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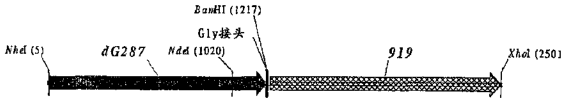
权利要求书 1 页 说明书 199 页 附图 6 页

(54) 发明名称

奈瑟球菌蛋白质的杂交表达

(57) 摘要

以单个杂交蛋白形式表达两种或多种奈瑟球菌的蛋白质（如 A 和 B），其可以式 NH_2-A-B-COOH 简单地表示。



权利要求书

1. 式NH_2-A-B-COOH的杂交蛋白，其特征在于，所述的A含ΔG287，B含953，所述杂交蛋白的氨基酸序列如SEQ ID NO:6所示。

2. 如权利要求1所述的蛋白质，其特征在于，所述的ΔG287来自脑膜炎奈瑟氏球菌菌株2996或394/98。

3. 如权利要求1所述的蛋白质，其特征在于，所述953来自脑膜炎奈瑟氏球菌菌株2996或394/98。

4. 如权利要求1所述的蛋白质，其特征在于，所述的A和B来自相同的菌株。

5. 如权利要求1所述的蛋白质，其特征在于，所述杂交蛋白的氨基酸序列如SEQ ID NO:6所示。

奈瑟球菌蛋白质的杂交表达

[0001] 本案是2001.02.28提交的申请号为01808738.8，名为奈瑟球菌蛋白质的杂交表达的分案申请。本文将所引用的全部文献都纳入作为参考。

技术领域

[0002] 本发明涉及蛋白质表达的领域。具体说，本发明涉及奈瑟球菌（如淋病奈瑟球菌或较佳地为脑膜炎奈瑟球菌）的蛋白质的异源表达。

背景技术

[0003] 国际专利申请WO99/24578、WO99/36544、WO99/57280和WO00/22430公开了脑膜炎奈瑟球菌(Neisseria meningitidis)和淋病奈瑟球菌(Neisseriagonorrhoeae)的蛋白质。这些蛋白质一般是以N-未端GST-融合体或C-未端His-标记融合体在大肠杆菌中表达的（即异源表达），虽然也公开了其它表达系统（包括在天然的奈瑟球菌中的表达）。

[0004] 本发明的目的是提供这些蛋白质的异源表达的其它或改进方法。这些方法通常影响表达的水平、纯化的简易程度、表达的细胞内定位和/或表达的蛋白质的免疫学特性。

[0005] 发明的公开

[0006] 在本发明中，以单杂交蛋白表达本发明的两种或多种（如3、4、5、6或更多）蛋白质。较佳地，不使用非奈瑟球菌的融合配体（如GST或聚-His）。

[0007] 这有两个优点。其一，可能不稳定或本身表达很差的蛋白质可以通过加入合适的克服该问题的杂交配体予以帮助。其二，简化工业生产，即制备两种分别有用的蛋白质只需要一次表达和纯化。

[0008] 因此，本发明提供了同时异源表达本发明的两种或多种蛋白质的方法，其中所述的本发明的两种或多种蛋白质是融合的（即，它们是作为单多肽链翻译的）。

[0009] 该方法通常包括如下步骤：获得编码本发明第一种蛋白质的第一核酸；获得编码本发明第二种蛋白质的第二核酸；连接第一和第二核酸。将得到的核酸插入表达载体中，或已作为表达载体的一部分。

[0010] 当仅连接两种蛋白质时，可以式NH_2-A-B-COOH简单地表示杂交蛋白。A和B各选自任何奈瑟球菌蛋白质，尤其是那些以SEQ#1-4326表示的。该方法非常适合表达蛋白质orf1、orf4、orf25、orf40、Orf46/46.1、orf83、233、287、292L、564、687、741、907、919、953、961和983。

[0011] 由式NH_2-A-B-COOH在下表中以‘X’表示的42个杂交体是优选的：

[0012]

↓ AB →	ORF46.1	287	741	919	953	961	983
ORF46.1		×	×	×	×	×	×
287	×		×	×	×	×	×
741	×	×		×	×	×	×
919	×	×	×		×	×	×
953	×	×	×	×		×	×

961	×	×	×	×	×		×
983	×	×	×	×	×	×	

[0013] 因此，优选的以杂交体表达的蛋白质是ORF46.1，287，741，919，953，961和983。它们可以全长形式或多-甘氨酸缺失（△G）形式使用（如△G-287、△GTbp2、△G741、△G983等）、或以截短形式使用（如△1-287、△2-287等），或以结构域缺失的形式使用（如287B、287C、287BC、ORF46$_{1-433}$、ORF46$_{433-608}$、ORF46、961c等）等。

[0014] 特别优选的是：(a)含919和287的杂交蛋白；(b)含953和287的杂交蛋白；(c)含287和ORF46.1的杂交蛋白；(d)含ORF1和ORF46.1的杂交蛋白；(e)含919和ORF46.1的杂交蛋白；(f)含ORF46.1和919的杂交蛋白；(g)含ORF46.1、287和919的杂交蛋白；(h)含919和519的杂交蛋白；和(i)含ORF97和225的杂交蛋白。

[0015] 附图中显示了其它优选例，它们包括△G287-919、△G287-953、△G287-961、△G983-ORF46.1、△G983-741、△G983-961、△G983-961C、△G741-961、△G741-961C、△G741-983、△G741-ORF46.1、ORF46.1-741、ORF46.1-961、ORF46.1-961C、961-ORF46.1、961-741、961-983、961C-ORF46.1、961C-741、961C-983、961CL-ORF46.1、961CL-741和961CL-983。

[0016] 当使用287时，其优先位于杂交体的C-末端；如果在N-末端使用它，则优先使用287的△G形式（如与ORF46.1、919、953或961杂交的杂交体的N-末端）。

[0017] 当使用287时，其优先为菌株2996或菌株394/98的。

[0018] 当使用961时，其优先在N-末端。可使用961的结构域形式。

[0019] WO99/66741公开了ORF46、287、919和953的多态形式的排序。本发明可以使用这些多态形式中的任一形式。

[0020] 较佳地，本发明杂交蛋白中的组成蛋白质(A和B)来源于是同一菌株。

[0021] 杂交体中的融合蛋白可以是直接相连的，或者是通过接头肽相连的，如通过聚-甘氨酸接头（即，Gn，其中n＝3、4、5、6、7、8、9、10或更多）或通过协助克隆的短肽序列相连。显然不宜将△G蛋白质连接于聚-甘氨酸接头的C-末端。

[0022] 融合蛋白可以缺失天然前导肽或可以包含N-末端融合配体的前导肽序列。

[0023] 宿主

[0024] 较佳地，利用异源宿主。异源宿主可以是原核的或真核的。优先为大肠杆菌，但其它合适的宿主包括枯草芽孢杆菌(Bacillus subtilis)、霍乱弧菌(Vibriocholerae)、伤寒沙门氏菌(Salmonella typhi)、鼠伤寒沙门氏菌(salmonellatyphimurium)、脑膜炎奈瑟球菌、淋病奈瑟球菌、乳糖奈瑟球菌(Neisserialactamica)、灰色奈瑟球菌(Neisseria cinerea)、分枝杆菌（如结核分枝杆菌(M.tuberculosis)、酵母等。

[0025] 载体、宿主等

[0026] 如上所述的方法，本发明提供了(a)用于这些方法的核酸和载体；(b)含所述载体的宿主细胞；(c)可用这些方法表达的或可表达的蛋白质；(d)包含这些蛋白质的组合物，其可能适合作为疫苗、或例如诊断剂或免疫原性的组合物；(e)用作药物（如疫苗）或诊断剂的组合物；(f)这些组合物在制备以下物质中的用途(1)用于治疗或预防奈瑟球菌引起的感染的药物(2)检测奈瑟球菌或由奈瑟球菌引起的抗体存在与否的诊断剂，和/或(3)能产生抗奈瑟球菌抗体的药物；和(g)治疗患者的方法，其包括对该患者施用治疗有效量

的这些组合物。

[0027] 序列

[0028] 本发明还提供了具有以下实施例中所列出的任何的蛋白质或核酸。本发明还提供了具有与这些序列是序列相同性的蛋白质和核酸。如上所述,“序列相同性”的程度最好大于 50%(如 60%、70%、80%、90%、95%、99%或更大)。

[0029] 本文的命名

[0030] 本文参考在 WO99/24578、WO99/36544 和 WO99/57280 中公开的 2166 个蛋白质序列,并将它们编号为如下的 SEQ#:

[0031]

申请	蛋白质序列	本文的 SEQ#
WO99/24578	偶 SEQ ID2-892	SEQ#1-446
WO99/36544	偶 SEQ ID2-90	SEQ#447-491
WO99/57280	偶 SEQ ID2-3020 偶 SEQ ID3040-3114 SEQ ID3115-3241	SEQ#492-2001 SEQ#2002-2039 SEQ#2040-2166

[0032] 除了这种 SEQ# 编号外,本文还使用了 WO99/24578、WO99/36544 和 WO99/27280 中的命名约定(如 WO99/24578 和 WO99/36544 中用的‘ORF4′、‘ORF40′、‘OFR40-1′等;WO99/57280 中用的‘m919′、‘g919′和‘a919′等)。

[0033] 在本文中将 Tettelin 等 [Science(2000)287:1809-1815] 中的从 NMB0001 到 NMB2160 的 2160 个蛋白质称为 SEQ#2167-4326[参见 WO00/66791]。

[0034] 本文采用的术语“本发明的蛋白质”指包含以下的蛋白质:

[0035] (a)SEQ#1-4326 中的一个序列;或

[0036] (b) 与 SEQ#1-4326 中的一个序列相同的序列;或

[0037] (c)SEQ#1-4326 中的一个序列的片段。

[0038] (b) 中的“序列相同性”的程度最好大于 50%(如 60%、70%、80%、90%、95%、99%或更大)。其包括突变体和等位基因变体 [如,参见 WO00/66741]。相同性最好用 Smith-Waterman 同源性搜寻算法确定,如在 MPSRCH 程序 (OxfordMolecular) 中执行的,采用参数“缺口罚分 (gap open penalty)”为 12,“缺口延伸罚分 (gap extension penalty)”为 1 进行缺口仿射搜索。通常,将两种蛋白质之间 50%或更高的相同性视为功能等效的指示。

[0039] (c) 中的“片段”应包含 SEQ#1-4326 中一个序列的至少 n 个连续的氨基酸,且根据具体的序列 n 为 7 或更高(如 8、10、12、14、16、18、20、25、30、35、40、50、60、70、80、90、100 或更高)。较佳地,片段包含 SEQ#1-4326 中一个序列的表位。优选的片段是在 WO00/71574 和 WO01/04316 中公开的那些。

[0040] 本发明优选的蛋白质是在脑膜炎奈瑟球菌血清群 B 中发现的。

[0041] 根据本发明使用的优选蛋白质是血清群 B 脑膜炎奈瑟球菌菌株 2996 或菌株 394/98(新西兰菌株)。除非特别指出,本文所述的蛋白质是脑膜炎奈瑟球菌菌株 2996 的蛋白质。但是,应该理解通常本发明并不受菌株的限制。参考具体的蛋白质(如‘287′、‘919′等)可以包括任何菌株的该蛋白质。

[0042] 应该理解术语“核酸”包括 DNA 和 RNA,以及它们的类似物,如含有修饰骨架的那些

类似物，还包括肽核酸（PNA）等。

[0043] 附图简述

[0044] 图 1-26 显示本发明的杂交蛋白。

[0045] 本发明的进行模式

[0046] 实施例 1-ORF46 的杂交体

[0047] 脑膜炎奈瑟球菌（血清群 B，菌株 2996）的完整 ORF46 蛋白质具有如下序列：

[0048] 1 LGISRKISLI LSILAVCLPM HAHASDLAND SFIRQVLDRQ HFEPDGKYHL

[0049] 51 FGSRGELAER SGHIGLGKIQ SHQLGNLMIQ QAAIKGNIGY IVRFSDHGHE

[0050] 101 VHSPFDNHAS HSDSDEAGSP VDGFSLYRIH WDGYEHHPAD GYDGPQGGGY

[0051] 151 PAPKGARDIY SYDIKGVAQN IRLNLTDATRS TGQRLADRFH NAGSMLTQGV

[0052] 201 GDGFKRATRY SPELDRSGNA AEAFNGTADI VKNIIGAAGE IVGAGDAVQG

[0053] 251 ISEGSNIAVM HGLGLLSTEN KMARINDLAD MAQLKDYAAA AIRDWAVQNP

[0054] 301 NAAQGIEAVS NIFMAAIPIK GICAVRGKYG LGGITAHPIK RSQMGAIALP

[0055] 351 KGKSAVSDNF ADAAYAKYPS PYHSRNIRSN LEQRYGKENI TSSTVPPSNG

[0056] 401 KNVKLADQRH PKTGVPFDGK GFPNFEKHVK YDTKLDIQEL SGGGIPKAKP

[0057] 451 VSDAKPRWEV DRKLNKLTTR EQVEKNVQET RNGNKNSNFS QHAQLEREIN

[0058] 501 KLKSADEINF ADGMGKFTDS MNDKAFSRLV KSVKENGFTN PVVEYVEING

[0059] 551 KAYIVRGNNR VFAAEYLGRI HELKFKKVDF PVPNTSWKNP TDVLNESGNV

[0060] 601 KRPRYRSK*

[0061] 在前导肽下加下划线。

[0062] 可以在 WO00/66741 中发现其它菌株的 ORF46 的序列。

[0063] ORF46 在其 C- 末端和 N- 末端与 287、919 和 ORF1 融合。该杂交蛋白通常是不溶解的，但产生一些良好的 ELISA 和杀菌结果（针对同源 2996 菌株）：

[0064]

蛋白质	ELISA	杀菌 Ab
Orf1-Orf46.1-His	850	256
919-Orf46.1-His	12900	512
919-287-Orf46-His	n. d.	n. d.
Orf46.1-287His	150	8192
Orf46.1-919His	2800	2048
Orf46.1-287-919His	3200	16384

[0065] 为了比较，构建了 ORF46.1、287（以 GST 融合体或△ G287 的形式）和 919 的“三”杂交体，并针对各种菌株（包括同源 2996 菌株）将其与三种抗原的简单混合物相比。FCA 用作佐剂：

[0066]

	2996	BZ232	MC58	NGH38	F6124	BZ133
混合物	8192	256	512	1024	>2048	>2048
ORF46.1-287-919his	16384	256	4096	8192	8192	8192
AG287-919-ORF46.1his	8192	64	4096	8192	8192	16384
AG287-ORF46.1-919his	4096	128	256	8192	512	1024

[0067] 同样，这些杂交体显示相当等的或更佳的免疫活性。

[0068] 针对各种异源菌株，将两种蛋白质（菌株 2996）的杂交体与单种蛋白质相比：

[0069]

	1000	MC58	F6124(MenA)
ORF46.1-His	<4	4096	<4
ORF1-His	8	256	128
ORF1—ORF46.1-His	1024	512	1024

[0070] 再次，这些杂交体显示相等的或更佳的免疫活性。

[0071] 实施例 2-△ G287 的杂交体

[0072] 发现 287 中 (Gly)$_6$ 序列的缺失对蛋白质的表达有显著影响。将缺失 N- 未端氨基酸多达 GGGGGG 的蛋白质称为‘△ G287’。在菌株 MC58 中，它的基本序列（前导肽有下划线）为：

[0073] SPDVKS ADTLSKPAAP VVSEKETEAK EDAPQAGSQG QGAPSAQGSQ DMAAVSEENT

[0074] GNGGAVTADN PKNEDEVAQN DMPQNAAGTD SSTPNHTPDP NMLAGNMENQ ATDAGESSQP

[0075] ANQPDMANAA DGMQGDDPSA GGQNAGNTAA QGANQAGNNQ AAGSSDPIPA SNPAPANGGS

[0076] NFGRVDLANG VLIDGPSQNI TLTHCKGDSC SGNNFLDEEV QLKSEFEKLS DADKISNYKK

[0077] DGKNDKFVGL VADSVQMKGI NQYIIFYKPK PTSFARFRRS ARSRRSLPAE MPLIPVNQAD

[0078] TLIVDGEAVS LTGHSGNIFA PEGNYRYLTY GAEKLPGGSY ALRVQGEPAK GEMLAGAAVY

[0079] NGEVLHFHTE NGRPYPTRGR FAAKVDFGSK SVDGIIDSGD DLHMGTQKFK AAIDGNGFKG

[0080] TWTENGSGDV SGKFYGPAGE EVAGKYSYRP TDAEKGGFGV FAGKEQD*

[0081] 与‘287-His’或‘287^{未标记的}’相比，有或无 His- 标记的△ G287（分别为‘△ G287-His’和‘△ G287K’）以很好的水平表达。

[0082] 在基因变异性数据的基础上，从许多 MenB 菌株（尤其是从菌株 2996、MC58、100 和 BZ232）的大肠杆菌中表达△ G287-His 的变体。结果也好 - 它们都具有很高的 ELISA 滴定度，且血清杀菌滴定度 >8192。由 pET-24b 表达的△ G287K 在 ELISA 和血清杀菌实验中有极佳滴定度。

[0083] 还将聚 -Gly 序列的缺失应用于 Tbp2(NMB0460)、741(NMB1870) 和 983(NMB1969)。在不编码其前导肽的序列且没有聚 -Gly（即，以“△ G 形式”），在 pET 载体中克隆并在大肠杆菌中表达时，观察到相同的作用 - 在携带聚 - 甘氨酸段缺失的克隆中表达很好，若在表达的蛋白中存在甘氨酸时则表达差或不表达。

[0084] 将△ G287 直接融合于 919、953、961（如下所示的序列）和 ORF46.1 的符合读框的上游：

[0085] ΔG287-919

[0086] ATGGCTAGCCCCGATGTTAAATCGGCCGGACACGCTGTCAAAACCGGCCGCTCCTGTTGTTGCTGAAAAGAGACAGAG

[0087] GTAAAAGAAGATCCGCCACAGGCAGGTTCTCAAGGACAGCCGCGCGCCATCCACACAAGGCAGCCAAGATATGCCGGCA

[0088] GTTTCGGCAGAAAATACACGCAATGGCGGTGCGGCAACAACGGACAAACCCAAAAATGAAGACGAGGGACCGCAAAAT

[0089] GATATGCCGCAAAATTCCGCCGAATCCGCAAATCAAACAGGGAACAACCAACCCGCCCATTCTTCAGATTCCGCCCCC

[0090] GCGTCAAACCCTGCACCTGCGAATGGCGGTAGCAATTTTGGAAGGGTTGATTTGGCTAATGGCGTTTTGATTGATGGG

[0091] CCGTCGCAAAATATAACGTTGACCCACTGTAAACGGCGATTCTTGTAATGGTGATAATTTATTGGATGAAGAAGCACCG

[0092] TCAAAATCAGAATTTGAAAATTTAAATGAGTCTGAACGAATTGAGAAATATAAGAAAGATGGGAAAAGCGATAAATTT

[0093] ACTAATTTGGTTGCGACAGCAGTTCAAGCTAATGGAACTAACAAATATGTCATCATTTATAAAGACAAGTCCGCTTCA

[0094] TCTTCATCTGCGCGATTCAGGCGTTCTGCACGGTCGAGGAGGTCGCTTCCTGCCGAGATGCCGCTAATCCCCGTCAAT

[0095] CAGGCGGATACGCTGATTGTCGATGGGGAAGCGGTCAGCCTGACGGGGCATTCCGGCAATATCTTCGCGCCCGAAGGG

[0096] AATTACCGGTATCTGACTTACGGGGCGGAAAAATTGCCCGGCGGATCGTATGCCCTCCGTGTGCAAGGCGAACCCGCA

[0097] AAAGGCGAAATGCTTGCTGGCACGGCCGTGTACAACGGCGAAGTGCTGCATTTTCATACGGAAAACGGCCGTCCGTAC

[0098] CCGACTAGAGGCAGGTTTGCCGCAAAAGTCGATTTCGGCAGCAAATCTGTGGACGGCATTATCGACAGCGGCGATGAT

[0099] TTGCATATGGGTACGCAAAAATTCAAAGCCGCCATCGATGGAAACGGCTTTAAGGGGACTTGGACGGAAAATGGCGGC

[0100] GGGGATGTTTCCGGAAGGTTTTACGGCCCGGCCGGCGAGGAAGTCGGCGGAAAATACAGCTATCGCCCGACAGATGCG

[0101] GAAAAGGGCGGATTCGGCGTGTTTGCCGGCAAAAAAGAGCAGGATGGATCCGGAGGAGGAGGATGCCAAAGCAAGAGC

[0102] ATCCAAACCTTTCCGCAACCCGACACATCCGTCATCAACGGCCCGGACCGGCCGGTCGGCATCCCCGACCCCGCCGGA

[0103] ACGACGGTCGGCGGCGGCGGGGCCGTCTATACCGTTGTACCGCACCTGTCCCTGCCCCACTGGGCGGCGCAGGATTTC

[0104] GCCAAAAGCCTGCAATCCTTCCGCCTCGGCTGCGCCAATTTGAAAAACCGCCAAGGCTGGCAGGATGTGTGCGCCCAA

[0105] GCCTTTCAAACCCCCGTCCATTCCTTTCAGGCAAAACAGTTTTTTGAACGCTATTTCACGCCGTGGCAGGTTGCAGGC

[0106] AACGGAAGCCTTGCCGGTACGGTTACCGGCTATTACGAGCCGGTGCTGAAGGGCGACGACAGGCGGACGGCACAAGCC

[0107] CGCTTCCCGATTTACGGTATTCCCGACGATTTTATCTCCGTCCCCCTGCCTGCCGGTTTGCGGAGCGGAAAAGCCCTT

[0108] GTCCGCATCAGGCAGACGGGAAAAAACAGCGGCACAATCGACAATACCGGCGGCACACATACCGCCGACCTCTCCCGA

[0109] TTCCCCATCACCGCGCGCACAACGGCAATCAAAGGCAGGTTTGAAGGAAGCCGCTTCCTCCCCTACCACACGCGCAAC

[0110] CAAATCAACGGCGGCGCGCTTGACGGCAAAGCCCCGATACTCGGTTACGCCGAAGACCCCGTCGAACTTTTTTTTATG

[0111] CACATCCAAGGCTCGGGCCGTCTGAAAACCCCGTCCGGCAAATACATCCGCATCGGCTATGCCGACAAAAACGAACAT

[0112] CCCTACGTTTCCATCGGACGCTATATGGCGGACAAAGGCTACCTCAAGCTCGGGCAGACCTCGATGCAGGGCATCAAA

[0113] GCCTATATGCGGCAAAATCCGCAACGCCTCGCCGAAGTTTTGGGTCAAAACCCCAGCTATATCTTTTTCCGCGAGCTT

[0114] GCCGGAAGCAGCAATGACGGTCCCGTCGGCGCACTGGGCACGCCGTTGATGGGGGAATATGCCGGCGCAGTCGACCGG

[0115] CACTACATTACCTTGGGCGCGCCCTTATTTGTCGCCACCGCCCATCCGGTTACCCGCAAAGCCCTCAACCGCCTGATT

[0116] ATGGCGCAGGATACCGGCAGCGCGATTAAAGGCGCGGTGCGCGTGGATTATTTTGGGGATACGGCGACGAAGCCGGC

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[0118] TAACTCGAG

[0119] 1 MASPDVKSAD TLSKPAAPVV AEKETEVKED APQAGSQGQG APSTQGSQDM

[0120] 51 AAVSAENTGN GGAATTDKPK NEDEGPQNDM PQNSAESANQ TGNNQPADSS

[0121] 101 DSAPASNPAP ANGGSNFGRV DLANGVLIDG PSQNITLTHC KGDSCNGDNL

[0122] 151 LDEEAPSKSE FENLNESERI EKYKKDGKSD KFTNLVATAV QANGTNKYVI

[0123] 201 IYKDKSASSS SARFRRSARS RRSLPAEMPL IPVNQADTLI VDGEAVSLTG

[0124] 251 HSGNIFAPEG NYRYLTYGAE KLPGGSYALR VQGEPAKGEM LAGTAVYNGE

[0125] 301 VLHFHTENGR PYPTRGRFAA KVDFGSKSVD GIIDSGDDLH MGTQKFKCAAI

[0126] 351 DGNGFKGTWT ENGGGDVSGR FYGPACEEVA GKYSYRPTDA EKGGFGVFAG

[0127] 401 KKEQDGSGGG GCQSKSIQTF PQPDTSVING PDRPVGIPDP AGTTVGGGGA

[0128] 451 VYTVVPHLSL PHWAAQDFAK SLQSFRLGCA NLKNRQGWQD VCAQAFQTPV

[0129] 501 HSFQAKQFFE RYFTPWQVAG NGSLAGTVTG YYEPVLKGDD RRTAQARFPI

[0130] 551 YGIPDDFISV PLPAGLRSGK ALVRIRQTGK NSGTIDNTGG THTADLSRFP

[0131] 601 ITARTTAIKG RFEGSRFLPY HTRNQINGGA LDGKAPILGY AEDPVELFFM

[0132] 651 HIQGSGRLKT PSGKYIRIGY ADKNEHPYVS IGRYMADKGY LKLGQTSMQG

[0133] 701 IKAYMRQNPQ RLAEVLGQNP SYIFFRELAG SSNDGPVGAL GTPLMGEYAG

[0134] 751 AVDRHYITLG APLFVATAHP VTRKALNRLI MAQDTGSAIK GAVRVDYFWG

[0135] 801 YGDEAGELAG KQKTTGYVWQ LLPNGMKPEY RP*

[0136] ΔG287-953

[0137] ATGGCTAGCCCCGATGTTAAATCGGCGGACACGCTGTCAAAACCGGCCGCTCCTGTTGTTGCTGAAAAAGAGACAGAG

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[0139] GTTTCGGCAGAAAATACAGGCAATGGCGGTGCGGCAACAACGGACAAACCCAAAAATGAAGACGAGGGACCGCAAAAT

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[0141] GCGTCAAACCCTGCACCTGCGAATGGCGGTAGCAATTTTGGAAGGGTTGATTTGGCTAATGGCGTTTTGATTGATGGG

[0142] CCGTCGCAAAATATAACGTTGACCCACTGTAAAGGCGATTCTTGTAATGGTGATAATTTATTGGATGAAGAAGCACCG

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[0144] ACTAATTTGGTTGCGACAGCAGTTCAAGCTAATGGAACTAACAAATATGTCATCATTTATAAAGACAAGTCCGCTTCA

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[0146] CAGGCGGATACGCTGATTGTCGATGGGGAAGCGGTCAGCCTGACGGGGCATTCCGGCAATATCTTCGCGCCCGAAGGG

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[0157] GTCAAACTCAAAGCCGAAAAATTCAACTGCTACCAAAGCCCGATGGCGAAAACCGAAGTTTGCGGCGGCGACTTCAGC

[0158] ACCACCATCGACCGCACCAAATGGGGCGTGGACTACCTCGTTAACGTTGGTATGACCAAAAGCGTCCGCATCGACATC

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[0160] 1 MASPDVKSAD TLSKPAAPVV AEKETEVKED APQAGSQGQG APSTQGSQDM

[0161] 51 AAVSAENTGN GGAATTDKPK NEDEGPQNDM PQNSAESANQ TGNNQPADSS

[0162] 101 DSAPASNPAP ANGGSNFGRV DLANGVLIDG PSQNITLTHC KGDSCNGDNL

[0163] 151 LDEEAPSKSE FENLNESERI EKYKKDGKSD KFTNLVATAV QANGTNKYVI

[0164] 201 IYKDKSASSS SARFRRSARS RRSLPAEMPL IPVNQADTLI VDGEAVSLTG

[0165] 251 HSGNIFAPEG NYRYLTYGAE KLPGGSYALR VQGEPAKGEM LAGTAVYNGE

[0166] 301 VLHFHTENGR PYPTRGRFAA KVDFGSKSVD GIIDSGDDLH MGTQKFKAAI

[0167] 351 DGNGFKGTWT ENGGGDVSGR FYGPAGEEVA GKYSYRPTDA EKGGFGVFAG

[0168] 401 KKEQDGSGGG GATYKVDEYH ANARFAIDHF NTSTNVGGFY GLTGSVEFDQ

[0169] 451 AKRDGKIDIT IPVANLQSGS QHFTDHLKSA DIFDAAQYPD IRFVSTKFNF

[0170] 501 NGKKLVSVDG NLTMHGKTAP VKLKAEKTNC YQSPMAKTEV CGGDFSTTID

[0171] 551 RTKWGVDYLV NVGMTKSVRI DIQIEAAKQ*

[0172] ΔG287-961

[0173] ATGGCTAGCCCCGATGTTAAATCGGCGGACACGCTGTCAAAACCGGCCGCTCCTGTTGTTGCTGAAAAAGAGACAGAG

[0174] GTAAAAGAAGATGCGCCACAGGCAGGTTCTCAAGGACAGGGCGCGCCATCCACACAAGGCAGCCAAGATATGGCGGCA

[0175] GTTTCGGCAGAAAATACAGGCAATGGCGGTGCGGCAACAACGGACAAACCCAAAAATGAAGACGAGGGACCGCAAAAT

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[0184] AAAGGCGAAATGCTTGCTGGCACGGCCGTGTACAACGGCGAAGTGCTGCATTTTCATACGGAAAACGGCCGTCCGTAC

[0185] CCGACTAGAGGCAGGTTTGCCGCAAAAGTCGATTTCGGCAGCAAATCTGTGGACGGCATTATCGACAGCGGCGATGAT

[0186] TTGCATATGGGTACGCAAAAATTCAAAGCCGCCATCGATGGAAACGGCTTTAAGGGGACTTGGACGGAAAATGGCGGC

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[0190] GAGACCATCTACGACATTGATGAAGACGGCACAATTACCAAAAAAGACGCAACTGCAGCCGATGTTGAAGCCGACGAC

[0191] TTTAAAGGTCTGGGTCTGAAAAAAGTCGTGACTAACCTGACCAAAACCGTCAATGAAAACAAACAAAACGTCGATGCC

[0192] AAAGTAAAAGCTGCAGAATCTGAAATAGAAAAGTTAACAACCAAGTTAGCAGACACTGATGCCGCTTTAGCAGATACT

[0193] GATGCCGCTCTGGATGCAACCACCAACGCCTTGAATAAATTGGGAGAAAATATAACGACATTTGCTGAAGAGACTAAG

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[0195] ATCGCCGATTCATTGGATGAAACCAACACTAAGGCAGACGAAGCCGTCAAAACCGCCAATGAAGCCAAACAGACGGCC

[0196] GAAGAAACCAAACAAAACGTCGATGCCAAAGTAAAAGCTGCAGAAACTGCAGCAGGCAAAGCCGAAGCTGCCGCTGGC

[0197] ACAGCTAATACTGCAGCCGACAAGGCCGAAGCTGTCGCTGCAAAAGTTACCGACATCAAAGCTGATATCGCTACGAAC

[0198] AAAGATAATATTGCTAAAAAAGCAAACAGTGCCGACGTGTACACCAGAGAAGAGTCTGACAGCAAATTTGTCAGAATT

[0199] GATGGTCTGAACGCTACTACCGAAAAATTGGACACACGCTTGGCTTCTGCTGAAAAATCCATTGCCGATCACGATACT

[0200] CGCCTGAACGGTTTGGATAAAACAGTGTCAGACCTGCGCAAAGAAACCCGCCAAGGCCTTGCAGAACAAGCCGCGCTC

[0201] TCCGGTCTGTTCCAACCTTACAACGTGGGTCGGTTCAATGTAACGGCTGCAGTCGGCGGCTACAAATCCGAATCGGCA

[0202] GTCGCCATCGGTACCGGCTTCCGCTTTACCGAAAACTTTGCCGCCAAAGCAGGCGTGGCAGTCGGCACTTCGTCCGGT

[0203] TCTTCCGCAGCCTACCATGTCGGCGTCAATTACGAGTGGTAACTCGAG

[0204] 1 MASPDVKSAD TLSKPAAPVV AEKETEVKED APQAGSQGQG APSTQGSQDM

[0205] 51 AAVSAENTGN GGAATTDKPK NEDEGPQNDM PQNSAESANQ TGNNQPADSS

[0206] 101 DSAPASNPAP ANGGSNFGRV DLANGVLIDG PSQNITLTHC KGDSCNGDNL

[0207] 151 LDEEAPSKSE FENLNESERI EKYKKDGKSD KFTNLVATAV QANGTNKYVI

[0208] 201 IYKDKSASSS SARFRRSARS RRSLPAEMPL IPVNQADTLI VDGGEAVSLTG

[0209] 251 HSGNIFAPEG NYRYLTYGAE KLPGGSYALR VQGEPAKGEM LAGTAVYNGE

[0210] 301 VLHFHTENGR PYPTRGRFAA KVDFGSKSVD GIIDSGDDLH MGTQKFKAAI

[0211] 351 DGNGFKGTWT ENGGGDVSGR FYGPAGEEVA GKYSYRPTDA EKGGFGVFAG

[0212] 401 KKEQDGSGGG GATNDDDVKK AATVAIAAAY NNGQEINGFK AGETIYDIDE

[0213] 451 DGTITKKDAT AADVEADDFK GLGLKKVVTN LTKTVNENKQ NVDAKVKAAE

[0214] 501 SEIEKLTTKL ADTDAALADT DAALDATTNA LNKLGENITT FAEETKTNIV

[0215] 551 KIDEKLEAVA DTVDKHAEAF NDIADSLDET NTKADEAVKT ANEAKQTAEE

[0216] 601 TKQNVDAKVK AAETAAGKAE AAAGTANTAA DKAEAVAAKV TDIKADIATN

[0217] 651 KDNIAKKANS ADVYTREESD SKFVRIDGLN ATTEKLDTRL ASAEKSIADH

[0218] 701 DTRLNGLDKT VSDLRKETRQ GLAEQAALSG LFQPYNVGRF NVTAAVGGYKC

[0219] 751 SESAVAIGTG FRFTENFAAK AGVAVGTSSG SSAAYHVGVN YEW*

[0220]

	ELISA	杀菌
△G287-953-His	3834	65536
△G287-961-His	108627	65536

[0221] 对 919 和 ORF46.1 而言，将针对杂交蛋白产生的抗体的杀菌效力（同源菌株）与针对组分抗原（用 287-GST）的简单混合物产生的抗体相比：

[0222]

	与 287 的混合物	与△G287 的杂交体
919	32000	128000
ORF46.1	128	16000

[0223] 还获得了针对异源 MenB 菌株和针对血清型 A 和 C 的杀菌活性的数据：

[0224]

	919		ORF46.1	
菌株	混合物	杂交体	混合物	杂交体
NGH38	**1024**	**32000**	**-**	**16384**
MC58	**512**	**8192**	**-**	**512**
BZ232	**512**	**512**	**-**	**-**
MenA (F6124)	**512**	**32000**	**-**	**8192**
MenC (C11)	**>2048**	**>2048**	**-**	**-**
MenC (BZ133)	**>4096**	**64000**	**-**	**8192**

[0225] 因此，在 N-末端与△G287 的杂交蛋白在免疫学上优于与△G287-ORF46.1 的简单混合物，即使针对异源菌株也特别有效。可以在 pET-24b 中表达△G287-ORF46.1。

[0226] 用新西兰菌株 394/98，而非 2996，制备相同的杂交蛋白：

[0227] ΔG287Nz-919

[0228] ATGGCTAGCCCCGATGTCAAGTCGGCGGACACGCTGTCAAAACCTGCCGCCCCTGTTGTTTCTGAAAAAGAGACAGAG

[0229] GCAAAGGAAGATGCGGCCACAGGCAGGTTCTCAAGGACAGGGCGCGCCATCCGCACAAGGCGGTCAAGATATGGCGGCG

[0230] GTTTCGGAAGAAAATACAGGCAATGGCGGTGCGGCAGCAACGGACAAACCCAAAAATGAAGACGAGGGGGCGCAAAAT

[0231] GATATGCCGCAAAATGCCGCCGATACAGATAGTTTGACACCGAATCACACCCCGGCTTCGAATATGCCGGCCGGAAAT

[0232] ATGGAAAACCAAGCACCGGATGCCGGGGAATCGGAGCAGCCGGCAAACCAACCGGATATGGCAAATACGGCGGACGGA

[0233] ATGCAGGGTGACGATCCGTCGGCAGGCGGGGAAAATGCCGGCAATACGGCTGCCCAAGGTACAAATCAAGCCGAAAAC

[0234] AATCAAACCGCCGGTTCTCAAAATCCTGCCTCTTCAACCAATCCTAGCGCCACGAATAGCGGTGGTGATTTTGGAAGG

[0235] ACGAACGTGGGCAATTCTGTTGTGATTGACGGGCCGTCGCAAAATATAACGTTGACCCACTGTAAAGGCGATTCTTGT

[0236] AGTGGCAATAATTTCTTGGATGAAGAAGTACAGCTAAAATCAGAATTTGAAAAATTAAGTGATGCAGACAAAATAAGT

[0237] AATTACAAGAAAGATGGGAAGAATGACGGGAAGAATGATAAATTTGTCGGTTTGGTTGCCGATAGTGTGCAGATGAAG

[0238] GGAATCAATCAATATATTATCTTTTATAAACCTAAACCCACTTCATTTGCGCGATTTAGGCGTTCTGCACGGTCGAGG

[0239] CGGTCGCTTCCGGCCGAGATGCCGCTGATTCCCGTCAATCAGGCGGATACGCTGATTGTCGATGGGGAAGCGGTCAGC

[0240] CTGACGGGGCATTCCGGCAATATCTTCGCGCCCGAAGGGAATTACCGGTATCTGACTTACGGGGCGGAAAAATTGCCC

[0241] GGCGGATCGTATGCCCTCCGTGTTCAAGGCGAACCTTCAAAAGGCGAAATGCTCGCGGGCACGGCAGTGTACAACGGC

[0242] GAAGTGCTGCATTTTCATACGGAAAACGGCCGTCCGTCCCCGTCCAGAGGCAGGTTTGCCGCAAAAGTCGATTTCGGC

[0243] AGCAAATCTGTGGACGGCATTATCGACAGCGGCGATGGTTTGCATATGGGTACGCAAAAATTCAAAGCCGCCATCGAT

[0244] GGAAACGGCTTTAAGGGGACTTGGACGGAAAATGGCGGCGGGGATGTTTCCGGAAAGTTTTACGGCCCGGCCGGCGAG

[0245] GAAGTGGCGGGAAAATACAGCTATCGCCCAACAGATGCGGAAAAGGGCGGATTCGGCGTGTTTGCCGGCAAAAAACAG

[0246] CAGGATGGATCCGGAGGAGGAGGATGCCAAAGCAAGAGCATCCAAACCTTTCCGCAACCCGACACATCCGTCATCAAC

[0247] GGCCCGGACCGGCCGGTCGGCATCCCCGACCCCGCCGGAACGACGGTCGGCGGCGGCGGGGCCGTCTATACCGTTGTA

[0248] CCGCACCTGTCCCTGCCCCACTGGGCGGCGCAGGATTTCGCCAAAAGCCTGCAATCCTTCCGCCTCGGCTGCGCCAAT

[0249] TTGAAAAACCGCCAAGGCTGGCAGGATGTGTGCGCCCAAGCCTTTCAAACCCCCGTCCATTCCTTTCAGGCAAAACAG

[0250] TTTTTTGAACGCTATTTCACGCCGTGGCAGGTTGCAGGCAACGGAAGCCTTGCCGGTACGGTTACCGGCTATTACGAG

[0251] CCGGTGCTGAAGGGCGACGACAGGCGGACGGCACAAGCCCGCTTCCCGATTTACGGTATTCCCGACGATTTTATCTCC

[0252] GTCCCCCTGCCTGCCGGTTTGCGGAGCGGAAAAGCCCTTGTCCGCATCAGGCAGACGGGAAAAAACAGCGGCACAATC

[0253] GACAATACCGGCGGCACACATACCGCCGACCTCTCCCGATTCCCCATCACCGCGCGCACAACGGCAATCAAAGGCAGG

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[0255] CTCGGTTACGCCGAAGACCCCGTCGAACTTTTTTTATGCACATCCAAGGCTCGGGCCGTCTGAAAACCCCGTCCGGC

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[0260] GCCCATCCGGTTACCCGCAAAGCCCTCAACCGCCTGATTATGGCGCAGGATACCGGCAGCGCGATTAAAGGCGCGGTG

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[0262] CAGCTCCTACCCAACGGTATGAAGCCCGAATACCGCCCGTAAAAGCTT

[0263] 1 MASPDVKSAD TLSKPAAPVV SEKETEAKED APQAGSQGQG APSAQGGQDM

[0264] 51 AAVSEENTGN GGAAATDKPK NEDEGAQNDM PQNAADTDSL TPNHTPASNM

[0265] 101 PAGNMENQAP DAGESEQPAN QPDMANTADG MQGDDPSAGG ENAGNTAAQG

[0266] 151 TNQAENNQTA GSQNPASSTN PSATNSGGDF GRTNVGNSVV IDGPSQNITL

[0267] 201 THCKGDSCSG NNFLDEEVQL KSEFEKLSDA DKISNYKKDG KNDGKNDKFV

[0268] 251 GLVADSVQMK GINQYIIFYK PKPTSFARFR RSARSRRSLP AEMPLIPVNQ

[0269] 301 ADTLIVDGEA VSLTGHSGNI FAPEGNYRYL TYGAEKLPGG SYALRVQGEP

[0270] 351 SKGEMLAGTA VYNGEVLHFH TENGRPSPSR GRFAAKVDFG SKSVDGIIDS

[0271] 401 GDGLHMGTQK FKAAIDGNGF KGTWTENGGG DVSGKFYGPA GEEVAGKCYSY

[0272] 451 RPTDAEKGGF GVFAGKKEQD GSGGGGCQSK SIQTFPQPDT SVINGPDRPV

[0273] 501 GIPDPAGTTV GGGGAVYTVV PHLSLPHWAA QDFAKSLQSF RLGCANLKNR

[0274] 551 QGWQDVCAQA FQTPVHSFQA KQFFERYFTP WQVAGNGSLA GTVTGYYEPV

[0275] 601 LKGDDRRTAQ ARFPIYGIPD DFISVPLPAG LRSGKALVRI RQTGKNSGTI

[0276] 651 DNTGGTHTAD LSRFPITART TAIKGRFEGS RFLPYHTRNQ INGGALDGKA

[0277] 701 PILGYAEDPV ELFFMHIQGS GRLKTPSGKY IRIGYADKNE HPYVSIGRYM

[0278] 751 ADKGYLKLGQ TSMQGIKAYM RQNPQRLAEV LGQNPSYIFF RELAGSSNDG

[0279] 801 PVGALGTPLM GEYAGAVDRH YITLGAPLFV ATAHPVTRKA LNRLIMAQDT

[0280] 851 GSAIKGAVRV DYFWGYGDEA GELAGKQKTT GYVWQLLPNG MKPEYRP*

[0281] ΔG287Nz-953

[0282] ATGGCTAGCCCCGATGTCAAGTCGGCGGACACGCTGTCAAAACCTGCCGCCCCTGTTGTTTCTGAAAAAGAGACAGAG

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[0285] GATATGCCGCAAAATGCCGCCGATACAGATAGTTTGACACCGAATCACACCCCGGCTTCGAATATGCCGGCCGGAAAT

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[0291] AATTACAAGAAAGATGGGAAGAATGACGGGAAGAATGATAAAATTTTGTCGGTTTGGTTGCCGATAGTGTGCAGATGAAG

[0292] GGAATCAATCAATATATTATCTTTTATAAACCTAAACCCACTTCATTTGCGCGATTTAGGCGTTCTGCACGGTCGAGG

[0293] CGGTCGCTTCCGGCCGAGATGCCGCTGATTCCCGTCAATCAGGCGGATACGCTGATTGTCGATGGGGAAGCGGTCAGC

[0294] CTGACGGGGCATTCCGGCAATATCTTCGCGCCCGAAGGGAATTACCGGTATCTGACTTACGGGGCGGAAAAATTGCCC

[0295] GGCGGATCGTATGCCCTCCGTGTTCAAGGCGAACCTTCAAAAGGCGAAATGCTCGCGGGCACGGCAGTGTACAACGGC

[0296] GAAGTGCTGCATTTTCATACGGAAAACGGCCGTCCGTCCCCGTCCAGAGGCAGGTTTGCCGCAAAAGTCGATTTCGGC

[0297] AGCAAATCTGTGCACGGCATTATCGACAGCGGCGATGGTTTGCATATGGGTACGCAAAAATTCAAAGCCGCCATCGAT

[0298] GGAAACGGCTTTAAGGGGACTTGGACGGAAAATGGCGGCGGGGATGTTTCCGGAAAGTTTTACGGCCCGGCCGGCGAG

[0299] GAAGTGGCGGGAAAATACAGCTATCGCCCAACAGATGCGGAAAAGGGCGGATTCGGCGTGTTTGCCGGCAAAAAAGAG

[0300] CAGGATGGATCCGGAGGAGGAGGAGCCACCTACAAAGTGGACGAATATCACGCCAACGCCCGTTTCGCCATCGACCAT

[0301] TTCAACACCAGCACCAACGTCGGCGGTTTTTACGGTCTGACCGGTTCCGTCGAGTTCGACCAAGCAAAACGCGACGGT

[0302] AAAATCGACATCACCATCCCCGTTGCCAACCTGCAAAGCGGTTCGCAACACTTTACCGACCACCTGAAATCAGCCGAC

[0303] ATCTTCGATGCCGCCCAATATCCGGACATCCGCTTTGTTTCCACCAAATTCAACTTCAACGGCAAAAAACTGGTTTCC

[0304] GTTGACGGCAACCTGACCATGCACGGCAAAACCGCCCCCGTCAAACTCAAAGCCGAAAAATTCAACTGCTACCAAAGC

[0305] CCGATGGCGAAAACCGAAGTTTGCGGCGGCGACTTCAGCACCACCATCGACCGCACCAAATGGGGCGTGGACTACCTC

[0306] GTTAACGTTGGTATGACCAAAAGCGTCCGCATCGACATCCAAATCGAGGCAGCCAAACAATAAAAGCTT

[0307] 1 MASPDVKSAD TLSKPAAPVV SEKETEAKED APQAGSQGQG APSAQGGQDM

[0308] 51 AAVSEENTGN GGAAATDKPK NEDEGAQNDM PQNAADTDSL TPNHTPASNM

[0309] 101 PAGNMENQAP DAGESEQPAN QPDMANTADG MQGDDPSAGG ENAGNTAAQG

[0310] 151 TNQAENNQTA GSQNPASSTN PSATNSGGDF GRTNVGNSVV IDGPSQNITL

[0311] 201 THCKGDSCSG NNFLDEEVQL KSEFEKLSDA DKISNYKKDG KNDGKNDKFV

[0312] 251 GLVADSVQMK GINQYIIFYK PKPTSFARFR RSARSRRSLP AEMPLIPVNQ

[0313] 301 ADTLIVDGEA VSLTGHSGNI FAPEGNYRYL TYGAEKLPGG SYALRVQGEP

[0314] 351 SKGEMLAGTA VYNGEVLHFH TENGRPSPSR GRFAAKVDFG SKSVDGITDS

[0315] 401 GDGLHMGTQK FKAAIDGNGF KGTWTENGGG DVSGKFYGPA GEEVAGKYSY

[0316] 451 RPTDAEKGGF GVFAGKKEQD GSGGGGATYK VDEYHANARF AIDHFNTSTN

[0317] 501 VGGFYGLTGS VEFDQAKRDG KIDITIPVAN LQSGSQHFTD HLKSADIFDA

[0318] 551 AQYPDIRFVS TKFNFNGKKL VSVDGNLTMH GKTAPVKLKA EKFNCYQSPM

[0319] 601 AKTEVCGGDF STTIDRTKWG VDYLVNVGMT KSVRIDIQIE AAKQ*

[0320] ΔG287Nz-961

[0321] ATGGCTAGCCCCGATGTCAAGTCGGCGGACACGCTGTCAAAACCTGCCGCCCCTGTTGTTTCTGAAAAAGAGACAGAG

[0322] GCAAAGGAAGATGCGCCACAGGCAGGTTCTCAAGGACAGGCGCGCCATCCGCACAAGGCGGTCAAGATATGGCGGCG

[0323] GTTTCGGAAGAAAATACAGGCAATGGCGGTGCGGCAGCAACGGACAAACCCAAAAATGAAGACGAGGGGGCGCAAAT

[0324] GATATGCCGCAAAATGCCGCCGATACAGATAGTTTGACACCGAATCACACCCCCGGCTTCGAATATGCCGGCCGGAAAT

[0325] ATGGAAAACCAAGCACCGGATGCCGGGGAATCGGAGCAGCCGGCAAACCAACCGGATATGGCAAATACGGCGGACGGA

[0326] ATGCAGGGTGACGATCCGTCGGCAGGCGGGGAAAATGCCGGCAATACGGCTGCCCAAGGTACAAATCAAGCCGAAAAC

[0327] AATCAAACCGCCGGTTCTCAAAATCCTGCCTCTTCAACCAATCCTAGCGCCACGAATAGCGGTGGTGATTTTGGAAGG

[0328] ACGAACGTGGGCAATTCTGTTGTGATTGACGGGCCGTCGCAAAATATAACGTTGACCCACTGTAAAGGCGATTCTTGT

[0329] AGTGGCAATAATTTCTTGGATGAAGAAGTACAGCTAAAATCAGAATTTGAAAAATTAAGTGATGCAGACAAAATAAGT

[0330] AATTACAAGAAAGATGGGAAGAATCACGGGAAGAATGATAAATTTGTCGGTTTGGTTGCCGATAGTGTGCAGATGAAG

[0331] GGAATCAATCAATATATTATCTTTTATAAACCTAAACCCACTTCATTTGCGCGATTTAGGCGTTCTGCACGGTCGAGG

[0332] CGGTCGCTTCCGGCCGAGATGCCGCTGATTCCCGTCAATCAGGCGGATACGCTGATTGTCGATGGGGAAGCGGTCAGC

[0333] CTGACGGGGCATTCCGGCAATATCTTCGCGCCCGAAGGGAATTACCGGTATCTGACTTACGGGGCGGAAAAATTGCCC

[0334] GGCGGATCGTATGCCCTCCGTGTTCAAGGCGAACCTTCAAAAGGCGAAATGCTCGCGGGCACGGCAGTGTACAACGGC

[0335] GAAGTGCTGCATTTTCATACGGAAAACGGCCGTCCGTCCCCGTCCAGAGGCAGGTTTGCCGCAAAAGTCGATTTCGGC

[0336] AGCAAATCTGTGGACGGCATTATCGACAGCGGCGATGGTTTGCATATGGGTACGCAAAAATTCAAAGCCGCCATCGAT

[0337] GGAAACGGCTTTAAGGGGACTTGGACGGAAAATGGCGGCGGGGATGTTTCCGGAAAGTTTTACGGCCCGGCCGGCGAG

[0338] GAAGTGGCGGGAAAATACAGCTATCGCCCAACAGATGCGGAAAAGGGCGGATTCGGCGTGTTTGCCGGCAAAAAAGAG

[0339] CAGGATGGATCCGGAGGAGGAGGAGCCACAAACGACGACGATGTTAAAAAAGCTGCCACTGTGGCCATTGCTGCTGCC

[0340] TACAACAATGGCCAAGAAATCAACGGTTTCAAAGCTGGAGAGACCATCTACGACATTGATGAAGACGGCACAATTACC

[0341] AAAAAAGACGCAACTGCAGCCGATGTTGAAGCCGACGACTTTAAAGGTCTGGGTCTGAAAAAAGTCGTGACTAACCTG

[0342] ACCAAAACCGTCAATGAAAACAAACAAAACGTCGATGCCAAAGTAAAAGCTGCAGAATCTGAAATAGAAAAGTTAACA

[0343] ACCAAGTTAGCAGACACTGATGCCGCTTTAGCAGATACTGATGCCGCTCTGGATGCAACCACCAACGCCTTGAATAAA

[0344] TTGGGAGAAAATATAACGACATTTGCTGAAGAGACTAAGACAAATATCGTAAAAATTGATGAAAAATTAGAAGCCGTG

[0345] GCTGATACCGTCGACAAGCATGCCGAAGCATTCAACGATATCGCCGATTCATTGGATGAAACCAACACTAAGGCAGAC

[0346] GAAGCCGTCAAAACCGCCAATGAAGCCAAACAGACGGCCGAAGAAACCAAACAAAACGTCGATGCCAAAGTAAAAGCT

[0347] GCAGAAACTGCAGCAGGCAAAGCCGAAGCTGCCGCTGGCACAGCTAATACTGCAGCCGACAAGGCCGAAGCTGTCGCT

[0348] GCAAAAGTTACCGACATCAAAGCTGATATCGCTACGAACAAAGATAATATTGCTAAAAAAGCAAACAGTGCCGACGTG

[0349] TACACCAGAGAAGAGTCTGACAGCAAATTTGTCAGAATTGATGGTCTGAACGCTACTACCGAAAAATTGGACACACGC

[0350] TTGGCTTCTGCTGAAAAATCCATTGCCGATCACGATACTCGCCTGAACGGTTTGGATAAAACAGTGTCAGACCTGCGC

[0351] AAAGAAACCCGCCAAGGCCTTGCAGAACAAGCCGCGCTCTCCGGTCTGTTCCAACCTTACAACGTGGGTCGGTTCAAT

[0352] GTAACGGCTGCAGTCGGCGGCTACAAATCCGAATCGGCAGTCGCCATCGGTACCGGCTTCCGCTTTACCGAAAACTTT

[0353] GCCGCCAAAGCAGGCGTGGCAGTCGGCACTTCGTCCGGTTCTTCCGCAGCCTACCATGTCGGCGTCAATTACGAGTGG

[0354] TAAAAGCTT

[0355] 1 MASPDVKSAD TLSKPAAPVV SEKETEAKED APQAGSQGQG APSAQGGQDM

[0356] 51 AAVSEENTGN GGAAATDKPK NEDEGAQNDM PQNAADTDSL TPNHTPASNM

[0357] 101 PAGNMENQAP DAGESEQPAN QPDMANTADG MQGDDPSAGG ENAGNTAAQG

[0358] 151 TNQAENNQTA GSQNPASSTN PSATNSGGDF GRTNVGNSVV IDGPSQNITL

[0359] 201 THCKGDSCSG NNFLDEEVQL KSEFEKLSDA DKISNYKKDG KNDGKNDKTV

[0360] 251 GLVADSVQMK GINQYIIFYK PKPTSFARFR RSARSRRSLP AEMPLIPVNQ

[0361] 301 ADTLIVDGEA VSLTGHSCNI FAPEGNYRYL TYGAEKLPGG SYALRVQGEP

[0362] 351 SKGEMLAGTA VYNGEVLHFH TENGRPSPSR GRFAAKVDFG SKSVDGIIDS

[0363] 401 GDGLHMGTQK FKAAIDGNGF KGTWTENGGG DVSGKTYGPA GEEVAGKYSY

[0364] 451 RPTDAEKGGF GVFAGKKEQD GSGGGGATND DDVKKAATVA IAAAYNNGQE

[0365] 501 INGFKAGETI YDIDEDGTIT KKDATAADVE ADDFKGLGLK KVVTNLTKTV

[0366] 551 NENKQNVDAK VKAAESEIEK LTTKLADTDA ALADTDAALD ATTMALNKLG

[0367] 601 ENITTFAEET KTNIVKIDEK IEAVADTVDK HAEAFNDIAD SLDETNTKAD

[0368] 651 EAVKTANEAK QTAEETKQNV DAKVKAAETA AGKAEAAAGT ANTAADKAEA

[0369] 701 VAAKVTDIKA DIATNKDNIA KKANSADVYT REESDSKFVR IDGLNATTEK

[0370] 751 LDTRLASAEK SIADHDTRLN GLDKTVSDLR KETRQGLAEQ AALSGLFQPY

[0371] 801 NVGRFNVTAA VGGYKSESAV AIGTGFRFTE NFAAKAGVAV GTSSGSSAAY

[0372] 851 HVGVNYEW*

[0373] 实施例 3-△G983 的杂交体

[0374] 蛋白质 983 具有如下序列：

[0375] 983 → △G983

[0376] 1 MRTTPTFPTK TFKPTAMALA VATTLSACLG GGGGGTSAPD FNAGGTGIGS

[0377] 51 NSRATTAKSA AVSYAGIKNE MCKDRSMLCA GRDDVAVTDR DAKINAPPPN

[0378] 101 LHTGDFPNPN DAYKNLINLK PAIEAGYTGR GVEVGIVDTG ESVGSISFPE

[0379] 151 LYGRKEHGYN ENYKNYTAYM RKEAPEDGGG KDIEASFDDE AVIETEAKPT

[0380] 201 DIRHVKEIGH IDLVSHIIGG RSVDGRPAGG IAPDATLHIM NTNDETKNEM

[0381] 251 MVAAIRNAWV KLGERGVRIV NNSFGTTSRA GTADLFQIAN SEEQYRQALL

[0382] 301 DYSGGDKTDE GIRLMQQSDY GNLSYHIRNK NMLFIFSTGN DAQAQPNTYA

[0383] 351 LLPFYEKDAQ KGIITVAGVD RSGEKFKREM YGEPGTEPLE YGSNHCGITA

[0384] 401 MWCLSAPYEA SVRFTRTNPI QIAGTSFSAP IVTGTAALLL QKYPWMSNDN

[0385] 451 LRTTLLTTAQ DIGAVGVDSK FGWGLLDAGK AMNGPASFPF GDFTADTKGT

[0386] 501 SDIAYSFRND ISGTGGLIKK GGSQLQLHGN NTYTGKTIIE GGSLVLYGNN

[0387] 551 KSDMRVETKG ALIYNGAASG GSLNSDGIVY LADTDQSGAN ETVHIKGSLQ

[0388] 601 LDGKGTLYTR LGKLLKVDGT AIIGGKLYMS ARGKGAGYLN STGRRVPFLS

[0389] 651 AAKIGQDYSF FTNIETDGGL LASLDSVEKT AGSEGDTLSY YVRRGNAART

[0390] 701 ASAAAHSAPA GLKHAVEQGG SNLENLMVEL DASESSATPE TVE TAAADRT

[0391] 751 DMPGIRPYGA TFRAAAAVQH ANAADGVRIF NSLAATVYAD STAAHADMQG

[0392] 801 RRLKAVSDGL DHNGTGLRVI AQTQQDGGTW EQGGVEGKMR GSTQTVGIAA

[0393] 851 KTGENTTAAA TLGMGRSTWS ENSANAKTDS ISLFAGIRHD AGDIGYLKGL

[0394] 901 FSYGRYKNSI SRSTGADEHA EGSVNGTLMQ LGALGGVNVP FAATGDLTVE

[0395] 9.51 GGLRYDLLKQ DAFAEKGSAL GWSGNSLTEG TLVGLAGLKL SQPLSDKAVL

[0396] 1001 FATAGVERDL NGRDYTVTGG FTGATAATGK TGARNMPHTR LVAGL GADVE

[0397] 1051 FGNGWNGLAR YSYAGSKQYG NHSGRVGVGY RF*

[0398] 因此△G983 具有如下基本序列：

[0399] TSAPD FNAGGTGIGS

[0400] NSRATTAKSA AVSYAGIKNE MCKDRSMLCA GRDDVAVTDR DAKINAPPPN

[0401] LHTGDFPNPN DAYKNLINLK PAIEAGYTGR GVEVGIVDTG ESVGSISFPE

[0402] LYGRKEHGYN ENYKNYTAYM RKEAPEDGGG KDIEASFDDE AVIETEAKPT

[0403] DIRHVKEIGH IDLVSHIIGG RSVDGRPAGG IAPDATLHTM NTNDETKNEM

[0404] MVAAIRNAWV KLGERGVRIV NNSFGTTSRA GTADLFQIAN SEEQYRQALL

[0405] DYSGGDKTDE GIRLMQQSDY GNLSYHIRNK NMLFIFSTGN DAQAQPNTYA

[0406] LLPFYEKDAQ KGIITVAGVD RSGEKFKREM YGEPGTEPLE YGSNHCGITA

[0407] MWCLSAPYEA SVRFTRTNPI QIAGTSFSAP IVTGTAALLL QKYPWMSNDN

[0408] LRTTLLTTAQ DIGAVGVDSK FGWGLLDAGK AMNGPASFPF GDFTADTKGT

[0409] SDIAYSFRND ISGTGGLIKK GGSQLQLHGN NTYTGKTIIE GGSLVLYGNN

[0410] KSDMRVETKG ALTYNGAASG GSLNSDGIVY LADTDQSGAN ETVHIKGSLQ

[0411] LDGKGTLYTR LGKLLKVDGT AIIGGKLYMS ARGKGAGYLN STGRRVPFLS

[0412] AAKIGQDYSF FTNIETDGGL LASLDSVEKT AGSEGDTLSY YVRRGNAART

[0413] ASAAAHSAPA GLKHAVEQGG SNLENLMVEL DASESSATPE TVETAAADRT

[0414] DMPGIRPYGA TFRAAAAVQH ANAADGVRIF NSLAATVYAD STAAHADMQG

[0415] RRLKAVSDGL DHNGTGLRVI AQTQQDGGTW EQGGVEGKMRGSTQTVGIAA

[0416] KTGENTTAAA TLGMGRSTWS ENSANAKTDS ISLFAGIRHD AGDIGYLKGL

[0417] FSYGRYKNSI SRSTGADEHA EGSVNGTLMQ LGALGGVNVP FAATGDLTVE

[0418] GGLRYDLLKQ DAFAEKGSAL GWSGNSLTEG TLVGLAGLKLSQPLSDKAVL

[0419] FATAGVERDL NGRDYTVTGG FTGATAATGK TGARNMPHTR LVAGLGADVE

[0420] FGNGWNGLAR YSYAGSKQYG NHSGRVGVGY RF*

[0421] 将△G983 作为在其 C- 末端与 ORF46.1、741、961 或 961C 的杂交体表达：

[0422] △G983-ORF46.1

[0423] ATGACTTCTGCGCCCGACTTCAATGCAGGCGGTACCGGTATCGGCAGCAACAGCAGAGCAACAACAGCGAAATCAGCA

[0424] GCAGTATCTTACGCCGGTATCAAGAACGAAATGTGCAAAGACAGAAGCATGCTCTGTGCCGGTCGGGATGACGTTGCG

[0425] GTTACAGACAGGGATGCCAAAATCAATGCCCCCCCCCCGAATCTGCATACCGGAGACTTTCCAAACCCAAATGACGCA

[0426] TACAAGAATTTGATCAACCTCAAACCTGCAATTGAAGCAGGCTATACAGGACGCGGGGTAGAGGTAGGTATCGTCGAC

[0427] ACAGGCGAATCCGTCGGCAGCATATCCTTTCCCGAACTGTATGGCAGAAAAGAACACGGCTATAACGAAAATTACAAA

[0428] AACTATACGGCGTATATGCGGAAGGAAGCGCCTGAAGACGGAGGCGGTAAAGACATTGAAGCTTCTTTCGACGATGAG

[0429] GCCGTTATAGAGACTGAAGCAAAGCCGACGGATATCCGCCACGTAAAAGAAATCGGACACATCGATTTGGTCTCCCAT

[0430] ATTATTGGCGGGCGTTCCGTGGACGGCAGACCTGCAGGCGGTATTGCGCCCGATGCGACGCTACACATAATGAATACG

[0431] AATGATGAAACCAAGAAACGAAATGATGGTTGCAGCCATCCGCAATGCATGGGTCAAGCTGGGCGAACGTGGCGTGCGC

[0432] ATCGTCAATAACAGTTTTGGAACAACATCGAGGGCAGGCACTGCCGACCTTTTCCAAATAGCCAATTCGGAGGAGCAG

[0433] TACCGCCAAGCGTTGCTCGACTATTCCGGCGGTGATAAAACAGACGAGGGTATCCGCCTGATGCAACAGAGCGATTAC

[0434] GGCAACCTGTCCTACCACATCCGTAATAAAAACATGCTTTTCATCTTTTCGACAGGCAATGACGCACAAGCTCAGCCC

[0435] AACACATATGCCCTATTGCCATTTTATGAAAAAGACGCTCAAAAAGGCATTATCACAGTCGCAGGCGTAGACCGCAGT

[0436] GGAGAAAAGTTCAAACGGGAAATGTATGGAGAACCGGGTACAGAACCGCTTGAGTATGGCTCCAACCATTGCGGAATT

[0437] ACTGCCATGTGGTGCCTGTCGGCACCCTATGAAGCAAGCGTCCGTTTCACCCGTACAAACCCGATTCAAATTGCCGGA

[0438] ACATCCTTTTCCGCACCCATCGTAACCGGCACGGCGGCTCTGCTGCTGCAGAAATACCCGTGGATGAGCAACGACAAC

[0439] CTGCGTACCACGTTGCTGACGACGGCTCAGGACATCGGTGCAGTCGGCGTGGACAGCAAGTTCGGCTGGGGACTGCTG

[0440] GATGCGGGTAAGGCCATGAACGGACCCGCGTCCTTTCCGTTCGGCGACTTTACCGCCGATACGAAAGGTACATCCGAT

[0441] ATTGCCTACTCCTTCCGTAACGACATTTCAGGCACGGGCGGCCTGATCAAAAAAGGCGGCAGCCAACTGCAACTGCAC

[0442] GGCAACAACACCTATACGGGCAAAACCATTATCGAAGGCGGTTCGCTGGTGTTGTACGGCAACAACAAATCGGATATG

[0443] CGCGTCGAAACCAAAGGTGCGCTGATTTATAACGGGGCGGCATCCGGCGGCAGCCTGAACAGCGACGGCATTGTCTAT

[0444] CTGGCAGATACCGACCAATCCGGCGCAAACGAAACCGTACACATCAAAGGCAGTCTGCAGCTGGACGGCAAAGGTACG

[0445] CTGTACACACGTTTGGGCAAACTGCTGAAAGTGGACGGTACGGCGATTATCGGCGGCAAGCTGTACATGTCGGCACGC

[0446] GGCAAGGGGGCAGGCTATCTCAACAGTACCGGACGACGTGTTCCCTTCCTGAGTGCCGCCAAAATCGGGCAGGATTAT

[0447] TCTTTCTTCACAAACATCGAAACCGACGGCGGCCTGCTGGCTTCCCTCGACAGCGTCGAAAAAACAGCGGGCAGTGAA

[0448] GGCGACACGCTGTCCTATTATGTCCGTCGCGGCAATGCGGCACGGACTGCTTCGGCAGCGGCACATTCCGCGCCCGCC

[0449] GGTCTGAAACACGCCGTAGAACAGGGCGGCAGCAATCTGGAAAACCTGATGGTCGAACTGGATGCCTCCGAATCATCC

[0450] GCAACACCCGAGACGGTTGAAACTGCGGCAGCCGACCGGACAGATATGCCGGGCATCCGCCCCTACGGCGCAACTTTC

[0451] CGCGCAGCGGCAGCCGTACAGCATGCGAATGCCGCCGACGGTGTACGCATCTTCAACAGTCTCGCCGCTACCGTCTAT

[0452] GCCGACAGTACCGCCGCCCATGCCGATATGCAGGGACGCCGCCTGAAAGCCGTATCGGACGGGTTGGACCACAACGGC

[0453] ACGGGTCTGCGCGTCATCGCGCAAACCCAACAGGACGGTGGAACGTGGAACAGGGCGGTGTTGAAGGCAAAATGCGC

[0454] GGCAGTACCCAAACCGTCGGCATTGCCGCGAAAACCGGCGAAAATACGACAGCAGCCGCCACACTGGGCATGGGACGC

[0455] AGCACATGGAGCGAAAACAGTGCAAATGCAAAAACCGACAGCATTAGTCTGTTTGCAGGCATACGGCACGATGCGGGC

[0456] GATATCGGCTATCTCAAAGGCCTGTTCTCCTACGGACGCTACAAAAACAGCATCAGCCGCAGCACCGGTGCGGACGAA

[0457] CATGCGGAAGGCAGCGTCAACGGCACGCTGATGCAGCTGGGCGCACTGGGCGGTGTCAACGTTCCGTTTGCCGCAACG

[0458] GGAGATTTGACGGTCGAAGGCGGTCTGCGCTACGACCTGCTCAAACAGGATGCATTCGCCGAAAAAGGCAGTGCTTTG

[0459] GGCTGGAGCGGCAACAGCCTCACTGAAGGCACGCTGGTCGGACTCGCGGGTCTGAAGCTGTCGCAACCCTTGAGCGAT

[0460] AAAGCCGTCCTGTTTGCAACGGCGGGCGTGGAACGCGACCTGAACGGACGCGACTACACGGTAACGGGCGGCTTTACC

[0461] GGCGCGACTGCAGCAACCGGCAAGACGGGGGCACGCAATATGCCGCACACCCGTCTGGTTGCCGGCCTGGGCGCGGAT

[0462] GTCGAATTCGGCAACGGCTGGAACGGCTTGGCACGTTACAGCTACGCCGGTTCCAAACAGTACGGCAACCACAGCGGA

[0463] CGAGTCGGCGTAGGCTACCGGTTCCTCGACGGTGGCGGAGGCACTGGATCCTCAGATTTGGCAAACGATTCTTTTATC

[0464] CGGCAGGTTCTCGACCGTCAGCATTTCGAACCCGACGGGAAATACCACCTATTCGGCAGCAGGGGGGAACTTGCCGAG

[0465] CGCAGCGGCCATATCGGATTGGGAAAAATACAAAGCCATCAGTTGGGCAACCTGATGATTCAACAGGCGGCCATTAAA

[0466] GGAAATATCGGCTACATTGTCCGCTTTTCCGATCACGGGCACGAAGTCCATTCCCCCTTCGACAACCATGCCTCACAT

[0467] TCCGATTCTGATGAAGCCGGTAGTCCCGTTGACGGATTTAGCCTTTACCGCATCCATTGGGACGGATACGAACACCAT

[0468] CCCGCCGACGGCTATGACGGGCCACAGGGCGGCGGCTATCCCGCTCCCAAAGGCGCGAGGGATATATACAGCTACGAC

[0469] ATAAAAGGCGTTGCCCAAAATATCCGCCTCAACCTGACCGACAACCGCAGCACCGGACAACGGCTTGCCGACCGTTTC

[0470] CACAATGCCGGTAGTATGCTGACGCAAGGAGTAGGCGACGGATTCAAACGCGCCACCCGATACAGCCCCGAGCTGGAC

[0471] AGATCGGGCAATGCCGCCGAAGCCTTCAACGGCACTGCAGATATCGTTAAAAACATCATCGGCGCGGCAGGAGAAATT

[0472] GTCGGCGCAGGCGATGCCGTGCAGGGCATAAGCGAAGGCTCAAACATTGCTGTCATGCACGGCTTGGGTCTGCTTTCC

[0473] ACCGAAAACAAGATGGCGCGCATCAACGATTTGGCAGATATGGCGCAACTCAAAGACTATGCCGCAGCAGCCATCCGC

[0474] GATTGGGCAGTCCAAAACCCCAATGCCGCACAAGGCATAGAAGCCGTCAGCAATATCTTTATGGCAGCCATCCCCATC

[0475] AAAGGGATTGGAGCTGTTCGGGGAAAATACGGCTTGGGCGGCATCACGGCACATCCTATCAAGCGGTCGCAGATGGGC

[0476] GCGATCGCATTGCCGAAAGGGAAATCCGCCGTCAGCGACAATTTTGCCGATGCGGCATACGCCAAATACCCGTCCCCT

[0477] TACCATTCCCGAAATATCCGTTCAAACTTGGAGCAGCGTTACGGCAAAGAAAACATCACCTCCTCAACCGTGCCGCCG

[0478] TCAAACGGCAAAAATGTCAAACTGGCAGACCAACGCCACCCGAAGACAGGCGTACCGTTTGACGGTAAAGGGTTTCCG

[0479] AATTTTGAGAAGCACGTGAAATATGATACGCTCGAGCACCACCACCACCACCACTGA

[0480] 1 MTSAPDFNAG GTGIGSNSRA TTAKSAAVSY AGIKNEMCKD RSMLCAGRDD

[0481] 51 VAVTDRDAKI NAPPPNLHTG DFPNPNDAYK NLINLKPAIE AGYTGRGVEV

[0482] 101 GIVDTGESVG SISFPELYGR KEHGYNENYK NYTAYMRKEA PEDGGGKDIE

[0483] 151 ASFDDEAVIE TEAKPTDIRH VKEIGHIDLV SHIIGGRSVD GRPAGGIAPD

[0484] 201 ATLHIMNTND ETKNEMMVAA IRNAWVKLGE RGVRIVNNSF GTTSRAGTAD

[0485] 251 LFQIANSEEQ YRQALLDYSG GDKTDEGIRL MQQSDYGNLS YHIRNKNMLF

[0486] 301 IFSTGNDAQA QPNTYALLPF YEKDAQKGII TVAGVDRSGE KFKREMYGEP

[0487] 351 GTEPLEYGSN HCGITAMWCL SAPYEASVRF TRTNPIQIAG TSFSAPIVTG

[0488] 401 TAALLLQKYP WMSNDNLRTT LLTTAQDIGA VGVDSKFGWG LLDAGKAMNG

[0489] 451 PASFPFGDFT ADTKGTSDIA YSFRNDISGT GGLIKKGGSQ LQLHGNNTYT

[0490] 501 GKTIIEGGSL VLYGNNKSDM RVETKGALIY NGAASGGSLN SDGIVYLADT

[0491] 551 DQSGANETVH IKGSLQLDGK GTLYTRLGKL LKVDGTAIIG GKLYMSARGK

[0492] 601 GAGYLNSTGR RVPFLSAAKI GQDYSFFTNI ETDGGLLASL DSVEKTAGSE

[0493] 651 GDTLSYYVRR GNAARTASAA AHSAPAGLKH AVEQGGSNLE NLMVELDASE

[0494] 701 SSATPETVET AAADRTDMPG IRPYGATFRA AAAVQHANAA DGVRIFNSLA

[0495] 751 ATVYADSTAA HADMQGRRLK AVSDGLDHNG TGLRVIAQTQ QDGGTWEQGG

[0496] 801 VEGKMRGSTQ TVGIAAKTGE NTTAAATLGM GRSTWSENSA NAKTDSISLF

[0497] 851 AGIRHDAGDI GYLKGLFSYG RYKNSISRST GADEHAEGSV NGTLMQLGAL

[0498] 901 GGVNVPFAAT GDLTVEGGLR YDLLKQDAFA EKGSALGWSG NSLTEGTLVG

[0499] 951 LAGLKLSQPL SDKAVLFATA GVERDLNGRD YTVTGGFTGA TAATGKTCAR

[0500] 1001 NMPHTRLVAG LGADVEFGNG WNGLARYSYA GSKQTGNHSG RVGVGYRFLD

[0501] 1051 GGGGTGSSDL ANDSFIRQVL DRQHFEPDGK YHLFGSRGEL AERSGHIGLG

[0502] 1101 KIQSHQLGNL MIQQAAIKGN IGYIVRFSDH GHEVHSPFDN HASHSDSDEA

[0503] 1151 GSPVDGFSLY RIHWDGYEHH PADGYDGPQG GGYPAPKGAR DIYSYDIKGV

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[0710] GCTGCCACTGTGGCCATTGCTGCTGCCTACAACAATGGCCAAGAAATCAACGGTTTCAAAGCTGGAGAGACCATCTAC

[0711] GACATTGATGAAGACGGCACAATTACCAAAAAAGACGCAACTGCAGCCGATGTTGAAGCCGACGACTTTAAAGGTCTG

[0712] GGTCTGAAAAAAGTCGTGACTAACCTGACCAAAACCGTCAATGAAAACAAACAAAACGTCGATGCCAAAGTAAAAGCT

[0713] GCAGAATCTGAAATAGAAAAGTTAACAACCAAGTTAGCAGACACTGATGCCGCTTTAGCAGATACTGATGCCGCTCTG

[0714] GATGCAACCACCAACGCCTTGAATAAATTGGGAGAAAATATAACGACATTTGCTGAAGAGACTAAGACAAATATCGTA

[0715] AAAATTGATGAAAAATTAGAAGCCGTGGCTGATACCGTCGACAAGCATGCCGAAGCATTCAACGATATCGCCGATTCA

[0716] TTGGATGAAACCAACACTAAGGCAGACGAAGCCGTCAAAACCGCCAATGAAGCCAAACAGACGGCCGAAGAAACCAAA

[0717] CAAAACGTCGATGCCAAAGTAAAAGCTGCAGAAACTGCAGCAGGCAAAGCCGAAGCTGCCGCTGGCACAGCTAATACT

[0718] GCAGCCGACAAGGCCGAAGCTGTCGCTGCAAAAGTTACCGACATCAAAGCTGATATCGCTACGAACAAAGATAATATT

[0719] GCTAAAAAAGCAAACAGTGCCGACGTGTACACCAGAGAAGAGTCTGACAGCAAATTTGTCAGAATTGATGGTCTGAAC

[0720] GCTACTACCGAAAAATTGGACACACGCTTGGCTTCTGCTGAAAAATCCATTGCCGATCACGATACTCGCCTGAACGGT

[0721] TTGGATAAAACAGTGTCAGACCTGCGCAAAGAAACCCGCCAAGGCCTTGCAGAACAAGCCGCGCTCTCCGGTCTGTTC

[0722] CAACCTTACAACGTGGGTCTCGAGCACCACCACCACCACCACTGA

[0723] 1 MTSAPDFNAG GTGIGSNSRA TTAKSAAVSY AGIKNEMCKD RSMLCAGRDD

[0724] 51 VAVTDRDAKI NAPPPNLHTG DFPNPNDAYK NLINLKPAIE AGYTGRGVEV

[0725] 101 GIVDTGESVG SISFPELYGR KEHGYNENYK NYTAYMRKEA PEDGGGKDIE

[0726] 151 ASFDDEAVIE TEAKPTDIRH VKEIGHIDLV SHIIGGRSVD GRPAGGIAPD

[0727] 201 ATLHIMNTND ETKNEMMVAA IRNAWVKLGE RGVRIVNNSF GTTSRAGTAD

[0728] 251 LFQIANSEEQ YRQALLDYSG GDKTDEGIRL MQQSDYGNLS YHIRNKNMLF

[0729] 301 IFSTGNDAQA QPNTYALLPF YEKDAQKGII TVAGVDRSGE KFKREMYGEP

[0730] 351 GTEPLEYGSN HCGITAMWCL SAPYEASVRF TRTNPIQIAG TSFSAPIVTG

[0731] 401 TAALLLQKYP WMSNDNLRTT LLTTAQDIGA VGVDSKTGWG LLDAGKAMNG

[0732] 451 PASFPFGDFT ADTKGTSDIA YSFRNDISGT GGLIKKGGSQ LQLHGNNTYT

[0733] 501 GKTIIEGGSL VLYGNNKSDM RVETKGALIY NGAASGGSLNSDGIVYLADT

[0734] 551 DQSGANETVH IKGSLQLDGK GTLYTRLGKL LKVDGTAIIG GKLYMSARGK

[0735] 601 GAGYLNSTGR RVPFLSAAKI GQDYSFFTNI ETDGGLLASL DSVEKTAGSE

[0736] 651 GDTLSYYVRR GNAARTASAA AHSAPAGLKH AVEQGGSNLE NLMVELDASE

[0737] 701 SSATPETVET AAADRTDMPG IRPYGATFRA AAAVQHANAA DGVRIFNSLA

[0738] 751 ATVYADSTAA HADMQGRRLK AVSDGLDHNG TGLRVIAQTQ QDGGTWEQGG

[0739] 801 VEGKMRGSTQ TVGIAAKTGE NTTAAATLGM GRSTWSENSA NAKTDSISLF

[0740] 851 AGIRHDAGDI GTLKGLFSYG RYKNSISRST GADEHAEGSV NGTLMQLGAL

[0741] 901 GGVNVPFAAT GDLTVEGGLR YDLLKQDAFA KKGSALGWSG NSLTTEGTLVG

[0742] 951 LAGLKLSQPL SDKAVLFATA GVERDLNGRD YTVTGGFTGA TAATGKTGAR

[0743] 1001 NMPHTRLVAG LGADVEFGNG WNGLARYSYA GSKQYGNHSG RVGVGYRFLE

[0744] 1051 GGGGTGSATN DDDVKKAATV AIAAAYNNGQ EINGFKAGET IYDIDEDGTI

[0745] 1101 TKKDATAADV EADDFKGLGL KKVVTNLTKT VNENKQNVDA KVKAAESEIE

[0746] 1151 KLTTKLADTD AALADTDAAL DATTNALNKL GENITTFAEE TKTNIVKIDE

[0747] 1201 KLEAVADTVD KHAEAFNDIA DSLDETNTKA DEAVKTANEA KQTAEETKQN

[0748] 1251 VDAKVKAAET AAGKAEAAAG TANTAADKAE AVAAKVTDIK ADIATNKDNI

[0749] 1301 AKKANSADVY TREESDSKFV RIDGLNATTE KLDTRLASAE KSIADHDTRL

[0750] 1351 NGLDKTVSDL RKETRQGLAE QAALSGLFQP YNVGLEHHHH HH*

[0751] 实施例 4-△G741 的杂交体

[0752] 蛋白质 741 具有如下序列：

[0753] 1 VNRTAFCCLS LTTALILTAC SSGGGGVAAD IGAGLADALT APLDHKDKGL

[0754] 51 QSLTLDQSVR KNEKLKLAAQ GAEKTYGNGD SLNTGKLKND KVSRFDFIRQ

[0755] 101 IEVDGQLITL ESGEFQVYKQ SHSALTAFQT EQIQDSEHSG KMVAKRQFRI

[0756] 151 GDIAGEHTSF DKLPEGGRAT YRGTAFGSDD AGGKLTYTID FAAKQGNGKI

[0757] 201 EHLKSPELNV DLAAADIKPD GKRHAVISGS VLYNQAEKGS YSLGIFGGKA

[0758] 251 QEVAGSAEVK TVNGIRHIGL AAKQ*

[0759] 因此，△G741 具有如下基本序列：

[0760] VAAD IGAGLADALT APLDHKDKGL

[0761] QSLTLDQSVR KNEKLKLAAQ GAEKTYGNGD SLNTGKLKND KVSRFDFIRQ

[0762] IEVDGQLITL ESGEFQVYKQ SHSALTAFQT EQIQDSEHSG KMVAKRQFRI

[0763] GDIAGEHTSF DKLPEGGRAT YRGTAFGSDD AGGKLTYTID FAAKQCNGKI

[0764] EHLKSPELNV DLAAADIKPD GKRHAVISGS VLYNQAEKGS YSLGIFGGKA

[0765] QEVAGSAEVK TVNGIRHIGL AAKQ*

[0766] 将△G741 直接融合于蛋白质 961、961C、983 和 ORF46.1 的符合读框的上游：

[0767] ΔG741-961

[0768] ATGGTCGCCGCCGACATCGGTGCGGGGCTTGCCGATGCACTAACCGCACCGCTCGACCATAAAGACAAAGGTTTGCAG

[0769] TCTTTGACGCTGGATCAGTCCGTCAGGAAAAACGAGAAACTGAAGCTGGCGGCACAAGGTGCGGAAAAAACTTATGGA

[0770] AACGGTGACAGCCTCAATACGGGCAAATTGAAGAACGACAAGGTCAGCCGTTTCGACTTTATCCGCCAAATCGAAGTG

[0771] GACGGGCAGCTCATTACCTTGGAGAGTGGAGAGTTCCAAGTATACAAACAAAGCCATTCCGCCTTAACCGCCTTTCAG

[0772] ACCGAGCAAATACAAGATTCGGAGCATTCCGGGAAGATGGTTGCGAAACGCCAGTTCAGAATCGGCGACATGGCGGGC

[0773] GAACATACATCTTTTGACAAGCTTCCCGAAGGCGGCAGGGCGACATATCGCGGGACGGCGTTCGGTTCAGACGATGCC

[0774] GGCGGAAAACTGACCTACACCATAGATTTCGCCGCCAAGCAGGGAAACGGCAAAATCGAACATTTGAAATCGCCAGAA

[0775] CTCAATGTCGACCTGGCCGCCGCCGATATCAAGCCGCATGGAAAACGCCATGCCGTCATCAGCGGTTCCGTCCTTTAC

[0776] AACCAAGCCGAGAAAGGCAGTTACTCCCTCGGTATCTTTGGCGGAAAAGCCCAGGAAGTTGCCGGCAGCGCGGAAGTG

[0777] AAAACCGTAAACGGCATACGCCATATCGGCCTTGCCGCCAAGCAACTCGAGGGTGGCGGAGGCACTGGATCCGCCACA

[0778] AACGACGACGATGTTAAAAAAGCTGCCACTGTGGCCATTGCTGCTGCCTACAACAATGGCCAAGAAATCAACGGTTTC

[0779] AAAGCTGGAGAGACCATCTACGACATTGATGAAGACGGCACAATTACCAAAAAAGACGCAACTGCAGCCGATGTTGAA

[0780] GCCGACGACTTTAAAGGTCTGGGTCTGAAAAAAGTCGTGACTAACCTGACCAAAACCGTCAATGAAAACAAACAAAAC

[0781] GTCGATGCCAAAGTAAAAGCTGCAGAATCTGAAATAGAAAAGTTAACAACCAAGTTAGCAGACACTGATGCCGCTTTA

[0782] GCAGATACTGATGCCGCTCTGGATGCAACCACCAACGCCTTGAATAAATTGGGAGAAAATATAACGACATTTGCTGAA

[0783] GAGACTAAGACAAATATCGTAAAAATTGATGAAAAATTAGAAGCCGTGGCTGATACCGTCGACAAGCATGCCGAAGCA

[0784] TTCAACGATATCGCCGATTCATTGGATGAAACCAACACTAAGGCAGACGAAGCCGTCAAAACCGCCAATGAAGCCAAA

[0785] CAGACGGCCGAAGAAACCAAACAAAACGTCGATGCCAAAGTAAAAGCTGCAGAAACTGCAGCAGGCAAAGCCGAAGCT

[0786] GCCGCTGGCACAGCTAATACTGCAGCCGACAAGGCCGAAGCTGTCGCTGCAAAAGTTACCGACATCAAAGCTGATATC

[0787] GCTACGAACAAAGATAATATTGCTAAAAAAGCAAACAGTGCCGACGTGTACACCAGAGAAGAGTCTGACAGCAAATTT

[0788] GTCAGAATTGATGGTCTGAACGCTACTACCGAAAAATTGGACACACGCTTGGCTTCTGCTGAAAAATCCATTGCCGAT

[0789] CACGATACTCGCCTGAACGGTTTGGATAAAACAGTGTCAGACCTGCGCAAAGAAACCCGCCAAGGCCTTGCAGAACAA

[0790] GCCGCGCTCTCCGGTCTGTTCCAACCTTACAACGTGGGTCGGTTCAATGTAACGGCTGCAGTCGGCGGCTACAAATCC

[0791] GAATCGGCAGTCGCCATCGGTACCGGCTTCCGCTTTACCGAAAACTTTGCCGCCAAAGCAGGCGTGGCAGTCGGCACT

[0792] TCGTCCGGTTCTTCCGCAGCCTACCATGTCGGCGTCAATTACGAGTGGCTCGAGCACCACCACCACCACCACTGA

[0793] 1 MVAADIGAGL ADALTAPLDH KDKGLQSLTL DQSVRKNEKL KLAAQGAEKT

[0794] 51 YGNGDSLNTG KLKNDKVSRF DFIRQIEVDG QLITLESGEF QVYKQSHSAL

[0795] 101 TAFQTEQIQD SEHSGKMVAK RQFRIGDIAG EHTSFDKLPE GGRATYRGTA

[0796] 151 FGSDDAGGKL TYTIDFAAKQ GNGKIEHLKS PELNVDLAAA DIKCPDGKRHA

[0797] 201 VISGSVLYNQ AEKGSYSLGI FGGKAQEVAG SAEVKTVNGI RHIGLAAKQL

[0798] 251 EGGGGTGSAT NDDDVKKAAT VAIAAAYNNG QEINGFKAGE TIYDIDEDGT

[0799] 301 ITKKDATAAD VEADDFKGLG LKKVVTNLTK TVNENKQNVD AKVKAAESEI

[0800] 351 EKLTTKLADT DAALADTDAA LDATTNALNK LGEKNTTFAE ETKTNIVKID

[0801] 401 EKLEAVADTV DKHAEAFNDI ADSLDETNTK ADEAVKTANE AKQTAEETKQ

[0802] 451 NVDAKVKAAE TAAGKAEAAA GTANTAADKA EAVAAKVTDI KADIATNKDN

[0803] 501 IAKKANSADV YTREESDSKF VRIDGLNATT EKLDTRLASA EKSIADHDTR

[0804] 551 LNGLDKTVSD LRKETRQGLA EQAALSGLFQ PYNVGRFNVT AAVGGYKSES

[0805] 601 AVAIGTGFRF TENFAAKAGV AVGTSSGSSA AYHVGVNYEW LEHHHHHH*

[0806] ΔG741-961c

[0807] ATGGTCGCCGCCGACATCGGTGCGGGGCTTGCCGATGCACTAACCGCACCGCTCGACCATAAAGACAAAGGTTTGCAG

[0808] TCTTTGACGCTGGATCAGTCCGTCAGGAAAAACGAGAAACTGAAGCTGGCGGCACAAGGTGCGGAAAAAACTTATGGA

[0809] AACGGTGACAGCCTCAATACGGGCAAATTGAAGAACGACAAGGTCAGCCGTTTCGACTTTATCCGCCAAATCGAAGTG

[0810] GACGGGCAGCTCATTACCTTGGAGAGTGGAGAGTTCCAAGTATACAAACAAAGCCATTCCGCCTTAACCGCCTTTCAG

[0811] ACCGAGCAAATACAAGATTCGGAGCATTCCGGGAAGATGGTTGCGAAACGCCAGTTCAGAATCGGCGACATAGCGGGC

[0812] GAACATACATCTTTTGACAAGCTTCCCGAAGGCGGCAGGGCGACATATCGCGGGACGGCGTTCGGTTCAGACGATGCC

[0813] GGCGGAAAACTGACCTACACCATAGATTTCGCCGCCAAGCAGGGAAACGGCAAAATCGAACATTTGAAATCGCCAGAA

[0814] CTCAATGTCGACCTGGCCGCCGCCGATATCAAGCCGGATGGAAAACGCCATGCCGTCATCAGCGGTTCCGTCCTTTAC

[0815] AACCAAGCCGAGAAAGGCAGTTACTCCCTCGGTATCTTTGGCGGAAAAGCCCAGGAAAGTTGCCGGCAGCGCGGAAGTG

[0816] AAAACCGTAAACGGCATACGCCATATCGGCCTTGCCGCCAAGCAACTCGAGGGTGGCGGAGGCACTGGATCCGCCACA

[0817] AACGACGACGATGTTAAAAAAGCTGCCACTGTGGCCATTGCTGCTGCCTACAACAATGGCCAAGAAATCAACGGTTTC

[0818] AAAGCTGGAGAGACCATCTACGACATTGATGAAGACGGCACAATTACCAAAAAAGACGCAACTGCAAGCCGATGTTGAA

[0819] GCCGACGACTTTAAAGGTCTGGGTCTGAAAAAAGTCGTGACTAACCTGACCAAAACCGTCAATGAAAACAAACAAAAC

[0820] GTCGATGCCAAAGTAAAAGCTGCAGAATCTGAAATAGAAAAGTTAACAACCAAGTTAGCAGACACTGATGCCGCTTTA

[0821] GCAGATACTGATGCCGCTCTGGATGCAACCACCAACGCCTTGAATAAATTGGGAGAAAATATAACGACATTTGCTGAA

[0822] GAGACTAAGACAAATATCGTAAAAATTGATGAAAAATTAGAAGCCGTGGCTGATACCGTCGACAAGCATGCCGAAGCA

[0823] TTCAACGATATCGCCGATTCATTGGATGAAACCAACACTAAGGCAGACGAAGCCGTCAAAACCGCCAATGAAAGCCAAA

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[0825] GCCGCTGGCACAGCTAATACTGCAGCCGACAAGGCCGAAGCTGTCGCTGCAAAAGTTACCGACATCAAAGCTGATATC

[0826] GCTACGAACAAAGATAATATTGCTAAAAAAGCAAACAGTGCCGACGTGTACACCAGAGAAGAGTCTGACAGCAAATTT

[0827] GTCAGAATTGATGGTCTGAACGCTACTACCGAAAAATTGGACACACGCTTGGCTTCTGCTGAAAAATCCATTGCCGAT

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[0829] GCCGCGCTCTCCGGTCTGTTCCAACCTTACAACGTGGGTCTCGAGCACCACCACCACCACCACTGA

[0830] 1 MVAADIGAGL ADALTAPLDH KDKGLQSLTL DQSVRKNEKL KLAAQGAEKT

[0831] 51 YGNGDSLNTG KLKNDKVSRF DFIRQIEVDG QLITLESGEF QVYKQSHSAL

[0832] 101 TAFQTEQIQD SEHSGKMVAK RQFRIGDIAG EHTSFDKLPE GGRATYRRGTA

[0833] 151 FGSDDAGGKL TYTIDFAAKQ GNGKIEHLKS PELNVDLAAA DIKPDGKRHA

[0834] 201 VISGSVLYNQ AEKGSYSLGI FGGKAQEVAG SAEVKTVNGI RHIGLAAKQL

[0835] 251 EGGGGTGSAT NDDDVKKAAT VAIAAAYNNG QEINGFKAGE TIYDIDEDGT

[0836] 301 ITKKDATAAD VEADDFKGLG LKKVVTNLTK TVNENKQNVD AKVKAAESEI

[0837] 351 EKLTTKLADT DAALADTDAA LDATTNALNK LGENITTFAE ETKTNIVKID

[0838] 401 EKLEAVADTV DKHAEAFNDI ADSLDETNTK ADEAVKTANE AKQTAEETKQ

[0839] 451 NVDAKVKAAE TAAGKAEAAA GTANTAADKA EAVAAKVTDI KADIATNKDN

[0840] 501 IAKKANSADV YTREESDSKF VRIDGLNATT EKLDTRLASA EKSIADHDTR

[0841] 551 LNGLDKTVSD LRKETRQGLA EQAALSGLFQ PYNVGLEHHH HHH*

[0842] <u>ΔG741-983</u>

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[0844] TCTTTGACGCTGGATCAGTCCGTCAGGAAAAACGAGAAACTGAAGCTGGCGGCACAAGGTGCGGAAAAAACTTATGGA

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[0846] GACGGGCAGCTCATTACCTTGGAGAGTGGAGAGTTCCAAGTATACAAACAAAGCCATTCCGCCTTAACCGCCTTTCAG

[0847] ACCGAGCAAATACAAGATTCGGAGCATTCCGGGAAGATGGTTGCGAAACGCCAGTTCAGAATCGGCGACATAGCGGGC

[0848] GAACATACATCTTTTGACAAGCTTCCCGAAGGCGGCAGGGCGACATATCGCGGGACGGCGTTCGGTTCAGACGATGCC

[0849] GGCGGAAAACTGACCTACACCATAGATTTCGCCGCCAAGCAGGGAAACGGCAAAATCGAACATTTGAAATCGCCAGAA

[0850] CTCAATGTCGACCTGGCCGCCGCCGATATCAAGCCGGATGGAAAACGCCATGCCGTCATCAGCGGTTCCGTCCTTTAC

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[0855] GATGCCAAAATCAATGCCCCCCCCCCGAATCTGCATACCGGAGACTTTCCAAACCCAAATGACGCATACAAGAATTTG

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[0875] TTGGGCAAACTGCTGAAAGTGGACGGTACGGCGATTATCGGCGGCAAGCTGTACATGTCGGCACGCGGCAAGGGGGCA

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[0898] 201 VISGSVLYNQ AKKGSYSLGI FGGKAQEVAG SAEVKTVNGI RHIGLAAKQL

[0899] 251 EGSGGGGTSA PDFNAGGTGI GSNSRATTAK SAAVSYAGIK NEMCKDRSML

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[0902] 401 GGKDIEASFD DEAVIETEAK PTDIRHVKEI GHIDLVSHII GGRSVDGRPA

[0903] 451 GGIAPDATLH IMNTNDETKN EMMVAAIRNA WVKLGERGVR IVNNSFGTTS

[0904] 501 RAGTADLFQI ANSEEQYRQA LLDYSGGDKT DEGIRLMQQS DYGNLSYHIR

[0905] 551 NKNMLFIFST GNDAQAQPNT YALLPFYEKD AQKGIITVAG VDRSGEKFKR

[0906] 601 EMYGEPGTEP LEYGSNHCGI TAMWCLSAPY EASVRFTRTN PIQIAGTSFS

[0907] 651 APIVTGTAAL LLQKYPWMSN DNLRTTLLTT AQDIGAVGVD SKFGWGLDA

[0908] 701 GKAMNGPASF PFGDFTADTK GTSDIAYSFR NDISGTGGLI KKGGSQLQLAH

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[0910] 801 VYLADTDQSG ANETVHIKGS LQLDGKGTLY TRLGKLLKVD GTAIIGGKLY

[0911] 851 MSARGKGAGY LNSTGRRVPF LSAAKIGQDY SFFTNIETDG GLLASLDSVE

[0912] 901 KTAGSEGDTL SYYVRRGNAA RTASAAAHSA PAGLKHAVEQ GGSNLENLMV

[0913] 951 ELDASESSAT PETVETAAAD RTDMPGIRPY GATFRAAAAV QHANAADGVR

[0914] 1001 IFNSLAATVY ADSTAAHADM QGRRLKAVSD GLDHNGTGLR VIAQTQQDGG

[0915] 1051 TWEQGGVEGK MRGSTQTVGI AAKTGENTTA AATLGMGRST WSENSANAKT

[0916] 1101 DSISLFAGIR HDAGDIGYLK GLFSYGRYKN SISRSTGADE HAEGSVNGTL

[0917] 1151 MQLGALGGVN VPFAATGDLT VEGGLRYDLL KQDAFAEKGS ALGWSGNSLT

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[0919] 1251 GKTGARNMPH TRLVAGLGAD VEFGNGWNGL ARYSYAGSKQ YGNHSGRVGV

[0920] 1301 GYRFLEHHHH HH*

[0921] ΔG741-ORF46.1

[0922] ATGGTCGCCGCCGACATCGGTGCGGGGCTTGCCGATGCACTAACCGCACCGCTCGACCATAAAGACAAAGGTTTGCAG

[0923] TCTTTGACGCTGGATCAGTCCGTCAGGAAAAACGAGAAACTGAAGCTGGCGGCACAAGGTGCGGAAAAAACTTATGGA

[0924] AACGGTGACAGCCTCAATACGGGCAAATTGAAGAACGACAAGGTCAGCCGTTTCGACTTTATCCGCCAAATCGAAGTG

[0925] GACGGGCAGCTCATTACCTTGGAGAGTGGAGAGTTCCAAGTATACAAACAAAGCCATTCCGCCTTAACCGCCTTTCAG

[0926] ACCGAGCAAATACAAGATTCGGAGCATTCCGGGAAGATGGTTGCGAAACGCCAGTTCAGAATCGGCGACATAGCGGGC

[0927] GAACATACATCTTTTGACAAGCTTCCCGAAGGCGGCAGGGCGACATATCGCGGGACGGCGTTCGGTTCAGACGATGCC

[0928] GGCGGAAAACTGACTACACCATAGATTTCGCCGCCAAGCAGGGAAACGGAAATCGAACATTTCGAAATCGCCAGAA

[0929] CTCAATGTCGACCTGGCCGCCGCCGATATCAAGCCGGATGGAAAACGCCATGCCGTCATCAGCGGTTCCGTCCTTTAC

[0930] AACCAAGCCGAGAAAGGCAGTTACTCCCTCGGTATCTTTGGCGGAAAAGCCCAGGAAGTTGCCGCCAGCGCGGAAGTG

[0931] AAAACCGTAAACGGCATACGCCATATCGGCCTTGCCGCCAAGCAACTCGACGGTGGCGGAGGCACTGGATCCTCAGAT

[0932] TTGGCAAACGATTCTTTTATCCGGCAGGTTCTCGACCGTCAGCATTTCGAACCCGACGGGAAATACCACCTATTCGGC

[0933] AGCAGGGGGGAACTTGCCGAGCGCAGCGGCCATATCGGATTGGGAAAAATACAAAGCCATCAGTTGGGCAACCTGATG

[0934] ATTCAACAGGCGGCCATTAAAGGAAATATCGGCTACATTGTCCGCTTTTCCGATCACGGGCACGAAGTCCATTCCCCC

[0935] TTCGACAACCATGCCTCACATTCCGATTCTGATGAAGCCGGTAGTCCCGTTGACGGATTTAGCCTTTACCGCATCCAT

[0936] TGGGACGGATACGAACACCATCCCCCCGACGGCTATGACGGGCCACAGGGCGGCGGCTATCCCGCTCCCAAAGGCGCG

[0937] AGGGATATATACAGCTACGACATAAAAGGCGTTGCCCAAAATATCCGCCTCAACCTGACCGACAACCGCAGCACCGGA

[0938] CAACGGCTTGCCGACCGTTTCCACAATGCCGGTAGTATGCTGACGCAAGGAGTAGGCGACGGATTCAAACGCGCCACC

[0939] CGATACAGCCCCGAGCTGGACAGATCGGGCAATGCCGCCCAAGCCTTCAACGGCACTGCAGATATCGTTAAAAACATC

[0940] ATCGGCGCGGCAGGAGAAATTGTCGGCGCAGGCGATGCCGTGCAGCGGCATAAGCGAAGGCTCAAACATTCCTGTCATG

[0941] CACGGCTTGGGTCTGCTTTCCACCGAAAACAAGATGGCGCGCATCAACGATTTGGCAGATATGGCGCAACTCAAAGAC

[0942] TATGCCGCAGCAGCCATCCGCGATTGGGCAGTCCAAAACCCCAATGCCGCACAAGGCATAGAAGCCGTCAGCAATATC

[0943] TTTATGGCAGCCATCCCCATCAAAGGGATTCGAGCTGTTCGGGGAAAATACGGCTTGGGCGGCATCACCGCACATCCT

[0944] ATCAACCGGTCGCAGATGGGCGCGATCGCATTGCCGAAAGGGAAATCCGCCGTCAGCGACAATTTTGCCGATGCGGCA

[0945] TACGCCAAATACCCGTCCCCTTACCATTCCCGAAATATCCGTTCAAACTTGGAGCAGCGTTACGGCAAAGAAAACATC

[0946] ACCTCCTCAACCGTGCCGCCGTCAAACGGCAAAAATGTCAAACTGGCAGACCAACGCCACCCGAAGACAGGCGTACCG

[0947] TTTGACGGTAAAGGGTTTCCGAATTTTGAGAAGCACGTGAAATATGATACGCTCGAGCACCACCACCACCACCACTCGA

[0948] 1 MVAADIGAGL ADALTAPLDH KDKGLQSLTL DQSVRKNEKL KLAAQGAEKT

[0949] 51 YGNGDSLNTG KLKNDKVSRF DFIRQIEVDG QLITLESGEF QVYKQSHSAL

[0950] 101 TAFQTEQIQD SEHSGKMVAK RQFRIGDIAG EHTSFDKLPE GGRATYRGTA

[0951] 151 FGSDDAGGKL TYTIDFAAKQ GNGKIEHLKS PELNVDLAAA DIKPDGKRHA

[0952] 201 VISGSVLYNQ AEKGSYSLGI FGGKAQEVAG SAEVKTVNGI RHIGLAAKQL

[0953] 251 DGGGGTGSSD LANDSFIRQV LDRQHFEPDG KYHLFGSRGE LAERSGHIGL

[0954] 301 GKIQSHQLGN LMIQQAAIKG NIGYIVRFSD HGHEVHSPFD NHASHSDSDE

[0955] 351 AGSPVDGFSL YRIHWDGYEH HPADGYDGPQ GGGYPAPKGA RDIYSYDIKG

[0956] 401 VAQNIRLNLT DNRSTGQRLA DRFHNAGSML TQGVGDGFKRATRYSPELDR

[0957] 451 SCNAAEAFNG TADIVKNIIG AAGEIVGAGD AVQGISEGSN IAVMHGLGLL

[0958] 501 STENKMARIN DLADMAQLKD YAAAAIRDWA VQNPNAAQGI EAVSNIFMAA

[0959] 551 IPIKGIGAVR GKYGLGGITA HPIKRSQMGA IALPKGKSAV SDNFADAAYA

[0960] 601 KYPSPYHSRN IRSNLEQRYG KENITSSTVP PSNGKNVKLA DQRHPKTGVP

[0961] 651 FDGKGFPNFE KHVKYDTLEH HHHHH*

[0962] 实施例5-287的杂交体

[0963] 以全长、具有C-末端His-标记或无其前导肽但具有C-末端His-标记的287的表达水平非常低。用N-末端GST-融合实现了较好的表达。将GST用作N-末端融合配体的替代方法，将287置于蛋白质919的C-末端（‘919-287′）、蛋白质953的C-端（‘953-287′）和蛋白质ORF46.1的C-末端（‘ORF46.1-287′）。在这两种方法中，前导肽都是缺失的，且杂交体是直接的符合读杠的融合。

[0964] 为了制备953-287杂交体，通过设计正向引物自各序列前导区的下游，除去两种蛋白质的前导肽；在953反向引物中除去终止密码子序列，但在287反向引物中包含终止密码子序列。对953基因而言，用于扩增的5′和3′引物分别包括NdeI和BamHI限制酶切位点，而对287基因的扩增而言，5′和3′引物分别包括BamHI和XhoI限制酶切位点。用这种方法，用NdeI-BamHI（克隆第一个基因）且随后用BamHI-XhoI（克隆第二个基因），可以实现pET21b+中两个基因的顺序定向克隆。

[0965] 通过将编码287的成熟部分的序列克隆入pET21b+中的919-His克隆的3′-端的XhoI位点，可以得到919-287杂交体。设计用于扩增287基因的引物，从而在PCR片段

的 5′ –引入 SalI 限制酶切位点并在 3′ –引入 XhoI 位点。因为由 SalI 和 XhoI 限制酶产生的粘性末端是相容的，因此可以将由 SalI-XhoI 消化的 287PCR 产物插入到由 XhoI 切割的 pET21b-919 克隆中。

[0966] 类似地得到 ORF46.1-287 杂交体。

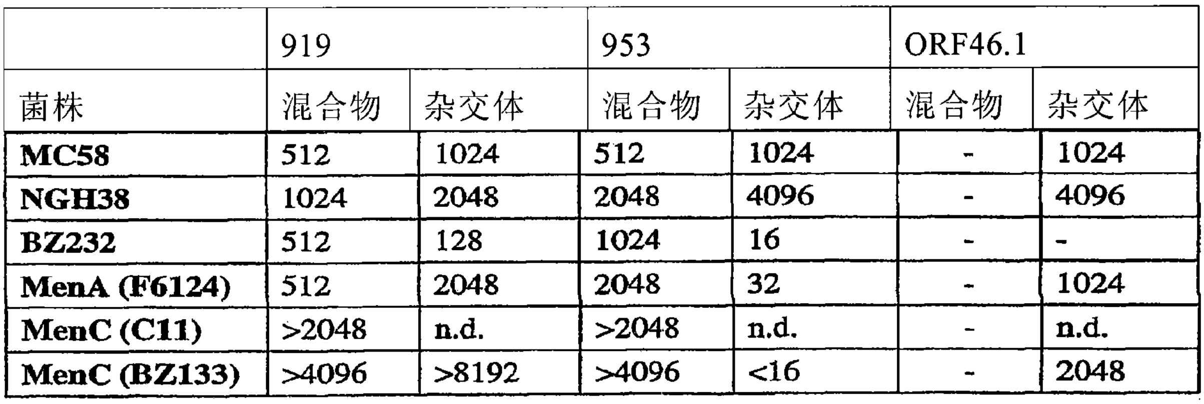
[0967] 将针对杂交蛋白产生的抗体的杀菌效力（同源菌株）与针对组分抗原的简单混合物产生的抗体相比：

[0968]

	与 287 的混合物	与 287 的杂交体
919	32000	16000
953	8192	8192
ORF46.1	128	8192

[0969] 对 919-287 和 953-287 而言，还获得了针对异源 MenB 菌株和针对血清型 A 和 C 的杀菌活性的数据：

[0970]



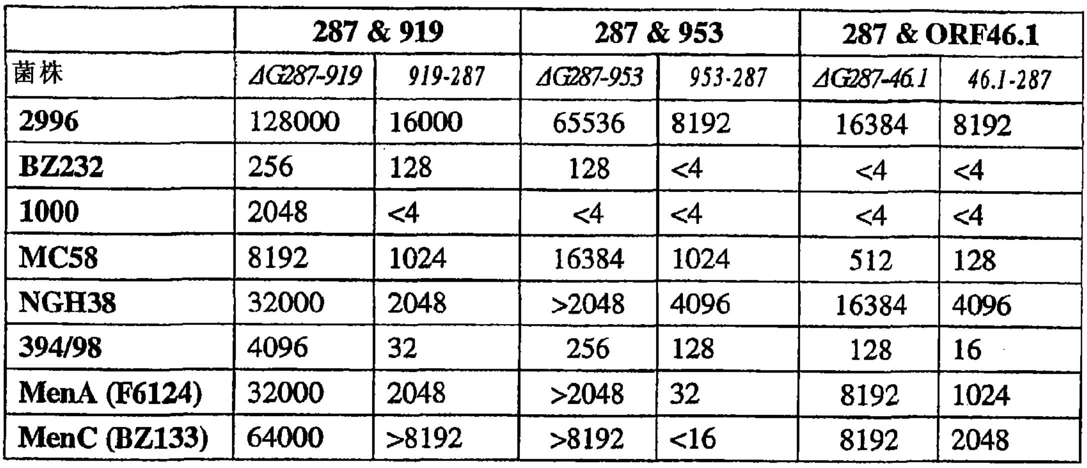
	919		953		ORF46.1	
菌株	混合物	杂交体	混合物	杂交体	混合物	杂交体
MC58	512	1024	512	1024	-	1024
NGH38	1024	2048	2048	4096	-	4096
BZ232	512	128	1024	16	-	-
MenA (F6124)	512	2048	2048	32	-	1024
MenC (C11)	>2048	n.d.	>2048	n.d.	-	n.d.
MenC (BZ133)	>4096	>8192	>4096	<16	-	2048

[0971] 还构建了 ORF46.1 和 919 的杂交体。在 N- 末端用 919 得到了最佳结果（高 4 倍的滴定度）。

[0972] 还测试了杂交体 919-519His、ORF97-225His 和 225-ORF97His。它们的 ELISA 滴定度和杀菌抗体应答结果中等。

[0973] 两种蛋白质 A 和 B 的杂交体可以是 NH_2-A-B-COOH 或 NH_2-B-A-COOH，用△ G287 还制得了在 N- 末端与 287“反向”杂交的杂交体。使用一系列菌株，包括同源菌株 2996。FCA 用作佐剂：

[0974]



	287 & 919		**287 & 953**		**287 & ORF46.1**	
菌株	*ΔG287-919*	*919-287*	*ΔG287-953*	*953-287*	*ΔG287-46.1*	*46.1-287*
2996	128000	16000	65536	8192	16384	8192
BZ232	256	128	128	<4	<4	<4
1000	2048	<4	<4	<4	<4	<4
MC58	8192	1024	16384	1024	512	128
NGH38	32000	2048	>2048	4096	16384	4096
394/98	4096	32	256	128	128	16
MenA (F6124)	32000	2048	>2048	32	8192	1024
MenC (BZ133)	64000	>8192	>8192	<16	8192	2048

[0975] 通常在N-末端用287观察到较好的杀菌滴定度。

[0976] 当融合于蛋白质961[如上所示的NH_2-△G287-961-COOH-序列]时，得到的蛋白质是不溶解的，纯化必须将其变性和复性。在复性后，发现约50％蛋白质仍不溶解。比较可溶和不溶蛋白质，用可溶蛋白质得到更好的杀菌滴定度(FCA作为佐剂)：

[0977]

	2996	BZ232	MC58	NGH38	F6124	BZ133
可溶的	65536	128	4096	>2048	>2048	4096
不溶的	8192	<4	<4	16	n. d.	n. d.

[0978] 但用明矾佐剂替代，可以改善不溶形式的蛋白质的滴定度：

[0979]

不溶的	32768	128	4096	>2048	>2048	2048

[0980] 还在杂交蛋白中使用961C(见上)。由于961及其结构域变体指导有效的表达，它们非常适合作为杂交蛋白的N-末端部分。

[0981] 实施例23-其它杂交体

[0982] 附图中显示本发明的其它杂交蛋白，它们具有如下所示的序列。当与单独蛋白质相比时，这此杂交蛋白是有利的：

[0983] <u>ORF46.1-741</u>

[0984] ATGTCAGATTTGGCAAACGATTCTTTTATCCGGCAGGTTCTCGACCGTCAGCATTTCGAACCCGACGGGAAATACCAC

[0985] CTATTCGGCAGCAGGGGGGAACTTGCCGAGCGCAGCGGCCATATCGGATTGGGAAAAATACAAAGCCATCAGTTGGGC

[0986] AACCTGATGATTCAACAGGCGGCCATTAAAGGAAATATCGGCTACATTGTCCGCTTTTCCGATCACGGGCACGAAAGTC

[0987] CATTCCCCCTTCGACAACCATGCCTCACATTCCGATTCTGATGAAGCCGGTAGTCCCGTTGACGCATTTAGCCTTTAC

[0988] CGCATCCATTGGGACGGATACGAACACCATCCCGCCGACGGCTATGACGGGCCACAGGGCGGCGGCTATCCCGCTCCC

[0989] AAAGGCGCGAGGGATATATACAGCTACGACATAAAAGGCGTTGCCCAAAATATCCGCCTCAACCTGACCGACAACCGC

[0990] AGCACCGGACAACGGCTTGCCGACCGTTTCCACAATGCCGGTAGTATGCTGACGCAAGGAGTAGGCGACGGATTCAAA

[0991] CGCGCCACCCGATACAGCCCCGAGCTGGACAGATCGGGCAATGCCGCCGAAGCCTTCAACGGCACTGCAGATATCGTT

[0992] AAAAACATCATCGGCGCGGCAGGAGAAATTGTCGGCGCAGGCGATGCCGTGCAGGGCATTAAGCGAAGGCTCAAACATT

[0993] GCTGTCATGCACGGCTTGGGTCTGCTTTCCACCGAAAACAAGATGGCGCGCATCAACGATTTGGCAGATATGGCGCAA

[0994] CTCAAAGACTATGCCGCAGCAGCCATCCGCGATTGGGCAGTCCAAAACCCCAATGCCGCACAAGGCATAGAAGCCGTC

[0995] AGCAATATCTTTATGGCAGCCATCCCCATCAAAGGGATTGGAGCTGTTCGGGGAAAATACGGCTTGGGCGGCATCACG

[0996] GCACATCCTATCAAGCGGTCGCAGATGGGCGCGATCGCATTGCCGAAAGGGAAATCCGCCGTCAGCGACAATTTTGCC

[0997] GATGCGGCATACGCCAAATACCCGTCCCCTTACCATTCCCGAAATATCCGTTCAAACTTGGAGCAGCGTTACGGCAAA

[0998] GAAAACATCACCTCCTCAACCGTGCCGCCGTCAAACGGCAAAAATGTCAAACTGGCAGACCAACGCCACCCGAAGACA

[0999] GGCGTACCGTTTCACGGTAAAGGGTTTCCGAATTTTGAGAAGCACGTGAAATATGATACGGGATCCGGAGGGGGTGGT

[1000] GTCGCCGCCGACATCGGTGCGGGGCTTGCCGATGCACTAACCGCACCGCTCGACCATAAAGACAAAGGTTTGCAGTCT

[1001] TTGACGCTGGATCAGTCCGTCAGGAAAAACGAGAAACTGAAGCTGGCGGCACAAGGTGCGGAAAAAACTTATGGAAAC

[1002] GGTGACAGCCTCAATACGGGCAAATTGAAGAACGACAAGGTCAGCCGTTTCGACTTTATCCGCCAAATCGAAGTGGAC

[1003] GGGCAGCTCATTACCTTGGAGAGTGGAGAGTTCCAAGTATACAAACAAAGCCATTCCGCCTTAACCGCCTTTCAGACC

[1004] GAGCAAATACAAGATTCGGAGCATTCCGGGAAGATGGTTGCGAAACGCCAGTTCAGAATCGGCGACATAGCGGGCGAA

[1005] CATACATCTTTTGACAAGCTTCCCGAAGGCGGCAGGGCGACATATCGCGGGACGGCGTTCGGTTCAGACGATGCCGGC

[1006] GGAAAACTGACCTACACCATAGATTTCGCCGCCAAGCAGGGAAACGGCAAAATCGAACATTTGAAATCGCCAGAACTC

[1007] AATGTCGACCTGGCCGCCGCCGATATCAAGCCGGATGGAAAACGCCATGCCGTCATCAGCGGTTCCGTCCTTTACAAC

[1008] CAAGCCGAGAAAGGCAGTTACTCCCTCGGTATCTTTGGCGGAAAAGCCCAGGAAGTTGCCGGCAGCGCGGAAGTGAAA

[1009] ACCGTAAACGGCATACGCCATATCGGCCTTGCCGCCAAGCAACTCGAGCACCACCACCACCACCACTGA

[1010] 1 MSDLANDSFI RQVLDRQHFE PDGKYHLFGS RGELAERSGH IGLGKIQSHQ

[1011] 51 LGNLMIQQAA IKGNIGYIVR FSDHGHEVHS PFDNHASHSD SDEAGSPVDG

[1012] 101 FSLYRIHWDG YEHHPADGYD GPQGGGYPAP KGARDIYSYD IKGVAQNIRL

[1013] 151 NLTDNRSTGQ RLADRFHNAG SMLTQGVGDG FKRATRYSPE LDRSGNAAEA

[1014] 201 FNGTADIVKN IIGAAGEIVG AGDAVQGISE GSNIAVMHGL GLLSTENKMA

[1015] 251 RINDLADMAQ LKDYAAAAIR DWAVQNPNAA QGIEAVSNIF MAAIPIKGIG

[1016] 301 AVRGKYGLGG ITAHPIKRSQ MGAIALPKGK SAVSDNFADA AYAKYPSPYH

[1017] 351 SRNIRSNLEQ RYGKENITSS TVPPSNGKNV KIADQRHPKT GVPFDGKGFP

[1018] 401 NFEKHVKYDT GSGGGGVAAD IGAGLADALT APLDHKDKGL QSLTLDQSVR

[1019] 451 KNEKLKLAAQ GAEKTYGNGD SLNTGKLKND KVSRFDFIRQ IEVDGQLITL

[1020] 501 ESGEFQVYKQ SHSALTAFQT EQIQDSEHSG KMVAKRQFRI GDIAGEHTSF

[1021] 551 DKLPEGGRAT YRGTAFGSDD AGGKLTYTID FAAKQGNGKI EHLKSPELNV

[1022] 601 DLAAADLKPD GKRHAVLSGS VLYNQAEKGS YSLGIFGGKA QEVAGSAEVK

[1023] 651 TVNGIRHIGL AAKQLEHHHH HH*

[1024] ORF46.1-961

[1025] ATGTCAGATTTGGCAAACGATTCTTTTATCCGGCAGGTTCTCGACCGTCAGCATTTCGAACCCGACGGGAAATACCAC

[1026] CTATTCGGCAGCAGGGGGGAACTTGCCGAGCGCAGCGGCCATATCGGATTGGGAAAAATACAAAGCCATCAGTTGGGC

[1027] AACCTGATGATTCAACAGGCGGCCATTAAAGGAAATATCGGCTACATTGTCCGCTTTTCCGATCACGGGCACGAAGTC

[1028] CATTCCCCCTTCGACAACCATGCCTCACATTCCGATTCTGATGAAGCCGGTAGTCCCGTTGACGGATTTAGCCTTTAC

[1029] CGCATCCATTGGGACGGATACGAACACCATCCCGCCGACGGCTATGACGGGCCACAGGGCGGCGGCTATCCCGCTCCC

[1030] AAAGGCGCGAGGGATATATACAGCTACGACATAAAAGGCGTTGCCCAAAATATCCGCCTCAACCTGACCGACAACCGC

[1031] AGCACCGGACAACGGCTTGCCGACCGTTTCCACAATGCCGGTAGTATGCTGACGCAAGGAGTAGGCGACGGATTCAAA

[1032] CGCGCCACCCGATACAGCCCCGAGCTGGACAGATCGGGCAATGCCGCCGAAGCCTTCAACGGCACTGCAGATATCGTT

[1033] AAAAACATCATCGGCGCGGCAGGAGAAATTGTCGGCGCAGGCGATGCCGTGCAGGGCATAAGCGAAGGCTCAAACATT

[1034] GCTGTCATGCACGGCTTGGGTCTGCTTTCCACCGAAAACAAGATGGCGCGCATCAACGATTTGGCAGATATGGCGCAA

[1035] CTCAAAGACTATGCCGCAGCAGCCATCCGCGATTGGGCAGTCCAAAACCCCAATGCCGCACAAGGCATAGAAGCCGTC

[1036] AGCAATATCTTTATGGCAGCCATCCCCATCAAAGGGATTGGAGCTGTTCGGGGAAAATACGGCTTGGGCGGCATCACG

[1037] GCACATCCTATCAAGCGGTCGCAGATGGGCGCGATCGCATTGCCGAAAGGGAAATCCGCCGTCAGCGACAATTTGCC

[1038] GATGCGGCATACGCCAAATACCCGTCCCCTTACCATTCCCGAAATATCCGTTCAAACTTGGAGCAGCGTTACGGCAAA

[1039] GAAAACATCACCTCCTCAACCGTGCCGCCGTCAAACGGCAAAAATGTCAAACTGGCAGACCAACGCCACCCGAAGACA

[1040] GGCGTACCGTTTGACGGTAAAGGGTTTCCGAATTTTGAGAAGCACGTGAAATATGATACGGGATCCGGAGGAGGAGGA

[1041] GCCACAAACGACGACGATGTTAAAAAAGCTGCCACTGTGGCCATTGCTGCTGCCTACAACAATGGCCAAGAAATCAAC

[1042] GGTTTCAAAGCTGGAGAGACCATCTACGACATTGATGAAGACGGCACAATTACCAAAAAAGACGCAACTGCAGCCGAT

[1043] GTTGAAGCCGACGACTTTAAAGGTCTGGGTCTGAAAAAAGTCGTGACTAACCTGACCAAAACCGTCAATGAAAACAAA

[1044] CAAAACGTCGATGCCAAAGTAAAAGCTGCAGAATCTGAAATAGAAAAGTTAACAACCAAGTTAGCAGACACTGATGCC

[1045] GCTTTAGCAGATACTGATGCCGCTCTGGATGCAACCACCAACGCCTTGAATAAATTGGGAGAAAATATAACGACATTT

[1046] GCTGAAGAGACTAAGACAAATATCGTAAAAATTGATGAAAAATTAGAAGCCGTGGCTGATACCGTCGACAAGCATGCC

[1047] GAAGCATTCAACGATATCGCCGATTCATTGGATGAAACCAACACTAAGGCAGACGAAGCCGTCAAAACCGCCAATGAA

[1048] GCCAAACAGACGGCCGAAGAAACCAAACAAAACGTCGATGCCAAAGTAAAAGCTGCAGAAACTGCAGCAGGCAAAGCC

[1049] GAAGCTGCCGCTGGCACAGCTAATACTGCAGCCGACAAGGCCGAAGCTGTCGCTGCAAAAGTTACCGACATCAAAGCT

[1050] GATATCGCTACGAACAAAGATAATATTGCTAAAAAAGCAAACAGTGCCGACGTGTACACCAGAGAAGAGTCTGACAGC

[1051] AAATTTGTCAGAATTGATGGTCTGAACGCTACTACCGAAAAATTGGACACACGCTTGGCTTCTGCTGAAAAATCCATT

[1052] GCCGATCACGATACTCGCCTGAACGGTTTGGATAAAACAGTGTCAGACCTGCGCAAAGAAACCCGCCAAGGCCTTGCA

[1053] GAACAAGCCGCGCTCTCCGGTCTGTTCCAACCTTACAACGTGGGTCGGTTCAATGTAACGGCTGCAGTCGGCGGCTAC

[1054] AAATCCGAATCGGCAGTCGCCATCGGTACCGGCTTCCGCTTTACCGAAAACTTTGCCGCCAAAGCAGGCGTGGCAGTC

[1055] GGCACTTCGTCCGGTTCTTCCGCAGCCTACCATGTCGGCGTCAATTACGAGTGGCTCGAGCACCACCACCACCACCAC

[1056] TGA

[1057] 1 MSDLANDSFI RQVLDRQHFE PDGKYHLFGS RGELAERSGH IGLGKIQSHQ

[1058] 51 LGNLMIQQAA IKGNIGYIVR FSDHGHEVHS PFDNHASHSD SDEAGSPVDG

[1059] 101 FSLYRIHWDG YEHHPADGYD GPQGGGYPAP KGARDIYSYD IKGVAQNIRL

[1060] 151 NLTDNRSTGQ RLADRFHNAG SMLTQGVGDG FKRATRYSPE LDRSGNAAEA

[1061] 201 FNGTADIVKN IIGAAGEIVG AGDAVQGISE GSNIAVMHGL GLLSTENKMA

[1062] 251 RINDLADMAQ LKDYAAAAIR DWAVQNPNAA QGIEAVSNIF MAAIPIKGIG

[1063] 301 AVRGKYGLGG ITAHPIKRSQ MGAIALPKGK SAVSDNFADA AYAKYPSPYH

[1064] 351 SRNIRSNLEQ RYGKENITSS TVPPSNGKNV KLADQRHPKT GVPFDGKGFP

[1065] 401 NFEKHVKYDT GSGGGGATND DDVKKAATVA IAAAYNNGQE INGFKAGETI

[1066] 451 YDIDEDGTIT KKDATAADVE ADDFKGLGLK KVVTNLTKTV NENKQNVDAK

[1067] 501 VKAAESEIEK LTTKLADTDA ALADTDAALD ATTNALNKLG ENITTFAEET

[1068] 551 KTNIVKIDEK LEAVADTVDK HAEAFNDIAD SLDETNTKAD EAVKTANEAK

[1069] 601 QTAEETKQNV DAKVKAAETA AGKAEAAAGT ANTAADKAEA VAAKVTDIKA

[1070] 651 DIATNKDNIA KKANSADVYT REESDSKFVR IDGLNATTEK LDTRLASAEK

[1071] 701 SIADHDTRLN GLDKTVSDLR KETRQGLAEQ AALSGLFQPY NVGRFNVTAA

[1072] 751 VGGYKSESAV AIGTGFRFTE NFAAKAGVAV GTSSGSSAAY HVGVNYEWLE

[1073] 801 HHHHHH*

[1074] ORF46.1-961c

[1075] ATGTCAGATTTGGCAAACGATTCTTTTATCCGGCAGGTTCTCGACCGTCAGCATTTCGAACCCGACGGGAAATACCAC

[1076] CTATTCGGCAGCAGGGGGGAACTTGCCGAGCGCAGCGGCCATATCGGATTGGGAAAAATACAAAGCCATCAGTTGGGC

[1077] AACCTGATGATTCAACAGGCGGCCATTAAAGGAAATATCGGCTACATTGTCCGCTTTTCCGATCACGGGCACGAAGTC

[1078] CATTCCCCCTTCGACAACCATGCCTCACATTCCGATTCTGATGAAGCCGGTAGTCCCGTTGACGGATTTAGCCTTTAC

[1079] CGCATCCATTGGGACGGATACGAACACCATCCCGCCGACGGCTATGACGGGCCACAGGGCGGCGGCTATCCCGCTCCC

[1080] AAAGGCGCGAGGGATATATACAGCTACGACATAAAAGGCGTTGCCCAAAATATCCGCCTCAACCTGACCGACAACCGC

[1081] AGCACCGGACAACGGCTTGCCGACCGTTTCCACAATGCCGGTAGTATGCTGACGCAAGGAGTAGGCGACGGATTCAAA

[1082] CGCGCCACCCGATACAGCCCCGAGCTGGACAGATCGGGCAATGCCGCCGAAGCCTTCAACGGCACTGCAGATATCGTT

[1083] AAAAACATCATCGGCGCGGCAGGAGAAATTGTCGGCGCAGGCGATGCCGTGCAGGGCATAAGCGAAGGCTCAAACATT

[1084] GCTGTCATGCACGGCTTGGGTCTGCTTTCCACCGAAAACAAGATGGCGCGCATCAACGATTTGGCAGATATGGCGCAA

[1085] CTCAAAGACTATGCCGCAGCAGCCATCCGCGATTGGGCAGTCCAAAACCCCAATGCCGCACAAGGCATAGAAGCCGTC

[1086] AGCAATATCTTTATGGCAGCCATCCCCATCAAAGGGATTGCAGCTGTTCGGGGAAAATACGGCTTGGGCGGCATCACG

[1087] GCACATCCTATCAAGCGGTCGCAGATGGGCGCGATCGCATTGCCGAAAGGGAAATCCGCCGTCAGCGACAATTTTGCC

[1088] GATGCGGCATACGCCAAATACCCGTCCCCTTACCATTCCCGAAATATCCGTTCAAACTTGGAGCAGCGTTACGGCAAA

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[1513] GATACTGATGCCGCTCTGGATGCAACCACCAACGCCTTGAATAAATTGGGAGAAAATATAACGACATTTGCTGAAGAG

[1514] ACTAAGACAAATATCGTAAAAATTGATGAAAAATTAGAAGCCGTGGCTGATACCGTCGACAAGCATGCCGAAGCATTC

[1515] AACGATATCGCCGATTCATTGGATGAAACCAACACTAAGGCAGACGAAGCCGTCAAAACCGCCAATGAAGCCAAACAG

[1516] ACGGCCGAAGAAACCAAACAAAACGTCGATGCCAAAGTAAAAGCTGCAGAAACTGCAGCAGGCAAAGCCGAAGCTGCC

[1517] GCTGGCACAGCTAATACTGCAGCCGACAAGGCCGAAGCTGTCGCTGCAAAAGTTACCGACATCAAAGCTGATATCGCT

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[1519] AGAATTGATGGTCTGAACGCTACTACCGAAAAATTGGACACACGCTTGGCTTCTGCTGAAAAATCCATTGCCGATCAC

[1520] GATACTCGCCTGAACGGTTTGGATAAAACAGTGTCAGACCTGCGCAAAGAAACCCGCCAAGGCCTTGCAGAACAAGCC

[1521] GCGCTCTCCGGTCTGTTCCAACCTTACAACGTGGGTGGATCCGGAGGGGGTGGTGTCGCCGCCGACATCGGTGCGGGG

[1522] CTTGCCGATGCACTAACCGCACCGCTCGACCATAAACACAAAGGTTTGCAGTCTTTGACGCTGGATCAGTCCGTCAGG

[1523] AAAAACGAGAAACTGAAGCTGGCGGCACAAGGTGCGGAAAAAACTTATGGAAACGGTGACAGCCTCAATACGGGCAAA

[1524] TTGAAGAACGACAAGGTCAGCCGTTTCGACTTTATCCGCCAAATCGAAGTGGACGGGCAGCTCATTACCTTGGAGAGT

[1525] GGAGAGTTCCAAGTATACAAACAAAGCCATTCCGCCTTAACCGCCTTTCAGACCGAGCAAATACAAGATTCGGAGCAT

[1526] TCCGGGAAGATGGTTGCGAAACGCCAGTTCAGAATCGGCGACATAGCGGGCGAACATACATCTTTTGACAAGCTTCCC

[1527] GAAGGCGGCAGGGCGACATATCGCGGGACGGCGTTCGGTTCAGACGATGCCGGCGGAAAACTGACCTACACCATAGAT

[1528] TTCGCCGCCAAGCAGGGAAACGGCAAAATCGAACATTTGAAATCGCCAGAACTCAATGTCGACCTGGCCGCCGCCGAT

[1529] ATCAAGCCGGATGGAAAACGCCATGCCGTCATCAGCGGTTCCGTCCTTTACAACCAAGCCGAGAAAGGCAGTTACTCC

[1530] CTCGGTATCTTTGGCGGAAAAGCCCAGGAAGTTGCCGGCAGCGCGGAAGTGAAAACCGTAAACGGCATACGCCATATC

[1531] GGCCTTGCCGCCAAGCAACTCGAGCACCACCACCACCACCACTGA

[1532] 1 MKHFPSKVLT TAILATFCSG ALAATNDDDV KKAATVAIAA AYNNGQEING

[1533] 51 FKAGETIYDI DEDGTITKKD ATAADVEADD FKGLGLKKVV TNLTKTVNEN

[1534] 101 KQNVDAKVKA AESEIEKLTT KLADTDAALA DTDAALDATT NALNKLGENI

[1535] 151 TTFAEETKTN IVKIDEKLEA VADTVDKHAE AFNDIADSLD ETNTKADEAV

[1536] 201 KTANEAKQTA EETKQNVDAK VKAAETAAGK AEAAAGTANT AADKAEAVAA

[1537] 251 KVTDIKADIA TNKDNIAKKA NSADVYTREE SDSKFVRIDG LNATTEKLDT

[1538] 301 RLASAEKSIA DHDTRLNGLD KTVSDLRKET RQGLAEQAAL SGLFQPYNVG

[1539] 351 GSGGGGVAAD IGAGLADALT APLDHKDKGL QSLTLDQSVR KNEKLKLAAQ

[1540] 401 GAEKTYGNGD SLNTGKLKND KVSRFDFIRQ IEVDGQLITL ESGEFQVYKQ

[1541] 451 SHSALTAFQT EQIQDSEHSG KMVAKRQFRI GDIAGEHTSF DKLPEGGRAT

[1542] 501 YRGTAFGSDD AGGKLTYTID FAAKQGNGKI EHLKSPELNV DLAAADIKPD

[1543] 551 GKRHAVISGS VLYNQAEKGS YSLGIFGGKA QEVAGSAEVK TVNGIRHIGL

[1544] 601 AAKQLEHHHHH HH *

[1545] 961cL-983

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[1547] GACGACGATGTTAAAAAAGCTGCCACTGTGGCCATTGCTGCTGCCTACAACAATGGCCAAGAAATCAACGGTTTCAAA

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[1549] GACGACTTTAAAGGTCTGGGTCTGAAAAAAGTCGTGACTAACCTGACCAAAACCGTCAATGAAAACAAACAAAACGTC

[1550] GATGCCAAAGTAAAAGCTGCAGAATCTGAAATAGAAAAGTTAACAACCAAGTTAGCAGACACTGATGCCGCTTTAGCA

[1551] GATACTGATGCCGCTCTGGATGCAACCACCAACGCCTTGAATAAATTGGGAGAAAATATAACGACATTTGCTGAAGAG

[1552] ACTAAGACAAATATCGTAAAAATTGATGAAAAATTAGAAGCCGTGGCTGATACCGTCGACAAGCATGCCGAAGCATTC

[1553] AACGATATCGCCGATTCATTGGATGAAACCAACACTAAGGCAGACGAAGCCGTCAAAACCGCCAATGAAGCCAAACAG

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[1557] AGAATTGATGGTCTGAACGCTACTACCGAAAAATTGGACACACGCTTGGCTTCTGCTGAAAAATCCATTGCCGATCAC

[1558] GATACTCGCCTGAACGGTTTGGATAAAACAGTGTCAGACCTGCGCAAAGAAACCCGCCAAGGCCTTGCAGAACAAGCC

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[1563] GCAATTGAAGCAGGCTATACAGGACGCGGGGTAGAGGTAGGTATCGTCGACACAGGCGAATCCGTCGGCAGCATATCC

[1564] TTTCCCGAACTGTATGGCAGAAAAGAACACGGCTATAACGAAAATTACAAAAACTATACGGCGTATATGCGGAAGGAA

[1565] GCGCCTGAAGACGGAGGCGGTAAAGACATTGAAGCTTCTTTCGACGATGAGGCCGTTATAGAGACTGAAGCAAAGCCG

[1566] ACGGATATCCGCCACGTAAAAGAAATCGGACACATCGATTTGGTCTCCCATATTATTGGCGGGCGTTCCGTGGACGGC

[1567] AGACCTGCAGGCGGTATTGCGCCCGATGCGACGCTACACATAATGAATACGAATGATGAAACCAAGAACGAAATGATG

[1568] GTTGCAGCCATCCGCAATGCATGGGTCAAGCTGGGCGAACGTGGCGTGCGCATCGTCAATAACAGTTTTGGAACAACA

[1569] TCGAGGGCAGGCACTGCCGACCTTTTCCAAATAGCCAATTCGGAGGAGCAGTACCGCCAAGCGTTGCTCGACTATTCC

[1570] GGCGGTGATAAAACAGACGAGGGTATCCGCCTGATGCAACAGAGCGATTACGGCAACCTGTCCTACCACATCCGTAAT

[1571] AAAAACATGCTTTTCATCTTTTCGACAGGCAATGACGCACAAGCTCAGCCCAACACATATGCCCTATTGCCATTTTAT

[1572] GAAAAAGACGCTCAAAAAGGCATTATCACAGTCGCAGGCGTAGACCGCAGTGGAGAAAAGTTCAAACGGGAAATGTAT

[1573] GGAGAACCGGGTACAGAACCGCTTGAGTATGGCTCCAACCATTGCGGAATTACTGCCATGTGGTGCCTGTCGGCACCC

[1574] TATGAAGCAAGCGTCCGTTTCACCCGTACAAACCCGATTCAAATTGCCGGAACATCCTTTTCCGCACCCATCGTAACC

[1575] GGCACGGCGGCTCTGCTGCTGCAGAAATACCCGTGGATGAGCAACGACAACCTGCGTACCACGTTGCTGACGACGGCT

[1576] CAGGACATCGGTGCAGTCGGCGTGGACAGCAAGTTCGGCTGGGGACTGCTGGATGCGGGTAAGGCCATGAACGGACCC

[1577] GCGTCCTTTCCGTTCGGCGACTTTACCGCCGATACGAAAGGTACATCCGATATTGCCTACTCCTTCCGTAACGACATT

[1578] TCAGGCACGGGCGGCCTGATCAAAAAGGCGGCAGCCAACTGCAACTGCACGGCAACAACACCTATACGGGCAAAACC

[1579] ATTATCGAAGGCGGTTCGCTGGTGTTGTACGGCAACAACAAATCGGATATGCGCGTCGAAACCAAAGGTGCGCTGATT

[1580] TATAACGGGGCGGCATCCGGCGGCAGCCTGAACAGCGACGGCATTGTCTATCTGGCAGATACCGACCAATCCGGCGCA

[1581] AACGAAACCGTACACATCAAAGGCAGTCTGCAGCTGGACGGCAAAGGTACGCTGTACACACGTTTGGGCAAACTGCTG

[1582] AAAGTGGACGGTACGGCGATTATCGGCGGCAAGCTGTACATGTCGGCACGCGGCAAGGGGGCAGGCTATCTCAACAGT

[1583] ACCGGACGACGTGTTCCCTTCCTGAGTGCCGCCAAAATCGGGCAGGATTATTCTTTCTTCACAAACATCGAAACCGAC

[1584] GGCGGCCTGCTGGCTTCCCTCGACAGCGTCGAAAAAACAGCGGGCAGTGAAGGCGACACGCTGTCCTATTATGTCCGT

[1585] CGCGGCAATGCGGCACGGACTGCTTCGGCAGCGGCACATTCCGCGCCCGCCGGTCTGAAACACGCCGTAGAACAGGGC

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[1590] CAACAGGACGGTGGAACGTGGAACAGGGCGGTGTTGAAGGCAAAATGCGCGGCAGTACCCAAACCGTCGGCATTGCC

[1591] GCGAAAACCGGCGAAAATACGACAGCAGCCGCCACACTGGGCATGGACGCAGCACATGGAGCGAAAACAGTGCAAAT

[1592] GCAAAAACCGACAGCATTAGTCTGTTTGCAGGCATACGGCACGATGCGGGCGATATCGGCTATCTCAAAGGCCTGTTC

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[1594] CTGATGCAGCTGGGCGCACTGGGCGGTGTCAACGTTCCGTTTGCCGCAACGGGAGATTTGACGGTCGAAGGCGGTCTG

[1595] CGCTACGACCTGCTCAAACAGGATGCATTCGCCGAAAAAGGCAGTGCTTTGGGCTGGAGCGGCAACAGCCTCACTGAA

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[1600] CTCGAG

[1601] 1 MKHFPSKVLT TAILATFCSG ALAATNDDDV KKAATVAIAA AYNNGQEING

[1602] 51 FKAGETIYDI DEDGTITKKD ATAADVEADD FKGLGLKKVV TNLTKTVNEN

[1603] 101 KQNVDAKVKA AESEIEKLTT KLADTDAALA DTDAALDATT NALNKLGENI

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[1605] 201 KTANEAKQTA EETKQNVDAK VKAAETAAGK AEAAAGTANT AADKAEAVAA

[1606] 251 KVTDIKADIA TNKDNIAKKA NSADVYTREE SDSKFVRIDG LNATTEKLDT

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[1608] 351 GSGGGGTSAP DFNAGGTGIG SNSRATTAKS AAVSYAGIKNEMCKDRSMLC

[1609] 401 AGRDDVAVTD RDAKINAPPP NLHTGDFPNP NDAYKNLINL KPAIEAGYTG

[1610] 451 RGVEVGIVDT GESVGSISFP ELYGRKEHGY NENYKNYTAY MRKEAPEDGG

[1611] 501 GKDIEASFDD EAVIETEAKP TDIRHVKEIG HIDLVSHIIG GRSVDGRPAG

[1612] 551 GIAPDATLHI MNTNDETKNE MMVAAIRNAW VKLGERGVRI VNNSFGTTSR

[1613] 601 AGTADLFQIA NSEEQYRQAL LDYSGGDKTD EGIRLMQQSD YGNLSYHIRN

[1614] 651 KNMLFIFSTG NDAQAQPNTY ALLPFYEKDA QKGIITVAGV DRSGEKFKRE

[1615] 701 MYGEPGTEPL EYGSNHCGIT AMWCLSAPYE ASVRFTRTNP IQIAGTSFSA

[1616] 751 PIVTGTAALL LQKYPWMSND NLRTTLLTTA QDIGAVGVDS KTGWGLLDAG

[1617] 801 KAMNGPASFP FGDFTADTKG TSDIAYSFRN DISGTGGLIK KGGSQLQLHG

[1618] 851 NNTYTGKTII EGGSLVLYGN NKSDMRVETK GALIYNGAAS GGSLNSDGIV

[1619] 901 YLADTDQSGA NETVHIKGSL QLDGKGTLYT RLGKLLKVDG TAIIGGKLYM

[1620] 951 SARGKGAGYL NSTGRRVPFL SAAKIGQDYS FFTNIETDGG LLASLDSVEK

[1621] 1001 TAGSEGDTLS YYVRRGNAAR TASAAAHSAP AGLKHAVEQG GSNLENLMVE

[1622] 1051 LDASESSATP ETVETAAADR TDMPGIRPYG ATFRAAAAVQ HANAADGVRI

[1623] 1101 FNSLAATVYA DSTAAHADMQ GRRLKVASDG LDHNGTGLRV IAQTQQDGGT

[1624] 1151 WEQGGVEGKM RGSTQTVGIA AKTGENTTAA ATLGMGRSTW SENSANAKTD

[1625] 1201 SISLFAGIRH DAGDIGYLKG LFSYGRYKNS ISRSTQADEH AEGSVNGTLM

[1626] 1251 QLGALGGVNV PFATGDLTV EGGLRYDLLK QDAFAEKGSA LGWSGNSLTE

[1627] 1301 GTLVGLAGLKC LSQPLSDKAV LFATAGVERD LNGRDYTVTG GFTGATAATG

[1628] 1351 KTGARNMPHT RLVAGLGADV EFGNGWNGLA RYSYAGSKQY GNHSGRVGVG

[1629] 1401 YRF*

[1630] 可以理解本发明仅以实施例的方式进行描述，在本发明的范围和精神内还可进行

改变。例如，设想可以使用其它菌株的蛋白质［如，参见 WO00/66741，ORF4、ORF40、ORF46、225、235、287、519、726、919 和 953 的多态序列］。

[1631] 实验详述

[1632] 克隆策略和寡核苷酸设计

[1633] 用以脑膜炎奈瑟球菌 B MC58 的基因组序列为基础设计的寡核苷酸，通过 PCR 扩增编码感兴趣的抗原的基因。除非特别指出，通常将菌株 2996 的基因组 DNA 用作 PCR 反应的模板，将扩增的片段克隆入表达载体 pET21b+(Novagen)，从而以 C- 末端 His 标记的产物形式表达该蛋白，或将其克隆入 pET-24b+(Novagen) 以‘未标记的’形式（如△ G287K）表达该蛋白。

[1634] 不用融合配体和用其自身前导肽（如果存在时）表达蛋白质，进行开放读框（ATG 到终止密码子）的扩增。

[1635] 当蛋白质以‘未标记的’的形式表达时，通过从预定的前导序列设计 5′ －端扩增引物下游除去前导肽。

[1636] 用于 PCR 的引物的解链温度取决于整个引物中杂交核苷酸的数量和类型，并用以下公式确定：

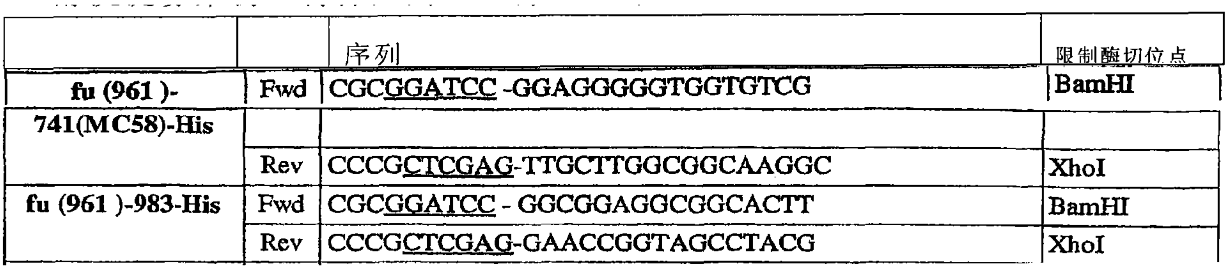
[1637] $T_{m1} = 4(G+C)+2(A+T)$ （除去尾部的）

[1638] $T_{m2} = 64.9+0.41(\% GC)-600/N$ （完整的引物）

[1639] 对整个低聚物而言，所选寡核苷酸的解链温度通常为 65-70℃，仅针对杂交区域，解链温度为 50-60℃。

[1640] 用 Perkin Elmer394DNA/RNA 合成仪合成寡核苷酸，将其从柱上洗脱到 2.0ml NH_4OH 中，在 56℃培育 5 小时以去保护。加入 0.3M 乙酸钠和 2 体积的乙醇沉淀寡聚物。将样品离心，将沉淀物重悬浮于水中。

[1641]



		序列	限制酶切位点
fu (961)-741(MC58)-His	Fwd	CGCGGATCC -GGAGGGGGTGGTGTCG	BamHI
	Rev	CCCGCTCGAG-TTGCTTGGCGGCAAGGC	XhoI
fu (961)-983-His	Fwd	CGCGGATCC - GGCGGAGGCGGCACTT	BamHI
	Rev	CCCGCTCGAG-GAACCGGTAGCCTACG	XhoI

[1642]

fu (961)- Orf46.1-His	Fwd	CGCGGATCCGGTGGTGGTGGT-TCAGATTTGGCAAACGATTC	BamHI
	Rev	CCCGCTCGAG-CGTATCATATTTCACGTGC	XhoI
fu (961 c-L)-741(MC58)	Fwd	CGCGGATCC -GGAGGGGGTGGTGTCG	BamHI
	Rev	CCCGCTCGAG-TTATTGCTTGGCGGCAAG	XhoI
fu (961c-L)-983	Fwd	CGCGGATCC - GGCGGAGGCGGCACTT	BamHI
	Rev	CCCGCTCGAG-TCAGAACCGGTAGCCTAC	XhoI
fu (961c-L)-Orf46.1	Fwd	CGCGGATCCGGTGGTGGTGGT-TCAGATTTGGCAAACGATTC	BamHI
	Rev	CCCGCTCGAG-TTACGTATCATATTTCACGTGC	XhoI
fu-(ΔG287)-919-His	Fwd	CGCGGATCCGGTGGTGGTGGT-CAAAGCAAGAGCATCCAAACC	BamHI
	Rev	CCCAAGCTT-TTCGGGCGGTATTCGGGCTTC	HindIII
fu-(ΔG287)-953-His	Fwd	CGCGGATCCGGTGGTGGTGGT-GCCACCTACAAAGTGGAC	BamHI
	Rev	GCCCAAGCTT-TTGTTTGGCTGCCTCGAT	HindIII
fu-(ΔG287)-961-His	Fwd	CGCGGATCCGGTGGTGGTGGT-ACAAGCGACGACG	BamHI
	Rev	GCCCAAGCTT-CCACTCGTAATTGACGCC	HindIII
fu-(ΔG287)-Orf46.1-His	Fwd	CGCGGATCCGGTGGTGGTGGT-TCAGATTTGGCAAACGATTC	BamHI
	Rev	CCCAAGCTT-CGTATCATATTTCACGTGC	HindIII
fu-(ΔG287-919)-Orf46.1-His	Fwd	CCCAAGCTTGGTGGTGGTGGTGGT-TCAGATTTGGCAAACGATTC	HindIII
	Rev	CCCGCTCGAG-CGTATCATATTTCACGTGC	XhoI
fu-(ΔG287-Orf46.1)-919-His	Fwd	CCCAAGCTTGGTGGTGGTGGTGGT-CAAAGCAAGAGCATCCAAACC	HindIII
	Rev	CCCGCTCGAG-CGGGCGGTATTCGGGCTT	XhoI
fu ΔG287(394.98)-...	Fwd	CGCGGATCCGCTAGC-CCCGATGTTAAATCGGC	NheI
	Rev	CGGGGATCC-ATCCTGCTCTTTTTTGCCGG	BamHI
fu Orf1-(Orf46.1)-His	Fwd	CGCGGATCCGCTAGC-GGACACACTTATTTCGGCATC	NheI
	Rev	CGCGGATCC-CCAGCGGTAGCCTAATTTGAT	
fu (Orf1)-Orf46.1-His	Fwd	CGCGGATCCGGTGGTGGTGGT-TCAGATTTGGCAAACGATTC	BamHI
	Rev	CCCAAGCTT-CGTATCATATTTCACGTGC	HindIII
fu (919)-Orf46.1-His	Fwd1	GCGGCGTCGACGGTGGCGGAGGCACTGGATCCTCAG	SalI
	Fwd2	GGAGGCACTGGATCCTCAGATTTGGCAAACGATTC	
	Rev	CCCGCTCGAG-CGTATCATATTTCACGTGC	XhoI
Fu (orf46)-287-His	Fwd	CGGGGATCCGGGGGCGGCGGTGGCG	BamHI
	Rev	CCCAAGCTTATCCTGCTCTTTTTTGCCGGC	HindIII
Fu (orf46)-919-His	Fwd	CGCGGATCCGGTGGTGGTGGTCAAAGCAAGAGCATCCAAACC	BamHI
	Rev	CCCAAGCTTCGGGCGGTATTCGGGCTTC	HindIII

[1643]

Fu (orf46-919)-287-His	Fwd	CCCCAAGCTTGGGGGCGGCGGTGGCG	HindIII
	Rev	CCCGCTCGAGATCCTGCTCTTTTTTGCCGGC	XhoI
Fu (orf46-287)-919-His	Fwd	CCCAAGCTTGGTGGTGGTGGTGGTCAAAGCAAGAGCATCCAAACC	HindIII
	Rev	CCCGCTCGAGCGGGCGGTATTCGGGCTT	XhoI
(ΔG741)-961c-His	Fwd1	GGAGGCACTGGATCCGCAGCCACAAACGACGACGA	XhoI
	Fwd2	GCGGCCTCGAG-GGTGGCGGAGGCACTGGATCCGCAG	
	Rev	CCCGCTCGAG-ACCCAGCTTGTAAGGTTG	XhoI
(ΔG741)-961-His	Fwd1	GGAGGCACTGGATCCGCAGCCACAAACGACGACGA	XhoI
	Fwd2	GCGGCCTCGAG-GGTGGCGGAGGCACTGGATCCGCAG	
	Rev	CCCGCTCGAG-CCACTCGTAATTGACGCC	XhoI
(ΔG741)-983-His	Fwd	GCGGCCTCGAG-GGATCCGGCGGAGGCGGCACTTCTGCG	XhoI
	Rev	CCCGCTCGAG-GAACCGGTAGCCTACG	XhoI
(ΔG741)-orf46.1-His	Fwd1	GGAGGCACTGGATCCTCAGATTTGGCAAACGATTC	SalI
	Fwd2	GCGGCGTCGACGGTGGCGGAGGCACTGGATCCTCAGA	
	Rev	CCCGCTCGAG-CGTATCATATTTCACGTGC	XhoI
(ΔG983)-741(MC58) -His	Fwd	GCGGCCTCGAG-GGATCCGGAGGGGGTGGTGTCGCC	XhoI
	Rev	CCCGCTCGAG-TTGCTTGGCGGCAAG	XhoI
(ΔG983)-961c-His	Fwd1	GGAGGCACTGGATCCGCAGCCACAAACGACGACGA	XhoI
	Fwd2	GCGGCCTCGAG-GGTGGCGGAGGCACTGGATCCGCAG	
	Rev	CCCGCTCGAG-ACCCAGCTTGTAAGGTTG	XhoI
(ΔG983)-961-His	Fwd1	GGAGGCACTGGATCCGCAGCCACAAACGACGACGA	XhoI
	Fwd2	GCGGCCTCGAG-GGTGGCGGAGGCACTGGATCCGCAG	
	Rev	CCCGCTCGAG-CCACTCGTAATTGACGCC	XhoI
(ΔG983)- Orf46.1-His	Fwd1	GGAGGCACTGGATCCTCAGATTTGGCAAACGATTC	SalI
	Fwd2	GCGGCGTCGACGGTGGCGGAGGCACTGGATCCTCAGA	
	Rev	CCCGCTCGAG-CGTATCATATTTCACGTGC	XhoI

[1644] *将该引物用作反向引物，将所有 287 的 C 未端融合于 His- 标记。

[1645] § 与 287-His 反向引物联用的正向引物。

[1646] NB- 所有 PCR 反应使用菌株 2996，除非特别指出（如菌株 MC58）。

[1647] 在所有以 ATG 起始不跟随唯一 NheI 位点的构建物中，ATG 密码子是用于克隆的 NdeI 位点的一部分。在 5′ 端用 NheI 作为克隆位点制备的构建物（如所有那些在 N- 未端包含 287 的）另有两个融合于抗原的编码序列的密码子 (GCTAGC)。

[1648] 染色体 DNA 模板的制备

[1649] 在 100ml GC 培养基中使脑膜炎奈瑟球菌前株 2996、MC58、394.98、1000 和 BZ232（及其它）生长至指数期，离心收获，并重悬浮于 5ml 缓冲液 (20% w/v 蔗糖、50mM Tris-HCl、50mM EDTA、pH8) 中。在冰上培育 10 分钟后，加入 10ml 裂解液 (50mM NaCl、1% 十二烷基肌氨酸钠 (Na-Sarkosyl)、50μg/ml 蛋白酶 K) 裂解细菌，悬浮液在 37℃培育 2 小时。进行 2 次苯酚提取（平衡至 pH8）和一次 $CHCl_3$/ 异戊醇 (24 :1) 提取。加入 0.3M 乙酸钠和 2 体积乙醇沉降 DNA，并离心收集。用 70% (v/v) 乙醇洗涤沉淀物 1 次，并重溶解于 4.0ml TE 缓冲液 (10mMTris-HCl、1mM EDTA、pH8.0)。读取 OD_{260} 测定 DNA 浓度。

[1650] PCR 扩增

[1651] 标准的 PCR 过程：进行如下在 40μM 各寡核苷酸引物、400-800μM dNTP 溶液、1x

PCR 缓冲液（包含 1.5mM $MgCl_2$）、2.5 单位 TaqI DNA 聚合酶（用 Perkin-Elmer AmpliTaQ，Boerhingher Mannheim Expand™ 长模板）存在时，将 200ng2996、MC581000、或 BZ232 菌株的基因组 DNA 或 10ng 重组克隆的质粒 DNA 制备物用作模板。

[1652] 将整个混合物在 95℃初步培育 3 分钟后，每份样品进行 2- 步的扩增：用除去引物 (T_{m1}) 的限制酶尾部的杂交温度进行前 5 轮。然后按全长低聚物 (T_{m2}) 计算的杂交温度进行 30 轮。根据要扩增的 Orf 的长度，在 68℃或 72℃进行的延伸时间各不相同。对 Orf1 而言，自 3 分钟开始的延伸时间每轮递增 15 秒。以在 72℃ 10 分钟延伸步骤完成循环。

[1653] 将扩增的 DNA 直接加到 1％琼脂糖凝胶上。按制造商的说明，用 Qiagen 凝胶提取试剂盒纯化相应于正确大小条带的 DNA 片段。

[1654] PCR 片段和克隆载体的消化

[1655] 用适合的限制酶消化相应于扩增片段的纯化 DNA，从而克隆入 pET-21b+、pET22b+、或 pET-24b+。用 QIAquick PCR 纯化试剂盒（按制造商的说明）纯化消化的片段，用 H_2O 或 10mM Tris(pH8.5) 洗脱。用适合的限制酶消化质粒载体，加到 1.0％琼脂糖凝胶上，用 Qiagen AIQquick 凝胶提取试剂盒纯化相应于消化的载体的条带。

[1656] 克隆

[1657] 将预先消化和纯化的、相应于各基因的片段连接到 pET21b+、pET22b+ 或 pET-24b+ 中。将在连接缓冲液（由制造商提供）中的 T4DNA 连接酶用于摩尔比为 3：1 的片段 / 载体。

[1658] 通过在冰上培育连接酶反应溶液和细菌 40 分钟，然后在 37℃培育 3 分钟，将重组质粒转化入感受态大肠杆菌 DH5 或 HB101 中。

[1659] 然后添加 800μl LB 肉汤，并在 37℃培育 20 分钟。在 Eppendorf 微型离心机中以最高速度离心这些细胞，并重悬浮于约 200μl 的上清液中，并涂布在 LB 氨苄青霉素 (100mg/ml) 琼脂上。

[1660] 在 4.0ml LB 肉汤 +100μg/ml 氨苄青霉素中培育随机选择的集落过夜，进行重组集落的筛选。使细胞沉淀，并按制造商的说明用 Qiagen QIAprep SpinMiniprep 试剂盒提取质粒 DNA。用适合的限制酶消化约 1μg 的各微型制备物，将消化物加到 1-1.5％琼脂糖凝胶（取决于预计的插入大小）与分子量标记 (1kbDNA Ladder,GIBCO) 平行。根据插入的大小选择阳性克隆。

[1661] 表达

[1662] 各基因克隆入表达载体后，将重组质粒转化入适合表达重组蛋白的大肠杆菌菌株中。如上所述，用 1μl 各构建物转化大肠杆菌 BL21-DE3。将单重组集落接种入 2ml LB+Amp(100μg/ml) 中，在 37℃培育过夜，然后在 100ml 烧瓶中用 20ml LB+Amp(100μg/ml) 以 1：30 稀释，使 OD_{600} 在 0.1-0.2 之间。将烧瓶置于旋转式水浴摇床中于 30℃或 37℃培育，直到 OD600 显示适合诱导表达的指数生长期 (0.4-0.8OD)。加入 1.0mM IPTG 诱导蛋白质表达。在 30℃或 37℃培育 3 小时后，测定 OD_{600} 并检测表达。用微型离心机离心 1.0ml 各样品，将沉淀物重悬浮于 PBS 中，用 SDS-PAGE 和考马斯蓝染色分析。

[1663] His- 标记的蛋白质的纯化

[1664] 从菌株 2996 和 MC58 中克隆了 287 的各种形式。用 C- 末端 His 标记的融合体进行构建，其包括成熟形式 (aa18-427)、含缺失（△ 1、△ 2、△ 3 和△ 4) 的构建物和由 B

或C结构域组成的克隆。对以His-融合体纯化的各克隆而言，划线接种单集落，并且在37℃ LB/Amp(100μg/ml)琼脂板上培育过夜。将从该平板上分离的集落接种到20ml LB/Amp(100μg/ml)的液体培养基中，并在37℃振荡生长过夜。以1:30将过夜培养物稀释到1.0L LB/Amp(100μg/ml)液体培养基中，让其在最佳温度(30或37℃)生长，直到OD_{550}达到0.6-0.8。添加IPTG(终浓度为1.0mM)诱导重组蛋白的表达，再培育培养物3小时。于4℃，以8000g离心15分钟收获细菌。将细菌沉淀物重悬浮于7.5ml(i)冷缓冲液A(300mM NaCl、50mM磷酸盐缓冲液、10mM咪唑、pH8.0)，用于可溶性蛋白质；或(ii)缓冲液B(10mM Tirs-HCl、100mM磷酸盐缓冲液，pH8.8和任选地8M尿素)，用于不溶性蛋白质。以可溶形式纯化的蛋白质包括287-His、△1、△2、△3和△4287-His、△4287MC58-His、287c-His和287cMC58-His。蛋白质287bMC58-His是不溶的并相应地纯化。用Branson Sonifier450，在冰上以40W、30秒超声处理破坏细胞4次，并于4℃以13000xg离心30分钟。对于不溶蛋白质，将沉淀物重悬浮于2.0ml缓冲液C(6M盐酸胍、100mM磷酸盐缓冲液、10mM Tris-HCl、pH7.5)，并用Dounce匀浆器处理10次。以13000g离心匀浆30分钟并保留上清液。将可溶的和不溶制备物的上清液与150μl Ni^{2+}-树脂(预先用缓冲液A或缓冲液B平衡)混合，并在室温温和振荡培育30分钟。树脂是按制造商说明制备的ChelatingSepharose Fast Flow(Pharmcia)。于4℃，以700g离心分批制备物5分钟，弃去上清液。用10ml缓冲液A或B洗涤树脂2次(分批)10分钟，重悬浮于1.0ml缓冲液A或B中，加到一次性柱上。用(i)缓冲液A(4℃)或(ii)缓冲液B(室温)持续洗涤树脂，直到流出物的OD_{280}达到0.02-0.01。再用(i)冷缓冲液C(300mMNaCl、50mM磷酸盐缓冲液、20mM咪唑、pH8.0)或(ii)缓冲液D(10mM Tris-HCl、100mM磷酸盐缓冲液、pH6.3和任选地8M尿素)进一步洗涤树脂，直到流出物的OD_{280}达到0.02-0.01。加入700μl(i)冷洗脱缓冲液A(300mM NaCl、50mM磷酸盐缓冲液、250mM咪唑、pH8.0)或(ii)洗脱缓冲液B(10mM Tris-HCl、100mM磷酸盐缓冲液、pH4.5和任选地8M尿素)洗脱His-融合蛋白，收集组分直到OD_{280}显示获得了所有重组蛋白。用SDS-PAGE分析20μl量的各洗脱组分。用Bradford试验法计算蛋白质浓度。

[1665] 变性的His-融合蛋白的复性

[1666] 需要变性以稳定287bMC8，因此在免疫接种前需进行复性步骤。将甘油加到上述得到的变性组分中，使终浓度为10％ v/v。用透析缓冲液I(10％ v/v甘油，0.5M精氨酸、50mM磷酸盐缓冲液、5.0mM还原的谷胱甘肽、0.5mM氧化的谷胱甘肽、2.0M尿素，pH8.8)将蛋白质稀释至200μg/ml，用相同的缓冲液在4℃透析12-14小时。于4℃，用缓冲液II(10％ v/v甘油，0.5M精氨酸、50mM磷酸盐缓冲液、5.0mM还原的谷胱甘肽、0.5mM氧化的谷胱甘肽、pH8.8)再进行透析12-14小时。用以下公式计算蛋白质的浓度：

[1667] 蛋白质(mg/ml) = $(1.55\times OD_{280})-(0.76\times OD_{260})$

[1668] 免疫接种

[1669] 在第0、21和35天，用抗原免疫接种Balb/C小鼠，在第49天分析血清。

[1670] 血清分析-ELISA

[1671] 将不包囊的MenB M7和包囊的菌株置于巧克力琼脂板上，在37℃、5％ CO_2中培育过夜。用无菌Dracon刷从琼脂板上收集细菌菌落，并接种到含有0.25％葡萄糖的Mueller-Hinton肉汤(Difco)中。每30分钟监测一次细菌的生长，随后测定OD_{620}。让细菌

生长直到OD达到0.4-0.5。将培养物以4000rpm离心10分钟。弃去上清液，用PBS洗涤细菌2次，重悬浮于含有0.025％甲醛的PBS中，并在37℃培育1小时，然后在4℃搅拌培育过夜。在96孔Greiner板的各孔中添加100μl细菌细胞，并在4℃培育过夜。然后用PBT洗涤缓冲液（0.1％ Tween-20的PBS溶液）冲洗这些孔3次。在各孔中加入200μl饱和缓冲液（2.7％聚乙烯吡咯烷酮10的水溶液），将这些平板在37℃培育2小时。用PBT冲洗这些孔3次。在各孔中加入200μl稀释的血清（稀释缓冲液：1％ BSA、0.1％ Tween-20、0.1％ NaN_3的PBS溶液），将这些平板在37℃培育2小时。用PBT冲洗这些孔3次。在各孔中加入100μl HRP-缀合的兔抗-小鼠（Dako）血清（用稀释缓冲液以1：2000稀释），将这些平板置于37℃培育90分钟。用PBT缓冲液洗涤这些孔3次。在各孔中加入100μl HRP的底物缓冲液（25ml柠檬酸缓冲液pH5，10mg邻-苯二胺（phenildiamine）和10μl H_2O_2），并将平板在室温中静置20分钟。在各孔中加入100μl12.5％ H_2SO_4，随后测定OD_{490}。计算ELISA滴定度，即高于预先免疫血清稀释度的、OD490值为0.4的血清稀释度。当OD490值为0.4的血清稀释度高于1：400时，将ELISA视为阳性。

[1672] 血清分析-FACS扫描细菌结合分析

[1673] 将不包囊的MenB M7菌株置于巧克力琼脂板上，在37℃、5％ CO_2中培育过夜。用无菌Dracon刷从琼脂板上收集菌落，并接种到4支装有0.25％葡萄糖的8ml Mueller-Hinton肉汤（Difco）试管中。每30分钟监测细菌的生长，然后测定OD_{620}。让细菌生长直到OD达到0.35-0.5。将培养物以4000rpm离心10分钟。弃去上清液，用封阻缓冲液（1％ BSA的PBS溶液，0.4％ NaN3）重悬浮沉淀物，并以4000rpm离心5分钟。将细胞重悬浮于封阻缓冲液，使OD_{620}达到0.05。在96孔Costar板的各孔中添加100μl细菌细胞。在各孔中加入100μl稀释的（1:100、1：200、1：400）血清（以封阻缓冲液配制），并将这些平板在4℃培育2小时。以4000rpm离心细胞5分钟，吸出上清液，在各孔中加入200μl/孔封阻缓冲液洗少涤细胞。在各孔中加入100μl R-Phicoerytrin缀合的F(ab)2山羊抗-小鼠（以1：100稀释），将平板置于4℃培育1小时。以4000rpm离心5分钟以沉淀细胞，添加200μl/孔封阻缓冲洗涤细胞。吸出上清液，细胞重悬浮于200μl/孔PBS、0.25％甲醛。将样品转移到FACScan管中并读数。FACScan(Laser Power15mW)的条件设定为：FL2开；FSC-H阈值：92；FSC PMT电压：E01；SSCPMT:474；Amp.Gains6.1；FL-2PMT:586；补偿值：0。

[1674] 血清分析-杀菌试验

[1675] 于37℃，在5％ CO_2、在巧克力琼脂板（以冷冻原液起始）上培育脑膜炎奈瑟球菌菌株2996过夜。收集菌落，并将其接种到7ml含有0.25％葡萄糖的Mueller-Hinton肉汤中，使OD_{620}达到0.05-0.08。在37℃振荡培育约1.5小时，直到OD_{620}达到0.23-0.24。用50mM磷酸盐缓冲液（pH7.2，含10mM $MgCl_2$、10mM$CaCl_2$和0.5％（w/v）BSA（分析缓冲液））以10^5CFU/ml工作稀释度稀释细菌。最终反应混合物的总体积为50μl，其中25μl连续2倍稀释的测试血清，12.5μl工作稀释度的细菌，12.5μl幼兔补体（终浓度25％）。

[1676] 对照包括：用补体血清培育的细菌、用细菌培育并在56℃加热30分钟补充灭活的免疫血清。在加入幼兔补体后，用斜置方法立即将10μl对照置于Mueller-Hinton琼脂板上（0时间）。37℃旋转培育96孔板1小时。将每份样品的7μl涂布在Mueller-Hinton琼脂板上作为斑点，而用斜置方法将10μl对照涂布在Mueller-Hinton琼脂板上（1时间）。37℃培育琼脂板18小时，计算相应于0时间和1时间的菌落数量。

[1677]　血清分析 -Western 印迹法

[1678]　将纯化的蛋白质 (500ng/ 泳道)、外膜小泡 (5μg) 和 MenB 菌株 2996 衍生的全细胞提取物 (25μg) 加到 12% SDS- 聚丙烯酰胺凝胶上，并转移到硝基纤维素膜上。用转化缓冲液 (0.3% Tris 碱，1.14% 甘氨酸、20% (v/v) 甲醇) 在 4℃、150mA 进行转化 2 小时。于 4℃，在饱和缓冲液 (10% 脱脂乳、0.1% Triton X100 的 PBS 溶液) 中培育过夜使膜饱和。用冲洗缓冲液 (3% 脱脂乳、0.1% Triton X100 的 PBS 溶液) 冲洗膜 2 次，并在 37℃与用洗涤缓冲液以 1 :200 稀释的小鼠血清一起培育 2 小时。冲洗膜 2 次，与 1 :2000 稀释的辣根过氧化物酶标记的抗 - 小鼠 Ig 一起培育 90 分钟。用 0.1% Triton X100 的 PBS 溶液冲洗膜 2 次，用 Opti-4CN 底物试剂盒 (Bio-Rad) 显色。加入水终止反应。

[1679]　如下制备 OMV :于 37℃、5% CO_2，在 5 个 GC 板上让脑膜炎奈瑟球菌 2996 生长过夜，用接种环收获，并重悬浮于 10ml20mM Tris-HCl pH7.5、2mM EDTA 中。在 56℃热灭活 45 分钟，在冰上超声处理破碎细胞 5 分钟 (50% 负载循环 (dutycycle)、50% 输出，Branson 超声仪 3mm 微型针头)。以 5000g 离心 10 分钟除去未被破坏的细胞，回收含有完整细胞包膜组分的上清液，于 4℃以 50000g 进一步离心过夜。将含有膜的沉淀物重悬浮于 2% 二烷基肌氨酸钠、20mM Tris-HClpH7.5、2mM EDTA 中，在室温培育 20 分钟以溶解内膜。以 10000g 离心上清液 10 分钟除去聚集体，以 50000g 进一步离心上清液 3 小时。用 PBS 冲洗含有外膜的沉淀物，并重悬浮于相同的缓冲液中。用 BSA 作为标准，由 D.C.Bio-Rad 蛋白分析 (改进的 Lowry 方法) 测定蛋白质的浓度。

[1680]　如下制备全细胞提取物 :使脑膜炎奈瑟球菌在 GC 板上培育过夜，用接种环收获，并重悬浮于 1ml20mM Tris-HCl 中。在 56℃热灭活 30 分钟。

[1681]　序列表

[1682]　<110> 启龙股份公司 (Chiron SpA)

[1683]　<120> 奈瑟球菌蛋白质的杂交表达

[1684]　<130>024941F2

[1685]　<150>GB0004695.3

[1686]　<151>2000-02-28

[1687]　<150>GB0027675.8

[1688]　<151>2000-11-13

[1689]　<160>121

[1690]　<170>SeqWin99，version1.02

[1691]　<210>1

[1692]　<211>608

[1693]　<212>PRT

[1694]　<213> 脑膜炎奈瑟氏菌 (Neisseria meningitidis)

[1695]　<400>1

[1696]

```
Leu Gly Ile Ser Arg Lys Ile Ser Leu Ile Leu Ser Ile Leu Ala Val
1               5                   10                  15
Cys Leu Pro Met His Ala His Ala Ser Asp Leu Ala Asn Asp Ser Phe
            20                  25                  30
Ile Arg Gln Val Leu Asp Arg Gln His Phe Glu Pro Asp Gly Lys Tyr
        35                  40                  45
His Leu Phe Gly Ser Arg Gly Glu Leu Ala Glu Arg Ser Gly His Ile
    50                  55                  60
Gly Leu Gly Lys Ile Gln Ser His Gln Leu Gly Asn Leu Met Ile Gln
65                  70                  75                  80
Gln Ala Ala Ile Lys Gly Asn Ile Gly Tyr Ile Val Arg Phe Ser Asp
                85                  90                  95
His Gly His Glu Val His Ser Pro Phe Asp Asn His Ala Ser His Ser
            100                 105                 110
Asp Ser Asp Glu Ala Gly Ser Pro Val Asp Gly Phe Ser Leu Tyr Arg
        115                 120                 125
Ile His Trp Asp Gly Tyr Glu His His Pro Ala Asp Gly Tyr Asp Gly
    130                 135                 140
Pro Gln Gly Gly Gly Tyr Pro Ala Pro Lys Gly Ala Arg Asp Ile Tyr
145                 150                 155                 160
Ser Tyr Asp Ile Lys Gly Val Ala Gln Asn Ile Arg Leu Asn Leu Thr
                165                 170                 175
Asp Asn Arg Ser Thr Gly Gln Arg Leu Ala Asp Arg Phe His Asn Ala
            180                 185                 190
Gly Ser Met Leu Thr Gln Gly Val Gly Asp Gly Phe Lys Arg Ala Thr
        195                 200                 205
Arg Tyr Ser Pro Glu Leu Asp Arg Ser Gly Asn Ala Ala Glu Ala Phe
    210                 215                 220
Asn Gly Thr Ala Asp Ile Val Lys Asn Ile Ile Gly Ala Ala Gly Glu
225                 230                 235                 240
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[1697]

```
Ile Val Gly Ala Gly Asp Ala Val Gln Gly Ile Ser Glu Gly Ser Asn
                245                 250                 255
Ile Ala Val Met His Gly Leu Gly Leu Leu Ser Thr Glu Asn Lys Met
            260                 265                 270
Ala Arg Ile Asn Asp Leu Ala Asp Met Ala Gln Leu Lys Asp Tyr Ala
        275                 280                 285
Ala Ala Ala Ile Arg Asp Trp Ala Val Gln Asn Pro Asn Ala Ala Gln
    290                 295                 300
Gly Ile Glu Ala Val Ser Asn Ile Phe Met Ala Ala Ile Pro Ile Lys
305                 310                 315                 320
Gly Ile Gly Ala Val Arg Gly Lys Tyr Gly Leu Gly Gly Ile Thr Ala
                325                 330                 335
His Pro Ile Lys Arg Ser Gln Met Gly Ala Ile Ala Leu Pro Lys Gly
            340                 345                 350
Lys Ser Ala Val Ser Asp Asn Phe Ala Asp Ala Ala Tyr Ala Lys Tyr
        355                 360                 365
Pro Ser Pro Tyr His Ser Arg Asn Ile Arg Ser Asn Leu Glu Gln Arg
    370                 375                 380
Tyr Gly Lys Glu Asn Ile Thr Ser Ser Thr Val Pro Pro Ser Asn Gly
385                 390                 395                 400
Lys Asn Val Lys Leu Ala Asp Gln Arg His Pro Lys Thr Gly Val Pro
                405                 410                 415
Phe Asp Gly Lys Gly Phe Pro Asn Phe Glu Lys His Val Lys Tyr Asp
            420                 425                 430
Thr Lys Leu Asp Ile Gln Glu Leu Ser Gly Gly Gly Ile Pro Lys Ala
        435                 440                 445
Lys Pro Val Ser Asp Ala Lys Pro Arg Trp Glu Val Asp Arg Lys Leu
    450                 455                 460
Asn Lys Leu Thr Thr Arg Glu Gln Val Glu Lys Asn Val Gln Glu Ile
465                 470                 475                 480
Arg Asn Gly Asn Lys Asn Ser Asn Phe Ser Gln His Ala Gln Leu Glu
                485                 490                 495
Arg Glu Ile Asn Lys Leu Lys Ser Ala Asp Glu Ile Asn Phe Ala Asp
            500                 505                 510
Gly Met Gly Lys Phe Thr Asp Ser Met Asn Asp Lys Ala Phe Ser Arg
        515                 520                 525
Leu Val Lys Ser Val Lys Glu Asn Gly Phe Thr Asn Pro Val Val Glu
    530                 535                 540
Tyr Val Glu Ile Asn Gly Lys Ala Tyr Ile Val Arg Gly Asn Asn Arg
545                 550                 555                 560
Val Phe Ala Ala Glu Tyr Leu Gly Arg Ile His Glu Leu Lys Phe Lys
                565                 570                 575
Lys Val Asp Phe Pro Val Pro Asn Thr Ser Trp Lys Asn Pro Thr Asp
            580                 585                 590
Val Leu Asn Glu Ser Gly Asn Val Lys Arg Pro Arg Tyr Arg Ser Lys
        595                 600                 605
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[1698] <210>2

[1699] <211>464

[1700] <212>PRT

[1701] <213> 人工序列

[1702] <220>

[1703] <223>ΔG287

[1704] <400>2

[1705]

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Ser Pro Asp Val Lys Ser Ala Asp Thr Leu Ser Lys Pro Ala Ala Pro
1               5                   10                  15
Val Val Ser Glu Lys Glu Thr Glu Ala Lys Glu Asp Ala Pro Gln Ala
            20                  25                  30
Gly Ser Gln Gly Gln Gly Ala Pro Ser Ala Gln Gly Ser Gln Asp Met
        35                  40                  45
Ala Ala Val Ser Glu Glu Asn Thr Gly Asn Gly Gly Ala Val Thr Ala
    50                  55                  60
Asp Asn Pro Lys Asn Glu Asp Glu Val Ala Gln Asn Asp Met Pro Gln
65                  70                  75                  80
Asn Ala Ala Gly Thr Asp Ser Ser Thr Pro Asn His Thr Pro Asp Pro
                85                  90                  95
Asn Met Leu Ala Gly Asn Met Glu Asn Gln Ala Thr Asp Ala Gly Glu
            100                 105                 110
Ser Ser Gln Pro Ala Asn Gln Pro Asp Met Ala Asn Ala Ala Asp Gly
        115                 120                 125
Met Gln Gly Asp Asp Pro Ser Ala Gly Gly Gln Asn Ala Gly Asn Thr
    130                 135                 140
Ala Ala Gln Gly Ala Asn Gln Ala Gly Asn Asn Gln Ala Ala Gly Ser
145                 150                 155                 160
Ser Asp Pro Ile Pro Ala Ser Asn Pro Ala Pro Ala Asn Gly Gly Ser
                165                 170                 175
Asn Phe Gly Arg Val Asp Leu Ala Asn Gly Val Leu Ile Asp Gly Pro
            180                 185                 190
Ser Gln Asn Ile Thr Leu Thr His Cys Lys Gly Asp Ser Cys Ser Gly
        195                 200                 205
Asn Asn Phe Leu Asp Glu Glu Val Gln Leu Lys Ser Glu Phe Glu Lys
    210                 215                 220
Leu Ser Asp Ala Asp Lys Ile Ser Asn Tyr Lys Lys Asp Gly Lys Asn
225                 230                 235                 240
Asp Lys Phe Val Gly Leu Val Ala Asp Ser Val Gln Met Lys Gly Ile
                245                 250                 255
Asn Gln Tyr Ile Ile Phe Tyr Lys Pro Lys Pro Thr Ser Phe Ala Arg
            260                 265                 270
Phe Arg Arg Ser Ala Arg Ser Arg Arg Ser Leu Pro Ala Glu Met Pro
        275                 280                 285
Leu Ile Pro Val Asn Gln Ala Asp Thr Leu Ile Val Asp Gly Glu Ala
    290                 295                 300
Val Ser Leu Thr Gly His Ser Gly Asn Ile Phe Ala Pro Glu Gly Asn
305                 310                 315                 320
Tyr Arg Tyr Leu Thr Tyr Gly Ala Glu Lys Leu Pro Gly Gly Ser Tyr
                325                 330                 335
Ala Leu Arg Val Gln Gly Glu Pro Ala Lys Gly Glu Met Leu Ala Gly
            340                 345                 350
Ala Ala Val Tyr Asn Gly Glu Val Leu His Phe His Thr Glu Asn Gly
        355                 360                 365
Arg Pro Tyr Pro Thr Arg Gly Arg Phe Ala Ala Lys Val Asp Phe Gly
    370                 375                 380
```

[1706]

```
Ser Lys Ser Val Asp Gly Ile Ile Asp Ser Gly Asp Asp Leu His Met
385                 390                 395                 400
Gly Thr Gln Lys Phe Lys Ala Ala Ile Asp Gly Asn Gly Phe Lys Gly
                405                 410                 415
Thr Trp Thr Glu Asn Gly Ser Gly Asp Val Ser Gly Lys Phe Tyr Gly
            420                 425                 430
Pro Ala Gly Glu Glu Val Ala Gly Lys Tyr Ser Tyr Arg Pro Thr Asp
        435                 440                 445
Ala Glu Lys Gly Gly Phe Gly Val Phe Ala Gly Lys Lys Glu Gln Asp
    450                 455                 460
```

[1707] <210>3

[1708] <211>2505

[1709] <212>DNA

[1710] <213> 人工序列

[1711] <220>

[1712] <223>ΔG287-919

[1713] <400>3

[1714]

atggctagcc ccgatgttaa atcggcggac acgctgtcaa aaccggccgc tcctgttgtt 60
gctgaaaaag agacagaggt aaaagaagat gcgccacagg caggttctca aggacagggc 120
gcgccatcca cacaaggcag ccaagatatg gcggcagttt cggcagaaaa tacaggcaat 180
ggcggtgcgg caacaacgga caaacccaaa aatgaagacg agggaccgca aaatgatatg 240
ccgcaaaatt ccgccgaatc cgcaaatcaa acagggaaca accaacccgc cgattcttca 300
gattccgccc ccgcgtcaaa ccctgcacct gcgaatggcg gtagcaattt tggaagggtt 360
gatttggcta atggcgtttt gattgatggg ccgtcgcaaa atataacgtt gacccactgt 420
aaaggcgatt cttgtaatgg tgataattta ttggatgaag aagcaccgtc aaaatcagaa 480
tttgaaaatt taaatgagtc tgaacgaatt gagaaatata agaaagatgg gaaaagcgat 540
aaatttacta atttggttgc gacagcagtt caagctaatg gaactaacaa atatgtcatc 600
atttataaag acaagtccgc ttcatcttca tctgcgcgat tcaggcgttc tgcacggtcg 660
aggaggtcgc ttcctgccga gatgccgcta atccccgtca atcaggcgga tacgctgatt 720
gtcgatgggg aagcggtcag cctgacgggg cattccggca atatcttcgc gcccgaaggg 780
aattaccggt atctgactta cggggcggaa aaattgcccg gcggatcgta tgccctccgt 840
gtgcaaggcg aaccggcaaa aggcgaaatg cttgctggca cggccgtgta caacggcgaa 900
gtgctgcatt ttcatacgga aaacggccgt ccgtacccga ctagaggcag gtttgccgca 960
aaagtcgatt tcggcagcaa atctgtggac ggcattatcg acagcggcga tgatttgcat 1020
atgggtacgc aaaaattcaa agccgccatc gatggaaacg gctttaaggg gacttggacg 1080
gaaaatggcg gcggggatgt ttccggaagg ttttacggcc cggccggcga ggaagtggcg 1140
ggaaaataca gctatcgccc gacagatgcg gaaaagggcg gattcggcgt gtttgccggc 1200
aaaaaagagc aggatggatc cggaggagga ggatgccaaa gcaagagcat ccaaaccttt 1260
ccgcaacccg acacatccgt catcaacggc ccggaccggc cggtcggcat ccccgacccc 1320
gccggaacga cggtcggcgg cggcggggcc gtctataccg ttgtaccgca cctgtccctg 1380
ccccactggg cggcgcagga tttcgccaaa agcctgcaat ccttccgcct cggctgcgcc 1440
aatttgaaaa accgccaagg ctggcaggat gtgtgcgccc aagcctttca aacccccgtc 1500
cattcctttc aggcaaaaca gtttttgaa cgctatttca cgccgtggca ggttgcaggc 1560
aacggaagcc ttgccggtac ggttaccggc tattacgagc cggtgctgaa gggcgacgac 1620
aggcggacgg cacaagcccg cttcccgatt tacggtattc ccgacgattt tatctccgtc 1680
cccctgcctg ccggtttgcg gagcggaaaa gcccttgtcc gcatcaggca gacgggaaaa 1740
aacagcggca caatcgacaa taccggcggc acacataccg ccgacctctc ccgattcccc 1800
atcaccgcgc gcacaacggc aatcaaaggc aggtttgaag gaagccgctt cctcccctac 1860

[1715] cacacgcgca accaaatcaa cggcggcgcg cttgacggca aagccccgat actcggttac 1920
gccgaagacc ccgtcgaact ttttttatg cacatccaag gctcgggccg tctgaaaacc 1980
ccgtccggca aatacatccg catcggctat gccgacaaaa acgaacatcc ctacgtttcc 2040
atcggacgct atatggcgga caaaggctac ctcaagctcg ggcagacctc gatgcagggc 2100
atcaaagcct atatgcggca aaatccgcaa cgcctcgccg aagttttggg tcaaaacccc 2160
agctatatct tttccgcga gcttgccgga agcagcaatg acggtcccgt cggcgcactg 2220
ggcacgccgt tgatgggggga atatgccggc gcagtcgacc ggcactacat taccttgggc 2280
gcgcccttat ttgtcgccac cgcccatccg gttacccgca aagccctcaa ccgcctgatt 2340
atggcgcagg ataccggcag cgcgattaaa ggcgcggtgc gcgtggatta tttttgggga 2400
tacggcgacg aagccggcga acttgccggc aaacagaaaa ccacgggtta cgtctggcag 2460
ctcctaccca acggtatgaa gcccgaatac cgcccgtaac tcgag 2505

[1716] <210>4

[1717] <211>832

[1718] <212>PRT

[1719] <213> 人工序列

[1720] <220>

[1721] <223>ΔG287-919

[1722] <400>4

[1723]

Met Ala Ser Pro Asp Val Lys Ser Ala Asp Thr Leu Ser Lys Pro Ala
1 5 10 15
Ala Pro Val Val Ala Glu Lys Glu Thr Glu Val Lys Glu Asp Ala Pro
20 25 30
Gln Ala Gly Ser Gln Gly Gln Gly Ala Pro Ser Thr Gln Gly Ser Gln
35 40 45
Asp Met Ala Ala Val Ser Ala Glu Asn Thr Gly Asn Gly Gly Ala Ala
50 55 60
Thr Thr Asp Lys Pro Lys Asn Glu Asp Glu Gly Pro Gln Asn Asp Met
65 70 75 80
Pro Gln Asn Ser Ala Glu Ser Ala Asn Gln Thr Gly Asn Asn Gln Pro
85 90 95
Ala Asp Ser Ser Asp Ser Ala Pro Ala Ser Asn Pro Ala Pro Ala Asn
100 105 110
Gly Gly Ser Asn Phe Gly Arg Val Asp Leu Ala Asn Gly Val Leu Ile
115 120 125
Asp Gly Pro Ser Gln Asn Ile Thr Leu Thr His Cys Lys Gly Asp Ser
130 135 140
Cys Asn Gly Asp Asn Leu Leu Asp Glu Glu Ala Pro Ser Lys Ser Glu
145 150 155 160
Phe Glu Asn Leu Asn Glu Ser Glu Arg Ile Glu Lys Tyr Lys Lys Asp
165 170 175
Gly Lys Ser Asp Lys Phe Thr Asn Leu Val Ala Thr Ala Val Gln Ala
180 185 190
Asn Gly Thr Asn Lys Tyr Val Ile Ile Tyr Lys Asp Lys Ser Ala Ser
195 200 205
Ser Ser Ser Ala Arg Phe Arg Arg Ser Ala Arg Ser Arg Arg Ser Leu
210 215 220
Pro Ala Glu Met Pro Leu Ile Pro Val Asn Gln Ala Asp Thr Leu Ile
225 230 235 240
Val Asp Gly Glu Ala Val Ser Leu Thr Gly His Ser Gly Asn Ile Phe
245 250 255

[1724]

Ala Pro Glu Gly Asn Tyr Arg Tyr Leu Thr Tyr Gly Ala Glu Lys Leu
260 265 270
Pro Gly Gly Ser Tyr Ala Leu Arg Val Gln Gly Glu Pro Ala Lys Gly
275 280 285
Glu Met Leu Ala Gly Thr Ala Val Tyr Asn Gly Glu Val Leu His Phe
290 295 300
His Thr Glu Asn Gly Arg Pro Tyr Pro Thr Arg Gly Arg Phe Ala Ala
305 310 315 320
Lys Val Asp Phe Gly Ser Lys Ser Val Asp Gly Ile Ile Asp Ser Gly
325 330 335
Asp Asp Leu His Met Gly Thr Gln Lys Phe Lys Ala Ala Ile Asp Gly
340 345 350
Asn Gly Phe Lys Gly Thr Trp Thr Glu Asn Gly Gly Gly Asp Val Ser
355 360 365
Gly Arg Phe Tyr Gly Pro Ala Gly Glu Glu Val Ala Gly Lys Tyr Ser
370 375 380
Tyr Arg Pro Thr Asp Ala Glu Lys Gly Gly Phe Gly Val Phe Ala Gly
385 390 395 400
Lys Lys Glu Gln Asp Gly Ser Gly Gly Gly Gly Cys Gln Ser Lys Ser
405 410 415
Ile Gln Thr Phe Pro Gln Pro Asp Thr Ser Val Ile Asn Gly Pro Asp
420 425 430
Arg Pro Val Gly Ile Pro Asp Pro Ala Gly Thr Thr Val Gly Gly Gly
435 440 445
Gly Ala Val Tyr Thr Val Val Pro His Leu Ser Leu Pro His Trp Ala
450 455 460
Ala Gln Asp Phe Ala Lys Ser Leu Gln Ser Phe Arg Leu Gly Cys Ala
465 470 475 480
Asn Leu Lys Asn Arg Gln Gly Trp Gln Asp Val Cys Ala Gln Ala Phe
485 490 495
Gln Thr Pro Val His Ser Phe Gln Ala Lys Gln Phe Phe Glu Arg Tyr
500 505 510
Phe Thr Pro Trp Gln Val Ala Gly Asn Gly Ser Leu Ala Gly Thr Val
515 520 525
Thr Gly Tyr Tyr Glu Pro Val Leu Lys Gly Asp Asp Arg Arg Thr Ala
530 535 540
Gln Ala Arg Phe Pro Ile Tyr Gly Ile Pro Asp Asp Phe Ile Ser Val
545 550 555 560
Pro Leu Pro Ala Gly Leu Arg Ser Gly Lys Ala Leu Val Arg Ile Arg
565 570 575
Gln Thr Gly Lys Asn Ser Gly Thr Ile Asp Asn Thr Gly Gly Thr His
580 585 590
Thr Ala Asp Leu Ser Arg Phe Pro Ile Thr Ala Arg Thr Thr Ala Ile
595 600 605
Lys Gly Arg Phe Glu Gly Ser Arg Phe Leu Pro Tyr His Thr Arg Asn
610 615 620
Gln Ile Asn Gly Gly Ala Leu Asp Gly Lys Ala Pro Ile Leu Gly Tyr
625 630 635 640
Ala Glu Asp Pro Val Glu Leu Phe Phe Met His Ile Gln Gly Ser Gly
645 650 655
Arg Leu Lys Thr Pro Ser Gly Lys Tyr Ile Arg Ile Gly Tyr Ala Asp
660 665 670

[1725]

Lys Asn Glu His Pro Tyr Val Ser Ile Gly Arg Tyr Met Ala Asp Lys
675 680 685
Gly Tyr Leu Lys Leu Gly Gln Thr Ser Met Gln Gly Ile Lys Ala Tyr
690 695 700
Met Arg Gln Asn Pro Gln Arg Leu Ala Glu Val Leu Gly Gln Asn Pro
705 710 715 720
Ser Tyr Ile Phe Phe Arg Glu Leu Ala Gly Ser Ser Asn Asp Gly Pro
725 730 735
Val Gly Ala Leu Gly Thr Pro Leu Met Gly Glu Tyr Ala Gly Ala Val
740 745 750
Asp Arg His Tyr Ile Thr Leu Gly Ala Pro Leu Phe Val Ala Thr Ala
755 760 765
His Pro Val Thr Arg Lys Ala Leu Asn Arg Leu Ile Met Ala Gln Asp
770 775 780
Thr Gly Ser Ala Ile Lys Gly Ala Val Arg Val Asp Tyr Phe Trp Gly
785 790 795 800
Tyr Gly Asp Glu Ala Gly Glu Leu Ala Gly Lys Gln Lys Thr Thr Gly
805 810 815
Tyr Val Trp Gln Leu Leu Pro Asn Gly Met Lys Pro Glu Tyr Arg Pro
820 825 830

[1726] <210>5

[1727] <211>1746

[1728] <212>DNA

[1729] <213> 人工序列

[1730] <220>

[1731] <223>ΔG287-953

[1732] <400>5

[1733]

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gctgaaaaag agacagaggt aaaagaagat gcgccacagg caggttctca aggacagggc 120
gcgccatcca cacaaggcag ccaagatatg gcggcagttt cggcagaaaa tacaggcaat 180
ggcggtgcgg caacaacgga caaacccaaa aatgaagacg agggaccgca aaatgatatg 240
ccgcaaaatt ccgccgaatc cgcaaatcaa acagggaaca accaacccgc cgattcttca 300
gattccgccc ccgcgtcaaa ccctgcacct gcgaatggcg gtagcaattt tggaagggtt 360
gatttggcta atggcgtttt gattgatggg ccgtcgcaaa atataacgtt gacccactgt 420
aaaggcgatt cttgtaatgg tgataattta ttggatgaag aagcaccgtc aaaatcagaa 480
tttgaaaatt taaatgagtc tgaacgaatt gagaaatata agaaagatgg gaaaagcgat 540
aaatttacta atttggttgc gacagcagtt caagctaatg gaactaacaa atatgtcatc 600
atttataaag acaagtccgc ttcatcttca tctgcgcgat tcaggcgttc tgcacggtcg 660
aggaggtcgc ttcctgccga gatgccgcta atccccgtca atcaggcgga tacgctgatt 720
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aattaccggt atctgactta cggggcggaa aaattgcccg gcggatcgta tgccctccgt 840
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gtgctgcatt ttcatacgga aaacggccgt ccgtacccga ctagaggcag gtttgccgca 960
aaagtcgatt tcggcagcaa atctgtggac ggcattatcg acagcggcga tgatttgcat 1020
atgggtacgc aaaaattcaa agccgccatc gatggaaacg gctttaaggg gacttggacg 1080
gaaaatggcg gcggggatgt ttccggaagg ttttacggcc cggccggcga ggaagtggcg 1140
ggaaaataca gctatcgccc gacagatgcg gaaaagggcg gattcggcgt gtttgccggc 1200
aaaaaagagc aggatggatc cggaggagga ggagccacct acaaagtgga cgaatatcac 1260

[1734]

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gccaacgccc gtttcgccat cgaccatttc aacaccagca ccaacgtcgg cggtttttac    1320
ggtctgaccg gttccgtcga gttcgaccaa gcaaaacgcg acggtaaaat cgacatcacc    1380
atccccgttg ccaacctgca aagcggttcg caacacttta ccgaccacct gaaatcagcc    1440
gacatcttcg atgccgccca atatccggac atccgctttg tttccaccaa attcaacttc    1500
aacggcaaaa aactggtttc cgttgacggc aacctgacca tgcacggcaa aaccgccccc    1560
gtcaaactca aagccgaaaa attcaactgc taccaaagcc cgatggcgaa aaccgaagtt    1620
tgcggcggcg acttcagcac caccatcgac cgcaccaaat ggggcgtgga ctacctcgtt    1680
aacgttggta tgaccaaaag cgtccgcatc gacatccaaa tcgaggcagc caaacaataa    1740
ctcgag                                                               1746
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[1735] <210>6

[1736] <211>579

[1737] <212>PRT

[1738] <213> 人工序列

[1739] <220>

[1740] <223>ΔG287-953

[1741] <400>6

[1742]

Met Ala Ser Pro Asp Val Lys Ser Ala Asp Thr Leu Ser Lys Pro Ala
1 5 10 15
Ala Pro Val Val Ala Glu Lys Glu Thr Glu Val Lys Glu Asp Ala Pro
20 25 30
Gln Ala Gly Ser Gln Gly Gln Gly Ala Pro Ser Thr Gln Gly Ser Gln
35 40 45
Asp Met Ala Ala Val Ser Ala Glu Asn Thr Gly Asn Gly Gly Ala Ala
50 55 60
Thr Thr Asp Lys Pro Lys Asn Glu Asp Glu Gly Pro Gln Asn Asp Met
65 70 75 80
Pro Gln Asn Ser Ala Glu Ser Ala Asn Gln Thr Gly Asn Asn Gln Pro
85 90 95
Ala Asp Ser Ser Asp Ser Ala Pro Ala Ser Asn Pro Ala Pro Ala Asn
100 105 110
Gly Gly Ser Asn Phe Gly Arg Val Asp Leu Ala Asn Gly Val Leu Ile
115 120 125
Asp Gly Pro Ser Gln Asn Ile Thr Leu Thr His Cys Lys Gly Asp Ser
130 135 140
Cys Asn Gly Asp Asn Leu Leu Asp Glu Glu Ala Pro Ser Lys Ser Glu
145 150 155 160
Phe Glu Asn Leu Asn Glu Ser Glu Arg Ile Glu Lys Tyr Lys Lys Asp
165 170 175
Gly Lys Ser Asp Lys Phe Thr Asn Leu Val Ala Thr Ala Val Gln Ala
180 185 190
Asn Gly Thr Asn Lys Tyr Val Ile Ile Tyr Lys Asp Lys Ser Ala Ser
195 200 205
Ser Ser Ser Ala Arg Phe Arg Arg Ser Ala Arg Ser Arg Arg Ser Leu
210 215 220
Pro Ala Glu Met Pro Leu Ile Pro Val Asn Gln Ala Asp Thr Leu Ile
225 230 235 240
Val Asp Gly Glu Ala Val Ser Leu Thr Gly His Ser Gly Asn Ile Phe
245 250 255
Ala Pro Glu Gly Asn Tyr Arg Tyr Leu Thr Tyr Gly Ala Glu Lys Leu

[1743]

260 265 270
Pro Gly Gly Ser Tyr Ala Leu Arg Val Gln Gly Glu Pro Ala Lys Gly
275 280 285
Glu Met Leu Ala Gly Thr Ala Val Tyr Asn Gly Glu Val Leu His Phe
290 295 300
His Thr Glu Asn Gly Arg Pro Tyr Pro Thr Arg Gly Arg Phe Ala Ala
305 310 315 320
Lys Val Asp Phe Gly Ser Lys Ser Val Asp Gly Ile Ile Asp Ser Gly
325 330 335
Asp Asp Leu His Met Gly Thr Gln Lys Phe Lys Ala Ala Ile Asp Gly
340 345 350
Asn Gly Phe Lys Gly Thr Trp Thr Glu Asn Gly Gly Gly Asp Val Ser
355 360 365
Gly Arg Phe Tyr Gly Pro Ala Gly Glu Glu Val Ala Gly Lys Tyr Ser
370 375 380
Tyr Arg Pro Thr Asp Ala Glu Lys Gly Gly Phe Gly Val Phe Ala Gly
385 390 395 400
Lys Lys Glu Gln Asp Gly Ser Gly Gly Gly Gly Ala Thr Tyr Lys Val
405 410 415
Asp Glu Tyr His Ala Asn Ala Arg Phe Ala Ile Asp His Phe Asn Thr
420 425 430
Ser Thr Asn Val Gly Gly Phe Tyr Gly Leu Thr Gly Ser Val Glu Phe
435 440 445
Asp Gln Ala Lys Arg Asp Gly Lys Ile Asp Ile Thr Ile Pro Val Ala
450 455 460
Asn Leu Gln Ser Gly Ser Gln His Phe Thr Asp His Leu Lys Ser Ala
465 470 475 480
Asp Ile Phe Asp Ala Ala Gln Tyr Pro Asp Ile Arg Phe Val Ser Thr
485 490 495
Lys Phe Asn Phe Asn Gly Lys Lys Leu Val Ser Val Asp Gly Asn Leu
500 505 510
Thr Met His Gly Lys Thr Ala Pro Val Lys Leu Lys Ala Glu Lys Phe
515 520 525
Asn Cys Tyr Gln Ser Pro Met Ala Lys Thr Glu Val Cys Gly Gly Asp
530 535 540
Phe Ser Thr Thr Ile Asp Arg Thr Lys Trp Gly Val Asp Tyr Leu Val
545 550 555 560
Asn Val Gly Met Thr Lys Ser Val Arg Ile Asp Ile Gln Ile Glu Ala
565 570 575
Ala Lys Gln

[1744] <210>7

[1745] <211>2388

[1746] <212>DNA

[1747] <213> 人工序列

[1748] <220>

[1749] <223> ΔG287-961

[1750] <400>7

[1751]

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[1752]

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gctgaaaaag agacagaggt aaaagaagat gcgccacagg caggttctca aggacagggc    120
gcgccatcca cacaaggcag ccaagatatg gcggcagttt cggcagaaaa tacaggcaat    180
ggcggtgcgg caacaacgga caaacccaaa aatgaagacg agggaccgca aaatgatatg    240
ccgcaaaatt ccgccgaatc cgcaaatcaa acagggaaca accaacccgc cgattcttca    300
gattccgccc ccgcgtcaaa ccctgcacct gcgaatggcg gtagcaattt tggaagggtt    360
gatttggcta atggcgtttt gattgatggg ccgtcgcaaa atataacgtt gacccactgt    420
aaaggcgatt cttgtaatgg tgataattta ttggatgaag aagcaccgtc aaaatcagaa    480
tttgaaaatt taaatgagtc tgaacgaatt gagaaatata agaaagatgg gaaaagcgat    540
aaatttacta atttggttgc gacagcagtt caagctaatg gaactaacaa atatgtcatc    600
atttataaag acaagtccgc ttcatcttca tctgcgcgat tcaggcgttc tgcacggtcg    660
aggaggtcgc ttcctgccga gatgccgcta atccccgtca atcaggcgga tacgctgatt    720
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aattaccggt atctgactta cggggcggaa aaattgcccg gcggatcgta tgccctccgt    840
gtgcaaggcg aaccggcaaa aggcgaaatg cttgctggca cggccgtgta caacggcgaa    900
gtgctgcatt ttcatacgga aaacggccgt ccgtacccga ctagaggcag gtttgccgca    960
aaagtcgatt tcggcagcaa atctgtggac ggcattatcg acagcggcga tgatttgcat    1020
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gaaaatggcg gcggggatgt ttccggaagg ttttacggcc cggccggcga ggaagtggcg    1140
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aaaaaagagc aggatggatc cggaggagga ggagccacaa acgacgacga tgttaaaaaa    1260
gctgccactg tggccattgc tgctgcctac aacaatggcc aagaaatcaa cggtttcaaa    1320
gctggagaga ccatctacga cattgatgaa gacggcacaa ttaccaaaaa agacgcaact    1380
gcagccgatg ttgaagccga cgactttaaa ggtctgggtc tgaaaaaagt cgtgactaac    1440
ctgaccaaaa ccgtcaatga aaacaaacaa aacgtcgatg ccaaagtaaa agctgcagaa    1500
tctgaaatag aaaagttaac aaccaagtta gcagacactg atgccgcttt agcagatact    1560
gatgccgctc tggatgcaac caccaacgcc ttgaataaat tgggagaaaa tataacgaca    1620
tttgctgaag agactaagac aaatatcgta aaaattgatg aaaaattaga agccgtggct    1680
gataccgtcg acaagcatgc cgaagcattc aacgatatcg ccgattcatt ggatgaaacc    1740
aacactaagg cagacgaagc cgtcaaaacc gccaatgaag ccaaacagac ggccgaagaa    1800
accaaacaaa acgtcgatgc caaagtaaaa gctgcagaaa ctgcagcagg caaagccgaa    1860
gctgccgctg gcacagctaa tactgcagcc gacaaggccg aagctgtcgc tgcaaaagtt    1920
accgacatca aagctgatat cgctacgaac aaagataata ttgctaaaaa agcaaacagt    1980
gccgacgtgt acaccagaga agagtctgac agcaaatttg tcagaattga tggtctgaac    2040
gctactaccg aaaaattgga cacacgcttg gcttctgctg aaaaatccat tgccgatcac    2100
gatactcgcc tgaacggttt ggataaaaca gtgtcagacc tgcgcaaaga aacccgccaa    2160
ggccttgcag aacaagccgc gctctccggt ctgttccaac cttacaacgt gggtcggttc    2220
aatgtaacgg ctgcagtcgg cggctacaaa tccgaatcgg cagtcgccat cggtaccggc    2280
ttccgcttta ccgaaaactt tgccgccaaa gcaggcgtgg cagtcggcac ttcgtccggt    2340
tcttccgcag cctaccatgt cggcgtcaat tacgagtggt aactcgag                2388
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[1753] 〈210〉8

[1754] 〈211〉793

[1755] 〈212〉PRT

[1756] 〈213〉人工序列

[1757] 〈220〉

[1758] 〈223〉ΔG287-961

[1759] 〈400〉8

[1760]

Met Ala Ser Pro Asp Val Lys Ser Ala Asp Thr Leu Ser Lys Pro Ala
1 5 10 15
Ala Pro Val Val Ala Glu Lys Glu Thr Glu Val Lys Glu Asp Ala Pro

[1761]

20 25 30
Gln Ala Gly Ser Gln Gly Gln Gly Ala Pro Ser Thr Gln Gly Ser Gln
35 40 45
Asp Met Ala Ala Val Ser Ala Glu Asn Thr Gly Asn Gly Gly Ala Ala
50 55 60
Thr Thr Asp Lys Pro Lys Asn Glu Asp Glu Gly Pro Gln Asn Asp Met
65 70 75 80
Pro Gln Asn Ser Ala Glu Ser Ala Asn Gln Thr Gly Asn Asn Gln Pro
85 90 95
Ala Asp Ser Ser Asp Ser Ala Pro Ala Ser Asn Pro Ala Pro Ala Asn
100 105 110
Gly Gly Ser Asn Phe Gly Arg Val Asp Leu Ala Asn Gly Val Leu Ile
115 120 125
Asp Gly Pro Ser Gln Asn Ile Thr Leu Thr His Cys Lys Gly Asp Ser
130 135 140
Cys Asn Gly Asp Asn Leu Leu Asp Glu Glu Ala Pro Ser Lys Ser Glu
145 150 155 160
Phe Glu Asn Leu Asn Glu Ser Glu Arg Ile Glu Lys Tyr Lys Lys Asp
165 170 175
Gly Lys Ser Asp Lys Phe Thr Asn Leu Val Ala Thr Ala Val Gln Ala
180 185 190
Asn Gly Thr Asn Lys Tyr Val Ile Ile Tyr Lys Asp Lys Ser Ala Ser
195 200 205
Ser Ser Ser Ala Arg Phe Arg Arg Ser Ala Arg Ser Arg Arg Ser Leu
210 215 220
Pro Ala Glu Met Pro Leu Ile Pro Val Asn Gln Ala Asp Thr Leu Ile
225 230 235 240
Val Asp Gly Glu Ala Val Ser Leu Thr Gly His Ser Gly Asn Ile Phe
245 250 255
Ala Pro Glu Gly Asn Tyr Arg Tyr Leu Thr Tyr Gly Ala Glu Lys Leu
260 265 270
Pro Gly Gly Ser Tyr Ala Leu Arg Val Gln Gly Glu Pro Ala Lys Gly
275 280 285
Glu Met Leu Ala Gly Thr Ala Val Tyr Asn Gly Glu Val Leu His Phe
290 295 300
His Thr Glu Asn Gly Arg Pro Tyr Pro Thr Arg Gly Arg Phe Ala Ala
305 310 315 320
Lys Val Asp Phe Gly Ser Lys Ser Val Asp Gly Ile Ile Asp Ser Gly
325 330 335
Asp Asp Leu His Met Gly Thr Gln Lys Phe Lys Ala Ala Ile Asp Gly
340 345 350
Asn Gly Phe Lys Gly Thr Trp Thr Glu Asn Gly Gly Gly Asp Val Ser
355 360 365
Gly Arg Phe Tyr Gly Pro Ala Gly Glu Glu Val Ala Gly Lys Tyr Ser
370 375 380
Tyr Arg Pro Thr Asp Ala Glu Lys Gly Gly Phe Gly Val Phe Ala Gly
385 390 395 400
Lys Lys Glu Gln Asp Gly Ser Gly Gly Gly Gly Ala Thr Asn Asp Asp
405 410 415
Asp Val Lys Lys Ala Ala Thr Val Ala Ile Ala Ala Ala Tyr Asn Asn
420 425 430
Gly Gln Glu Ile Asn Gly Phe Lys Ala Gly Glu Thr Ile Tyr Asp Ile

[1762]

435 440 445
Asp Glu Asp Gly Thr Ile Thr Lys Lys Asp Ala Thr Ala Ala Asp Val
450 455 460
Glu Ala Asp Asp Phe Lys Gly Leu Gly Leu Lys Lys Val Val Thr Asn
465 470 475 480
Leu Thr Lys Thr Val Asn Glu Asn Lys Gln Asn Val Asp Ala Lys Val
485 490 495
Lys Ala Ala Glu Ser Glu Ile Glu Lys Leu Thr Thr Lys Leu Ala Asp
500 505 510
Thr Asp Ala Ala Leu Ala Asp Thr Asp Ala Ala Leu Asp Ala Thr Thr
515 520 525
Asn Ala Leu Asn Lys Leu Gly Glu Asn Ile Thr Thr Phe Ala Glu Glu
530 535 540
Thr Lys Thr Asn Ile Val Lys Ile Asp Glu Lys Leu Glu Ala Val Ala
545 550 555 560
Asp Thr Val Asp Lys His Ala Glu Ala Phe Asn Asp Ile Ala Asp Ser
565 570 575
Leu Asp Glu Thr Asn Thr Lys Ala Asp Glu Ala Val Lys Thr Ala Asn
580 585 590
Glu Ala Lys Gln Thr Ala Glu Glu Thr Lys Gln Asn Val Asp Ala Lys
595 600 605
Val Lys Ala Ala Glu Thr Ala Ala Gly Lys Ala Glu Ala Ala Ala Gly
610 615 620
Thr Ala Asn Thr Ala Ala Asp Lys Ala Glu Ala Val Ala Ala Lys Val
625 630 635 640
Thr Asp Ile Lys Ala Asp Ile Ala Thr Asn Lys Asp Asn Ile Ala Lys
645 650 655
Lys Ala Asn Ser Ala Asp Val Tyr Thr Arg Glu Glu Ser Asp Ser Lys
660 665 670
Phe Val Arg Ile Asp Gly Leu Asn Ala Thr Thr Glu Lys Leu Asp Thr
675 680 685
Arg Leu Ala Ser Ala Glu Lys Ser Ile Ala Asp His Asp Thr Arg Leu
690 695 700
Asn Gly Leu Asp Lys Thr Val Ser Asp Leu Arg Lys Glu Thr Arg Gln
705 710 715 720
Gly Leu Ala Glu Gln Ala Ala Leu Ser Gly Leu Phe Gln Pro Tyr Asn
725 730 735
Val Gly Arg Phe Asn Val Thr Ala Ala Val Gly Gly Tyr Lys Ser Glu
740 745 750
Ser Ala Val Ala Ile Gly Thr Gly Phe Arg Phe Thr Glu Asn Phe Ala
755 760 765
Ala Lys Ala Gly Val Ala Val Gly Thr Ser Ser Gly Ser Ser Ala Ala
770 775 780
Tyr His Val Gly Val Asn Tyr Glu Trp
785 790

[1763] <210>9

[1764] <211>2700

[1765] <212>DNA

[1766] <213> 人工序列

[1767] <220>

[1768] <223>ΔG287NZ-919

[1769] <400>9

[1770]

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atggctagcc ccgatgtcaa gtcggcggac acgctgtcaa aacctgccgc ccctgttgtt    60
tctgaaaaag agacagaggc aaaggaagat gcgccacagg caggttctca aggacagggc   120
gcgccatccg cacaaggcgg tcaagatatg gcggcggttt cggaagaaaa tacaggcaat   180
ggcggtgcgg cagcaacgga caaacccaaa aatgaagacg agggggcgca aaatgatatg   240
ccgcaaaatg ccgccgatac agatagtttg acaccgaatc acaccccggc ttcgaatatg   300
ccggccggaa atatggaaaa ccaagcaccg gatgccgggg aatcggagca gccggcaaac   360
caaccggata tggcaaatac ggcggacgga atgcagggtg acgatccgtc ggcaggcggg   420
gaaaatgccg gcaatacggc tgcccaaggt acaaatcaag ccgaaaacaa tcaaaccgcc   480
ggttctcaaa atcctgcctc ttcaaccaat cctagcgcca cgaatagcgg tggtgatttt   540
ggaaggacga acgtgggcaa ttctgttgtg attgacgggc cgtcgcaaaa tataacgttg   600
acccactgta aaggcgattc ttgtagtggc aataatttct tggatgaaga agtacagcta   660
aaatcagaat ttgaaaaatt aagtgatgca gacaaaataa gtaattacaa gaaagatggg   720
aagaatgacg ggaagaatga taaatttgtc ggtttggttg ccgatagtgt gcagatgaag   780
ggaatcaatc aatatattat cttttataaa cctaaaccca cttcatttgc gcgatttagg   840
cgttctgcac ggtcgaggcg gtcgcttccg gccgagatgc cgctgattcc cgtcaatcag   900
gcggatacgc tgattgtcga tggggaagcg gtcagcctga cggggcattc cggcaatatc   960
ttcgcgcccg aagggaatta ccggtatctg acttacgggg cggaaaaatt gcccggcgga  1020
tcgtatgccc tccgtgttca aggcgaacct tcaaaaggcg aaatgctcgc gggcacggca  1080
gtgtacaacg gcgaagtgct gcattttcat acggaaaacg gccgtccgtc cccgtccaga  1140
ggcaggtttg ccgcaaaagt cgatttcggc agcaaatctg tggacggcat tatcgacagc  1200
ggcgatggtt tgcatatggg tacgcaaaaa ttcaaagccg ccatcgatgg aaacggcttt  1260
aaggggactt ggacggaaaa tggcggcggg gatgtttccg gaaagtttta cggcccggcc  1320
ggcgaggaag tggcgggaaa atacagctat cgcccaacag atgcggaaaa gggcggattc  1380
ggcgtgtttg ccggcaaaaa agagcaggat ggatccggag gaggaggatg ccaaagcaag  1440
agcatccaaa cctttccgca acccgacaca tccgtcatca acggcccgga ccggccggtc  1500
ggcatccccg accccgccgg aacgacggtc ggcggcggcg gggccgtcta taccgttgta  1560
ccgcacctgt ccctgcccca ctgggcggcg caggatttcg ccaaaagcct gcaatccttc  1620
cgcctcggct gcgccaattt gaaaaaccgc caaggctggc aggatgtgtg cgcccaagcc  1680
tttcaaaccc ccgtccattc ctttcaggca aaacagtttt ttgaacgcta tttcacgccg  1740
tggcaggttg caggcaacgg aagccttgcc ggtacggtta ccggctatta cgagccggtg  1800
ctgaagggcg acgacaggcg gacggcacaa gcccgcttcc cgatttacgg tattcccgac  1860
gattttatct ccgtcccccct gcctgccggt ttgcggagcg gaaaagccct tgtccgcatc  1920
aggcagacgg gaaaaaacag cggcacaatc gacaataccg gcggcacaca taccgccgac  1980
ctctcccgat tccccatcac cgcgcgcaca acggcaatca aaggcaggtt tgaaggaagc  2040
cgcttcctcc cctaccacac gcgcaaccaa atcaacggcg gcgcgcttga cggcaaagcc  2100
ccgatactcg gttacgccga agaccccgtc gaactttttt ttatgcacat ccaaggctcg  2160
ggccgtctga aaaccccgtc cggcaaatac atccgcatcg gctatgccga caaaaacgaa  2220
catccctacg tttccatcgg acgctatatg gcggacaaag gctacctcaa gctcgggcag  2280
acctcgatgc agggcatcaa agcctatatg cggcaaaatc cgcaacgcct cgccgaagtt  2340
ttgggtcaaa accccagcta tatctttttc cgcgagcttg ccggaagcag caatgacggt  2400
cccgtcggcg cactgggcac gccgttgatg gggggaatatg ccggcgcagt cgaccggcac  2460
tacattacct tgggcgcgcc cttatttgtc gccaccgccc atccggttac ccgcaaagcc  2520
ctcaaccgcc tgattatggc gcaggatacc ggcagcgcga ttaaaggcgc ggtgcgcgtg  2580
gattattttt ggggatacgg cgacgaagcc ggcgaacttg ccggcaaaca gaaaaccacg  2640
ggttacgtct ggcagctcct acccaacggt atgaagcccg aataccgccc gtaaaagctt  2700
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[1771] <210>10

[1772] <211>897

[1773] <212>PRT

[1774] <213> 人工序列

[1775] <220>

[1776] <223>ΔG287NZ-919

[1777] <400>10

[1778]

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Met Ala Ser Pro Asp Val Lys Ser Ala Asp Thr Leu Ser Lys Pro Ala
1               5                   10                  15
Ala Pro Val Val Ser Glu Lys Glu Thr Glu Ala Lys Glu Asp Ala Pro
            20                  25                  30
Gln Ala Gly Ser Gln Gly Gln Gly Ala Pro Ser Ala Gln Gly Gly Gln
        35                  40                  45
Asp Met Ala Ala Val Ser Glu Glu Asn Thr Gly Asn Gly Gly Ala Ala
    50                  55                  60
Ala Thr Asp Lys Pro Lys Asn Glu Asp Glu Gly Ala Gln Asn Asp Met
65                  70                  75                  80
Pro Gln Asn Ala Ala Asp Thr Asp Ser Leu Thr Pro Asn His Thr Pro
                85                  90                  95
Ala Ser Asn Met Pro Ala Gly Asn Met Glu Asn Gln Ala Pro Asp Ala
            100                 105                 110
Gly Glu Ser Glu Gln Pro Ala Asn Gln Pro Asp Met Ala Asn Thr Ala
        115                 120                 125
Asp Gly Met Gln Gly Asp Asp Pro Ser Ala Gly Gly Glu Asn Ala Gly
    130                 135                 140
Asn Thr Ala Ala Gln Gly Thr Asn Gln Ala Glu Asn Asn Gln Thr Ala
145                 150                 155                 160
Gly Ser Gln Asn Pro Ala Ser Ser Thr Asn Pro Ser Ala Thr Asn Ser
                165                 170                 175
Gly Gly Asp Phe Gly Arg Thr Asn Val Gly Asn Ser Val Val Ile Asp
            180                 185                 190
Gly Pro Ser Gln Asn Ile Thr Leu Thr His Cys Lys Gly Asp Ser Cys
        195                 200                 205
Ser Gly Asn Asn Phe Leu Asp Glu Glu Val Gln Leu Lys Ser Glu Phe
    210                 215                 220
Glu Lys Leu Ser Asp Ala Asp Lys Ile Ser Asn Tyr Lys Lys Asp Gly
225                 230                 235                 240
Lys Asn Asp Gly Lys Asn Asp Lys Phe Val Gly Leu Val Ala Asp Ser
                245                 250                 255
Val Gln Met Lys Gly Ile Asn Gln Tyr Ile Ile Phe Tyr Lys Pro Lys
            260                 265                 270
Pro Thr Ser Phe Ala Arg Phe Arg Arg Ser Ala Arg Ser Arg Arg Ser
        275                 280                 285
Leu Pro Ala Glu Met Pro Leu Ile Pro Val Asn Gln Ala Asp Thr Leu
    290                 295                 300
Ile Val Asp Gly Glu Ala Val Ser Leu Thr Gly His Ser Gly Asn Ile
305                 310                 315                 320
Phe Ala Pro Glu Gly Asn Tyr Arg Tyr Leu Thr Tyr Gly Ala Glu Lys
                325                 330                 335
Leu Pro Gly Gly Ser Tyr Ala Leu Arg Val Gln Gly Glu Pro Ser Lys
            340                 345                 350
Gly Glu Met Leu Ala Gly Thr Ala Val Tyr Asn Gly Glu Val Leu His
        355                 360                 365
```

[1779]

```
Phe His Thr Glu Asn Gly Arg Pro Ser Pro Ser Arg Gly Arg Phe Ala
    370                 375                 380
Ala Lys Val Asp Phe Gly Ser Lys Ser Val Asp Gly Ile Ile Asp Ser
385                 390                 395                 400
Gly Asp Gly Leu His Met Gly Thr Gln Lys Phe Lys Ala Ala Ile Asp
                405                 410                 415
Gly Asn Gly Phe Lys Gly Thr Trp Thr Glu Asn Gly Gly Gly Asp Val
            420                 425                 430
Ser Gly Lys Phe Tyr Gly Pro Ala Gly Glu Glu Val Ala Gly Lys Tyr
        435                 440                 445
Ser Tyr Arg Pro Thr Asp Ala Glu Lys Gly Gly Phe Gly Val Phe Ala
    450                 455                 460
Gly Lys Lys Glu Gln Asp Gly Ser Gly Gly Gly Gly Cys Gln Ser Lys
465                 470                 475                 480
Ser Ile Gln Thr Phe Pro Gln Pro Asp Thr Ser Val Ile Asn Gly Pro
                485                 490                 495
Asp Arg Pro Val Gly Ile Pro Asp Pro Ala Gly Thr Thr Val Gly Gly
            500                 505                 510
Gly Gly Ala Val Tyr Thr Val Val Pro His Leu Ser Leu Pro His Trp
        515                 520                 525
Ala Ala Gln Asp Phe Ala Lys Ser Leu Gln Ser Phe Arg Leu Gly Cys
    530                 535                 540
Ala Asn Leu Lys Asn Arg Gln Gly Trp Gln Asp Val Cys Ala Gln Ala
545                 550                 555                 560
Phe Gln Thr Pro Val His Ser Phe Gln Ala Lys Gln Phe Phe Glu Arg
                565                 570                 575
Tyr Phe Thr Pro Trp Gln Val Ala Gly Asn Gly Ser Leu Ala Gly Thr
            580                 585                 590
Val Thr Gly Tyr Tyr Glu Pro Val Leu Lys Gly Asp Asp Arg Arg Thr
        595                 600                 605
Ala Gln Ala Arg Phe Pro Ile Tyr Gly Ile Pro Asp Asp Phe Ile Ser
    610                 615                 620
Val Pro Leu Pro Ala Gly Leu Arg Ser Gly Lys Ala Leu Val Arg Ile
625                 630                 635                 640
Arg Gln Thr Gly Lys Asn Ser Gly Thr Ile Asp Asn Thr Gly Gly Thr
                645                 650                 655
His Thr Ala Asp Leu Ser Arg Phe Pro Ile Thr Ala Arg Thr Thr Ala
            660                 665                 670
Ile Lys Gly Arg Phe Glu Gly Ser Arg Phe Leu Pro Tyr His Thr Arg
        675                 680                 685
Asn Gln Ile Asn Gly Gly Ala Leu Asp Gly Lys Ala Pro Ile Leu Gly
    690                 695                 700
Tyr Ala Glu Asp Pro Val Glu Leu Phe Phe Met His Ile Gln Gly Ser
705                 710                 715                 720
Gly Arg Leu Lys Thr Pro Ser Gly Lys Tyr Ile Arg Ile Gly Tyr Ala
                725                 730                 735
Asp Lys Asn Glu His Pro Tyr Val Ser Ile Gly Arg Tyr Met Ala Asp
            740                 745                 750
Lys Gly Tyr Leu Lys Leu Gly Gln Thr Ser Met Gln Gly Ile Lys Ala
        755                 760                 765
Tyr Met Arg Gln Asn Pro Gln Arg Leu Ala Glu Val Leu Gly Gln Asn
    770                 775                 780
```

[1780]

```
Pro Ser Tyr Ile Phe Phe Arg Glu Leu Ala Gly Ser Ser Asn Asp Gly
785                 790                 795                 800
Pro Val Gly Ala Leu Gly Thr Pro Leu Met Gly Glu Tyr Ala Gly Ala
                805                 810                 815
Val Asp Arg His Tyr Ile Thr Leu Gly Ala Pro Leu Phe Val Ala Thr
            820                 825                 830
Ala His Pro Val Thr Arg Lys Ala Leu Asn Arg Leu Ile Met Ala Gln
        835                 840                 845
Asp Thr Gly Ser Ala Ile Lys Gly Ala Val Arg Val Asp Tyr Phe Trp
    850                 855                 860
Gly Tyr Gly Asp Glu Ala Gly Glu Leu Ala Gly Lys Gln Lys Thr Thr
865                 870                 875                 880
Gly Tyr Val Trp Gln Leu Leu Pro Asn Gly Met Lys Pro Glu Tyr Arg
                885                 890                 895
Pro
```

[1781] <210>11

[1782] <211>1941

[1783] <212>DNA

[1784] <213> 人工序列

[1785] <220>

[1786] <223>ΔG287NZ-953

[1787] <400>11

[1788]

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atggctagcc ccgatgtcaa gtcggcggac acgctgtcaa aacctgccgc ccctgttgtt    60
tctgaaaaag agacagaggc aaaggaagat gcgccacagg caggttctca aggacagggc   120
gcgccatccg cacaaggcgg tcaagatatg gcggcggttt cggaagaaaa tacaggcaat   180
ggcggtgcgg cagcaacgga caaacccaaa aatgaagacg agggggcgca aaatgatatg   240
ccgcaaaatg ccgccgatac agatagtttg acaccgaatc acaccccggc ttcgaatatg   300
ccggccggaa atatggaaaa ccaagcaccg gatgccgggg aatcggagca gccggcaaac   360
caaccggata tggcaaatac ggcggacgga atgcagggtg acgatccgtc ggcaggcggg   420
gaaaatgccg gcaatacggc tgcccaaggt acaaatcaag ccgaaaacaa tcaaaccgcc   480
ggttctcaaa atcctgcctc ttcaaccaat cctagcgcca cgaatagcgg tggtgatttt   540
ggaaggacga acgtgggcaa ttctgttgtg attgacgggc cgtcgcaaaa tataacgttg   600
acccactgta aaggcgattc ttgtagtggc aataatttct tggatgaaga agtacagcta   660
aaatcagaat ttgaaaaatt aagtgatgca gacaaaataa gtaattacaa gaaagatggg   720
aagaatgacg ggaagaatga taaatttgtc ggtttggttg ccgatagtgt gcagatgaag   780
ggaatcaatc aatatattat cttttataaa cctaaaccca cttcatttgc gcgatttagg   840
cgttctgcac ggtcgaggcg gtcgcttccg gccgagatgc cgctgattcc cgtcaatcag   900
gcggatacgc tgattgtcga tggggaagcg gtcagcctga cggggcattc cggcaatatc   960
ttcgcgcccg aagggaatta ccggtatctg acttacgggg cggaaaaatt gcccggcgga  1020
tcgtatgccc tccgtgttca aggcgaacct tcaaaaggcg aaatgctcgc gggcacggca  1080
gtgtacaacg gcgaagtgct gcattttcat acggaaaacg gccgtccgtc cccgtccaga  1140
ggcaggtttg ccgcaaaagt cgatttcggc agcaaatctg tggacggcat tatcgacagc  1200
ggcgatggtt tgcatatggg tacgcaaaaa ttcaaagccg ccatcgatgg aaacggcttt  1260
aaggggactt ggacggaaaa tggcggcggg gatgtttccg gaaagtttta cggcccggcc  1320
ggcgaggaag tggcgggaaa atacagctat cgcccaacag atgcggaaaa gggcggattc  1380
ggcgtgtttg ccggcaaaaa agagcaggat ggatccggag gaggaggagc cacctacaaa  1440
gtggacgaat atcacgccaa cgcccgtttc gccatcgacc atttcaacac cagcaccaac  1500
gtcggcggtt tttacggtct gaccggttcc gtcgagttcg accaagcaaa acgcgacggt  1560
```

[1789]

```
aaaatcgaca tcaccatccc cgttgccaac ctgcaaagcg gttcgcaaca ctttaccgac    1620
cacctgaaat cagccgacat cttcgatgcc gcccaatatc cggacatccg ctttgtttcc    1680
accaaattca acttcaacgg caaaaaactg gtttccgttg acggcaacct gaccatgcac    1740
ggcaaaaccg cccccgtcaa actcaaagcc gaaaaattca actgctacca aagcccgatg    1800
gcgaaaaccg aagtttgcgg cggcgacttc agcaccacca tcgaccgcac caaatggggc    1860
gtggactacc tcgttaacgt tggtatgacc aaaagcgtcc gcatcgacat ccaaatcgag    1920
gcagccaaac aataaaagct t                                              1941
```

[1790] <210>12

[1791] <211>644

[1792] <212>PRT

[1793] <213> 人工序列

[1794] <220>

[1795] <223>ΔG287NZ-953

[1796] <400>12

[1797]

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Met Ala Ser Pro Asp Val Lys Ser Ala Asp Thr Leu Ser Lys Pro Ala
1               5                   10                  15
Ala Pro Val Val Ser Glu Lys Glu Thr Glu Ala Lys Glu Asp Ala Pro
            20                  25                  30
Gln Ala Gly Ser Gln Gly Gln Gly Ala Pro Ser Ala Gln Gly Gly Gln
        35                  40                  45
Asp Met Ala Ala Val Ser Glu Glu Asn Thr Gly Asn Gly Gly Ala Ala
    50                  55                  60
Ala Thr Asp Lys Pro Lys Asn Glu Asp Glu Gly Ala Gln Asn Asp Met
65                  70                  75                  80
Pro Gln Asn Ala Ala Asp Thr Asp Ser Leu Thr Pro Asn His Thr Pro
                85                  90                  95
Ala Ser Asn Met Pro Ala Gly Asn Met Glu Asn Gln Ala Pro Asp Ala
            100                 105                 110
Gly Glu Ser Glu Gln Pro Ala Asn Gln Pro Asp Met Ala Asn Thr Ala
        115                 120                 125
Asp Gly Met Gln Gly Asp Asp Pro Ser Ala Gly Gly Glu Asn Ala Gly
    130                 135                 140
Asn Thr Ala Ala Gln Gly Thr Asn Gln Ala Glu Asn Asn Gln Thr Ala
145                 150                 155                 160
Gly Ser Gln Asn Pro Ala Ser Ser Thr Asn Pro Ser Ala Thr Asn Ser
                165                 170                 175
Gly Gly Asp Phe Gly Arg Thr Asn Val Gly Asn Ser Val Val Ile Asp
            180                 185                 190
Gly Pro Ser Gln Asn Ile Thr Leu Thr His Cys Lys Gly Asp Ser Cys
        195                 200                 205
Ser Gly Asn Asn Phe Leu Asp Glu Glu Val Gln Leu Lys Ser Glu Phe
    210                 215                 220
Glu Lys Leu Ser Asp Ala Asp Lys Ile Ser Asn Tyr Lys Lys Asp Gly
225                 230                 235                 240
Lys Asn Asp Gly Lys Asn Asp Lys Phe Val Gly Leu Val Ala Asp Ser
                245                 250                 255
Val Gln Met Lys Gly Ile Asn Gln Tyr Ile Ile Phe Tyr Lys Pro Lys
            260                 265                 270
Pro Thr Ser Phe Ala Arg Phe Arg Arg Ser Ala Arg Ser Arg Arg Ser
```

[1798]

275 280 285
Leu Pro Ala Glu Met Pro Leu Ile Pro Val Asn Gln Ala Asp Thr Leu
290 295 300
Ile Val Asp Gly Glu Ala Val Ser Leu Thr Gly His Ser Gly Asn Ile
305 310 315 320
Phe Ala Pro Glu Gly Asn Tyr Arg Tyr Leu Thr Tyr Gly Ala Glu Lys
325 330 335
Leu Pro Gly Gly Ser Tyr Ala Leu Arg Val Gln Gly Glu Pro Ser Lys
340 345 350
Gly Glu Met Leu Ala Gly Thr Ala Val Tyr Asn Gly Glu Val Leu His
355 360 365
Phe His Thr Glu Asn Gly Arg Pro Ser Pro Ser Arg Gly Arg Phe Ala
370 375 380
Ala Lys Val Asp Phe Gly Ser Lys Ser Val Asp Gly Ile Ile Asp Ser
385 390 395 400
Gly Asp Gly Leu His Met Gly Thr Gln Lys Phe Lys Ala Ala Ile Asp
405 410 415
Gly Asn Gly Phe Lys Gly Thr Trp Thr Glu Asn Gly Gly Gly Asp Val
420 425 430
Ser Gly Lys Phe Tyr Gly Pro Ala Gly Glu Glu Val Ala Gly Lys Tyr
435 440 445
Ser Tyr Arg Pro Thr Asp Ala Glu Lys Gly Gly Phe Gly Val Phe Ala
450 455 460
Gly Lys Lys Glu Gln Asp Gly Ser Gly Gly Gly Gly Ala Thr Tyr Lys
465 470 475 480
Val Asp Glu Tyr His Ala Asn Ala Arg Phe Ala Ile Asp His Phe Asn
485 490 495
Thr Ser Thr Asn Val Gly Gly Phe Tyr Gly Leu Thr Gly Ser Val Glu
500 505 510
Phe Asp Gln Ala Lys Arg Asp Gly Lys Ile Asp Ile Thr Ile Pro Val
515 520 525
Ala Asn Leu Gln Ser Gly Ser Gln His Phe Thr Asp His Leu Lys Ser
530 535 540
Ala Asp Ile Phe Asp Ala Ala Gln Tyr Pro Asp Ile Arg Phe Val Ser
545 550 555 560
Thr Lys Phe Asn Phe Asn Gly Lys Lys Leu Val Ser Val Asp Gly Asn
565 570 575
Leu Thr Met His Gly Lys Thr Ala Pro Val Lys Leu Lys Ala Glu Lys
580 585 590
Phe Asn Cys Tyr Gln Ser Pro Met Ala Lys Thr Glu Val Cys Gly Gly
595 600 605
Asp Phe Ser Thr Thr Ile Asp Arg Thr Lys Trp Gly Val Asp Tyr Leu
610 615 620
Val Asn Val Gly Met Thr Lys Ser Val Arg Ile Asp Ile Gln Ile Glu
625 630 635 640
Ala Ala Lys Gln

[1799] <210>13

[1800] <211>2583

[1801] <212>DNA

[1802] <213> 人工序列

[1803] <220>

[1804] <223>ΔG287NZ-961

[1805] <400>13

[1806]

atggctagcc ccgatgtcaa gtcggcggac acgctgtcaa aacctgccgc ccctgttgtt 60
tctgaaaaag agacagaggc aaaggaagat gcgccacagg caggttctca aggacagggc 120
gcgccatccg cacaaggcgg tcaagatatg gcggcggttt cggaagaaaa tacaggcaat 180
ggcggtgcgg cagcaacgga caaacccaaa aatgaagacg agggggcgca aaatgatatg 240
ccgcaaaatg ccgccgatac agatagtttg acaccgaatc acaccccggc ttcgaatatg 300
ccggccggaa atatggaaaa ccaagcaccg gatgccgggg aatcggagca gccggcaaac 360
caaccggata tggcaaatac ggcggacgga atgcagggtg acgatccgtc ggcaggcggg 420
gaaaatgccg gcaatacggc tgcccaaggt acaaatcaag ccgaaaacaa tcaaaccgcc 480
ggttctcaaa atcctgcctc ttcaaccaat cctagcgcca cgaatagcgg tggtgatttt 540
ggaaggacga acgtgggcaa ttctgttgtg attgacgggc cgtcgcaaaa tataacgttg 600
acccactgta aaggcgattc ttgtagtggc aataatttct tggatgaaga agtacagcta 660
aaatcagaat ttgaaaaatt aagtgatgca gacaaaataa gtaattacaa gaaagatggg 720
aagaatgacg ggaagaatga taaatttgtc ggtttggttg ccgatagtgt gcagatgaag 780
ggaatcaatc aatatattat cttttataaa cctaaaccca cttcatttgc gcgatttagg 840
cgttctgcac ggtcgaggcg gtcgcttccg gccgagatgc cgctgattcc cgtcaatcag 900
gcggatacgc tgattgtcga tggggaagcg gtcagcctga cggggcattc cggcaatatc 960
ttcgcgcccg aagggaatta ccggtatctg acttacgggg cggaaaaatt gcccggcgga 1020
tcgtatgccc tccgtgttca aggcgaacct tcaaaaggcg aaatgctcgc gggcacggca 1080
gtgtacaacg gcgaagtgct gcattttcat acggaaaacg gccgtccgtc cccgtccaga 1140
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ggcgatggtt tgcatatggg tacgcaaaaa ttcaaagccg ccatcgatgg aaacggcttt 1260
aaggggactt ggacggaaaa tggcggcggg gatgtttccg gaaagtttta cggcccggcc 1320
ggcgaggaag tggcgggaaa atacagctat cgcccaacag atgcggaaaa gggcggattc 1380
ggcgtgtttg ccggcaaaaa agagcaggat ggatccggag gaggaggagc cacaaacgac 1440
gacgatgtta aaaaagctgc cactgtggcc attgctgctg cctacaacaa tggccaagaa 1500
atcaacggtt tcaaagctgg agagaccatc tacgacattg atgaagacgg cacaattacc 1560
aaaaaagacg caactgcagc cgatgttgaa gccgacgact ttaaaggtct gggtctgaaa 1620
aaagtcgtga ctaacctgac caaaaccgtc aatgaaaaca aacaaaacgt cgatgccaaa 1680
gtaaaagctg cagaatctga aatagaaaag ttaacaacca agttagcaga cactgatgcc 1740
gctttagcag atactgatgc cgctctggat gcaaccacca acgccttgaa taaattggga 1800
gaaaatataa cgacatttgc tgaagagact aagacaaata tcgtaaaaat tgatgaaaaa 1860
ttagaagccg tggctgatac cgtcgacaag catgccgaag cattcaacga tatcgccgat 1920
tcattggatg aaaccaacac taaggcagac gaagccgtca aaaccgccaa tgaagccaaa 1980
cagacggccg aagaaaccaa acaaaacgtc gatgccaaag taaaagctgc agaaactgca 2040
gcaggcaaag ccgaagctgc cgctggcaca gctaatactg cagccgacaa ggccgaagct 2100
gtcgctgcaa aagttaccga catcaaagct gatatcgcta cgaacaaaga taatattgct 2160
aaaaaagcaa acagtgccga cgtgtacacc agagaagagt ctgacagcaa atttgtcaga 2220
attgatggtc tgaacgctac taccgaaaaa ttggacacac gcttggcttc tgctgaaaaa 2280
tccattgccg atcacgatac tcgcctgaac ggtttggata aaacagtgtc agacctgcgc 2340
aaagaaaccc gccaaggcct tgcagaacaa gccgcgctct ccggtctgtt ccaaccttac 2400
aacgtgggtc ggttcaatgt aacggctgca gtcggcggct acaaatccga atcggcagtc 2460
gccatcggta ccggcttccg ctttaccgaa aactttgccg ccaaagcagg cgtggcagtc 2520
ggcacttcgt ccggttcttc cgcagcctac catgtcggcg tcaattacga gtggtaaaag 2580
ctt 2583

[1807] <210>14

[1808] <211>858

[1809] <212>PRT

[1810] <213> 人工序列

[1811] <220>

[1812] <223>ΔG287NZ-961

[1813] <400>14

[1814]

```
Met Ala Ser Pro Asp Val Lys Ser Ala Asp Thr Leu Ser Lys Pro Ala
1               5                   10                  15
Ala Pro Val Val Ser Glu Lys Glu Thr Glu Ala Lys Glu Asp Ala Pro
            20                  25                  30
Gln Ala Gly Ser Gln Gly Gln Gly Ala Pro Ser Ala Gln Gly Gly Gln
        35                  40                  45
Asp Met Ala Ala Val Ser Glu Glu Asn Thr Gly Asn Gly Gly Ala Ala
    50                  55                  60
Ala Thr Asp Lys Pro Lys Asn Glu Asp Glu Gly Ala Gln Asn Asp Met
65                  70                  75                  80
Pro Gln Asn Ala Ala Asp Thr Asp Ser Leu Thr Pro Asn His Thr Pro
                85                  90                  95
Ala Ser Asn Met Pro Ala Gly Asn Met Glu Asn Gln Ala Pro Asp Ala
            100                 105                 110
Gly Glu Ser Glu Gln Pro Ala Asn Gln Pro Asp Met Ala Asn Thr Ala
        115                 120                 125
Asp Gly Met Gln Gly Asp Asp Pro Ser Ala Gly Gly Glu Asn Ala Gly
    130                 135                 140
Asn Thr Ala Ala Gln Gly Thr Asn Gln Ala Glu Asn Asn Gln Thr Ala
145                 150                 155                 160
Gly Ser Gln Asn Pro Ala Ser Ser Thr Asn Pro Ser Ala Thr Asn Ser
                165                 170                 175
Gly Gly Asp Phe Gly Arg Thr Asn Val Gly Asn Ser Val Val Ile Asp
            180                 185                 190
Gly Pro Ser Gln Asn Ile Thr Leu Thr His Cys Lys Gly Asp Ser Cys
        195                 200                 205
Ser Gly Asn Asn Phe Leu Asp Glu Glu Val Gln Leu Lys Ser Glu Phe
    210                 215                 220
Glu Lys Leu Ser Asp Ala Asp Lys Ile Ser Asn Tyr Lys Lys Asp Gly
225                 230                 235                 240
Lys Asn Asp Gly Lys Asn Asp Lys Phe Val Gly Leu Val Ala Asp Ser
                245                 250                 255
Val Gln Met Lys Gly Ile Asn Gln Tyr Ile Ile Phe Tyr Lys Pro Lys
            260                 265                 270
Pro Thr Ser Phe Ala Arg Phe Arg Arg Ser Ala Arg Ser Arg Arg Ser
        275                 280                 285
Leu Pro Ala Glu Met Pro Leu Ile Pro Val Asn Gln Ala Asp Thr Leu
    290                 295                 300
Ile Val Asp Gly Glu Ala Val Ser Leu Thr Gly His Ser Gly Asn Ile
305                 310                 315                 320
Phe Ala Pro Glu Gly Asn Tyr Arg Tyr Leu Thr Tyr Gly Ala Glu Lys
                325                 330                 335
Leu Pro Gly Gly Ser Tyr Ala Leu Arg Val Gln Gly Glu Pro Ser Lys
            340                 345                 350
Gly Glu Met Leu Ala Gly Thr Ala Val Tyr Asn Gly Glu Val Leu His
```

[1815]

```
        355                 360                 365
Phe His Thr Glu Asn Gly Arg Pro Ser Pro Ser Arg Gly Arg Phe Ala
    370                 375                 380
Ala Lys Val Asp Phe Gly Ser Lys Ser Val Asp Gly Ile Ile Asp Ser
385                 390                 395                 400
Gly Asp Gly Leu His Met Gly Thr Gln Lys Phe Lys Ala Ala Ile Asp
                405                 410                 415
Gly Asn Gly Phe Lys Gly Thr Trp Thr Glu Asn Gly Gly Gly Asp Val
            420                 425                 430
Ser Gly Lys Phe Tyr Gly Pro Ala Gly Glu Glu Val Ala Gly Lys Tyr
        435                 440                 445
Ser Tyr Arg Pro Thr Asp Ala Glu Lys Gly Gly Phe Gly Val Phe Ala
    450                 455                 460
Gly Lys Lys Glu Gln Asp Gly Ser Gly Gly Gly Gly Ala Thr Asn Asp
465                 470                 475                 480
Asp Asp Val Lys Lys Ala Ala Thr Val Ala Ile Ala Ala Ala Tyr Asn
                485                 490                 495
Asn Gly Gln Glu Ile Asn Gly Phe Lys Ala Gly Glu Thr Ile Tyr Asp
            500                 505                 510
Ile Asp Glu Asp Gly Thr Ile Thr Lys Lys Asp Ala Thr Ala Ala Asp
        515                 520                 525
Val Glu Ala Asp Asp Phe Lys Gly Leu Gly Leu Lys Lys Val Val Thr
    530                 535                 540
Asn Leu Thr Lys Thr Val Asn Glu Asn Lys Gln Asn Val Asp Ala Lys
545                 550                 555                 560
Val Lys Ala Ala Glu Ser Glu Ile Glu Lys Leu Thr Thr Lys Leu Ala
                565                 570                 575
Asp Thr Asp Ala Ala Leu Ala Asp Thr Asp Ala Ala Leu Asp Ala Thr
            580                 585                 590
Thr Asn Ala Leu Asn Lys Leu Gly Glu Asn Ile Thr Thr Phe Ala Glu
        595                 600                 605
Glu Thr Lys Thr Asn Ile Val Lys Ile Asp Glu Lys Leu Glu Ala Val
    610                 615                 620
Ala Asp Thr Val Asp Lys His Ala Glu Ala Phe Asn Asp Ile Ala Asp
625                 630                 635                 640
Ser Leu Asp Glu Thr Asn Thr Lys Ala Asp Glu Ala Val Lys Thr Ala
                645                 650                 655
Asn Glu Ala Lys Gln Thr Ala Glu Glu Thr Lys Gln Asn Val Asp Ala
            660                 665                 670
Lys Val Lys Ala Ala Glu Thr Ala Ala Gly Lys Ala Glu Ala Ala Ala
        675                 680                 685
Gly Thr Ala Asn Thr Ala Ala Asp Lys Ala Glu Ala Val Ala Ala Lys
    690                 695                 700
Val Thr Asp Ile Lys Ala Asp Ile Ala Thr Asn Lys Asp Asn Ile Ala
705                 710                 715                 720
Lys Lys Ala Asn Ser Ala Asp Val Tyr Thr Arg Glu Glu Ser Asp Ser
                725                 730                 735
Lys Phe Val Arg Ile Asp Gly Leu Asn Ala Thr Thr Glu Lys Leu Asp
            740                 745                 750
Thr Arg Leu Ala Ser Ala Glu Lys Ser Ile Ala Asp His Asp Thr Arg
        755                 760                 765
Leu Asn Gly Leu Asp Lys Thr Val Ser Asp Leu Arg Lys Glu Thr Arg
```

[1816]

```
        770                 775                 780
Gln Gly Leu Ala Glu Gln Ala Ala Leu Ser Gly Leu Phe Gln Pro Tyr
785                 790                 795                 800
Asn Val Gly Arg Phe Asn Val Thr Ala Ala Val Gly Gly Tyr Lys Ser
                805                 810                 815
Glu Ser Ala Val Ala Ile Gly Thr Gly Phe Arg Phe Thr Glu Asn Phe
            820                 825                 830
Ala Ala Lys Ala Gly Val Ala Val Gly Thr Ser Ser Gly Ser Ser Ala
        835                 840                 845
Ala Tyr His Val Gly Val Asn Tyr Glu Trp
    850                 855
```

[1817] <210>15

[1818] <211>1082

[1819] <212>PRT

[1820] <213> 人工序列

[1821] <220>

[1822] <223>983

[1823] <400>15

[1824]

```
Met Arg Thr Thr Pro Thr Phe Pro Thr Lys Thr Phe Lys Pro Thr Ala
1               5                   10                  15
Met Ala Leu Ala Val Ala Thr Thr Leu Ser Ala Cys Leu Gly Gly Gly
            20                  25                  30
Gly Gly Gly Thr Ser Ala Pro Asp Phe Asn Ala Gly Gly Thr Gly Ile
        35                  40                  45
Gly Ser Asn Ser Arg Ala Thr Thr Ala Lys Ser Ala Ala Val Ser Tyr
    50                  55                  60
Ala Gly Ile Lys Asn Glu Met Cys Lys Asp Arg Ser Met Leu Cys Ala
65                  70                  75                  80
Gly Arg Asp Asp Val Ala Val Thr Asp Arg Asp Ala Lys Ile Asn Ala
                85                  90                  95
Pro Pro Pro Asn Leu His Thr Gly Asp Phe Pro Asn Pro Asn Asp Ala
            100                 105                 110
Tyr Lys Asn Leu Ile Asn Leu Lys Pro Ala Ile Glu Ala Gly Tyr Thr
        115                 120                 125
Gly Arg Gly Val Glu Val Gly Ile Val Asp Thr Gly Glu Ser Val Gly
    130                 135                 140
Ser Ile Ser Phe Pro Glu Leu Tyr Gly Arg Lys Glu His Gly Tyr Asn
145                 150                 155                 160
Glu Asn Tyr Lys Asn Tyr Thr Ala Tyr Met Arg Lys Glu Ala Pro Glu
                165                 170                 175
Asp Gly Gly Gly Lys Asp Ile Glu Ala Ser Phe Asp Asp Glu Ala Val
            180                 185                 190
Ile Glu Thr Glu Ala Lys Pro Thr Asp Ile Arg His Val Lys Glu Ile
        195                 200                 205
Gly His Ile Asp Leu Val Ser His Ile Ile Gly Gly Arg Ser Val Asp
    210                 215                 220
Gly Arg Pro Ala Gly Gly Ile Ala Pro Asp Ala Thr Leu His Ile Met
225                 230                 235                 240
Asn Thr Asn Asp Glu Thr Lys Asn Glu Met Met Val Ala Ala Ile Arg
```

[1825]

```
                245                 250                 255
Asn Ala Trp Val Lys Leu Gly Glu Arg Gly Val Arg Ile Val Asn Asn
            260                 265                 270
Ser Phe Gly Thr Thr Ser Arg Ala Gly Thr Ala Asp Leu Phe Gln Ile
        275                 280                 285
Ala Asn Ser Glu Glu Gln Tyr Arg Gln Ala Leu Leu Asp Tyr Ser Gly
    290                 295                 300
Gly Asp Lys Thr Asp Glu Gly Ile Arg Leu Met Gln Gln Ser Asp Tyr
305                 310                 315                 320
Gly Asn Leu Ser Tyr His Ile Arg Asn Lys Asn Met Leu Phe Ile Phe
                325                 330                 335
Ser Thr Gly Asn Asp Ala Gln Ala Gln Pro Asn Thr Tyr Ala Leu Leu
            340                 345                 350
Pro Phe Tyr Glu Lys Asp Ala Gln Lys Gly Ile Ile Thr Val Ala Gly
        355                 360                 365
Val Asp Arg Ser Gly Glu Lys Phe Lys Arg Glu Met Tyr Gly Glu Pro
    370                 375                 380
Gly Thr Glu Pro Leu Glu Tyr Gly Ser Asn His Cys Gly Ile Thr Ala
385                 390                 395                 400
Met Trp Cys Leu Ser Ala Pro Tyr Glu Ala Ser Val Arg Phe Thr Arg
                405                 410                 415
Thr Asn Pro Ile Gln Ile Ala Gly Thr Ser Phe Ser Ala Pro Ile Val
            420                 425                 430
Thr Gly Thr Ala Ala Leu Leu Leu Gln Lys Tyr Pro Trp Met Ser Asn
        435                 440                 445
Asp Asn Leu Arg Thr Thr Leu Leu Thr Thr Ala Gln Asp Ile Gly Ala
    450                 455                 460
Val Gly Val Asp Ser Lys Phe Gly Trp Gly Leu Leu Asp Ala Gly Lys
465                 470                 475                 480
Ala Met Asn Gly Pro Ala Ser Phe Pro Phe Gly Asp Phe Thr Ala Asp
                485                 490                 495
Thr Lys Gly Thr Ser Asp Ile Ala Tyr Ser Phe Arg Asn Asp Ile Ser
            500                 505                 510
Gly Thr Gly Gly Leu Ile Lys Lys Gly Gly Ser Gln Leu Gln Leu His
        515                 520                 525
Gly Asn Asn Thr Tyr Thr Gly Lys Thr Ile Ile Glu Gly Gly Ser Leu
    530                 535                 540
Val Leu Tyr Gly Asn Asn Lys Ser Asp Met Arg Val Glu Thr Lys Gly
545                 550                 555                 560
Ala Leu Ile Tyr Asn Gly Ala Ala Ser Gly Gly Ser Leu Asn Ser Asp
                565                 570                 575
Gly Ile Val Tyr Leu Ala Asp Thr Asp Gln Ser Gly Ala Asn Glu Thr
            580                 585                 590
Val His Ile Lys Gly Ser Leu Gln Leu Asp Gly Lys Gly Thr Leu Tyr
        595                 600                 605
Thr Arg Leu Gly Lys Leu Leu Lys Val Asp Gly Thr Ala Ile Ile Gly
    610                 615                 620
Gly Lys Leu Tyr Met Ser Ala Arg Gly Lys Gly Ala Gly Tyr Leu Asn
625                 630                 635                 640
Ser Thr Gly Arg Arg Val Pro Phe Leu Ser Ala Ala Lys Ile Gly Gln
                645                 650                 655
Asp Tyr Ser Phe Phe Thr Asn Ile Glu Thr Asp Gly Gly Leu Leu Ala
```

[1826]

660 665 670
Ser Leu Asp Ser Val Glu Lys Thr Ala Gly Ser Glu Gly Asp Thr Leu
675 680 685
Ser Tyr Tyr Val Arg Arg Gly Asn Ala Ala Arg Thr Ala Ser Ala Ala
690 695 700
Ala His Ser Ala Pro Ala Gly Leu Lys His Ala Val Glu Gln Gly Gly
705 710 715 720
Ser Asn Leu Glu Asn Leu Met Val Glu Leu Asp Ala Ser Glu Ser Ser
725 730 735
Ala Thr Pro Glu Thr Val Glu Thr Ala Ala Ala Asp Arg Thr Asp Met
740 745 750
Pro Gly Ile Arg Pro Tyr Gly Ala Thr Phe Arg Ala Ala Ala Ala Val
755 760 765
Gln His Ala Asn Ala Ala Asp Gly Val Arg Ile Phe Asn Ser Leu Ala
770 775 780
Ala Thr Val Tyr Ala Asp Ser Thr Ala Ala His Ala Asp Met Gln Gly
785 790 795 800
Arg Arg Leu Lys Ala Val Ser Asp Gly Leu Asp His Asn Gly Thr Gly
805 810 815
Leu Arg Val Ile Ala Gln Thr Gln Gln Asp Gly Gly Thr Trp Glu Gln
820 825 830
Gly Gly Val Glu Gly Lys Met Arg Gly Ser Thr Gln Thr Val Gly Ile
835 840 845
Ala Ala Lys Thr Gly Glu Asn Thr Thr Ala Ala Ala Thr Leu Gly Met
850 855 860
Gly Arg Ser Thr Trp Ser Glu Asn Ser Ala Asn Ala Lys Thr Asp Ser
865 870 875 880
Ile Ser Leu Phe Ala Gly Ile Arg His Asp Ala Gly Asp Ile Gly Tyr
885 890 895
Leu Lys Gly Leu Phe Ser Tyr Gly Arg Tyr Lys Asn Ser Ile Ser Arg
900 905 910
Ser Thr Gly Ala Asp Glu His Ala Glu Gly Ser Val Asn Gly Thr Leu
915 920 925
Met Gln Leu Gly Ala Leu Gly Gly Val Asn Val Pro Phe Ala Ala Thr
930 935 940
Gly Asp Leu Thr Val Glu Gly Gly Leu Arg Tyr Asp Leu Leu Lys Gln
945 950 955 960
Asp Ala Phe Ala Glu Lys Gly Ser Ala Leu Gly Trp Ser Gly Asn Ser
965 970 975
Leu Thr Glu Gly Thr Leu Val Gly Leu Ala Gly Leu Lys Leu Ser Gln
980 985 990
Pro Leu Ser Asp Lys Ala Val Leu Phe Ala Thr Ala Gly Val Glu Arg
995 1000 1005
Asp Leu Asn Gly Arg Asp Tyr Thr Val Thr Gly Gly Phe Thr Gly Ala
1010 1015 1020
Thr Ala Ala Thr Gly Lys Thr Gly Ala Arg Asn Met Pro His Thr Arg
1025 1030 1035 1040
Leu Val Ala Gly Leu Gly Ala Asp Val Glu Phe Gly Asn Gly Trp Asn
1045 1050 1055
Gly Leu Ala Arg Tyr Ser Tyr Ala Gly Ser Lys Gln Tyr Gly Asn His
1060 1065 1070
[1827] Ser Gly Arg Val Gly Val Gly Tyr Arg Phe
1075 1080

[1828]　<210>16

[1829]　<211>1047

[1830]　<212>PRT

[1831]　<213> 人工序列

[1832]　<220>

[1833]　<223>ΔG983

[1834]　<400>16

[1835]

```
Thr Ser Ala Pro Asp Phe Asn Ala Gly Gly Thr Gly Ile Gly Ser Asn
1               5                   10                  15
Ser Arg Ala Thr Thr Ala Lys Ser Ala Ala Val Ser Tyr Ala Gly Ile
            20                  25                  30
Lys Asn Glu Met Cys Lys Asp Arg Ser Met Leu Cys Ala Gly Arg Asp
        35                  40                  45
Asp Val Ala Val Thr Asp Arg Asp Ala Lys Ile Asn Ala Pro Pro Pro
    50                  55                  60
Asn Leu His Thr Gly Asp Phe Pro Asn Pro Asn Asp Ala Tyr Lys Asn
65                  70                  75                  80
Leu Ile Asn Leu Lys Pro Ala Ile Glu Ala Gly Tyr Thr Gly Arg Gly
                85                  90                  95
Val Glu Val Gly Ile Val Asp Thr Gly Glu Ser Val Gly Ser Ile Ser
            100                 105                 110
Phe Pro Glu Leu Tyr Gly Arg Lys Glu His Gly Tyr Asn Glu Asn Tyr
        115                 120                 125
Lys Asn Tyr Thr Ala Tyr Met Arg Lys Glu Ala Pro Glu Asp Gly Gly
    130                 135                 140
Gly Lys Asp Ile Glu Ala Ser Phe Asp Asp Glu Ala Val Ile Glu Thr
145                 150                 155                 160
Glu Ala Lys Pro Thr Asp Ile Arg His Val Lys Glu Ile Gly His Ile
                165                 170                 175
Asp Leu Val Ser His Ile Ile Gly Gly Arg Ser Val Asp Gly Arg Pro
            180                 185                 190
Ala Gly Gly Ile Ala Pro Asp Ala Thr Leu His Ile Met Asn Thr Asn
        195                 200                 205
Asp Glu Thr Lys Asn Glu Met Met Val Ala Ala Ile Arg Asn Ala Trp
    210                 215                 220
Val Lys Leu Gly Glu Arg Gly Val Arg Ile Val Asn Asn Ser Phe Gly
225                 230                 235                 240
Thr Thr Ser Arg Ala Gly Thr Ala Asp Leu Phe Gln Ile Ala Asn Ser
                245                 250                 255
Glu Glu Gln Tyr Arg Gln Ala Leu Leu Asp Tyr Ser Gly Gly Asp Lys
            260                 265                 270
Thr Asp Glu Gly Ile Arg Leu Met Gln Gln Ser Asp Tyr Gly Asn Leu
        275                 280                 285
Ser Tyr His Ile Arg Asn Lys Asn Met Leu Phe Ile Phe Ser Thr Gly
    290                 295                 300
Asn Asp Ala Gln Ala Gln Pro Asn Thr Tyr Ala Leu Leu Pro Phe Tyr
305                 310                 315                 320
Glu Lys Asp Ala Gln Lys Gly Ile Ile Thr Val Ala Gly Val Asp Arg
```

[1836]

```
                325                 330                 335
Ser Gly Glu Lys Phe Lys Arg Glu Met Tyr Gly Glu Pro Gly Thr Glu
            340                 345                 350
Pro Leu Glu Tyr Gly Ser Asn His Cys Gly Ile Thr Ala Met Trp Cys
        355                 360                 365
Leu Ser Ala Pro Tyr Glu Ala Ser Val Arg Phe Thr Arg Thr Asn Pro
    370                 375                 380
Ile Gln Ile Ala Gly Thr Ser Phe Ser Ala Pro Ile Val Thr Gly Thr
385                 390                 395                 400
Ala Ala Leu Leu Leu Gln Lys Tyr Pro Trp Met Ser Asn Asp Asn Leu
                405                 410                 415
Arg Thr Thr Leu Leu Thr Thr Ala Gln Asp Ile Gly Ala Val Gly Val
            420                 425                 430
Asp Ser Lys Phe Gly Trp Gly Leu Leu Asp Ala Gly Lys Ala Met Asn
        435                 440                 445
Gly Pro Ala Ser Phe Pro Phe Gly Asp Phe Thr Ala Asp Thr Lys Gly
    450                 455                 460
Thr Ser Asp Ile Ala Tyr Ser Phe Arg Asn Asp Ile Ser Gly Thr Gly
465                 470                 475                 480
Gly Leu Ile Lys Lys Gly Gly Ser Gln Leu Gln Leu His Gly Asn Asn
                485                 490                 495
Thr Tyr Thr Gly Lys Thr Ile Ile Glu Gly Gly Ser Leu Val Leu Tyr
            500                 505                 510
Gly Asn Asn Lys Ser Asp Met Arg Val Glu Thr Lys Gly Ala Leu Ile
        515                 520                 525
Tyr Asn Gly Ala Ala Ser Gly Gly Ser Leu Asn Ser Asp Gly Ile Val
    530                 535                 540
Tyr Leu Ala Asp Thr Asp Gln Ser Gly Ala Asn Glu Thr Val His Ile
545                 550                 555                 560
Lys Gly Ser Leu Gln Leu Asp Gly Lys Gly Thr Leu Tyr Thr Arg Leu
                565                 570                 575
Gly Lys Leu Leu Lys Val Asp Gly Thr Ala Ile Ile Gly Gly Lys Leu
            580                 585                 590
Tyr Met Ser Ala Arg Gly Lys Gly Ala Gly Tyr Leu Asn Ser Thr Gly
        595                 600                 605
Arg Arg Val Pro Phe Leu Ser Ala Ala Lys Ile Gly Gln Asp Tyr Ser
    610                 615                 620
Phe Phe Thr Asn Ile Glu Thr Asp Gly Gly Leu Leu Ala Ser Leu Asp
625                 630                 635                 640
Ser Val Glu Lys Thr Ala Gly Ser Glu Gly Asp Thr Leu Ser Tyr Tyr
                645                 650                 655
Val Arg Arg Gly Asn Ala Ala Arg Thr Ala Ser Ala Ala Ala His Ser
            660                 665                 670
Ala Pro Ala Gly Leu Lys His Ala Val Glu Gln Gly Gly Ser Asn Leu
        675                 680                 685
Glu Asn Leu Met Val Glu Leu Asp Ala Ser Glu Ser Ser Ala Thr Pro
    690                 695                 700
Glu Thr Val Glu Thr Ala Ala Ala Asp Arg Thr Asp Met Pro Gly Ile
705                 710                 715                 720
Arg Pro Tyr Gly Ala Thr Phe Arg Ala Ala Ala Ala Val Gln His Ala
                725                 730                 735
Asn Ala Ala Asp Gly Val Arg Ile Phe Asn Ser Leu Ala Ala Thr Val
```

[1837]

```
            740                 745                 750
Tyr Ala Asp Ser Thr Ala Ala His Ala Asp Met Gln Gly Arg Arg Leu
        755                 760                 765
Lys Ala Val Ser Asp Gly Leu Asp His Asn Gly Thr Gly Leu Arg Val
    770                 775                 780
Ile Ala Gln Thr Gln Gln Asp Gly Gly Thr Trp Glu Gln Gly Gly Val
785                 790                 795                 800
Glu Gly Lys Met Arg Gly Ser Thr Gln Thr Val Gly Ile Ala Ala Lys
                805                 810                 815
Thr Gly Glu Asn Thr Thr Ala Ala Ala Thr Leu Gly Met Gly Arg Ser
            820                 825                 830
Thr Trp Ser Glu Asn Ser Ala Asn Ala Lys Thr Asp Ser Ile Ser Leu
        835                 840                 845
Phe Ala Gly Ile Arg His Asp Ala Gly Asp Ile Gly Tyr Leu Lys Gly
    850                 855                 860
Leu Phe Ser Tyr Gly Arg Tyr Lys Asn Ser Ile Ser Arg Ser Thr Gly
865                 870                 875                 880
Ala Asp Glu His Ala Glu Gly Ser Val Asn Gly Thr Leu Met Gln Leu
                885                 890                 895
Gly Ala Leu Gly Gly Val Asn Val Pro Phe Ala Ala Thr Gly Asp Leu
            900                 905                 910
Thr Val Glu Gly Gly Leu Arg Tyr Asp Leu Leu Lys Gln Asp Ala Phe
        915                 920                 925
Ala Glu Lys Gly Ser Ala Leu Gly Trp Ser Gly Asn Ser Leu Thr Glu
    930                 935                 940
Gly Thr Leu Val Gly Leu Ala Gly Leu Lys Leu Ser Gln Pro Leu Ser
945                 950                 955                 960
Asp Lys Ala Val Leu Phe Ala Thr Ala Gly Val Glu Arg Asp Leu Asn
                965                 970                 975
Gly Arg Asp Tyr Thr Val Thr Gly Gly Phe Thr Gly Ala Thr Ala Ala
            980                 985                 990
Thr Gly Lys Thr Gly Ala Arg Asn Met Pro His Thr Arg Leu Val Ala
        995                 1000                1005
Gly Leu Gly Ala Asp Val Glu Phe Gly Asn Gly Trp Asn Gly Leu Ala
    1010                1015                1020
Arg Tyr Ser Tyr Ala Gly Ser Lys Gln Tyr Gly Asn His Ser Gly Arg
1025                1030                1035                1040
Val Gly Val Gly Tyr Arg Phe
                1045
```

[1838] <210>17

[1839] <211>4425

[1840] <212>DNA

[1841] <213> 人工序列

[1842] <220>

[1843] <223>ΔG983-ORF46.1

[1844] <400>17

[1845]

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atgacttctg cgccccgactt caatgcaggc ggtaccggta tcggcagcaa cagcagagca    60
acaacagcga aatcagcagc agtatcttac gccggtatca agaacgaaat gtgcaaagac   120
agaagcatgc tctgtgccgg tcgggatgac gttgcggtta cagacaggga tgccaaaatc   180
```

```
aatgcccccc ccccgaatct gcataccgga gactttccaa acccaaatga cgcatacaag    240
aatttgatca acctcaaacc tgcaattgaa gcaggctata caggacgcgg ggtagaggta    300
ggtatcgtcg acacaggcga atccgtcggc agcatatcct ttcccgaact gtatggcaga    360
aaagaacacg gctataacga aaattacaaa aactatacgg cgtatatgcg gaaggaagcg    420
cctgaagacg gaggcggtaa agacattgaa gcttctttcg acgatgaggc cgttatagag    480
actgaagcaa agccgacgga tatccgccac gtaaaagaaa tcggacacat cgatttggtc    540
tcccatatta ttggcgggcg ttccgtggac ggcagacctg caggcggtat tgcgcccgat    600
gcgacgctac acataatgaa tacgaatgat gaaaccaaga acgaaatgat ggttgcagcc    660
atccgcaatg catgggtcaa gctgggcgaa cgtggcgtgc gcatcgtcaa taacagtttt    720
ggaacaacat cgagggcagg cactgccgac cttttccaaa tagccaattc ggaggagcag    780
taccgccaag cgttgctcga ctattccggc ggtgataaaa cagacgaggg tatccgcctg    840
atgcaacaga gcgattacgg caacctgtcc taccacatcc gtaataaaaa catgcttttc    900
atcttttcga caggcaatga cgcacaagct cagcccaaca catatgccct attgccattt    960
tatgaaaaag acgctcaaaa aggcattatc acagtcgcag gcgtagaccg cagtggagaa   1020
aagttcaaac gggaaatgta tggagaaccg ggtacagaac cgcttgagta tggctccaac   1080
cattgcggaa ttactgccat gtggtgcctg tcggcaccct atgaagcaag cgtccgtttc   1140
acccgtacaa acccgattca aattgccgga acatcctttt ccgcacccat cgtaaccggc   1200
acggcggctc tgctgctgca gaaatacccg tggatgagca acgacaacct gcgtaccacg   1260
ttgctgacga cggctcagga catcggtgca gtcggcgtgg acagcaagtt cggctgggga   1320
ctgctggatg cgggtaaggc catgaacgga cccgcgtcct ttccgttcgg cgactttacc   1380
gccgatacga aaggtacatc cgatattgcc tactccttcc gtaacgacat ttcaggcacg   1440
ggcggcctga tcaaaaaagg cggcagccaa ctgcaactgc acggcaacaa cacctatacg   1500
ggcaaaacca ttatcgaagg cggttcgctg gtgttgtacg gcaacaacaa atcggatatg   1560
cgcgtcgaaa ccaaaggtgc gctgatttat aacggggcgg catccggcgg cagcctgaac   1620
agcgacggca ttgtctatct ggcagatacc gaccaatccg gcgcaaacga aaccgtacac   1680
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ctgaaagtgg acggtacggc gattatcggc ggcaagctgt acatgtcggc acgcggcaag   1800
ggggcaggct atctcaacag taccggacga cgtgttccct tcctgagtgc cgccaaaatc   1860
gggcaggatt attctttctt cacaaacatc gaaaccgacg gcggcctgct ggcttccctc   1920
gacagcgtcg aaaaaacagc gggcagtgaa ggcgacacgc tgtcctatta tgtccgtcgc   1980
ggcaatgcgg cacggactgc ttcggcagcg gcacattccg cgcccgccgg tctgaaacac   2040
gccgtagaac agggcggcag caatctggaa aacctgatgg tcgaactgga tgcctccgaa   2100
tcatccgcaa cacccgagac ggttgaaact gcggcagccg accgcacaga tatgccgggc   2160
atccgcccct acggcgcaac tttccgcgca gcggcagccg tacagcatgc gaatgccgcc   2220
gacggtgtac gcatcttcaa cagtctcgcc gctaccgtct atgccgacag taccgccgcc   2280
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gttgaaggca aaatgcgcgg cagtacccaa accgtcggca ttgccgcgaa aaccggcgaa   2460
aatacgacag cagccgccac actgggcatg ggacgcagca catggagcga aaacagtgca   2520
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agcgataaag ccgtcctgtt tgcaacggcg ggcgtggaac gcgacctgaa cggacgcgac   2940
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aatatgccgc acacccgtct ggttgccggc ctgggcgcgg atgtcgaatt cggcaacggc   3060
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cgagtcggcg taggctaccg gttcctcgac ggtggcggag gcactggatc ctcagatttg   3180
gcaaacgatt cttttatccg gcaggttctc gaccgtcagc atttcgaacc cgacgggaaa   3240
taccacctat tcggcagcag gggggaactt gccgagcgca gcggccatat cggattggga   3300
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[1846]

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catgcctcac attccgattc tgatgaagcc ggtagtcccg ttgacggatt tagcctttac   3480
cgcatccatt gggacggata cgaacaccat cccgccgacg gctatgacgg gccacagggc   3540
ggcggctatc ccgctcccaa aggcgcgagg gatatataca gctacgacat aaaaggcgtt   3600
gcccaaaata tccgcctcaa cctgaccgac aaccgcagca ccggacaacg gcttgccgac   3660
cgtttccaca atgccggtag tatgctgacg caaggagtag gcgacggatt caaacgcgcc   3720
acccgataca gccccgagct ggacagatcg ggcaatgccg ccgaagcctt caacggcact   3780
gcagatatcg ttaaaaacat catcggcgcg gcaggagaaa ttgtcggcgc aggcgatgcc   3840
gtgcagggca taagcgaagg ctcaaacatt gctgtcatgc acggcttggg tctgctttcc   3900
accgaaaaca agatggcgcg catcaacgat ttggcagata tggcgcaact caaagactat   3960
gccgcagcag ccatccgcga ttgggcagtc caaaacccca atgccgcaca aggcatagaa   4020
gccgtcagca atatctttat ggcagccatc cccatcaaag ggattggagc tgttcgggga   4080
aaatacggct tgggcggcat cacggcacat cctatcaagc ggtcgcagat gggcgcgatc   4140
gcattgccga aagggaaatc cgccgtcagc gacaattttg ccgatgcggc atacgccaaa   4200
tacccgtccc cttaccattc ccgaaatatc cgttcaaact tggagcagcg ttacggcaaa   4260
gaaaacatca cctcctcaac cgtgccgccg tcaaacggca aaaatgtcaa actggcagac   4320
caacgccacc cgaagacagg cgtaccgttt gacggtaaag ggtttccgaa ttttgagaag   4380
cacgtgaaat atgatacgct cgagcaccac caccaccacc actga                   4425
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[1847] <210>18

[1848] <211>1474

[1849] <212>PRT

[1850] <213> 人工序列

[1851] <220>

[1852] <223>ΔG983-ORF46.1

[1853] <400>18

[1854]

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Met Thr Ser Ala Pro Asp Phe Asn Ala Gly Gly Thr Gly Ile Gly Ser
1               5                   10                  15
Asn Ser Arg Ala Thr Thr Ala Lys Ser Ala Ala Val Ser Tyr Ala Gly
            20                  25                  30
Ile Lys Asn Glu Met Cys Lys Asp Arg Ser Met Leu Cys Ala Gly Arg
        35                  40                  45
Asp Asp Val Ala Val Thr Asp Arg Asp Ala Lys Ile Asn Ala Pro Pro
    50                  55                  60
Pro Asn Leu His Thr Gly Asp Phe Pro Asn Pro Asn Asp Ala Tyr Lys
65                  70                  75                  80
Asn Leu Ile Asn Leu Lys Pro Ala Ile Glu Ala Gly Tyr Thr Gly Arg
                85                  90                  95
Gly Val Glu Val Gly Ile Val Asp Thr Gly Glu Ser Val Gly Ser Ile
            100                 105                 110
Ser Phe Pro Glu Leu Tyr Gly Arg Lys Glu His Gly Tyr Asn Glu Asn
        115                 120                 125
Tyr Lys Asn Tyr Thr Ala Tyr Met Arg Lys Glu Ala Pro Glu Asp Gly
    130                 135                 140
Gly Gly Lys Asp Ile Glu Ala Ser Phe Asp Asp Glu Ala Val Ile Glu
145                 150                 155                 160
Thr Glu Ala Lys Pro Thr Asp Ile Arg His Val Lys Glu Ile Gly His
                165                 170                 175
```

[1855]

```
Ile Asp Leu Val Ser His Ile Ile Gly Gly Arg Ser Val Asp Gly Arg
            180                 185                 190
Pro Ala Gly Gly Ile Ala Pro Asp Ala Thr Leu His Ile Met Asn Thr
        195                 200                 205
Asn Asp Glu Thr Lys Asn Glu Met Met Val Ala Ala Ile Arg Asn Ala
    210                 215                 220
Trp Val Lys Leu Gly Glu Arg Gly Val Arg Ile Val Asn Asn Ser Phe
225                 230                 235                 240
Gly Thr Thr Ser Arg Ala Gly Thr Ala Asp Leu Phe Gln Ile Ala Asn
                245                 250                 255
Ser Glu Glu Gln Tyr Arg Gln Ala Leu Leu Asp Tyr Ser Gly Gly Asp
            260                 265                 270
Lys Thr Asp Glu Gly Ile Arg Leu Met Gln Gln Ser Asp Tyr Gly Asn
        275                 280                 285
Leu Ser Tyr His Ile Arg Asn Lys Asn Met Leu Phe Ile Phe Ser Thr
    290                 295                 300
Gly Asn Asp Ala Gln Ala Gln Pro Asn Thr Tyr Ala Leu Leu Pro Phe
305                 310                 315                 320
Tyr Glu Lys Asp Ala Gln Lys Gly Ile Ile Thr Val Ala Gly Val Asp
                325                 330                 335
Arg Ser Gly Glu Lys Phe Lys Arg Glu Met Tyr Gly Glu Pro Gly Thr
            340                 345                 350
Glu Pro Leu Glu Tyr Gly Ser Asn His Cys Gly Ile Thr Ala Met Trp
        355                 360                 365
Cys Leu Ser Ala Pro Tyr Glu Ala Ser Val Arg Phe Thr Arg Thr Asn
    370                 375                 380
Pro Ile Gln Ile Ala Gly Thr Ser Phe Ser Ala Pro Ile Val Thr Gly
385                 390                 395                 400
Thr Ala Ala Leu Leu Leu Gln Lys Tyr Pro Trp Met Ser Asn Asp Asn
                405                 410                 415
Leu Arg Thr Thr Leu Leu Thr Thr Ala Gln Asp Ile Gly Ala Val Gly
            420                 425                 430
Val Asp Ser Lys Phe Gly Trp Gly Leu Leu Asp Ala Gly Lys Ala Met
        435                 440                 445
Asn Gly Pro Ala Ser Phe Pro Phe Gly Asp Phe Thr Ala Asp Thr Lys
    450                 455                 460
Gly Thr Ser Asp Ile Ala Tyr Ser Phe Arg Asn Asp Ile Ser Gly Thr
465                 470                 475                 480
Gly Gly Leu Ile Lys Lys Gly Gly Ser Gln Leu Gln Leu His Gly Asn
                485                 490                 495
Asn Thr Tyr Thr Gly Lys Thr Ile Ile Glu Gly Gly Ser Leu Val Leu
            500                 505                 510
Tyr Gly Asn Asn Lys Ser Asp Met Arg Val Glu Thr Lys Gly Ala Leu
        515                 520                 525
Ile Tyr Asn Gly Ala Ala Ser Gly Gly Ser Leu Asn Ser Asp Gly Ile
    530                 535                 540
Val Tyr Leu Ala Asp Thr Asp Gln Ser Gly Ala Asn Glu Thr Val His
545                 550                 555                 560
Ile Lys Gly Ser Leu Gln Leu Asp Gly Lys Gly Thr Leu Tyr Thr Arg
                565                 570                 575
Leu Gly Lys Leu Leu Lys Val Asp Gly Thr Ala Ile Ile Gly Gly Lys
            580                 585                 590
```

[1856]

Leu Tyr Met Ser Ala Arg Gly Lys Gly Ala Gly Tyr Leu Asn Ser Thr
595 600 605
Gly Arg Arg Val Pro Phe Leu Ser Ala Ala Lys Ile Gly Gln Asp Tyr
610 615 620
Ser Phe Phe Thr Asn Ile Glu Thr Asp Gly Gly Leu Leu Ala Ser Leu
625 630 635 640
Asp Ser Val Glu Lys Thr Ala Gly Ser Glu Gly Asp Thr Leu Ser Tyr
645 650 655
Tyr Val Arg Arg Gly Asn Ala Ala Arg Thr Ala Ser Ala Ala Ala His
660 665 670
Ser Ala Pro Ala Gly Leu Lys His Ala Val Glu Gln Gly Gly Ser Asn
675 680 685
Leu Glu Asn Leu Met Val Glu Leu Asp Ala Ser Glu Ser Ser Ala Thr
690 695 700
Pro Glu Thr Val Glu Thr Ala Ala Ala Asp Arg Thr Asp Met Pro Gly
705 710 715 720
Ile Arg Pro Tyr Gly Ala Thr Phe Arg Ala Ala Ala Ala Val Gln His
725 730 735
Ala Asn Ala Ala Asp Gly Val Arg Ile Phe Asn Ser Leu Ala Ala Thr
740 745 750
Val Tyr Ala Asp Ser Thr Ala Ala His Ala Asp Met Gln Gly Arg Arg
755 760 765
Leu Lys Ala Val Ser Asp Gly Leu Asp His Asn Gly Thr Gly Leu Arg
770 775 780
Val Ile Ala Gln Thr Gln Gln Asp Gly Gly Thr Trp Glu Gln Gly Gly
785 790 795 800
Val Glu Gly Lys Met Arg Gly Ser Thr Gln Thr Val Gly Ile Ala Ala
805 810 815
Lys Thr Gly Glu Asn Thr Thr Ala Ala Ala Thr Leu Gly Met Gly Arg
820 825 830
Ser Thr Trp Ser Glu Asn Ser Ala Asn Ala Lys Thr Asp Ser Ile Ser
835 840 845
Leu Phe Ala Gly Ile Arg His Asp Ala Gly Asp Ile Gly Tyr Leu Lys
850 855 860
Gly Leu Phe Ser Tyr Gly Arg Tyr Lys Asn Ser Ile Ser Arg Ser Thr
865 870 875 880
Gly Ala Asp Glu His Ala Glu Gly Ser Val Asn Gly Thr Leu Met Gln
885 890 895
Leu Gly Ala Leu Gly Gly Val Asn Val Pro Phe Ala Ala Thr Gly Asp
900 905 910
Leu Thr Val Glu Gly Gly Leu Arg Tyr Asp Leu Leu Lys Gln Asp Ala
915 920 925
Phe Ala Glu Lys Gly Ser Ala Leu Gly Trp Ser Gly Asn Ser Leu Thr
930 935 940
Glu Gly Thr Leu Val Gly Leu Ala Gly Leu Lys Leu Ser Gln Pro Leu
945 950 955 960
Ser Asp Lys Ala Val Leu Phe Ala Thr Ala Gly Val Glu Arg Asp Leu
965 970 975
Asn Gly Arg Asp Tyr Thr Val Thr Gly Gly Phe Thr Gly Ala Thr Ala
980 985 990
Ala Thr Gly Lys Thr Gly Ala Arg Asn Met Pro His Thr Arg Leu Val
995 1000 1005

[1857]

Ala Gly Leu Gly Ala Asp Val Glu Phe Gly Asn Gly Trp Asn Gly Leu
1010 1015 1020
Ala Arg Tyr Ser Tyr Ala Gly Ser Lys Gln Tyr Gly Asn His Ser Gly
1025 1030 1035 1040
Arg Val Gly Val Gly Tyr Arg Phe Leu Asp Gly Gly Gly Gly Thr Gly
1045 1050 1055
Ser Ser Asp Leu Ala Asn Asp Ser Phe Ile Arg Gln Val Leu Asp Arg
1060 1065 1070
Gln His Phe Glu Pro Asp Gly Lys Tyr His Leu Phe Gly Ser Arg Gly
1075 1080 1085
Glu Leu Ala Glu Arg Ser Gly His Ile Gly Leu Gly Lys Ile Gln Ser
1090 1095 1100
His Gln Leu Gly Asn Leu Met Ile Gln Gln Ala Ala Ile Lys Gly Asn
1105 1110 1115 1120
Ile Gly Tyr Ile Val Arg Phe Ser Asp His Gly His Glu Val His Ser
1125 1130 1135
Pro Phe Asp Asn His Ala Ser His Ser Asp Ser Asp Glu Ala Gly Ser
1140 1145 1150
Pro Val Asp Gly Phe Ser Leu Tyr Arg Ile His Trp Asp Gly Tyr Glu
1155 1160 1165
His His Pro Ala Asp Gly Tyr Asp Gly Pro Gln Gly Gly Gly Tyr Pro
1170 1175 1180
Ala Pro Lys Gly Ala Arg Asp Ile Tyr Ser Tyr Asp Ile Lys Gly Val
1185 1190 1195 1200
Ala Gln Asn Ile Arg Leu Asn Leu Thr Asp Asn Arg Ser Thr Gly Gln
1205 1210 1215
Arg Leu Ala Asp Arg Phe His Asn Ala Gly Ser Met Leu Thr Gln Gly
1220 1225 1230
Val Gly Asp Gly Phe Lys Arg Ala Thr Arg Tyr Ser Pro Glu Leu Asp
1235 1240 1245
Arg Ser Gly Asn Ala Ala Glu Ala Phe Asn Gly Thr Ala Asp Ile Val
1250 1255 1260
Lys Asn Ile Ile Gly Ala Ala Gly Glu Ile Val Gly Ala Gly Asp Ala
1265 1270 1275 1280
Val Gln Gly Ile Ser Glu Gly Ser Asn Ile Ala Val Met His Gly Leu
1285 1290 1295
Gly Leu Leu Ser Thr Glu Asn Lys Met Ala Arg Ile Asn Asp Leu Ala
1300 1305 1310
Asp Met Ala Gln Leu Lys Asp Tyr Ala Ala Ala Ala Ile Arg Asp Trp
1315 1320 1325
Ala Val Gln Asn Pro Asn Ala Ala Gln Gly Ile Glu Ala Val Ser Asn
1330 1335 1340
Ile Phe Met Ala Ala Ile Pro Ile Lys Gly Ile Gly Ala Val Arg Gly
1345 1350 1355 1360
Lys Tyr Gly Leu Gly Gly Ile Thr Ala His Pro Ile Lys Arg Ser Gln
1365 1370 1375
Met Gly Ala Ile Ala Leu Pro Lys Gly Lys Ser Ala Val Ser Asp Asn
1380 1385 1390
Phe Ala Asp Ala Ala Tyr Ala Lys Tyr Pro Ser Pro Tyr His Ser Arg
1395 1400 1405
Asn Ile Arg Ser Asn Leu Glu Gln Arg Tyr Gly Lys Glu Asn Ile Thr
1410 1415 1420

[1858]

```
Ser Ser Thr Val Pro Pro Ser Asn Gly Lys Asn Val Lys Leu Ala Asp
1425                1430                1435                1440
Gln Arg His Pro Lys Thr Gly Val Pro Phe Asp Gly Lys Gly Phe Pro
                1445                1450                1455
Asn Phe Glu Lys His Val Lys Tyr Asp Thr Leu Glu His His His His
            1460                1465                1470
His His
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[1859] <210>19

[1860] <211>3939

[1861] <212>DNA

[1862] <213>人工序列

[1863] <220>

[1864] <223>ΔG983-741

[1865] <400>19

[1866]

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acaacagcga aatcagcagc agtatcttac gccggtatca agaacgaaat gtgcaaagac   120
agaagcatgc tctgtgccgg tcgggatgac gttgcggtta cagacaggga tgccaaaatc   180
aatgcccccc ccccgaatct gcataccgga gactttccaa acccaaatga cgcatacaag   240
aatttgatca acctcaaacc tgcaattgaa gcaggctata caggacgcgg ggtagaggta   300
ggtatcgtcg acacaggcga atccgtcggc agcatatcct ttcccgaact gtatggcaga   360
aaagaacacg gctataacga aaattacaaa aactatacgg cgtatatgcg gaaggaagcg   420
cctgaagacg gaggcggtaa agacattgaa gcttctttcg acgatgaggc cgttatagag   480
actgaagcaa agccgacgga tatccgccac gtaaaagaaa tcggacacat cgatttggtc   540
tcccatatta ttggcgggcg ttccgtggac ggcagacctg caggcggtat tgcgcccgat   600
gcgacgctac acataatgaa tacgaatgat gaaaccaaga acgaaatgat ggttgcagcc   660
atccgcaatg catgggtcaa gctgggcgaa cgtggcgtgc gcatcgtcaa taacagtttt   720
ggaacaacat cgagggcagg cactgccgac cttttccaaa tagccaattc ggaggagcag   780
taccgccaag cgttgctcga ctattccggc ggtgataaaa cagacgaggg tatccgcctg   840
atgcaacaga gcgattacgg caacctgtcc taccacatcc gtaataaaaa catgcttttc   900
atcttttcga caggcaatga cgcacaagct cagcccaaca catatgccct attgccattt   960
tatgaaaaag acgctcaaaa aggcattatc acagtcgcag gcgtagaccg cagtggagaa  1020
aagttcaaac gggaaatgta tggagaaccg ggtacagaac cgcttgagta tggctccaac  1080
cattgcggaa ttactgccat gtggtgcctg tcggcaccct atgaagcaag cgtccgtttc  1140
acccgtacaa acccgattca aattgccgga acatcctttt ccgcacccat cgtaaccggc  1200
acggcggctc tgctgctgca gaaatacccg tggatgagca acgacaacct gcgtaccacg  1260
ttgctgacga cggctcagga catcggtgca gtcggcgtgg acagcaagtt cggctgggga  1320
ctgctggatg cgggtaaggc catgaacgga cccgcgtcct ttccgttcgg cgactttacc  1380
gccgatacga aaggtacatc cgatattgcc tactccttcc gtaacgacat ttcaggcacg  1440
ggcggcctga tcaaaaaagg cggcagccaa ctgcaactgc acggcaacaa cacctatacg  1500
ggcaaaacca ttatcgaagg cggttcgctg gtgttgtacg gcaacaacaa atcggatatg  1560
cgcgtcgaaa ccaaaggtgc gctgatttat aacggggcgg catccggcgg cagcctgaac  1620
agcgacggca ttgtctatct ggcagatacc gaccaatccg gcgcaaacga aaccgtacac  1680
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gggcaggatt attctttctt cacaaacatc gaaaccgacg gcggcctgct ggcttccctc  1920
gacagcgtcg aaaaaacagc gggcagtgaa ggcgacacgc tgtcctatta tgtccgtcgc  1980
ggcaatgcgg cacggactgc ttcggcagcg gcacattccg cgcccgccgg tctgaaacac  2040
```

[1867]

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gccgtagaac agggcggcag caatctggaa aacctgatgg tcgaactgga tgcctccgaa   2100
tcatccgcaa caccccgagac ggttgaaact gcggcagccg accgcacaga tatgccgggc   2160
atccgcccct acggcgcaac tttccgcgca gcggcagccg tacagcatgc gaatgccgcc   2220
gacggtgtac gcatcttcaa cagtctcgcc gctaccgtct atgccgacag taccgccgcc   2280
catgccgata tgcagggacg ccgcctgaaa gccgtatcgg acgggttgga ccacaacggc   2340
acgggtctgc gcgtcatcgc gcaaacccaa caggacggtg gaacgtggga acagggcggt   2400
gttgaaggca aaatgcgcgg cagtacccaa accgtcggca ttgccgcgaa aaccggcgaa   2460
aatacgacag cagccgccac actgggcatg ggacgcagca catggagcga aaacagtgca   2520
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ggctatctca aaggcctgtt ctcctacgga cgctacaaaa acagcatcag ccgcagcacc   2640
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tacgacctgc tcaaacagga tgcattcgcc gaaaaaggca gtgctttggg ctggagcggc   2820
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agcgataaag ccgtcctgtt tgcaacggcg ggcgtggaac gcgacctgaa cggacgcgac   2940
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tggaacggct tggcacgtta cagctacgcc ggttccaaac agtacggcaa ccacagcgga   3120
cgagtcggcg taggctaccg gttcctcgag ggatccggag ggggtggtgt cgccgccgac   3180
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cagtctttga cgctggatca gtccgtcagg aaaaacgaga aactgaagct ggcggcacaa   3300
ggtgcggaaa aaacttatgg aaacggtgac agcctcaata cgggcaaatt gaagaacgac   3360
aaggtcagcc gtttcgactt tatccgccaa atcgaagtgg acgggcagct cattaccttg   3420
gagagtggag agttccaagt atacaaacaa agccattccg ccttaaccgc ctttcagacc   3480
gagcaaatac aagattcgga gcattccggg aagatggttg cgaaacgcca gttcagaatc   3540
ggcgacatag cgggcgaaca tacatctttt gacaagcttc ccgaaggcgg cagggcgaca   3600
tatcgcggga cggcgttcgg ttcagacgat gccggcggaa aactgaccta caccatagat   3660
ttcgccgcca agcagggaaa cggcaaaatc gaacatttga aatcgccaga actcaatgtc   3720
gacctggccg ccgccgatat caagccggat ggaaaacgcc atgccgtcat cagcggttcc   3780
gtcctttaca accaagccga gaaaggcagt tactccctcg gtatctttgg cggaaaagcc   3840
caggaagttg ccggcagcgc ggaagtgaaa accgtaaacg gcatacgcca tatcggcctt   3900
gccgccaagc aactcgagca ccaccaccac caccactga                          3939
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[1868] <210>20

[1869] <211>1312

[1870] <212>PRT

[1871] <213> 人工序列

[1872] <220>

[1873] <223>ΔG983-741

[1874] <400>20

[1875]

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Met Thr Ser Ala Pro Asp Phe Asn Ala Gly Gly Thr Gly Ile Gly Ser
1               5                   10                  15
Asn Ser Arg Ala Thr Thr Ala Lys Ser Ala Ala Val Ser Tyr Ala Gly
            20                  25                  30
Ile Lys Asn Glu Met Cys Lys Asp Arg Ser Met Leu Cys Ala Gly Arg
        35                  40                  45
Asp Asp Val Ala Val Thr Asp Arg Asp Ala Lys Ile Asn Ala Pro Pro
    50                  55                  60
Pro Asn Leu His Thr Gly Asp Phe Pro Asn Pro Asn Asp Ala Tyr Lys
65                  70                  75                  80
```

[1876]

```
Asn Leu Ile Asn Leu Lys Pro Ala Ile Glu Ala Gly Tyr Thr Gly Arg
                85                  90                  95
Gly Val Glu Val Gly Ile Val Asp Thr Gly Glu Ser Val Gly Ser Ile
            100                 105                 110
Ser Phe Pro Glu Leu Tyr Gly Arg Lys Glu His Gly Tyr Asn Glu Asn
        115                 120                 125
Tyr Lys Asn Tyr Thr Ala Tyr Met Arg Lys Glu Ala Pro Glu Asp Gly
    130                 135                 140
Gly Gly Lys Asp Ile Glu Ala Ser Phe Asp Asp Glu Ala Val Ile Glu
145                 150                 155                 160
Thr Glu Ala Lys Pro Thr Asp Ile Arg His Val Lys Glu Ile Gly His
                165                 170                 175
Ile Asp Leu Val Ser His Ile Ile Gly Gly Arg Ser Val Asp Gly Arg
            180                 185                 190
Pro Ala Gly Gly Ile Ala Pro Asp Ala Thr Leu His Ile Met Asn Thr
        195                 200                 205
Asn Asp Glu Thr Lys Asn Glu Met Met Val Ala Ala Ile Arg Asn Ala
    210                 215                 220
Trp Val Lys Leu Gly Glu Arg Gly Val Arg Ile Val Asn Asn Ser Phe
225                 230                 235                 240
Gly Thr Thr Ser Arg Ala Gly Thr Ala Asp Leu Phe Gln Ile Ala Asn
                245                 250                 255
Ser Glu Glu Gln Tyr Arg Gln Ala Leu Leu Asp Tyr Ser Gly Gly Asp
            260                 265                 270
Lys Thr Asp Glu Gly Ile Arg Leu Met Gln Gln Ser Asp Tyr Gly Asn
        275                 280                 285
Leu Ser Tyr His Ile Arg Asn Lys Asn Met Leu Phe Ile Phe Ser Thr
    290                 295                 300
Gly Asn Asp Ala Gln Ala Gln Pro Asn Thr Tyr Ala Leu Leu Pro Phe
305                 310                 315                 320
Tyr Glu Lys Asp Ala Gln Lys Gly Ile Ile Thr Val Ala Gly Val Asp
                325                 330                 335
Arg Ser Gly Glu Lys Phe Lys Arg Glu Met Tyr Gly Glu Pro Gly Thr
            340                 345                 350
Glu Pro Leu Glu Tyr Gly Ser Asn His Cys Gly Ile Thr Ala Met Trp
        355                 360                 365
Cys Leu Ser Ala Pro Tyr Glu Ala Ser Val Arg Phe Thr Arg Thr Asn
    370                 375                 380
Pro Ile Gln Ile Ala Gly Thr Ser Phe Ser Ala Pro Ile Val Thr Gly
385                 390                 395                 400
Thr Ala Ala Leu Leu Leu Gln Lys Tyr Pro Trp Met Ser Asn Asp Asn
                405                 410                 415
Leu Arg Thr Thr Leu Leu Thr Thr Ala Gln Asp Ile Gly Ala Val Gly
            420                 425                 430
Val Asp Ser Lys Phe Gly Trp Gly Leu Leu Asp Ala Gly Lys Ala Met
        435                 440                 445
Asn Gly Pro Ala Ser Phe Pro Phe Gly Asp Phe Thr Ala Asp Thr Lys
    450                 455                 460
Gly Thr Ser Asp Ile Ala Tyr Ser Phe Arg Asn Asp Ile Ser Gly Thr
465                 470                 475                 480
Gly Gly Leu Ile Lys Lys Gly Gly Ser Gln Leu Gln Leu His Gly Asn
                485                 490                 495
```

[1877]

Asn Thr Tyr Thr Gly Lys Thr Ile Ile Glu Gly Gly Ser Leu Val Leu
500 505 510
Tyr Gly Asn Asn Lys Ser Asp Met Arg Val Glu Thr Lys Gly Ala Leu
515 520 525
Ile Tyr Asn Gly Ala Ala Ser Gly Gly Ser Leu Asn Ser Asp Gly Ile
530 535 540
Val Tyr Leu Ala Asp Thr Asp Gln Ser Gly Ala Asn Glu Thr Val His
545 550 555 560
Ile Lys Gly Ser Leu Gln Leu Asp Gly Lys Gly Thr Leu Tyr Thr Arg
565 570 575
Leu Gly Lys Leu Leu Lys Val Asp Gly Thr Ala Ile Ile Gly Gly Lys
580 585 590
Leu Tyr Met Ser Ala Arg Gly Lys Gly Ala Gly Tyr Leu Asn Ser Thr
595 600 605
Gly Arg Arg Val Pro Phe Leu Ser Ala Ala Lys Ile Gly Gln Asp Tyr
610 615 620
Ser Phe Phe Thr Asn Ile Glu Thr Asp Gly Gly Leu Leu Ala Ser Leu
625 630 635 640
Asp Ser Val Glu Lys Thr Ala Gly Ser Glu Gly Asp Thr Leu Ser Tyr
645 650 655
Tyr Val Arg Arg Gly Asn Ala Ala Arg Thr Ala Ser Ala Ala Ala His
660 665 670
Ser Ala Pro Ala Gly Leu Lys His Ala Val Glu Gln Gly Gly Ser Asn
675 680 685
Leu Glu Asn Leu Met Val Glu Leu Asp Ala Ser Glu Ser Ser Ala Thr
690 695 700
Pro Glu Thr Val Glu Thr Ala Ala Ala Asp Arg Thr Asp Met Pro Gly
705 710 715 720
Ile Arg Pro Tyr Gly Ala Thr Phe Arg Ala Ala Ala Ala Val Gln His
725 730 735
Ala Asn Ala Ala Asp Gly Val Arg Ile Phe Asn Ser Leu Ala Ala Thr
740 745 750
Val Tyr Ala Asp Ser Thr Ala Ala His Ala Asp Met Gln Gly Arg Arg
755 760 765
Leu Lys Ala Val Ser Asp Gly Leu Asp His Asn Gly Thr Gly Leu Arg
770 775 780
Val Ile Ala Gln Thr Gln Gln Asp Gly Gly Thr Trp Glu Gln Gly Gly
785 790 795 800
Val Glu Gly Lys Met Arg Gly Ser Thr Gln Thr Val Gly Ile Ala Ala
805 810 815
Lys Thr Gly Glu Asn Thr Thr Ala Ala Ala Thr Leu Gly Met Gly Arg
820 825 830
Ser Thr Trp Ser Glu Asn Ser Ala Asn Ala Lys Thr Asp Ser Ile Ser
835 840 845
Leu Phe Ala Gly Ile Arg His Asp Ala Gly Asp Ile Gly Tyr Leu Lys
850 855 860
Gly Leu Phe Ser Tyr Gly Arg Tyr Lys Asn Ser Ile Ser Arg Ser Thr
865 870 875 880
Gly Ala Asp Glu His Ala Glu Gly Ser Val Asn Gly Thr Leu Met Gln
885 890 895
Leu Gly Ala Leu Gly Gly Val Asn Val Pro Phe Ala Ala Thr Gly Asp
900 905 910

[1878]

Leu Thr Val Glu Gly Gly Leu Arg Tyr Asp Leu Leu Lys Gln Asp Ala
915 920 925
Phe Ala Glu Lys Gly Ser Ala Leu Gly Trp Ser Gly Asn Ser Leu Thr
930 935 940
Glu Gly Thr Leu Val Gly Leu Ala Gly Leu Lys Leu Ser Gln Pro Leu
945 950 955 960
Ser Asp Lys Ala Val Leu Phe Ala Thr Ala Gly Val Glu Arg Asp Leu
965 970 975
Asn Gly Arg Asp Tyr Thr Val Thr Gly Gly Phe Thr Gly Ala Thr Ala
980 985 990
Ala Thr Gly Lys Thr Gly Ala Arg Asn Met Pro His Thr Arg Leu Val
995 1000 1005
Ala Gly Leu Gly Ala Asp Val Glu Phe Gly Asn Gly Trp Asn Gly Leu
1010 1015 1020
Ala Arg Tyr Ser Tyr Ala Gly Ser Lys Gln Tyr Gly Asn His Ser Gly
1025 1030 1035 1040
Arg Val Gly Val Gly Tyr Arg Phe Leu Glu Gly Ser Gly Gly Gly Gly
1045 1050 1055
Val Ala Ala Asp Ile Gly Ala Gly Leu Ala Asp Ala Leu Thr Ala Pro
1060 1065 1070
Leu Asp His Lys Asp Lys Gly Leu Gln Ser Leu Thr Leu Asp Gln Ser
1075 1080 1085
Val Arg Lys Asn Glu Lys Leu Lys Leu Ala Ala Gln Gly Ala Glu Lys
1090 1095 1100
Thr Tyr Gly Asn Gly Asp Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp
1105 1110 1115 1120
Lys Val Ser Arg Phe Asp Phe Ile Arg Gln Ile Glu Val Asp Gly Gln
1125 1130 1135
Leu Ile Thr Leu Glu Ser Gly Glu Phe Gln Val Tyr Lys Gln Ser His
1140 1145 1150
Ser Ala Leu Thr Ala Phe Gln Thr Glu Gln Ile Gln Asp Ser Glu His
1155 1160 1165
Ser Gly Lys Met Val Ala Lys Arg Gln Phe Arg Ile Gly Asp Ile Ala
1170 1175 1180
Gly Glu His Thr Ser Phe Asp Lys Leu Pro Glu Gly Gly Arg Ala Thr
1185 1190 1195 1200
Tyr Arg Gly Thr Ala Phe Gly Ser Asp Asp Ala Gly Gly Lys Leu Thr
1205 1210 1215
Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly Asn Gly Lys Ile Glu His
1220 1225 1230
Leu Lys Ser Pro Glu Leu Asn Val Asp Leu Ala Ala Ala Asp Ile Lys
1235 1240 1245
Pro Asp Gly Lys Arg His Ala Val Ile Ser Gly Ser Val Leu Tyr Asn
1250 1255 1260
Gln Ala Glu Lys Gly Ser Tyr Ser Leu Gly Ile Phe Gly Gly Lys Ala
1265 1270 1275 1280
Gln Glu Val Ala Gly Ser Ala Glu Val Lys Thr Val Asn Gly Ile Arg
1285 1290 1295
His Ile Gly Leu Ala Ala Lys Gln Leu Glu His His His His His His
1300 1305 1310

[1879] <210>21

[1880] <211>4344

[1881] <212>DNA

[1882] <213> 人工序列

[1883] <220>

[1884] <223>ΔG983-961

[1885] <400>21

[1886]

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atgacttctg cgcccgactt caatgcaggc ggtaccggta tcggcagcaa cagcagagca    60
acaacagcga aatcagcagc agtatcttac gccggtatca agaacgaaat gtgcaaagac   120
agaagcatgc tctgtgccgg tcgggatgac gttgcggtta cagacaggga tgccaaaatc   180
aatgcccccc ccccgaatct gcataccgga gactttccaa acccaaatga cgcatacaag   240
aatttgatca acctcaaacc tgcaattgaa gcaggctata caggacgcgg ggtagaggta   300
ggtatcgtcg acacaggcga atccgtcggc agcatatcct ttcccgaact gtatggcaga   360
aaagaacacg gctataacga aaattacaaa aactatacgg cgtatatgcg gaaggaagcg   420
cctgaagacg gaggcggtaa agacattgaa gcttctttcg acgatgaggc cgttatagag   480
actgaagcaa agccgacgga tatccgccac gtaaaagaaa tcggacacat cgatttggtc   540
tcccatatta ttggcgggcg ttccgtggac ggcagacctg caggcggtat tgcgcccgat   600
gcgacgctac acataatgaa tacgaatgat gaaaccaaga acgaaatgat ggttgcagcc   660
atccgcaatg catgggtcaa gctgggcgaa cgtggcgtgc gcatcgtcaa taacagtttt   720
ggaacaacat cgagggcagg cactgccgac cttttccaaa tagccaattc ggaggagcag   780
taccgccaag cgttgctcga ctattccggc ggtgataaaa cagacgaggg tatccgcctg   840
atgcaacaga gcgattacgg caacctgtcc taccacatcc gtaataaaaa catgcttttc   900
atcttttcga caggcaatga cgcacaagct cagcccaaca catatgccct attgccattt   960
tatgaaaaag acgctcaaaa aggcattatc acagtcgcag gcgtagaccg cagtggagaa  1020
aagttcaaac gggaaatgta tggagaaccg ggtacagaac cgcttgagta tggctccaac  1080
cattgcggaa ttactgccat gtggtgcctg tcggcaccct atgaagcaag cgtccgtttc  1140
acccgtacaa acccgattca aattgccgga acatcctttt ccgcacccat cgtaaccggc  1200
acggcggctc tgctgctgca gaaatacccg tggatgagca acgacaacct gcgtaccacg  1260
ttgctgacga cggctcagga catcggtgca gtcggcgtgg acagcaagtt cggctgggga  1320
ctgctggatg cgggtaaggc catgaacgga cccgcgtcct ttccgttcgg cgactttacc  1380
gccgatacga aaggtacatc cgatattgcc tactccttcc gtaacgacat ttcaggcacg  1440
ggcggcctga tcaaaaaagg cggcagccaa ctgcaactgc acggcaacaa cacctatacg  1500
ggcaaaacca ttatcgaagg cggttcgctg gtgttgtacg gcaacaacaa atcggatatg  1560
cgcgtcgaaa ccaaaggtgc gctgatttat aacggggcgg catccggcgg cagcctgaac  1620
agcgacggca ttgtctatct ggcagatacc gaccaatccg gcgcaaacga aaccgtacac  1680
atcaaaggca gtctgcagct ggacggcaaa ggtacgctgt acacacgttt gggcaaactg  1740
ctgaaagtgg acggtacggc gattatcggc ggcaagctgt acatgtcggc acgcggcaag  1800
ggggcaggct atctcaacag taccggacga cgtgttccct tcctgagtgc cgccaaaatc  1860
gggcaggatt attctttctt cacaaacatc gaaaccgacg gcggcctgct ggcttccctc  1920
gacagcgtcg aaaaaacagc gggcagtgaa ggcgacacgc tgtcctatta tgtccgtcgc  1980
ggcaatgcgg cacggactgc ttcggcagcg gcacattccg cgcccgccgg tctgaaacac  2040
gccgtagaac agggcggcag caatctggaa aacctgatgg tcgaactgga tgcctccgaa  2100
tcatccgcaa cacccgagac ggttgaaact gcggcagccg accgcacaga tatgccgggc  2160
atccgcccct acggcgcaac tttccgcgca gcggcagccg tacagcatgc gaatgccgcc  2220
gacggtgtac gcatcttcaa cagtctcgcc gctaccgtct atgccgacag taccgccgcc  2280
catgccgata tgcagggacg ccgcctgaaa gccgtatcgg acgggttgga ccacaacggc  2340
acgggtctgc gcgtcatcgc gcaaacccaa caggacggtg gaacgtggga acagggcggt  2400
gttgaaggca aaatgcgcgg cagtacccaa accgtcggca ttgccgcgaa aaccggcgaa  2460
aatacgacag cagccgccac actgggcatg ggacgcagca catggagcga aaacagtgca  2520
aatgcaaaaa ccgacagcat tagtctgttt gcaggcatac ggcacgatgc gggcgatatc  2580
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[1887]

ggctatctca aaggcctgtt ctcctacgga cgctacaaaa acagcatcag ccgcagcacc 2640
ggtgcggacg aacatgcgga aggcagcgtc aacggcacgc tgatgcagct gggcgcactg 2700
ggcggtgtca acgttccgtt tgccgcaacg ggagatttga cggtcgaagg cggtctgcgc 2760
tacgacctgc tcaaacagga tgcattcgcc gaaaaaggca gtgctttggg ctggagcggc 2820
aacagcctca ctgaaggcac gctggtcgga ctcgcgggtc tgaagctgtc gcaacccttg 2880
agcgataaag ccgtcctgtt tgcaacggcg ggcgtggaac gcgacctgaa cggacgcgac 2940
tacacggtaa cgggcggctt taccggcgcg actgcagcaa ccggcaagac gggggcacgc 3000
aatatgccgc acacccgtct ggttgccggc ctgggcgcgg atgtcgaatt cggcaacggc 3060
tggaacggct tggcacgtta cagctacgcc ggttccaaac agtacggcaa ccacagcgga 3120
cgagtcggcg taggctaccg gttcctcgag ggtggcggag gcactggatc cgccacaaac 3180
gacgacgatg ttaaaaaagc tgccactgtg gccattgctg ctgcctacaa caatggccaa 3240
gaaatcaacg gtttcaaagc tggagagacc atctacgaca ttgatgaaga cggcacaatt 3300
accaaaaaag acgcaactgc agccgatgtt gaagccgacg actttaaagg tctgggtctg 3360
aaaaaagtcg tgactaacct gaccaaaacc gtcaatgaaa acaaacaaaa cgtcgatgcc 3420
aaagtaaaag ctgcagaatc tgaaatagaa aagttaacaa ccaagttagc agacactgat 3480
gccgctttag cagatactga tgccgctctg gatgcaacca ccaacgcctt gaataaattg 3540
ggagaaaata taacgacatt tgctgaagag actaagacaa atatcgtaaa aattgatgaa 3600
aaattagaag ccgtggctga taccgtcgac aagcatgccg aagcattcaa cgatatcgcc 3660
gattcattgg atgaaaccaa cactaaggca gacgaagccg tcaaaaccgc caatgaagcc 3720
aaacagacgg ccgaagaaac caaacaaaac gtcgatgcca aagtaaaagc tgcagaaact 3780
gcagcaggca aagccgaagc tgccgctggc acagctaata ctgcagccga caaggccgaa 3840
gctgtcgctg caaaagttac cgacatcaaa gctgatatcg ctacgaacaa agataatatt 3900
gctaaaaaag caaacagtgc cgacgtgtac accagagaag agtctgacag caaatttgtc 3960
agaattgatg gtctgaacgc tactaccgaa aaattggaca cacgcttggc ttctgctgaa 4020
aaatccattg ccgatcacga tactcgcctg aacggtttgg ataaaacagt gtcagacctg 4080
cgcaaagaaa cccgccaagg ccttgcagaa caagccgcgc tctccggtct gttccaacct 4140
tacaacgtgg gtcggttcaa tgtaacggct gcagtcggcg gctacaaatc cgaatcggca 4200
gtcgccatcg gtaccggctt ccgctttacc gaaaactttg ccgccaaagc aggcgtggca 4260
gtcggcactt cgtccggttc ttccgcagcc taccatgtcg gcgtcaatta cgagtggctc 4320
gagcaccacc accaccacca ctga 4344

[1888] <210>22

[1889] <211>1447

[1890] <212>PRT

[1891] <213> 人工序列

[1892] <220>

[1893] <223>ΔG983-961

[1894] <400>22

[1895]

```
Met Thr Ser Ala Pro Asp Phe Asn Ala Gly Gly Thr Gly Ile Gly Ser
1               5                   10                  15
Asn Ser Arg Ala Thr Thr Ala Lys Ser Ala Ala Val Ser Tyr Ala Gly
            20                  25                  30
Ile Lys Asn Glu Met Cys Lys Asp Arg Ser Met Leu Cys Ala Gly Arg
        35                  40                  45
Asp Asp Val Ala Val Thr Asp Arg Asp Ala Lys Ile Asn Ala Pro Pro
    50                  55                  60
Pro Asn Leu His Thr Gly Asp Phe Pro Asn Pro Asn Asp Ala Tyr Lys
65                  70                  75                  80
Asn Leu Ile Asn Leu Lys Pro Ala Ile Glu Ala Gly Tyr Thr Gly Arg
                85                  90                  95
```

[1896]

```
Gly Val Glu Val Gly Ile Val Asp Thr Gly Glu Ser Val Gly Ser Ile
            100                 105                 110
Ser Phe Pro Glu Leu Tyr Gly Arg Lys Glu His Gly Tyr Asn Glu Asn
        115                 120                 125
Tyr Lys Asn Tyr Thr Ala Tyr Met Arg Lys Glu Ala Pro Glu Asp Gly
    130                 135                 140
Gly Gly Lys Asp Ile Glu Ala Ser Phe Asp Asp Glu Ala Val Ile Glu
145                 150                 155                 160
Thr Glu Ala Lys Pro Thr Asp Ile Arg His Val Lys Glu Ile Gly His
                165                 170                 175
Ile Asp Leu Val Ser His Ile Ile Gly Gly Arg Ser Val Asp Gly Arg
            180                 185                 190
Pro Ala Gly Gly Ile Ala Pro Asp Ala Thr Leu His Ile Met Asn Thr
        195                 200                 205
Asn Asp Glu Thr Lys Asn Glu Met Met Val Ala Ala Ile Arg Asn Ala
    210                 215                 220
Trp Val Lys Leu Gly Glu Arg Gly Val Arg Ile Val Asn Asn Ser Phe
225                 230                 235                 240
Gly Thr Thr Ser Arg Ala Gly Thr Ala Asp Leu Phe Gln Ile Ala Asn
                245                 250                 255
Ser Glu Glu Gln Tyr Arg Gln Ala Leu Leu Asp Tyr Ser Gly Gly Asp
            260                 265                 270
Lys Thr Asp Glu Gly Ile Arg Leu Met Gln Gln Ser Asp Tyr Gly Asn
        275                 280                 285
Leu Ser Tyr His Ile Arg Asn Lys Asn Met Leu Phe Ile Phe Ser Thr
    290                 295                 300
Gly Asn Asp Ala Gln Ala Gln Pro Asn Thr Tyr Ala Leu Leu Pro Phe
305                 310                 315                 320
Tyr Glu Lys Asp Ala Gln Lys Gly Ile Ile Thr Val Ala Gly Val Asp
                325                 330                 335
Arg Ser Gly Glu Lys Phe Lys Arg Glu Met Tyr Gly Glu Pro Gly Thr
            340                 345                 350
Glu Pro Leu Glu Tyr Gly Ser Asn His Cys Gly Ile Thr Ala Met Trp
        355                 360                 365
Cys Leu Ser Ala Pro Tyr Glu Ala Ser Val Arg Phe Thr Arg Thr Asn
    370                 375                 380
Pro Ile Gln Ile Ala Gly Thr Ser Phe Ser Ala Pro Ile Val Thr Gly
385                 390                 395                 400
Thr Ala Ala Leu Leu Leu Gln Lys Tyr Pro Trp Met Ser Asn Asp Asn
                405                 410                 415
Leu Arg Thr Thr Leu Leu Thr Thr Ala Gln Asp Ile Gly Ala Val Gly
            420                 425                 430
Val Asp Ser Lys Phe Gly Trp Gly Leu Leu Asp Ala Gly Lys Ala Met
        435                 440                 445
Asn Gly Pro Ala Ser Phe Pro Phe Gly Asp Phe Thr Ala Asp Thr Lys
    450                 455                 460
Gly Thr Ser Asp Ile Ala Tyr Ser Phe Arg Asn Asp Ile Ser Gly Thr
465                 470                 475                 480
Gly Gly Leu Ile Lys Lys Gly Gly Ser Gln Leu Gln Leu His Gly Asn
                485                 490                 495
Asn Thr Tyr Thr Gly Lys Thr Ile Ile Glu Gly Gly Ser Leu Val Leu
            500                 505                 510
```

[1897]

```
Tyr Gly Asn Asn Lys Ser Asp Met Arg Val Glu Thr Lys Gly Ala Leu
        515                 520                 525
Ile Tyr Asn Gly Ala Ala Ser Gly Gly Ser Leu Asn Ser Asp Gly Ile
    530                 535                 540
Val Tyr Leu Ala Asp Thr Asp Gln Ser Gly Ala Asn Glu Thr Val His
545                 550                 555                 560
Ile Lys Gly Ser Leu Gln Leu Asp Gly Lys Gly Thr Leu Tyr Thr Arg
                565                 570                 575
Leu Gly Lys Leu Leu Lys Val Asp Gly Thr Ala Ile Ile Gly Gly Lys
            580                 585                 590
Leu Tyr Met Ser Ala Arg Gly Lys Gly Ala Gly Tyr Leu Asn Ser Thr
        595                 600                 605
Gly Arg Arg Val Pro Phe Leu Ser Ala Ala Lys Ile Gly Gln Asp Tyr
    610                 615                 620
Ser Phe Phe Thr Asn Ile Glu Thr Asp Gly Gly Leu Leu Ala Ser Leu
625                 630                 635                 640

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

[1898]

```
        915                 920                 925
Phe Ala Glu Lys Gly Ser Ala Leu Gly Trp Ser Gly Asn Ser Leu Thr
    930                 935                 940
Glu Gly Thr Leu Val Gly Leu Ala Gly Leu Lys Leu Ser Gln Pro Leu
945                 950                 955                 960
Ser Asp Lys Ala Val Leu Phe Ala Thr Ala Gly Val Glu Arg Asp Leu
                965                 970                 975
Asn Gly Arg Asp Tyr Thr Val Thr Gly Gly Phe Thr Gly Ala Thr Ala
            980                 985                 990
Ala Thr Gly Lys Thr Gly Ala Arg Asn Met Pro His Thr Arg Leu Val
        995                 1000                1005
Ala Gly Leu Gly Ala Asp Val Glu Phe Gly Asn Gly Trp Asn Gly Leu
    1010                1015                1020
Ala Arg Tyr Ser Tyr Ala Gly Ser Lys Gln Tyr Gly Asn His Ser Gly
1025                1030                1035                1040
Arg Val Gly Val Gly Tyr Arg Phe Leu Glu Gly Gly Gly Gly Thr Gly
                1045                1050                1055
Ser Ala Thr Asn Asp Asp Asp Val Lys Lys Ala Ala Thr Val Ala Ile
            1060                1065                1070
Ala Ala Ala Tyr Asn Asn Gly Gln Glu Ile Asn Gly Phe Lys Ala Gly
        1075                1080                1085
Glu Thr Ile Tyr Asp Ile Asp Glu Asp Gly Thr Ile Thr Lys Lys Asp
    1090                1095                1100
Ala Thr Ala Ala Asp Val Glu Ala Asp Asp Phe Lys Gly Leu Gly Leu
1105                1110                1115                1120
Lys Lys Val Val Thr Asn Leu Thr Lys Thr Val Asn Glu Asn Lys Gln
                1125                1130                1135
Asn Val Asp Ala Lys Val Lys Ala Ala Glu Ser Glu Ile Glu Lys Leu
            1140                1145                1150
Thr Thr Lys Leu Ala Asp Thr Asp Ala Ala Leu Ala Asp Thr Asp Ala
        1155                1160                1165
Ala Leu Asp Ala Thr Thr Asn Ala Leu Asn Lys Leu Gly Glu Asn Ile
    1170                1175                1180
Thr Thr Phe Ala Glu Glu Thr Lys Thr Asn Ile Val Lys Ile Asp Glu
1185                1190                1195                1200
Lys Leu Glu Ala Val Ala Asp Thr Val Asp Lys His Ala Glu Ala Phe
                1205                1210                1215
Asn Asp Ile Ala Asp Ser Leu Asp Glu Thr Asn Thr Lys Ala Asp Glu
            1220                1225                1230
Ala Val Lys Thr Ala Asn Glu Ala Lys Gln Thr Ala Glu Glu Thr Lys
        1235                1240                1245
Gln Asn Val Asp Ala Lys Val Lys Ala Ala Glu Thr Ala Ala Gly Lys
    1250                1255                1260
Ala Glu Ala Ala Ala Gly Thr Ala Asn Thr Ala Ala Asp Lys Ala Glu
1265                1270                1275                1280
Ala Val Ala Ala Lys Val Thr Asp Ile Lys Ala Asp Ile Ala Thr Asn
                1285                1290                1295
Lys Asp Asn Ile Ala Lys Lys Ala Asn Ser Ala Asp Val Tyr Thr Arg
            1300                1305                1310
Glu Glu Ser Asp Ser Lys Phe Val Arg Ile Asp Gly Leu Asn Ala Thr
        1315                1320                1325
Thr Glu Lys Leu Asp Thr Arg Leu Ala Ser Ala Glu Lys Ser Ile Ala
```

[1899]

```
    1330                1335                1340
Asp His Asp Thr Arg Leu Asn Gly Leu Asp Lys Thr Val Ser Asp Leu
1345                1350                1355                1360
Arg Lys Glu Thr Arg Gln Gly Leu Ala Glu Gln Ala Ala Leu Ser Gly
                1365                1370                1375
Leu Phe Gln Pro Tyr Asn Val Gly Arg Phe Asn Val Thr Ala Ala Val
            1380                1385                1390
Gly Gly Tyr Lys Ser Glu Ser Ala Val Ala Ile Gly Thr Gly Phe Arg
        1395                1400                1405
Phe Thr Glu Asn Phe Ala Ala Lys Ala Gly Val Ala Val Gly Thr Ser
    1410                1415                1420
Ser Gly Ser Ser Ala Ala Tyr His Val Gly Val Asn Tyr Glu Trp Leu
1425                1430                1435                1440
Glu His His His His His His
                1445
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[1900] <210>23

[1901] <211>4179

[1902] <212>DNA

[1903] <213> 人工序列

[1904] <220>

[1905] <223>ΔG983-961c

[1906] <400>23

[1907]

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atgacttctg cgcccgactt caatgcaggc ggtaccggta tcggcagcaa cagcagagca    60
acaacagcga aatcagcagc agtatcttac gccggtatca agaacgaaat gtgcaaagac   120
agaagcatgc tctgtgccgg tcgggatgac gttgcggtta cagacaggga tgccaaaatc   180
aatgcccccc ccccgaatct gcataccgga gactttccaa acccaaatga cgcatacaag   240
aatttgatca acctcaaacc tgcaattgaa gcaggctata caggacgcgg ggtagaggta   300
ggtatcgtcg acacaggcga atccgtcggc agcatatcct ttcccgaact gtatggcaga   360
aaagaacacg gctataacga aaattacaaa aactatacgg cgtatatgcg gaaggaagcg   420
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gcgacgctac acataatgaa tacgaatgat gaaaccaaga acgaaatgat ggttgcagcc   660
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ggcaaaacca ttatcgaagg cggttcgctg gtgttgtacg gcaacaacaa atcggatatg  1560
cgcgtcgaaa ccaaaggtgc gctgatttat aacggggcgg catccggcgg cagcctgaac  1620
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[1908]

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[1909] <210>24

[1910] <211>1392

[1911] <212>PRT

[1912] <213> 人工序列

[1913] <220>

[1914] <223>ΔG983-961c

[1915] <400>24

[1916]

Met Thr Ser Ala Pro Asp Phe Asn Ala Gly Gly Thr Gly Ile Gly Ser
1 5 10 15
Asn Ser Arg Ala Thr Thr Ala Lys Ser Ala Ala Val Ser Tyr Ala Gly
20 25 30
Ile Lys Asn Glu Met Cys Lys Asp Arg Ser Met Leu Cys Ala Gly Arg
35 40 45
Asp Asp Val Ala Val Thr Asp Arg Asp Ala Lys Ile Asn Ala Pro Pro
50 55 60
Pro Asn Leu His Thr Gly Asp Phe Pro Asn Pro Asn Asp Ala Tyr Lys
65 70 75 80
Asn Leu Ile Asn Leu Lys Pro Ala Ile Glu Ala Gly Tyr Thr Gly Arg
85 90 95
Gly Val Glu Val Gly Ile Val Asp Thr Gly Glu Ser Val Gly Ser Ile
100 105 110
Ser Phe Pro Glu Leu Tyr Gly Arg Lys Glu His Gly Tyr Asn Glu Asn
115 120 125
Tyr Lys Asn Tyr Thr Ala Tyr Met Arg Lys Glu Ala Pro Glu Asp Gly
130 135 140
Gly Gly Lys Asp Ile Glu Ala Ser Phe Asp Asp Glu Ala Val Ile Glu
145 150 155 160
Thr Glu Ala Lys Pro Thr Asp Ile Arg His Val Lys Glu Ile Gly His
165 170 175
Ile Asp Leu Val Ser His Ile Ile Gly Gly Arg Ser Val Asp Gly Arg
180 185 190
Pro Ala Gly Gly Ile Ala Pro Asp Ala Thr Leu His Ile Met Asn Thr
195 200 205
Asn Asp Glu Thr Lys Asn Glu Met Met Val Ala Ala Ile Arg Asn Ala
210 215 220
Trp Val Lys Leu Gly Glu Arg Gly Val Arg Ile Val Asn Asn Ser Phe
225 230 235 240
Gly Thr Thr Ser Arg Ala Gly Thr Ala Asp Leu Phe Gln Ile Ala Asn
245 250 255
Ser Glu Glu Gln Tyr Arg Gln Ala Leu Leu Asp Tyr Ser Gly Gly Asp
260 265 270
Lys Thr Asp Glu Gly Ile Arg Leu Met Gln Gln Ser Asp Tyr Gly Asn
275 280 285
Leu Ser Tyr His Ile Arg Asn Lys Asn Met Leu Phe Ile Phe Ser Thr
290 295 300
Gly Asn Asp Ala Gln Ala Gln Pro Asn Thr Tyr Ala Leu Leu Pro Phe
305 310 315 320
Tyr Glu Lys Asp Ala Gln Lys Gly Ile Ile Thr Val Ala Gly Val Asp
325 330 335
Arg Ser Gly Glu Lys Phe Lys Arg Glu Met Tyr Gly Glu Pro Gly Thr
340 345 350
Glu Pro Leu Glu Tyr Gly Ser Asn His Cys Gly Ile Thr Ala Met Trp
355 360 365
Cys Leu Ser Ala Pro Tyr Glu Ala Ser Val Arg Phe Thr Arg Thr Asn
370 375 380
Pro Ile Gln Ile Ala Gly Thr Ser Phe Ser Ala Pro Ile Val Thr Gly
385 390 395 400
Thr Ala Ala Leu Leu Leu Gln Lys Tyr Pro Trp Met Ser Asn Asp Asn

[1917]

```
                405                 410                 415
Leu Arg Thr Thr Leu Leu Thr Thr Ala Gln Asp Ile Gly Ala Val Gly
            420                 425                 430
Val Asp Ser Lys Phe Gly Trp Gly Leu Leu Asp Ala Gly Lys Ala Met
        435                 440                 445
Asn Gly Pro Ala Ser Phe Pro Phe Gly Asp Phe Thr Ala Asp Thr Lys
    450                 455                 460
Gly Thr Ser Asp Ile Ala Tyr Ser Phe Arg Asn Asp Ile Ser Gly Thr
465                 470                 475                 480
Gly Gly Leu Ile Lys Lys Gly Gly Ser Gln Leu Gln Leu His Gly Asn
                485                 490                 495
Asn Thr Tyr Thr Gly Lys Thr Ile Ile Glu Gly Gly Ser Leu Val Leu
            500                 505                 510
Tyr Gly Asn Asn Lys Ser Asp Met Arg Val Glu Thr Lys Gly Ala Leu
        515                 520                 525
Ile Tyr Asn Gly Ala Ala Ser Gly Gly Ser Leu Asn Ser Asp Gly Ile
    530                 535                 540
Val Tyr Leu Ala Asp Thr Asp Gln Ser Gly Ala Asn Glu Thr Val His
545                 550                 555                 560
Ile Lys Gly Ser Leu Gln Leu Asp Gly Lys Gly Thr Leu Tyr Thr Arg
                565                 570                 575
Leu Gly Lys Leu Leu Lys Val Asp Gly Thr Ala Ile Ile Gly Gly Lys
            580                 585                 590
Leu Tyr Met Ser Ala Arg Gly Lys Gly Ala Gly Tyr Leu Asn Ser Thr
        595                 600                 605
Gly Arg Arg Val Pro Phe Leu Ser Ala Ala Lys Ile Gly Gln Asp Tyr
    610                 615                 620
Ser Phe Phe Thr Asn Ile Glu Thr Asp Gly Gly Leu Leu Ala Ser Leu
625                 630                 635                 640
Asp Ser Val Glu Lys Thr Ala Gly Ser Glu Gly Asp Thr Leu Ser Tyr
                645                 650                 655
Tyr Val Arg Arg Gly Asn Ala Ala Arg Thr Ala Ser Ala Ala Ala His
            660                 665                 670
Ser Ala Pro Ala Gly Leu Lys His Ala Val Glu Gln Gly Gly Ser Asn
        675                 680                 685
Leu Glu Asn Leu Met Val Glu Leu Asp Ala Ser Glu Ser Ser Ala Thr
    690                 695                 700
Pro Glu Thr Val Glu Thr Ala Ala Ala Asp Arg Thr Asp Met Pro Gly
705                 710                 715                 720
Ile Arg Pro Tyr Gly Ala Thr Phe Arg Ala Ala Ala Ala Val Gln His
                725                 730                 735
Ala Asn Ala Ala Asp Gly Val Arg Ile Phe Asn Ser Leu Ala Ala Thr
            740                 745                 750
Val Tyr Ala Asp Ser Thr Ala Ala His Ala Asp Met Gln Gly Arg Arg
        755                 760                 765
Leu Lys Ala Val Ser Asp Gly Leu Asp His Asn Gly Thr Gly Leu Arg
    770                 775                 780
Val Ile Ala Gln Thr Gln Gln Asp Gly Gly Thr Trp Glu Gln Gly Gly
785                 790                 795                 800
Val Glu Gly Lys Met Arg Gly Ser Thr Gln Thr Val Gly Ile Ala Ala
                805                 810                 815
Lys Thr Gly Glu Asn Thr Thr Ala Ala Ala Thr Leu Gly Met Gly Arg
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[1918]

820 825 830
Ser Thr Trp Ser Glu Asn Ser Ala Asn Ala Lys Thr Asp Ser Ile Ser
835 840 845
Leu Phe Ala Gly Ile Arg His Asp Ala Gly Asp Ile Gly Tyr Leu Lys
850 855 860
Gly Leu Phe Ser Tyr Gly Arg Tyr Lys Asn Ser Ile Ser Arg Ser Thr
865 870 875 880
Gly Ala Asp Glu His Ala Glu Gly Ser Val Asn Gly Thr Leu Met Gln
885 890 895
Leu Gly Ala Leu Gly Gly Val Asn Val Pro Phe Ala Ala Thr Gly Asp
900 905 910
Leu Thr Val Glu Gly Gly Leu Arg Tyr Asp Leu Leu Lys Gln Asp Ala
915 920 925
Phe Ala Glu Lys Gly Ser Ala Leu Gly Trp Ser Gly Asn Ser Leu Thr
930 935 940
Glu Gly Thr Leu Val Gly Leu Ala Gly Leu Lys Leu Ser Gln Pro Leu
945 950 955 960
Ser Asp Lys Ala Val Leu Phe Ala Thr Ala Gly Val Glu Arg Asp Leu
965 970 975
Asn Gly Arg Asp Tyr Thr Val Thr Gly Gly Phe Thr Gly Ala Thr Ala
980 985 990
Ala Thr Gly Lys Thr Gly Ala Arg Asn Met Pro His Thr Arg Leu Val
995 1000 1005
Ala Gly Leu Gly Ala Asp Val Glu Phe Gly Asn Gly Trp Asn Gly Leu
1010 1015 1020
Ala Arg Tyr Ser Tyr Ala Gly Ser Lys Gln Tyr Gly Asn His Ser Gly
1025 1030 1035 1040
Arg Val Gly Val Gly Tyr Arg Phe Leu Glu Gly Gly Gly Gly Thr Gly
1045 1050 1055
Ser Ala Thr Asn Asp Asp Asp Val Lys Lys Ala Ala Thr Val Ala Ile
1060 1065 1070
Ala Ala Ala Tyr Asn Asn Gly Gln Glu Ile Asn Gly Phe Lys Ala Gly
1075 1080 1085
Glu Thr Ile Tyr Asp Ile Asp Glu Asp Gly Thr Ile Thr Lys Lys Asp
1090 1095 1100
Ala Thr Ala Ala Asp Val Glu Ala Asp Asp Phe Lys Gly Leu Gly Leu
1105 1110 1115 1120
Lys Lys Val Val Thr Asn Leu Thr Lys Thr Val Asn Glu Asn Lys Gln
1125 1130 1135
Asn Val Asp Ala Lys Val Lys Ala Ala Glu Ser Glu Ile Glu Lys Leu
1140 1145 1150
Thr Thr Lys Leu Ala Asp Thr Asp Ala Ala Leu Ala Asp Thr Asp Ala
1155 1160 1165
Ala Leu Asp Ala Thr Thr Asn Ala Leu Asn Lys Leu Gly Glu Asn Ile
1170 1175 1180
Thr Thr Phe Ala Glu Glu Thr Lys Thr Asn Ile Val Lys Ile Asp Glu
1185 1190 1195 1200
Lys Leu Glu Ala Val Ala Asp Thr Val Asp Lys His Ala Glu Ala Phe
1205 1210 1215
Asn Asp Ile Ala Asp Ser Leu Asp Glu Thr Asn Thr Lys Ala Asp Glu
1220 1225 1230
Ala Val Lys Thr Ala Asn Glu Ala Lys Gln Thr Ala Glu Glu Thr Lys

[1919]

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

[1920] <210>25

[1921] <211>274

[1922] <212>PRT

[1923] <213> 人工序列

[1924] <220>

[1925] <223>741

[1926] <400>25

[1927]

Val Asn Arg Thr Ala Phe Cys Cys Leu Ser Leu Thr Thr Ala Leu Ile
1 5 10 15
Leu Thr Ala Cys Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly
20 25 30
Ala Gly Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys
35 40 45
Gly Leu Gln Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys
50 55 60
Leu Lys Leu Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp
65 70 75 80
Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp
85 90 95
Phe Ile Arg Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser
100 105 110
Gly Glu Phe Gln Val Tyr Lys Gln Ser His Ser Ala Leu Thr Ala Phe
115 120 125
Gln Thr Glu Gln Ile Gln Asp Ser Glu His Ser Gly Lys Met Val Ala
130 135 140
Lys Arg Gln Phe Arg Ile Gly Asp Ile Ala Gly Glu His Thr Ser Phe
145 150 155 160
Asp Lys Leu Pro Glu Gly Gly Arg Ala Thr Tyr Arg Gly Thr Ala Phe
165 170 175

[1928]

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Gly Ser Asp Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala
            180                 185                 190
Ala Lys Gln Gly Asn Gly Lys Ile Glu His Leu Lys Ser Pro Glu Leu
        195                 200                 205
Asn Val Asp Leu Ala Ala Ala Asp Ile Lys Pro Asp Gly Lys Arg His
    210                 215                 220
Ala Val Ile Ser Gly Ser Val Leu Tyr Asn Gln Ala Glu Lys Gly Ser
225                 230                 235                 240
Tyr Ser Leu Gly Ile Phe Gly Gly Lys Ala Gln Glu Val Ala Gly Ser
                245                 250                 255
Ala Glu Val Lys Thr Val Asn Gly Ile Arg His Ile Gly Leu Ala Ala
            260                 265                 270
Lys Gln
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[1929] <210>26

[1930] <211>248

[1931] <212>PRT

[1932] <213> 人工序列

[1933] <220>

[1934] <223>ΔG741

[1935] <400>26

[1936]

Val Ala Ala Asp Ile Gly Ala Gly Leu Ala Asp Ala Leu Thr Ala Pro
1 5 10 15
Leu Asp His Lys Asp Lys Gly Leu Gln Ser Leu Thr Leu Asp Gln Ser
20 25 30
Val Arg Lys Asn Glu Lys Leu Lys Leu Ala Ala Gln Gly Ala Glu Lys
35 40 45
Thr Tyr Gly Asn Gly Asp Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp
50 55 60
Lys Val Ser Arg Phe Asp Phe Ile Arg Gln Ile Glu Val Asp Gly Gln
65 70 75 80
Leu Ile Thr Leu Glu Ser Gly Glu Phe Gln Val Tyr Lys Gln Ser His
85 90 95
Ser Ala Leu Thr Ala Phe Gln Thr Glu Gln Ile Gln Asp Ser Glu His
100 105 110
Ser Gly Lys Met Val Ala Lys Arg Gln Phe Arg Ile Gly Asp Ile Ala
115 120 125
Gly Glu His Thr Ser Phe Asp Lys Leu Pro Glu Gly Gly Arg Ala Thr
130 135 140
Tyr Arg Gly Thr Ala Phe Gly Ser Asp Asp Ala Gly Gly Lys Leu Thr
145 150 155 160
Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly Asn Gly Lys Ile Glu His
165 170 175
Leu Lys Ser Pro Glu Leu Asn Val Asp Leu Ala Ala Ala Asp Ile Lys
180 185 190
Pro Asp Gly Lys Arg His Ala Val Ile Ser Gly Ser Val Leu Tyr Asn
195 200 205
Gln Ala Glu Lys Gly Ser Tyr Ser Leu Gly Ile Phe Gly Gly Lys Ala
[1937] 210 215 220
Gln Glu Val Ala Gly Ser Ala Glu Val Lys Thr Val Asn Gly Ile Arg
225 230 235 240
His Ile Gly Leu Ala Ala Lys Gln
245

[1938] <210>27

[1939] <211>1947

[1940] <212>DNA

[1941] <213> 人工序列

[1942] <220>

[1943] <223>ΔG741-961

[1944] <400>27

[1945]

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aagctggcgg cacaaggtgc ggaaaaaact tatggaaacg gtgacagcct caatacgggc 180
aaattgaaga acgacaaggt cagccgtttc gactttatcc gccaaatcga agtggacggg 240
cagctcatta ccttggagag tggagagttc caagtataca aacaaagcca ttccgcctta 300
accgcctttc agaccgagca aatacaagat tcggagcatt ccgggaagat ggttgcgaaa 360
cgccagttca gaatcggcga catagcgggc gaacatacat cttttgacaa gcttcccgaa 420
ggcggcaggg cgacatatcg cgggacggcg ttcggttcag acgatgccgg cggaaaactg 480
acctacacca tagatttcgc cgccaagcag ggaaacggca aaatcgaaca tttgaaatcg 540
ccagaactca atgtcgacct ggccgccgcc gatatcaagc cggatggaaa acgccatgcc 600
gtcatcagcg gttccgtcct ttacaaccaa gccgagaaag gcagttactc cctcggtatc 660
tttggcggaa aagcccagga agttgccggc agcgcggaag tgaaaaccgt aaacggcata 720
cgccatatcg gccttgccgc caagcaactc gagggtggcg gaggcactgg atccgccaca 780
aacgacgacg atgttaaaaa agctgccact gtggccattg ctgctgccta caacaatggc 840
caagaaatca acggtttcaa agctggagag accatctacg acattgatga agacggcaca 900
attaccaaaa aagacgcaac tgcagccgat gttgaagccg acgactttaa aggtctgggt 960
ctgaaaaaag tcgtgactaa cctgaccaaa accgtcaatg aaaacaaaca aaacgtcgat 1020
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gaaaaattag aagccgtggc tgataccgtc gacaagcatg ccgaagcatt caacgatatc 1260
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ccttacaacg tgggtcggtt caatgtaacg gctgcagtcg gcggctacaa atccgaatcg 1800
gcagtcgcca tcggtaccgg cttccgcttt accgaaaact ttgccgccaa agcaggcgtg 1860
gcagtcggca cttcgtccgg ttcttccgca gcctaccatg tcggcgtcaa ttacgagtgg 1920
ctcgagcacc accaccacca ccactga 1947

[1946] <210>28

[1947] <211>648

[1948] <212>PRT

[1949] <213> 人工序列

[1950] <220>

[1951] <223>ΔG741-961

[1952] <400>28

[1953]

Met Val Ala Ala Asp Ile Gly Ala Gly Leu Ala Asp Ala Leu Thr Ala
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Pro Leu Asp His Lys Asp Lys Gly Leu Gln Ser Leu Thr Leu Asp Gln
20 25 30
Ser Val Arg Lys Asn Glu Lys Leu Lys Leu Ala Ala Gln Gly Ala Glu
35 40 45
Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn Thr Gly Lys Leu Lys Asn
50 55 60
Asp Lys Val Ser Arg Phe Asp Phe Ile Arg Gln Ile Glu Val Asp Gly
65 70 75 80
Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe Gln Val Tyr Lys Gln Ser
85 90 95
His Ser Ala Leu Thr Ala Phe Gln Thr Glu Gln Ile Gln Asp Ser Glu
100 105 110
His Ser Gly Lys Met Val Ala Lys Arg Gln Phe Arg Ile Gly Asp Ile
115 120 125
Ala Gly Glu His Thr Ser Phe Asp Lys Leu Pro Glu Gly Gly Arg Ala
130 135 140
Thr Tyr Arg Gly Thr Ala Phe Gly Ser Asp Asp Ala Gly Gly Lys Leu
145 150 155 160
Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly Asn Gly Lys Ile Glu
165 170 175
His Leu Lys Ser Pro Glu Leu Asn Val Asp Leu Ala Ala Ala Asp Ile
180 185 190
Lys Pro Asp Gly Lys Arg His Ala Val Ile Ser Gly Ser Val Leu Tyr
195 200 205
Asn Gln Ala Glu Lys Gly Ser Tyr Ser Leu Gly Ile Phe Gly Gly Lys
210 215 220
Ala Gln Glu Val Ala Gly Ser Ala Glu Val Lys Thr Val Asn Gly Ile
225 230 235 240
Arg His Ile Gly Leu Ala Ala Lys Gln Leu Glu Gly Gly Gly Gly Thr
245 250 255
Gly Ser Ala Thr Asn Asp Asp Asp Val Lys Lys Ala Ala Thr Val Ala
260 265 270
Ile Ala Ala Ala Tyr Asn Asn Gly Gln Glu Ile Asn Gly Phe Lys Ala
275 280 285
Gly Glu Thr Ile Tyr Asp Ile Asp Glu Asp Gly Thr Ile Thr Lys Lys
290 295 300
Asp Ala Thr Ala Ala Asp Val Glu Ala Asp Asp Phe Lys Gly Leu Gly
305 310 315 320
Leu Lys Lys Val Val Thr Asn Leu Thr Lys Thr Val Asn Glu Asn Lys
325 330 335
Gln Asn Val Asp Ala Lys Val Lys Ala Ala Glu Ser Glu Ile Glu Lys
340 345 350
Leu Thr Thr Lys Leu Ala Asp Thr Asp Ala Ala Leu Ala Asp Thr Asp
355 360 365
Ala Ala Leu Asp Ala Thr Thr Asn Ala Leu Asn Lys Leu Gly Glu Asn

[1954]

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

[1955] <210>29

[1956] <211>1782

[1957] <212>DNA

[1958] <213> 人工序列

[1959] <220>

[1960] <223>ΔG741-961c

[1961] <400>29

[1962]

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aaagacaaag gtttgcagtc tttgacgctg gatcagtccg tcaggaaaaa cgagaaactg 120
aagctggcgg cacaaggtgc ggaaaaaact tatggaaacg gtgacagcct caatacgggc 180
aaattgaaga acgacaaggt cagccgtttc gactttatcc gccaaatcga agtggacggg 240
cagctcatta ccttggagag tggagagttc caagtataca aacaaagcca ttccgcctta 300
accgcctttc agaccgagca aatacaagat tcggagcatt ccgggaagat ggttgcgaaa 360
[1963] cgccagttca gaatcggcga catagcgggc gaacatacat cttttgacaa gcttcccgaa 420
ggcggcaggg cgacatatcg cgggacggcg ttcggttcag acgatgccgg cggaaaactg 480
acctacacca tagatttcgc cgccaagcag ggaaacggca aaatcgaaca tttgaaatcg 540
ccagaactca atgtcgacct ggccgccgcc gatatcaagc cggatggaaa acgccatgcc 600
gtcatcagcg gttccgtcct ttacaaccaa gccgagaaag gcagttactc cctcggtatc 660
tttggcggaa aagcccagga agttgccggc agcgcggaag tgaaaaccgt aaacggcata 720
cgccatatcg gccttgccgc caagcaactc gagggtggcg gaggcactgg atccgccaca 780
aacgacgacg atgttaaaaa agctgccact gtggccattg ctgctgccta caacaatggc 840
caagaaatca acggtttcaa agctggagag accatctacg acattgatga agacggcaca 900
attaccaaaa aagacgcaac tgcagccgat gttgaagccg acgactttaa aggtctgggt 960
ctgaaaaaag tcgtgactaa cctgaccaaa accgtcaatg aaaacaaaca aaacgtcgat 1020
gccaaagtaa aagctgcaga atctgaaata gaaaagttaa caaccaagtt agcagacact 1080
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ttgggagaaa atataacgac atttgctgaa gagactaaga caaatatcgt aaaaattgat 1200
gaaaaattag aagccgtggc tgataccgtc gacaagcatg ccgaagcatt caacgatatc 1260
gccgattcat tggatgaaac caacactaag gcagacgaag ccgtcaaaac cgccaatgaa 1320
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gaaaaatcca ttgccgatca cgatactcgc ctgaacggtt tggataaaac agtgtcagac 1680
ctgcgcaaag aaacccgcca aggccttgca gaacaagccg cgctctccgg tctgttccaa 1740
ccttacaacg tgggtctcga gcaccaccac caccaccact ga 1782

[1964] 〈210〉30

[1965] 〈211〉593

[1966] 〈212〉PRT

[1967] 〈213〉人工序列

[1968] 〈220〉

[1969] 〈223〉ΔG741-961c

[1970] 〈400〉30

[1971]

Met Val Ala Ala Asp Ile Gly Ala Gly Leu Ala Asp Ala Leu Thr Ala
1 5 10 15
Pro Leu Asp His Lys Asp Lys Gly Leu Gln Ser Leu Thr Leu Asp Gln
20 25 30
Ser Val Arg Lys Asn Glu Lys Leu Lys Leu Ala Ala Gln Gly Ala Glu
35 40 45
Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn Thr Gly Lys Leu Lys Asn
50 55 60
Asp Lys Val Ser Arg Phe Asp Phe Ile Arg Gln Ile Glu Val Asp Gly
65 70 75 80
Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe Gln Val Tyr Lys Gln Ser
85 90 95
His Ser Ala Leu Thr Ala Phe Gln Thr Glu Gln Ile Gln Asp Ser Glu
100 105 110
His Ser Gly Lys Met Val Ala Lys Arg Gln Phe Arg Ile Gly Asp Ile
115 120 125
Ala Gly Glu His Thr Ser Phe Asp Lys Leu Pro Glu Gly Gly Arg Ala
130 135 140
Thr Tyr Arg Gly Thr Ala Phe Gly Ser Asp Asp Ala Gly Gly Lys Leu

[1972]

```
145                 150                 155                 160
Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly Asn Gly Lys Ile Glu
                165                 170                 175
His Leu Lys Ser Pro Glu Leu Asn Val Asp Leu Ala Ala Ala Asp Ile
            180                 185                 190
Lys Pro Asp Gly Lys Arg His Ala Val Ile Ser Gly Ser Val Leu Tyr
        195                 200                 205
Asn Gln Ala Glu Lys Gly Ser Tyr Ser Leu Gly Ile Phe Gly Gly Lys
    210                 215                 220
Ala Gln Glu Val Ala Gly Ser Ala Glu Val Lys Thr Val Asn Gly Ile
225                 230                 235                 240
Arg His Ile Gly Leu Ala Ala Lys Gln Leu Glu Gly Gly Gly Gly Thr
                245                 250                 255
Gly Ser Ala Thr Asn Asp Asp Asp Val Lys Lys Ala Ala Thr Val Ala
            260                 265                 270
Ile Ala Ala Ala Tyr Asn Asn Gly Gln Glu Ile Asn Gly Phe Lys Ala
        275                 280                 285
Gly Glu Thr Ile Tyr Asp Ile Asp Glu Asp Gly Thr Ile Thr Lys Lys
    290                 295                 300
Asp Ala Thr Ala Ala Asp Val Glu Ala Asp Asp Phe Lys Gly Leu Gly
305                 310                 315                 320
Leu Lys Lys Val Val Thr Asn Leu Thr Lys Thr Val Asn Glu Asn Lys
                325                 330                 335
Gln Asn Val Asp Ala Lys Val Lys Ala Ala Glu Ser Glu Ile Glu Lys
            340                 345                 350
Leu Thr Thr Lys Leu Ala Asp Thr Asp Ala Ala Leu Ala Asp Thr Asp
        355                 360                 365
Ala Ala Leu Asp Ala Thr Thr Asn Ala Leu Asn Lys Leu Gly Glu Asn
    370                 375                 380
Ile Thr Thr Phe Ala Glu Glu Thr Lys Thr Asn Ile Val Lys Ile Asp
385                 390                 395                 400
Glu Lys Leu Glu Ala Val Ala Asp Thr Val Asp Lys His Ala Glu Ala
                405                 410                 415
Phe Asn Asp Ile Ala Asp Ser Leu Asp Glu Thr Asn Thr Lys Ala Asp
            420                 425                 430
Glu Ala Val Lys Thr Ala Asn Glu Ala Lys Gln Thr Ala Glu Glu Thr
        435                 440                 445
Lys Gln Asn Val Asp Ala Lys Val Lys Ala Ala Glu Thr Ala Ala Gly
    450                 455                 460
Lys Ala Glu Ala Ala Ala Gly Thr Ala Asn Thr Ala Ala Asp Lys Ala
465                 470                 475                 480
Glu Ala Val Ala Ala Lys Val Thr Asp Ile Lys Ala Asp Ile Ala Thr
                485                 490                 495
Asn Lys Asp Asn Ile Ala Lys Lys Ala Asn Ser Ala Asp Val Tyr Thr
            500                 505                 510
Arg Glu Glu Ser Asp Ser Lys Phe Val Arg Ile Asp Gly Leu Asn Ala
        515                 520                 525
Thr Thr Glu Lys Leu Asp Thr Arg Leu Ala Ser Ala Glu Lys Ser Ile
    530                 535                 540
Ala Asp His Asp Thr Arg Leu Asn Gly Leu Asp Lys Thr Val Ser Asp
545                 550                 555                 560
Leu Arg Lys Glu Thr Arg Gln Gly Leu Ala Glu Gln Ala Ala Leu Ser
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[1973]

565 570 575
Gly Leu Phe Gln Pro Tyr Asn Val Gly Leu Glu His His His His His
580 585 590
His

[1974] <210>31

[1975] <211>3939

[1976] <212>DNA

[1977] <213>人工序列

[1978] <220>

[1979] <223>ΔG741-983

[1980] <400>31

[1981]

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aaagacaaag gtttgcagtc tttgacgctg gatcagtccg tcaggaaaaa cgagaaactg 120
aagctggcgg cacaaggtgc ggaaaaaact tatggaaacg gtgacagcct caatacgggc 180
aaattgaaga acgacaaggt cagccgtttc gactttatcc gccaaatcga agtggacggg 240
cagctcatta ccttggagag tggagagttc caagtataca aacaaagcca ttccgcctta 300
accgcctttc agaccgagca aatacaagat tcggagcatt ccgggaagat ggttgcgaaa 360
cgccagttca gaatcggcga catagcgggc gaacatacat cttttgacaa gcttcccgaa 420
ggcggcaggg cgacatatcg cgggacggcg ttcggttcag acgatgccgg cggaaaactg 480
acctacacca tagatttcgc cgccaagcag ggaaacggca aaatcgaaca tttgaaatcg 540
ccagaactca atgtcgacct ggccgccgcc gatatcaagc cggatggaaa acgccatgcc 600
gtcatcagcg gttccgtcct ttacaaccaa gccgagaaag gcagttactc cctcggtatc 660
tttggcggaa aagcccagga agttgccggc agcgcggaag tgaaaaccgt aaacggcata 720
cgccatatcg gccttgccgc caagcaactc gagggatccg gcggaggcgg cacttctgcg 780
cccgacttca atgcaggcgg taccggtatc ggcagcaaca gcagagcaac aacagcgaaa 840
tcagcagcag tatcttacgc cggtatcaag aacgaaatgt gcaaagacag aagcatgctc 900
tgtgccggtc gggatgacgt tgcggttaca gacagggatg ccaaaatcaa tgcccccccc 960
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ggcggtaaag acattgaagc ttctttcgac gatgaggccg ttatagagac tgaagcaaag 1260
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ggcaatgacg cacaagctca gcccaacaca tatgccctat tgccatttta tgaaaaagac 1740
gctcaaaaag gcattatcac agtcgcaggc gtagaccgca gtggagaaaa gttcaaacgg 1800
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actgccatgt ggtgcctgtc ggcaccctat gaagcaagcg tccgtttcac ccgtacaaac 1920
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[1982]

aaaaaaggcg gcagccaact gcaactgcac ggcaacaaca cctatacggg caaaaccatt 2280
atcgaaggcg gttcgctggt gttgtacggc aacaacaaat cggatatgcg cgtcgaaacc 2340
aaaggtgcgc tgatttataa cggggcggca tccggcggca gcctgaacag cgacggcatt 2400
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cggactgctt cggcagcggc acattccgcg cccgccggtc tgaaacacgc cgtagaacag 2820
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cccgagacgg ttgaaactgc ggcagccgac cgcacagata tgccgggcat ccgcccctac 2940
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ggctaccggt tcctcgagca ccaccaccac caccactga 3939

[1983] <210>32

[1984] <211>1312

[1985] <212>PRT

[1986] <213> 人工序列

[1987] <220>

[1988] <223>ΔG741-983

[1989] <400>32

[1990]

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

[1991]

```
            100                 105                 110
His Ser Gly Lys Met Val Ala Lys Arg Gln Phe Arg Ile Gly Asp Ile
        115                 120                 125
Ala Gly Glu His Thr Ser Phe Asp Lys Leu Pro Glu Gly Gly Arg Ala
    130                 135                 140
Thr Tyr Arg Gly Thr Ala Phe Gly Ser Asp Asp Ala Gly Gly Lys Leu
145                 150                 155                 160
Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly Asn Gly Lys Ile Glu
                165                 170                 175
His Leu Lys Ser Pro Glu Leu Asn Val Asp Leu Ala Ala Ala Asp Ile
            180                 185                 190
Lys Pro Asp Gly Lys Arg His Ala Val Ile Ser Gly Ser Val Leu Tyr
        195                 200                 205
Asn Gln Ala Glu Lys Gly Ser Tyr Ser Leu Gly Ile Phe Gly Gly Lys
    210                 215                 220
Ala Gln Glu Val Ala Gly Ser Ala Glu Val Lys Thr Val Asn Gly Ile
225                 230                 235                 240
Arg His Ile Gly Leu Ala Ala Lys Gln Leu Glu Gly Ser Gly Gly Gly
                245                 250                 255
Gly Thr Ser Ala Pro Asp Phe Asn Ala Gly Gly Thr Gly Ile Gly Ser
            260                 265                 270
Asn Ser Arg Ala Thr Thr Ala Lys Ser Ala Ala Val Ser Tyr Ala Gly
        275                 280                 285
Ile Lys Asn Glu Met Cys Lys Asp Arg Ser Met Leu Cys Ala Gly Arg
    290                 295                 300
Asp Asp Val Ala Val Thr Asp Arg Asp Ala Lys Ile Asn Ala Pro Pro
305                 310                 315                 320
Pro Asn Leu His Thr Gly Asp Phe Pro Asn Pro Asn Asp Ala Tyr Lys
                325                 330                 335
Asn Leu Ile Asn Leu Lys Pro Ala Ile Glu Ala Gly Tyr Thr Gly Arg
            340                 345                 350
Gly Val Glu Val Gly Ile Val Asp Thr Gly Glu Ser Val Gly Ser Ile
        355                 360                 365
Ser Phe Pro Glu Leu Tyr Gly Arg Lys Glu His Gly Tyr Asn Glu Asn
    370                 375                 380
Tyr Lys Asn Tyr Thr Ala Tyr Met Arg Lys Glu Ala Pro Glu Asp Gly
385                 390                 395                 400
Gly Gly Lys Asp Ile Glu Ala Ser Phe Asp Asp Glu Ala Val Ile Glu
                405                 410                 415
Thr Glu Ala Lys Pro Thr Asp Ile Arg His Val Lys Glu Ile Gly His
            420                 425                 430
Ile Asp Leu Val Ser His Ile Ile Gly Gly Arg Ser Val Asp Gly Arg
        435                 440                 445
Pro Ala Gly Gly Ile Ala Pro Asp Ala Thr Leu His Ile Met Asn Thr
    450                 455                 460
Asn Asp Glu Thr Lys Asn Glu Met Met Val Ala Ala Ile Arg Asn Ala
465                 470                 475                 480
Trp Val Lys Leu Gly Glu Arg Gly Val Arg Ile Val Asn Asn Ser Phe
                485                 490                 495
Gly Thr Thr Ser Arg Ala Gly Thr Ala Asp Leu Phe Gln Ile Ala Asn
            500                 505                 510
Ser Glu Glu Gln Tyr Arg Gln Ala Leu Leu Asp Tyr Ser Gly Gly Asp
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[1992]

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        515                 520                 525
Lys Thr Asp Glu Gly Ile Arg Leu Met Gln Gln Ser Asp Tyr Gly Asn
    530                 535                 540
Leu Ser Tyr His Ile Arg Asn Lys Asn Met Leu Phe Ile Phe Ser Thr
545                 550                 555                 560
Gly Asn Asp Ala Gln Ala Gln Pro Asn Thr Tyr Ala Leu Leu Pro Phe
                565                 570                 575
Tyr Glu Lys Asp Ala Gln Lys Gly Ile Ile Thr Val Ala Gly Val Asp
            580                 585                 590
Arg Ser Gly Glu Lys Phe Lys Arg Glu Met Tyr Gly Glu Pro Gly Thr
        595                 600                 605
Glu Pro Leu Glu Tyr Gly Ser Asn His Cys Gly Ile Thr Ala Met Trp
    610                 615                 620
Cys Leu Ser Ala Pro Tyr Glu Ala Ser Val Arg Phe Thr Arg Thr Asn
625                 630                 635                 640
Pro Ile Gln Ile Ala Gly Thr Ser Phe Ser Ala Pro Ile Val Thr Gly
                645                 650                 655
Thr Ala Ala Leu Leu Leu Gln Lys Tyr Pro Trp Met Ser Asn Asp Asn
            660                 665                 670
Leu Arg Thr Thr Leu Leu Thr Thr Ala Gln Asp Ile Gly Ala Val Gly
        675                 680                 685
Val Asp Ser Lys Phe Gly Trp Gly Leu Leu Asp Ala Gly Lys Ala Met
    690                 695                 700
Asn Gly Pro Ala Ser Phe Pro Phe Gly Asp Phe Thr Ala Asp Thr Lys
705                 710                 715                 720
Gly Thr Ser Asp Ile Ala Tyr Ser Phe Arg Asn Asp Ile Ser Gly Thr
                725                 730                 735
Gly Gly Leu Ile Lys Lys Gly Gly Ser Gln Leu Gln Leu His Gly Asn
            740                 745                 750
Asn Thr Tyr Thr Gly Lys Thr Ile Ile Glu Gly Gly Ser Leu Val Leu
        755                 760                 765
Tyr Gly Asn Asn Lys Ser Asp Met Arg Val Glu Thr Lys Gly Ala Leu
    770                 775                 780
Ile Tyr Asn Gly Ala Ala Ser Gly Gly Ser Leu Asn Ser Asp Gly Ile
785                 790                 795                 800
Val Tyr Leu Ala Asp Thr Asp Gln Ser Gly Ala Asn Glu Thr Val His
                805                 810                 815
Ile Lys Gly Ser Leu Gln Leu Asp Gly Lys Gly Thr Leu Tyr Thr Arg
            820                 825                 830
Leu Gly Lys Leu Leu Lys Val Asp Gly Thr Ala Ile Ile Gly Gly Lys
        835                 840                 845
Leu Tyr Met Ser Ala Arg Gly Lys Gly Ala Gly Tyr Leu Asn Ser Thr
    850                 855                 860
Gly Arg Arg Val Pro Phe Leu Ser Ala Ala Lys Ile Gly Gln Asp Tyr
865                 870                 875                 880
Ser Phe Phe Thr Asn Ile Glu Thr Asp Gly Gly Leu Leu Ala Ser Leu
                885                 890                 895
Asp Ser Val Glu Lys Thr Ala Gly Ser Glu Gly Asp Thr Leu Ser Tyr
            900                 905                 910
Tyr Val Arg Arg Gly Asn Ala Ala Arg Thr Ala Ser Ala Ala Ala His
        915                 920                 925
Ser Ala Pro Ala Gly Leu Lys His Ala Val Glu Gln Gly Gly Ser Asn
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[1993]

930 935 940

Leu Glu Asn Leu Met Val Glu Leu Asp Ala Ser Glu Ser Ser Ala Thr
945 950 955 960

Pro Glu Thr Val Glu Thr Ala Ala Ala Asp Arg Thr Asp Met Pro Gly
965 970 975

Ile Arg Pro Tyr Gly Ala Thr Phe Arg Ala Ala Ala Ala Val Gln His
980 985 990

Ala Asn Ala Ala Asp Gly Val Arg Ile Phe Asn Ser Leu Ala Ala Thr
995 1000 1005

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

Leu Lys Ala Val Ser Asp Gly Leu Asp His Asn Gly Thr Gly Leu Arg
1025 1030 1035 1040

Val Ile Ala Gln Thr Gln Gln Asp Gly Gly Thr Trp Glu Gln Gly Gly
1045 1050 1055

Val Glu Gly Lys Met Arg Gly Ser Thr Gln Thr Val Gly Ile Ala Ala
1060 1065 1070

Lys Thr Gly Glu Asn Thr Thr Ala Ala Ala Thr Leu Gly Met Gly Arg
1075 1080 1085

Ser Thr Trp Ser Glu Asn Ser Ala Asn Ala Lys Thr Asp Ser Ile Ser
1090 1095 1100

Leu Phe Ala Gly Ile Arg His Asp Ala Gly Asp Ile Gly Tyr Leu Lys
1105 1110 1115 1120

Gly Leu Phe Ser Tyr Gly Arg Tyr Lys Asn Ser Ile Ser Arg Ser Thr
1125 1130 1135

Gly Ala Asp Glu His Ala Glu Gly Ser Val Asn Gly Thr Leu Met Gln
1140 1145 1150

Leu Gly Ala Leu Gly Gly Val Asn Val Pro Phe Ala Ala Thr Gly Asp
1155 1160 1165

Leu Thr Val Glu Gly Gly Leu Arg Tyr Asp Leu Leu Lys Gln Asp Ala
1170 1175 1180

Phe Ala Glu Lys Gly Ser Ala Leu Gly Trp Ser Gly Asn Ser Leu Thr
1185 1190 1195 1200

Glu Gly Thr Leu Val Gly Leu Ala Gly Leu Lys Leu Ser Gln Pro Leu
1205 1210 1215

Ser Asp Lys Ala Val Leu Phe Ala Thr Ala Gly Val Glu Arg Asp Leu
1220 1225 1230

Asn Gly Arg Asp Tyr Thr Val Thr Gly Gly Phe Thr Gly Ala Thr Ala
1235 1240 1245

Ala Thr Gly Lys Thr Gly Ala Arg Asn Met Pro His Thr Arg Leu Val
1250 1255 1260

Ala Gly Leu Gly Ala Asp Val Glu Phe Gly Asn Gly Trp Asn Gly Leu
1265 1270 1275 1280

Ala Arg Tyr Ser Tyr Ala Gly Ser Lys Gln Tyr Gly Asn His Ser Gly
1285 1290 1295

Arg Val Gly Val Gly Tyr Arg Phe Leu Glu His His His His His His
1300 1305 1310

[1994] <210>33

[1995] <211>2028

[1996] <212>DNA

[1997] <213> 人工序列

[1998] <220>

[1999] <223> ΔG741-ORF46.1

[2000] <400>33

[2001]

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aagctggcgg cacaaggtgc ggaaaaaact tatggaaacg gtgacagcct caatacgggc  180
aaattgaaga acgacaaggt cagccgtttc gactttatcc gccaaatcga agtggacggg  240
cagctcatta ccttggagag tggagagttc caagtataca aacaaagcca ttccgcctta  300
accgcctttc agaccgagca aatacaagat tcggagcatt ccgggaagat ggttgcgaaa  360
cgccagttca gaatcggcga catagcgggc gaacatacat cttttgacaa gcttcccgaa  420
ggcggcaggg cgacatatcg cgggacggcg ttcggttcag acgatgccgg cggaaaactg  480
acctacacca tagatttcgc cgccaagcag ggaaacggca aaatcgaaca tttgaaatcg  540
ccagaactca atgtcgacct ggccgccgcc gatatcaagc cggatggaaa acgccatgcc  600
gtcatcagcg gttccgtcct ttacaaccaa gccgagaaag gcagttactc cctcggtatc  660
tttggcggaa aagcccagga agttgccggc agcgcggaag tgaaaaccgt aaacggcata  720
cgccatatcg gccttgccgc caagcaactc gacggtggcg gaggcactgg atcctcagat  780
ttggcaaacg attcttttat ccggcaggtt ctcgaccgtc agcatttcga acccgacggg  840
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ggaaaaatac aaagccatca gttgggcaac ctgatgattc aacaggcggc cattaaagga  960
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aaccatgcct cacattccga ttctgatgaa gccggtagtc ccgttgacgg atttagcctt 1080
taccgcatcc attgggacgg atacgaacac catcccgccg acggctatga cgggccacag 1140
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gaccaacgcc acccgaagac aggcgtaccg tttgacggta aagggtttcc gaattttgag 1980
aagcacgtga aatatgatac gctcgagcac caccaccacc accactga             2028
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[2002] <210>34

[2003] <211>675

[2004] <212>PRT

[2005] <213> 人工序列

[2006] <220>

[2007] <223> Δ6741-ORF46.1

[2008] <400>34

[2009]

Met Val Ala Ala Asp Ile Gly Ala Gly Leu Ala Asp Ala Leu Thr Ala
1 5 10 15
Pro Leu Asp His Lys Asp Lys Gly Leu Gln Ser Leu Thr Leu Asp Gln

[2010]

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            20                  25                  30
Ser Val Arg Lys Asn Glu Lys Leu Lys Leu Ala Ala Gln Gly Ala Glu
        35                  40                  45
Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn Thr Gly Lys Leu Lys Asn
    50                  55                  60
Asp Lys Val Ser Arg Phe Asp Phe Ile Arg Gln Ile Glu Val Asp Gly
65                  70                  75                  80
Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe Gln Val Tyr Lys Gln Ser
                85                  90                  95
His Ser Ala Leu Thr Ala Phe Gln Thr Glu Gln Ile Gln Asp Ser Glu
            100                 105                 110
His Ser Gly Lys Met Val Ala Lys Arg Gln Phe Arg Ile Gly Asp Ile
        115                 120                 125
Ala Gly Glu His Thr Ser Phe Asp Lys Leu Pro Glu Gly Gly Arg Ala
    130                 135                 140
Thr Tyr Arg Gly Thr Ala Phe Gly Ser Asp Asp Ala Gly Gly Lys Leu
145                 150                 155                 160
Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly Asn Gly Lys Ile Glu
                165                 170                 175
His Leu Lys Ser Pro Glu Leu Asn Val Asp Leu Ala Ala Ala Asp Ile
            180                 185                 190
Lys Pro Asp Gly Lys Arg His Ala Val Ile Ser Gly Ser Val Leu Tyr
        195                 200                 205
Asn Gln Ala Glu Lys Gly Ser Tyr Ser Leu Gly Ile Phe Gly Gly Lys
    210                 215                 220
Ala Gln Glu Val Ala Gly Ser Ala Glu Val Lys Thr Val Asn Gly Ile
225                 230                 235                 240
Arg His Ile Gly Leu Ala Ala Lys Gln Leu Asp Gly Gly Gly Gly Thr
                245                 250                 255
Gly Ser Ser Asp Leu Ala Asn Asp Ser Phe Ile Arg Gln Val Leu Asp
            260                 265                 270
Arg Gln His Phe Glu Pro Asp Gly Lys Tyr His Leu Phe Gly Ser Arg
        275                 280                 285
Gly Glu Leu Ala Glu Arg Ser Gly His Ile Gly Leu Gly Lys Ile Gln
    290                 295                 300
Ser His Gln Leu Gly Asn Leu Met Ile Gln Gln Ala Ala Ile Lys Gly
305                 310                 315                 320
Asn Ile Gly Tyr Ile Val Arg Phe Ser Asp His Gly His Glu Val His
                325                 330                 335
Ser Pro Phe Asp Asn His Ala Ser His Ser Asp Ser Asp Glu Ala Gly
            340                 345                 350
Ser Pro Val Asp Gly Phe Ser Leu Tyr Arg Ile His Trp Asp Gly Tyr
        355                 360                 365
Glu His His Pro Ala Asp Gly Tyr Asp Gly Pro Gln Gly Gly Gly Tyr
    370                 375                 380
Pro Ala Pro Lys Gly Ala Arg Asp Ile Tyr Ser Tyr Asp Ile Lys Gly
385                 390                 395                 400
Val Ala Gln Asn Ile Arg Leu Asn Leu Thr Asp Asn Arg Ser Thr Gly
                405                 410                 415
Gln Arg Leu Ala Asp Arg Phe His Asn Ala Gly Ser Met Leu Thr Gln
            420                 425                 430
Gly Val Gly Asp Gly Phe Lys Arg Ala Thr Arg Tyr Ser Pro Glu Leu
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[2011]

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

[2012] <210>35

[2013] <211>2019

[2014] <212>DNA

[2015] <213> 人工序列

[2016] <220>

[2017] <223>ORF46.1-741

[2018] <400>35

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atcggattgg gaaaaataca aagccatcag ttgggcaacc tgatgattca acaggcggcc 180
attaaaggaa atatcggcta cattgtccgc ttttccgatc acgggcacga agtccattcc 240
cccttcgaca accatgcctc acattccgat tctgatgaag ccggtagtcc cgttgacgga 300
tttagccttt accgcatcca ttgggacgga tacgaacacc atcccgccga cggctatgac 360
gggccacagg gcggcggcta tcccgctccc aaaggcgcga gggatatata cagctacgac 420
ataaaaggcg ttgcccaaaa tatccgcctc aacctgaccg acaaccgcag caccggacaa 480
cggcttgccg accgtttcca caatgccggt agtatgctga cgcaaggagt aggcgacgga 540
ttcaaacgcg ccacccgata cagccccgag ctggacagat cgggcaatgc cgccgaagcc 600

[2020] ttcaacggca ctgcagatat cgttaaaaac atcatcggcg cggcaggaga aattgtcggc 660
gcaggcgatg ccgtgcaggg cataagcgaa ggctcaaaca ttgctgtcat gcacggcttg 720
ggtctgcttt ccaccgaaaa caagatggcg cgcatcaacg atttggcaga tatggcgcaa 780
ctcaaagact atgccgcagc agccatccgc gattgggcag tccaaaaccc caatgccgca 840
caaggcatag aagccgtcag caatatcttt atggcagcca tccccatcaa agggattgga 900
gctgttcggg gaaaatacgg cttgggcggc atcacggcac atcctatcaa gcggtcgcag 960
atgggcgcga tcgcattgcc gaaagggaaa tccgccgtca gcgacaattt tgccgatgcg 1020
gcatacgcca aatacccgtc cccttaccat tcccgaaata tccgttcaaa cttggagcag 1080
cgttacggca aagaaaacat cacctcctca accgtgccgc cgtcaaacgg caaaaatgtc 1140
aaactggcag accaacgcca cccgaagaca ggcgtaccgt ttgacggtaa agggtttccg 1200
aattttgaga agcacgtgaa atatgatacg ggatccggag gggtggtgt cgccgccgac 1260
atcggtgcgg ggcttgccga tgcactaacc gcaccgctcg accataaaga caaaggtttg 1320
cagtctttga cgctggatca gtccgtcagg aaaaacgaga aactgaagct ggcggcacaa 1380
ggtgcggaaa aaacttatgg aaacggtgac agcctcaata cgggcaaatt gaagaacgac 1440
aaggtcagcc gtttcgactt tatccgccaa atcgaagtgg acgggcagct cattaccttg 1500
gagagtggag agttccaagt atacaaacaa agccattccg ccttaaccgc ctttcagacc 1560
gagcaaatac aagattcgga gcattccggg aagatggttg cgaaacgcca gttcagaatc 1620
ggcgacatag cgggcgaaca tacatctttt gacaagcttc ccgaaggcgg cagggcgaca 1680
tatcgcggga cggcgttcgg ttcagacgat gccggcggaa aactgaccta caccatagat 1740
ttcgccgcca agcagggaaa cggcaaaatc gaacatttga aatcgccaga actcaatgtc 1800
gacctggccg ccgccgatat caagccggat ggaaaacgcc atgccgtcat cagcggttcc 1860
gtcctttaca accaagccga gaaaggcagt tactccctcg gtatctttgg cggaaaagcc 1920
caggaagttg ccggcagcgc ggaagtgaaa accgtaaacg gcatacgcca tatcggcctt 1980
gccgccaagc aactcgagca ccaccaccac caccactga 2019

[2021] <210>36

[2022] <211>672

[2023] <212>PRT

[2024] <213>人工序列

[2025] <220>

[2026] <223>ORF46.1-741

[2027] <400>36

[2028]

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1               5                   10                  15
Gln His Phe Glu Pro Asp Gly Lys Tyr His Leu Phe Gly Ser Arg Gly
            20                  25                  30
Glu Leu Ala Glu Arg Ser Gly His Ile Gly Leu Gly Lys Ile Gln Ser
        35                  40                  45
His Gln Leu Gly Asn Leu Met Ile Gln Gln Ala Ala Ile Lys Gly Asn
    50                  55                  60
Ile Gly Tyr Ile Val Arg Phe Ser Asp His Gly His Glu Val His Ser
65                  70                  75                  80
Pro Phe Asp Asn His Ala Ser His Ser Asp Ser Asp Glu Ala Gly Ser
                85                  90                  95
Pro Val Asp Gly Phe Ser Leu Tyr Arg Ile His Trp Asp Gly Tyr Glu
            100                 105                 110
His His Pro Ala Asp Gly Tyr Asp Gly Pro Gln Gly Gly Gly Tyr Pro
        115                 120                 125
Ala Pro Lys Gly Ala Arg Asp Ile Tyr Ser Tyr Asp Ile Lys Gly Val
    130                 135                 140
Ala Gln Asn Ile Arg Leu Asn Leu Thr Asp Asn Arg Ser Thr Gly Gln
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[2029]

145 150 155 160
Arg Leu Ala Asp Arg Phe His Asn Ala Gly Ser Met Leu Thr Gln Gly
165 170 175
Val Gly Asp Gly Phe Lys Arg Ala Thr Arg Tyr Ser Pro Glu Leu Asp
180 185 190
Arg Ser Gly Asn Ala Ala Glu Ala Phe Asn Gly Thr Ala Asp Ile Val
195 200 205
Lys Asn Ile Ile Gly Ala Ala Gly Glu Ile Val Gly Ala Gly Asp Ala
210 215 220
Val Gln Gly Ile Ser Glu Gly Ser Asn Ile Ala Val Met His Gly Leu
225 230 235 240
Gly Leu Leu Ser Thr Glu Asn Lys Met Ala Arg Ile Asn Asp Leu Ala
245 250 255
Asp Met Ala Gln Leu Lys Asp Tyr Ala Ala Ala Ala Ile Arg Asp Trp
260 265 270
Ala Val Gln Asn Pro Asn Ala Ala Gln Gly Ile Glu Ala Val Ser Asn
275 280 285
Ile Phe Met Ala Ala Ile Pro Ile Lys Gly Ile Gly Ala Val Arg Gly
290 295 300
Lys Tyr Gly Leu Gly Gly Ile Thr Ala His Pro Ile Lys Arg Ser Gln
305 310 315 320
Met Gly Ala Ile Ala Leu Pro Lys Gly Lys Ser Ala Val Ser Asp Asn
325 330 335
Phe Ala Asp Ala Ala Tyr Ala Lys Tyr Pro Ser Pro Tyr His Ser Arg
340 345 350
Asn Ile Arg Ser Asn Leu Glu Gln Arg Tyr Gly Lys Glu Asn Ile Thr
355 360 365
Ser Ser Thr Val Pro Pro Ser Asn Gly Lys Asn Val Lys Leu Ala Asp
370 375 380
Gln Arg His Pro Lys Thr Gly Val Pro Phe Asp Gly Lys Gly Phe Pro
385 390 395 400
Asn Phe Glu Lys His Val Lys Tyr Asp Thr Gly Ser Gly Gly Gly Gly
405 410 415
Val Ala Ala Asp Ile Gly Ala Gly Leu Ala Asp Ala Leu Thr Ala Pro
420 425 430
Leu Asp His Lys Asp Lys Gly Leu Gln Ser Leu Thr Leu Asp Gln Ser
435 440 445
Val Arg Lys Asn Glu Lys Leu Lys Leu Ala Ala Gln Gly Ala Glu Lys
450 455 460
Thr Tyr Gly Asn Gly Asp Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp
465 470 475 480
Lys Val Ser Arg Phe Asp Phe Ile Arg Gln Ile Glu Val Asp Gly Gln
485 490 495
Leu Ile Thr Leu Glu Ser Gly Glu Phe Gln Val Tyr Lys Gln Ser His
500 505 510
Ser Ala Leu Thr Ala Phe Gln Thr Glu Gln Ile Gln Asp Ser Glu His
515 520 525
Ser Gly Lys Met Val Ala Lys Arg Gln Phe Arg Ile Gly Asp Ile Ala
530 535 540
Gly Glu His Thr Ser Phe Asp Lys Leu Pro Glu Gly Gly Arg Ala Thr
545 550 555 560
Tyr Arg Gly Thr Ala Phe Gly Ser Asp Asp Ala Gly Gly Lys Leu Thr

[2030]

```
                  565                 570                 575
Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly Asn Gly Lys Ile Glu His
              580                 585                 590
Leu Lys Ser Pro Glu Leu Asn Val Asp Leu Ala Ala Ala Asp Ile Lys
          595                 600                 605
Pro Asp Gly Lys Arg His Ala Val Ile Ser Gly Ser Val Leu Tyr Asn
    610                 615                 620
Gln Ala Glu Lys Gly Ser Tyr Ser Leu Gly Ile Phe Gly Gly Lys Ala
625                 630                 635                 640
Gln Glu Val Ala Gly Ser Ala Glu Val Lys Thr Val Asn Gly Ile Arg
                  645                 650                 655
His Ile Gly Leu Ala Ala Lys Gln Leu Glu His His His His His His
              660                 665                 670
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[2031] <210>37

[2032] <211>2421

[2033] <212>DNA

[2034] <213> 人工序列

[2035] <220>

[2036] <223>ORF46.1-961

[2037] <400>37

[2038]

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cccgacggga aataccacct attcggcagc agggggggaac ttgccgagcg cagcggccat 120
atcggattgg gaaaaataca aagccatcag ttgggcaacc tgatgattca acaggcggcc 180
attaaaggaa atatcggcta cattgtccgc ttttccgatc acgggcacga agtccattcc 240
cccttcgaca accatgcctc acattccgat tctgatgaag ccggtagtcc cgttgacgga 300
tttagccttt accgcatcca ttgggacgga tacgaacacc atcccgccga cggctatgac 360
gggccacagg gcggcggcta tcccgctccc aaaggcgcga gggatatata cagctacgac 420
ataaaaggcg ttgcccaaaa tatccgcctc aacctgaccg acaaccgcag caccggacaa 480
cggcttgccg accgtttcca caatgccggt agtatgctga cgcaaggagt aggcgacgga 540
ttcaaacgcg ccacccgata cagccccgag ctggacagat cgggcaatgc cgccgaagcc 600
ttcaacggca ctgcagatat cgttaaaaac atcatcggcg cggcaggaga aattgtcggc 660
gcaggcgatg ccgtgcaggg cataagcgaa ggctcaaaca ttgctgtcat gcacggcttg 720
ggtctgcttt ccaccgaaaa caagatggcg cgcatcaacg atttggcaga tatggcgcaa 780
ctcaaagact atgccgcagc agccatccgc gattgggcag tccaaaaccc caatgccgca 840
caaggcatag aagccgtcag caatatcttt atggcagcca tccccatcaa agggattgga 900
gctgttcggg gaaaatacgg cttgggcggc atcacggcac atcctatcaa gcggtcgcag 960
atgggcgcga tcgcattgcc gaaagggaaa tccgccgtca gcgacaattt tgccgatgcg 1020
gcatacgcca aatacccgtc cccttaccat tcccgaaata tccgttcaaa cttggagcag 1080
cgttacggca aagaaaacat cacctcctca accgtgccgc cgtcaaacgg caaaaatgtc 1140
aaactggcag accaacgcca cccgaagaca ggcgtaccgt ttgacggtaa agggtttccg 1200
aattttgaga agcacgtgaa atatgatacg ggatccggag gaggaggagc cacaaacgac 1260
gacgatgtta aaaaagctgc cactgtggcc attgctgctg cctacaacaa tggccaagaa 1320
atcaacggtt tcaaagctgg agagaccatc tacgacattg atgaagacgg cacaattacc 1380
aaaaaagacg caactgcagc cgatgttgaa gccgacgact ttaaaggtct gggtctgaaa 1440
aaagtcgtga ctaacctgac caaaaccgtc aatgaaaaca aacaaaacgt cgatgccaaa 1500
gtaaaagctg cagaatctga aatagaaaag ttaacaacca agttagcaga cactgatgcc 1560
gctttagcag atactgatgc cgctctggat gcaaccacca acgccttgaa taaattggga 1620
gaaaatataa cgacatttgc tgaagagact aagacaaata tcgtaaaaat tgatgaaaaa 1680

[2039] ttagaagccg tggctgatac cgtcgacaag catgccgaag cattcaacga tatcgccgat 1740
tcattggatg aaaccaacac taaggcagac gaagccgtca aaaccgccaa tgaagccaaa 1800
cagacggccg aagaaaccaa acaaaacgtc gatgccaaag taaaagctgc agaaactgca 1860
gcaggcaaag ccgaagctgc cgctggcaca gctaatactg cagccgacaa ggccgaagct 1920
gtcgctgcaa aagttaccga catcaaagct gatatcgcta cgaacaaaga taatattgct 1980
aaaaaagcaa acagtgccga cgtgtacacc agagaagagt ctgacagcaa atttgtcaga 2040
attgatggtc tgaacgctac taccgaaaaa ttggacacac gcttggcttc tgctgaaaaa 2100
tccattgccg atcacgatac tcgcctgaac ggtttggata aaacagtgtc agacctgcgc 2160
aaagaaaccc gccaaggcct tgcagaacaa gccgcgctct ccggtctgtt ccaaccttac 2220
aacgtgggtc ggttcaatgt aacggctgca gtcggcggct acaaatccga atcggcagtc 2280
gccatcggta ccggcttccg ctttaccgaa aactttgccg ccaaagcagg cgtggcagtc 2340
ggcacttcgt ccggttcttc cgcagcctac catgtcggcg tcaattacga gtggctcgag 2400
caccaccacc accaccactg a 2421

[2040] <210>38

[2041] <211>806

[2042] <212>PRT

[2043] <213> 人工序列

[2044] <220>

[2045] <223>ORF46.1-961

[2046] <400>38

[2047]

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Met Ser Asp Leu Ala Asn Asp Ser Phe Ile Arg Gln Val Leu Asp Arg
1               5                   10                  15
Gln His Phe Glu Pro Asp Gly Lys Tyr His Leu Phe Gly Ser Arg Gly
            20                  25                  30
Glu Leu Ala Glu Arg Ser Gly His Ile Gly Leu Gly Lys Ile Gln Ser
        35                  40                  45
His Gln Leu Gly Asn Leu Met Ile Gln Gln Ala Ala Ile Lys Gly Asn
    50                  55                  60
Ile Gly Tyr Ile Val Arg Phe Ser Asp His Gly His Glu Val His Ser
65                  70                  75                  80
Pro Phe Asp Asn His Ala Ser His Ser Asp Ser Asp Glu Ala Gly Ser
                85                  90                  95
Pro Val Asp Gly Phe Ser Leu Tyr Arg Ile His Trp Asp Gly Tyr Glu
            100                 105                 110
His His Pro Ala Asp Gly Tyr Asp Gly Pro Gln Gly Gly Gly Tyr Pro
        115                 120                 125
Ala Pro Lys Gly Ala Arg Asp Ile Tyr Ser Tyr Asp Ile Lys Gly Val
    130                 135                 140
Ala Gln Asn Ile Arg Leu Asn Leu Thr Asp Asn Arg Ser Thr Gly Gln
145                 150                 155                 160
Arg Leu Ala Asp Arg Phe His Asn Ala Gly Ser Met Leu Thr Gln Gly
                165                 170                 175
Val Gly Asp Gly Phe Lys Arg Ala Thr Arg Tyr Ser Pro Glu Leu Asp
            180                 185                 190
Arg Ser Gly Asn Ala Ala Glu Ala Phe Asn Gly Thr Ala Asp Ile Val
        195                 200                 205
Lys Asn Ile Ile Gly Ala Ala Gly Glu Ile Val Gly Ala Gly Asp Ala
    210                 215                 220
Val Gln Gly Ile Ser Glu Gly Ser Asn Ile Ala Val Met His Gly Leu
225                 230                 235                 240
```

[2048]

Gly Leu Leu Ser Thr Glu Asn Lys Met Ala Arg Ile Asn Asp Leu Ala
245 250 255
Asp Met Ala Gln Leu Lys Asp Tyr Ala Ala Ala Ala Ile Arg Asp Trp
260 265 270
Ala Val Gln Asn Pro Asn Ala Ala Gln Gly Ile Glu Ala Val Ser Asn
275 280 285
Ile Phe Met Ala Ala Ile Pro Ile Lys Gly Ile Gly Ala Val Arg Gly
290 295 300
Lys Tyr Gly Leu Gly Gly Ile Thr Ala His Pro Ile Lys Arg Ser Gln
305 310 315 320
Met Gly Ala Ile Ala Leu Pro Lys Gly Lys Ser Ala Val Ser Asp Asn
325 330 335
Phe Ala Asp Ala Ala Tyr Ala Lys Tyr Pro Ser Pro Tyr His Ser Arg
340 345 350
Asn Ile Arg Ser Asn Leu Glu Gln Arg Tyr Gly Lys Glu Asn Ile Thr
355 360 365
Ser Ser Thr Val Pro Pro Ser Asn Gly Lys Asn Val Lys Leu Ala Asp
370 375 380
Gln Arg His Pro Lys Thr Gly Val Pro Phe Asp Gly Lys Gly Phe Pro
385 390 395 400
Asn Phe Glu Lys His Val Lys Tyr Asp Thr Gly Ser Gly Gly Gly Gly
405 410 415
Ala Thr Asn Asp Asp Asp Val Lys Lys Ala Ala Thr Val Ala Ile Ala
420 425 430
Ala Ala Tyr Asn Asn Gly Gln Glu Ile Asn Gly Phe Lys Ala Gly Glu
435 440 445
Thr Ile Tyr Asp Ile Asp Glu Asp Gly Thr Ile Thr Lys Lys Asp Ala
450 455 460
Thr Ala Ala Asp Val Glu Ala Asp Asp Phe Lys Gly Leu Gly Leu Lys
465 470 475 480
Lys Val Val Thr Asn Leu Thr Lys Thr Val Asn Glu Asn Lys Gln Asn
485 490 495
Val Asp Ala Lys Val Lys Ala Ala Glu Ser Glu Ile Glu Lys Leu Thr
500 505 510
Thr Lys Leu Ala Asp Thr Asp Ala Ala Leu Ala Asp Thr Asp Ala Ala
515 520 525
Leu Asp Ala Thr Thr Asn Ala Leu Asn Lys Leu Gly Glu Asn Ile Thr
530 535 540
Thr Phe Ala Glu Glu Thr Lys Thr Asn Ile Val Lys Ile Asp Glu Lys
545 550 555 560
Leu Glu Ala Val Ala Asp Thr Val Asp Lys His Ala Glu Ala Phe Asn
565 570 575
Asp Ile Ala Asp Ser Leu Asp Glu Thr Asn Thr Lys Ala Asp Glu Ala
580 585 590
Val Lys Thr Ala Asn Glu Ala Lys Gln Thr Ala Glu Glu Thr Lys Gln
595 600 605
Asn Val Asp Ala Lys Val Lys Ala Ala Glu Thr Ala Ala Gly Lys Ala
610 615 620
Glu Ala Ala Ala Gly Thr Ala Asn Thr Ala Ala Asp Lys Ala Glu Ala
625 630 635 640
Val Ala Ala Lys Val Thr Asp Ile Lys Ala Asp Ile Ala Thr Asn Lys
645 650 655

[2049]

Asp Asn Ile Ala Lys Lys Ala Asn Ser Ala Asp Val Tyr Thr Arg Glu
660 665 670
Glu Ser Asp Ser Lys Phe Val Arg Ile Asp Gly Leu Asn Ala Thr Thr
675 680 685
Glu Lys Leu Asp Thr Arg Leu Ala Ser Ala Glu Lys Ser Ile Ala Asp
690 695 700
His Asp Thr Arg Leu Asn Gly Leu Asp Lys Thr Val Ser Asp Leu Arg
705 710 715 720
Lys Glu Thr Arg Gln Gly Leu Ala Glu Gln Ala Ala Leu Ser Gly Leu
725 730 735
Phe Gln Pro Tyr Asn Val Gly Arg Phe Asn Val Thr Ala Ala Val Gly
740 745 750
Gly Tyr Lys Ser Glu Ser Ala Val Ala Ile Gly Thr Gly Phe Arg Phe
755 760 765
Thr Glu Asn Phe Ala Ala Lys Ala Gly Val Ala Val Gly Thr Ser Ser
770 775 780
Gly Ser Ser Ala Ala Tyr His Val Gly Val Asn Tyr Glu Trp Leu Glu
785 790 795 800
His His His His His His
805

[2050] <210>39

[2051] <211>2256

[2052] <212>DNA

[2053] <213> 人工序列

[2054] <220>

[2055] <223>ORF46.1-961c

[2056] <400>39

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atcggattgg gaaaaataca aagccatcag ttgggcaacc tgatgattca acaggcggcc 180
attaaaggaa atatcggcta cattgtccgc ttttccgatc acgggcacga agtccattcc 240
cccttcgaca accatgcctc acattccgat tctgatgaag ccggtagtcc cgttgacgga 300
tttagccttt accgcatcca ttgggacgga tacgaacacc atcccgccga cggctatgac 360
gggccacagg gcggcggcta tcccgctccc aaaggcgcga gggatatata cagctacgac 420
ataaaaggcg ttgcccaaaa tatccgcctc aacctgaccg acaaccgcag caccggacaa 480
cggcttgccg accgtttcca caatgccggt agtatgctga cgcaaggagt aggcgacgga 540
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gcaggcgatg ccgtgcaggg cataagcgaa ggctcaaaca ttgctgtcat gcacggcttg 720
ggtctgcttt ccaccgaaaa caagatggcg cgcatcaacg atttggcaga tatggcgcaa 780
ctcaaagact atgccgcagc agccatccgc gattgggcag tccaaaaccc caatgccgca 840
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gctgttcggg gaaaatacgg cttgggcggc atcacggcac atcctatcaa gcggtcgcag 960
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aaactggcag accaacgcca cccgaagaca ggcgtaccgt ttgacggtaa agggtttccg 1200
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cagacggccg aagaaaccaa acaaaacgtc gatgccaaag taaaagctgc agaaactgca 1860
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gtcgctgcaa aagttaccga catcaaagct gatatcgcta cgaacaaaga taatattgct 1980
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tccattgccg atcacgatac tcgcctgaac ggtttggata aaacagtgtc agacctgcgc 2160
aaagaaaccc gccaaggcct tgcagaacaa gccgcgctct ccggtctgtt ccaaccttac 2220
aacgtgggtc tcgagcacca ccaccaccac cactga 2256

[2059] <210>40

[2060] <211>751

[2061] <212>PRT

[2062] <213>人工序列

[2063] <220>

[2064] <223>ORF46.1-961c

[2065] <400>40

[2066]

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1               5                   10                  15
Gln His Phe Glu Pro Asp Gly Lys Tyr His Leu Phe Gly Ser Arg Gly
            20                  25                  30
Glu Leu Ala Glu Arg Ser Gly His Ile Gly Leu Gly Lys Ile Gln Ser
        35                  40                  45
His Gln Leu Gly Asn Leu Met Ile Gln Gln Ala Ala Ile Lys Gly Asn
    50                  55                  60
Ile Gly Tyr Ile Val Arg Phe Ser Asp His Gly His Glu Val His Ser
65                  70                  75                  80
Pro Phe Asp Asn His Ala Ser His Ser Asp Ser Asp Glu Ala Gly Ser
                85                  90                  95
Pro Val Asp Gly Phe Ser Leu Tyr Arg Ile His Trp Asp Gly Tyr Glu
            100                 105                 110
His His Pro Ala Asp Gly Tyr Asp Gly Pro Gln Gly Gly Gly Tyr Pro
        115                 120                 125
Ala Pro Lys Gly Ala Arg Asp Ile Tyr Ser Tyr Asp Ile Lys Gly Val
    130                 135                 140
Ala Gln Asn Ile Arg Leu Asn Leu Thr Asp Asn Arg Ser Thr Gly Gln
145                 150                 155                 160
Arg Leu Ala Asp Arg Phe His Asn Ala Gly Ser Met Leu Thr Gln Gly
                165                 170                 175
Val Gly Asp Gly Phe Lys Arg Ala Thr Arg Tyr Ser Pro Glu Leu Asp
            180                 185                 190
Arg Ser Gly Asn Ala Ala Glu Ala Phe Asn Gly Thr Ala Asp Ile Val
        195                 200                 205
```

[2067]

Lys Asn Ile Ile Gly Ala Ala Gly Glu Ile Val Gly Ala Gly Asp Ala
210 215 220
Val Gln Gly Ile Ser Glu Gly Ser Asn Ile Ala Val Met His Gly Leu
225 230 235 240
Gly Leu Leu Ser Thr Glu Asn Lys Met Ala Arg Ile Asn Asp Leu Ala
245 250 255
Asp Met Ala Gln Leu Lys Asp Tyr Ala Ala Ala Ile Arg Asp Trp
260 265 270
Ala Val Gln Asn Pro Asn Ala Ala Gln Gly Ile Glu Ala Val Ser Asn
275 280 285
Ile Phe Met Ala Ala Ile Pro Ile Lys Gly Ile Gly Ala Val Arg Gly
290 295 300
Lys Tyr Gly Leu Gly Gly Ile Thr Ala His Pro Ile Lys Arg Ser Gln
305 310 315 320
Met Gly Ala Ile Ala Leu Pro Lys Gly Lys Ser Ala Val Ser Asp Asn
325 330 335
Phe Ala Asp Ala Ala Tyr Ala Lys Tyr Pro Ser Pro Tyr His Ser Arg
340 345 350
Asn Ile Arg Ser Asn Leu Glu Gln Arg Tyr Gly Lys Glu Asn Ile Thr
355 360 365
Ser Ser Thr Val Pro Pro Ser Asn Gly Lys Asn Val Lys Leu Ala Asp
370 375 380
Gln Arg His Pro Lys Thr Gly Val Pro Phe Asp Gly Lys Gly Phe Pro
385 390 395 400
Asn Phe Glu Lys His Val Lys Tyr Asp Thr Gly Ser Gly Gly Gly Gly
405 410 415
Ala Thr Asn Asp Asp Asp Val Lys Lys Ala Ala Thr Val Ala Ile Ala
420 425 430
Ala Ala Tyr Asn Asn Gly Gln Glu Ile Asn Gly Phe Lys Ala Gly Glu
435 440 445
Thr Ile Tyr Asp Ile Asp Glu Asp Gly Thr Ile Thr Lys Lys Asp Ala
450 455 460
Thr Ala Ala Asp Val Glu Ala Asp Asp Phe Lys Gly Leu Gly Leu Lys
465 470 475 480
Lys Val Val Thr Asn Leu Thr Lys Thr Val Asn Glu Asn Lys Gln Asn
485 490 495
Val Asp Ala Lys Val Lys Ala Ala Glu Ser Glu Ile Glu Lys Leu Thr
500 505 510
Thr Lys Leu Ala Asp Thr Asp Ala Ala Leu Ala Asp Thr Asp Ala Ala
515 520 525
Leu Asp Ala Thr Thr Asn Ala Leu Asn Lys Leu Gly Glu Asn Ile Thr
530 535 540
Thr Phe Ala Glu Glu Thr Lys Thr Asn Ile Val Lys Ile Asp Glu Lys
545 550 555 560
Leu Glu Ala Val Ala Asp Thr Val Asp Lys His Ala Glu Ala Phe Asn
565 570 575
Asp Ile Ala Asp Ser Leu Asp Glu Thr Asn Thr Lys Ala Asp Glu Ala
580 585 590
Val Lys Thr Ala Asn Glu Ala Lys Gln Thr Ala Glu Glu Thr Lys Gln
595 600 605
Asn Val Asp Ala Lys Val Lys Ala Ala Glu Thr Ala Ala Gly Lys Ala
610 615 620

[2068]

Glu Ala Ala Ala Gly Thr Ala Asn Thr Ala Ala Asp Lys Ala Glu Ala
625 630 635 640
Val Ala Ala Lys Val Thr Asp Ile Lys Ala Asp Ile Ala Thr Asn Lys
645 650 655
Asp Asn Ile Ala Lys Lys Ala Asn Ser Ala Asp Val Tyr Thr Arg Glu
660 665 670
Glu Ser Asp Ser Lys Phe Val Arg Ile Asp Gly Leu Asn Ala Thr Thr
675 680 685
Glu Lys Leu Asp Thr Arg Leu Ala Ser Ala Glu Lys Ser Ile Ala Asp
690 695 700
His Asp Thr Arg Leu Asn Gly Leu Asp Lys Thr Val Ser Asp Leu Arg
705 710 715 720
Lys Glu Thr Arg Gln Gly Leu Ala Glu Gln Ala Ala Leu Ser Gly Leu
725 730 735
Phe Gln Pro Tyr Asn Val Gly Leu Glu His His His His His His
740 745 750

[2069] <210>41

[2070] <211>2421

[2071] <212>DNA

[2072] <213> 人工序列

[2073] <220>

[2074] <223>961-ORF46.1

[2075] <400>41

[2076]

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aacaatggcc aagaaatcaa cggtttcaaa gctggagaga ccatctacga cattgatgaa 120
gacggcacaa ttaccaaaaa agacgcaact gcagccgatg ttgaagccga cgactttaaa 180
ggtctgggtc tgaaaaaagt cgtgactaac ctgaccaaaa ccgtcaatga aaacaaacaa 240
aacgtcgatg ccaaagtaaa agctgcagaa tctgaaatag aaaagttaac aaccaagtta 300
gcagacactg atgccgcttt agcagatact gatgccgctc tggatgcaac caccaacgcc 360
ttgaataaat tgggagaaaa tataacgaca tttgctgaag agactaagac aaatatcgta 420
aaaattgatg aaaaattaga agccgtggct gataccgtcg acaagcatgc cgaagcattc 480
aacgatatcg ccgattcatt ggatgaaacc aacactaagg cagacgaagc cgtcaaaacc 540
gccaatgaag ccaaacagac ggccgaagaa accaaacaaa acgtcgatgc caaagtaaaa 600
gctgcagaaa ctgcagcagg caaagccgaa gctgccgctg gcacagctaa tactgcagcc 660
gacaaggccg aagctgtcgc tgcaaaagtt accgacatca aagctgatat cgctacgaac 720
aaagataata ttgctaaaaa agcaaacagt gccgacgtgt acaccagaga agagtctgac 780
agcaaatttg tcagaattga tggtctgaac gctactaccg aaaaattgga cacacgcttg 840
gcttctgctg aaaaatccat tgccgatcac gatactcgcc tgaacggttt ggataaaaca 900
gtgtcagacc tgcgcaaaga aacccgccaa ggccttgcag aacaagccgc gctctccggt 960
ctgttccaac cttacaacgt gggtcggttc aatgtaacgg ctgcagtcgg cggctacaaa 1020
tccgaatcgg cagtcgccat cggtaccggc ttccgcttta ccgaaaactt tgccgccaaa 1080
gcaggcgtgg cagtcggcac ttcgtccggt tcttccgcag cctaccatgt cggcgtcaat 1140
tacgagtggg gatccggagg aggaggatca gatttggcaa acgattcttt tatccggcag 1200
gttctcgacc gtcagcattt cgaacccgac gggaaatacc acctattcgg cagcaggggg 1260
gaacttgccg agcgcagcgg ccatatcgga ttgggaaaaa tacaaagcca tcagttgggc 1320
aacctgatga ttcaacaggc ggccattaaa ggaaatatcg gctacattgt ccgcttttcc 1380
gatcacgggc acgaagtcca ttcccccttc gacaaccatg cctcacattc cgattctgat 1440
gaagccggta gtcccgttga cggatttagc ctttaccgca tccattggga cggatacgaa 1500

[2077] caccatcccg ccgacggcta tgacgggcca cagggcggcg gctatcccgc tcccaaaggc 1560

gcgagggata tatacagcta cgacataaaa ggcgttgccc aaaatatccg cctcaacctg 1620
accgacaacc gcagcaccgg acaacggctt gccgaccgtt tccacaatgc cggtagtatg 1680
ctgacgcaag gagtaggcga cggattcaaa cgcgccaccc gatacagccc cgagctggac 1740
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aacgatttgg cagatatggc gcaactcaaa gactatgccg cagcagccat ccgcgattgg 1980
gcagtccaaa accccaatgc cgcacaaggc atagaagccg tcagcaatat ctttatggca 2040
gccatcccca tcaaagggat tggagctgtt cggggaaaat acggcttggg cggcatcacg 2100
gcacatccta tcaagcggtc gcagatgggc gcgatcgcat tgccgaaagg gaaatccgcc 2160
gtcagcgaca attttgccga tgcggcatac gccaaatacc cgtcccctta ccattcccga 2220
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ccgccgtcaa acggcaaaaa tgtcaaactg gcagaccaac gccacccgaa gacaggcgta 2340
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[2078] <210>42

[2079] <211>806

[2080] <212>PRT

[2081] <213> 人工序列

[2082] <220>

[2083] <223>961-ORF46.1

[2084] <400>42

[2085]

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

[2086]

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    210                 215                 220
Ala Val Ala Ala Lys Val Thr Asp Ile Lys Ala Asp Ile Ala Thr Asn
225                 230                 235                 240
Lys Asp Asn Ile Ala Lys Lys Ala Asn Ser Ala Asp Val Tyr Thr Arg
                245                 250                 255
Glu Glu Ser Asp Ser Lys Phe Val Arg Ile Asp Gly Leu Asn Ala Thr
            260                 265                 270
Thr Glu Lys Leu Asp Thr Arg Leu Ala Ser Ala Glu Lys Ser Ile Ala
        275                 280                 285
Asp His Asp Thr Arg Leu Asn Gly Leu Asp Lys Thr Val Ser Asp Leu
    290                 295                 300
Arg Lys Glu Thr Arg Gln Gly Leu Ala Glu Gln Ala Ala Leu Ser Gly
305                 310                 315                 320
Leu Phe Gln Pro Tyr Asn Val Gly Arg Phe Asn Val Thr Ala Ala Val
                325                 330                 335
Gly Gly Tyr Lys Ser Glu Ser Ala Val Ala Ile Gly Thr Gly Phe Arg
            340                 345                 350
Phe Thr Glu Asn Phe Ala Ala Lys Ala Gly Val Ala Val Gly Thr Ser
        355                 360                 365
Ser Gly Ser Ser Ala Ala Tyr His Val Gly Val Asn Tyr Glu Trp Gly
    370                 375                 380
Ser Gly Gly Gly Gly Ser Asp Leu Ala Asn Asp Ser Phe Ile Arg Gln
385                 390                 395                 400
Val Leu Asp Arg Gln His Phe Glu Pro Asp Gly Lys Tyr His Leu Phe
                405                 410                 415
Gly Ser Arg Gly Glu Leu Ala Glu Arg Ser Gly His Ile Gly Leu Gly
            420                 425                 430
Lys Ile Gln Ser His Gln Leu Gly Asn Leu Met Ile Gln Gln Ala Ala
        435                 440                 445
Ile Lys Gly Asn Ile Gly Tyr Ile Val Arg Phe Ser Asp His Gly His
    450                 455                 460
Glu Val His Ser Pro Phe Asp Asn His Ala Ser His Ser Asp Ser Asp
465                 470                 475                 480
Glu Ala Gly Ser Pro Val Asp Gly Phe Ser Leu Tyr Arg Ile His Trp
                485                 490                 495
Asp Gly Tyr Glu His His Pro Ala Asp Gly Tyr Asp Gly Pro Gln Gly
            500                 505                 510
Gly Gly Tyr Pro Ala Pro Lys Gly Ala Arg Asp Ile Tyr Ser Tyr Asp
        515                 520                 525
Ile Lys Gly Val Ala Gln Asn Ile Arg Leu Asn Leu Thr Asp Asn Arg
    530                 535                 540
Ser Thr Gly Gln Arg Leu Ala Asp Arg Phe His Asn Ala Gly Ser Met
545                 550                 555                 560
Leu Thr Gln Gly Val Gly Asp Gly Phe Lys Arg Ala Thr Arg Tyr Ser
                565                 570                 575
Pro Glu Leu Asp Arg Ser Gly Asn Ala Ala Glu Ala Phe Asn Gly Thr
            580                 585                 590
Ala Asp Ile Val Lys Asn Ile Ile Gly Ala Ala Gly Glu Ile Val Gly
        595                 600                 605
Ala Gly Asp Ala Val Gln Gly Ile Ser Glu Gly Ser Asn Ile Ala Val
    610                 615                 620
Met His Gly Leu Gly Leu Leu Ser Thr Glu Asn Lys Met Ala Arg Ile
```

[2087]

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625                 630                 635                 640
Asn Asp Leu Ala Asp Met Ala Gln Leu Lys Asp Tyr Ala Ala Ala Ala
                645                 650                 655
Ile Arg Asp Trp Ala Val Gln Asn Pro Asn Ala Ala Gln Gly Ile Glu
            660                 665                 670
Ala Val Ser Asn Ile Phe Met Ala Ala Ile Pro Ile Lys Gly Ile Gly
        675                 680                 685
Ala Val Arg Gly Lys Tyr Gly Leu Gly Gly Ile Thr Ala His Pro Ile
    690                 695                 700
Lys Arg Ser Gln Met Gly Ala Ile Ala Leu Pro Lys Gly Lys Ser Ala
705                 710                 715                 720
Val Ser Asp Asn Phe Ala Asp Ala Ala Tyr Ala Lys Tyr Pro Ser Pro
                725                 730                 735
Tyr His Ser Arg Asn Ile Arg Ser Asn Leu Glu Gln Arg Tyr Gly Lys
            740                 745                 750
Glu Asn Ile Thr Ser Ser Thr Val Pro Pro Ser Asn Gly Lys Asn Val
        755                 760                 765
Lys Leu Ala Asp Gln Arg His Pro Lys Thr Gly Val Pro Phe Asp Gly
    770                 775                 780
Lys Gly Phe Pro Asn Phe Glu Lys His Val Lys Tyr Asp Thr Leu Glu
785                 790                 795                 800
His His His His His His
                805
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[2088] <210>43

[2089] <211>1938

[2090] <212>DNA

[2091] <213> 人工序列

[2092] <220>

[2093] <223>961-741

[2094] <400>43

[2095]

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aacaatggcc aagaaatcaa cggtttcaaa gctggagaga ccatctacga cattgatgaa 120
gacggcacaa ttaccaaaaa agacgcaact gcagccgatg ttgaagccga cgactttaaa 180
ggtctgggtc tgaaaaaagt cgtgactaac ctgaccaaaa ccgtcaatga aaacaaacaa 240
aacgtcgatg ccaaagtaaa agctgcagaa tctgaaatag aaaagttaac aaccaagtta 300
gcagacactg atgccgcttt agcagatact gatgccgctc tggatgcaac caccaacgcc 360
ttgaataaat tgggagaaaa tataacgaca tttgctgaag agactaagac aaatatcgta 420
aaaattgatg aaaaattaga agccgtggct gataccgtcg acaagcatgc cgaagcattc 480
aacgatatcg ccgattcatt ggatgaaacc aacactaagg cagacgaagc cgtcaaaacc 540
gccaatgaag ccaaacagac ggccgaagaa accaaacaaa acgtcgatgc caaagtaaaa 600
gctgcagaaa ctgcagcagg caaagccgaa gctgccgctg gcacagctaa tactgcagcc 660
gacaaggccg aagctgtcgc tgcaaaagtt accgacatca aagctgatat cgctacgaac 720
aaagataata ttgctaaaaa agcaaacagt gccgacgtgt acaccagaga agagtctgac 780
agcaaatttg tcagaattga tggtctgaac gctactaccg aaaaattgga cacacgcttg 840
gcttctgctg aaaaatccat tgccgatcac gatactcgcc tgaacggttt ggataaaaca 900
gtgtcagacc tgcgcaaaga aacccgccaa ggccttgcag aacaagccgc gctctccggt 960
ctgttccaac cttacaacgt gggtcggttc aatgtaacgg ctgcagtcgg cggctacaaa 1020
tccgaatcgg cagtcgccat cggtaccggc ttccgcttta ccgaaaactt tgccgccaaa 1080

[2096] gcaggcgtgg cagtcggcac ttcgtccggt tcttccgcag cctaccatgt cggcgtcaat 1140
tacgagtggg gatccggagg gggtggtgtc gccgccgaca tcggtgcggg gcttgccgat 1200
gcactaaccg caccgctcga ccataaagac aaaggtttgc agtctttgac gctggatcag 1260
tccgtcagga aaaacgagaa actgaagctg gcggcacaag gtgcggaaaa aacttatgga 1320
aacggtgaca gcctcaatac gggcaaattg aagaacgaca aggtcagccg tttcgacttt 1380
atccgccaaa tcgaagtgga cgggcagctc attaccttgg agagtggaga gttccaagta 1440
tacaaacaaa gccattccgc cttaaccgcc tttcagaccg agcaaataca agattcggag 1500
cattccggga agatggttgc gaaacgccag ttcagaatcg gcgacatagc gggcgaacat 1560
acatcttttg acaagcttcc cgaaggcggc agggcgacat atcgcgggac ggcgttcggt 1620
tcagacgatg ccggcggaaa actgacctac accatagatt tcgccgccaa gcagggaaac 1680
ggcaaaatcg aacatttgaa atcgccagaa ctcaatgtcg acctggccgc cgccgatatc 1740
aagccggatg gaaaacgcca tgccgtcatc agcggttccg tcctttacaa ccaagccgag 1800
aaaggcagtt actccctcgg tatctttggc ggaaaagccc aggaagttgc cggcagcgcg 1860
gaagtgaaaa ccgtaaacgg catacgccat atcggccttg ccgccaagca actcgagcac 1920
caccaccacc accactga 1938

[2097] <210>44

[2098] <211>645

[2099] <212>PRT

[2100] <213> 人工序列

[2101] <220>

[2102] <223>961741

[2103] <400>44

[2104]

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Ala Ala Ala Tyr Asn Asn Gly Gln Glu Ile Asn Gly Phe Lys Ala Gly
            20                  25                  30
Glu Thr Ile Tyr Asp Ile Asp Glu Asp Gly Thr Ile Thr Lys Lys Asp
        35                  40                  45
Ala Thr Ala Ala Asp Val Glu Ala Asp Asp Phe Lys Gly Leu Gly Leu
    50                  55                  60
Lys Lys Val Val Thr Asn Leu Thr Lys Thr Val Asn Glu Asn Lys Gln
65                  70                  75                  80
Asn Val Asp Ala Lys Val Lys Ala Ala Glu Ser Glu Ile Glu Lys Leu
                85                  90                  95
Thr Thr Lys Leu Ala Asp Thr Asp Ala Ala Leu Ala Asp Thr Asp Ala
            100                 105                 110
Ala Leu Asp Ala Thr Thr Asn Ala Leu Asn Lys Leu Gly Glu Asn Ile
        115                 120                 125
Thr Thr Phe Ala Glu Glu Thr Lys Thr Asn Ile Val Lys Ile Asp Glu
    130                 135                 140
Lys Leu Glu Ala Val Ala Asp Thr Val Asp Lys His Ala Glu Ala Phe
145                 150                 155                 160
Asn Asp Ile Ala Asp Ser Leu Asp Glu Thr Asn Thr Lys Ala Asp Glu
                165                 170                 175
Ala Val Lys Thr Ala Asn Glu Ala Lys Gln Thr Ala Glu Glu Thr Lys
            180                 185                 190
Gln Asn Val Asp Ala Lys Val Lys Ala Ala Glu Thr Ala Ala Gly Lys
        195                 200                 205
Ala Glu Ala Ala Ala Gly Thr Ala Asn Thr Ala Ala Asp Lys Ala Glu
    210                 215                 220
```

[2105]

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       Ala Val Ala Ala Lys Val Thr Asp Ile Lys Ala Asp Ile Ala Thr Asn
       225                 230                 235                 240
       Lys Asp Asn Ile Ala Lys Lys Ala Asn Ser Ala Asp Val Tyr Thr Arg
                       245                 250                 255
       Glu Glu Ser Asp Ser Lys Phe Val Arg Ile Asp Gly Leu Asn Ala Thr
                   260                 265                 270
       Thr Glu Lys Leu Asp Thr Arg Leu Ala Ser Ala Glu Lys Ser Ile Ala
               275                 280                 285
       Asp His Asp Thr Arg Leu Asn Gly Leu Asp Lys Thr Val Ser Asp Leu
           290                 295                 300
       Arg Lys Glu Thr Arg Gln Gly Leu Ala Glu Gln Ala Ala Leu Ser Gly
       305                 310                 315                 320
       Leu Phe Gln Pro Tyr Asn Val Gly Arg Phe Asn Val Thr Ala Ala Val
                       325                 330                 335
       Gly Gly Tyr Lys Ser Glu Ser Ala Val Ala Ile Gly Thr Gly Phe Arg
                   340                 345                 350
       Phe Thr Glu Asn Phe Ala Ala Lys Ala Gly Val Ala Val Gly Thr Ser
               355                 360                 365
       Ser Gly Ser Ser Ala Ala Tyr His Val Gly Val Asn Tyr Glu Trp Gly
           370                 375                 380
       Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu Ala Asp
       385                 390                 395                 400
       Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Gly Leu Gln Ser Leu
                       405                 410                 415
       Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu Ala Ala
                   420                 425                 430
       Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn Thr Gly
               435                 440                 445
       Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg Gln Ile
           450                 455                 460
       Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe Gln Val
       465                 470                 475                 480
       Tyr Lys Gln Ser His Ser Ala Leu Thr Ala Phe Gln Thr Glu Gln Ile
                       485                 490                 495
       Gln Asp Ser Glu His Ser Gly Lys Met Val Ala Lys Arg Gln Phe Arg
                   500                 505                 510
       Ile Gly Asp Ile Ala Gly Glu His Thr Ser Phe Asp Lys Leu Pro Glu
               515                 520                 525
       Gly Gly Arg Ala Thr Tyr Arg Gly Thr Ala Phe Gly Ser Asp Asp Ala
           530                 535                 540
       Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly Asn
       545                 550                 555                 560
       Gly Lys Ile Glu His Leu Lys Ser Pro Glu Leu Asn Val Asp Leu Ala
                       565                 570                 575
       Ala Ala Asp Ile Lys Pro Asp Gly Lys Arg His Ala Val Ile Ser Gly
                   580                 585                 590
       Ser Val Leu Tyr Asn Gln Ala Glu Lys Gly Ser Tyr Ser Leu Gly Ile
               595                 600                 605
       Phe Gly Gly Lys Ala Gln Glu Val Ala Gly Ser Ala Glu Val Lys Thr
           610                 615                 620
       Val Asn Gly Ile Arg His Ile Gly Leu Ala Ala Lys Gln Leu Glu His
[2106] 625                 630                 635                 640
       His His His His His
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[2107] <210>45

[2108] <211>4335

[2109] <212>DNA

[2110] <213> 人工序列

[2111] <220>

[2112] <223>961-983

[2113] <400>45

[2114]

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gacggcacaa ttaccaaaaa agacgcaact gcagccgatg ttgaagccga cgactttaaa   180
ggtctgggtc tgaaaaaagt cgtgactaac ctgaccaaaa ccgtcaatga aaacaaacaa   240
aacgtcgatg ccaaagtaaa agctgcagaa tctgaaatag aaaagttaac aaccaagtta   300
gcagacactg atgccgcttt agcagatact gatgccgctc tggatgcaac caccaacgcc   360
ttgaataaat tgggagaaaa tataacgaca tttgctgaag agactaagac aaatatcgta   420
aaaattgatg aaaaattaga agccgtggct gataccgtcg acaagcatgc cgaagcattc   480
aacgatatcg ccgattcatt ggatgaaacc aacactaagg cagacgaagc cgtcaaaacc   540
gccaatgaag ccaaacagac ggccgaagaa accaaacaaa acgtcgatgc caaagtaaaa   600
gctgcagaaa ctgcagcagg caaagccgaa gctgccgctg gcacagctaa tactgcagcc   660
gacaaggccg aagctgtcgc tgcaaaagtt accgacatca aagctgatat cgctacgaac   720
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agcaaatttg tcagaattga tggtctgaac gctactaccg aaaaattgga cacacgcttg   840
gcttctgctg aaaaatccat tgccgatcac gatactcgcc tgaacggttt ggataaaaca   900
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ggtatcggca gcaacagcag agcaacaaca gcgaaatcag cagcagtatc ttacgccggt  1260
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gaaatcggac acatcgattt ggtctcccat attattggcg ggcgttccgt ggacggcaga  1740
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aagaacgaaa tgatggttgc agccatccgc aatgcatggg tcaagctggg cgaacgtggc  1860
gtgcgcatcg tcaataacag ttttggaaca acatcgaggg caggcactgc cgaccttttc  1920
caaatagcca attcggagga gcagtaccgc caagcgttgc tcgactattc cggcggtgat  1980
aaaacagacg agggtatccg cctgatgcaa cagagcgatt acggcaacct gtcctaccac  2040
atccgtaata aaaacatgct tttcatcttt tcgacaggca atgacgcaca agctcagccc  2100
aacacatatg ccctattgcc attttatgaa aaagacgctc aaaaaggcat tatcacagtc  2160
gcaggcgtag accgcagtgg agaaaagttc aaacgggaaa tgtatggaga accgggtaca  2220
gaaccgcttg agtatggctc caaccattgc ggaattactg ccatgtggtg cctgtcggca  2280
ccctatgaag caagcgtccg tttcacccgt acaaacccga ttcaaattgc cggaacatcc  2340
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[2115]

agcaacgaca acctgcgtac cacgttgctg acgacggctc aggacatcgg tgcagtcggc 2460
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tcctttccgt tcggcgactt taccgccgat acgaaaggta catccgatat tgcctactcc 2580
ttccgtaacg acatttcagg cacgggcggc ctgatcaaaa aaggcggcag ccaactgcaa 2640
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gcggatgtcg aattcggcaa cggctggaac ggcttggcac gttacagcta cgccggttcc 4260
aaacagtacg gcaaccacag cggacgagtc ggcgtaggct accggttcct cgagcaccac 4320
caccaccacc actga 4335

[2116] <210>46

[2117] <211>1444

[2118] <212>PRT

[2119] <213> 人工序列

[2120] <220>

[2121] <223>961-983

[2122] <400>46

[2123]

Met Ala Thr Asn Asp Asp Asp Val Lys Lys Ala Ala Thr Val Ala Ile
1 5 10 15
Ala Ala Ala Tyr Asn Asn Gly Gln Glu Ile Asn Gly Phe Lys Ala Gly
20 25 30
Glu Thr Ile Tyr Asp Ile Asp Glu Asp Gly Thr Ile Thr Lys Lys Asp
35 40 45
Ala Thr Ala Ala Asp Val Glu Ala Asp Asp Phe Lys Gly Leu Gly Leu
50 55 60
Lys Lys Val Val Thr Asn Leu Thr Lys Thr Val Asn Glu Asn Lys Gln

[2124]

```
65                  70                  75                  80
Asn Val Asp Ala Lys Val Lys Ala Ala Glu Ser Glu Ile Glu Lys Leu
                85                  90                  95
Thr Thr Lys Leu Ala Asp Thr Asp Ala Ala Leu Ala Asp Thr Asp Ala
            100                 105                 110
Ala Leu Asp Ala Thr Thr Asn Ala Leu Asn Lys Leu Gly Glu Asn Ile
        115                 120                 125
Thr Thr Phe Ala Glu Glu Thr Lys Thr Asn Ile Val Lys Ile Asp Glu
    130                 135                 140
Lys Leu Glu Ala Val Ala Asp Thr Val Asp Lys His Ala Glu Ala Phe
145                 150                 155                 160
Asn Asp Ile Ala Asp Ser Leu Asp Glu Thr Asn Thr Lys Ala Asp Glu
                165                 170                 175
Ala Val Lys Thr Ala Asn Glu Ala Lys Gln Thr Ala Glu Glu Thr Lys
            180                 185                 190
Gln Asn Val Asp Ala Lys Val Lys Ala Ala Glu Thr Ala Ala Gly Lys
        195                 200                 205
Ala Glu Ala Ala Ala Gly Thr Ala Asn Thr Ala Ala Asp Lys Ala Glu
    210                 215                 220
Ala Val Ala Ala Lys Val Thr Asp Ile Lys Ala Asp Ile Ala Thr Asn
225                 230                 235                 240
Lys Asp Asn Ile Ala Lys Lys Ala Asn Ser Ala Asp Val Tyr Thr Arg
                245                 250                 255
Glu Glu Ser Asp Ser Lys Phe Val Arg Ile Asp Gly Leu Asn Ala Thr
            260                 265                 270
Thr Glu Lys Leu Asp Thr Arg Leu Ala Ser Ala Glu Lys Ser Ile Ala
        275                 280                 285
Asp His Asp Thr Arg Leu Asn Gly Leu Asp Lys Thr Val Ser Asp Leu
    290                 295                 300
Arg Lys Glu Thr Arg Gln Gly Leu Ala Glu Gln Ala Ala Leu Ser Gly
305                 310                 315                 320
Leu Phe Gln Pro Tyr Asn Val Gly Arg Phe Asn Val Thr Ala Ala Val
                325                 330                 335
Gly Gly Tyr Lys Ser Glu Ser Ala Val Ala Ile Gly Thr Gly Phe Arg
            340                 345                 350
Phe Thr Glu Asn Phe Ala Ala Lys Ala Gly Val Ala Val Gly Thr Ser
        355                 360                 365
Ser Gly Ser Ser Ala Ala Tyr His Val Gly Val Asn Tyr Glu Trp Gly
    370                 375                 380
Ser Gly Gly Gly Gly Thr Ser Ala Pro Asp Phe Asn Ala Gly Gly Thr
385                 390                 395                 400
Gly Ile Gly Ser Asn Ser Arg Ala Thr Thr Ala Lys Ser Ala Ala Val
                405                 410                 415
Ser Tyr Ala Gly Ile Lys Asn Glu Met Cys Lys Asp Arg Ser Met Leu
            420                 425                 430
Cys Ala Gly Arg Asp Asp Val Ala Val Thr Asp Arg Asp Ala Lys Ile
        435                 440                 445
Asn Ala Pro Pro Pro Asn Leu His Thr Gly Asp Phe Pro Asn Pro Asn
    450                 455                 460
Asp Ala Tyr Lys Asn Leu Ile Asn Leu Lys Pro Ala Ile Glu Ala Gly
465                 470                 475                 480
Tyr Thr Gly Arg Gly Val Glu Val Gly Ile Val Asp Thr Gly Glu Ser
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[2125]

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                485                 490                 495
Val Gly Ser Ile Ser Phe Pro Glu Leu Tyr Gly Arg Lys Glu His Gly
            500                 505                 510
Tyr Asn Glu Asn Tyr Lys Asn Tyr Thr Ala Tyr Met Arg Lys Glu Ala
        515                 520                 525
Pro Glu Asp Gly Gly Gly Lys Asp Ile Glu Ala Ser Phe Asp Asp Glu
    530                 535                 540
Ala Val Ile Glu Thr Glu Ala Lys Pro Thr Asp Ile Arg His Val Lys
545                 550                 555                 560
Glu Ile Gly His Ile Asp Leu Val Ser His Ile Ile Gly Gly Arg Ser
                565                 570                 575
Val Asp Gly Arg Pro Ala Gly Gly Ile Ala Pro Asp Ala Thr Leu His
            580                 585                 590
Ile Met Asn Thr Asn Asp Glu Thr Lys Asn Glu Met Met Val Ala Ala
        595                 600                 605
Ile Arg Asn Ala Trp Val Lys Leu Gly Glu Arg Gly Val Arg Ile Val
    610                 615                 620
Asn Asn Ser Phe Gly Thr Thr Ser Arg Ala Gly Thr Ala Asp Leu Phe
625                 630                 635                 640
Gln Ile Ala Asn Ser Glu Glu Gln Tyr Arg Gln Ala Leu Leu Asp Tyr
                645                 650                 655
Ser Gly Gly Asp Lys Thr Asp Glu Gly Ile Arg Leu Met Gln Gln Ser
            660                 665                 670
Asp Tyr Gly Asn Leu Ser Tyr His Ile Arg Asn Lys Asn Met Leu Phe
        675                 680                 685
Ile Phe Ser Thr Gly Asn Asp Ala Gln Ala Gln Pro Asn Thr Tyr Ala
    690                 695                 700
Leu Leu Pro Phe Tyr Glu Lys Asp Ala Gln Lys Gly Ile Ile Thr Val
705                 710                 715                 720
Ala Gly Val Asp Arg Ser Gly Glu Lys Phe Lys Arg Glu Met Tyr Gly
                725                 730                 735
Glu Pro Gly Thr Glu Pro Leu Glu Tyr Gly Ser Asn His Cys Gly Ile
            740                 745                 750
Thr Ala Met Trp Cys Leu Ser Ala Pro Tyr Glu Ala Ser Val Arg Phe
        755                 760                 765
Thr Arg Thr Asn Pro Ile Gln Ile Ala Gly Thr Ser Phe Ser Ala Pro
    770                 775                 780
Ile Val Thr Gly Thr Ala Ala Leu Leu Leu Gln Lys Tyr Pro Trp Met
785                 790                 795                 800
Ser Asn Asp Asn Leu Arg Thr Thr Leu Leu Thr Thr Ala Gln Asp Ile
                805                 810                 815
Gly Ala Val Gly Val Asp Ser Lys Phe Gly Trp Gly Leu Leu Asp Ala
            820                 825                 830
Gly Lys Ala Met Asn Gly Pro Ala Ser Phe Pro Phe Gly Asp Phe Thr
        835                 840                 845
Ala Asp Thr Lys Gly Thr Ser Asp Ile Ala Tyr Ser Phe Arg Asn Asp
    850                 855                 860
Ile Ser Gly Thr Gly Gly Leu Ile Lys Lys Gly Gly Ser Gln Leu Gln
865                 870                 875                 880
Leu His Gly Asn Asn Thr Tyr Thr Gly Lys Thr Ile Ile Glu Gly Gly
                885                 890                 895
Ser Leu Val Leu Tyr Gly Asn Asn Lys Ser Asp Met Arg Val Glu Thr
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[2126]

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            900                 905                 910
Lys Gly Ala Leu Ile Tyr Asn Gly Ala Ala Ser Gly Gly Ser Leu Asn
        915                 920                 925
Ser Asp Gly Ile Val Tyr Leu Ala Asp Thr Asp Gln Ser Gly Ala Asn
    930                 935                 940
Glu Thr Val His Ile Lys Gly Ser Leu Gln Leu Asp Gly Lys Gly Thr
945                 950                 955                 960
Leu Tyr Thr Arg Leu Gly Lys Leu Leu Lys Val Asp Gly Thr Ala Ile
                965                 970                 975
Ile Gly Gly Lys Leu Tyr Met Ser Ala Arg Gly Lys Gly Ala Gly Tyr
            980                 985                 990
Leu Asn Ser Thr Gly Arg Arg Val Pro Phe Leu Ser Ala Ala Lys Ile
        995                 1000                1005
Gly Gln Asp Tyr Ser Phe Phe Thr Asn Ile Glu Thr Asp Gly Gly Leu
    1010                1015                1020
Leu Ala Ser Leu Asp Ser Val Glu Lys Thr Ala Gly Ser Glu Gly Asp
1025                1030                1035                1040
Thr Leu Ser Tyr Tyr Val Arg Arg Gly Asn Ala Ala Arg Thr Ala Ser
                1045                1050                1055
Ala Ala Ala His Ser Ala Pro Ala Gly Leu Lys His Ala Val Glu Gln
            1060                1065                1070
Gly Gly Ser Asn Leu Glu Asn Leu Met Val Glu Leu Asp Ala Ser Glu
        1075                1080                1085
Ser Ser Ala Thr Pro Glu Thr Val Glu Thr Ala Ala Ala Asp Arg Thr
    1090                1095                1100
Asp Met Pro Gly Ile Arg Pro Tyr Gly Ala Thr Phe Arg Ala Ala Ala
1105                1110                1115                1120
Ala Val Gln His Ala Asn Ala Ala Asp Gly Val Arg Ile Phe Asn Ser
                1125                1130                1135
Leu Ala Ala Thr Val Tyr Ala Asp Ser Thr Ala Ala His Ala Asp Met
            1140                1145                1150
Gln Gly Arg Arg Leu Lys Ala Val Ser Asp Gly Leu Asp His Asn Gly
        1155                1160                1165
Thr Gly Leu Arg Val Ile Ala Gln Thr Gln Gln Asp Gly Gly Thr Trp
    1170                1175                1180
Glu Gln Gly Gly Val Glu Gly Lys Met Arg Gly Ser Thr Gln Thr Val
1185                1190                1195                1200
Gly Ile Ala Ala Lys Thr Gly Glu Asn Thr Thr Ala Ala Ala Thr Leu
                1205                1210                1215
Gly Met Gly Arg Ser Thr Trp Ser Glu Asn Ser Ala Asn Ala Lys Thr
            1220                1225                1230
Asp Ser Ile Ser Leu Phe Ala Gly Ile Arg His Asp Ala Gly Asp Ile
        1235                1240                1245
Gly Tyr Leu Lys Gly Leu Phe Ser Tyr Gly Arg Tyr Lys Asn Ser Ile
    1250                1255                1260
Ser Arg Ser Thr Gly Ala Asp Glu His Ala Glu Gly Ser Val Asn Gly
1265                1270                1275                1280
Thr Leu Met Gln Leu Gly Ala Leu Gly Gly Val Asn Val Pro Phe Ala
                1285                1290                1295
Ala Thr Gly Asp Leu Thr Val Glu Gly Gly Leu Arg Tyr Asp Leu Leu
            1300                1305                1310
Lys Gln Asp Ala Phe Ala Glu Lys Gly Ser Ala Leu Gly Trp Ser Gly
```

[2127]

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        1315                1320                1325
Asn Ser Leu Thr Glu Gly Thr Leu Val Gly Leu Ala Gly Leu Lys Leu
    1330                1335                1340
Ser Gln Pro Leu Ser Asp Lys Ala Val Leu Phe Ala Thr Ala Gly Val
1345                1350                1355                1360
Glu Arg Asp Leu Asn Gly Arg Asp Tyr Thr Val Thr Gly Gly Phe Thr
                1365                1370                1375
Gly Ala Thr Ala Ala Thr Gly Lys Thr Gly Ala Arg Asn Met Pro His
            1380                1385                1390
Thr Arg Leu Val Ala Gly Leu Gly Ala Asp Val Glu Phe Gly Asn Gly
        1395                1400                1405
Trp Asn Gly Leu Ala Arg Tyr Ser Tyr Ala Gly Ser Lys Gln Tyr Gly
    1410                1415                1420
Asn His Ser Gly Arg Val Gly Val Gly Tyr Arg Phe Leu Glu His His
1425                1430                1435                1440
His His His His
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[2128] <210>47

[2129] <211>2256

[2130] <212>DNA

[2131] <213>人工序列

[2132] <220>

[2133] <223>961c-ORF46.1

[2134] <400>47

[2135]

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aacaatggcc aagaaatcaa cggtttcaaa gctggagaga ccatctacga cattgatgaa   120
gacggcacaa ttaccaaaaa agacgcaact gcagccgatg ttgaagccga cgactttaaa   180
ggtctgggtc tgaaaaaagt cgtgactaac ctgaccaaaa ccgtcaatga aaacaaacaa   240
aacgtcgatg ccaaagtaaa agctgcagaa tctgaaatag aaaagttaac aaccaagtta   300
gcagacactg atgccgcttt agcagatact gatgccgctc tggatgcaac caccaacgcc   360
ttgaataaat tgggagaaaa tataacgaca tttgctgaag agactaagac aaatatcgta   420
aaaattgatg aaaaattaga agccgtggct gataccgtcg acaagcatgc cgaagcattc   480
aacgatatcg ccgattcatt ggatgaaacc aacactaagg cagacgaagc cgtcaaaacc   540
gccaatgaag ccaaacagac ggccgaagaa accaaacaaa acgtcgatgc caaagtaaaa   600
gctgcagaaa ctgcagcagg caaagccgaa gctgccgctg gcacagctaa tactgcagcc   660
gacaaggccg aagctgtcgc tgcaaaagtt accgacatca aagctgatat cgctacgaac   720
aaagataata ttgctaaaaa agcaaacagt gccgacgtgt acaccagaga agagtctgac   780
agcaaatttg tcagaattga tggtctgaac gctactaccg aaaaattgga cacacgcttg   840
gcttctgctg aaaaatccat tgccgatcac gatactcgcc tgaacggttt ggataaaaca   900
gtgtcagacc tgcgcaaaga aacccgccaa ggccttgcag aacaagccgc gctctccggt   960
ctgttccaac cttacaacgt gggtggatcc ggaggaggag gatcagattt ggcaaacgat  1020
tcttttatcc ggcaggttct cgaccgtcag catttcgaac ccgacgggaa ataccaccta  1080
ttcggcagca gggggggaact tgccgagcgc agcggccata tcggattggg aaaaatacaa  1140
agccatcagt tgggcaacct gatgattcaa caggcggcca ttaaaggaaa tatcggctac  1200
attgtccgct tttccgatca cgggcacgaa gtccattccc ccttcgacaa ccatgcctca  1260
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tgggacggat acgaacacca tcccgccgac ggctatgacg ggccacaggg cggcggctat  1380
cccgctccca aaggcgcgag ggatatatac agctacgaca taaaaggcgt tgcccaaaat  1440
atccgcctca acctgaccga caaccgcagc accggacaac ggcttgccga ccgtttccac  1500
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[2136]

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agcccccgagc tggacagatc gggcaatgcc gccgaagcct tcaacggcac tgcagatatc 1620
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acctcctcaa ccgtgccgcc gtcaaacggc aaaaatgtca aactggcaga ccaacgccac 2160
ccgaagacag gcgtaccgtt tgacggtaaa gggtttccga attttgagaa gcacgtgaaa 2220
tatgatacgc tcgagcacca ccaccaccac cactga 2256

[2137] <210>48

[2138] <211>751

[2139] <212>PRT

[2140] <213> 人工序列

[2141] <220>

[2142] <223>961c-ORF46.1

[2143] <400>48

[2144]

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Ala Ala Ala Tyr Asn Asn Gly Gln Glu Ile Asn Gly Phe Lys Ala Gly
20 25 30
Glu Thr Ile Tyr Asp Ile Asp Glu Asp Gly Thr Ile Thr Lys Lys Asp
35 40 45
Ala Thr Ala Ala Asp Val Glu Ala Asp Asp Phe Lys Gly Leu Gly Leu
50 55 60
Lys Lys Val Val Thr Asn Leu Thr Lys Thr Val Asn Glu Asn Lys Gln
65 70 75 80
Asn Val Asp Ala Lys Val Lys Ala Ala Glu Ser Glu Ile Glu Lys Leu
85 90 95
Thr Thr Lys Leu Ala Asp Thr Asp Ala Ala Leu Ala Asp Thr Asp Ala
100 105 110
Ala Leu Asp Ala Thr Thr Asn Ala Leu Asn Lys Leu Gly Glu Asn Ile
115 120 125
Thr Thr Phe Ala Glu Glu Thr Lys Thr Asn Ile Val Lys Ile Asp Glu
130 135 140
Lys Leu Glu Ala Val Ala Asp Thr Val Asp Lys His Ala Glu Ala Phe
145 150 155 160
Asn Asp Ile Ala Asp Ser Leu Asp Glu Thr Asn Thr Lys Ala Asp Glu
165 170 175
Ala Val Lys Thr Ala Asn Glu Ala Lys Gln Thr Ala Glu Glu Thr Lys
180 185 190
Gln Asn Val Asp Ala Lys Val Lys Ala Ala Glu Thr Ala Ala Gly Lys
195 200 205
Ala Glu Ala Ala Ala Gly Thr Ala Asn Thr Ala Ala Asp Lys Ala Glu
210 215 220
Ala Val Ala Ala Lys Val Thr Asp Ile Lys Ala Asp Ile Ala Thr Asn

[2145]

225 230 235 240
Lys Asp Asn Ile Ala Lys Lys Ala Asn Ser Ala Asp Val Tyr Thr Arg
245 250 255
Glu Glu Ser Asp Ser Lys Phe Val Arg Ile Asp Gly Leu Asn Ala Thr
260 265 270
Thr Glu Lys Leu Asp Thr Arg Leu Ala Ser Ala Glu Lys Ser Ile Ala
275 280 285
Asp His Asp Thr Arg Leu Asn Gly Leu Asp Lys Thr Val Ser Asp Leu
290 295 300
Arg Lys Glu Thr Arg Gln Gly Leu Ala Glu Gln Ala Ala Leu Ser Gly
305 310 315 320
Leu Phe Gln Pro Tyr Asn Val Gly Gly Ser Gly Gly Gly Gly Ser Asp
325 330 335
Leu Ala Asn Asp Ser Phe Ile Arg Gln Val Leu Asp Arg Gln His Phe
340 345 350
Glu Pro Asp Gly Lys Tyr His Leu Phe Gly Ser Arg Gly Glu Leu Ala
355 360 365
Glu Arg Ser Gly His Ile Gly Leu Gly Lys Ile Gln Ser His Gln Leu
370 375 380
Gly Asn Leu Met Ile Gln Gln Ala Ala Ile Lys Gly Asn Ile Gly Tyr
385 390 395 400
Ile Val Arg Phe Ser Asp His Gly His Glu Val His Ser Pro Phe Asp
405 410 415
Asn His Ala Ser His Ser Asp Ser Asp Glu Ala Gly Ser Pro Val Asp
420 425 430
Gly Phe Ser Leu Tyr Arg Ile His Trp Asp Gly Tyr Glu His His Pro
435 440 445
Ala Asp Gly Tyr Asp Gly Pro Gln Gly Gly Gly Tyr Pro Ala Pro Lys
450 455 460
Gly Ala Arg Asp Ile Tyr Ser Tyr Asp Ile Lys Gly Val Ala Gln Asn
465 470 475 480
Ile Arg Leu Asn Leu Thr Asp Asn Arg Ser Thr Gly Gln Arg Leu Ala
485 490 495
Asp Arg Phe His Asn Ala Gly Ser Met Leu Thr Gln Gly Val Gly Asp
500 505 510
Gly Phe Lys Arg Ala Thr Arg Tyr Ser Pro Glu Leu Asp Arg Ser Gly
515 520 525
Asn Ala Ala Glu Ala Phe Asn Gly Thr Ala Asp Ile Val Lys Asn Ile
530 535 540
Ile Gly Ala Ala Gly Glu Ile Val Gly Ala Gly Asp Ala Val Gln Gly
545 550 555 560
Ile Ser Glu Gly Ser Asn Ile Ala Val Met His Gly Leu Gly Leu Leu
565 570 575
Ser Thr Glu Asn Lys Met Ala Arg Ile Asn Asp Leu Ala Asp Met Ala
580 585 590
Gln Leu Lys Asp Tyr Ala Ala Ala Ala Ile Arg Asp Trp Ala Val Gln
595 600 605
Asn Pro Asn Ala Ala Gln Gly Ile Glu Ala Val Ser Asn Ile Phe Met
610 615 620
Ala Ala Ile Pro Ile Lys Gly Ile Gly Ala Val Arg Gly Lys Tyr Gly
625 630 635 640
Leu Gly Gly Ile Thr Ala His Pro Ile Lys Arg Ser Gln Met Gly Ala

[2146]

645 650 655
Ile Ala Leu Pro Lys Gly Lys Ser Ala Val Ser Asp Asn Phe Ala Asp
660 665 670
Ala Ala Tyr Ala Lys Tyr Pro Ser Pro Tyr His Ser Arg Asn Ile Arg
675 680 685
Ser Asn Leu Glu Gln Arg Tyr Gly Lys Glu Asn Ile Thr Ser Ser Thr
690 695 700
Val Pro Pro Ser Asn Gly Lys Asn Val Lys Leu Ala Asp Gln Arg His
705 710 715 720
Pro Lys Thr Gly Val Pro Phe Asp Gly Lys Gly Phe Pro Asn Phe Glu
725 730 735
Lys His Val Lys Tyr Asp Thr Leu Glu His His His His His His
740 745 750

[2147] <210>49

[2148] <211>1773

[2149] <212>DNA

[2150] <213> 人工序列

[2151] <220>

[2152] <223>961c-741

[2153] <400>49

[2154]

atggccacaa acgacgacga tgttaaaaaa gctgccactg tggccattgc tgctgcctac 60
aacaatggcc aagaaatcaa cggtttcaaa gctggagaga ccatctacga cattgatgaa 120
gacggcacaa ttaccaaaaa agacgcaact gcagccgatg ttgaagccga cgactttaaa 180
ggtctgggtc tgaaaaaagt cgtgactaac ctgaccaaaa ccgtcaatga aaacaaacaa 240
aacgtcgatg ccaaagtaaa agctgcagaa tctgaaatag aaaagttaac aaccaagtta 300
gcagacactg atgccgcttt agcagatact gatgccgctc tggatgcaac caccaacgcc 360
ttgaataaat tgggagaaaa tataacgaca tttgctgaag agactaagac aaatatcgta 420
aaaattgatg aaaaattaga agccgtggct gataccgtcg acaagcatgc cgaagcattc 480
aacgatatcg ccgattcatt ggatgaaacc aacactaagg cagacgaagc cgtcaaaacc 540
gccaatgaag ccaaacagac ggccgaagaa accaaacaaa acgtcgatgc caaagtaaaa 600
gctgcagaaa ctgcagcagg caaagccgaa gctgccgctg gcacagctaa tactgcagcc 660
gacaaggccg aagctgtcgc tgcaaaagtt accgacatca aagctgatat cgctacgaac 720
aaagataata ttgctaaaaa agcaaacagt gccgacgtgt acaccagaga agagtctgac 780
agcaaatttg tcagaattga tggtctgaac gctactaccg aaaaattgga cacacgcttg 840
gcttctgctg aaaaatccat tgccgatcac gatactcgcc tgaacggttt ggataaaaca 900
gtgtcagacc tgcgcaaaga aacccgccaa ggccttgcag aacaagccgc gctctccggt 960
ctgttccaac cttacaacgt gggtggatcc ggaggggtg gtgtcgccgc cgacatcggt 1020
gcggggcttg ccgatgcact aaccgcaccg ctcgaccata aagacaaagg tttgcagtct 1080
ttgacgctgg atcagtccgt caggaaaaac gagaaactga agctggcggc acaaggtgcg 1140
gaaaaaactt atggaaacgg tgacagcctc aatacgggca aattgaagaa cgacaaggtc 1200
agccgtttcg actttatccg ccaaatcgaa gtggacgggc agctcattac cttggagagt 1260
ggagagttcc aagtatacaa acaaagccat tccgccttaa ccgcctttca gaccgagcaa 1320
atacaagatt cggagcattc cgggaagatg gttgcgaaac gccagttcag aatcggcgac 1380
atagcgggcg aacatacatc ttttgacaag cttcccgaag gcggcagggc gacatatcgc 1440
gggacggcgt tcggttcaga cgatgccggc ggaaaactga cctacaccat agatttcgcc 1500
gccaagcagg gaaacggcaa aatcgaacat ttgaaatcgc cagaactcaa tgtcgacctg 1560
gccgccgccg atatcaagcc ggatggaaaa cgccatgccg tcatcagcgg ttccgtcctt 1620
tacaaccaag ccgagaaagg cagttactcc ctcggtatct ttggcggaaa agcccaggaa 1680
[2155] gttgccggca gcgcggaagt gaaaaccgta aacggcatac gccatatcgg ccttgccgcc 1740
aagcaactcg agcaccacca ccaccaccac tga 1773

[2156] <210>50

[2157] <211>590

[2158] <212>PRT

[2159] <213>人工序列

[2160] <220>

[2161] <223>961c-741

[2162] <400>50

[2163]

Met Ala Thr Asn Asp Asp Asp Val Lys Lys Ala Ala Thr Val Ala Ile
1 5 10 15
Ala Ala Ala Tyr Asn Asn Gly Gln Glu Ile Asn Gly Phe Lys Ala Gly
20 25 30
Glu Thr Ile Tyr Asp Ile Asp Glu Asp Gly Thr Ile Thr Lys Lys Asp
35 40 45
Ala Thr Ala Ala Asp Val Glu Ala Asp Asp Phe Lys Gly Leu Gly Leu
50 55 60
Lys Lys Val Val Thr Asn Leu Thr Lys Thr Val Asn Glu Asn Lys Gln
65 70 75 80
Asn Val Asp Ala Lys Val Lys Ala Ala Glu Ser Glu Ile Glu Lys Leu
85 90 95
Thr Thr Lys Leu Ala Asp Thr Asp Ala Ala Leu Ala Asp Thr Asp Ala
100 105 110
Ala Leu Asp Ala Thr Thr Asn Ala Leu Asn Lys Leu Gly Glu Asn Ile
115 120 125
Thr Thr Phe Ala Glu Glu Thr Lys Thr Asn Ile Val Lys Ile Asp Glu
130 135 140
Lys Leu Glu Ala Val Ala Asp Thr Val Asp Lys His Ala Glu Ala Phe
145 150 155 160
Asn Asp Ile Ala Asp Ser Leu Asp Glu Thr Asn Thr Lys Ala Asp Glu
165 170 175
Ala Val Lys Thr Ala Asn Glu Ala Lys Gln Thr Ala Glu Glu Thr Lys
180 185 190
Gln Asn Val Asp Ala Lys Val Lys Ala Ala Glu Thr Ala Ala Gly Lys
195 200 205
Ala Glu Ala Ala Ala Gly Thr Ala Asn Thr Ala Ala Asp Lys Ala Glu
210 215 220
Ala Val Ala Ala Lys Val Thr Asp Ile Lys Ala Asp Ile Ala Thr Asn
225 230 235 240
Lys Asp Asn Ile Ala Lys Lys Ala Asn Ser Ala Asp Val Tyr Thr Arg
245 250 255
Glu Glu Ser Asp Ser Lys Phe Val Arg Ile Asp Gly Leu Asn Ala Thr
260 265 270
Thr Glu Lys Leu Asp Thr Arg Leu Ala Ser Ala Glu Lys Ser Ile Ala
275 280 285
Asp His Asp Thr Arg Leu Asn Gly Leu Asp Lys Thr Val Ser Asp Leu
290 295 300
Arg Lys Glu Thr Arg Gln Gly Leu Ala Glu Gln Ala Ala Leu Ser Gly
305 310 315 320
Leu Phe Gln Pro Tyr Asn Val Gly Gly Ser Gly Gly Gly Gly Val Ala

[2164]

```
                325                 330                 335
Ala Asp Ile Gly Ala Gly Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp
            340                 345                 350
His Lys Asp Lys Gly Leu Gln Ser Leu Thr Leu Asp Gln Ser Val Arg
        355                 360                 365
Lys Asn Glu Lys Leu Lys Leu Ala Ala Gln Gly Ala Glu Lys Thr Tyr
    370                 375                 380
Gly Asn Gly Asp Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp Lys Val
385                 390                 395                 400
Ser Arg Phe Asp Phe Ile Arg Gln Ile Glu Val Asp Gly Gln Leu Ile
                405                 410                 415
Thr Leu Glu Ser Gly Glu Phe Gln Val Tyr Lys Gln Ser His Ser Ala
            420                 425                 430
Leu Thr Ala Phe Gln Thr Glu Gln Ile Gln Asp Ser Glu His Ser Gly
        435                 440                 445
Lys Met Val Ala Lys Arg Gln Phe Arg Ile Gly Asp Ile Ala Gly Glu
    450                 455                 460
His Thr Ser Phe Asp Lys Leu Pro Glu Gly Gly Arg Ala Thr Tyr Arg
465                 470                 475                 480
Gly Thr Ala Phe Gly Ser Asp Asp Ala Gly Gly Lys Leu Thr Tyr Thr
                485                 490                 495
Ile Asp Phe Ala Ala Lys Gln Gly Asn Gly Lys Ile Glu His Leu Lys
            500                 505                 510
Ser Pro Glu Leu Asn Val Asp Leu Ala Ala Ala Asp Ile Lys Pro Asp
        515                 520                 525
Gly Lys Arg His Ala Val Ile Ser Gly Ser Val Leu Tyr Asn Gln Ala
    530                 535                 540
Glu Lys Gly Ser Tyr Ser Leu Gly Ile Phe Gly Gly Lys Ala Gln Glu
545                 550                 555                 560
Val Ala Gly Ser Ala Glu Val Lys Thr Val Asn Gly Ile Arg His Ile
                565                 570                 575
Gly Leu Ala Ala Lys Gln Leu Glu His His His His His His
            580                 585                 590
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[2165] <210>51

[2166] <211>4170

[2167] <212>DNA

[2168] <213> 人工序列

[2169] <220>

[2170] <223>961c-983

[2171] <400>51

[2172]

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atggccacaa acgacgacga tgttaaaaaa gctgccactg tggccattgc tgctgcctac   60
aacaatggcc aagaaatcaa cggtttcaaa gctggagaga ccatctacga cattgatgaa  120
gacggcacaa ttaccaaaaa agacgcaact gcagccgatg ttgaagccga cgactttaaa  180
ggtctgggtc tgaaaaaagt cgtgactaac ctgaccaaaa ccgtcaatga aaacaaacaa  240
aacgtcgatg ccaaagtaaa agctgcagaa tctgaaatag aaaagttaac aaccaagtta  300
gcagacactg atgccgcttt agcagatact gatgccgctc tggatgcaac caccaacgcc  360
ttgaataaat tgggagaaaa tataacgaca tttgctgaag agactaagac aaatatcgta  420
aaaattgatg aaaaattaga agccgtggct gataccgtcg acaagcatgc cgaagcattc  480
aacgatatcg ccgattcatt ggatgaaacc aacactaagg cagacgaagc cgtcaaaacc  540
```

[2173]

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gccaatgaag ccaaacagac ggccgaagaa accaaacaaa acgtcgatgc caaagtaaaa    600
gctgcagaaa ctgcagcagg caaagccgaa gctgccgctg gcacagctaa tactgcagcc    660
gacaaggccg aagctgtcgc tgcaaaagtt accgacatca aagctgatat cgctacgaac    720
aaagataata ttgctaaaaa agcaaacagt gccgacgtgt acaccagaga agagtctgac    780
agcaaatttg tcagaattga tggtctgaac gctactaccg aaaaattgga cacacgcttg    840
gcttctgctg aaaaatccat tgccgatcac gatactcgcc tgaacggttt ggataaaaca    900
gtgtcagacc tgcgcaaaga aacccgccaa ggccttgcag aacaagccgc gctctccggt    960
ctgttccaac cttacaacgt gggtggatcc ggcggaggcg gcacttctgc gcccgacttc   1020
aatgcaggcg gtaccggtat cggcagcaac agcagagcaa caacagcgaa atcagcagca   1080
gtatcttacg ccggtatcaa gaacgaaatg tgcaaagaca gaagcatgct ctgtgccggt   1140
cgggatgacg ttgcggttac agacagggat gccaaaatca atgccccccc cccgaatctg   1200
cataccggag actttccaaa cccaaatgac gcatacaaga atttgatcaa cctcaaacct   1260
gcaattgaag caggctatac aggacgcggg gtagaggtag gtatcgtcga cacaggcgaa   1320
tccgtcggca gcatatcctt tcccgaactg tatggcagaa aagaacacgg ctataacgaa   1380
aattacaaaa actatacggc gtatatgcgg aaggaagcgc ctgaagacgg aggcggtaaa   1440
gacattgaag cttctttcga cgatgaggcc gttatagaga ctgaagcaaa gccgacggat   1500
atccgccacg taaaagaaat cggacacatc gatttggtct cccatattat tggcgggcgt   1560
tccgtggacg gcagacctgc aggcggtatt gcgcccgatg cgacgctaca cataatgaat   1620
acgaatgatg aaaccaagaa cgaaatgatg gttgcagcca tccgcaatgc atgggtcaag   1680
ctgggcgaac gtggcgtgcg catcgtcaat aacagttttg gaacaacatc gagggcaggc   1740
actgccgacc ttttccaaat agccaattcg gaggagcagt accgccaagc gttgctcgac   1800
tattccggcg gtgataaaac agacgagggt atccgcctga tgcaacagag cgattacggc   1860
aacctgtcct accacatccg taataaaaac atgcttttca tcttttcgac aggcaatgac   1920
gcacaagctc agcccaacac atatgcccta ttgccatttt atgaaaaaga cgctcaaaaa   1980
ggcattatca cagtcgcagg cgtagaccgc agtggagaaa agttcaaacg ggaaatgtat   2040
ggagaaccgg gtacagaacc gcttgagtat ggctccaacc attgcggaat tactgccatg   2100
tggtgcctgt cggcacccta tgaagcaagc gtccgtttca cccgtacaaa cccgattcaa   2160
attgccggaa catccttttc cgcacccatc gtaaccggca cggcggctct gctgctgcag   2220
aaatacccgt ggatgagcaa cgacaacctg cgtaccacgt tgctgacgac ggctcaggac   2280
atcggtgcag tcggcgtgga cagcaagttc ggctggggac tgctggatgc gggtaaggcc   2340
atgaacggac ccgcgtcctt tccgttcggc gactttaccg ccgatacgaa aggtacatcc   2400
gatattgcct actccttccg taacgacatt tcaggcacgg gcggcctgat caaaaaaggc   2460
ggcagccaac tgcaactgca cggcaacaac acctatacgg gcaaaaccat tatcgaaggc   2520
ggttcgctgg tgttgtacgg caacaacaaa tcggatatgc gcgtcgaaac caaaggtgcg   2580
ctgatttata acggggcggc atccggcggc agcctgaaca gcgacggcat tgtctatctg   2640
gcagataccg accaatccgg cgcaaacgaa accgtacaca tcaaaggcag tctgcagctg   2700
gacggcaaag gtacgctgta cacacgtttg ggcaaactgc tgaaagtgga cggtacggcg   2760
attatcggcg gcaagctgta catgtcggca cgcggcaagg gggcaggcta tctcaacagt   2820
accggacgac gtgttccctt cctgagtgcc gccaaaatcg ggcaggatta ttctttcttc   2880
acaaacatcg aaaccgacgg cggcctgctg gcttccctcg acagcgtcga aaaaacagcg   2940
ggcagtgaag gcgacacgct gtcctattat gtccgtcgcg gcaatgcggc acggactgct   3000
tcggcagcgg cacattccgc gcccgccggt ctgaaacacg ccgtagaaca gggcggcagc   3060
aatctggaaa acctgatggt cgaactggat gcctccgaat catccgcaac acccgagacg   3120
gttgaaactg cggcagccga ccgcacagat atgccgggca tccgccccta cggcgcaact   3180
ttccgcgcag cggcagccgt acagcatgcg aatgccgccg acggtgtacg catcttcaac   3240
agtctcgccg ctaccgtcta tgccgacagt accgccgccc atgccgatat gcagggacgc   3300
cgcctgaaag ccgtatcgga cgggttggac cacaacggca cgggtctgcg cgtcatcgcg   3360
caaacccaac aggacggtgg aacgtgggaa cagggcggtg ttgaaggcaa aatgcgcggc   3420
agtacccaaa ccgtcggcat tgccgcgaaa accggcgaaa atacgacagc agccgccaca   3480
ctgggcatgg gacgcagcac atggagcgaa aacagtgcaa atgcaaaaac cgacagcatt   3540
agtctgtttg caggcatacg gcacgatgcg ggcgatatcg gctatctcaa aggcctgttc   3600
tcctacggac gctacaaaaa cagcatcagc cgcagcaccg gtgcggacga acatgcggaa   3660
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[2174]

ggcagcgtca acggcacgct gatgcagctg ggcgcactgg gcggtgtcaa cgttccgttt 3720
gccgcaacgg gagatttgac ggtcgaaggc ggtctgcgct acgacctgct caaacaggat 3780
gcattcgccg aaaaaggcag tgctttgggc tggagcggca acagcctcac tgaaggcacg 3840
ctggtcggac tcgcgggtct gaagctgtcg caacccttga gcgataaagc cgtcctgttt 3900
gcaacggcgg gcgtggaacg cgacctgaac ggacgcgact acacggtaac gggcggcttt 3960
accggcgcga ctgcagcaac cggcaagacg ggggcacgca atatgccgca cacccgtctg 4020
gttgccggcc tgggcgcgga tgtcgaattc ggcaacggct ggaacggctt ggcacgttac 4080
agctacgccg gttccaaaca gtacggcaac cacagcggac gagtcggcgt aggctaccgg 4140
ttcctcgagc accaccacca ccaccactga 4170

[2175] <210>52

[2176] <211>1389

[2177] <212>PRT

[2178] <213> 人工序列

[2179] <220>

[2180] <223>961c-983

[2181] <400>52

[2182]

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Met Ala Thr Asn Asp Asp Asp Val Lys Lys Ala Ala Thr Val Ala Ile
1               5                   10                  15
Ala Ala Ala Tyr Asn Asn Gly Gln Glu Ile Asn Gly Phe Lys Ala Gly
            20                  25                  30
Glu Thr Ile Tyr Asp Ile Asp Glu Asp Gly Thr Ile Thr Lys Lys Asp
        35                  40                  45
Ala Thr Ala Ala Asp Val Glu Ala Asp Asp Phe Lys Gly Leu Gly Leu
    50                  55                  60
Lys Lys Val Val Thr Asn Leu Thr Lys Thr Val Asn Glu Asn Lys Gln
65                  70                  75                  80
Asn Val Asp Ala Lys Val Lys Ala Ala Glu Ser Glu Ile Glu Lys Leu
                85                  90                  95
Thr Thr Lys Leu Ala Asp Thr Asp Ala Ala Leu Ala Asp Thr Asp Ala
            100                 105                 110
Ala Leu Asp Ala Thr Thr Asn Ala Leu Asn Lys Leu Gly Glu Asn Ile
        115                 120                 125
Thr Thr Phe Ala Glu Glu Thr Lys Thr Asn Ile Val Lys Ile Asp Glu
    130                 135                 140
Lys Leu Glu Ala Val Ala Asp Thr Val Asp Lys His Ala Glu Ala Phe
145                 150                 155                 160
Asn Asp Ile Ala Asp Ser Leu Asp Glu Thr Asn Thr Lys Ala Asp Glu
                165                 170                 175
Ala Val Lys Thr Ala Asn Glu Ala Lys Gln Thr Ala Glu Glu Thr Lys
            180                 185                 190
Gln Asn Val Asp Ala Lys Val Lys Ala Ala Glu Thr Ala Ala Gly Lys
        195                 200                 205
Ala Glu Ala Ala Ala Gly Thr Ala Asn Thr Ala Ala Asp Lys Ala Glu
    210                 215                 220
Ala Val Ala Ala Lys Val Thr Asp Ile Lys Ala Asp Ile Ala Thr Asn
225                 230                 235                 240
Lys Asp Asn Ile Ala Lys Lys Ala Asn Ser Ala Asp Val Tyr Thr Arg
                245                 250                 255
Glu Glu Ser Asp Ser Lys Phe Val Arg Ile Asp Gly Leu Asn Ala Thr
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[2183]

260 265 270
Thr Glu Lys Leu Asp Thr Arg Leu Ala Ser Ala Glu Lys Ser Ile Ala
275 280 285
Asp His Asp Thr Arg Leu Asn Gly Leu Asp Lys Thr Val Ser Asp Leu
290 295 300
Arg Lys Glu Thr Arg Gln Gly Leu Ala Glu Gln Ala Ala Leu Ser Gly
305 310 315 320
Leu Phe Gln Pro Tyr Asn Val Gly Gly Ser Gly Gly Gly Gly Thr Ser
325 330 335
Ala Pro Asp Phe Asn Ala Gly Gly Thr Gly Ile Gly Ser Asn Ser Arg
340 345 350
Ala Thr Thr Ala Lys Ser Ala Ala Val Ser Tyr Ala Gly Ile Lys Asn
355 360 365

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

[2184]

```
Glu Lys Phe Lys Arg Glu Met Tyr Gly Glu Pro Gly Thr Glu Pro Leu
        675                 680                 685
Glu Tyr Gly Ser Asn His Cys Gly Ile Thr Ala Met Trp Cys Leu Ser
    690                 695                 700
Ala Pro Tyr Glu Ala Ser Val Arg Phe Thr Arg Thr Asn Pro Ile Gln
705                 710                 715                 720
Ile Ala Gly Thr Ser Phe Ser Ala Pro Ile Val Thr Gly Thr Ala Ala
                725                 730                 735
Leu Leu Leu Gln Lys Tyr Pro Trp Met Ser Asn Asp Asn Leu Arg Thr
            740                 745                 750
Thr Leu Leu Thr Thr Ala Gln Asp Ile Gly Ala Val Gly Val Asp Ser
        755                 760                 765
Lys Phe Gly Trp Gly Leu Leu Asp Ala Gly Lys Ala Met Asn Gly Pro
    770                 775                 780
Ala Ser Phe Pro Phe Gly Asp Phe Thr Ala Asp Thr Lys Gly Thr Ser
785                 790                 795                 800
Asp Ile Ala Tyr Ser Phe Arg Asn Asp Ile Ser Gly Thr Gly Gly Leu
                805                 810                 815
Ile Lys Lys Gly Gly Ser Gln Leu Gln Leu His Gly Asn Asn Thr Tyr
            820                 825                 830
Thr Gly Lys Thr Ile Ile Glu Gly Gly Ser Leu Val Leu Tyr Gly Asn
        835                 840                 845
Asn Lys Ser Asp Met Arg Val Glu Thr Lys Gly Ala Leu Ile Tyr Asn
    850                 855                 860
Gly Ala Ala Ser Gly Gly Ser Leu Asn Ser Asp Gly Ile Val Tyr Leu
865                 870                 875                 880
Ala Asp Thr Asp Gln Ser Gly Ala Asn Glu Thr Val His Ile Lys Gly
                885                 890                 895
Ser Leu Gln Leu Asp Gly Lys Gly Thr Leu Tyr Thr Arg Leu Gly Lys
            900                 905                 910
Leu Leu Lys Val Asp Gly Thr Ala Ile Ile Gly Gly Lys Leu Tyr Met
        915                 920                 925
Ser Ala Arg Gly Lys Gly Ala Gly Tyr Leu Asn Ser Thr Gly Arg Arg
    930                 935                 940
Val Pro Phe Leu Ser Ala Ala Lys Ile Gly Gln Asp Tyr Ser Phe Phe
945                 950                 955                 960
Thr Asn Ile Glu Thr Asp Gly Gly Leu Leu Ala Ser Leu Asp Ser Val
                965                 970                 975
Glu Lys Thr Ala Gly Ser Glu Gly Asp Thr Leu Ser Tyr Tyr Val Arg
            980                 985                 990
Arg Gly Asn Ala Ala Arg Thr Ala Ser Ala Ala Ala His Ser Ala Pro
        995                 1000                1005
Ala Gly Leu Lys His Ala Val Glu Gln Gly Gly Ser Asn Leu Glu Asn
    1010                1015                1020
Leu Met Val Glu Leu Asp Ala Ser Glu Ser Ser Ala Thr Pro Glu Thr
1025                1030                1035                1040
Val Glu Thr Ala Ala Ala Asp Arg Thr Asp Met Pro Gly Ile Arg Pro
                1045                1050                1055
Tyr Gly Ala Thr Phe Arg Ala Ala Ala Ala Val Gln His Ala Asn Ala
            1060                1065                1070
Ala Asp Gly Val Arg Ile Phe Asn Ser Leu Ala Ala Thr Val Tyr Ala
        1075                1080                1085
```

[2185]

Asp Ser Thr Ala Ala His Ala Asp Met Gln Gly Arg Arg Leu Lys Ala
    1090   1095   1100
Val Ser Asp Gly Leu Asp His Asn Gly Thr Gly Leu Arg Val Ile Ala
1105   1110   1115   1120
Gln Thr Gln Gln Asp Gly Gly Thr Trp Glu Gln Gly Gly Val Glu Gly
                1125   1130   1135
Lys Met Arg Gly Ser Thr Gln Thr Val Gly Ile Ala Ala Lys Thr Gly
            1140   1145   1150
Glu Asn Thr Thr Ala Ala Ala Thr Leu Gly Met Gly Arg Ser Thr Trp
        1155   1160   1165
Ser Glu Asn Ser Ala Asn Ala Lys Thr Asp Ser Ile Ser Leu Phe Ala
    1170   1175   1180
Gly Ile Arg His Asp Ala Gly Asp Ile Gly Tyr Leu Lys Gly Leu Phe
1185   1190   1195   1200
Ser Tyr Gly Arg Tyr Lys Asn Ser Ile Ser Arg Ser Thr Gly Ala Asp
                1205   1210   1215
Glu His Ala Glu Gly Ser Val Asn Gly Thr Leu Met Gln Leu Gly Ala
            1220   1225   1230
Leu Gly Gly Val Asn Val Pro Phe Ala Ala Thr Gly Asp Leu Thr Val
        1235   1240   1245
Glu Gly Gly Leu Arg Tyr Asp Leu Leu Lys Gln Asp Ala Phe Ala Glu
    1250   1255   1260
Lys Gly Ser Ala Leu Gly Trp Ser Gly Asn Ser Leu Thr Glu Gly Thr
1265   1270   1275   1280
Leu Val Gly Leu Ala Gly Leu Lys Leu Ser Gln Pro Leu Ser Asp Lys
                1285   1290   1295
Ala Val Leu Phe Ala Thr Ala Gly Val Glu Arg Asp Leu Asn Gly Arg
            1300   1305   1310
Asp Tyr Thr Val Thr Gly Gly Phe Thr Gly Ala Thr Ala Ala Thr Gly
        1315   1320   1325
Lys Thr Gly Ala Arg Asn Met Pro His Thr Arg Leu Val Ala Gly Leu
    1330   1335   1340
Gly Ala Asp Val Glu Phe Gly Asn Gly Trp Asn Gly Leu Ala Arg Tyr
1345   1350   1355   1360
Ser Tyr Ala Gly Ser Lys Gln Tyr Gly Asn His Ser Gly Arg Val Gly
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Val Gly Tyr Arg Phe Leu Glu His His His His His His
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[2186] <210>53

[2187] <211>2304

[2188] <212>DNA

[2189] <213>人工序列

[2190] <220>

[2191] <223>961cL-ORF46.1

[2192] <400>53

[2193]

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aaacaaaacg tcgatgccaa agtaaaagct gcagaatctg aaatagaaaa gttaacaacc 360
aagttagcag acactgatgc cgctttagca gatactgatg ccgctctgga tgcaaccacc 420
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[2195] <210>54

[2196] <211>765

[2197] <212>PRT

[2198] <213> 人工序列

[2199] <220>

[2200] <223>961cL-ORF46.1

[2201] <400>54

[2202]

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

[2203]

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    50                  55                  60
Thr Ile Thr Lys Lys Asp Ala Thr Ala Ala Asp Val Glu Ala Asp Asp
65                  70                  75                  80
Phe Lys Gly Leu Gly Leu Lys Lys Val Val Thr Asn Leu Thr Lys Thr
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Val Asn Glu Asn Lys Gln Asn Val Asp Ala Lys Val Lys Ala Ala Glu
            100                 105                 110
Ser Glu Ile Glu Lys Leu Thr Thr Lys Leu Ala Asp Thr Asp Ala Ala
        115                 120                 125
Leu Ala Asp Thr Asp Ala Ala Leu Asp Ala Thr Thr Asn Ala Leu Asn
    130                 135                 140
Lys Leu Gly Glu Asn Ile Thr Thr Phe Ala Glu Glu Thr Lys Thr Asn
145                 150                 155                 160
Ile Val Lys Ile Asp Glu Lys Leu Glu Ala Val Ala Asp Thr Val Asp
                165                 170                 175
Lys His Ala Glu Ala Phe Asn Asp Ile Ala Asp Ser Leu Asp Glu Thr
            180                 185                 190
Asn Thr Lys Ala Asp Glu Ala Val Lys Thr Ala Asn Glu Ala Lys Gln
        195                 200                 205
Thr Ala Glu Glu Thr Lys Gln Asn Val Asp Ala Lys Val Lys Ala Ala
    210                 215                 220
Glu Thr Ala Ala Gly Lys Ala Glu Ala Ala Ala Gly Thr Ala Asn Thr
225                 230                 235                 240
Ala Ala Asp Lys Ala Glu Ala Val Ala Ala Lys Val Thr Asp Ile Lys
                245                 250                 255
Ala Asp Ile Ala Thr Asn Lys Asp Asn Ile Ala Lys Lys Ala Asn Ser
            260                 265                 270
Ala Asp Val Tyr Thr Arg Glu Glu Ser Asp Ser Lys Phe Val Arg Ile
        275                 280                 285
Asp Gly Leu Asn Ala Thr Thr Glu Lys Leu Asp Thr Arg Leu Ala Ser
    290                 295                 300
Ala Glu Lys Ser Ile Ala Asp His Asp Thr Arg Leu Asn Gly Leu Asp
305                 310                 315                 320
Lys Thr Val Ser Asp Leu Arg Lys Glu Thr Arg Gln Gly Leu Ala Glu
                325                 330                 335
Gln Ala Ala Leu Ser Gly Leu Phe Gln Pro Tyr Asn Val Gly Gly Ser
            340                 345                 350
Gly Gly Gly Gly Ser Asp Leu Ala Asn Asp Ser Phe Ile Arg Gln Val
        355                 360                 365
Leu Asp Arg Gln His Phe Glu Pro Asp Gly Lys Tyr His Leu Phe Gly
    370                 375                 380
Ser Arg Gly Glu Leu Ala Glu Arg Ser Gly His Ile Gly Leu Gly Lys
385                 390                 395                 400
Ile Gln Ser His Gln Leu Gly Asn Leu Met Ile Gln Gln Ala Ala Ile
                405                 410                 415
Lys Gly Asn Ile Gly Tyr Ile Val Arg Phe Ser Asp His Gly His Glu
            420                 425                 430
Val His Ser Pro Phe Asp Asn His Ala Ser His Ser Asp Ser Asp Glu
        435                 440                 445
Ala Gly Ser Pro Val Asp Gly Phe Ser Leu Tyr Arg Ile His Trp Asp
    450                 455                 460
Gly Tyr Glu His His Pro Ala Asp Gly Tyr Asp Gly Pro Gln Gly Gly
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[2204]

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465                 470                 475                 480
Gly Tyr Pro Ala Pro Lys Gly Ala Arg Asp Ile Tyr Ser Tyr Asp Ile
                485                 490                 495
Lys Gly Val Ala Gln Asn Ile Arg Leu Asn Leu Thr Asp Asn Arg Ser
            500                 505                 510
Thr Gly Gln Arg Leu Ala Asp Arg Phe His Asn Ala Gly Ser Met Leu
        515                 520                 525
Thr Gln Gly Val Gly Asp Gly Phe Lys Arg Ala Thr Arg Tyr Ser Pro
    530                 535                 540
Glu Leu Asp Arg Ser Gly Asn Ala Ala Glu Ala Phe Asn Gly Thr Ala
545                 550                 555                 560
Asp Ile Val Lys Asn Ile Ile Gly Ala Ala Gly Glu Ile Val Gly Ala
                565                 570                 575
Gly Asp Ala Val Gln Gly Ile Ser Glu Gly Ser Asn Ile Ala Val Met
            580                 585                 590
His Gly Leu Gly Leu Leu Ser Thr Glu Asn Lys Met Ala Arg Ile Asn
        595                 600                 605
Asp Leu Ala Asp Met Ala Gln Leu Lys Asp Tyr Ala Ala Ala Ala Ile
    610                 615                 620
Arg Asp Trp Ala Val Gln Asn Pro Asn Ala Ala Gln Gly Ile Glu Ala
625                 630                 635                 640
Val Ser Asn Ile Phe Met Ala Ala Ile Pro Ile Lys Gly Ile Gly Ala
                645                 650                 655
Val Arg Gly Lys Tyr Gly Leu Gly Gly Ile Thr Ala His Pro Ile Lys
            660                 665                 670
Arg Ser Gln Met Gly Ala Ile Ala Leu Pro Lys Gly Lys Ser Ala Val
        675                 680                 685
Ser Asp Asn Phe Ala Asp Ala Ala Tyr Ala Lys Tyr Pro Ser Pro Tyr
    690                 695                 700
His Ser Arg Asn Ile Arg Ser Asn Leu Glu Gln Arg Tyr Gly Lys Glu
705                 710                 715                 720
Asn Ile Thr Ser Ser Thr Val Pro Pro Ser Asn Gly Lys Asn Val Lys
                725                 730                 735
Leu Ala Asp Gln Arg His Pro Lys Thr Gly Val Pro Phe Asp Gly Lys
            740                 745                 750
Gly Phe Pro Asn Phe Glu Lys His Val Lys Tyr Asp Thr
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[2205] <210>55

[2206] <211>1839

[2207] <212>DNA

[2208] <213> 人工序列

[2209] <220>

[2210] <223>961cL-741

[2211] <400>55

[2212]

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gcctacaaca atggccaaga aatcaacggt ttcaaagctg gagagaccat ctacgacatt 180
gatgaagacg gcacaattac caaaaaagac gcaactgcag ccgatgttga agccgacgac 240
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aagttagcag acactgatgc cgctttagca gatactgatg ccgctctgga tgcaaccacc 420
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[2214] <210>56

[2215] <211>612

[2216] <212>PRT

[2217] <213> 人 T 序列

[2218] <220>

[2219] <223>961cL-741

[2220] <400>56

[2221]

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

[2222]

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Leu Ala Asp Thr Asp Ala Ala Leu Asp Ala Thr Thr Asn Ala Leu Asn
    130                 135                 140
Lys Leu Gly Glu Asn Ile Thr Thr Phe Ala Glu Glu Thr Lys Thr Asn
145                 150                 155                 160
Ile Val Lys Ile Asp Glu Lys Leu Glu Ala Val Ala Asp Thr Val Asp
                165                 170                 175
Lys His Ala Glu Ala Phe Asn Asp Ile Ala Asp Ser Leu Asp Glu Thr
            180                 185                 190
Asn Thr Lys Ala Asp Glu Ala Val Lys Thr Ala Asn Glu Ala Lys Gln
        195                 200                 205
Thr Ala Glu Glu Thr Lys Gln Asn Val Asp Ala Lys Val Lys Ala Ala
    210                 215                 220
Glu Thr Ala Ala Gly Lys Ala Glu Ala Ala Ala Gly Thr Ala Asn Thr
225                 230                 235                 240
Ala Ala Asp Lys Ala Glu Ala Val Ala Ala Lys Val Thr Asp Ile Lys
                245                 250                 255
Ala Asp Ile Ala Thr Asn Lys Asp Asn Ile Ala Lys Lys Ala Asn Ser
            260                 265                 270
Ala Asp Val Tyr Thr Arg Glu Glu Ser Asp Ser Lys Phe Val Arg Ile
        275                 280                 285
Asp Gly Leu Asn Ala Thr Thr Glu Lys Leu Asp Thr Arg Leu Ala Ser
    290                 295                 300
Ala Glu Lys Ser Ile Ala Asp His Asp Thr Arg Leu Asn Gly Leu Asp
305                 310                 315                 320
Lys Thr Val Ser Asp Leu Arg Lys Glu Thr Arg Gln Gly Leu Ala Glu
                325                 330                 335
Gln Ala Ala Leu Ser Gly Leu Phe Gln Pro Tyr Asn Val Gly Gly Ser
            340                 345                 350
Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu Ala Asp Ala
        355                 360                 365
Leu Thr Ala Pro Leu Asp His Lys Asp Lys Gly Leu Gln Ser Leu Thr
    370                 375                 380
Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu Ala Ala Gln
385                 390                 395                 400
Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn Thr Gly Lys
                405                 410                 415
Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg Gln Ile Glu
            420                 425                 430
Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe Gln Val Tyr
        435                 440                 445
Lys Gln Ser His Ser Ala Leu Thr Ala Phe Gln Thr Glu Gln Ile Gln
    450                 455                 460
Asp Ser Glu His Ser Gly Lys Met Val Ala Lys Arg Gln Phe Arg Ile
465                 470                 475                 480
Gly Asp Ile Ala Gly Glu His Thr Ser Phe Asp Lys Leu Pro Glu Gly
                485                 490                 495
Gly Arg Ala Thr Tyr Arg Gly Thr Ala Phe Gly Ser Asp Asp Ala Gly
            500                 505                 510
Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly Asn Gly
        515                 520                 525
Lys Ile Glu His Leu Lys Ser Pro Glu Leu Asn Val Asp Leu Ala Ala
    530                 535                 540
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[2223]

Ala Asp Ile Lys Pro Asp Gly Lys Arg His Ala Val Ile Ser Gly Ser
545 550 555 560
Val Leu Tyr Asn Gln Ala Glu Lys Gly Ser Tyr Ser Leu Gly Ile Phe
565 570 575
Gly Gly Lys Ala Gln Glu Val Ala Gly Ser Ala Glu Val Lys Thr Val
580 585 590
Asn Gly Ile Arg His Ile Gly Leu Ala Ala Lys Gln Leu Glu His His
595 600 605
His His His His
610

[2224] <210>57

[2225] <211>4218

[2226] <212>DNA

[2227] <213> 人工序列

[2228] <220>

[2229] <223>961cL-983

[2230] <400>57

[2231]

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gatgaagacg gcacaattac caaaaaagac gcaactgcag ccgatgttga agccgacgac   240
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[2232]

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[2234] <211>1403

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Phe Cys Ser Gly Ala Leu Ala Ala Thr Asn Asp Asp Asp Val Lys Lys
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Thr Ile Thr Lys Lys Asp Ala Thr Ala Ala Asp Val Glu Ala Asp Asp
65 70 75 80
Phe Lys Gly Leu Gly Leu Lys Lys Val Val Thr Asn Leu Thr Lys Thr
85 90 95
Val Asn Glu Asn Lys Gln Asn Val Asp Ala Lys Val Lys Ala Ala Glu
100 105 110
Ser Glu Ile Glu Lys Leu Thr Thr Lys Leu Ala Asp Thr Asp Ala Ala
115 120 125
Leu Ala Asp Thr Asp Ala Ala Leu Asp Ala Thr Thr Asn Ala Leu Asn
130 135 140
Lys Leu Gly Glu Asn Ile Thr Thr Phe Ala Glu Glu Thr Lys Thr Asn
145 150 155 160
Ile Val Lys Ile Asp Glu Lys Leu Glu Ala Val Ala Asp Thr Val Asp
165 170 175
Lys His Ala Glu Ala Phe Asn Asp Ile Ala Asp Ser Leu Asp Glu Thr
180 185 190
Asn Thr Lys Ala Asp Glu Ala Val Lys Thr Ala Asn Glu Ala Lys Gln
195 200 205
Thr Ala Glu Glu Thr Lys Gln Asn Val Asp Ala Lys Val Lys Ala Ala
210 215 220
Glu Thr Ala Ala Gly Lys Ala Glu Ala Ala Ala Gly Thr Ala Asn Thr
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Ala Ala Asp Lys Ala Glu Ala Val Ala Ala Lys Val Thr Asp Ile Lys
245 250 255
Ala Asp Ile Ala Thr Asn Lys Asp Asn Ile Ala Lys Lys Ala Asn Ser
260 265 270
Ala Asp Val Tyr Thr Arg Glu Glu Ser Asp Ser Lys Phe Val Arg Ile
275 280 285
Asp Gly Leu Asn Ala Thr Thr Glu Lys Leu Asp Thr Arg Leu Ala Ser
290 295 300
Ala Glu Lys Ser Ile Ala Asp His Asp Thr Arg Leu Asn Gly Leu Asp
305 310 315 320
Lys Thr Val Ser Asp Leu Arg Lys Glu Thr Arg Gln Gly Leu Ala Glu
325 330 335
Gln Ala Ala Leu Ser Gly Leu Phe Gln Pro Tyr Asn Val Gly Gly Ser
340 345 350
Gly Gly Gly Gly Thr Ser Ala Pro Asp Phe Asn Ala Gly Gly Thr Gly
355 360 365
Ile Gly Ser Asn Ser Arg Ala Thr Thr Ala Lys Ser Ala Ala Val Ser
370 375 380
Tyr Ala Gly Ile Lys Asn Glu Met Cys Lys Asp Arg Ser Met Leu Cys
385 390 395 400
Ala Gly Arg Asp Asp Val Ala Val Thr Asp Arg Asp Ala Lys Ile Asn
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420 425 430
Ala Tyr Lys Asn Leu Ile Asn Leu Lys Pro Ala Ile Glu Ala Gly Tyr

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Gly Ser Ile Ser Phe Pro Glu Leu Tyr Gly Arg Lys Glu His Gly Tyr
465                 470                 475                 480
Asn Glu Asn Tyr Lys Asn Tyr Thr Ala Tyr Met Arg Lys Glu Ala Pro
                485                 490                 495
Glu Asp Gly Gly Gly Lys Asp Ile Glu Ala Ser Phe Asp Asp Glu Ala
            500                 505                 510
Val Ile Glu Thr Glu Ala Lys Pro Thr Asp Ile Arg His Val Lys Glu
        515                 520                 525
Ile Gly His Ile Asp Leu Val Ser His Ile Ile Gly Gly Arg Ser Val
    530                 535                 540
Asp Gly Arg Pro Ala Gly Gly Ile Ala Pro Asp Ala Thr Leu His Ile
545                 550                 555                 560
Met Asn Thr Asn Asp Glu Thr Lys Asn Glu Met Met Val Ala Ala Ile
                565                 570                 575
Arg Asn Ala Trp Val Lys Leu Gly Glu Arg Gly Val Arg Ile Val Asn
            580                 585                 590
Asn Ser Phe Gly Thr Thr Ser Arg Ala Gly Thr Ala Asp Leu Phe Gln
        595                 600                 605
Ile Ala Asn Ser Glu Glu Gln Tyr Arg Gln Ala Leu Leu Asp Tyr Ser
    610                 615                 620
Gly Gly Asp Lys Thr Asp Glu Gly Ile Arg Leu Met Gln Gln Ser Asp
625                 630                 635                 640
Tyr Gly Asn Leu Ser Tyr His Ile Arg Asn Lys Asn Met Leu Phe Ile
                645                 650                 655
Phe Ser Thr Gly Asn Asp Ala Gln Ala Gln Pro Asn Thr Tyr Ala Leu
            660                 665                 670
Leu Pro Phe Tyr Glu Lys Asp Ala Gln Lys Gly Ile Ile Thr Val Ala
        675                 680                 685
Gly Val Asp Arg Ser Gly Glu Lys Phe Lys Arg Glu Met Tyr Gly Glu
    690                 695                 700
Pro Gly Thr Glu Pro Leu Glu Tyr Gly Ser Asn His Cys Gly Ile Thr
705                 710                 715                 720
Ala Met Trp Cys Leu Ser Ala Pro Tyr Glu Ala Ser Val Arg Phe Thr
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Arg Thr Asn Pro Ile Gln Ile Ala Gly Thr Ser Phe Ser Ala Pro Ile
            740                 745                 750
Val Thr Gly Thr Ala Ala Leu Leu Leu Gln Lys Tyr Pro Trp Met Ser
        755                 760                 765
Asn Asp Asn Leu Arg Thr Thr Leu Leu Thr Thr Ala Gln Asp Ile Gly
    770                 775                 780
Ala Val Gly Val Asp Ser Lys Phe Gly Trp Gly Leu Leu Asp Ala Gly
785                 790                 795                 800
Lys Ala Met Asn Gly Pro Ala Ser Phe Pro Phe Gly Asp Phe Thr Ala
                805                 810                 815
Asp Thr Lys Gly Thr Ser Asp Ile Ala Tyr Ser Phe Arg Asn Asp Ile
            820                 825                 830
Ser Gly Thr Gly Gly Leu Ile Lys Lys Gly Gly Ser Gln Leu Gln Leu
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His Gly Asn Asn Thr Tyr Thr Gly Lys Thr Ile Ile Glu Gly Gly Ser
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[2243]

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885 890 895
Asp Gly Ile Val Tyr Leu Ala Asp Thr Asp Gln Ser Gly Ala Asn Glu
900 905 910
Thr Val His Ile Lys Gly Ser Leu Gln Leu Asp Gly Lys Gly Thr Leu
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Tyr Thr Arg Leu Gly Lys Leu Leu Lys Val Asp Gly Thr Ala Ile Ile
930 935 940
Gly Gly Lys Leu Tyr Met Ser Ala Arg Gly Lys Gly Ala Gly Tyr Leu
945 950 955 960
Asn Ser Thr Gly Arg Arg Val Pro Phe Leu Ser Ala Ala Lys Ile Gly
965 970 975
Gln Asp Tyr Ser Phe Phe Thr Asn Ile Glu Thr Asp Gly Gly Leu Leu
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Ala Ser Leu Asp Ser Val Glu Lys Thr Ala Gly Ser Glu Gly Asp Thr
995 1000 1005
Leu Ser Tyr Tyr Val Arg Arg Gly Asn Ala Ala Arg Thr Ala Ser Ala
1010 1015 1020
Ala Ala His Ser Ala Pro Ala Gly Leu Lys His Ala Val Glu Gln Gly
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1075 1080 1085
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Gly Arg Arg Leu Lys Ala Val Ser Asp Gly Leu Asp His Asn Gly Thr
1125 1130 1135
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1140 1145 1150
Gln Gly Gly Val Glu Gly Lys Met Arg Gly Ser Thr Gln Thr Val Gly
1155 1160 1165
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Met Gly Arg Ser Thr Trp Ser Glu Asn Ser Ala Asn Ala Lys Thr Asp
1185 1190 1195 1200
Ser Ile Ser Leu Phe Ala Gly Ile Arg His Asp Ala Gly Asp Ile Gly
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Tyr Leu Lys Gly Leu Phe Ser Tyr Gly Arg Tyr Lys Asn Ser Ile Ser
1220 1225 1230
Arg Ser Thr Gly Ala Asp Glu His Ala Glu Gly Ser Val Asn Gly Thr
1235 1240 1245
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1250 1255 1260
Thr Gly Asp Leu Thr Val Glu Gly Gly Leu Arg Tyr Asp Leu Leu Lys

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Ser Leu Thr Glu Gly Thr Leu Val Gly Leu Ala Gly Leu Lys Leu Ser
            1300                1305                1310
Gln Pro Leu Ser Asp Lys Ala Val Leu Phe Ala Thr Ala Gly Val Glu
        1315                1320                1325
Arg Asp Leu Asn Gly Arg Asp Tyr Thr Val Thr Gly Gly Phe Thr Gly
    1330                1335                1340
Ala Thr Ala Ala Thr Gly Lys Thr Gly Ala Arg Asn Met Pro His Thr
1345                1350                1355                1360
Arg Leu Val Ala Gly Leu Gly Ala Asp Val Glu Phe Gly Asn Gly Trp
                1365                1370                1375
Asn Gly Leu Ala Arg Tyr Ser Tyr Ala Gly Ser Lys Gln Tyr Gly Asn
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His Ser Gly Arg Val Gly Val Gly Tyr Arg Phe
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图 1 —ΔG287—919

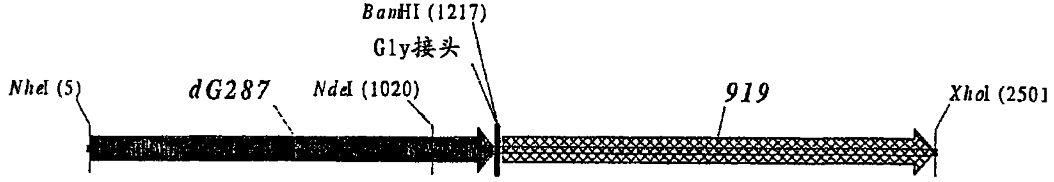

图 2 —ΔG287—953

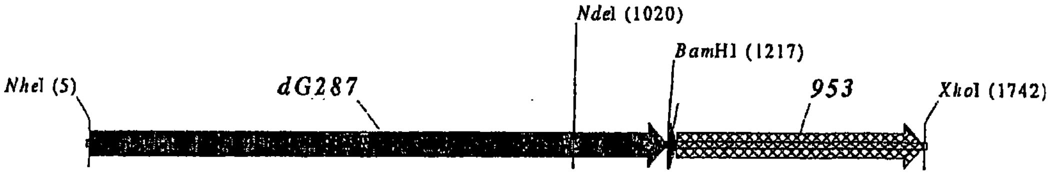

图 3 —ΔG287—961

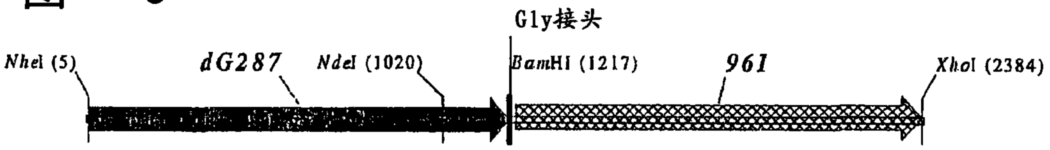

图 4 —ΔG287NZ—919

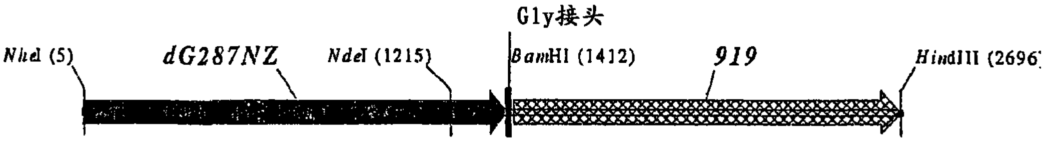

图 5 —ΔG287NZ—953

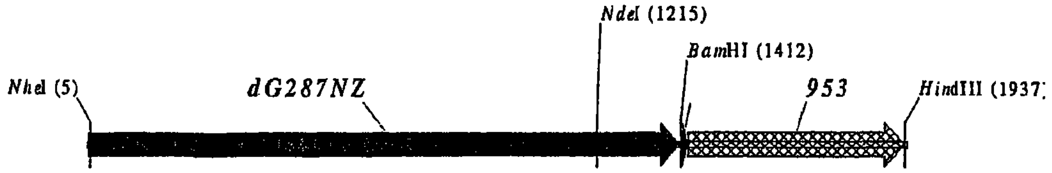

图 6 —ΔG287NZ—961

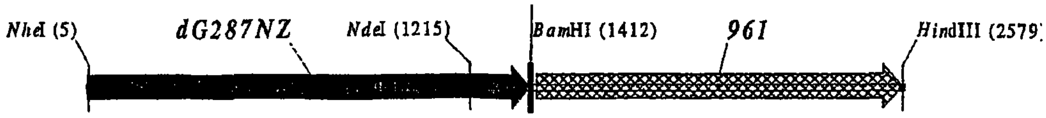

图 7 —ΔG983-ORF46.1

图 8 —ΔG983-741

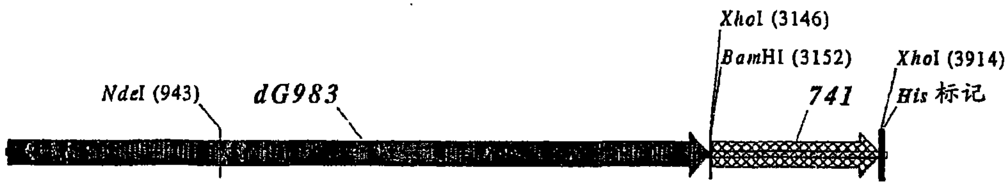

图 9 — ΔG983-961

图 10 — ΔG983-961c

图 11 — ΔG741-961

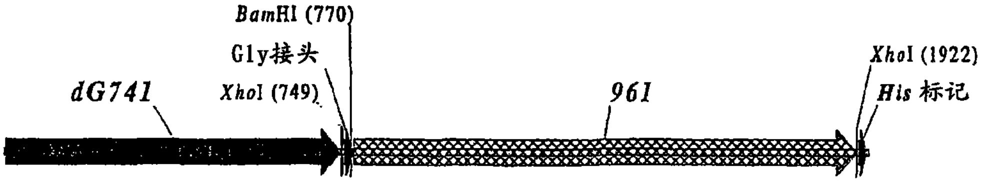

图 12 — ΔG741-961c

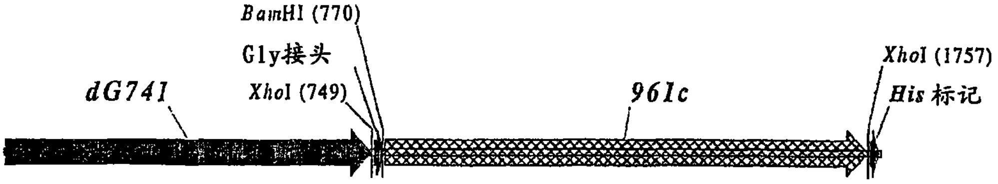

图 13 —ΔG741-983

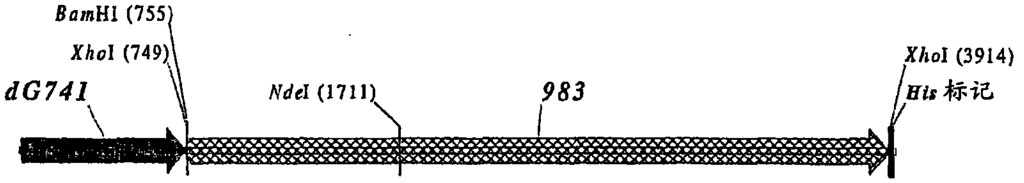

图 14 —ΔG741-ORF46.1

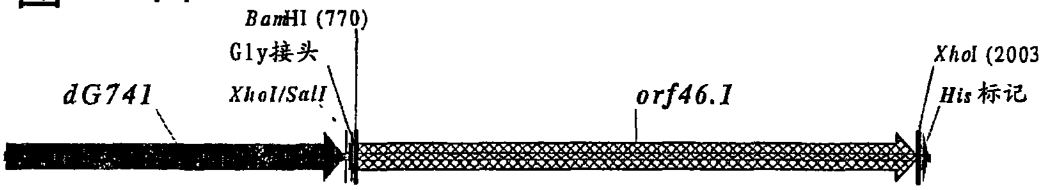

图 15 —ORF46.1-741

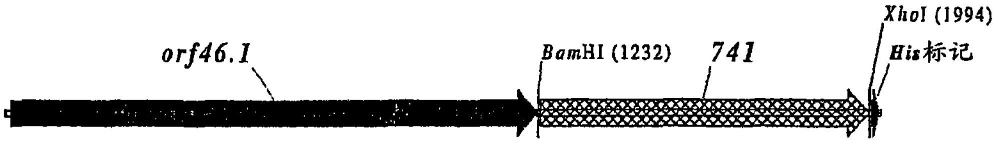

图 16 —ORF46.1-961

图 17 —ORF46.1—961c

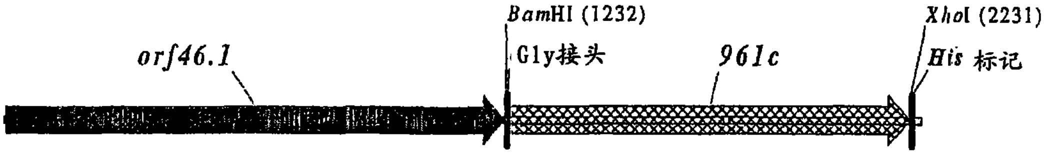

图 18 — **961-ORF46.1**

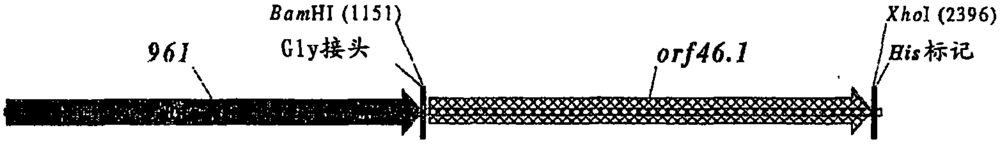

图 19 — **961-741**

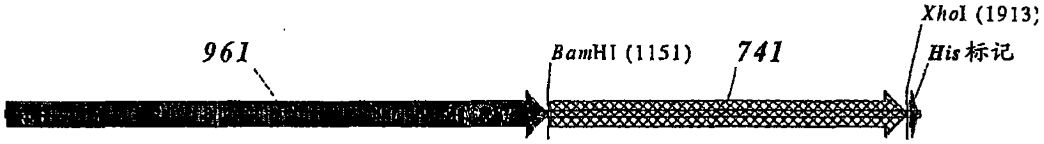

图 20 — **961-983**

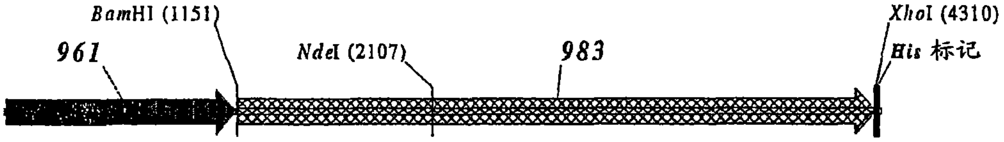

图 21 — **961c-ORF46.1**

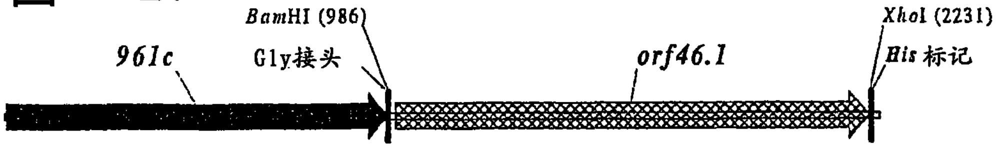

图 22 — **961c-741**

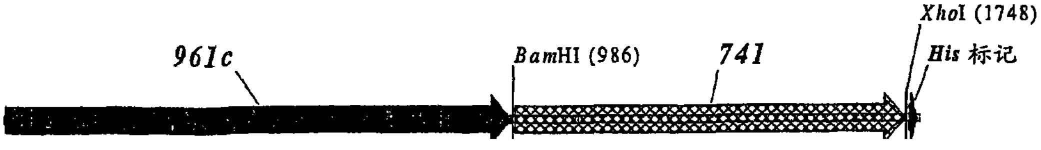

图 23 — **961c-983**

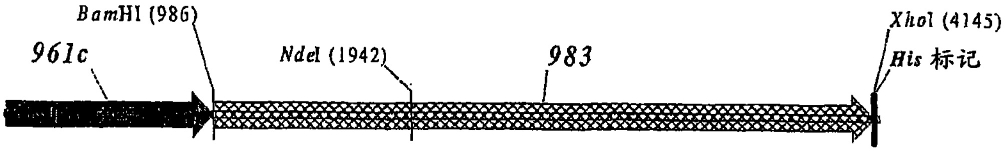

图 24 — **961cL-ORF46.1**

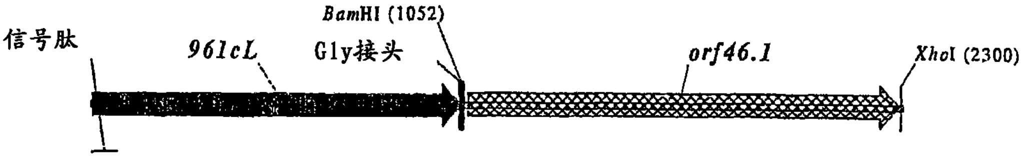

图 25 — **961cL-741**

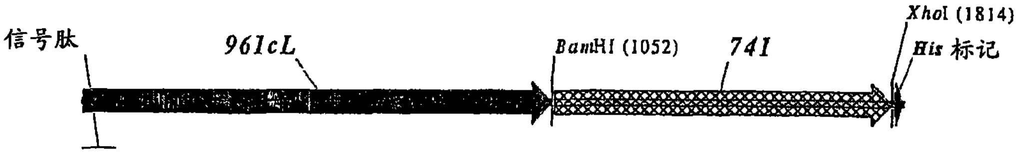

图 26 — **961cL-983**