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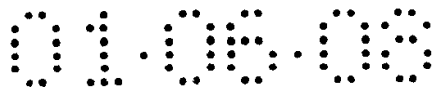
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[54]发明名称 改变植物木质素含量的材料和方法

[57]摘要

提供了与木质素生物合成途径相关的新型分离多核苷酸和多肽,以及包括所述序列的结构。还披露了用于在目标生物中改变木质素含量、木质素结构和木质素组成的方法,该方法包括将本发明的一种或多种多核苷酸整合到目标生物的基因组中。

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权 利 要 求 书

- 1.一种分离的多核苷酸，包括选自下列一组的核苷酸序列：（1）序列 89-266 和 350-375 所示序列；（2）序列 89-266 和 350-375 所示序列的互补物；（3）序列 89-266 和 350-375 所示序列的反向互补物；（4）序列 89-266 和 350-375 所示序列的反向序列；（5）与上述（1）-（4）所示序列相比，所产生的预期（E）值为 0.01 或更低的核苷酸序列；（6）与上述（1）-（4）所示核苷酸序列的相同性至少为 50%的核苷酸序列；（7）在严格杂交条件下，能与上述（1）-（4）所示序列杂交的核苷酸序列；（8）作为上述（1）-（4）所示序列的 200-聚体的核苷酸序列；（9）作为上述（1）-（4）所示序列的 100-聚体的核苷酸序列；（10）作为上述（1）-（4）所示序列的 40-聚体的核苷酸序列；（11）作为上述（1）-（4）所示序列的 20-聚体的核苷酸序列；（12）作为上述（1）-（4）所示序列的简并性等同物的核苷酸序列；和（13）作为上述（1）-（4）所示序列的等位变体的核苷酸序列。
- 2.一种分离的寡核苷酸探针或引物，含有与权利要求 1 所述核苷酸序列的 10 个连续残基互补的至少 10 个连续的残基。
- 3.一种包括权利要求 2 的多种寡核苷酸探针或引物的试剂盒。
- 4.一种在它上面记录了多种多核苷酸的储存介质，至少有一种多核苷酸包括权利要求 1 或 2 所示的核苷酸序列。
- 5.一种包括权利要求 1 的多核苷酸的结构。
- 6.一种含有权利要求 5 所述结构的转基因细胞。
- 7.一种结构，沿 5'-3'方向包括：
 - （a）基因启动子序列；
 - （b）多核苷酸序列，至少包括下列一种：（1）编码由权利要求 1 的核苷酸序列所编码的多肽的至少一个功能性部分的多核苷酸；和（2）包括编码由选自权利要求 1 所示一组序列的核苷酸序列所编码的多肽的基因的非编码区的多核苷酸；和
 - （c）基因终止序列。
- 8.如权利要求 7 的结构，其中，所述多核苷酸为有义方向。
- 9.如权利要求 7 的结构，其中，所述多核苷酸为反义方向。
- 10.如权利要求 7 的结构，其中，所述基因启动子序列在植物宿主中是有功能的，以便在木质部进行转录。

11.一种含有权利要求 7 结构的转基因植物细胞。

12.一种含有权利要求 11 所述的转基因植物细胞的植物或其部分或繁殖体或后代。

5 13.一种改变植物木质素含量、木质素组成和木质素结构中的一种或多种的方法,包括将权利要求 1 的多核苷酸稳定地整合到该植物的基因组中。

14.如权利要求 20 的方法,其中,所述植物选自桉树和松树。

15.如权利要求 20 的方法,包括将权利要求 7 的结构稳定地整合到所述植物的基因组中。

10 16.一种用于生产具有改变了的木质素含量、改变了的木质素组成和改变了的木质素结构中的一种或多种的植物的方法,包括:

(a) 用权利要求 7 的结构转化植物细胞,以便提供转基因细胞;
和

15 (b) 在有利于再生和成熟植物生长的条件下培养所述转基因细胞。

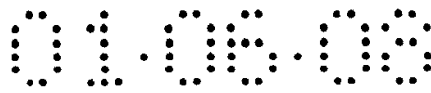
17.一种改变与植物中木质素生物合成途径相关的多肽活性的方法,包括将权利要求 7 的结构稳定地整合到该植物的基因组中。

18.一种分离的多肽,包括选自下列一组的氨基酸序列:

(a) 序列 267-349 和 376-401 的序列;

20 (b) 与 (a) 的序列至少具有 50%的相同性的序列;与 (a) 的序列至少具有 70%的相同性的序列;与 (a) 的序列至少具有 90%的相同性的序列。

19.一种分离的多肽,由权利要求 1 的分离的多核苷酸序列编码。



说明书

改变植物木质素含量的材料和方法

技术领域

5 本发明涉及被认为是新型的多核苷酸,包括部分序列和延长的序列以及探针和引物,含有所述多核苷酸的结构,含有所述多核苷酸的生物材料(包括植物、微生物和多细胞生物),由所述多核苷酸编码的多肽,以及使用所述多核苷酸和多肽的方法。更具体地讲,本发明涉及在包括植物的生物材料中改变木质素含量和组成,涉及与木质素生物合成途径10 相关的多肽,并涉及编码所述酶的多核苷酸。

发明背景

木质素是一种不溶性聚合物,它主要是决定植物茎干的硬度。具体地讲,木质素在某些植物细胞的多糖成分周围起着基质作用。木质素的含量越高,植物的硬度越大。例如,树木能合成大量的木质素,木质素15 占木材干重的 20%-30%。除了产生硬度之外,木质素还通过使得细胞壁疏水和不渗透水而有助于水分在植物内部的运输。木质素还通过阻止致病剂的穿透和繁殖,在植物抗病性方面起着作用。

树木中高浓度的木质素在造纸业中造成了很大的问题,其中,相当多的资源必须用于从造纸所需的纤维素纤维中分离木质素。常用于除去20 木质素的方法,要花费大量的能量和化合物,导致成本的增加和产生大量不需要的废物。仅在美国,每年就要从木材中除去大约 2000 万吨的木质素。

木质素主要决定饲料作物的可消化性,植物木质素含量的小的增加,就会导致可消化性的相当高的降低。例如,具有较低木质素含量的25 作物能够为牲畜提供更有效的饲料,相对所消耗的饲料作物量而言,奶和肉的产量较高。在正常植物生长中,干物质重量的增加伴随着可消化性的相应降低。在决定饲料作物的最佳收获时间时,农民必须在高产的具有较差可消化性的材料,和较低产量的具有较高可消化性材料之间进行选择。

30 对某些用途来说,木质素含量的增加是理想的,因为增加植物木质素的含量可导致木材机械强度的增强,改变其颜色并增加抗腐能力。菌根类的组成和含量通过改变木质素的含量和结构组成也有利于操作。

如下面所要详细讨论的,木质素是通过至少三种不同的单木纤维醇聚合形成的,所述木质素是在多步骤的途径中合成的,该途径中的每一个步骤是由不同的酶催化的。业已证实,控制编码某些酶,如肉桂基醇脱氢酶(CAD)和咖啡酸 3-O-甲基转移酶(COMT)的基因的拷贝数,会导致木质素产量的改变;例如,参见 US5,451,514 和 PCT 公开号 WO94/23044。另外,业已证实编码 CAD 的序列在白杨中的反义表达,会导致具有改变了的组成的木质素的产生(Grand C 等,植物(柏林) 163: 232-237 (1985))。

尽管业已分离了某些植物种的编码与木质素生物合成途径相关的某些酶的多核苷酸,但尚未鉴定多种植物中编码多种酶的基因。因此,本领域仍然需要可用于改变植物木质素含量和组成的材料,以及使用该材料的方法。

发明概述

简单地讲,本发明提供了所附序列表中序列 1-266 和 35-375 所示的分离的多核苷酸,所述序列的变体,含有所述序列的结构,含有序列 1-266 和 350-375 的序列的延长序列,及其变体,与序列 1-266、350-375 所示序列相应的探针和引物及其变体,以及至少含有序列 1-266 和 350-375 所示多种多核苷酸的特定数量连续残基的多核苷酸(x-聚体),以上这些在本文中统称为“本发明的多核苷酸”。本发明的多核苷酸优选可从桉树和松树中获得,并优选编码与木质素生物合成途径相关的酶。提供了含有所述序列的结构,使用所述序列和结构的方法,以及生物材料,包括具有改变了的基因组和/或木质素含量和组成的植物细胞和植物。本发明还提供了所附序列表中序列 267-349 和 376-401 所示的分离的多肽序列;所述序列的多肽变体;以及含有所述多肽序列及所述序列变体的多肽。

一方面,本发明提供了编码以下酶或以下酶的部分的分离的多核苷酸:肉桂酸 4-羟化酶(C4H),香豆酸 3-羟化酶(C3H),酚酶(PNL), O-甲基转移酶(OMT),肉桂基醇脱氢酶(CAD),肉桂酰-辅酶 A 还原酶(CCR),苯丙氨酸氨裂解酶(PAL),4-香豆酸:辅酶 A 连接酶(4CL),松柏醇葡萄糖基转移酶(CGT),松柏苷 β -葡萄糖苷酶(CBG),漆酶(LAC),过氧化物酶(POX),阿魏酸-5-羟化酶(F5H), α 淀粉酶,咖啡酸甲基转移酶,咖啡酰辅酶 A 甲基转移酶,香豆酸 6A 连接

酶，细胞色素 P450 LXX1A，联苯酚氧化酶，黄酮醇葡萄糖基转移酶，类黄酮羟化酶，和异黄酮还原酶。

在一种实施方案中，本发明的多核苷酸包括含有选自下列一组的核苷酸序列的多核苷酸：（a）序列 1-266 和 350-375 所示多核苷酸；（b）序列 1-266 和 350-375 所示多核苷酸的互补物；（c）序列 1-266 和 350-375 所示序列的反向互补物；（d）序列 1-266 和 350-375 所示序列的反向序列；和（e）序列 1-266 和 350-375 所示多核苷酸的变体。在本发明的另一种实施方案中，多核苷酸至少包括序列 1-266 和 350-375 的多种多核苷酸的特定数量的连续残基（x-聚体）。在另一方面，多核苷酸包括相应于序列 1-266 和 350-375 的多种多核苷酸的探针和引物。

另一方面，本发明提供了含有本发明多核苷酸的结构，所述多核苷酸是独立的或者与一种或多种本发明序列组合，或者与一种或多种已知多核苷酸组合；同时，还提供了含有所述结构的宿主细胞和转基因细胞。

在一个有关方面，本发明提供了沿 5'-3' 方向包括基因启动子序列；编码由本发明的多核苷酸编码的酶的至少一个功能性部分的开放读框；和基因终止序列的结构。开放读框可以沿有义和反义方向取向。还提供了包括由上述多核苷酸编码的酶的编码基因的非编码区或与非编码区互补的多核苷酸，以及基因启动子序列和基因终止序列的 DNA 结构。所述基因启动子和终止序列优选在诸如植物细胞的宿主细胞中有功能，所述基因启动子和终止序列最优选是原始酶基因的启动子和终止序列，不过，其他本领域常用的，如花椰菜花叶病毒（CMV）启动子，有或没有增强子，如 Kozak 序列或 Ω 增强子，以及根癌农杆菌胭脂氨酸合成酶终止子也可被用于本发明。为了在一种或多种需要的组织中进行定向表达，可以采用组织专一性启动子。在一种优选实施方案中，所述基因启动子序列可以在木质部转录。所述结构还可以包括鉴定转化细胞的标记。

在另一方面，提供了转基因细胞，如含有本发明结构的转基因植物细胞，还提供了含有所述转基因细胞的植物以及所述植物的果实和种子。

另一方面，提供了改变诸如植物的目标生物的木质素含量和组成的方法，所述方法包括将含有本发明多核苷酸的结构稳定地整合到目标植

物的基因组中。在一种优选实施方案中，所述目标植物是木本植物，优选选自桉树和松树，最优选选自巨桉（*Eucalyptus grandis*）和辐射松（*Pinus radiata*）。在相关方面，提供了用于生产具有改变了的木质素含量的植物的方法，该方法包括用含有本发明多核苷酸的结构转化植物细胞，以便提供转基因细胞，并在有利于再生和成熟植物生长的条件下培养所述转基因细胞。

另一方面，本发明提供了用于改变诸如植物的目标生物中一种酶的活性的方法，包括将本发明的结构稳定地整合到所述目标生物的基因组中。在一种优选实施方案中，所述目标植物是木本植物，优选选自桉树和松树，最优选选自巨桉和辐射松。本发明还提供了含有序列 267-349, 376-401 所示分离的多肽的多肽，以及所述多肽的变体。

附图的简要说明

通过结合附图阅读下面的更详细的说明可以了解本发明的上述特征和其他特征，以及获得这些特征的方法，并能最好地理解本发明。

图 1 是木质素生物合成途径的示意图。

图 2 是来自烟草植物的基因组 DNA 样品，所述植物是在标记实验中用来自松属的单一序列识别物（左图）和来自桉属的单一序列识别物（右图）产生的。在以上两幅图中，泳道 A 和 B 含有来自用空载体转化的对照植物的 DNA 样品，泳道 C-E 含有来自用单一序列识别物转化的植物的 DNA 样品。

图 3 表示在转化的烟草植物中检测松属单一序列识别物。泳道 A 和 B 表示来自序列 402 的探针与缺乏所述松属单一序列识别物的烟草植物（空载体转化的对照植物）的基因组 DNA 的杂交。泳道 C-E 表示所述探针与含有 1-3 个拷贝的松属单一序列识别物的烟草植物的基因组 DNA 杂交。

图 4 表示在转化的烟草植物中检测桉属单一序列识别物。泳道 A 和 B 表示来自序列 403 的探针与缺乏所述桉属单一序列识别物的烟草植物（空载体转化的对照植物）的基因组 DNA 的杂交。泳道 C-E 表示所述探针与含有 1-2 个拷贝的桉属单一序列识别物的烟草植物的基因组 DNA 杂交。

图 5 表示存在于用本发明的有义和反义遗传结构转化过的烟草植物中的可提取木质素量，以野生型木质素含量的百分比形式表示。

详细说明

木质素是由至少三种不同的单木质醇聚合而成的，主要是对-香豆醇、松柏醇和芥子醇。尽管这三种类型的木质醇亚基是众所周知的，但在各种植物的木质素生物合成途径中有可能出现所述亚基的略有不同的变体。在不同的植物种之间以及在同一物种之内，木质素中所述残基的相对浓度不同。另外，在特定植物的不同组织之间，木质素的组成也会改变。以上三种单木质醇是在多步骤的过程中由苯丙氨酸产生，被认为是通过自由基机制聚合成木质素。

图 1 表示松柏醇生物合成途径的不同步骤以及负责催化每一步的酶。对-香豆醇和芥子醇是通过类似途径合成的。首先通过苯丙氨酸氨裂解酶 (PAL) 使苯丙氨酸脱氨，以便得到肉桂酸，然后由肉桂酸 4-羟化酶 (C4H) 对肉桂酸进行羟化，以便形成对-香豆酸。由香豆酸 3-羟化酶将对-香豆酸羟化成咖啡酸。然后由 O-甲基转移酶 (OMT) 对新加上去的羟基进行甲基化，以便得到阿魏酸，阿魏酸通过 4-香豆酸：辅酶 A 连接酶 (4CL) 与辅酶 A 缀合，形成阿魏酰辅酶 A。通过肉桂酰辅酶 A 还原酶 (CCR) 催化将阿魏酰辅酶 A 还原成松柏醛。在肉桂基醇脱氢酶 (CAD) 的作用下，将阿魏酰辅酶 A 进一步还原成松柏醇，然后将其转化成葡萄糖基化形式，以便通过松柏醇葡萄糖基转移酶 (CGT) 从细胞质中外泌到细胞壁中。在外泌之后，在松柏苷 β -葡萄糖苷酶 (CBG) 的作用下获得松柏醇的脱葡萄糖基化形式。最后，在酚酶 (PNL)、漆酶 (LAC) 和过氧化物酶 (POX) 的作用下将三种单木质醇聚合成木质素。

芥子醇的形成还涉及到另一种酶——阿魏酸-5-羟化酶 (F5H)。为了更详细地了解木质素生物合成途径，可以参见 Whetton R 和 Sederoff R. 植物细胞, 7: 1001-1013, 1995。

已知植物木质素含量的定量和定性改变受诸如光线刺激, 低钙含量和机械胁迫的外部因素的诱导。还可以通过病原体感染诱导新型木质素的形成, 有时是在正常情况下不木质化的组织中形成。除了木质素之外, 若干其他类型的植物产品也是由苯丙氨酸产生的, 包括类黄酮、香豆素、芪和苯甲酸衍生物, 所有这些化合物合成的第一步都相同。因此, 改变与木质素生物合成途径有关的 PAL、C4H、4CL 和其他酶的作用, 可以影响除木质素之外的其他产物的合成。

使用本发明的方法和材料,通过改变本发明多核苷酸的表达或通过改变由多核苷酸编码的多肽或改变所述多核苷酸可以改变植物的木质素含量。例如,可以通过将编码与木质素生物合成途径相关的酶的基因的额外的拷贝整合到目标植物基因组中,改变诸如植物的目标生物的木质素含量。类似地,通过用所述基因的反义拷贝转化所述目标植物,可以实现木质素含量的改变。另外,可以操纵编码木质素生物合成途径中不同酶的基因的拷贝数量,改变所合成的每一种单木质醇的相对含量,从而导致具有改变了的组成的木质素的形成。所述木质素组成的改变可能是有利的,例如,在用于纸张的木材加工应用中,并且还能有效改变木质材料对腐霉菌的易感性。

在第一方面,本发明提供了在序列表中序列 1-266 和 250-375 所示分离的多核苷酸序列,所述序列的变体,含有序列 1-266, 350-375 所示序列的延长序列及其变体,相应于序列 1-266, 350-375 所示序列的探针和引物及其变体,至少含有序列 1-266, 350-375 所示多种多核苷酸的特定数量的连续残基的多核苷酸(x-聚体),以及含有序列 1-266, 350-375 所示序列的部分的延长序列,以上所有序列在本文中被统称为“本发明的多核苷酸”。本发明还提供了序列表中序列 267-349 和 376-401 所示的分离的多肽,所述序列的多肽变体,以及含有所述分离的多肽序列和所述序列变体的多肽。

本文所披露的多核苷酸源于森林植物资源,即来自巨桉和辐射松。本发明的某些多核苷酸为“部分”序列,就是说它不代表编码一种完整长度多肽的完整长度的基因。所述部分序列可以通过用引物和/或探针以及众所周知的杂交和/或 PCR 技术对各种 DNA 文库进行分析和测序延长。部分序列可以一直延长到编码一种多肽的开放读框、完整长度的多核苷酸和/或基因能够表达一种多肽,或者鉴定到该基因组的其他有用部分为止。所述延长序列(包括完整长度多核苷酸和基因),在所述延长的多核苷酸包括鉴定的序列或其变体或序列 1-266, 350-375 之一的鉴定的连续部分(x-聚体),或其变体时,被称为“相应于”序列 1-266, 350-375 所示序列之一,或其变体,或序列 1-266, 350-375 所示序列的一部分。类似地,可以用序列 1-266 和 350-375 所示 cDNA 序列通过常规方法确定并获得相应于本发明多核苷酸的 RNA 序列、反向序列、互补序列、反义序列等。

序列 1-266 和 350-375 所示的多核苷酸可以包括编码多肽的开放读框（“ORFs”）或部分开放读框。另外，编码多肽的开放读框还可以在相应于序列 1-266 和 350-375 所示序列的延长的或完整长度序列中鉴定。可以用本领域公知技术鉴定开放读框。例如，所述技术包括分析已知起始和终止密码子的位置，根据密码子频率鉴定最有可能的读框等。例如，适于 ORF 分析的工具和软件可以在互联网上获得

<http://www.ncbi.nlm.nih.gov/gorf/gorf.html>。可以在本发明多核苷酸上鉴定开放读框和部分开放读框。一旦鉴定到部分开放读框，就可以用本领域众所周知的技术对所述部分开放读框部位进行延长，直到鉴定到编码完整开放读框的多核苷酸。因此，可以用本发明的多核苷酸鉴定编码多肽的开放读框。

一旦在本发明的多核苷酸上鉴定到开放读框，即可分离和/或合成所述开放读框。然后，可以构建可以表达的遗传结构，该结构包括所述开放读框和合适的启动子、起始密码子、终止密码子等。可将所述遗传结构导入宿主细胞，以便表达由所述开放读框编码的多肽。合适的宿主细胞可以包括各种原核和真核细胞，包括植物细胞、哺乳动物细胞、细菌细胞、和藻类等。

可以表达由本发明多核苷酸所编码的多肽，并用于各种实验中，以便确定其生物学活性。所述多肽可用于产生抗体，分离相应的相互作用蛋白或其他化合物，并用于定量测定相互作用蛋白或其他化合物的含量。

本发明还涉及调节树木的多核苷酸和/或多肽含量和组成的方法，该方法包括将含有本发明的一种或多种多核苷酸的遗传结构稳定地整合到所述生物的基因组中。在一种实施方案中，目标生物是树木，优选为木本植物，更优选为松属和桉属的木本植物，最优选为巨桉和辐射松。在一个相关方面，提供了用于生产具有改变了的基因型和表现型的树木植物的方法，该方法包括用本发明的遗传结构转化植物细胞，以便提供转基因细胞，并在有利于再生和成熟植物生长的条件下培养所述转基因细胞。本发明还涉及并包括由于改变了本发明多核苷酸或多肽的水平或含量，因而与野生型生物相比具有改变了的基因型或表现型的树木植物，以及所述树木植物的成分（种子等），和所述树木植物的后代。

本发明的分离的多核苷酸还可用于基因组作图、物理作图、和基因

的定位克隆。另外，序列 1-266 和 350-375 所示的多核苷酸序列及其变体还可用于设计寡核苷酸探针和引物。寡核苷酸探针和引物的序列与感兴趣的多核苷酸的特定部分大体上互补。用本发明多核苷酸设计的寡核苷酸探针，可用于在其细胞中具有充分相似的 DNA 和 RNA 的任何生物中检测基因的存在，并检查基因的表达方式，使用本领域公知技术，如狭线印迹 DNA 杂交技术。用本发明多核苷酸设计的寡核苷酸探针可用于 PCR 扩增。用本发明多核苷酸设计的寡核苷酸探针和引物，还可以与各种微阵列技术结合使用，包括由 Synteni 所使用的微阵列技术（Palo Alto，加利弗尼亚）。

本发明的多核苷酸还可用于标记或鉴定一种生物或其繁殖材料。例如，所述标记可以通过将一种非破坏性、无功能的外源多核苷酸识别物稳定地整合到一种生物中。所述多核苷酸含有本发明的一种多核苷酸。

本发明的多肽和编码所述多肽的多核苷酸在植物的木质素和生物合成途径中具有活性。所述多核苷酸是通过 DNA 和多肽相似性检索而推测性鉴定的。业已证实本发明的多核苷酸和多肽与下面的已知与木质素生物合成过程相关的多肽具有相似性：

表 1

多肽身份	多肽序列	多核苷酸序列
肉桂酸 4-羟化酶 (C4H)	2, 3, 17, 48, 49, 92, 124, 125, 153-163	
香豆酸 3-羟化酶 (C3H)	4, 18, 50-52, 93, 101, 126, 127, 149-152	
酚酶(PNL)	5, 35, 36, 81, 116, 183	
O-甲基转移酶 (OMT)	6, 22-25, 53-55, 94, 104-107, 173-175	
肉桂醇脱氢酶 (CAD)	1, 7, 30, 71, 95, 112, 164	
肉桂酰-辅酶 A 还原酶 (CCR)	8, 26-29, 58-70, 96, 108-111, 128-134, 167	
苯丙氨酸氨裂解酶(PAL)	9-11, 16, 45-47, 97, 98, 100, 122, 123, 176 242-248	325-331

多肽身份	多肽序列	多核苷酸序列
4-香豆酸:辅酶 A 连接酶 (4CL)	2, 56-57, 90, 147, 158 265-266	348-349
松柏醇葡萄糖基转移酶(CGT)	31-33, 72, 113-115, 135, 168	
松柏苷 β -葡萄糖苷酶(CBG)	34, 73-80, 1360141, 165, 166	
漆酶 (LAC)	37-41, 82-84, 117, 118, 142-144, 172	
过氧化物酶(POX)	13, 42-44, 85-89, 91, 119-121, 145, 146, 177-182, 249-250, 264, 350-375	332-333 347, 376-401
阿魏酸-5-羟化酶 (F5H)	19-21, 102, 103, 169-171	
α 淀粉酶	184-186	267-269
咖啡酸甲基转移酶	187-192	270-275
咖啡酰辅酶 A 甲基转移酶	193-195	276-278
香豆酸辅酶 A 连接酶	196-200	279-283
细胞色素 P450 LXXIA	201-206	284-289
联酚氧化酶	207-217 251-263	290-300 334-346
黄酮醇葡萄糖基转移酶	218	301
类黄酮羟化酶	219-233	302-316
异黄酮还原酶	234-241	317-324

在一种实施方案中, 本发明的分离的多核苷酸包括选自下列一组的序列: (a) 序列 1-266 和 350-375 所示序列; (b) 序列 1-266 和 350-375 所示序列的互补物; (c) 序列 1-266 和 350-375 所示序列的反向互补物; (d) 序列 1-266 和 350-375 所示序列的反向序列; 和 (e) 在本文中所确定的与 (a) - (d) 的序列或 (a) - (d) 的序列的特定部位具有至少 50%、75%、90%或 98%相同性的序列。

在另一方面, 提供了由本发明的多核苷酸编码的分离的多肽。在一种实施方案中, 所述多肽包括序列 267-349 和 376-401 所示的氨基酸序

列, 及其变体, 以及由本发明的多核苷酸(包括含有序列 1-266 和 350-375 所示序列的多核苷酸) 所表达的多肽。

5 另一方面, 本发明提供了单独含有、与本发明的一种或多种其他多核苷酸组合、或与一种或多种已知多核苷酸组合的本发明多核苷酸的遗传结构, 同时提供了含有所述结构的细胞和目标生物。

10 在一个相关方面, 本发明提供了遗传结构, 该结构沿 5'-3' 方向含有基因启动子序列、编码由本发明的多核苷酸编码的多肽的至少一个功能性部分的开放读框、以及基因终止序列。所述开放读框可以沿有义和反义方向取向。还涉及含有基因启动子序列、本发明多核苷酸、和基因终止序列的遗传结构, 以及含有基因启动子序列、本发明多核苷酸的非翻译区、或互补于非翻译区的核苷酸序列、和基因终止序列的遗传结构。所述遗传结构还可以包括用于鉴定转化细胞的标记。

15 所述基因启动子和终止序列优选在宿主植物中具有功能, 最优选是所述宿主植物所固有的。可以使用本领域常用的启动子和终止序列, 如花椰菜花叶病毒 (CMV) 启动子, 有或没有增强子, 如 Kozak 序列或 Ω 增强子, 以及根癌农杆菌胭脂氨酸合成酶终止子。为了在一种或多种需要的组织中进行定向表达, 可以使用组织专一性启动子。

20 另一方面, 提供了用于生产与天然生物相比具有改变了的多核苷酸或多肽含量的本发明的树木植物的方法。所述方法包括用本发明的遗传结构转化目标树木植物, 以便提供转基因细胞, 并在有利于再生和成熟植物生长的条件下培养所述转基因细胞。提供了含有本发明遗传结构的细胞, 同时提供了含有所述转基因细胞的组织和树木植物, 以及果实、种子和其他产品、衍生物、或所述树木植物的后代。本发明还包括本发明转基因植物的繁殖体。在本文中, 术语“繁殖体”表示可用于进行有性或无性生殖或繁殖的植物的任何部分, 包括切穗。

植物品种, 特别是可以按照植物育种者权利注册的植物品种可以从本发明中排除。不能仅仅因为一种植物在其基因组中含有导入该植物或其祖先的细胞中的、稳定的转基因, 就将该植物视为“植物品种”。

30 本文所使用的术语“多核苷酸”表示核苷酸的统称, 并包括 DNA 和相应的 RNA 分子, 可以是单链和双链分子, 包括 HnRNA 和 mRNA 分子, DNA 和 RNA 分子的有义和反义链, 以及 cDNA、基因组 DNA 和完全或部分合成的多核苷酸。HnRNA 分子含有内含子, 并且以大体

上的一对一的方式“相应于”一种 DNA 分子。mRNA 分子“相应于”切除了其中的内含子的 HnRNA 和 DNA 分子。本发明的多核苷酸可以是完整的基因，或其任何部分。基因是编码有功能的蛋白或 RNA 分子的 DNA 序列。可操作的反义多核苷酸可以包括相应多核苷酸的一个片段，因此，“多核苷酸”的定义包括所有可操作的反义片段。反义多核苷酸和与反义多核苷酸相关的技术在本领域中是众所周知的，并且披露于，例如，Robinson-Benion 等，“反义技术”，酶学方法 254(23):363-375, 1995；和 Kawasaki 等，Artific. Organs 20(8):836-848, 1996。

还提供了所述分离的多核苷酸的互补物、所述分离的多核苷酸的反向互补物、和所述分离的多核苷酸的反向序列、以及所述序列的变体。本文所使用的术语“互补物”、“反向互补物”、和“反向序列”的定义可以通过下面的例子得到最佳理解。对于序列 5'AGGACC3'来说，其互补物、反向互补物和反向序列如下：

互补物 3' TCCTGG 5'

反向互补物 3' GGTCCT 5'

反向序列 5' CCAGGA 3'。

在本文中，术语“寡核苷酸”是指多核苷酸序列的较短的片段，通常包括 6-60 个核苷酸，并且包括用于杂交试验的探针和用于通过聚合酶链式反应进行 DNA 扩增的引物。

基因组 DNA 和异源 DNA 的鉴定，可以用一种 cDNA 序列的全部或部分作为探针，在合适严格的条件下，通过标准 DNA/DNA 杂交技术筛选合适的文库完成。或者，可将使用根据已知基因组 DNA、cDNA 和蛋白序列设计的寡核苷酸引物的 PCR 技术用于扩增和鉴定基因组和 cDNA 序列。可以通过常规合成方法生产相应于所述鉴定序列和变体的合成 DNA。本文所述的所有多核苷酸是分离的和纯化的，正如这些术语在本领域中所常用的形式。

在另一方面，本发明提供了由上述多核苷酸编码的或部分编码的分离的多肽。在本文中，术语“多肽”包括任何长度的氨基酸链，包括完整长度的蛋白，其中，所述氨基酸残基是通过共价肽键连接的。本文所说的术语“由多核苷酸编码的多肽”，包括由含有本文所提供的分离的 DNA 序列或变体的多核苷酸所编码的多肽。在特定实施方案中，本发明的多肽包括选自序列 267-349 和 376-401 所示序列的氨基酸序列，以

及所述序列的变体。

本发明的多肽可以通过将编码所述多肽的 DNA 序列插入一种表达载体，并在合适的宿主中表达所述多肽而通过重组方法产生。可以采用本领域普通技术人员所公知的多种表达载体中的任一种。表达可以在业
5 已用含有编码一种重组多肽的 DNA 分子转化或转染过的任何合适的宿主细胞中完成。合适的宿主细胞包括原核细胞、酵母和高等真核细胞。所采用的宿主细胞优选为大肠杆菌、昆虫、酵母或哺乳动物细胞系，如 COS 或 CHO。以这种方式表达的 DNA 序列可以编码天然存在的多肽，天然存在的多肽部分，或其变体。

10 在一个相关方面，提供了至少包括具有选自序列 267-349 和 376-401 所示序列的氨基酸序列的多肽的功能性部分的多肽，及其变体。在本文中，一种多肽的“功能性部分”是含有影响该多肽功能所必须的活性位点的部分，例如，该分子的能够结合一种或多种反应物的部分。所述活性位点可以由存在于一个或多个多肽链上的分离的部分组成，并且通常
15 具有高的结合力。

可以通过以下方法鉴定一种多肽的功能性部分：首先通过化学或酶解消化所述多肽，制备该多肽的片段，或者对编码所述多肽的多核苷酸进行诱变分析，然后表达所得到的突变型多肽。然后对所述多肽片段或突变型多肽进行试验，以便确定哪一部分保留了生物学活性，例如，使
20 用下面所提供的代表性试验方法。

所述活性位点可以由存在于一个或多个多肽链上的分离的部分组成，并且通常具有高的底物专一性。本文所使用的术语“由一种多核苷酸编码的多肽”，包括由含有本发明的部分分离的多核苷酸的多核苷酸所编码的多肽。

25 还可以通过合成或重组方法制备本发明多肽的部分和其他变体。可以用本领域普通技术人员所公知的技术制备具有少于大约 100 个氨基酸，通常含有少于大约 50 个氨基酸的多肽。例如，所述多肽可以用任一种商业化的固相技术合成，如 Merrifield 固相合成方法，其中，将氨基酸顺序添加到生长的氨基酸链上。参见 Merrifield，美国化学协会杂
30 志 85: 2149-2146, 1963, 用于多肽自动化合成的设备可以从诸如 Perkin Elmer / Applied Biosystems, Inc. (Foster 市，加利福尼亚)的供应商那里购买，并可以按照生产商的说明进行操作。可以用标准诱变技术制备天

然多肽的变体，如寡核苷酸定向的位点专一性诱变(Kunkel, T., 美国科学院院报 82:488-492, 1985)。还可以用标准技术从 DNA 序列中除去片段，以便能够制备截短的多肽。

一般，本文所述的多肽是以分离的大体上纯化的形式制备的。所述多肽的纯度优选为至少大约 80%；更优选为至少大约 90%；最优选为至少大约 99%。在下文所披露的某些优选实施方案中，将所述分离的多肽掺入药用组合物或疫苗中，以便用于治疗皮肤病。

在本文中，术语“变体”包括不同于特定序列的核苷酸或氨基酸序列，其中，有一个或多个核苷酸或氨基酸残基的缺失、取代或添加。变体可以是天然存在的等位变体或非天然存在的变体，变体序列（多核苷酸或多肽）与本发明的序列相比，优选具有至少 50%，更优选至少 75%，最优选至少 90%的相同性。所述百分相同性是通过按如下方法比较两个要比较的序列，测定在比较部分相同残基的数量，用本发明（查询）序列上的残基总数去除所述数量，并用 100 乘以所得结果而测定的。

可以用可公开获得的计算机程序比较多核苷酸和多肽序列，并测定在特定部位上与另一种多核苷酸相同的核苷酸的百分比。用于比较并鉴定多核苷酸序列相似性的两种代表性程序是 BLASTN 和 FASTA 程序。还可以用 BLASTX 程序分析多核苷酸，该程序能比较一种核苷酸的查询序列（两条链）的六框概念翻译产物和蛋白质序列数据库。可以用 BLASTP 程序检查多肽序列的相似性。BLASTN、BLASTX 和 BLASTP 程序可以在 NCBI 匿名 FTP 服务器上获得(<ftp://ncbi.nlm.nih.gov>), </blast/executables/>。被设定为在有关文献中所披露的预设参数、并用该程序分配的 BLASTN 程序 2.0.4 版[1998 年 2 月 24 日]和 2.0.6 版[1998 年 9 月 16 日]，可优选用于测定本发明多核苷酸变体。被设定为在有关文献中所披露的预设参数的 BLASTP 程序、并用该程序分配的 BLASTP 程序，可优选用于测定本发明的多肽变体。包括 BLASTN，BLASTP 和 BLASTX 在内的 BLAST 程序家族的使用披露于 NCBI's 网站 URL <http://www.ncbi.nlm.nih.gov/BLAST/newblast.html> 并披露于 Altschul Stephen F 等的文献中，“缺口 BLAST 和 PSI-BLAST: 新一代蛋白数据库检索程序”核酸研究 25: 3389-3402, 1997。

计算机程序 FASTA 可以在互联网上从 ftp 网站 <ftp://ftp.virginia.edu/pub/fasta/> 获得。被设定为在有关文献中披露的预

设参数并用有关程序分配的 1996 年 2 月的 2.0.4 版, 可用于本发明变体的测定。FASTA 程序的使用披露于 Pearson WR 和 Lipman DJ, “用于生物学序列分析的改进工具”, 美国科学院院报 85: 2444-2448, 1988; 和 Pearson WR, “用 FASTP 和 FASTA 进行快速和灵敏的序列比较”, 酶学方法 183:63-98, 1990。

10 优选将以下运行参数用于比较和相似性的测定, 使用 BLASTN, 它能得出多核苷酸序列的 E 值和百分相同性: Unix 运行指令: blastall -p blastn -d embldb -e 10 -G0 -E0 -r 1 -v 30 -b 30 -i queryseq -o results; 参数为: -p 程序名 [String]; -d 数据库 [String]; -e 预期值 (E) [Real]; -G 打开一个缺口的费用 (零引起的预设行为) [整数]; -E 延长一个缺口的费用 (零引起的预设行为) [整数]; -r 核苷酸比较的报酬(仅用 blastn) [整数]; -v 单线描述数量(V) [整数]; -b 要显示的比较数量 (B) [整数]; -i 查询文件[File In]; 和 -o BLAST 报告输出文件 [File Out] Optional. 优选将以下运行参数用于通过 BLASTP 15 进行比较和相似性的测定, 由此可以得到多肽序列的 E 值和百分相同性: blastall -p blastp -d swissprotodb -e 10 -G0 -E 0 -v 30 -b 30 -i queryseq -o results; 参数为: -p 程序名 [String]; -d 数据库 [String]; -e 预期值(E) [Real]; -G 打开一个缺口的费用 (零引起的预设行为) [整数]; -E 延长一个缺口的费用 (零引起的预设行为) [整数]; -v 单线描述的数量 (v) [整数]; -b 要显示的比较数量 (b) [整数]; -I 查询文件 [File In]; 20 -o BLAST 报告输出文件 [File Out] Optional. 通过由 BLASTN, FASTA, BLASTP 或类似序列产生的查询序列“点击”一个或多个数据库序列, 可以比较并鉴定序列的相似部分。所述点击是按照相似性程度和序列重叠的长度排列的。对一个数据库序列的点击通常表示仅在查询序列的一部分 25 部分序列长度上重叠。

BLASTN, FASTA, BLASTP 程序还能产生排比的“预期”值 (E)。预期值 (E) 表示在检索特定大小的数据库时, 在特定数量的连续序列上“预期”随机出现点击的次数。所述预期值被用作显著性阈值, 用于确定对诸如优选的 EMBL 数据库的数据库的点击是否表示真实的相似 30 性。例如, 赋予一次多核苷酸点击的 0.1 的 E 值, 被理解成意味着在 EMBL 数据库大小的数据库中, 人们预期在有关序列的比较部分上看到 0.1 的匹配, 具有仅通过随机方式得到的类似得分。根据该标准, 所述

多核苷酸序列的比较和匹配部分有 90% 的可能性相同。对于在比较和匹配部分的 E 值为 0.01 或更低的序列来说，用 BLASTN 或 FASTA 在程序 EMBL 数据库中随机发现匹配的可能性为 1% 或更低。

根据一种实施方案，对于本发明的每一种多核苷酸和多肽来说，多核苷酸和多肽的“变体”优选包括与本发明的多核苷酸或多肽相比具有相同数量或较少数量核酸或氨基酸的序列，并且与本发明的多核苷酸或多肽相比能产生 0.01 或更低的 E 值。就是说，变体多核苷酸或多肽是至少有 99% 的可能性与本发明的多核苷酸或多肽相同的任何序列，用设定为上述参数的 BLASTN、FSATA 或 BLASTP 程序测定具有 0.01 或更低的 E 值。根据一种优选实施方案，变体多核苷酸是具有与本发明的多核苷酸相同数量或较少核酸的序列，它与本发明的多核苷酸至少有 99% 的可能性相同，用被设定为上述参数的 BLASTN 或 FASTA 程序测定，具有 0.01 或更低的 E 值。类似地，根据一种优选实施方案，变体多肽是与本发明的多肽相比具有相同数量或较少氨基酸的序列，它至少有 99% 的可能性与本发明的多肽相同，用被设定为上述参数的 BLASTN 或 FASTA 程序测定，具有 0.01 或更低的 E 值。

或者，本发明的变体多核苷酸能与序列 1-266 和 350-375 所示多核苷酸序列或这些序列的互补物、或反向序列、或反向互补物在严格条件下杂交。在本文中，“严格条件”是指在 $6 \times \text{SSC}$ ，0.2% SDS 中预洗涤，在 65°C 下，在 $6 \times \text{SSC}$ ，0.2% SDS 中杂交过夜；然后进行 2 次 30 分钟的洗涤，每次在 65°C 下，在 $1 \times \text{SSC}$ ，0.1% SDS 中进行，然后再进行 2 次 30 分钟的洗涤，分别在 65°C 下，在 $0.2 \times \text{SSC}$ ，0.1% SDS 中进行。

本发明还包括不同于所披露的序列的多核苷酸，由于遗传密码的简并性，该序列能编码与本发明所涉及的氨基酸相同的序列。所述多核苷酸被称为本文所披露的多核苷酸的“简并性等同物”。类似地，本发明还包括与所披露的序列不同，但它所编码的多肽与由本发明多核苷酸所编码的多肽具有相似的酶促活性的多核苷酸。因此，本发明涉及并包括由于保守性取代而不同于序列 1-266 和 350-375 所示多核苷酸序列或所述序列的互补物、反向序列、或反向互补物的序列的多核苷酸。另外，本发明还涉及并包括含有由于占总序列长度 10% 以下的缺失和/或插入而不同于序列 1-266 和 350-375 所示多核苷酸序列或所述序列的互补物、反向互补物、或反向序列的序列的多核苷酸。类似地，本发明涉及

并还包括含有由于占总序列长度 10% 以下的氨基酸取代、插入和/或缺失而不同于序列 267-349 和 376-401 所示多肽序列的序列的多肽，只要所述变体多肽在木质素生物合成途径中具有活性即可。

5 本发明的多核苷酸（包括变体）可以从由植物或非植物生物组建的各种文库中分离，或者用本领域公知的技术合成。本发明的多核苷酸，可以通过对按照下面的例 1 和例 2 所述方法由巨桉和辐射松制备的 cDNA 文库进行高通量测序分离。或者，可以合成基于序列 1-266 和 350-375 所示序列的寡核苷酸探针，并用于通过杂交或 PCR 技术在来自巨桉和辐射松的 cDNA 和基因组 DNA 中鉴定阳性克隆。探针可以短于
10 本文所提供的序列，但长度应当至少为大约 10 个，优选至少大约 15 个，最优选至少大约 20 个氨基酸。适用于所述寡核苷酸探针的杂交和 PCR 技术是本领域所熟知的。可以通过限制酶消化、DNA 测序等分析阳性克隆。

本发明的多核苷酸的变体源于其他桉属和松属植物，以及源于木材
15 行业所使用的其他商业上重要的物种。其中，举例来说，包括以下裸子植物：火炬松（*Pinus taeda*），湿地松（*Pinus elliotti*），沙松（*Pinus clausa*），长叶松（*Pinus palustris*），短叶松（*Pinus echinata*），西黄松（*Pinus ponderosa*），约弗松（*Pinus jeffrey*），美加红松（*Pinus resinosa*），刚松（*Pinus rigida*），美国短叶松（*Pinus banksiana*），
20 晚松（*Pinus serotina*），北美乔松（*Pinus strobus*），山白松（*Pinus monticola*），糖松（*Pinus lambertiana*），矮松（*Pinus virginiana*），小干松 *Pinus contorta*），加勒比松（*Pinus caribaea*），海岸松（*P. pinaster*），土耳其松（*P. brutia*），阿富汗松（*P. eldarica*），大果松（*P. coulteri*），欧洲黑松（*P. nigra*）和欧洲赤松（*P. sylvestris*）；花旗松（*Pseudotsuga menziesii*）；铁杉包括异叶铁杉（*Tsuga heterophylla*）；加拿大铁杉（*Tsuga canadensis*）；西美山铁杉（*Tsuga mertensiana*）；云杉包括挪威云杉（*Picea abies*），红云杉（*Picea rubens*），白云杉（*Picea glauca*），黑云杉（*Picea mariana*），北美云杉（*Picea sitchensis*），恩格曼氏云杉（*Picea engelmanni*）和蓝叶云杉（*Picea pungens*）；北美红杉（*Sequoia sempervirens*）；冷
30 杉包括洛杉矶冷杉（*Abies lasiocarpa*），银杉（*Abies amabilis*），巨冷杉（*Abies gr. and is*），壮丽冷杉（*Abies procera*），白云杉（*Abies concolor*），红果冷杉（*Abies magnifica*），和胶冷杉（*Abies balsamea*），

柏包括北美乔柏 (*Thuja plicata*), 下延香松 (*libocedrus decurrens*), 北美香柏 (*Thuja occidentalis*), 美国扁柏 (*Chamaecyparis lawsoniana*), 美国尖叶扁柏 (*Chamaecyparis thyoides*), 黄扁柏 (*Chamaecyparis nootkatensis*), 和铅笔柏 (*Huniperus virginiana*); 落叶松包括美洲落叶松 (*Larix laricina*), Western 落叶松 (*Larix occidentalis*), 欧洲落叶松 (*Larix decidua*), 日本落叶松 (*Larix leptolepis*), 和新疆落叶松 (*Larix siberica*); 落羽杉 (*Taxodium distichum*) 和巨杉 (*Sequoia gigantea*); 和以下被子植物, 例如: 白桉 (*Eucalyptus alba*), *E. bancroftii*, *E. botyroides*, *E. bridgesiana*, 美叶桉 (*E. calophylla*), 赤桉 (*E. camaldulensis*), 柠檬桉 (*E. citriodora*), 棒萼桉 (*E. cladocalyx*), *E. coccifera*, *E. curtisii*, 山桉 (*E. dalrympleana*), 棉芝老桉 (*E. deglupta*), *E. delagatensis*, *E. diversicolor*, *E. dunnii*,), 美丽花桉 (*E. ficifolia*), 蓝桉 (*E. globulus*), 棒头桉 (*E. gomphocephala*), *E. gunnii*, *E. henryi*, *E. laevopinea*, *E. macarthurii*, *E. macrorhyncha*, 花皮桉 (*E. maculata*), *E. marginata*, *E. megacarpa*, *E. melliodora*, *E. nicholii*, *E. nitens*, *E. nova-angelica*, 斜叶桉 (*E. obliqua*), *E. obtusiflora*, *E. oreades*, *E. pauciflora*, *E. polybractea*, 王桉 (*E. regnans*), 树脂桉 (*E. resinifera*), 大叶桉 (*E. robusta*), 野桉 (*E. rudis*), 悉尼蓝桉 (*E. saligna*), 铁木桉 (*E. sideroxylon*), *E. stuartiana*, 细叶桉 (*E. tereticornis*), 毛叶桉 (*E. torelliana*), *E. urnigera*, *E. urophylla*, 多枝桉 (*E. viminalis*), *E. viridis*, *E. wandoo* 和 *E. youmanni*.

本发明的多核苷酸还可以合成, 例如, 用自动寡核苷酸合成仪合成 (例如, Beckman Oligo 1000M DNA 合成仪), 以便获得高达 50 或更多核苷酸的核苷酸片段。然后可以用分子生物学领域所公知的标准 DNA 操作技术, 将多个这样的多核苷酸片段连接在一起。一种常用的代表性多核苷酸合成技术包括合成具有例如 80 个核酸的单链多核苷酸片段, 并让该片段与合成的互补的 85 个核酸的片段杂交, 以便形成 5 个核苷酸的突出端。然后以类似方式合成下一个片段, 在相反的链上具有 5 个核苷酸的突出端。所述“粘性”末端能确保以上两个部分在杂交时能正确连接。这样, 可以在体外完全合成本发明的完整的多核苷酸。

序列 1-266 和 350-375 所示的多核苷酸可以是“部分”或完整长度的序列。部分序列不代表编码天然多肽的基因的完整编码部分。本文所披露的部分多核苷酸序列可用于获得各种物种和生物的相应的完整长

度的基因，例如，通过用基于本发明多核苷酸的探针杂交或用基于本发明多核苷酸的引物进行 PCR 扩增筛选 DNA 表达文库获得。这样，人们可以用本领域公知的方法将本发明多核苷酸的相应 mRNA 向上游和下游延伸，并鉴定相应的基因组 DNA，包括完整基因的启动子和增强子区。

因此，本发明包括含有序列 1-266 和 350-375 所示序列的分离的多核苷酸，或编码一种功能性多肽的所述序列之一的变体，包括完整长度的基因。所述延长的多核苷酸的长度可以为大约 50-大约 4000 个核酸或碱基对，其长度优选为低于大约 4000 个核酸或碱基对，更优选低于大约 3000 个核酸或碱基对，更优选低于大约 2000 个核酸或碱基对。在某些场合下，本发明延长的多核苷酸的长度低于大约 1800 个核酸或碱基对，优选低于大约 1600 个核酸或碱基对，更优选低于大约 1400 个核酸或碱基对，更优选低于大约 1200 个核酸或碱基对，最优选低于大约 1000 个核酸或碱基对。

本发明的多核苷酸还包括至少含有序列 1-266 和 350-375 所示多核苷酸的任一种或其变体的特定数量的连续残基的多核苷酸（x-聚体）。根据优选实施方案，x 的值优选为至少 20，更优选至少 40，更优选至少 60，最优选至少 80。因此，本发明的多核苷酸包括含有序列 1-266 和 350-375 所示多核苷酸的 20-聚体、40-聚体、60-聚体、80-聚体、100-聚体、120-聚体、150-聚体、180-聚体、220-聚体、250-聚体或 300-聚体、400-聚体、500-聚体、或 600-聚体或任何 x-聚体的变体的多核苷酸。就是说，就 E 值、百分相似性和杂交而言，上述变体的定义还适用于本发明多核苷酸的任何 x-聚体。

本发明还包括与序列 1-266 和 350-375 以及这些序列的变体互补和/或相应的多核苷酸探针和引物。所述寡核苷酸探针和引物大体上互补于感兴趣的多核苷酸。如果一种寡核苷酸探针或引物或其互补物包括在序列 1-266 和 350-375 所示序列之一或所述序列之一的变体中，该寡核苷酸探针或引物则被称为“相应于”本发明的多核苷酸，包括序列 1-266 和 350-375 所示序列之一或变体。

如果一条链的核苷酸在进行合适的核苷酸插入和/或缺失之后与另一股链的核苷酸配对的比例为至少 80%，优选至少 90%-95%，更优选至少 98%-100%的话，则认为这两个单链序列大体上互补。或者，如果

第一股 DNA 链能在严格杂交条件下与第二股 DNA 链杂交，则存在明显的互补性。用于测定互补性的严格杂交条件包括至少大约 1M 的盐条件，更常见的是低于大约 500mM，优选低于大约 200mM。杂交温度可以低至 5℃，但通常高于大约 22℃，更优选高于大约 30℃，最优选高于大约 37℃。对于特定杂交来说，较长的 DNA 片段可能需要更高的杂交温度。由于杂交的严格性受诸如探针组成、有机溶剂的存在和碱基错配程度的其他因素的影响，参数的组合比任一种参数单独的绝对作用更重要。来自植物或含有植物材料的样品或产品的 DNA，可以通过用存在于该样品中的 RNA 制备 cDNA 而产生的基因组 DNA。

除了 DNA-DNA 杂交之外，还可以进行 DNA-RNA、RNA-RNA 杂交实验。在第一种情况下，检测来自表达基因的 mRNA，而不是检测所述样品 mRNA 的基因组 DNA 或 cDNA。在第二种情况下，可以使用 RNA 探针。另外，还可以使用能与目标序列专一性杂交的 DNA 的人工类似物。

在具体实施方案中，所述寡核苷酸探针和/或引物包括与本发明多核苷酸序列互补的至少大约 6 个连续的残基，更优选至少大约 10 个连续残基，最优选至少大约 20 个连续残基。本发明的探针和引物的长度可以为大约 8-100 个碱基对，优选为大约 10-50 个碱基对，更优选为大约 15-40 个碱基对。所述探针可以用本领域公知的方法方便地加以选择，要考虑 DNA-DNA 杂交严格性，退火和解链温度，形成环的潜力和其他因素，这些内容是本领域所公知的。适用于设计探针，特别是适用于设计 PCR 引物的工具和软件，可以从互联网上获得，例如，在 <http://www.horizonpress.com/pcr/>。用于设计 PCR 引物的优选技术还披露于 Dieffenbach CW 和 Dvksler GS, PCR 引物：实验室手册，CSHL 出版社：冷泉港，纽约，1995。

相应于本发明多核苷酸的多种寡核苷酸探针或引物可以试剂盒形式提供。所述试剂盒通常包括多种 DNA 或寡核苷酸探针，每一种探针针对一种多核苷酸序列专一。本发明的试剂盒可以包括相应于本发明多核苷酸，包括序列 1-266 和 350-375 所示的一种或多种的探针或引物。

在一种可用于高处理量实验的实施方案中，本发明的寡核苷酸探针试剂盒包括阵列形式中的多种探针，其中，每一种探针被固定在一固体底物表面上预定的、空间上可寻找到的位置上。例如，可用于本发明

中的阵列形式披露于 US5412087, US5545531 和 PCT 公开号 WO95/00530 中, 以上文献的内容被收作本文参考。

对于诸如植物育种和质量控制操作的用途来说, 高处理量筛选系统的重要性是显而易见的, 其中, 有必要鉴定大量的种子样品和植物幼苗, 以便检查不希望的植物材料的样品或产品, 为了检疫目的等鉴定植物或含有植物材料的样品或产品, 或证实植物或含有植物材料的样品或产品的真实来源。筛选用作标记植物的识别物的本发明多核苷酸的存在或不存在, 对于随后在植物育种通过分散的花粉进行基因渐渗中检测基因流量来说是有价值的。

这样, 本发明的寡核苷酸探针试剂盒可用于以快速和节省费用的方式检查本发明多核苷酸在含有不同材料的不同样品或产品中的存在/缺乏 (或在混合存在的情况下其相对量)。可以用本发明检查的植物物种的例子包括树木, 如松树和桉树, 其他树木, 农用植物, 包括作物和牧草植物, 以及园艺植物。

本发明的另一方面包括本发明多核苷酸的收集, 本发明多核苷酸, 特别是序列 1-266, 350-375 所示的多核苷酸及其变体和 x-聚体的收集, 可以记录和/或保存记录和/或保存在介质上, 并随后用于分析和比较目的等。合适的储存介质包括磁性介质, 如磁盘, 磁带, CD-ROM 储存介质, 和光学储存介质等。适用于记录和保存信息, 以及获取信息, 如记录在所述介质上的多核苷酸序列的储存介质和方法在本领域中是众所周知的。记录在储存介质上的多核苷酸信息优选是计算机可读的, 并可用于分析和比较所述多核苷酸信息。

因此, 本发明的另一方面包括在它上面记录了本发明的多核苷酸, 特别是记录了序列 1-266, 350-375 所示所有多核苷酸及其变体, 以及序列 1-266 和 350-375 的多核苷酸的 x-聚体, 以及含有或相应于序列 1-266 和 350-375 的多核苷酸的延长序列、探针和引物的储存介质。根据一种实施方案, 所述储存介质包括本发明的一共至少 20, 优选至少 50, 更优选至少 100, 最优选至少 200 种多核苷酸。优选序列 1-266 和 350-375 所示多核苷酸或所示多核苷酸的变体。

另一方面, 本发明提供了沿 5'-3' 方向包括基因启动子序列; 编码由本发明的多核苷酸编码的多肽的至少一个功能性部分的开放读框; 和基因终止序列的遗传结构。在本文中, 一种酶的“功能性部分”是含有

影响一个代谢步骤所必需的活性位点的部分,即所述分子能够结合一种或多种反应剂或能够改善或调节反应速度的部分。活性位点可以由存在于一个或多个多肽链上的分离的部分组成,并且通常具有高的底物专一性。本文所使用的术语“由核苷酸序列编码的酶”包括由包括本发明的部分分离的多核苷酸的核苷酸序列编码的酶。

所述开放读框可以沿有义或反义方向取向,对于需要增加木质素合成的用途来说,所述开放读框可以沿有义方向插入所述结构,以使用所述结构转化目标生物可导致有关基因拷贝数量的增加,并因此增加酶的量。当需要下调木质素合成时,可将所述开放读框沿反义方向插入所述结构,以便由所述多核苷酸转录所产生的 RNA 互补于内源 mRNA 序列。这反过来又会导致有关基因拷贝数量的减少,并因此减少酶的量。或者,可以通过将合适的亚序列(例如 DNA 或 RNA)插入核酶结构中而实现调节。

还提供了含有编码由上述 DNA 序列编码的酶的基因的非编码区或互补于非编码区的核苷酸序列,以及基因启动子序列和基因终止序列的遗传结构。在本文中,术语“非编码区”包括距离翻译序列或开放读框的 5'或 3'末端大约 2000 个碱基对的不被翻译的转录序列和非转录序列。可用于本发明结构中的非编码区的例子包括内含子和 5'非编码前导序列。用这样的 DNA 结构转化目标植物能通过共抑制过程导致由该植物合成的木质素量的减少,类似于披露于以下文献中的方式,例如, Napoli 等,植物细胞 2: 279-290, 1990; 和 Carvalho Niebel 等,植物细胞 7: 347-358, 1995。

本发明的遗传结构还包括可操作地连接于待转录的多核苷酸上的基因启动子序列和基因终止序列,由它们控制该基因的表达。基因启动子序列通常位于待转录多核苷酸的 5'末端,并被用于启动该多核苷酸的转录。基因启动子序列通常存在于一个基因的 5'非编码区,不过,它们可以存在于内含子中(Luehrsen KR, 分子基因遗传学, 225:81-93, 1991),或存在于编码区,例如,存在于番茄的 PAL 上(Bloksberg, 苯丙氨酸氨裂解酶和植物病原体相互作用的生物学研究, 博士论文, 加利福尼亚大学, Davis, 1991, University Microfilms International Order No.9217564)。当所述结构包括一个沿有义方向的开放读框时,所述基因启动子序列还能启动所述开放读框的翻译。对于包括沿反义方向的开

放读框或非编码区的 DNA 结构来说, 所述基因启动子序列仅包括具有 RNA 聚合酶结合位点的转录起始位点。

可用于本发明 DNA 结构的多种基因启动子序列为本领域所熟知。所述启动子基因序列和基因终止序列可以是目标植物宿主本身所具有的, 或者可以是外源性的, 只要所述启动子能在所述目标宿主中起作用即可。例如, 所述启动子和终止序列可源于其他植物、植物病毒、和细菌质粒。基因启动子和终止序列优选源于本发明的序列本身。

影响启动子选择的因素包括所需要的该结构的组织专一性, 以及转录和翻译的时间。例如, 诸如 35S 花椰菜花叶病毒 (CaMV35S) 启动子的组成型启动子, 能影响所述酶在植物的所有部分中的活性。使用组织专一型启动子, 会导致仅在感兴趣的组织中产生所需要的有义或反义 RNA。采用使用了诱导型基因启动子序列的 DNA 结构, 可以通过诸如光照、加热、厌氧胁迫、和改变营养条件等的外部刺激调节 RNA 聚合酶结合和启动的速度。可将时序调节启动子用于实现在转化细胞的发育过程的特定时间调节 RNA 聚合酶结合和启动的速度。优选使用来自相关酶基因的原始启动子, 或来自待转化生物 (如桉树或松树) 中的特定组织-定向基因的启动子。可用于本发明的基因启动子的其他例子包括甘露氨酸合成酶 (mas), 章鱼氨酸合成酶 (ocs), 以及由 Chua 等所披露的启动子, 科学 244: 174-181, 1989。

基因终止序列位于待转录多核苷酸的 3' 末端, 这些序列可来自与基因启动子序列相同的基因, 或来自不同基因。本领域已知的很多基因终止序列可被用于本发明, 如根癌农杆菌胭脂氨酸合成酶基因的 3' 末端, 不过, 优选的基因终止序列是源于原有酶基因或源于待转化的目标生物物的序列。

本发明的遗传结构还可以含有一种选择标记, 该标记能在植物细胞中起作用, 以便检测含有本发明结构的转化细胞。所述标记是本领域所公知的, 通常能赋予对一种或多种毒素的抗性。所述标记的一种例子是 NPTII 基因, 该基因的表达会产生对卡那霉素或潮霉素的抗性, 这两种抗生素在中等浓度下通常对植物细胞具有毒性 (Rogers 等, Weissbach A 和 H 著, 植物分子生物学方法, 学术出版公司: San Diego, CA, 1988)。

或者, 可以通过本领域已知的其他技术, 如 Southern 和 Western 印迹确定目标结构在转化细胞中的存在。

用于可操作地连接本发明遗传结构的成分的技术为本领域所熟知，并包括使用含有一种或多种所披露的限制性内切酶位点的合成接头，例如，Maniatis 等，（分子克隆：实验室手册，CSHL 出版社：冷泉港，NY, 1989）。本发明的 DNA 结构可以连接到具有至少一种复制系统的载体上，例如，大肠杆菌，以便在每一次操作之后，所得到的结构能被克隆和测序，并确保操作的正确性。

本发明的遗传结构可用于转化多种植物，包括单子叶植物（例如，牧草，玉米，谷类，燕麦，小麦和大麦），双子叶植物（例如，拟南芥属，烟草，豆类，苜蓿，橡树，桉树，槭树），和裸子植物（例如，苏格兰松；参见 Aronen, Finnish Forest Res. Papers, Vol. 595, 1996), 白云杉（Ellis 等，生物技术 11:94-92, 1993）和落叶松（黄等，体外细胞 27:201-207, 1991）。在一种优选实施方案中，本发明的遗传结构被用于转化木本植物，在本文中被定义为其茎干生活多年，并且每一年通过木本组织的增加而增大直径的树木或灌木。优选的目标植物选自桉树和松树，最优选选自巨桉和辐射松。如上文所述，用包括编码由本发明的多核苷酸编码的酶的开放读框的遗传结构转化植物，会导致该植物木质素含量的改变，其中，所述开放读框的取向为有义方向。用含有反义方向的开放读框或一个基因的非编码（非翻译）区的遗传结构转化植物也会产生转化植物木质素含量的改变。

可以通过选择启动子序列，或通过选择将所述多核苷酸整合到目标生物基因组上的功能性拷贝或位点的数量控制 RNA 在目标细胞中的产生。可以用一种以上本发明的结构转化目标植物，以便改变木质素生物合成途径的一种以上酶的活性，在一种以上组织中影响酶的活性或在一个以上的表达时间影响酶的活性。类似地，可将一种结构组建成含有一个以上编码由本发明多核苷酸编码的酶的开放读框或一个以上编码所述酶的基因的非编码区。本发明的多核苷酸还可以编码与木质素生物合成途径相关的酶的其他已知序列组合使用。这样，有可能将木质素生物合成途径增加到非木本植物中，以便产生一种新的木本植物。

用于将 DNA 稳定整合到目标植物基因组中的技术为本领域所熟知，并包括根癌农杆菌介导的导入，电穿孔，原生质体融合，向生殖器官中注射，向未成熟胚胎中注射，以及高速轰击导入。技术的选择取决于要转化的目标植物。例如，双子叶植物和某些单子叶植物以及裸子植

物可以用农杆菌属 Ti 质粒技术转化，例如由 Bevan 所披露的（核酸研究 12: 8711-8721, 1984）。用于导入本发明 DNA 结构的目标包括组织，如叶片组织，分散的细胞，原生质体，种子，胚胎，分生组织；子叶，和下胚轴等。用于转化桉树和松树的一种优选方法是使用花粉（例如，参见 Aronen, Finnish Forest Res. Papers, Vol. 595, 1996）或容易再生的胚胎组织的 biolistic 方法。可用于本发明方法中的其他转化技术包括在以下文献中所披露的：Ellis 等（植物细胞报导，8: 16-20, 1989），Wilson 等（植物细胞报导，7: 704-707, 1989）和 Tautorius 等（理论应用遗传学 78: 531-536, 1989）。

一旦细胞被转化，就可以通过诸如上文所述的卡那霉素抗性标记的标记筛选在其基因组中整合了本发明 DNA 结构的细胞。然后可以在适于再生全植株的培养基中用本领域公知技术培养转基因细胞。对于原生质体来说，在合适的渗透压条件下再生细胞壁。对于种子或胚胎来说，使用合适的萌发或愈伤组织启动培养基。例如，使用合适的再生培养基。对很多物种来说，植物的再生方法业已完善。有关树木的再生的综述可以参见 Dunstan 等，“木本植物的体细胞胚发生” Thorpe TA 著，植物体外胚胎发生，农业上的当代植物科学和生物技术 20(12):471-540, 1995。Roberts 等披露了专门用于云杉再生的方法（“云杉体细胞胚发生” Redenbaugh K 著，合成种子：将合成种子用于作物改良，CRC 出版社：23 章，427-449 页，1993）。所得到的转化植物可以用本领域公知方法有性或无性方式再生，以便得到转基因植物的连续的世代。

在另一方面，本发明提供了改变一种多肽在宿主生物中的含量（浓度）或活性的方法，包括将含有本发明多核苷酸的结构稳定地整合到该植物的基因组中。本发明的遗传 NA 结构可用于转化多种生物。所述生物包括植物，如单子叶被子植物（例如，牧草、玉米、谷类、燕麦、小麦和大麦），和双子叶被子植物（例如，拟南芥属、烟草、豆类、苜蓿、橡树、桉树、槭树），以及裸子植物（例如，苏格兰松；参见 Aronen, Finnish Forest Res. Papers, Vol. 595, 1996），白云杉（Ellis 等，生物技术 11: 94-92, 1993），和落叶松（Huang 等，体外细胞 27: 201-207, 1991）。

在优选实施方案中，本发明的遗传结构被用于转化木本植物，在本文中被定义为其茎干能生活多年，并在每一年由于木质组织的增加而增

大直径的树木或灌木。目标植物优选选自桉树和松树，最优选选自巨桉和辐射松，但也可以包括下面所列举的物种的任一种：

松树：美国短叶松树（*Pinus banksiana*），土耳其松（*P. brutia*），加勒比松（*Pinus caribaea*），沙松（*Pinus clausa*），小干松（*Pinus contorta*），大果松（*P. coulteri*），短叶松（*Pinus echinata*），阿富汗松（*P. eldarica*），湿地松（*Pinus elliotti*），约弗松（*Pinus jeffrey*），糖松（*Pinus lambertiana*），山白松（*Pinus monticola*），欧洲黑松（*P. nigra*），长叶松（*Pinus palustris*），海岸松（*P. pinaster*），西黄松（*Pinus ponderosa*），美加红松（*Pinus resinosa*），刚松（*Pinus rigida*），晚松（*Pinus serotina*），北美乔松（*Pinus strobus*），欧洲赤松（*P. sylvestris*），火炬松（*Pinus taeda*），矮松（*Pinus virginiana*）。

其他裸子植物：银杉（*Abies amabilis*），胶冷杉（*Abies balsamea*），白云杉（*Abies concolor*），巨冷杉（*Abies grandis*），洛杉矶冷杉（*Abies lasiocarpa*），红果冷杉（*Abies magnifica*），壮丽冷杉（*Abies procera*），美国扁柏（*Chamaecyparis lawsoniana*），黄扁柏（*Chamaecyparis nootkatensis*），美国尖叶扁柏（*Chamaecyparis thyoides*），铅笔柏（*Huniperus virginiana*），欧洲落叶松（*Larix decidua*），美洲落叶松（*Larix laricina*），日本落叶松（*Larix leptolepis*），Western 落叶松（*Larix occidentalis*），新疆落叶松（*Larix siberica*），下延香松（*libocedrus decurrens*），挪威云杉（*Picea abies*），恩格曼氏云杉（*Picea engelmanni*），白云杉（*Picea glauca*），黑云杉（*Picea mariana*），蓝叶云杉（*Picea pungens*），红云杉（*Picea rubens*），北美云杉（*Picea sitchensis*），北美红杉（*Sequoia sempervirens*），花旗松（*Pseudotsuga menziesii*），巨杉（*Sequoia gigantea*），北美红杉（*Sequoia sempervirens*）；落羽杉（*Taxodium distichum*），加拿大铁杉（*Tsuga canadensis*），异叶铁杉（*Tsuga heterophylla*），西美山铁杉（*Tsuga mertensiana*），北美香柏（*Thuja occidentalis*），北美乔柏（*Thuja plicata*）。

桉属：白桉（*Eucalyptus alba*），*E. bancroftii*，*E. botyroides*，*E. bridgesiana*，美叶桉（*E. calophylla*），赤桉（*E. camaldulensis*），柠檬桉（*E. citriodora*），棒萼桉（*E. cladocalyx*），*E. coccifera*，*E. curtisii*，山桉（*E. dalrympleana*），棉芝老桉（*E. deglupta*），*E. delagatensis*，*E. diversicolor*，*E. dunnii*，），美丽花桉（*E. ficifolia*），蓝桉（*E. globulus*），

棒头桉 (*E. gomphocephala*), *E. gunnii*, *E. henryi*, *E. laevopinea*, *E. macarthurii*, *E. macrorhyncha*, 花皮桉 (*E. maculata*), *E. marginata*, *E. megacarpa*, *E. melliodora*, *E. nicholii*, *E. nitens*, *E. nova-angelica*, 斜叶桉 (*E. obliqua*), *E. obtusiflora*, *E. oreades*, *E. pauciflora*, *E. polybractea*, 王桉 (*E. regnans*), 树脂桉 (*E. resinifera*), 大叶桉 (*E. robusta*), 野桉 (*E. rudis*), 悉尼蓝桉 (*E. saligna*), 铁木桉 (*E. sideroxylon*), *E. stuartiana*, 细叶桉 (*E. tereticornis*), 毛叶桉 (*E. torelliana*), *E. urnigera*, *E. urophylla*, 多枝桉 (*E. viminalis*), *E. viridis*, *E. wandoo*, *E. Youmanni*, 和上述任一物种的杂交种。

10 本发明的多核苷酸具有作为标记生物,特别是植物的非破坏性标记的特殊用途。不过,其他生物也可以用本发明的多核苷酸标记,其中包括有商业价值的动物、鱼、细菌和酵母。含有本发明多核苷酸的结构可以作为外源、非功能性、非破坏性标记物稳定地导入生物中。日后通过测定该标记在材料样品中的存在与否,可以证实所述生物的起源或来源。

15 标记的检测可以用多种常规技术完成,并且通常包括使用核酸探针。通过使用分支寡核苷酸可以提高检测探针存在的灵敏度,如 Horn T, Chang CA 和 Urdea MS,“在核酸定量分析中用作信号放大物的分支寡脱氧核糖核苷酸 (bdNA)的化学合成和鉴定”,核酸研究 25(23):4842-20 4849, 1997),从而能够检测样品中少到 50 个 DNA 分子。

提供以下的实施例是为了说明而不是为了限定。

实施例 1

分离并鉴定来自巨桉的 cDNA 克隆

25 按以下方法构建并筛选两个巨桉 cDNA 表达文库(一个来自同一棵树的各组织的混合物,另一个来自同一棵树的叶片)。

使用 Chang 等的方法(植物分子生物学报 11:113-116, 1993),仅做过小的改进,从植物组织中提取 mRNA。具体地讲,将样品溶解在 CPC-RNAXB (100 mM Tris-Cl, pH 8.0; 25 mM EDTA; 2.0 M NaCl; 2% 30 CTAB; 2% PVP 和 0.05% 亚精胺*3 HCl) 中,并用 24: 1 的氯仿:异戊醇提取,用乙醇沉淀 mRNA,并用 Poly(A) Quik mRNA 分离试剂盒 (Stratagene, La Jolla, CA) 纯化总 RNA 制备物。通过逆转录酶合成,由

纯化的 mRNA 构建 cDNA 表达文库，然后按照生产商的方案用 ZAP 表达 cDNA 合成试剂盒 (Stratagene) 插入 λ ZAP 中。用 Gigapack II 包装提取物 (Stratagene) 包装所得到的 cDNA，使用来自 5 μ l 连接混合物的 1 μ l DNA 样品。用 XL1-Blue MRF' 细胞和 XL0LR 细胞 (Stratagene) 以及 ExAssist 辅助噬菌体 (Stratagene) 对所述文库进行总体切除。用 NZY 培养液 (Gibco BRL, Gaithersburg, MD) 稀释切除的噬菌粒，并铺平板到含有 X-gal 和异丙基-硫代-半乳糖苷 (IPTG) 的 LB-卡那霉素琼脂平板上。

在被铺平板并挑选用于 DNA 微量制备的克隆中，99% 含有适合筛选的插入片段。在含有卡那霉素的 NZY 培养液中培养阳性克隆，并通过碱性裂解和聚乙二醇 (PEG) 沉淀纯化 cDNA。用 1% 的琼脂糖凝胶筛选染色体污染的测序模板。按照生产商的方案，用 Catalyst 800 仪器 (Perkin Elmer/Applied Biosystems, Foster City, CA) 制备染料引物序列。

用 Perkin Elmer/Applied Biosystems Prism 377 测序仪获得阳性克隆的 DNA 序列。首先从 5' 末端对 cDNA 克隆进行测序，在某些情况下还可以从 3' 末端开始测序。对某些克隆来说，用亚克隆片段获得内部序列。用限制作图的标准方法进行亚克隆，并亚克隆到 pBluescript II SK+ 载体上。

用被设定为上述优选参数的 1996 年 2 月的 FASTA 程序 (2.0.4 版) (可以从互联网站 <ftp://ftp.virginia.edu/pub/fasta/> 获得) 或 BLASTN 程序 2.0.4 版 [1998 年 2 月 24 日]，或 2.0.6 版 [1998 年 9 月 16 日] 比较测定的 cDNA 序列和 EMBL 数据库 (Release46, 1996 年 3 月) 中的已知序列。用多种序列的多种排列构建可靠的共有序列。根据来自其他植物中的已知序列的相似性，确定分离的本发明的多核苷酸编码一种独特的酶。

使用上述方法分离了源于巨桉文库的编码以下多肽的 cDNA 序列：PAL (序列 16, 100, 242-246); C4H (序列 17, 153, 154, 和 161); C3H (序列 18, 101, 149 和 150); F5H (序列 19-21, 102, 103 和 169-171); OMT (序列 22-25, 104-107, 173 和 174); CCR (序列 26-29 和 108-111); CAD (序列 1, 30 和 112); CGT (序列 31-33 和 113-115); CBG (序列 34, 165 和 166); PNL (序列 35, 36 和 116); LAC (序列

37-41, 117 和 118); POX (序列 42-44, 119-121, 179, 249-250 和 350-358); 咖啡酸甲基转移酶(序列 187-192); 咖啡酰辅酶 A 甲基转移酶(序列 193-195); 香豆酸 Co-A 连接酶(序列 196-198); 细胞色素 P450 LXX1A (序列 201-206); 联酚氧化酶(序列 207-217); 黄酮醇葡萄糖基转移酶(序列 218); 类黄酮羟化酶(序列 219-223); 和异黄酮还原酶(序列 234-240)。

实施例 2

源于辐射松的 cDNA 克隆的分离和鉴定

10 a) 通过高处理量筛选分离 cDNA 克隆

从木质部构建辐射松 cDNA 表达文库，并按例 1 所述方法筛选。使用正向和反向引物在 Perkin Elmer/Applied Biosystems Prism 377 测序仪上获得阳性克隆的 DNA 序列，并按上述方法将测定的序列与 EMBL 数据库中的已知序列进行比较。根据与其他植物总的已知序列的相似性，所分离的 DNA 序列被确定为编码以下酶 C4H (序列 2, 3, 48, 49, 92, 124, 125, 155-160, 162 和 163); C3H (序列 4, 50-52, 93, 126, 127, 151 和 152); PNL (序列 5, 81 和 183); OMT (序列 6, 53-55, 94 和 175); CAD (序列 7, 71, 95 和 164); CCR (序列 8, 58-70, 96, 128-134 和 167); PAL (序列 9-11, 45-47, 97, 98, 122, 123 和 176, 247 和 20 248); 4CL (序列 12, 56, 57, 90, 99, 147, 148, 265 和 266); CGT (序列 72, 135 和 168); CBG (序列 73-80 和 136-141); LAC (序列 82-84, 142-144 和 172); POX (序列 85-89, 91, 145, 146, 177, 178, 180-182, 264, 359-375); α 淀粉酶 (序列 184-186); 香豆酸 6A 连接酶 (序列 199 和 200); 类黄酮羟化酶(序列 224-233); 异黄酮还原酶 (序列 241); 和联酚氧化酶(序列 251-263)。

25 b) 通过 PCR 分离 cDNA 克隆

根据下面的以前在其他物种中鉴定的过氧化物酶序列上的保守结构域设计两种 PCR 探针，以下称之为 LNB010 和 LNB011 (分别为序列 14 和 15): vanpox, hvupox6, taepox, hvupox1, osapox, ntopox2, ntopox1, 30 lespox, pokpox, luspox, athpox, hrpox, spopox, 和 tvepox (Genbank 保藏号分别为 D11337, M83671, X56011, X58396, X66125, J02979, D11396, X71593, D11102, L07554, M58381, X57564, Z22920, 和 Z31011)。

从松树木质部分离 RNA, 并按上述方法合成第一股 cDNA 链。使用 4 μ M LNB010, 4 μ M LNB011, 1 x Kogen's 缓冲液, 0.1 mg/ml BSA, 200 mM dNTP, 2 mM Mg^{2+} , 和 0.1 U/ μ l of Taq 聚合酶 (Gibco BRL) 对该 DNA 进行 PCR。条件为: 94°C 下 2 分钟, 55°C 下 1 分钟和 72°C 下 1 分钟, 进行 2 轮; 94°C 下 1 分钟, 55°C 下 1 分钟, 和 72°C 下 1 分钟, 进行 25 轮; 和 94°C 下 1 分钟, 55°C 下 1 分钟, 和 72°C 下 3 分钟, 进行 18 轮, 在 Stratagene Robocycler 中进行。以相同方式对该基因进行再次扩增。使用 Schleicher & Schuell Elu-Quik DNA 纯化试剂盒从 TAE 琼脂糖凝胶中纯化大约 200bp 的带, 并克隆到 T-尾 pBluescript 载体上 (Marchuk D 等, 核酸研究 19:1154, 1991)。根据与已知序列的相似性, 分离的基因 (序列 13) 被确定为编码松树过氧化物酶 (POX)。

实施例 3

使用 O-甲基转移酶 (OMT) 基因改变木质素生物合成
用辐射松 OMT 基因转化烟草植物

通过用公开的方法直接转化(参见 An G, Ebert PR, Mitra A, Ha SB, “二元载体” Gelvin SB, Schilperoort RA, 著, 植物分子生物学手册, Kluwer 学术出版社: Dordrecht, 1988)将含有包括源于辐射松的 OMT 编码区 (序列 53) 的多核苷酸的有义和反义结构插入 LBA4301 中 (由 University of California, Davis, CA 的 Dr. C. Kado 馈赠)。通过限制性消化和 DNA 测序证实所述转基因结构的存在和完整性。

用 Horsch 等的方法 (科学 227:1229-1231, 1985) 转化烟草 (Nicotiana tabacum cv. Samsun) 叶子切片。建立 OMT 的有义结构的 5 个独立的转化植物品系, 并建立 OMT 的反义结构的 8 个独立的转化植物品系。用“Southern”印迹实验证实含有合适的木质素基因结构的转化植物。在下面的表 2 中被标明为“Southern”一栏中的“+”表示转化的植物品系被证实为独立的转化品系。

在转化植物中表达松属 OMT

从用 OMT 有义和反义结构产生的每一个独立的转化植物品系中分离总 RNA。在 Northern 印迹实验中分析 RNA 样品, 以便测定所述转基因在每一个转化品系中的表达水平。在表 2 中被标明为 Northern 一栏中的数据, 表示含有 OMT 的有义和反义结构的转化植物品系, 相对

Northern 印迹上的背景而言，都表现出高水平的表达。在 2 号有义植物品系中未测出 OMT 的表达，因为 RNA 样品表现出降解的迹象。与来自空载体转化的对照植物的样品没有可检测的杂交。

在转化植物中改变 OMT 酶活性

5 分析用 OMT 有义和反义结构产生的转化植物品系，分析转化烟草植物中由松属 OMT 基因和内源烟草 OMT 基因编码的 OMT 酶的总的活性。从每一种转化植物制备粗制蛋白提取物，并用 Zhang 等的方法（植物生理学，113:65-74, 1997）分析。在表 1 中被标明为“酶”的一栏中的数据表示含有 OMT 有义结构的转化植物品系通常具有较高的 OMT 酶活性，最高为 199%，而含有 OMT 反义结构的转化植物品系通常具有较低的 OMT 活性，最低为 35%，以上百分比是相对空载体转化的对照植物而言。3 号有义植物品系中的 OMT 酶的活性没有测定。

转化植物中松属 OMT 对木质素浓度的影响

15 用已经完善的硫代乙醇酸提取方法（参见 Freudenberg 等，木质素的构建和生物合成，Springer-Verlag: 柏林，1968）测定转化植物木质素的浓度。简单地讲，在液氮中冷冻平均大小为 38 日龄的烟草全植株，并用研钵和研棒研磨成细粉。分别用甲醇提取 100 毫克来自空载体转化过的对照植物品系，含有 OMT 有义结构的 5 个独立的转化植物品系和含有 OMT 反义结构的 8 个独立的转化植物品系的冷冻粉末，然后用 20 10% 的硫代乙醇酸提取，最后溶解在 1 M NaOH 中。测定最终提取物在 280nm 下的吸收值。表 2 中被标明为“TGA”一栏中的数据表示含有有义和反义 OMT 基因结构的转化植物品系，相对空载体转化的对照植物品系而言，均表现出木质素的显著减少。

表 2

	植物品系	转基因	方向	Southern	Northern	酶	TGA
5	1	对照	na	+	空白	100	104
	1	OMT	有义	+	2.9E+6	86	55
	2	OMT	有义	+	na	162	58
	3	OMT	有义	+	4.1E+6	na	63
	4	OMT	有义	+	2.3E+6	142	66
10	5	OMT	有义	+	3.6E+5	199	75
	1	OMT	反义	+	1.6E+4	189	66
	2	OMT	反义	+	5.7E+3	35	70
	3	OMT	反义	+	8.0E+3	105	73
	4	OMT	反义	+	1.4E+4	109	74
15	5	OMT	反义	+	2.5E+4	87	78
	6	OMT	反义	+	2.5E+4	58	84
	7	OMT	反义	+	2.5E+4	97	92
	8	OMT	反义	+	1.1E+4	151	94

20 以上数据清楚地表明, 通过 OMT 的木质素合成基因的有义或反义表达可以直接操纵通过 TGA 分析测定的木质素的浓度。

实施例 4

用 4-香豆酸: 辅酶 A 连接酶(4CL)基因改变木质素生物合成

25 a) 用辐射松 4CL 基因转化烟草植物

按照上述方法, 通过直接转化将含有包括源于辐射松的 4CL 编码区(序列 56)的多核苷酸的有义和反义结构插入根癌农杆菌 LBA4301, 通过限制性消化和 DNA 测序证实该转基因结构的存在和完整性。

30 按上述方法转化烟草(*Nicotiana tabacum* cv. Samsun) 叶子切片。建立 4CL 的有义结构的 5 个独立的转化植物品系, 并建立 4CL 反义结构的 8 个独立的转化植物品系。用 Southern 印迹实验证实含有合成的木质素基因结构的转化植物。表 3 中被标明为“Southern”一栏中的“+”表示所列举的转化植物品系被证实为独立的转化品系。

b) 在转化植物中表达松属 4CL

从用 4CL 有义和反义结构产生的每一个独立的转化植物品系中分离总 RNA。在 Northern 印迹实验中分析 RNA 样品，以便测定所述转基因在每一个转化品系中的表达水平。在表 3 中被标明为 Northern 一栏中的数据表示含有 4CL 的有义和反义结构的转化植物品系，相对 Northern 印迹上的背景而言，都表现出高水平的表达。在 1 号反义植物品系中未测出 4CL 的表达，因为在进行该实验时是没有它的。与源于空载体转化的对照植物的 RNA 样品不存在可检测的杂交。

c) 在转化植物中改变 4CL 酶活性

分析用 4CL 有义和反义结构产生的转化植物品系，分析转化烟草植物中由松属 4CL 基因和内源烟草 4CL 基因编码的 4CL 酶的总的活性。从每一种转化植物制备粗制蛋白提取物，并用 Zhang 等的方法(植物生理学, 113:65-74, 1997) 分析。在表 3 中被标明为“酶”的一栏中的数据表示含有 4CL 有义结构的转化植物品系通常具有较高的 4CL 酶活性，最高为 258%，而含有 4CL 反义结构的转化植物品系通常具有较低的 4CL 活性，最低为 59%，以上百分比是相对空载体转化的对照植物而言。

d) 转化植物中松属 4CL 对木质素浓度的影响

按例 3 所述方法测定转化植物材料样品中木质素的浓度。表 3 中被标明为“TGA”一栏中的数据表示含有有义和反义 4CL 基因结构的转化植物品系，相对空载体转化的对照植物品系而言，均表现出木质素的显著减少。以上数据清楚地表明，通过 4CL 的木质素合成基因的有义或反义表达可以直接操纵通过 TGA 分析测定的木质素的浓度。

表 3

	植物品系	转基因	方向	Southern	Northern	酶	TGA
5	1	对照	na	+	空白	100	92
	2	对照	na	+	空白	100	104
	1	4CL	有义	+	2.3E+4	169	64
	2	4CL	有义	+	4.5E+4	258	73
	3	4CL	有义	+	3.1E+4	174	77
10	4	4CL	有义	+	1.7E+4	164	80
	5	4CL	有义	+	1.6E+4	184	92
	1	4CL	反义	+	na	59	75
	2	4CL	反义	+	1.0E+4	70	75
	3	4CL	反义	+	9.6E+3	81	80
15	4	4CL	反义	+	1.2E+4	90	83
	5	4CL	反义	+	4.7E+3	101	88
	6	4CL	反义	+	3.9E+3	116	89
	7	4CL	反义	+	1.8E+3	125	94
	8	4CL	反义	+	1.7E+4	106	97

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实施例 5

用本发明的木质素生物合成基因转化烟草

通过上述直接转化将含有包括源于巨桉的 C3H (序列 18), F5H (序列 19), CCR (序列 26) 和 CGT (序列 31) 的编码区和源于辐射松的 OMT (序列 6), PAL (序列 45 和 47), C4H (序列 48 和 49), PNL (序列 81) 和 LAC (序列 83) 的编码区的多核苷酸的有义和反义结构插入根癌农杆菌 LBA4301 中。通过限制性消化和 DNA 测序证实该转基因结构的存在和完整性。

用例 3 所述方法转化烟草 (*Nicotiana tabacum* cv. Samsun) 叶子切片。建立 12 个上述所列举的每一种有义和反义结构独立的转化植物品系。用 Southern 印迹实验证实含有合适的木质素基因结构的转化植物。分析过的所有转化植物品系都被证实为独立的转化品系。

实施例 6

操纵转化植物中木质素的含量

a) 通过 Northern 印迹实验测定转基因表达

从例 5 中所述每一个独立的转化植物品系中分离总 RNA。在 Northern 印迹实验中分析 RNA 样品，以便测定每一个转化品系中转基因的表达式。表 4 中被标明为“Northern”的一栏表示测定的所有植物品系相对 Northern 印迹上背景的转基因表达水平。与来自空载体转化的对照植物的 RNA 样品不存在可检测的杂交。

b) 测定转化植物中木质素浓度

按例 3 所述方法测定了空载体转化的对照植物品系和多达 12 个例 5 所示每一种有义结构和每一种反义结构的独立转化品系的木质素浓度。表 4 中被标明为“TGA”的一栏表示用 C3H, F5H, CCR, PAL, C4H, PNL 和 LAC 转化过的植物品系的硫代乙醇酸可提取的木质素，以转化植物相对对照植物的 TGA 的可提取的木质素的平均百分比表示。波动范围用括号表示。

表 4

转基因	方向	品系数量	Northern	TGA
对照	na	3	空白	100 (92-104)
C3H	有义	5	3.7E+4	74 (67-85)
20 F5H	有义	10	5.8E+4	70 (63-79)
F5H	反义	9	5.8E+4	73 (35-93)
CCR	有义	1	na	74
CCR	反义	2	na	74 (62-86)
PAL	有义	5	1.9E+5	77 (71-86)
25 PAL	反义	4	1.5E+4	62 (37-77)
C4H	反义	10	5.8E+4	86 (52-113)
PNL	反义	6	1.2E+4	88 (70-114)
LAC	有义	5	1.7E+5	na
30 LAC	反义	12	1.7E+5	88 (73-114)

图 5 表示可提取的木质素的量，以通过例 5 所示方法用 PAL (有义和反义), C4H (反义), C3H (有义), F5H (有义 和反义), C5H (有义 和

反义) C3H (有义; 在图 5 中被称为 COMT), OMT (有义 和 反义; 在图 5 中被称为 CCOMT), 4CL (有义 和 反义), CCR (有义 和 反义) 和 CGT (反义) 结构转化的烟草植物相对野生型木质素的百分比表示。测定转基因植物中硫代乙醇酸可提取的木质素的量, 归一化为空载体对照植物。三种提取物分别来自大约 10 个独立产生的转基因植物的每一种。三种提取物的平均值用黑点表示, 作为这种植物的木质素值。用特定 cDNA 结构转化的 10 个独立转基因植物的平均值用线条表示。空载体转化的对照植物的平均值用 X 表示。对照的值被外推通过有关区域, 以便于比较。黑色线条表示平均值, 该平均值相对对照植物而言, 木质素的含量显著降低($p < 0.05$)。灰色线条表示相对对照植物没有明显变化的平均值。

含有有义和反义木质素生物合成基因结构的转化品系所表现出的平均木质素含量显著低于空载体转化的对照植物品系的含量。对木质素浓度最明显的影响出现在 OMT 有义植物中, 和 PAL 有义植物中。以上数据清楚地表明, 通过 TGA 分析测定的木质素浓度可以通过常规的反义方法, 还可以通过用本发明的木质素生物合成基因进行有义超量表达而进行直接操纵。

实施例 7

操纵转化植物中木质素酶活性

分析含有源于辐射松的 PAL (序列 45), PNL (序列 81) 和 LAC (序列 83) 和源于巨桉的 CGT (序列 31) 的有义和反义结构的转化的烟草植物的组织提取物中特定木质素生物合成酶的活性和底物专一性。

用公开的方法对 PAL (Southerton SG 和 Deverall BJ, 植物病理学 39:223-230, 1990), CGT (Vellekoop P 等, FEBS, 330:36-40, 1993), PNL (Espin CJ 等, 植物化学 44:17-22, 1997) 和 LAC (Bao W 等, 科学, 260:672-674, 1993) 进行酶分析。表 5 中被标明为“酶”一栏中的数据表示来自分析过的所有植物品系的重复测定值, 以相对空载体转化的对照植物的酶活性的百分比表示。波动范围用括号表示。

表 5

	转基因	方向	品系数量	酶
	对照	na	3	100
5	PAL	有义	5	87 (60-124)
	PAL	反义	3	53 (38-80)
	CGT	反义	1	89
	PNL	反义	6	144 (41-279)
	LAC	有义	5	78 (16-240)
10	LAC	反义	11	64 (14-106)

除了 PNL 反义转化植物品系之外，所有转化的植物品系所表现出的平均木质素酶活性都明显低于在空载体转化的对照植物中所观察到的活性。对木质素酶活性最明显的影响出现在 PAL 反义转化植物品系中。其中，所有的品系都表现出降低了的 PAL 活性，并且在 LAC 反义转化植物品系中所表现出的 LAC 活性仅为空载体转化的对照植物品系的 14%。

实施例 8

20 木质素生物合成基因的功能鉴定

将含有包括源于辐射松的 PAL (序列 47), OMT (序列 53), 4CL (序列 56 和 57) 和 POX (序列 86), 以及源于巨桉的 OMT (序列 23 和 24), CCR (序列 26-28), CGT (序列 31 和 33) 和 POX (序列 42 和 44) 的编码区的多核苷酸的有义结构插入商业出售的蛋白表达载体 pProEX-1 (Gibco BRL) 中。将所得到的结构转入大肠杆菌 XL1-Blue (Stratagene) 中，然后通过添加 IPTG 对其进行诱导，以便产生重组蛋白。用 Ni 柱层析(Janknecht R 等，美国科学院院报 88:8972-8976, 1991) 生产松属 OMT 和 4CL 结构以及桉属 OMT 和 POX 结构的纯化蛋白。对每一种纯化蛋白的酶分析，结论性地证实了测试基因的预期的底物专一性和酶促活性。

在表 6 中示出了表明证实辐射是 4CL 基因 (序列 56) 和 辐射松

OMT 基因 (序列 53)的酶促活性的两个代表性酶分析实验。对于 4CL 酶来说,一个单位等于以每分钟 0.1 个吸收单位的速度将底物转化成产物所需要的蛋白量。对于 OMT 酶来说,一个单位等于每分钟将 1 皮摩尔底物转化成产物所需要的蛋白量。

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表 6

转基因	纯化 步骤	提取物 总 ml	蛋白 总 mg	总活性 单位	%产物 活性	纯化 倍数
4CL	粗制物	10 ml	51 mg	4200	100	1
	Ni 柱	4 ml	0.84 mg	3680	88	53
OMT	粗制物	10 ml	74 mg	4600	100	1
	Ni 柱	4 ml	1.2 mg	4487	98	60

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表 6 中的数据表明,纯化的 4CL 和纯化的 OMT 酶在酶分析中都表现出高的活性,证实了在该申请中所披露的对 4CL 和 OMT 基因的鉴定。来自用空载体转化的大肠杆菌的粗制蛋白制剂,在 4CL 或 OMT 酶分析中未表现出活性。

实施例 9

证实植物中特殊序列识别物的存在/缺乏

用不存在于烟草中的独特的识别序列生产转基因烟草植物。所插入的独特的识别序列是从辐射松 (序列 402) 和巨桉 (序列 403) 中分离的。通过用公开的方法(参见 An G, Ebert PR, Mitra A, Ha SB, “二元载体”, Gelvin SB, Schilperoort RA, 著, 植物分子生物学手册, Kluwer 学术出版社, Dordrecht, 1988)通过直接转化将所述独特的识别序列插入根癌农杆菌 LBA4301(由 University of California, Davis, CA 的 Dr.C.Kado 馈赠)。通过限制性消化和 DNA 测序,证实所述独特的识别序列在农杆菌属转基因结构上的存在和完整性。

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用 Horsch 等(科学 227:1229-1231, 1985)的方法转化烟草 (Nicotiana

tabacum cv. Samsun) 叶子切片。建立所使用的每一种独特的序列识别物的三种独立的转化植物品系。用缺乏独特的序列识别物的空基因转移载体建立两个空载体对照植物品系。

5 用 Southern 印迹分析确定所述序列识别物的独特性，以便检验该序列识别物在有关植物基因组中的存在。如果所述序列识别物是独特的，并因此被用作标记物，那么该序列识别物应当明确不存在于未被标记过的植物中，并且应当明确地存在于标记过的植物中。在本实施例中，所述独特的识别物预期不存在于空载体转化的对照植物中。该独特的识别物应当预期存在于用该独特序列识别物转化过的转基因植物
10 中。

用 Murray 和 Thompson 的十六烷基三甲基溴化铵 (CTAB) 方法 (核酸研究 8:4321-4325, 1980) 制备来自空载体转化的对照植物和用独特序列识别物转化过的植物的基因组 DNA。用限制性酶消化所述 DNA 样品，对于用松属独特序列识别物 (序列 402) 转化过的植物来说使用
15 EcoRI，对于用桉属独特序列识别物 (序列 403) 转化过的植物来说使用限制酶 XbaI。在 1% 的琼脂糖凝胶上分离所述限制性消化所产生的 DNA 片段；图 2 的左侧照片和图 2 的右侧照片分别表示来自松属和桉属实验的 DNA 样品的 DNA 片段形式。

在所述琼脂糖凝胶电泳步骤之后，用由 Southern 建立的方法 (分子
20 生物学方法 98:503-517) 将所述 DNA 样品转移到 Hybond-N+ 牌尼龙膜 (Amersham Life Science, Little Chalfont, Buckinghamshire, England) 上。用放射性标记过的探针检测所述尼龙膜上上述独特序列识别物，并在高严格条件下洗涤 (最终洗涤：0.5 X 柠檬酸钠盐缓冲液 (SSC) 加 0.1% 十二烷基硫酸钠 (SDS), 15 分钟，65°C)。用放射性自显影检测探
25 针与基因组 DNA 样品中的互补序列杂交。结果如图 3 和 4 所示。

图 3 (相应于图 2 的左侧照片) 表示用源于松属序列识别物 (序列 402) 的探针进行的 Southern 印迹分析中检测到的杂交形式。泳道 A-B 含有源于空载体转化的对照植物的 DNA 样品，而泳道 C-E 含有源于用序列 402 转化过的植物的 DNA。在泳道 A-B 中没有杂交，这表明序列
30 402 不存在于空载体转化的烟草植物中；就是说序列 402 是适用于烟草植物的非普遍性标记的独特标记。在泳道 C-E 中存在强的杂交，这表明通过转化接受了序列 402 的植物业已明确地、并非普遍性地被序列

402 所包含的独特序列所标记。

图 4（相应于图 2 的右侧照片）表示用源于桉属序列识别物（序列 403）的探针进行的 Southern 印迹分析中检测到的杂交形式。泳道 A-B 含有源于空载体转化的对照植物的 DNA 样品，而泳道 C-E 含有源于用序列 403 转化过的植物的 DNA。在泳道 A-B 中没有杂交，这表明序列 403 不存在于空载体转化的烟草植物中；就是说序列 403 是适用于烟草植物的非普遍性标记的独特标记。在泳道 C-E 中存在强的杂交，这表明通过转化接受了序列 403 的植物业已明确地、并非普遍性地被序列 403 所包含的独特序列所标记。

本实施例清楚地表明了在本说明书中所披露的序列在非普遍性标记转基因材料方面的用途。从大量的潜在标记中选择独特的序列，并证实其在要标记的生物的基因组中的缺乏。将该标记插入要标记的生物的基因组中，并使用业已完善的 DNA 检测方法明确地检测被用作标记物的所述独特序列识别物。

由于在本实施例中所使用的序列专一性检测方法，本说明书所披露的本发明的用户有很大可能性在所披露的序列中间发现一种序列识别物，该识别物可用于标记任何特定生物，并且该方法是一种用于证实被标记的生物只可能获得了特定标记的明确方法，该生物是通过将所述独特序列专门加入到要标记的生物的基因组中而标记过的。如果本发明的用户将用于特定生物中的标记的准确序列作为秘密保守，那么有关该生物的起源和历史的任何争议，都可以通过在本实施例中所证实的标记检测技术得到明确无误的解决。

在所附序列表中示出了序列 1-403。在所附序列表中使用的核苷酸密码包括符号“n,”符合 WIPO 标准 ST.25 (1998), 附录 2, 表 1。

本文所引用的所有文献（包括专利文献和非专利文献）被以全文形式收作本文参考。

尽管在以上说明中已经结合某些优选实施方案对本发明进行了说明，并且为了说明目的提供了许多细节，但本领域技术人员显而易见的是，本发明还有其他实施方案，并且在不超出本发明基本原则的前提下，可以对本文所披露的细节进行大的改变。

序列表

<110> Bloksberg, Leonard N.
Havukkala, Ilkka

<120> 改变植物木质素含量的材料和方法

<130> 11000.1003c4PCT

<150> US 09/169,789

<151> 1998-10-09

<150> US 60/143,811

<151> 1999-07-14

<160> 403

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 535

<212> DNA

<213>

<220>

<221>

<222> (110)...(110)

<400> 1

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aggattgcct	cggttgggct	gcccgggacc	cttctggggt	cctctcccn	tacaaattca	120
cccgaggcc	gtgggaagcg	aagacgtctc	gattaagatc	acgcactgtg	gagtgtgcta	180
cgcagatgtg	gcttggacta	ggaatgtgca	gggacactcc	aagtatcctc	tggtgccggg	240
gcacgagata	gttggaattg	tgaaacaggt	tggtccagt	gtccaacgct	tcaaagttgg	300
cgatcatgtg	ggggtgggaa	cttatgtcaa	ttcatgcaga	gagtgcgagt	attgcaatga	360
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<211> 671

<212> DNA

<213>

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<211> 940

<212> DNA

<213>

<220>

<221>

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<400> 3

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aacaaccccg	ccaactggaa	gaaccccgag	gagttccgcc	ccgagcgggt	cttcgaggag	420
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<210> 4

<211> 949

<212> DNA

<213>

<220>

<221>

<222> (1) ... (949)

<223> n

<400> 4

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<211> 959

<212> DNA

<213>

<220>

<221>

<222> (697) ... (697)

<400> 5

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<210> 6

<211> 1026

<212> DNA

<213>

<400> 6

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 <211> 624
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cactccatcg	agcgggagat	caattccgtc	aacgacaatc	cgtaaatcga	tgtctccagg	600
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<210> 10

<211> 278

<212> DNA

<213>

<400> 10

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gtcaattccc	tcggcttgat	ctccgccaga	aagactgccg	aggccgttga	gattttaaag	180
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<210> 11

<211> 765

<212> DNA

<213>

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<210> 12

<211> 453

<212> DNA

<213>

<400> 12

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tccggaacgc	tcaataaa	atcctcgatt	acaggaactg	gcgagtctct	cccgcacaat	180
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gcttccaggt	ggatcctgct	aatcgaattc	ctgcagcccg	gggtccact	agttctagag	420
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<210> 13
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<210> 14
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<210> 15
 <211> 22
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<210> 16
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<210> 17
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<210> 18
 <211> 414
 <212> DNA
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<400> 18
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tctccggcaa gtccacacc ttctgtgtcg gcgacctcaa ggagaacctg cggatgctca      360
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<210> 19
 <211> 469
 <212> DNA
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cttctccgaa caaaccacaa ggtactgcct taccctcgga gctgccgggc gcatggccga      180
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taagcagccg tgaggcggtc cgggagtgtc tcaccaccca cgacaaggac ctcgcttctc      360
gccccaaatc caaggcgggg atccacttgg gctacgggta tgccgggttt ggcttcgtag      420
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<210> 20
 <211> 341
 <212> DNA
 <213>

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<400> 20
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agaagtatgg cgggatcttc cacctccgca tgggcttctt gcacatggtt gccgtgtcgt      180
cccccgacgt ggcccgccag gtccctccagg tccacgacgg gatcttctcg aaccggcctg      240
ccaccatcgc gatcagctac ctacagtatg accgggcgga catggccttc gcgcactacg      300
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<210> 21
 <211> 387
 <212> DNA
 <213>

<400> 21

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cgcgagtctg	gcgaagaagt	atggcgggat	cttccacctc	cgcatgggct	tcctgcacat	180
ggttgccgtg	tcgtccccc	acgtggcccc	ccaggtcctc	caggtccacg	acgggatctt	240
ctcgaaccgg	cctgccacca	tcgcgatcag	ctacctcacg	tatgaccggg	ccgacatggc	300
cttcgcgcac	tacggcccgt	tctggcggca	gatgcggaag	ctgtgcgtga	tgaaagctct	360
tcagcgggaag	cgggctgagt	cgtggga				387

<210> 22

<211> 443

<212> DNA

<213>

<400> 22

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aaagcccaaa	ctcgtacaga	aggagagaga	gagagagaat	agaagcatga	gtgcatgcac	180
gaaccaagca	atcacgacgg	ccagtgaaga	tgaagagttc	ttgttcgcca	tggaatgaa	240
tgctctgata	gcactcccct	tggtcttgaa	ggccaccatc	gaactgggga	tcctcgaaat	300
actggccgag	tgccgggccta	tggtccact	ttcgctgct	cagattgcct	cccgtctctc	360
cgaaagaac	ccggaagccc	ccgtaaccct	tgaccggatc	ctccggtttc	tcgccagcta	420
ctccatcctc	tcttgcactc	tcg				443

<210> 23

<211> 607

<212> DNA

<213>

<400> 23

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acttaggtca	actgcaacat	ttcttgatca	caacatatta	caatattcct	aagcagagag	180
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tgatgctctt	taccaatata	ttttggagac	cagcgtgtac	ccaagagagc	ctgagcccat	360
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cgaagggcag	ttcttgaaca	tgcttctcaa	gctcatcaaa	gccaagaaca	ccatggagat	480
tggtgtcttc	actggctact	ctctcctcgc	caccgctctt	gctcttctctg	atgacggaaa	540
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<210> 24

<211> 421

<212> DNA

<213>

<400> 24

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ccaagtctcg	gacgaggagg	cgaacctctt	cgccatgcag	ctggcgagcg	cctccgtgct	180
ccccatggtc	ctcaaggccg	ccatcgagct	cgacctcctc	gagatcatgg	ccaaggccgg	240
gccgggcgcg	ttcctctccc	cgggggaagt	cgcgccccag	ctcccgaccc	agaaccccca	300
ggcaccgcgt	atgctcgacc	ggatcttccg	gctgctggcc	agctactccg	tgctcacgtg	360
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421

<210> 25
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 <212> DNA
 <213>

<400> 25

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cgaagcattc	ggaagtcggc	cacaagagcc	tcttgagag	cgatgctctc	taccagtata	180
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cagccaaaca	tccatggaac	ctgatgacca	catcggcgga	tgaagggcag	ttcctgaaca	300
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tcaatggttc	aaagacaaca	taagacagaa	gatggaaaaa	atagaaagga	aggaaagtat	660
taagggtagt	ttctcatttc	atcaatgctt	gatttttgaga	tctcctttct	ggtgcatca	720
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<210> 26
 <211> 508
 <212> DNA
 <213>

<400> 26

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agggacgggc	tacgtcggca	agttcatcgt	ggaagcgagt	gcaaaagcag	ggcatccac	240
gttcgcgctg	gttaggcaga	gcacggcttc	cgaccccgtc	aaggggccagc	tcgtcgagag	300
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gaaggcaatc	aagcaagccg	acgtggtgat	atcgacagtg	gggcacatgc	aaatggcgga	420
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<210> 27
 <211> 495
 <212> DNA
 <213>

<400> 27

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aagaggaagg	tggggcagcc	taaaggggca	ctgcgggtca	ctgcatcaag	caataagaag	180
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ggtgagtcgg	acaaggactt	cgctgatttt	tcattccaaga	tcctgcattt	gaaaggagac	360
agaaaggatt	ttgattttgt	taaatctagt	cttgctgcag	aaggctttga	cgttgtttat	420
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<210> 28
 <211> 472

<212> DNA

<213>

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gggccacccc	acgtacgtcc	tccagcgtcc	ggagaccggc	ctcgacattg	agaagctcca	180
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tggaaatgtc	aagcggtttt	tgccgtcaga	gttcggaatg	gacccggccc	tcatgggtca	420
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<210> 29

<211> 396

<212> DNA

<213>

<400> 29

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cgtccggtta	catcgctcgt	tggtcgtca	agctcctcct	ccagcgcggc	tacaccgtca	180
aggccaccgt	ccgcgatccg	aatgatccaa	aaaagactga	acatttgctt	ggacttgatg	240
gagcgaaaga	tagacttcaa	ctgttcaaag	caaacctgct	ggaagagggt	tcatttgatc	300
ctattgttga	gggttggtgca	ggcgtttttc	aaactgcctc	tcccttttat	catgatgtca	360
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<210> 30

<211> 592

<212> DNA

<213>

<400> 30

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tgctcgggtt	gggctgccc	ggacccttct	gggttcctct	ccccctacaa	attcaccgcg	180
agggccgtgg	gaagcgaaga	cgtctcgatt	aagatcacgc	actgtggagt	gtgctacgca	240
gatgtggctt	ggactaggaa	tgtgcaggga	cactccaagt	atcctctggt	gccagggcac	300
gagatagtgt	gaattgtgaa	acaggttggc	tccagtgtcc	aacgcttcaa	agttggcgat	360
catgtggggg	tgggaaactta	tgtcaattca	tgagagaggt	gcgagtattg	caatgacagg	420
ctagaagtcc	aatgtgaaaa	gtcggttatg	acttttgatg	gaattgatgc	agatgggtaca	480
gtgacaaagg	gaggatattc	tagtcacatt	gtcgtccatg	aaaggatttg	cgtcaggatt	540
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<210> 31

<211> 468

<212> DNA

<213>

<400> 31

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taccctgcac	aaagccacat	tggcgccatg	ctcaagctag	caaagctcct	ccatcacaag	180
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ggccccgagt	tcacaaatgg	aatgctgagc	gactttcagt	tcctgacaa	ccccgatgg	300
cttcctcctt	cggacttgga	tgcgatccaa	gacatcaaga	tgctctgcga	atcgtccagg	360

aactatatgg tcagcccat caacgatctt gtatcgagcc tgggctcgaa cccgagcgtc 420
cctccggtga cttgcatcaa tctcggtagg ttatcatgaca ctctgtgac 468

<210> 32
<211> 405
<212> DNA
<213>

<400> 32
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agcaagcccc taactcagt gtctatgtga gtcttgggag catcgctct gtgaacgagt 180
cggaattttc cgaaatagct ttaggttttag ccgatagcca gcagccattc ttgtgggtgg 240
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<210> 33
<211> 380
<212> DNA
<213>

<400> 33
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aggagctcac aagcattggc gacatcttctg aggaggagaa gaagcatgag ggccctcagg 180
tcccgaacct cgacctcgag gacatagcgt cttaaagacc cgtggtgagg gagagggtgc 240
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tcgaggagaa ggacaagcat 380

<210> 34
<211> 305
<212> DNA
<213>

<400> 34
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cgtcgtggtc ggccggcgcc gcgtggtgga cctcatcgcc gtccatgctg aaggcgtcga 180
aggaagcgga catggctggg ggatcgatcg accgatccga tcggccggag gatttcgaga 240
tcggagatgg agagatggaa atgaaagaga gagagagaga gagatccggt ggactggtgg 300
tggtt 305

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<211> 693
<212> DNA
<213>

<400> 35
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ggcattcccc aatgtgggtc aggcctgtt tgggtgtcaac tctggccgtg gcagagtgc 180
tgccatggcc gcttacaagg tcacctgct caccctgaa ggcaaagtcg aactcgacgt 240
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ctgccgtgcc ggctcttgct cctcctgcgc gggcaaggtc gtggcgggga gcgtcgacca 360

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cgcctaccct	aagtctgagg	tcaccattga	gaccacaag	gaagaggagc	tcactgcttg	480
aagctctcct	atatttgctt	ttgcataaat	cagtctcact	ctacgcaact	ttctccactc	540
tctccccct	tcactacatg	tttgtttagt	ccttttagtct	cttccttttt	tactgtacga	600
gggatgattt	gatgttattc	tgagtctaata	gtaatggctt	ttctttttcc	tatttctgta	660
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<210> 36
 <211> 418
 <212> DNA
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<400> 36						
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atgccttagt	ttgaaaaatt	aaccaactat	taaaattaat	gatgatgaat	atggattatg	180
tgtgaaaaac	tatatagact	taaaattgac	tcagaagaca	ttcttttctt	cttattttat	240
gatatgatga	attcgggtcta	aacaggcaaa	tggtgtcaaa	cgggaagtcg	gcaaaactct	300
tcctcggcag	tgactaccgg	gcgggcgatg	atgcggatcc	gggggccggg	tcgctggaga	360
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<210> 37
 <211> 777
 <212> DNA
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<400> 37						
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ggacaccggg	ataatcgcg	cggagaccca	ccccatccat	ctgcacggat	tcaacttctt	180
cgggtgtggc	aaaggagtg	ggaattatga	cccaaagaag	gatccaaga	agttcaatct	240
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<210> 38
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 <212> DNA
 <213>

<400> 38						
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tcgatgttca	cgtgggccaa	tccatggctg	tcttagtgac	cttaaatcag	cctccaaagg	180
actactacat	tgctgcattc	acccggttca	ccaagacggt	tctcaatgca	actgcagtgc	240
tacactacac	caactcgctt	acccagttt	cggggccact	accagctggt	ccaacttacc	300
aaaaacattg	gtccatgaag	caagcaagaa	caatcaggtg	gaac		344

<210> 39
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<212> DNA

<213>

<400> 39

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ggtgaacggg	caattcccgg	gtccgacttt	ggaagttaac	gacggcgaca	ccctcgttgt	240
caatgtcgtc	aacaaagctc	gctacaacgt	caccattcac	tggcacggcg	tccggcaggt	300
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<210> 40

<211> 358

<212> DNA

<213>

<400> 40

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catgtatgat	tcaatcgatg	ttcacgtggg	ccaatccatg	gctgtcttag	tgaccttaaa	180
tcagcctcca	aaggactact	acattgtcgc	atccacccgg	ttcaccaaga	cggttctcaa	240
tgcaactgca	gtgctacact	acaccaactc	gcttacccca	gtttccgggc	cactaccagc	300
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<210> 41

<211> 409

<212> DNA

<213>

<400> 41

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ttcctcttgg	gagctctcct	cctcttctct	gtggcggtga	cattggcaga	tgcaaaagtt	180
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ctcgttgtca	atgtcgtcaa	caaagctcgc	tacaacgtca	ccattcactg	gcacggcgctc	360
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<210> 42

<211> 515

<212> DNA

<213>

<400> 42

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tttcccagct	tacctgtgct	gatttccttc	gggcaccagg	agttcaaaca	cccgtgattg	360
tccgtttctc	cactgtcatc	cacgaaaggg	gcagccctga	aaccctgagg	gaccctcgag	420
gttttgctgt	gaagttctac	acaagagagg	gtaactttga	tctggtggga	aacaatttcc	480
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<210> 43

<211> 471

<212> DNA

<213>

<400> 43

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gtaagccagg	agtacaagaa	ggctgtcgag	aaatgcaaga	agaagttgag	aggcctcatc	180
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<213>

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<211> 418

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1785

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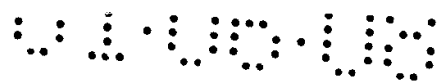
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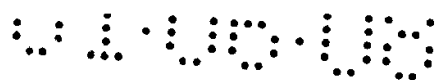
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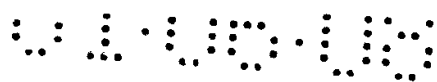
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<210> 58
<211> 741
<212> DNA
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<210> 59
<211> 643
<212> DNA
<213>

<400> 59

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<210> 60
<211> 441
<212> DNA
<213>

<400> 60

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<210> 61
<211> 913
<212> DNA
<213>

<400> 61

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<210> 62
<211> 680
<212> DNA
<213>

<400> 62

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<210> 63
<211> 492
<212> DNA
<213>

<400> 63

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<210> 64
<211> 524
<212> DNA
<213>

<400> 64

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atacgactat	aatagcttag	agcgttcctt	gctggactga	gtca		524

<210> 65
<211> 417
<212> DNA
<213>

<400> 65

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gagagacgct	ggcgagggtg	agtctctcag	aaaattgcat	ggggatcgat	tgcagatctt	360
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<210> 66

<211> 511

<212> DNA

<213>

<400> 66

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<210> 67

<211> 609

<212> DNA

<213>

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<210> 68

<211> 474

<212> DNA

<213>

<400> 68

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cgtccaacaa	ttgaaggatg	ccgggggtcca	tatcctttat	gggtctttga	gtgatcacia	420

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474

<210> 69
<211> 474
<212> DNA
<213>

<400> 69

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<210> 70
<211> 608
<212> DNA
<213>

<400> 70

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<210> 71
<211> 1474
<212> DNA
<213>

<400> 71

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 <211> 1038
 <212> DNA
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<400> 72						
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<210> 73
 <211> 372
 <212> DNA
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<400> 73						
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<210> 74
 <211> 545
 <212> DNA
 <213>

<400> 74

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ccaacaagcc	tttgctccct	ttggagaaga	atgcttccaa	ggttcttggt	gcaggaaccc	180
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gaaacataac	cgtaggaact	acaattctgg	aagctatcaa	actagctgtc	agccccctca	300
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atgccattgt	ggttgtgggt	gaggcaccat	acgcagaaac	gtttggagac	aatcttaatt	420
tgaccattcc	cctaggcgga	ggggacacga	ttaagacggg	ctgtggctcc	ttgaaatgcc	480
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gtttt						545

<210> 75
 <211> 463
 <212> DNA
 <213>

<400> 75

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tgtagagcct	tttgttactc	tgtatcactg	ggacttgcca	caagctctgg	aggacgaata	180
cgggtgattt	cgtagcaaaa	aagtgtgga	tgactttggc	atattctcag	agaatgctt	240
tcgtgctttt	ggagaccgtg	tgaagtactg	ggtaactgtt	aacgaaccgt	tgatcttctc	300
atattttttc	tacgatgtgg	ggcttcacgc	accggggccg	tgttcgcttg	gatttggaaa	360
ctgcactgcg	ggaaattcag	cgacagagcc	ttatattgta	gcccataaca	tgcttcttgc	420
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<210> 76
 <211> 435
 <212> DNA
 <213>

<400> 76

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tcgagctact	ggcattcaat	acacatttgc	tccatgtggt	gctgtttgca	gagatcctcg	180
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attacccccca	atttt					435

<210> 77
 <211> 451
 <212> DNA
 <213>

<400> 77

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cactgcttat	tacatgtatg	atcctaaaca	acctaaacaa	aatgtaacag	attaccagac	180
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aacactatgg	aaatccaact	atgattctct	ctgaaaatgg	aatggacgac	ctggaaacgt	360
gacacttcca	gcaggactgc	atgataccat	caggggtaac	tactataaaa	gctattttgca	420
aaatttgatt	aatgcacgtg	aatgaccggg	g			451

<210> 78
 <211> 374
 <212> DNA
 <213>

<400> 78

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cttcagaaaa	atggcaatgg	cacaagcatt	cagaggccgt	gtcttgcaag	ctgcccgttt	180
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agctcttagc	ctgctctcat	caaaagcctt	catctctttc	tctgttgaac	ggcatcggt	300
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gacaggacaa	tctg					374

<210> 79
 <211> 457
 <212> DNA
 <213>

<400> 79

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aaggcccaag	catctgggac	tcattttcac	gaacaccagg	caaaattctt	gatggaagca	180
acggtgatgt	agcagtggat	cagtatcatc	gttataaggc	agatgtaaaa	ctgatgaaag	240
atatgggctg	ggctacctac	agattctcga	tttcatggcc	tctgtatatt	ccaaagggaa	300
aaggagagat	caatgaggaa	ggagtagcct	attacaataa	cctcatcaat	gaactcctcc	360
agaatggaat	ccaagcgtct	gtcaactttg	tttcaactgg	atactcccca	gtctctggag	420
gatgaatatg	gcggattttc	gaggccaacc	attgtga			457

<210> 80
 <211> 346
 <212> DNA
 <213>

<400> 80

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ggtttcaaat	ttggtgcagg	gtcatctgct	tatcaggcgg	aaggagctgc	tcatgagggg	180
ggcaaaggcc	caagcatttg	ggatacatte	tcccacactc	caggtaaaat	cgctgatggg	240
aatattggga	tggttcagta	gatcaatacc	accgttataa	ggaagatgtg	cagcttctca	300
aatacatggg	aatggacgtc	tatcgtttct	ctatctcctg	gtcacg		346

<210> 81
 <211> 957
 <212> DNA
 <213>

<400> 81

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ctttaactgc	aataactgtg	gaagcgtaca	aaaagtttgt	cctagtttct	ctcattcaga	120
ctggtcaggt	tccagcattt	ccaaaataca	cacctgctgt	tgtccaaaga	aatttgaaat	180
cttgcaactca	gccctacatt	gatttagcaa	acaactacag	tagtgggaaa	atttctgtat	240
tggaagcttg	tgtcaacacg	aacacagaga	agttcaagaa	tgatagtaat	ttgggggttag	300
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aactccatgt	tctgcagatg	attcaagatg	gtgagatttt	tgcaaccata	aatcagaaag	480

01.05.09

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<210> 82
 <211> 489
 <212> DNA
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<400> 82						
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ggactagagt	aaaagtcctt	ccctttaaca	caactgttca	attgattctt	caagacacca	180
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gccaagggtgt	tggaaactac	aatgaatcaa	cagatgcacc	aaattttaac	ctcattgacc	300
ctgtcgagag	aaacactgtg	ggagttccca	aaggaggttg	ggctgctata	agatttcgtg	360
cagacaatcc	aggggtttgg	ttcatgcact	gtcatttgga	ggttcacaca	tcgtggggac	420
tgaaaatggc	gtgggtagta	aagaacggaa	aagggcccat	cgattttcca	cccggttggg	480
taccagtaa						489

<210> 83
 <211> 471
 <212> DNA
 <213>

<400> 83						
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tgtccggggc	agtcttgtgg	aggtccaacg	gatcaagatt	tgcagcaagt	atgaatacat	420
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<210> 84
 <211> 338
 <212> DNA
 <213>

<400> 84						
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aatcagtgcg	tctatcttct	gctctccttg	ttttgctact	agcatttgtt	gcttacttag	180
ttgctgtaac	aaacgcagat	gtccacaatt	ataccttcat	tattagaaaag	agacagttac	240
caggctatgc	aataagcgta	taatcgccac	cgtcaatggc	agctaccagg	cccaactatt	300
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<210> 85
 <211> 1229
 <212> DNA

<213>

<400> 85

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cttgaacctta	catgtttttg	aaaagtatcg	atgttcttta	aaatgaacat	tgaatacaac	1140
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<210> 86

<211> 1410

<212> DNA

<213>

<400> 86

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<210> 87
 <211> 687
 <212> DNA
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<400> 87

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<210> 88
 <211> 688
 <212> DNA
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<400> 88

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<210> 89
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 <212> DNA
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<400> 89

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<210> 90
 <211> 1960
 <212> DNA
 <213>

<400> 90

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<213>

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<211> 660

<212> DNA

<213>

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<223> n

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<211> 1012

<212> DNA

<213>

<400> 94

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 <211> 492
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 <211> 391
 <212> DNA
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 <211> 567
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<400> 100

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<211> 612

<212> DNA

<213>

<400> 101

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<210> 102

<211> 455

<212> DNA

<213>

<400> 102

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<210> 103

<211> 1866

<212> DNA

<213>

<400> 103

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<210> 104

<211> 519

<212> DNA

<213>

<400> 104

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<210> 105

<211> 594

<212> DNA

<213>

<400> 105

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<210> 106

<211> 407

<212> DNA

<213>

<400> 106

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tcgaccggat	cttcgggctg	ctggccagct	actccgtgct	cacgtgcacc	ctccgcgacc	360
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<210> 107

<211> 1630

<212> DNA

<213>

<400> 107

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<210> 108

<211> 1248

<212> DNA

<213>

<400> 108

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<210> 109

<211> 481

<212> DNA

<213>

<400> 109

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gcagcctaaa	ggggcactgc	gggtcactgc	atcaagcaat	aagaagatcc	tcattcatggg	180
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ttttgttaaa	tctagtcttg	ctgcagaagg	ctttgacgtt	gtttatgaca	ttaacggcga	420
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<210> 110

<211> 458

<212> DNA

<213>

<400> 110

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ggtttttgcc	gtcagagttc	ggaatggacc	cggccctcat	gggtcatgca	attgagccgg	420
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<210> 111
 <211> 448
 <212> DNA
 <213>

<400> 111

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gttggtgcagg	cgtttttcac	actgcctctc	ccttttatca	tgatgtcaag	gatccgcagg	360
cagaattact	tgatccgggt	gtgaaggga	cactcaatgt	cctgaagtca	tgttccaaag	420
accttctctg	cagcgtgtgg	cttgacat				448

<210> 112
 <211> 578
 <212> DNA
 <213>

<400> 112

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tgaaaagtgc	gttatgactt	ttgatggaat	tgatgcagat	ggtacagtga	caaaggagg	480
atattctagt	cacattgtcg	tccatgaaag	gtattgcgtc	aggattccag	aaaactaccc	540
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<210> 113
 <211> 454
 <212> DNA
 <213>

<400> 113

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ccccatcaac	gatcttgtat	cgagcctggg	ctcgaaccgg	agcgtccctc	cggtgacttg	420
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<210> 114
 <211> 479
 <212> DNA
 <213>

<400> 114

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cggttgcttt	ctggaggcat	tacaggagag	ggggaagatt	gtgaaatggg	cgcctcaaca	420
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<210> 115

<211> 420

<212> DNA

<213>

<400> 115

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<210> 116

<211> 679

<212> DNA

<213>

<400> 116

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<210> 117

<211> 763

<212> DNA

<213>

<400> 117

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acaataaaatt	aaggaagaca	aggaattttg	tttttttcat	tggaggagt	taattttgtt	720
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<210> 118
 <211> 538
 <212> DNA
 <213>

<400> 118

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<210> 119
 <211> 515
 <212> DNA
 <213>

<400> 119

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<210> 120
 <211> 458
 <212> DNA
 <213>

<400> 120

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<210> 121
 <211> 1243
 <212> DNA
 <213>

<400> 121

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cgatatcgcc	ttggaccaaa	ctaccttcaa	ctccccgtta	atgtcccaag	tgcgtcatca	1200
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<210> 122

<211> 404

<212> DNA

<213>

<400> 122

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tttgggtagc	atgcagatca	gttgggtgat	cgtgtactgc	tttcactatt	acttacatat	360
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<210> 123

<211> 415

<212> DNA

<213>

<400> 123

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tttgggagcc	aaggagattt	ccattgaagg	gaaatctctg	acaatctcag	acgttgctgc	240
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cgaggagagt	tcaaactggg	ttctcaccca	gatgaccaag	gggacggata	cctatgggtg	360
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<210> 124

<211> 1659

<212> DNA

<213>

<400> 124

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cgccaaggag	gtcctgcaca	cccagggcgt	cgagtttggg	tctcgaaccc	ggaacgtggt	180
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ttcaaaagtt	tgctaggatt	tcaataacag	acaccgtcaa	ttatgtcatg	tttcaataaa	1560
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<210> 125

<211> 461

<212> DNA

<213>

<400> 125

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aggacccccg	gcatggccga	tcgtagggaa	cgctcttcag	attggatttt	ccagcggcgc	180
gttcgagacc	tcagtgaaga	aattccatga	gagatacggg	ccaatattca	ctgtgtggct	240
cggttcccg	cctctgctga	tgatcaccga	ccgcgagctt	gcccacgagg	cgctcgtaca	300
gaagggtccc	gtcttcgctt	gaccgcccgc	ccgcctcgg	gatgcagaaa	atcttcagta	360
gcaaccagca	caacatcact	tcggctgaat	acggcccgt	gtggcggagc	ttcgcaggaa	420
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<210> 126

<211> 569

<212> DNA

<213>

<400> 126

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ttaatttagt	tcagtctatg	ttgggacacc	tgcttcatca	ttcgtatgg	gcacctcctg	180
agggaatgaa	ggcagaagac	atagatctca	cagagaatcc	agggcttggt	actttcatgg	240
ccaagcctgt	gcaggccatt	gctattcctc	gattgcctga	tcattctctac	aagcgacagc	300
cactcaattg	atcaattgat	ctgatagtaa	gtttgaattt	tgttttgata	caaaacgaaa	360

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<210> 127

<211> 661

<212> DNA

<213>

<400> 127

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gtctgagaat	tctaccatgt	tgatgaacaa	gattttggat	acttacgagg	gttttaagga	180
ggttcaggag	ttggtggatg	tgggaggagg	tattgggtcg	actctcaatc	tcatagtgtc	240
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tcactaccca	gctgtgaaac	atgtgggtgg	agacatgttt	gatagtgtac	caagtggcca	360
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gaagaattgt	cacaaggcgt	tgccagagaa	ggggaagggt	attgcgggtg	acaccattct	480
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gttggcatat	aaccacgggg	gcaaggaacg	cacagagcaa	gaatttcaag	atttagctaa	600
ggagacggga	tttgcagggt	gtgttgaacc	tgtatgttgt	gtcaatggaa	tgtgggtaat	660
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<210> 128

<211> 427

<212> DNA

<213>

<400> 128

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atcaagcgtc	tcctccagtg	tggttaccaa	gtgagaggaa	ctgtgcggga	tcctggcaat	180
gagaaaaaga	tggtctcattt	atggaagtta	gatggggcga	aagagagact	gcaactaatg	240
aaagctgatt	taatggacga	gggcagcttc	gatgagggtc	tcagaggctg	ccatggtgtt	300
tttcacacag	cgtctccagt	cgtgggtgtc	aaatcagatc	ccaagatatg	gtatgctctg	360
gccaagactt	tagcagaaaa	agcagcatgg	gattttgccc	aagaaaacca	tctggacatg	420
gttgacag						427

<210> 129

<211> 1412

<212> DNA

<213>

<400> 129

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tcgaggaaca	gtgtgcgtta	caggagctgc	tgggttcata	gggtcatggc	tcacatgcg	180
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tttggatgat	gaaggaagct	ttgatgctgc	cattgatggg	tgtgagggtg	ttttccatgt	360
tgccactccc	atggattttcg	agtcaggaga	tcccagagaat	gagataatta	agccaacaat	420
caacgggggtc	ttgaatgtta	tgagatcgtg	tgcaaaaagcc	aagtccgtga	agcgagttgt	480
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ttttgacgaa	tcatgctgga	ccaacgtgga	tctttgcaga	aaagttaaaa	tgacaggatg	600
gatgtacttt	gtatcgaaga	cattagcaga	gaaagctgct	tgggattttg	cagaggagaa	660

caagatcgat	ctcattactg	ttatccccac	attggtcggt	ggaccattca	ttatgcagac	720
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atagaaataa	gaagaatacc	ggctgatcgc	tgttgtttat	taatgcgaat	tttattgatg	1320
ttgacaaggt	cataccaggg	ctcctggaat	gctacatatg	tacggctgat	tctagctcca	1380
gtaatataat	ttttcaaatt	ctaaaaaaaa	aa			1412

<210> 130

<211> 666

<212> DNA

<213>

<400> 130

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aagagaacaa	gagagtgggt	tgtgtaactg	gggcaaattg	gtacatcggc	tcttggctgg	180
tcatgagatt	actggaacat	ggctattatg	ttcatggaac	tgtaggggac	ccagaagaca	240
cagggaaaggt	tgggcatttg	ctgcggctcc	caggggcaag	tgagaagcta	aagctgttca	300
aggcagagct	taacgacgaa	atggccctttg	atgatgctgt	gagcggttgt	caagggggtt	360
tccacgttgc	caagcctggt	aatctggact	caaacgctct	tcagggggag	gttggttggtc	420
ctgcggtgag	gggaacagta	aatctgcttc	gagcctgcga	acgatcgggc	actgtgaaac	480
gagtgataca	tacctcgtcc	gtttcagcag	tgagattcac	tggaacacct	gacccccctg	540
atactgtgct	ggatgaatct	cattggactt	cggtcgagta	ttgcagaaag	acaaagatgg	600
tcggatggat	gtactacatc	gccaacactt	atgcagaaga	gggagcccat	aagttcggat	660
cagaga						666

<210> 131

<211> 478

<212> DNA

<213>

<400> 131

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ctgctaaatc	atgagatcca	tcaaggaagt	acagtatgtg	tgacaggagc	tgctggcttc	120
ataggatcat	ggctcgtcat	gcgtttgctt	gagcgaggat	atactgttag	aggaactgtg	180
cgagacactg	gtaatccggt	gaagacgaag	catctattgg	atctgcctgg	ggcgaatgag	240
aggttaaactc	tctggaaagc	agattttgat	gatgaaggaa	gctttgacgc	cgccattgat	300
ggttgtagag	gagttttcca	tgttgccact	cccattggatt	ttgaatccga	ggacccccgag	360
aacgagataa	ttaaacccgc	tgtcaatggg	atgttgaaatg	ttttgagatc	gtgtgggaaa	420
accaagtcta	tgaagcgagt	tgttttccag	tcgtctgctg	ggactctgct	ttttacgg	478

<210> 132

<211> 510

<212> DNA

<213>

<400> 132

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ctacctccct	gaaaagatga	gcgagggtatg	cgtgacagga	ggcacaggct	tcatagctgc	120

ttatctcatt	cgtagtcttc	tccagaaagg	ttacagagtt	cgcactacag	ttcgcaaccc	180
agataatgtg	gagaagttta	gttatctgtg	ggatctgcct	ggtgcaaacg	aaagactcaa	240
catcgtgaga	gcagatttgc	tagaggaagg	cagttttgat	gcagcagtag	atggtgtaga	300
tggagtattc	catactgcat	cacctgtctt	agtcccatat	aacgagcgct	tgaaggaaac	360
cctaatagat	ccttgtgtga	agggcactat	caatgtcctc	aggtcctgtt	caagatcacc	420
ttcagtaaag	cgggtggtgc	ttacatcctc	ctgctcatca	ataccgatac	gactataata	480
gcttagagcg	ttccctgctg	gactgagtca				510

<210> 133

<211> 890

<212> DNA

<213>

<400> 133

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gttggtcatg	cagtgcctagc	aggaggagca	gcgttgcaat	tggggaaaat	tccaaaatca	120
ataacgagag	gacagaagta	agtttgtgga	aatagcaacc	atgccggtgt	ttccttctgg	180
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gagagacgct	ggcgagggtg	agtctctcag	aaaattgcat	ggggatcgat	tgcagatctt	360
ctatgcagat	gtcttggatt	atcacagcat	tactgatgcg	ctcaagggtc	gttctggtct	420
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gaagtacaag	cagcccacaa	tgcactggaa	gcgtgtgctc	agactgagac	cattgagaaa	540
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ttgaatatgg	tgacaatcaa	cgcatctctg	attgtaggac	ctggcatcac	atacaaaagc	780
tcaggatcta	ccattgcata	tcttaaagg	gctgcacaaa	tgtatgagaa	gggcacttta	840
gctagtgtgg	acataagggt	tctagcggat	gcacatatat	gcgcttatga		890

<210> 134

<211> 955

<212> DNA

<213>

<400> 134

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tattggagga	acaggctaca	ttggtcgtca	tataaccaa	gccagccttg	ctcttggtca	180
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gacggatcaa	cagaatatta	tcaaggctat	taaggagggt	ggaacatca	agagggtttt	420
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gaaaaaaatt	gcagagtgcg	cattcccact	caatgctata	atgtcaaccg	gccactctat	900
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<210> 135

<211> 1024

<212> DNA

<213>

<400> 135

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agtatttcac  cgataatttc  tggtagggatc ccgcattatc caagaccttt gagggaaaaa      180
aaccctgcta  cttcaacaca ggcgtaatgg tgatcgatct tgaaaaatgg cgggcagggg      240
aattcacaag  aaagatcgaa atctggatgg acatacagaa ggaacgccgt atctatgagc      300
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gcaagcaatg  ccgctgcaag tcatgtaggg aaggcgttgt gaactcaatt ttcggcgact      900
gtacaggatg  taaatttttg gaacattaat atcattatga taagttcctg aaccaacaac      960
tgtataatac  cttataaatg tatctgcaac tccatttttg cataaaaaaa aaaaaaaaaa     1020
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<210> 136

<211> 497

<212> DNA

<213>

<400> 136

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agaacataaa  tccgaacaat gaacttgcaa atttcctgca ttgccatcgc cagcccaaga      60
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tataggttct  aggggtcttg ggggctcctg atgcccaatt gttgctgtgc ttggcatgac      180
ccaaacatgc  aagagatctg tagtcagtag tcttgttgga tctatagctt ttagaaaaga      240
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ttcaacggga  ggaggagcaa gatattcagc attgcttttg gcaccagatg gataggcatt      360
attttccatc  ggaattcagc cgagctcgcc ccctcagtc aatcgctcgtg aaaatccctc      420
aaaattgggc  aattctggct cgaaatcgcc aaattatggg ctacaacagg attaaaattg      480
cacagaaatc  tgccagt                                           497

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<210> 137

<211> 528

<212> DNA

<213>

<400> 137

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ggcaatccga  gcctagccaa ccaacttggc agcaaggagc acagggagtt ggcgagagaa      60
gctgttagga  aatctttggt attgttgaaa aatgggaagt cagccaacaa gcctttgctc      120
cctttggaga  agaatgcttc caaggttctt gttgcaggaa cccatcctga taatctgggt      180
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ggaggggaca  cgattaagac ggtctgtggc tccttgaaat gccttgtaat cttgatatct      480
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<210> 138

<211> 424

<212> DNA

<213>

<400> 138

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acaagctctg	gaggacgaat	acggtggatt	tcgtagcaaa	aaagttgtgg	atgactttgg	180
catattctca	gaagaatgct	ttcgtgcttt	tggagaccgt	gtgaagtact	gggtaactgt	240
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ctgttcgcct	ggatttgga	actgcactgc	gggaaattca	gcgacagagc	cttatattgt	360
agcccataac	atgcttcttg	cacatagtag	cgctgttaaa	aatatatagc	ataaatatccc	420
aggg						424

<210> 139

<211> 404

<212> DNA

<213>

<400> 139

gctaccatct	tccctcataa	tattgggctt	ggagctacca	gggatcctga	tctggctaga	60
agaatagggg	ctgctacggc	tttggaagtt	cgagctactg	gcattcaata	cacatttgct	120
ccatgtgttg	ctgtttgcag	agatcctcga	tggggccgct	gctatgagag	ctacagttag	180
gatccaaaaa	ttgtcaaggc	catgactgag	attatcgttg	gcctgcaagg	gaatcctcct	240
gctaattcta	caaaaggggg	gccttttata	gctggacagt	caaagtgttg	agcttgtgct	300
aagcattttg	tgggttatgg	tggaacaacc	aaaggtatcg	atgagaataa	tactgttatc	360
aactatcaag	ggttatattca	acattccaaa	ttacccccaa	tttt		404

<210> 140

<211> 437

<212> DNA

<213>

<400> 140

cctagaattc	tatggtgaaa	attggttgga	caaggctgcc	caagtttaca	aaggaacagt	60
cccaaattgg	taaaggttca	atagactatc	taggcgttaa	ccaatacact	gcttattaca	120
tgtatgatcc	taaacaacct	aaacaaaatg	taacagatta	ccagactgga	ctggaataca	180
ggctttgcat	atgctcgcaa	tggagtgcct	attggacca	gggcgaactc	caattggctt	240
tacattgtgc	cttggggctc	atacaaggcc	gtcacatacg	taaaagaaca	ctatggaaat	300
ccaactatga	ttctctctga	aatggaatg	gacgacctgg	aaacgtgaca	cttccagcag	360
gactgcatga	taccatcagg	ggtaactact	ataaaagcta	tttgcaaaat	ttgattaatg	420
cacgtgaatg	accggggg					437

<210> 141

<211> 470

<212> DNA

<213>

<400> 141

gatacatcca	agctgagaat	ggaagagatt	aatggtgata	acgcagtaag	gaggagctgc	60
tttctccag	gtttcatggt	tgggatagca	acttctgctt	atcagtgtga	aggagctgcc	120
aacgaagggt	gaaaaggccc	aagcatcttg	gactcatttt	cacgaacacc	aggcaaaatt	180
cttgatggaa	gcaacggtga	tgtagcagtg	gatcagtatc	atcgttataa	ggcagatgta	240
aaactgatga	aagatatggg	cgtggctacc	tacagattct	cgatttcatg	gcctcgatata	300
tttccaaagg	gaaaaggaga	gatcaatgag	gaaggagtag	cctattacaa	taacctcatc	360
aatgaactcc	tccagaatgg	aatccaagcg	tctgtcaact	ttgtttcact	gggatactcc	420
ccagtctctg	gaggatgaat	atggcggatt	tctgaggcca	accattgtga		470

<210> 142
 <211> 413
 <212> DNA
 <213>

<400> 142

ataagactaa	ttttccagac	aatcctccat	tcccattcaa	ttacactggt	actccaccca	60
ataatacaca	ggctgtgaat	gggactagag	taaaagtcct	tccctttaac	acaactgttc	120
aattgattct	tcaagacacc	agcatcttca	gcacagacag	ccaccctgtc	catctccatg	180
gtttcaattt	ctttgtggtg	ggccaaggtg	ttggaaacta	caatgaatca	acagatgcac	240
caaattttta	cctcattgac	cctgtcgaga	gaaacactgt	gggagttccc	aaaggaggtt	300
gggctgctat	aagatttcgt	gcagacaatc	caggggtttg	gttcatgcac	tgtcatttgg	360
aggttcacac	atcgtgggga	ctgaaaatgg	cgtgggtagt	aaagaacgga	aaa	413

<210> 143
 <211> 457
 <212> DNA
 <213>

<400> 143

aaaacctttt	cagacgaatg	ttctgatgct	cggccccggc	cagacaacag	acatacttct	60
cactgccaat	caggctacag	gtagatacta	catggctgct	cgagcatatt	ccaacgggca	120
aggagttccc	ttcgataaca	ccactaccac	tgccatttta	gaatacgagg	gaagctctaa	180
gacttcaact	ccagtcattg	ctaactcttc	attctataac	gacaccaaca	gtgctactag	240
cttcgcta	ggtcttagaa	gcttgggctc	acacgaccac	ccagtcttcg	ttcctcagag	300
tgtggaggag	aatctgttct	acaccatcgg	tttgggggtg	atcaaagtgc	cggggcagtc	360
ttgtggagg	ccaacggatc	aagatttgca	gcaagtatga	atacatatca	tttgtcccgc	420
aaccacttct	tccaatcctt	caagctcagc	attttgg			457

<210> 144
 <211> 598
 <212> DNA
 <213>

<400> 144

gttcggcact	gagagatcca	tttctttcaa	tgttgagaca	gtgagtagta	ttagtttgat	60
atctctttca	ggaatatatc	gtgcttgacg	gatctttagt	ttctgcaaca	atgtcgttgc	120
aatcagtgcg	tctatcttct	gttctccttg	ttttgctact	agcattttgt	gcttacttag	180
ttgctgtaac	aaacgcagat	gtccacaatt	ataccttcat	tattagaaag	aagacagtta	240
ccaggctatg	caataagcgt	ataatcgcca	ccgtcaatgg	acagctacca	ggcccaacta	300
ttcatgtacg	tgatggagac	gttggttaata	tcaaagctta	taacaaagct	gggtacaatg	360
ccactcttca	ctggcatgga	gtcgagcagt	tgcgtacagg	atgggccgat	ggacctgcat	420
atgttacaca	gtgccccatt	ccaccaggtg	gtcgttatac	atacagattc	accatttctg	480
aacaggaagg	caccgtgtgg	tggcacgctc	atgtgtcatg	gctccgagct	acggtgcatg	540
gagctttcgt	aatccttcct	aagagaggca	aaccatatcc	ctttcctaaa	ccccgtgc	598

<210> 145
 <211> 1080
 <212> DNA
 <213>

<400> 145

aagatcttgg	ttcgagtctc	tcagctctct	ccaaaggaat	tttgtgggtc	atthtcaggt	60
gaagacacca	tggtgaaggc	ttatcccacc	gtaagcgagg	agtacaaggc	tgccattgac	120
aaatgcaaga	ggaagctccg	agctctcatt	gcagagaaga	actgtgcgcc	gatcatggtt	180

cgaatcgc	at	ggcacagcgc	tgggacttac	gatgtcaaga	ccaagaccgg	agggcccttc	240
gggacgatga	gatatggggc	cgagcttgcc	cacgggtgcta	acagtgggtct	ggacatcgca		300
gttaggctcc	tggagccaat	caaggaacag	ttccccataa	tcacctatgc	tgacctttat		360
cagttggctg	gtgtgggtggc	tgttgaagtg	accggggggac	ctgacattcc	gttccatcct		420
ggaagagaag	acaagcctga	gcctccagaa	gaaggccgcc	ttcctgatgc	tacaaaagga		480
cctgatcatc	tgagggatgt	ttttgggtcac	atgggggttga	atgataagga	aattgtggcc		540
ttgtctgggtg	cccacacctt	ggggagatgc	cacaaggaga	gatctggttt	tgaaggacca		600
tggacctcta	accccccttat	ctttgacaac	tcttacttca	cagagcttgt	gactggagag		660
aaggaaggcc	tgcttcagtt	gccatctgat	aaggcactgc	ttgctgatcc	tagttttgca		720
gtttatgttc	agaagtatgc	acaggacgaa	gacgctttct	ttgctgacta	tgcggaagct		780
cacctgaagc	tttctgaact	tgggtttgct	gatgcgtaga	ttcatacctt	ctgcagagac		840
aattccttgc	tagatagctt	cgttttgtat	ttcatcta	cttttcgatt	atatagtcac		900
atagaagttg	gtgttatgcg	ccatagtgat	acttgaacct	acatgttttt	gaaaagtatc		960
gatgttcttt	aaaatgaaca	ttgaatacaa	cattttggaa	tctgggtgtg	ttctatcaag	1020	
cgcataat	aatcgaatgc	ttcgttcctg	ttaaaaaaaa	aaataaaata	aaaaaaaaaa	1080	

<210> 146

<211> 701

<212> DNA

<213>

<400> 146

gtagtttcgt	tttacaacaa	tctcaggttt	tgaatctcag	aatagttgcg	aaaggaagcg	60
atgacgaagt	acgtgatcgt	tagctccatt	gtatgtttct	ttgtatttgt	ttctgcgtgc	120
ataattttctg	tcaatggatt	agttgtccat	gaagatgatc	tgtcaaagcc	tgtgcatggg	180
ctttcgtgga	cattttataa	ggacagttgc	cccgaacttg	aggccatagt	gaaatcggta	240
cttgagccgg	cgttggacga	agatatcact	caggccgcag	gttgctgaga	cttcatttcc	300
atgactgttt	tgtgcagggg	tgcgatgggt	ccgtgttgct	gacaggaact	aaaagaaacc	360
ccgagtgagc	aacaggctca	gccaaaactta	acactaagag	cccgggcctt	gcagctgatc	420
gacgaaatta	aaacgcgtgt	agaagctagc	tgcagtgggg	ttgtaacttg	tgcagacatt	480
ctggcctttg	ctgctcgtga	ctccgctcgt	caggaggccc	aaaatttcca	gtaccacttg	540
gccgcagaga	tagcctaaag	tttgccagtc	aatccgtagt	tctcgccaat	ataccaactc	600
caactttaaa	tttgacacag	ctgatgaaca	tttttggtc	caaaggattc	agtttggccg	660
aaatgggttg	tctttcaggt	ggacacacaa	tcggcattgg	t		701

<210> 147

<211> 338

<212> DNA

<213>

<400> 147

ctcaattctg	tgtgtctctg	ctcgctcagg	gccgggtctg	ctattctgct	catgcacaag	60
tttgagatcg	ggagcctgct	ggatctgggt	cagaggttca	aggtcacggt	agcgcctgtc	120
gtgcctccca	ttgttctcgc	ctttgccaag	aacgcgctcg	tggaaagcta	tgatctgtcg	180
tccattaggg	ttgtgctgtc	cggtgccgcg	cctctcgga	aggagctgga	ggatgcatta	240
aggctacgac	ttcccaaagc	cacttttggt	cagggatacg	gtatgacaga	ggcaggaccg	300
gtgctatcaa	tgtgtctggc	cttcgctaag	gagccctt			338

<210> 148

<211> 357

<212> DNA

<213>

<400> 148

ctcaattctg	tgtgtctctg	ctcgctcagg	gccgggtctg	ctattctgct	catgcacaag	60
tttgagatcg	ggagcctgct	ggatctgggt	cagaggttca	aggtcacggt	agcgcctgtc	120

gtgcctccca	ttgtttctgc	ctttgccaa	aacgcgctcg	tggaaaagcta	tgatctgtcg	180
tccattaggg	ttgtgctgtc	cggtgccgcg	cctctcgga	aggagctgga	ggatgcatta	240
aggctacgac	ttcccaaagc	cacttttgg	cagggatacg	gtatgacaga	ggcaggaccg	300
gtgctatcaa	tgtgtctggc	cttcgctaag	gagccctttc	cgatgaagtc	cggtgcg	357

<210> 149

<211> 470

<212> DNA

<213>

<220>

<221>

<222> (437) ... (437)

<400> 149

gagaaattca	caagcttcac	agcacgagag	ttaaagagcg	agacacgggt	tgatccagt	60
aagggccggc	ccccggagat	ggcgaagacg	ctcaccgcgc	tggctggggg	agaagaccct	120
ccagtccaaa	gttcgtccgc	gataaggatg	agcgcccac	ggtggcctac	aaccagttca	180
gcaacgtgat	ccccgtgata	tccctggcgg	ggattgacga	ggccggcgcc	cggaagggcc	240
gagatctgca	agaagatcgt	ggaggcgtgc	gaggactggg	gcgtcttcca	ggtggttgac	300
cacgggggtg	atacggggct	catcactgac	atgaccggc	tcgcgcgtaa	gtntctcgct	360
ctgccctcgg	aggaaaagct	ccggttcgac	atgactggcg	gaaaaagggg	gggttatcgt	420
ctccagcatc	tcaaggngaa	caagttcagg	actggtgcaa	aagtacgaac		470

<210> 150

<211> 380

<212> DNA

<213>

<400> 150

ggaggtcgg	gacagagcag	tacagcgaga	agctcatggc	cctcgcttgc	aagctcttgg	60
aggctctctc	ggaggcaatg	ggactggaga	aggaggcact	gaccaaggca	tgcgtggaca	120
tggaccagaa	ggtggtggtc	aactactacc	ccaaatgcc	gcagcccgac	ctcacgctcg	180
ggctgaagcg	ccacactgac	ccgggaacca	tactcttct	gctccaggac	caggtggggg	240
gcctccaggc	caccagagat	ggcggcaaga	gctggatcac	cgtccagcct	gtggaagggg	300
cttttgtggt	caacctaggc	gatcatggtc	atttctgag	caacgggagg	ttcaagaacg	360
cggaccacca	ggcgggtggtg					380

<210> 151

<211> 349

<212> DNA

<213>

<220>

<221>

<222> (212) ... (212)

<400> 151

ttggactcca	tacctctcgt	ggacctccaa	ggtcttttac	gcgattctgc	tagagccac	60
gttattcaac	aaattggccg	ggcctgcgct	gaatatggct	tcttcagat	aatcaatcat	120
ggcatcccag	atgcagttat	caacaggatg	ctggaagtag	cgaaggagtt	tttcagaatg	180
cctgtggagg	accgaatgga	atactattcc	gncgatccgt	ccagaaaaac	acgtttgtcg	240
acgagcttca	acatccataa	agaacaagtc	ttcaactggg	gggctatctc	agacatcatt	300
gttatccgtt	agaagatcat	gttcacactt	ggccttcaaa	acctgcggg		349

<210> 152

<211> 427

<212> DNA

<213>

<220>

<221>

<222> (234) ... (234)

<221>

<222> (240) ... (240)

<400> 152

atggtctggg	cagcatacgg	aggacgatgg	aagatggaac	gcaaggtgtg	caacatgcac	60
atgttgggag	ggaaggcgtt	ggaagattgg	cagccggtga	gggacgccga	aatgggcttc	120
atgctccgga	atattctcag	tcactcgcag	cgcggcgaga	cggtgaatgt	gccggacctc	180
ctgaacatct	gcgcgcgcaa	catgatcggg	cagatcattc	taagcaagcg	ggtnttcgan	240
acagaagggg	acgaggccaa	cgagttcaag	gacatgggtg	tggaactcat	gacctgcgct	300
ggatacttca	atatcggaga	cttcattcca	tcgctagcgt	ggatggactt	gcagggcatt	360
cagcggggta	tgaagaagct	ccacaagaaa	tgggacgcac	tcatacagag	gattattgat	420
taacacc						427

<210> 153

<211> 298

<212> DNA

<213>

<220>

<221>

<222> (214) ... (214)

<400> 153

gttaccaaag	ggcagcaacg	tattcttaaa	catgggttct	atccacaggg	atcccaagat	60
ttgggacaaa	ccgttggagt	ttagaccgga	gaggttcttg	gaaggtccta	gcaagtatga	120
tttctcaggt	aacaacttcg	catacatgcc	attcggttct	ggtcgaaggg	tgtgtgcagg	180
gcttgcgctg	gcagagagga	tgctaccata	tgtnttggcc	tctcttttgc	actcattcaa	240
gtgggaaata	ccaccagggt	ctgagctgga	tttacctgga	caagttcggc	cttgtggt	298

<210> 154

<211> 251

<212> DNA

<213>

<400> 154

gacttcaaag	ggcaggattt	tgagctgata	cccttcggtg	caggtagaag	gagctgcccg	60
gctattgcat	ttggaaatgc	cagtgttgag	cttgcttttag	ctcaacttct	tcacagtttc	120
gattgggagc	ttcctgatgg	gatccagcct	agggacttgg	atatgaccga	agtttttggc	180
atcacaatgc	acagaattgc	caacctcatg	gttgtagcca	aaccccgctt	ctcctagacg	240
atactcgtgc	c					251

<210> 155

<211> 411

<212> DNA

<213>

<220>

<221>

<222> (198) ... (198)

<400> 155

acgggggctcc	ggtgacgaga	tactggcagg	tcggtgaagc	tggttgagg	ttcgaatata	60
cgagagggat	cctgtttctt	gtccccttac	cttggttttc	ctcatccttc	cgaatgcagt	120
ctaattcgaa	gaccgtggaa	gagcggcgcc	cggggcctgg	gtaagagctt	gctggagata	180
tctcggcttg	actatgtntt	ggctcttttc	gtgaatggca	agggggatct	aggggcgatg	240
atggggctcg	ctgtcgtttt	gagggaaaat	tcgcaactgt	tgatggctct	gactacatct	300
ctggccgtct	tgattggttg	cgttttgttc	tttgtttggc	ggagaggggg	atcggctccc	360
tcgaagcagc	cggagaagcc	aactcccctg	gtgaaagaag	aggaagagga	g	411

<210> 156

<211> 404

<212> DNA

<213>

<400> 156

gctgaagtta	ataaaaactaa	gtacattgag	ggtgacatgg	aggcagaatt	ttcaaatacta	60
gctttggaca	ttattggatt	gtgtgtattt	aactatgatt	ttggatccgt	tactcgagaa	120
tcaccagtaa	tcaaggcagt	ctatggtaca	ttgtttgaag	ctgagcatag	atcaaccttt	180
tacataccat	actggaaatt	tccgctggca	agatggttag	ttcctcgcca	acgaaagtcc	240
catgaagacc	taaaggtcat	taatgaatgt	cttgataatc	tgatagcagg	ggccaaggaa	300
acaagacagg	aagacgatat	cgaggctctt	caaggaagag	attactctaa	agtgaatat	360
gcaagtttgc	tcagatttct	agttgatatg	agggagaaga	tggt		404

<210> 157

<211> 259

<212> DNA

<213>

<220>

<221>

<222> (116) ... (116)

<221>

<222> (246) ... (246)

<400> 157

ccaatcatcg	gcaattttcca	ccaagtgaga	cttcctcttc	accgtgctct	caaaaatctt	60
gctgagaaat	atgggtcccat	tttgtttctg	cgctttggct	ctgtacccac	tgtgngtgtt	120
tcttcatctg	agatggccaa	acactttctt	aaaactcatg	atttgatatt	tgccagccga	180
cctccaacat	cggtaggaaa	atattttctt	tataacttca	aagatattgc	cttcagtcct	240
tatgngatc	actggagga					259

<210> 158

<211> 338

<212> DNA

<213>

<400> 158

aatggcagtt	gggggtcaag	gaaatgtggt	ctcagcttgc	aggcagccat	ggaagctaca	60
atcgtctggt	gggtgttttg	gtagtaatat	tttctctggc	agttttttat	ttgaagagta	120
gaggttcgaa	gaagcgtctg	cctccagggc	cgaagggttg	cctctggttg	gaaatttggt	180
tcaggttgca	ttctccggga	agcccttcat	gtatgtggtg	cgagatctga	gggagcagtt	240
tggctcgatt	ttcacgctcc	aaatggggca	aaaaacgccc	caaattacca	cctccccgaa	300

atttccaaca cggggcctct taaaaaagag ggggcccc

338

<210> 159

<211> 539

<212> DNA

<213>

<220>

<221>

<222> (1)...(539)

<223> n

<400> 159

aatgtggccg	aggagttcct	gnaagactca	tggatctggc	tttcgccagc	agacctccaa	60
ccatcggtaa	cgaatatttt	ggtataattc	ctccgacgtc	gcattttccc	cctatggtcc	120
ttactggagg	cagatgcgta	aaatctgtgt	gttaaagttg	ctgagctcaa	gacgcataga	180
ttccttccgc	cacataagag	aagaggaagt	ctcttctatg	gttcgctcta	ttgctaattc	240
ggatctgcat	cctgtgaaca	ttagcagggc	cgtgtcagcc	cttgggattg	atataatctg	300
caggatggcc	ttcggtaaaa	agtactgtga	ccaagaccta	attggtggca	ttgggatnaa	360
gtcaatgata	aaggaaacgt	ttgtgtnagc	agggtcnttg	aacatgggag	attttatacc	420
atacttggca	tggattgatc	ttcaaggtct	caaccgtcga	ttgaagaaca	tacacaagat	480
ccaagacgac	ttgttagggg	aagatactag	aggcacacgc	ttcgccaacc	gcagaataa	539

<210> 160

<211> 310

<212> DNA

<213>

<220>

<221>

<222> (16)...(16)

<400> 160

cgaatgggtg	gtcggnaaag	accgcacagt	aaaggagtct	gatttggtaa	gtctgaaata	60
ccttcagtgt	gtggtgaaag	agacgctacg	attatacccg	ggaggacctc	tagcacttcc	120
ccatgagtct	gtggaggctg	tgacagtaga	agggtactat	atacctaaga	agacgatgct	180
gttggtgaat	gtgtgggcta	taggaaggga	cccaaagtgt	tgggggattg	atgcttcaga	240
attcaagcca	gagagattta	tggaggaatt	aggtgggcat	ctgcatgata	atgtcatgga	300
tttagcaggc						310

<210> 161

<211> 412

<212> DNA

<213>

<400> 161

cgccacctcc	ctctctctct	tccccctcct	cctgtctctc	ctggtcgccc	cgcaaaagcc	60
ctccgcctct	gtccgcagtc	accgccagcc	atggatctcc	tcttcctgga	gaagaccctc	120
ctgggcctct	tcgcgcgcgc	catcgtggcc	atcgcggtct	ccaagctccg	gggcaagcgg	180
ttccgcctcc	ccccgggccc	cctccccgtg	cccatcttcg	gcaactggct	ccaggtcggc	240
gacgacctca	accaccgcaa	cctcaccgac	ctcgccaaga	ggttcggcga	catcctctct	300
ctccgcatgg	ggcagcgcaa	cctcgtggtc	gtctcgtccc	cggacctctc	caaggaggtg	360
ctccacacgc	agggcgctcg	gttcgggtcc	cgcacccgga	acgtcgtctt	ct	412

<210> 162

<211> 329

<212> DNA

<213>

<400> 162

actttttacaa	tgagtgatca	caaacaattt	tttccaaaat	tcataacaaa	attttgata	60
cagtgcata	tggggcaaac	aatctgacgg	acttcaaaac	tactgacaac	aaaacaaacc	120
atctggggat	gaattacaat	ggaaatccac	acttcatttg	gctgcaactg	tatatataaa	180
gtgtttattg	cttccagctc	ctccagactt	tggaagaaat	tctatatattt	tttttcagga	240
tctgagcttc	aggctattgg	tttggccaca	acaacggagt	ggttgagaat	gtgcaggctg	300
aattgccctc	ctttctctgt	cacatccac				329

<210> 163

<211> 475

<212> DNA

<213>

<400> 163

atttgcgtca	gtctctacct	ttgcctgcaa	cattcacagt	cgctgatgga	gggcctcccg	60
cagcaactgt	cctgtgctta	ctctgggctt	tcttcatgat	atggtttttg	ggcaagagaa	120
gaactagtgc	cacgctgcca	ccaggaccct	atgcatggcc	catcatagga	aacctctacc	180
aattaatact	gcccgtctac	cgttctctta	gaggccttgc	tgacaaatat	gtccccatta	240
tgtttctgcg	cttaggetct	gtccctaccg	tcgtcgtttc	ttcttctgag	acggccaaag	300
agtttctcaa	aactcatgac	ttgatttttg	ccagccgacc	cccaacagcc	gctgggagat	360
tgatgttttc	caactctaaa	gacgtggtgt	tcgctccgta	tggagatcac	tggaggcaaa	420
tgagaaaaat	atgcgtgtta	gaactactga	ctgccaaaag	aatcgagctc	gtgcc	475

<210> 164

<211> 372

<212> DNA

<213>

<220>

<221>

<222> (22)...(22)

<400> 164

tggaataaca	gttcgactct	gngatttcat	aaaatatgat	gaggaaagga	gaatcaggtg	60
gatttgaggt	taagggatgg	gctgccatgg	atgactccgg	cgtcctctcg	cctttcaact	120
ttactcgag	gaaaacggga	tcccacgatg	tactttcaag	gtagcatact	gtggaatctg	180
tcactccgat	ctgcatcaaa	ttcggaatga	atggaaaaat	tccttatacc	caaatgggtt	240
ccaggccacg	aaatcgtagg	aactgttget	tgaagtccgg	tcagaagtga	agaatttttg	300
ctggctggag	aatcggcggg	gggtgtaagg	ggtgcatggg	tttggaggtg	ccagccaatt	360
ggtgaattct	tg					372

<210> 165

<211> 307

<212> DNA

<213>

<400> 165

tctctctctc	tctccctctt	gagagtgttg	aagtgttagg	atgaggattc	gagtgccgtc	60
gatgctgttg	ttgtggtcac	tgttgggcct	cgtggcgagg	tcgacaatgg	ccgaagagac	120
ggtgatcccc	gagacaacgc	gtttcgacac	cgggtgggctg	agcagatcgg	ccttcccga	180
gggcttcgtc	tgggggacgg	cgacctcggc	ttatcaagtc	gaaggcatgg	ccgacaaaga	240
gggacgcggg	cctagcatct	gggacgtctt	cgtcaagatt	ccaggaattg	tggccggtaa	300
tgcaact						307

<210> 166
 <211> 454
 <212> DNA
 <213>

<400> 166

gaagaaatta	ggttttctt	gtcggtcttt	ggtagtgggt	ctggtgatag	cagagacggt	60
ccatggtgct	tatgagttca	gcagatacga	ctttcctcct	ggctttgtgt	ttggtgctgg	120
cacttcagct	tatcagggtcg	aaggagcagc	aaatgaggat	gggaagactc	caagtataat	180
ggacacctgg	gccactctg	actcagggtg	tacaagcgga	gcaaattggag	atattgcctg	240
tgatcaatat	cacaaatata	aggtagatgt	ccaactcatg	gcagaaatgg	gattagacgc	300
ataccggttt	tccatctcat	ggtcaaggct	catcccaa	gggagaggct	ctgtgaatcc	360
gaagggattg	cagtactaca	acaacctcat	caatgaactg	atcagccatg	ggattgaacc	420
cgcacgtgac	cctgcacccat	tttgatctgc	caca			454

<210> 167
 <211> 433
 <212> DNA
 <213>

<400> 167

gagaagcaat	aggaaaatat	ggccctggag	aatggtgaaa	gaagcagagt	actgatcatt	60
ggaggaaccg	gttatttttg	cagaaggtta	gtgaaggcca	gccttgcctt	cggacatgag	120
acttatgtcc	agtatcgtgc	ccaggcagcc	tctgatataca	acaaagtggg	gacgcttatt	180
tccttcaaat	ctcaaggagc	acacctggtg	gatgcttcca	ttgacaatca	cacaagcctc	240
gtaaatgccg	tgaaacgagt	ggaagtgtga	atatcggcga	tgggtgccga	gggtctgaga	300
gaggggcagc	tgaaagtgat	cgaggccatt	aaagaggcag	gaaccgtcaa	gcgctttctt	360
ccttctgagt	tcgggatggc	ccagacagaa	tggtgcacgc	catctatccg	ggcaacgagg	420
ttttctctga	ttaa					433

<210> 168
 <211> 330
 <212> DNA
 <213>

<400> 168

cggggagctt	gacttgggac	tggaaagcag	cgggcatcgt	ttcctgtggg	ttctccgcgg	60
tcaccccttc	aatccaaact	tatctgcgct	gctgcccccg	ggtttcgaac	agcggaccaa	120
agatcgtggt	ctcgtgggta	cctcatgggc	tccgcagggt	tctatccttg	cacaccgcgc	180
aacaggaggt	tttgtgagtc	actgcggttg	gaactcgatg	ctggagagca	tttggttttg	240
agttccatt	atcgcttggc	ccctccaagc	tgaccaaagg	ccgatcgggt	tactttctgg	300
tgaatgatag	tagaatagac	ggtaggcttg				330

<210> 169
 <211> 398
 <212> DNA
 <213>

<400> 169

ggaaaatttg	gtatcggtag	agagatcctg	tgagatcgac	gcgtgggtcg	accttcaaaa	60
tttgaccggt	gaggtgatct	ctcgaacagc	gtttggcagt	agcttcgaag	aaggcaaaag	120
gatctccgaa	cttcaggggg	aacaagccca	gctcacgata	atagcccttc	aatcgggtcta	180
catccctggt	tgaggttttg	tgccaactaa	gatgaacagg	aggatgaaga	gcatagataa	240
ggaagtgcgg	gctctgctca	tggaacatcat	ccgcagaaga	gagaaagcaa	taagggaagg	300
ggaagctgct	ggcgatgatc	tgctggggct	gttgctggag	tcaaacatga	aggagaatgt	360

cgggatgagc cttcacgatg tgatggacgg agttgcag

398

<210> 170

<211> 432

<212> DNA

<213>

<220>

<221>

<222> (214)...(214)

<400> 170

gttaccaaag	ggcagcaacg	tattcttaaa	catgggttct	atccacaggg	atcccaagat	60
ttgggacaaa	ccgttggagt	ttagaccgga	gaggttcttg	gaaggtccta	gcaagtatga	120
tttctcaggt	aacaacttcg	catacatgcc	attcggttct	ggtcgaaggg	tgtgtgcagg	180
gcttgcgctg	gcagagagga	tgcaaccata	tgtnttggcc	tctcttttgc	actcattcaa	240
gtgggaaata	ccaccagggg	ctgagctgga	tttactggac	aagttcggcc	ttgtgggtcaa	300
gaaaatgaag	ccccttgtcg	ccattccaag	accaagattg	tccactctgg	agctctacat	360
gtcgagatag	atatttcatt	agagtcccaa	agctcttcat	ttcaattcta	agaaataaac	420
gtatcctgcc	ag					432

<210> 171

<211> 303

<212> DNA

<213>

<220>

<221>

<222> (105)...(105)

<400> 171

ccatcgcggc	cctggcccgg	acctacgggc	cgctcatgca	cctgcggctc	gggttcgtac	60
gacgtggttg	tgccgcgctc	ggcctccgtg	gccgcgaggt	tccnaagac	ccacgacgcc	120
aacttctcga	gccggccgcc	caactccggg	gcgaacacat	cgcgtacaac	taccaggacc	180
tgatgttcgc	gccctacggc	ccgcggtggc	ggatgctaag	gaagataagc	tccgtccacc	240
tcttctccgg	caaggctctt	aagcattaca	gacacgttcg	ccagaaaaag	gtcgcaatcc	300
tca						303

<210> 172

<211> 518

<212> DNA

<213>

<400> 172

cattagatat	atatatatag	acacgcattt	acgatatcat	tgcaacaatg	tcattggtag	60
gctgggttgt	ttttctaata	gctttgattt	cgtatttggc	tgccatcaca	aatgcagcaa	120
tcgtcaatta	taccttcata	attgaagcga	agacagttac	caggctatgc	aaggagaata	180
caataatcac	cgtcaatggg	cagctaccag	gtccgaccat	ctatgtccat	gacggagaca	240
ctgttattgt	tgaaacttat	aacaaggccg	agtacaatgc	cactcttcac	tggcatggag	300
tggagcagtt	gcgtacacca	tgggctgatg	gacctgcata	tgttactcaa	tgtcccatte	360
caccaggttg	tcgttatata	tacagattca	acatctcttg	acaagaagga	accgtgtggg	420
ggcatgccca	ttactcatgg	ctccgagcta	cggctccatg	agcttttgta	atccttccta	480
aggaaggaag	ctcatatccc	ttttctaaac	ccaatgcc			518

<210> 173

<211> 309

<212> DNA

<213>

<220>

<221>

<222> (284)...(284)

<221>

<222> (294)...(294)

<400> 173

gccgctgata	ctaggattga	gatctgcatg	ctccccgtgg	gtgatggcat	cactctctgc	60
cgtcggatca	gctgagcatc	taatctcaag	tccttatgat	cagggttcat	tcttaatgta	120
gaacccacga	aaaagagagg	gatttatgta	tatcttggtg	ctgtttcttt	tccatgaacc	180
tagaaacggg	attcgcaatt	aaatgccaaa	ttatggtgct	gtttctcttt	agtgtctctg	240
atttcttttt	attttttaat	ttttttgatc	agtttctctg	aatnatctca	agtncttcca	300
aaaaaaaa						309

<210> 174

<211> 381

<212> DNA

<213>

<400> 174

taagacgaag	aaatggaaac	aacggccaag	ccatcgcgaa	acgcctttcc	gcatatggaa	60
tgcactatat	ttgatcttcc	gcatgtggtg	gccaatntag	aagttagcga	gaacgtgaga	120
tgtgttccctg	gggacatgtt	tgagtcata	ccaccagcag	atgcaataat	attgaagtgg	180
atactccatg	attggagcga	tgaagacgct	gtgaagatac	tgaagcgatg	caaggaggcc	240
ttaggcaagg	gcaagggcaa	gaaacagaag	gtaattataa	ttgacatggt	gatggacaac	300
acgaagagcg	ccaaagagac	ggtcgaaacc	cagctcttct	atgacatggt	gattgatgaa	360
ccctcgccgt	cgggaaaggg	g				381

<210> 175

<211> 236

<212> DNA

<213>

<220>

<221>

<222> (37)...(37)

<400> 175

tgaattacca	catgcggctg	atagatctgg	tgaaggncgg	aggattgatt	gcgtatgaca	60
atactctgtg	gcaaggatcc	gttgcgcttc	ccccagaagt	cgccatgagc	gaaggcatga	120
gttatgggga	agacagagag	catatgttgg	aactaaacag	ggcccttgct	gcagaccctc	180
gcatcgagat	tgctcagatc	ccaattgccg	atggagtgtg	gctgtgcagg	cgctt	236

<210> 176

<211> 404

<212> DNA

<213>

<220>

<221>

<222> (1)...(404)

<223> n

<400> 176

gtcgggaatt	ccacttacca	gaccattaat	tcacgattca	tcccacctca	gcctggaaat	60
ttggtctgaa	tctggagccc	aatactgtac	aagtagcctt	ggtctcttcg	ggaatccgtg	120
tntggaaaga	agaaattgag	atccggccaa	agatggttgc	agggtcagac	ctgggcgctg	180
tgcaggccaa	tggaaatcaa	aatggaaatg	gatttcatca	tgtgcattct	gttgatctct	240
gcattcagaa	tggncagac	cctctgaact	gggggcaggc	tgccaaggcc	ctgcagggt	300
cccactttga	agaagtgaag	ctcatggtgg	ngtcctat	cggtatccng	gaagtttcca	360
ttgaaggcaa	atcngtcaca	atcgcggtg	tgaccgcagt	tgcc		404

<210> 177

<211> 415

<212> DNA

<213>

<220>

<221>

<222> (20)...(20)

<400> 177

cccaacgcta	tgcgtctgan	caggcaactt	tcttcagtgc	atttgtggcg	gccatggata	60
aattgggcag	tgtgggtgta	aaaactggca	cacaggggga	ggtcaggagg	agatgtgatg	120
cgttcaattg	agaagagtaa	agttcaaatt	ctctccatta	ttaagggtgg	attgtatgca	180
tggttgagat	taatgaacgg	aacaaagaaa	atttaatgtt	ttgtaactag	tgagattgat	240
gaattgaata	aagaattttt	cctgtcctct	gattcaacct	gttttgcact	ctgtgaagca	300
ctttacagtc	tggactctgg	aaggaatcca	tcaaactcgt	actaagaaaa	gggtaatgat	360
tttaaagaga	ttccgttgcg	ctcattccat	tgggggattc	ctgaaaaatat	ctgcc	415

<210> 178

<211> 409

<212> DNA

<213>

<400> 178

gatgggcgcg	caattctttt	cagccggctg	gtgtagttgc	tgttgaggtt	acgggaggtc	60
ccacaattga	gtttgtccct	ggtcgtaagg	attcactggc	atcaccacga	gaagggcggc	120
ttcctgatgc	gaagaaagg	tcacaacacc	taagggtat	cttttatagg	atgggcctat	180
ctgacaagga	tatagttgct	ctttctggag	cgcacaccat	tgggaaaagc	acatccagaa	240
aggtcaggct	ttgatggagc	atggaccgag	cagcctctga	agtttgataa	ttcatatttt	300
gtagagcttc	tcaaaggcga	gtctgaagga	ttactccaat	tgcttacgga	caaatgcttg	360
gtagaggatc	ccagtttccg	cccttatgtg	gatctttatg	ccaaggatg		409

<210> 179

<211> 411

<212> DNA

<213>

<220>

<221>

<222> (393)...(393)

<400> 179

agagcttctc	ccagagaggc	ctctctatgg	aagatctcgt	cgctcttttcg	ggaggccaca	60
cactaggatt	ttcccactgc	tcctccttcg	caggcaggat	ccgcaacttc	aacaccacgc	120
acgacatcga	cccacgatg	cacccatccc	tggcagcgag	cctaaggaggc	gtgtgcccga	180


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gcaagaacag gccaaaaaac gcagggacca ccatggaccc ttctctgacc accttcgaca      240
acacgtacta cgggctgata ctccagggga agggcctgtt ctcttcggac caggccctcc      300
tggcagtgcc caagacgaag gatctggtcg agaagttcgc aggctcgac aaggaattca      360
cggatgcatt cgtcaagtcc atgatcaaga ttnagcagca tcacaggcgg a              411

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<210> 180

<211> 334

<212> DNA

<213>

<400> 180

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gcatcatggg aagtacaact gggaagaaga gacagcctaa cagcaagcaa aacagcagca      60
aataacaaca ttccagcccc cacatcaaatt gttgcaacac ttaactccaa gtttcagaat      120
gtaggcctca ctgaacaaga catggtcaca ctctcaggag ccatacaat aggaaaggcg      180
cgttgtgcaa cattcaactc taggctcacg ggacaaccgg atcccactct tcagaaagag      240
tttttgacat cgctccaaca aatctgcttt caagggctag ccagtaataa caacaccgta      300
acttcactgg atgtggagac tcccgtcatt ttgt              334

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<210> 181

<211> 343

<212> DNA

<213>

<400> 181

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atttcgctga actggatctg gatcgaagaa ggtattgcat atcaaagaaa gaggcaaata      60
tgactccggc cactgttttg ctttctatat ttgtgattgt atatggtagt gctgtgaacg      120
ctctgccaac tcccgtggcg ggtctttcgt ggacgttcta caacacaagt tgcccgtcat      180
tggagtcgat agtgcggaag cgcattggaag cctatttgag tgcagacatc acacaagctg      240
caggattgct gaggtccac ttccacgact gttttgtcca gggatgcgac ggggtctgtg      300
tgctgaactc aacatcgggg gagcaaacag ttgcgccccaa ctt              343

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<210> 182

<211> 443

<212> DNA

<213>

<220>

<221>

<222> (164)...(164)

<400> 182

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atttcgctga actggatctg gatcgaagaa ggtattgcat atcaaagaaa gacgcaaata      60
tgactccggc cactgttttg ctttctatat ttgtgattgt atatggtagt gctgtgaacg      120
ctctgccaat tcccgtggcg ggtctttcgt ggaccgtttt acanacaaag ttgcccgtca      180
ttggagtcca tagtgcgga ggcattggaa gcctatttga gtgcagacat cacacaagct      240
gcaggattgc tgaggctcca cttccacgac tgttttgtcc agggatgcga cgggtctgtg      300
ttgctgaact caacatcggg ggagcaaac gttgcgcca acttatcact cagagcggag      360
gctctgaaaa tcatcaatga catcaaagag aacgtagaag cggcgtgcag cggaactgtg      420
tcgtgtgcag acattcttgc ctt              443

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<210> 183

<211> 243

<212> DNA

<213>

<400> 183

acattgatga	ttgtgctacg	cgtatTTTTT	tcaatctcta	gcacttgga	aggtctggag	60
gaggcggtc	caaggTTGCC	tgaggGCCGT	gaccgttctt	cactataaac	accatattca	120
gtccccatac	taaatggtcg	tctaaatggc	agtggagaaa	ccacactcct	ggattgtcag	180
ctttgaatct	tatcgcaacc	caaccgctca	caggagctat	tactgtgttg	cgtagtgggg	240
atc						243

<210> 184

<211> 473

<212> DNA

<213>

<400> 184

ggtggccccct	agaagaaaca	cactcagaga	gtttgatcta	taagaggaga	gattcactcc	60
aaaatgcaca	gggagattca	ctccaccatc	aaattttaat	cattggcctt	tttcctctca	120
acggccgatg	gcgtaaacac	gcgtaagcaa	acaccaagat	cctgaaacag	tcgactgatc	180
gattcagaat	aatttgaaag	gaaactggac	tactcaatca	atttgTTGAC	atttatcaag	240
aaatggatga	ttcagtacag	gaggtatcca	aggaaggcaa	tcaatgggca	ggattcattg	300
agggtgagaa	tgtaatccga	agaggaagg	agattcttct	acagcatgat	aaccgggagg	360
cacataactg	ggagtcacat	aaacataagt	ggtggccaca	tttggaagaa	aaaatcccgc	420
acattgccaa	agcaggattt	acatctatat	ggctgccgcc	tgcttttgat	tcg	473

<210> 185

<211> 641

<212> DNA

<213>

<400> 185

ggcaccgagc	tgggataccc	ctgctgcgac	ttgatccctt	ttgaacagga	attattttaat	60
tttcctaatt	atTTTAGTTT	gcaaggaaac	ttgactactc	catcaatttg	tttacagttt	120
tcgaaaaatg	ggctatccag	ttcaggaggt	atccaaggaa	cacgatcaat	gggcaggatt	180
tgTTGAAGGT	gaaagtgtgc	ttcaaagagg	aaggagagatt	cttctccagg	gttttaactg	240
ggagtcacat	aaatacaagt	ggtggccaaa	tttggaagaa	aagatcccgc	acattgctaa	300
agcaggattt	acatctgtat	ggctgccacc	tgcttttgat	tctgctgcac	cccaaggTTA	360
cttgcCCCGA	aacattttatt	ctctgaactc	tgcatatggT	tcagaatatc	agctgaaaag	420
cttactttatg	acaatgcgaa	agaaaaatgt	gagagccatg	gctgacatag	ttatcaatca	480
tcgcatggga	agctctcagg	ggTTTGGAGG	cttgTATAAT	cgctattatg	gttgCCTGCC	540
ttgggatgaa	cgtgctgtta	cacgttgTTC	tggtggactt	ggaaactgga	gcacagggga	600
taattttcat	ggagtaccaa	acgttgatca	caccaagat	t		641

<210> 186

<211> 655

<212> DNA

<213>

<400> 186

agaatggcca	agtttctgac	tctgtcttta	ttgttatggT	tctcctgcat	catagtcaat	60
gcagcctctc	ctgcacaagc	agaagctaca	acgcctcctc	tgaataccct	cttacttcag	120
ggcttcaatt	gggattcagc	ccagagttct	actccttggT	ataatgtatt	gaagggaatt	180
gtagacgatg	cagcggacgc	cggcattacg	tacgtctggT	ttccgcgcgc	ctcacaatcc	240
ggcgcCCCTC	aaggTTATTT	gccagcgaag	ctctatgatt	tagactcgTc	ctacgggagc	300
gagcaacaac	taaaggatgc	cgtgaatgcg	ttccaccaa	aggggaattgc	gattatgggc	360
gacatcgtga	taaaccatcg	gaacgggacg	aagcaggacg	ataaaggata	ttggtgcgtg	420
tttgagggcg	ggaaggggga	cggTactctg	gactggggac	cctgggcggT	caccgtgaag	480
gaccaacat	atccgttgtg	cggctccggc	caggcggaca	ccggagggga	cttcaagtac	540

gccccggacg tggaccacac caatcccaag atacagcaag atttgtcggg gtggatgaat 600
 tggctcaagt ccatgtcggg tttgatggct ggagggttcga ctacgtcaag gctac 655

<210> 187

<211> 438

<212> DNA

<213>

<400> 187

ctgggggtggg gaggctgggc gacgtggggc ggagcgcggg ggactgcctc cggatgatca 60
 tggggaagca cagcacgctc cgggaaggga tcaacttcga cttgcccag gtcgtggcca 120
 aagcgctcc cattcctggg gtgacccatg ttgggtggcg catgttcaag tccatccctg 180
 ctggtgatgc cattttcatg aggtggatac tgacgacatg gacggacgac gagtgaagc 240
 agatactgga aaactgcttc aaggcactcc ctgctggagg gaagctgatt gcctgcgagc 300
 cgggtctacc gcagcactca gatgatagcc acaggactcg agcacttctt gagggcgaca 360
 tcttcgtgat gaccatctac agggccaagg gcaagcatag gactgagcag gaattccagc 420
 agctcgggct ctctaccg 438

<210> 188

<211> 597

<212> DNA

<213>

<400> 188

acccaacaat ggccgacaac caagaacgcg aaggcgcgga tcaagaagag gaagtcggga 60
 agctggcggg ccagctgggc agcgcggtgg tgctcccgat gacctcaag tcggccctcg 120
 agctcggcat catcgacgcc ctgctctccg ccggtgggtt cctctcggct gccgagatag 180
 cgagccgggt tggcgccaag aaccgggggg cccagctcct ggtggaccgg atgatgcgcc 240
 tcctggcgag ccacggcggt atcgagtggc ggttgaggag gggcgacggc aacggagatg 300
 gaggggagag agagtacggt ccaggaccca tgtgcagggt ctttgccaag gaccaagaag 360
 gtggagatgt tggtcctctg tttctgctaa ttcacgacaa ggtcttcatg gagagtgggt 420
 accacttgaa cgatgtcatc atggaaggag ggttccggt cgagagggca tacgggatga 480
 cggcgttcga gtatcctgcc gttgacgata ggttcaatca agttttcaac cgggccatgg 540
 cgagtcatac ttccctcatc atgaagaaaa tactcgatgt ctacagaggg tttgaag 597

<210> 189

<211> 470

<212> DNA

<213>

<400> 189

cccgacccc ctttacatga acaagatcct cgagtcgtac cgtgggtttg agggcgcaaa 60
 gacgattgcc gacctagggt gcggcgtcgg ccagaacctt cggctcatat tggacaagtt 120
 cccaaatctc aggggcatac tctatgatct gcctcatgtg atcaaagatg cacctgccca 180
 tctctgatag gagcgtgtcg gaggagacct gttaaagtct gttccgaaag cagatatact 240
 cttcatgaag tggcttttcc atggtctacg agacgatttc tgcaaaatgc tactccagaa 300
 ctgttacgag gcgctgccac caaatggcaa ggtggtcatc gtggaccoga tccttcccg 360
 ataccccgag acagacatag tgtcgaggaa ctcgttcacc tccgacatga tcatgctata 420
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<211> 499

<212> DNA

<213>

<400> 190

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taacaggaga	caaatcccaa	gtcagggtgc	tgagtggggc	aggatgagca	tgtgtgatgc	360
agagaaaaga	ctcctagcca	acgcattgct	agacatatcc	aatgagcggg	tcattcttct	420
ttctgaatca	tgcattccgc	tgtataactt	cagcctcatc	tatcactaca	ttatgaagtc	480
cggatatagc	ttcatgggt					499

<210> 191
 <211> 1036
 <212> DNA
 <213>

<400> 191

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gaagccccag	tcattacaac	ttcccatgaa	gatgaagaaa	ttttgaatgc	ctttgaggtc	180
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<210> 192
 <211> 682
 <212> DNA
 <213>

<400> 192

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aactggtggg	aaggagagaa	cagaggaaga	attcaaaggg	ttgttccagc	gcgcagggtt	420
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atcatgcagt	atatgcctta	tgttttatgt	tatctggcag	tataagattt	ctgaagacat	600
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<210> 193
 <211> 399

<212> DNA

<213>

<400> 193

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ccggttgatg	aggggcagct	gatctccatg	atgttgaagc	tcatgaatgc	gaagaagaca		300
atcgagatcg	gagtcttcac	cggctactct	cttctgacca	ccgcacttgc	acttccggcc		360
gacggcaaga	taatagcgat	agaccaggat	aaggaggcc				399

<210> 194

<211> 399

<212> DNA

<213>

<400> 194

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ggagtcttca	cgggctattc	tcttctcacc	accgcacttg	cacttccggc	cgacggcaag	300
ataatagcaa	tagaccggga	taaggaggcc	tatgaaattg	gcctgccata	tatcaaaaaa	360
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<210> 195

<211> 296

<212> DNA

<213>

<400> 195

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gtcttcaccg	gctgtttctc	tctcaccacc	gcacttgac	ttccggccga	tggcaagata	240
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<210> 196

<211> 474

<212> DNA

<213>

<400> 196

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cttcgagaac	atctccgagt	tcgcccagcg	cccctgcgtc	atcaacgggg	ccaccggccg	240
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gttcgcgttc	ctcggcgcg	cctaccgggg	cgccatcagc	acgaccgcga	acccgttcta	420
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<210> 197

<211> 543

<212> DNA

<213>

<400> 197

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ggtggaccgg	tacgacctgt	cgtcgatccg	gaccatcatg	tcgggtgcgg	cccgatgggg	540
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<210> 198

<211> 564

<212> DNA

<213>

<400> 198

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caaagtctgc	ttccggcaaa	atfffagac	gtgagctgat	tgcaaaagta	cgagcaaaga	540
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<210> 199

<211> 455

<212> DNA

<213>

<400> 199

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gcaaagaaat	atatcatttt	ttctggtatc	atgatacaaa	gttgacacaaa	cttatttgta	420
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<210> 200

<211> 569

<212> DNA

<213>

<400> 200

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cttttttttc	ttgctaagag	tagccatgat	tgaggtacag	tcagctcccc	ccatggcacg	180
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<210> 201

<211> 993

<212> DNA

<213>

<400> 201

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<210> 202

<211> 349

<212> DNA

<213>

<400> 202

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<210> 203

<211> 432

<212> DNA

<213>

<400> 203

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agaagttgct cg 432

<210> 204
<211> 407
<212> DNA
<213>

<400> 204

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<210> 205
<211> 384
<212> DNA
<213>

<400> 205

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<210> 206
<211> 543
<212> DNA
<213>

<400> 206

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<210> 207
<211> 1320
<212> DNA
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<400> 207

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<210> 208

<211> 980

<212> DNA

<213>

<400> 208

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<210> 209

<211> 305

<212> DNA

<213>

<400> 209

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caccatccat	tggcatggta	ttcggcagct	gaggtcgggg	tgggccgacg	ggccggcata	180
catcacccaa	tgcccaattc	agccaggcca	aagctatgtg	tacaatttca	ccatcacggg	240
ccaacggggc	accctccttt	ggcatgcgca	catactctgg	ctcagggcaa	ccctgcacgg	300

agcca

305

<210> 210
 <211> 411
 <212> DNA
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<400> 210

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cgacgacagc	cattctccaa	gcacatttct	tcaacaaaag	cggcgtcttc	acgagcgatt	180
tccccggtaa	cccgccaacc	attttcaact	acacggggtc	accgccatca	aatttgcgga	240
ccacaagcgg	gacaaaggtg	taccggttgc	gttataactc	gacggtccag	ctgggtgttc	300
aagacaccgg	gattatcgcc	ccagagaacc	acccaattca	tcttcacggg	ttcaatttct	360
tcgccattgg	gaaggggatta	ggaaattata	atccgaaagt	ggatcagaag	a	411

<210> 211
 <211> 311
 <212> DNA
 <213>

<400> 211

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catccagggc	caagttccaa	ttgcccttcc	caggggtggat	ttacattgcc	tgttgagagt	180
ggcaagaagt	acatgctccg	aatcatcaat	gctgcgctca	atgaggagct	cttcttcaag	240
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accaacacgg	g					311

<210> 212
 <211> 334
 <212> DNA
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<400> 212

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cccaggggtgg	atttacattg	cctgttgaga	gtggcaagaa	gtacatgctc	cgaatcatca	240
atgctgcgct	caatgaggag	ctcttcttca	agattgctgg	gcaccagctg	accatcgtgg	300
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<210> 213
 <211> 1374
 <212> DNA
 <213>

<400> 213

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aagcaaagac	accgtcatag	ttccgatcga	ttccggggag	acccacctcc	tccgagtcac	120
caacgctgcg	ctcaatcagg	aactcttctt	caccgtagcg	aaccatagggt	tactgtgggt	180
cggtgccgac	gcctcctacc	tgaaacctt	caccacctcg	gtgatcatgc	ttgggccagg	240
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cgaaccttac	cagagtgtct	agggagcgcc	ttttgacaac	accacgacca	cggccatact	360
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aaataaggtt	gacgtcccga	ccgacatcga	cgaaaacctc	tttatcacgg	tcggcctagg	540
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cgcgagattt	cagttcagtg	attgtttccc	ctgaattcag	ggagccacca	gttgtttgct	1320
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<210> 214

<211> 418

<212> DNA

<213>

<400> 214

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gatgagagcc	gccttcttca	cactgtgcgc	tctcgtgttc	ttgccggctc	ttgctcaggc	180
gaagcacgga	ggtgtcacca	ggcattacaa	gtttgatatac	aagatgcaga	atgtgacgag	240
gttggtgccag	acgaagagca	ttgtcacggt	caatggccag	ctcccggggc	ctcgaatcat	300
cgctagagaa	ggcgaccggc	tcctaataca	agtcgttaac	aatgtccagt	acaatgtcac	360
aatccactgg	catggagtcc	gacaactcag	aagcgggtgg	gctgacggac	cggcatac	418

<210> 215

<211> 466

<212> DNA

<213>

<400> 215

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ctctttttatg	atthttgtggt	aaatgagaca	cctattgaga	tgctatgtga	gacaaatcgg	180
agcgtactaa	ctgtgaacgg	tctatttcct	gggccggaga	tccatgctca	caaggggtgac	240
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gtgagacaaa	tacggtatcc	ttggtctgat	ggcccagaat	atgtcacgca	atgccccatc	360
cctacaaact	cgagctttct	tcaaaaaatc	aaactcaccg	aggaagaggg	cacggtgtgg	420
tggcacgccc	acagcgactg	gtcacgtgcc	acaatacatg	gcctat		466

<210> 216

<211> 757

<212> DNA

<213>

<400> 216

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gtgtacctgc	attgtcttca	aggaggacat	ctaaagcaac	tactgtaaga	ctttggaccg	180
gcacgagcac	aagtctcctt	ctttgttctg	gatcaagtga	ttgttacaag	ttcatttttc	240
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gctcttttgc	atggctcaag	gcgaagtc	catctactat	gttctcgt	gtaggagac	360
tattcagatg	ttatgtggga	cgaatcagac	cgtattgact	gtgaatggtc	tgtttcctgg	420
gccagagatt	catgctcaca	aaggcgacac	catctacgtt	aatgtcacca	acacaggacc	480
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tatacacggc	cctataatca	ttttgcctgt	caacggcacc	aactaccctt	acaagtttga	720
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<210> 217

<211> 251

<212> DNA

<213>

<400> 217

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tgagagagag	agatgggaac	atctctaggg	tttgtgggtc	ccatgaccct	gctcttttgc	120
atggctcaag	gcgaagtcct	ctactatgat	ttcgtgggtg	aggagacacc	tattcagatg	180
ttatgtggga	cgaatcagac	cgtattgact	gtgaatggtc	tgtttcctgg	gccagagatt	240
catgctcaca	a					251

<210> 218

<211> 762

<212> DNA

<213>

<400> 218

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ccaaagagtt	cattgaggaa	accaaggata	gaggtatgct	ggtgggttgg	gcgcctcaga	180
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tgaagagaga	agagttggcg	atactgggtg	ggaattcgat	caaagggtgaa	gaaggagatg	420
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gaaaacatcc	cagtacccca	agcgttcata	tttctgcatt	tcgcattaaa	tttactttgt	660
attgttccgc	acatatgtat	tttcagggtt	tcaggtttcc	ccagagttga	acctcatttt	720
caattagatt	gtttcacgct	tttacggcgc	aggggggtt	ga		762

<210> 219

<211> 1144

<212> DNA

<213>

<400> 219

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caaccgtcgg	aagcgaccca	agcttcccc	tcagccccca	gcattggccc	tgatcggtcaa	180
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gtttactgct	ctcggctatg	accaaggctc	gctcgtctct	ggtcgtcatg	gtgactactg	420
gcgcgctctc	cggcgtctct	gctccgcgga	gctcctcgtg	aacaagcgcg	tcaacgatac	480
ggcccacctc	aggcaaaagt	gtgtcgacag	catgatcatg	tatatagaag	aagaaatggc	540

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<210> 220

<211> 563

<212> DNA

<213>

<400> 220

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cccagcatg gcccgatgac ggcaacattt tcgacctcg gaccatgccg caccagaacc 180
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tcgtgaacaa gcgcgtcaac gagacggccc acctcaggca aaagtgtgtc gacagcatga 480
tcatgtacat agaggaagaa atggcagtc aacaagcaac aaaagggcaa ggaatcgact 540
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<210> 221

<211> 447

<212> DNA

<213>

<400> 221

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cgacggcacc acttctcttc ccacacgcgt catcggtgta ttgcactata ggaggatact 180
tcgtcccacg cgacactatt gtgatggtga atgcatgggc cattcacaaa gaccctcagt 240
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aacaaaagct actattgcct tttggactgg gacggagggc atgccctggt gcccccttgg 360
ctcatcgggt catggggtgg acgttgggct tgttgattca gtgttttgat tggaaaagag 420
taagcgaaga agagattgac atgacgg 447

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<210> 222

<211> 494

<212> DNA

<213>

<400> 222

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gaggaagaag ggcgaccag agctcgaga cagcatgatc agtcatcttc tgcactaca 180
agaatctcag ccggaagact actcggactc catgatcaaa gggcttgctc ttgttttggt 240
agttgcggga acagacacgt catcgcttac attagaatgg ataatgacaa acttactaaa 300
caatcctgaa aagttagaga aggcccgaag tgagattgat tctgttattg gccacgatcg 360

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tctggtagaa	gaatcggatg	tttcgaatct	accttacctt	cagtgcacat	tcttagagac	420
ccttcgacta	aacaccacgg	tgccacttct	cgtcccgac	gcatcatcag	ctgattgcac	480
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<210> 223

<211> 492

<212> DNA

<213>

<400> 223

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gaagagattg	tcttgcctca	aagacgacag	agagcaagat	ttcatggatt	ggatgatcaa	180
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cgtcaaggaa	gcaactgcgtt	tatatcctcc	agtaccgggtg	aacggcctta	gaagctccat	480
ggaagagtgc	ac					492

<210> 224

<211> 391

<212> DNA

<213>

<400> 224

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ctctcggaat	gaaaactaca	gtggtagtct	cctctccggc	catggcaaag	caagttctca	180
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tatccaatac	aaagctcttc	agcgtcaaga	ggttagaagc	cctggaacat	ttgagaagag	360
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<210> 225

<211> 536

<212> DNA

<213>

<400> 225

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aatactctcg	ttctcgtgaa	tgtttgggcg	attgggagga	accctaagtc	atgggaggac	180
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aatggagtca	cgctgcgcaa	agctcgtgag	ctctcggcta	ttccgacacc	acgccttgaa	480
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<210> 226

<211> 463

<212> DNA

<213>

<400> 226

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atcatgcatg	gagcaacttg	tccaggaaaa	gaaaaggcag	actgcccccg	gggcctttct	180
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tcgtctcttc	tccagaaata	gccagtgaat	ttctcaaaac	ccatgatcag	ctttttgcca	360
gcagaattcc	ctctgctgct	attaaggtat	tgacctacaa	tttgtccggc	ctcatatttt	420
ccccgtatgg	cccttgctgg	aggcaagtgc	gtaaactttg	cgt		463

<210> 227

<211> 463

<212> DNA

<213>

<400> 227

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acagtgaacc	atctaaaaaa	ctggcgatgg	agtttgtaga	gtttttgtata	acactcgtca	180
ctgctcttct	ttttgttgta	ttggtagcag	catggagcaa	cttgttcagg	aaaagaaaag	240
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agattcctca	ccgatcactg	gcagagctgt	ctatgaaata	cgggcctctc	ctgtctctcc	360
gcctcgggtc	tactcccgc	ttagtcgtct	cttctccaga	aatagccagt	gaattttctca	420
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<210> 228

<211> 463

<212> DNA

<213>

<400> 228

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ccacaccaag	caattacagc	tctctctatg	aaatatgggc	ctctcatgtc	tctccgcctc	240
ggctcctatc	tacttttgg	cgtttcttct	ccagatgtgg	ccgaggagtt	cctgaagact	300
catgatctgg	ctttcgccag	cagacctcca	accatcggtg	cgaagtactt	ttggtataat	360
tcctccgacg	tcgcattttc	cccctatgg	ccttactgga	ggcagatgcg	taaaatctgt	420
gtgttacagt	tgctgagctc	aagacgcata	gattccttcc	gcc		463

<210> 229

<211> 463

<212> DNA

<213>

<400> 229

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aaggtctcaa	ccgtcgattg	aagaacatac	acaagatcca	agacgacttg	ttagggaaga	180
tactagagga	acacgcttcg	ccaccgcaga	ataaccccaa	ctacatgcc	gatctcgtgg	240
atgttttgct	cgcgccctct	gcggatgaag	atctggagtt	cgaattact	cgagacaata	300
taaaatctgt	catctatgta	tatattgtcc	atgcaattat	tagatttcaa	tgacttaa	360
aaaacatgac	acggtgatta	tatcttgaca	tttgttttg	atttgttttg	ttggtaggat	420
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<210> 230

<211> 543

<212> DNA

<213>

<400> 230

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gccgatttta	ttccgccact	tgtcttcgga	gccctgcaat	gtcctgggct	atgaaatctc	180
tcaaaacact	caagttcttg	ttaatatattg	ggcgattgga	aggaactctg	agtcattgga	240
agatgccgga	agcttcaaac	ctgagagatt	catggaaaga	gttgggtctg	aggtagatac	300
aaatggagat	caaaattctg	cgtggcttcc	cttcggagca	gggaggagaa	gatgcccgag	360
acagcaattg	ggaacgcttg	ttgcagaaat	tgggctggca	cagctcttgc	actgtttcaa	420
atggaggctt	cccgaagctg	atatggatgg	cccaaatcaa	gaacttgaca	tgatggaaag	480
gtttaatgga	atcacatcgc	cgagggctaa	ggaactgttt	gcgattccga	cacccgcct	540
tga						543

<210> 231

<211> 381

<212> DNA

<213>

<400> 231

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cgcgctgttg	gattggatcg	catggcatgc	gaatctgac	tgctcagct	cgtttattta	180
caagctatgg	taaaagaaac	gcttcgactt	cacccagcgg	ggcctctttt	gaaccgtcgc	240
ttatccgctg	agtctgcaa	tgtgttgggg	tacgaattcc	ctaaaaacac	tcgtgttctc	300
gttaatgctt	gggcgattgg	gaggaacca	aagttatggg	aggacgctga	aactttcaag	360
ccagaaagat	tcacgggaag	a				381

<210> 232

<211> 384

<212> DNA

<213>

<400> 232

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acatagcaaa	attgccctat	ctacaagcag	tagtgaagga	ggtactcaga	ttgcacccag	180
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tcccagagaa	cacgcaggtg	tttgtgaata	tctggggcat	cggaagagat	cccaacgttt	300
ggaaggaacc	tctgaaattc	aaaccgga	ggtttttaga	ctgtaatact	gactacagag	360
gccaggattt	tgaactgata	ccat				384

<210> 233

<211> 405

<212> DNA

<213>

<400> 233

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tgaccttcgg	taaaaagtat	tcggaccggg	attcaggagc	attcagttca	atgatcaaa	180
aaagtttact	gttactcggc	tcctttaata	ttggagaata	cataccttac	ttgaactgga	240
tggatttgca	aggtctcaac	cgccggctga	agaagctacg	tacaacacaa	gaccagttgc	300
tagagaaagt	aatagaggaa	catgctgccc	agaatcggag	caacatgacg	catgatcttg	360
tggatgcctt	acttgcagcc	tctgcggata	aagatagaga	gctcc		405

<210> 234

<211> 348

<212> DNA

<213>

<400> 234

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gaatatcaag	agattcttgc	cttcagagtt	tggaaatgat	gtggatcgtg	tccatgctgt	180
ggagccagta	aaaactggat	ttgctctcaa	ggccaagatc	cgcgccttg	ttgaggccga	240
gggaatccct	tatacctatg	tgtcttctaa	ctcttttgca	ggttactacc	ttcaaacatt	300
gtcacagccc	ggggctacag	ctccccctag	agataacggt	gttatctt		348

<210> 235

<211> 640

<212> DNA

<213>

<400> 235

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cagatgaaga	tttggagtct	caattatact	gtgtgttaag	ctagtagtca	gtcaagcatt	120
gaaggcatga	acaccttaaa	gacatgaaca	gatgaagatt	tggagtctca	atggtattat	180
tgectacctt	atctccagtc	acagcagagt	cgcttctaga	aaccgatcga	gttcgccgga	240
aaacaccgcg	cctccgccgt	gaaaaccact	cagagatggc	tgcgaagagc	aaggtcctgg	300
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gtctattgaa	tgcgatcaag	caggtcgatg	tggtaatctc	tgctgtgggg	cgagcacaaa	540
tagaggacca	agacaggatt	gttgctgcc	tcaaagcagc	cgggaatatc	aagagatttg	600
tgcttcaga	gtttggaaac	aacgtggatc	gtgtccatgc			640

<210> 236

<211> 464

<212> DNA

<213>

<400> 236

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gccaagatcc	gccgcctcgt	tgaggccgag	ggaatccctt	atacctatgt	gtcttctaac	180
tcttttgcag	gttactacct	tcaaacattg	tcacagcccg	gggctacagc	ttcccctaga	240
gataacgttg	ttatcttagg	ggatggaaat	gccaaagtgg	tgtttaacaa	ggaggatgac	300
atcggcacct	ataccatcaa	agctgtggat	gatccaagga	ccttgaacaa	aattctgtac	360
atcaggcctc	ctgccaacac	ctactcaatg	aatgagctcg	tgtctttgtg	ggagagaaag	420
atcggcaagg	ctctggagag	ggtgtatgtt	ccagaggagc	aaat		464

<210> 237

<211> 315

<212> DNA

<213>

<400> 237

cttctagaaa	ccgatcgagt	tgcgccgaaa	acaccgcgcc	tccgccgtga	aaaccacttc	60
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catcgtggaa	gccagtgtca	agtcgggtcg	ccctaccttc	gttctcgcca	gggagtccac	180

tctctccaac	cccgccaagg	ccaagatcgt	ccaaggtttc	aagagcctcg	gcgtcacttt	240
agttcacgga	gacatatacg	atcaagagag	tctgttgaat	gcgatcaagc	aggtcgatgt	300
ggtaatctct	gctga					315

<210> 238

<211> 376

<212> DNA

<213>

<400> 238

caaagtcacg	tcagagaccg	atcaagttcg	ccggaaaaca	ccacgcgcgc	tatgaaaaga	60
ccctccaaga	tggcagagat	gagcagagtc	ttggtgattg	gaggcgccgg	atacatcgga	120
aagttcattg	tgaagcgtg	tgctaagtcc	ggtcacccta	cctttgttct	cgagacggag	180
tccactctct	ccaaccccg	caacgccgaa	atcatcaaag	gtttcaagag	cttaggcgtg	240
aacctagtcc	atggagacat	atacgatcaa	aaaagtctgt	tgagtgcgat	taagcaagtt	300
gatgtggtaa	tatctactgt	ggggcaagca	cagctagaag	accaagacag	gattgttgca	360
gccatcaaag	cagccg					376

<210> 239

<211> 297

<212> DNA

<213>

<400> 239

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tgctaagtcc	ggtcacccta	cctttgttct	cgagacggag	tccactctct	ccaaccccg	180
caacgccgaa	atcatcaaag	gtttcaagag	cttaggcgtg	aacctagtcc	atggagacat	240
atacgatcaa	aagagtctgt	tgagtgcgat	taagcaagtt	gatgtggtaa	tctctac	297

<210> 240

<211> 951

<212> DNA

<213>

<400> 240

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cagcatggga	ggagagaccg	cccggtcgat	caacctcacc	tgcaatggcc	tctccccgcc	180
tcaaccgcag	tacaacgccg	agaacaacca	tgatcaggac	accacagttg	ccacaagggg	240
tctcattatt	ggcgccaccg	ggttcatcgg	tcggtttgtt	gcagaggcca	gtgtgaaatc	300
cgggcgcccc	acttatgccc	ttgtgcggcc	gacaacatta	agttcgaagc	ccaaggtcat	360
tcagtctctg	gtggattcgg	gtattcaagt	tgtttatgga	tgtctacatg	atcacaaatc	420
tttggtgaaa	gccatcaggc	aggttgacgt	tgttatttct	actgttggtg	gagcccta	480
tcttgatcag	ctcaagattg	tggatgccat	caaggaagtt	ggcactgtca	agagatttct	540
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ttacatagaa	aagagaaaag	tccggcgtgc	agtggaggaa	gcaaagattc	cttacacata	660
catctgctgc	aactccatag	ctggctggcc	atactattat	cacacacatc	caactgagct	720
ccccccacca	aaggaacagt	ttgagatcta	tggggatgga	agcgttaaa	cctttttcgt	780
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caagtctatt	catttcagac	caccaaagaa	ttttctcaac	ttaaacgaac	tcgcagacat	900
atgggagaat	aagattaaca	gaactctgcc	aagagtatct	gtctcagcag	a	951

<210> 241

<211> 371

<212> DNA

<213>

<400> 241

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ttcacagggc	tatccaacct	acgttcttgt	ccgtcctgct	acagcagctg	cccctgattc	180
cttcaaagca	aagctacttc	agcaattcaa	agatattggc	attcatattc	ttgaaggatc	240
attagatgat	cacaacagcc	ttgtggatgc	aatcaagcaa	gtagacatag	taatatccgc	300
agttgccatt	cctcagcatt	tggatcagtt	taatatcata	aacgccatta	aggatgttgg	360
aatggaata	t					371

<210> 242

<211> 687

<212> DNA

<213>

<400> 242

taatggcgag	ctccacccgt	ctcactactg	tgagagggac	ctgctcaaag	tggtcgaccg	60
cgagcatgtg	ttcacctacg	ctgatgacgc	ctgcagcgcc	acctacccgc	tgatgcagaa	120
gctgaggcaa	gtcctggtcg	accaggcact	ggtgaatggc	gagagcgagc	tgaacccgag	180
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ttgccaahta	aatctcatgt	atccaatctt	ttctatcaag	agacaattgt	atttcttggt	600
ttctgttttg	tcctttttgt	ctcctcccaa	gtgaagaaat	tggagaatat	aagtaattga	660
gtaaaattttt	acatggaaaa	aaaaaaa				687

<210> 243

<211> 344

<212> DNA

<213>

<400> 243

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tccaaaagat	cgtggccttc	gaggaggagc	tcaaggccca	gttgccgaag	gacgtcgagg	120
gcgttcgagt	ccagtacgag	acaggaaacc	tcgccatccc	caaccagatc	aaggaatgca	180
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agggcgatg	atcccctggc	gaggacttcg	acaaggctct	cactgcgatc	tgtgctggaa	300
aactgattga	tccgctgctg	gagtgcctaa	gcggttgga	cggt		344

<210> 244

<211> 681

<212> DNA

<213>

<400> 244

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gctgcagttc	cttgccaacc	ctgtgaccaa	ccatgtccag	agcgcggagc	aacacaacca	120
ggacgtgaac	tccttgggccc	tgatctcgtc	gaggaagact	gccgaggcca	tcgatgtgct	180
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ctacgtcggg	tccaacggcg	agctccaccc	gtcgcggttc	agcgagaaa	acctgatcaa	360
ggtggtcgac	cgggagtagc	tcttcgccta	catcgatgac	ccctgcagcg	ccacgtaccc	420

cctgatgcag	aaactgaggc	aggtcctcgt	ggacgatgcg	ctggacgacg	tcgaccggga	480
gaagaacccc	agcacctcca	tcttccagaa	gattggggct	ttcgaggagg	agctcaaggc	540
actcctcccg	aaggagggtcg	agaacgcgag	agctcagttc	gagagcggga	actcggcgat	600
cgctaacaag	atcagggggt	gcagggtcgta	cccattgtac	aggttcgtga	gggaagagct	660
cgggaccggt	ttgctcacgg	g				681

<210> 245
 <211> 1455
 <212> DNA
 <213>

<400> 245

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<210> 246
 <211> 294
 <212> DNA
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<400> 246

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acccgctggg	gagaccctca	cggccaaaca	agcctttgag	ctcgtcggga	tcagtgggtg	180
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<210> 247
 <211> 1520
 <212> DNA
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<400> 247

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aattatttac	tgtctctttt	tttttccgga	gcttgcgacc	gccttcgatt	ccgtgcacta	1500
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<210> 248

<211> 449

<212> DNA

<213>

<400> 248

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ggaattcaca	ggcgaagtga	aattctgtgc	gggaaatggc	ggtacggcgt	ctttgaacga	180
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tgcccagggtg	gcagccgtgg	ccaggagaac	gggatccgtg	agagtcgaac	ttgagaccgg	360
cgcgaaaggc	cggttagatg	agagcagtaa	ttgggtgatg	gacagtatgg	cgaacgggac	420
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<210> 249

<211> 512

<212> DNA

<213>

<400> 249

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gacctgtccc	aatgctgagt	tgatcgctgc	aaatgctgtc	agaatgcgg	caatgaagga	180
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512

<210> 250

<211> 354

<212> DNA

<213>

<400> 250

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gcggagaagg	tggcggttcc	gaaccagtcg	ctaaccgggt	tcgacgtaat	agacgagatc	300
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<210> 251

<211> 195

<212> DNA

<213>

<400> 251

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acattccggt	ttctgggtcaa	acaaggagaa	acttaccttc	tacggatggt	caatgctgca	180
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<210> 252

<211> 377

<212> DNA

<213>

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<210> 253

<211> 387

<212> DNA

<213>

<400> 253

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<210> 254

<211> 534

<212> DNA

<213>

<400> 254

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tataacttca	ctgtcacagg	acagagggga	actctctggt	ggcacgctca	catctcttgg	420
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<210> 255

<211> 1076

<212> DNA

<213>

<400> 255

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<210> 256

<211> 483

<212> DNA

<213>

<400> 256

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gcacgggata	aggcagttgc	ggactgggtg	ggctgatggg	cctgcttata	ttacgcagtg	360
ccccattcaa	acaggccaaa	cttatgtata	taactttaca	atcacagggc	agcgaggcac	420
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tct						483

<210> 257

01.05.08

<211> 470
<212> DNA
<213>

<400> 257

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ggtcctggtt	atatcactca	atgtccactt	caaaccggaa	tgagttacgt	ttataatttc	420
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<210> 258
<211> 472
<212> DNA
<213>

<400> 258

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tccctggaca	acatatcttc	ttcgtatcat	caatgctgca	ctcaatgatg	aactcttcc	180
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agggacattt	gataattcca	ctgttgacag	aattgtgagt	tataattctc	ataagtttaa	420
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<211> 405
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<210> 262
 <211> 279
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<210> 263
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<213>

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<211> 1790

<212> DNA

<213>

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<210> 266

<211> 2043

<212> DNA

<213>

<400> 266

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<211> 92

<212> PRT

<213>

<400> 267

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Phe Ile Glu Gly Glu Asn Val Ile Arg Arg Gly Arg Glu Ile Leu Leu
35     40     45
Gln His Asp Asn Arg Glu Ala His Asn Trp Glu Ser His Lys His Lys
50     55     60
Trp Trp Pro His Leu Glu Glu Lys Ile Pro His Ile Ala Lys Ala Gly
65     70     75     80
Phe Thr Ser Ile Trp Leu Pro Pro Ala Phe Asp Ser
85     90

```

<210> 268

<211> 182

<212> PRT

<213>

<400> 268

```

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

```

<210> 269

<211> 218

<212> PRT

<213>

<400> 269

```

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

```

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                165                170                175
Asp Phe Lys Tyr Ala Pro Asp Val Asp His Thr Asn Pro Lys Ile Gln
                180                185                190
Gln Asp Leu Ser Glu Trp Met Asn Trp Leu Lys Ser Met Ser Asp Leu
                195                200                205
Met Ala Gly Gly Ser Thr Thr Ser Arg Leu
                210                215

```

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<210> 270
<211> 145
<212> PRT
<213>

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```

<400> 270
Gly Val Gly Arg Leu Val Asp Val Gly Gly Ser Ala Gly Asp Cys Leu
 1      5      10      15
Arg Met Ile Met Gly Lys His Thr His Val Arg Glu Gly Ile Asn Phe
 20      25      30
Asp Leu Pro Glu Val Val Ala Lys Ala Pro Pro Ile Pro Gly Val Thr
 35      40      45
His Val Gly Gly Asp Met Phe Lys Ser Ile Pro Ala Gly Asp Ala Ile
 50      55      60
Phe Met Arg Trp Ile Leu Thr Thr Trp Thr Asp Asp Glu Cys Lys Gln
 65      70      75      80
Ile Leu Glu Asn Cys Phe Lys Ala Leu Pro Ala Gly Gly Lys Leu Ile
      85      90      95
Ala Cys Glu Pro Val Leu Pro Gln His Ser Asp Asp Ser His Arg Thr
      100      105      110
Arg Ala Leu Leu Glu Gly Asp Ile Phe Val Met Thr Ile Tyr Arg Ala
      115      120      125
Lys Gly Lys His Arg Thr Glu Gln Glu Phe Gln Gln Leu Gly Leu Ser
      130      135      140
Thr
145

```

```

<210> 271
<211> 198
<212> PRT
<213>

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```

<400> 271
Pro Thr Met Ala Asp Asn Gln Glu Arg Glu Gly Arg Asp Gln Glu Glu
 1      5      10      15
Glu Val Gly Lys Leu Ala Val Gln Leu Ala Ser Ala Val Val Leu Pro
 20      25      30
Met Thr Leu Lys Ser Ala Leu Glu Leu Gly Ile Ile Asp Ala Leu Val
 35      40      45
Ser Ala Gly Gly Phe Leu Ser Ala Ala Glu Ile Ala Ser Arg Val Gly
 50      55      60
Ala Lys Asn Pro Gly Ala Pro Val Leu Val Asp Arg Met Met Arg Leu
 65      70      75      80
Leu Ala Ser His Gly Val Ile Glu Trp Arg Leu Arg Arg Gly Asp Gly
      85      90      95
Asn Gly Asp Gly Gly Glu Arg Glu Tyr Gly Pro Gly Pro Met Cys Arg
      100      105      110
Phe Phe Ala Lys Asp Gln Glu Gly Gly Asp Val Gly Pro Leu Phe Leu

```

```

      115              120              125
Leu Ile His Asp Lys Val Phe Met Glu Ser Trp Tyr His Leu Asn Asp
      130              135              140
Val Ile Met Glu Gly Gly Val Pro Phe Glu Arg Ala Tyr Gly Met Thr
145              150              155              160
Ala Phe Glu Tyr Pro Ala Val Asp Asp Arg Phe Asn Gln Val Phe Asn
      165              170              175
Arg Ala Met Ala Ser His Thr Ser Leu Ile Met Lys Lys Ile Leu Asp
      180              185              190
Val Tyr Arg Gly Phe Glu
      195

```

<210> 272

<211> 156

<212> PRT

<213>

<400> 272

```

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

```

<210> 273

<211> 166

<212> PRT

<213>

<400> 273

```

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

```

				85					90					95			
Trp	Ser	Val	Phe	Asn	Arg	Arg	Gln	Ile	Pro	Ser	Gln	Val	Ser	Glu	Trp		
			100					105					110				
Gly	Arg	Met	Ser	Met	Cys	Asp	Ala	Glu	Lys	Arg	Leu	Leu	Ala	Asn	Ala		
		115					120					125					
Leu	Leu	Asp	Ile	Ser	Asn	Glu	Arg	Phe	Ile	Leu	Leu	Ser	Glu	Ser	Cys		
		130				135					140						
Ile	Pro	Leu	Tyr	Asn	Phe	Ser	Leu	Ile	Tyr	His	Tyr	Ile	Met	Lys	Ser		
145					150					155					160		
Gly	Tyr	Ser	Phe	Met	Gly												
				165													

<210> 274

<211> 328

<212> PRT

<213>

<400> 274

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

305 310 315 320
 Asp Asp Val Ser Gln Thr Thr Leu
 325

<210> 275
 <211> 160
 <212> PRT
 <213>

<400> 275

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

<210> 276
 <211> 112
 <212> PRT
 <213>

<400> 276

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

<210> 277
 <211> 133
 <212> PRT
 <213>

<400> 277

```

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

```

<210> 278

<211> 98

<212> PRT

<213>

<400> 278

```

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

```

<210> 279

<211> 157

<212> PRT

<213>

<400> 279

```

Arg His His Gln Thr Leu Thr Phe Ser Ser Ser Ala Leu Cys Leu Cys
 1          5          10          15
Leu Cys Leu Ser Ile Leu Arg Pro Ala Thr Thr Met Glu Ala Lys Pro
          20          25          30
Ser Glu Gln Pro Arg Glu Phe Ile Phe Arg Ser Lys Leu Pro Asp Ile
          35          40          45
Tyr Ile Pro Asp Asn Leu Ser Leu His Ala Tyr Cys Phe Glu Asn Ile
          50          55          60

```

Ser Glu Phe Ala Asp Arg Pro Cys Val Ile Asn Gly Ala Thr Gly Arg
65 70 75 80
Thr Tyr Thr Tyr Ala Glu Val Glu Leu Ile Ser Arg Arg Val Ser Ala
85 90 95
Gly Leu Asn Gly Leu Gly Val Gly Gln Gly Asp Val Ile Met Leu Leu
100 105 110
Leu Gln Asn Cys Pro Glu Phe Val Phe Ala Phe Leu Gly Ala Ser Tyr
115 120 125
Arg Gly Ala Ile Ser Thr Thr Ala Asn Pro Phe Tyr Thr Pro Gly Glu
130 135 140
Ile Ala Lys Gln Ala Ser Ala Ala Arg Ala Lys Ile Val
145 150 155

<210> 280

<211> 180

<212> PRT

<213>

<400> 280

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

<210> 281

<211> 180

<212> PRT

<213>

<400> 281

Gly Gln Leu Val Ala Gly Val Glu Ala Gln Val Ile Ser Val Asp Thr
1 5 10 15
Leu Lys Ser Leu Pro Pro Asn Gln Leu Gly Glu Ile Trp Val Arg Gly
20 25 30
Pro Asn Met Met Lys Gly Tyr Tyr Asn Asn Pro Gln Ala Thr Lys Leu
35 40 45

Thr Ile Asp Asn Lys Gly Trp Val His Thr Gly Asp Leu Gly Tyr Phe
 50 55 60
 Asp Glu Glu Gly Gln Leu Tyr Val Val Asp Arg Ile Lys Glu Leu Ile
 65 70 75 80
 Lys Tyr Lys Gly Phe Gln Ile Ala Pro Ala Glu Leu Glu Gly Leu Leu
 85 90 95
 Leu Ser His Pro Glu Ile Leu Asp Ala Val Val Ile Pro Phe Pro Asp
 100 105 110
 Ala Glu Ala Gly Glu Val Pro Ile Ala Tyr Val Val Arg Ser Pro Thr
 115 120 125
 Ser Ser Leu Thr Glu Glu Glu Val Gln Lys Phe Ile Ala Asn Gln Val
 130 135 140
 Ala Pro Phe Lys Arg Leu Arg Arg Val Thr Phe Val Asn Ser Val Pro
 145 150 155 160
 Lys Ser Ala Ser Gly Lys Ile Leu Arg Arg Glu Leu Ile Ala Lys Val
 165 170 175
 Arg Ala Lys Ile
 180

<210> 282

<211> 119

<212> PRT

<213>

<400> 282

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

<210> 283

<211> 152

<212> PRT

<213>

<400> 283

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

His Ser Tyr Cys Phe Glu Lys Leu Asp Glu Leu Arg Glu Lys Pro Cys
 65 70 75 80
 Leu Ile Gln Gly Ser Asn Gly Lys Ile Tyr Ser Tyr Gly Glu Val Glu
 85 90 95
 Leu Ile Ser Arg Lys Val Ala Ser Gly Leu Ala Lys Leu Gly Phe Lys
 100 105 110
 Lys Gly Asp Val Val Met Leu Leu Leu Pro Asn Cys Pro Glu Phe Val
 115 120 125
 Phe Val Phe Leu Gly Ala Ser Met Ala Gly Ala Ile Ala Thr Thr Ala
 130 135 140
 Asn Pro Phe Tyr Thr Pro Ser Asp
 145 150

<210> 284

<211> 330

<212> PRT

<213>

<400> 284

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

Leu Met Asn Ile Phe Leu Gly Gly Val Asp Thr Gly Ala Val Ser Trp
 305 310 315 320
 Thr Gly Gln Trp Leu Ser Ser Leu Gly Thr
 325 330

<210> 285
 <211> 115
 <212> PRT
 <213>

<400> 285
 Thr Glu Leu Glu Asp Glu Gly Phe Met Asp Met Val His Glu Gly Met
 1 5 10 15
 Ala Met Leu Gly Ser Phe Ser Ala Ser Asp Tyr Phe Pro Arg Leu Gly
 20 25 30
 Trp Ile Val Asp Arg Phe Thr Gly Leu His Ser Arg Leu Glu Lys Ser
 35 40 45
 Phe Arg Asn Leu Asp Asp Leu Tyr Gln Lys Val Ile Glu Glu His Arg
 50 55 60
 Asn Ala Asn Lys Ser Asn Glu Gly Lys Glu Asp Ile Val Asp Val Leu
 65 70 75 80
 Leu Lys Met Glu Lys Asp Gln Thr Glu Leu Ala Gly Val Arg Leu Lys
 85 90 95
 Glu Asp Asn Ile Lys Ala Ile Leu Met Val Tyr His Thr Ile Ser Thr
 100 105 110
 Tyr Tyr Leu
 115

<210> 286
 <211> 143
 <212> PRT
 <213>

<400> 286
 Leu Val Val Ala Ala Leu Leu Ile Val Leu Leu Arg Ser Lys Ser Arg
 1 5 10 15
 Lys Arg Lys Ser Asn Leu Pro Pro Ser Pro Pro Lys Leu Pro Ile Ile
 20 25 30
 Gly Asn Leu His Gln Leu Gly Lys Ser Pro His Ile Ser Leu His Arg
 35 40 45
 Leu Ala Arg Asn Tyr Gly Pro Ile Met Ser Leu Gln Leu Gly Glu Val
 50 55 60
 Pro Thr Ile Val Val Ser Ser Ala Ala Met Ala Lys Glu Val Met Lys
 65 70 75 80
 Thr His Asp Leu Val Leu Ala Asn Arg Pro Gln Ile Phe Ser Ala Lys
 85 90 95
 His Leu Phe Tyr Asp Cys Thr Asp Met Ala Phe Ser Pro Tyr Gly Ala
 100 105 110
 Tyr Trp Arg His Ile Arg Lys Ile Cys Ile Leu Glu Val Leu Ser Ala
 115 120 125
 Lys Arg Val Gln Ser Phe Ser His Val Arg Glu Glu Glu Val Ala
 130 135 140

<210> 287
 <211> 135
 <212> PRT

<213>

<400> 287

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

<210> 288

<211> 128

<212> PRT

<213>

<400> 288

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

<210> 289

<211> 179

<212> PRT

<213>

<400> 289

Ile	Arg	Met	Val	Asn	Glu	Leu	Gly	Ser	Glu	Lys	Pro	Phe	Leu	Val	Cys
1				5					10					15	
Leu	Glu	Phe	Tyr	Met	Lys	Leu	Ala	Ile	Ala	Leu	Val	Ala	Leu	Val	Val
		20						25					30		
Ala	Trp	Ser	Phe	Phe	Val	Lys	Gly	Arg	Asn	Arg	Lys	Leu	Pro	Pro	Gly

```

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

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<210> 290
<211> 440
<212> PRT
<213>

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<400> 290
Ser Ser Leu Ala Phe Gly Gln His Ile Ile Ala Thr Ser Tyr Ser Cys
  1              5              10              15
Asn Leu His Gln Ile Gly Glu Met Ser Phe Gln Asn Gln Leu Phe Ile
      20              25              30
Phe Cys Thr Leu Leu Leu Gly Phe Leu Lys Leu Ala Glu Gly Lys Thr
      35              40              45
Arg His Tyr Thr Phe His Ile Asp Ser His Asn Met Thr Arg Leu Cys
      50              55              60
His Thr Arg Ser Val Leu Ser Val Asn Lys Gln Tyr Pro Gly Pro Pro
65              70              75              80
Leu Val Ala Arg Glu Gly Asp Asn Ile Leu Val Lys Val Val Asn His
      85              90              95
Val Ala Ala Asn Val Thr Ile His Trp His Gly Val Arg Gln Leu Arg
      100              105              110
Thr Gly Trp Ala Asp Gly Pro Ala Tyr Val Thr Gln Cys Pro Ile Gln
      115              120              125
Thr Asn Gln Ser Tyr Thr Tyr Asn Phe Thr Leu Thr Gly Gln Arg Gly
      130              135              140
Thr Leu Leu Trp His Ala His Val Ser Trp Leu Arg Ser Ser Ile His
145              150              155              160
Gly Pro Ile Ile Ile Leu Pro Lys Arg Asn Glu Ser Tyr Pro Phe Glu
      165              170              175
Lys Pro Ser Lys Glu Val Pro Ile Ile Phe Gly Glu Trp Phe Asn Val
      180              185              190
Asp Pro Glu Ala Val Ile Ala Gln Ala Leu Gln Ser Gly Gly Gly Pro
      195              200              205
Asn Val Ser Asp Ala Tyr Thr Ile Asn Gly Leu Pro Gly Pro Leu Tyr
      210              215              220
Asn Cys Ser Ser Lys Asp Thr Phe Lys Leu Lys Val Lys Pro Gly Lys
225              230              235              240
Thr Tyr Leu Leu Arg Leu Ile Asn Ala Ala Leu Asn Asp Glu Leu Phe

```

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

<210> 291

<211> 326

<212> PRT

<213>

<400> 291

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


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      195              200              205
Ala Ala Leu Asn Glu Glu Leu Phe Phe Lys Ile Ala Gly His Gln Leu
  210              215              220
Thr Ile Val Glu Val Asp Ala Thr Tyr Val Lys Pro Phe Lys Thr Asp
225              230              235              240
Thr Ile Val Ile Ala Pro Gly Gln Thr Thr Asn Ala Leu Ile Ser Thr
      245              250              255
Asp Gln Ser Ser Gly Lys Tyr Met Val Ala Ala Ser Pro Phe Met Asp
      260              265              270
Ser Pro Ile Ala Val Asp Asn Met Thr Ala Thr Ala Thr Leu His Tyr
      275              280              285
Ser Gly Thr Leu Ala Ala Thr Ser Thr Thr Leu Thr Lys Thr Pro Pro
290              295              300
Gln Asn Ala Thr Ala Val Ala Asn Asn Phe Val Asn Ser Leu Arg Ser
305              310              315              320
Leu Asn Ser Lys Arg Tyr
      325

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<210> 292

<211> 101

<212> PRT

<213>

<400> 292

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

```

<210> 293

<211> 136

<212> PRT

<213>

<400> 293

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

```

				85					90					95			
Leu	Val	Phe	Gln	Asp	Thr	Gly	Ile	Ile	Ala	Pro	Glu	Asn	His	Pro	Ile		
			100					105					110				
His	Leu	His	Gly	Phe	Asn	Phe	Phe	Ala	Ile	Gly	Lys	Gly	Leu	Gly	Asn		
		115					120					125					
Tyr	Asn	Pro	Lys	Val	Asp	Gln	Lys										
	130					135											

<210> 294
 <211> 104
 <212> PRT
 <213>

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

<210> 295
 <211> 110
 <212> PRT
 <213>

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

<210> 296
 <211> 384
 <212> PRT
 <213>

<400> 296

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

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<210> 297

<211> 139

<212> PRT

<213>

<400> 297

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Ser Cys Leu Ser Leu His His His Leu Arg Gln Val Thr Ser Asp Phe
 1          5          10          15

```

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

<210> 298
 <211> 155
 <212> PRT
 <213>

<400> 298
 Pro Asp Arg Val Ile Ser Thr Ser Ser Ile Leu Tyr Gln Gly Glu Arg
 1 5 10 15
 Gly Thr Met Gly Thr Phe Leu Gly Phe Ala Val Thr Ala Thr Leu Leu
 20 25 30
 Phe Cys Val Ala Gln Gly Glu Val Leu Phe Tyr Asp Phe Val Val Asn
 35 40 45
 Glu Thr Pro Ile Glu Met Leu Cys Glu Thr Asn Arg Ser Val Leu Thr
 50 55 60
 Val Asn Gly Leu Phe Pro Gly Pro Glu Ile His Ala His Lys Gly Asp
 65 70 75 80
 Thr Ile Tyr Val Asn Val Thr Asn Leu Gly Pro Tyr Gly Val Thr Ile
 85 90 95
 His Trp His Gly Val Arg Gln Ile Arg Tyr Pro Trp Ser Asp Gly Pro
 100 105 110
 Glu Tyr Val Thr Gln Cys Pro Ile Pro Thr Asn Ser Ser Phe Leu Gln
 115 120 125
 Lys Ile Lys Leu Thr Glu Glu Glu Gly Thr Val Trp Trp His Ala His
 130 135 140
 Ser Asp Trp Ser Arg Ala Thr Ile His Gly Leu
 145 150 155

<210> 299
 <211> 179
 <212> PRT
 <213>

<400> 299
 Leu Leu Gln Val His Phe Ser Leu Val Glu Arg Glu Arg Glu Met Gly
 1 5 10 15
 Thr Phe Leu Gly Phe Val Val Thr Met Thr Leu Leu Phe Cys Met Ala
 20 25 30
 Gln Gly Glu Val Ile Tyr Tyr Asp Phe Val Val Lys Glu Thr Pro Ile
 35 40 45

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

<210> 300
 <211> 62
 <212> PRT
 <213>

<400> 300

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

<210> 301
 <211> 190
 <212> PRT
 <213>

<400> 301

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

Val	Arg	Asn	Ser	Ile	Lys	Gly	Glu	Glu	Gly	Asp	Glu	Met	Arg	Lys	Arg
130						135					140				
Ile	Gly	Lys	Leu	Lys	Glu	Thr	Ala	Lys	Arg	Ala	Val	Ser	Glu	Gly	Gly
145					150					155					160
Ser	Ser	Lys	Asn	Asn	Leu	Asp	Lys	Leu	Leu	His	His	Ile	Phe	Leu	Lys
			165						170					175	
Gly	Met	His	Gln	Met	Ile	Val	Gln	Asn	Val	Glu	Ala	Asn	Asn		
			180					185					190		

<210> 302

<211> 365

<212> PRT

<213>

<400> 302

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

Lys Asp Glu Ile Asp Gln Val Val Gly Leu Asn Arg Lys Leu Glu Glu
 340 345 350
 Asn Asp Thr Glu Lys Met Pro Phe Leu Gln Ala Val Val
 355 360 365

<210> 303
 <211> 183
 <212> PRT
 <213>

<400> 303

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

<210> 304
 <211> 148
 <212> PRT
 <213>

<400> 304

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

Ala Cys Pro Gly Ala Pro Leu Ala His Arg Val Met Gly Trp Thr Leu
 115 120 125
 Gly Leu Leu Ile Gln Cys Phe Asp Trp Lys Arg Val Ser Glu Glu Glu
 130 135 140
 Ile Asp Met Thr
 145

<210> 305
 <211> 164
 <212> PRT
 <213>

<400> 305

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

<210> 306
 <211> 163
 <212> PRT
 <213>

<400> 306

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

Gln Gln Glu Leu Asp Thr His Val Gly Arg Ser Arg Pro Val Glu Glu
 115 120 125
 Ser Asp Val Lys Asn Leu Thr Tyr Leu Gln Ala Ile Val Lys Glu Ala
 130 135 140
 Leu Arg Leu Tyr Pro Pro Val Pro Val Asn Gly Leu Arg Ser Ser Met
 145 150 155 160
 Glu Glu Cys

<210> 307

<211> 129

<212> PRT

<213>

<400> 307

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

<210> 308

<211> 166

<212> PRT

<213>

<400> 308

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

Gly Glu Asn Gln Glu Val Asp Met Asn Glu Met Phe Asn Gly Val Thr
 130 135 140
 Leu Arg Lys Ala Arg Glu Leu Ser Ala Ile Pro Thr Pro Arg Leu Glu
 145 150 155 160
 Cys Ile Ala His Leu Lys
 165

<210> 309
 <211> 123
 <212> PRT
 <213>

<400> 309
 Ser Cys Trp Arg Cys Val Ala Glu Pro Asn His Ala Trp Ser Asn Leu
 1 5 10 15
 Ser Arg Lys Arg Lys Gly Arg Leu Pro Pro Gly Pro Phe Ser Leu Pro
 20 25 30
 Ile Ile Gly Asn Leu His Met Leu Gly Lys Ile Pro His Arg Ser Leu
 35 40 45
 Ala Glu Leu Ser Met Lys Tyr Gly Pro Leu Leu Ser Leu Arg Leu Gly
 50 55 60
 Ser Thr Pro Ala Leu Val Val Ser Ser Pro Glu Ile Ala Ser Glu Phe
 65 70 75 80
 Leu Lys Thr His Asp Gln Leu Phe Ala Ser Arg Ile Pro Ser Ala Ala
 85 90 95
 Ile Lys Val Leu Thr Tyr Asn Leu Ser Gly Leu Ile Phe Ser Pro Tyr
 100 105 110
 Gly Pro Cys Trp Arg Gln Val Arg Lys Leu Cys
 115 120

<210> 310
 <211> 114
 <212> PRT
 <213>

<400> 310
 Tyr Ser Glu Pro Ser Lys Lys Leu Ala Met Glu Phe Val Glu Phe Cys
 1 5 10 15
 Ile Thr Leu Val Thr Ala Leu Leu Phe Val Val Leu Val Ala Ala Trp
 20 25 30
 Ser Asn Leu Phe Arg Lys Arg Lys Gly Arg Leu Pro Pro Gly Pro Phe
 35 40 45
 Ser Leu Pro Ile Ile Gly Asn Leu His Met Leu Gly Lys Ile Pro His
 50 55 60
 Arg Ser Leu Ala Glu Leu Ser Met Lys Tyr Gly Pro Leu Leu Ser Leu
 65 70 75 80
 Arg Leu Gly Ser Thr Pro Ala Leu Val Val Ser Ser Pro Glu Ile Ala
 85 90 95
 Ser Glu Phe Leu Lys Thr His Asp Gln Leu Phe Ala Ser Arg Ile Pro
 100 105 110
 Ser Ala

<210> 311
 <211> 154
 <212> PRT

<213>

<400> 311

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

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<210> 312

<211> 116

<212> PRT

<213>

<400> 312

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

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<210> 313

<211> 180

<212> PRT

<213>

<400> 313

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Ala Pro Asp Glu Leu Glu Arg Val Val Gly Leu Gly Arg Met Val Arg
 1          5          10          15
Glu Ser Asp Leu Pro Arg Leu Val Tyr Leu Gln Ala Val Val Lys Glu

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

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<210> 314
<211> 127
<212> PRT
<213>

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      <400> 314
Gly Ile Leu Phe Asp Met Leu Leu Gly Gly Ser Asp Thr Ala Pro Thr
1      5      10      15
Ile Ile Glu Trp Ala Ile Ser Glu Ala Leu Ile Asn Pro Pro Val Met
      20      25      30
Lys Lys Leu Gln Asp Glu Leu Glu Arg Val Val Gly Leu Asp Arg Met
      35      40      45
Ala Cys Glu Ser Asp Leu Pro Gln Leu Val Tyr Leu Gln Ala Met Val
      50      55      60
Lys Glu Thr Leu Arg Leu His Pro Ala Gly Pro Leu Leu Asn Arg Arg
65      70      75      80
Leu Ser Ala Glu Ser Cys Asn Val Leu Gly Tyr Glu Phe Pro Lys Asn
      85      90      95
Thr Arg Val Leu Val Asn Ala Trp Ala Ile Gly Arg Asn Pro Lys Leu
      100      105      110
Trp Glu Asp Ala Glu Thr Phe Lys Pro Glu Arg Phe Thr Gly Arg
      115      120      125

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<210> 315
<211> 127
<212> PRT
<213>

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      <400> 315
Thr Ser Ala Thr Val Glu Trp Ala Met Ala Glu Leu Ile Arg Lys Pro
1      5      10      15
Thr Leu Leu Lys Lys Ala Gln Ala Glu Leu Asp Glu Val Val Gly Arg
      20      25      30
Glu Lys Arg Met Glu Glu Ser Asp Ile Ala Lys Leu Pro Tyr Leu Gln

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

<210>	316
<211>	134
<212>	PRT
<213>	

<400> 316															
Glu 1	Asp	Glu	Val	Ser 5	Ala	Met	Ile	Arg	Ser 10	Ile	Val	Asn	Ser	Asp 15	Ala
His	Lys	Asp	Ser	Arg	Pro	Val	Asn 20	Ile 25	Lys	Gln	Leu	Ala	Ser 30	Ser	Leu
Val	Thr	Ala 35	Ile	Val	Leu	Arg	Met 40	Thr	Phe	Gly	Lys	Lys 45	Tyr	Ser	Asp
Arg	Asp 50	Ser	Gly	Ala	Phe	Ser 55	Ser	Met	Ile	Lys	Glu 60	Ser	Leu	Leu	Leu
Leu 65	Gly	Ser	Phe	Asn 70	Ile	Gly	Glu	Tyr	Ile	Pro	Tyr 75	Leu	Asn	Trp	Met 80
Asp	Leu	Gln	Gly	Leu 85	Asn	Arg	Arg	Leu	Lys 90	Lys	Leu	Arg	Thr	Thr 95	Gln
Asp	Gln	Leu	Leu 100	Glu	Lys	Val	Ile	Glu 105	Glu	His	Ala	Ala	Gln 110	Asn	Arg
Ser	Asn	Met 115	Thr	His	Asp	Leu	Val 120	Asp	Ala	Leu	Leu	Ala 125	Ala	Ser	Ala
Asp	Lys 130	Asp	Arg	Glu	Leu										

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<210> 317
<211> 115
<212> PRT
<213>
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	<400> 317															
Ile	Tyr	Asp	Gln	Glu	Ser	Leu	Leu	Asn	Ala	Ile	Lys	Gln	Val	Asp	Val	
1				5					10					15		
Val	Ile	Ser	Ala	Val	Gly	Gln	Ala	Gln	Thr	Glu	Asp	Gln	Asp	Arg	Ile	
			20					25					30			
Val	Ala	Ala	Ile	Lys	Ala	Ala	Gly	Asn	Ile	Lys	Arg	Phe	Leu	Pro	Ser	
		35					40					45				
Glu	Phe	Gly	Asn	Asp	Val	Asp	Arg	Val	His	Ala	Val	Glu	Pro	Val	Lys	
	50					55					60					
Thr	Gly	Phe	Ala	Leu	Lys	Ala	Lys	Ile	Arg	Arg	Leu	Val	Glu	Ala	Glu	
65					70					75					80	
Gly	Ile	Pro	Tyr	Thr	Tyr	Val	Ser	Ser	Asn	Ser	Phe	Ala	Gly	Tyr	Tyr	
				85					90					95		
Leu	Gln	Thr	Leu	Ser	Gln	Pro	Gly	Ala	Thr	Ala	Pro	Pro	Arg	Asp	Asn	

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100 105 110

Val Val Ile
115

<210> 318
<211> 161
<212> PRT
<213>

<400> 318

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

<210> 319
<211> 141
<212> PRT
<213>

<400> 319

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

130

135

140

<210> 320

<211> 102

<212> PRT

<213>

<400> 320

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

<210> 321

<211> 125

<212> PRT

<213>

<400> 321

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

<210> 322

<211> 98

<212> PRT

<213>

<400> 322

Ser	Ser	Ser	Pro	Glu	Asn	Thr	Thr	Pro	Ala	Val	Lys	Arg	Pro	Ser	Lys
1				5					10					15	
Met	Ala	Glu	Met	Ser	Arg	Val	Leu	Val	Ile	Gly	Gly	Ala	Gly	Tyr	Ile
		20						25					30		

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Gly	Lys	Phe	Ile	Val	Lys	Ala	Cys	Ala	Lys	Ser	Gly	His	Pro	Thr	Phe
		35					40					45			
Val	Leu	Glu	Thr	Glu	Ser	Thr	Leu	Ser	Asn	Pro	Ala	Asn	Ala	Glu	Ile
	50					55				60					
Ile	Lys	Gly	Phe	Lys	Ser	Leu	Gly	Val	Asn	Leu	Val	His	Gly	Asp	Ile
65					70				75						80
Tyr	Asp	Gln	Lys	Ser	Leu	Leu	Ser	Ala	Ile	Lys	Gln	Val	Asp	Val	Val
				85					90					95	
Ile	Ser														

<210> 323
 <211> 319
 <212> PRT
 <213>

<400> 323

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

<210> 324
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 <212> PRT
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<400> 324

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

<210> 325
 <211> 164
 <212> PRT
 <213>

<400> 325

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

<210> 326
 <211> 114
 <212> PRT

<213>

<400> 326

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

```

<210> 327

<211> 226

<212> PRT

<213>

<400> 327

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

```

<210> 328
 <211> 424
 <212> PRT
 <213>

<400> 328

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

Gly Thr Pro Ile Gly Val Ser Met Asp Asn Thr Arg Leu Ala Val Ala
 405 410 415
 Ser Ile Gly Lys Leu Met Phe Ala
 420

<210> 329
 <211> 97
 <212> PRT
 <213>

<400> 329
 Asn Ser Gly Ile Thr Pro Cys Leu Pro Leu Arg Gly Ser Ile Ser Ala
 1 5 10 15
 Ser Gly Asp Leu Val Pro Phe Ser Tyr Ile Ala Gly Leu Leu Thr Gly
 20 25 30
 Arg Pro Asn Ser Lys Ala Val Gly Pro Ala Gly Glu Thr Leu Thr Ala
 35 40 45
 Lys Gln Ala Phe Glu Leu Ala Gly Ile Ser Gly Gly Phe Phe Glu Leu
 50 55 60
 Gln Pro Lys Glu Gly Leu Ala Leu Val Asn Gly Thr Gly Val Gly Ser
 65 70 75 80
 Ala Leu Ala Ala Ile Val Leu Phe Glu Ala Asn Met Leu Thr Val Leu
 85 90 95
 Ser

<210> 330
 <211> 412
 <212> PRT
 <213>

<400> 330
 Val Tyr Arg Ser Ile Asn Ser Gln Ala Glu Ala Pro Ser Trp Pro Asn
 1 5 10 15
 Gly Ser Cys Ser Asp His Gly Val Cys Leu Gly Arg Glu Ser Tyr Met
 20 25 30
 Lys His Ala Ala Lys Leu His Glu Met Asn Pro Leu Gln Lys Pro Lys
 35 40 45
 Gln Asp Arg Tyr Ala Leu Arg Thr Ser Pro Gln Trp Leu Gly Pro Gln
 50 55 60
 Val Glu Ile Ile Arg Ser Ala Thr His Met Ile Glu Arg Glu Ile Asn
 65 70 75 80
 Ser Val Asn Asp Asn Pro Val Ile Asp Val Ala Arg Asp Lys Ala Leu
 85 90 95
 His Gly Gly Asn Phe Gln Gly Thr Pro Ile Gly Val Ser Met Asp Asn
 100 105 110
 Leu Arg Leu Ser Ile Ser Ala Ile Gly Lys Leu Met Phe Ala Gln Phe
 115 120 125
 Ser Glu Leu Val Asn Asp Tyr Tyr Asn Gly Gly Leu Pro Ser Asn Leu
 130 135 140
 Ser Gly Gly Pro Asn Pro Ser Leu Asp Tyr Gly Leu Lys Gly Ala Glu
 145 150 155 160
 Ile Ala Met Ala Ser Tyr Thr Ser Glu Leu Leu Tyr Leu Ala Asn Pro
 165 170 175
 Val Thr Ser His Val Gln Ser Ala Glu Gln His Asn Gln Asp Val Asn
 180 185 190

```

Ser Leu Gly Leu Val Ser Ala Arg Lys Ser Ala Glu Ala Ile Asp Ile
    195                200                205
Leu Lys Leu Met Leu Ser Thr Tyr Leu Thr Ala Leu Cys Gln Ala Val
    210                215                220
Asp Leu Arg His Leu Glu Glu Asn Met Leu Ala Thr Val Lys Gln Ile
225                230                235                240
Val Ser Gln Val Ala Lys Lys Thr Leu Ser Thr Gly Leu Asn Gly Glu
                245                250                255
Leu Leu Pro Gly Arg Phe Cys Glu Lys Asp Leu Leu Gln Val Val Asp
    260                265                270
Asn Glu His Val Phe Ser Tyr Ile Asp Asp Pro Cys Asn Ala Ser Tyr
    275                280                285
Pro Leu Thr Gln Lys Leu Arg Asn Ile Leu Val Glu His Ala Phe Lys
    290                295                300
Asn Ala Glu Gly Glu Lys Asp Pro Asn Thr Ser Ile Phe Asn Lys Ile
305                310                315                320
Pro Val Phe Glu Ala Glu Leu Lys Ala Gln Leu Glu Pro Gln Val Ser
                325                330                335
Leu Ala Arg Glu Ser Tyr Asp Lys Gly Thr Ser Pro Leu Pro Asn Arg
    340                345                350
Ile Gln Glu Cys Arg Ser Tyr Pro Leu Tyr Glu Phe Val Arg Asn Gln
    355                360                365
Leu Gly Thr Leu Gln Ala Trp Leu Phe His Ile Asn Ile Val Met Arg
    370                375                380
Cys Leu Ile Ile Tyr Cys Ser Leu Phe Phe Pro Glu Leu Ala Thr Ala
385                390                395                400
Phe Asp Ser Val His Tyr Ala Arg Thr Lys Pro Leu
                405                410

```

<210> 331
 <211> 132
 <212> PRT
 <213>

<400> 331

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

```

<210> 332
 <211> 170
 <212> PRT

<213>

<400> 332

```

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

```

<210> 333

<211> 118

<212> PRT

<213>

<400> 333

```

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

```

<210> 334

<211> 65

<212> PRT

<213>

<400> 334

```

Asn Ala Asp Pro Ile Ala Val Ile Asp Glu Ala Leu Ser Thr Gly Gly

```

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

<210> 335
 <211> 104
 <212> PRT
 <213>

<400> 335
 Lys Pro His Gly Glu Thr Pro Leu Ile Ile Gly Glu Trp Trp Asn Ala
 1 5 10 15
 Asp Pro Ile Ala Val Ile Asp Glu Ala Leu Arg Thr Gly Gly Ala Pro
 20 25 30
 Asn Leu Ser Asp Ala Tyr Thr Leu Asn Gly Gln Pro Gly Asp Leu Tyr
 35 40 45
 Asn Cys Ser Arg Ala Gly Thr Phe Arg Phe Pro Val Lys Gln Gly Glu
 50 55 60
 Thr Tyr Leu Leu Arg Met Val Asn Ala Ala Leu Asn Ser Ala His Phe
 65 70 75 80
 Phe Lys Ile Ala Gly His Lys Phe Thr Val Val Ala Val Asp Ala Ser
 85 90 95
 Tyr Thr Lys Pro Tyr Lys Gln Met
 100

<210> 336
 <211> 125
 <212> PRT
 <213>

<400> 336
 Asp Ala His Thr Ile Asn Gly Lys Pro Gly Pro Leu Phe Lys Cys Pro
 1 5 10 15
 Thr Lys Asp Thr Phe Val Val Pro Val Glu His Gly Lys Thr Tyr Leu
 20 25 30
 Leu Arg Ile Ile Asn Ala Ala Leu Asn Asp Glu Leu Phe Phe Asp Val
 35 40 45
 Ala Asn His His Leu Lys Val Val Glu Ile Asp Ala Val Tyr Thr Lys
 50 55 60
 Pro Leu Ile Thr Asn Ser Ile Val Ile Ala Pro Gly Gln Thr Thr Asn
 65 70 75 80
 Ala Leu Ile His Thr Asn Lys Arg Ser Gly Arg Tyr Phe Met Ala Ala
 85 90 95
 Arg Ser Phe Met Asp Ala Pro Val Ser Val Asp Asn Lys Thr Ala Thr
 100 105 110
 Ala Ile Leu Gln Tyr Val Asn Ser Ile Gln Ile Leu Leu
 115 120 125

<210> 337
 <211> 178

<212> PRT

<213>

<400> 337

```

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

```

<210> 338

<211> 358

<212> PRT

<213>

<400> 338

```

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

```


				165					170					175			
Arg	Tyr	Tyr	Met	Ala	Ala	Arg	Ala	Tyr	Gln	Asn	Gln	Ala	Ala	Gly	Asp		
			180					185						190			
Phe	Thr	Asn	Thr	Thr	Thr	Thr	Ala	Ile	Leu	Glu	Tyr	Ile	Gly	Ser	Glu		
		195					200					205					
Asn	Ser	Thr	Arg	Pro	Ile	Leu	Pro	Ser	Leu	Pro	Ala	Tyr	Asn	Asp	Thr		
	210					215					220						
Ala	Thr	Val	Thr	Arg	Phe	Ser	Arg	Ala	Leu	Arg	Ser	Leu	Ala	Ser	Gln		
225					230					235					240		
Glu	His	Pro	Val	Asn	Val	Pro	His	Thr	Ile	Asp	Glu	Ser	Leu	Ile	Ser		
				245					250					255			
Thr	Val	Gly	Leu	Gly	Leu	Leu	Pro	Cys	Gly	Ala	Gly	Asn	Thr	Cys	Glu		
		260						265					270				
Gly	Pro	Asn	Gly	Thr	Arg	Leu	Ser	Ala	Ser	Ile	Asn	Asn	Ile	Ser	Tyr		
	275						280					285					
Val	Glu	Pro	Thr	Ile	Ser	Leu	Leu	Gln	Ala	Tyr	Tyr	Tyr	Thr	Ala	Asn		
	290					295					300						
Gly	Ile	Phe	Thr	Gly	Asp	Phe	Pro	Ser	Lys	Pro	Glu	Val	Arg	Phe	Asn		
305					310					315					320		
Tyr	Thr	Gly	Asp	Asp	Ile	Pro	Arg	Lys	Phe	Trp	Ala	Pro	Asp	Pro	Ala		
				325					330					335			
Thr	Lys	Val	Lys	Val	Leu	Glu	Tyr	Asn	Ser	Thr	Val	Gln	Leu	Val	Phe		
			340					345					350				
Gln	Ser	Thr	Asn	Ile	Phe												
			355														

<210> 339

<211> 160

<212> PRT

<213>

<400> 339

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

<210> 340

<211> 156

<212> PRT

<213>

<400> 340

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

<210> 341

<211> 157

<212> PRT

<213>

<400> 341

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

<210> 342

<211> 134

<212> PRT

<213>

<400> 342

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

<210> 343

<211> 419

<212> PRT

<213>

<400> 343

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

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

<210> 344
 <211> 111
 <212> PRT
 <213>

				<400> 344													
Leu	Asn	Tyr	Asn	Ala	Thr	Val	Gln	Val	Ile	Leu	Gln	Gly	Thr	Asn	Ile		
1				5					10					15			
Phe	Ala	Gly	Glu	Ser	His	Pro	Ile	His	Leu	His	Gly	Tyr	Asp	Phe	Tyr		
			20					25					30				
Ile	Val	Gly	Ala	Gly	Phe	Gly	Asn	Tyr	Asn	Ala	Gln	Thr	Asp	Pro	Gln		
		35				40						45					
Lys	Phe	Asn	Leu	Val	Asp	Pro	Pro	Met	Arg	Asn	Thr	Val	Asn	Val	Pro		
		50				55					60						
Val	Asn	Gly	Trp	Ala	Ala	Ile	Arg	Phe	Val	Ala	Asp	Asn	Pro	Gly	Ala		
65					70					75					80		
Trp	Val	Met	His	Cys	His	Leu	Asp	Val	His	Ile	Thr	Trp	Gly	Leu	Ala		
			85						90					95			
Met	Val	Phe	Val	Val	Asn	Asn	Gly	Pro	Asp	Pro	Leu	Leu	Ser	Leu			
			100					105					110				

<210> 345
 <211> 93
 <212> PRT
 <213>

				<400> 345													
Thr	Arg	Val	Lys	Val	Leu	Asn	Tyr	Asn	Thr	Thr	Val	Gln	Val	Ile	Leu		
1				5					10					15			
Gln	Gly	Thr	Asn	Ile	Phe	Ala	Gly	Glu	Ser	His	Pro	Ile	His	Leu	His		
			20					25					30				
Gly	Tyr	Asp	Phe	Tyr	Ile	Val	Gly	Ala	Gly	Phe	Gly	Asn	Tyr	Asn	Pro		

```

      35              40              45
Gln Thr Asp Pro Gln Lys Phe Asn Leu Ala Asp Pro Pro Met Arg Asn
  50              55              60
Thr Val Asn Val Pro Val Asn Gly Trp Ala Ala Ile Arg Phe Val Ala
65              70              75              80
Asp Asn Pro Gly Ala Trp Val Met His Cys His Leu Asp
      85              90

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<210> 346
 <211> 93
 <212> PRT
 <213>

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      <400> 346
Lys Thr Phe Ser Asp Glu Cys Ser Asp Ala Arg Pro Arg Pro Asp Asn
  1              5              10              15
Arg His Ser Gly Arg Val Asp Gln Leu Ala Asp Thr Phe Ser Val Ser
      20              25              30
Met Lys Gly Gly Glu Thr Asn Leu Leu Arg Val Ile Asn Ala Ala Leu
      35              40              45
Asn Thr Asp Leu Phe Phe Ser Ile Ala Ser His Thr Met Thr Val Val
  50              55              60
Ala Val Asp Ala Leu Tyr Thr Lys Pro Phe Gln Thr Asn Val Leu Met
65              70              75              80
Leu Gly Pro Gly Gln Thr Thr Asp Ile Ala Ala Ala Asn
      85              90

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<210> 347
 <211> 114
 <212> PRT
 <213>

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      <400> 347
Pro Asp Ser Thr Ile Asn Thr Ser Phe Leu Gln Gln Leu Gln Gly Gln
  1              5              10              15
Cys Pro Arg Ala Gly Gly Asp Glu Leu Pro Ser Ser Leu Asp Tyr Val
      20              25              30
Thr Pro Ala Arg Phe Asp Asn Thr Tyr Phe Ala Asn Leu Lys Gln Gln
      35              40              45
Lys Gly Val Leu His Ser Asp Arg Thr Leu Tyr Asp Pro Ala Ala Ser
  50              55              60
Gly Ser Val Thr Ser Ser Thr Val Asp His Phe Ser Ser Asp Gln Thr
65              70              75              80
Ala Phe Phe Glu Ser Phe Lys Gly Ala Met Ile Lys Met Gly Asn Leu
      85              90              95
Ser Pro Ser Ala Gly Thr Gln Gly Glu Ile Arg Arg Asp Cys Arg Lys
      100              105              110
Val Asn

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<210> 348
 <211> 551
 <212> PRT
 <213>

<400> 348

Met	Glu	Gly	Gln	Ile	Ala	Ala	Leu	Ser	Lys	Glu	Asp	Glu	Phe	Ile	Phe	1	5	10	15
His	Ser	Pro	Phe	Pro	Ala	Val	Pro	Val	Pro	Glu	Asn	Ile	Ser	Leu	Phe	20	25	30	
Gln	Phe	Val	Leu	Glu	Gly	Ala	Glu	Lys	Tyr	Arg	Asp	Lys	Val	Ala	Leu	35	40	45	
Val	Glu	Ala	Ser	Thr	Gly	Lys	Glu	Tyr	Asn	Tyr	Gly	Gln	Val	Ile	Ser	50	55	60	
Leu	Thr	Arg	Asn	Val	Ala	Ala	Gly	Leu	Val	Asp	Lys	Gly	Ile	Gln	Lys	65	70	75	80
Gly	Asp	Val	Val	Phe	Val	Leu	Leu	Pro	Asn	Met	Ala	Glu	Tyr	Pro	Ile	85	90	95	
Ile	Val	Leu	Gly	Ile	Met	Leu	Ala	Gly	Ala	Val	Phe	Ser	Gly	Ala	Asn	100	105	110	
Pro	Ser	Ala	His	Ile	Asn	Glu	Val	Glu	Lys	His	Ile	Gln	Asp	Ser	Gly	115	120	125	
Ala	Lys	Ile	Val	Val	Thr	Val	Gly	Ser	Ala	Tyr	Glu	Lys	Val	Arg	Gln	130	135	140	
Val	Lys	Leu	Pro	Val	Ile	Ile	Ala	Asp	Asn	Glu	His	Val	Met	Asn	Thr	145	150	155	160
Ile	Pro	Leu	Gln	Glu	Ile	Phe	Glu	Arg	Asn	Tyr	Glu	Ala	Ala	Gly	Pro	165	170	175	
Phe	Val	Gln	Ile	Cys	Gln	Asp	Asp	Leu	Cys	Ala	Leu	Pro	Tyr	Ser	Ser	180	185	190	
Gly	Thr	Thr	Gly	Ala	Ser	Lys	Gly	Val	Met	Leu	Thr	His	Arg	Asn	Leu	195	200	205	
Ile	Ala	Asn	Leu	Cys	Ser	Ser	Leu	Phe	Asp	Val	His	Glu	Ser	Leu	Val	210	215	220	
Gly	Asn	Phe	Thr	Thr	Leu	Gly	Leu	Met	Pro	Phe	Phe	His	Ile	Tyr	Gly	225	230	235	240
Ile	Thr	Gly	Ile	Cys	Cys	Ala	Thr	Leu	Arg	Asn	Gly	Gly	Lys	Val	Val	245	250	255	
Val	Met	Ser	Arg	Phe	Asp	Leu	Arg	His	Phe	Ile	Ser	Ser	Leu	Ile	Thr	260	265	270	
Tyr	Glu	Val	Asn	Phe	Ala	Pro	Ile	Val	Pro	Pro	Ile	Met	Leu	Ser	Leu	275	280	285	
Val	Lys	Asn	Pro	Ile	Val	Asn	Glu	Phe	Asp	Leu	Ser	Arg	Leu	Lys	Leu	290	295	300	
Lys	Ala	Val	Met	Thr	Ala	Ala	Ala	Pro	Leu	Ala	Pro	Asp	Leu	Leu	Arg	305	310	315	320
Ala	Phe	Glu	Glu	Lys	Phe	Pro	Gly	Val	Glu	Val	Gln	Glu	Ala	Tyr	Gly	325	330	335	
Leu	Thr	Glu	His	Ser	Cys	Ile	Thr	Leu	Thr	His	Cys	Ala	Pro	Gly	Asn	340	345	350	
Ile	Arg	Gly	Arg	Ala	Lys	Lys	Ser	Ser	Val	Gly	Phe	Ile	Ile	Pro	Asn	355	360	365	
Leu	Glu	Val	Lys	Phe	Ile	Asp	Pro	Glu	Thr	Gly	Lys	Ser	Leu	Pro	Arg	370	375	380	
Asn	Ser	Ile	Gly	Glu	Val	Cys	Val	Arg	Ser	Gln	Cys	Val	Met	Arg	Gly	385	390	395	400
Tyr	Tyr	Lys	Lys	Pro	Thr	Glu	Thr	Glu	Lys	Thr	Val	Asp	Ser	Asp	Gly	405	410	415	
Trp	Leu	His	Thr	Gly	Asp	Val	Gly	Phe	Ile	Asp	Asp	Asp	Asp	Asp	Val	420	425	430	
Phe	Ile	Val	Asp	Arg	Ile	Lys	Glu	Leu	Ile	Lys	Tyr	Lys	Gly	Phe	Gln	435	440	445	
Val	Ala	Pro	Ala	Glu	Leu	Glu	Ala	Ile	Leu	Leu	Ser	His	Pro	Ser	Val				

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      450              455              460
Glu Asp Ala Ala Val Val Pro Leu Pro Asp Glu Glu Ala Gly Glu Ile
465              470              475              480
Pro Ala Ala Cys Val Val Met Ala Ala Ser Ala Thr Glu Thr Glu Asp
              485              490              495
Asp Ile Ser Lys Phe Val Ala Ser Gln Val Ala Thr Tyr Lys Arg Val
              500              505              510
Arg Leu Val Lys Phe Val Ser Thr Ile Pro Lys Ser Ser Ser Gly Lys
              515              520              525
Ile Leu Arg Arg Leu Leu Arg Asp Asn Leu Arg Glu Thr Leu Lys Asn
              530              535              540
Gln His Gln Pro Leu Ser Thr
545              550

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<210> 349

<211> 544

<212> PRT

<213>

<400> 349

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

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290	295	300
Arg Thr Ile Met Ser Gly Ala Ala Pro Met Gly Lys Glu Leu Glu Asp		
305	310	315
Thr Val Arg Ala Lys Leu Pro Asn Ala Lys Leu Gly Gln Gly Tyr Gly		
	325	330
Met Thr Glu Ala Gly Pro Val Leu Ala Met Cys Pro Ala Phe Ala Lys		
	340	345
Glu Pro Phe Glu Ile Lys Ser Gly Ala Cys Gly Thr Val Val Arg Asn		
	355	360
Ala Glu Met Lys Ile Val Asp Pro Glu Thr Gly Ala Ser Leu Pro Arg		
	370	375
Asn Gln Ala Gly Glu Ile Cys Ile Arg Gly His Gln Ile Met Lys Gly		
385	390	395
Tyr Leu Asn Asp Ala Glu Ala Thr Ala Asn Thr Ile Asp Lys Glu Gly		
	405	410
Trp Leu His Thr Gly Asp Ile Gly Tyr Ile Asp Asp Asp Asp Glu Leu		
	420	425
Phe Ile Val Asp Arg Leu Lys Glu Leu Ile Lys Tyr Lys Gly Phe Gln		
	435	440
Val Ala Pro Ala Glu Leu Glu Ala Met Leu Ile Ala His Pro Ser Ile		
	450	455
Ser Asp Ala Ala Val Val Pro Met Lys Asp Glu Val Ala Gly Glu Val		
465	470	475
Pro Val Ala Phe Val Val Lys Ser Asn Gly Ser Val Ile Thr Glu Asp		
	485	490
Glu Ile Lys Gln Tyr Ile Ser Lys Gln Val Val Phe Tyr Lys Arg Ile		
	500	505
Lys Arg Val Phe Phe Thr Asp Ala Ile Pro Lys Ala Pro Ser Gly Lys		
	515	520
Ile Leu Arg Lys Asp Leu Arg Ala Lys Leu Ala Ser Gly Val Tyr Asn		
530	535	540

<210> 350

<211> 717

<212> DNA

<213>

<400> 350

cctgttttgg caacaactcc agcagctctc tgctcttttt actataaaaa aacccatctt	60
cacttcttct gtacttgcac acgaacatta agcgcttgat cagaacttgt atcagctccc	120
caccaccacc aaacagaaga gaaacagaag aaaaggaaaa gttcgaacaa cttcgaacga	180
tgcgagccct tgctgtttgtg ctcggttctg ctatcttgct ggcgtatgtc gcgagcagtg	240
cgggtgcgct gagcttggat tactatgacc agacgtgccc gaagctcgag ttttcggtga	300
ggggggctgt gaagaaagcg atgaagaacg acaacaccgt tcctgctgct ttacttcgca	360
tgcacttcca cgactgcttc atcagaggat gtgacggttc cgtgctcttg aactcgacgg	420
caaagaacac agccgaaaaa gacgggcccgc cgaacatctc actccacgca ttctatgtga	480
tcgaccttgc gaaggaagcg gtggaagctc agtgccctgg ggtcgtctct tgcgccgaca	540
tcttggccct ggccgctcgg gatgctgtcg ctctgtctgg aggaccgcat tgggatgtgc	600
cgaaaggaag aaaagatggg aggattcgaa agcgaatgac acaaggcaat taccagctcc	660
gaccttcaac atctctcaac tacagcaagc ttctctcaag aggcctttcc atggaga	717

<210> 351
 <211> 369
 <212> DNA
 <213>

<400> 351

ggcgtctctc	ctctgtctag	tcatgtttct	gaaatacctc	tccgcgcac	tcatctctct	60
tgcaacgatt	cgctctgctt	acggtgcctc	cactccgaag	cgaagagcaa	catgcgcggg	120
cgggcagacc	gtgaaaaacg	aggcctgttg	cgcttggttc	cccgtcctgg	aagacattct	180
gcccaacatg	ttcgacaacg	aatgtggcga	cgacgcccat	ggcgtctctg	gtctgagctt	240
ccacgacgcg	atcggtttct	ctccttctca	aggtggagga	ggcgcggacg	gatccatttt	300
gtcttcagt	acaccgaact	gcagttcccc	gcgaacgctg	gcctcgacga	cccgatcgac	360
actgagctt						369

<210> 352
 <211> 1391
 <212> DNA
 <213>

<400> 352

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ctgcccggaa	aaagccggaa	aaggaaactgt	tattttcaag	cttttatctc	accacaatca	120
cggagttata	tattatacca	agatttccgc	gttaacctta	cgcgcggaga	acttcatctg	180
agtgtgtgct	cttgctgggt	ttcaacagga	acatatcgat	aatttatgtc	atggctacac	240
acgatatggt	cggtttttcc	gtcgtcgttg	tcctccttgc	cacttcgggt	atcaccactg	300
cccgttgtaa	gctctcaccg	agtcattatc	aatcaacatg	tccgaaagca	ttgtcgattg	360
ttcgagctgg	agtagcaaaa	gcaatcaaga	atgagaccgc	gacgggcgcg	tccttgcttc	420
ggctgcactt	ccatgactgc	ttcgtcaatg	ggtgcgatgc	gtcgatattg	ttggatgaca	480
cgcttagctt	cgtgggcgag	aaaacagcag	ctccgaacaa	caattccgtg	agagggttcg	540
aagtgatcga	ccgcatcaag	gctagtctgg	agaaggagtg	ccctggagtg	gtttcctgtg	600
cagatatcgt	tgcctgggt	gctcgcgact	cagtcgttca	tttgggaggt	ccttcatgga	660
ccgtaagctt	aggagaaaag	gattccatta	ctgctagcag	gagccttgct	aacacctcca	720
tacctccacc	tactttctaata	ctcagtgtctc	tcataaccag	cttcgctgct	cagggtcttt	780
cagtcaagaa	catggtggct	ctttctgggt	cacataccat	tggcctagcg	agatgcactt	840
ccttccgaag	acggatctac	aacgactcga	acatagatac	atccttcgcc	cataaattgc	900
agaagatatg	tcccaggatt	ggaaatgata	gtgtccttca	aaggctagac	atccaaacgc	960
cgaccttctt	tgacaacctt	tactaccaca	atttactgca	gaagaagggc	cttcttctact	1020
ctgatcaaga	gctcttcaat	ggcagttctg	tggattcact	ggtcaagaag	tatgcatgcg	1080
acacaggaaa	atttttccga	gattttgcca	aggcaatgat	caaaatgagc	gaaattaagc	1140
cccccaaagg	aagcaatggt	caaataagga	aaaattgcag	gaaagtgaac	taagtatgaa	1200
gctcatatat	gcaatttgaa	actgccacat	atgaacacgg	tagtgaaatc	agggctcgat	1260
aatgtcccct	gacaatttgt	cgtcatgtat	ctgtcttctt	gactaatttg	tggttgctgc	1320
ttgaaaaata	aaggagctcg	tctcagtttc	tgtaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	1380
aaaaaaaaaa	a					1391

<210> 353
 <211> 337
 <212> DNA
 <213>

<400> 353

cagaatgcct	agtcgtcatc	cgatttgggt	aattgtcgcc	atagcttttg	taaccgcact	60
cgggtgggga	agtgccctccg	cacaactctc	tacaaacttc	tactccaaaa	gttgtcccaa	120
tgttttgagc	acggtgaaat	ctgttggtccg	gtccgcgggtg	tcgaaagagc	gccgcatggg	180
tgcttctctc	ctgcgcctct	tctttcatga	ttgcttcgtc	aatgggtgcg	atggctcgat	240

actcctggac gacacatcct cgttccaagg ggagaagacg gccggcccaa ataataagtc 300
 tttagagagga tacaacgtca ttgaccggat caagtcc 337

<210> 354

<211> 368

<212> DNA

<213>

<400> 354

ctcacttccg agcgcgccat gcagttcacc ttttcgcgcg ctttcctcgc tctcgtcaca 60
 gtcgcggccg ctatgccac caagcgtgcg gcgtgcagca acggacgaac ggccactcat 120
 gcctcgtgct gtgtgtggtt cgacgtcctc gacgatattc aagagaatct gttcgacggg 180
 ggagagtgcg gagaggaaac acacgagtct ctgcggtcga ctttcacga tgccatcggc 240
 ttctccccga gcctgtttct cgagggaaaa ttcggtggtc tcggcgctga tggttccatc 300
 atggtcact ctgacatcga gaccgtgttc ccgcgaaca atggaattga tgatatcgtc 360
 gacgcgca 368

<210> 355

<211> 955

<212> DNA

<213>

<400> 355

aagaaactca gacccagacc cagaccacat catggcctcc cgtttcagct ctttcgtttt 60
 ggtttctttt cttgtgatag ctgcatcaca tgttcatgtt acgagctctg ctcacttggt 120
 gaaggggctc tcgtggctct tctacgagaa gagctgtccc aaggtggagt ccgtcatcaa 180
 gaaacatctc aagaagggtg tcgaggagga tattggccaa gctgctgggc tgcttcgtct 240
 gcacttccat gactgctttg ttaagggatg tgatgcttcg gtgttgctgg atggatcagc 300
 cagtggacca agtgagcagg acgtccacc gaaccggagc ttgagaccat cagcattcaa 360
 gatcatcgat gacctccgtg agctcgtgga caagaagtgt ggtcgagtag tctcttgctc 420
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 atcacccaac cgattcgaca acaagtactt tgctgatttg gtgaaccgcc aaggcctgtt 840
 cacctcagac caagatctgt atgaggatcc cacaaccagg gacattgtca ctagctttgc 900
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<210> 356

<211> 308

<212> DNA

<213>

<400> 356

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 ttcgacaacg aatgcggcga tgacgccccat gctgccctgc gtctgagttt ccacgatgca 240
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<210> 357

<211> 373

<212> DNA

<213>

<400> 357

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tccggcgtgc	tgcgcatctt	tctcactgag	agatgacttg	cttacaaatc	tcttcggggg	180
tgtgtgcggc	gaagaggcgc	acgagtctct	ccgattgtct	ttccatgatg	ccattgcgtt	240
ttcgcccgca	ttaattaggc	aaggcaaacc	gggaggtgga	ggtgctgatg	gctctatgat	300
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<210> 358

<211> 417

<212> DNA

<213>

<400> 358

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cacctttgga	cgtgcacagt	gcaggacatt	cagccctagg	ctctacaact	tcaacgcgag	300
tggcagccca	gatccaacca	taagtccttc	atacttgacc	actctccaac	aactttgccc	360
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<210> 359

<211> 659

<212> DNA

<213>

<400> 359

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acaacgacat	tcctgcaccc	aactcaaccc	atcagactct	ggaaaccaa	ttcaacctca	600
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<210> 360

<211> 669

<212> DNA

<213>

<400> 360

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cattaaggag	gccatcgagg	tggaatgtcc	tggagtgggtg	tcgtgtgctg	acattattgt	420

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<210> 361

<211> 916

<212> DNA

<213>

<400> 361

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accttcacta	gcgagaaaata	tgctcttccc	aataacaatt	ccgcgagggg	tttcgaggtg	360
atcgatagca	taaagagcca	actcgagaat	gcttgcaccg	gcgtcgtttc	ttgtgcagac	420
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aagtgtccta	gtaccacagg	ctccggagac	agcaacctgt	cgccactgga	ttatacgact	780
cccactgtgt	ttgacaaaaa	ctattactac	aactctgaaa	gcaaaagagg	acttctccac	840
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<210> 362

<211> 586

<212> DNA

<213>

<400> 362

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aattaaaatt	tgtaaagatt	gtattatcta	tagcttttct	ctgaagttat	aagcgaagct	540
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<210> 363

<211> 1224

<212> DNA

<213>

<400> 363

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<210> 364

<211> 519

<212> DNA

<213>

<400> 364

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agtttggtga	ctatttggtt	gatttcgatg	taccaagtac	aaagtttctc	aacagattaa	480
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<210> 365

<211> 646

<212> DNA

<213>

<400> 365

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<210> 366

<211> 364

<212> DNA

<213>

<400> 366

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<210> 367

<211> 364

<212> DNA

<213>

<400> 367

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<210> 368

<211> 801

<212> DNA

<213>

<400> 368

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<210> 369

<211> 1171

<212> DNA

<213>

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<210> 370

<211> 1073

<212> DNA

<213>

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<210> 371

<211> 1522

<212> DNA

<213>

<400> 371

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actatataac	agcaccaccg	gtacacaaat	gcgggatccc	acgatggacc	agagtttcgc	780
taagaatctt	tatctcacct	gccctaccag	taccaccgtt	aacaccacca	aattggatat	840
tcgcactcca	aatgtgttcg	acaacaaata	ctacgtcgat	ctcctcaacc	gacagaccct	900
cttcacttct	gaccagactc	tttacaccga	cactcgaacc	cgcgacattg	tgatcaattt	960
tgcggtgaat	cagagcctct	tctttgaaca	gtttgtgctg	agcatgctca	aaatggggca	1020
gctggatgtg	ctcacaggaa	gcgagggaga	gatccgtaag	aactgctggg	ctgcgaatcc	1080
ttcaacattt	tcgattatgg	atccagaggc	gtctcaagaa	tcaacatctt	actctatgtg	1140
agattaggg	tatgagcgaa	tctcaaatat	aagcaagcag	cgtaatttcc	cagcaaagtc	1200
taataaatat	atatataacc	ggcatcttgt	aaaccctttg	caatgctggg	tctacaaatt	1260
actttttccc	ttttgacctt	ctgaaagagc	agaaatcaag	cctgaataca	gtgcattctc	1320
gttgaaaata	aatagcgttt	cttggttgata	atcagatttc	caaccgattc	cggcaatttc	1380
caataagaaa	ctttactgaa	tttaaaactca	aatgctggcc	aattttgttt	agggcgtttt	1440
tgaaatcggt	ggactgttat	ctttggaaac	ctacattaga	cttatattta	tctaaaatat	1500
tgaccccaaa	aaaaaaaaaa	aa				1522

<210> 372

<211> 311

<212> DNA

<213>

<400> 372

ctcaatttcg	ctcttatctt	ctgtgtttca	tcgttttctt	cccaatatga	tgatgaggac	60
tctagtgtgc	attgggttaa	tggctgtgtt	tgtagccttc	atacatataa	acgcttgaat	120
gggcagctga	gctcaacgtt	ttatgccaaa	tcgtgtccga	ggttgccatc	gatagtgaag	180
tcagtgggtga	agcaagcggg	cgctaaggag	aaaagaatgg	gagcgtcctt	ggtccgcctt	240
cactttcacg	attgcttcgt	caatgggtgc	gatggttcaa	tcttattgga	tgacaacgcg	300
acgtttaccg	g					311

<210> 373

<211> 474

<212> DNA

<213>

<400> 373

catcgatgct	atcaagacag	ccctcgagag	ttcttgcaac	gccactgttt	cttgccgaga	60
tattctcgct	attgcagcgc	gggattcagt	ataccttagc	ggtgggcctt	actggcaagt	120
gcagatgggg	agaagagatg	gcaccactgc	cagcaaaagt	gcagcaaatg	ccgacatccc	180
ttctcctatt	gagtcgcttg	gttcaactcat	atcccaattc	caaggtgttg	ggctttctgt	240
tcatgatctt	gtagtgtttt	caggggctca	caccataggc	cgtgcccact	gtggcacctt	300
cagctcacgc	ctattcaatt	tcagcggctc	aaacagtgcg	gacccaacta	ttcaccaatc	360
tctactgcaa	gacctgcata	gtttatgcc	agatggaac	agtgatccaa	ataccctggc	420
gccactggac	cctgtgacca	aagacaagct	ccataatgtg	tatttcagaa	atct	474

<210> 374

<211> 353

<212> DNA

<213>

<400> 374

ctttctgtta	cggtatgcgt	tgtttgttca	gggggacata	caattgggag	agctcgggtgc	60
acagtgttca	gcggtagact	ctacaatttc	agcggaacgg	gcagtccgga	tccgacactg	120
aattcctcct	atctatccac	cttgcaaagc	acgtgcccgc	agaatggaag	cgcgaatacg	180
ttaacgtcac	tggatccagg	gactccaaat	acgttcgaca	acaactactt	tgcaaatctg	240

cagattgaga tgggtctgct tcagtcgacg aagaacttct ttccacatcg ggagcaagca 300
ccatctctac tgtcaatgat tatgccagta gtcaatccga tttcttcttc aac 353

<210> 375
<211> 461
<212> DNA
<213>

<400> 375

caaagcagag ttgcgtttga agcgcaagaa atggccgctt taatgaaaag ctccgcatgc 60
attgctgtaa ttgtgtttat tgtgtgttcg attaataaca ctgtgcatgg gcagctgagc 120
tcaacatttt atgacaaatc ttgcccgcgac gtgctgtcgg tagtgaaagc cggggtgaag 180
caagcggtcg ccaaggagca aaggatgggg gcgtcgcttc tccgacttca cttccacgac 240
tgcttcgtta atggtttgcga tgggtccgtt ctggttgatg actcttcgaa aattactggc 300
gagaaaacgg ctattcccaa tgccaattcg gcgagggggg tcgatgtgat cgataccata 360
aagagtcagg tcgagaaatc ttgcagcgca gtcgtttcct gttctgacat tctagccatt 420
gctgctcgtg attctgttgt tgaactgggc ggcccttcac g 461

<210> 376
<211> 179
<212> PRT
<213>

<400> 376

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

<210> 377
<211> 115
<212> PRT
<213>

<400> 377

Met Phe Leu Lys Tyr Leu Ser Ala Ala Leu Ile Ser Leu Ala Thr Ile

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

<210> 378

<211> 315

<212> PRT

<213>

<400> 378

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

275 280 285
 Lys Ala Met Ile Lys Met Ser Glu Ile Lys Pro Pro Lys Gly Ser Asn
 290 295 300
 Gly Gln Ile Arg Lys Asn Cys Arg Lys Val Asn
 305 310 315

<210> 379
 <211> 111
 <212> PRT
 <213>

<400> 379
 Met Pro Ser Arg His Pro Ile Trp Val Ile Val Ala Ile Ala Phe Val
 1 5 10 15
 Thr Ala Leu Gly Trp Gly Ser Ala Ser Ala Gln Leu Ser Thr Asn Phe
 20 25 30
 Tyr Ser Lys Ser Cys Pro Asn Val Leu Ser Thr Val Lys Ser Val Val
 35 40 45
 Arg Ser Ala Val Ser Lys Glu Arg Arg Met Gly Ala Ser Leu Leu Arg
 50 55 60
 Leu Phe Phe His Asp Cys Phe Val Asn Gly Cys Asp Gly Ser Ile Leu
 65 70 75 80
 Leu Asp Asp Thr Ser Ser Phe Gln Gly Glu Lys Thr Ala Gly Pro Asn
 85 90 95
 Asn Lys Ser Leu Arg Gly Tyr Asn Val Ile Asp Arg Ile Lys Ser
 100 105 110

<210> 380
 <211> 116
 <212> PRT
 <213>

<400> 380
 Met Gln Phe Thr Phe Ser Ala Ala Phe Leu Ala Leu Val Thr Val Ala
 1 5 10 15
 Ala Ala Met Pro Thr Lys Arg Ala Ala Cys Ser Asn Gly Arg Thr Ala
 20 25 30
 Thr His Ala Ser Cys Cys Val Trp Phe Asp Val Leu Asp Asp Ile Gln
 35 40 45
 Glu Asn Leu Phe Asp Gly Gly Glu Cys Gly Glu Glu Thr His Glu Ser
 50 55 60
 Leu Arg Leu Thr Phe His Asp Ala Ile Gly Phe Ser Pro Ser Leu Phe
 65 70 75 80
 Leu Glu Gly Lys Phe Gly Gly Leu Gly Ala Asp Gly Ser Ile Met Ala
 85 90 95
 His Ser Asp Ile Glu Thr Val Phe Pro Ala Asn Asn Gly Ile Asp Asp
 100 105 110
 Ile Val Asp Ala
 115

<210> 381
 <211> 308
 <212> PRT
 <213>

<400> 381

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

<210> 382

<211> 98

<212> PRT

<213>

<400> 382

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

Arg Ser Lys Gly Gly Gly Gly Ala Asp Gly Ser Ile Ile Ala Phe Asn
 85 90 95
 Lys Thr

<210> 383
 <211> 119
 <212> PRT
 <213>

<400> 383
 Met Ala Phe Lys Leu Val Val Asn Leu Val Ser Leu Ala Leu Ala Val
 1 5 10 15
 Ser Ala Ala Asn Phe Lys Arg Val Ala Cys Pro Gly Thr Thr Ala Thr
 20 25 30
 Ala Arg Asn Pro Ala Cys Cys Ala Phe Phe Ser Leu Arg Asp Asp Leu
 35 40 45
 Leu Thr Asn Leu Phe Gly Gly Val Cys Gly`Glu Glu Ala His Glu Ser
 50 55 60
 Leu Arg Leu Ser Phe His Asp Ala Ile Ala Phe Ser Pro Ala Leu Ile
 65 70 75 80
 Arg Gln Gly Lys Pro Gly Gly Gly Gly Ala Asp Gly Ser Met Ile Thr
 85 90 95
 Phe Pro Asn Val Glu Pro Asn Phe Asn Ala Asn Asn Gly Ile Ile Asp
 100 105 110
 Ser Val Asp Phe Leu Thr Pro
 115

<210> 384
 <211> 138
 <212> PRT
 <213>

<400> 384
 Ser Cys Pro Gly Thr Val Ser Cys Ala Asp Ile Leu Ala Leu Gly Ala
 1 5 10 15
 Gln Ala Ser Val Val Leu Ser Gly Gly Pro Ser Trp Arg Val Leu Ser
 20 25 30
 Gly Arg Arg Asp Ser Leu Thr Ala Asn Gln Ala Gly Ala Asn Thr Ser
 35 40 45
 Ile Pro Ser Pro Phe Asp Ser Leu Ala Asn Leu Thr Ser Lys Phe Ala
 50 55 60
 Ala Val Gly Leu Asp Thr Asn Asp Leu Val Thr Leu Ser Gly Ala His
 65 70 75 80
 Thr Phe Gly Arg Ala Gln Cys Arg Thr Phe Ser Pro Arg Leu Tyr Asn
 85 90 95
 Phe Asn Ala Ser Gly Ser Pro Asp Pro Thr Ile Ser Pro Ser Tyr Leu
 100 105 110
 Thr Thr Leu Gln Gln Leu Cys Pro Gln Asn Gly Ser Gly Ser Val Leu
 115 120 125
 Ala Asn Leu Asp Pro Thr Thr Val Asn Thr
 130 135

<210> 385
 <211> 208
 <212> PRT

<213>

<400> 385

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

<210> 386

<211> 202

<212> PRT

<213>

<400> 386

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

Tyr Val Pro Leu His Asn Gly Ser Ile Ser Ser Leu Leu Ser Ala Phe
 165 170 175
 Ala Ser Val Gly Ile Asp Ala Glu Gly Ala Val Ala Leu Leu Gly Leu
 180 185 190
 Ile Leu Ile His Ser Val Leu His Tyr Thr
 195 200

<210> 387

<211> 287

<212> PRT

<213>

<400> 387

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

<210> 388

<211> 161

<212> PRT

<213>

<400> 388

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

<210> 389

<211> 318

<212> PRT

<213>

<400> 389

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

Cys Pro Ser Ala Gly Gly Asp Ser Asn Leu Ser Pro Leu Asp Ala Val
 225 230 235 240
 Thr Ser Ile Thr Phe Asp Asn Lys Tyr Tyr Ser Asn Leu Lys Ile Gln
 245 250 255
 Lys Gly Leu Leu His Ser Asp Gln Gln Leu Phe Asn Gly Gly Ser Thr
 260 265 270
 Asp Ser Gln Val Thr Ala Tyr Ser Ser Asn Gln Asn Ser Phe Phe Ile
 275 280 285
 Asp Phe Thr Ala Ala Met Val Lys Met Gly Asn Ile Ser Pro Leu Thr
 290 295 300
 Gly Thr Asn Gly Gln Ile Arg Lys Asn Cys Arg Lys Ser Asn
 305 310 315

<210> 390

<211> 95

<212> PRT

<213>

<400> 390

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

<210> 391

<211> 201

<212> PRT

<213>

<400> 391

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

Leu Gly Arg Arg Asp Ser Ala Thr Ala Ser Leu Ser Ala Ala Asn Thr
 145 150 155 160
 Asn Ile Pro Ala Pro Thr Ser Asn Leu Ser Gly Leu Ile Ser Ser Phe
 165 170 175
 Gln Ala Gln Gly Leu Ser Thr Lys Asp Met Ile Val Leu Ser Gly Ala
 180 185 190
 His Thr Ile Gly Gln Ala Arg Cys Thr
 195 200

<210> 392
 <211> 120
 <212> PRT
 <213>

<400> 392
 Leu Ile Ser Ser Phe Thr Ala His Gly Leu Ser Thr Lys Asp Leu Gly
 1 5 10 15
 Ala Leu Ser Gly Ala His Thr Ile Gly Gln Ala Arg Cys Thr Thr Phe
 20 25 30
 Arg Ala Arg Val Tyr Asn Glu Ser Asn Ile Asp Thr Ser Phe Ala Thr
 35 40 45
 Ser Val Lys Ala Asn Trp Pro Ser Ala Gly Gly Asp Asn Thr Leu Ser
 50 55 60
 Pro Leu Asp Leu Ala Thr Pro Thr Thr Phe Asp Asn Lys Tyr Tyr Thr
 65 70 75 80
 Asp Leu Arg Ser Gln Lys Gly Leu Leu His Ser Asp Gln Gln Met Phe
 85 90 95
 Ser Gly Gly Ser Thr Asn Ser Gln Val Thr Thr Tyr Ser Ser Asn Gln
 100 105 110
 Lys His Leu Leu Tyr Arg Leu Tyr
 115 120

<210> 393
 <211> 120
 <212> PRT
 <213>

<400> 393
 Lys Arg Ile Asn Phe His Leu Lys Glu Asp Ile Thr Gln Ala Ala Gly
 1 5 10 15
 Leu Leu Arg Val His Phe His Asp Cys Phe Val Gln Gly Cys Asp Gly
 20 25 30
 Ser Val Leu Leu Asp Gly Ser Ala Ser Gly Pro Ser Glu Gln Asp Ala
 35 40 45
 Pro Pro Asn Leu Thr Leu Arg Ala Lys Ala Phe Glu Ile Ile Asn Asp
 50 55 60
 Ile Lys Lys His Val Glu Lys Ala Cys Ser Gly Val Val Ser Cys Ala
 65 70 75 80
 Asp Leu Thr Ala Leu Ala Ala Arg Glu Ser Val Arg Ala Val Gly Gly
 85 90 95
 Pro Glu Tyr Arg Val Pro Leu Gly Arg Asp Ser Leu Lys Phe Ala
 100 105 110
 Thr Arg Lys Val Thr Leu Ala Asn
 115 120

<210> 394

<211> 266

<212> PRT

<213>

<400> 394

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

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<210> 395

<211> 323

<212> PRT

<213>

<400> 395

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

```

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

<210> 396

<211> 223

<212> PRT

<213>

<400> 396

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

```

Thr Lys Phe Asp Asn Tyr Tyr Phe Lys Ser Leu Leu Ser Gly Gln Gly
145                150                155                160
Leu Leu Asn Thr Asp Glu Glu Leu Phe Ala Lys Gly Ser Gly Lys Thr
                165                170                175
Lys Glu Leu Val Lys Leu Tyr Ala Ala Asn Glu Glu Leu Phe Leu Lys
                180                185                190
Gln Phe Ala Leu Ser Met Val Lys Met Gly Asn Ile Lys Pro Leu Thr
                195                200                205
Gly Thr Val Gly Glu Ile Arg Val Asn Cys Arg Lys Val Asn Ser
210                215                220

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<210> 397

<211> 351

<212> PRT

<213>

<400> 397

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

```

Gly Glu Ile Arg Lys Asn Cys Trp Ala Ala Asn Pro Ser Thr Phe Ser
 325 330 335
 Ile Met Asp Pro Glu Ala Ser Gln Glu Ser Thr Ser Tyr Ser Met
 340 345 350

<210> 398
 <211> 103
 <212> PRT
 <213>

<400> 398

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

<210> 399
 <211> 157
 <212> PRT
 <213>

<400> 399

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

<210> 400
 <211> 117
 <212> PRT

<213>

<400> 400

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

```

<210> 401

<211> 143

<212> PRT

<213>

<400> 401

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

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<210> 402

<211> 1474

<212> DNA

<213>

<400> 402

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gaattcggca cgagaaaacg tccatagctt ccttgccaac tgcaagcaat acagtacaag      60
agccagacga tcgaatcctg tgaagtgggt ctgaagtgat gggaagcttg gaatctgaaa      120
aaactgttac aggatatgca gctcgggact ccagtggcca cttgtcccct tacacttaca      180
atctcagaaa gaaaggacct gaggatgtaa ttgtaaaagg catttactgc ggaatctgcc      240

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actctgattt	agttcaaatg	cgtaatgaaa	tggacatgtc	tcattaccca	atgggtccctg	300
ggcatgaagt	ggtggggatt	gtaacagaga	ttggcagcga	ggtgaagaaa	ttcaaagtgg	360
gagagcatgt	aggggttggg	tgcattgttg	ggtcctgtcg	cagttgcggt	aattgcaatc	420
agagcatgga	acaatactgc	agcaagagga	tttggaccta	caatgatgtg	aaccatgacg	480
gcacacctac	tcagggcgga	tttgcaagca	gtatgggtgg	tgatcagatg	tttgtgggtc	540
gaatcccgga	gaatcttcct	ctggaacaag	cggccccctc	gttatgtgca	ggggttacag	600
ttttcagccc	aatgaagcat	ttcgccatga	cagagccccg	gaagaaatgt	gggattttgg	660
gttttaggagg	cgtggggcac	atgggtgtca	agattgccaa	agcctttgga	ctccacgtga	720
cggttatcag	ttcgtctgat	aaaaagaaa	aagaagccat	ggaagtcctc	ggcgccgatg	780
cttatcttgt	tagcaaggat	actgaaaaga	tgatggaagc	agcagagagc	ctagattaca	840
taatggacac	cattccagtt	gctcatcctc	tggaaaccata	tcttgccctt	ctgaagacaa	900
atggaaagct	agtgatgctg	ggcgttggtc	cagagccggt	gcacttcgtg	actcctctct	960
taatacttgg	gagaaggagc	atagctggaa	gtttcattgg	cagcatggag	gaaacacagg	1020
aaactctaga	tttctgtgca	gagaagaagg	tatcatcgat	gattgagggt	gtgggcctgg	1080
actacatcaa	cacggccatg	gaaaggttgg	agaagaacga	tgtccgttac	agatttgtgg	1140
tggatgttgc	tagaagcaag	ttggataatt	agtctgcaat	caatcaatca	gatcaatgcc	1200
tgcatgcaag	atgaatagat	ctggactagt	agcttaacat	gaaagggaaa	ttaaattttt	1260
atttaggaac	tcgatactgg	tttttggttac	tttagtttag	cttttgtgag	gttgaaacaa	1320
ttcagatgtt	tttttaactt	gtatatgtaa	agatcaattt	ctcgtgacag	taaataataa	1380
tccaatgtct	tctgccaaat	taatatatgt	attcgtattt	ttatatgaaa	aaaaaaaaaa	1440
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaa			1474

<210> 403

<211> 414

<212> DNA

<213>

<400> 403

cacgctcgac	gaattcggta	ccccgggttc	gaaatcgata	agcttggatc	caaagcaaca	60
cattgaactc	tctctctctc	tctctctctc	tctctctctc	tccccaccc	ccccttccca	120
accccaacca	catacagaca	agtagatacg	cgcacacaga	agaagaaaag	atgggggttt	180
caatgcagtc	aatcgcacta	gcgacgggtc	tggccgtcct	aacgacatgg	gcgtggaggg	240
cgggtgaactg	ggtgtggctg	aggccgaaga	ggctcgagag	gcttctgaga	cagcaaggtc	300
tctccggcaa	gtcctacacc	ttcctggtcg	gcgacctcaa	ggagaacctg	cggatgctca	360
aggaagccaa	gtccaagccc	atcgccgtct	ccgatgacat	caagcctcgt	ctct	414

说明书附图



图 1

松属 桉属
IKb A B C D E IKb A B C D E



图 2

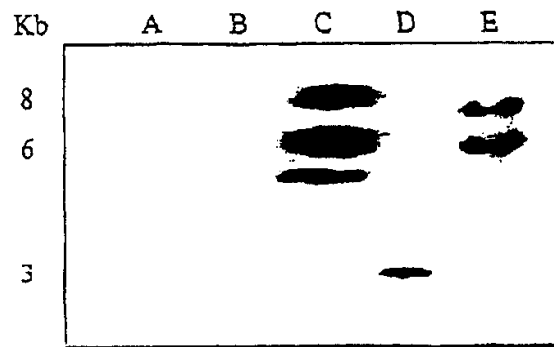


图 3

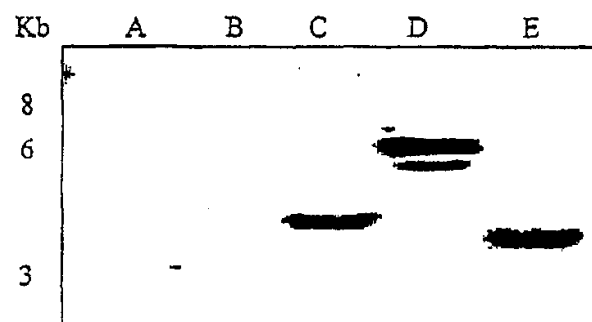


图 4

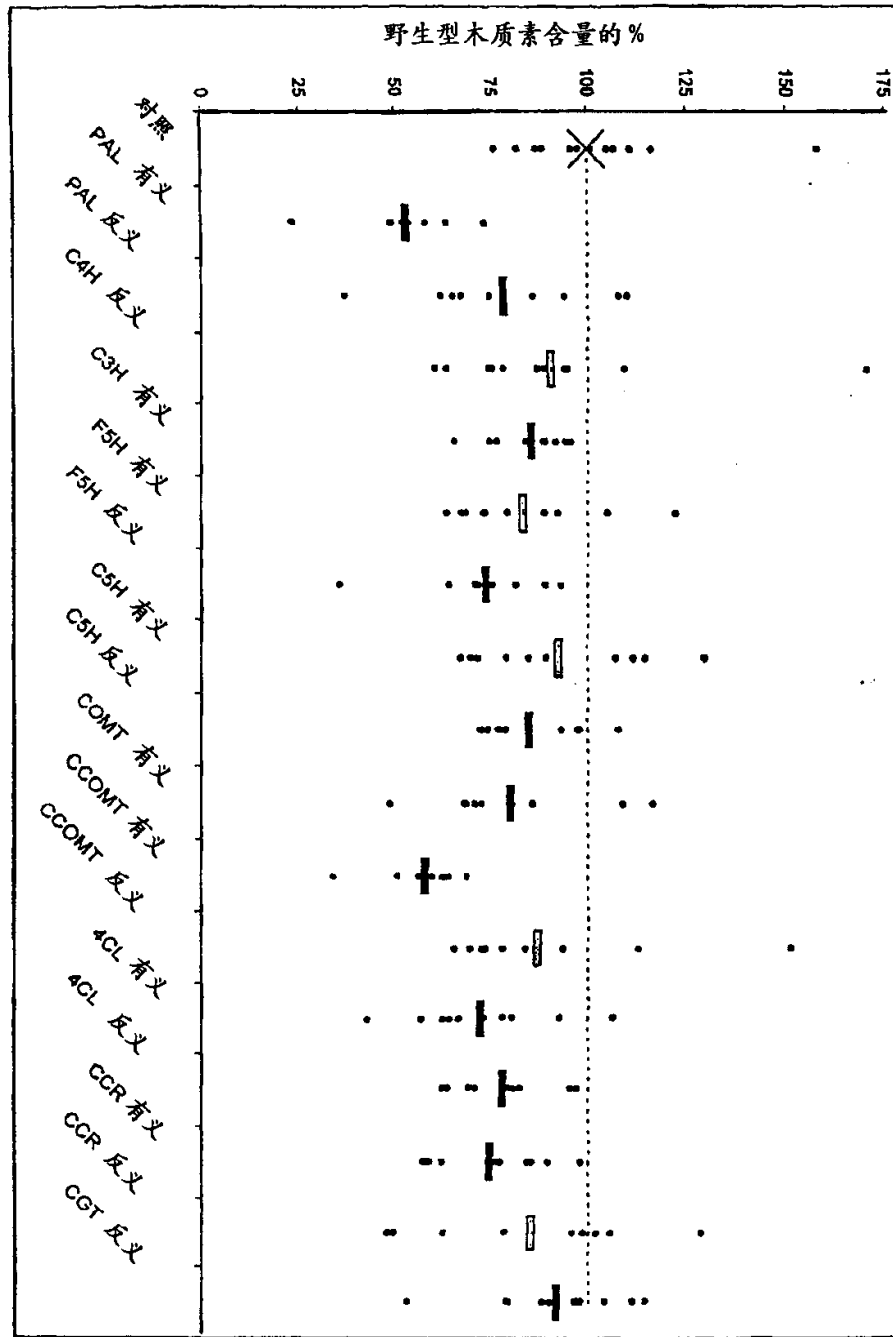


图 5