCC	2
BEtag-19bp	CATAAAATACAGAAGCGGGCAAAGG ^{*1} ATTAGTCTATTTGGGAAGACG ^{*2} GATATCTCC	3
BEtag-25bp	CATAAAATACAGAAGCGGGCAAAGG ^{*1} TTCAGGATTAGTCTATTTGGGAAGACG ^{*2} GATATCTCC	4
BEtag-31bp	CATAAAATACAGAAGCGGGCAAAGG ^{*1} AGTCTATTCAGGATTAGTCTATTTGGGAAGACG ^{*2} GATATCTCC	5
PAM	ATCTCTGCAGGGGGGGGG ^{*3} CCGGC	6

[0187] *1:TALE识别序列、*2:含有目标碱基的目标密码子、*3:PAM部

[0188] 在图1中,示出表示已完成的报告质粒的结构的概念图。另外,在图2中示出含有TALE识别序列、间隔区1、目标位点、PAM部以及向导RNA目标序列的从NheI识别位点到XhoI识别位点的序列。在该报告质粒中,目标密码子位于相当于NanoLuc荧光素酶起始密码子的位置,根据该报告质粒,通过与TALE识别序列结合的TALE-脱氨酶,目标密码子ACG转变为ATG(目标碱基(目标位点)C被T取代)时,表达NanoLuc荧光素酶(图3)。

[0189] 2.TALE载体组和TALE表达质粒的制作

[0190] TALE载体组的序列及结构以TALE重复单元与上述1.中制作的报告质粒的TALE识别序列对应的方式,按照Sakuma et al. (2013)构建。首先,对编码由第12个和第13个的2个氨基酸构成的可变残基的4种(RVD:HD、NG、NI、NN)的序列以外的模块序列(非重复可变双残基(non-repeat-variable di-residue(non-RVD)))进行改变(特别是第4个和第32个),进一步将在其两端附加了限制酶BsaI识别位点的序列(模块序列)人工DNA合成(共计16种:1HD~4HD、1NG~4NG、1NI~4NI、1NN~4NN)。接着,将这些模块序列插入到pEX-A2J2(Eurofins Genomics公司制,Tokyo,Japan)中,制作模块质粒组(共计16种:pEX1HD~pEX4HD、pEX1NG~pEX4NG、pEX1NI~pEX4NI及pEX1NN~pEX4NN)。

[0191] 另外,通过人工DNA合成,制作构成阵列质粒的DNA序列FUS2_aXX(共计7种:XX=1a、2a、2b、3a、3b、4a、4b)及FUS2_b(1-4)(共计4种)。将它们插入到pCR8/GW/TOPO(Thermo Fisher Scientific公司制,Waltham,MA,USA)中,制作pCR8_FUS2_aXX和pCR8_FUS_b(1-4)。接着,将其用作Sakuma et al. (2013)中记载的铂金门系统中的最初的组装步骤(步骤1)的捕获载体,根据该文献中记载的方法,制作连接TALE序列的阵列质粒。

[0192] 接着,制作目标载体(TALE-WT、TALE-63、TALE-47),其是在从pcDNA 3.1(+)(Thermo Fisher Scientific公司制)中去除了耐药基因表达单元的pcDNA3.1s中,插入了通过人工DNA合成制作的、编码TALE的N末端结构域的序列以外,还插入了所述模块序列1个和编码紧连着其3'末端的TALE的C末端结构域的序列。作为TALE的C末端结构域,使用野生型(WT:C末端结构域的氨基酸数量=180)、C末端结构域的氨基酸数量为63的结构域(63)、C末端结构域的氨基酸数量为47的结构域(47)这3种,编码“WT”的序列是参照Addgene的pTALETF_v2(ID:32185~32188)中所含的C末端结构域的序列,编码“63”的序列是参照Addgene的pTALEN_v2(ID:32189~32192)中所含的C末端结构域的序列,编码“47”的序列是参照Addgene的ptCMV-153/47-VR-NG(Addgene ID:50704)中所含的C末端结构域的序列进行人工DNA合成。另外,作为TALE的N末端结构域,对应于这些C末端结构域,分别参照WT: Addgene的pTALETF_v2(ID:32185~32188)中所含的N末端结构域的序列;63: Addgene的ptCMV-136/63-VR-HD(ID:50699)中所含的N末端结构域的序列;47: Addgene的ptCMV-153/

47-VR-HD (ID:50703)中所含的N末端结构域的序列进行人工DNA合成。使用上述中制作的阵列质粒和目标载体,按照Sakuma et al. (2013)中记载的方法,并通过Golden Gate法制作TALE表达质粒。

[0193] 3. TALE-脱氨酶表达质粒的制作(1)

[0194] (1) 104个氨基酸接头系列

[0195] 首先,将通过人工DNA合成制作的AncBE4max基因(Koblan et al., “Improving cytidine and adenine base editors by expression optimization and ancestral reconstruction”, Nat Biotechnol, 36, p.843-846 (2018) 和Target-AID基因(Nishida et al., “Targeted nucleotide editing using hybrid prokaryotic and vertebrate adaptive immune systems.”, Science 353, aaf8729 (2016) 分别插入到pcDNA3.1s的BamHI识别位点与EcoRV识别位点之间,由此制作AncBE4max表达质粒和Target-AID表达质粒。

[0196] 接着,通过以下方法制作具有104个氨基酸接头1的TALE-脱氨酶表达质粒。即,以上述AncBE4max表达质粒的AncBE4max基因作为模板,使用下述表2中记载的引物,将Anc689脱氨酶基因(Anc689脱氨酶:引物序列号7~8)、10个氨基酸接头2及UGI基因的2次重复序列(10aa接头-β内酰胺酶:引物序列号11~12)分别通过PCR扩增。另外,将上述Target-AID表达质粒的Target-AID基因作为模板,使用下述表2中记载的引物,将PmCDA1脱氨酶基因(PmCDA1:引物序列号9~10)和编码104个氨基酸接头1的序列(104aa接头:引物序列号13~17)通过PCR扩增。进而,通过PCR扩增含有从内酰胺酶到编码TALE的N末端结构域(WT、63或47)的序列的序列(引物序列号22~25)。在下述表2中,示出用于构建TALE-脱氨酶表达质粒的各引物及其序列号。表2中,在104aa接头用以下,例如“WT-104-BE4”表示该序列是,TALE的C末端结构域为WT、并且编码含有所述104个氨基酸接头1和Anc689脱氨酶(BE4)的TALE-脱氨酶用的接头1的序列。此外,在下述各表中,“AID”并不表示脱氨酶为AID,而是表示来自“Target-AID”的PmCDA1。

[0197] [表2]

[0198]

产物	正向引物 (5'-3')	序列号	反向引物 (5'-3')	序列号
Anc689 脱氨酶	anc689 脱氨酶 _F	7	anc689 脱氨酶 _R_inf10aa	8
PmCDA1	PmCDA1_F	9	PmCDA1_R_inf10aa	10
10aa 接头 -β- 内酰胺酶	10aa_F	11	Amp_F	12
WT-104-BE4 用 104aa 接头	104aa_F_infWT	13	AID_R3_infAnc689	15
47-104-BE4 用 104aa 接头	104aa_F_inf47	14		
WT-104-AID 用 104aa 接头	104aa_F_infWT	13	AID_R3_infCDA1	17
63-104-AID 用 104aa 接头	104aa_F_inf63	16		
47-104-AID 用 104aa 接头	104aa_F_inf47	14		
TALE_WT-β-内酰胺酶	TALE_WT_R	22	Amp_R	25
TALE_63-β-内酰胺酶	TALE_63_R	23		
TALE_47-β-内酰胺酶	TALE_47_R	24		

[0199] 将编码各脱氨酶、104个氨基酸接头1的序列和10个氨基酸接头2及UGI基因的2次重复序列通过In-Fusion法(TaKaRa Bio Inc, Shiga, Japan)插入到上述2.中制作的含有从 β -内酰胺酶到编码TALE的N末端结构域(WT、63或47)的序列的序列与编码TALE的C末端结构域(WT、63或47)的下游(3'侧)序列之间,制作从N末端依次结合了TALE(N末端结构域(WT、63或47)-TALE重复结构域-C末端结构域(WT、63或47))、104个氨基酸接头1(104aa)、脱氨酶(Anc689脱氨酶(BE4)或PmCDA1脱氨酶(AID))、10个氨基酸接头2(10aa)、UGI基因(UGI)、10个接头2(10aa)和UGI基因(UGI)的表达TALE-脱氨酶的质粒(TALE-脱氨酶表达质粒)。在图4中,示出所述TALE-脱氨酶结构的概念图。

[0200] (2) 12个氨基酸接头系列

[0201] 另外,将代替所述104个氨基酸接头1而具有12个氨基酸接头1(12aa)的TALE-脱氨酶表达质粒通过以下方法制作。即,首先,使下述表3中记载的寡核苷酸分别退火,制作编码12个氨基酸接头1的序列。表3中,在12aa接头(序列号18~21)用以下,例如“TALE_12-AID”表示该序列是,TALE的C末端结构域为WT、并且编码含有所述12个氨基酸接头1和PmCDA1脱氨酶(AID)的TALE-脱氨酶用的接头1的序列。该12个氨基酸接头1由Yang L et al., “Engineering and optimising deaminase fusions for genomic editing.” Nat Commun 713330 (2016) 中记载的12个氨基酸组成。接着,使用下述表4所示的引物(序列号9、22~24),分别用反向PCR扩增上述TALE-脱氨酶表达质粒的编码104个氨基酸接头1的序列以外的序列,通过In-Fusion法插入编码所述12个氨基酸接头1的序列。在下述表3中,示出编码12个氨基酸接头1的序列及其序列号,在表4中,示出使用于反向PCR的引物及其序列号。

[0202] [表3]

产物	正义寡核苷酸	序列号	反义寡核苷酸	序列号
TALE_WT-12-AID用12 aa 接头	12aa_infWT	18	12aa_infCDA1	21
TALE_63-12-AID用12 aa 接头	12aa_inf63	19		
TALE_47-12-AID用12 aa 接头	12aa_inf47	20		

[0204] [表4]

最终产物	正向引物 (5'-3')	序列号	反向引物 (5'-3')	序列号
TALE_WT-12-AID	PmCDA1_F	9	TALE_WT_R	22
TALE_63-12-AID			TALE_63_R	23
TALE_12-12-AID			TALE_47_R	24

[0206] (3) 氨基酸长度调节接头系列

[0207] 进而,将在TALE-47-104-AID中代替104个氨基酸接头1而编码从该104个氨基酸接

头1的C末端侧依次缺失氨基酸、使氨基酸长度成为12、24、36、48、60或84的各氨基酸接头1的TALE-脱氨酶表达质粒通过以下方法制作。即,使用下述表5中记载的引物(序列号9、26~31),用反向PCR中扩增上述TALE-脱氨酶表达质粒的编码缺失氨基酸的序列以外的序列,通过In-Fusion法使其自我连接(self-ligation)而制作。在下述表5中,示出使用于TALE-47-104-AID的氨基酸接头1缺失突变体制作的引物及其序列号。

[0208] [表5]

最终产物	正向引物 (5'-3')	序列号	反向引物 (5'-3')	序列号
TALE_47-12'-AID	PmCDA1_F	9	12aa_R_infCDA1	26
TALE_47-24'-AID			24aa_R_infCDA1	27
TALE_47-36'-AID			36aa_R_infCDA1	28
TALE_47-48'-AID			48aa_R_infCDA1	29
TALE_47-60'-AID			60aa_R_infCDA1	30
TALE_47-84'-AID			84aa_R_infCDA1	31

[0210] 另外,作为TALE-脱氨酶的阴性对照(NC),为了TALE重复单元不与人基因组结合,代替上述1.中制作的报告质粒的TALE识别序列,表达以识别并结合下面的NC序列:5'-tTGGCGTATAGTCGCG-3'(序列号:32)的方式构建的TALE-脱氨酶-NC,除此之外,与上述同样地分别制作表达对应于各TALE-脱氨酶的TALE-脱氨酶-NC的质粒(TALE-脱氨酶-NC表达质粒)。

[0211] 在下述表6中,分别示出制作的各表达质粒中的TALE-脱氨酶及其阴性对照(TALE-脱氨酶-NC)的结构及表示其序列的序列号(碱基序列的序列号、氨基酸序列的序列号)的一览。

[0212] [表6]

[0213]

TALE- 脱氢酶						TALE- 脱氢酶 -NC (阴性对照)					
ID	TALE 识别 序列	TALE C末端 结构域	接头1 长度 (a.a.)	脱氢酶	序列 号	ID	TALE 识别 序列	TALE C末端 结构域	接头1 长度 (a.a.)	脱氢酶	序列 号
WT-104-BE4	人	WT	104	Anc689	33,34	WT-104-BE4- NC	非人	WT	104	Anc689	35,36
47-104-BE4		47			37,38	47-104-BE4- NC		47			39,40
WT-104-AID		WT	104	PmCDA1	41,42	WT-104-AID- NC		WT	104	PmCDA1	43,44
63-104-AID		63			45,46	63-104-AID- NC		63			47,48
47-104-AID		47			49,50	47-104-AID- NC		47			51,52
WT-12-AID		WT	12	PmCDA1	53,54	WT-12-AID- NC		WT	12	PmCDA1	55,56
63-12-AID		63			57,58	63-12-AID- NC		63			59,60
47-12-AID		47			61,62	47-12-AID- NC		47			63,64
47-12'-84'- AID		47	12,24,36,48, 60 或 84	PmCDA1	—	47-12'-84'- AID-NC		47	12,24,36,48, 60 或 84	PmCDA1	—
AncBE4max	—	—	—	Anc689	—	—					

[0214] 4. Cas9表达质粒的制作

[0215] 首先,将pX330(Addgene,Cambridge,MA;Plasmid 42230)的从U6启动子到BGH多A附加序列的区域进行人工DNA合成,通过In-Fusion法插入到pBlueScriptH(SK+)(Stratagene,La Jolla,CA,USA)的EcoRV识别位点与BamHI识别位点之间,由此制作将Cas9表达质粒pX330_BS。接着,通过对pX330_BS的Cas9基因进行基于PCR的位点特异性突变导入法,分别制作切口酶类型的nCas9(D10A)表达质粒和无切割活性的dCas9(D10A+H840A)表达质粒。

[0216] 5. 向导RNA表达质粒的制作(1)

[0217] 首先,用XbaI和NotI处理上述4.中制作的pX330_BS而去除Cas9基因,在填补反应后,通过自我连接,制作质粒(pX330_BS-ΔCas9)。接着,使以与下述表7所示的向导RNA的目标序列(在表7中,表示向导RNA的目标序列(反义链上)的互补序列)(表7的下划线以外的序列)对应的方式设计的寡核苷酸退火,通过bpiI处理和连接,插入到pX330_BS-ΔCas9中,制作表达各向导RNA(sgRNA-1~8)的质粒(向导RNA表达质粒1~8)。在下述表7中,示出向导RNA的目标序列的互补序列(除下划线外)和Cas9的PAM序列(下划线)。

[0218] [表7]

[0219]

PAM序列的位置	向导 RNA	向导RNA的目标序列的互补序列和PAM序列	序列号
PAM1	sgRNA-1	GGAAGACGGATATCTCCTGC <u>AGG</u>	65
PAM2	sgRNA-2	GAAGACGGATATCTCCTGCA <u>GGG</u>	66
PAM3	sgRNA-3	AAGACGGATATCTCCTGCAG <u>GGG</u>	67
PAM4	sgRNA-4	AGACGGATATCTCCTGCAGG <u>GGG</u>	68
PAM5	sgRNA-5	GACGGATATCTCCTGCAGGG <u>GGG</u>	69
PAM6	sgRNA-6	ACGGATATCTCCTGCAGGGG <u>GGG</u>	70
PAM7	sgRNA-7	CGGATATCTCCTGCAGGGGG <u>GGG</u>	71
PAM8	sgRNA-8	GGATATCTCCTGCAGGGGGG <u>GGG</u>	72

[0220] 下划线:PAM序列

[0221] 6. 向HEK细胞的转化(1)

[0222] 将在含有10%FBS的DMEM培养基中生长的HEK293T细胞以 5×10^4 个细胞接种到96孔板的各孔中。使用脂质体LTX(Thermo Fisher Scientific公司制),将表6中记载的TALE-脱氨酶表达质粒和TALE-脱氨酶-NC表达质粒中的任一种75ng;上述4.中制作的nCas9表达质粒或dCas9表达质粒50ng;上述5.中制作的向导RNA表达质粒1~8和pX330_BS- Δ Cas9(无向导RNA)中的任一种10ng;上述1.中制作的报告质粒中的任一种20ng;以及作为参考质粒的pGL4.54 (PROMEGA公司制) 5ng导入HEK293T细胞中。参考质粒是表达萤火虫荧光素酶fLuc)的质粒。

[0223] 另外,作为阳性对照,将上述3.中制作的AncBE4max表达质粒75ng;上述5.中制作的向导RNA表达质粒1~8和pX330_BS- Δ Cas9(无向导RNA)中的任一种10ng;上述1.中制作的报告质粒中的任一种20ng;pGL4.545ng组合并导入HEK293T细胞中。

[0224] 7. NanoLuc荧光素酶活性值的测定

[0225] 转化后培养24小时,然后去除培养基,用PBS(-)洗涤后,用被动裂解液(Passive Lysis Buffer (PROMEGA公司制))处理,溶解细胞,制成细胞溶解液。将所述细胞溶解液在DMEM培养基稀释100倍,使用Nano-Glo双荧光素报告基因检测系统(Dual-Luciferase Reporter Assay System (PROMEGA公司制)),通过TriStar S LB942盘判读器(Berthold Technologies公司制,Bad Wildbad,Germany)测定了NanoLuc荧光素酶活性-和萤火虫荧光素酶活性分数。

[0226] 作为各分数的阴性对照,测定关于导入TALE-脱氨酶-NC表达质粒的细胞的NanoLuc荧光素酶活性分数。此外,对于阳性对照(导入了AncBE4max表达质粒的细胞),测定关于导入pX330_BS- Δ Cas9表达质粒的细胞(不表达向导RNA的细胞)的活性分数,作为阴性对照(AncBE4max-NC)。

[0227] 活性的数值化如下进行。首先,使用基于参考质粒的萤火虫荧光素酶活性分数,将各NanoLuc荧光素酶活性分数标准化。接着,使用标准化的活性分数,从导入TALE-脱氨酶表达质粒的细胞的活性分数中减去导入TALE-脱氨酶-NC表达质粒的细胞的活性分数,作为

TALE-脱氨酶活性的活性值。另外,从导入AncBE4max的表达质粒的细胞的活性分数中减去AncBE4max-NC,作为AncBE4max活性值。进而,为了在各试验之间比较TALE-脱氨酶活性,TALE-脱氨酶活性值用以后述PAM2条件下的AncBE4max活性值为1时的相对活性来表示。试验至少重复进行3次,对平均值赋予标准偏差进行图表化。

[0228] <试验1>PAM序列位置对碱基编辑器活性的影响

[0229] 作为阳性对照,为了检查现有的碱基编辑器AncBE4max显示最高活性的PAM序列的位置,将PAM序列的位置每一个碱基向3'侧(下游)移动(PAM1~PAM8),检查碱基编辑活性。

[0230] 在AncBE4max中,在将PAM序列位置设为目标DNA序列中第21~23个位置的情况下,已知有碱基编辑活性高的目标碱基的位置成为同一目标DNA序列的第4~8个的关系(Rees, H.A. and Liu, D.R., Nat Rev Genet 19, 770-788 (2018))。在本研究中所使用的报告基因中,如上所述,通过以向导RNA的目标序列改变的方式设计,可以将PAM序列的位置从表7中记载的PAM1到PAM8进行变更,因此可相应地变更目标碱基的位置。

[0231] 在上述6.中,将上述3.中制作的AncBE4max表达质粒、上述5.中制作的向导RNA表达质粒1~8中的任一种、上述1.中制作的报告质粒(间隔区1:19bp)、作为参考质粒的pGL4.54组合并导入HEK293T细胞中,通过上述7.分别取得AncBE4max活性值。另外,作为阴性对照,代替向导RNA表达质粒,使用pX330_BS-ΔCas9。

[0232] 将结果示于图5。在图5中,示出以使用向导RNA表达质粒2时即PAM2时的AncBE4max活性值为1.0的情况下的、使用各向导RNA表达质粒1~8时即PAM1~8时的AncBE4max活性值。如图5所示,可知AncBE4max活性值在PAM2时示出最大活性。因此,将PAM2时的AncBE4max活性值确定为用于以下活性评价的阳性对照。

[0233] <试验2>间隔区1长度对TALE-脱氨酶活性的影响

[0234] (BE4系列)

[0235] 关于TALE的C末端结构域为WT或47-氨基酸接头1为104个氨基酸、脱氨酶为BE4(Anc689)的2种TALE-脱氨酶(WT-104-BE4、47-104-BE4),将PAM序列的位置固定在PAM2,检查报告基因的间隔区1的长度对活性的影响。间隔区1的长度设为7bp、13bp、19bp、25bp、31bp。另外,作为Cas9/向导RNA,对有nCas9(D10A)及向导RNA的表达(nCas9)、有dCas9(D10A+H840A)及向导RNA的表达(dCas9)、有nCas9表达和无向导RNA表达(nCas9/无向导)的3个条件进行了研究。

[0236] 在上述6.中,将上述3.(1)中制作的TALE-脱氨酶表达质粒(WT-104-BE4或47-104-BE4)或与其对应的TALE-脱氨酶-NC表达质粒、上述4.中制作的nCas9表达质粒或dCas9表达质粒、上述5.中制作的向导RNA表达质粒2或pX330_BS-ΔCas9、上述1.中制作的报告质粒(间隔区1:7~31bp)和作为参考质粒的pGL4.54组合并导入HEK293T细胞中,通过上述7.分别取得TALE-脱氨酶活性值(相对于AncBE4max活性值的比例)。

[0237] 将结果示于图6。如图6所示,即使在任一TALE-脱氨酶(BE4)中,在不存在向导RNA的情况下,即在nCas9不结合于目标碱基附近的情况下,也没有观察到活性。另外,使用nCas9在底链中加缺口的活性比使用dCas9不加缺口时的活性高。关于间隔区1的长度,在13bp和25bp的情况下显示出特别高的活性,在25bp的情况下显示出更高的活性。关于TALE的C末端结构域,47(0.29±0.03)的活性高于WT(例如,nCas9,间隔区1长度:25bp时,是0.19±0.01)。

[0238] (AID系列)

[0239] 关于TALE的C末端结构域为WT、63或47,氨基酸接头1为104个氨基酸或12个氨基酸,脱氨酶为AID(PmCDA1)的6种TALE-脱氨酶(WT-104/12-AID、63—104/12-AID、47—104/12-AID),与上述BE4同样地检查报告基因的间隔区1的长度对活性的影响。

[0240] 将结果示于图7。如图7所示,即使在任一TALE-脱氨酶(AID)中,在不存在向导RNA的情况下,即在nCas9不结合于目标碱基附近的情况下,也没有观察到活性。另外,在WT-104-AID、63—104-AID、WT-12-AID、63—12-AID中,与脱氨酶为BE4的情况同样地,使用nCas9在底链中加缺口的活性比使用dCas9不加缺口时的活性高。另一方面,在47-104-AID、47-12-AID中,缺口的效果并不显著。

[0241] 关于间隔区1的长度,在所有TALE-脱氨酶(AID)中,在25bp时显示出高活性,在63-104-AID、47-12-AID中,即使是19bp也显示出高活性。关于TALE的C末端结构域,在104个氨基酸接头1的情况下,活性为WT(例如,nCas9,间隔区1长度:25bp时,是 0.09 ± 0.00)、63(0.16 ± 0.01)、47(0.4 ± 0.03)(图7-A、B、C);在12个氨基酸接头1中,活性为WT(0.32 ± 0.02)、63(0.38 ± 0.03)、47(0.57 ± 0.02)(图7-D、E、F),在氨基酸接头1的长度相同的情况下,有 $47 > 63 > \text{WT}$ 的关系。另外,TALE的C末端结构域用同样的结构进行比较时,12个氨基酸接头1的活性比104个氨基酸接头1高。显示出最高活性的TALE-脱氨酶(AID)为47-12-AID(例如,nCas9,间隔区1长度:19bp时,是 0.57 ± 0.2)。

[0242] <试验3>PAM序列位置对TALE-脱氨酶活性的影响

[0243] 固定报告基因的间隔区1的长度,将PAM序列的位置每一个碱基向3'侧(下游)移动,检查PAM序列的位置(即对应于Cas9的位置)对TALE-脱氨酶活性的影响。作为间隔区1长度,对试验2中进行活性评价时活性比较高的13bp、19bp、25bp进行了研究。

[0244] 在上述6.中,将上述3.(1)(2)中制作的TALE-脱氨酶表达质粒(AID系列:WT-104/12-AID、63-104/12-AID、47-104/12-AID)或与其对应的TALE-脱氨酶-NC表达质粒、上述4.中制作的nCas9表达质粒、上述5.中制作的向导RNA表达质粒1~8、上述1.中制作的报告质粒(间隔区1:13、19或25bp)和作为参考质粒的pGL4.54组合并导入HEK293T细胞中,通过上述7.分别取得TALE-脱氨酶活性值(相对于AncBE4max活性值的比例)。

[0245] 将结果示于图8。如图8所示,在47-12-AID以外的TALE-脱氨酶(AID系列)中,间隔区1长度为19bp时显示出高活性。作为PAM序列的位置,在WT-104-AID中是PAM6(例如,间隔区1长度:19bp时,是 0.42 ± 0.08)或PAM7(0.38 ± 0.05)(图8-A)时显示出高活性,在63-104-AID中是PAM7(0.39 ± 0.00)(图8-B)时显示出高活性,在47-104-AID中也是PAM7(0.90 ± 0.10)(图8-C)时显示出高活性,在WT-12-AID中也是PAM7(0.91 ± 0.04)(图8-D)时显示出高活性,在63—12-AID中是PAM6(0.49 ± 0.02)(图8-E)时显示出高活性。另一方面,在47—12-AID中,间隔区1长度为13bp时,在PAM4(0.86 ± 0.02)或PAM7(0.96 ± 0.03)显示出高活性,间隔区1长度为19bp时,在PAM1(0.79 ± 0.05)显示出高活性,间隔区1长度为25bp时,在PAM6(0.74 ± 0.13)显示出高活性(图8-F)。其中活性高的是47-104-AID的间隔区1长度:19bp/PAM7(0.90 ± 0.10)、WT-12-AID的间隔区1长度:19bp/PAM7(0.91 ± 0.04)、47-12-AID的间隔区1长度:13bp/PAM7(0.96 ± 0.03)。

[0246] <试验4>氨基酸接头1长度对TALE-脱氨酶活性的影响

[0247] 从上述试验3已判明,作为氨基酸接头1,12个氨基酸的活性比104个氨基酸高,但

关于其氨基酸长度本身没有进行研究。因此,使用上述3.(3)中制作的TALE-脱氨酶表达质粒(47-12'~84'-AID:氨基酸接头1长度:84个氨基酸、60个氨基酸、36个氨基酸、24个氨基酸、12个氨基酸),检查氨基酸接头1长度的影响。

[0248] 在上述6.中,将上述3.(3)中制作的各TALE-脱氨酶表达质粒或与其对应的TALE-脱氨酶-NC表达质粒、上述4.中制作的nCas9表达质粒、上述5.中制作的向导RNA表达质粒2、上述1.中制作的报告质粒(间隔区1:25bp)和作为参考质粒的pGL4.54组合并导入HEK293T细胞中,通过上述7.分别取得TALE-脱氨酶活性值(相对于AncBE4max活性值的比例)。

[0249] 将结果示于图9。在图9中,作为TALE-脱氨酶表达质粒,使用上述3.(1)中制作的47-104-AID或(2)中制作的47-12-AID或与其对应的TALE-脱氨酶-NC表达质粒时的结果也一同示出。如图9所示,判明了将氨基酸接头1的长度缩短至12个氨基酸时的TALE-脱氨酶(AID)的活性稍低,但氨基酸接头1的长度对活性的影响不大。

[0250] 8.TALE-脱氨酶表达质粒的制作(2)

[0251] (1)BE4系列(BE4-TALE)

[0252] (2)32个氨基酸接头系列(BE4-32-TALE)

[0253] 将从N末端依次配置Anc689脱氨酶(BE4)、接头1(32个氨基酸)、TALE(C末端结构域:WT、63或47)的TALE-脱氨酶(以下,根据情况称为“BE4-32-TALE”)的表达质粒通过以下方法制作。即,首先,以3.(1)中制作的AncBE4max表达质粒作为模板,使用下述表8中记载的引物,将包括编码32个氨基酸接头1的序列的5'侧(引物序列号25、73~74)、包括编码10个氨基酸接头2和UGI的2次重复序列的3'侧(引物序列号12、75~77)通过PCR分别扩增。另外,以2.中制作的目标载体(TALE-WT、TALE-63、TALE-47)分别作为模板,通过PCR扩增编码各TALE的序列(引物序列号22~24、78~79)。在下述表8中,示出用于构建BE4-32-TALE表达质粒的各引物及其序列号。

[0254] [表8]

产物	正向引物 (5'-3')		反向引物 (5'-3')	序列号
BE4-32-WT, BE4-32-63用 β-内酰胺酶-Anc689脱氨酶-32aa接头	BE4_32aa+infTALEW	73	Amp_R	25
BE4-32-47用 β-内酰胺酶-Anc689脱氨酶-32aa接头	BE4_32aa+infTALE47	74		
BE4-32-WT用10aa-UGI-10aa- UGI-NLS-β-内酰胺酶	10aa_F+infWT	75	Amp_F	12
BE4-32-63用10aa-UGI-10aa- UGI-NLS-β-内酰胺酶	10aa_F+inf63	76		
BE4-32-47用10aa-UGI-10aa- UGI-NLS-β-内酰胺酶	10aa_F+inf47	77		
TALE-WT	TALE_WT_F	78	TALE_WT_R	22
TALE-63			TALE_63_R	23
TALE-47			TALE_47_R	24

[0256] 将上述3个片段组合,与3.(1)同样地,通过In-Fusion法,分别制作用于表达从N末端依次配置脱氨酶(Anc689脱氨酶(BE4))、接头1(32个氨基酸)、TALE(C末端结构域:WT、63或47)的BE4-32-TALE表达质粒的目标载体(BE4-32-WT、BE4-32-63、BE4-32-47)。与2.同样地,使用它们连接1.中制作的TALE序列的阵列质粒或连接3.中制作的NC序列的阵列质粒,

通过Golden Gate法制作各TALE-脱氨酶表达质粒或-TALE-脱氨酶-NC表达质粒。在图11(A)中,示出所述TALE-脱氨酶结构的概念图。另外,在下述表12中,分别示出制作的各表达质粒中的TALE-脱氨酶及其阴性对照(TALE-脱氨酶-NC)的结构及表示其序列的序列号(碱基序列的序列号、氨基酸序列的序列号)的一览。

[0257] (3)氨基酸长度调节接头系列(BE4-135/234-TALE)

[0258] 接着,将在编码脱氨酶与TALE之间的接头1长度(32个氨基酸)的序列的下游侧插入了编码已知的接头序列即HTS95氨基酸序列(Sun,N.and Zhao,H.,Mol BioSyst10,p.446-453(2014),Doi:10.1039/c3mb70412b)的序列或编码其2次重复序列的序列的TALE-脱氨酶(以下,根据情况称为“BE4-135-TALE”或“BE4-234-TALE”)的表达质粒(接头1长度:包括在HTS95氨基酸序列前后附加的连接序列,135或234个氨基酸)通过以下方法制作。即,以8.(1)(a)中制作的BE4-32-WT、BE4-32-63、BE4-32-47的各目标载体作为模板,使用下述表9中记载的引物,将编码32个氨基酸接头1的序列5'侧(引物序列号25、80)、编码各TALE的序列以后的3'侧(引物序列号12、81~82)通过PCR分别扩增。在下述表9中,示出使用的各引物及其序列号。

[0259] [表9]

产物	正向引物 (5'-3')	序列号	反向引物 (5'-3')	序列号
在β-内酰胺酶-Anc689脱氨酶-32aa接头插入了HTS95aa接头	BE4_32aa+inf95aa5'-2	80	Amp_R	25
在TALE WT 10aa-UGI-10aa-UGI-NLS β-内酰胺酶插入了HTS95aa接头	TALEWT_F+inf95aa3'-2	81	Amp_F	12
在TALE 63 10aa-UGI-10aa-UGI-NLS β-内酰胺酶插入了HTS95aa接头				
在TALE 47 10aa-UGI-10aa-UGI-NLS β-内酰胺酶插入了HTS95aa接头				
	TALE47_F+inf95aa3'-2	82		

[0261] 另外,将含有编码经合成的HTS95氨基酸序列和前后连接序列的序列(HTS95:碱基序列的序列号105、氨基酸序列的序列号106)的质粒用限制酶A1eI及PshI双重切割,通过琼脂糖凝胶电泳回收含有编码HTS95的序列的目标DNA片段,利用T4连接酶进行连接后,利用限制酶XmaI及SacII进行双重切割,通过琼脂糖凝胶电泳回收含有HTS95×2的目标DNA片段。

[0262] 将上述3个片段组合,与3.(1)同样地,通过In-Fusion法,分别制作用于表达从N末端依次配置脱氨酶(Anc689脱氨酶(BE4))、接头1(135个氨基酸或234个氨基酸)、TALE(C末端结构域:WT、63或47)的BE4-135-TALE或BE4-234-TALE表达质粒的目标载体(BE4-135-WT、BE4-135-63、BE4-135-47、BE4-234-WT、BE4-234-63、BE4-234-47)。与2.同样地,使用它们连接1.中制作的TALE序列的阵列质粒或连接3.中制作的NC序列的阵列质粒,通过Golden Gate法制作各TALE-脱氨酶表达质粒或-TALE-脱氨酶-NC表达质粒。示出所述TALE-脱氨酶结构的概念图与图11(a)相同。另外,在下述表12中,分别示出制作的各表达质粒中的TALE-脱氨酶及其阴性对照(TALE-脱氨酶-NC)的结构及表示其序列的序列号(碱基序列的序列号、氨基酸序列的序列号)的一览。

[0263] (2)ABE8e系列(ABE8e-TALE)

[0264] 首先,将通过人工DNA合成制作的ABEmax基因(Koblan et al.,Nat Biotechnol,

36, p.843-846 (2018)) 分别插入到pcDNA3, 1s的BamHI识别位点与EcoRV识别位点之间, 由此制作ABEmax表达质粒2。

[0265] 接着, 制作ABEmax的改进型ABE8e (V106W) (Richter, M.F, et al., Nat Biotechnol 38, p.883-891 (2020), Doi: 10.1038/s41587-020-0453-z) 表达质粒。即, 以ABEmax表达质粒2作为模板, 使用下述表10中记载的引物, 将编码3'-ABEmax基因的N末端的NLS的序列~编码32个氨基酸接头1的C末端的序列-5'通过PCR扩增(引物序列号83~84), 并将其作为受体。另外, 在ABE7.10基因上以包含成为V106W、A109S、T111R、D119N、H122N、Y147D、F149Y、T166I、D167N的突变的方式设计引物, 以ABEmax表达质粒2作为模板, 通过PCR扩增2个片段A(引物序列号85~86)和片段B(引物序列号87~88)。接着, 通过In-Fusion法将2个片段插入所述受体中, 制作ABE8e (TadA-8e (V106W)) 表达质粒。在下述表10中, 示出使用的各引物及其序列号。此外, 在下述各表中, “ABE8e”表示脱氨酶为TadA-8e (V106W)。

[0266] [表10]

产物	正向引物 (5'-3')	序列号	反向引物 (5'-3')	序列号
ABE8e用N-末端 NLS和32aa 接头-Cas9(D10A)-NLS	5'NLS_R-infTadA	83	ABE8e_F2	84
ABE8e用 A 片段	TadA7.1_F	85	ABE8e_R1	86
ABE8e用 B 片段	ABE8e_F1	87	ABE8e_R2	88

[0268] 接着, 将从N末端依次配置ABE脱氨酶(ABE8e)、接头1(32个氨基酸、135个氨基酸或234个氨基酸)、TALE (C末端结构域: 47)的TALE-脱氨酶(以下, 根据情况称为“ABE8e-32-47”、“ABE8e-135-47”或“ABE8e-234-47”)的表达质粒通过以下方法制作。即, 以8. (1) (a) 和(b)中制作的BE4-32-47、BE4-135-47、BE4-234-47的各目标载体作为模板, 使用下述表11中记载的引物, 将含有编码N末端的NLS的序列的5'侧和含有编码从32个氨基酸接头到C末端侧的序列的3'侧在包含载体的状态下通过PCR扩增(引物序列号89~90), 并将其作为受体。另外, 通过In-Fusion法, 将以ABE8e (TadA-8e (V106W)) 表达质粒作为模板通过PCR进行扩增(引物序列号追加91~92)的ABE8e (TadA-8e (V106W)) 基因部分插入到所述受体, 制作用于表达ABE8e-32-47、ABE8e-135-47或ABE8e-234-47的目标载体。在下述表11中, 示出使用的各引物及其序列号。

[0269] [表11]

产物	正向引物 (5'-3')	序列号	反向引物 (5'-3')	序列号
ABE8e-TALE用N-末端 NLS和32aa 接头-TALE-NLS	SV40NLS_R	89	32aa 接头_F	90
ABE8e-TALE用ABE8e-V82G	ABE8e_Rinf32aa	91	ABE8e_FinfNLS	92

[0271] 与2.同样地, 使用各目标载体连接1.中制作的TALE序列的阵列质粒或连接3.中制作的NC序列的阵列质粒, 通过Golden Gate法制作各TALE-脱氨酶表达质粒或-TALE-脱氨酶-NC表达质粒。在图11 (B) 中, 示出所述TALE-脱氨酶结构的概念图。另外, 在下述表12中, 分别示出制作的各表达质粒中的TALE-脱氨酶及其阴性对照(TALE-脱氨酶-NC)的结构及表示其序列的序列号(碱基序列的序列号、氨基酸序列的序列号)的一览。

[0272] [表12]

[0273]

TALE-脱氨酶						TALE- 脱氨酶 -NC (阴性对照)					
ID	TALE 识别 序列	TALE C末端 结构域	接头1 长度 (a. a.)	脱氨酶	序列 号	ID	TALE 识别 序列	TALE C末端 结构域	接头1 长度 (a. a.)	脱氨酶	序列 号
BE4-32-WT	人	WT	32	Anc689	93,94	BE4-32-WT- NC	非人	WT	32	Anc689	95,96
BE4-135-WT			135		107,108	BE4-135-WT- NC			135		109,110
BE4-234-WT			234		119,120	BE4-234-WT- NC			234		121,122
BE4-32-63		63	32		97,98	BE4-32-63- NC		32	99,100		
BE4-135-63			135		111,112	BE4-135-63- NC		135	113,114		
BE4-234-63			234		123,124	BE4-234-63- NC		234	125,126		
BE4-32-47		47	32		101,102	BE4-32-47- NC		32	103,104		
BE4-135-47			135		115,116	BE4-135-47- NC		135	117,118		
BE4-234-47			234		127,128	BE4-234-47- NC		234	129,130		
ABE8e-32-47	人	47	32	TadA-8e (V106W)	131,132	ABE8e-32-47- NC	47	32	TadA-8e (V106W)	133,134	
ABE8e-135-47			135		135,136	ABE8e-135-47- NC		135		137,138	
ABE8e-234-47			234		139,140	ABE8e-234-47- NC		234		141,142	

[0274] 9. 以内源性DNA(基因组DNA)作为目标的TALE-脱氨酶表达质粒的制作

[0275] 作为TALE识别序列,以下述表13中记载的8种内源性DNA上的序列成为目标的方式,通过与2.同样的方法,制作连接TALE序列的阵列质粒。作为所述内源性DNA,设定了存在

相同性高的家族基因 (CCR2及HBD) 的CCR5和HBB。

[0276] 除了使用上述各阵列质粒以外,与3.同样地,通过Golden Gate法,制作从N末端依次配置TALE (C末端结构域:WT或47)、接头1 (12个氨基酸或104个氨基酸)、脱氨酶 (AID) 的TALE-脱氨酶 (WT (*) -12-AID、47 (*) -12-AID、47 (*) -104-AID:*分别是目标) 的表达质粒 (TALE-AID表达质粒)。另外,除了使用各阵列质粒以外,与8.同样地,通过Golden Gate法,制作从N末端依次配置脱氨酶 (BE4或ABE8e)、接头1 (32个氨基酸或135个氨基酸)、TALE (C末端结构域:63或47) 的TALE-脱氨酶 (BE4-32-47 (*)、BE4—135-63 (*)、ABE8e-135-47 (*) :*分别是目标) 的表达质粒 (BE4-TALE表达质粒、ABE8e-TALE表达质粒)。在下述表13中,示出作为目标的TALE识别序列,在表14中,分别示出制作的各表达质粒中的目标、TALE-脱氨酶的结构及表示其序列的序列号 (碱基序列的序列号、氨基酸序列的序列号) 的一览。

[0277] [表13]

[0278]

TALE	TALE识别序列 (5'-3')	序列号
TALE-AS3	tGAGCCCAGAAGGGGACA	143
TALEE-AS14-1	tAGCTTGGtCCAACCTGT	144
TALE-AS14-2	tGGTCAACCTGTTAGAGC	145
TALE-AS14-3	tCTAACAGGTTGGACCAA	146
TALE-AS5	tGCAGTAGCTCTAACAGG	147
TALE-AS6	tCTGCCGTTACTGCCCTG	148
TALE-AS7	tTTGCCACACTGAGTGAG	149
TALE-S2	tGCCACACTGAGTGAGC	150

[0279] [表14]

[0280]

ID	目标	TALE的名称	TALE C末端 结构域	接头1 长度 (a. a.)	脱氢酶	序列号
WT(AS3)-12-AID	AS3	TALE-AS3	WT	12	PmCDA1	151,152
47(AS3)-104-AID			47	104		153,154
WT(AS14-1)-12-AID	AS14	TALE-AS14-1	WT	12		155,156
47(AS14-1)-104-AID			47	104		157,158
47(AS14-2)-12-AID		TALE-AS14-2	47	12		159,160
WT(S2)-12-AID	S2	TALE-S2	WT	12		161,162
47(S2)-104-AID			47	104		163,164
BE4-32-47(AS14-3)	AS14	TALE-AS14-3	47	32	Anc689	165,166
BE4-135-63(AS14-3)			63	135		167,168
BE4-32-47(AS5)	AS5	TALE-AS5	47	32		169,170
BE4-135-63(AS5)			63	135		171,172
BE4-32-47(AS6)	AS6	TALE-AS6	47	32		173,174
BE4-135-63(AS6)			63	135		175,176
BE4-32-47(AS7)	AS7	TALE-AS7	47	32		177,178
BE4-135-63(AS7)			63	135		179,180
ABE8e-135-47(AS5)	AS5	TALE-AS5	47	135	TadA-8e (V106W)	181,182
ABE8e-135-47(AS6)	AS6	TALE-AS6				183,184
ABE8e-135-47(AS7)	AS7	TALE-AS7				185,186

[0281] 10. BE4-TALE用及ABE8e-TALE用报告质粒的制作

[0282] 作为报告基因,在1.中制作的pNLF-M/A中插入下述表15所示的序列(N-CBE(BE4-TALE用)或N-ABE(ABE8e-TALE用),分别制作BE4-TALE用和ABE8e-TALE用的报告质粒。插入序列含有TALE识别序列的互补序列(表15中的下划线(*1):5'-CCTTTGCCCGCTTCTGTa-3';小写字母表示TALE的N末端结构域所识别的胸腺嘧啶的互补碱基)、目标密码子(表15中的下划线(*2):5'-ACG-3'或5'-TAG-3')及它们之间的间隔区1序列,间隔区1的长度包括位于目标密码子5'的碱基,为7bp、13bp、19bp、25bp或31bp。在下述表15中,示出插入pNLF-M/A质粒中的各序列。

[0283] [表15]

[0284]

产物	序列 (5'-3')	序列号
N-CBE-7bp	CTAGCATAAAACCTTTGGCCGCTTCTGTa ^{*1} GGGAAGACG ^{*2} GATATCTCTGCGGGG ^{*3} GAGCT	187
N-CBE-13bp	CTAGCATAAAACCTTTGGCCGCTTCTGTa ^{*1} CTATTGGGAAGACG ^{*2} GATATCTCTGCGGGG ^{*3} GAGCT	188
N-CBE-19bp	CTAGCATAAAACCTTTGGCCGCTTCTGTa ^{*1} ATTAGTCTATTGGGAAGACG ^{*2} GATATCTCTGCGGGG ^{*3} GAGCT	189
N-CBE-25bp	CTAGCATAAAACCTTTGGCCGCTTCTGTa ^{*1} TTCAGGATTAGTCTATTGGGAAGACG ^{*2} GATATCTCTGCGGGG ^{*3} GAGCT	190
N-CBE-31bp	CTAGCATAAAACCTTTGGCCGCTTCTGTa ^{*1} AGTCTATTGAGGATTAGTCTATTGGGAAGACG ^{*2} GATATCTCTGCGGGG ^{*3} GAGCT	191
N-ABE-7bp	CTAGCACCATGGCGCCTTTGGCCGCTTCTGTa ^{*1} CGCGCTTAG ^{*2} TCTTTGCGC	192
N-ABE-13bp	CTAGCACCATGGCGCCTTTGGCCGCTTCTGTa ^{*1} GCCTCCCGCGCTTAG ^{*2} TCTTTGCGC	193
N-ABE-19bp	CTAGCACCATGGCGCCTTTGGCCGCTTCTGTa ^{*1} CCCAACGCTCCCGCGCTTAG ^{*2} TCTTTGCGC	194
N-ABE-25bp	CTAGCACCATGGCGCCTTTGGCCGCTTCTGTa ^{*1} GCAGGCCCAACGCTCCCGCGCTTAG ^{*2} TCTTTGCGC	195
N-ABE-31bp	CTAGCACCATGGCGCCTTTGGCCGCTTCTGTa ^{*1} GCTGGAGCAGGCCCAACGCTCCCGCGCTTAG ^{*2} TCTTTGCGC	196

*1: TALE 识别序列的互补序列、*2: 含有目标碱基的目标密码子

、*3: PAM

[0285] 在该BE4-TALE用报告质粒中,目标密码子位于相当于Nano荧光素酶起始密码子的位置,根据该报告质粒,通过与TALE识别序列结合的TALE-脱氨酶,目标密码子ACG转变为

ATG(目标碱基(目标位点)C被T取代)时,表达NanoLuc荧光素酶(图10)。另一方面,在ABE8e-TALE用报告质粒中,目标密码子位于相当于插入到NanoLuc荧光素酶的上游的终止密码子的位置,根据该报告质粒,通过与TALE识别序列结合的TALE-脱氨酶,目标密码子TAG转变为TGG(目标碱基(目标位点)A被G取代)时,表达NanoLuc荧光素酶。

[0286] 11. 向导RNA表达质粒的制作(2)

[0287] 除了将表达向导RNA的质粒设计成对应于向导RNA的目标序列(表16中,示出向导RNA的目标序列(反义链上)的互补序列)之外,与5.同样地,制作表达各向导RNA的质粒(向导RNA表达质粒)。在下述表16中,示出向导RNA的目标序列的互补序列。

[0288] [表16]

向导 RNA	目标	向导RNA的目标序列的互补序列	序列号
sgRNA-N-CBE	BE4-TALE用报告基因	GAAGACGGATATCTCCTGCG	197
sgRNA-N-ABE	ABE8e-TALE用报告基因	GCTTAGTCTTTCGGCTCGAG	198
sgRNA-AS3	AS3	CAGAGATGGCCAGGTTGAGC	199
sgRNA-AS14	AS14	CAGGCCAAAGAATTCCTGGA	200
sgRNA-AS5	AS5	AGAATTCCTGGAAGGTGTTC	201
sgRNA-AS6	AS6	TGCACCATGGTGTCTGTTTG	202
sgRNA-AS7	AS7	GTGAGCCAGGCCATCACTAA	203
sgRNA-S2	S2	CGTGGATCCTGAGAACTTCA	204

[0290] 12. 向HEK细胞的转化(2)

[0291] 在将上述10.中制作的各报告质粒作为目标DNA时,与6.所示的方法同样地进行。即,使用脂质体LTX,将8.中制作的BE4-TALE表达质粒或ABE8e-TALE表达质粒中的任一种75ng;4.中制作的nCas9表达质粒或dCas9表达质粒50ng;11.中制作的向导RNA表达质粒10ng、10.中制作的报告质粒中的任一种20ng;以及作为参考质粒的pGL4.545ng以 5×10^4 个/孔导入HEK293T细胞中,并培养24小时。

[0292] 另外,在将上述9.中记载的内源性DNA作为目标DNA时,如下所述。即,在使用AID作为脱氨酶的情况下,将9.中制作的TALE-AID表达质粒中的任一种30ng;4.中制作的nCas9表达质粒或dCas9表达质粒20ng;11.中制作的向导RNA表达质粒5ng以 3×10^4 个/孔导入HEK293T细胞中,并培养48小时,在使用BE4或ABE8e作为脱氨酶的情况下,将9.中制作的BE4-TALE表达质粒或ABE8e-TALE表达质粒中的任一种60ng;4.中制作的nCas9表达质粒或dCas9表达质粒40ng;11.中制作的向导RNA表达质粒10ng以 3×10^4 个/孔导入HEK293T细胞中,并培养48小时。另外,作为此时的对照,将Target-AID表达质粒、AncBE4max表达质粒及ABE8e表达质粒中的任一种30ng与11.中制作的向导RNA表达质粒10ng的组合、或者Target-AID表达质粒、AncBE4max表达质粒和ABE8e表达质粒中的任一种60ng与11.中制作的向导RNA表达质粒20ng的组合中的任一种导入HEK293T细胞中。

[0293] 13. 碱基编辑活性的分析

[0294] 转化48小时后,去除培养基,用PBS(-)洗涤后,添加DNAzol (Molecular Research Center, INC, Ohio, USA) 50 μ L,溶解细胞。以细胞溶解液作为模板,使用下述表17中记载的引物,通过PrimeSTAR Max (Takara Bio Inc., Siga, Japan),扩增含有所述内源性DNA的目标位点的区域。将得到的PCR产物纯化后,委托FASMAC株式会社进行测序。使用EditR (Kluesner et al., The CRISPR J1, p.239-250 (2018), DOI:10.1089/crispr.2018.0014) 分析序列数据,计算目标位点的碱基编辑效率(T或G的比例)。

[0295] [表17]

目标	目标基因	正向引物 (5'-3')	序列号	反向引物 (5'-3')	序列号
AS3	CCR5	CCR5-AS3-F2	205	CCR5-AS3-R2	206
	CCR2	CCR2-AS3-F	207	CCR2-AS3-R	208
AS14/AS5	CCR5	CCR5-AS14-F1	209	CCR5-AS14-R	210
	CCR2	CCR2-AS14-F1	211	CCR2-AS14-R1	212
AS6	HBB	HBB-AS6-F2	213	HBB-AS6-R2	214
	HBD	HBD-AS6-F	215	HBD-AS6-R	216
AS7/S2	HBB	HBB-S2-F	217	HBB-S2-R	218
	HBD	HBD-S2-F	219	HBD-S2-R	220

[0297] <试验5>间隔区1长度及接头1长度对TALE-脱氨酶(N末端融合体)活性的影响

[0298] 通过上述12.进行向HEK细胞的转化,通过上述7.分别取得TALE-脱氨酶活性值(相对于AncBE4max活性值或ABE8e活性值的比例)。

[0299] (BE4系列)

[0300] 关于从N末端依次配置Anc689脱氨酶(BE4)、接头1(32个氨基酸、135个氨基酸或234个氨基酸)、TALE(C末端结构域:WT、63或47)的TALE脱氨酶(BE4-TALE-WT、BE4-TALE-63、BE4-TALE-47),检查报告基因的间隔区1的长度以及接头1的长度对活性的影响。间隔区1的长度设为7bp、13bp、19bp、25bp、31bp。另外,作为Cas9/向导RNA,对有nCas9(D10A)及向导RNA的表达(nCas9)、有dCas9(D10A+H840A)及向导RNA的表达(dCas9)、有nCas9表达和无向导RNA表达(nCas9/无向导)的3个条件进行了研究。

[0301] 将结果分别示于图12A的(A)(B)和图12B的(C)中。即使在任一BE4-TALE,在不存在向导RNA的情况下,即在nCas9不结合于目标碱基附近的情况下,也没有观察到活性。另一方面,在nCas9或dCas9的存在下,观察到了活性。关于nCas9对缺口的活性促进效果,没有TALE-脱氨酶的C末端融合体(在C末端侧配置有脱氨酶)那么显著。

[0302] 关于间隔区1的长度,在TALE的C末端结构域是WT和63的情况下为25bp时,显示特别高的活性,在TALE的C末端结构域是47的情况下为19bp和25bp时,显示出特别高的活性。关于接头1的长度,在TALE的C末端结构域是WT和47的情况下为32个氨基酸时,活性特别高,在TALE的C末端结构域是63的情况下为135个氨基酸时,活性特别高。关于活性特别高的组合,在TALE的C末端结构域为WT的情况下,是接头1长度为32个氨基酸且间隔区1长度为25bp时(0.75 ± 0.10),在TALE的C末端结构域为63的情况下,是接头1长度为135个氨基酸且间隔区1长度为25bp时(0.86 ± 0.11),在TALE的C末端结构域为47的情况下,是接头1长度为32个

氨基酸且间隔区1长度为19bp和25bp时 (0.80 ± 0.14 和 0.85 ± 0.13)。

[0303] (ABE8e系列)

[0304] 关于从N末端依次配置ABE8e脱氨酶 (ABE8e)、接头1 (32个氨基酸、135个氨基酸或234个氨基酸)、TALE (C末端结构域:47)的TALE脱氨酶 (ABE8e-TALE-47),也与上述BE4系列同样地,检查报告基因的间隔区1的长度以及接头1的长度对活性的影响。

[0305] 将其结果示于图12B (D) 中。即使在任一ABE8e-TALE中,在不存在向导RNA的情况下,即在nCas9不结合于目标碱基附近的情况下,也没有观察到活性。另一方面,在nCas9或dCas9的存在下,观察到了活性。此外,在nCas9和dCas9的比较中,活性为相同程度或dCas9更高。

[0306] 关于间隔区1的长度,在19bp时显示出特别高的活性。关于接头1的长度,nCas9的情况下为135个氨基酸 (0.54 ± 0.03) 时,显示出特别高的活性,dCas9的情况下为32个氨基酸 (0.55 ± 0.13) 和135个氨基酸 (0.57 ± 0.09) 时,显示出特别高的活性。

[0307] <试验6>内源性DNA中的碱基编辑活性

[0308] 关于上述中得到特别高活性的TALE-脱氨酶,通过上述12.和13.中记载的方法,检查对内源性DNA的碱基编辑活性。作为所述内源性DNA,设定了存在相同性高的家族基因 (CCR2及HBD) 的CCR5和HBB。在图13A及图13B中,分别示出所述内源性DNA (CCR5、HBB) 上的目标区域 (AS3 (a:序列号221)、AS14 (b:序列号222) (e:序列号225)、S2 (c:序列号223)、AS5 (d:序列号224)、AS6 (f:序列号226)、AS7 (g:序列号227))、TALE识别序列或其互补序列的位置、向导RNA的目标序列的互补序列的位置。另外,在图13A和图13B中,作为(a)、(b)、(d)、(e)所示的与CCR5相同性高的CCR2、(c)、(f)、(g)所示的与HBB相同性高的HBD的对准,还分别示出与各区域的碱基不同的碱基。

[0309] (AID系列)

[0310] 将使用从N末端依次配置TALE (C末端结构域:WT或47)、接头1 (12个氨基酸或104个氨基酸)、脱氨酶 (AID) 的TALE-AID (WT (*) -12-AID、47 (*) -12-AID、47 (*) -104-AID:*分别是目标) 时的结果示于图14~图16中。在各TALE-AID中,TALE识别序列分别位于图13A所示的AS3 (a)、AS14 (b)、S2 (c) 上。在图14中,示出目标AS3上的、向导RNA (sgRNA-AS3) 的目标序列的互补序列的第1碱基 (A)、第10碱基 (B)、第11碱基 (C) 中的T的比例 (即,碱基从C编辑成T的比例),在图15中,示出目标AS14上的、向导RNA (sgRNA-AS14) 的目标序列的互补序列的第1碱基 (A)、第5碱基 (B)、第6碱基 (C) 中的T的比例,在图16中,示出目标S2上的、向导RNA (sgRNA-S2) 的目标序列的互补序列的第1碱基 (A)、第8碱基 (B)、第9碱基 (C) 中的T的比例。

[0311] TALE-AID与现有的碱基编辑器即Target-AID和AncBE4max相比,对于目标CCR5基因或HBB基因,显示出相同程度或更高的活性。另一方面,对于不是目标的CCR2基因或HBD基因,Target-AID和AncBE4max显示出碱基编辑活性,而TALE-AID几乎没有显示出碱基编辑活性。因此,可确认到TALE-AID比现有Target-AID或AncBE4max目标特异性高。

[0312] (BE4系列)

[0313] 将使用从N末端依次配置脱氨酶 (BE4)、接头1 (32个氨基酸或135个氨基酸)、TALE (C末端结构域:47或63) 的BE4-TALE (BE4-32-47 (*)、BE4-135-63 (*) :*分别是目标) 时的结果示于图17~图20中。在各BE4-TALE中,TALE识别序列分别位于图13B所示的AS5 (d)、AS14 (e)、AS6 (f)、AS7 (g) 的互补序列上。在图17中,示出目标AS5上的、向导RNA (sgRNA-AS5) 的目

标序列的互补序列的第7碱基(A)、第8碱基(B)中的T的比例,在图18中,示出目标AS14上的、向导RNA(sgRNA-AS14)的目标序列的互补序列的第1碱基(A)、第5碱基(B)、第6碱基(C)中的T的比例,在图19中,示出目标AS6上的、向导RNA(sgRNA-AS6)的目标序列的互补序列的第5碱基(A)、第6碱基(B)中的T的比例,在图20中,示出目标AS7上的、向导RNA(sgRNA-AS7)的目标序列的互补序列的第6碱基(A)、第7碱基(B)中的T的比例。

[0314] BE4-TALE与现有的碱基编辑器即Target-AID和AncBE4max相比,对于目标CCR5基因或HBB基因,显示出大致相同程度的活性。另一方面,对于不是目标的CCR2基因或HBD基因,Target-AID和AncBE4max显示出碱基编辑活性,而BE4-TALE几乎没有显示出碱基编辑活性。因此,可确认到BE4-TALE比现有Target-AID或AncBE4max目标特异性高。

[0315] (ABE8e系列)

[0316] 将使用从N末端依次配置ABE8e脱氨酶(ABE8e)、接头1(135个氨基酸)、TALE(C末端结构域:47)的ABE8e-TALE(ABE8e-135-47)时的结果示于图21~图23中。在各ABE8e-TALE中,TALE识别序列分别位于图13B所示的AS5(d)、AS6(f)、AS7(g)的互补序列上。在图21中,示出目标AS5上的、向导RNA(sgRNA-AS5)的目标序列的互补序列的第3碱基(A)、第4碱基(B)中的G的比例(即,碱基从A编辑成G的比例),在图22中,示出目标AS6上的、向导RNA(sgRNA-AS6)的目标序列的互补序列的第4碱基(A)、第7碱基(B)中的G的比例,在图23中,示出目标AS7上的、向导RNA(sgRNA-AS7)的目标序列的互补序列的第4碱基(A)、第8碱基(B)中的G的比例。

[0317] ABE8e-TALE与现有的碱基编辑器即ABE8e(TadA-8e(V106W))相比,对于目标CCR5基因或HBB基因,显示出相同程度的活性。另一方面,对于不是目标的CCR2基因或HBD基因,ABE8e(TadA-8e(V106W))显示出碱基编辑活性,而ABE8e几乎没有显示出碱基编辑活性。因此,可确认到ABE8e-TALE比现有的ABE8e(TadA-8e(V106W))目标特异性高。

[0318] 产业上的可利用性

[0319] 如上所述,根据本发明,可以提供一种能够特异性且有效率地进行利用核碱基转化酶的目标DNA的编辑的方法、制备使用该方法编辑了基因组的细胞的方法、以及用于它们的DNA编辑系统。因此,本发明可期待在要求高编辑效率和高安全性的基因编辑治疗等领域中的利用、应用。

序列表

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<223> WT-104-BE4

<400> 33

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<210> 34

<211> 1459

<212> PRT

<213> 人工序列(Artificial Sequence)

<220>

<223> WT-104-BE4

<400> 34

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

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Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala		
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Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu		
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Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala		
305	310	315
Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg		
	325	330
Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val		
	340	345
Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val		
	355	360
Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp		
	370	375
Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu		
385	390	395
Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr		
	405	410
Pro Ala Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala		
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Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly		
	435	440
Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys		
	450	455
Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp		
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His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Asn Gly		
	485	490
Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys		
	500	505
Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn		
	515	520
Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val		
	530	535
Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala		
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Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu		
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Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala		

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Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val		
625	630	635
Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp		
645	650	655
Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu		
660	665	670
Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr		
675	680	685
Pro Ala Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala		
690	695	700
Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly		
705	710	715
Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Arg		
725	730	735
Pro Ala Leu Glu Ser Ile Val Ala Gln Leu Ser Arg Pro Asp Pro Ala		
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Leu Ala Ala Leu Thr Asn Asp His Leu Val Ala Leu Ala Cys Leu Gly		
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Gly Arg Pro Ala Leu Asp Ala Val Lys Lys Gly Leu Pro His Ala Pro		
770	775	780
Ala Leu Ile Lys Arg Thr Asn Arg Arg Ile Pro Glu Arg Thr Ser His		
785	790	795
Arg Val Ala Asp His Ala Gln Val Val Arg Val Leu Gly Phe Phe Gln		
805	810	815
Cys His Ser His Pro Ala Gln Ala Phe Asp Asp Ala Met Thr Gln Phe		
820	825	830
Gly Met Ser Arg His Gly Leu Leu Gln Leu Phe Arg Arg Val Gly Val		
835	840	845
Thr Glu Leu Glu Ala Arg Ser Gly Thr Leu Pro Pro Ala Ser Gln Arg		
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Trp Asp Arg Ile Leu Gln Ala Ser Gly Met Lys Arg Ala Lys Pro Ser		
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Pro Thr Ser Thr Gln Thr Pro Asp Gln Ala Ser Leu His Ala Phe Ala		
885	890	895

Asp Ser Leu Glu Arg Asp Leu Asp Ala Pro Ser Pro Met His Glu Gly		
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Asp Gln Thr Arg Ala Ser Ala Ser Ser Arg Ala Asp Pro Lys Lys Lys		
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Arg Lys Val Gly Gly Gly Gly Thr Gly Gly Gly Gly Ser Ala Glu Tyr		
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Val Arg Ala Leu Phe Asp Phe Asn Gly Asn Asp Glu Glu Asp Leu Pro		
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Phe Lys Lys Gly Asp Ile Leu Arg Ile Arg Asp Lys Pro Glu Glu Gln		
965	970	975
Trp Trp Asn Ala Glu Asp Ser Glu Gly Lys Arg Gly Met Ile Leu Val		
980	985	990
Pro Tyr Val Glu Lys Tyr Ser Gly Asp Tyr Lys Asp His Asp Gly Asp		
995	1000	1005
Tyr Lys Asp His Asp Ile Asp Tyr Lys Asp Asp Asp Asp Lys Ser		
1010	1015	1020
Gly Ser Ser Glu Thr Gly Pro Val Ala Val Asp Pro Thr Leu Arg		
1025	1030	1035
Arg Arg Ile Glu Pro His Glu Phe Glu Val Phe Phe Asp Pro Arg		
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Glu Leu Arg Lys Glu Thr Cys Leu Leu Tyr Glu Ile Lys Trp Gly		
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Thr Ser His Lys Ile Trp Arg His Ser Ser Lys Asn Thr Thr Lys		
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His Val Glu Val Asn Phe Ile Glu Lys Phe Thr Ser Glu Arg His		
1085	1090	1095
Phe Cys Pro Ser Thr Ser Cys Ser Ile Thr Trp Phe Leu Ser Trp		
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Ser Pro Cys Gly Glu Cys Ser Lys Ala Ile Thr Glu Phe Leu Ser		
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Gln His Pro Asn Val Thr Leu Val Ile Tyr Val Ala Arg Leu Tyr		
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His His Met Asp Gln Gln Asn Arg Gln Gly Leu Arg Asp Leu Val		
1145	1150	1155
Asn Ser Gly Val Thr Ile Gln Ile Met Thr Ala Pro Glu Tyr Asp		
1160	1165	1170
Tyr Cys Trp Arg Asn Phe Val Asn Tyr Pro Pro Gly Lys Glu Ala		
1175	1180	1185
His Trp Pro Arg Tyr Pro Pro Leu Trp Met Lys Leu Tyr Ala Leu		

1190	1195	1200
Glu Leu His Ala Gly Ile	Leu Gly Leu Pro Pro	Cys Leu Asn Ile
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Leu Arg Arg Lys Gln Pro	Gln Leu Thr Phe Phe	Thr Ile Ala Leu
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Gln Ser Cys His Tyr Gln	Arg Leu Pro Pro His	Ile Leu Trp Ala
1235	1240	1245
Thr Gly Leu Lys Ser Gly	Gly Ser Gly Gly Ser	Gly Gly Ser Thr
1250	1255	1260
Asn Leu Ser Asp Ile Ile	Glu Lys Glu Thr Gly	Lys Gln Leu Val
1265	1270	1275
Ile Gln Glu Ser Ile Leu	Met Leu Pro Glu Glu	Val Glu Glu Val
1280	1285	1290
Ile Gly Asn Lys Pro Glu	Ser Asp Ile Leu Val	His Thr Ala Tyr
1295	1300	1305
Asp Glu Ser Thr Asp Glu	Asn Val Met Leu Leu	Thr Ser Asp Ala
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Pro Glu Tyr Lys Pro Trp	Ala Leu Val Ile Gln	Asp Ser Asn Gly
1325	1330	1335
Glu Asn Lys Ile Lys Met	Leu Ser Gly Gly Ser	Gly Gly Ser Gly
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Gly Ser Thr Asn Leu Ser	Asp Ile Ile Glu Lys	Glu Thr Gly Lys
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Gln Leu Val Ile Gln Glu	Ser Ile Leu Met Leu	Pro Glu Glu Val
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Glu Glu Val Ile Gly Asn	Lys Pro Glu Ser Asp	Ile Leu Val His
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Thr Ala Tyr Asp Glu Ser	Thr Asp Glu Asn Val	Met Leu Leu Thr
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Ser Asp Ala Pro Glu Tyr	Lys Pro Trp Ala Leu	Val Ile Gln Asp
1415	1420	1425
Ser Asn Gly Glu Asn Lys	Ile Lys Met Leu Ser	Gly Gly Ser Lys
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Arg Thr Ala Asp Gly Ser	Glu Phe Glu Pro Lys	Lys Lys Arg Lys
1445	1450	1455

Val

<210> 35

<211> 4377

<212> DNA

<213> 人工序列(Artificial Sequence)

<220>

<223> WT-104-BE4-NC

<400> 35

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<211> 1459
 <212> PRT
 <213> 人工序列(Artificial Sequence)
 <220>
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 20 25 30
 Gly Ile His Gly Val Pro Ala Ala Val Asp Leu Arg Thr Leu Gly Tyr
 35 40 45
 Ser Gln Gln Gln Gln Glu Lys Ile Lys Pro Lys Val Arg Ser Thr Val
 50 55 60
 Ala Gln His His Glu Ala Leu Val Gly His Gly Phe Thr His Ala His
 65 70 75 80
 Ile Val Ala Leu Ser Gln His Pro Ala Ala Leu Gly Thr Val Ala Val
 85 90 95
 Lys Tyr Gln Asp Met Ile Ala Ala Leu Pro Glu Ala Thr His Glu Ala
 100 105 110
 Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg Ala Leu Glu Ala
 115 120 125
 Leu Leu Thr Val Ala Gly Glu Leu Arg Gly Pro Pro Leu Gln Leu Asp
 130 135 140
 Thr Gly Gln Leu Leu Lys Ile Ala Lys Arg Gly Gly Val Thr Ala Val
 145 150 155 160
 Glu Ala Val His Ala Trp Arg Asn Ala Leu Thr Gly Ala Pro Leu Asn
 165 170 175
 Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys
 180 185 190
 Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp
 195 200 205
 His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Asn Gly
 210 215 220
 Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
 225 230 235 240
 Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser His
 245 250 255
 Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val

260	265	270
Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala		
275	280	285
Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu		
290	295	300
Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala		
305	310	315
Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg		
325	330	335
Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val		
340	345	350
Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val		
355	360	365
Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp		
370	375	380
Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu		
385	390	395
Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr		
405	410	415
Pro Ala Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala		
420	425	430
Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly		
435	440	445
Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys		
450	455	460
Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp		
465	470	475
His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly		
485	490	495
Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys		
500	505	510
Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn		
515	520	525
Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val		
530	535	540
Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala		
545	550	555
Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu		
565	570	575

Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala		
580	585	590
Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg		
595	600	605
Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val		
610	615	620
Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val		
625	630	635
Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp		
645	650	655
Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu		
660	665	670
Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr		
675	680	685
Pro Ala Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala		
690	695	700
Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly		
705	710	715
Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Arg		
725	730	735
Pro Ala Leu Glu Ser Ile Val Ala Gln Leu Ser Arg Pro Asp Pro Ala		
740	745	750
Leu Ala Ala Leu Thr Asn Asp His Leu Val Ala Leu Ala Cys Leu Gly		
755	760	765
Gly Arg Pro Ala Leu Asp Ala Val Lys Lys Gly Leu Pro His Ala Pro		
770	775	780
Ala Leu Ile Lys Arg Thr Asn Arg Arg Ile Pro Glu Arg Thr Ser His		
785	790	795
Arg Val Ala Asp His Ala Gln Val Val Arg Val Leu Gly Phe Phe Gln		
805	810	815
Cys His Ser His Pro Ala Gln Ala Phe Asp Asp Ala Met Thr Gln Phe		
820	825	830
Gly Met Ser Arg His Gly Leu Leu Gln Leu Phe Arg Arg Val Gly Val		
835	840	845
Thr Glu Leu Glu Ala Arg Ser Gly Thr Leu Pro Pro Ala Ser Gln Arg		
850	855	860
Trp Asp Arg Ile Leu Gln Ala Ser Gly Met Lys Arg Ala Lys Pro Ser		
865	870	875
Pro Thr Ser Thr Gln Thr Pro Asp Gln Ala Ser Leu His Ala Phe Ala		

	885		890		895
Asp Ser Leu Glu Arg Asp Leu Asp Ala Pro Ser Pro Met His Glu Gly					
	900		905		910
Asp Gln Thr Arg Ala Ser Ala Ser Ser Arg Ala Asp Pro Lys Lys Lys					
	915		920		925
Arg Lys Val Gly Gly Gly Gly Thr Gly Gly Gly Gly Ser Ala Glu Tyr					
	930		935		940
Val Arg Ala Leu Phe Asp Phe Asn Gly Asn Asp Glu Glu Asp Leu Pro					
945		950		955	960
Phe Lys Lys Gly Asp Ile Leu Arg Ile Arg Asp Lys Pro Glu Glu Gln					
	965		970		975
Trp Trp Asn Ala Glu Asp Ser Glu Gly Lys Arg Gly Met Ile Leu Val					
	980		985		990
Pro Tyr Val Glu Lys Tyr Ser Gly Asp Tyr Lys Asp His Asp Gly Asp					
	995		1000		1005
Tyr Lys Asp His Asp Ile Asp Tyr Lys Asp Asp Asp Asp Lys Ser					
	1010		1015		1020
Gly Ser Ser Glu Thr Gly Pro Val Ala Val Asp Pro Thr Leu Arg					
	1025		1030		1035
Arg Arg Ile Glu Pro His Glu Phe Glu Val Phe Phe Asp Pro Arg					
	1040		1045		1050
Glu Leu Arg Lys Glu Thr Cys Leu Leu Tyr Glu Ile Lys Trp Gly					
	1055		1060		1065
Thr Ser His Lys Ile Trp Arg His Ser Ser Lys Asn Thr Thr Lys					
	1070		1075		1080
His Val Glu Val Asn Phe Ile Glu Lys Phe Thr Ser Glu Arg His					
	1085		1090		1095
Phe Cys Pro Ser Thr Ser Cys Ser Ile Thr Trp Phe Leu Ser Trp					
	1100		1105		1110
Ser Pro Cys Gly Glu Cys Ser Lys Ala Ile Thr Glu Phe Leu Ser					
	1115		1120		1125
Gln His Pro Asn Val Thr Leu Val Ile Tyr Val Ala Arg Leu Tyr					
	1130		1135		1140
His His Met Asp Gln Gln Asn Arg Gln Gly Leu Arg Asp Leu Val					
	1145		1150		1155
Asn Ser Gly Val Thr Ile Gln Ile Met Thr Ala Pro Glu Tyr Asp					
	1160		1165		1170
Tyr Cys Trp Arg Asn Phe Val Asn Tyr Pro Pro Gly Lys Glu Ala					
	1175		1180		1185

His Trp	Pro Arg Tyr Pro Pro	Leu Trp Met Lys Leu	Tyr Ala Leu
1190	1195	1200	
Glu Leu	His Ala Gly Ile Leu	Gly Leu Pro Pro Cys	Leu Asn Ile
1205	1210	1215	
Leu Arg	Arg Lys Gln Pro Gln	Leu Thr Phe Phe Thr	Ile Ala Leu
1220	1225	1230	
Gln Ser	Cys His Tyr Gln Arg	Leu Pro Pro His Ile	Leu Trp Ala
1235	1240	1245	
Thr Gly	Leu Lys Ser Gly Gly	Ser Gly Gly Ser Gly	Gly Ser Thr
1250	1255	1260	
Asn Leu	Ser Asp Ile Ile Glu	Lys Glu Thr Gly Lys	Gln Leu Val
1265	1270	1275	
Ile Gln	Glu Ser Ile Leu Met	Leu Pro Glu Glu Val	Glu Glu Val
1280	1285	1290	
Ile Gly	Asn Lys Pro Glu Ser	Asp Ile Leu Val His	Thr Ala Tyr
1295	1300	1305	
Asp Glu	Ser Thr Asp Glu Asn	Val Met Leu Leu Thr	Ser Asp Ala
1310	1315	1320	
Pro Glu	Tyr Lys Pro Trp Ala	Leu Val Ile Gln Asp	Ser Asn Gly
1325	1330	1335	
Glu Asn	Lys Ile Lys Met Leu	Ser Gly Gly Ser Gly	Gly Ser Gly
1340	1345	1350	
Gly Ser	Thr Asn Leu Ser Asp	Ile Ile Glu Lys Glu	Thr Gly Lys
1355	1360	1365	
Gln Leu	Val Ile Gln Glu Ser	Ile Leu Met Leu Pro	Glu Glu Val
1370	1375	1380	
Glu Glu	Val Ile Gly Asn Lys	Pro Glu Ser Asp Ile	Leu Val His
1385	1390	1395	
Thr Ala	Tyr Asp Glu Ser Thr	Asp Glu Asn Val Met	Leu Leu Thr
1400	1405	1410	
Ser Asp	Ala Pro Glu Tyr Lys	Pro Trp Ala Leu Val	Ile Gln Asp
1415	1420	1425	
Ser Asn	Gly Glu Asn Lys Ile	Lys Met Leu Ser Gly	Gly Ser Lys
1430	1435	1440	
Arg Thr	Ala Asp Gly Ser Glu	Phe Glu Pro Lys Lys	Lys Arg Lys
1445	1450	1455	

Val

<210> 37

<211> 4023

<212> DNA

<213> 人工序列(Artificial Sequence)

<220>

<223> 47-104-BE4

<400> 37

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<212>	PRT					
<213>	人工序列(Artificial Sequence)					
<220>						

<223> 47-104-BE4

<400> 38

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

290	295	300
Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu		
305	310	315
Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser		
325	330	335
Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro		
340	345	350
Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile		
355	360	365
Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu		
370	375	380
Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val		
385	390	395
Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln		
405	410	415
Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln		
420	425	430
Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr		
435	440	445
Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro		
450	455	460
Asp Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu		
465	470	475
Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu		
485	490	495
Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln		
500	505	510
Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His		
515	520	525
Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly		
530	535	540
Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln		
545	550	555
Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser His Asp		
565	570	575
Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu		
580	585	590
Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser		
595	600	605

Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro		
610	615	620
Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile		
625	630	635
Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu		
	645	650
Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val		
	660	665
Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln		
	675	680
Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln		
	690	695
Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr		
705	710	715
Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro		
	725	730
Glu Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Arg Pro Ala Leu		
	740	745
Glu Ser Ile Val Ala Gln Leu Ser Arg Pro Asp Pro Ala Leu Ala Ala		
	755	760
Leu Thr Asn Asp His Leu Val Ala Leu Ala Cys Leu Gly Gly Arg Pro		
	770	775
Ala Met Asp Ala Val Lys Lys Gly Leu Pro His Ala Pro Glu Leu Ile		
785	790	795
Arg Ser Ser Arg Ala Asp Pro Lys Lys Lys Arg Lys Val Gly Gly Gly		
	805	810
Gly Thr Gly Gly Gly Gly Ser Ala Glu Tyr Val Arg Ala Leu Phe Asp		
	820	825
Phe Asn Gly Asn Asp Glu Glu Asp Leu Pro Phe Lys Lys Gly Asp Ile		
	835	840
Leu Arg Ile Arg Asp Lys Pro Glu Glu Gln Trp Trp Asn Ala Glu Asp		
	850	855
Ser Glu Gly Lys Arg Gly Met Ile Leu Val Pro Tyr Val Glu Lys Tyr		
865	870	875
Ser Gly Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His Asp Ile		
	885	890
Asp Tyr Lys Asp Asp Asp Asp Lys Ser Gly Ser Ser Glu Thr Gly Pro		
	900	905
Val Ala Val Asp Pro Thr Leu Arg Arg Arg Ile Glu Pro His Glu Phe		

915	920	925
Glu Val Phe Phe Asp Pro Arg	Glu Leu Arg Lys	Glu Thr Cys Leu Leu
930	935	940
Tyr Glu Ile Lys Trp Gly Thr Ser His Lys Ile Trp Arg His Ser Ser		
945	950	955
Lys Asn Thr Thr Lys His Val Glu Val Asn Phe Ile Glu Lys Phe Thr		
965	970	975
Ser Glu Arg His Phe Cys Pro Ser Thr Ser Cys Ser Ile Thr Trp Phe		
980	985	990
Leu Ser Trp Ser Pro Cys Gly Glu Cys Ser Lys Ala Ile Thr Glu Phe		
995	1000	1005
Leu Ser Gln His Pro Asn Val Thr Leu Val Ile Tyr Val Ala Arg		
1010	1015	1020
Leu Tyr His His Met Asp Gln Gln Asn Arg Gln Gly Leu Arg Asp		
1025	1030	1035
Leu Val Asn Ser Gly Val Thr Ile Gln Ile Met Thr Ala Pro Glu		
1040	1045	1050
Tyr Asp Tyr Cys Trp Arg Asn Phe Val Asn Tyr Pro Pro Gly Lys		
1055	1060	1065
Glu Ala His Trp Pro Arg Tyr Pro Pro Leu Trp Met Lys Leu Tyr		
1070	1075	1080
Ala Leu Glu Leu His Ala Gly Ile Leu Gly Leu Pro Pro Cys Leu		
1085	1090	1095
Asn Ile Leu Arg Arg Lys Gln Pro Gln Leu Thr Phe Phe Thr Ile		
1100	1105	1110
Ala Leu Gln Ser Cys His Tyr Gln Arg Leu Pro Pro His Ile Leu		
1115	1120	1125
Trp Ala Thr Gly Leu Lys Ser Gly Gly Ser Gly Gly Ser Gly Gly		
1130	1135	1140
Ser Thr Asn Leu Ser Asp Ile Ile Glu Lys Glu Thr Gly Lys Gln		
1145	1150	1155
Leu Val Ile Gln Glu Ser Ile Leu Met Leu Pro Glu Glu Val Glu		
1160	1165	1170
Glu Val Ile Gly Asn Lys Pro Glu Ser Asp Ile Leu Val His Thr		
1175	1180	1185
Ala Tyr Asp Glu Ser Thr Asp Glu Asn Val Met Leu Leu Thr Ser		
1190	1195	1200
Asp Ala Pro Glu Tyr Lys Pro Trp Ala Leu Val Ile Gln Asp Ser		
1205	1210	1215

Asn Gly	Glu Asn Lys Ile Lys	Met Leu Ser Gly Gly	Ser Gly Gly
1220	1225	1230	
Ser Gly	Gly Ser Thr Asn Leu	Ser Asp Ile Ile Glu	Lys Glu Thr
1235	1240	1245	
Gly Lys	Gln Leu Val Ile Gln	Glu Ser Ile Leu Met	Leu Pro Glu
1250	1255	1260	
Glu Val	Glu Glu Val Ile Gly	Asn Lys Pro Glu Ser	Asp Ile Leu
1265	1270	1275	
Val His	Thr Ala Tyr Asp Glu	Ser Thr Asp Glu Asn	Val Met Leu
1280	1285	1290	
Leu Thr	Ser Asp Ala Pro Glu	Tyr Lys Pro Trp Ala	Leu Val Ile
1295	1300	1305	
Gln Asp	Ser Asn Gly Glu Asn	Lys Ile Lys Met Leu	Ser Gly Gly
1310	1315	1320	
Ser Lys	Arg Thr Ala Asp Gly	Ser Glu Phe Glu Pro	Lys Lys Lys
1325	1330	1335	
Arg Lys	Val		
1340			

<210> 39

<211> 4023

<212> DNA

<213> 人工序列(Artificial Sequence)

<220>

<223> 47-104-BE4-NC

<400> 39

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cgtgctgcgc aaccctccga cgcttcgccc gccgcgcagg tggatctacg cacgctcggc	180
tacagtcagc agcagcaaga gaagatcaaa ccgaaggtgc gttcgacagt ggcgacgac	240
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ccggcagcgt tagggaccgt cgctgtcacg tatcagcaca taatcacggc gttgccagag	360
gcgacacacg aagacatcgt tggcgtcggc aaacagtggg ccggcgacg cgccctggag	420
gccttgctca cggatgcggg ggagttgaga ggtccgccgt tacagttgga cacaggccaa	480
cttgtgaaga ttgcaaaacg tggcggcggt accgcaatgg aggcagtgc tgcattgcgc	540
aatgcgctca cgggagcacc cctcaacctg acccccgacc aggttgctgc tattgctagt	600
aacggcggag gcaaacaggc gctggaaaca gtccagcgcc tcttgccggg cttgtgtcag	660
gaccacggcc tgaccccgaga acaagttgtc gcgattgcaa gcaacaacgg aggcaacaa	720
gccttagaaa cagtccagag attgttgccg gtgctgtgcc aagccacgg cctgaccccg	780
gaccaggtgg ttgcaatcgc gtcacacgat gggggaaagc aggcctaga aaccgttcag	840

cgactcctgc	ccgtcctgtg	ccaggcccac	ggcctgaccc	cagcccaagt	tgctcgcgatt	900
gcaagcaaca	acggaggcaa	acaagcctta	gaaacagtcc	agagattgtt	gccggtgctg	960
tgccaagacc	acggcctgac	cccggaccag	gtggttgcaa	tcgcgtcaca	cgatggggga	1020
aagcaggccc	tagaaaccgt	tcagcgactc	ctgcccgtcc	tgtgccagga	ccacggcctg	1080
accccagaac	aagttgtcgc	gattgcaagc	aacaacggag	gcaaacaagc	cttagaaaca	1140
gtccagagat	tgttgccggt	gctgtgccaa	gccacaggcc	tgacccccga	ccaggttgctc	1200
gctattgcta	gtaacggcgg	aggcaaacag	gcgctggaaa	cagttcagcg	cctcttgccg	1260
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gtggccaggc	tgtatcacca	catggaccag	cagaacaggc	agggcctgcg	ggatctggtg	3120
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actgcctacg acgagagtac cgacgaaaat gtgatgttac tgacctccga cgcccctgag 3900
tataagccat gggctctggt catccaggac tccaatggag aaaataagat caagatgtta 3960
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gtg 4023

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<210> 40

<211> 1341

<212> PRT

<213> 人工序列(Artificial Sequence)

<220>

<223> 47-104-BE4-NC

<400> 40

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Tyr Lys Asp Asp Asp Asp Lys Ser Trp Lys Asp Ala Ser Gly Trp Ser
           20           25           30
Arg Met His Ala Ala Pro Arg Arg Arg Ala Ala Gln Pro Ser Asp Ala
           35           40           45
Ser Pro Ala Ala Gln Val Asp Leu Arg Thr Leu Gly Tyr Ser Gln Gln
           50           55           60
Gln Gln Glu Lys Ile Lys Pro Lys Val Arg Ser Thr Val Ala Gln His
65           70           75           80
His Glu Ala Leu Val Gly His Gly Phe Thr His Ala His Ile Val Ala
           85           90           95
Leu Ser Gln His Pro Ala Ala Leu Gly Thr Val Ala Val Thr Tyr Gln
           100          105          110
His Ile Ile Thr Ala Leu Pro Glu Ala Thr His Glu Asp Ile Val Gly
           115          120          125
Val Gly Lys Gln Trp Ser Gly Ala Arg Ala Leu Glu Ala Leu Leu Thr

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130	135	140
Asp Ala Gly Glu Leu Arg Gly Pro Pro Leu Gln Leu Asp Thr Gly Gln		
145	150	155
Leu Val Lys Ile Ala Lys Arg Gly Gly Val Thr Ala Met Glu Ala Val		
165	170	175
His Ala Ser Arg Asn Ala Leu Thr Gly Ala Pro Leu Asn Leu Thr Pro		
180	185	190
Asp Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu		
195	200	205
Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu		
210	215	220
Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln		
225	230	235
Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His		
245	250	255
Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser His Asp Gly Gly		
260	265	270
Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln		
275	280	285
Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser Asn Asn		
290	295	300
Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu		
305	310	315
Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser		
325	330	335
His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro		
340	345	350
Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile		
355	360	365
Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu		
370	375	380
Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val		
385	390	395
Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln		
405	410	415
Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln		
420	425	430
Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr		
435	440	445

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

755	760	765
Leu Thr Asn Asp His Leu Val Ala Leu Ala Cys Leu Gly Gly Arg Pro		
770	775	780
Ala Met Asp Ala Val Lys Lys Gly Leu Pro His Ala Pro Glu Leu Ile		
785	790	795
Arg Ser Ser Arg Ala Asp Pro Lys Lys Lys Arg Lys Val Gly Gly Gly		800
805	810	815
Gly Thr Gly Gly Gly Gly Ser Ala Glu Tyr Val Arg Ala Leu Phe Asp		
820	825	830
Phe Asn Gly Asn Asp Glu Glu Asp Leu Pro Phe Lys Lys Gly Asp Ile		
835	840	845
Leu Arg Ile Arg Asp Lys Pro Glu Glu Gln Trp Trp Asn Ala Glu Asp		
850	855	860
Ser Glu Gly Lys Arg Gly Met Ile Leu Val Pro Tyr Val Glu Lys Tyr		
865	870	875
Ser Gly Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His Asp Ile		
885	890	895
Asp Tyr Lys Asp Asp Asp Asp Lys Ser Gly Ser Ser Glu Thr Gly Pro		
900	905	910
Val Ala Val Asp Pro Thr Leu Arg Arg Arg Ile Glu Pro His Glu Phe		
915	920	925
Glu Val Phe Phe Asp Pro Arg Glu Leu Arg Lys Glu Thr Cys Leu Leu		
930	935	940
Tyr Glu Ile Lys Trp Gly Thr Ser His Lys Ile Trp Arg His Ser Ser		
945	950	955
Lys Asn Thr Thr Lys His Val Glu Val Asn Phe Ile Glu Lys Phe Thr		
965	970	975
Ser Glu Arg His Phe Cys Pro Ser Thr Ser Cys Ser Ile Thr Trp Phe		
980	985	990
Leu Ser Trp Ser Pro Cys Gly Glu Cys Ser Lys Ala Ile Thr Glu Phe		
995	1000	1005
Leu Ser Gln His Pro Asn Val Thr Leu Val Ile Tyr Val Ala Arg		
1010	1015	1020
Leu Tyr His His Met Asp Gln Gln Asn Arg Gln Gly Leu Arg Asp		
1025	1030	1035
Leu Val Asn Ser Gly Val Thr Ile Gln Ile Met Thr Ala Pro Glu		
1040	1045	1050
Tyr Asp Tyr Cys Trp Arg Asn Phe Val Asn Tyr Pro Pro Gly Lys		
1055	1060	1065

Glu Ala	His Trp Pro Arg Tyr	Pro Pro Leu Trp Met	Lys Leu Tyr
1070	1075	1080	
Ala Leu	Glu Leu His Ala Gly	Ile Leu Gly Leu Pro	Pro Cys Leu
1085	1090	1095	
Asn Ile	Leu Arg Arg Lys Gln	Pro Gln Leu Thr Phe	Phe Thr Ile
1100	1105	1110	
Ala Leu	Gln Ser Cys His Tyr	Gln Arg Leu Pro Pro	His Ile Leu
1115	1120	1125	
Trp Ala	Thr Gly Leu Lys Ser	Gly Gly Ser Gly Gly	Ser Gly Gly
1130	1135	1140	
Ser Thr	Asn Leu Ser Asp Ile	Ile Glu Lys Glu Thr	Gly Lys Gln
1145	1150	1155	
Leu Val	Ile Gln Glu Ser Ile	Leu Met Leu Pro Glu	Glu Val Glu
1160	1165	1170	
Glu Val	Ile Gly Asn Lys Pro	Glu Ser Asp Ile Leu	Val His Thr
1175	1180	1185	
Ala Tyr	Asp Glu Ser Thr Asp	Glu Asn Val Met Leu	Leu Thr Ser
1190	1195	1200	
Asp Ala	Pro Glu Tyr Lys Pro	Trp Ala Leu Val Ile	Gln Asp Ser
1205	1210	1215	
Asn Gly	Glu Asn Lys Ile Lys	Met Leu Ser Gly Gly	Ser Gly Gly
1220	1225	1230	
Ser Gly	Gly Ser Thr Asn Leu	Ser Asp Ile Ile Glu	Lys Glu Thr
1235	1240	1245	
Gly Lys	Gln Leu Val Ile Gln	Glu Ser Ile Leu Met	Leu Pro Glu
1250	1255	1260	
Glu Val	Glu Glu Val Ile Gly	Asn Lys Pro Glu Ser	Asp Ile Leu
1265	1270	1275	
Val His	Thr Ala Tyr Asp Glu	Ser Thr Asp Glu Asn	Val Met Leu
1280	1285	1290	
Leu Thr	Ser Asp Ala Pro Glu	Tyr Lys Pro Trp Ala	Leu Val Ile
1295	1300	1305	
Gln Asp	Ser Asn Gly Glu Asn	Lys Ile Lys Met Leu	Ser Gly Gly
1310	1315	1320	
Ser Lys	Arg Thr Ala Asp Gly	Ser Glu Phe Glu Pro	Lys Lys Lys
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Arg Lys	Val		
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<211> 4320

<212> DNA

<213> 人工序列(Artificial Sequence)

<220>

<223> WT-104-AID

<400> 41

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

Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val			
260	265	270	
Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala			
275	280	285	
Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu			
290	295	300	
Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala			
305	310	315	320
Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg			
325	330	335	
Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val			
340	345	350	
Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val			
355	360	365	
Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp			
370	375	380	
Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu			
385	390	395	400
Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr			
405	410	415	
Pro Ala Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala			
420	425	430	
Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly			
435	440	445	
Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys			
450	455	460	
Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp			
465	470	475	480
His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Asn Gly			
485	490	495	
Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys			
500	505	510	
Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn			
515	520	525	
Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val			
530	535	540	
Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala			
545	550	555	560
Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu			

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Pro	Val	Leu	Cys	Gln	Asp	His	Gly	Leu	Thr	Pro	Asp	Gln	Val	Val	Ala		
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Ile	Ala	Ser	Asn	Ile	Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg		
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Leu	Leu	Pro	Val	Leu	Cys	Gln	Asp	His	Gly	Leu	Thr	Pro	Glu	Gln	Val		
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Val	Ala	Ile	Ala	Ser	Asn	Ile	Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val		
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Gln	Arg	Leu	Leu	Pro	Val	Leu	Cys	Gln	Ala	His	Gly	Leu	Thr	Pro	Asp		
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Gln	Val	Val	Ala	Ile	Ala	Ser	Asn	Ile	Gly	Gly	Lys	Gln	Ala	Leu	Glu		
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Thr	Val	Gln	Arg	Leu	Leu	Pro	Val	Leu	Cys	Gln	Ala	His	Gly	Leu	Thr		
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Pro	Ala	Gln	Val	Val	Ala	Ile	Ala	Ser	Asn	Asn	Gly	Gly	Lys	Gln	Ala		
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Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu	Pro	Val	Leu	Cys	Gln	Asp	His	Gly		
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Pro	Ala	Leu	Glu	Ser	Ile	Val	Ala	Gln	Leu	Ser	Arg	Pro	Asp	Pro	Ala		
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Ala	Leu	Ile	Lys	Arg	Thr	Asn	Arg	Arg	Ile	Pro	Glu	Arg	Thr	Ser	His		
785					790					795					800		
Arg	Val	Ala	Asp	His	Ala	Gln	Val	Val	Arg	Val	Leu	Gly	Phe	Phe	Gln		
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Gly	Met	Ser	Arg	His	Gly	Leu	Leu	Gln	Leu	Phe	Arg	Arg	Val	Gly	Val		
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Thr	Glu	Leu	Glu	Ala	Arg	Ser	Gly	Thr	Leu	Pro	Pro	Ala	Ser	Gln	Arg		
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Trp	Asp	Arg	Ile	Leu	Gln	Ala	Ser	Gly	Met	Lys	Arg	Ala	Lys	Pro	Ser		
865					870					875					880		

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

1175	1180	1185
Gln Ser Ser His Asn Gln Leu Asn Glu Asn Arg Trp Leu Glu Lys		
1190	1195	1200
Thr Leu Lys Arg Ala Glu Lys Trp Arg Ser Glu Leu Ser Ile Met		
1205	1210	1215
Ile Gln Val Lys Ile Leu His Thr Thr Lys Ser Pro Ala Val Gly		
1220	1225	1230
Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Thr Asn Leu Ser Asp		
1235	1240	1245
Ile Ile Glu Lys Glu Thr Gly Lys Gln Leu Val Ile Gln Glu Ser		
1250	1255	1260
Ile Leu Met Leu Pro Glu Glu Val Glu Glu Val Ile Gly Asn Lys		
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Pro Glu Ser Asp Ile Leu Val His Thr Ala Tyr Asp Glu Ser Thr		
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Asp Glu Asn Val Met Leu Leu Thr Ser Asp Ala Pro Glu Tyr Lys		
1295	1300	1305
Pro Trp Ala Leu Val Ile Gln Asp Ser Asn Gly Glu Asn Lys Ile		
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Lys Met Leu Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Thr Asn		
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Leu Ser Asp Ile Ile Glu Lys Glu Thr Gly Lys Gln Leu Val Ile		
1340	1345	1350
Gln Glu Ser Ile Leu Met Leu Pro Glu Glu Val Glu Glu Val Ile		
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Gly Asn Lys Pro Glu Ser Asp Ile Leu Val His Thr Ala Tyr Asp		
1370	1375	1380
Glu Ser Thr Asp Glu Asn Val Met Leu Leu Thr Ser Asp Ala Pro		
1385	1390	1395
Glu Tyr Lys Pro Trp Ala Leu Val Ile Gln Asp Ser Asn Gly Glu		
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Asn Lys Ile Lys Met Leu Ser Gly Gly Ser Lys Arg Thr Ala Asp		
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Gly Ser Glu Phe Glu Pro Lys Lys Lys Arg Lys Val		
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<213> 人工序列(Artificial Sequence)		

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<223> WT-104-AID-NC

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<211>	1440					
<212>	PRT					

<213> 人工序列(Artificial Sequence)

<220>

<223> WT-104-AID-NC

<400> 44

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Gly	Ile	His	Gly	Val	Pro	Ala	Ala	Val	Asp	Leu	Arg	Thr	Leu	Gly	Tyr
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Ser	Gln	Gln	Gln	Gln	Glu	Lys	Ile	Lys	Pro	Lys	Val	Arg	Ser	Thr	Val
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Ala	Gln	His	His	Glu	Ala	Leu	Val	Gly	His	Gly	Phe	Thr	His	Ala	His
65					70					75					80
Ile	Val	Ala	Leu	Ser	Gln	His	Pro	Ala	Ala	Leu	Gly	Thr	Val	Ala	Val
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Lys	Tyr	Gln	Asp	Met	Ile	Ala	Ala	Leu	Pro	Glu	Ala	Thr	His	Glu	Ala
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Ile	Val	Gly	Val	Gly	Lys	Gln	Trp	Ser	Gly	Ala	Arg	Ala	Leu	Glu	Ala
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Leu	Leu	Thr	Val	Ala	Gly	Glu	Leu	Arg	Gly	Pro	Pro	Leu	Gln	Leu	Asp
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Thr	Gly	Gln	Leu	Leu	Lys	Ile	Ala	Lys	Arg	Gly	Gly	Val	Thr	Ala	Val
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Glu	Ala	Val	His	Ala	Trp	Arg	Asn	Ala	Leu	Thr	Gly	Ala	Pro	Leu	Asn
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Leu	Thr	Pro	Asp	Gln	Val	Val	Ala	Ile	Ala	Ser	Asn	Gly	Gly	Gly	Lys
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Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu	Pro	Val	Leu	Cys	Gln	Asp
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His	Gly	Leu	Thr	Pro	Glu	Gln	Val	Val	Ala	Ile	Ala	Ser	Asn	Asn	Gly
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Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu	Pro	Val	Leu	Cys
225					230				235					240	
Gln	Ala	His	Gly	Leu	Thr	Pro	Asp	Gln	Val	Val	Ala	Ile	Ala	Ser	His
			245						250				255		
Asp	Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu	Pro	Val
		260					265					270			
Leu	Cys	Gln	Ala	His	Gly	Leu	Thr	Pro	Ala	Gln	Val	Val	Ala	Ile	Ala

275	280	285
Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu		
290	295	300
Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala		
305	310	315
Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg		
325	330	335
Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val		
340	345	350
Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val		
355	360	365
Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp		
370	375	380
Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu		
385	390	395
Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr		
405	410	415
Pro Ala Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala		
420	425	430
Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly		
435	440	445
Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys		
450	455	460
Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp		
465	470	475
His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly		
485	490	495
Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys		
500	505	510
Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn		
515	520	525
Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val		
530	535	540
Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala		
545	550	555
Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu		
565	570	575
Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala		
580	585	590

Ile	Ala	Ser	His	Asp	Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg
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Leu	Leu	Pro	Val	Leu	Cys	Gln	Asp	His	Gly	Leu	Thr	Pro	Glu	Gln	Val
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Val	Ala	Ile	Ala	Ser	Asn	Asn	Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val
625					630					635					640
Gln	Arg	Leu	Leu	Pro	Val	Leu	Cys	Gln	Ala	His	Gly	Leu	Thr	Pro	Asp
				645					650					655	
Gln	Val	Val	Ala	Ile	Ala	Ser	His	Asp	Gly	Gly	Lys	Gln	Ala	Leu	Glu
			660					665						670	
Thr	Val	Gln	Arg	Leu	Leu	Pro	Val	Leu	Cys	Gln	Ala	His	Gly	Leu	Thr
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Pro	Ala	Gln	Val	Val	Ala	Ile	Ala	Ser	Asn	Asn	Gly	Gly	Lys	Gln	Ala
690					695						700				
Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu	Pro	Val	Leu	Cys	Gln	Asp	His	Gly
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Leu	Thr	Pro	Glu	Gln	Val	Val	Ala	Ile	Ala	Ser	Asn	Asn	Gly	Gly	Arg
			725					730					735		
Pro	Ala	Leu	Glu	Ser	Ile	Val	Ala	Gln	Leu	Ser	Arg	Pro	Asp	Pro	Ala
		740					745					750			
Leu	Ala	Ala	Leu	Thr	Asn	Asp	His	Leu	Val	Ala	Leu	Ala	Cys	Leu	Gly
	755				760						765				
Gly	Arg	Pro	Ala	Leu	Asp	Ala	Val	Lys	Lys	Gly	Leu	Pro	His	Ala	Pro
770					775					780					
Ala	Leu	Ile	Lys	Arg	Thr	Asn	Arg	Arg	Ile	Pro	Glu	Arg	Thr	Ser	His
785				790						795					800
Arg	Val	Ala	Asp	His	Ala	Gln	Val	Val	Arg	Val	Leu	Gly	Phe	Phe	Gln
			805					810					815		
Cys	His	Ser	His	Pro	Ala	Gln	Ala	Phe	Asp	Asp	Ala	Met	Thr	Gln	Phe
		820						825				830			
Gly	Met	Ser	Arg	His	Gly	Leu	Leu	Gln	Leu	Phe	Arg	Arg	Val	Gly	Val
	835					840					845				
Thr	Glu	Leu	Glu	Ala	Arg	Ser	Gly	Thr	Leu	Pro	Pro	Ala	Ser	Gln	Arg
	850					855				860					
Trp	Asp	Arg	Ile	Leu	Gln	Ala	Ser	Gly	Met	Lys	Arg	Ala	Lys	Pro	Ser
865				870						875					880
Pro	Thr	Ser	Thr	Gln	Thr	Pro	Asp	Gln	Ala	Ser	Leu	His	Ala	Phe	Ala
			885					890				895			
Asp	Ser	Leu	Glu	Arg	Asp	Leu	Asp	Ala	Pro	Ser	Pro	Met	His	Glu	Gly

900	905	910
Asp Gln Thr Arg Ala Ser Ala Ser Ser Arg Ala Asp Pro Lys Lys Lys		
915	920	925
Arg Lys Val Gly Gly Gly Gly Thr Gly Gly Gly Gly Ser Ala Glu Tyr		
930	935	940
Val Arg Ala Leu Phe Asp Phe Asn Gly Asn Asp Glu Glu Asp Leu Pro		
945	950	955
Phe Lys Lys Gly Asp Ile Leu Arg Ile Arg Asp Lys Pro Glu Glu Gln		
965	970	975
Trp Trp Asn Ala Glu Asp Ser Glu Gly Lys Arg Gly Met Ile Leu Val		
980	985	990
Pro Tyr Val Glu Lys Tyr Ser Gly Asp Tyr Lys Asp His Asp Gly Asp		
995	1000	1005
Tyr Lys Asp His Asp Ile Asp Tyr Lys Asp Asp Asp Asp Lys Ser		
1010	1015	1020
Gly Met Thr Asp Ala Glu Tyr Val Arg Ile His Glu Lys Leu Asp		
1025	1030	1035
Ile Tyr Thr Phe Lys Lys Gln Phe Phe Asn Asn Lys Lys Ser Val		
1040	1045	1050
Ser His Arg Cys Tyr Val Leu Phe Glu Leu Lys Arg Arg Gly Glu		
1055	1060	1065
Arg Arg Ala Cys Phe Trp Gly Tyr Ala Val Asn Lys Pro Gln Ser		
1070	1075	1080
Gly Thr Glu Arg Gly Ile His Ala Glu Ile Phe Ser Ile Arg Lys		
1085	1090	1095
Val Glu Glu Tyr Leu Arg Asp Asn Pro Gly Gln Phe Thr Ile Asn		
1100	1105	1110
Trp Tyr Ser Ser Trp Ser Pro Cys Ala Asp Cys Ala Glu Lys Ile		
1115	1120	1125
Leu Glu Trp Tyr Asn Gln Glu Leu Arg Gly Asn Gly His Thr Leu		
1130	1135	1140
Lys Ile Trp Ala Cys Lys Leu Tyr Tyr Glu Lys Asn Ala Arg Asn		
1145	1150	1155
Gln Ile Gly Leu Trp Asn Leu Arg Asp Asn Gly Val Gly Leu Asn		
1160	1165	1170
Val Met Val Ser Glu His Tyr Gln Cys Cys Arg Lys Ile Phe Ile		
1175	1180	1185
Gln Ser Ser His Asn Gln Leu Asn Glu Asn Arg Trp Leu Glu Lys		
1190	1195	1200

Thr Leu	Lys Arg	Ala Glu	Lys Trp	Arg Ser	Glu Leu	Ser Ile	Met
1205			1210			1215	
Ile Gln	Val Lys	Ile Leu	His Thr	Thr Lys	Ser Pro	Ala Val	Gly
1220			1225			1230	
Ser Gly	Gly Ser	Gly Gly	Ser Gly	Gly Gly	Ser Thr	Asn Leu	Ser Asp
1235			1240			1245	
Ile Ile	Glu Lys	Glu Thr	Gly Lys	Gln Leu	Val Ile	Gln Glu	Ser
1250			1255			1260	
Ile Leu	Met Leu	Pro Glu	Glu Val	Glu Glu	Val Ile	Gly Asn	Lys
1265			1270			1275	
Pro Glu	Ser Asp	Ile Leu	Val His	Thr Ala	Tyr Asp	Glu Ser	Thr
1280			1285			1290	
Asp Glu	Asn Val	Met Leu	Leu Thr	Ser Asp	Ala Pro	Glu Tyr	Lys
1295			1300			1305	
Pro Trp	Ala Leu	Val Ile	Gln Asp	Ser Asn	Gly Glu	Asn Lys	Ile
1310			1315			1320	
Lys Met	Leu Ser	Gly Gly	Ser Gly	Gly Gly	Ser Gly	Gly Ser	Thr Asn
1325			1330			1335	
Leu Ser	Asp Ile	Ile Glu	Lys Glu	Thr Gly	Lys Gln	Leu Val	Ile
1340			1345			1350	
Gln Glu	Ser Ile	Leu Met	Leu Pro	Glu Glu	Val Glu	Glu Val	Ile
1355			1360			1365	
Gly Asn	Lys Pro	Glu Ser	Asp Ile	Leu Val	His Thr	Ala Tyr	Asp
1370			1375			1380	
Glu Ser	Thr Asp	Glu Asn	Val Met	Leu Leu	Thr Ser	Asp Ala	Pro
1385			1390			1395	
Glu Tyr	Lys Pro	Trp Ala	Leu Val	Ile Gln	Asp Ser	Asn Gly	Glu
1400			1405			1410	
Asn Lys	Ile Lys	Met Leu	Ser Gly	Gly Ser	Lys Arg	Thr Ala	Asp
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Gly Ser	Glu Phe	Glu Pro	Lys Lys	Lys Arg	Lys Val		
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<210> 45

<211> 3975

<212> DNA

<213> 人工序列(Artificial Sequence)

<220>

<223> 63-104-AID

<400> 45

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<210> 46

<211> 1325

<212> PRT

<213> 人工序列(Artificial Sequence)

<220>

<223> 63-104-AID

<400> 46

Met Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His Asp Ile Asp

1 5 10 15

Tyr Lys Asp Asp Asp Asp Lys Met Ala Pro Lys Lys Lys Arg Lys Val

20 25 30

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

340	345	350
Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val		
355	360	365
Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp		
370	375	380
Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu		
385	390	395
Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr		
405	410	415
Pro Ala Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala		
420	425	430
Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly		
435	440	445
Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys		
450	455	460
Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp		
465	470	475
His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Asn Gly		
485	490	495
Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys		
500	505	510
Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn		
515	520	525
Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val		
530	535	540
Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala		
545	550	555
Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu		
565	570	575
Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala		
580	585	590
Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg		
595	600	605
Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val		
610	615	620
Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val		
625	630	635
Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp		
645	650	655

Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu		
660	665	670
Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr		
675	680	685
Pro Ala Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala		
690	695	700
Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly		
705	710	715
Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Arg		
725	730	735
Pro Ala Leu Glu Ser Ile Val Ala Gln Leu Ser Arg Pro Asp Pro Ala		
740	745	750
Leu Ala Ala Leu Thr Asn Asp His Leu Val Ala Leu Ala Cys Leu Gly		
755	760	765
Gly Arg Pro Ala Leu Asp Ala Val Lys Lys Gly Leu Pro His Ala Pro		
770	775	780
Ala Leu Ile Lys Arg Thr Asn Arg Arg Ile Pro Glu Arg Thr Ser His		
785	790	795
Arg Val Ala Gly Ser Ser Arg Ala Asp Pro Lys Lys Lys Arg Lys Val		
805	810	815
Gly Gly Gly Gly Thr Gly Gly Gly Gly Ser Ala Glu Tyr Val Arg Ala		
820	825	830
Leu Phe Asp Phe Asn Gly Asn Asp Glu Glu Asp Leu Pro Phe Lys Lys		
835	840	845
Gly Asp Ile Leu Arg Ile Arg Asp Lys Pro Glu Glu Gln Trp Trp Asn		
850	855	860
Ala Glu Asp Ser Glu Gly Lys Arg Gly Met Ile Leu Val Pro Tyr Val		
865	870	875
Glu Lys Tyr Ser Gly Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp		
885	890	895
His Asp Ile Asp Tyr Lys Asp Asp Asp Asp Lys Ser Gly Met Thr Asp		
900	905	910
Ala Glu Tyr Val Arg Ile His Glu Lys Leu Asp Ile Tyr Thr Phe Lys		
915	920	925
Lys Gln Phe Phe Asn Asn Lys Lys Ser Val Ser His Arg Cys Tyr Val		
930	935	940
Leu Phe Glu Leu Lys Arg Arg Gly Glu Arg Arg Ala Cys Phe Trp Gly		
945	950	955
Tyr Ala Val Asn Lys Pro Gln Ser Gly Thr Glu Arg Gly Ile His Ala		

965							970					975				
Glu	Ile	Phe	Ser	Ile	Arg	Lys	Val	Glu	Glu	Tyr	Leu	Arg	Asp	Asn	Pro	
980							985					990				
Gly	Gln	Phe	Thr	Ile	Asn	Trp	Tyr	Ser	Ser	Trp	Ser	Pro	Cys	Ala	Asp	
995							1000					1005				
Cys	Ala	Glu	Lys	Ile	Leu	Glu	Trp	Tyr	Asn	Gln	Glu	Leu	Arg	Gly		
1010							1015					1020				
Asn	Gly	His	Thr	Leu	Lys	Ile	Trp	Ala	Cys	Lys	Leu	Tyr	Tyr	Glu		
1025							1030					1035				
Lys	Asn	Ala	Arg	Asn	Gln	Ile	Gly	Leu	Trp	Asn	Leu	Arg	Asp	Asn		
1040							1045					1050				
Gly	Val	Gly	Leu	Asn	Val	Met	Val	Ser	Glu	His	Tyr	Gln	Cys	Cys		
1055							1060					1065				
Arg	Lys	Ile	Phe	Ile	Gln	Ser	Ser	His	Asn	Gln	Leu	Asn	Glu	Asn		
1070							1075					1080				
Arg	Trp	Leu	Glu	Lys	Thr	Leu	Lys	Arg	Ala	Glu	Lys	Trp	Arg	Ser		
1085							1090					1095				
Glu	Leu	Ser	Ile	Met	Ile	Gln	Val	Lys	Ile	Leu	His	Thr	Thr	Lys		
1100							1105					1110				
Ser	Pro	Ala	Val	Gly	Ser	Gly	Gly	Ser	Gly	Gly	Ser	Gly	Gly	Ser		
1115							1120					1125				
Thr	Asn	Leu	Ser	Asp	Ile	Ile	Glu	Lys	Glu	Thr	Gly	Lys	Gln	Leu		
1130							1135					1140				
Val	Ile	Gln	Glu	Ser	Ile	Leu	Met	Leu	Pro	Glu	Glu	Val	Glu	Glu		
1145							1150					1155				
Val	Ile	Gly	Asn	Lys	Pro	Glu	Ser	Asp	Ile	Leu	Val	His	Thr	Ala		
1160							1165					1170				
Tyr	Asp	Glu	Ser	Thr	Asp	Glu	Asn	Val	Met	Leu	Leu	Thr	Ser	Asp		
1175							1180					1185				
Ala	Pro	Glu	Tyr	Lys	Pro	Trp	Ala	Leu	Val	Ile	Gln	Asp	Ser	Asn		
1190							1195					1200				
Gly	Glu	Asn	Lys	Ile	Lys	Met	Leu	Ser	Gly	Gly	Ser	Gly	Gly	Ser		
1205							1210					1215				
Gly	Gly	Ser	Thr	Asn	Leu	Ser	Asp	Ile	Ile	Glu	Lys	Glu	Thr	Gly		
1220							1225					1230				
Lys	Gln	Leu	Val	Ile	Gln	Glu	Ser	Ile	Leu	Met	Leu	Pro	Glu	Glu		
1235							1240					1245				
Val	Glu	Glu	Val	Ile	Gly	Asn	Lys	Pro	Glu	Ser	Asp	Ile	Leu	Val		
1250							1255					1260				

His Thr Ala Tyr Asp Glu Ser Thr Asp Glu Asn Val Met Leu Leu
1265 1270 1275
Thr Ser Asp Ala Pro Glu Tyr Lys Pro Trp Ala Leu Val Ile Gln
1280 1285 1290
Asp Ser Asn Gly Glu Asn Lys Ile Lys Met Leu Ser Gly Gly Ser
1295 1300 1305
Lys Arg Thr Ala Asp Gly Ser Glu Phe Glu Pro Lys Lys Lys Arg
1310 1315 1320
Lys Val
1325

<210> 47

<211> 3975

<212> DNA

<213> 人工序列(Artificial Sequence)

<220>

<223> 63-104-AID-NC

<400> 47

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gtagatttga gaactttggg atattcacag cagcagcagg aaaagatcaa gccc aaagtg	180
aggctgcagag tcgcgcagca tcacgaagcg ctggtgggtc atgggtttac acatgcccac	240
atcgtagcct tgtcgcagca ccctgcagcc cttggcacgg tcgccgtcaa gtaccaggac	300
atgattgcgg cggttgcgga agccacacat gaggcgatcg tcggtgtggg gaaacagtgg	360
agcggagccc gagcgcttga ggccctgttg acggtcgcgg gagagctgag agggcctccc	420
cttcagctgg acacgggcca gttgctgaag atcgcgaagc ggggaggagt cacggcggtc	480
gaggcggtag acgcgtggcg caatgcgctc acgggagcac ccctcaacct gacccccgac	540
caggttgtcg ctattgctag taacggcgga ggcaaacagg cgctggaaac agttcagcgc	600
ctcttgccgg tcttgtgtca ggaccacggc ctgacccag aacaagttgt cgcgattgca	660
agcaacaacg gaggcaaaca agccttagaa acagtccaga gattgttgcc ggtgctgtgc	720
caagccccacg gcctgacccc ggaccagggtg gttgcaatcg cgtcacacga tgggggaaag	780
caggccctag aaaccgttca gcgactcctg cccgtcctgt gccaggccca cggcctgacc	840
ccagcccaag ttgtcgcgat tgcaagcaac aacggaggca aacaagcctt agaaacagtc	900
cagagattgt tgccggtgct gtgccaagac cacggcctga ccccggaaca ggtggttgca	960
atcgcgtcac acgatggggg aaagcaggcc ctagaaaccg ttcagcgact cctgcccgtc	1020
ctgtgccagg accacggcct gacccagaa caagttgtcg cgattgcaag caacaacgga	1080
ggcaaacaag ccttagaaac agtccagaga ttgttgccgg tgctgtgcca agcccacggc	1140
ctgacccccg accaggttgt cgctattgct agtaacggcg gaggcaaaca ggcgtggaa	1200
acagttcagc gcctcttgcc ggtcttgtgt caggccacg gcctgacccc agcccaggtt	1260
gtggccatcg ccagcaacat aggtggcaag caggccctcg aaaccgtcca gagactgtta	1320

ccggttctct	gccaggacca	cggcctgacc	cccgaccagg	ttgtcgctat	tgctagtaac	1380
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cacggcctga	ccccagaaca	ggttgtggcc	atcgccagca	acataggtgg	caagcaggcc	1500
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tacaaggacg	atgacgataa	gtctggcatg	accgacgccg	agtatgtgcg	gatccacgag	2760
aagctggata	tctacacctt	caagaagcag	ttctttaaca	ataagaagtc	cgtgtctcac	2820
agatgctatg	tgctgttcga	gctgaagcgg	agaggagaga	ggcgcgcatg	tttttggggc	2880
tacgccgtga	ataagccaca	gagcggaaac	gagaggggaa	tccacgccga	gatcttctcc	2940
atcaggaaaag	tggaggagta	tctgcgcgac	aaccctggcc	agtttacaat	caattggtac	3000
agctcctgga	gccccatgcg	cgattgtgcc	gagaagatcc	tggagtggta	taaccaggag	3060
ctgagaggca	atggccacac	cctgaagatc	tgggcctgca	agctgtacta	tgagaagaac	3120
gcccggaaatc	agatcggcct	gtggaacctg	agagacaatg	gcgtgggcct	gaacgtgatg	3180
gtgtctgagc	actaccagtg	ctgtaggaag	atcttcatcc	agtctagcca	caatcagctg	3240
aacgagaatc	gctggctgga	gaagacactg	aagagggccg	agaagtggcg	cagcgagctg	3300
tccatcatga	tccagtgtaa	gatcctgcac	accacaaaga	gcccagcagt	gggatccgga	3360
ggatctggag	gaagcggagg	atccaccaac	ctgtctgaca	tcatcgagaa	ggagacaggc	3420
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ggcaacaagc	ctgagtccga	tatcctggtg	cacaccgcct	acgacgagtc	cacagatgag	3540
aatgtgatgc	tgctgacctc	tgacgcccc	gagtataagc	cctgggccct	ggtcatccag	3600
gatagcaacg	gcgagaataa	gatcaagatg	ctgtccggcg	gaagcggagg	atccggaggc	3660

tctaccaatc tgtccgatat tattgaaaa gagacaggca agcaactggt catccaggag 3720
 tctatcctga tgctgccaga agaagtcgaa gaagtgatcg gaaacaagcc cgaaagcgac 3780
 atcctgggtcc atactgccta cgacgagagt accgacgaaa atgtgatgtt actgacctcc 3840
 gacgccccctg agtataagcc atgggctctg gtcattccagg actccaatgg agaaaataag 3900
 atcaagatgt taagcggcgg ctccaagaga acagccgacg gctccgagtt cgagcccaag 3960
 aagaagcgga aagtg 3975

<210> 48

<211> 1325

<212> PRT

<213> 人工序列(Artificial Sequence)

<220>

<223> 63-104-AID-NC

<400> 48

Met Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His Asp Ile Asp

1 5 10 15

Tyr Lys Asp Asp Asp Asp Lys Met Ala Pro Lys Lys Lys Arg Lys Val

20 25 30

Gly Ile His Gly Val Pro Ala Ala Val Asp Leu Arg Thr Leu Gly Tyr

35 40 45

Ser Gln Gln Gln Gln Glu Lys Ile Lys Pro Lys Val Arg Ser Thr Val

50 55 60

Ala Gln His His Glu Ala Leu Val Gly His Gly Phe Thr His Ala His

65 70 75 80

Ile Val Ala Leu Ser Gln His Pro Ala Ala Leu Gly Thr Val Ala Val

85 90 95

Lys Tyr Gln Asp Met Ile Ala Ala Leu Pro Glu Ala Thr His Glu Ala

100 105 110

Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg Ala Leu Glu Ala

115 120 125

Leu Leu Thr Val Ala Gly Glu Leu Arg Gly Pro Pro Leu Gln Leu Asp

130 135 140

Thr Gly Gln Leu Leu Lys Ile Ala Lys Arg Gly Gly Val Thr Ala Val

145 150 155 160

Glu Ala Val His Ala Trp Arg Asn Ala Leu Thr Gly Ala Pro Leu Asn

165 170 175

Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys

180 185 190

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp

195 200 205

His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Asn Gly			
210	215	220	
Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys			
225	230	235	240
Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser His			
	245	250	255
Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val			
	260	265	270
Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala			
	275	280	285
Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu			
	290	295	300
Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala			
305	310	315	320
Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg			
	325	330	335
Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val			
	340	345	350
Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val			
	355	360	365
Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp			
370	375	380	
Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu			
385	390	395	400
Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr			
	405	410	415
Pro Ala Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala			
	420	425	430
Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly			
	435	440	445
Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys			
450	455	460	
Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp			
465	470	475	480
His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly			
	485	490	495
Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys			
	500	505	510
Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn			

515	520	525
Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val		
530	535	540
Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala		
545	550	555
Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu		
565	570	575
Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala		
580	585	590
Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg		
595	600	605
Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val		
610	615	620
Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val		
625	630	635
Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp		
645	650	655
Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu		
660	665	670
Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr		
675	680	685
Pro Ala Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala		
690	695	700
Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly		
705	710	715
Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Arg		
725	730	735
Pro Ala Leu Glu Ser Ile Val Ala Gln Leu Ser Arg Pro Asp Pro Ala		
740	745	750
Leu Ala Ala Leu Thr Asn Asp His Leu Val Ala Leu Ala Cys Leu Gly		
755	760	765
Gly Arg Pro Ala Leu Asp Ala Val Lys Lys Gly Leu Pro His Ala Pro		
770	775	780
Ala Leu Ile Lys Arg Thr Asn Arg Arg Ile Pro Glu Arg Thr Ser His		
785	790	795
Arg Val Ala Gly Ser Ser Arg Ala Asp Pro Lys Lys Lys Arg Lys Val		
805	810	815
Gly Gly Gly Gly Thr Gly Gly Gly Gly Ser Ala Glu Tyr Val Arg Ala		
820	825	830

Leu Phe Asp Phe Asn Gly Asn Asp Glu Glu Asp Leu Pro Phe Lys Lys		
835	840	845
Gly Asp Ile Leu Arg Ile Arg Asp Lys Pro Glu Glu Gln Trp Trp Asn		
850	855	860
Ala Glu Asp Ser Glu Gly Lys Arg Gly Met Ile Leu Val Pro Tyr Val		
865	870	875
Glu Lys Tyr Ser Gly Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp		
	885	890
His Asp Ile Asp Tyr Lys Asp Asp Asp Asp Lys Ser Gly Met Thr Asp		
	900	905
Ala Glu Tyr Val Arg Ile His Glu Lys Leu Asp Ile Tyr Thr Phe Lys		
	915	920
Lys Gln Phe Phe Asn Asn Lys Lys Ser Val Ser His Arg Cys Tyr Val		
	930	935
Leu Phe Glu Leu Lys Arg Arg Gly Glu Arg Arg Ala Cys Phe Trp Gly		
945	950	955
Tyr Ala Val Asn Lys Pro Gln Ser Gly Thr Glu Arg Gly Ile His Ala		
	965	970
Glu Ile Phe Ser Ile Arg Lys Val Glu Glu Tyr Leu Arg Asp Asn Pro		
	980	985
Gly Gln Phe Thr Ile Asn Trp Tyr Ser Ser Trp Ser Pro Cys Ala Asp		
	995	1000
Cys Ala Glu Lys Ile Leu Glu Trp Tyr Asn Gln Glu Leu Arg Gly		
1010	1015	1020
Asn Gly His Thr Leu Lys Ile Trp Ala Cys Lys Leu Tyr Tyr Glu		
1025	1030	1035
Lys Asn Ala Arg Asn Gln Ile Gly Leu Trp Asn Leu Arg Asp Asn		
1040	1045	1050
Gly Val Gly Leu Asn Val Met Val Ser Glu His Tyr Gln Cys Cys		
1055	1060	1065
Arg Lys Ile Phe Ile Gln Ser Ser His Asn Gln Leu Asn Glu Asn		
1070	1075	1080
Arg Trp Leu Glu Lys Thr Leu Lys Arg Ala Glu Lys Trp Arg Ser		
1085	1090	1095
Glu Leu Ser Ile Met Ile Gln Val Lys Ile Leu His Thr Thr Lys		
1100	1105	1110
Ser Pro Ala Val Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser		
1115	1120	1125
Thr Asn Leu Ser Asp Ile Ile Glu Lys Glu Thr Gly Lys Gln Leu		

1130	1135	1140
Val Ile Gln Glu Ser Ile Leu Met Leu Pro Glu Glu Val Glu Glu		
1145	1150	1155
Val Ile Gly Asn Lys Pro Glu Ser Asp Ile Leu Val His Thr Ala		
1160	1165	1170
Tyr Asp Glu Ser Thr Asp Glu Asn Val Met Leu Leu Thr Ser Asp		
1175	1180	1185
Ala Pro Glu Tyr Lys Pro Trp Ala Leu Val Ile Gln Asp Ser Asn		
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Val Glu Glu Val Ile Gly Asn Lys Pro Glu Ser Asp Ile Leu Val		
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His Thr Ala Tyr Asp Glu Ser Thr Asp Glu Asn Val Met Leu Leu		
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Thr Ser Asp Ala Pro Glu Tyr Lys Pro Trp Ala Leu Val Ile Gln		
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Asp Ser Asn Gly Glu Asn Lys Ile Lys Met Leu Ser Gly Gly Ser		
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Arg Met His Ala Ala Pro Arg Arg Arg Ala Ala Gln Pro Ser Asp Ala

35 40 45

Ser Pro Ala Ala Gln Val Asp Leu Arg Thr Leu Gly Tyr Ser Gln Gln

50 55 60

Gln Gln Glu Lys Ile Lys Pro Lys Val Arg Ser Thr Val Ala Gln His

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His Glu Ala Leu Val Gly His Gly Phe Thr His Ala His Ile Val Ala			
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Leu Ser Gln His Pro Ala Ala Leu Gly Thr Val Ala Val Thr Tyr Gln			
	100	105	110
His Ile Ile Thr Ala Leu Pro Glu Ala Thr His Glu Asp Ile Val Gly			
	115	120	125
Val Gly Lys Gln Trp Ser Gly Ala Arg Ala Leu Glu Ala Leu Leu Thr			
	130	135	140
Asp Ala Gly Glu Leu Arg Gly Pro Pro Leu Gln Leu Asp Thr Gly Gln			
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Leu Val Lys Ile Ala Lys Arg Gly Gly Val Thr Ala Met Glu Ala Val			
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His Ala Ser Arg Asn Ala Leu Thr Gly Ala Pro Leu Asn Leu Thr Pro			
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Asp Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu			
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Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu			
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Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln			
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Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly			
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Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln			
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Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser Asn Asn			
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Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu			
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Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser			
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Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro			
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Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile			
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Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln			
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Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr			
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Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro			
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Asp Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu			
465	470	475	480
Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu			
	485	490	495
Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln			
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Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His			
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Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly			
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Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln			
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Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser His Asp			
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Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu			
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Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser			
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Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro			
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Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile			
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Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu			
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Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val			
	660	665	670
Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln			
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Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln			

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Glu Ser Ile Val Ala Gln Leu Ser Arg Pro Asp Pro Ala Leu Ala Ala		
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Gly Thr Gly Gly Gly Gly Ser Ala Glu Tyr Val Arg Ala Leu Phe Asp		
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Phe Asn Gly Asn Asp Glu Glu Asp Leu Pro Phe Lys Lys Gly Asp Ile		
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Val Arg Ile His Glu Lys Leu Asp Ile Tyr Thr Phe Lys Lys Gln Phe		
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Phe Asn Asn Lys Lys Ser Val Ser His Arg Cys Tyr Val Leu Phe Glu		
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Thr Ile Asn Trp Tyr Ser Ser Trp Ser Pro Cys Ala Asp Cys Ala Glu		
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Leu Asn	Val Met Val Ser Glu	His Tyr Gln Cys Cys	Arg Lys Ile
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Phe Ile	Gln Ser Ser His Asn	Gln Leu Asn Glu Asn	Arg Trp Leu
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Glu Lys	Thr Leu Lys Arg Ala	Glu Lys Trp Arg Ser	Glu Leu Ser
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Val Gly	Ser Gly Gly Ser Gly	Gly Ser Gly Gly Ser	Thr Asn Leu
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Asn Lys	Pro Glu Ser Asp Ile	Leu Val His Thr Ala	Tyr Asp Glu
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Ser Thr	Asp Glu Asn Val Met	Leu Leu Thr Ser Asp	Ala Pro Glu
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Tyr Lys	Pro Trp Ala Leu Val	Ile Gln Asp Ser Asn	Gly Glu Asn
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Lys Ile	Lys Met Leu Ser Gly	Gly Ser Gly Gly Ser	Gly Gly Ser
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Thr Asn	Leu Ser Asp Ile Ile	Glu Lys Glu Thr Gly	Lys Gln Leu
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Val Ile	Gln Glu Ser Ile Leu	Met Leu Pro Glu Glu	Val Glu Glu
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Tyr Asp	Glu Ser Thr Asp Glu	Asn Val Met Leu Leu	Thr Ser Asp
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gtcatccagg	agagcatcct	gatgtgccc	gaggaggtgg	aggaagtgat	cggcaacaag	3480
cctgagtccg	atatcctggt	gcacaccgcc	tacgacgagt	ccacagatga	gaatgtgatg	3540
ctgctgacct	ctgacgcccc	agagtataag	ccctggggcc	tggtcatcca	ggatagcaac	3600
ggcgagaata	agatcaagat	gctgtccggc	ggaagcggag	gatccggagg	ctctaccaat	3660
ctgtccgata	ttattgaaaa	agagacaggc	aagcaactgg	tcattccagga	gtctatcctg	3720
atgctgccag	aagaagtcga	agaagtgatc	ggaacaagc	ccgaaagcga	catcctggtc	3780
catactgcct	acgacgagag	taccgacgaa	aatgtgatgt	tactgacctc	cgacgcccct	3840
gagtataagc	catgggctct	ggtcatccag	gactccaatg	gagaaaataa	gatcaagatg	3900
ttaagcggcg	gctccaagag	aacagccgac	ggctccgagt	tcgagcccaa	gaagaagcgg	3960
aaagtg						3966

<210> 52

<211> 1322
 <212> PRT
 <213> 人工序列(Artificial Sequence)
 <220>
 <223> 47-104-AID-NC
 <400> 52
 Met Ala Ser Ser Pro Pro Lys Lys Lys Arg Lys Val Ala Ala Ala Asp
 1 5 10 15
 Tyr Lys Asp Asp Asp Asp Lys Ser Trp Lys Asp Ala Ser Gly Trp Ser
 20 25 30
 Arg Met His Ala Ala Pro Arg Arg Arg Ala Ala Gln Pro Ser Asp Ala
 35 40 45
 Ser Pro Ala Ala Gln Val Asp Leu Arg Thr Leu Gly Tyr Ser Gln Gln
 50 55 60
 Gln Gln Glu Lys Ile Lys Pro Lys Val Arg Ser Thr Val Ala Gln His
 65 70 75 80
 His Glu Ala Leu Val Gly His Gly Phe Thr His Ala His Ile Val Ala
 85 90 95
 Leu Ser Gln His Pro Ala Ala Leu Gly Thr Val Ala Val Thr Tyr Gln
 100 105 110
 His Ile Ile Thr Ala Leu Pro Glu Ala Thr His Glu Asp Ile Val Gly
 115 120 125
 Val Gly Lys Gln Trp Ser Gly Ala Arg Ala Leu Glu Ala Leu Leu Thr
 130 135 140
 Asp Ala Gly Glu Leu Arg Gly Pro Pro Leu Gln Leu Asp Thr Gly Gln
 145 150 155 160
 Leu Val Lys Ile Ala Lys Arg Gly Gly Val Thr Ala Met Glu Ala Val
 165 170 175
 His Ala Ser Arg Asn Ala Leu Thr Gly Ala Pro Leu Asn Leu Thr Pro
 180 185 190
 Asp Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu
 195 200 205
 Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu
 210 215 220
 Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln
 225 230 235 240
 Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His
 245 250 255
 Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser His Asp Gly Gly

260	265	270
Lys Gln Ala Leu Glu Thr Val	Gln Arg Leu Leu Pro Val	Leu Cys Gln
275	280	285
Ala His Gly Leu Thr Pro Ala	Gln Val Val Ala Ile Ala	Ser Asn Asn
290	295	300
Gly Gly Lys Gln Ala Leu Glu Thr	Val Gln Arg Leu Leu Pro Val	Leu
305	310	315
Cys Gln Asp His Gly Leu Thr Pro	Asp Gln Val Val Ala Ile Ala	Ser
325	330	335
His Asp Gly Gly Lys Gln Ala Leu	Glu Thr Val Gln Arg Leu Leu Pro	
340	345	350
Val Leu Cys Gln Asp His Gly Leu	Thr Pro Glu Gln Val Val Ala Ile	
355	360	365
Ala Ser Asn Asn Gly Gly Lys Gln	Ala Leu Glu Thr Val Gln Arg Leu	
370	375	380
Leu Pro Val Leu Cys Gln Ala His	Gly Leu Thr Pro Asp Gln Val Val	
385	390	395
Ala Ile Ala Ser Asn Gly Gly Gly	Lys Gln Ala Leu Glu Thr Val Gln	
405	410	415
Arg Leu Leu Pro Val Leu Cys Gln	Ala His Gly Leu Thr Pro Ala Gln	
420	425	430
Val Val Ala Ile Ala Ser Asn Ile	Gly Gly Lys Gln Ala Leu Glu Thr	
435	440	445
Val Gln Arg Leu Leu Pro Val Leu	Cys Gln Asp His Gly Leu Thr Pro	
450	455	460
Asp Gln Val Val Ala Ile Ala Ser	Asn Gly Gly Gly Lys Gln Ala Leu	
465	470	475
Glu Thr Val Gln Arg Leu Leu Pro	Val Leu Cys Gln Asp His Gly Leu	
485	490	495
Thr Pro Glu Gln Val Val Ala Ile	Ala Ser Asn Ile Gly Gly Lys Gln	
500	505	510
Ala Leu Glu Thr Val Gln Arg Leu	Leu Leu Pro Val Leu Cys Gln Ala His	
515	520	525
Gly Leu Thr Pro Asp Gln Val Val	Ala Ile Ala Ser Asn Asn Gly Gly	
530	535	540
Lys Gln Ala Leu Glu Thr Val Gln	Arg Leu Leu Pro Val Leu Cys Gln	
545	550	555
Ala His Gly Leu Thr Pro Ala Gln	Val Val Ala Ile Ala Ser Asn Gly	
565	570	575

Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu			
580	585	590	
Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser			
595	600	605	
His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro			
610	615	620	
Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile			
625	630	635	640
Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu			
645	650	655	
Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val			
660	665	670	
Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln			
675	680	685	
Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln			
690	695	700	
Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr			
705	710	715	720
Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro			
725	730	735	
Glu Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Arg Pro Ala Leu			
740	745	750	
Glu Ser Ile Val Ala Gln Leu Ser Arg Pro Asp Pro Ala Leu Ala Ala			
755	760	765	
Leu Thr Asn Asp His Leu Val Ala Leu Ala Cys Leu Gly Gly Arg Pro			
770	775	780	
Ala Met Asp Ala Val Lys Lys Gly Leu Pro His Ala Pro Glu Leu Ile			
785	790	795	800
Arg Ser Ser Arg Ala Asp Pro Lys Lys Lys Arg Lys Val Gly Gly Gly			
805	810	815	
Gly Thr Gly Gly Gly Gly Ser Ala Glu Tyr Val Arg Ala Leu Phe Asp			
820	825	830	
Phe Asn Gly Asn Asp Glu Glu Asp Leu Pro Phe Lys Lys Gly Asp Ile			
835	840	845	
Leu Arg Ile Arg Asp Lys Pro Glu Glu Gln Trp Trp Asn Ala Glu Asp			
850	855	860	
Ser Glu Gly Lys Arg Gly Met Ile Leu Val Pro Tyr Val Glu Lys Tyr			
865	870	875	880
Ser Gly Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His Asp Ile			

	885		890		895
Asp Tyr Lys Asp Asp Asp Asp Lys Ser Gly Met Thr Asp Ala Glu Tyr					
900		905		910	
Val Arg Ile His Glu Lys Leu Asp Ile Tyr Thr Phe Lys Lys Gln Phe					
915		920		925	
Phe Asn Asn Lys Lys Ser Val Ser His Arg Cys Tyr Val Leu Phe Glu					
930		935		940	
Leu Lys Arg Arg Gly Glu Arg Arg Ala Cys Phe Trp Gly Tyr Ala Val					
945		950		955	960
Asn Lys Pro Gln Ser Gly Thr Glu Arg Gly Ile His Ala Glu Ile Phe					
965		970		975	
Ser Ile Arg Lys Val Glu Glu Tyr Leu Arg Asp Asn Pro Gly Gln Phe					
980		985		990	
Thr Ile Asn Trp Tyr Ser Ser Trp Ser Pro Cys Ala Asp Cys Ala Glu					
995		1000		1005	
Lys Ile Leu Glu Trp Tyr Asn Gln Glu Leu Arg Gly Asn Gly His					
1010		1015		1020	
Thr Leu Lys Ile Trp Ala Cys Lys Leu Tyr Tyr Glu Lys Asn Ala					
1025		1030		1035	
Arg Asn Gln Ile Gly Leu Trp Asn Leu Arg Asp Asn Gly Val Gly					
1040		1045		1050	
Leu Asn Val Met Val Ser Glu His Tyr Gln Cys Cys Arg Lys Ile					
1055		1060		1065	
Phe Ile Gln Ser Ser His Asn Gln Leu Asn Glu Asn Arg Trp Leu					
1070		1075		1080	
Glu Lys Thr Leu Lys Arg Ala Glu Lys Trp Arg Ser Glu Leu Ser					
1085		1090		1095	
Ile Met Ile Gln Val Lys Ile Leu His Thr Thr Lys Ser Pro Ala					
1100		1105		1110	
Val Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Thr Asn Leu					
1115		1120		1125	
Ser Asp Ile Ile Glu Lys Glu Thr Gly Lys Gln Leu Val Ile Gln					
1130		1135		1140	
Glu Ser Ile Leu Met Leu Pro Glu Glu Val Glu Glu Val Ile Gly					
1145		1150		1155	
Asn Lys Pro Glu Ser Asp Ile Leu Val His Thr Ala Tyr Asp Glu					
1160		1165		1170	
Ser Thr Asp Glu Asn Val Met Leu Leu Thr Ser Asp Ala Pro Glu					
1175		1180		1185	

Tyr Lys	Pro Trp	Ala Leu	Val Ile	Gln Asp	Ser Asn	Gly Glu	Asn
1190			1195			1200	
Lys Ile	Lys Met	Leu Ser	Gly Gly	Ser Gly	Gly Ser	Gly Gly	Ser
1205			1210			1215	
Thr Asn	Leu Ser	Asp Ile	Ile Ile	Glu Lys	Glu Thr	Gly Lys	Gln Leu
1220			1225			1230	
Val Ile	Gln Glu	Ser Ile	Leu Met	Leu Pro	Glu Glu	Val Glu	Glu
1235			1240			1245	
Val Ile	Gly Asn	Lys Pro	Glu Ser	Asp Ile	Leu Val	His Thr	Ala
1250			1255			1260	
Tyr Asp	Glu Ser	Thr Asp	Glu Asn	Val Met	Leu Leu	Thr Ser	Asp
1265			1270			1275	
Ala Pro	Glu Tyr	Lys Pro	Trp Ala	Leu Val	Ile Gln	Asp Ser	Asn
1280			1285			1290	
Gly Glu	Asn Lys	Ile Lys	Met Leu	Ser Gly	Gly Ser	Lys Arg	Thr
1295			1300			1305	
Ala Asp	Gly Ser	Glu Phe	Glu Pro	Lys Lys	Lys Arg	Lys Val	
1310			1315			1320	

<210> 53

<211> 4044

<212> DNA

<213> 人工序列(Artificial Sequence)

<220>

<223> WT-12-AID

<400> 53

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gacgataaga tggcccaaaa gaagaagcgg aaggtcggtg tccacggagt cccagcagcc	120
gtagatttga gaactttggg atattcacag cagcagcagg aaaagatcaa gcccaaagtg	180
aggtcgacag tcgcgcagca tcacgaagcg ctggtgggtc atgggtttac acatgcccac	240
atcgtagcct tgtcgcagca ccctgcagcc cttggcacgg tcgccgtcaa gtaccaggac	300
atgattgcgg cgttgccgga agccacacat gaggcgatcg tcggtgtggg gaaacagtgg	360
agcggagccc gagcgcttga ggccctgttg acggtcgcgg gagagctgag agggcctccc	420
cttcagctgg acacgggcca gttgctgaag atcgcaagc ggggaggagt cacggcggtc	480
gaggcggtac acgcgtggcg caatgcgtc acgggagcac ccctcaacct gacccagac	540
caggttgtgg ccatcgccag caacataggt ggcaagcagg ccctcgaaac cgtccagaga	600
ctgttaccgg ttctctgcca ggaccacggc ctgaccccg aacaggtggt tgcaatcgcg	660
tcacacgatg ggggaaagca ggccctagaa accgttcagc gactcctgcc cgtcctgtgc	720
caggccccacg gcctgacccc agaccaggtt gtggccatcg ccagcaacat aggtggcaag	780
caggccctcg aaaccgtcca gagactgtta ccggttctct gccaggccca cggcctgacc	840

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cagagattgt	tgccggtgct	gtgccaagac	cacggcctga	ccccagacca	ggttgtggcc	960
atcgccagca	acataggtgg	caagcaggcc	ctcgaaaccg	tccagagact	gttaccggtt	1020
ctctgccagg	accacggcct	gaccccagaa	caggttgtgg	ccatcgccag	caacataggt	1080
ggcaagcagg	ccctcgaaac	cgtccagaga	ctgttaccgg	ttctctgcca	ggcccacggc	1140
ctgaccccgag	accaagttgt	cgcgattgca	agcaacaacg	gaggcaaaca	agccttagaa	1200
acagtccaga	gattgttgcc	tgtgctgtgc	caagcccacg	gcctgacccc	ggcccaggtg	1260
gttgcaatcg	cgtcacacga	tgggggaaag	caggccctag	aaaccgttca	gcgactcctg	1320
cccgctcctgt	gccaggacca	cggcctgacc	ccagaccaag	ttgtcgcgat	tgcaagcaac	1380
aacggaggca	aacaagcctt	agaaacagtc	cagagattgt	tgccggtgct	gtgccaagac	1440
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ttagaaacag	tccagagatt	gttgccggtg	ctgtgccaa	cccacggcct	gaccccagac	1560
caagttgtcg	cgattgcaag	caacaacgga	ggcaaacaag	ccttagaaac	agtccagaga	1620
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tcacacgatg	ggggaaagca	ggccctagaa	accgttcagc	gactcctgcc	cgctcctgtgc	1740
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ggcaaacaag	ccttagaaac	agtccagaga	ttgttgccgg	tgctgtgcca	agaccacggc	2160
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cttgtagcgc	tggcctgcct	cggcggacga	cccgccttgg	atgcggtgaa	gaaggggctc	2340
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gctagcccca	agaagaagag	aaaggtggag	gccagcatga	ccgacgccga	gtatgtgcgg	2820
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aattggtaca	gctcctggag	cccatgcgcc	gattgtgccg	agaagatcct	ggagtggtat	3120
aaccaggagc	tgagaggcaa	tggccacacc	ctgaagatct	gggcctgcaa	gctgtactat	3180

gagaagaacg cccggaatca gatcggcctg tggaacctga gagacaatgg cgtgggcctg 3240
 aacgtgatgg tgtctgagca ctaccagtgc tgtaggaaga tcttcatcca gtctagccac 3300
 aatcagctga acgagaatcg ctggctggag aagacactga agagggccga gaagtggcgc 3360
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 gaagtgatcg gcaacaagcc tgagtccgat atcctgggtgc acaccgccta cgacgagtcc 3600
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 gtcattccagg atagcaacgg cgagaataag atcaagatgc tgtccggcgg aagcggagga 3720
 tccggaggct ctaccaatct gtccgatatt attgaaaaag agacaggcaa gcaactggtc 3780
 atccaggagt ctatcctgat gctgccagaa gaagtcgaag aagtgatcgg aaacaagccc 3840
 gaaagcgaca tcctgggtcca tactgcctac gacgagagta ccgacgaaaa tgtgatgtta 3900
 ctgacctccg acgcccctga gtataagcca tgggtctctgg tcattccagga ctccaatgga 3960
 gaaaataaga tcaagatgtt aagcggcggc tccaagagaa cagccgacgg ctccgagttc 4020
 gagcccaaga agaagcggaa agtg 4044

<210> 54

<211> 1348

<212> PRT

<213> 人工序列(Artificial Sequence)

<220>

<223> WT-12-AID

<400> 54

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

130	135	140
Thr Gly Gln Leu Leu Lys	Ile Ala Lys Arg Gly Gly Val Thr Ala Val	
145	150	155
Glu Ala Val His Ala Trp Arg Asn Ala Leu Thr Gly Ala Pro Leu Asn		160
	165	170
Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys		175
	180	185
Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp		190
	195	200
His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly		205
	210	220
Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys		225
	230	235
Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn		240
	245	250
Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val		255
	260	265
Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala		270
	275	280
Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu		285
	290	295
Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala		300
	305	310
Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg		315
	320	325
Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val		330
	335	340
Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val		345
	350	355
Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp		360
	365	370
Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu		375
	380	385
Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr		390
	395	400
	405	410
Pro Ala Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala		415
	420	425
Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly		430
	435	440
	445	

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

755	760	765
Gly Arg Pro Ala Leu Asp	Ala Val Lys Lys Gly	Leu Pro His Ala Pro
770	775	780
Ala Leu Ile Lys Arg Thr	Asn Arg Arg Ile Pro	Glu Arg Thr Ser His
785	790	795
Arg Val Ala Asp His	Ala Gln Val Val Arg	Val Leu Gly Phe Phe Gln
805	810	815
Cys His Ser His Pro	Ala Gln Ala Phe Asp	Asp Ala Met Thr Gln Phe
820	825	830
Gly Met Ser Arg His	Gly Leu Leu Gln Leu	Phe Arg Arg Val Gly Val
835	840	845
Thr Glu Leu Glu Ala	Arg Ser Gly Thr Leu	Pro Pro Ala Ser Gln Arg
850	855	860
Trp Asp Arg Ile Leu	Gln Ala Ser Gly Met	Lys Arg Ala Lys Pro Ser
865	870	875
Pro Thr Ser Thr Gln	Thr Pro Asp Gln Ala	Ser Leu His Ala Phe Ala
885	890	895
Asp Ser Leu Glu Arg	Asp Leu Asp Ala Pro	Ser Pro Met His Glu Gly
900	905	910
Asp Gln Thr Arg Ala	Ser Ala Ser Ala Ser	Pro Lys Lys Lys Arg Lys
915	920	925
Val Glu Ala Ser Met	Thr Asp Ala Glu Tyr	Val Arg Ile His Glu Lys
930	935	940
Leu Asp Ile Tyr Thr	Phe Lys Lys Gln Phe	Phe Asn Asn Lys Lys Ser
945	950	955
Val Ser His Arg Cys	Tyr Val Leu Phe Glu	Leu Lys Arg Arg Gly Glu
965	970	975
Arg Arg Ala Cys Phe	Trp Gly Tyr Ala Val	Asn Lys Pro Gln Ser Gly
980	985	990
Thr Glu Arg Gly Ile	His Ala Glu Ile Phe	Ser Ile Arg Lys Val Glu
995	1000	1005
Glu Tyr Leu Arg Asp	Asn Pro Gly Gln Phe	Thr Ile Asn Trp Tyr
1010	1015	1020
Ser Ser Trp Ser Pro	Cys Ala Asp Cys Ala	Glu Lys Ile Leu Glu
1025	1030	1035
Trp Tyr Asn Gln Glu	Leu Arg Gly Asn Gly	His Thr Leu Lys Ile
1040	1045	1050
Trp Ala Cys Lys Leu	Tyr Tyr Glu Lys Asn	Ala Arg Asn Gln Ile
1055	1060	1065

Gly Leu Trp Asn Leu Arg Asp Asn Gly Val Gly Leu Asn Val Met		
1070	1075	1080
Val Ser Glu His Tyr Gln Cys Cys Arg Lys Ile Phe Ile Gln Ser		
1085	1090	1095
Ser His Asn Gln Leu Asn Glu Asn Arg Trp Leu Glu Lys Thr Leu		
1100	1105	1110
Lys Arg Ala Glu Lys Trp Arg Ser Glu Leu Ser Ile Met Ile Gln		
1115	1120	1125
Val Lys Ile Leu His Thr Thr Lys Ser Pro Ala Val Gly Ser Gly		
1130	1135	1140
Gly Ser Gly Gly Ser Gly Gly Ser Thr Asn Leu Ser Asp Ile Ile		
1145	1150	1155
Glu Lys Glu Thr Gly Lys Gln Leu Val Ile Gln Glu Ser Ile Leu		
1160	1165	1170
Met Leu Pro Glu Glu Val Glu Glu Val Ile Gly Asn Lys Pro Glu		
1175	1180	1185
Ser Asp Ile Leu Val His Thr Ala Tyr Asp Glu Ser Thr Asp Glu		
1190	1195	1200
Asn Val Met Leu Leu Thr Ser Asp Ala Pro Glu Tyr Lys Pro Trp		
1205	1210	1215
Ala Leu Val Ile Gln Asp Ser Asn Gly Glu Asn Lys Ile Lys Met		
1220	1225	1230
Leu Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Thr Asn Leu Ser		
1235	1240	1245
Asp Ile Ile Glu Lys Glu Thr Gly Lys Gln Leu Val Ile Gln Glu		
1250	1255	1260
Ser Ile Leu Met Leu Pro Glu Glu Val Glu Glu Val Ile Gly Asn		
1265	1270	1275
Lys Pro Glu Ser Asp Ile Leu Val His Thr Ala Tyr Asp Glu Ser		
1280	1285	1290
Thr Asp Glu Asn Val Met Leu Leu Thr Ser Asp Ala Pro Glu Tyr		
1295	1300	1305
Lys Pro Trp Ala Leu Val Ile Gln Asp Ser Asn Gly Glu Asn Lys		
1310	1315	1320
Ile Lys Met Leu Ser Gly Gly Ser Lys Arg Thr Ala Asp Gly Ser		
1325	1330	1335
Glu Phe Glu Pro Lys Lys Lys Arg Lys Val		
1340	1345	

<210> 55

<211> 4044

<212> DNA

<213> 人工序列(Artificial Sequence)

<220>

<223> WT-12-AID-NC

<400> 55

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gtagatttga	gaactttggg	atattcacag	cagcagcagg	aaaagatcaa	gcccaaagtg	180
aggtcgacag	tcgcgcagca	tcacgaagcg	ctggtgggtc	atgggtttac	acatgcccac	240
atcgtagcct	tgtcgcagca	ccctgcagcc	cttggcacgg	tcgccgtcaa	gtaccaggac	300
atgattgcgg	cgttgccgga	agccacacat	gaggcgatcg	tcggtgtggg	gaaacagtgg	360
agcggagccc	gagcgcttga	ggccctgttg	acggtcgcgg	gagagctgag	agggcctccc	420
cttcagctgg	acacgggcca	gttgctgaag	atcgcaagc	ggggaggagt	cacggcggtc	480
gaggcggtac	acgcgtggcg	caatgcgctc	acgggagcac	ccctcaacct	gacccccgac	540
caggttgtcg	ctattgctag	taacggcgga	ggcaaacagg	cgctggaaac	agttcagcgc	600
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caagcccacg	gcctgacccc	ggaccagggtg	gttgcaatcg	cgtcacacga	tgggggaaag	780
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<210> 56

<211> 1348

<212> PRT

<213> 人工序列(Artificial Sequence)

<220>

<223> WT-12-AID-NC

<400> 56

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

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Ser	Asn	Asn	Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu	
290				295				300								
Pro	Val	Leu	Cys	Gln	Asp	His	Gly	Leu	Thr	Pro	Asp	Gln	Val	Val	Ala	
305				310				315				320				
Ile	Ala	Ser	His	Asp	Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg	
				325				330				335				
Leu	Leu	Pro	Val	Leu	Cys	Gln	Asp	His	Gly	Leu	Thr	Pro	Glu	Gln	Val	
				340				345				350				
Val	Ala	Ile	Ala	Ser	Asn	Asn	Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val	
355				360				365								
Gln	Arg	Leu	Leu	Pro	Val	Leu	Cys	Gln	Ala	His	Gly	Leu	Thr	Pro	Asp	
370				375				380								
Gln	Val	Val	Ala	Ile	Ala	Ser	Asn	Gly	Gly	Gly	Lys	Gln	Ala	Leu	Glu	
385				390				395				400				
Thr	Val	Gln	Arg	Leu	Leu	Pro	Val	Leu	Cys	Gln	Ala	His	Gly	Leu	Thr	
				405				410				415				
Pro	Ala	Gln	Val	Val	Ala	Ile	Ala	Ser	Asn	Ile	Gly	Gly	Lys	Gln	Ala	
420				425				430								
Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu	Pro	Val	Leu	Cys	Gln	Asp	His	Gly	
435				440				445								
Leu	Thr	Pro	Asp	Gln	Val	Val	Ala	Ile	Ala	Ser	Asn	Gly	Gly	Gly	Lys	
450				455				460								
Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu	Pro	Val	Leu	Cys	Gln	Asp	
465				470				475				480				
His	Gly	Leu	Thr	Pro	Glu	Gln	Val	Val	Ala	Ile	Ala	Ser	Asn	Ile	Gly	
				485				490				495				
Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu	Pro	Val	Leu	Cys	
500				505				510								
Gln	Ala	His	Gly	Leu	Thr	Pro	Asp	Gln	Val	Val	Ala	Ile	Ala	Ser	Asn	
515				520				525								
Asn	Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu	Pro	Val	
530				535				540								
Leu	Cys	Gln	Ala	His	Gly	Leu	Thr	Pro	Ala	Gln	Val	Val	Ala	Ile	Ala	
545				550				555				560				
Ser	Asn	Gly	Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu	
				565				570				575				
Pro	Val	Leu	Cys	Gln	Asp	His	Gly	Leu	Thr	Pro	Asp	Gln	Val	Val	Ala	
580				585				590								
Ile	Ala	Ser	His	Asp	Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg	

595	600	605
Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val		
610	615	620
Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val		
625	630	635
Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp		
645	650	655
Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu		
660	665	670
Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr		
675	680	685
Pro Ala Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala		
690	695	700
Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly		
705	710	715
Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Arg		
725	730	735
Pro Ala Leu Glu Ser Ile Val Ala Gln Leu Ser Arg Pro Asp Pro Ala		
740	745	750
Leu Ala Ala Leu Thr Asn Asp His Leu Val Ala Leu Ala Cys Leu Gly		
755	760	765
Gly Arg Pro Ala Leu Asp Ala Val Lys Lys Gly Leu Pro His Ala Pro		
770	775	780
Ala Leu Ile Lys Arg Thr Asn Arg Arg Ile Pro Glu Arg Thr Ser His		
785	790	795
Arg Val Ala Asp His Ala Gln Val Val Arg Val Leu Gly Phe Phe Gln		
805	810	815
Cys His Ser His Pro Ala Gln Ala Phe Asp Asp Ala Met Thr Gln Phe		
820	825	830
Gly Met Ser Arg His Gly Leu Leu Gln Leu Phe Arg Arg Val Gly Val		
835	840	845
Thr Glu Leu Glu Ala Arg Ser Gly Thr Leu Pro Pro Ala Ser Gln Arg		
850	855	860
Trp Asp Arg Ile Leu Gln Ala Ser Gly Met Lys Arg Ala Lys Pro Ser		
865	870	875
Pro Thr Ser Thr Gln Thr Pro Asp Gln Ala Ser Leu His Ala Phe Ala		
885	890	895
Asp Ser Leu Glu Arg Asp Leu Asp Ala Pro Ser Pro Met His Glu Gly		
900	905	910

Asp Gln Thr Arg Ala Ser Ala Ser Ala Ser Pro Lys Lys Lys Arg Lys		
915	920	925
Val Glu Ala Ser Met Thr Asp Ala Glu Tyr Val Arg Ile His Glu Lys		
930	935	940
Leu Asp Ile Tyr Thr Phe Lys Lys Gln Phe Phe Asn Asn Lys Lys Ser		
945	950	955
Val Ser His Arg Cys Tyr Val Leu Phe Glu Leu Lys Arg Arg Gly Glu		
	965	970
Arg Arg Ala Cys Phe Trp Gly Tyr Ala Val Asn Lys Pro Gln Ser Gly		
	980	985
Thr Glu Arg Gly Ile His Ala Glu Ile Phe Ser Ile Arg Lys Val Glu		
	995	1000
Glu Tyr Leu Arg Asp Asn Pro Gly Gln Phe Thr Ile Asn Trp Tyr		
1010	1015	1020
Ser Ser Trp Ser Pro Cys Ala Asp Cys Ala Glu Lys Ile Leu Glu		
1025	1030	1035
Trp Tyr Asn Gln Glu Leu Arg Gly Asn Gly His Thr Leu Lys Ile		
1040	1045	1050
Trp Ala Cys Lys Leu Tyr Tyr Glu Lys Asn Ala Arg Asn Gln Ile		
1055	1060	1065
Gly Leu Trp Asn Leu Arg Asp Asn Gly Val Gly Leu Asn Val Met		
1070	1075	1080
Val Ser Glu His Tyr Gln Cys Cys Arg Lys Ile Phe Ile Gln Ser		
1085	1090	1095
Ser His Asn Gln Leu Asn Glu Asn Arg Trp Leu Glu Lys Thr Leu		
1100	1105	1110
Lys Arg Ala Glu Lys Trp Arg Ser Glu Leu Ser Ile Met Ile Gln		
1115	1120	1125
Val Lys Ile Leu His Thr Thr Lys Ser Pro Ala Val Gly Ser Gly		
1130	1135	1140
Gly Ser Gly Gly Ser Gly Gly Ser Thr Asn Leu Ser Asp Ile Ile		
1145	1150	1155
Glu Lys Glu Thr Gly Lys Gln Leu Val Ile Gln Glu Ser Ile Leu		
1160	1165	1170
Met Leu Pro Glu Glu Val Glu Glu Val Ile Gly Asn Lys Pro Glu		
1175	1180	1185
Ser Asp Ile Leu Val His Thr Ala Tyr Asp Glu Ser Thr Asp Glu		
1190	1195	1200
Asn Val Met Leu Leu Thr Ser Asp Ala Pro Glu Tyr Lys Pro Trp		

1205	1210	1215
Ala Leu Val Ile Gln Asp Ser Asn Gly Glu Asn Lys Ile Lys Met		
1220	1225	1230
Leu Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Thr Asn Leu Ser		
1235	1240	1245
Asp Ile Ile Glu Lys Glu Thr Gly Lys Gln Leu Val Ile Gln Glu		
1250	1255	1260
Ser Ile Leu Met Leu Pro Glu Glu Val Glu Glu Val Ile Gly Asn		
1265	1270	1275
Lys Pro Glu Ser Asp Ile Leu Val His Thr Ala Tyr Asp Glu Ser		
1280	1285	1290
Thr Asp Glu Asn Val Met Leu Leu Thr Ser Asp Ala Pro Glu Tyr		
1295	1300	1305
Lys Pro Trp Ala Leu Val Ile Gln Asp Ser Asn Gly Glu Asn Lys		
1310	1315	1320
Ile Lys Met Leu Ser Gly Gly Ser Lys Arg Thr Ala Asp Gly Ser		
1325	1330	1335
Glu Phe Glu Pro Lys Lys Lys Arg Lys Val		
1340	1345	

<210> 57

<211> 3699

<212> DNA

<213> 人工序列(Artificial Sequence)

<220>

<223> 63-12-AID

<400> 57

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cgagtggcag	gttccgctag	ccccaagaag	aagagaaagg	tggaggccag	catgaccgac	2460
gccgagtatg	tgcggatcca	cgagaagctg	gatatctaca	cettcaagaa	gcagttcttt	2520
aacaataaga	agtcctgtgc	tcacagatgc	tatgtgctgt	tcgagctgaa	gcggagagga	2580
gagaggcgcg	catgtttttg	gggctacgcc	gtgaataagc	cacagagcgg	aaccgagagg	2640
ggaatccacg	ccgagatctt	ctccatcagg	aaagtggagg	agtatctgcg	cgacaaccct	2700
ggccagttta	caatcaattg	gtacagctcc	tggagcccat	gcgccgattg	tgccgagaag	2760
atcctggagt	ggtataacca	ggagctgaga	ggcaatggcc	acaccctgaa	gatctgggcc	2820
tgcaagctgt	actatgagaa	gaacgcccgg	aatcagatcg	gcctgtggaa	cctgagagac	2880
aatggcgtag	gcctgaacgt	gatggtgtct	gagcactacc	agtgtcttag	gaagatcttc	2940
atccagtcta	gccacaatca	gctgaacgag	aatcgctggc	tggagaagac	actgaagagg	3000
gccgagaagt	ggcgcagcga	gctgtccatc	atgatccagg	tgaagatcct	gcacaccaca	3060
aagagcccag	cagtgggatc	cggaggatct	ggaggaagcg	gaggatccac	caacctgtct	3120

gacatcatcg agaaggagac aggcaagcag ctggtcatcc aggagagcat cctgatgctg 3180
 cccgaggagg tggaggaagt gatcggcaac aagcctgagt ccgatatcct ggtgcacacc 3240
 gcctacgacg agtccacaga tgagaatgtg atgctgctga cctctgacgc cccagagtat 3300
 aagccctggg ccctggtcat ccaggatagc aacggcgaga ataagatcaa gatgctgtcc 3360
 ggcggaagcg gaggatccgg aggctctacc aatctgtccg atattattga aaaagagaca 3420
 ggcaagcaac tggatcatcca ggagtctatc ctgatgctgc cagaagaagt cgaagaagtg 3480
 atcggaaca agcccgaag cgacatcctg gtccatactg cctacgacga gaggaccgac 3540
 gaaaatgtga tgttactgac ctccgacgcc cctgagtata agccatgggc tctggtcatc 3600
 caggactcca atggagaaaa taagatcaag atgttaagcg gcggctccaa gagaacagcc 3660
 gacggctccg agttcgagcc caagaagaag cggaaagtg 3699

<210> 58

<211> 1233

<212> PRT

<213> 人工序列(Artificial Sequence)

<220>

<223> 63-12-AID

<400> 58

Met Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His Asp Ile Asp
 1 5 10 15

Tyr Lys Asp Asp Asp Asp Lys Met Ala Pro Lys Lys Lys Arg Lys Val
 20 25 30

Gly Ile His Gly Val Pro Ala Ala Val Asp Leu Arg Thr Leu Gly Tyr
 35 40 45

Ser Gln Gln Gln Gln Glu Lys Ile Lys Pro Lys Val Arg Ser Thr Val
 50 55 60

Ala Gln His His Glu Ala Leu Val Gly His Gly Phe Thr His Ala His
 65 70 75 80

Ile Val Ala Leu Ser Gln His Pro Ala Ala Leu Gly Thr Val Ala Val
 85 90 95

Lys Tyr Gln Asp Met Ile Ala Ala Leu Pro Glu Ala Thr His Glu Ala
 100 105 110

Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg Ala Leu Glu Ala
 115 120 125

Leu Leu Thr Val Ala Gly Glu Leu Arg Gly Pro Pro Leu Gln Leu Asp
 130 135 140

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

Glu Ala Val His Ala Trp Arg Asn Ala Leu Thr Gly Ala Pro Leu Asn
 165 170 175

Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys			
180	185	190	
Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp			
195	200	205	
His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly			
210	215	220	
Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys			
225	230	235	240
Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn			
245	250	255	
Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val			
260	265	270	
Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala			
275	280	285	
Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu			
290	295	300	
Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala			
305	310	315	320
Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg			
325	330	335	
Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val			
340	345	350	
Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val			
355	360	365	
Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp			
370	375	380	
Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu			
385	390	395	400
Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr			
405	410	415	
Pro Ala Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala			
420	425	430	
Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly			
435	440	445	
Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys			
450	455	460	
Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp			
465	470	475	480
His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Asn Gly			

	485		490		495
Gly Lys Gln Ala Leu Glu Thr Val	Gln Arg Leu Leu Pro Val Leu Cys				
500	505	510			
Gln Ala His Gly Leu Thr Pro Asp	Gln Val Val Ala Ile Ala Ser Asn				
515	520	525			
Asn Gly Gly Lys Gln Ala Leu Glu Thr Val	Gln Arg Leu Leu Pro Val				
530	535	540			
Leu Cys Gln Ala His Gly Leu Thr Pro Ala	Gln Val Val Ala Ile Ala				
545	550	555	560		
Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val	Gln Arg Leu Leu				
565	570	575			
Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp	Gln Val Val Ala				
580	585	590			
Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val	Gln Arg				
595	600	605			
Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro	Glu Gln Val				
610	615	620			
Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val					
625	630	635	640		
Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp					
645	650	655			
Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu					
660	665	670			
Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr					
675	680	685			
Pro Ala Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala					
690	695	700			
Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly					
705	710	715	720		
Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Arg					
725	730	735			
Pro Ala Leu Glu Ser Ile Val Ala Gln Leu Ser Arg Pro Asp Pro Ala					
740	745	750			
Leu Ala Ala Leu Thr Asn Asp His Leu Val Ala Leu Ala Cys Leu Gly					
755	760	765			
Gly Arg Pro Ala Leu Asp Ala Val Lys Lys Gly Leu Pro His Ala Pro					
770	775	780			
Ala Leu Ile Lys Arg Thr Asn Arg Arg Ile Pro Glu Arg Thr Ser His					
785	790	795	800		

Arg Val Ala Gly Ser Ala Ser Pro Lys Lys Lys Arg Lys Val Glu Ala		
805	810	815
Ser Met Thr Asp Ala Glu Tyr Val Arg Ile His Glu Lys Leu Asp Ile		
820	825	830
Tyr Thr Phe Lys Lys Gln Phe Phe Asn Asn Lys Lys Ser Val Ser His		
835	840	845
Arg Cys Tyr Val Leu Phe Glu Leu Lys Arg Arg Gly Glu Arg Arg Ala		
850	855	860
Cys Phe Trp Gly Tyr Ala Val Asn Lys Pro Gln Ser Gly Thr Glu Arg		
865	870	875
Gly Ile His Ala Glu Ile Phe Ser Ile Arg Lys Val Glu Glu Tyr Leu		
885	890	895
Arg Asp Asn Pro Gly Gln Phe Thr Ile Asn Trp Tyr Ser Ser Trp Ser		
900	905	910
Pro Cys Ala Asp Cys Ala Glu Lys Ile Leu Glu Trp Tyr Asn Gln Glu		
915	920	925
Leu Arg Gly Asn Gly His Thr Leu Lys Ile Trp Ala Cys Lys Leu Tyr		
930	935	940
Tyr Glu Lys Asn Ala Arg Asn Gln Ile Gly Leu Trp Asn Leu Arg Asp		
945	950	955
Asn Gly Val Gly Leu Asn Val Met Val Ser Glu His Tyr Gln Cys Cys		
965	970	975
Arg Lys Ile Phe Ile Gln Ser Ser His Asn Gln Leu Asn Glu Asn Arg		
980	985	990
Trp Leu Glu Lys Thr Leu Lys Arg Ala Glu Lys Trp Arg Ser Glu Leu		
995	1000	1005
Ser Ile Met Ile Gln Val Lys Ile Leu His Thr Thr Lys Ser Pro		
1010	1015	1020
Ala Val Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Thr Asn		
1025	1030	1035
Leu Ser Asp Ile Ile Glu Lys Glu Thr Gly Lys Gln Leu Val Ile		
1040	1045	1050
Gln Glu Ser Ile Leu Met Leu Pro Glu Glu Val Glu Glu Val Ile		
1055	1060	1065
Gly Asn Lys Pro Glu Ser Asp Ile Leu Val His Thr Ala Tyr Asp		
1070	1075	1080
Glu Ser Thr Asp Glu Asn Val Met Leu Leu Thr Ser Asp Ala Pro		
1085	1090	1095
Glu Tyr Lys Pro Trp Ala Leu Val Ile Gln Asp Ser Asn Gly Glu		

1100	1105	1110
Asn Lys Ile Lys Met Leu Ser Gly Gly Ser Gly Gly Ser Gly Gly		
1115	1120	1125
Ser Thr Asn Leu Ser Asp Ile Ile Glu Lys Glu Thr Gly Lys Gln		
1130	1135	1140
Leu Val Ile Gln Glu Ser Ile Leu Met Leu Pro Glu Glu Val Glu		
1145	1150	1155
Glu Val Ile Gly Asn Lys Pro Glu Ser Asp Ile Leu Val His Thr		
1160	1165	1170
Ala Tyr Asp Glu Ser Thr Asp Glu Asn Val Met Leu Leu Thr Ser		
1175	1180	1185
Asp Ala Pro Glu Tyr Lys Pro Trp Ala Leu Val Ile Gln Asp Ser		
1190	1195	1200
Asn Gly Glu Asn Lys Ile Lys Met Leu Ser Gly Gly Ser Lys Arg		
1205	1210	1215
Thr Ala Asp Gly Ser Glu Phe Glu Pro Lys Lys Lys Arg Lys Val		
1220	1225	1230

<210> 59

<211> 3699

<212> DNA

<213> 人工序列(Artificial Sequence)

<220>

<223> 63-12-AID-NC

<400> 59

atggactata aggaccacga cggagactac aaggatcatg atattgatta caaagacgat	60
gacgataaga tggccccaaa gaagaagcgg aaggtcggta tccacggagt cccagcagcc	120
gtagatttga gaactttggg atattcacag cagcagcagg aaaagatcaa gccc aaagtg	180
aggtcgacag tcgcgacagca tcacgaagcg ctgggtgggtc atgggtttac acatgcccac	240
atcgtagcct tgtcgacagca ccctgcagcc cttggcacgg tcgccgtcaa gtaccaggac	300
atgattgcgg cgttgccgga agccacacat gaggcgatcg tcggtgtggg gaaacagtgg	360
agcggagccc gagcgcttga ggccctgttg acggtcgcgg gagagctgag agggcctccc	420
cttcagctgg acacgggcca gttgctgaag atcgcgaaag ggggaggagt cacggcgggtc	480
gaggcggtac acgcgtggcg caatgcgctc acgggagcac ccctcaacct gacccccgac	540
caggttgtcg ctattgctag taacggcgga ggcaaacagg cgctggaaac agttcagcgc	600
ctcttgccgg tcttgtgtca ggaccacggc ctgaccccag aacaagttgt cgcgattgca	660
agcaacaacg gaggcaaaca agccttagaa acagtccaga gattgttgcc ggtgctgtgc	720
caagcccacg gcctgacccc ggaccaggtg gttgcaatcg cgtcacacga tgggggaaag	780
caggccctag aaaccgttca gcgactcctg cccgtcctgt gccaggccca cggcctgacc	840
ccagcccaag ttgtcgcgat tgcaagcaac aacggaggca aacaagcctt agaaacagtc	900

cagagattgt	tgccggtgct	gtgccaagac	cacggcctga	ccccggacca	ggtggttgca	960
atcgcgtcac	acgatggggg	aaagcaggcc	ctagaaaccg	ttcagcgact	cctgccccgtc	1020
ctgtgccagg	accacggcct	gaccccagaa	caagttgtcg	cgattgcaag	caacaacgga	1080
ggcaaacaag	ccttagaaac	agtccagaga	ttgttgccgg	tgctgtgcca	agccccacggc	1140
ctgacccccg	accaggttgt	cgctattgct	agtaacggcg	gaggcaaaca	ggcgctggaa	1200
acagttcagc	gcctcttgcc	ggtcttgtgt	caggccccacg	gcctgacccc	agcccaggtt	1260
gtggccatcg	ccagcaacat	aggtggcaag	caggccctcg	aaaccgtcca	gagactgtta	1320
ccggttctct	gccaggacca	cggcctgacc	cccgaccagg	ttgtcgctat	tgctagtaac	1380
ggcggaggca	aacaggcgct	ggaaacagtt	cagcgctctt	tgccggtctt	gtgtcaggac	1440
cacggcctga	ccccagaaca	ggttgtggcc	atcgccagca	acataggtgg	caagcaggcc	1500
ctcgaaccg	tccagagact	gttaccggtt	ctctgccagg	cccacggcct	gaccccagac	1560
caagttgtcg	cgattgcaag	caacaacgga	ggcaaacaag	ccttagaaac	agtccagaga	1620
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cagagattgt	tgccggtgct	gtgccaagcc	cacggcctga	ccccggacca	ggtggttgca	1980
atcgcgtcac	acgatggggg	aaagcaggcc	ctagaaaccg	ttcagcgact	cctgccccgtc	2040
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ggcaaacaag	ccttagaaac	agtccagaga	ttgttgccgg	tgctgtgcca	agaccacggc	2160
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tcaatcgtag	cccagctttc	gaggccggac	cccgcgtggg	ccgcactcac	taatgatcat	2280
cttgtagcgc	tggcctgcct	cggcggacga	cccgccttgg	atgcggtgaa	gaaggggctc	2340
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cgagtggcag	gttccgctag	ccccaagaag	aagagaaagg	tggaggccag	catgaccgac	2460
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gccgagaagt	ggcgcagcga	gctgtccatc	atgatccagg	tgaagatcct	gcacaccaca	3060
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gacatcatcg	agaaggagac	aggcaagcag	ctggtcatcc	aggagagcat	cctgatgctg	3180
cccgaggagg	tggagggaagt	gatcggcaac	aagcctgagt	ccgatatcct	ggtgcacacc	3240

gcctacgacg agtccacaga tgagaatgtg atgctgctga cctctgacgc cccagagtat 3300
aagccctggg ccctgggtcat ccaggatagc aacggcgaga ataagatcaa gatgctgtcc 3360
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gaaaatgtga tgttactgac ctccgacgcc cctgagtata agccatgggc tctgggtcatc 3600
caggactcca atggagaaaa taagatcaag atgttaagcg gcggctccaa gagaacagcc 3660
gacggctccg agttcgagcc caagaagaag cggaaagtg 3699

<210> 60

<211> 1233

<212> PRT

<213> 人工序列(Artificial Sequence)

<220>

<223> 63-12-AID-NC

<400> 60

Met Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His Asp Ile Asp

1 5 10 15

Tyr Lys Asp Asp Asp Asp Lys Met Ala Pro Lys Lys Lys Arg Lys Val

20 25 30

Gly Ile His Gly Val Pro Ala Ala Val Asp Leu Arg Thr Leu Gly Tyr

35 40 45

Ser Gln Gln Gln Gln Glu Lys Ile Lys Pro Lys Val Arg Ser Thr Val

50 55 60

Ala Gln His His Glu Ala Leu Val Gly His Gly Phe Thr His Ala His

65 70 75 80

Ile Val Ala Leu Ser Gln His Pro Ala Ala Leu Gly Thr Val Ala Val

85 90 95

Lys Tyr Gln Asp Met Ile Ala Ala Leu Pro Glu Ala Thr His Glu Ala

100 105 110

Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg Ala Leu Glu Ala

115 120 125

Leu Leu Thr Val Ala Gly Glu Leu Arg Gly Pro Pro Leu Gln Leu Asp

130 135 140

Thr Gly Gln Leu Leu Lys Ile Ala Lys Arg Gly Gly Val Thr Ala Val

145 150 155 160

Glu Ala Val His Ala Trp Arg Asn Ala Leu Thr Gly Ala Pro Leu Asn

165 170 175

Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys

180 185 190

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp		
195	200	205
His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Asn Gly		
210	215	220
Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys		
225	230	235
Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser His		
245	250	255
Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val		
260	265	270
Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala		
275	280	285
Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu		
290	295	300
Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala		
305	310	315
Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg		
325	330	335
Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val		
340	345	350
Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val		
355	360	365
Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp		
370	375	380
Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu		
385	390	395
Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr		
405	410	415
Pro Ala Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala		
420	425	430
Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly		
435	440	445
Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys		
450	455	460
Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp		
465	470	475
His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly		
485	490	495
Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys		

500	505	510
Gln Ala His Gly Leu Thr Pro Asp	Gln Val Val Ala Ile Ala Ser Asn	
515	520	525
Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val		
530	535	540
Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala		
545	550	555
Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu		
565	570	575
Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala		
580	585	590
Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg		
595	600	605
Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val		
610	615	620
Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val		
625	630	635
Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp		
645	650	655
Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu		
660	665	670
Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr		
675	680	685
Pro Ala Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala		
690	695	700
Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly		
705	710	715
Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Arg		
725	730	735
Pro Ala Leu Glu Ser Ile Val Ala Gln Leu Ser Arg Pro Asp Pro Ala		
740	745	750
Leu Ala Ala Leu Thr Asn Asp His Leu Val Ala Leu Ala Cys Leu Gly		
755	760	765
Gly Arg Pro Ala Leu Asp Ala Val Lys Lys Gly Leu Pro His Ala Pro		
770	775	780
Ala Leu Ile Lys Arg Thr Asn Arg Arg Ile Pro Glu Arg Thr Ser His		
785	790	795
Arg Val Ala Gly Ser Ala Ser Pro Lys Lys Lys Arg Lys Val Glu Ala		
805	810	815

Ser Met Thr Asp Ala Glu Tyr Val Arg Ile His Glu Lys Leu Asp Ile		
820	825	830
Tyr Thr Phe Lys Lys Gln Phe Phe Asn Asn Lys Lys Ser Val Ser His		
835	840	845
Arg Cys Tyr Val Leu Phe Glu Leu Lys Arg Arg Gly Glu Arg Arg Ala		
850	855	860
Cys Phe Trp Gly Tyr Ala Val Asn Lys Pro Gln Ser Gly Thr Glu Arg		
865	870	875
Gly Ile His Ala Glu Ile Phe Ser Ile Arg Lys Val Glu Glu Tyr Leu		
885	890	895
Arg Asp Asn Pro Gly Gln Phe Thr Ile Asn Trp Tyr Ser Ser Trp Ser		
900	905	910
Pro Cys Ala Asp Cys Ala Glu Lys Ile Leu Glu Trp Tyr Asn Gln Glu		
915	920	925
Leu Arg Gly Asn Gly His Thr Leu Lys Ile Trp Ala Cys Lys Leu Tyr		
930	935	940
Tyr Glu Lys Asn Ala Arg Asn Gln Ile Gly Leu Trp Asn Leu Arg Asp		
945	950	955
Asn Gly Val Gly Leu Asn Val Met Val Ser Glu His Tyr Gln Cys Cys		
965	970	975
Arg Lys Ile Phe Ile Gln Ser Ser His Asn Gln Leu Asn Glu Asn Arg		
980	985	990
Trp Leu Glu Lys Thr Leu Lys Arg Ala Glu Lys Trp Arg Ser Glu Leu		
995	1000	1005
Ser Ile Met Ile Gln Val Lys Ile Leu His Thr Thr Lys Ser Pro		
1010	1015	1020
Ala Val Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Thr Asn		
1025	1030	1035
Leu Ser Asp Ile Ile Glu Lys Glu Thr Gly Lys Gln Leu Val Ile		
1040	1045	1050
Gln Glu Ser Ile Leu Met Leu Pro Glu Glu Val Glu Glu Val Ile		
1055	1060	1065
Gly Asn Lys Pro Glu Ser Asp Ile Leu Val His Thr Ala Tyr Asp		
1070	1075	1080
Glu Ser Thr Asp Glu Asn Val Met Leu Leu Thr Ser Asp Ala Pro		
1085	1090	1095
Glu Tyr Lys Pro Trp Ala Leu Val Ile Gln Asp Ser Asn Gly Glu		
1100	1105	1110
Asn Lys Ile Lys Met Leu Ser Gly Gly Ser Gly Gly Ser Gly Gly		

1115	1120	1125
Ser Thr Asn Leu Ser Asp Ile	Ile Glu Lys Glu Thr	Gly Lys Gln
1130	1135	1140
Leu Val Ile Gln Glu Ser Ile	Leu Met Leu Pro Glu	Glu Val Glu
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Glu Val Ile Gly Asn Lys Pro	Glu Ser Asp Ile Leu	Val His Thr
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Ala Tyr Asp Glu Ser Thr Asp	Glu Asn Val Met Leu	Leu Thr Ser
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Asp Ala Pro Glu Tyr Lys Pro	Trp Ala Leu Val Ile	Gln Asp Ser
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Asn Gly Glu Asn Lys Ile Lys	Met Leu Ser Gly Gly	Ser Lys Arg
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<211> 3690

<212> DNA

<213> 人工序列(Artificial Sequence)

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<223> 47-12-AID

<400> 61

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<213> 人工序列(Artificial Sequence)

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<223> 47-12-AID

<400> 62

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           35           40           45
Ser Pro Ala Ala Gln Val Asp Leu Arg Thr Leu Gly Tyr Ser Gln Gln
           50           55           60
Gln Gln Glu Lys Ile Lys Pro Lys Val Arg Ser Thr Val Ala Gln His
65           70           75           80
His Glu Ala Leu Val Gly His Gly Phe Thr His Ala His Ile Val Ala
           85           90           95
Leu Ser Gln His Pro Ala Ala Leu Gly Thr Val Ala Val Thr Tyr Gln
           100          105          110
His Ile Ile Thr Ala Leu Pro Glu Ala Thr His Glu Asp Ile Val Gly
           115          120          125
Val Gly Lys Gln Trp Ser Gly Ala Arg Ala Leu Glu Ala Leu Leu Thr
           130          135          140
Asp Ala Gly Glu Leu Arg Gly Pro Pro Leu Gln Leu Asp Thr Gly Gln
145          150          155          160
Leu Val Lys Ile Ala Lys Arg Gly Gly Val Thr Ala Met Glu Ala Val
           165          170          175
His Ala Ser Arg Asn Ala Leu Thr Gly Ala Pro Leu Asn Leu Thr Pro
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Asp Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu
           195          200          205

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Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln		
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Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser		
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Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro		
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Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile		
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Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val		
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Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln		
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Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro		
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Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu		
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Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val		
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Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln		
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Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr		
705	710	715
Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro		
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Glu Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Arg Pro Ala Leu		
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Glu Ser Ile Val Ala Gln Leu Ser Arg Pro Asp Pro Ala Leu Ala Ala		
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Leu Thr Asn Asp His Leu Val Ala Leu Ala Cys Leu Gly Gly Arg Pro		
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Ala Met Asp Ala Val Lys Lys Gly Leu Pro His Ala Pro Glu Leu Ile		
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Arg Ser Ala Ser Pro Lys Lys Lys Arg Lys Val Glu Ala Ser Met Thr		
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Asp Ala Glu Tyr Val Arg Ile His Glu Lys Leu Asp Ile Tyr Thr Phe		
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Ser Pro Ala Ala Gln Val Asp Leu Arg Thr Leu Gly Tyr Ser Gln Gln
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Gln Gln Glu Lys Ile Lys Pro Lys Val Arg Ser Thr Val Ala Gln His
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His Glu Ala Leu Val Gly His Gly Phe Thr His Ala His Ile Val Ala
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His Ile Ile Thr Ala Leu Pro Glu Ala Thr His Glu Asp Ile Val Gly
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Asp Ala Gly Glu Leu Arg Gly Pro Pro Leu Gln Leu Asp Thr Gly Gln
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Leu Val Lys Ile Ala Lys Arg Gly Gly Val Thr Ala Met Glu Ala Val
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His Ala Ser Arg Asn Ala Leu Thr Gly Ala Pro Leu Asn Leu Thr Pro
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Asp Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu
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Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu
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Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu	Pro	Val	Leu	Cys	Gln
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Ala	His	Gly	Leu	Thr	Pro	Ala	Gln	Val	Val	Ala	Ile	Ala	Ser	Asn	Asn
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Cys	Gln	Asp	His	Gly	Leu	Thr	Pro	Asp	Gln	Val	Val	Ala	Ile	Ala	Ser
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His	Asp	Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu	Pro
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Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu		
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Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser		
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His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro		
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Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu		
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Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val		
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Lys Lys Gln Phe Phe Asn Asn Lys Lys Ser Val Ser His Arg Cys Tyr		
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<211> 1406

<212> PRT

<213> 人工序列(Artificial Sequence)

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<223> BE4-32-WT

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 Glu Leu Arg Lys Glu Thr Cys Leu Leu Tyr Glu Ile Lys Trp Gly Thr
 50 55 60
 Ser His Lys Ile Trp Arg His Ser Ser Lys Asn Thr Thr Lys His Val
 65 70 75 80
 Glu Val Asn Phe Ile Glu Lys Phe Thr Ser Glu Arg His Phe Cys Pro
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 Ser Thr Ser Cys Ser Ile Thr Trp Phe Leu Ser Trp Ser Pro Cys Gly
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 Glu Cys Ser Lys Ala Ile Thr Glu Phe Leu Ser Gln His Pro Asn Val
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 Thr Leu Val Ile Tyr Val Ala Arg Leu Tyr His His Met Asp Gln Gln
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 Asn Arg Gln Gly Leu Arg Asp Leu Val Asn Ser Gly Val Thr Ile Gln
 145 150 155 160
 Ile Met Thr Ala Pro Glu Tyr Asp Tyr Cys Trp Arg Asn Phe Val Asn
 165 170 175
 Tyr Pro Pro Gly Lys Glu Ala His Trp Pro Arg Tyr Pro Pro Leu Trp
 180 185 190
 Met Lys Leu Tyr Ala Leu Glu Leu His Ala Gly Ile Leu Gly Leu Pro
 195 200 205
 Pro Cys Leu Asn Ile Leu Arg Arg Lys Gln Pro Gln Leu Thr Phe Phe
 210 215 220
 Thr Ile Ala Leu Gln Ser Cys His Tyr Gln Arg Leu Pro Pro His Ile
 225 230 235 240
 Leu Trp Ala Thr Gly Leu Lys Ser Gly Gly Ser Ser Gly Gly Ser Ser

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Tyr	Lys	Asp	His	Asp	Ile	Asp	Tyr	Lys	Asp	Asp	Asp	Asp	Lys	Met	Ala
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Pro	Lys	Lys	Lys	Arg	Lys	Val	Gly	Ile	His	Gly	Val	Pro	Ala	Ala	Val
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Pro	Lys	Val	Arg	Ser	Thr	Val	Ala	Gln	His	His	Glu	Ala	Leu	Val	Gly
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His	Gly	Phe	Thr	His	Ala	His	Ile	Val	Ala	Leu	Ser	Gln	His	Pro	Ala
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Gly	Pro	Pro	Leu	Gln	Leu	Asp	Thr	Gly	Gln	Leu	Leu	Lys	Ile	Ala	Lys
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Arg	Gly	Gly	Val	Thr	Ala	Val	Glu	Ala	Val	His	Ala	Trp	Arg	Asn	Ala
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Leu	Pro	Val	Leu	Cys	Gln	Asp	His	Gly	Leu	Thr	Pro	Glu	Gln	Val	Val
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Ala	Ile	Ala	Ser	His	Asp	Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln
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Arg	Leu	Leu	Pro	Val	Leu	Cys	Gln	Ala	His	Gly	Leu	Thr	Pro	Asp	Gln
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Val	Val	Ala	Ile	Ala	Ser	Asn	Ile	Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr
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Val	Gln	Arg	Leu	Leu	Pro	Val	Leu	Cys	Gln	Ala	His	Gly	Leu	Thr	Pro
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Ala Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu		
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Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu		
580	585	590
Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln		
595	600	605
Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His		
610	615	620
Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly		
625	630	635
Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln		
645	650	655
Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Asn		
660	665	670
Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu		
675	680	685
Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser		
690	695	700
His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro		
705	710	715
Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile		
725	730	735
Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu		
740	745	750
Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val		
755	760	765
Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln		
770	775	780
Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln		
785	790	795
Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr		
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Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro		
820	825	830
Ala Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu		
835	840	845
Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu		
850	855	860
Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln		

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Ala Leu Glu Thr Val	Gln Arg Leu Leu Pro	Val Leu Cys Gln Asp His	
	885	890	895
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Lys Gln Ala Leu Glu	Thr Val Gln Arg Leu Leu Pro	Val Leu Cys Gln	
	915	920	925
Ala His Gly Leu Thr	Pro Asp Gln Val Val Ala Ile	Ala Ser Asn Ile	
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Gly Gly Lys Gln Ala	Leu Glu Thr Val Gln Arg Leu Leu Pro	Val Leu	
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Cys Gln Ala His Gly	Leu Thr Pro Ala Gln Val Val Ala Ile	Ala Ser	
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Asn Asn Gly Gly Lys	Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro		
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Val Leu Cys Gln Asp	His Gly Leu Thr Pro Glu Gln Val Val Ala Ile		
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Gln Leu Ser Arg Pro	Asp Pro Ala Leu Ala Ala Leu Thr Asn Asp		
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His Leu Val Ala Leu	Ala Cys Leu Gly Gly Arg Pro Ala Leu Asp		
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Ala Val Lys Lys Gly	Leu Pro His Ala Pro Ala Leu Ile Lys Arg		
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Thr Asn Arg Arg Ile	Pro Glu Arg Thr Ser His Arg Val Ala Asp		
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His Ala Gln Val Val	Arg Val Leu Gly Phe Phe Gln Cys His Ser		
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His Pro Ala Gln Ala	Phe Asp Asp Ala Met Thr Gln Phe Gly Met		
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Ser Arg His Gly Leu	Leu Gln Leu Phe Arg Arg Val Gly Val Thr		
	1115	1120	1125
Glu Leu Glu Ala Arg	Ser Gly Thr Leu Pro Pro Ala Ser Gln Arg		
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Trp Asp Arg Ile Leu	Gln Ala Ser Gly Met Lys Arg Ala Lys Pro		
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Ser Pro Thr Ser Thr	Gln Thr Pro Asp Gln Ala Ser Leu His Ala		
	1160	1165	1170

Phe Ala	Asp Ser Leu Glu Arg	Asp Leu Asp Ala Pro	Ser Pro Met
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His Glu	Gly Asp Gln Thr Arg	Ala Ser Ala Ser Ser	Gly Gly Ser
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Gly Gly	Ser Gly Gly Ser Thr	Asn Leu Ser Asp Ile	Ile Glu Lys
1205	1210	1215	
Glu Thr	Gly Lys Gln Leu Val	Ile Gln Glu Ser Ile	Leu Met Leu
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Pro Glu	Glu Val Glu Glu Val	Ile Gly Asn Lys Pro	Glu Ser Asp
1235	1240	1245	
Ile Leu	Val His Thr Ala Tyr	Asp Glu Ser Thr Asp	Glu Asn Val
1250	1255	1260	
Met Leu	Leu Thr Ser Asp Ala	Pro Glu Tyr Lys Pro	Trp Ala Leu
1265	1270	1275	
Val Ile	Gln Asp Ser Asn Gly	Glu Asn Lys Ile Lys	Met Leu Ser
1280	1285	1290	
Gly Gly	Ser Gly Gly Ser Gly	Gly Ser Thr Asn Leu	Ser Asp Ile
1295	1300	1305	
Ile Glu	Lys Glu Thr Gly Lys	Gln Leu Val Ile Gln	Glu Ser Ile
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Leu Met	Leu Pro Glu Glu Val	Glu Glu Val Ile Gly	Asn Lys Pro
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Glu Ser	Asp Ile Leu Val His	Thr Ala Tyr Asp Glu	Ser Thr Asp
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Glu Asn	Val Met Leu Leu Thr	Ser Asp Ala Pro Glu	Tyr Lys Pro
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Trp Ala	Leu Val Ile Gln Asp	Ser Asn Gly Glu Asn	Lys Ile Lys
1370	1375	1380	
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Arg	Arg	Arg	Ile	Glu	Pro	His	Glu	Phe	Glu	Val	Phe	Phe	Asp	Pro	Arg
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Glu	Leu	Arg	Lys	Glu	Thr	Cys	Leu	Leu	Tyr	Glu	Ile	Lys	Trp	Gly	Thr
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Ser	His	Lys	Ile	Trp	Arg	His	Ser	Ser	Lys	Asn	Thr	Thr	Lys	His	Val
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Glu	Val	Asn	Phe	Ile	Glu	Lys	Phe	Thr	Ser	Glu	Arg	His	Phe	Cys	Pro
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Ser	Thr	Ser	Cys	Ser	Ile	Thr	Trp	Phe	Leu	Ser	Trp	Ser	Pro	Cys	Gly
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Glu	Cys	Ser	Lys	Ala	Ile	Thr	Glu	Phe	Leu	Ser	Gln	His	Pro	Asn	Val
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Thr	Leu	Val	Ile	Tyr	Val	Ala	Arg	Leu	Tyr	His	His	Met	Asp	Gln	Gln
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Asn	Arg	Gln	Gly	Leu	Arg	Asp	Leu	Val	Asn	Ser	Gly	Val	Thr	Ile	Gln
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Ile	Met	Thr	Ala	Pro	Glu	Tyr	Asp	Tyr	Cys	Trp	Arg	Asn	Phe	Val	Asn
				165					170					175	
Tyr	Pro	Pro	Gly	Lys	Glu	Ala	His	Trp	Pro	Arg	Tyr	Pro	Pro	Leu	Trp
				180				185					190		
Met	Lys	Leu	Tyr	Ala	Leu	Glu	Leu	His	Ala	Gly	Ile	Leu	Gly	Leu	Pro
				195				200				205			
Pro	Cys	Leu	Asn	Ile	Leu	Arg	Arg	Lys	Gln	Pro	Gln	Leu	Thr	Phe	Phe
				210				215				220			
Thr	Ile	Ala	Leu	Gln	Ser	Cys	His	Tyr	Gln	Arg	Leu	Pro	Pro	His	Ile
225					230					235					240
Leu	Trp	Ala	Thr	Gly	Leu	Lys	Ser	Gly	Gly	Ser	Ser	Gly	Gly	Ser	Ser
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Gly	Ser	Glu	Thr	Pro	Gly	Thr	Ser	Glu	Ser	Ala	Thr	Pro	Glu	Ser	Ser
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Tyr	Lys	Asp	His	Asp	Ile	Asp	Tyr	Lys	Asp	Asp	Asp	Asp	Lys	Met	Ala
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Pro	Lys	Lys	Lys	Arg	Lys	Val	Gly	Ile	His	Gly	Val	Pro	Ala	Ala	Val

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	325	330	335
Pro Lys Val Arg Ser Thr Val Ala Gln His His Glu Ala Leu Val Gly			
	340	345	350
His Gly Phe Thr His Ala His Ile Val Ala Leu Ser Gln His Pro Ala			
	355	360	365
Ala Leu Gly Thr Val Ala Val Lys Tyr Gln Asp Met Ile Ala Ala Leu			
	370	375	380
Pro Glu Ala Thr His Glu Ala Ile Val Gly Val Gly Lys Gln Trp Ser			
385	390	395	400
Gly Ala Arg Ala Leu Glu Ala Leu Leu Thr Val Ala Gly Glu Leu Arg			
	405	410	415
Gly Pro Pro Leu Gln Leu Asp Thr Gly Gln Leu Leu Lys Ile Ala Lys			
	420	425	430
Arg Gly Gly Val Thr Ala Val Glu Ala Val His Ala Trp Arg Asn Ala			
	435	440	445
Leu Thr Gly Ala Pro Leu Asn Leu Thr Pro Asp Gln Val Val Ala Ile			
	450	455	460
Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu			
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Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val			
	485	490	495
Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln			
	500	505	510
Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln			
	515	520	525
Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr			
	530	535	540
Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro			
545	550	555	560
Ala Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu			
	565	570	575
Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu			
	580	585	590
Thr Pro Asp Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln			
	595	600	605
Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His			
610	615	620	

Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly			
625	630	635	640
Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln			
	645	650	655
Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Gly			
	660	665	670
Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu			
	675	680	685
Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser			
	690	695	700
Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro			
705	710	715	720
Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile			
	725	730	735
Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu			
	740	745	750
Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val			
	755	760	765
Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln			
	770	775	780
Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln			
785	790	795	800
Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr			
	805	810	815
Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro			
	820	825	830
Ala Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu			
	835	840	845
Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu			
	850	855	860
Thr Pro Asp Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln			
865	870	875	880
Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His			
	885	890	895
Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly			
	900	905	910
Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln			
	915	920	925
Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser His Asp			

930	935	940
Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu		
945	950	955
Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser		
965	970	975
Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro		
980	985	990
Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile		
995	1000	1005
Ala Ser Asn Asn Gly Gly Arg Pro Ala Leu Glu Ser Ile Val Ala		
1010	1015	1020
Gln Leu Ser Arg Pro Asp Pro Ala Leu Ala Ala Leu Thr Asn Asp		
1025	1030	1035
His Leu Val Ala Leu Ala Cys Leu Gly Gly Arg Pro Ala Leu Asp		
1040	1045	1050
Ala Val Lys Lys Gly Leu Pro His Ala Pro Ala Leu Ile Lys Arg		
1055	1060	1065
Thr Asn Arg Arg Ile Pro Glu Arg Thr Ser His Arg Val Ala Asp		
1070	1075	1080
His Ala Gln Val Val Arg Val Leu Gly Phe Phe Gln Cys His Ser		
1085	1090	1095
His Pro Ala Gln Ala Phe Asp Asp Ala Met Thr Gln Phe Gly Met		
1100	1105	1110
Ser Arg His Gly Leu Leu Gln Leu Phe Arg Arg Val Gly Val Thr		
1115	1120	1125
Glu Leu Glu Ala Arg Ser Gly Thr Leu Pro Pro Ala Ser Gln Arg		
1130	1135	1140
Trp Asp Arg Ile Leu Gln Ala Ser Gly Met Lys Arg Ala Lys Pro		
1145	1150	1155
Ser Pro Thr Ser Thr Gln Thr Pro Asp Gln Ala Ser Leu His Ala		
1160	1165	1170
Phe Ala Asp Ser Leu Glu Arg Asp Leu Asp Ala Pro Ser Pro Met		
1175	1180	1185
His Glu Gly Asp Gln Thr Arg Ala Ser Ala Ser Ser Gly Gly Ser		
1190	1195	1200
Gly Gly Ser Gly Gly Ser Thr Asn Leu Ser Asp Ile Ile Glu Lys		
1205	1210	1215
Glu Thr Gly Lys Gln Leu Val Ile Gln Glu Ser Ile Leu Met Leu		
1220	1225	1230

Pro Glu	Glu Val	Glu Glu	Val Ile	Gly Asn	Lys Pro	Glu Ser	Asp
1235			1240			1245	
Ile Leu	Val His	Thr Ala	Tyr Asp	Glu Ser	Thr Asp	Glu Asn	Val
1250			1255			1260	
Met Leu	Leu Thr	Ser Asp	Ala Pro	Glu Tyr	Lys Pro	Trp Ala	Leu
1265			1270			1275	
Val Ile	Gln Asp	Ser Asn	Gly Glu	Asn Lys	Ile Lys	Met Leu	Ser
1280			1285			1290	
Gly Gly	Ser Gly	Gly Ser	Gly Gly	Ser Thr	Asn Leu	Ser Asp	Ile
1295			1300			1305	
Ile Glu	Lys Glu	Thr Gly	Lys Gln	Leu Val	Ile Gln	Glu Ser	Ile
1310			1315			1320	
Leu Met	Leu Pro	Glu Glu	Val Glu	Glu Val	Ile Gly	Asn Lys	Pro
1325			1330			1335	
Glu Ser	Asp Ile	Leu Val	His Thr	Ala Tyr	Asp Glu	Ser Thr	Asp
1340			1345			1350	
Glu Asn	Val Met	Leu Leu	Thr Ser	Asp Ala	Pro Glu	Tyr Lys	Pro
1355			1360			1365	
Trp Ala	Leu Val	Ile Gln	Asp Ser	Asn Gly	Glu Asn	Lys Ile	Lys
1370			1375			1380	
Met Leu	Ser Gly	Gly Ser	Lys Arg	Thr Ala	Asp Gly	Ser Glu	Phe
1385			1390			1395	
Glu Pro	Lys Lys	Lys Arg	Lys Val				
1400			1405				

<210> 97

<211> 3873

<212> DNA

<213> 人工序列(Artificial Sequence)

<220>

<223> BE4-32-63

<400> 97

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aagtggggca	catctcacia	gatctggcgc	cactctagca	agaacaccac	aaagcacgtg	240
gaagtgaatt	tcatcgagaa	gtttaccagc	gagcggcact	tctgccctag	cacctcctgt	300
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ttcctgtccc	agcacccaaa	cgtgaccctg	gtcatctacg	tggccaggct	gtatcaccac	420
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cacgcaggaa	tcctgggcct	gcctccatgc	ctgaatatcc	tgcgccgga	gcagccccag	660
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<210> 98

<211> 1291

<212> PRT

<213> 人工序列(Artificial Sequence)

<220>

<223> BE4-32-63

<400> 98

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Arg Lys Val Ser Ser Glu Thr Gly Pro Val Ala Val Asp Pro Thr Leu
          20           25           30
Arg Arg Arg Ile Glu Pro His Glu Phe Glu Val Phe Phe Asp Pro Arg
          35           40           45
Glu Leu Arg Lys Glu Thr Cys Leu Leu Tyr Glu Ile Lys Trp Gly Thr
          50           55           60
Ser His Lys Ile Trp Arg His Ser Ser Lys Asn Thr Thr Lys His Val
65           70           75           80
Glu Val Asn Phe Ile Glu Lys Phe Thr Ser Glu Arg His Phe Cys Pro
          85           90           95
Ser Thr Ser Cys Ser Ile Thr Trp Phe Leu Ser Trp Ser Pro Cys Gly
          100          105          110

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Glu Cys Ser Lys Ala Ile Thr Glu Phe Leu Ser Gln His Pro Asn Val		
115	120	125
Thr Leu Val Ile Tyr Val Ala Arg Leu Tyr His His Met Asp Gln Gln		
130	135	140
Asn Arg Gln Gly Leu Arg Asp Leu Val Asn Ser Gly Val Thr Ile Gln		
145	150	155
Ile Met Thr Ala Pro Glu Tyr Asp Tyr Cys Trp Arg Asn Phe Val Asn		
165	170	175
Tyr Pro Pro Gly Lys Glu Ala His Trp Pro Arg Tyr Pro Pro Leu Trp		
180	185	190
Met Lys Leu Tyr Ala Leu Glu Leu His Ala Gly Ile Leu Gly Leu Pro		
195	200	205
Pro Cys Leu Asn Ile Leu Arg Arg Lys Gln Pro Gln Leu Thr Phe Phe		
210	215	220
Thr Ile Ala Leu Gln Ser Cys His Tyr Gln Arg Leu Pro Pro His Ile		
225	230	235
Leu Trp Ala Thr Gly Leu Lys Ser Gly Gly Ser Ser Gly Gly Ser Ser		
245	250	255
Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Ser		
260	265	270
Gly Gly Ser Ser Gly Gly Ser Met Asp Tyr Lys Asp His Asp Gly Asp		
275	280	285
Tyr Lys Asp His Asp Ile Asp Tyr Lys Asp Asp Asp Asp Lys Met Ala		
290	295	300
Pro Lys Lys Lys Arg Lys Val Gly Ile His Gly Val Pro Ala Ala Val		
305	310	315
Asp Leu Arg Thr Leu Gly Tyr Ser Gln Gln Gln Gln Glu Lys Ile Lys		
325	330	335
Pro Lys Val Arg Ser Thr Val Ala Gln His His Glu Ala Leu Val Gly		
340	345	350
His Gly Phe Thr His Ala His Ile Val Ala Leu Ser Gln His Pro Ala		
355	360	365
Ala Leu Gly Thr Val Ala Val Lys Tyr Gln Asp Met Ile Ala Ala Leu		
370	375	380
Pro Glu Ala Thr His Glu Ala Ile Val Gly Val Gly Lys Gln Trp Ser		
385	390	395
Gly Ala Arg Ala Leu Glu Ala Leu Leu Thr Val Ala Gly Glu Leu Arg		
405	410	415
Gly Pro Pro Leu Gln Leu Asp Thr Gly Gln Leu Leu Lys Ile Ala Lys		

420	425	430
Arg Gly Gly Val Thr Ala Val	Glu Ala Val His Ala Trp	Arg Asn Ala
435	440	445
Leu Thr Gly Ala Pro Leu Asn	Leu Thr Pro Asp Gln Val	Val Ala Ile
450	455	460
Ala Ser Asn Ile Gly Gly Lys	Gln Ala Leu Glu Thr Val	Gln Arg Leu
465	470	475
480		
Leu Pro Val Leu Cys Gln Asp	His Gly Leu Thr Pro Glu	Gln Val Val
485	490	495
Ala Ile Ala Ser His Asp Gly	Gly Lys Gln Ala Leu Glu	Thr Val Gln
500	505	510
Arg Leu Leu Pro Val Leu Cys	Gln Ala His Gly Leu Thr	Pro Asp Gln
515	520	525
Val Val Ala Ile Ala Ser Asn	Ile Gly Gly Lys Gln Ala	Leu Glu Thr
530	535	540
Val Gln Arg Leu Leu Pro Val	Leu Cys Gln Ala His Gly	Leu Thr Pro
545	550	555
560		
Ala Gln Val Val Ala Ile Ala	Ser Asn Asn Gly Gly Lys	Gln Ala Leu
565	570	575
Glu Thr Val Gln Arg Leu Leu	Pro Val Leu Cys Gln Asp	His Gly Leu
580	585	590
Thr Pro Asp Gln Val Val Ala	Ile Ala Ser Asn Ile Gly	Gly Lys Gln
595	600	605
Ala Leu Glu Thr Val Gln Arg	Leu Leu Pro Val Leu Cys	Gln Asp His
610	615	620
Gly Leu Thr Pro Glu Gln Val	Val Ala Ile Ala Ser Asn	Ile Gly Gly
625	630	635
640		
Lys Gln Ala Leu Glu Thr Val	Gln Arg Leu Leu Pro Val	Leu Cys Gln
645	650	655
Ala His Gly Leu Thr Pro Asp	Gln Val Val Ala Ile Ala	Ser Asn Asn
660	665	670
Gly Gly Lys Gln Ala Leu Glu	Thr Val Gln Arg Leu Leu	Pro Val Leu
675	680	685
Cys Gln Ala His Gly Leu Thr	Pro Ala Gln Val Val Ala	Ile Ala Ser
690	695	700
His Asp Gly Gly Lys Gln Ala	Leu Glu Thr Val Gln Arg	Leu Leu Pro
705	710	715
720		
Val Leu Cys Gln Asp His Gly	Leu Thr Pro Asp Gln Val	Val Ala Ile
725	730	735

Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu			
740	745	750	
Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val			
755	760	765	
Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln			
770	775	780	
Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln			
785	790	795	800
Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr			
805	810	815	
Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro			
820	825	830	
Ala Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu			
835	840	845	
Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu			
850	855	860	
Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln			
865	870	875	880
Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His			
885	890	895	
Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly			
900	905	910	
Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln			
915	920	925	
Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile			
930	935	940	
Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu			
945	950	955	960
Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser			
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Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro			
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Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile			
995	1000	1005	
Ala Ser Asn Asn Gly Gly Arg Pro Ala Leu Glu Ser Ile Val Ala			
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Gln Leu Ser Arg Pro Asp Pro Ala Leu Ala Ala Leu Thr Asn Asp			
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His Leu Val Ala Leu Ala Cys Leu Gly Gly Arg Pro Ala Leu Asp			

1040	1045	1050
Ala Val Lys Lys Gly Leu Pro His Ala Pro Ala Leu Ile Lys Arg		
1055	1060	1065
Thr Asn Arg Arg Ile Pro Glu Arg Thr Ser His Arg Val Ala Gly		
1070	1075	1080
Ser Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Thr Asn Leu Ser		
1085	1090	1095
Asp Ile Ile Glu Lys Glu Thr Gly Lys Gln Leu Val Ile Gln Glu		
1100	1105	1110
Ser Ile Leu Met Leu Pro Glu Glu Val Glu Glu Val Ile Gly Asn		
1115	1120	1125
Lys Pro Glu Ser Asp Ile Leu Val His Thr Ala Tyr Asp Glu Ser		
1130	1135	1140
Thr Asp Glu Asn Val Met Leu Leu Thr Ser Asp Ala Pro Glu Tyr		
1145	1150	1155
Lys Pro Trp Ala Leu Val Ile Gln Asp Ser Asn Gly Glu Asn Lys		
1160	1165	1170
Ile Lys Met Leu Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Thr		
1175	1180	1185
Asn Leu Ser Asp Ile Ile Glu Lys Glu Thr Gly Lys Gln Leu Val		
1190	1195	1200
Ile Gln Glu Ser Ile Leu Met Leu Pro Glu Glu Val Glu Glu Val		
1205	1210	1215
Ile Gly Asn Lys Pro Glu Ser Asp Ile Leu Val His Thr Ala Tyr		
1220	1225	1230
Asp Glu Ser Thr Asp Glu Asn Val Met Leu Leu Thr Ser Asp Ala		
1235	1240	1245
Pro Glu Tyr Lys Pro Trp Ala Leu Val Ile Gln Asp Ser Asn Gly		
1250	1255	1260
Glu Asn Lys Ile Lys Met Leu Ser Gly Gly Ser Lys Arg Thr Ala		
1265	1270	1275
Asp Gly Ser Glu Phe Glu Pro Lys Lys Lys Arg Lys Val		
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<210> 99

<211> 3873

<212> DNA

<213> 人工序列(Artificial Sequence)

<220>

<223> BE4-32-63-NC

<400> 99

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<212> PRT

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Glu Val Asn Phe Ile Glu Lys	Phe Thr Ser Glu Arg His	Phe Cys Pro
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Ser Thr Ser Cys Ser Ile Thr	Trp Phe Leu Ser Trp Ser	Pro Cys Gly
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Glu Cys Ser Lys Ala Ile Thr	Glu Phe Leu Ser Gln His	Pro Asn Val
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Tyr Pro Pro Gly Lys Glu Ala	His Trp Pro Arg Tyr Pro	Pro Leu Trp
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Met Lys Leu Tyr Ala Leu Glu	Leu His Ala Gly Ile Leu	Gly Leu Pro
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Pro Cys Leu Asn Ile Leu Arg	Arg Lys Gln Pro Gln Leu	Thr Phe Phe
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Gly Pro Pro Leu Gln Leu Asp Thr Gly Gln Leu Leu Lys Ile Ala Lys		
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Arg Gly Gly Val Thr Ala Val Glu Ala Val His Ala Trp Arg Asn Ala		
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Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln		
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Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln		
	515	520 525
Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr		
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Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln		
	645	650 655
Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Gly		

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Val	Leu	Cys	Gln	Asp	His	Gly	Leu	Thr	Pro	Asp	Gln	Val	Val	Ala	Ile												
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Gln Leu Ser Arg Pro Asp Pro Ala Leu Ala Ala Leu Thr Asn Asp		
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<213> 人工序列(Artificial Sequence)

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<223> BE4-32-47

<400> 102

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Thr	Ile	Ala	Leu	Gln	Ser	Cys	His	Tyr	Gln	Arg	Leu	Pro	Pro	His	Ile
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Leu	Trp	Ala	Thr	Gly	Leu	Lys	Ser	Gly	Gly	Ser	Ser	Gly	Gly	Ser	Ser
				245					250				255		
Gly	Ser	Glu	Thr	Pro	Gly	Thr	Ser	Glu	Ser	Ala	Thr	Pro	Glu	Ser	Ser
			260					265					270		
Gly	Gly	Ser	Ser	Gly	Gly	Ser	Met	Ala	Ser	Ser	Pro	Pro	Lys	Lys	Lys

275	280	285
Arg Lys Val Ala Ala Ala Asp Tyr Lys Asp Asp Asp Asp Lys Ser Trp		
290	295	300
Lys Asp Ala Ser Gly Trp Ser Arg Met His Ala Ala Pro Arg Arg Arg		
305	310	315
Ala Ala Gln Pro Ser Asp Ala Ser Pro Ala Ala Gln Val Asp Leu Arg		
325	330	335
Thr Leu Gly Tyr Ser Gln Gln Gln Gln Glu Lys Ile Lys Pro Lys Val		
340	345	350
Arg Ser Thr Val Ala Gln His His Glu Ala Leu Val Gly His Gly Phe		
355	360	365
Thr His Ala His Ile Val Ala Leu Ser Gln His Pro Ala Ala Leu Gly		
370	375	380
Thr Val Ala Val Thr Tyr Gln His Ile Ile Thr Ala Leu Pro Glu Ala		
385	390	395
Thr His Glu Asp Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg		
405	410	415
Ala Leu Glu Ala Leu Leu Thr Asp Ala Gly Glu Leu Arg Gly Pro Pro		
420	425	430
Leu Gln Leu Asp Thr Gly Gln Leu Val Lys Ile Ala Lys Arg Gly Gly		
435	440	445
Val Thr Ala Met Glu Ala Val His Ala Ser Arg Asn Ala Leu Thr Gly		
450	455	460
Ala Pro Leu Asn Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn		
465	470	475
Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val		
485	490	495
Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala		
500	505	510
Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu		
515	520	525
Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala		
530	535	540
Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg		
545	550	555
Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val		
565	570	575
Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val		
580	585	590

Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp		
595	600	605
Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu		
610	615	620
Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr		
625	630	635
Pro Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala		
	645	650
Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly		
	660	665
Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys		
	675	680
Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala		
	690	695
His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser His Asp Gly		
705	710	715
Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys		
	725	730
Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn		
	740	745
Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val		
	755	760
Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala		
	770	775
Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu		
785	790	795
Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala		
	805	810
Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg		
	820	825
Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val		
	835	840
Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val		
	850	855
Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp		
865	870	875
Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu		
	885	890
Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr		
		895

900	905	910
Pro Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala		
915	920	925
Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly		
930	935	940
Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys		
945	950	955
Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala		
965	970	975
His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser Asn Asn Gly		
980	985	990
Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys		
995	1000	1005
Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser		
1010	1015	1020
Asn Asn Gly Gly Arg Pro Ala Leu Glu Ser Ile Val Ala Gln Leu		
1025	1030	1035
Ser Arg Pro Asp Pro Ala Leu Ala Ala Leu Thr Asn Asp His Leu		
1040	1045	1050
Val Ala Leu Ala Cys Leu Gly Gly Arg Pro Ala Met Asp Ala Val		
1055	1060	1065
Lys Lys Gly Leu Pro His Ala Pro Glu Leu Ile Arg Ser Ser Gly		
1070	1075	1080
Gly Ser Gly Gly Ser Gly Gly Ser Thr Asn Leu Ser Asp Ile Ile		
1085	1090	1095
Glu Lys Glu Thr Gly Lys Gln Leu Val Ile Gln Glu Ser Ile Leu		
1100	1105	1110
Met Leu Pro Glu Glu Val Glu Glu Val Ile Gly Asn Lys Pro Glu		
1115	1120	1125
Ser Asp Ile Leu Val His Thr Ala Tyr Asp Glu Ser Thr Asp Glu		
1130	1135	1140
Asn Val Met Leu Leu Thr Ser Asp Ala Pro Glu Tyr Lys Pro Trp		
1145	1150	1155
Ala Leu Val Ile Gln Asp Ser Asn Gly Glu Asn Lys Ile Lys Met		
1160	1165	1170
Leu Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Thr Asn Leu Ser		
1175	1180	1185
Asp Ile Ile Glu Lys Glu Thr Gly Lys Gln Leu Val Ile Gln Glu		
1190	1195	1200

Ser Ile	Leu Met Leu Pro Glu	Glu Val Glu Glu Val	Ile Gly Asn
1205		1210	1215
Lys Pro	Glu Ser Asp Ile Leu	Val His Thr Ala Tyr	Asp Glu Ser
1220		1225	1230
Thr Asp	Glu Asn Val Met Leu	Leu Thr Ser Asp Ala	Pro Glu Tyr
1235		1240	1245
Lys Pro	Trp Ala Leu Val Ile	Gln Asp Ser Asn Gly	Glu Asn Lys
1250		1255	1260
Ile Lys	Met Leu Ser Gly Gly	Ser Lys Arg Thr Ala	Asp Gly Ser
1265		1270	1275
Glu Phe	Glu Pro Lys Lys Lys	Arg Lys Val	
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<210> 103

<211> 3864

<212> DNA

<213> 人工序列(Artificial Sequence)

<220>

<223> BE4-32-47-NC

<400> 103

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tttgaggtgt	tctttgatcc	aagagagctg	aggaaggaga	catgcctgct	gtacgagatc	180
aagtggggca	catctcacia	gatctggcgc	cactctagca	agaacaccac	aaagcacgtg	240
gaagtgaatt	tcatcgagaa	gtttaccagc	gagcggcact	tctgccctag	cacctcctgt	300
tctatcacat	ggtttctgag	ctgggtccca	tgcggcgagt	gtagcaaggc	catcaccgag	360
ttcctgtccc	agcacccaaa	cgtgaccctg	gtcatctacg	tggccaggct	gtatcaccac	420
atggaccagc	agaacaggca	gggctgcg	gatctggatga	attccggcgt	gaccatccag	480
atcatgacag	cccccgagta	cgattactgt	tggagaaact	tcgtgaacta	cccacctggc	540
aaggaggcac	actggcctag	gtaccacccc	ctgtggatga	agctgtatgc	actggagctg	600
cacgcaggaa	tcctgggcct	gcctccatgc	ctgaatatcc	tgcgccgga	gcagccccag	660
ctgaccttct	ttacaatcgc	cctgcagagc	tgctactacc	agcggctgcc	acctcacatc	720
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gcttcctccc	ctccaaagaa	aaagagaaag	gttgcgggcg	ctgactacaa	ggatgacgac	900
gataaaagtt	ggaaggacgc	aagtggttgg	tctagaatgc	atgcggcccc	gcgacggcgt	960
gctgcgcaac	cctccgacgc	ttcgccggcc	gcgcaggtgg	atctacgcac	gctcggctac	1020
agtcagcagc	agcaagagaa	gatcaaaccg	aaggtgcgtt	cgacagtggc	gcagcaccac	1080
gaggcactgg	tgggccatgg	gtttacacac	gcgcacatcg	ttgcgctcag	ccaacacccg	1140
gcagcgtag	ggaccgtcgc	tgtcacgtat	cagcacataa	tcacggcggt	gccagaggcg	1200

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gtgaagattg	caaaacgtgg	cggcgtgacc	gcaatggagg	cagtgcacgc	atcgcgcaat	1380
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cagagattgt	tgccgggtgct	gtgccaagac	cacggcctga	cccctgagca	ggtagtggct	3060
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gaagtgatcg	gcaacaagcc	tgagtccgat	atcctggtgc	acaccgccta	cgacaggtcc	3420
acagatgaga	atgtgatgct	gctgacctct	gacgccccag	agtataagcc	ctgggcccctg	3480
gtcatccagg	atagcaacgg	cgagaataag	atcaagatgc	tgtccggcgg	aagcggagga	3540

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gaaagcgaca tcctgggtcca tactgcctac gacgagagta cgcacgaaaa tgtgatgtta 3720
ctgacctccg acgccccctga gtataagcca tgggctctgg tcatccagga ctccaatgga 3780
gaaaataaga tcaagatgtt aagcggcggc tccaagagaa cagccgacgg ctccgagttc 3840
gagcccaaga agaagcggaa agtg 3864

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<210> 104

<211> 1288

<212> PRT

<213> 人工序列(Artificial Sequence)

<220>

<223> BE4-32-47-NC

<400> 104

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Arg Lys Val Ser Ser Glu Thr Gly Pro Val Ala Val Asp Pro Thr Leu
          20           25           30
Arg Arg Arg Ile Glu Pro His Glu Phe Glu Val Phe Phe Asp Pro Arg
          35           40           45
Glu Leu Arg Lys Glu Thr Cys Leu Leu Tyr Glu Ile Lys Trp Gly Thr
          50           55           60
Ser His Lys Ile Trp Arg His Ser Ser Lys Asn Thr Thr Lys His Val
65           70           75           80
Glu Val Asn Phe Ile Glu Lys Phe Thr Ser Glu Arg His Phe Cys Pro
          85           90           95
Ser Thr Ser Cys Ser Ile Thr Trp Phe Leu Ser Trp Ser Pro Cys Gly
          100          105          110
Glu Cys Ser Lys Ala Ile Thr Glu Phe Leu Ser Gln His Pro Asn Val
          115          120          125
Thr Leu Val Ile Tyr Val Ala Arg Leu Tyr His His Met Asp Gln Gln
          130          135          140
Asn Arg Gln Gly Leu Arg Asp Leu Val Asn Ser Gly Val Thr Ile Gln
145          150          155          160
Ile Met Thr Ala Pro Glu Tyr Asp Tyr Cys Trp Arg Asn Phe Val Asn
          165          170          175
Tyr Pro Pro Gly Lys Glu Ala His Trp Pro Arg Tyr Pro Pro Leu Trp
          180          185          190
Met Lys Leu Tyr Ala Leu Glu Leu His Ala Gly Ile Leu Gly Leu Pro
          195          200          205

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Pro Cys Leu Asn Ile Leu Arg Arg Lys Gln Pro Gln Leu Thr Phe Phe		
210	215	220
Thr Ile Ala Leu Gln Ser Cys His Tyr Gln Arg Leu Pro Pro His Ile		
225	230	235 240
Leu Trp Ala Thr Gly Leu Lys Ser Gly Gly Ser Ser Gly Gly Ser Ser		
245	250	255
Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Ser		
260	265	270
Gly Gly Ser Ser Gly Gly Ser Met Ala Ser Ser Pro Pro Lys Lys Lys		
275	280	285
Arg Lys Val Ala Ala Ala Asp Tyr Lys Asp Asp Asp Lys Ser Trp		
290	295	300
Lys Asp Ala Ser Gly Trp Ser Arg Met His Ala Ala Pro Arg Arg Arg		
305	310	315 320
Ala Ala Gln Pro Ser Asp Ala Ser Pro Ala Ala Gln Val Asp Leu Arg		
325	330	335
Thr Leu Gly Tyr Ser Gln Gln Gln Gln Glu Lys Ile Lys Pro Lys Val		
340	345	350
Arg Ser Thr Val Ala Gln His His Glu Ala Leu Val Gly His Gly Phe		
355	360	365
Thr His Ala His Ile Val Ala Leu Ser Gln His Pro Ala Ala Leu Gly		
370	375	380
Thr Val Ala Val Thr Tyr Gln His Ile Ile Thr Ala Leu Pro Glu Ala		
385	390	395 400
Thr His Glu Asp Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg		
405	410	415
Ala Leu Glu Ala Leu Leu Thr Asp Ala Gly Glu Leu Arg Gly Pro Pro		
420	425	430
Leu Gln Leu Asp Thr Gly Gln Leu Val Lys Ile Ala Lys Arg Gly Gly		
435	440	445
Val Thr Ala Met Glu Ala Val His Ala Ser Arg Asn Ala Leu Thr Gly		
450	455	460
Ala Pro Leu Asn Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn		
465	470	475 480
Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val		
485	490	495
Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala		
500	505	510
Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu		

515	520	525
Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala		
530	535	540
Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg		
545	550	555
Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val		
565	570	575
Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val		
580	585	590
Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp		
595	600	605
Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu		
610	615	620
Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr		
625	630	635
Pro Glu Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala		
645	650	655
Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly		
660	665	670
Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys		
675	680	685
Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala		
690	695	700
His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser Asn Ile Gly		
705	710	715
Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys		
725	730	735
Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn		
740	745	750
Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val		
755	760	765
Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala		
770	775	780
Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu		
785	790	795
Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala		
805	810	815
Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg		
820	825	830

Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val		
835	840	845
Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val		
850	855	860
Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp		
865	870	875
		880
Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu		
	885	890
		895
Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr		
	900	905
		910
Pro Glu Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala		
	915	920
		925
Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly		
	930	935
		940
Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys		
945	950	955
		960
Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala		
	965	970
		975
His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser Asn Asn Gly		
	980	985
		990
Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys		
	995	1000
		1005
Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser		
1010	1015	1020
Asn Asn Gly Gly Arg Pro Ala Leu Glu Ser Ile Val Ala Gln Leu		
1025	1030	1035
Ser Arg Pro Asp Pro Ala Leu Ala Ala Leu Thr Asn Asp His Leu		
1040	1045	1050
Val Ala Leu Ala Cys Leu Gly Gly Arg Pro Ala Met Asp Ala Val		
1055	1060	1065
Lys Lys Gly Leu Pro His Ala Pro Glu Leu Ile Arg Ser Ser Gly		
1070	1075	1080
Gly Ser Gly Gly Ser Gly Gly Ser Thr Asn Leu Ser Asp Ile Ile		
1085	1090	1095
Glu Lys Glu Thr Gly Lys Gln Leu Val Ile Gln Glu Ser Ile Leu		
1100	1105	1110
Met Leu Pro Glu Glu Val Glu Glu Val Ile Gly Asn Lys Pro Glu		
1115	1120	1125
Ser Asp Ile Leu Val His Thr Ala Tyr Asp Glu Ser Thr Asp Glu		

1130	1135	1140
Asn Val Met Leu Leu Thr Ser Asp Ala Pro Glu Tyr Lys Pro Trp		
1145	1150	1155
Ala Leu Val Ile Gln Asp Ser Asn Gly Glu Asn Lys Ile Lys Met		
1160	1165	1170
Leu Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Thr Asn Leu Ser		
1175	1180	1185
Asp Ile Ile Glu Lys Glu Thr Gly Lys Gln Leu Val Ile Gln Glu		
1190	1195	1200
Ser Ile Leu Met Leu Pro Glu Glu Val Glu Glu Val Ile Gly Asn		
1205	1210	1215
Lys Pro Glu Ser Asp Ile Leu Val His Thr Ala Tyr Asp Glu Ser		
1220	1225	1230
Thr Asp Glu Asn Val Met Leu Leu Thr Ser Asp Ala Pro Glu Tyr		
1235	1240	1245
Lys Pro Trp Ala Leu Val Ile Gln Asp Ser Asn Gly Glu Asn Lys		
1250	1255	1260
Ile Lys Met Leu Ser Gly Gly Ser Lys Arg Thr Ala Asp Gly Ser		
1265	1270	1275
Glu Phe Glu Pro Lys Lys Lys Arg Lys Val		
1280	1285	

<210> 105

<211> 309

<212> DNA

<213> 人工序列(Artificial Sequence)

<220>

<223> HTS95

<400> 105

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aacagcatcc agccaaccct gtggacaatc ggatccatca atggagtggc accactggcc	180
aagtctatca agctgggcat cctgtgacc ggcagcgct acacagacca gaccacagcc	240
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accgcggtc	309

<210> 106

<211> 103

<212> PRT

<213> 人工序列(Artificial Sequence)

<220>

<223> HTS95

<400> 106

Tyr Thr Arg Val Gly Ser Gly Ser Gly Ser Gly Ser Ile Thr Arg Thr

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Thr Asn Pro Arg Asn Val Val Pro Lys Ile Tyr Met Ser Ala Gly Ser

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Ile Pro Leu Thr Thr His Ile Thr Asn Ser Ile Gln Pro Thr Leu Trp

35 40 45

Thr Ile Gly Ser Ile Asn Gly Val Ala Pro Leu Ala Lys Ser Ile Lys

50 55 60

Leu Gly Ile Pro Val Thr Gly Ser Ala Tyr Thr Asp Gln Thr Thr Ala

65 70 75 80

Met Val Arg Lys Lys Val Ser Val Phe Met Gly Ser Gly Ser Gly Ser

85 90 95

Gly Ser Ser Met Thr Ala Val

100

<210> 107

<211> 4527

<212> DNA

<213> 人工序列(Artificial Sequence)

<220>

<223> BE4-135-WT

<400> 107

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<212> PRT

<213> 人工序列(Artificial Sequence)

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 35 40 45
 Glu Leu Arg Lys Glu Thr Cys Leu Leu Tyr Glu Ile Lys Trp Gly Thr
 50 55 60
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 65 70 75 80
 Glu Val Asn Phe Ile Glu Lys Phe Thr Ser Glu Arg His Phe Cys Pro

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Glu	Cys	Ser	Lys	Ala	Ile	Thr	Glu	Phe	Leu	Ser	Gln	His	Pro	Asn	Val		
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Thr	Leu	Val	Ile	Tyr	Val	Ala	Arg	Leu	Tyr	His	His	Met	Asp	Gln	Gln		
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Asn	Arg	Gln	Gly	Leu	Arg	Asp	Leu	Val	Asn	Ser	Gly	Val	Thr	Ile	Gln		
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Ile	Met	Thr	Ala	Pro	Glu	Tyr	Asp	Tyr	Cys	Trp	Arg	Asn	Phe	Val	Asn		
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Tyr	Pro	Pro	Gly	Lys	Glu	Ala	His	Trp	Pro	Arg	Tyr	Pro	Pro	Leu	Trp		
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Met	Lys	Leu	Tyr	Ala	Leu	Glu	Leu	His	Ala	Gly	Ile	Leu	Gly	Leu	Pro		
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Pro	Cys	Leu	Asn	Ile	Leu	Arg	Arg	Lys	Gln	Pro	Gln	Leu	Thr	Phe	Phe		
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Thr	Ile	Ala	Leu	Gln	Ser	Cys	His	Tyr	Gln	Arg	Leu	Pro	Pro	His	Ile		
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Ile	Tyr	Met	Ser	Ala	Gly	Ser	Ile	Pro	Leu	Thr	Thr	His	Ile	Thr	Asn		
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Tyr	Thr	Asp	Gln	Thr	Thr	Ala	Met	Val	Arg	Lys	Lys	Val	Ser	Val	Phe		
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Tyr	Lys	Asp	His	Asp	Gly	Asp	Tyr	Lys	Asp	His	Asp	Ile	Asp	Tyr	Lys		
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Asp Asp Asp Asp Lys Met Ala Pro Lys Lys Lys Arg Lys Val Gly Ile			
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His Gly Val Pro Ala Ala Val Asp Leu Arg Thr Leu Gly Tyr Ser Gln			
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Gln Gln Gln Glu Lys Ile Lys Pro Lys Val Arg Ser Thr Val Ala Gln			
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His His Glu Ala Leu Val Gly His Gly Phe Thr His Ala His Ile Val			
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Ala Leu Ser Gln His Pro Ala Ala Leu Gly Thr Val Ala Val Lys Tyr			
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Gln Asp Met Ile Ala Ala Leu Pro Glu Ala Thr His Glu Ala Ile Val			
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Gly Val Gly Lys Gln Trp Ser Gly Ala Arg Ala Leu Glu Ala Leu Leu			
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Thr Val Ala Gly Glu Leu Arg Gly Pro Pro Leu Gln Leu Asp Thr Gly			
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Gln Leu Leu Lys Ile Ala Lys Arg Gly Gly Val Thr Ala Val Glu Ala			
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Val His Ala Trp Arg Asn Ala Leu Thr Gly Ala Pro Leu Asn Leu Thr			
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Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala			
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Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly			
	580	585	590
Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys			
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Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala			
	610	615	620
His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile Gly			
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Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys			
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Gln Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser Asn			
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Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val			
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Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala			
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Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu			

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Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg			
	740	745	750
Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val			
	755	760	765
Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val			
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Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu			
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Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr			
	820	825	830
Pro Asp Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala			
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Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly			
	850	855	860
Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys			
865	870	875	880
Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala			
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His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Asn Gly			
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Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys			
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Gln Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser His			
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Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val			
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Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala			
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Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu			
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Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala			
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Lys Gln	Ala Leu Glu	Thr Val	Gln Arg Leu	Leu Pro	Val Leu Cys
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Gln Asp	His Gly Leu	Thr Pro	Glu Gln Val	Val Ala	Ile Ala Ser
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Gln Val	Val Arg Val	Leu Gly	Phe Phe Gln	Cys His	Ser His Pro
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Gly Asp	Gln Thr Arg	Ala Ser	Ala Ser Ser	Gly Gly	Ser Gly Gly
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Glu Val Glu Glu Val Ile Gly Asn Lys Pro Glu Ser Asp Ile Leu		
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Val His Thr Ala Tyr Asp Glu Ser Thr Asp Glu Asn Val Met Leu		
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Leu Thr Ser Asp Ala Pro Glu Tyr Lys Pro Trp Ala Leu Val Ile		
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Gln Asp Ser Asn Gly Glu Asn Lys Ile Lys Met Leu Ser Gly Gly		
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Leu Val Ile Gln Asp Ser Asn Gly Glu Asn Lys Ile Lys Met Leu		
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Ser	His	Lys	Ile	Trp	Arg	His	Ser	Ser	Lys	Asn	Thr	Thr	Lys	His	Val
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Ser	Thr	Ser	Cys	Ser	Ile	Thr	Trp	Phe	Leu	Ser	Trp	Ser	Pro	Cys	Gly
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Thr	Leu	Val	Ile	Tyr	Val	Ala	Arg	Leu	Tyr	His	His	Met	Asp	Gln	Gln
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Ser	Gly	Ser	Ile	Thr	Arg	Thr	Thr	Asn	Pro	Arg	Asn	Val	Val	Pro	Lys
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Pro Leu Ala Lys Ser	Ile Lys Leu Gly Ile	Pro Val Thr Gly	Ser Ala
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Tyr Thr Asp Gln Thr	Thr Ala Met Val Arg	Lys Lys Val Ser	Val Phe
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Met Gly Ser Gly Ser	Gly Ser Gly Ser Met	Thr Ala Val Met	Asp
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Tyr Lys Asp His Asp	Gly Asp Tyr Lys Asp	His Asp Ile Asp	Tyr Lys
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Asp Asp Asp Asp Lys	Met Ala Pro Lys Lys	Lys Arg Lys Val Gly	Ile
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His Gly Val Pro Ala	Ala Val Asp Leu Arg	Thr Leu Gly Tyr	Ser Gln
420	425	430	
Gln Gln Gln Glu Lys	Ile Lys Pro Lys Val	Arg Ser Thr Val	Ala Gln
435	440	445	
His His Glu Ala Leu	Val Gly His Gly Phe	Thr His Ala His	Ile Val
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Ala Leu Ser Gln His	Pro Ala Ala Leu Gly	Thr Val Ala Val	Lys Tyr
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Gln Asp Met Ile Ala	Ala Leu Pro Glu Ala	Thr His Glu Ala	Ile Val
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Gly Val Gly Lys Gln	Trp Ser Gly Ala Arg	Ala Leu Glu Ala	Leu Leu
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Thr Val Ala Gly Glu	Leu Arg Gly Pro Pro	Leu Gln Leu Asp	Thr Gly
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Gln Leu Leu Lys Ile	Ala Lys Arg Gly Gly	Val Thr Ala Val	Glu Ala
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Val His Ala Trp Arg	Asn Ala Leu Thr Gly	Ala Pro Leu Asn	Leu Thr
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Pro Asp Gln Val Val	Ala Ile Ala Ser Asn	Gly Gly Gly Lys	Gln Ala
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Leu Glu Thr Val Gln	Arg Leu Leu Pro Val	Leu Cys Gln Asp	His Gly
580	585	590	
Leu Thr Pro Glu Gln	Val Val Ala Ile Ala	Ser Asn Asn Gly	Gly Lys
595	600	605	
Gln Ala Leu Glu Thr	Val Gln Arg Leu Leu	Pro Val Leu Cys	Gln Ala
610	615	620	

His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser His Asp Gly			
625	630	635	640
Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys			
	645	650	655
Gln Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser Asn			
	660	665	670
Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val			
	675	680	685
Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala			
	690	695	700
Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu			
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Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala			
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Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg			
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Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val			
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Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val			
	770	775	780
Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala			
785	790	795	800
Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu			
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Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr			
	820	825	830
Pro Asp Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala			
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Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly			
	850	855	860
Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys			
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Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala			
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His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Asn Gly			
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Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys			
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Gln Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser Asn			

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Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu		
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Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala		
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Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu		
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Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly		
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Ser Arg Pro Asp Pro Ala Leu Ala Ala Leu Thr Asn Asp His Leu		
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His Gly Leu Leu Gln Leu Phe Arg Arg Val Gly Val Thr Glu Leu		
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Ser Gly	Gly Ser Thr Asn Leu	Ser Asp Ile Ile Glu	Lys Glu Thr
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Gly Lys	Gln Leu Val Ile Gln	Glu Ser Ile Leu Met	Leu Pro Glu
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Glu Val	Glu Glu Val Ile Gly	Asn Lys Pro Glu Ser	Asp Ile Leu
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Val His	Thr Ala Tyr Asp Glu	Ser Thr Asp Glu Asn	Val Met Leu
1355	1360	1365	
Leu Thr	Ser Asp Ala Pro Glu	Tyr Lys Pro Trp Ala	Leu Val Ile
1370	1375	1380	
Gln Asp	Ser Asn Gly Glu Asn	Lys Ile Lys Met Leu	Ser Gly Gly
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Ser Gly	Gly Ser Gly Gly Ser	Thr Asn Leu Ser Asp	Ile Ile Glu
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Lys Glu	Thr Gly Lys Gln Leu	Val Ile Gln Glu Ser	Ile Leu Met
1415	1420	1425	
Leu Pro	Glu Glu Val Glu Glu	Val Ile Gly Asn Lys	Pro Glu Ser
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Asp Ile	Leu Val His Thr Ala	Tyr Asp Glu Ser Thr	Asp Glu Asn
1445	1450	1455	
Val Met	Leu Leu Thr Ser Asp	Ala Pro Glu Tyr Lys	Pro Trp Ala
1460	1465	1470	
Leu Val	Ile Gln Asp Ser Asn	Gly Glu Asn Lys Ile	Lys Met Leu
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<213> 人工序列(Artificial Sequence)

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<223> BE4-135-63

<400> 111

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<212> PRT

<213> 人工序列(Artificial Sequence)

<220>

<223> BE4-135-63

<400> 112

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

Gly Gly Ser Ser Gly Gly Ser Tyr Thr Arg Val Gly Ser Gly Ser Gly	275	280	285
Ser Gly Ser Ile Thr Arg Thr Thr Asn Pro Arg Asn Val Val Pro Lys	290	295	300
Ile Tyr Met Ser Ala Gly Ser Ile Pro Leu Thr Thr His Ile Thr Asn	305	310	315
Ser Ile Gln Pro Thr Leu Trp Thr Ile Gly Ser Ile Asn Gly Val Ala	325	330	335
Pro Leu Ala Lys Ser Ile Lys Leu Gly Ile Pro Val Thr Gly Ser Ala	340	345	350
Tyr Thr Asp Gln Thr Thr Ala Met Val Arg Lys Lys Val Ser Val Phe	355	360	365
Met Gly Ser Gly Ser Gly Ser Gly Ser Ser Met Thr Ala Val Met Asp	370	375	380
Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His Asp Ile Asp Tyr Lys	385	390	395
Asp Asp Asp Asp Lys Met Ala Pro Lys Lys Lys Arg Lys Val Gly Ile	405	410	415
His Gly Val Pro Ala Ala Val Asp Leu Arg Thr Leu Gly Tyr Ser Gln	420	425	430
Gln Gln Gln Glu Lys Ile Lys Pro Lys Val Arg Ser Thr Val Ala Gln	435	440	445
His His Glu Ala Leu Val Gly His Gly Phe Thr His Ala His Ile Val	450	455	460
Ala Leu Ser Gln His Pro Ala Ala Leu Gly Thr Val Ala Val Lys Tyr	465	470	475
Gln Asp Met Ile Ala Ala Leu Pro Glu Ala Thr His Glu Ala Ile Val	485	490	495
Gly Val Gly Lys Gln Trp Ser Gly Ala Arg Ala Leu Glu Ala Leu Leu	500	505	510
Thr Val Ala Gly Glu Leu Arg Gly Pro Pro Leu Gln Leu Asp Thr Gly	515	520	525
Gln Leu Leu Lys Ile Ala Lys Arg Gly Gly Val Thr Ala Val Glu Ala	530	535	540
Val His Ala Trp Arg Asn Ala Leu Thr Gly Ala Pro Leu Asn Leu Thr	545	550	555
Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala	565	570	575
Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly			

580	585	590
Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys		
595	600	605
Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala		
610	615	620
His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile Gly		
625	630	635
Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys		
645	650	655
Gln Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser Asn		
660	665	670
Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val		
675	680	685
Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala		
690	695	700
Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu		
705	710	715
Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala		
725	730	735
Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg		
740	745	750
Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val		
755	760	765
Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val		
770	775	780
Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala		
785	790	795
Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu		
805	810	815
Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr		
820	825	830
Pro Asp Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala		
835	840	845
Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly		
850	855	860
Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys		
865	870	875
Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala		
885	890	895

His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Asn Gly		
900	905	910
Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys		
915	920	925
Gln Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser His		
930	935	940
Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val		
945	950	955
Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala		
965	970	975
Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu		
980	985	990
Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala		
995	1000	1005
Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln		
1010	1015	1020
Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp		
1025	1030	1035
Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu		
1040	1045	1050
Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly		
1055	1060	1065
Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly		
1070	1075	1080
Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys		
1085	1090	1095
Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser		
1100	1105	1110
Asn Asn Gly Gly Arg Pro Ala Leu Glu Ser Ile Val Ala Gln Leu		
1115	1120	1125
Ser Arg Pro Asp Pro Ala Leu Ala Ala Leu Thr Asn Asp His Leu		
1130	1135	1140
Val Ala Leu Ala Cys Leu Gly Gly Arg Pro Ala Leu Asp Ala Val		
1145	1150	1155
Lys Lys Gly Leu Pro His Ala Pro Ala Leu Ile Lys Arg Thr Asn		
1160	1165	1170
Arg Arg Ile Pro Glu Arg Thr Ser His Arg Val Ala Gly Ser Ser		
1175	1180	1185
Gly Gly Ser Gly Gly Ser Gly Gly Ser Thr Asn Leu Ser Asp Ile		

1190	1195	1200
Ile Glu Lys Glu Thr Gly Lys	Gln Leu Val Ile Gln	Glu Ser Ile
1205	1210	1215
Leu Met Leu Pro Glu Glu Val	Glu Glu Val Ile Gly	Asn Lys Pro
1220	1225	1230
Glu Ser Asp Ile Leu Val His	Thr Ala Tyr Asp Glu	Ser Thr Asp
1235	1240	1245
Glu Asn Val Met Leu Leu Thr	Ser Asp Ala Pro Glu	Tyr Lys Pro
1250	1255	1260
Trp Ala Leu Val Ile Gln Asp	Ser Asn Gly Glu Asn	Lys Ile Lys
1265	1270	1275
Met Leu Ser Gly Gly Ser Gly	Gly Ser Gly Gly Ser	Thr Asn Leu
1280	1285	1290
Ser Asp Ile Ile Glu Lys Glu	Thr Gly Lys Gln Leu	Val Ile Gln
1295	1300	1305
Glu Ser Ile Leu Met Leu Pro	Glu Glu Val Glu Glu	Val Ile Gly
1310	1315	1320
Asn Lys Pro Glu Ser Asp Ile	Leu Val His Thr Ala	Tyr Asp Glu
1325	1330	1335
Ser Thr Asp Glu Asn Val Met	Leu Leu Thr Ser Asp	Ala Pro Glu
1340	1345	1350
Tyr Lys Pro Trp Ala Leu Val	Ile Gln Asp Ser Asn	Gly Glu Asn
1355	1360	1365
Lys Ile Lys Met Leu Ser Gly	Gly Ser Lys Arg Thr	Ala Asp Gly
1370	1375	1380
Ser Glu Phe Glu Pro Lys Lys	Lys Arg Lys Val	
1385	1390	

<210> 113

<211> 4182

<212> DNA

<213> 人工序列(Artificial Sequence)

<220>

<223> BE4-135-63-NC

<400> 113

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tccgagacag gaccagtggc agtggaccct aactgcgga gaaggatcga gcctcacgag	120
tttgaggtgt tctttgatcc aagagagctg aggaaggaga catgcctgct gtacgagatc	180
aagtggggca catctcacia gatctggcgc cactctagca agaacaccac aaagcacgtg	240
gaagtgaatt tcatcgagaa gtttaccagc gagcggcact tctgccctag cacctcctgt	300

tctatcacat	ggtttctgag	ctggtcccca	tgcggcgagt	gtagcaaggc	catcaccgag	360
ttcctgtccc	agcacccaaa	cgtgaccctg	gtcatctacg	tggccaggct	gtatcaccac	420
atggaccagc	agaacaggca	gggcctgcgg	gatctggtga	attccggcgt	gaccatccag	480
atcatgacag	cccccgagta	cgattactgt	tggagaaact	tcgtgaacta	cccacctggc	540
aaggaggcac	actggcctag	gtacccaccc	ctgtggatga	agctgtatgc	actggagctg	600
cacgcaggaa	tcctgggcct	gcctccatgc	ctgaatatcc	tgcgccggaa	gcagccccag	660
ctgaccttct	ttacaatcgc	cctgcagagc	tgtcactacc	agcggctgcc	acctcacatc	720
ctgtgggcaa	ccggcctgaa	gtctggagga	tcctctggag	gaagctccgg	aagcgagaca	780
ccaggcacat	ctgagagcgc	cacaccagag	tctagcggcg	gctcctctgg	aggatcctac	840
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gtggtgccaa	agatctacat	gtccgccggc	tctatccctc	tgaccacaca	catcacaaac	960
agcatccagc	caaccctgtg	gacaatcgga	tccatcaatg	gagtggcacc	actggccaag	1020
tctatcaagc	tgggcatccc	tgtgaccggc	agcgctaca	cagaccagac	cacagccatg	1080
gtgcggaaga	aggtgagcgt	gttcatgggc	agcggatctg	gaagcggatc	tagcatgacc	1140
gcggtcatgg	actataagga	ccacgacgga	gactacaagg	atcatgatat	tgattacaaa	1200
gacgatgacg	ataagatggc	cccaaagaag	aagcgggaag	tcggtatcca	cggagtccca	1260
gcagccgtag	atttgagaac	tttgggatat	tcacagcagc	agcaggaaaa	gatcaagccc	1320
aaagtgaggt	cgacagtcgc	gcagcatcac	gaagcgtgg	tgggtcatgg	gtttacacat	1380
gcccacatcg	tagccttgtc	gcagcaccct	gcagcccttg	gcacggtcgc	cgtcaagtac	1440
caggacatga	ttgcggcggt	gccggaagcc	acacatgagg	cgatcgtcgg	tgtggggaaa	1500
cagtggagcg	gagcccagc	gcttgaggcc	ctgttgacgg	tcgcgggaga	gctgagaggg	1560
cctccccctt	agctggacac	gggccagttg	ctgaagatcg	cgaagcgggg	aggagtcacg	1620
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ggaaagcagg	ccctagaaac	cgttcagcga	ctcctgcccc	tcctgtgcca	ggcccacggc	1980
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caggccctcg aaaccgtcca gagactgtta ccggttctct gccaggccca cggcctgacc 2700
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 cagagattgt tgcctgtgct gtgccaagcc cacggcctga ccccgccca ggttgtcgt 2820
 attgctagta acggcggagg caaacaggcg ctggaaacag ttcagcgcct cttgccggtc 2880
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 acagtccaga gattgttgcc ggtgctgtgc caagcccacg gcctgacccc ggaccaggtg 3120
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 cccgtcctgt gccaggccca cggcctgacc ccagcccaag ttgtcgcgat tgcaagcaac 3240
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 tataagccct gggccctggt catccaggat agcaacggcg agaataagat caagatgctg 3840
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 gacgaaaatg tgatgttact gacctccgac gcccctgagt ataagccatg ggctctggtc 4080
 atccaggact ccaatggaga aaataagatc aagatgtaa gcggcggctc caagagaaca 4140
 gccgacggct ccgagttcga gccaagaag aagcggaaag tg 4182

<210> 114

<211> 1394

<212> PRT

<213> 人工序列(Artificial Sequence)

<220>

<223> BE4-135-63-NC

<400> 114

Met Lys Arg Thr Ala Asp Gly Ser Glu Phe Glu Ser Pro Lys Lys Lys

1 5 10 15

Arg Lys Val Ser Ser Glu Thr Gly Pro Val Ala Val Asp Pro Thr Leu

20 25 30

Arg Arg Arg Ile Glu Pro His Glu Phe Glu Val Phe Phe Asp Pro Arg

35 40 45

Glu Leu Arg Lys Glu Thr Cys Leu Leu Tyr Glu Ile Lys Trp Gly Thr		
50	55	60
Ser His Lys Ile Trp Arg His Ser Ser Lys Asn Thr Thr Lys His Val		
65	70	75 80
Glu Val Asn Phe Ile Glu Lys Phe Thr Ser Glu Arg His Phe Cys Pro		
	85	90 95
Ser Thr Ser Cys Ser Ile Thr Trp Phe Leu Ser Trp Ser Pro Cys Gly		
	100	105 110
Glu Cys Ser Lys Ala Ile Thr Glu Phe Leu Ser Gln His Pro Asn Val		
	115	120 125
Thr Leu Val Ile Tyr Val Ala Arg Leu Tyr His His Met Asp Gln Gln		
	130	135 140
Asn Arg Gln Gly Leu Arg Asp Leu Val Asn Ser Gly Val Thr Ile Gln		
145	150	155 160
Ile Met Thr Ala Pro Glu Tyr Asp Tyr Cys Trp Arg Asn Phe Val Asn		
	165	170 175
Tyr Pro Pro Gly Lys Glu Ala His Trp Pro Arg Tyr Pro Pro Leu Trp		
	180	185 190
Met Lys Leu Tyr Ala Leu Glu Leu His Ala Gly Ile Leu Gly Leu Pro		
	195	200 205
Pro Cys Leu Asn Ile Leu Arg Arg Lys Gln Pro Gln Leu Thr Phe Phe		
210	215	220
Thr Ile Ala Leu Gln Ser Cys His Tyr Gln Arg Leu Pro Pro His Ile		
225	230	235 240
Leu Trp Ala Thr Gly Leu Lys Ser Gly Gly Ser Ser Gly Gly Ser Ser		
	245	250 255
Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Ser		
	260	265 270
Gly Gly Ser Ser Gly Gly Ser Tyr Thr Arg Val Gly Ser Gly Ser Gly		
	275	280 285
Ser Gly Ser Ile Thr Arg Thr Thr Asn Pro Arg Asn Val Val Pro Lys		
290	295	300
Ile Tyr Met Ser Ala Gly Ser Ile Pro Leu Thr Thr His Ile Thr Asn		
305	310	315 320
Ser Ile Gln Pro Thr Leu Trp Thr Ile Gly Ser Ile Asn Gly Val Ala		
	325	330 335
Pro Leu Ala Lys Ser Ile Lys Leu Gly Ile Pro Val Thr Gly Ser Ala		
	340	345 350
Tyr Thr Asp Gln Thr Thr Ala Met Val Arg Lys Lys Val Ser Val Phe		

355	360	365
Met Gly Ser Gly Ser Gly Ser Gly Ser Ser Met Thr Ala Val Met Asp		
370	375	380
Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His Asp Ile Asp Tyr Lys		
385	390	395
Asp Asp Asp Asp Lys Met Ala Pro Lys Lys Lys Arg Lys Val Gly Ile		400
405	410	415
His Gly Val Pro Ala Ala Val Asp Leu Arg Thr Leu Gly Tyr Ser Gln		
420	425	430
Gln Gln Gln Glu Lys Ile Lys Pro Lys Val Arg Ser Thr Val Ala Gln		
435	440	445
His His Glu Ala Leu Val Gly His Gly Phe Thr His Ala His Ile Val		
450	455	460
Ala Leu Ser Gln His Pro Ala Ala Leu Gly Thr Val Ala Val Lys Tyr		
465	470	475
Gln Asp Met Ile Ala Ala Leu Pro Glu Ala Thr His Glu Ala Ile Val		
485	490	495
Gly Val Gly Lys Gln Trp Ser Gly Ala Arg Ala Leu Glu Ala Leu Leu		
500	505	510
Thr Val Ala Gly Glu Leu Arg Gly Pro Pro Leu Gln Leu Asp Thr Gly		
515	520	525
Gln Leu Leu Lys Ile Ala Lys Arg Gly Gly Val Thr Ala Val Glu Ala		
530	535	540
Val His Ala Trp Arg Asn Ala Leu Thr Gly Ala Pro Leu Asn Leu Thr		
545	550	555
Pro Asp Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala		
565	570	575
Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly		
580	585	590
Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys		
595	600	605
Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala		
610	615	620
His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser His Asp Gly		
625	630	635
Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys		
645	650	655
Gln Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser Asn		
660	665	670

Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val		
675	680	685
Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala		
690	695	700
Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu		
705	710	715
Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala		
725	730	735
Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg		
740	745	750
Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val		
755	760	765
Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val		
770	775	780
Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala		
785	790	795
Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu		
805	810	815
Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr		
820	825	830
Pro Asp Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala		
835	840	845
Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly		
850	855	860
Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys		
865	870	875
Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala		
885	890	895
His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Asn Gly		
900	905	910
Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys		
915	920	925
Gln Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser Asn		
930	935	940
Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val		
945	950	955
Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala		
965	970	975
Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu		

980						985				990					
Pro	Val	Leu	Cys	Gln	Asp	His	Gly	Leu	Thr	Pro	Glu	Gln	Val	Val	Ala
995						1000				1005					
Ile	Ala	Ser	Asn	Asn	Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln	
1010						1015				1020					
Arg	Leu	Leu	Pro	Val	Leu	Cys	Gln	Ala	His	Gly	Leu	Thr	Pro	Asp	
1025						1030				1035					
Gln	Val	Val	Ala	Ile	Ala	Ser	His	Asp	Gly	Gly	Lys	Gln	Ala	Leu	
1040						1045				1050					
Glu	Thr	Val	Gln	Arg	Leu	Leu	Pro	Val	Leu	Cys	Gln	Ala	His	Gly	
1055						1060				1065					
Leu	Thr	Pro	Ala	Gln	Val	Val	Ala	Ile	Ala	Ser	Asn	Asn	Gly	Gly	
1070						1075				1080					
Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu	Pro	Val	Leu	Cys	
1085						1090				1095					
Gln	Asp	His	Gly	Leu	Thr	Pro	Glu	Gln	Val	Val	Ala	Ile	Ala	Ser	
1100						1105				1110					
Asn	Asn	Gly	Gly	Arg	Pro	Ala	Leu	Glu	Ser	Ile	Val	Ala	Gln	Leu	
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Ser	Arg	Pro	Asp	Pro	Ala	Leu	Ala	Ala	Leu	Thr	Asn	Asp	His	Leu	
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Gly	Gly	Ser	Gly	Gly	Ser	Gly	Gly	Ser	Thr	Asn	Leu	Ser	Asp	Ile	
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Ile	Glu	Lys	Glu	Thr	Gly	Lys	Gln	Leu	Val	Ile	Gln	Glu	Ser	Ile	
1205						1210				1215					
Leu	Met	Leu	Pro	Glu	Glu	Val	Glu	Glu	Val	Ile	Gly	Asn	Lys	Pro	
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Glu	Ser	Asp	Ile	Leu	Val	His	Thr	Ala	Tyr	Asp	Glu	Ser	Thr	Asp	
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Met Leu	Ser Gly Gly Ser Gly	Gly Ser Gly Gly Ser	Thr Asn Leu
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Ser Asp	Ile Ile Glu Lys Glu	Thr Gly Lys Gln Leu	Val Ile Gln
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Glu Ser	Ile Leu Met Leu Pro	Glu Glu Val Glu Glu	Val Ile Gly
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Asn Lys	Pro Glu Ser Asp Ile	Leu Val His Thr Ala	Tyr Asp Glu
1325		1330	1335
Ser Thr	Asp Glu Asn Val Met	Leu Leu Thr Ser Asp	Ala Pro Glu
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Tyr Lys	Pro Trp Ala Leu Val	Ile Gln Asp Ser Asn	Gly Glu Asn
1355		1360	1365
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<210> 115

<211> 4173

<212> DNA

<213> 人工序列(Artificial Sequence)

<220>

<223> BE4-135-47

<400> 115

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<210> 116

<211> 1391

<212> PRT

<213> 人工序列(Artificial Sequence)

<220>

<223> BE4-135-47

<400> 116

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

130	135	140
Asn Arg Gln Gly Leu Arg Asp Leu Val Asn Ser Gly Val Thr Ile Gln		
145	150	155
Ile Met Thr Ala Pro Glu Tyr Asp Tyr Cys Trp Arg Asn Phe Val Asn		
165	170	175
Tyr Pro Pro Gly Lys Glu Ala His Trp Pro Arg Tyr Pro Pro Leu Trp		
180	185	190
Met Lys Leu Tyr Ala Leu Glu Leu His Ala Gly Ile Leu Gly Leu Pro		
195	200	205
Pro Cys Leu Asn Ile Leu Arg Arg Lys Gln Pro Gln Leu Thr Phe Phe		
210	215	220
Thr Ile Ala Leu Gln Ser Cys His Tyr Gln Arg Leu Pro Pro His Ile		
225	230	235
Leu Trp Ala Thr Gly Leu Lys Ser Gly Gly Ser Ser Gly Gly Ser Ser		
245	250	255
Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Ser		
260	265	270
Gly Gly Ser Ser Gly Gly Ser Tyr Thr Arg Val Gly Ser Gly Ser Gly		
275	280	285
Ser Gly Ser Ile Thr Arg Thr Thr Asn Pro Arg Asn Val Val Pro Lys		
290	295	300
Ile Tyr Met Ser Ala Gly Ser Ile Pro Leu Thr Thr His Ile Thr Asn		
305	310	315
Ser Ile Gln Pro Thr Leu Trp Thr Ile Gly Ser Ile Asn Gly Val Ala		
325	330	335
Pro Leu Ala Lys Ser Ile Lys Leu Gly Ile Pro Val Thr Gly Ser Ala		
340	345	350
Tyr Thr Asp Gln Thr Thr Ala Met Val Arg Lys Lys Val Ser Val Phe		
355	360	365
Met Gly Ser Gly Ser Gly Ser Gly Ser Ser Met Thr Ala Val Met Ala		
370	375	380
Ser Ser Pro Pro Lys Lys Lys Arg Lys Val Ala Ala Ala Asp Tyr Lys		
385	390	395
Asp Asp Asp Asp Lys Ser Trp Lys Asp Ala Ser Gly Trp Ser Arg Met		
405	410	415
His Ala Ala Pro Arg Arg Arg Ala Ala Gln Pro Ser Asp Ala Ser Pro		
420	425	430
Ala Ala Gln Val Asp Leu Arg Thr Leu Gly Tyr Ser Gln Gln Gln Gln		
435	440	445

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

755	760	765
Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile		
770	775	780
Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu		
785	790	795
Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val		
805	810	815
Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln		
820	825	830
Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln		
835	840	845
Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr		
850	855	860
Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro		
865	870	875
Glu Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu		
885	890	895
Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu		
900	905	910
Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln		
915	920	925
Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His		
930	935	940
Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser His Asp Gly Gly		
945	950	955
Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln		
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Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile		
980	985	990
Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu		
995	1000	1005
Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala		
1010	1015	1020
Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu		
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Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val		
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Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr		
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Pro Ala Gln Val Val Ala Ile	Ala Ser Asn Asn Gly	Gly Lys Gln
1085	1090	1095
Ala Leu Glu Thr Val Gln Arg	Leu Leu Pro Val Leu	Cys Gln Asp
1100	1105	1110
His Gly Leu Thr Pro Glu Gln	Val Val Ala Ile Ala	Ser Asn Asn
1115	1120	1125
Gly Gly Arg Pro Ala Leu Glu	Ser Ile Val Ala Gln	Leu Ser Arg
1130	1135	1140
Pro Asp Pro Ala Leu Ala Ala	Leu Thr Asn Asp His	Leu Val Ala
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Leu Ala Cys Leu Gly Gly Arg	Pro Ala Met Asp Ala	Val Lys Lys
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Gly Leu Pro His Ala Pro Glu	Leu Ile Arg Ser Ser	Gly Gly Ser
1175	1180	1185
Gly Gly Ser Gly Gly Ser Thr	Asn Leu Ser Asp Ile	Ile Glu Lys
1190	1195	1200
Glu Thr Gly Lys Gln Leu Val	Ile Gln Glu Ser Ile	Leu Met Leu
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Pro Glu Glu Val Glu Glu Val	Ile Gly Asn Lys Pro	Glu Ser Asp
1220	1225	1230
Ile Leu Val His Thr Ala Tyr	Asp Glu Ser Thr Asp	Glu Asn Val
1235	1240	1245
Met Leu Leu Thr Ser Asp Ala	Pro Glu Tyr Lys Pro	Trp Ala Leu
1250	1255	1260
Val Ile Gln Asp Ser Asn Gly	Glu Asn Lys Ile Lys	Met Leu Ser
1265	1270	1275
Gly Gly Ser Gly Gly Ser Gly	Gly Ser Thr Asn Leu	Ser Asp Ile
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Ile Glu Lys Glu Thr Gly Lys	Gln Leu Val Ile Gln	Glu Ser Ile
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Leu Met Leu Pro Glu Glu Val	Glu Glu Val Ile Gly	Asn Lys Pro
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Glu Ser Asp Ile Leu Val His	Thr Ala Tyr Asp Glu	Ser Thr Asp
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Glu Asn Val Met Leu Leu Thr	Ser Asp Ala Pro Glu	Tyr Lys Pro
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Trp Ala Leu Val Ile Gln Asp	Ser Asn Gly Glu Asn	Lys Ile Lys

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<210> 118

<211> 1391

<212> PRT

<213> 人工序列(Artificial Sequence)

<220>

<223> BE4-135-47-NC

<400> 118

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

Glu Leu Arg Lys Glu Thr Cys Leu Leu Tyr Glu Ile Lys Trp Gly Thr
50 55 60

Ser His Lys Ile Trp Arg His Ser Ser Lys Asn Thr Thr Lys His Val
65 70 75 80

Glu Val Asn Phe Ile Glu Lys Phe Thr Ser Glu Arg His Phe Cys Pro
85 90 95

Ser Thr Ser Cys Ser Ile Thr Trp Phe Leu Ser Trp Ser Pro Cys Gly
100 105 110

Glu Cys Ser Lys Ala Ile Thr Glu Phe Leu Ser Gln His Pro Asn Val
115 120 125

Thr Leu Val Ile Tyr Val Ala Arg Leu Tyr His His Met Asp Gln Gln
130 135 140

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

Ile Met Thr Ala Pro Glu Tyr Asp Tyr Cys Trp Arg Asn Phe Val Asn
165 170 175

Tyr Pro Pro Gly Lys Glu Ala His Trp Pro Arg Tyr Pro Pro Leu Trp
180 185 190

Met Lys Leu Tyr Ala Leu Glu Leu His Ala Gly Ile Leu Gly Leu Pro
195 200 205

Pro Cys Leu Asn Ile Leu Arg Arg Lys Gln Pro Gln Leu Thr Phe Phe
210 215 220

Thr	Ile	Ala	Leu	Gln	Ser	Cys	His	Tyr	Gln	Arg	Leu	Pro	Pro	His	Ile
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Leu	Trp	Ala	Thr	Gly	Leu	Lys	Ser	Gly	Gly	Ser	Ser	Gly	Gly	Ser	Ser
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Gly	Ser	Glu	Thr	Pro	Gly	Thr	Ser	Glu	Ser	Ala	Thr	Pro	Glu	Ser	Ser
				260				265					270		
Gly	Gly	Ser	Ser	Gly	Gly	Ser	Tyr	Thr	Arg	Val	Gly	Ser	Gly	Ser	Gly
				275				280					285		
Ser	Gly	Ser	Ile	Thr	Arg	Thr	Thr	Asn	Pro	Arg	Asn	Val	Val	Pro	Lys
				290				295					300		
Ile	Tyr	Met	Ser	Ala	Gly	Ser	Ile	Pro	Leu	Thr	Thr	His	Ile	Thr	Asn
305					310					315					320
Ser	Ile	Gln	Pro	Thr	Leu	Trp	Thr	Ile	Gly	Ser	Ile	Asn	Gly	Val	Ala
				325					330					335	
Pro	Leu	Ala	Lys	Ser	Ile	Lys	Leu	Gly	Ile	Pro	Val	Thr	Gly	Ser	Ala
				340				345					350		
Tyr	Thr	Asp	Gln	Thr	Thr	Ala	Met	Val	Arg	Lys	Lys	Val	Ser	Val	Phe
				355				360					365		
Met	Gly	Ser	Gly	Ser	Gly	Ser	Gly	Ser	Ser	Met	Thr	Ala	Val	Met	Ala
				370				375					380		
Ser	Ser	Pro	Pro	Lys	Lys	Lys	Arg	Lys	Val	Ala	Ala	Ala	Asp	Tyr	Lys
385					390					395					400
Asp	Asp	Asp	Asp	Lys	Ser	Trp	Lys	Asp	Ala	Ser	Gly	Trp	Ser	Arg	Met
				405					410					415	
His	Ala	Ala	Pro	Arg	Arg	Arg	Ala	Ala	Gln	Pro	Ser	Asp	Ala	Ser	Pro
				420					425				430		
Ala	Ala	Gln	Val	Asp	Leu	Arg	Thr	Leu	Gly	Tyr	Ser	Gln	Gln	Gln	Gln
				435				440					445		
Glu	Lys	Ile	Lys	Pro	Lys	Val	Arg	Ser	Thr	Val	Ala	Gln	His	His	Glu
				450				455				460			
Ala	Leu	Val	Gly	His	Gly	Phe	Thr	His	Ala	His	Ile	Val	Ala	Leu	Ser
465					470					475					480
Gln	His	Pro	Ala	Ala	Leu	Gly	Thr	Val	Ala	Val	Thr	Tyr	Gln	His	Ile
				485					490					495	
Ile	Thr	Ala	Leu	Pro	Glu	Ala	Thr	His	Glu	Asp	Ile	Val	Gly	Val	Gly
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Lys	Gln	Trp	Ser	Gly	Ala	Arg	Ala	Leu	Glu	Ala	Leu	Leu	Thr	Asp	Ala
				515				520					525		
Gly	Glu	Leu	Arg	Gly	Pro	Pro	Leu	Gln	Leu	Asp	Thr	Gly	Gln	Leu	Val

530	535	540
Lys Ile Ala Lys Arg Gly Gly Val Thr Ala Met Glu Ala Val His Ala		
545	550	555
Ser Arg Asn Ala Leu Thr Gly Ala Pro Leu Asn Leu Thr Pro Asp Gln		
565	570	575
Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr		
580	585	590
Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro		
595	600	605
Glu Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu		
610	615	620
Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu		
625	630	635
Thr Pro Asp Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln		
645	650	655
Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His		
660	665	670
Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly		
675	680	685
Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln		
690	695	700
Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser His Asp		
705	710	715
Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu		
725	730	735
Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser		
740	745	750
Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro		
755	760	765
Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile		
770	775	780
Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu		
785	790	795
Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val		
805	810	815
Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln		
820	825	830
Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln		
835	840	845

Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr		
850	855	860
Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro		
865	870	875 880
Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu		
885	890	895
Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu		
900	905	910
Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln		
915	920	925
Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His		
930	935	940
Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly		
945	950	955 960
Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln		
965	970	975
Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser His Asp		
980	985	990
Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu		
995	1000	1005
Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala		
1010	1015	1020
Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu		
1025	1030	1035
Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val		
1040	1045	1050
Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr		
1055	1060	1065
Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr		
1070	1075	1080
Pro Ala Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln		
1085	1090	1095
Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp		
1100	1105	1110
His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Asn		
1115	1120	1125
Gly Gly Arg Pro Ala Leu Glu Ser Ile Val Ala Gln Leu Ser Arg		
1130	1135	1140
Pro Asp Pro Ala Leu Ala Ala Leu Thr Asn Asp His Leu Val Ala		

1145	1150	1155
Leu Ala Cys Leu Gly Gly Arg Pro Ala Met Asp Ala Val Lys Lys		
1160	1165	1170
Gly Leu Pro His Ala Pro Glu Leu Ile Arg Ser Ser Gly Gly Ser		
1175	1180	1185
Gly Gly Ser Gly Gly Ser Thr Asn Leu Ser Asp Ile Ile Glu Lys		
1190	1195	1200
Glu Thr Gly Lys Gln Leu Val Ile Gln Glu Ser Ile Leu Met Leu		
1205	1210	1215
Pro Glu Glu Val Glu Glu Val Ile Gly Asn Lys Pro Glu Ser Asp		
1220	1225	1230
Ile Leu Val His Thr Ala Tyr Asp Glu Ser Thr Asp Glu Asn Val		
1235	1240	1245
Met Leu Leu Thr Ser Asp Ala Pro Glu Tyr Lys Pro Trp Ala Leu		
1250	1255	1260
Val Ile Gln Asp Ser Asn Gly Glu Asn Lys Ile Lys Met Leu Ser		
1265	1270	1275
Gly Gly Ser Gly Gly Ser Gly Gly Ser Thr Asn Leu Ser Asp Ile		
1280	1285	1290
Ile Glu Lys Glu Thr Gly Lys Gln Leu Val Ile Gln Glu Ser Ile		
1295	1300	1305
Leu Met Leu Pro Glu Glu Val Glu Glu Val Ile Gly Asn Lys Pro		
1310	1315	1320
Glu Ser Asp Ile Leu Val His Thr Ala Tyr Asp Glu Ser Thr Asp		
1325	1330	1335
Glu Asn Val Met Leu Leu Thr Ser Asp Ala Pro Glu Tyr Lys Pro		
1340	1345	1350
Trp Ala Leu Val Ile Gln Asp Ser Asn Gly Glu Asn Lys Ile Lys		
1355	1360	1365
Met Leu Ser Gly Gly Ser Lys Arg Thr Ala Asp Gly Ser Glu Phe		
1370	1375	1380
Glu Pro Lys Lys Lys Arg Lys Val		
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<210> 119		
<211> 4824		
<212> DNA		
<213> 人工序列(Artificial Sequence)		
<220>		
<223> BE4-234-WT		

<400> 119

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<210> 120

<211> 1608

<212> PRT

<213> 人工序列(Artificial Sequence)

<220>

<223> BE4-234-WT

<400> 120

Met Lys Arg Thr Ala Asp Gly Ser Glu Phe Glu Ser Pro Lys Lys Lys
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Arg Lys Val Ser Ser Glu Thr Gly Pro Val Ala Val Asp Pro Thr Leu
 20 25 30

Arg Arg Arg Ile Glu Pro His Glu Phe Glu Val Phe Phe Asp Pro Arg
 35 40 45

Glu Leu Arg Lys Glu Thr Cys Leu Leu Tyr Glu Ile Lys Trp Gly Thr
 50 55 60

Ser His Lys Ile Trp Arg His Ser Ser Lys Asn Thr Thr Lys His Val
 65 70 75 80

Glu Val Asn Phe Ile Glu Lys Phe Thr Ser Glu Arg His Phe Cys Pro
 85 90 95

Ser Thr Ser Cys Ser Ile Thr Trp Phe Leu Ser Trp Ser Pro Cys Gly
 100 105 110

Glu Cys Ser Lys Ala Ile Thr Glu Phe Leu Ser Gln His Pro Asn Val
 115 120 125

Thr Leu Val Ile Tyr Val Ala Arg Leu Tyr His His Met Asp Gln Gln
 130 135 140

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

Ile Met Thr Ala Pro Glu Tyr Asp Tyr Cys Trp Arg Asn Phe Val Asn
 165 170 175

Tyr Pro Pro Gly Lys Glu Ala His Trp Pro Arg Tyr Pro Pro Leu Trp
 180 185 190

Met Lys Leu Tyr Ala Leu Glu Leu His Ala Gly Ile Leu Gly Leu Pro
 195 200 205

Pro Cys Leu Asn Ile Leu Arg Arg Lys Gln Pro Gln Leu Thr Phe Phe
 210 215 220

Thr	Ile	Ala	Leu	Gln	Ser	Cys	His	Tyr	Gln	Arg	Leu	Pro	Pro	His	Ile
225					230					235					240
Leu	Trp	Ala	Thr	Gly	Leu	Lys	Ser	Gly	Gly	Ser	Ser	Gly	Gly	Ser	Ser
				245					250					255	
Gly	Ser	Glu	Thr	Pro	Gly	Thr	Ser	Glu	Ser	Ala	Thr	Pro	Glu	Ser	Ser
				260					265					270	
Gly	Gly	Ser	Ser	Gly	Gly	Ser	Tyr	Thr	Arg	Val	Gly	Ser	Gly	Ser	Gly
				275					280					285	
Ser	Gly	Ser	Ile	Thr	Arg	Thr	Thr	Asn	Pro	Arg	Asn	Val	Val	Pro	Lys
				290					295					300	
Ile	Tyr	Met	Ser	Ala	Gly	Ser	Ile	Pro	Leu	Thr	Thr	His	Ile	Thr	Asn
305					310					315					320
Ser	Ile	Gln	Pro	Thr	Leu	Trp	Thr	Ile	Gly	Ser	Ile	Asn	Gly	Val	Ala
				325					330					335	
Pro	Leu	Ala	Lys	Ser	Ile	Lys	Leu	Gly	Ile	Pro	Val	Thr	Gly	Ser	Ala
				340					345					350	
Tyr	Thr	Asp	Gln	Thr	Thr	Ala	Met	Val	Arg	Lys	Lys	Val	Ser	Val	Phe
				355					360					365	
Met	Gly	Ser	Gly	Ser	Gly	Ser	Gly	Ser	Ser	Met	Thr	Gly	Val	Gly	Ser
				370					375					380	
Gly	Ser	Gly	Ser	Gly	Ser	Ile	Thr	Arg	Thr	Thr	Asn	Pro	Arg	Asn	Val
385					390					395					400
Val	Pro	Lys	Ile	Tyr	Met	Ser	Ala	Gly	Ser	Ile	Pro	Leu	Thr	Thr	His
				405					410					415	
Ile	Thr	Asn	Ser	Ile	Gln	Pro	Thr	Leu	Trp	Thr	Ile	Gly	Ser	Ile	Asn
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Gly	Val	Ala	Pro	Leu	Ala	Lys	Ser	Ile	Lys	Leu	Gly	Ile	Pro	Val	Thr
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Gly	Ser	Ala	Tyr	Thr	Asp	Gln	Thr	Thr	Ala	Met	Val	Arg	Lys	Lys	Val
				450					455					460	
Ser	Val	Phe	Met	Gly	Ser	Gly	Ser	Gly	Ser	Gly	Ser	Ser	Met	Thr	Ala
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Val	Met	Asp	Tyr	Lys	Asp	His	Asp	Gly	Asp	Tyr	Lys	Asp	His	Asp	Ile
				485					490					495	
Asp	Tyr	Lys	Asp	Asp	Asp	Asp	Lys	Met	Ala	Pro	Lys	Lys	Lys	Arg	Lys
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Val	Gly	Ile	His	Gly	Val	Pro	Ala	Ala	Val	Asp	Leu	Arg	Thr	Leu	Gly
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His Ile Val Ala Leu Ser Gln His Pro Ala Ala Leu Gly Thr Val Ala		560
	565	570
Val Lys Tyr Gln Asp Met Ile Ala Ala Leu Pro Glu Ala Thr His Glu		575
	580	585
Ala Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg Ala Leu Glu		590
	595	600
Ala Leu Leu Thr Val Ala Gly Glu Leu Arg Gly Pro Pro Leu Gln Leu		605
610	615	620
Asp Thr Gly Gln Leu Leu Lys Ile Ala Lys Arg Gly Gly Val Thr Ala		
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Val Glu Ala Val His Ala Trp Arg Asn Ala Leu Thr Gly Ala Pro Leu		
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Asn Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly		655
	660	665
Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln		670
	675	680
Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp		
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Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu		
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Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser		
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Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro		735
	740	745
Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile		
	755	760
Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu		765
	770	775
Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val		
785	790	795
Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln		
	805	810
Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln		815
	820	825
Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr		
835	840	845

Val	Gln	Arg	Leu	Leu	Pro	Val	Leu	Cys	Gln	Ala	His	Gly	Leu	Thr	Pro
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Gly	Leu	Thr	Pro	Asp	Gln	Val	Val	Ala	Ile	Ala	Ser	Asn	Asn	Gly	Gly
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Asp	His	Gly	Leu	Thr	Pro	Glu	Gln	Val	Val	Ala	Ile	Ala	Ser	Asn	Asn
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Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu	Pro	Val	Leu
			980						985					990	
Cys	Gln	Ala	His	Gly	Leu	Thr	Pro	Asp	Gln	Val	Val	Ala	Ile	Ala	Ser
		995							1000					1005	
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Pro	Val	Leu	Cys	Gln	Ala	His	Gly	Leu	Thr	Pro	Ala	Gln	Val	Val	
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Ala	Ile	Ala	Ser	His	Asp	Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val	
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Gln	Arg	Leu	Leu	Pro	Val	Leu	Cys	Gln	Asp	His	Gly	Leu	Thr	Pro	
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Asp	Gln	Val	Val	Ala	Ile	Ala	Ser	Asn	Ile	Gly	Gly	Lys	Gln	Ala	
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Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu	Pro	Val	Leu	Cys	Gln	Asp	His	
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Cys	Gln	Ala	His	Gly	Leu	Thr	Pro	Asp	Gln	Val	Val	Ala	Ile	Ala	
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Ser	Asn	Ile	Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu	

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Leu Pro Val Leu Cys Gln Ala	His Gly Leu Thr Pro	Ala Gln Val
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Val Ala Ile Ala Ser Asn Asn	Gly Gly Lys Gln Ala	Leu Glu Thr
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Val Gln Arg Leu Leu Pro Val	Leu Cys Gln Asp His	Gly Leu Thr
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Pro Glu Gln Val Val Ala Ile	Ala Ser Asn Asn Gly	Gly Arg Pro
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Ala Leu Glu Ser Ile Val Ala	Gln Leu Ser Arg Pro	Asp Pro Ala
1220	1225	1230
Leu Ala Ala Leu Thr Asn Asp	His Leu Val Ala Leu	Ala Cys Leu
1235	1240	1245
Gly Gly Arg Pro Ala Leu Asp	Ala Val Lys Lys Gly	Leu Pro His
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Ala Pro Ala Leu Ile Lys Arg	Thr Asn Arg Arg Ile	Pro Glu Arg
1265	1270	1275
Thr Ser His Arg Val Ala Asp	His Ala Gln Val Val	Arg Val Leu
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Gly Phe Phe Gln Cys His Ser	His Pro Ala Gln Ala	Phe Asp Asp
1295	1300	1305
Ala Met Thr Gln Phe Gly Met	Ser Arg His Gly Leu	Leu Gln Leu
1310	1315	1320
Phe Arg Arg Val Gly Val Thr	Glu Leu Glu Ala Arg	Ser Gly Thr
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Leu Pro Pro Ala Ser Gln Arg	Trp Asp Arg Ile Leu	Gln Ala Ser
1340	1345	1350
Gly Met Lys Arg Ala Lys Pro	Ser Pro Thr Ser Thr	Gln Thr Pro
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Asp Gln Ala Ser Leu His Ala	Phe Ala Asp Ser Leu	Glu Arg Asp
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Leu Asp Ala Pro Ser Pro Met	His Glu Gly Asp Gln	Thr Arg Ala
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Ser Ala Ser Ser Gly Gly Ser	Gly Gly Ser Gly Gly	Ser Thr Asn
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Leu Ser Asp Ile Ile Glu Lys	Glu Thr Gly Lys Gln	Leu Val Ile
1415	1420	1425
Gln Glu Ser Ile Leu Met Leu	Pro Glu Glu Val Glu	Glu Val Ile
1430	1435	1440

Gly Asn	Lys Pro	Glu Ser	Asp Ile	Leu Val	His Thr	Ala Tyr	Asp
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Glu Ser	Thr Asp	Glu Asn	Val Met	Leu Leu	Thr Ser	Asp Ala	Pro
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Glu Tyr	Lys Pro	Trp Ala	Leu Val	Ile Gln	Asp Ser	Asn Gly	Glu
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Asn Lys	Ile Lys	Met Leu	Ser Gly	Gly Ser	Gly Gly	Ser Gly	Gly
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Ser Thr	Asn Leu	Ser Asp	Ile Ile	Glu Lys	Glu Thr	Gly Lys	Gln
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Leu Val	Ile Gln	Glu Ser	Ile Leu	Met Leu	Pro Glu	Glu Val	Glu
1520			1525			1530	
Glu Val	Ile Gly	Asn Lys	Pro Glu	Ser Asp	Ile Leu	Val His	Thr
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Ala Tyr	Asp Glu	Ser Thr	Asp Glu	Asn Val	Met Leu	Leu Thr	Ser
1550			1555			1560	
Asp Ala	Pro Glu	Tyr Lys	Pro Trp	Ala Leu	Val Ile	Gln Asp	Ser
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Asn Gly	Glu Asn	Lys Ile	Lys Met	Leu Ser	Gly Gly	Ser Lys	Arg
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Thr Ala	Asp Gly	Ser Glu	Phe Glu	Pro Lys	Lys Lys	Arg Lys	Val
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<211> 4824

<212> DNA

<213> 人工序列(Artificial Sequence)

<220>

<223> BE4-234-WT-NC

<400> 121

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tttgaggtgt tctttgatcc aagagagctg aggaaggaga catgcctgct gtacgagatc	180
aagtggggca catctcacia gatctggcgc cactctagca agaacaccac aaagcacgtg	240
gaagtgaatt tcatcgagaa gtttaccage gagcggcact tctgccctag cacctcctgt	300
tctatcacat ggtttctgag ctggtcccca tgcggcgagt gtagcaaggc catcaccgag	360
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<220>	
<223> BE4-234-WT-NC	
<400> 122	

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Arg	Arg	Arg	Ile	Glu	Pro	His	Glu	Phe	Glu	Val	Phe	Phe	Asp	Pro	Arg
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Glu	Leu	Arg	Lys	Glu	Thr	Cys	Leu	Leu	Tyr	Glu	Ile	Lys	Trp	Gly	Thr
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Ser	His	Lys	Ile	Trp	Arg	His	Ser	Ser	Lys	Asn	Thr	Thr	Lys	His	Val
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Glu	Val	Asn	Phe	Ile	Glu	Lys	Phe	Thr	Ser	Glu	Arg	His	Phe	Cys	Pro
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Ser	Thr	Ser	Cys	Ser	Ile	Thr	Trp	Phe	Leu	Ser	Trp	Ser	Pro	Cys	Gly
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Glu	Cys	Ser	Lys	Ala	Ile	Thr	Glu	Phe	Leu	Ser	Gln	His	Pro	Asn	Val
				115				120					125		
Thr	Leu	Val	Ile	Tyr	Val	Ala	Arg	Leu	Tyr	His	His	Met	Asp	Gln	Gln
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Asn	Arg	Gln	Gly	Leu	Arg	Asp	Leu	Val	Asn	Ser	Gly	Val	Thr	Ile	Gln
145					150					155					160
Ile	Met	Thr	Ala	Pro	Glu	Tyr	Asp	Tyr	Cys	Trp	Arg	Asn	Phe	Val	Asn
				165					170					175	
Tyr	Pro	Pro	Gly	Lys	Glu	Ala	His	Trp	Pro	Arg	Tyr	Pro	Pro	Leu	Trp
				180				185					190		
Met	Lys	Leu	Tyr	Ala	Leu	Glu	Leu	His	Ala	Gly	Ile	Leu	Gly	Leu	Pro
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Pro	Cys	Leu	Asn	Ile	Leu	Arg	Arg	Lys	Gln	Pro	Gln	Leu	Thr	Phe	Phe
				210				215				220			
Thr	Ile	Ala	Leu	Gln	Ser	Cys	His	Tyr	Gln	Arg	Leu	Pro	Pro	His	Ile
225					230					235					240
Leu	Trp	Ala	Thr	Gly	Leu	Lys	Ser	Gly	Gly	Ser	Ser	Gly	Gly	Ser	Ser
				245					250					255	
Gly	Ser	Glu	Thr	Pro	Gly	Thr	Ser	Glu	Ser	Ala	Thr	Pro	Glu	Ser	Ser
				260				265					270		
Gly	Gly	Ser	Ser	Gly	Gly	Ser	Tyr	Thr	Arg	Val	Gly	Ser	Gly	Ser	Gly
				275				280				285			
Ser	Gly	Ser	Ile	Thr	Arg	Thr	Thr	Asn	Pro	Arg	Asn	Val	Val	Pro	Lys
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Ile	Tyr	Met	Ser	Ala	Gly	Ser	Ile	Pro	Leu	Thr	Thr	His	Ile	Thr	Asn

305	310	315	320
Ser Ile Gln Pro Thr	Leu Trp Thr Ile Gly	Ser Ile Asn Gly Val Ala	
	325	330	335
Pro Leu Ala Lys Ser	Ile Lys Leu Gly Ile	Pro Val Thr Gly Ser Ala	
	340	345	350
Tyr Thr Asp Gln Thr	Thr Ala Met Val Arg	Lys Lys Val Ser Val Phe	
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Met Gly Ser Gly Ser	Gly Ser Gly Ser Met	Thr Gly Val Gly Ser	
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Gly Ser Gly Ser Gly	Ser Ile Thr Arg Thr	Thr Asn Pro Arg Asn Val	
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Val Pro Lys Ile Tyr	Met Ser Ala Gly Ser	Ile Pro Leu Thr Thr His	
	405	410	415
Ile Thr Asn Ser Ile	Gln Pro Thr Leu Trp	Thr Ile Gly Ser Ile Asn	
	420	425	430
Gly Val Ala Pro Leu	Ala Lys Ser Ile Lys	Leu Gly Ile Pro Val Thr	
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Gly Ser Ala Tyr Thr	Asp Gln Thr Thr Ala	Met Val Arg Lys Lys Val	
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Ser Val Phe Met Gly	Ser Gly Ser Gly Ser	Gly Ser Ser Met Thr Ala	
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Val Met Asp Tyr Lys	Asp His Asp Gly Asp	Tyr Lys Asp His Asp Ile	
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Asp Tyr Lys Asp Asp	Asp Asp Lys Met Ala	Pro Lys Lys Lys Arg Lys	
	500	505	510
Val Gly Ile His Gly	Val Pro Ala Ala Val	Asp Leu Arg Thr Leu Gly	
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Tyr Ser Gln Gln Gln	Gln Glu Lys Ile Lys	Pro Lys Val Arg Ser Thr	
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Val Ala Gln His His	Glu Ala Leu Val Gly	His Gly Phe Thr His Ala	
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His Ile Val Ala Leu	Ser Gln His Pro Ala	Ala Leu Gly Thr Val Ala	
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Val Lys Tyr Gln Asp	Met Ile Ala Ala Leu	Pro Glu Ala Thr His Glu	
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Ala Ile Val Gly Val	Gly Lys Gln Trp Ser	Gly Ala Arg Ala Leu Glu	
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Ala Leu Leu Thr Val	Ala Gly Glu Leu Arg	Gly Pro Pro Leu Gln Leu	
610	615	620	

Asp Thr Gly Gln Leu Leu Lys Ile Ala Lys Arg Gly Gly Val Thr Ala			
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Val Glu Ala Val His Ala Trp Arg Asn Ala Leu Thr Gly Ala Pro Leu			
	645	650	655
Asn Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly			
	660	665	670
Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln			
	675	680	685
Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Asn			
	690	695	700
Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu			
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Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser			
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His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro			
	740	745	750
Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile			
	755	760	765
Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu			
	770	775	780
Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val			
785	790	795	800
Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln			
	805	810	815
Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln			
	820	825	830
Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr			
	835	840	845
Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro			
	850	855	860
Asp Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu			
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Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu			
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Thr Pro Ala Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln			
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Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His			
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Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly			

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Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Ile		
965	970	975
Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu		
980	985	990
Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser		
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Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu		
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Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro		
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Asp Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala		
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Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu		
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Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val		
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Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr		
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Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr		
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Pro Glu Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Arg Pro		
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Ala Leu Glu Ser Ile Val Ala Gln Leu Ser Arg Pro Asp Pro Ala		
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Leu Ala	Ala Leu Thr Asn Asp	His Leu Val Ala Leu	Ala Cys Leu
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Gly Gly	Arg Pro Ala Leu Asp	Ala Val Lys Lys Gly	Leu Pro His
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Thr Ser	His Arg Val Ala Asp	His Ala Gln Val Val	Arg Val Leu
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Gly Phe	Phe Gln Cys His Ser	His Pro Ala Gln Ala	Phe Asp Asp
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Ala Met	Thr Gln Phe Gly Met	Ser Arg His Gly Leu	Leu Gln Leu
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Phe Arg	Arg Val Gly Val Thr	Glu Leu Glu Ala Arg	Ser Gly Thr
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Leu Pro	Pro Ala Ser Gln Arg	Trp Asp Arg Ile Leu	Gln Ala Ser
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Gly Met	Lys Arg Ala Lys Pro	Ser Pro Thr Ser Thr	Gln Thr Pro
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Asp Gln	Ala Ser Leu His Ala	Phe Ala Asp Ser Leu	Glu Arg Asp
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Leu Asp	Ala Pro Ser Pro Met	His Glu Gly Asp Gln	Thr Arg Ala
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Ser Ala	Ser Ser Gly Gly Ser	Gly Gly Ser Gly Gly	Ser Thr Asn
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Leu Ser	Asp Ile Ile Glu Lys	Glu Thr Gly Lys Gln	Leu Val Ile
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Gln Glu	Ser Ile Leu Met Leu	Pro Glu Glu Val Glu	Glu Val Ile
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Gly Asn	Lys Pro Glu Ser Asp	Ile Leu Val His Thr	Ala Tyr Asp
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Glu Ser	Thr Asp Glu Asn Val	Met Leu Leu Thr Ser	Asp Ala Pro
1460	1465	1470	
Glu Tyr	Lys Pro Trp Ala Leu	Val Ile Gln Asp Ser	Asn Gly Glu
1475	1480	1485	
Asn Lys	Ile Lys Met Leu Ser	Gly Gly Ser Gly Gly	Ser Gly Gly
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Ser Thr	Asn Leu Ser Asp Ile	Ile Glu Lys Glu Thr	Gly Lys Gln
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Leu Val	Ile Gln Glu Ser Ile	Leu Met Leu Pro Glu	Glu Val Glu

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<211> 1493

<212> PRT

<213> 人工序列(Artificial Sequence)

<220>

<223> BE4-234-63

<400> 124

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

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Ile Met Thr Ala Pro Glu Tyr Asp Tyr Cys Trp Arg Asn Phe Val Asn		
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Tyr Pro Pro Gly Lys Glu Ala His Trp Pro Arg Tyr Pro Pro Leu Trp		
180	185	190
Met Lys Leu Tyr Ala Leu Glu Leu His Ala Gly Ile Leu Gly Leu Pro		
195	200	205
Pro Cys Leu Asn Ile Leu Arg Arg Lys Gln Pro Gln Leu Thr Phe Phe		
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Thr Ile Ala Leu Gln Ser Cys His Tyr Gln Arg Leu Pro Pro His Ile		
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Leu Trp Ala Thr Gly Leu Lys Ser Gly Gly Ser Ser Gly Gly Ser Ser		
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Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Ser		
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Gly Gly Ser Ser Gly Gly Ser Tyr Thr Arg Val Gly Ser Gly Ser Gly		
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Ser Gly Ser Ile Thr Arg Thr Thr Asn Pro Arg Asn Val Val Pro Lys		
290	295	300
Ile Tyr Met Ser Ala Gly Ser Ile Pro Leu Thr Thr His Ile Thr Asn		
305	310	315
Ser Ile Gln Pro Thr Leu Trp Thr Ile Gly Ser Ile Asn Gly Val Ala		
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Pro Leu Ala Lys Ser Ile Lys Leu Gly Ile Pro Val Thr Gly Ser Ala		
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Tyr Thr Asp Gln Thr Thr Ala Met Val Arg Lys Lys Val Ser Val Phe		
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Met Gly Ser Gly Ser Gly Ser Gly Ser Ser Met Thr Gly Val Gly Ser		
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385	390	395
Val Pro Lys Ile Tyr Met Ser Ala Gly Ser Ile Pro Leu Thr Thr His		
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Ile Thr Asn Ser Ile Gln Pro Thr Leu Trp Thr Ile Gly Ser Ile Asn		
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Asp Tyr Lys Asp Asp Asp Asp Lys Met Ala Pro Lys Lys Lys Arg Lys		
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His Ile Val Ala Leu Ser Gln His Pro Ala Ala Leu Gly Thr Val Ala		
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Val Lys Tyr Gln Asp Met Ile Ala Ala Leu Pro Glu Ala Thr His Glu		
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Ala Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg Ala Leu Glu		
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Ala Leu Leu Thr Val Ala Gly Glu Leu Arg Gly Pro Pro Leu Gln Leu		
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Val Glu Ala Val His Ala Trp Arg Asn Ala Leu Thr Gly Ala Pro Leu		
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Asn Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly		
	660	665 670
Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln		
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Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp		
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Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu		
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Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser		
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Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro		
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Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile		

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Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln		
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Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu		
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Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser		
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Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val		
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1040	1045	1050
Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro		
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Gly Leu	Thr Pro	Glu Gln	Val Val	Ala Ile	Ala Ser	Asn Ile	Gly
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Gly Lys	Gln Ala	Leu Glu	Thr Val	Gln Arg	Leu Leu	Pro Val	Leu
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Cys Gln	Ala His	Gly Leu	Thr Pro	Asp Gln	Val Val	Ala Ile	Ala
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Val Ala	Ile Ala	Ser Asn	Asn Gly	Gly Lys	Gln Ala	Leu Glu	Thr
1175			1180		1185		
Val Gln	Arg Leu	Leu Pro	Val Leu	Cys Gln	Asp His	Gly Leu	Thr
1190			1195		1200		
Pro Glu	Gln Val	Val Ala	Ile Ala	Ser Asn	Asn Gly	Gly Arg	Pro
1205			1210		1215		
Ala Leu	Glu Ser	Ile Val	Ala Gln	Leu Ser	Arg Pro	Asp Pro	Ala
1220			1225		1230		
Leu Ala	Ala Leu	Thr Asn	Asp His	Leu Val	Ala Leu	Ala Cys	Leu
1235			1240		1245		
Gly Gly	Arg Pro	Ala Leu	Asp Ala	Val Lys	Lys Gly	Leu Pro	His
1250			1255		1260		
Ala Pro	Ala Leu	Ile Lys	Arg Thr	Asn Arg	Arg Ile	Pro Glu	Arg
1265			1270		1275		
Thr Ser	His Arg	Val Ala	Gly Ser	Ser Gly	Gly Ser	Gly Gly	Ser
1280			1285		1290		
Gly Gly	Ser Thr	Asn Leu	Ser Asp	Ile Ile	Glu Lys	Glu Thr	Gly
1295			1300		1305		
Lys Gln	Leu Val	Ile Gln	Glu Ser	Ile Leu	Met Leu	Pro Glu	Glu
1310			1315		1320		
Val Glu	Glu Val	Ile Gly	Asn Lys	Pro Glu	Ser Asp	Ile Leu	Val
1325			1330		1335		
His Thr	Ala Tyr	Asp Glu	Ser Thr	Asp Glu	Asn Val	Met Leu	Leu
1340			1345		1350		
Thr Ser	Asp Ala	Pro Glu	Tyr Lys	Pro Trp	Ala Leu	Val Ile	Gln

1355	1360	1365
Asp Ser Asn Gly Glu Asn Lys Ile Lys Met Leu Ser Gly Gly Ser		
1370	1375	1380
Gly Gly Ser Gly Gly Ser Thr Asn Leu Ser Asp Ile Ile Glu Lys		
1385	1390	1395
Glu Thr Gly Lys Gln Leu Val Ile Gln Glu Ser Ile Leu Met Leu		
1400	1405	1410
Pro Glu Glu Val Glu Glu Val Ile Gly Asn Lys Pro Glu Ser Asp		
1415	1420	1425
Ile Leu Val His Thr Ala Tyr Asp Glu Ser Thr Asp Glu Asn Val		
1430	1435	1440
Met Leu Leu Thr Ser Asp Ala Pro Glu Tyr Lys Pro Trp Ala Leu		
1445	1450	1455
Val Ile Gln Asp Ser Asn Gly Glu Asn Lys Ile Lys Met Leu Ser		
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Gly Gly Ser Lys Arg Thr Ala Asp Gly Ser Glu Phe Glu Pro Lys		
1475	1480	1485
Lys Lys Arg Lys Val		
1490		

<210> 125

<211> 4479

<212> DNA

<213> 人工序列(Artificial Sequence)

<220>

<223> BE4-234-63-NC

<400> 125

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tttgaggtgt tctttgatcc aagagagctg aggaaggaga catgcctgct gtacgagatc	180
aagtggggca catctcacia gatctggcgc cactctagca agaacaccac aaagcacgtg	240
gaagtgaatt tcatcgagaa gtttaccagc gagcggcact tctgccctag cacctcctgt	300
tctatcacat ggtttctgag ctggtcccca tgcggcgagt gtagcaaggc catcaccgag	360
ttcctgtccc agcacccaaa cgtgaccctg gtcactacg tggccaggct gtatcaccac	420
atggaccagc agaacaggca gggcctgcgg gatctggtga attccggcgt gaccatccag	480
atcatgacag ccccccagta cgattactgt tggagaaact tcgtgaacta cccacctggc	540
aaggaggcac actggcctag gtacccaccc ctgtggatga agctgtatgc actggagctg	600
cacgcaggaa tcctgggcct gcctccatgc ctgaatatcc tgcgccgga gcagccccag	660
ctgaccttct ttacaatcgc cctgcagagc tgtcactacc agcggctgcc acctcacatc	720
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<210> 126

<211> 1493

<212> PRT

<213> 人工序列(Artificial Sequence)

<220>

<223> BE4-234-63-NC

<400> 126

Met Lys Arg Thr Ala Asp Gly Ser Glu Phe Glu Ser Pro Lys Lys Lys

1 5 10 15

Arg Lys Val Ser Ser Glu Thr Gly Pro Val Ala Val Asp Pro Thr Leu

20 25 30

Arg Arg Arg Ile Glu Pro His Glu Phe Glu Val Phe Phe Asp Pro Arg

35 40 45

Glu Leu Arg Lys Glu Thr Cys Leu Leu Tyr Glu Ile Lys Trp Gly Thr

50 55 60

Ser His Lys Ile Trp Arg His Ser Ser Lys Asn Thr Thr Lys His Val

65	70	75	80
Glu Val Asn Phe Ile Glu Lys Phe Thr Ser Glu Arg His Phe Cys Pro			
	85	90	95
Ser Thr Ser Cys Ser Ile Thr Trp Phe Leu Ser Trp Ser Pro Cys Gly			
	100	105	110
Glu Cys Ser Lys Ala Ile Thr Glu Phe Leu Ser Gln His Pro Asn Val			
	115	120	125
Thr Leu Val Ile Tyr Val Ala Arg Leu Tyr His His Met Asp Gln Gln			
	130	135	140
Asn Arg Gln Gly Leu Arg Asp Leu Val Asn Ser Gly Val Thr Ile Gln			
145	150	155	160
Ile Met Thr Ala Pro Glu Tyr Asp Tyr Cys Trp Arg Asn Phe Val Asn			
	165	170	175
Tyr Pro Pro Gly Lys Glu Ala His Trp Pro Arg Tyr Pro Pro Leu Trp			
	180	185	190
Met Lys Leu Tyr Ala Leu Glu Leu His Ala Gly Ile Leu Gly Leu Pro			
	195	200	205
Pro Cys Leu Asn Ile Leu Arg Arg Lys Gln Pro Gln Leu Thr Phe Phe			
210	215	220	
Thr Ile Ala Leu Gln Ser Cys His Tyr Gln Arg Leu Pro Pro His Ile			
225	230	235	240
Leu Trp Ala Thr Gly Leu Lys Ser Gly Gly Ser Ser Gly Gly Ser Ser			
	245	250	255
Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Ser			
	260	265	270
Gly Gly Ser Ser Gly Gly Ser Tyr Thr Arg Val Gly Ser Gly Ser Gly			
	275	280	285
Ser Gly Ser Ile Thr Arg Thr Thr Asn Pro Arg Asn Val Val Pro Lys			
290	295	300	
Ile Tyr Met Ser Ala Gly Ser Ile Pro Leu Thr Thr His Ile Thr Asn			
305	310	315	320
Ser Ile Gln Pro Thr Leu Trp Thr Ile Gly Ser Ile Asn Gly Val Ala			
	325	330	335
Pro Leu Ala Lys Ser Ile Lys Leu Gly Ile Pro Val Thr Gly Ser Ala			
	340	345	350
Tyr Thr Asp Gln Thr Thr Ala Met Val Arg Lys Lys Val Ser Val Phe			
	355	360	365
Met Gly Ser Gly Ser Gly Ser Gly Ser Ser Met Thr Gly Val Gly Ser			
370	375	380	

Gly Ser Gly Ser Gly Ser Ile Thr Arg Thr Thr Asn Pro Arg Asn Val															
385						390					395				400
Val Pro Lys Ile Tyr Met Ser Ala Gly Ser Ile Pro Leu Thr Thr His															
						405					410				415
Ile Thr Asn Ser Ile Gln Pro Thr Leu Trp Thr Ile Gly Ser Ile Asn															
						420					425				430
Gly Val Ala Pro Leu Ala Lys Ser Ile Lys Leu Gly Ile Pro Val Thr															
						435					440				445
Gly Ser Ala Tyr Thr Asp Gln Thr Thr Ala Met Val Arg Lys Lys Val															
						450					455				460
Ser Val Phe Met Gly Ser Gly Ser Gly Ser Gly Ser Ser Met Thr Ala															
465						470					475				480
Val Met Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His Asp Ile															
						485					490				495
Asp Tyr Lys Asp Asp Asp Asp Lys Met Ala Pro Lys Lys Lys Arg Lys															
						500					505				510
Val Gly Ile His Gly Val Pro Ala Ala Val Asp Leu Arg Thr Leu Gly															
						515					520				525
Tyr Ser Gln Gln Gln Gln Glu Lys Ile Lys Pro Lys Val Arg Ser Thr															
						530					535				540
Val Ala Gln His His Glu Ala Leu Val Gly His Gly Phe Thr His Ala															
545						550					555				560
His Ile Val Ala Leu Ser Gln His Pro Ala Ala Leu Gly Thr Val Ala															
						565					570				575
Val Lys Tyr Gln Asp Met Ile Ala Ala Leu Pro Glu Ala Thr His Glu															
						580					585				590
Ala Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg Ala Leu Glu															
						595					600				605
Ala Leu Leu Thr Val Ala Gly Glu Leu Arg Gly Pro Pro Leu Gln Leu															
						610					615				620
Asp Thr Gly Gln Leu Leu Lys Ile Ala Lys Arg Gly Gly Val Thr Ala															
625						630					635				640
Val Glu Ala Val His Ala Trp Arg Asn Ala Leu Thr Gly Ala Pro Leu															
						645					650				655
Asn Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly															
						660					665				670
Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln															
						675					680				685
Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Asn															

690	695	700
Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu		
705	710	715
Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser		
725	730	735
His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro		
740	745	750
Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile		
755	760	765
Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu		
770	775	780
Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val		
785	790	795
Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln		
805	810	815
Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln		
820	825	830
Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr		
835	840	845
Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro		
850	855	860
Asp Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu		
865	870	875
Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu		
885	890	895
Thr Pro Ala Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln		
900	905	910
Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His		
915	920	925
Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly		
930	935	940
Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln		
945	950	955
Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Ile		
965	970	975
Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu		
980	985	990
Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser		
995	1000	1005

Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu		
1010	1015	1020
Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val		
1025	1030	1035
Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val		
1040	1045	1050
Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro		
1055	1060	1065
Asp Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala		
1070	1075	1080
Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His		
1085	1090	1095
Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Asn Gly		
1100	1105	1110
Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu		
1115	1120	1125
Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala		
1130	1135	1140
Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu		
1145	1150	1155
Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val		
1160	1165	1170
Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr		
1175	1180	1185
Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr		
1190	1195	1200
Pro Glu Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Arg Pro		
1205	1210	1215
Ala Leu Glu Ser Ile Val Ala Gln Leu Ser Arg Pro Asp Pro Ala		
1220	1225	1230
Leu Ala Ala Leu Thr Asn Asp His Leu Val Ala Leu Ala Cys Leu		
1235	1240	1245
Gly Gly Arg Pro Ala Leu Asp Ala Val Lys Lys Gly Leu Pro His		
1250	1255	1260
Ala Pro Ala Leu Ile Lys Arg Thr Asn Arg Arg Ile Pro Glu Arg		
1265	1270	1275
Thr Ser His Arg Val Ala Gly Ser Ser Gly Gly Ser Gly Gly Ser		
1280	1285	1290
Gly Gly Ser Thr Asn Leu Ser Asp Ile Ile Glu Lys Glu Thr Gly		

1295	1300	1305
Lys Gln Leu Val Ile Gln Glu Ser Ile Leu Met Leu Pro Glu Glu		
1310	1315	1320
Val Glu Glu Val Ile Gly Asn Lys Pro Glu Ser Asp Ile Leu Val		
1325	1330	1335
His Thr Ala Tyr Asp Glu Ser Thr Asp Glu Asn Val Met Leu Leu		
1340	1345	1350
Thr Ser Asp Ala Pro Glu Tyr Lys Pro Trp Ala Leu Val Ile Gln		
1355	1360	1365
Asp Ser Asn Gly Glu Asn Lys Ile Lys Met Leu Ser Gly Gly Ser		
1370	1375	1380
Gly Gly Ser Gly Gly Ser Thr Asn Leu Ser Asp Ile Ile Glu Lys		
1385	1390	1395
Glu Thr Gly Lys Gln Leu Val Ile Gln Glu Ser Ile Leu Met Leu		
1400	1405	1410
Pro Glu Glu Val Glu Glu Val Ile Gly Asn Lys Pro Glu Ser Asp		
1415	1420	1425
Ile Leu Val His Thr Ala Tyr Asp Glu Ser Thr Asp Glu Asn Val		
1430	1435	1440
Met Leu Leu Thr Ser Asp Ala Pro Glu Tyr Lys Pro Trp Ala Leu		
1445	1450	1455
Val Ile Gln Asp Ser Asn Gly Glu Asn Lys Ile Lys Met Leu Ser		
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Gly Gly Ser Lys Arg Thr Ala Asp Gly Ser Glu Phe Glu Pro Lys		
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Lys Lys Arg Lys Val		
1490		
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<211> 4470		
<212> DNA		
<213> 人工序列(Artificial Sequence)		
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<223> BE4-234-47		
<400> 127		
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<210> 128

<211> 1490

<212> PRT

<213> 人工序列(Artificial Sequence)

<220>

<223> BE4-234-47

<400> 128

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

Ser Ile Gln Pro Thr Leu Trp Thr Ile Gly Ser Ile Asn Gly Val Ala		
325	330	335
Pro Leu Ala Lys Ser Ile Lys Leu Gly Ile Pro Val Thr Gly Ser Ala		
340	345	350
Tyr Thr Asp Gln Thr Thr Ala Met Val Arg Lys Lys Val Ser Val Phe		
355	360	365
Met Gly Ser Gly Ser Gly Ser Gly Ser Ser Met Thr Gly Val Gly Ser		
370	375	380
Gly Ser Gly Ser Gly Ser Ile Thr Arg Thr Thr Asn Pro Arg Asn Val		
385	390	395
Val Pro Lys Ile Tyr Met Ser Ala Gly Ser Ile Pro Leu Thr Thr His		
405	410	415
Ile Thr Asn Ser Ile Gln Pro Thr Leu Trp Thr Ile Gly Ser Ile Asn		
420	425	430
Gly Val Ala Pro Leu Ala Lys Ser Ile Lys Leu Gly Ile Pro Val Thr		
435	440	445
Gly Ser Ala Tyr Thr Asp Gln Thr Thr Ala Met Val Arg Lys Lys Val		
450	455	460
Ser Val Phe Met Gly Ser Gly Ser Gly Ser Gly Ser Ser Met Thr Ala		
465	470	475
Val Met Ala Ser Ser Pro Pro Lys Lys Lys Arg Lys Val Ala Ala Ala		
485	490	495
Asp Tyr Lys Asp Asp Asp Asp Lys Ser Trp Lys Asp Ala Ser Gly Trp		
500	505	510
Ser Arg Met His Ala Ala Pro Arg Arg Arg Ala Ala Gln Pro Ser Asp		
515	520	525
Ala Ser Pro Ala Ala Gln Val Asp Leu Arg Thr Leu Gly Tyr Ser Gln		
530	535	540
Gln Gln Gln Glu Lys Ile Lys Pro Lys Val Arg Ser Thr Val Ala Gln		
545	550	555
His His Glu Ala Leu Val Gly His Gly Phe Thr His Ala His Ile Val		
565	570	575
Ala Leu Ser Gln His Pro Ala Ala Leu Gly Thr Val Ala Val Thr Tyr		
580	585	590
Gln His Ile Ile Thr Ala Leu Pro Glu Ala Thr His Glu Asp Ile Val		
595	600	605
Gly Val Gly Lys Gln Trp Ser Gly Ala Arg Ala Leu Glu Ala Leu Leu		
610	615	620
Thr Asp Ala Gly Glu Leu Arg Gly Pro Pro Leu Gln Leu Asp Thr Gly		

625	630	635	640
Gln Leu Val Lys Ile Ala Lys Arg Gly Gly Val Thr Ala Met Glu Ala			
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Val His Ala Ser Arg Asn Ala Leu Thr Gly Ala Pro Leu Asn Leu Thr			
	660	665	670
Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala			
	675	680	685
Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly			
	690	695	700
Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys			
705	710	715	720
Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala			
	725	730	735
His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile Gly			
	740	745	750
Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys			
	755	760	765
Gln Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser Asn			
	770	775	780
Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val			
785	790	795	800
Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala			
	805	810	815
Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu			
	820	825	830
Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala			
	835	840	845
Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg			
	850	855	860
Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val			
865	870	875	880
Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val			
	885	890	895
Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala			
	900	905	910
Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu			
	915	920	925
Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr			
	930	935	940

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

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Ala Leu Thr Asn Asp His	Leu Val Ala Leu Ala	Cys Leu Gly Gly
1250	1255	1260
Arg Pro Ala Met Asp Ala	Val Lys Lys Gly Leu	Pro His Ala Pro
1265	1270	1275
Glu Leu Ile Arg Ser Ser	Gly Gly Ser Gly Gly	Ser Gly Gly Ser
1280	1285	1290
Thr Asn Leu Ser Asp Ile	Ile Glu Lys Glu Thr	Gly Lys Gln Leu
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Val Ile Gln Glu Ser Ile	Leu Met Leu Pro Glu	Glu Val Glu Glu
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Val Ile Gly Asn Lys Pro	Glu Ser Asp Ile Leu	Val His Thr Ala
1325	1330	1335
Tyr Asp Glu Ser Thr Asp	Glu Asn Val Met Leu	Leu Thr Ser Asp
1340	1345	1350
Ala Pro Glu Tyr Lys Pro	Trp Ala Leu Val Ile	Gln Asp Ser Asn
1355	1360	1365
Gly Glu Asn Lys Ile Lys	Met Leu Ser Gly Gly	Ser Gly Gly Ser
1370	1375	1380
Gly Gly Ser Thr Asn Leu	Ser Asp Ile Ile Glu	Lys Glu Thr Gly
1385	1390	1395
Lys Gln Leu Val Ile Gln	Glu Ser Ile Leu Met	Leu Pro Glu Glu
1400	1405	1410
Val Glu Glu Val Ile Gly	Asn Lys Pro Glu Ser	Asp Ile Leu Val
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His Thr Ala Tyr Asp Glu	Ser Thr Asp Glu Asn	Val Met Leu Leu
1430	1435	1440
Thr Ser Asp Ala Pro Glu	Tyr Lys Pro Trp Ala	Leu Val Ile Gln
1445	1450	1455
Asp Ser Asn Gly Glu Asn	Lys Ile Lys Met Leu	Ser Gly Gly Ser
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Lys Arg Thr Ala Asp Gly	Ser Glu Phe Glu Pro	Lys Lys Lys Arg
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1490		
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<211>	4470	
<212>	DNA	
<213>	人工序列(Artificial Sequence)	

<220>

<223> BE4-234-47-NC

<400> 129

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

Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Ser		
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Gly Gly Ser Ser Gly Gly Ser Tyr Thr Arg Val Gly Ser Gly Ser Gly		
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Ser Gly Ser Ile Thr Arg Thr Thr Asn Pro Arg Asn Val Val Pro Lys		
290	295	300
Ile Tyr Met Ser Ala Gly Ser Ile Pro Leu Thr Thr His Ile Thr Asn		
305	310	315
Ser Ile Gln Pro Thr Leu Trp Thr Ile Gly Ser Ile Asn Gly Val Ala		
325	330	335
Pro Leu Ala Lys Ser Ile Lys Leu Gly Ile Pro Val Thr Gly Ser Ala		
340	345	350
Tyr Thr Asp Gln Thr Thr Ala Met Val Arg Lys Lys Val Ser Val Phe		
355	360	365
Met Gly Ser Gly Ser Gly Ser Gly Ser Ser Met Thr Gly Val Gly Ser		
370	375	380
Gly Ser Gly Ser Gly Ser Ile Thr Arg Thr Thr Asn Pro Arg Asn Val		
385	390	395
Val Pro Lys Ile Tyr Met Ser Ala Gly Ser Ile Pro Leu Thr Thr His		
405	410	415
Ile Thr Asn Ser Ile Gln Pro Thr Leu Trp Thr Ile Gly Ser Ile Asn		
420	425	430
Gly Val Ala Pro Leu Ala Lys Ser Ile Lys Leu Gly Ile Pro Val Thr		
435	440	445
Gly Ser Ala Tyr Thr Asp Gln Thr Thr Ala Met Val Arg Lys Lys Val		
450	455	460
Ser Val Phe Met Gly Ser Gly Ser Gly Ser Gly Ser Ser Met Thr Ala		
465	470	475
Val Met Ala Ser Ser Pro Pro Lys Lys Lys Arg Lys Val Ala Ala Ala		
485	490	495
Asp Tyr Lys Asp Asp Asp Asp Lys Ser Trp Lys Asp Ala Ser Gly Trp		
500	505	510
Ser Arg Met His Ala Ala Pro Arg Arg Arg Ala Ala Gln Pro Ser Asp		
515	520	525
Ala Ser Pro Ala Ala Gln Val Asp Leu Arg Thr Leu Gly Tyr Ser Gln		
530	535	540
Gln Gln Gln Glu Lys Ile Lys Pro Lys Val Arg Ser Thr Val Ala Gln		
545	550	555
His His Glu Ala Leu Val Gly His Gly Phe Thr His Ala His Ile Val		

				565				570				575			
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Gln	His	Ile	Ile	Thr	Ala	Leu	Pro	Glu	Ala	Thr	His	Glu	Asp	Ile	Val
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Gly	Val	Gly	Lys	Gln	Trp	Ser	Gly	Ala	Arg	Ala	Leu	Glu	Ala	Leu	Leu
				610				615				620			
Thr	Asp	Ala	Gly	Glu	Leu	Arg	Gly	Pro	Pro	Leu	Gln	Leu	Asp	Thr	Gly
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Gln	Leu	Val	Lys	Ile	Ala	Lys	Arg	Gly	Gly	Val	Thr	Ala	Met	Glu	Ala
				645				650				655			
Val	His	Ala	Ser	Arg	Asn	Ala	Leu	Thr	Gly	Ala	Pro	Leu	Asn	Leu	Thr
				660				665				670			
Pro	Asp	Gln	Val	Val	Ala	Ile	Ala	Ser	Asn	Gly	Gly	Gly	Lys	Gln	Ala
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Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu	Pro	Val	Leu	Cys	Gln	Asp	His	Gly
				690				695				700			
Leu	Thr	Pro	Glu	Gln	Val	Val	Ala	Ile	Ala	Ser	Asn	Asn	Gly	Gly	Lys
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Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu	Pro	Val	Leu	Cys	Gln	Ala
				725				730				735			
His	Gly	Leu	Thr	Pro	Asp	Gln	Val	Val	Ala	Ile	Ala	Ser	His	Asp	Gly
				740				745				750			
Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu	Pro	Val	Leu	Cys
				755				760				765			
Gln	Ala	His	Gly	Leu	Thr	Pro	Ala	Gln	Val	Val	Ala	Ile	Ala	Ser	Asn
				770				775				780			
Asn	Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu	Pro	Val
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Leu	Cys	Gln	Asp	His	Gly	Leu	Thr	Pro	Asp	Gln	Val	Val	Ala	Ile	Ala
				805				810				815			
Ser	His	Asp	Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu
				820				825				830			
Pro	Val	Leu	Cys	Gln	Asp	His	Gly	Leu	Thr	Pro	Glu	Gln	Val	Val	Ala
				835				840				845			
Ile	Ala	Ser	Asn	Asn	Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg
				850				855				860			
Leu	Leu	Pro	Val	Leu	Cys	Gln	Ala	His	Gly	Leu	Thr	Pro	Asp	Gln	Val
865				870				875				880			

Val	Ala	Ile	Ala	Ser	Asn	Gly	Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val
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Gln	Arg	Leu	Leu	Pro	Val	Leu	Cys	Gln	Ala	His	Gly	Leu	Thr	Pro	Ala
				900				905				910			
Gln	Val	Val	Ala	Ile	Ala	Ser	Asn	Ile	Gly	Gly	Lys	Gln	Ala	Leu	Glu
				915				920				925			
Thr	Val	Gln	Arg	Leu	Leu	Pro	Val	Leu	Cys	Gln	Asp	His	Gly	Leu	Thr
				930				935				940			
Pro	Asp	Gln	Val	Val	Ala	Ile	Ala	Ser	Asn	Gly	Gly	Gly	Lys	Gln	Ala
945				950				955				960			
Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu	Pro	Val	Leu	Cys	Gln	Asp	His	Gly
				965				970				975			
Leu	Thr	Pro	Glu	Gln	Val	Val	Ala	Ile	Ala	Ser	Asn	Ile	Gly	Gly	Lys
				980				985				990			
Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu	Pro	Val	Leu	Cys	Gln	Ala
				995				1000				1005			
His	Gly	Leu	Thr	Pro	Asp	Gln	Val	Val	Ala	Ile	Ala	Ser	Asn	Asn	
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Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu	Pro	Val	
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Leu	Cys	Gln	Ala	His	Gly	Leu	Thr	Pro	Ala	Gln	Val	Val	Ala	Ile	
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Ala	Ser	Asn	Gly	Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg	
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Leu	Leu	Pro	Val	Leu	Cys	Gln	Asp	His	Gly	Leu	Thr	Pro	Asp	Gln	
1070				1075				1080							
Val	Val	Ala	Ile	Ala	Ser	His	Asp	Gly	Gly	Lys	Gln	Ala	Leu	Glu	
1085				1090				1095							
Thr	Val	Gln	Arg	Leu	Leu	Pro	Val	Leu	Cys	Gln	Asp	His	Gly	Leu	
1100				1105				1110							
Thr	Pro	Glu	Gln	Val	Val	Ala	Ile	Ala	Ser	Asn	Asn	Gly	Gly	Lys	
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Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu	Pro	Val	Leu	Cys	Gln	
1130				1135				1140							
Ala	His	Gly	Leu	Thr	Pro	Asp	Gln	Val	Val	Ala	Ile	Ala	Ser	His	
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Asp	Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu	Pro	
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Val	Leu	Cys	Gln	Ala	His	Gly	Leu	Thr	Pro	Ala	Gln	Val	Val	Ala	

1175	1180	1185
Ile Ala Ser Asn Asn Gly Gly	Lys Gln Ala Leu Glu	Thr Val Gln
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Arg Leu Leu Pro Val Leu Cys	Gln Asp His Gly Leu	Thr Pro Glu
1205	1210	1215
Gln Val Val Ala Ile Ala Ser	Asn Asn Gly Gly Arg	Pro Ala Leu
1220	1225	1230
Glu Ser Ile Val Ala Gln Leu	Ser Arg Pro Asp Pro	Ala Leu Ala
1235	1240	1245
Ala Leu Thr Asn Asp His Leu	Val Ala Leu Ala Cys	Leu Gly Gly
1250	1255	1260
Arg Pro Ala Met Asp Ala Val	Lys Lys Gly Leu Pro	His Ala Pro
1265	1270	1275
Glu Leu Ile Arg Ser Ser Gly	Gly Ser Gly Gly Ser	Gly Gly Ser
1280	1285	1290
Thr Asn Leu Ser Asp Ile Ile	Glu Lys Glu Thr Gly	Lys Gln Leu
1295	1300	1305
Val Ile Gln Glu Ser Ile Leu	Met Leu Pro Glu Glu	Val Glu Glu
1310	1315	1320
Val Ile Gly Asn Lys Pro Glu	Ser Asp Ile Leu Val	His Thr Ala
1325	1330	1335
Tyr Asp Glu Ser Thr Asp Glu	Asn Val Met Leu Leu	Thr Ser Asp
1340	1345	1350
Ala Pro Glu Tyr Lys Pro Trp	Ala Leu Val Ile Gln	Asp Ser Asn
1355	1360	1365
Gly Glu Asn Lys Ile Lys Met	Leu Ser Gly Gly Ser	Gly Gly Ser
1370	1375	1380
Gly Gly Ser Thr Asn Leu Ser	Asp Ile Ile Glu Lys	Glu Thr Gly
1385	1390	1395
Lys Gln Leu Val Ile Gln Glu	Ser Ile Leu Met Leu	Pro Glu Glu
1400	1405	1410
Val Glu Glu Val Ile Gly Asn	Lys Pro Glu Ser Asp	Ile Leu Val
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His Thr Ala Tyr Asp Glu Ser	Thr Asp Glu Asn Val	Met Leu Leu
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Thr Ser Asp Ala Pro Glu Tyr	Lys Pro Trp Ala Leu	Val Ile Gln
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Asp Ser Asn Gly Glu Asn Lys	Ile Lys Met Leu Ser	Gly Gly Ser
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Lys Val
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<211> 3678

<212> DNA

<213> 人工序列(Artificial Sequence)

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<400> 131

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gagggatgga	acagggcaat	cggcctgcac	gaccctacag	cccatgccga	aattatggcc	240
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<223> ABE8e-32-47

<400> 132

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

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305	310	315
Leu Gly Thr Val Ala Val Thr Tyr Gln His Ile Ile Thr Ala Leu Pro		
325	330	335
Glu Ala Thr His Glu Asp Ile Val Gly Val Gly Lys Gln Trp Ser Gly		
340	345	350
Ala Arg Ala Leu Glu Ala Leu Leu Thr Asp Ala Gly Glu Leu Arg Gly		
355	360	365
Pro Pro Leu Gln Leu Asp Thr Gly Gln Leu Val Lys Ile Ala Lys Arg		
370	375	380
Gly Gly Val Thr Ala Met Glu Ala Val His Ala Ser Arg Asn Ala Leu		
385	390	395
Thr Gly Ala Pro Leu Asn Leu Thr Pro Asp Gln Val Val Ala Ile Ala		
405	410	415
Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu		
420	425	430
Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala		
435	440	445
Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg		
450	455	460
Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val		
465	470	475
Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val		
485	490	495
Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala		
500	505	510
Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu		
515	520	525
Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr		
530	535	540
Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala		
545	550	555
Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly		
565	570	575
Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys		
580	585	590
Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala		
595	600	605

His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Asn Gly			
610	615	620	
Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys			
625	630	635	640
Gln Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser His			
645	650	655	
Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val			
660	665	670	
Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala			
675	680	685	
Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu			
690	695	700	
Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala			
705	710	715	720
Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg			
725	730	735	
Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val			
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Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val			
755	760	765	
Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala			
770	775	780	
Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu			
785	790	795	800
Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr			
805	810	815	
Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala			
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Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly			
835	840	845	
Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys			
850	855	860	
Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala			
865	870	875	880
His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile Gly			
885	890	895	
Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys			
900	905	910	
Gln Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser Asn			

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Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val		
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Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala		
945	950	955
Ser Asn Asn Gly Gly Arg Pro Ala Leu Glu Ser Ile Val Ala Gln Leu		
965	970	975
Ser Arg Pro Asp Pro Ala Leu Ala Ala Leu Thr Asn Asp His Leu Val		
980	985	990
Ala Leu Ala Cys Leu Gly Gly Arg Pro Ala Met Asp Ala Val Lys Lys		
995	1000	1005
Gly Leu Pro His Ala Pro Glu Leu Ile Arg Ser Ser Gly Gly Ser		
1010	1015	1020
Gly Gly Ser Gly Gly Ser Thr Asn Leu Ser Asp Ile Ile Glu Lys		
1025	1030	1035
Glu Thr Gly Lys Gln Leu Val Ile Gln Glu Ser Ile Leu Met Leu		
1040	1045	1050
Pro Glu Glu Val Glu Glu Val Ile Gly Asn Lys Pro Glu Ser Asp		
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Ile Leu Val His Thr Ala Tyr Asp Glu Ser Thr Asp Glu Asn Val		
1070	1075	1080
Met Leu Leu Thr Ser Asp Ala Pro Glu Tyr Lys Pro Trp Ala Leu		
1085	1090	1095
Val Ile Gln Asp Ser Asn Gly Glu Asn Lys Ile Lys Met Leu Ser		
1100	1105	1110
Gly Gly Ser Gly Gly Ser Gly Gly Ser Thr Asn Leu Ser Asp Ile		
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Ile Glu Lys Glu Thr Gly Lys Gln Leu Val Ile Gln Glu Ser Ile		
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Leu Met Leu Pro Glu Glu Val Glu Glu Val Ile Gly Asn Lys Pro		
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Glu Ser Asp Ile Leu Val His Thr Ala Tyr Asp Glu Ser Thr Asp		
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Glu Asn Val Met Leu Leu Thr Ser Asp Ala Pro Glu Tyr Lys Pro		
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Trp Ala Leu Val Ile Gln Asp Ser Asn Gly Glu Asn Lys Ile Lys		
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Glu Pro Lys Lys Lys Arg Lys Val

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1225

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<212> DNA

<213> 人工序列(Artificial Sequence)

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Ala	Leu	Thr	Leu	Ala	Lys	Arg	Ala	Arg	Asp	Glu	Arg	Glu	Val	Pro	Val
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Gly	Ala	Val	Leu	Val	Leu	Asn	Asn	Arg	Val	Ile	Gly	Glu	Gly	Trp	Asn
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Arg	Ala	Ile	Gly	Leu	His	Asp	Pro	Thr	Ala	His	Ala	Glu	Ile	Met	Ala
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Leu	Arg	Gln	Gly	Gly	Leu	Val	Met	Gln	Asn	Tyr	Arg	Leu	Ile	Asp	Ala
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Thr	Leu	Tyr	Val	Thr	Phe	Glu	Pro	Cys	Val	Met	Cys	Ala	Gly	Ala	Met
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Ile	His	Ser	Arg	Ile	Gly	Arg	Val	Val	Phe	Gly	Trp	Arg	Asn	Ser	Lys
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Arg	Gly	Ala	Ala	Gly	Ser	Leu	Met	Asn	Val	Leu	Asn	Tyr	Pro	Gly	Met
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Ala	Leu	Leu	Cys	Asp	Phe	Tyr	Arg	Met	Pro	Arg	Gln	Val	Phe	Asn	Ala
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Gln	Lys	Lys	Ala	Gln	Ser	Ser	Ile	Asn	Ser	Gly	Gly	Ser	Ser	Gly	Gly
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Ser	Ser	Gly	Gly	Ser	Ser	Gly	Gly	Ser	Met	Ala	Ser	Ser	Pro	Pro	Lys
									210					215	
Lys	Lys	Arg	Lys	Val	Ala	Ala	Ala	Asp	Tyr	Lys	Asp	Asp	Asp	Asp	Lys
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Ser	Trp	Lys	Asp	Ala	Ser	Gly	Trp	Ser	Arg	Met	His	Ala	Ala	Pro	Arg
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Arg	Arg	Ala	Ala	Gln	Pro	Ser	Asp	Ala	Ser	Pro	Ala	Ala	Gln	Val	Asp
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Lys	Val	Arg	Ser	Thr	Val	Ala	Gln	His	His	Glu	Ala	Leu	Val	Gly	His
									285					290	
Gly	Phe	Thr	His	Ala	His	Ile	Val	Ala	Leu	Ser	Gln	His	Pro	Ala	Ala
									295					300	

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Glu Ala Thr His Glu Asp Ile Val Gly Val Gly Lys Gln Trp Ser Gly			
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Ala Arg Ala Leu Glu Ala Leu Leu Thr Asp Ala Gly Glu Leu Arg Gly			
	355	360	365
Pro Pro Leu Gln Leu Asp Thr Gly Gln Leu Val Lys Ile Ala Lys Arg			
	370	375	380
Gly Gly Val Thr Ala Met Glu Ala Val His Ala Ser Arg Asn Ala Leu			
385	390	395	400
Thr Gly Ala Pro Leu Asn Leu Thr Pro Asp Gln Val Val Ala Ile Ala			
	405	410	415
Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu			
	420	425	430
Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala			
	435	440	445
Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg			
450	455	460	
Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val			
465	470	475	480
Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val			
	485	490	495
Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala			
	500	505	510
Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu			
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Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr			
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Pro Asp Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala			
545	550	555	560
Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly			
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Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys			
	580	585	590
Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala			
	595	600	605
His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Gly Gly			
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Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu	Pro	Val	Leu	Cys
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Ile	Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu	Pro	Val
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Leu	Cys	Gln	Asp	His	Gly	Leu	Thr	Pro	Asp	Gln	Val	Val	Ala	Ile	Ala
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Ser	Asn	Gly	Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu
690									695						700
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Val	Ala	Ile	Ala	Ser	Asn	Asn	Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val
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785									790						800
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Gln	Ala	His	Gly	Leu	Thr	Pro	Ala	Gln	Val	Val	Ala	Ile	Ala	Ser	Asn
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Glu Thr Gly Lys Gln Leu Val Ile Gln Glu Ser Ile Leu Met Leu		
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Pro Glu Glu Val Glu Glu Val Ile Gly Asn Lys Pro Glu Ser Asp		
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Met Leu Leu Thr Ser Asp Ala Pro Glu Tyr Lys Pro Trp Ala Leu		
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Val Ile Gln Asp Ser Asn Gly Glu Asn Lys Ile Lys Met Leu Ser		
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Ile Glu Lys Glu Thr Gly Lys Gln Leu Val Ile Gln Glu Ser Ile		
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Trp Ala Leu Val Ile Gln Asp Ser Asn Gly Glu Asn Lys Ile Lys		
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<400> 136

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Ala	Leu	Thr	Leu	Ala	Lys	Arg	Ala	Arg	Asp	Glu	Arg	Glu	Val	Pro	Val
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Gly	Ala	Val	Leu	Val	Leu	Asn	Asn	Arg	Val	Ile	Gly	Glu	Gly	Trp	Asn
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Arg	Ala	Ile	Gly	Leu	His	Asp	Pro	Thr	Ala	His	Ala	Glu	Ile	Met	Ala
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Leu	Arg	Gln	Gly	Gly	Leu	Val	Met	Gln	Asn	Tyr	Arg	Leu	Ile	Asp	Ala
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Ala	Leu	Leu	Cys	Asp	Phe	Tyr	Arg	Met	Pro	Arg	Gln	Val	Phe	Asn	Ala
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Gln	Lys	Lys	Ala	Gln	Ser	Ser	Ile	Asn	Ser	Gly	Gly	Ser	Ser	Gly	Gly
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Gln	Gln	Glu	Lys	Ile	Lys	Pro	Lys	Val	Arg	Ser	Thr	Val	Ala	Gln	His
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His	Glu	Ala	Leu	Val	Gly	His	Gly	Phe	Thr	His	Ala	His	Ile	Val	Ala
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Leu	Ser	Gln	His	Pro	Ala	Ala	Leu	Gly	Thr	Val	Ala	Val	Thr	Tyr	Gln
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His	Ile	Ile	Thr	Ala	Leu	Pro	Glu	Ala	Thr	His	Glu	Asp	Ile	Val	Gly
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Leu	Val	Lys	Ile	Ala	Lys	Arg	Gly	Gly	Val	Thr	Ala	Met	Glu	Ala	Val
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Asp	Gln	Val	Val	Ala	Ile	Ala	Ser	Asn	Ile	Gly	Gly	Lys	Gln	Ala	Leu
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Glu	Thr	Val	Gln	Arg	Leu	Leu	Pro	Val	Leu	Cys	Gln	Asp	His	Gly	Leu
	530					535					540				
Thr	Pro	Glu	Gln	Val	Val	Ala	Ile	Ala	Ser	His	Asp	Gly	Gly	Lys	Gln
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Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu	Pro	Val	Leu	Cys	Gln	Ala	His
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Gly	Leu	Thr	Pro	Asp	Gln	Val	Val	Ala	Ile	Ala	Ser	Asn	Ile	Gly	Gly
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Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu	Pro	Val	Leu	Cys	Gln

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Cys Gln Asp His Gly Leu	Thr Pro Asp Gln Val	Val Ala Ile Ala Ser
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Asn Ile Gly Gly Lys Gln	Ala Leu Glu Thr Val	Gln Arg Leu Leu Pro
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Val Leu Cys Gln Asp His	Gly Leu Thr Pro Glu	Gln Val Val Ala Ile
675	680	685
Ala Ser Asn Ile Gly Gly	Lys Gln Ala Leu Glu	Thr Val Gln Arg Leu
690	695	700
Leu Pro Val Leu Cys Gln	Ala His Gly Leu Thr	Pro Asp Gln Val Val
705	710	715
Ala Ile Ala Ser Asn Asn	Gly Gly Lys Gln Ala	Leu Glu Thr Val Gln
725	730	735
Arg Leu Leu Pro Val Leu	Cys Gln Ala His Gly	Leu Thr Pro Ala Gln
740	745	750
Val Val Ala Ile Ala Ser	His Asp Gly Gly Lys	Gln Ala Leu Glu Thr
755	760	765
Val Gln Arg Leu Leu Pro	Val Leu Cys Gln Asp	His Gly Leu Thr Pro
770	775	780
Asp Gln Val Val Ala Ile	Ala Ser Asn Asn Gly	Gly Lys Gln Ala Leu
785	790	795
Glu Thr Val Gln Arg Leu	Leu Leu Pro Val Leu	Cys Gln Asp His Gly
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Thr Pro Glu Gln Val Val	Ala Ile Ala Ser Asn	Asn Gly Gly Lys Gln
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Ala Leu Glu Thr Val Gln	Arg Leu Leu Pro Val	Leu Cys Gln Ala His
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Gly Leu Thr Pro Asp Gln	Val Val Ala Ile Ala	Ser Asn Asn Gly Gly
850	855	860
Lys Gln Ala Leu Glu Thr	Val Gln Arg Leu Leu	Pro Val Leu Cys Gln
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Ala His Gly Leu Thr Pro	Ala Gln Val Val Ala	Ile Ala Ser His Asp
885	890	895
Gly Gly Lys Gln Ala Leu	Glu Thr Val Gln Arg	Leu Leu Pro Val Leu
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Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser		
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Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro		
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Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile		
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Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val		
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Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala		
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Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu		
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Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly		
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Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly		
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Arg Pro Ala Leu Glu Ser Ile Val Ala Gln Leu Ser Arg Pro Asp		
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Pro Ala Leu Ala Ala Leu Thr Asn Asp His Leu Val Ala Leu Ala		
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Cys Leu Gly Gly Arg Pro Ala Met Asp Ala Val Lys Lys Gly Leu		
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Pro His Ala Pro Glu Leu Ile Arg Ser Ser Gly Gly Ser Gly Gly		
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Gly Lys Gln Leu Val Ile Gln Glu Ser Ile Leu Met Leu Pro Glu		
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Glu Val Glu Glu Val Ile Gly Asn Lys Pro Glu Ser Asp Ile Leu		
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Val His Thr Ala Tyr Asp Glu Ser Thr Asp Glu Asn Val Met Leu		
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Gln Asp Ser Asn Gly Glu Asn Lys Ile Lys Met Leu Ser Gly Gly		

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Asp Ile Leu Val His Thr Ala Tyr Asp Glu Ser Thr Asp Glu Asn		
1265	1270	1275
Val Met Leu Leu Thr Ser Asp Ala Pro Glu Tyr Lys Pro Trp Ala		
1280	1285	1290
Leu Val Ile Gln Asp Ser Asn Gly Glu Asn Lys Ile Lys Met Leu		
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<212> PRT

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35 40 45

Gly Ala Val Leu Val Leu Asn Asn Arg Val Ile Gly Glu Gly Trp Asn

50 55 60

Arg Ala Ile Gly Leu His Asp Pro Thr Ala His Ala Glu Ile Met Ala

65 70 75 80

Leu Arg Gln Gly Gly Leu Val Met Gln Asn Tyr Arg Leu Ile Asp Ala

85 90 95

Thr Leu Tyr Val Thr Phe Glu Pro Cys Val Met Cys Ala Gly Ala Met

100 105 110

Ile His Ser Arg Ile Gly Arg Val Val Phe Gly Trp Arg Asn Ser Lys

115 120 125

Arg Gly Ala Ala Gly Ser Leu Met Asn Val Leu Asn Tyr Pro Gly Met

130 135 140

Asn His Arg Val Glu Ile Thr Glu Gly Ile Leu Ala Asp Glu Cys Ala

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Gln Lys Lys Ala Gln Ser Ser Ile Asn Ser Gly Gly Ser Ser Gly Gly			
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Pro Lys Ile Tyr Met Ser Ala Gly Ser Ile Pro Leu Thr Thr His Ile			
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Val Ala Pro Leu Ala Lys Ser Ile Lys Leu Gly Ile Pro Val Thr Gly			
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Ser Ala Tyr Thr Asp Gln Thr Thr Ala Met Val Arg Lys Lys Val Ser			
	290	295	300
Val Phe Met Gly Ser Gly Ser Gly Ser Gly Ser Ser Met Thr Ala Val			
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Met Ala Ser Ser Pro Pro Lys Lys Lys Arg Lys Val Ala Ala Ala Asp			
	325	330	335
Tyr Lys Asp Asp Asp Lys Ser Trp Lys Asp Ala Ser Gly Trp Ser			
	340	345	350
Arg Met His Ala Ala Pro Arg Arg Arg Ala Ala Gln Pro Ser Asp Ala			
	355	360	365
Ser Pro Ala Ala Gln Val Asp Leu Arg Thr Leu Gly Tyr Ser Gln Gln			
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Gln Gln Glu Lys Ile Lys Pro Lys Val Arg Ser Thr Val Ala Gln His			
385	390	395	400
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Leu Ser Gln His Pro Ala Ala Leu Gly Thr Val Ala Val Thr Tyr Gln			
	420	425	430
His Ile Ile Thr Ala Leu Pro Glu Ala Thr His Glu Asp Ile Val Gly			
	435	440	445
Val Gly Lys Gln Trp Ser Gly Ala Arg Ala Leu Glu Ala Leu Leu Thr			
450	455	460	

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Leu	Val	Lys	Ile	Ala	Lys	Arg	Gly	Gly	Val	Thr	Ala	Met	Glu	Ala	Val
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His	Ala	Ser	Arg	Asn	Ala	Leu	Thr	Gly	Ala	Pro	Leu	Asn	Leu	Thr	Pro
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Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu	Pro	Val	Leu	Cys	Gln	Ala	His
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Gly	Leu	Thr	Pro	Asp	Gln	Val	Val	Ala	Ile	Ala	Ser	His	Asp	Gly	Gly
			580					585					590		
Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu	Pro	Val	Leu	Cys	Gln
		595						600					605		
Ala	His	Gly	Leu	Thr	Pro	Ala	Gln	Val	Val	Ala	Ile	Ala	Ser	Asn	Asn
		610					615					620			
Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu	Pro	Val	Leu
625					630					635					640
Cys	Gln	Asp	His	Gly	Leu	Thr	Pro	Asp	Gln	Val	Val	Ala	Ile	Ala	Ser
			645						650					655	
His	Asp	Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu	Pro
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Val	Leu	Cys	Gln	Asp	His	Gly	Leu	Thr	Pro	Glu	Gln	Val	Val	Ala	Ile
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Ala	Ser	Asn	Asn	Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu
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Leu	Pro	Val	Leu	Cys	Gln	Ala	His	Gly	Leu	Thr	Pro	Asp	Gln	Val	Val
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Ala	Ile	Ala	Ser	Asn	Gly	Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln
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Arg	Leu	Leu	Pro	Val	Leu	Cys	Gln	Ala	His	Gly	Leu	Thr	Pro	Ala	Gln
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Val	Val	Ala	Ile	Ala	Ser	Asn	Ile	Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr
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Val	Gln	Arg	Leu	Leu	Pro	Val	Leu	Cys	Gln	Asp	His	Gly	Leu	Thr	Pro

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Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu		800
	805	810
Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln		815
	820	825
Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His		830
	835	840
Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly		845
	850	860
Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln		865
	870	875
Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser Asn Gly		880
	885	890
Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu		895
	900	905
Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser		910
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His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro		925
	930	935
Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile		940
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Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu		955
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Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu		970
	975	980
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	990	995
Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln		1000
	1005	1010
Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala		1015
	1020	1025
Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu		1030
	1035	1040
Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly		1045
	1050	1055
Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly		1060
	1065	1070
Arg Pro Ala Leu Glu Ser Ile Val Ala Gln Leu Ser Arg Pro Asp		1075
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Pro Ala	Leu Ala Ala Leu Thr	Asn Asp His Leu Val	Ala Leu Ala
1085	1090	1095	
Cys Leu	Gly Gly Arg Pro Ala	Met Asp Ala Val Lys	Lys Gly Leu
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Pro His	Ala Pro Glu Leu Ile	Arg Ser Ser Gly Gly	Ser Gly Gly
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Ser Gly	Gly Ser Thr Asn Leu	Ser Asp Ile Ile Glu	Lys Glu Thr
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Gly Lys	Gln Leu Val Ile Gln	Glu Ser Ile Leu Met	Leu Pro Glu
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Glu Val	Glu Glu Val Ile Gly	Asn Lys Pro Glu Ser	Asp Ile Leu
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Val His	Thr Ala Tyr Asp Glu	Ser Thr Asp Glu Asn	Val Met Leu
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Leu Thr	Ser Asp Ala Pro Glu	Tyr Lys Pro Trp Ala	Leu Val Ile
1190	1195	1200	
Gln Asp	Ser Asn Gly Glu Asn	Lys Ile Lys Met Leu	Ser Gly Gly
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Ser Gly	Gly Ser Gly Gly Ser	Thr Asn Leu Ser Asp	Ile Ile Glu
1220	1225	1230	
Lys Glu	Thr Gly Lys Gln Leu	Val Ile Gln Glu Ser	Ile Leu Met
1235	1240	1245	
Leu Pro	Glu Glu Val Glu Glu	Val Ile Gly Asn Lys	Pro Glu Ser
1250	1255	1260	
Asp Ile	Leu Val His Thr Ala	Tyr Asp Glu Ser Thr	Asp Glu Asn
1265	1270	1275	
Val Met	Leu Leu Thr Ser Asp	Ala Pro Glu Tyr Lys	Pro Trp Ala
1280	1285	1290	
Leu Val	Ile Gln Asp Ser Asn	Gly Glu Asn Lys Ile	Lys Met Leu
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Ser Gly	Gly Ser Lys Arg Thr	Ala Asp Gly Ser Glu	Phe Glu Pro
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Lys Lys	Lys Arg Lys Val		
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<223> ABE8e-234-47

<400> 139

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<213>	人工序列(Artificial Sequence)					

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<400> 140

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

Ser	Ala	Tyr	Thr	Asp	Gln	Thr	Thr	Ala	Met	Val	Arg	Lys	Lys	Val	Ser
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Val	Phe	Met	Gly	Ser	Gly	Ser	Gly	Ser	Gly	Ser	Ser	Met	Thr	Gly	Val
305					310					315					320
Gly	Ser	Gly	Ser	Gly	Ser	Gly	Ser	Ile	Thr	Arg	Thr	Thr	Asn	Pro	Arg
				325					330					335	
Asn	Val	Val	Pro	Lys	Ile	Tyr	Met	Ser	Ala	Gly	Ser	Ile	Pro	Leu	Thr
			340						345					350	
Thr	His	Ile	Thr	Asn	Ser	Ile	Gln	Pro	Thr	Leu	Trp	Thr	Ile	Gly	Ser
		355					360					365			
Ile	Asn	Gly	Val	Ala	Pro	Leu	Ala	Lys	Ser	Ile	Lys	Leu	Gly	Ile	Pro
	370					375					380				
Val	Thr	Gly	Ser	Ala	Tyr	Thr	Asp	Gln	Thr	Thr	Ala	Met	Val	Arg	Lys
385					390					395					400
Lys	Val	Ser	Val	Phe	Met	Gly	Ser	Gly	Ser	Gly	Ser	Gly	Ser	Ser	Met
				405					410					415	
Thr	Ala	Val	Met	Ala	Ser	Ser	Pro	Pro	Lys	Lys	Lys	Arg	Lys	Val	Ala
			420						425					430	
Ala	Ala	Asp	Tyr	Lys	Asp	Asp	Asp	Asp	Lys	Ser	Trp	Lys	Asp	Ala	Ser
		435							440				445		
Gly	Trp	Ser	Arg	Met	His	Ala	Ala	Pro	Arg	Arg	Arg	Ala	Ala	Gln	Pro
	450					455						460			
Ser	Asp	Ala	Ser	Pro	Ala	Ala	Gln	Val	Asp	Leu	Arg	Thr	Leu	Gly	Tyr
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Ser	Gln	Gln	Gln	Gln	Glu	Lys	Ile	Lys	Pro	Lys	Val	Arg	Ser	Thr	Val
				485						490				495	
Ala	Gln	His	His	Glu	Ala	Leu	Val	Gly	His	Gly	Phe	Thr	His	Ala	His
			500						505					510	
Ile	Val	Ala	Leu	Ser	Gln	His	Pro	Ala	Ala	Leu	Gly	Thr	Val	Ala	Val
		515						520					525		
Thr	Tyr	Gln	His	Ile	Ile	Thr	Ala	Leu	Pro	Glu	Ala	Thr	His	Glu	Asp
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Ile	Val	Gly	Val	Gly	Lys	Gln	Trp	Ser	Gly	Ala	Arg	Ala	Leu	Glu	Ala
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Leu	Leu	Thr	Asp	Ala	Gly	Glu	Leu	Arg	Gly	Pro	Pro	Leu	Gln	Leu	Asp
				565						570				575	
Thr	Gly	Gln	Leu	Val	Lys	Ile	Ala	Lys	Arg	Gly	Gly	Val	Thr	Ala	Met
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Glu	Ala	Val	His	Ala	Ser	Arg	Asn	Ala	Leu	Thr	Gly	Ala	Pro	Leu	Asn

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Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys		
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Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp		
625	630	635
His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly		
645	650	655
Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys		
660	665	670
Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn		
675	680	685
Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val		
690	695	700
Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala		
705	710	715
Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu		
725	730	735
Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala		
740	745	750
Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg		
755	760	765
Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val		
770	775	780
Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val		
785	790	795
Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp		
805	810	815
Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu		
820	825	830
Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr		
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Pro Ala Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala		
850	855	860
Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly		
865	870	875
Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys		
885	890	895
Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp		
900	905	910

His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Asn Gly		
915	920	925
Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys		
930	935	940
Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn		
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Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val		
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Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala		
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Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu		
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Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val		
1010	1015	1020
Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val		
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Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro		
1040	1045	1050
Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala		
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Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His		
1070	1075	1080
Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile Gly		
1085	1090	1095
Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu		
1100	1105	1110
Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala		
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Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu		
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Ile Val Ala Gln Leu Ser Arg Pro Asp Pro Ala Leu Ala Ala Leu		
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Thr Asn Asp His Leu Val Ala Leu Ala Cys Leu Gly Gly Arg Pro		
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Ala Met Asp Ala Val Lys Lys Gly Leu Pro His Ala Pro Glu Leu		

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Gln Glu Ser Ile Leu Met Leu Pro Glu Glu Val Glu Glu Val Ile		
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Gly Asn Lys Pro Glu Ser Asp Ile Leu Val His Thr Ala Tyr Asp		
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Glu Ser Thr Asp Glu Asn Val Met Leu Leu Thr Ser Asp Ala Pro		
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Glu Tyr Lys Pro Trp Ala Leu Val Ile Gln Asp Ser Asn Gly Glu		
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Asn Lys Ile Lys Met Leu Ser Gly Gly Ser Gly Gly Ser Gly Gly		
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Ser Thr Asn Leu Ser Asp Ile Ile Glu Lys Glu Thr Gly Lys Gln		
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Leu Val Ile Gln Glu Ser Ile Leu Met Leu Pro Glu Glu Val Glu		
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Glu Val Ile Gly Asn Lys Pro Glu Ser Asp Ile Leu Val His Thr		
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312

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Arg	Ala	Ile	Gly	Leu	His	Asp	Pro	Thr	Ala	His	Ala	Glu	Ile	Met	Ala
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Asn	Val	Val	Pro	Lys	Ile	Tyr	Met	Ser	Ala	Gly	Ser	Ile	Pro	Leu	Thr		
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Thr	His	Ile	Thr	Asn	Ser	Ile	Gln	Pro	Thr	Leu	Trp	Thr	Ile	Gly	Ser		
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Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val			
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Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu			
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Lys	Tyr	Gln	Asp	Met	Ile	Ala	Ala	Leu	Pro	Glu	Ala	Thr	His	Glu	Ala
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His	Gly	Leu	Thr	Pro	Glu	Gln	Val	Val	Ala	Ile	Ala	Ser	Asn	Ile	Gly
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Gln	Ala	His	Gly	Leu	Thr	Pro	Asp	Gln	Val	Val	Ala	Ile	Ala	Ser	Asn
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	340		345		350
Val Ala Ile Ala	Ser His Asp Gly Gly Lys Gln	Ala Leu Glu Thr	Val		
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Gln Arg Leu Leu	Pro Val Leu Cys Gln Ala His	Gly Leu Thr Pro	Asp		
	370		375		380
Gln Val Val Ala	Ile Ala Ser Asn Ile Gly Gly Lys Gln	Ala Leu Glu			
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Thr Val Gln Arg	Leu Leu Pro Val Leu Cys Gln	Ala His Gly Leu	Thr		
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Pro Ala Gln Val	Val Ala Ile Ala Ser Asn Asn	Gly Gly Lys Gln	Ala		
	420		425		430
Leu Glu Thr Val	Gln Arg Leu Leu Pro Val Leu Cys	Gln Asp His Gly			
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Leu Thr Pro Asp	Gln Val Val Ala Ile Ala Ser Asn	Ile Gly Gly Lys			
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Gln Ala Leu Glu	Thr Val Gln Arg Leu Leu Pro	Val Leu Cys Gln	Asp		
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His Gly Leu Thr	Pro Glu Gln Val Val Ala Ile	Ala Ser Asn Ile	Gly		
	485		490		495
Gly Lys Gln Ala	Leu Glu Thr Val Gln Arg Leu Leu	Pro Val Leu Cys			
	500		505		510
Gln Ala His Gly	Leu Thr Pro Asp Gln Val Val	Ala Ile Ala Ser	Asn		
	515		520		525
Asn Gly Gly Lys	Gln Ala Leu Glu Thr Val Gln	Arg Leu Leu Pro	Val		
	530		535		540
Leu Cys Gln Ala	His Gly Leu Thr Pro Ala Gln	Val Val Ala Ile	Ala		
545		550		555	560
Ser Asn Asn Gly	Gly Lys Gln Ala Leu Glu Thr	Val Gln Arg Leu	Leu		
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Pro Val Leu Cys	Gln Asp His Gly Leu Thr Pro	Asp Gln Val Val	Ala		
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Ile Ala Ser Asn	Asn Gly Gly Lys Gln Ala Leu	Glu Thr Val Gln	Arg		
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Leu Leu Pro Val	Leu Cys Gln Asp His Gly Leu	Thr Pro Glu Gln	Val		
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Val Ala Ile Ala	Ser Asn Asn Gly Gly Lys Gln	Ala Leu Glu Thr	Val		
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Thr	Val	Gln	Arg	Leu	Leu	Pro	Val	Leu	Cys	Gln	Ala	His	Gly	Leu	Thr
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Pro	Ala	Gln	Val	Val	Ala	Ile	Ala	Ser	His	Asp	Gly	Gly	Lys	Gln	Ala
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Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu	Pro	Val	Leu	Cys	Gln	Asp	His	Gly
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Leu	Thr	Pro	Glu	Gln	Val	Val	Ala	Ile	Ala	Ser	Asn	Ile	Gly	Gly	Arg
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Pro	Ala	Leu	Glu	Ser	Ile	Val	Ala	Gln	Leu	Ser	Arg	Pro	Asp	Pro	Ala
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Leu	Ala	Ala	Leu	Thr	Asn	Asp	His	Leu	Val	Ala	Leu	Ala	Cys	Leu	Gly
				755				760				765			
Gly	Arg	Pro	Ala	Leu	Asp	Ala	Val	Lys	Lys	Gly	Leu	Pro	His	Ala	Pro
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Ala	Leu	Ile	Lys	Arg	Thr	Asn	Arg	Arg	Ile	Pro	Glu	Arg	Thr	Ser	His
785				790				795				800			
Arg	Val	Ala	Asp	His	Ala	Gln	Val	Val	Arg	Val	Leu	Gly	Phe	Phe	Gln
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Cys	His	Ser	His	Pro	Ala	Gln	Ala	Phe	Asp	Asp	Ala	Met	Thr	Gln	Phe
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Glu Tyr Leu Arg Asp Asn Pro Gly Gln Phe Thr Ile Asn Trp Tyr			
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Ser His Asn Gln Leu Asn Glu Asn Arg Trp Leu Glu Lys Thr Leu			
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Lys Arg Ala Glu Lys Trp Arg Ser Glu Leu Ser Ile Met Ile Gln			
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Val Lys Ile Leu His Thr Thr Lys Ser Pro Ala Val Gly Ser Gly			
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Gly Ser Gly Gly Ser Gly Gly Ser Thr Asn Leu Ser Asp Ile Ile			
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Glu Lys Glu Thr Gly Lys Gln Leu Val Ile Gln Glu Ser Ile Leu			
1160	1165	1170	
Met Leu Pro Glu Glu Val Glu Glu Val Ile Gly Asn Lys Pro Glu			
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Ser Asp Ile Leu Val His Thr Ala Tyr Asp Glu Ser Thr Asp Glu			
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Asn Val Met Leu Leu Thr Ser Asp Ala Pro Glu Tyr Lys Pro Trp			
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Ala Leu Val Ile Gln Asp Ser Asn Gly Glu Asn Lys Ile Lys Met			
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Asp Ile	Ile Glu Lys Glu Thr	Gly Lys Gln Leu Val	Ile Gln Glu
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Ser Ile	Leu Met Leu Pro Glu	Glu Val Glu Glu Val	Ile Gly Asn
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Lys Pro	Glu Ser Asp Ile Leu	Val His Thr Ala Tyr	Asp Glu Ser
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Thr Asp	Glu Asn Val Met Leu	Leu Thr Ser Asp Ala	Pro Glu Tyr
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Lys Pro	Trp Ala Leu Val Ile	Gln Asp Ser Asn Gly	Glu Asn Lys
1310	1315	1320	
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<211> 3966

<212> DNA

<213> 人工序列(Artificial Sequence)

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<223> 47(AS3)-104-AID

<400> 153

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<210> 154

<211> 1322

<212> PRT

<213> 人工序列(Artificial Sequence)

<220>

<223> 47(AS3)-104-AID

<400> 154

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Ser Pro Ala Ala Gln Val Asp Leu Arg Thr Leu Gly Tyr Ser Gln Gln
          50           55           60
Gln Gln Glu Lys Ile Lys Pro Lys Val Arg Ser Thr Val Ala Gln His
65           70           75           80
His Glu Ala Leu Val Gly His Gly Phe Thr His Ala His Ile Val Ala
          85           90           95
Leu Ser Gln His Pro Ala Ala Leu Gly Thr Val Ala Val Thr Tyr Gln
          100          105          110
His Ile Ile Thr Ala Leu Pro Glu Ala Thr His Glu Asp Ile Val Gly
          115          120          125
Val Gly Lys Gln Trp Ser Gly Ala Arg Ala Leu Glu Ala Leu Leu Thr
          130          135          140
Asp Ala Gly Glu Leu Arg Gly Pro Pro Leu Gln Leu Asp Thr Gly Gln
145          150          155          160
Leu Val Lys Ile Ala Lys Arg Gly Gly Val Thr Ala Met Glu Ala Val
          165          170          175

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His	Ala	Ser	Arg	Asn	Ala	Leu	Thr	Gly	Ala	Pro	Leu	Asn	Leu	Thr	Pro	
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Asp	Gln	Val	Val	Ala	Ile	Ala	Ser	Asn	Asn	Gly	Gly	Lys	Gln	Ala	Leu	
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Glu	Thr	Val	Gln	Arg	Leu	Leu	Pro	Val	Leu	Cys	Gln	Asp	His	Gly	Leu	
			210						215						220	
Thr	Pro	Glu	Gln	Val	Val	Ala	Ile	Ala	Ser	Asn	Ile	Gly	Gly	Lys	Gln	
225						230						235			240	
Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu	Pro	Val	Leu	Cys	Gln	Ala	His	
			245						250						255	
Gly	Leu	Thr	Pro	Asp	Gln	Val	Val	Ala	Ile	Ala	Ser	Asn	Asn	Gly	Gly	
			260						265						270	
Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu	Pro	Val	Leu	Cys	Gln	
			275						280						285	
Ala	His	Gly	Leu	Thr	Pro	Ala	Gln	Val	Val	Ala	Ile	Ala	Ser	His	Asp	
290						295						300				
Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu	Pro	Val	Leu	
305						310						315			320	
Cys	Gln	Asp	His	Gly	Leu	Thr	Pro	Asp	Gln	Val	Val	Ala	Ile	Ala	Ser	
			325						330						335	
His	Asp	Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu	Pro	
			340						345						350	
Val	Leu	Cys	Gln	Asp	His	Gly	Leu	Thr	Pro	Glu	Gln	Val	Val	Ala	Ile	
			355						360						365	
Ala	Ser	His	Asp	Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu	
370						375						380				
Leu	Pro	Val	Leu	Cys	Gln	Ala	His	Gly	Leu	Thr	Pro	Asp	Gln	Val	Val	
385						390						395			400	
Ala	Ile	Ala	Ser	Asn	Ile	Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln	
			405						410						415	
Arg	Leu	Leu	Pro	Val	Leu	Cys	Gln	Ala	His	Gly	Leu	Thr	Pro	Ala	Gln	
			420						425						430	
Val	Val	Ala	Ile	Ala	Ser	Asn	Asn	Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr	
			435						440						445	
Val	Gln	Arg	Leu	Leu	Pro	Val	Leu	Cys	Gln	Asp	His	Gly	Leu	Thr	Pro	
450						455						460				
Asp	Gln	Val	Val	Ala	Ile	Ala	Ser	Asn	Ile	Gly	Gly	Lys	Gln	Ala	Leu	
465						470						475			480	
Glu	Thr	Val	Gln	Arg	Leu	Leu	Pro	Val	Leu	Cys	Gln	Asp	His	Gly	Leu	

				485				490				495			
Thr	Pro	Glu	Gln	Val	Val	Ala	Ile	Ala	Ser	Asn	Ile	Gly	Gly	Lys	Gln
				500				505				510			
Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu	Pro	Val	Leu	Cys	Gln	Ala	His
				515				520				525			
Gly	Leu	Thr	Pro	Asp	Gln	Val	Val	Ala	Ile	Ala	Ser	Asn	Asn	Gly	Gly
				530				535				540			
Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu	Pro	Val	Leu	Cys	Gln
545				550				555				560			
Ala	His	Gly	Leu	Thr	Pro	Ala	Gln	Val	Val	Ala	Ile	Ala	Ser	Asn	Asn
				565				570				575			
Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu	Pro	Val	Leu
				580				585				590			
Cys	Gln	Asp	His	Gly	Leu	Thr	Pro	Asp	Gln	Val	Val	Ala	Ile	Ala	Ser
				595				600				605			
Asn	Asn	Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu	Pro
610				615				620							
Val	Leu	Cys	Gln	Asp	His	Gly	Leu	Thr	Pro	Glu	Gln	Val	Val	Ala	Ile
625				630				635				640			
Ala	Ser	Asn	Asn	Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu
				645				650				655			
Leu	Pro	Val	Leu	Cys	Gln	Ala	His	Gly	Leu	Thr	Pro	Asp	Gln	Val	Val
				660				665				670			
Ala	Ile	Ala	Ser	Asn	Ile	Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln
				675				680				685			
Arg	Leu	Leu	Pro	Val	Leu	Cys	Gln	Ala	His	Gly	Leu	Thr	Pro	Ala	Gln
690				695				700							
Val	Val	Ala	Ile	Ala	Ser	His	Asp	Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr
705				710				715				720			
Val	Gln	Arg	Leu	Leu	Pro	Val	Leu	Cys	Gln	Asp	His	Gly	Leu	Thr	Pro
				725				730				735			
Glu	Gln	Val	Val	Ala	Ile	Ala	Ser	Asn	Ile	Gly	Gly	Arg	Pro	Ala	Leu
				740				745				750			
Glu	Ser	Ile	Val	Ala	Gln	Leu	Ser	Arg	Pro	Asp	Pro	Ala	Leu	Ala	Ala
				755				760				765			
Leu	Thr	Asn	Asp	His	Leu	Val	Ala	Leu	Ala	Cys	Leu	Gly	Gly	Arg	Pro
770				775				780							
Ala	Met	Asp	Ala	Val	Lys	Lys	Gly	Leu	Pro	His	Ala	Pro	Glu	Leu	Ile
785				790				795				800			

Arg Ser Ser Arg Ala Asp Pro Lys Lys Lys Arg Lys Val Gly Gly Gly		
805	810	815
Gly Thr Gly Gly Gly Ser Ala Glu Tyr Val Arg Ala Leu Phe Asp		
820	825	830
Phe Asn Gly Asn Asp Glu Glu Asp Leu Pro Phe Lys Lys Gly Asp Ile		
835	840	845
Leu Arg Ile Arg Asp Lys Pro Glu Glu Gln Trp Trp Asn Ala Glu Asp		
850	855	860
Ser Glu Gly Lys Arg Gly Met Ile Leu Val Pro Tyr Val Glu Lys Tyr		
865	870	875
Ser Gly Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His Asp Ile		
885	890	895
Asp Tyr Lys Asp Asp Asp Asp Lys Ser Gly Met Thr Asp Ala Glu Tyr		
900	905	910
Val Arg Ile His Glu Lys Leu Asp Ile Tyr Thr Phe Lys Lys Gln Phe		
915	920	925
Phe Asn Asn Lys Lys Ser Val Ser His Arg Cys Tyr Val Leu Phe Glu		
930	935	940
Leu Lys Arg Arg Gly Glu Arg Arg Ala Cys Phe Trp Gly Tyr Ala Val		
945	950	955
Asn Lys Pro Gln Ser Gly Thr Glu Arg Gly Ile His Ala Glu Ile Phe		
965	970	975
Ser Ile Arg Lys Val Glu Glu Tyr Leu Arg Asp Asn Pro Gly Gln Phe		
980	985	990
Thr Ile Asn Trp Tyr Ser Ser Trp Ser Pro Cys Ala Asp Cys Ala Glu		
995	1000	1005
Lys Ile Leu Glu Trp Tyr Asn Gln Glu Leu Arg Gly Asn Gly His		
1010	1015	1020
Thr Leu Lys Ile Trp Ala Cys Lys Leu Tyr Tyr Glu Lys Asn Ala		
1025	1030	1035
Arg Asn Gln Ile Gly Leu Trp Asn Leu Arg Asp Asn Gly Val Gly		
1040	1045	1050
Leu Asn Val Met Val Ser Glu His Tyr Gln Cys Cys Arg Lys Ile		
1055	1060	1065
Phe Ile Gln Ser Ser His Asn Gln Leu Asn Glu Asn Arg Trp Leu		
1070	1075	1080
Glu Lys Thr Leu Lys Arg Ala Glu Lys Trp Arg Ser Glu Leu Ser		
1085	1090	1095
Ile Met Ile Gln Val Lys Ile Leu His Thr Thr Lys Ser Pro Ala		

1100	1105	1110
Val Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Thr Asn Leu		
1115	1120	1125
Ser Asp Ile Ile Glu Lys Glu Thr Gly Lys Gln Leu Val Ile Gln		
1130	1135	1140
Glu Ser Ile Leu Met Leu Pro Glu Glu Val Glu Glu Val Ile Gly		
1145	1150	1155
Asn Lys Pro Glu Ser Asp Ile Leu Val His Thr Ala Tyr Asp Glu		
1160	1165	1170
Ser Thr Asp Glu Asn Val Met Leu Leu Thr Ser Asp Ala Pro Glu		
1175	1180	1185
Tyr Lys Pro Trp Ala Leu Val Ile Gln Asp Ser Asn Gly Glu Asn		
1190	1195	1200
Lys Ile Lys Met Leu Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser		
1205	1210	1215
Thr Asn Leu Ser Asp Ile Ile Glu Lys Glu Thr Gly Lys Gln Leu		
1220	1225	1230
Val Ile Gln Glu Ser Ile Leu Met Leu Pro Glu Glu Val Glu Glu		
1235	1240	1245
Val Ile Gly Asn Lys Pro Glu Ser Asp Ile Leu Val His Thr Ala		
1250	1255	1260
Tyr Asp Glu Ser Thr Asp Glu Asn Val Met Leu Leu Thr Ser Asp		
1265	1270	1275
Ala Pro Glu Tyr Lys Pro Trp Ala Leu Val Ile Gln Asp Ser Asn		
1280	1285	1290
Gly Glu Asn Lys Ile Lys Met Leu Ser Gly Gly Ser Lys Arg Thr		
1295	1300	1305
Ala Asp Gly Ser Glu Phe Glu Pro Lys Lys Lys Arg Lys Val		
1310	1315	1320

<210> 155

<211> 4044

<212> DNA

<213> 人工序列(Artificial Sequence)

<220>

<223> WT(AS14-1)-12-AID

<400> 155

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gacgataaga tggcccaaaa gaagaagcgg aaggtcggta tccacggagt cccagcagcc	120
gtagatttga gaactttggg atattcacag cagcagcagg aaaagatcaa gcccaaagtg	180

aggtcgacag	tcgcgacagca	tcacgaagcg	ctggtgggtc	atgggtttac	acatgcccac	240
atcgtagcct	tgctgcagca	ccctgcagcc	cttggcacgg	tcgccgtcaa	gtaccaggac	300
atgattgcgg	cggtgccgga	agccacacat	gaggcgatcg	tcggtgtggg	gaaacagtgg	360
agcggagccc	gagcgcttga	ggccctgttg	acggtcgcgg	gagagctgag	agggcctccc	420
cttcagctgg	acacgggcca	gttgctgaag	atcgcggaagc	ggggaggagt	cacggcggtc	480
gaggcggtac	acgcgtggcg	caatgcgctc	acgggagcac	ccctcaacct	gaccccagac	540
caggttgtgg	ccatcgccag	caacataggt	ggcaagcagg	ccctcgaaac	cgtccagaga	600
ctgttaccgg	ttctctgcca	ggaccacggc	ctgaccccag	aacaagttgt	cgcgattgca	660
agcaacaacg	gaggcaaaca	agccttagaa	acagtccaga	gattgttgcc	ggtgctgtgc	720
caagcccacg	gcctgacccc	ggaccaggtg	gttgcaatcg	cgtcacacga	tgggggaaag	780
caggccctag	aaaccgttca	gcgactcctg	ccgctcctgt	gccaggccca	cggcctgacc	840
cccggcccagg	ttgtcgctat	tgctagtaac	ggcggaggca	aacaggcgct	ggaaacagtt	900
cagcgctctt	tgccggtctt	gtgtcaggac	cacggcctga	ccccgacca	ggttgctgct	960
attgctagta	acggcggagg	caaacaggcg	ctggaaacag	ttcagcgctt	cttgccggtc	1020
ttgtgtcagg	accacggcct	gaccccagaa	caagttgtcg	cgattgcaag	caacaacgga	1080
ggcaaacaag	ccttagaaaac	agtccagaga	ttgttgccgg	tgctgtgcca	agcccacggc	1140
ctgaccccag	accaagttgt	cgcgattgca	agcaacaacg	gaggcaaaca	agccttagaa	1200
acagtccaga	gattgttgcc	tgtgctgtgc	caagcccacg	gcctgacccc	cgcccaggtt	1260
gtcgtatttg	ctagtaacgg	cggaggcaaa	caggcgctgg	aaacagttca	gcgcctcttg	1320
ccggtcttgt	gtcaggacca	cggcctgacc	ccggaccagg	tggttgcaat	cgcgtcacac	1380
gatgggggaa	agcaggccct	agaaaccgtt	cagcgactcc	tgcccgtcct	gtgccaggac	1440
cacggcctga	ccccggaaca	ggtggttgca	atcgcgtcac	acgatggggg	aaagcaggcc	1500
ctagaaaccg	ttcagcgact	cctgcccgtc	ctgtgccagg	cccacggcct	gaccccagac	1560
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ccggaacagg	tggttgcaat	cgcgtcacac	gatgggggaa	agcaggccct	agaaaccgtt	1920
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attgctagta	acggcggagg	caaacaggcg	ctggaaacag	ttcagcgctt	cttgccggtc	2040
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ctgacccctg	agcaggtagt	ggctattgca	tccaacggag	ggggcagacc	cgcactggag	2220
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cttgtagcgc	tgccctgcct	cggcggacga	cccgccttgg	atgcggtgaa	gaaggggctc	2340
ccgcacgcgc	ctgcattgat	taagcggacc	aacagaagga	tccccgagag	gacatcacat	2400
cgagtggcag	atcacgcgca	agtgtccgc	gtgctcggat	tcttccagtg	tactcccac	2460
ccgcacaaag	cgttcgatga	cgccatgact	caatttggtg	tgctcagaca	cggactgctg	2520

cagctctttc gtagagtcgg tgtcacagaa ctggaggccc gctcgggcac actgcctccc 2580
 gcctcccagc ggtgggacag gattctccaa gcgagcggta tgaaacgcgc gaagccttca 2640
 cctacgtcaa ctcagacacc tgaccaggcg agccttcatg cgttcgcaga ctcgctggag 2700
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 gtgtctcaca gatgctatgt gctgttcgag ctgaagcgga gaggagagag gcgcgcatgt 2940
 ttttggggct acgccgtgaa taagccacag agcggaaacc agaggggaat ccacgccgag 3000
 atcttctcca tcaggaaaagt ggaggagtat ctgcgcgaca accctggcca gtttacaatc 3060
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 aaccaggagc tgagaggcaa tggccacacc ctgaagatct gggcctgcaa gctgtactat 3180
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 agcgagctgt ccatcatgat ccaggtgaag atcctgcaca ccacaaagag cccagcagt 3420
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 gaaagcgaca tcctggtcca tactgcctac gacgagagta ccgacgaaaa tgtgatgtta 3900
 ctgacctccg acgcccctga gtataagcca tgggctctgg tcatccagga ctccaatgga 3960
 gaaaataaga tcaagatgtt aagcggcggc tccaagagaa cagccgacgg ctccgagttc 4020
 gagcccaaga agaagcggaa agtg 4044

<210> 156

<211> 1348

<212> PRT

<213> 人工序列(Artificial Sequence)

<220>

<223> WT(AS14-1)-12-AID

<400> 156

Met Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His Asp Ile Asp

1 5 10 15

Tyr Lys Asp Asp Asp Asp Lys Met Ala Pro Lys Lys Lys Arg Lys Val

20 25 30

Gly Ile His Gly Val Pro Ala Ala Val Asp Leu Arg Thr Leu Gly Tyr

35 40 45

Ser	Gln	Gln	Gln	Gln	Glu	Lys	Ile	Lys	Pro	Lys	Val	Arg	Ser	Thr	Val
50						55					60				
Ala	Gln	His	His	Glu	Ala	Leu	Val	Gly	His	Gly	Phe	Thr	His	Ala	His
65					70					75					80
Ile	Val	Ala	Leu	Ser	Gln	His	Pro	Ala	Ala	Leu	Gly	Thr	Val	Ala	Val
				85					90					95	
Lys	Tyr	Gln	Asp	Met	Ile	Ala	Ala	Leu	Pro	Glu	Ala	Thr	His	Glu	Ala
			100					105					110		
Ile	Val	Gly	Val	Gly	Lys	Gln	Trp	Ser	Gly	Ala	Arg	Ala	Leu	Glu	Ala
		115					120					125			
Leu	Leu	Thr	Val	Ala	Gly	Glu	Leu	Arg	Gly	Pro	Pro	Leu	Gln	Leu	Asp
		130				135					140				
Thr	Gly	Gln	Leu	Leu	Lys	Ile	Ala	Lys	Arg	Gly	Gly	Val	Thr	Ala	Val
145					150					155					160
Glu	Ala	Val	His	Ala	Trp	Arg	Asn	Ala	Leu	Thr	Gly	Ala	Pro	Leu	Asn
				165					170					175	
Leu	Thr	Pro	Asp	Gln	Val	Val	Ala	Ile	Ala	Ser	Asn	Ile	Gly	Gly	Lys
			180					185					190		
Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu	Pro	Val	Leu	Cys	Gln	Asp
		195						200					205		
His	Gly	Leu	Thr	Pro	Glu	Gln	Val	Val	Ala	Ile	Ala	Ser	Asn	Asn	Gly
		210					215					220			
Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu	Pro	Val	Leu	Cys
225					230					235					240
Gln	Ala	His	Gly	Leu	Thr	Pro	Asp	Gln	Val	Val	Ala	Ile	Ala	Ser	His
				245					250					255	
Asp	Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu	Pro	Val
			260					265					270		
Leu	Cys	Gln	Ala	His	Gly	Leu	Thr	Pro	Ala	Gln	Val	Val	Ala	Ile	Ala
		275					280						285		
Ser	Asn	Gly	Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu
		290					295					300			
Pro	Val	Leu	Cys	Gln	Asp	His	Gly	Leu	Thr	Pro	Asp	Gln	Val	Val	Ala
305					310					315					320
Ile	Ala	Ser	Asn	Gly	Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg
				325					330					335	
Leu	Leu	Pro	Val	Leu	Cys	Gln	Asp	His	Gly	Leu	Thr	Pro	Glu	Gln	Val
			340						345				350		
Val	Ala	Ile	Ala	Ser	Asn	Asn	Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val

355	360	365
Gln Arg Leu Leu Pro Val	Leu Cys Gln Ala His	Gly Leu Thr Pro Asp
370	375	380
Gln Val Val Ala Ile Ala	Ser Asn Asn Gly Gly Lys	Gln Ala Leu Glu
385	390	395
Thr Val Gln Arg Leu Leu	Pro Val Leu Cys Gln Ala	His Gly Leu Thr
405	410	415
Pro Ala Gln Val Val Ala	Ile Ala Ser Asn Gly Gly	Gly Lys Gln Ala
420	425	430
Leu Glu Thr Val Gln Arg	Leu Leu Pro Val Leu Cys	Gln Asp His Gly
435	440	445
Leu Thr Pro Asp Gln Val	Val Ala Ile Ala Ser His	Asp Gly Gly Lys
450	455	460
Gln Ala Leu Glu Thr Val	Gln Arg Leu Leu Pro Val	Leu Cys Gln Asp
465	470	475
His Gly Leu Thr Pro Glu	Gln Val Val Ala Ile Ala	Ser His Asp Gly
485	490	495
Gly Lys Gln Ala Leu Glu	Thr Val Gln Arg Leu Leu	Pro Val Leu Cys
500	505	510
Gln Ala His Gly Leu Thr	Pro Asp Gln Val Val Ala	Ile Ala Ser Asn
515	520	525
Ile Gly Gly Lys Gln Ala	Leu Glu Thr Val Gln Arg	Leu Leu Pro Val
530	535	540
Leu Cys Gln Ala His Gly	Leu Thr Pro Ala Gln Val	Val Ala Ile Ala
545	550	555
Ser Asn Ile Gly Gly Lys	Gln Ala Leu Glu Thr Val	Gln Arg Leu Leu
565	570	575
Pro Val Leu Cys Gln Asp	His Gly Leu Thr Pro Asp	Gln Val Val Ala
580	585	590
Ile Ala Ser His Asp Gly	Gly Lys Gln Ala Leu Glu	Thr Val Gln Arg
595	600	605
Leu Leu Pro Val Leu Cys	Gln Asp His Gly Leu Thr	Pro Glu Gln Val
610	615	620
Val Ala Ile Ala Ser His	Asp Gly Gly Lys Gln Ala	Leu Glu Thr Val
625	630	635
Gln Arg Leu Leu Pro Val	Leu Cys Gln Ala His Gly	Leu Thr Pro Asp
645	650	655
Gln Val Val Ala Ile Ala	Ser Asn Gly Gly Gly Lys	Gln Ala Leu Glu
660	665	670

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr		
675	680	685
Pro Ala Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala		
690	695	700
Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly		
705	710	715
Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Arg		
	725	730
Pro Ala Leu Glu Ser Ile Val Ala Gln Leu Ser Arg Pro Asp Pro Ala		
	740	745
Leu Ala Ala Leu Thr Asn Asp His Leu Val Ala Leu Ala Cys Leu Gly		
	755	760
Gly Arg Pro Ala Leu Asp Ala Val Lys Lys Gly Leu Pro His Ala Pro		
	770	775
Ala Leu Ile Lys Arg Thr Asn Arg Arg Ile Pro Glu Arg Thr Ser His		
785	790	795
Arg Val Ala Asp His Ala Gln Val Val Arg Val Leu Gly Phe Phe Gln		
	805	810
Cys His Ser His Pro Ala Gln Ala Phe Asp Asp Ala Met Thr Gln Phe		
	820	825
Gly Met Ser Arg His Gly Leu Leu Gln Leu Phe Arg Arg Val Gly Val		
	835	840
Thr Glu Leu Glu Ala Arg Ser Gly Thr Leu Pro Pro Ala Ser Gln Arg		
	850	855
Trp Asp Arg Ile Leu Gln Ala Ser Gly Met Lys Arg Ala Lys Pro Ser		
865	870	875
Pro Thr Ser Thr Gln Thr Pro Asp Gln Ala Ser Leu His Ala Phe Ala		
	885	890
Asp Ser Leu Glu Arg Asp Leu Asp Ala Pro Ser Pro Met His Glu Gly		
	900	905
Asp Gln Thr Arg Ala Ser Ala Ser Ala Ser Pro Lys Lys Lys Arg Lys		
	915	920
Val Glu Ala Ser Met Thr Asp Ala Glu Tyr Val Arg Ile His Glu Lys		
	930	935
Leu Asp Ile Tyr Thr Phe Lys Lys Gln Phe Phe Asn Asn Lys Lys Ser		
945	950	955
Val Ser His Arg Cys Tyr Val Leu Phe Glu Leu Lys Arg Arg Gly Glu		
	965	970
Arg Arg Ala Cys Phe Trp Gly Tyr Ala Val Asn Lys Pro Gln Ser Gly		

980	985	990
Thr Glu Arg Gly Ile His Ala Glu	Ile Phe Ser Ile Arg	Lys Val Glu
995	1000	1005
Glu Tyr Leu Arg Asp Asn Pro	Gly Gln Phe Thr Ile	Asn Trp Tyr
1010	1015	1020
Ser Ser Trp Ser Pro Cys Ala	Asp Cys Ala Glu Lys	Ile Leu Glu
1025	1030	1035
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Gly Leu Trp Asn Leu Arg Asp	Asn Gly Val Gly Leu	Asn Val Met
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Val Ser Glu His Tyr Gln Cys	Cys Arg Lys Ile Phe	Ile Gln Ser
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Ser His Asn Gln Leu Asn Glu	Asn Arg Trp Leu Glu	Lys Thr Leu
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Lys Arg Ala Glu Lys Trp Arg	Ser Glu Leu Ser Ile	Met Ile Gln
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1130	1135	1140
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Glu Lys Glu Thr Gly Lys Gln	Leu Val Ile Gln Glu	Ser Ile Leu
1160	1165	1170
Met Leu Pro Glu Glu Val Glu	Glu Val Ile Gly Asn	Lys Pro Glu
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Ala Leu Val Ile Gln Asp Ser	Asn Gly Glu Asn Lys	Ile Lys Met
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Leu Ser Gly Gly Ser Gly Gly	Ser Gly Gly Ser Thr	Asn Leu Ser
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Asp Ile Ile Glu Lys Glu Thr	Gly Lys Gln Leu Val	Ile Gln Glu
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Ser Ile Leu Met Leu Pro Glu	Glu Val Glu Glu Val	Ile Gly Asn
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Lys Pro Glu Ser Asp Ile Leu Val His Thr Ala Tyr Asp Glu Ser
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 Lys Pro Trp Ala Leu Val Ile Gln Asp Ser Asn Gly Glu Asn Lys
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<212> DNA

<213> 人工序列(Artificial Sequence)

<220>

<223> 47(AS14-1) -104-AID

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Ser Pro Ala Ala Gln Val Asp Leu Arg Thr Leu Gly Tyr Ser Gln Gln	
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Gln Gln Glu Lys Ile Lys Pro Lys Val Arg Ser Thr Val Ala Gln His	
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His Glu Ala Leu Val Gly His Gly Phe Thr His Ala His Ile Val Ala	
85 90 95	
Leu Ser Gln His Pro Ala Ala Leu Gly Thr Val Ala Val Thr Tyr Gln	
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His Ile Ile Thr Ala Leu Pro Glu Ala Thr His Glu Asp Ile Val Gly	
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Val Gly Lys Gln Trp Ser Gly Ala Arg Ala Leu Glu Ala Leu Leu Thr	
130 135 140	
Asp Ala Gly Glu Leu Arg Gly Pro Pro Leu Gln Leu Asp Thr Gly Gln	
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Leu Val Lys Ile Ala Lys Arg Gly Gly Val Thr Ala Met Glu Ala Val	
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His Ala Ser Arg Asn Ala Leu Thr Gly Ala Pro Leu Asn Leu Thr Pro	
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Asp Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu	
195 200 205	

Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu		
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Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln		
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Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His		
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Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser His Asp Gly Gly		
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Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln		
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Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser Asn Gly		
290	295	300
Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu		
305	310	315 320
Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser		
325	330	335
Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro		
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Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile		
355	360	365
Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu		
370	375	380
Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val		
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Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln		
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Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln		
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Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr		
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Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro		
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Asp Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu		
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Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu		
485	490	495
Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln		
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Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His		

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545	550	555
Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser Asn Ile		
565	570	575
Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu		
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Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser		
595	600	605
His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro		
610	615	620
Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile		
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Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu		
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Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val		
660	665	670
Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln		
675	680	685
Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln		
690	695	700
Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr		
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Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro		
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Glu Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Arg Pro Ala Leu		
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Glu Ser Ile Val Ala Gln Leu Ser Arg Pro Asp Pro Ala Leu Ala Ala		
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Leu Thr Asn Asp His Leu Val Ala Leu Ala Cys Leu Gly Gly Arg Pro		
770	775	780
Ala Met Asp Ala Val Lys Lys Gly Leu Pro His Ala Pro Glu Leu Ile		
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Arg Ser Ser Arg Ala Asp Pro Lys Lys Lys Arg Lys Val Gly Gly Gly		
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Gly Thr Gly Gly Gly Gly Ser Ala Glu Tyr Val Arg Ala Leu Phe Asp		
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Ser Gly Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His Asp Ile		
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Val Arg Ile His Glu Lys Leu Asp Ile Tyr Thr Phe Lys Lys Gln Phe		
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Asn Lys Pro Glu Ser Asp Ile	Leu Val His Thr Ala	Tyr Asp Glu
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Ser Thr Asp Glu Asn Val Met	Leu Leu Thr Ser Asp	Ala Pro Glu
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Thr Asn Leu Ser Asp Ile Ile	Glu Lys Glu Thr Gly	Lys Gln Leu
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Val Ile Gln Glu Ser Ile Leu	Met Leu Pro Glu Glu	Val Glu Glu
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Val Ile Gly Asn Lys Pro Glu	Ser Asp Ile Leu Val	His Thr Ala
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Ala Pro Glu Tyr Lys Pro Trp	Ala Leu Val Ile Gln	Asp Ser Asn
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<213> 人工序列(Artificial Sequence)

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gcccctgagt ataagccatg ggctctggtc atccaggact ccaatggaga aaataagatc 3720
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<210> 160

<211> 1264

<212> PRT

<213> 人工序列(Artificial Sequence)

<220>

<223> 47(AS14-2)-12-AID

<400> 160

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Tyr Lys Asp Asp Asp Asp Lys Ser Trp Lys Asp Ala Ser Gly Trp Ser
          20           25           30
Arg Met His Ala Ala Pro Arg Arg Arg Ala Ala Gln Pro Ser Asp Ala
          35           40           45
Ser Pro Ala Ala Gln Val Asp Leu Arg Thr Leu Gly Tyr Ser Gln Gln
          50           55           60
Gln Gln Glu Lys Ile Lys Pro Lys Val Arg Ser Thr Val Ala Gln His
65           70           75           80
His Glu Ala Leu Val Gly His Gly Phe Thr His Ala His Ile Val Ala
          85           90           95
Leu Ser Gln His Pro Ala Ala Leu Gly Thr Val Ala Val Thr Tyr Gln
          100          105          110

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His Ile Ile Thr Ala Leu Pro Glu Ala Thr His Glu Asp Ile Val Gly		
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Val Gly Lys Gln Trp Ser Gly Ala Arg Ala Leu Glu Ala Leu Leu Thr		
130	135	140
Asp Ala Gly Glu Leu Arg Gly Pro Pro Leu Gln Leu Asp Thr Gly Gln		
145	150	155
Leu Val Lys Ile Ala Lys Arg Gly Gly Val Thr Ala Met Glu Ala Val		
165	170	175
His Ala Ser Arg Asn Ala Leu Thr Gly Ala Pro Leu Asn Leu Thr Pro		
180	185	190
Asp Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu		
195	200	205
Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu		
210	215	220
Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln		
225	230	235
Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His		
245	250	255
Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly		
260	265	270
Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln		
275	280	285
Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser His Asp		
290	295	300
Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu		
305	310	315
Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser		
325	330	335
His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro		
340	345	350
Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile		
355	360	365
Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu		
370	375	380
Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val		
385	390	395
Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln		
405	410	415
Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln		

	420		425		430
Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr					
	435		440		445
Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro					
	450		455		460
Asp Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu					
465			470		480
Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu					
	485		490		495
Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln					
	500		505		510
Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His					
	515		520		525
Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly					
	530		535		540
Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln					
545			550		560
Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser Asn Gly					
	565		570		575
Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu					
	580		585		590
Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser					
	595		600		605
Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro					
	610		615		620
Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile					
625			630		640
Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu					
	645		650		655
Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val					
	660		665		670
Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln					
	675		680		685
Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln					
	690		695		700
Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr					
705			710		720
Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro					
	725		730		735

Asp Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu		
740	745	750
Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu		
755	760	765
Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Arg Pro		
770	775	780
Ala Leu Glu Ser Ile Val Ala Gln Leu Ser Arg Pro Asp Pro Ala Leu		
785	790	795
Ala Ala Leu Thr Asn Asp His Leu Val Ala Leu Ala Cys Leu Gly Gly		
805	810	815
Arg Pro Ala Met Asp Ala Val Lys Lys Gly Leu Pro His Ala Pro Glu		
820	825	830
Leu Ile Arg Ser Ala Ser Pro Lys Lys Lys Arg Lys Val Glu Ala Ser		
835	840	845
Met Thr Asp Ala Glu Tyr Val Arg Ile His Glu Lys Leu Asp Ile Tyr		
850	855	860
Thr Phe Lys Lys Gln Phe Phe Asn Asn Lys Lys Ser Val Ser His Arg		
865	870	875
Cys Tyr Val Leu Phe Glu Leu Lys Arg Arg Gly Glu Arg Arg Ala Cys		
885	890	895
Phe Trp Gly Tyr Ala Val Asn Lys Pro Gln Ser Gly Thr Glu Arg Gly		
900	905	910
Ile His Ala Glu Ile Phe Ser Ile Arg Lys Val Glu Glu Tyr Leu Arg		
915	920	925
Asp Asn Pro Gly Gln Phe Thr Ile Asn Trp Tyr Ser Ser Trp Ser Pro		
930	935	940
Cys Ala Asp Cys Ala Glu Lys Ile Leu Glu Trp Tyr Asn Gln Glu Leu		
945	950	955
Arg Gly Asn Gly His Thr Leu Lys Ile Trp Ala Cys Lys Leu Tyr Tyr		
965	970	975
Glu Lys Asn Ala Arg Asn Gln Ile Gly Leu Trp Asn Leu Arg Asp Asn		
980	985	990
Gly Val Gly Leu Asn Val Met Val Ser Glu His Tyr Gln Cys Cys Arg		
995	1000	1005
Lys Ile Phe Ile Gln Ser Ser His Asn Gln Leu Asn Glu Asn Arg		
1010	1015	1020
Trp Leu Glu Lys Thr Leu Lys Arg Ala Glu Lys Trp Arg Ser Glu		
1025	1030	1035
Leu Ser Ile Met Ile Gln Val Lys Ile Leu His Thr Thr Lys Ser		

1040	1045	1050
Pro Ala Val Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Thr		
1055	1060	1065
Asn Leu Ser Asp Ile Ile Glu Lys Glu Thr Gly Lys Gln Leu Val		
1070	1075	1080
Ile Gln Glu Ser Ile Leu Met Leu Pro Glu Glu Val Glu Glu Val		
1085	1090	1095
Ile Gly Asn Lys Pro Glu Ser Asp Ile Leu Val His Thr Ala Tyr		
1100	1105	1110
Asp Glu Ser Thr Asp Glu Asn Val Met Leu Leu Thr Ser Asp Ala		
1115	1120	1125
Pro Glu Tyr Lys Pro Trp Ala Leu Val Ile Gln Asp Ser Asn Gly		
1130	1135	1140
Glu Asn Lys Ile Lys Met Leu Ser Gly Gly Ser Gly Gly Ser Gly		
1145	1150	1155
Gly Ser Thr Asn Leu Ser Asp Ile Ile Glu Lys Glu Thr Gly Lys		
1160	1165	1170
Gln Leu Val Ile Gln Glu Ser Ile Leu Met Leu Pro Glu Glu Val		
1175	1180	1185
Glu Glu Val Ile Gly Asn Lys Pro Glu Ser Asp Ile Leu Val His		
1190	1195	1200
Thr Ala Tyr Asp Glu Ser Thr Asp Glu Asn Val Met Leu Leu Thr		
1205	1210	1215
Ser Asp Ala Pro Glu Tyr Lys Pro Trp Ala Leu Val Ile Gln Asp		
1220	1225	1230
Ser Asn Gly Glu Asn Lys Ile Lys Met Leu Ser Gly Gly Ser Lys		
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Arg Thr Ala Asp Gly Ser Glu Phe Glu Pro Lys Lys Lys Arg Lys		
1250	1255	1260
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<400> 161		
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gtagatttga	gaactttggg	atattcacag	cagcagcagg	aaaagatcaa	gccccaaagtg	180
aggctgcacag	tcgcgcagca	tcacgaagcg	ctgggtgggtc	atgggttttac	acatgcccac	240
atcgtagcct	tgctgcagca	ccctgcagcc	cttggcacgg	tcgccgtcaa	gtaccaggac	300
atgattgcgg	cggttgccgga	agccacacat	gaggcgatcg	tcggtgtggg	gaaacagtgg	360
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<210> 162

<211> 1314

<212> PRT

<213> 人工序列(Artificial Sequence)

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<223> WT(S2) -12-AID

<400> 162

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Tyr Lys Asp Asp Asp Asp Lys Met Ala Pro Lys Lys Lys Arg Lys Val

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Gly Ile His Gly Val Pro Ala Ala Val Asp Leu Arg Thr Leu Gly Tyr

35 40 45

Ser Gln Gln Gln Gln Glu Lys Ile Lys Pro Lys Val Arg Ser Thr Val

50	55	60
Ala Gln His His Glu	Ala Leu Val Gly His Gly	Phe Thr His Ala His
65	70	75
Ile Val Ala Leu Ser Gln	His Pro Ala Ala Leu Gly	Thr Val Ala Val
85	90	95
Lys Tyr Gln Asp Met Ile	Ala Ala Leu Pro Glu Ala	Thr His Glu Ala
100	105	110
Ile Val Gly Val Gly Lys	Gln Trp Ser Gly Ala Arg	Ala Leu Glu Ala
115	120	125
Leu Leu Thr Val Ala Gly	Glu Leu Arg Gly Pro Pro	Leu Gln Leu Asp
130	135	140
Thr Gly Gln Leu Leu Lys	Ile Ala Lys Arg Gly Gly	Val Thr Ala Val
145	150	155
Glu Ala Val His Ala Trp	Arg Asn Ala Leu Thr Gly	Ala Pro Leu Asn
165	170	175
Leu Thr Pro Asp Gln Val	Val Ala Ile Ala Ser Asn	Asn Gly Gly Lys
180	185	190
Gln Ala Leu Glu Thr Val	Gln Arg Leu Leu Pro Val	Leu Cys Gln Asp
195	200	205
His Gly Leu Thr Pro Glu	Gln Val Val Ala Ile Ala	Ser His Asp Gly
210	215	220
Gly Lys Gln Ala Leu Glu	Thr Val Gln Arg Leu Leu	Pro Val Leu Cys
225	230	235
Gln Ala His Gly Leu Thr	Pro Asp Gln Val Val Ala	Ile Ala Ser His
245	250	255
Asp Gly Gly Lys Gln Ala	Leu Glu Thr Val Gln Arg	Leu Leu Pro Val
260	265	270
Leu Cys Gln Ala His Gly	Leu Thr Pro Ala Gln Val	Val Ala Ile Ala
275	280	285
Ser Asn Ile Gly Gly Lys	Gln Ala Leu Glu Thr Val	Gln Arg Leu Leu
290	295	300
Pro Val Leu Cys Gln Asp	His Gly Leu Thr Pro Asp	Gln Val Val Ala
305	310	315
Ile Ala Ser His Asp Gly	Gly Lys Gln Ala Leu Glu	Thr Val Gln Arg
325	330	335
Leu Leu Pro Val Leu Cys	Gln Asp His Gly Leu Thr	Pro Glu Gln Val
340	345	350
Val Ala Ile Ala Ser Asn	Ile Gly Gly Lys Gln Ala	Leu Glu Thr Val
355	360	365

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp			
370	375	380	
Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu			
385	390	395	400
Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr			
	405	410	415
Pro Ala Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala			
	420	425	430
Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly			
	435	440	445
Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys			
	450	455	460
Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp			
465	470	475	480
His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly			
	485	490	495
Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys			
	500	505	510
Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn			
	515	520	525
Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val			
	530	535	540
Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala			
545	550	555	560
Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu			
	565	570	575
Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala			
	580	585	590
Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg			
	595	600	605
Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val			
	610	615	620
Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val			
625	630	635	640
Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp			
	645	650	655
Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu			
	660	665	670
Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr			

675	680	685
Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Arg Pro Ala		
690	695	700
Leu Glu Ser Ile Val Ala Gln Leu Ser Arg Pro Asp Pro Ala Leu Ala		
705	710	715
Ala Leu Thr Asn Asp His Leu Val Ala Leu Ala Cys Leu Gly Gly Arg		
725	730	735
Pro Ala Leu Asp Ala Val Lys Lys Gly Leu Pro His Ala Pro Ala Leu		
740	745	750
Ile Lys Arg Thr Asn Arg Arg Ile Pro Glu Arg Thr Ser His Arg Val		
755	760	765
Ala Asp His Ala Gln Val Val Arg Val Leu Gly Phe Phe Gln Cys His		
770	775	780
Ser His Pro Ala Gln Ala Phe Asp Asp Ala Met Thr Gln Phe Gly Met		
785	790	795
Ser Arg His Gly Leu Leu Gln Leu Phe Arg Arg Val Gly Val Thr Glu		
805	810	815
Leu Glu Ala Arg Ser Gly Thr Leu Pro Pro Ala Ser Gln Arg Trp Asp		
820	825	830
Arg Ile Leu Gln Ala Ser Gly Met Lys Arg Ala Lys Pro Ser Pro Thr		
835	840	845
Ser Thr Gln Thr Pro Asp Gln Ala Ser Leu His Ala Phe Ala Asp Ser		
850	855	860
Leu Glu Arg Asp Leu Asp Ala Pro Ser Pro Met His Glu Gly Asp Gln		
865	870	875
Thr Arg Ala Ser Ala Ser Ala Ser Pro Lys Lys Lys Arg Lys Val Glu		
885	890	895
Ala Ser Met Thr Asp Ala Glu Tyr Val Arg Ile His Glu Lys Leu Asp		
900	905	910
Ile Tyr Thr Phe Lys Lys Gln Phe Phe Asn Asn Lys Lys Ser Val Ser		
915	920	925
His Arg Cys Tyr Val Leu Phe Glu Leu Lys Arg Arg Gly Glu Arg Arg		
930	935	940
Ala Cys Phe Trp Gly Tyr Ala Val Asn Lys Pro Gln Ser Gly Thr Glu		
945	950	955
Arg Gly Ile His Ala Glu Ile Phe Ser Ile Arg Lys Val Glu Glu Tyr		
965	970	975
Leu Arg Asp Asn Pro Gly Gln Phe Thr Ile Asn Trp Tyr Ser Ser Trp		
980	985	990

Ser Pro Cys Ala Asp Cys Ala Glu	Lys Ile Leu Glu Trp	Tyr Asn Gln
995	1000	1005
Glu Leu Arg Gly Asn Gly His	Thr Leu Lys Ile Trp	Ala Cys Lys
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Leu Tyr Tyr Glu Lys Asn Ala	Arg Asn Gln Ile Gly	Leu Trp Asn
1025	1030	1035
Leu Arg Asp Asn Gly Val Gly	Leu Asn Val Met Val	Ser Glu His
1040	1045	1050
Tyr Gln Cys Cys Arg Lys Ile	Phe Ile Gln Ser Ser	His Asn Gln
1055	1060	1065
Leu Asn Glu Asn Arg Trp Leu	Glu Lys Thr Leu Lys	Arg Ala Glu
1070	1075	1080
Lys Trp Arg Ser Glu Leu Ser	Ile Met Ile Gln Val	Lys Ile Leu
1085	1090	1095
His Thr Thr Lys Ser Pro Ala	Val Gly Ser Gly Gly	Ser Gly Gly
1100	1105	1110
Ser Gly Gly Ser Thr Asn Leu	Ser Asp Ile Ile Glu	Lys Glu Thr
1115	1120	1125
Gly Lys Gln Leu Val Ile Gln	Glu Ser Ile Leu Met	Leu Pro Glu
1130	1135	1140
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Val His Thr Ala Tyr Asp Glu	Ser Thr Asp Glu Asn	Val Met Leu
1160	1165	1170
Leu Thr Ser Asp Ala Pro Glu	Tyr Lys Pro Trp Ala	Leu Val Ile
1175	1180	1185
Gln Asp Ser Asn Gly Glu Asn	Lys Ile Lys Met Leu	Ser Gly Gly
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Ser Gly Gly Ser Gly Gly Ser	Thr Asn Leu Ser Asp	Ile Ile Glu
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Lys Glu Thr Gly Lys Gln Leu	Val Ile Gln Glu Ser	Ile Leu Met
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Leu Pro Glu Glu Val Glu Glu	Val Ile Gly Asn Lys	Pro Glu Ser
1235	1240	1245
Asp Ile Leu Val His Thr Ala	Tyr Asp Glu Ser Thr	Asp Glu Asn
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Val Met Leu Leu Thr Ser Asp	Ala Pro Glu Tyr Lys	Pro Trp Ala
1265	1270	1275
Leu Val Ile Gln Asp Ser Asn	Gly Glu Asn Lys Ile	Lys Met Leu

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

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Lys Gln Ala Leu Glu Thr Val	Gln Arg Leu Leu Pro Val	Leu Cys Gln
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Ala His Gly Leu Thr Pro Ala	Gln Val Val Ala Ile Ala	Ser Asn Ile
290	295	300
Gly Gly Lys Gln Ala Leu Glu Thr	Val Gln Arg Leu Leu Pro Val	Leu
305	310	315
Cys Gln Asp His Gly Leu Thr Pro	Asp Gln Val Val Ala Ile Ala	Ser
325	330	335
His Asp Gly Gly Lys Gln Ala Leu	Glu Thr Val Gln Arg Leu Leu Pro	
340	345	350
Val Leu Cys Gln Asp His Gly Leu	Thr Pro Glu Gln Val Val Ala Ile	
355	360	365
Ala Ser Asn Ile Gly Gly Lys Gln	Ala Leu Glu Thr Val Gln Arg Leu	
370	375	380
Leu Pro Val Leu Cys Gln Ala His	Gly Leu Thr Pro Asp Gln Val Val	
385	390	395
Ala Ile Ala Ser His Asp Gly Gly	Lys Gln Ala Leu Glu Thr Val Gln	
405	410	415
Arg Leu Leu Pro Val Leu Cys Gln	Ala His Gly Leu Thr Pro Ala Gln	
420	425	430
Val Val Ala Ile Ala Ser Asn Gly	Gly Gly Lys Gln Ala Leu Glu Thr	
435	440	445
Val Gln Arg Leu Leu Pro Val Leu	Cys Gln Asp His Gly Leu Thr Pro	
450	455	460
Asp Gln Val Val Ala Ile Ala Ser	Asn Asn Gly Gly Lys Gln Ala Leu	
465	470	475
Glu Thr Val Gln Arg Leu Leu Pro	Val Leu Cys Gln Asp His Gly Leu	
485	490	495
Thr Pro Glu Gln Val Val Ala Ile	Ala Ser Asn Ile Gly Gly Lys Gln	
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Ala Leu Glu Thr Val Gln Arg Leu	Leu Leu Pro Val Leu Cys Gln Ala His	
515	520	525
Gly Leu Thr Pro Asp Gln Val Val	Ala Ile Ala Ser Asn Asn Gly Gly	
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Lys Gln Ala Leu Glu Thr Val Gln	Arg Leu Leu Pro Val Leu Cys Gln	
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Ala His Gly Leu Thr Pro Ala Gln	Val Val Ala Ile Ala Ser Asn Gly	
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Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu			
580	585	590	
Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser			
595	600	605	
Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro			
610	615	620	
Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile			
625	630	635	640
Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu			
645	650	655	
Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val			
660	665	670	
Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln			
675	680	685	
Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln			
690	695	700	
Val Val Ala Ile Ala Ser His Asp Gly Gly Arg Pro Ala Leu Glu Ser			
705	710	715	720
Ile Val Ala Gln Leu Ser Arg Pro Asp Pro Ala Leu Ala Ala Leu Thr			
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Asn Asp His Leu Val Ala Leu Ala Cys Leu Gly Gly Arg Pro Ala Met			
740	745	750	
Asp Ala Val Lys Lys Gly Leu Pro His Ala Pro Glu Leu Ile Arg Ser			
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Ser Arg Ala Asp Pro Lys Lys Lys Arg Lys Val Gly Gly Gly Gly Thr			
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Gly Asn Asp Glu Glu Asp Leu Pro Phe Lys Lys Gly Asp Ile Leu Arg			
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Ile Arg Asp Lys Pro Glu Glu Gln Trp Trp Asn Ala Glu Asp Ser Glu			
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Gly Lys Arg Gly Met Ile Leu Val Pro Tyr Val Glu Lys Tyr Ser Gly			
835	840	845	
Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His Asp Ile Asp Tyr			
850	855	860	
Lys Asp Asp Asp Asp Lys Ser Gly Met Thr Asp Ala Glu Tyr Val Arg			
865	870	875	880
Ile His Glu Lys Leu Asp Ile Tyr Thr Phe Lys Lys Gln Phe Phe Asn			

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Asn Lys Lys Ser Val Ser His Arg Cys Tyr Val Leu Phe Glu Leu Lys			
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Arg Arg Gly Glu Arg Arg Ala Cys Phe Trp Gly Tyr Ala Val Asn Lys			
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Pro Gln Ser Gly Thr Glu Arg Gly Ile His Ala Glu Ile Phe Ser Ile			
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Arg Lys Val Glu Glu Tyr Leu Arg Asp Asn Pro Gly Gln Phe Thr Ile			
945	950	955	960
Asn Trp Tyr Ser Ser Trp Ser Pro Cys Ala Asp Cys Ala Glu Lys Ile			
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Ile Trp Ala Cys Lys Leu Tyr Tyr Glu Lys Asn Ala Arg Asn Gln Ile			
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Gly Leu Trp Asn Leu Arg Asp Asn Gly Val Gly Leu Asn Val Met			
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Val Ser Glu His Tyr Gln Cys Cys Arg Lys Ile Phe Ile Gln Ser			
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Ser His Asn Gln Leu Asn Glu Asn Arg Trp Leu Glu Lys Thr Leu			
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Lys Arg Ala Glu Lys Trp Arg Ser Glu Leu Ser Ile Met Ile Gln			
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Val Lys Ile Leu His Thr Thr Lys Ser Pro Ala Val Gly Ser Gly			
1070	1075	1080	
Gly Ser Gly Gly Ser Gly Gly Ser Thr Asn Leu Ser Asp Ile Ile			
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Glu Lys Glu Thr Gly Lys Gln Leu Val Ile Gln Glu Ser Ile Leu			
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Met Leu Pro Glu Glu Val Glu Glu Val Ile Gly Asn Lys Pro Glu			
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Asn Val Met Leu Leu Thr Ser Asp Ala Pro Glu Tyr Lys Pro Trp			
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Ala Leu Val Ile Gln Asp Ser Asn Gly Glu Asn Lys Ile Lys Met			
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Leu Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Thr Asn Leu Ser			
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Asp Ile	Ile Glu Lys Glu Thr	Gly Lys Gln Leu Val	Ile Gln Glu
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Lys Pro	Glu Ser Asp Ile Leu	Val His Thr Ala Tyr	Asp Glu Ser
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Thr Asp	Glu Asn Val Met Leu	Leu Thr Ser Asp Ala	Pro Glu Tyr
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Lys Pro	Trp Ala Leu Val Ile	Gln Asp Ser Asn Gly	Glu Asn Lys
1250	1255	1260	
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<211> 3864

<212> DNA

<213> 人工序列(Artificial Sequence)

<220>

<223> BE4-32-47(AS14-3)

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gaagtgatcg	gcaacaagcc	tgagtccgat	atcctggtgc	acaccgccta	cgacgagtcc	3420


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acagatgaga atgtgatgct gctgacctct gacgccccag agtataagcc ctgggccctg      3480
gtcatccagg atagcaacgg cgagaataag atcaagatgc tgtccggcgg aagcggagga      3540
tccggaggct ctaccaatct gtccgatatt attgaaaaag agacaggcaa gcaactggtc      3600
atccaggagt ctatcctgat gctgccagaa gaagtcgaag aagtgatcgg aaacaagccc      3660
gaaagcgaca tcctgggtcca tactgcctac gacgagagta cgcacgaaaa tgtgatgtta      3720
ctgacctccg acgccccctga gtataagcca tgggctctgg tcatccagga ctccaatgga      3780
gaaaataaga tcaagatgtt aagcggcggc tccaagagaa cagccgacgg ctccgagttc      3840
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<210> 166

<211> 1288

<212> PRT

<213> 人工序列(Artificial Sequence)

<220>

<223> BE4-32-47(AS14-3)

<400> 166

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1 5 10 15

Arg Lys Val Ser Ser Glu Thr Gly Pro Val Ala Val Asp Pro Thr Leu

20 25 30

Arg Arg Arg Ile Glu Pro His Glu Phe Glu Val Phe Phe Asp Pro Arg

35 40 45

Glu Leu Arg Lys Glu Thr Cys Leu Leu Tyr Glu Ile Lys Trp Gly Thr

50 55 60

Ser His Lys Ile Trp Arg His Ser Ser Lys Asn Thr Thr Lys His Val

65 70 75 80

Glu Val Asn Phe Ile Glu Lys Phe Thr Ser Glu Arg His Phe Cys Pro

85 90 95

Ser Thr Ser Cys Ser Ile Thr Trp Phe Leu Ser Trp Ser Pro Cys Gly

100 105 110

Glu Cys Ser Lys Ala Ile Thr Glu Phe Leu Ser Gln His Pro Asn Val

115 120 125

Thr Leu Val Ile Tyr Val Ala Arg Leu Tyr His His Met Asp Gln Gln

130 135 140

Asn Arg Gln Gly Leu Arg Asp Leu Val Asn Ser Gly Val Thr Ile Gln

145 150 155 160

Ile Met Thr Ala Pro Glu Tyr Asp Tyr Cys Trp Arg Asn Phe Val Asn

165 170 175

Tyr Pro Pro Gly Lys Glu Ala His Trp Pro Arg Tyr Pro Pro Leu Trp

180 185 190

Met Lys Leu Tyr Ala Leu Glu Leu His Ala Gly Ile Leu Gly Leu Pro		
195	200	205
Pro Cys Leu Asn Ile Leu Arg Arg Lys Gln Pro Gln Leu Thr Phe Phe		
210	215	220
Thr Ile Ala Leu Gln Ser Cys His Tyr Gln Arg Leu Pro Pro His Ile		
225	230	235
Leu Trp Ala Thr Gly Leu Lys Ser Gly Gly Ser Ser Gly Gly Ser Ser		
245	250	255
Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Ser		
260	265	270
Gly Gly Ser Ser Gly Gly Ser Met Ala Ser Ser Pro Pro Lys Lys Lys		
275	280	285
Arg Lys Val Ala Ala Ala Asp Tyr Lys Asp Asp Asp Asp Lys Ser Trp		
290	295	300
Lys Asp Ala Ser Gly Trp Ser Arg Met His Ala Ala Pro Arg Arg Arg		
305	310	315
Ala Ala Gln Pro Ser Asp Ala Ser Pro Ala Ala Gln Val Asp Leu Arg		
325	330	335
Thr Leu Gly Tyr Ser Gln Gln Gln Gln Glu Lys Ile Lys Pro Lys Val		
340	345	350
Arg Ser Thr Val Ala Gln His His Glu Ala Leu Val Gly His Gly Phe		
355	360	365
Thr His Ala His Ile Val Ala Leu Ser Gln His Pro Ala Ala Leu Gly		
370	375	380
Thr Val Ala Val Thr Tyr Gln His Ile Ile Thr Ala Leu Pro Glu Ala		
385	390	395
Thr His Glu Asp Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg		
405	410	415
Ala Leu Glu Ala Leu Leu Thr Asp Ala Gly Glu Leu Arg Gly Pro Pro		
420	425	430
Leu Gln Leu Asp Thr Gly Gln Leu Val Lys Ile Ala Lys Arg Gly Gly		
435	440	445
Val Thr Ala Met Glu Ala Val His Ala Ser Arg Asn Ala Leu Thr Gly		
450	455	460
Ala Pro Leu Asn Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser His		
465	470	475
Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val		
485	490	495
Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala		

500	505	510
Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu		
515	520	525
Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala		
530	535	540
Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg		
545	550	555
Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val		
565	570	575
Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val		
580	585	590
Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp		
595	600	605
Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu		
610	615	620
Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr		
625	630	635
Pro Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala		
645	650	655
Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly		
660	665	670
Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys		
675	680	685
Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala		
690	695	700
His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser Asn Asn Gly		
705	710	715
Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys		
725	730	735
Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn		
740	745	750
Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val		
755	760	765
Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala		
770	775	780
Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu		
785	790	795
Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala		
805	810	815

Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg		
820	825	830
Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val		
835	840	845
Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val		
850	855	860
Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp		
865	870	875
880		
Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu		
885	890	895
Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr		
900	905	910
Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala		
915	920	925
Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly		
930	935	940
Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys		
945	950	955
960		
Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala		
965	970	975
His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser Asn Ile Gly		
980	985	990
Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys		
995	1000	1005
Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser		
1010	1015	1020
Asn Asn Gly Gly Arg Pro Ala Leu Glu Ser Ile Val Ala Gln Leu		
1025	1030	1035
Ser Arg Pro Asp Pro Ala Leu Ala Ala Leu Thr Asn Asp His Leu		
1040	1045	1050
Val Ala Leu Ala Cys Leu Gly Gly Arg Pro Ala Met Asp Ala Val		
1055	1060	1065
Lys Lys Gly Leu Pro His Ala Pro Glu Leu Ile Arg Ser Ser Gly		
1070	1075	1080
Gly Ser Gly Gly Ser Gly Gly Ser Thr Asn Leu Ser Asp Ile Ile		
1085	1090	1095
Glu Lys Glu Thr Gly Lys Gln Leu Val Ile Gln Glu Ser Ile Leu		
1100	1105	1110
Met Leu Pro Glu Glu Val Glu Glu Val Ile Gly Asn Lys Pro Glu		

1115	1120	1125
Ser Asp Ile Leu Val His Thr Ala Tyr Asp Glu Ser Thr Asp Glu		
1130	1135	1140
Asn Val Met Leu Leu Thr Ser Asp Ala Pro Glu Tyr Lys Pro Trp		
1145	1150	1155
Ala Leu Val Ile Gln Asp Ser Asn Gly Glu Asn Lys Ile Lys Met		
1160	1165	1170
Leu Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Thr Asn Leu Ser		
1175	1180	1185
Asp Ile Ile Glu Lys Glu Thr Gly Lys Gln Leu Val Ile Gln Glu		
1190	1195	1200
Ser Ile Leu Met Leu Pro Glu Glu Val Glu Glu Val Ile Gly Asn		
1205	1210	1215
Lys Pro Glu Ser Asp Ile Leu Val His Thr Ala Tyr Asp Glu Ser		
1220	1225	1230
Thr Asp Glu Asn Val Met Leu Leu Thr Ser Asp Ala Pro Glu Tyr		
1235	1240	1245
Lys Pro Trp Ala Leu Val Ile Gln Asp Ser Asn Gly Glu Asn Lys		
1250	1255	1260
Ile Lys Met Leu Ser Gly Gly Ser Lys Arg Thr Ala Asp Gly Ser		
1265	1270	1275
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1280	1285	

<210> 167

<211> 4182

<212> DNA

<213> 人工序列(Artificial Sequence)

<220>

<223> BE4-135-63(AS14-3)

<400> 167

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tttgaggtgt tctttgatcc aagagagctg aggaaggaga catgcctgct gtacgagatc	180
aagtggggca catctcacia gatctggcgc cactctagca agaacaccac aaagcacgtg	240
gaagtgaatt tcatcgagaa gtttaccagc gagcggcact tctgccctag cacctcctgt	300
tctatcacat ggtttctgag ctggtcccca tgcggcgagt gtagcaaggc catcaccgag	360
ttcctgtccc agcacccaaa cgtgaccctg gtcacttacg tggccaggct gtatcaccac	420
atggaccagc agaacaggca gggcctgcgg gatctggtga attccggcgt gaccatccag	480
atcatgacag cccccgagta cgattactgt tggagaaact tcgtgaacta cccacctggc	540

aaggaggcac	actggcctag	gtaccacccc	ctgtggatga	agctgtatgc	actggagctg	600
cacgcaggaa	tcctgggcct	gcctccatgc	ctgaatatcc	tgcgccggaa	gcagccccag	660
ctgaccttct	ttacaatcgc	cctgcagagc	tgtcactacc	agcggctgcc	acctcacatc	720
ctgtgggcaa	ccggcctgaa	gtctggagga	tcctctggag	gaagctccgg	aagcgagaca	780
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gtggtgccaa	agatctacat	gtccgccggc	tctatccctc	tgaccacaca	catcacaaac	960
agcatccagc	caaccctgtg	gacaatcgga	tccatcaatg	gagtggcacc	actggccaag	1020
tctatcaagc	tgggcatccc	tgtgaccggc	agcgcctaca	cagaccagac	cacagccatg	1080
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 gacgaaaatg tgatgttact gacctccgac gccctgagt ataagccatg ggctctggtc 4080
 atccaggact ccaatggaga aaataagatc aagatgtaa gcggcggtc caagagaaca 4140
 gccgacggct ccgagttcga gccaagaag aagcggaaag tg 4182

<210> 168

<211> 1394

<212> PRT

<213> 人工序列(Artificial Sequence)

<220>

<223> BE4-135-63(AS14-3)

<400> 168

Met Lys Arg Thr Ala Asp Gly Ser Glu Phe Glu Ser Pro Lys Lys Lys

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Arg Lys Val Ser Ser Glu Thr Gly Pro Val Ala Val Asp Pro Thr Leu

20 25 30

Arg Arg Arg Ile Glu Pro His Glu Phe Glu Val Phe Phe Asp Pro Arg

35 40 45

Glu Leu Arg Lys Glu Thr Cys Leu Leu Tyr Glu Ile Lys Trp Gly Thr

50 55 60

Ser His Lys Ile Trp Arg His Ser Ser Lys Asn Thr Thr Lys His Val

65 70 75 80

Glu	Val	Asn	Phe	Ile	Glu	Lys	Phe	Thr	Ser	Glu	Arg	His	Phe	Cys	Pro		
					85				90					95			
Ser	Thr	Ser	Cys	Ser	Ile	Thr	Trp	Phe	Leu	Ser	Trp	Ser	Pro	Cys	Gly		
			100					105					110				
Glu	Cys	Ser	Lys	Ala	Ile	Thr	Glu	Phe	Leu	Ser	Gln	His	Pro	Asn	Val		
			115				120					125					
Thr	Leu	Val	Ile	Tyr	Val	Ala	Arg	Leu	Tyr	His	His	Met	Asp	Gln	Gln		
						130		135				140					
Asn	Arg	Gln	Gly	Leu	Arg	Asp	Leu	Val	Asn	Ser	Gly	Val	Thr	Ile	Gln		
145					150				155						160		
Ile	Met	Thr	Ala	Pro	Glu	Tyr	Asp	Tyr	Cys	Trp	Arg	Asn	Phe	Val	Asn		
					165				170					175			
Tyr	Pro	Pro	Gly	Lys	Glu	Ala	His	Trp	Pro	Arg	Tyr	Pro	Pro	Leu	Trp		
			180					185						190			
Met	Lys	Leu	Tyr	Ala	Leu	Glu	Leu	His	Ala	Gly	Ile	Leu	Gly	Leu	Pro		
			195				200					205					
Pro	Cys	Leu	Asn	Ile	Leu	Arg	Arg	Lys	Gln	Pro	Gln	Leu	Thr	Phe	Phe		
			210				215					220					
Thr	Ile	Ala	Leu	Gln	Ser	Cys	His	Tyr	Gln	Arg	Leu	Pro	Pro	His	Ile		
225					230				235						240		
Leu	Trp	Ala	Thr	Gly	Leu	Lys	Ser	Gly	Gly	Ser	Ser	Gly	Gly	Ser	Ser		
				245				250						255			
Gly	Ser	Glu	Thr	Pro	Gly	Thr	Ser	Glu	Ser	Ala	Thr	Pro	Glu	Ser	Ser		
			260					265					270				
Gly	Gly	Ser	Ser	Gly	Gly	Ser	Tyr	Thr	Arg	Val	Gly	Ser	Gly	Ser	Gly		
			275				280					285					
Ser	Gly	Ser	Ile	Thr	Arg	Thr	Thr	Asn	Pro	Arg	Asn	Val	Val	Pro	Lys		
			290				295				300						
Ile	Tyr	Met	Ser	Ala	Gly	Ser	Ile	Pro	Leu	Thr	Thr	His	Ile	Thr	Asn		
305				310				315						320			
Ser	Ile	Gln	Pro	Thr	Leu	Trp	Thr	Ile	Gly	Ser	Ile	Asn	Gly	Val	Ala		
				325				330					335				
Pro	Leu	Ala	Lys	Ser	Ile	Lys	Leu	Gly	Ile	Pro	Val	Thr	Gly	Ser	Ala		
			340				345						350				
Tyr	Thr	Asp	Gln	Thr	Thr	Ala	Met	Val	Arg	Lys	Lys	Val	Ser	Val	Phe		
			355				360					365					
Met	Gly	Ser	Gly	Ser	Gly	Ser	Gly	Ser	Ser	Met	Thr	Ala	Val	Met	Asp		
			370				375				380						
Tyr	Lys	Asp	His	Asp	Gly	Asp	Tyr	Lys	Asp	His	Asp	Ile	Asp	Tyr	Lys		

385	390	395	400
Asp Asp Asp Asp Lys Met Ala Pro Lys Lys Lys Arg Lys Val Gly Ile			
	405	410	415
His Gly Val Pro Ala Ala Val Asp Leu Arg Thr Leu Gly Tyr Ser Gln			
	420	425	430
Gln Gln Gln Glu Lys Ile Lys Pro Lys Val Arg Ser Thr Val Ala Gln			
	435	440	445
His His Glu Ala Leu Val Gly His Gly Phe Thr His Ala His Ile Val			
	450	455	460
Ala Leu Ser Gln His Pro Ala Ala Leu Gly Thr Val Ala Val Lys Tyr			
465	470	475	480
Gln Asp Met Ile Ala Ala Leu Pro Glu Ala Thr His Glu Ala Ile Val			
	485	490	495
Gly Val Gly Lys Gln Trp Ser Gly Ala Arg Ala Leu Glu Ala Leu Leu			
	500	505	510
Thr Val Ala Gly Glu Leu Arg Gly Pro Pro Leu Gln Leu Asp Thr Gly			
	515	520	525
Gln Leu Leu Lys Ile Ala Lys Arg Gly Gly Val Thr Ala Val Glu Ala			
	530	535	540
Val His Ala Trp Arg Asn Ala Leu Thr Gly Ala Pro Leu Asn Leu Thr			
545	550	555	560
Pro Asp Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala			
	565	570	575
Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly			
	580	585	590
Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys			
	595	600	605
Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala			
	610	615	620
His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile Gly			
625	630	635	640
Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys			
	645	650	655
Gln Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser Asn			
	660	665	670
Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val			
	675	680	685
Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala			
690	695	700	

Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu			
705	710	715	720
Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala			
	725	730	735
Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg			
	740	745	750
Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val			
	755	760	765
Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val			
	770	775	780
Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala			
	785	790	795
Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu			
	805	810	815
Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr			
	820	825	830
Pro Asp Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala			
	835	840	845
Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly			
	850	855	860
Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys			
	865	870	875
Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala			
	885	890	895
His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Asn Gly			
	900	905	910
Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys			
	915	920	925
Gln Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser Asn			
	930	935	940
Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val			
	945	950	955
Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala			
	965	970	975
Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu			
	980	985	990
Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala			
	995	1000	1005
Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln			

1010	1015	1020
Arg Leu Leu Pro Val Leu Cys	Gln Ala His Gly	Leu Thr Pro Asp
1025	1030	1035
Gln Val Val Ala Ile Ala Ser	His Asp Gly Gly	Lys Gln Ala Leu
1040	1045	1050
Glu Thr Val Gln Arg Leu Leu	Pro Val Leu Cys	Gln Ala His Gly
1055	1060	1065
Leu Thr Pro Ala Gln Val Val	Ala Ile Ala Ser	Asn Ile Gly Gly
1070	1075	1080
Lys Gln Ala Leu Glu Thr Val	Gln Arg Leu Leu	Pro Val Leu Cys
1085	1090	1095
Gln Asp His Gly Leu Thr Pro	Glu Gln Val Val	Ala Ile Ala Ser
1100	1105	1110
Asn Asn Gly Gly Arg Pro Ala	Leu Glu Ser Ile	Val Ala Gln Leu
1115	1120	1125
Ser Arg Pro Asp Pro Ala Leu	Ala Ala Leu Thr	Asn Asp His Leu
1130	1135	1140
Val Ala Leu Ala Cys Leu Gly	Gly Arg Pro Ala	Leu Asp Ala Val
1145	1150	1155
Lys Lys Gly Leu Pro His Ala	Pro Ala Leu Ile	Lys Arg Thr Asn
1160	1165	1170
Arg Arg Ile Pro Glu Arg Thr	Ser His Arg Val	Ala Gly Ser Ser
1175	1180	1185
Gly Gly Ser Gly Gly Ser Gly	Gly Ser Thr Asn	Leu Ser Asp Ile
1190	1195	1200
Ile Glu Lys Glu Thr Gly Lys	Gln Leu Val Ile	Gln Glu Ser Ile
1205	1210	1215
Leu Met Leu Pro Glu Glu Val	Glu Glu Val Ile	Gly Asn Lys Pro
1220	1225	1230
Glu Ser Asp Ile Leu Val His	Thr Ala Tyr Asp	Glu Ser Thr Asp
1235	1240	1245
Glu Asn Val Met Leu Leu Thr	Ser Asp Ala Pro	Glu Tyr Lys Pro
1250	1255	1260
Trp Ala Leu Val Ile Gln Asp	Ser Asn Gly Glu	Asn Lys Ile Lys
1265	1270	1275
Met Leu Ser Gly Gly Ser Gly	Gly Ser Gly Gly	Ser Thr Asn Leu
1280	1285	1290
Ser Asp Ile Ile Glu Lys Glu	Thr Gly Lys Gln	Leu Val Ile Gln
1295	1300	1305

Glu Ser Ile Leu Met Leu Pro	Glu Glu Val Glu Glu Val Ile Gly
1310	1315 1320
Asn Lys Pro Glu Ser Asp Ile	Leu Val His Thr Ala Tyr Asp Glu
1325	1330 1335
Ser Thr Asp Glu Asn Val Met	Leu Leu Thr Ser Asp Ala Pro Glu
1340	1345 1350
Tyr Lys Pro Trp Ala Leu Val	Ile Gln Asp Ser Asn Gly Glu Asn
1355	1360 1365
Lys Ile Lys Met Leu Ser Gly	Gly Ser Lys Arg Thr Ala Asp Gly
1370	1375 1380
Ser Glu Phe Glu Pro Lys Lys	Lys Arg Lys Val
1385	1390

<210> 169

<211> 3864

<212> DNA

<213> 人工序列(Artificial Sequence)

<220>

<223> BE4-32-47(AS5)

<400> 169

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aagtggggca catctcacia gatctggcgc cactctagca agaacaccac aaagcacgtg	240
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ctgaccttct ttacaatcgc cctgcagagc tgtcactacc agcggctgcc acctcacatc	720
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gaggcactgg tgggccatgg gtttacacac gcgcacatcg ttgcgctcag ccaacacccg	1140
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<210> 170

<211> 1288

<212> PRT

<213> 人工序列(Artificial Sequence)

<220>

<223> BE4-32-47(AS5)

<400> 170

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          20           25           30
Arg Arg Arg Ile Glu Pro His Glu Phe Glu Val Phe Phe Asp Pro Arg
          35           40           45
Glu Leu Arg Lys Glu Thr Cys Leu Leu Tyr Glu Ile Lys Trp Gly Thr
          50           55           60
Ser His Lys Ile Trp Arg His Ser Ser Lys Asn Thr Thr Lys His Val
65           70           75           80
Glu Val Asn Phe Ile Glu Lys Phe Thr Ser Glu Arg His Phe Cys Pro
          85           90           95
Ser Thr Ser Cys Ser Ile Thr Trp Phe Leu Ser Trp Ser Pro Cys Gly
          100          105          110
Glu Cys Ser Lys Ala Ile Thr Glu Phe Leu Ser Gln His Pro Asn Val
          115          120          125
Thr Leu Val Ile Tyr Val Ala Arg Leu Tyr His His Met Asp Gln Gln
          130          135          140
Asn Arg Gln Gly Leu Arg Asp Leu Val Asn Ser Gly Val Thr Ile Gln
145          150          155          160
Ile Met Thr Ala Pro Glu Tyr Asp Tyr Cys Trp Arg Asn Phe Val Asn
          165          170          175
Tyr Pro Pro Gly Lys Glu Ala His Trp Pro Arg Tyr Pro Pro Leu Trp
          180          185          190
Met Lys Leu Tyr Ala Leu Glu Leu His Ala Gly Ile Leu Gly Leu Pro
          195          200          205

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Pro	Cys	Leu	Asn	Ile	Leu	Arg	Arg	Lys	Gln	Pro	Gln	Leu	Thr	Phe	Phe
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Thr	Ile	Ala	Leu	Gln	Ser	Cys	His	Tyr	Gln	Arg	Leu	Pro	Pro	His	Ile
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Leu	Trp	Ala	Thr	Gly	Leu	Lys	Ser	Gly	Gly	Ser	Ser	Gly	Gly	Ser	Ser
			245					250						255	
Gly	Ser	Glu	Thr	Pro	Gly	Thr	Ser	Glu	Ser	Ala	Thr	Pro	Glu	Ser	Ser
			260					265					270		
Gly	Gly	Ser	Ser	Gly	Gly	Ser	Met	Ala	Ser	Ser	Pro	Pro	Lys	Lys	Lys
		275					280					285			
Arg	Lys	Val	Ala	Ala	Ala	Asp	Tyr	Lys	Asp	Asp	Asp	Asp	Lys	Ser	Trp
290						295					300				
Lys	Asp	Ala	Ser	Gly	Trp	Ser	Arg	Met	His	Ala	Ala	Pro	Arg	Arg	Arg
305				310						315					320
Ala	Ala	Gln	Pro	Ser	Asp	Ala	Ser	Pro	Ala	Ala	Gln	Val	Asp	Leu	Arg
			325						330				335		
Thr	Leu	Gly	Tyr	Ser	Gln	Gln	Gln	Gln	Glu	Lys	Ile	Lys	Pro	Lys	Val
		340						345					350		
Arg	Ser	Thr	Val	Ala	Gln	His	His	Glu	Ala	Leu	Val	Gly	His	Gly	Phe
	355					360						365			
Thr	His	Ala	His	Ile	Val	Ala	Leu	Ser	Gln	His	Pro	Ala	Ala	Leu	Gly
370						375					380				
Thr	Val	Ala	Val	Thr	Tyr	Gln	His	Ile	Ile	Thr	Ala	Leu	Pro	Glu	Ala
385				390						395					400
Thr	His	Glu	Asp	Ile	Val	Gly	Val	Gly	Lys	Gln	Trp	Ser	Gly	Ala	Arg
		405						410					415		
Ala	Leu	Glu	Ala	Leu	Leu	Thr	Asp	Ala	Gly	Glu	Leu	Arg	Gly	Pro	Pro
		420						425					430		
Leu	Gln	Leu	Asp	Thr	Gly	Gln	Leu	Val	Lys	Ile	Ala	Lys	Arg	Gly	Gly
	435						440					445			
Val	Thr	Ala	Met	Glu	Ala	Val	His	Ala	Ser	Arg	Asn	Ala	Leu	Thr	Gly
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Ala	Pro	Leu	Asn	Leu	Thr	Pro	Asp	Gln	Val	Val	Ala	Ile	Ala	Ser	Asn
465				470						475					480
Asn	Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu	Pro	Val
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Leu	Cys	Gln	Asp	His	Gly	Leu	Thr	Pro	Glu	Gln	Val	Val	Ala	Ile	Ala
		500						505					510		
Ser	His	Asp	Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu

515	520	525
Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala		
530	535	540
Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg		
545	550	555
Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val		
565	570	575
Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val		
580	585	590
Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp		
595	600	605
Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu		
610	615	620
Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr		
625	630	635
Pro Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala		
645	650	655
Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly		
660	665	670
Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys		
675	680	685
Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala		
690	695	700
His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser His Asp Gly		
705	710	715
Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys		
725	730	735
Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn		
740	745	750
Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val		
755	760	765
Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala		
770	775	780
Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu		
785	790	795
Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala		
805	810	815
Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg		
820	825	830

Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val		
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Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val		
850	855	860
Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp		
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Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu		
	885	890
Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr		
	900	910
Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala		
	915	925
Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly		
	930	940
Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys		
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Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala		
	965	975
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	980	990
Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys		
	995	1005
Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser		
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Asn Asn Gly Gly Arg Pro Ala Leu Glu Ser Ile Val Ala Gln Leu		
	1025	1035
Ser Arg Pro Asp Pro Ala Leu Ala Ala Leu Thr Asn Asp His Leu		
	1040	1050
Val Ala Leu Ala Cys Leu Gly Gly Arg Pro Ala Met Asp Ala Val		
	1055	1065
Lys Lys Gly Leu Pro His Ala Pro Glu Leu Ile Arg Ser Ser Gly		
	1070	1080
Gly Ser Gly Gly Ser Gly Gly Ser Thr Asn Leu Ser Asp Ile Ile		
	1085	1095
Glu Lys Glu Thr Gly Lys Gln Leu Val Ile Gln Glu Ser Ile Leu		
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Met Leu Pro Glu Glu Val Glu Glu Val Ile Gly Asn Lys Pro Glu		
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Ser Asp Ile Leu Val His Thr Ala Tyr Asp Glu Ser Thr Asp Glu		

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Asn Val Met Leu Leu Thr Ser Asp Ala Pro Glu Tyr Lys Pro Trp		
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Ala Leu Val Ile Gln Asp Ser Asn Gly Glu Asn Lys Ile Lys Met		
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Leu Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Thr Asn Leu Ser		
1175	1180	1185
Asp Ile Ile Glu Lys Glu Thr Gly Lys Gln Leu Val Ile Gln Glu		
1190	1195	1200
Ser Ile Leu Met Leu Pro Glu Glu Val Glu Glu Val Ile Gly Asn		
1205	1210	1215
Lys Pro Glu Ser Asp Ile Leu Val His Thr Ala Tyr Asp Glu Ser		
1220	1225	1230
Thr Asp Glu Asn Val Met Leu Leu Thr Ser Asp Ala Pro Glu Tyr		
1235	1240	1245
Lys Pro Trp Ala Leu Val Ile Gln Asp Ser Asn Gly Glu Asn Lys		
1250	1255	1260
Ile Lys Met Leu Ser Gly Gly Ser Lys Arg Thr Ala Asp Gly Ser		
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Glu Phe Glu Pro Lys Lys Lys Arg Lys Val		
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<210> 171

<211> 4182

<212> DNA

<213> 人工序列(Artificial Sequence)

<220>

<223> BE4-135-63(AS5)

<400> 171

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ctctgccagg	accacggcct	gaccccagac	caggttgttg	ccatcgccag	caacataggt	2940
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<210> 172

<211> 1394

<212> PRT

<213> 人工序列(Artificial Sequence)

<220>

<223> BE4-135-63(AS5)

<400> 172

Met Lys Arg Thr Ala Asp Gly Ser Glu Phe Glu Ser Pro Lys Lys Lys

1 5 10 15

Arg Lys Val Ser Ser Glu Thr Gly Pro Val Ala Val Asp Pro Thr Leu

20 25 30

Arg Arg Arg Ile Glu Pro His Glu Phe Glu Val Phe Phe Asp Pro Arg

35 40 45

Glu Leu Arg Lys Glu Thr Cys Leu Leu Tyr Glu Ile Lys Trp Gly Thr

50 55 60

Ser His Lys Ile Trp Arg His Ser Ser Lys Asn Thr Thr Lys His Val

65 70 75 80

Glu Val Asn Phe Ile Glu Lys Phe Thr Ser Glu Arg His Phe Cys Pro

85 90 95

Ser Thr Ser Cys Ser Ile Thr Trp Phe Leu Ser Trp Ser Pro Cys Gly		
100	105	110
Glu Cys Ser Lys Ala Ile Thr Glu Phe Leu Ser Gln His Pro Asn Val		
115	120	125
Thr Leu Val Ile Tyr Val Ala Arg Leu Tyr His His Met Asp Gln Gln		
130	135	140
Asn Arg Gln Gly Leu Arg Asp Leu Val Asn Ser Gly Val Thr Ile Gln		
145	150	155
Ile Met Thr Ala Pro Glu Tyr Asp Tyr Cys Trp Arg Asn Phe Val Asn		
165	170	175
Tyr Pro Pro Gly Lys Glu Ala His Trp Pro Arg Tyr Pro Pro Leu Trp		
180	185	190
Met Lys Leu Tyr Ala Leu Glu Leu His Ala Gly Ile Leu Gly Leu Pro		
195	200	205
Pro Cys Leu Asn Ile Leu Arg Arg Lys Gln Pro Gln Leu Thr Phe Phe		
210	215	220
Thr Ile Ala Leu Gln Ser Cys His Tyr Gln Arg Leu Pro Pro His Ile		
225	230	235
Leu Trp Ala Thr Gly Leu Lys Ser Gly Gly Ser Ser Gly Gly Ser Ser		
245	250	255
Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Ser		
260	265	270
Gly Gly Ser Ser Gly Gly Ser Tyr Thr Arg Val Gly Ser Gly Ser Gly		
275	280	285
Ser Gly Ser Ile Thr Arg Thr Thr Asn Pro Arg Asn Val Val Pro Lys		
290	295	300
Ile Tyr Met Ser Ala Gly Ser Ile Pro Leu Thr Thr His Ile Thr Asn		
305	310	315
Ser Ile Gln Pro Thr Leu Trp Thr Ile Gly Ser Ile Asn Gly Val Ala		
325	330	335
Pro Leu Ala Lys Ser Ile Lys Leu Gly Ile Pro Val Thr Gly Ser Ala		
340	345	350
Tyr Thr Asp Gln Thr Thr Ala Met Val Arg Lys Lys Val Ser Val Phe		
355	360	365
Met Gly Ser Gly Ser Gly Ser Gly Ser Ser Met Thr Ala Val Met Asp		
370	375	380
Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His Asp Ile Asp Tyr Lys		
385	390	395
Asp Asp Asp Asp Lys Met Ala Pro Lys Lys Lys Arg Lys Val Gly Ile		

	405	410	415
His Gly Val Pro Ala Ala Val Asp Leu Arg Thr Leu Gly Tyr Ser Gln			
	420	425	430
Gln Gln Gln Glu Lys Ile Lys Pro Lys Val Arg Ser Thr Val Ala Gln			
	435	440	445
His His Glu Ala Leu Val Gly His Gly Phe Thr His Ala His Ile Val			
	450	455	460
Ala Leu Ser Gln His Pro Ala Ala Leu Gly Thr Val Ala Val Lys Tyr			
465	470	475	480
Gln Asp Met Ile Ala Ala Leu Pro Glu Ala Thr His Glu Ala Ile Val			
	485	490	495
Gly Val Gly Lys Gln Trp Ser Gly Ala Arg Ala Leu Glu Ala Leu Leu			
	500	505	510
Thr Val Ala Gly Glu Leu Arg Gly Pro Pro Leu Gln Leu Asp Thr Gly			
	515	520	525
Gln Leu Leu Lys Ile Ala Lys Arg Gly Gly Val Thr Ala Val Glu Ala			
	530	535	540
Val His Ala Trp Arg Asn Ala Leu Thr Gly Ala Pro Leu Asn Leu Thr			
545	550	555	560
Pro Asp Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala			
	565	570	575
Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly			
	580	585	590
Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys			
	595	600	605
Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala			
	610	615	620
His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile Gly			
625	630	635	640
Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys			
	645	650	655
Gln Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser Asn			
	660	665	670
Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val			
	675	680	685
Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala			
	690	695	700
Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu			
705	710	715	720

Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala		
725	730	735
Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg		
740	745	750
Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val		
755	760	765
Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val		
770	775	780
Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala		
785	790	795
Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu		
805	810	815
Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr		
820	825	830
Pro Asp Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala		
835	840	845
Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly		
850	855	860
Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys		
865	870	875
Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala		
885	890	895
His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Gly Gly		
900	905	910
Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys		
915	920	925
Gln Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser Asn		
930	935	940
Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val		
945	950	955
Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala		
965	970	975
Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu		
980	985	990
Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala		
995	1000	1005
Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln		
1010	1015	1020
Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp		

1025	1030	1035
Gln Val Val Ala Ile Ala Ser	Asn Ile Gly Gly Lys	Gln Ala Leu
1040	1045	1050
Glu Thr Val Gln Arg Leu Leu	Pro Val Leu Cys Gln	Ala His Gly
1055	1060	1065
Leu Thr Pro Ala Gln Val Val	Ala Ile Ala Ser Asn	Asn Gly Gly
1070	1075	1080
Lys Gln Ala Leu Glu Thr Val	Gln Arg Leu Leu Pro	Val Leu Cys
1085	1090	1095
Gln Asp His Gly Leu Thr Pro	Glu Gln Val Val Ala	Ile Ala Ser
1100	1105	1110
Asn Asn Gly Gly Arg Pro Ala	Leu Glu Ser Ile Val	Ala Gln Leu
1115	1120	1125
Ser Arg Pro Asp Pro Ala Leu	Ala Ala Leu Thr Asn	Asp His Leu
1130	1135	1140
Val Ala Leu Ala Cys Leu Gly	Gly Arg Pro Ala Leu	Asp Ala Val
1145	1150	1155
Lys Lys Gly Leu Pro His Ala	Pro Ala Leu Ile Lys	Arg Thr Asn
1160	1165	1170
Arg Arg Ile Pro Glu Arg Thr	Ser His Arg Val Ala	Gly Ser Ser
1175	1180	1185
Gly Gly Ser Gly Gly Ser Gly	Gly Ser Thr Asn Leu	Ser Asp Ile
1190	1195	1200
Ile Glu Lys Glu Thr Gly Lys	Gln Leu Val Ile Gln	Glu Ser Ile
1205	1210	1215
Leu Met Leu Pro Glu Glu Val	Glu Glu Val Ile Gly	Asn Lys Pro
1220	1225	1230
Glu Ser Asp Ile Leu Val His	Thr Ala Tyr Asp Glu	Ser Thr Asp
1235	1240	1245
Glu Asn Val Met Leu Leu Thr	Ser Asp Ala Pro Glu	Tyr Lys Pro
1250	1255	1260
Trp Ala Leu Val Ile Gln Asp	Ser Asn Gly Glu Asn	Lys Ile Lys
1265	1270	1275
Met Leu Ser Gly Gly Ser Gly	Gly Ser Gly Gly Ser	Thr Asn Leu
1280	1285	1290
Ser Asp Ile Ile Glu Lys Glu	Thr Gly Lys Gln Leu	Val Ile Gln
1295	1300	1305
Glu Ser Ile Leu Met Leu Pro	Glu Glu Val Glu Glu	Val Ile Gly
1310	1315	1320

Asn Lys	Pro Glu	Ser Asp	Ile Leu	Val His	Thr Ala	Tyr Asp	Glu
1325			1330			1335	
Ser Thr	Asp Glu	Asn Val	Met Leu	Leu Thr	Ser Asp	Ala Pro	Glu
1340			1345			1350	
Tyr Lys	Pro Trp	Ala Leu	Val Ile	Gln Asp	Ser Asn	Gly Glu	Asn
1355			1360			1365	
Lys Ile	Lys Met	Leu Ser	Gly Gly	Ser Lys	Arg Thr	Ala Asp	Gly
1370			1375			1380	
Ser Glu	Phe Glu	Pro Lys	Lys Lys	Arg Lys	Val		
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<210> 173

<211> 3864

<212> DNA

<213> 人工序列(Artificial Sequence)

<220>

<223> BE4-32-47(AS6)

<400> 173

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aagtggggca	catctcacia	gatctggcgc	cactctagca	agaacaccac	aaagcacgtg	240
gaagtgaatt	tcatcgagaa	gtttaccagc	gagcggcact	tctgccctag	cacctcctgt	300
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ttcctgtccc	agcacccaaa	cgtgaccctg	gtcatctacg	tggccaggct	gtatcaccac	420
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atcatgacag	cccccgagta	cgattactgt	tggagaaact	tcgtgaacta	cccacctggc	540
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<210> 174

<211> 1288

<212> PRT

<213> 人工序列(Artificial Sequence)

<220>

<223> BE4-32-47(AS6)

<400> 174

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Arg Arg Arg Ile Glu Pro His Glu Phe Glu Val Phe Phe Asp Pro Arg
 35 40 45

Glu Leu Arg Lys Glu Thr Cys Leu Leu Tyr Glu Ile Lys Trp Gly Thr
 50 55 60

Ser His Lys Ile Trp Arg His Ser Ser Lys Asn Thr Thr Lys His Val
 65 70 75 80

Glu Val Asn Phe Ile Glu Lys Phe Thr Ser Glu Arg His Phe Cys Pro
 85 90 95

Ser Thr Ser Cys Ser Ile Thr Trp Phe Leu Ser Trp Ser Pro Cys Gly
 100 105 110

Glu Cys Ser Lys Ala Ile Thr Glu Phe Leu Ser Gln His Pro Asn Val
 115 120 125

Thr Leu Val Ile Tyr Val Ala Arg Leu Tyr His His Met Asp Gln Gln
 130 135 140

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

Ile Met Thr Ala Pro Glu Tyr Asp Tyr Cys Trp Arg Asn Phe Val Asn
 165 170 175

Tyr Pro Pro Gly Lys Glu Ala His Trp Pro Arg Tyr Pro Pro Leu Trp
 180 185 190

Met Lys Leu Tyr Ala Leu Glu Leu His Ala Gly Ile Leu Gly Leu Pro
 195 200 205

Pro Cys Leu Asn Ile Leu Arg Arg Lys Gln Pro Gln Leu Thr Phe Phe
 210 215 220

Thr	Ile	Ala	Leu	Gln	Ser	Cys	His	Tyr	Gln	Arg	Leu	Pro	Pro	His	Ile
225						230				235					240
Leu	Trp	Ala	Thr	Gly	Leu	Lys	Ser	Gly	Gly	Ser	Ser	Gly	Gly	Ser	Ser
				245					250					255	
Gly	Ser	Glu	Thr	Pro	Gly	Thr	Ser	Glu	Ser	Ala	Thr	Pro	Glu	Ser	Ser
				260					265					270	
Gly	Gly	Ser	Ser	Gly	Gly	Ser	Met	Ala	Ser	Ser	Pro	Pro	Lys	Lys	Lys
				275				280						285	
Arg	Lys	Val	Ala	Ala	Ala	Asp	Tyr	Lys	Asp	Asp	Asp	Asp	Lys	Ser	Trp
						295								300	
Lys	Asp	Ala	Ser	Gly	Trp	Ser	Arg	Met	His	Ala	Ala	Pro	Arg	Arg	Arg
305					310					315					320
Ala	Ala	Gln	Pro	Ser	Asp	Ala	Ser	Pro	Ala	Ala	Gln	Val	Asp	Leu	Arg
					325					330				335	
Thr	Leu	Gly	Tyr	Ser	Gln	Gln	Gln	Gln	Glu	Lys	Ile	Lys	Pro	Lys	Val
				340					345					350	
Arg	Ser	Thr	Val	Ala	Gln	His	His	Glu	Ala	Leu	Val	Gly	His	Gly	Phe
				355				360						365	
Thr	His	Ala	His	Ile	Val	Ala	Leu	Ser	Gln	His	Pro	Ala	Ala	Leu	Gly
				370				375						380	
Thr	Val	Ala	Val	Thr	Tyr	Gln	His	Ile	Ile	Thr	Ala	Leu	Pro	Glu	Ala
385					390					395					400
Thr	His	Glu	Asp	Ile	Val	Gly	Val	Gly	Lys	Gln	Trp	Ser	Gly	Ala	Arg
				405					410					415	
Ala	Leu	Glu	Ala	Leu	Leu	Thr	Asp	Ala	Gly	Glu	Leu	Arg	Gly	Pro	Pro
				420					425					430	
Leu	Gln	Leu	Asp	Thr	Gly	Gln	Leu	Val	Lys	Ile	Ala	Lys	Arg	Gly	Gly
				435					440					445	
Val	Thr	Ala	Met	Glu	Ala	Val	His	Ala	Ser	Arg	Asn	Ala	Leu	Thr	Gly
				450				455						460	
Ala	Pro	Leu	Asn	Leu	Thr	Pro	Asp	Gln	Val	Val	Ala	Ile	Ala	Ser	His
465					470					475					480
Asp	Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu	Pro	Val
				485					490					495	
Leu	Cys	Gln	Asp	His	Gly	Leu	Thr	Pro	Glu	Gln	Val	Val	Ala	Ile	Ala
				500					505					510	
Ser	Asn	Gly	Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu
				515					520					525	
Pro	Val	Leu	Cys	Gln	Ala	His	Gly	Leu	Thr	Pro	Asp	Gln	Val	Val	Ala

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Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg		
545	550	555
Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val		
565	570	575
Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val		
580	585	590
Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp		
595	600	605
Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu		
610	615	620
Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr		
625	630	635
Pro Glu Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala		
645	650	655
Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly		
660	665	670
Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys		
675	680	685
Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala		
690	695	700
His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser Asn Gly Gly		
705	710	715
Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys		
725	730	735
Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn		
740	745	750
Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val		
755	760	765
Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala		
770	775	780
Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu		
785	790	795
Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala		
805	810	815
Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg		
820	825	830
Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val		
835	840	845

Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val		
850	855	860
Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp		
865	870	875
Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu		
	885	890
Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr		
	900	905
Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala		
	915	920
Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly		
	930	935
Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys		
945	950	955
Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala		
	965	970
His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser Asn Gly Gly		
	980	985
Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys		
	995	1000
Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser		
1010	1015	1020
Asn Asn Gly Gly Arg Pro Ala Leu Glu Ser Ile Val Ala Gln Leu		
1025	1030	1035
Ser Arg Pro Asp Pro Ala Leu Ala Ala Leu Thr Asn Asp His Leu		
1040	1045	1050
Val Ala Leu Ala Cys Leu Gly Gly Arg Pro Ala Met Asp Ala Val		
1055	1060	1065
Lys Lys Gly Leu Pro His Ala Pro Glu Leu Ile Arg Ser Ser Gly		
1070	1075	1080
Gly Ser Gly Gly Ser Gly Gly Ser Thr Asn Leu Ser Asp Ile Ile		
1085	1090	1095
Glu Lys Glu Thr Gly Lys Gln Leu Val Ile Gln Glu Ser Ile Leu		
1100	1105	1110
Met Leu Pro Glu Glu Val Glu Glu Val Ile Gly Asn Lys Pro Glu		
1115	1120	1125
Ser Asp Ile Leu Val His Thr Ala Tyr Asp Glu Ser Thr Asp Glu		
1130	1135	1140
Asn Val Met Leu Leu Thr Ser Asp Ala Pro Glu Tyr Lys Pro Trp		

1145	1150	1155
Ala Leu Val Ile Gln Asp Ser Asn Gly Glu Asn Lys Ile Lys Met		
1160	1165	1170
Leu Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Thr Asn Leu Ser		
1175	1180	1185
Asp Ile Ile Glu Lys Glu Thr Gly Lys Gln Leu Val Ile Gln Glu		
1190	1195	1200
Ser Ile Leu Met Leu Pro Glu Glu Val Glu Glu Val Ile Gly Asn		
1205	1210	1215
Lys Pro Glu Ser Asp Ile Leu Val His Thr Ala Tyr Asp Glu Ser		
1220	1225	1230
Thr Asp Glu Asn Val Met Leu Leu Thr Ser Asp Ala Pro Glu Tyr		
1235	1240	1245
Lys Pro Trp Ala Leu Val Ile Gln Asp Ser Asn Gly Glu Asn Lys		
1250	1255	1260
Ile Lys Met Leu Ser Gly Gly Ser Lys Arg Thr Ala Asp Gly Ser		
1265	1270	1275
Glu Phe Glu Pro Lys Lys Lys Arg Lys Val		
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<210>	175	
<211>	4182	
<212>	DNA	
<213>	人工序列(Artificial Sequence)	
<220>		
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tttgaggtgt tctttgatcc aagagagctg aggaaggaga catgcctgct gtacgagatc		180
aagtggggca catctcacia gatctggcgc cactctagca agaacaccac aaagcacgtg		240
gaagtgaatt tcatcgagaa gtttaccagc gagcggcact tctgccctag cacctcctgt		300
tctatcacat ggtttctgag ctggtcccca tgcggcgagt gtagcaaggc catcaccgag		360
ttcctgtccc agcacccaaa cgtgaccctg gtcactacg tggccaggct gtatcaccac		420
atggaccagc agaacaggca gggcctgcgg gatctggtga attccggcgt gaccatccag		480
atcatgacag ccccccagta cgattactgt tggagaaact tcgtgaacta cccacctggc		540
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cacgcaggaa tcctgggcct gcctccatgc ctgaatatcc tgcgccgga gcagccccag		660
ctgaccttct ttacaatcgc cctgcagagc tgtcactacc agcggctgcc acctcacatc		720
ctgtgggcaa ccggcctgaa gtctggagga tcctctggag gaagctccgg aagcgagaca		780

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gtggtgccaa	agatctacat	gtccgccggc	tctatccctc	tgaccacaca	catcacaaac	960
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tctatcaagc	tgggcatccc	tgtgaccggc	agcgcctaca	cagaccagac	cacagccatg	1080
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gttgcaatcg	cgtcacacga	tgggggaaag	caggccctag	aaaccgttca	gcgactcctg	2160
cccgtcctgt	gccaggacca	cggcctgacc	ccagaacaag	ttgtcgcgat	tgcaagcaac	2220
aacggaggca	aacaagcctt	agaaacagtc	cagagattgt	tgccggtgct	gtgccaagcc	2280
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 gacgaaaatg tgatgttact gacctccgac gccctgagt ataagccatg ggctctggtc 4080
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 gccgacggct ccgagttcga gccaagaag aagcggaaag tg 4182

<210> 176

<211> 1394

<212> PRT

<213> 人工序列(Artificial Sequence)

<220>

<223> BE4-135-63(AS6)

<400> 176

Met Lys Arg Thr Ala Asp Gly Ser Glu Phe Glu Ser Pro Lys Lys Lys
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 Arg Lys Val Ser Ser Glu Thr Gly Pro Val Ala Val Asp Pro Thr Leu
 20 25 30
 Arg Arg Arg Ile Glu Pro His Glu Phe Glu Val Phe Phe Asp Pro Arg
 35 40 45
 Glu Leu Arg Lys Glu Thr Cys Leu Leu Tyr Glu Ile Lys Trp Gly Thr
 50 55 60
 Ser His Lys Ile Trp Arg His Ser Ser Lys Asn Thr Thr Lys His Val
 65 70 75 80
 Glu Val Asn Phe Ile Glu Lys Phe Thr Ser Glu Arg His Phe Cys Pro
 85 90 95
 Ser Thr Ser Cys Ser Ile Thr Trp Phe Leu Ser Trp Ser Pro Cys Gly
 100 105 110

Glu Cys Ser Lys Ala Ile Thr Glu Phe Leu Ser Gln His Pro Asn Val		
115	120	125
Thr Leu Val Ile Tyr Val Ala Arg Leu Tyr His His Met Asp Gln Gln		
130	135	140
Asn Arg Gln Gly Leu Arg Asp Leu Val Asn Ser Gly Val Thr Ile Gln		
145	150	155
Ile Met Thr Ala Pro Glu Tyr Asp Tyr Cys Trp Arg Asn Phe Val Asn		
165	170	175
Tyr Pro Pro Gly Lys Glu Ala His Trp Pro Arg Tyr Pro Pro Leu Trp		
180	185	190
Met Lys Leu Tyr Ala Leu Glu Leu His Ala Gly Ile Leu Gly Leu Pro		
195	200	205
Pro Cys Leu Asn Ile Leu Arg Arg Lys Gln Pro Gln Leu Thr Phe Phe		
210	215	220
Thr Ile Ala Leu Gln Ser Cys His Tyr Gln Arg Leu Pro Pro His Ile		
225	230	235
Leu Trp Ala Thr Gly Leu Lys Ser Gly Gly Ser Ser Gly Gly Ser Ser		
245	250	255
Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Ser		
260	265	270
Gly Gly Ser Ser Gly Gly Ser Tyr Thr Arg Val Gly Ser Gly Ser Gly		
275	280	285
Ser Gly Ser Ile Thr Arg Thr Thr Asn Pro Arg Asn Val Val Pro Lys		
290	295	300
Ile Tyr Met Ser Ala Gly Ser Ile Pro Leu Thr Thr His Ile Thr Asn		
305	310	315
Ser Ile Gln Pro Thr Leu Trp Thr Ile Gly Ser Ile Asn Gly Val Ala		
325	330	335
Pro Leu Ala Lys Ser Ile Lys Leu Gly Ile Pro Val Thr Gly Ser Ala		
340	345	350
Tyr Thr Asp Gln Thr Thr Ala Met Val Arg Lys Lys Val Ser Val Phe		
355	360	365
Met Gly Ser Gly Ser Gly Ser Gly Ser Ser Met Thr Ala Val Met Asp		
370	375	380
Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His Asp Ile Asp Tyr Lys		
385	390	395
Asp Asp Asp Asp Lys Met Ala Pro Lys Lys Lys Arg Lys Val Gly Ile		
405	410	415
His Gly Val Pro Ala Ala Val Asp Leu Arg Thr Leu Gly Tyr Ser Gln		

420	425	430
Gln Gln Gln Glu Lys Ile Lys Pro Lys Val Arg Ser Thr Val Ala Gln		
435	440	445
His His Glu Ala Leu Val Gly His Gly Phe Thr His Ala His Ile Val		
450	455	460
Ala Leu Ser Gln His Pro Ala Ala Leu Gly Thr Val Ala Val Lys Tyr		
465	470	475
Gln Asp Met Ile Ala Ala Leu Pro Glu Ala Thr His Glu Ala Ile Val		
485	490	495
Gly Val Gly Lys Gln Trp Ser Gly Ala Arg Ala Leu Glu Ala Leu Leu		
500	505	510
Thr Val Ala Gly Glu Leu Arg Gly Pro Pro Leu Gln Leu Asp Thr Gly		
515	520	525
Gln Leu Leu Lys Ile Ala Lys Arg Gly Gly Val Thr Ala Val Glu Ala		
530	535	540
Val His Ala Trp Arg Asn Ala Leu Thr Gly Ala Pro Leu Asn Leu Thr		
545	550	555
Pro Asp Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala		
565	570	575
Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly		
580	585	590
Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys		
595	600	605
Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala		
610	615	620
His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Asn Gly		
625	630	635
Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys		
645	650	655
Gln Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser His		
660	665	670
Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val		
675	680	685
Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala		
690	695	700
Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu		
705	710	715
Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala		
725	730	735

Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg			
740	745	750	
Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val			
755	760	765	
Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val			
770	775	780	
Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala			
785	790	795	800
Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu			
	805	810	815
Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr			
	820	825	830
Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala			
	835	840	845
Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly			
	850	855	860
Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys			
865	870	875	880
Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala			
	885	890	895
His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Gly Gly			
	900	905	910
Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys			
	915	920	925
Gln Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser Asn			
	930	935	940
Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val			
945	950	955	960
Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala			
	965	970	975
Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu			
	980	985	990
Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala			
	995	1000	1005
Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln			
	1010	1015	1020
Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp			
	1025	1030	1035
Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu			

1040	1045	1050
Glu Thr Val Gln Arg Leu	Leu Pro Val Leu Cys	Gln Ala His Gly
1055	1060	1065
Leu Thr Pro Ala Gln Val	Val Ala Ile Ala Ser	Asn Gly Gly Gly
1070	1075	1080
Lys Gln Ala Leu Glu Thr	Val Gln Arg Leu Leu	Pro Val Leu Cys
1085	1090	1095
Gln Asp His Gly Leu Thr	Pro Glu Gln Val Val	Ala Ile Ala Ser
1100	1105	1110
Asn Asn Gly Gly Arg Pro	Ala Leu Glu Ser Ile	Val Ala Gln Leu
1115	1120	1125
Ser Arg Pro Asp Pro Ala	Leu Ala Ala Leu Thr	Asn Asp His Leu
1130	1135	1140
Val Ala Leu Ala Cys Leu	Gly Gly Arg Pro Ala	Leu Asp Ala Val
1145	1150	1155
Lys Lys Gly Leu Pro His	Ala Pro Ala Leu Ile	Lys Arg Thr Asn
1160	1165	1170
Arg Arg Ile Pro Glu Arg	Thr Ser His Arg Val	Ala Gly Ser Ser
1175	1180	1185
Gly Gly Ser Gly Gly Ser	Gly Gly Ser Thr Asn	Leu Ser Asp Ile
1190	1195	1200
Ile Glu Lys Glu Thr Gly	Lys Gln Leu Val Ile	Gln Glu Ser Ile
1205	1210	1215
Leu Met Leu Pro Glu Glu	Val Glu Glu Val Ile	Gly Asn Lys Pro
1220	1225	1230
Glu Ser Asp Ile Leu Val	His Thr Ala Tyr Asp	Glu Ser Thr Asp
1235	1240	1245
Glu Asn Val Met Leu Leu	Thr Ser Asp Ala Pro	Glu Tyr Lys Pro
1250	1255	1260
Trp Ala Leu Val Ile Gln	Asp Ser Asn Gly Glu	Asn Lys Ile Lys
1265	1270	1275
Met Leu Ser Gly Gly Ser	Gly Gly Ser Gly Gly	Ser Thr Asn Leu
1280	1285	1290
Ser Asp Ile Ile Glu Lys	Glu Thr Gly Lys Gln	Leu Val Ile Gln
1295	1300	1305
Glu Ser Ile Leu Met Leu	Pro Glu Glu Val Glu	Glu Val Ile Gly
1310	1315	1320
Asn Lys Pro Glu Ser Asp	Ile Leu Val His Thr	Ala Tyr Asp Glu
1325	1330	1335

Ser Thr	Asp Glu	Asn Val	Met	Leu Leu	Thr Ser	Asp	Ala Pro	Glu
1340			1345			1350		
Tyr Lys	Pro Trp	Ala Leu	Val	Ile Gln	Asp Ser	Asn	Gly Glu	Asn
1355			1360			1365		
Lys Ile	Lys Met	Leu Ser	Gly	Gly Ser	Lys Arg	Thr	Ala Asp	Gly
1370			1375			1380		
Ser Glu	Phe Glu	Pro Lys	Lys	Lys Arg	Lys Val			
1385			1390					

<210> 177

<211> 3864

<212> DNA

<213> 人工序列(Artificial Sequence)

<220>

<223> BE4-32-47(AS7)

<400> 177

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tttgaggtgt	tctttgatcc	aagagagctg	aggaaggaga	catgcctgct	gtacgagatc	180
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gaagtgaatt	tcatcgagaa	gtttaccagc	gagcggcact	tctgccctag	cacctcctgt	300
tctatcacat	ggtttctgag	ctggtcccca	tgcggcgagt	gtagcaaggc	catcaccgag	360
ttcctgtccc	agcacccaaa	cgtgaccctg	gtcatctacg	tggccaggct	gtatcaccac	420
atggaccagc	agaacaggca	gggcctgcgg	gatctggtga	attccggcgt	gaccatccag	480
atcatgacag	cccccgagta	cgattactgt	tggagaaact	tcgtgaacta	cccacctggc	540
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gataaaaagt	ggaaggacgc	aagtggttgg	tctagaatgc	atgcggcccc	gcgacggcgt	960
gctgcgcaac	cctccgacgc	ttcgccggcc	gcgcagggtg	atctacgcac	gctcggctac	1020
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35 40 45
Glu Leu Arg Lys Glu Thr Cys Leu Leu Tyr Glu Ile Lys Trp Gly Thr
50 55 60
Ser His Lys Ile Trp Arg His Ser Ser Lys Asn Thr Thr Lys His Val
65 70 75 80
Glu Val Asn Phe Ile Glu Lys Phe Thr Ser Glu Arg His Phe Cys Pro
85 90 95
Ser Thr Ser Cys Ser Ile Thr Trp Phe Leu Ser Trp Ser Pro Cys Gly
100 105 110
Glu Cys Ser Lys Ala Ile Thr Glu Phe Leu Ser Gln His Pro Asn Val
115 120 125
Thr Leu Val Ile Tyr Val Ala Arg Leu Tyr His His Met Asp Gln Gln
130 135 140
Asn Arg Gln Gly Leu Arg Asp Leu Val Asn Ser Gly Val Thr Ile Gln
145 150 155 160
Ile Met Thr Ala Pro Glu Tyr Asp Tyr Cys Trp Arg Asn Phe Val Asn
165 170 175
Tyr Pro Pro Gly Lys Glu Ala His Trp Pro Arg Tyr Pro Pro Leu Trp
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195 200 205
Pro Cys Leu Asn Ile Leu Arg Arg Lys Gln Pro Gln Leu Thr Phe Phe
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Thr Ile Ala Leu Gln Ser Cys His Tyr Gln Arg Leu Pro Pro His Ile
225 230 235 240

Leu Trp Ala Thr Gly Leu Lys Ser Gly Gly Ser Ser Gly Gly Ser Ser		
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Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Ser		
260	265	270
Gly Gly Ser Ser Gly Gly Ser Met Ala Ser Ser Pro Pro Lys Lys Lys		
275	280	285
Arg Lys Val Ala Ala Ala Asp Tyr Lys Asp Asp Asp Asp Lys Ser Trp		
290	295	300
Lys Asp Ala Ser Gly Trp Ser Arg Met His Ala Ala Pro Arg Arg Arg		
305	310	315
Ala Ala Gln Pro Ser Asp Ala Ser Pro Ala Ala Gln Val Asp Leu Arg		
325	330	335
Thr Leu Gly Tyr Ser Gln Gln Gln Gln Glu Lys Ile Lys Pro Lys Val		
340	345	350
Arg Ser Thr Val Ala Gln His His Glu Ala Leu Val Gly His Gly Phe		
355	360	365
Thr His Ala His Ile Val Ala Leu Ser Gln His Pro Ala Ala Leu Gly		
370	375	380
Thr Val Ala Val Thr Tyr Gln His Ile Ile Thr Ala Leu Pro Glu Ala		
385	390	395
Thr His Glu Asp Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg		
405	410	415
Ala Leu Glu Ala Leu Leu Thr Asp Ala Gly Glu Leu Arg Gly Pro Pro		
420	425	430
Leu Gln Leu Asp Thr Gly Gln Leu Val Lys Ile Ala Lys Arg Gly Gly		
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Val Thr Ala Met Glu Ala Val His Ala Ser Arg Asn Ala Leu Thr Gly		
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Ala Pro Leu Asn Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn		
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Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val		
485	490	495
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Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu		
515	520	525
Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala		
530	535	540
Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg		

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Val Ala Ile Ala	Ser His Asp Gly Gly Lys Gln Ala	Leu Glu Thr Val	
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Gln Arg Leu Leu	Pro Val Leu Cys Gln Asp His Gly	Leu Thr Pro Asp	
	595	600	605
Gln Val Val Ala	Ile Ala Ser His Asp Gly Gly Lys Gln Ala	Leu Glu	
	610	615	620
Thr Val Gln Arg	Leu Leu Pro Val Leu Cys Gln Asp His Gly	Leu Thr	
625	630	635	640
Pro Glu Gln Val	Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala		
	645	650	655
Leu Glu Thr Val	Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly		
	660	665	670
Leu Thr Pro Asp	Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys		
	675	680	685
Gln Ala Leu Glu	Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala		
	690	695	700
His Gly Leu Thr	Pro Ala Gln Val Val Ala Ile Ala Ser Asn Ile Gly		
705	710	715	720
Gly Lys Gln Ala	Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys		
	725	730	735
Gln Asp His Gly	Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser His		
	740	745	750
Asp Gly Gly Lys	Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val		
	755	760	765
Leu Cys Gln Asp	His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala		
	770	775	780
Ser Asn Gly Gly	Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu		
785	790	795	800
Pro Val Leu Cys	Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala		
	805	810	815
Ile Ala Ser Asn	Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg		
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Val Ala Ile Ala	Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val		
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	885	890	895
Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr			
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Pro Glu Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala			
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Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly			
	930	935	940
Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys			
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Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala			
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His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser Asn Ile Gly			
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Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys			
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Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser			
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Val Ala Leu Ala Cys Leu Gly Gly Arg Pro Ala Met Asp Ala Val			
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Lys Lys Gly Leu Pro His Ala Pro Glu Leu Ile Arg Ser Ser Gly			
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Gly Ser Gly Gly Ser Gly Gly Ser Thr Asn Leu Ser Asp Ile Ile			
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Glu Lys Glu Thr Gly Lys Gln Leu Val Ile Gln Glu Ser Ile Leu			
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Lys Pro Glu Ser Asp Ile Leu	Val His Thr Ala Tyr	Asp Glu Ser
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Thr Asp Glu Asn Val Met Leu	Leu Thr Ser Asp Ala	Pro Glu Tyr
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Lys Pro Trp Ala Leu Val Ile	Gln Asp Ser Asn Gly	Glu Asn Lys
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Arg Arg Arg Ile Glu Pro His Glu Phe Glu Val Phe Phe Asp Pro Arg

35 40 45

Glu Leu Arg Lys Glu Thr Cys Leu Leu Tyr Glu Ile Lys Trp Gly Thr

50 55 60

Ser His Lys Ile Trp Arg His Ser Ser Lys Asn Thr Thr Lys His Val

65 70 75 80

Glu Val Asn Phe Ile Glu Lys Phe Thr Ser Glu Arg His Phe Cys Pro

85 90 95

Ser Thr Ser Cys Ser Ile Thr Trp Phe Leu Ser Trp Ser Pro Cys Gly

100 105 110

Glu Cys Ser Lys Ala Ile Thr Glu Phe Leu Ser Gln His Pro Asn Val

115 120 125

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

435	440	445
His His Glu Ala Leu Val Gly	His Gly Phe Thr	His Ala His Ile Val
450	455	460
Ala Leu Ser Gln His Pro Ala	Ala Leu Gly Thr Val	Ala Val Lys Tyr
465	470	475
Gln Asp Met Ile Ala Ala Leu Pro	Glu Ala Thr His Glu Ala Ile Val	
485	490	495
Gly Val Gly Lys Gln Trp Ser Gly	Ala Arg Ala Leu Glu Ala Leu Leu	
500	505	510
Thr Val Ala Gly Glu Leu Arg Gly	Pro Pro Leu Gln Leu Asp Thr Gly	
515	520	525
Gln Leu Leu Lys Ile Ala Lys Arg	Gly Gly Val Thr Ala Val Glu Ala	
530	535	540
Val His Ala Trp Arg Asn Ala Leu Thr	Gly Ala Pro Leu Asn Leu Thr	
545	550	555
Pro Asp Gln Val Val Ala Ile Ala Ser	Asn Gly Gly Gly Lys Gln Ala	
565	570	575
Leu Glu Thr Val Gln Arg Leu Leu Pro	Val Leu Cys Gln Asp His Gly	
580	585	590
Leu Thr Pro Glu Gln Val Val Ala Ile	Ala Ser Asn Gly Gly Gly Lys	
595	600	605
Gln Ala Leu Glu Thr Val Gln Arg Leu Leu	Pro Val Leu Cys Gln Ala	
610	615	620
His Gly Leu Thr Pro Asp Gln Val Val	Ala Ile Ala Ser Asn Asn Gly	
625	630	635
Gly Lys Gln Ala Leu Glu Thr Val Gln	Arg Leu Leu Pro Val Leu Cys	
645	650	655
Gln Ala His Gly Leu Thr Pro Ala Gln	Val Val Ala Ile Ala Ser His	
660	665	670
Asp Gly Gly Lys Gln Ala Leu Glu Thr	Val Gln Arg Leu Leu Pro Val	
675	680	685
Leu Cys Gln Asp His Gly Leu Thr Pro	Asp Gln Val Val Ala Ile Ala	
690	695	700
Ser His Asp Gly Gly Lys Gln Ala Leu Glu	Thr Val Gln Arg Leu Leu	
705	710	715
Pro Val Leu Cys Gln Asp His Gly Leu Thr	Pro Glu Gln Val Val Ala	
725	730	735
Ile Ala Ser Asn Ile Gly Gly Lys Gln	Ala Leu Glu Thr Val Gln Arg	
740	745	750

Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val		
755	760	765
Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val		
770	775	780
Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala		
785	790	795
Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu		
	805	810
Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr		
	820	825
Pro Asp Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala		
	835	840
Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly		
	850	855
Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys		
865	870	875
Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala		
	885	890
His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Asn Gly		
	900	905
Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys		
	915	920
Gln Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser Asn		
	930	935
Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val		
945	950	955
Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala		
	965	970
Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu		
	980	985
Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala		
	995	1000
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Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp		
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Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu		
	1040	1045
Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly		
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Lys Gln Ala Leu Glu Thr	Val Gln Arg Leu Leu	Pro Val Leu Cys
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Gln Asp His Gly Leu Thr	Pro Glu Gln Val Val	Ala Ile Ala Ser
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Ser Arg Pro Asp Pro Ala	Leu Ala Ala Leu Thr	Asn Asp His Leu
1130	1135	1140
Val Ala Leu Ala Cys Leu	Gly Gly Arg Pro Ala	Leu Asp Ala Val
1145	1150	1155
Lys Lys Gly Leu Pro His	Ala Pro Ala Leu Ile	Lys Arg Thr Asn
1160	1165	1170
Arg Arg Ile Pro Glu Arg	Thr Ser His Arg Val	Ala Gly Ser Ser
1175	1180	1185
Gly Gly Ser Gly Gly Ser	Gly Gly Ser Thr Asn	Leu Ser Asp Ile
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Ile Glu Lys Glu Thr Gly	Lys Gln Leu Val Ile	Gln Glu Ser Ile
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Leu Met Leu Pro Glu Glu	Val Glu Glu Val Ile	Gly Asn Lys Pro
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Glu Ser Asp Ile Leu Val	His Thr Ala Tyr Asp	Glu Ser Thr Asp
1235	1240	1245
Glu Asn Val Met Leu Leu	Thr Ser Asp Ala Pro	Glu Tyr Lys Pro
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Trp Ala Leu Val Ile Gln	Asp Ser Asn Gly Glu	Asn Lys Ile Lys
1265	1270	1275
Met Leu Ser Gly Gly Ser	Gly Gly Ser Gly Gly	Ser Thr Asn Leu
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Ser Asp Ile Ile Glu Lys	Glu Thr Gly Lys Gln	Leu Val Ile Gln
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Glu Ser Ile Leu Met Leu	Pro Glu Glu Val Glu	Glu Val Ile Gly
1310	1315	1320
Asn Lys Pro Glu Ser Asp	Ile Leu Val His Thr	Ala Tyr Asp Glu
1325	1330	1335
Ser Thr Asp Glu Asn Val	Met Leu Leu Thr Ser	Asp Ala Pro Glu
1340	1345	1350

Tyr Lys Pro Trp Ala Leu Val Ile Gln Asp Ser Asn Gly Glu Asn
 1355 1360 1365
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<212> DNA

<213> 人工序列(Artificial Sequence)

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<223> ABE8e-135-47(AS5)

<400> 181

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gtcatccagg	agtctatcct	gatgctgcca	gaagaagtcg	aagaagtgat	cggaacaag	3780
cccgaaagcg	acatcctggt	ccatactgcc	tacgacgaga	gtaccgacga	aaatgtgatg	3840
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          35           40           45
Gly Ala Val Leu Val Leu Asn Asn Arg Val Ile Gly Glu Gly Trp Asn
          50           55           60
Arg Ala Ile Gly Leu His Asp Pro Thr Ala His Ala Glu Ile Met Ala
65           70           75           80
Leu Arg Gln Gly Gly Leu Val Met Gln Asn Tyr Arg Leu Ile Asp Ala
          85           90           95
Thr Leu Tyr Val Thr Phe Glu Pro Cys Val Met Cys Ala Gly Ala Met
          100          105          110
Ile His Ser Arg Ile Gly Arg Val Val Phe Gly Trp Arg Asn Ser Lys
          115          120          125
Arg Gly Ala Ala Gly Ser Leu Met Asn Val Leu Asn Tyr Pro Gly Met
          130          135          140
Asn His Arg Val Glu Ile Thr Glu Gly Ile Leu Ala Asp Glu Cys Ala
145          150          155          160
Ala Leu Leu Cys Asp Phe Tyr Arg Met Pro Arg Gln Val Phe Asn Ala
          165          170          175
Gln Lys Lys Ala Gln Ser Ser Ile Asn Ser Gly Gly Ser Ser Gly Gly
          180          185          190
Ser Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu
          195          200          205
Ser Ser Gly Gly Ser Ser Gly Gly Ser Tyr Thr Arg Val Gly Ser Gly
          210          215          220
Ser Gly Ser Gly Ser Ile Thr Arg Thr Thr Asn Pro Arg Asn Val Val
225          230          235          240

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Pro Lys Ile Tyr Met Ser Ala Gly Ser Ile Pro Leu Thr Thr His Ile		
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Thr Asn Ser Ile Gln Pro Thr Leu Trp Thr Ile Gly Ser Ile Asn Gly		
260	265	270
Val Ala Pro Leu Ala Lys Ser Ile Lys Leu Gly Ile Pro Val Thr Gly		
275	280	285
Ser Ala Tyr Thr Asp Gln Thr Thr Ala Met Val Arg Lys Lys Val Ser		
290	295	300
Val Phe Met Gly Ser Gly Ser Gly Ser Gly Ser Ser Met Thr Ala Val		
305	310	315
Met Ala Ser Ser Pro Pro Lys Lys Lys Arg Lys Val Ala Ala Ala Asp		
325	330	335
Tyr Lys Asp Asp Asp Asp Lys Ser Trp Lys Asp Ala Ser Gly Trp Ser		
340	345	350
Arg Met His Ala Ala Pro Arg Arg Arg Ala Ala Gln Pro Ser Asp Ala		
355	360	365
Ser Pro Ala Ala Gln Val Asp Leu Arg Thr Leu Gly Tyr Ser Gln Gln		
370	375	380
Gln Gln Glu Lys Ile Lys Pro Lys Val Arg Ser Thr Val Ala Gln His		
385	390	395
His Glu Ala Leu Val Gly His Gly Phe Thr His Ala His Ile Val Ala		
405	410	415
Leu Ser Gln His Pro Ala Ala Leu Gly Thr Val Ala Val Thr Tyr Gln		
420	425	430
His Ile Ile Thr Ala Leu Pro Glu Ala Thr His Glu Asp Ile Val Gly		
435	440	445
Val Gly Lys Gln Trp Ser Gly Ala Arg Ala Leu Glu Ala Leu Leu Thr		
450	455	460
Asp Ala Gly Glu Leu Arg Gly Pro Pro Leu Gln Leu Asp Thr Gly Gln		
465	470	475
Leu Val Lys Ile Ala Lys Arg Gly Gly Val Thr Ala Met Glu Ala Val		
485	490	495
His Ala Ser Arg Asn Ala Leu Thr Gly Ala Pro Leu Asn Leu Thr Pro		
500	505	510
Asp Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu		
515	520	525
Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu		
530	535	540
Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln		

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Ala Leu Glu Thr Val	Gln Arg Leu Leu Pro	Val Leu Cys Gln Ala	His
565	570	575	
Gly Leu Thr Pro Asp	Gln Val Val Ala Ile	Ala Ser Asn Ile	Gly Gly
580	585	590	
Lys Gln Ala Leu Glu Thr	Val Gln Arg Leu Leu Pro	Val Leu Cys Gln	
595	600	605	
Ala His Gly Leu Thr Pro	Ala Gln Val Val Ala Ile	Ala Ser Asn Asn	
610	615	620	
Gly Gly Lys Gln Ala Leu	Glu Thr Val Gln Arg Leu	Leu Leu Pro Val Leu	
625	630	635	640
Cys Gln Asp His Gly Leu	Thr Pro Asp Gln Val Val	Ala Ile Ala Ser	
645	650	655	
Asn Gly Gly Gly Lys Gln	Ala Leu Glu Thr Val Gln	Arg Leu Leu Pro	
660	665	670	
Val Leu Cys Gln Asp His	Gly Leu Thr Pro Glu Gln	Val Val Ala Ile	
675	680	685	
Ala Ser Asn Ile Gly Gly	Lys Gln Ala Leu Glu Thr	Val Gln Arg Leu	
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Leu Pro Val Leu Cys Gln	Ala His Gly Leu Thr Pro	Asp Gln Val Val	
705	710	715	720
Ala Ile Ala Ser Asn Asn	Gly Gly Lys Gln Ala Leu	Glu Thr Val Gln	
725	730	735	
Arg Leu Leu Pro Val Leu	Cys Gln Ala His Gly Leu	Thr Pro Ala Gln	
740	745	750	
Val Val Ala Ile Ala Ser	His Asp Gly Gly Lys Gln	Ala Leu Glu Thr	
755	760	765	
Val Gln Arg Leu Leu Pro	Val Leu Cys Gln Asp His	Gly Leu Thr Pro	
770	775	780	
Asp Gln Val Val Ala Ile	Ala Ser Asn Gly Gly Gly	Lys Gln Ala Leu	
785	790	795	800
Glu Thr Val Gln Arg Leu	Leu Leu Pro Val Leu	Cys Gln Asp His Gly	Leu
805	810	815	
Thr Pro Glu Gln Val Val	Ala Ile Ala Ser His Asp	Gly Gly Lys Gln	
820	825	830	
Ala Leu Glu Thr Val Gln	Arg Leu Leu Pro Val Leu	Cys Gln Ala His	
835	840	845	
Gly Leu Thr Pro Asp Gln	Val Val Ala Ile Ala Ser	Asn Gly Gly Gly	
850	855	860	

Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln			
865	870	875	880
Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser Asn Ile			
	885	890	895
Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu			
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Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser			
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Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro			
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Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile			
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Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val			
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Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln			
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Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala			
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Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu			
	1025	1030	1035
Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly			
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Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly			
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Arg Pro Ala Leu Glu Ser Ile Val Ala Gln Leu Ser Arg Pro Asp			
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Pro Ala Leu Ala Ala Leu Thr Asn Asp His Leu Val Ala Leu Ala			
	1085	1090	1095
Cys Leu Gly Gly Arg Pro Ala Met Asp Ala Val Lys Lys Gly Leu			
	1100	1105	1110
Pro His Ala Pro Glu Leu Ile Arg Ser Ser Gly Gly Ser Gly Gly			
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Ser Gly Gly Ser Thr Asn Leu Ser Asp Ile Ile Glu Lys Glu Thr			
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Ser Gly Gly Ser Gly Gly Ser Thr Asn Leu Ser Asp Ile Ile Glu		
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Lys Glu Thr Gly Lys Gln Leu Val Ile Gln Glu Ser Ile Leu Met		
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1250	1255	1260
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1265	1270	1275
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Leu Val Ile Gln Asp Ser Asn Gly Glu Asn Lys Ile Lys Met Leu		
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<211> 1329

<212> PRT

<213> 人工序列(Artificial Sequence)

<220>

<223> ABE8e-135-47(AS6)

<400> 184

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Arg Lys Val Ser Glu Val Glu Phe Ser His Glu Tyr Trp Met Arg His

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Ala Leu Thr Leu Ala Lys Arg Ala Arg Asp Glu Arg Glu Val Pro Val

35 40 45

Gly Ala Val Leu Val Leu Asn Asn Arg Val Ile Gly Glu Gly Trp Asn

50 55 60

Arg Ala Ile Gly Leu His Asp Pro Thr Ala His Ala Glu Ile Met Ala

65 70 75 80

Leu Arg Gln Gly Gly Leu Val Met Gln Asn Tyr Arg Leu Ile Asp Ala

85 90 95

Thr Leu Tyr Val Thr Phe Glu Pro Cys Val Met Cys Ala Gly Ala Met

100	105	110
Ile His Ser Arg Ile Gly Arg Val Val Phe Gly Trp Arg Asn Ser Lys		
115	120	125
Arg Gly Ala Ala Gly Ser Leu Met Asn Val Leu Asn Tyr Pro Gly Met		
130	135	140
Asn His Arg Val Glu Ile Thr Glu Gly Ile Leu Ala Asp Glu Cys Ala		
145	150	155
Ala Leu Leu Cys Asp Phe Tyr Arg Met Pro Arg Gln Val Phe Asn Ala		
165	170	175
Gln Lys Lys Ala Gln Ser Ser Ile Asn Ser Gly Gly Ser Ser Gly Gly		
180	185	190
Ser Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu		
195	200	205
Ser Ser Gly Gly Ser Ser Gly Gly Ser Tyr Thr Arg Val Gly Ser Gly		
210	215	220
Ser Gly Ser Gly Ser Ile Thr Arg Thr Thr Asn Pro Arg Asn Val Val		
225	230	235
Pro Lys Ile Tyr Met Ser Ala Gly Ser Ile Pro Leu Thr Thr His Ile		
245	250	255
Thr Asn Ser Ile Gln Pro Thr Leu Trp Thr Ile Gly Ser Ile Asn Gly		
260	265	270
Val Ala Pro Leu Ala Lys Ser Ile Lys Leu Gly Ile Pro Val Thr Gly		
275	280	285
Ser Ala Tyr Thr Asp Gln Thr Thr Ala Met Val Arg Lys Lys Val Ser		
290	295	300
Val Phe Met Gly Ser Gly Ser Gly Ser Gly Ser Ser Met Thr Ala Val		
305	310	315
Met Ala Ser Ser Pro Pro Lys Lys Lys Arg Lys Val Ala Ala Ala Asp		
325	330	335
Tyr Lys Asp Asp Asp Asp Lys Ser Trp Lys Asp Ala Ser Gly Trp Ser		
340	345	350
Arg Met His Ala Ala Pro Arg Arg Arg Ala Ala Gln Pro Ser Asp Ala		
355	360	365
Ser Pro Ala Ala Gln Val Asp Leu Arg Thr Leu Gly Tyr Ser Gln Gln		
370	375	380
Gln Gln Glu Lys Ile Lys Pro Lys Val Arg Ser Thr Val Ala Gln His		
385	390	395
His Glu Ala Leu Val Gly His Gly Phe Thr His Ala His Ile Val Ala		
405	410	415

Leu Ser Gln His Pro Ala Ala Leu Gly Thr Val Ala Val Thr Tyr Gln		
420	425	430
His Ile Ile Thr Ala Leu Pro Glu Ala Thr His Glu Asp Ile Val Gly		
435	440	445
Val Gly Lys Gln Trp Ser Gly Ala Arg Ala Leu Glu Ala Leu Leu Thr		
450	455	460
Asp Ala Gly Glu Leu Arg Gly Pro Pro Leu Gln Leu Asp Thr Gly Gln		
465	470	475
Leu Val Lys Ile Ala Lys Arg Gly Gly Val Thr Ala Met Glu Ala Val		
485	490	495
His Ala Ser Arg Asn Ala Leu Thr Gly Ala Pro Leu Asn Leu Thr Pro		
500	505	510
Asp Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu		
515	520	525
Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu		
530	535	540
Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln		
545	550	555
Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His		
565	570	575
Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly		
580	585	590
Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln		
595	600	605
Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser His Asp		
610	615	620
Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu		
625	630	635
Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser		
645	650	655
His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro		
660	665	670
Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile		
675	680	685
Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu		
690	695	700
Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val		
705	710	715
Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln		

	725	730	735
Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln			
740	745	750	
Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr			
755	760	765	
Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro			
770	775	780	
Asp Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu			
785	790	795	800
Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu			
805	810	815	
Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln			
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Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His			
835	840	845	
Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly			
850	855	860	
Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln			
865	870	875	880
Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser Asn Asn			
885	890	895	
Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu			
900	905	910	
Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser			
915	920	925	
His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro			
930	935	940	
Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile			
945	950	955	960
Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu			
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Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val			
980	985	990	
Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln			
995	1000	1005	
Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala			
1010	1015	1020	
Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu			
1025	1030	1035	

Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly		
1040	1045	1050
Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly		
1055	1060	1065
Arg Pro Ala Leu Glu Ser Ile Val Ala Gln Leu Ser Arg Pro Asp		
1070	1075	1080
Pro Ala Leu Ala Ala Leu Thr Asn Asp His Leu Val Ala Leu Ala		
1085	1090	1095
Cys Leu Gly Gly Arg Pro Ala Met Asp Ala Val Lys Lys Gly Leu		
1100	1105	1110
Pro His Ala Pro Glu Leu Ile Arg Ser Ser Gly Gly Ser Gly Gly		
1115	1120	1125
Ser Gly Gly Ser Thr Asn Leu Ser Asp Ile Ile Glu Lys Glu Thr		
1130	1135	1140
Gly Lys Gln Leu Val Ile Gln Glu Ser Ile Leu Met Leu Pro Glu		
1145	1150	1155
Glu Val Glu Glu Val Ile Gly Asn Lys Pro Glu Ser Asp Ile Leu		
1160	1165	1170
Val His Thr Ala Tyr Asp Glu Ser Thr Asp Glu Asn Val Met Leu		
1175	1180	1185
Leu Thr Ser Asp Ala Pro Glu Tyr Lys Pro Trp Ala Leu Val Ile		
1190	1195	1200
Gln Asp Ser Asn Gly Glu Asn Lys Ile Lys Met Leu Ser Gly Gly		
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Ser Gly Gly Ser Gly Gly Ser Thr Asn Leu Ser Asp Ile Ile Glu		
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Lys Glu Thr Gly Lys Gln Leu Val Ile Gln Glu Ser Ile Leu Met		
1235	1240	1245
Leu Pro Glu Glu Val Glu Glu Val Ile Gly Asn Lys Pro Glu Ser		
1250	1255	1260
Asp Ile Leu Val His Thr Ala Tyr Asp Glu Ser Thr Asp Glu Asn		
1265	1270	1275
Val Met Leu Leu Thr Ser Asp Ala Pro Glu Tyr Lys Pro Trp Ala		
1280	1285	1290
Leu Val Ile Gln Asp Ser Asn Gly Glu Asn Lys Ile Lys Met Leu		
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<213>	人工序列(Artificial Sequence)
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<213> 人工序列(Artificial Sequence)

<220>

<223> ABE8e-135-47(AS7)

<400> 186

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

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Ser Ala Tyr Thr Asp Gln Thr Thr Ala Met Val Arg Lys Lys Val Ser		
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Val Phe Met Gly Ser Gly Ser Gly Ser Gly Ser Ser Met Thr Ala Val		
305	310	315
Met Ala Ser Ser Pro Pro Lys Lys Lys Arg Lys Val Ala Ala Ala Asp		
325	330	335
Tyr Lys Asp Asp Asp Asp Lys Ser Trp Lys Asp Ala Ser Gly Trp Ser		
340	345	350
Arg Met His Ala Ala Pro Arg Arg Arg Ala Ala Gln Pro Ser Asp Ala		
355	360	365
Ser Pro Ala Ala Gln Val Asp Leu Arg Thr Leu Gly Tyr Ser Gln Gln		
370	375	380
Gln Gln Glu Lys Ile Lys Pro Lys Val Arg Ser Thr Val Ala Gln His		
385	390	395
His Glu Ala Leu Val Gly His Gly Phe Thr His Ala His Ile Val Ala		
405	410	415
Leu Ser Gln His Pro Ala Ala Leu Gly Thr Val Ala Val Thr Tyr Gln		
420	425	430
His Ile Ile Thr Ala Leu Pro Glu Ala Thr His Glu Asp Ile Val Gly		
435	440	445
Val Gly Lys Gln Trp Ser Gly Ala Arg Ala Leu Glu Ala Leu Leu Thr		
450	455	460
Asp Ala Gly Glu Leu Arg Gly Pro Pro Leu Gln Leu Asp Thr Gly Gln		
465	470	475
Leu Val Lys Ile Ala Lys Arg Gly Gly Val Thr Ala Met Glu Ala Val		
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His Ala Ser Arg Asn Ala Leu Thr Gly Ala Pro Leu Asn Leu Thr Pro		
500	505	510
Asp Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu		
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Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu		
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Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln		
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Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His		
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Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly		
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Cys	Gln	Asp	His	Gly	Leu	Thr	Pro	Asp	Gln	Val	Val	Ala	Ile	Ala	Ser
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Ala	Ser	Asn	Ile	Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu
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Leu	Pro	Val	Leu	Cys	Gln	Ala	His	Gly	Leu	Thr	Pro	Asp	Gln	Val	Val
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Ala	Ile	Ala	Ser	His	Asp	Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln
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Arg	Leu	Leu	Pro	Val	Leu	Cys	Gln	Ala	His	Gly	Leu	Thr	Pro	Ala	Gln
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Val	Val	Ala	Ile	Ala	Ser	Asn	Ile	Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr
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Glu	Thr	Val	Gln	Arg	Leu	Leu	Pro	Val	Leu	Cys	Gln	Asp	His	Gly	Leu
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Ala	His	Gly	Leu	Thr	Pro	Ala	Gln	Val	Val	Ala	Ile	Ala	Ser	Asn	Ile
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Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro		
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Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile		
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Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu		
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Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val		
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Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala		
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Arg Pro Ala Leu Glu Ser Ile Val Ala Gln Leu Ser Arg Pro Asp		
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Pro Ala Leu Ala Ala Leu Thr Asn Asp His Leu Val Ala Leu Ala		
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Cys Leu Gly Gly Arg Pro Ala Met Asp Ala Val Lys Lys Gly Leu		
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Pro His Ala Pro Glu Leu Ile Arg Ser Ser Gly Gly Ser Gly Gly		
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Gly Lys Gln Leu Val Ile Gln Glu Ser Ile Leu Met Leu Pro Glu		
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Glu Val Glu Glu Val Ile Gly Asn Lys Pro Glu Ser Asp Ile Leu		
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Val His Thr Ala Tyr Asp Glu Ser Thr Asp Glu Asn Val Met Leu		
1175	1180	1185
Leu Thr Ser Asp Ala Pro Glu Tyr Lys Pro Trp Ala Leu Val Ile		
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Ser Gly	Gly Ser Gly Gly Ser	Thr Asn Leu Ser Asp	Ile Ile Glu
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Lys Glu	Thr Gly Lys Gln Leu	Val Ile Gln Glu Ser	Ile Leu Met
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Leu Pro	Glu Glu Val Glu Glu	Val Ile Gly Asn Lys	Pro Glu Ser
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Asp Ile	Leu Val His Thr Ala	Tyr Asp Glu Ser Thr	Asp Glu Asn
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Val Met	Leu Leu Thr Ser Asp	Ala Pro Glu Tyr Lys	Pro Trp Ala
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Leu Val	Ile Gln Asp Ser Asn	Gly Glu Asn Lys Ile	Lys Met Leu
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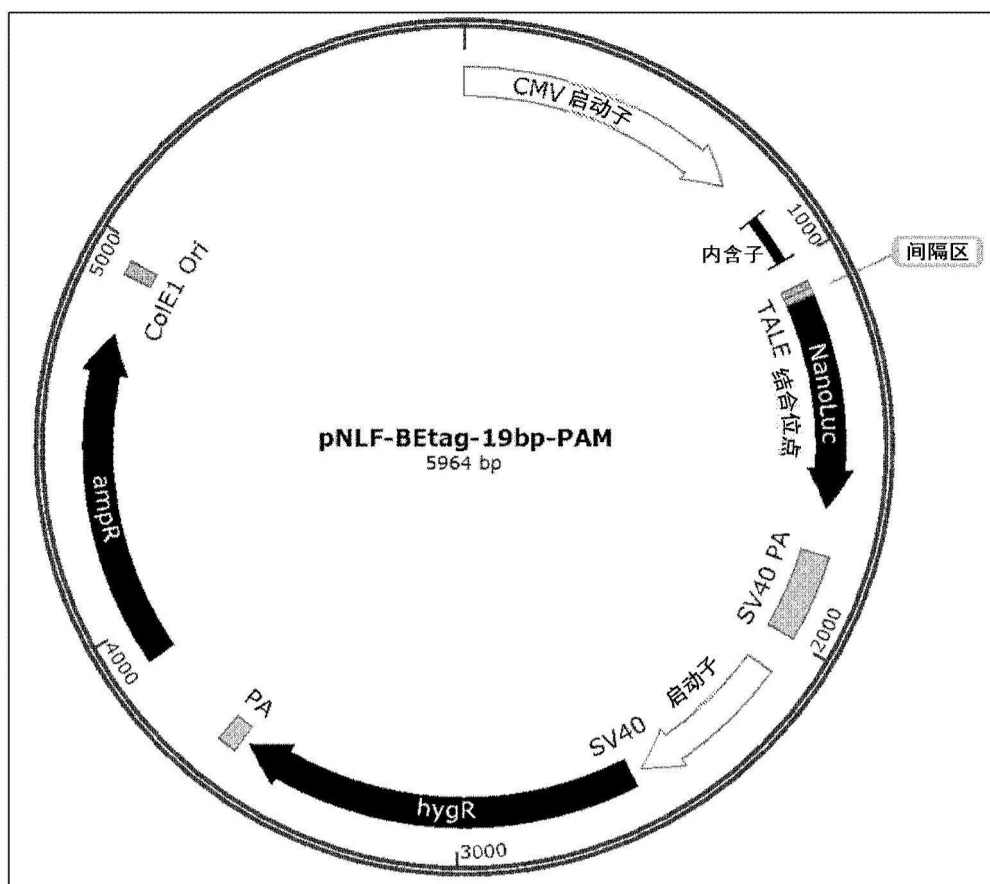


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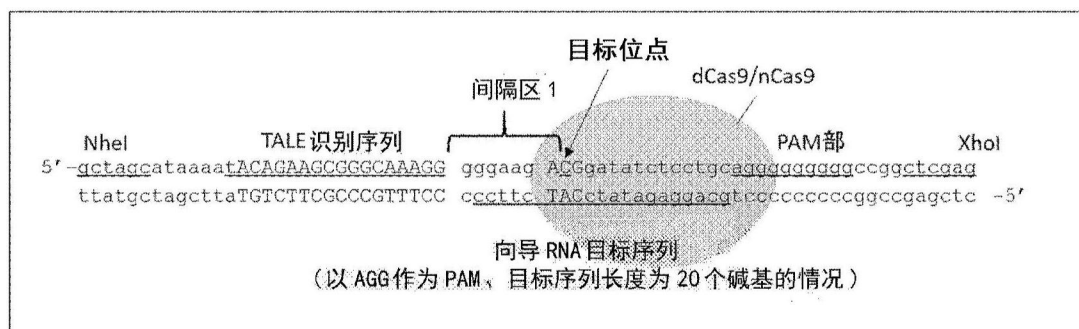


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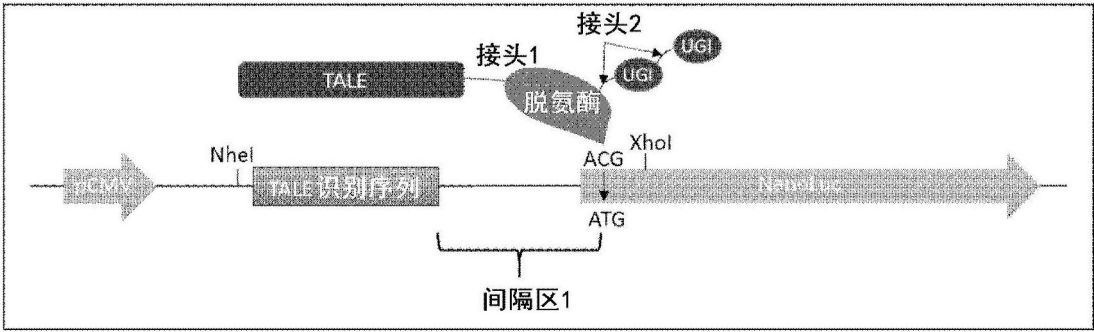


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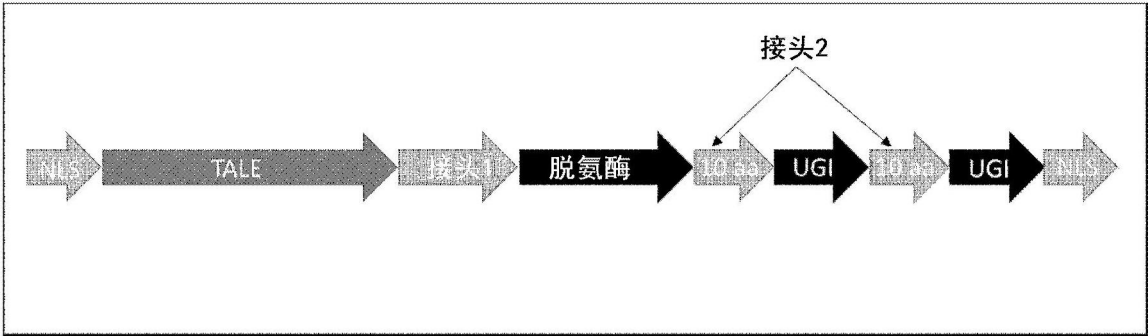


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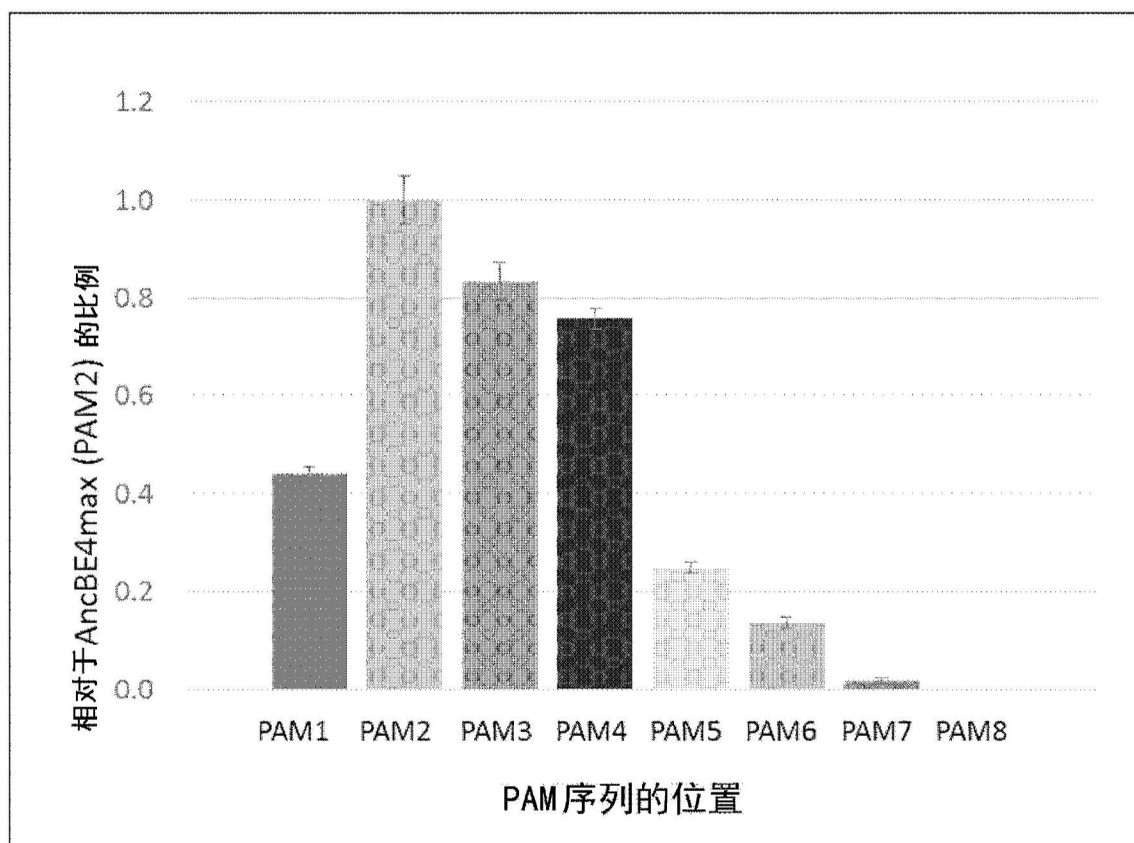


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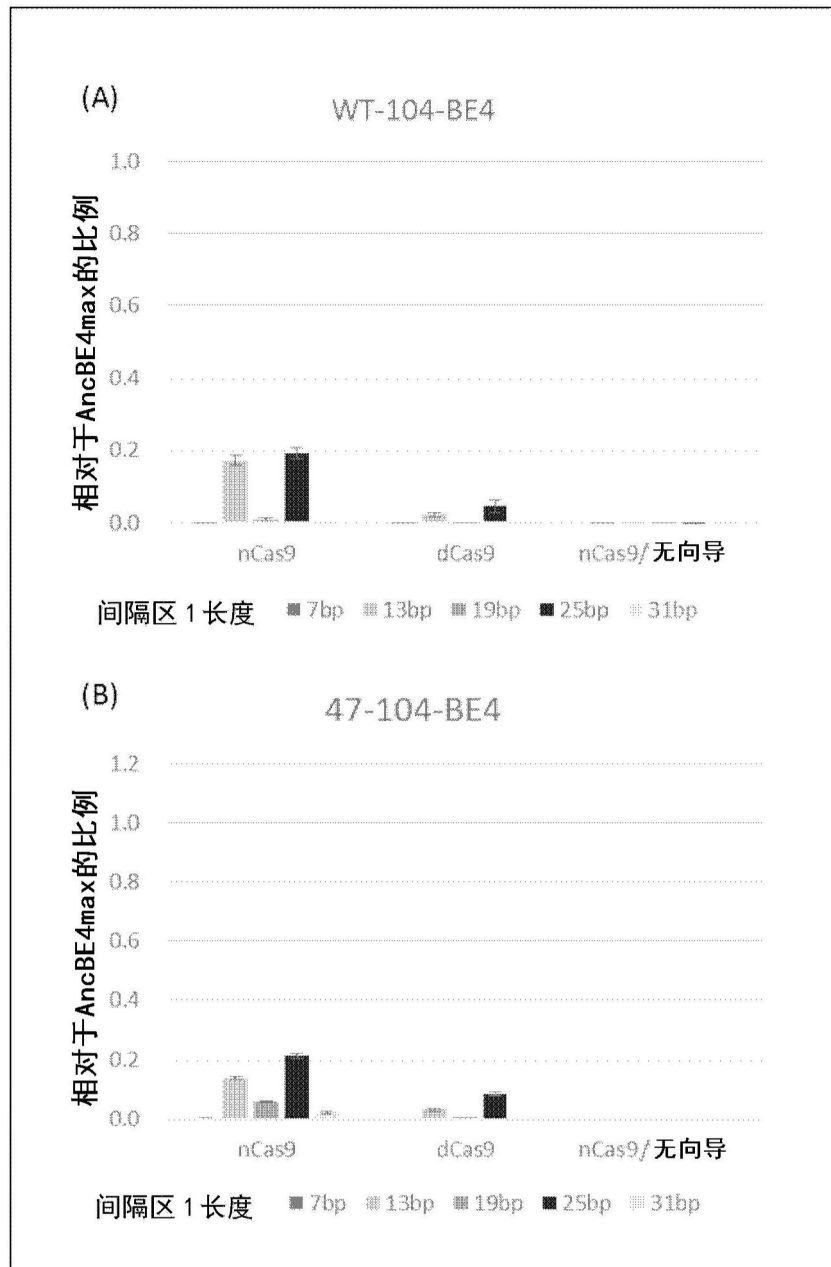


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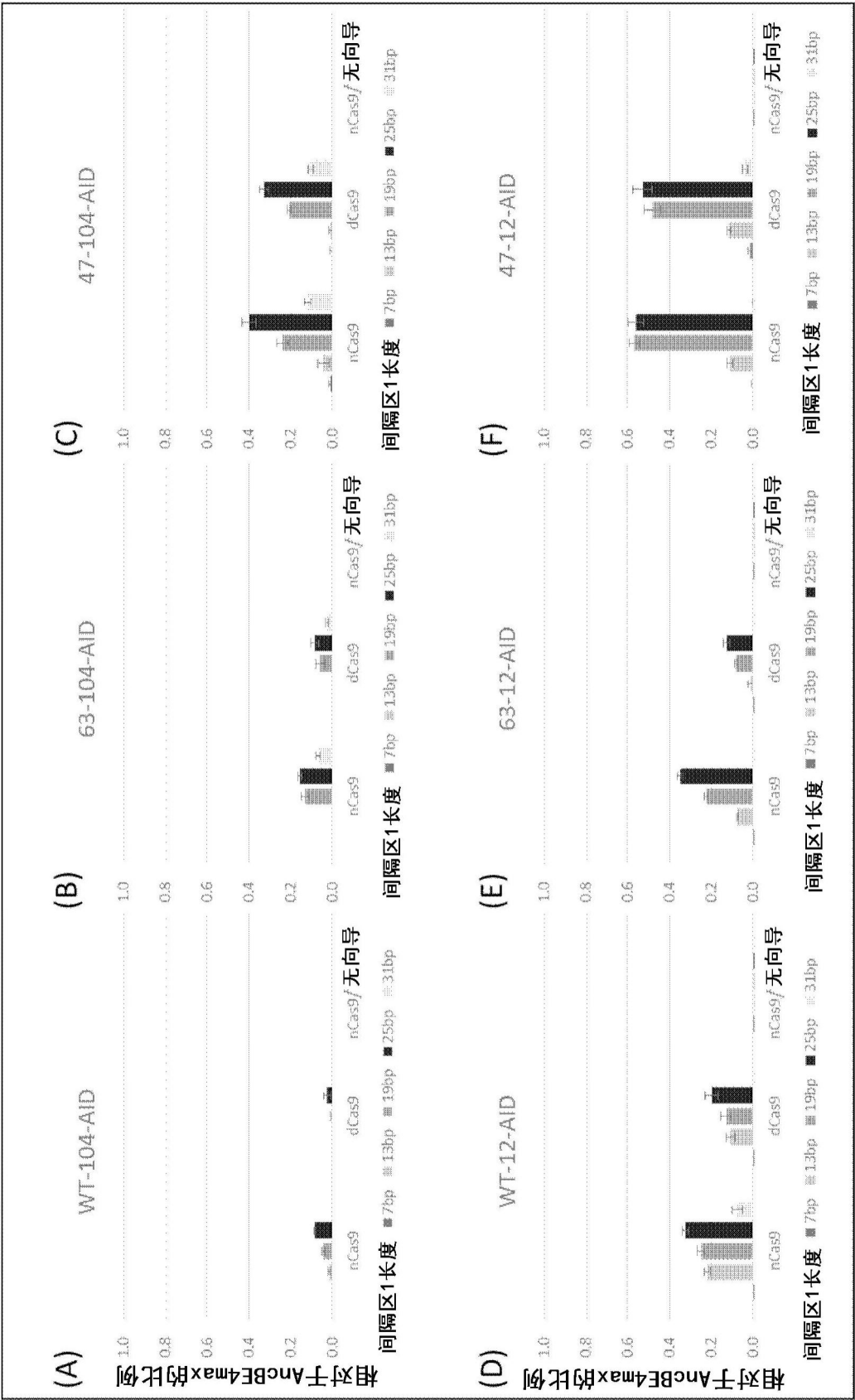


图7

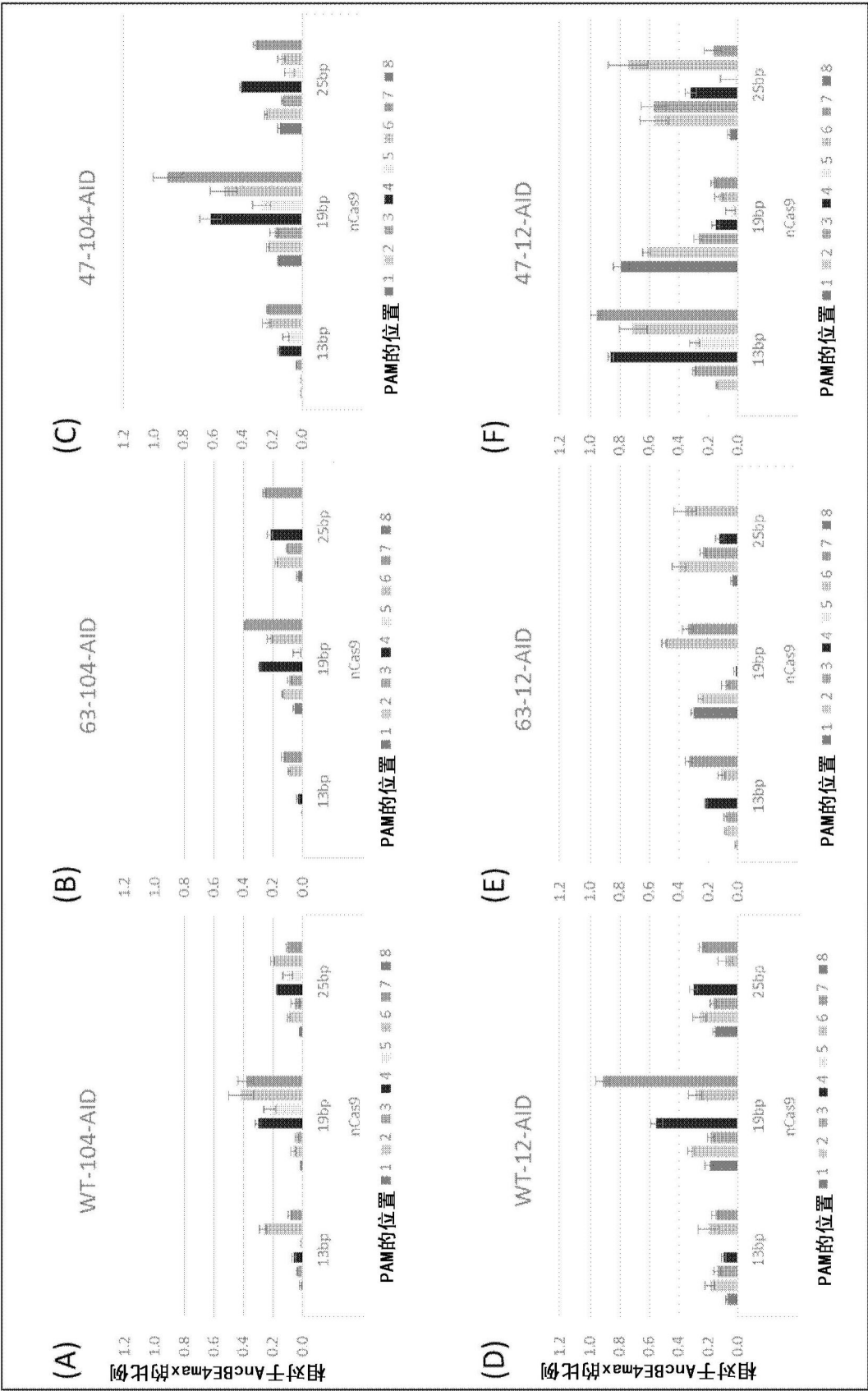


图8

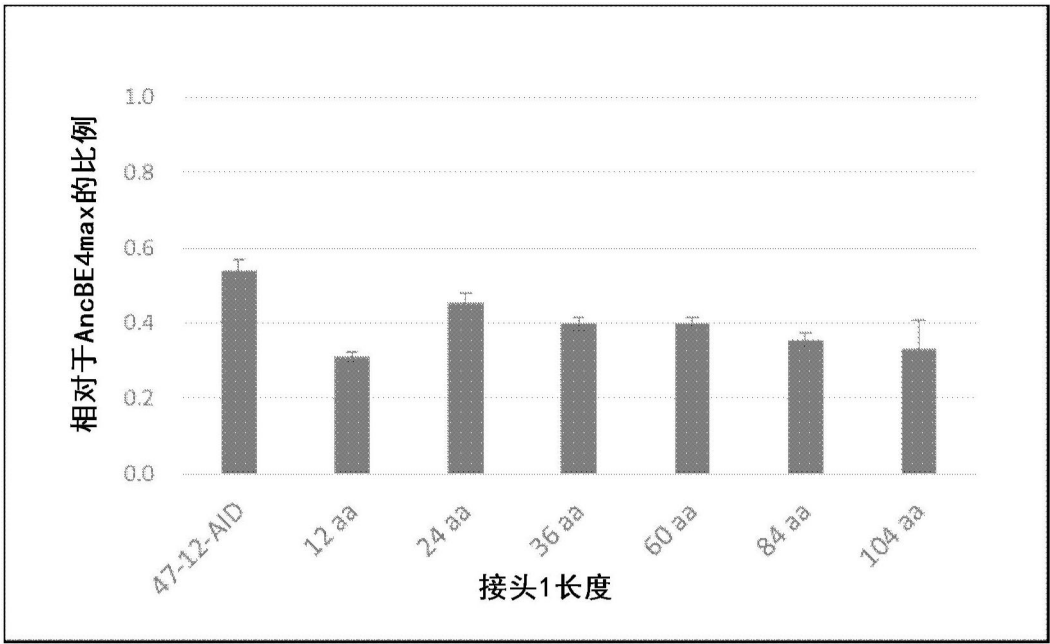


图9

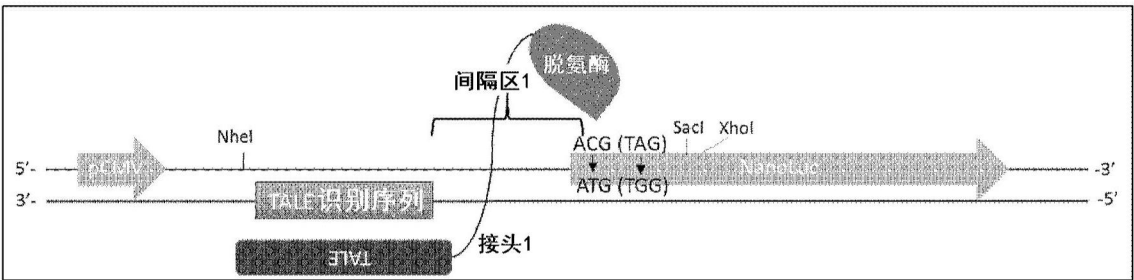


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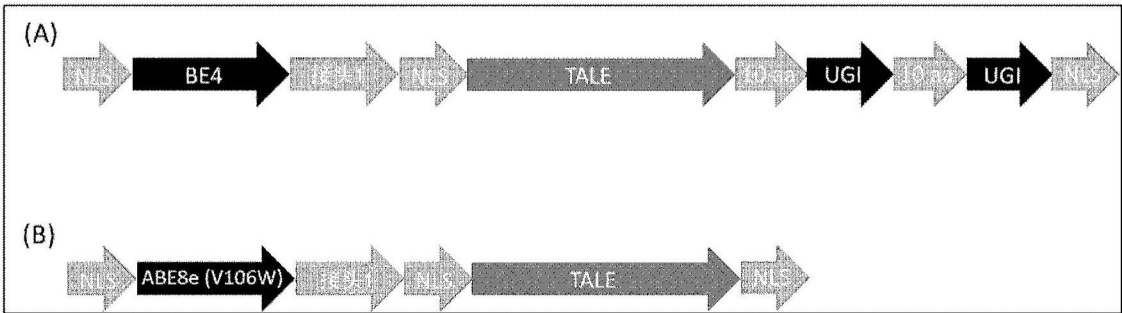


图11

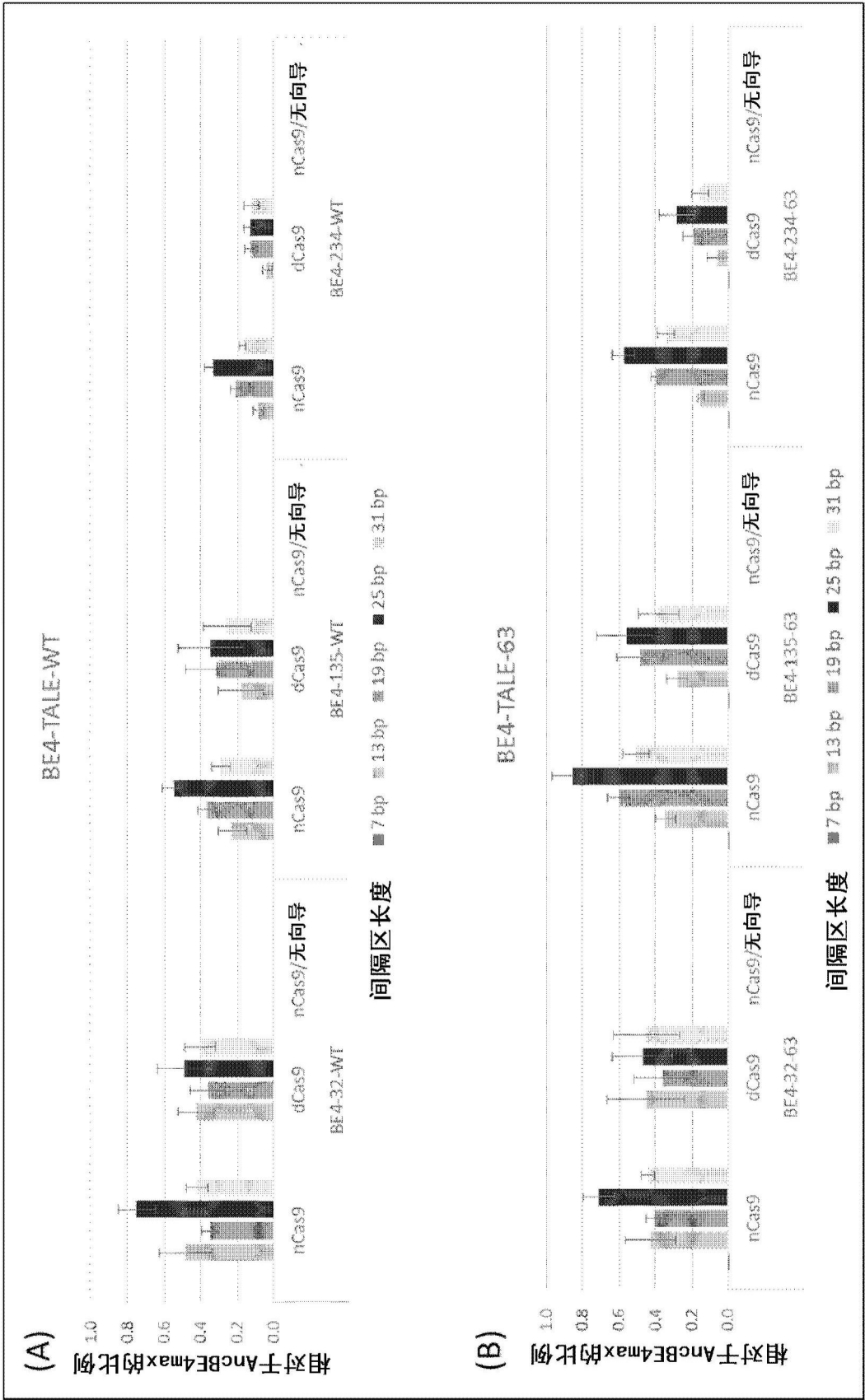


图12A

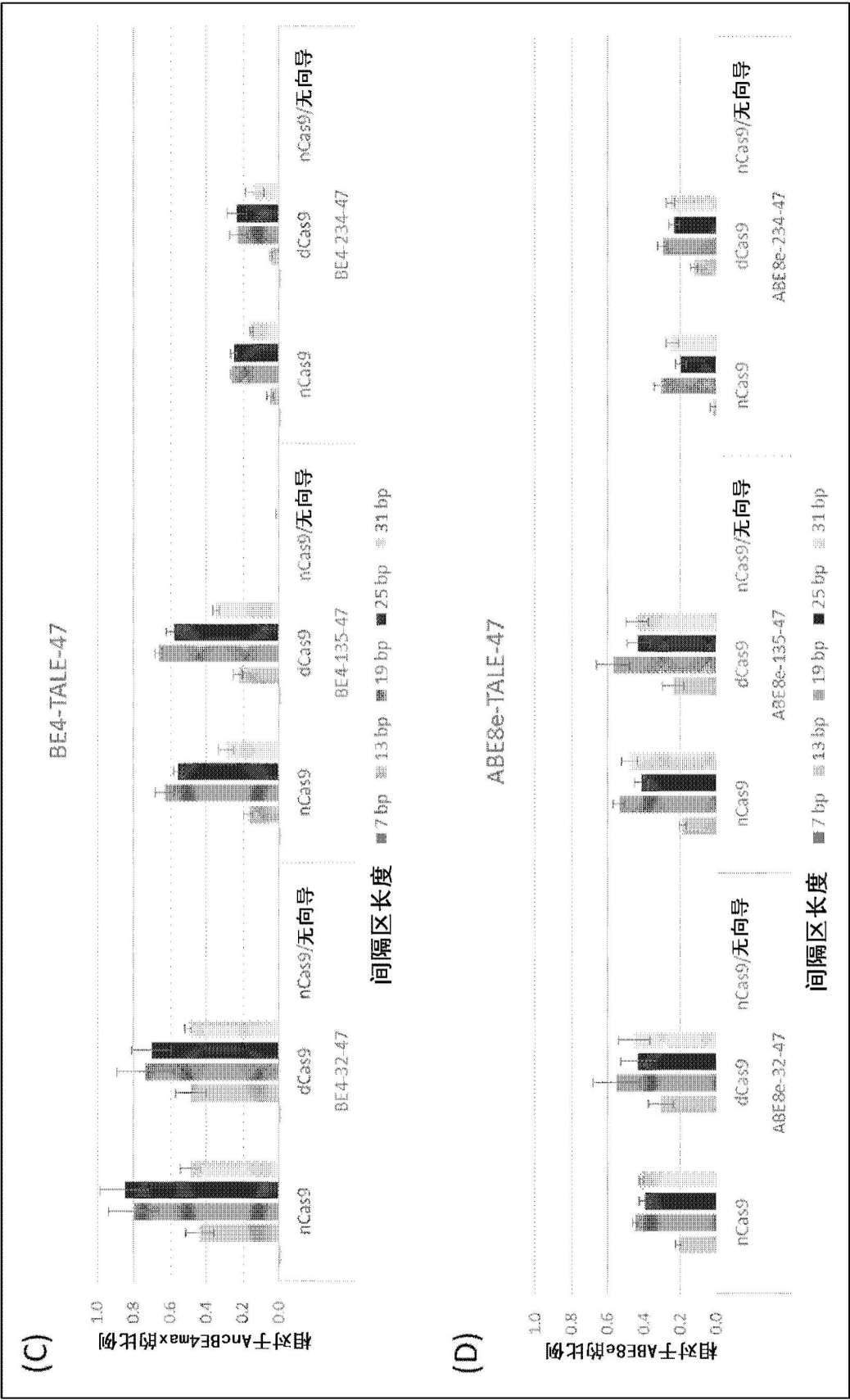


图12B

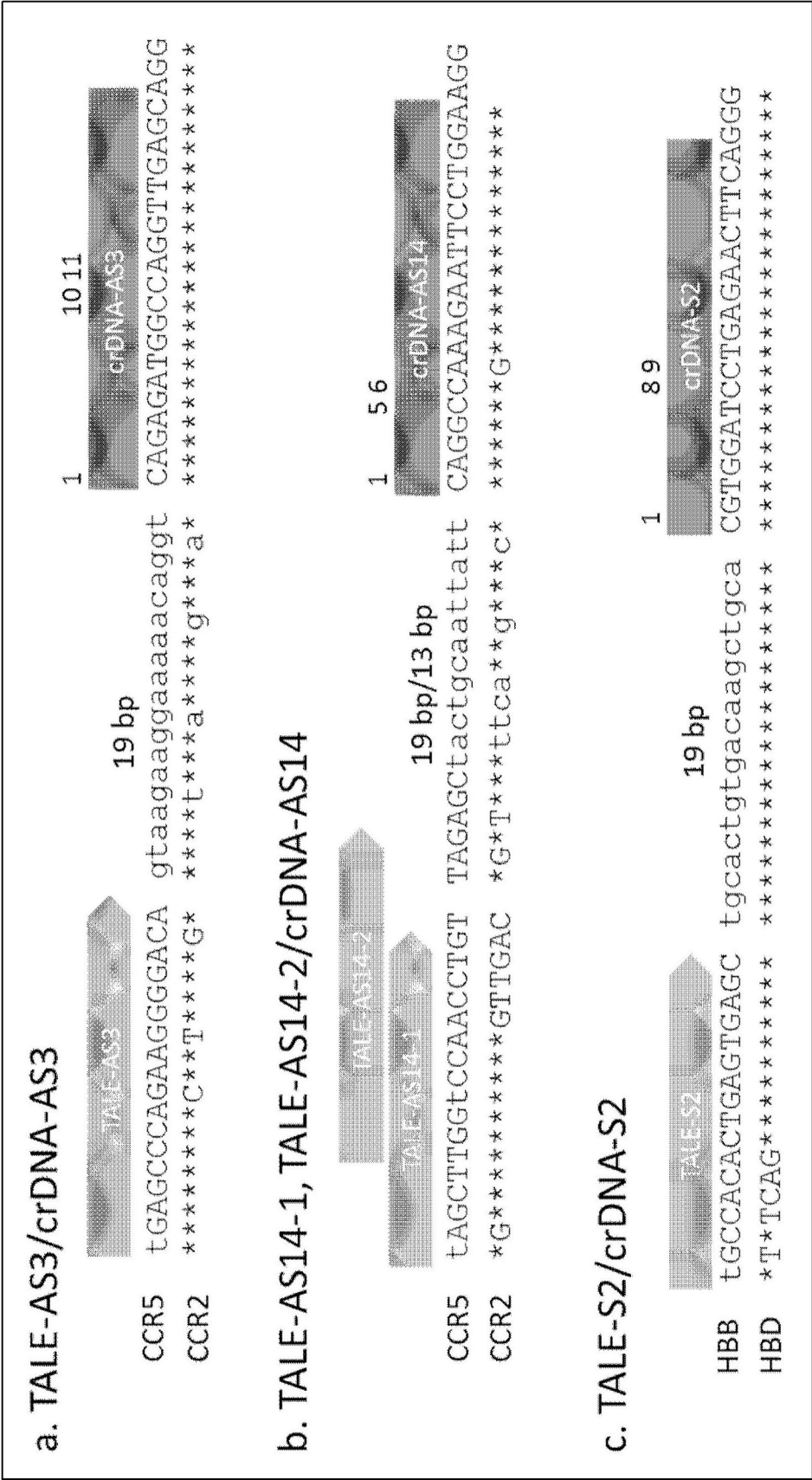


图13A

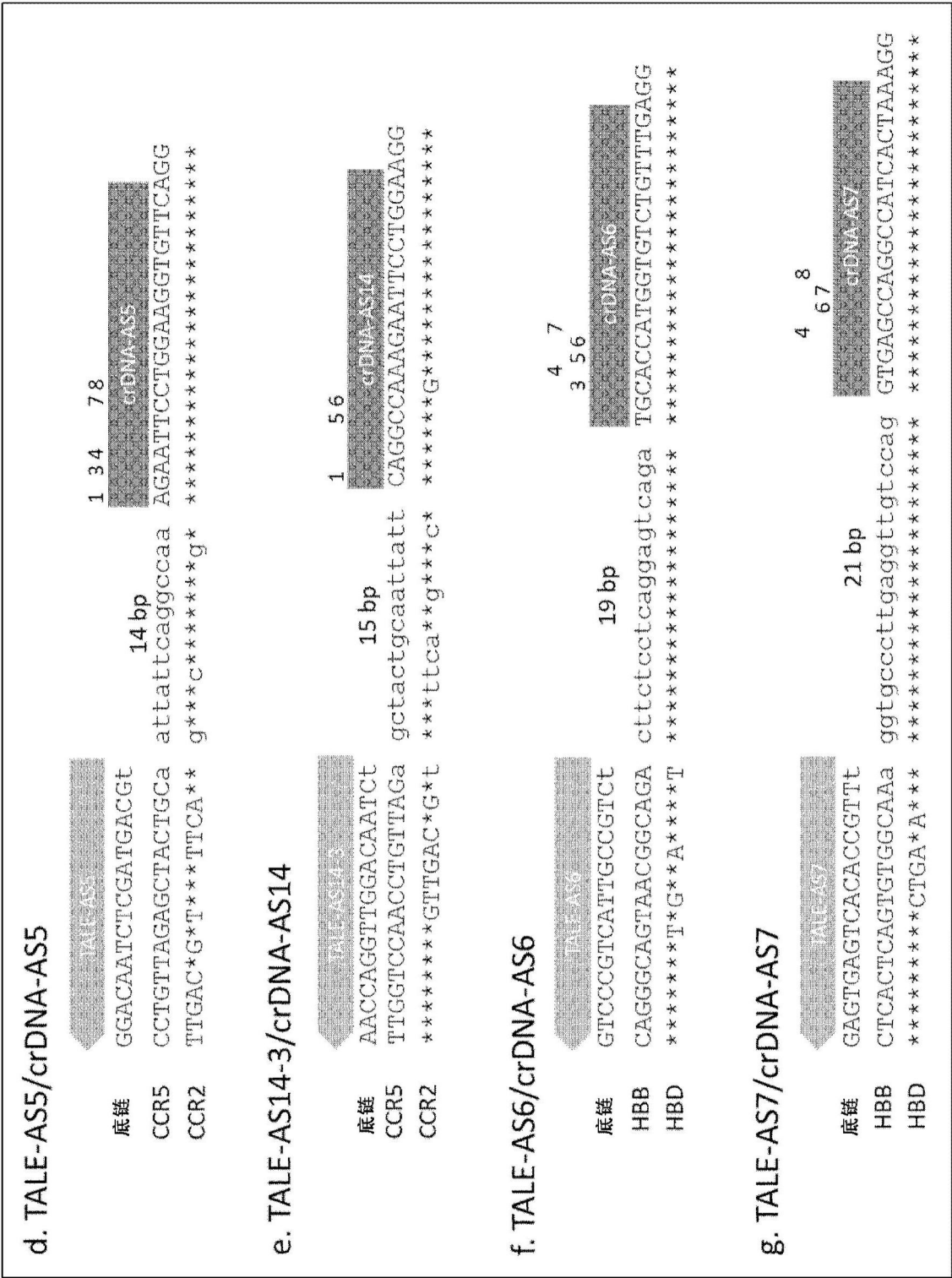


图13B

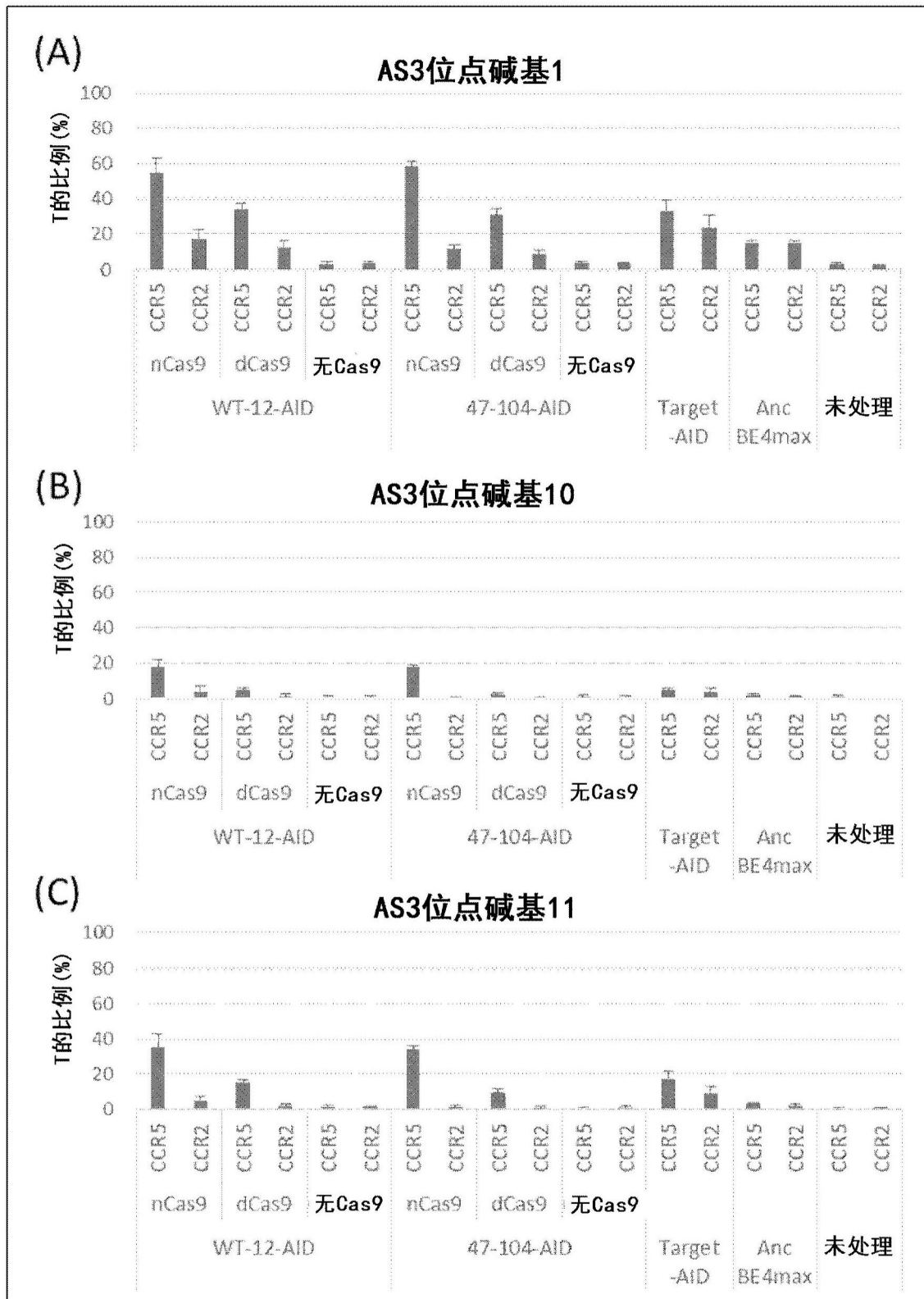


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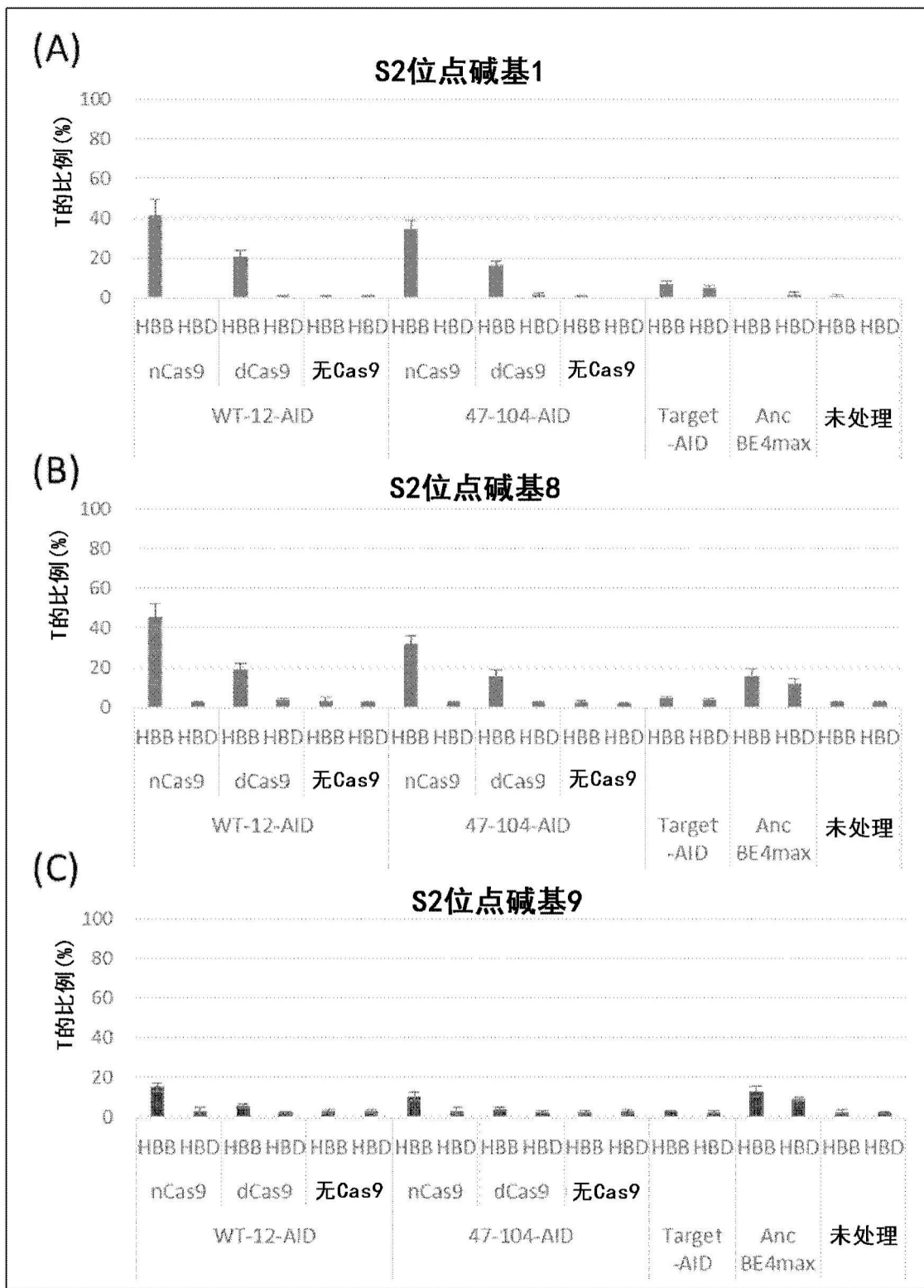


图16

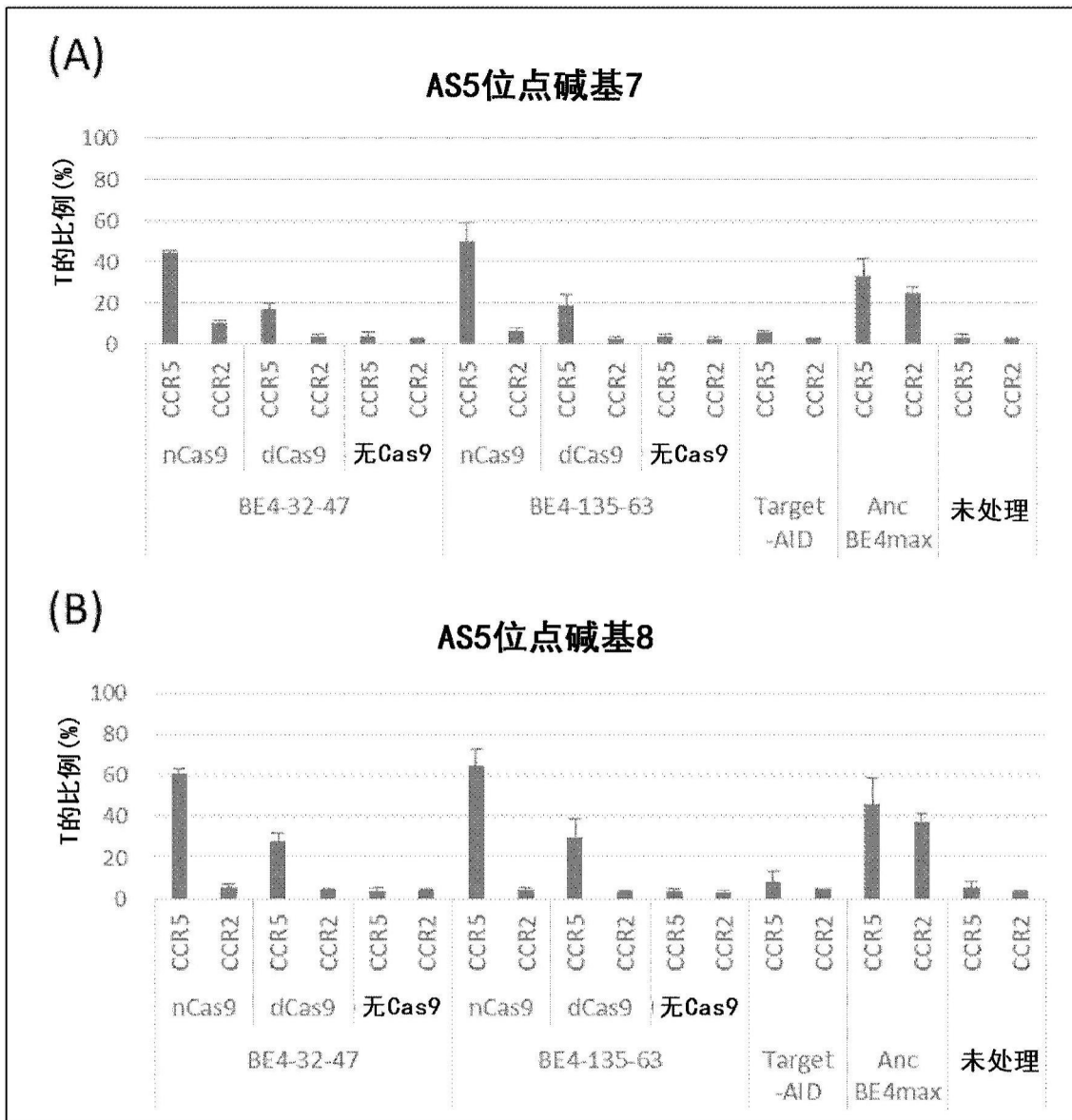


图17

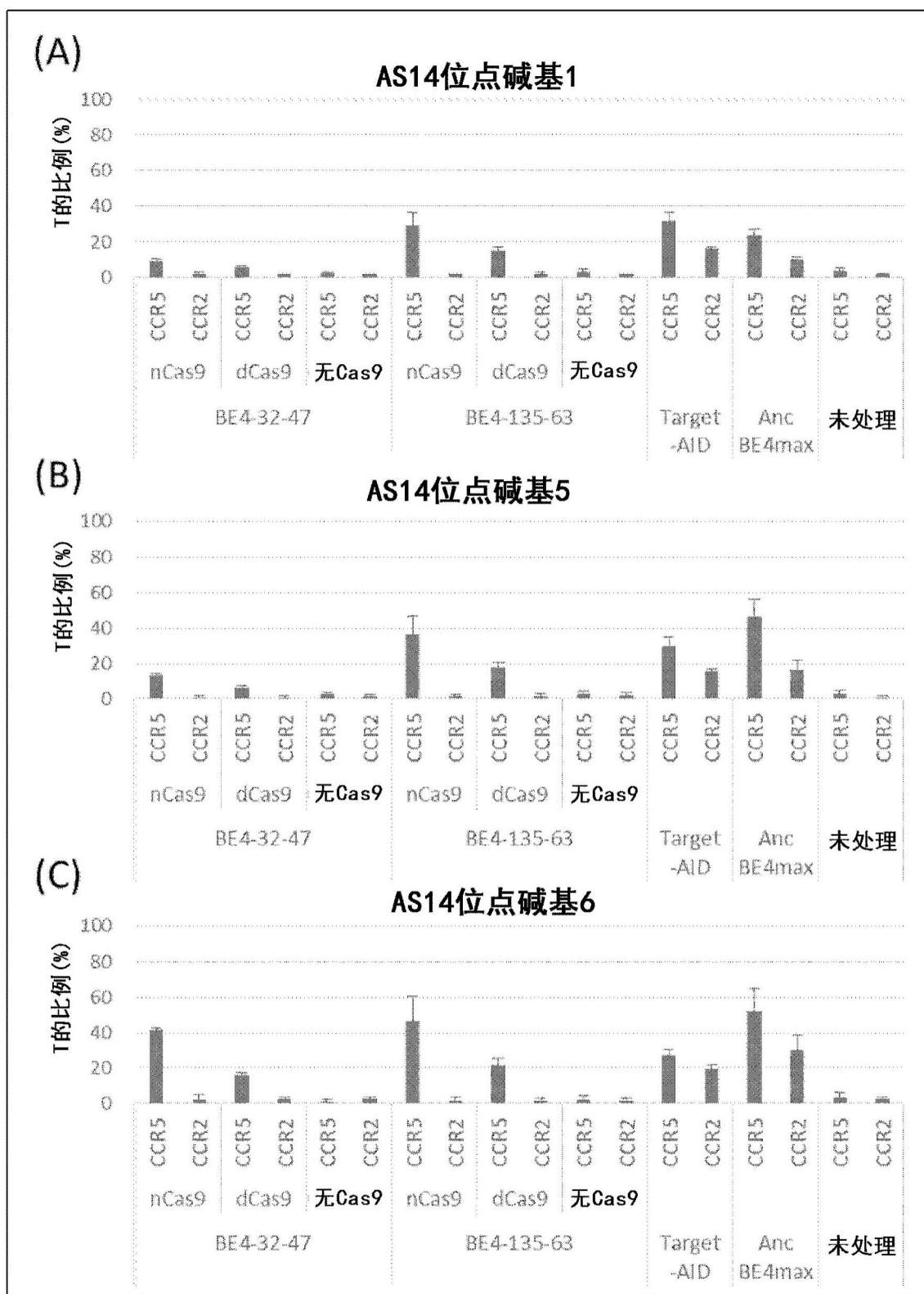


图18

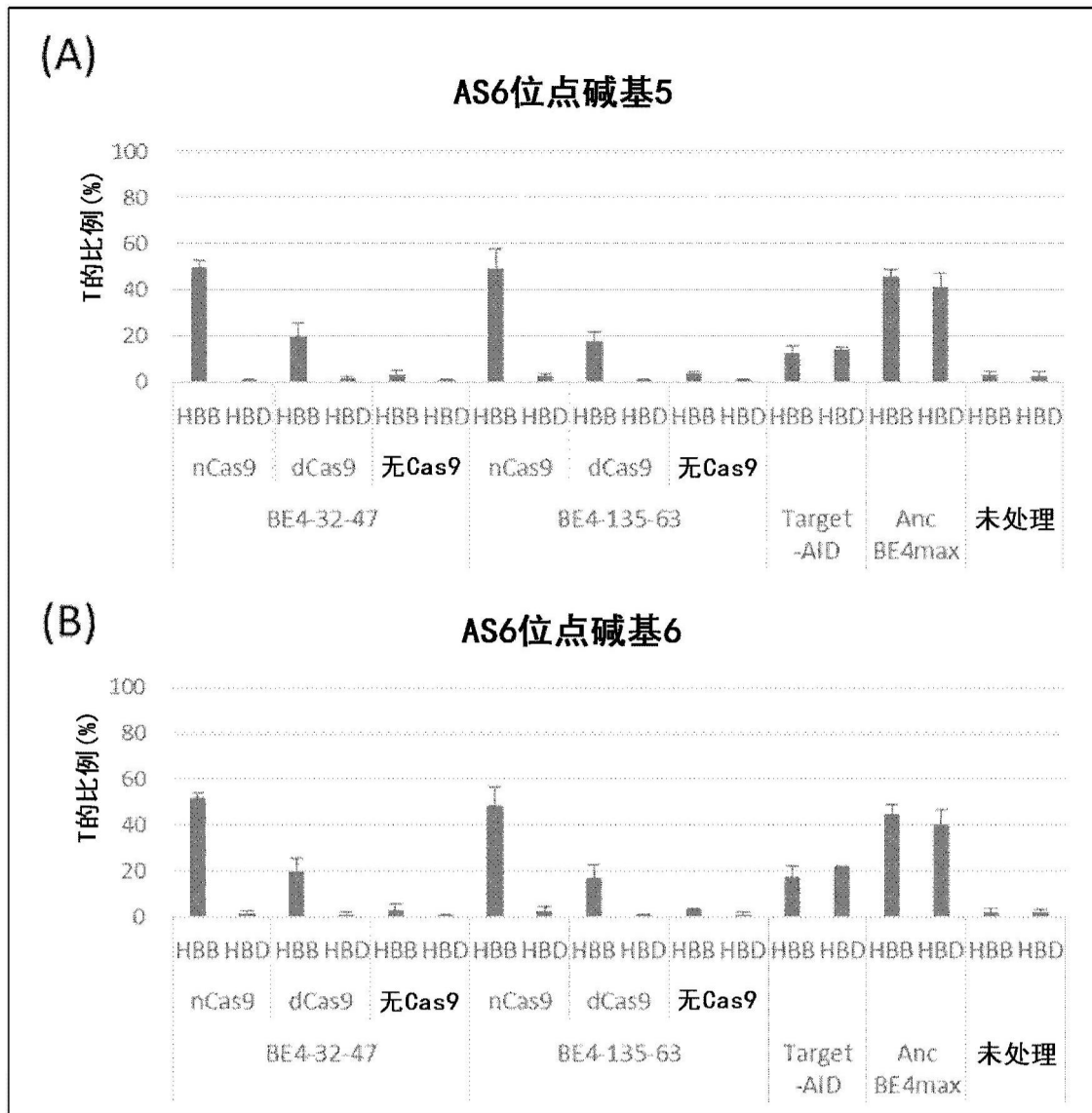


图19

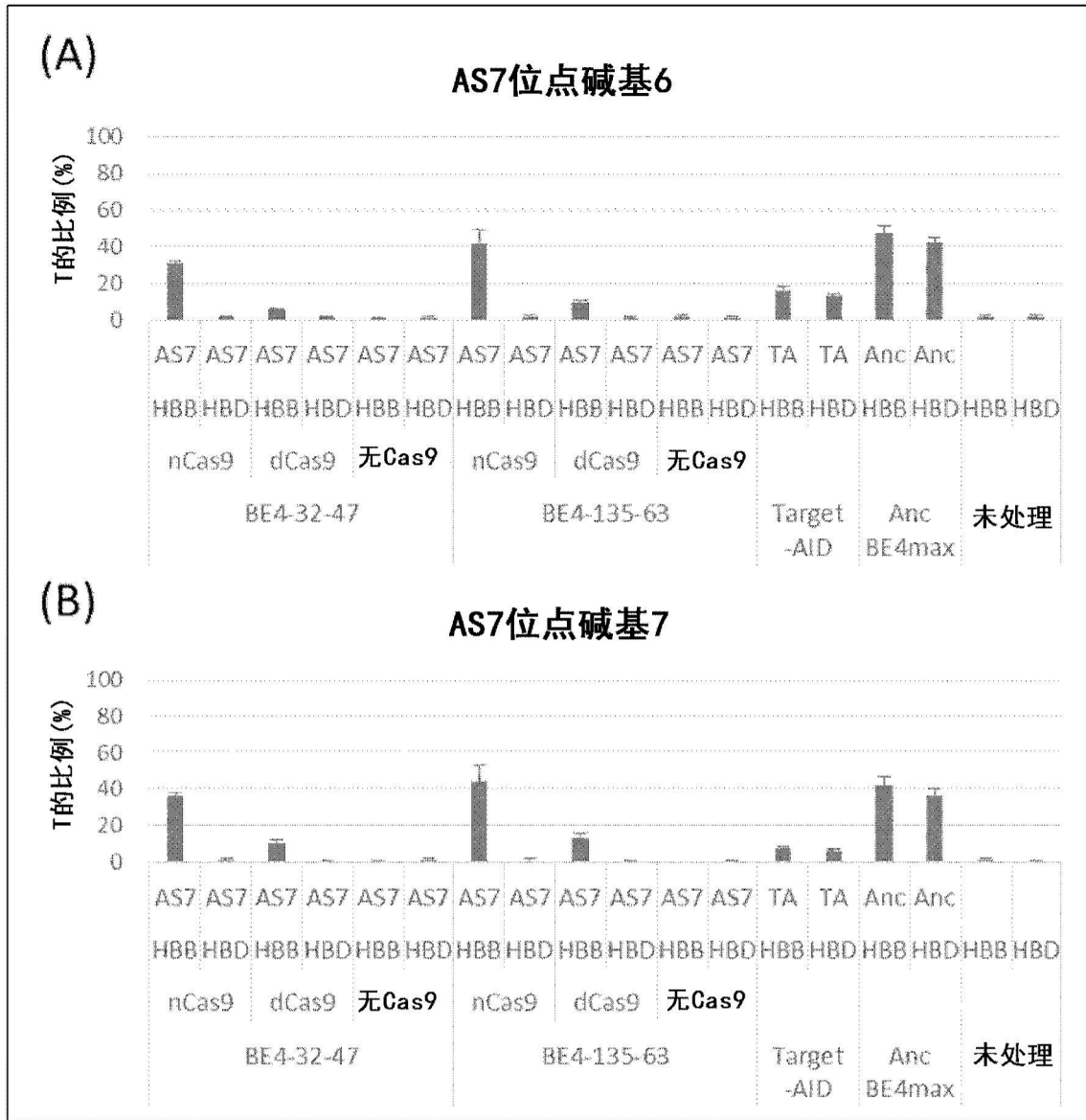


图20

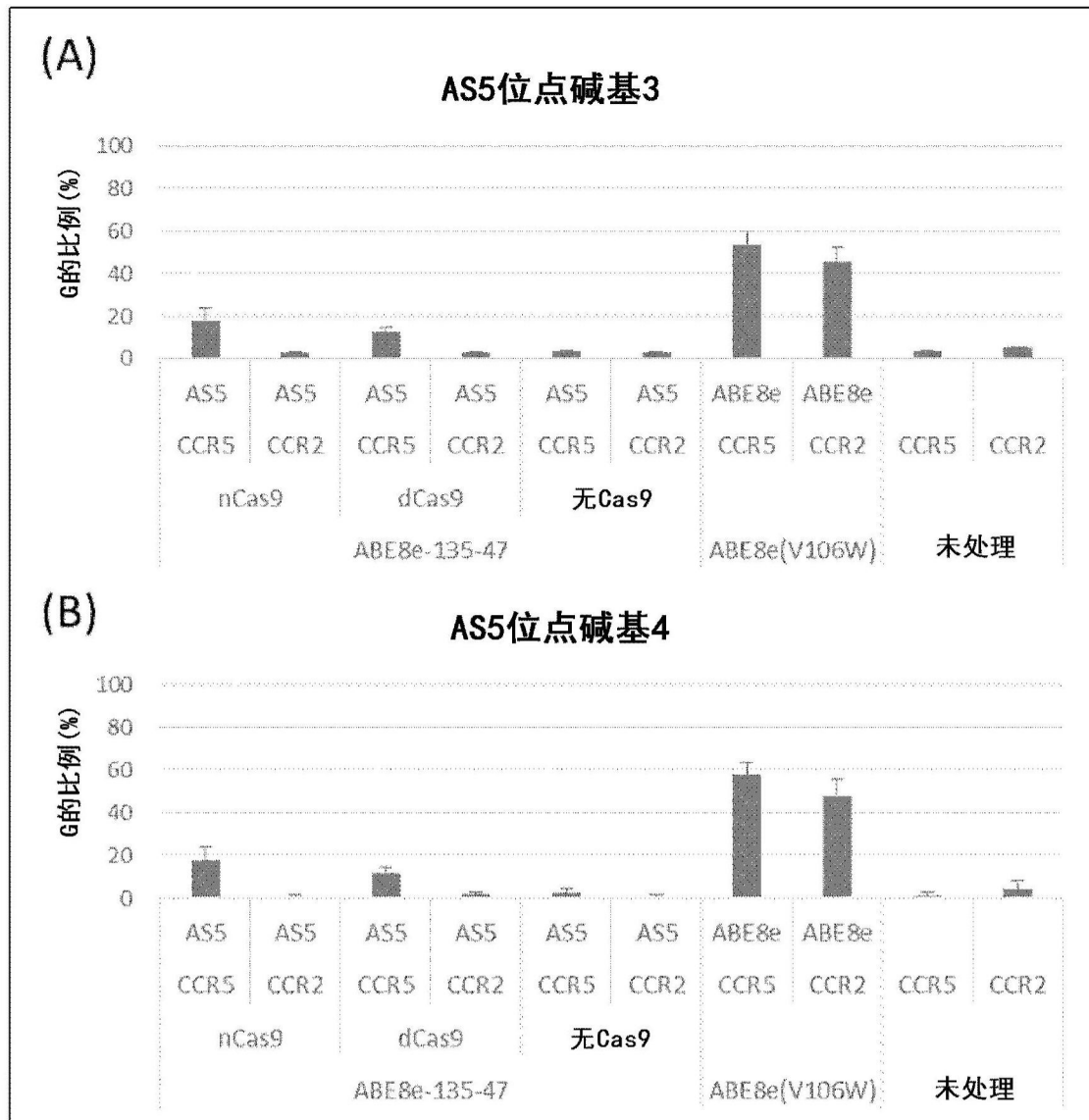


图21

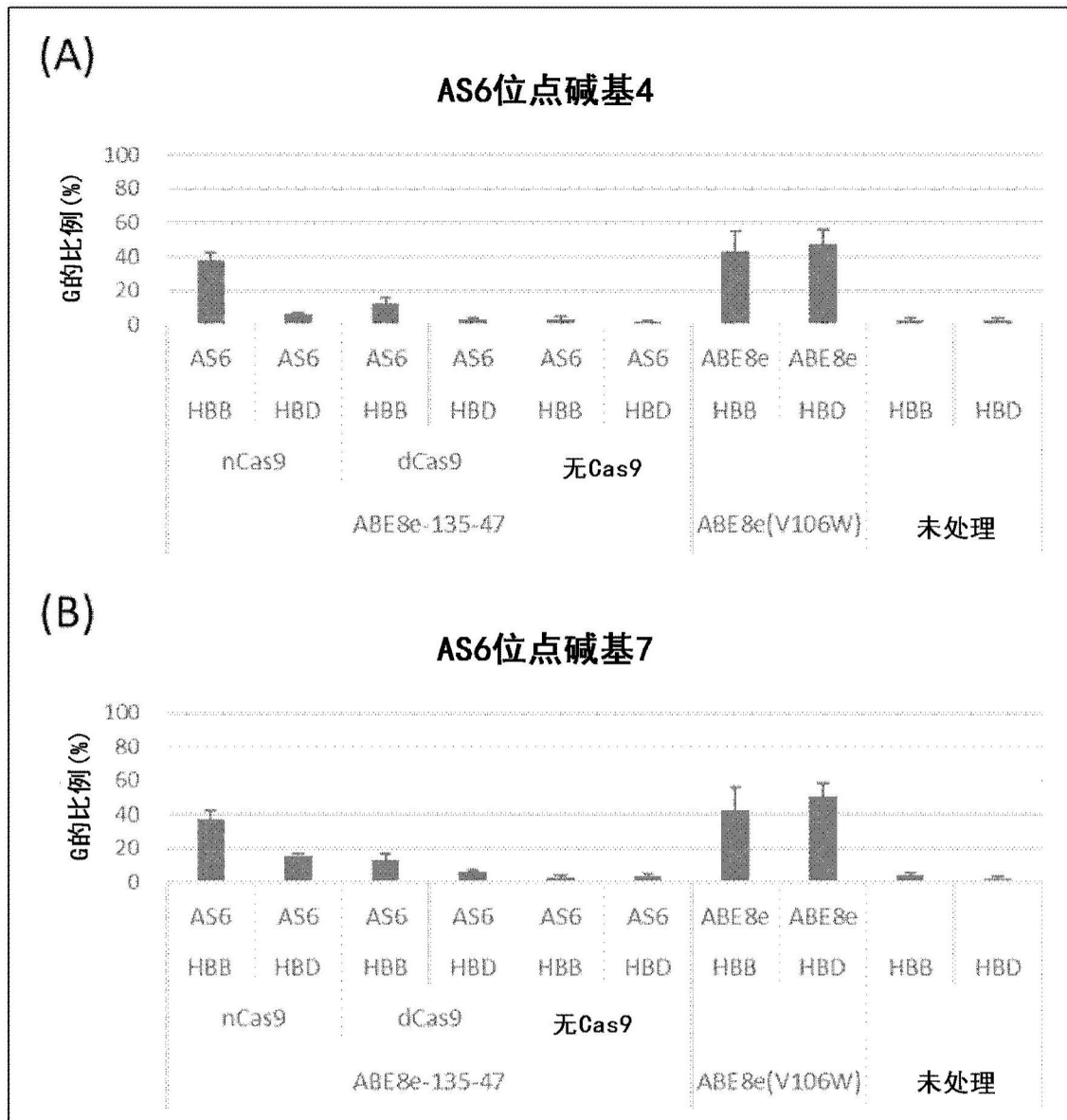


图22

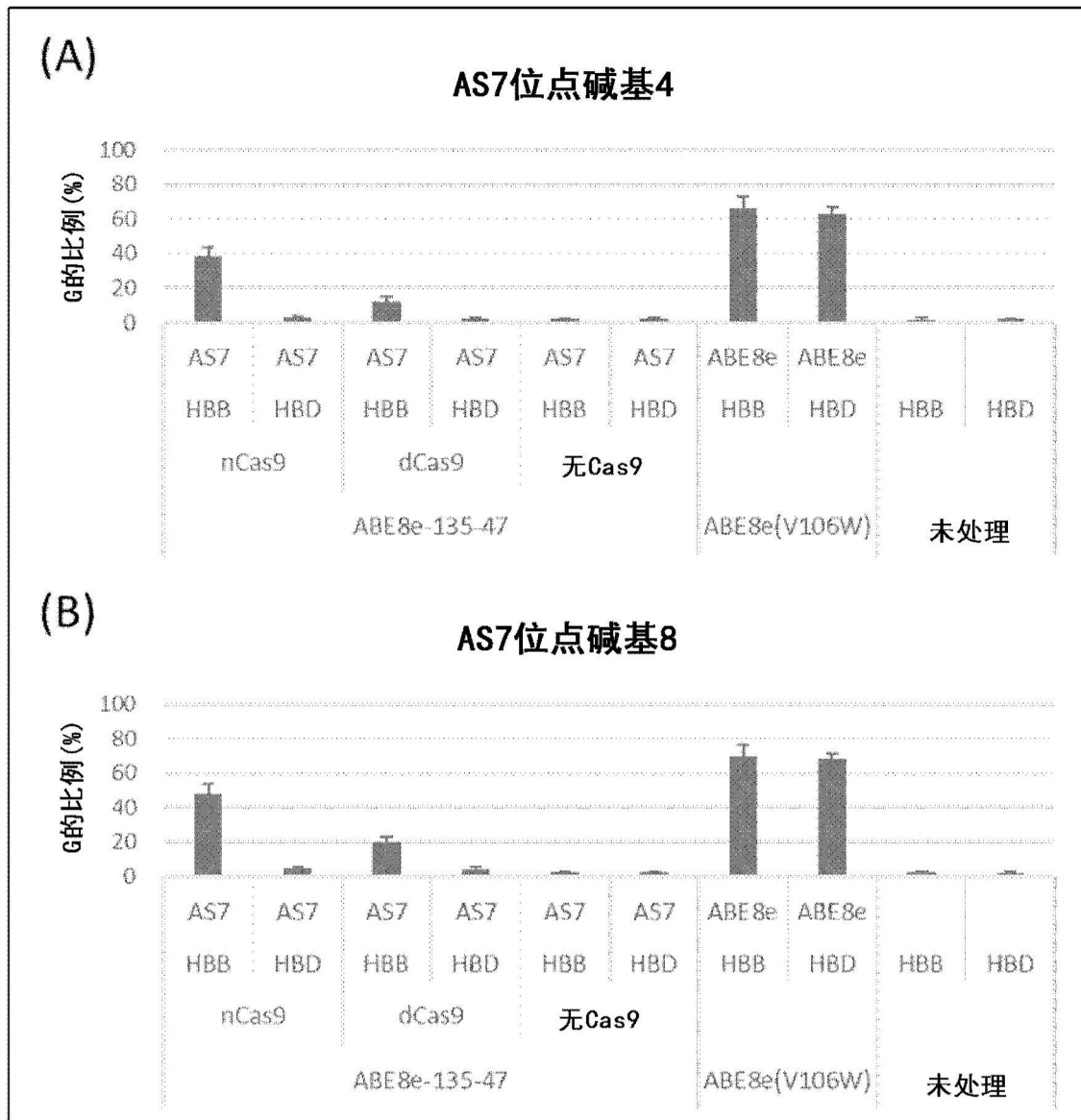


图23