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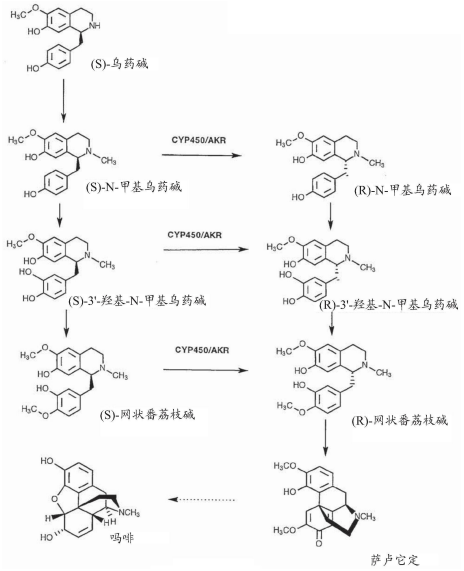
(54)发明名称

用于制备(R)-网状番荔枝碱及其前体的组合物和方法

(57)摘要

可用于制造化合物(R)-网状番荔枝碱及其合成前体的方法。还提供可用于合成(R)-网状番荔枝碱和合成前体的组合物。



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1.一种宿主细胞,其包含嵌合核酸序列,所述嵌合核酸序列包含作为可操作地连接部件的编码选自由CYP450和AKR组成的组的一种或多种多肽的一种或多种核酸序列。

2.根据权利要求1所述的宿主细胞,其不能天然产生苄基异喹啉衍生物、(S)-网状番荔枝碱、或(R)-网状番荔枝碱或(R)-网状番荔枝碱前体。

3.根据权利要求1所述的宿主细胞,其能够天然产生(S)-网状番荔枝碱但不是(R)-网状番荔枝碱或(R)-网状番荔枝碱前体。

4.根据权利要求1所述的宿主细胞,其中所述嵌合核酸序列包含连接至编码CYP450和AKR的核酸序列的能够在所述宿主细胞中控制表达的启动子。

5.根据权利要求1所述的宿主细胞,其中所述嵌合核酸序列包含作为可操作地连接部件的以下各项:

(i)一种编码CYP450多肽的第一核酸序列;

(ii)一种编码AKR多肽的第二核酸序列;以及

(iii)能够控制在宿主细胞中的表达的一种或多种核酸序列。

6.根据权利要求5所述的宿主细胞,其中所述第一核酸序列和所述第二核酸序列被可操作地连接以便产生一种包含CYP450和AKR的融合多肽。

7.一种用于制备(R)-网状番荔枝碱或(R)-网状番荔枝碱前体的方法,该方法包括:

(a)提供一种嵌合核酸序列,所述嵌合核酸序列包含作为可操作地连接部件的以下各项:

(i)一种编码CYP450多肽的第一核酸序列;

(ii)一种编码AKR多肽的第二核酸序列;以及

(iii)能够控制在宿主细胞中的表达的一种或多种核酸序列;

(b)将所述嵌合核酸序列引入宿主细胞中并且使所述宿主细胞生长以产生CYP450和AKR,并且产生(R)-网状番荔枝碱或该(R)-网状番荔枝碱前体;并且

(c)回收(R)-网状番荔枝碱或该(R)-网状番荔枝碱前体。

8.一种制备(R)-网状番荔枝碱或(R)-网状番荔枝碱前体的方法,该方法包括:

(a)提供一种苄基异喹啉衍生物;

(b)使该苄基异喹啉衍生物与一种酶混合物接触,该酶混合物能够在允许将该苄基异喹啉衍生物转化成(R)-网状番荔枝碱或(R)-网状番荔枝碱前体的条件下将该苄基异喹啉衍生物转化成(R)-网状番荔枝碱或(R)-网状番荔枝碱前体。

9.一种制备(R)-网状番荔枝碱的方法,该方法包括:

(a)提供(S)-网状番荔枝碱;并且

(b)使(S)-网状番荔枝碱与一种酶混合物接触,该酶混合物能够在允许将(S)-网状番荔枝碱转化成(R)-网状番荔枝碱的条件下将(S)-网状番荔枝碱转化成(R)-网状番荔枝碱。

10.一种用于制备(R)-网状番荔枝碱的方法,该方法包括:

(a)提供一种嵌合核酸序列,该嵌合核酸序列包含作为可操作地连接部件的以下各项:

(i)一种编码CYP450多肽的第一核酸序列;

(ii)一种编码AKR多肽的第二核酸序列;以及

(iii)能够控制在宿主细胞中的表达的一种或多种核酸序列;

(b)将该嵌合核酸序列引入一个宿主细胞中并且使该宿主细胞生长以产生CYP450和

AKR,并且产生(R)-网状番荔枝碱;并且

(c)回收(R)-网状番荔枝碱。

用于制备(R)-网状番荔枝碱及其前体的组合物和方法

相关申请

[0001] 本申请是申请号为201480071559.1、申请日为2014年12月03日、发明名称为“用于制备(R)-网状番荔枝碱及其前体的组合物和方法”的中国发明专利申请的分案申请，原申请为国际申请号为PCT/CA2014/051164的国家阶段申请，其要求来自2013年12月4日提交的美国临时专利申请号61/911,759和2014年9月15日提交的美国临时专利申请号62/050,399的根据35USC§119(e)的权益，这两个专利都通过引用以其全文结合在此。

披露领域

[0002] 在此披露的组合物和方法涉及次级代谢物和用于制造这些次级代谢物的方法。更具体地说，本披露涉及(R)-网状番荔枝碱及其某些前体以及用于制造(R)-网状番荔枝碱和此类前体的方法和组合物。

披露背景

[0003] 以下段落通过背景的方式提供给本披露。然而，它们并不是承认在此所讨论的任何内容是现有技术或是本领域技术人员常识的一部分。

[0004] 生命体的生物化学途径通常被分类为初级代谢的一部分或次级代谢的一部分。为活细胞初级代谢的一部分的途径涉及用于能量产生的分解代谢或涉及用于细胞的结构单元(building block)产生的合成代谢。另一方面，次级代谢物由不具有任何明显的合成代谢或分解代谢功能的活细胞产生。然而很久以前就已经认识到，许多次级代谢物可用于许多方面，包括例如作为治疗剂或天然忌避剂。

[0005] 次级代谢物(R)-网状番荔枝碱由罂粟(罂粟(Papaver somniferum))和植物家族罂粟科、樟科、番荔枝科、大戟科以及桑科的其他成员产生，并且可被用作一种用于产生药物活性化合物(包括吗啡和可待因)的源材料。

[0006] 已知的是，植物中的(R)-网状番荔枝碱是由(S)-网状番荔枝碱产生的。然而还不清楚是哪些基因和多肽涉及催化一个或多个转化反应。

[0007] 目前可从天然来源(诸如罂粟)收获(R)-网状番荔枝碱。可替代地可以合成制备(R)-网状番荔枝碱。然而现有的用于制造(R)-网状番荔枝碱的方法受(R)-网状番荔枝碱产率低的困扰和/或是昂贵的。不存在由(S)-网状番荔枝碱生物合成制备(R)-网状番荔枝碱的方法。因此在本领域中存在对于合成(R)-网状番荔枝碱的改进方法的需要。

披露概述

[0008] 以下段落意在向读者介绍随后的更详细说明并且不限定或限制本披露所要求保护的主题。

[0009] 本披露涉及次级代谢物(R)-网状番荔枝碱及其某些前体，以及涉及制备(R)-网状番荔枝碱及其某些前体的方法。

[0010] 因此，本披露在至少一个方面中提供一种制备(R)-网状番荔枝碱或(R)-网状番荔枝碱前体的方法的至少一个实施例，该方法包括：

(a)提供一种苄基异喹啉衍生物；

(b)使该苄基异喹啉衍生物与一种酶混合物接触，该酶混合物能够在允许将该苄

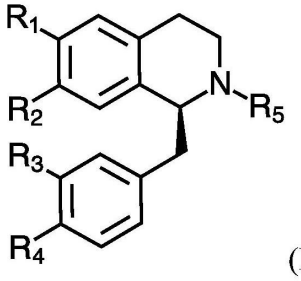
基异喹啉衍生物转化成(R)-网状番荔枝碱或(R)-网状番荔枝碱前体的条件下将该苄基异喹啉衍生物转化成(R)-网状番荔枝碱或(R)-网状番荔枝碱前体。

[0011] 本披露进一步在至少一个方面中提供一种制备(R)-网状番荔枝碱或其前体的方法的至少一个实施例,该方法包括:

(a)提供一种苄基异喹啉衍生物;

(b)使该苄基异喹啉衍生物与一种酶混合物接触,该酶混合物能够在允许将该苄基异喹啉衍生物转化成(R)-网状番荔枝碱或(R)-网状番荔枝碱前体的条件下将该苄基异喹啉衍生物转化成(R)-网状番荔枝碱或(R)-网状番荔枝碱前体;

其中该苄基异喹啉衍生物具有化学式(I):

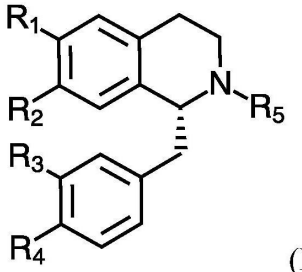


(I)

其中R_1、R_2、R_3以及R_4各自表示氢原子、羟基基团或甲氧基基团;

并且其中R_5表示氢原子或甲基基团;并且

其中该(R)-网状番荔枝碱前体具有化学式(II):

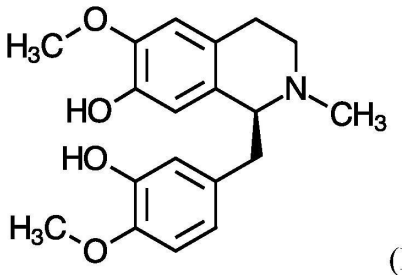


(II)

其中R_1、R_2、R_3以及R_4各自表示氢原子、羟基基团或甲氧基基团;

并且其中R_5表示氢原子或甲基基团,其条件是化学式(II)将(R)-网状番荔枝碱除外。

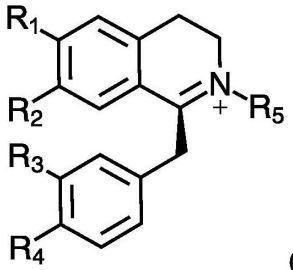
[0012] 在优选实施例中,在该苄基异喹啉衍生物中,R_1是甲氧基基团;R_2是羟基基团;R_3是羟基基团;R_4是甲氧基基团并且R_5是甲基基团,从而提供化学式:



(III)

也称为(S)-网状番荔枝碱。

[0013] 在另外的优选实施例中,该酶混合物包含一种第一多肽,该第一多肽能够将该苄基异喹啉衍生物氧化以形成一种具有化学式(IV)的氧化苄基异喹啉衍生物:

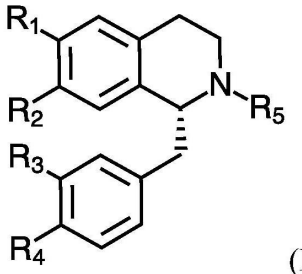


(IV)

其中R_1、R_2、R_3以及R_4各自表示氢原子、羟基或甲氧基基团；

并且其中R_5表示氢原子或甲基基团;以及

一种第二多肽,该第二多肽能够将该氧化苄基异喹啉衍生物(IV)还原以形成具有化学式(II)的(R)-网状番荔枝碱或(R)-网状番荔枝碱前体：



(II)

其中R_1、R_2、R_3以及R_4各自表示氢原子、羟基基团或甲氧基基团；

并且其中R_5表示氢原子或甲基基团,其条件是化学式(II)将(R)-网状番荔枝碱除外。

[0014] 在另外的优选实施例中,该酶混合物包含一种能够将(S)-网状番荔枝碱氧化以形成1,2-脱氢网状番荔枝碱的第一多肽和一种能够将1,2-脱氢网状番荔枝碱还原以形成(R)-网状番荔枝碱的第二多肽。

[0015] 在另外的优选实施例中,能够将该苄基异喹啉衍生物氧化以形成该氧化苄基异喹啉衍生物的该第一多肽是一种细胞色素P450,并且能够将该氧化苄基异喹啉衍生物还原以形成(R)-网状番荔枝碱或(R)-网状番荔枝碱前体的该第二多肽是一种醛-酮还原酶(AKR)。

[0016] 根据本披露,这些方法可以在体外或体内进行,包括但不限于在植物、植物细胞培养物、微生物以及无细胞系统中进行。

[0017] 在此进一步提供一种用于制备选自由CYP450和AKR或其混合物组成的组的酶的方法,该方法包括：

(a)提供一种嵌合核酸序列,该嵌合核酸序列包含作为可操作地连接部件的以下各项：

(i)编码选自由CYP450和AKR组成的组的一种或多种多肽的一种或多种核酸序列；以及

(ii)能够控制在宿主细胞中的表达的一种或多种核酸序列；

(b)将该嵌合核酸序列引入一个宿主细胞中并且使该宿主细胞生长以产生选自由CYP450和AKR组成的组的该多肽;并且

(c)从该宿主细胞中回收选自由CYP450和AKR组成的组的多肽。

[0018] 在此进一步提供一种用于制备具有化学式(II)的(R)-网状番荔枝碱或(R)-网状番荔枝碱前体的方法,该方法包括：

(a)提供一种嵌合核酸序列，该嵌合核酸序列包含作为可操作地连接部件的以下各项：

(i)一种编码CYP450多肽的第一核酸序列；

(ii)一种编码AKR多肽的第二核酸序列；以及

(iii)能够控制在宿主细胞中的表达的一种或多种核酸序列；

(b)将该嵌合核酸序列引入一个宿主细胞中并且使该宿主细胞生长以产生CYP450和AKR，并且产生具有化学式(II)的(R)-网状番荔枝碱或(R)-网状番荔枝碱前体；并且

(c)回收具有化学式(II)的(R)-网状番荔枝碱或(R)-网状番荔枝碱前体。

[0019] 在优选实施例中，该第一核酸序列和该第二核酸序列被可操作地连接以便产生一种包含CYP450和AKR的融合多肽。

[0020] 在此进一步提供一种用于制备具有化学式(II)的(R)-网状番荔枝碱或(R)-网状番荔枝碱前体的方法，该方法包括：

(a)提供一种第一嵌合核酸序列，该第一嵌合核酸序列包含作为可操作地连接部件的一种编码CYP450多肽的第一核酸序列和一种控制该第一核酸序列在细胞中的表达的第一核酸序列；

(b)提供一种第二嵌合核酸序列，该第二嵌合核酸序列包含作为可操作地连接部件的一种编码AKR多肽的第二核酸序列和一种控制该第二核酸序列在细胞中的表达的第二核酸序列；

(c)将该第一嵌合核酸序列和该第二嵌合核酸序列引入一个宿主细胞中并且使该宿主细胞生长以产生CYP450和AKR，并且产生具有化学式(II)的(R)-网状番荔枝碱或(R)-网状番荔枝碱前体；并且

(d)回收具有化学式(II)的(R)-网状番荔枝碱或(R)-网状番荔枝碱前体。

[0021] 本披露进一步提供用于制备(R)-网状番荔枝碱的组合物，这些组合物包含一种酶混合物，该酶混合物包含一种能够将(S)-网状番荔枝碱氧化以形成1,2-脱氢网状番荔枝碱的第一多肽和一种能够将1,2-脱氢网状番荔枝碱还原以形成(R)-网状番荔枝碱的第二多肽。

[0022] 在优选实施例中，该酶混合物包含一种能够将(S)-网状番荔枝碱氧化以形成1,2-脱氢网状番荔枝碱的第一多肽和一种能够将1,2-脱氢网状番荔枝碱还原以形成(R)-网状番荔枝碱的第二多肽。

[0023] 在另外的优选实施例中，能够将(S)-网状番荔枝碱氧化以形成1,2-脱氢网状番荔枝碱的该第一多肽是一种细胞色素P450，并且能够将1,2-脱氢网状番荔枝碱还原以形成(R)-网状番荔枝碱的该第二多肽是一种醛-酮还原酶(AKR)。

[0024] 本发明还进一步提供包含核酸序列的组合物，这些核酸序列编码一种能够将(S)-网状番荔枝碱氧化以形成1,2-脱氢网状番荔枝碱的第一多肽和一种能够将1,2-脱氢网状番荔枝碱还原以形成(R)-网状番荔枝碱的第二多肽。在优选实施例中，这些核酸序列是一种编码能够一起将(S)-网状番荔枝碱氧化以形成1,2-脱氢网状番荔枝碱的细胞色素P450和醛-酮还原酶，以及能够将1,2-脱氢网状番荔枝碱还原以形成(R)-网状番荔枝碱的第二多肽的核酸序列。

[0025] 本披露进一步包括使用编码AKR和/或CYP450的核酸序列的方法，以便检测其在样

品(例如包含植物细胞的样品)中的存在或不存在,以便调节AKR和/或CYP450在植物细胞和其他细胞中的表达,并且作为一种标记物以便评估植物群体中基因遗传连接AKR和/或CYP450的分离。

[0026] 在一个另外的实施例中,本披露提供一种检测编码AKR和/或CYP450的核酸序列的存在或不存在的方法,该方法包括:

(a)提供一种怀疑包含编码AKR和/或CYP450的核酸序列的样品;并且

(b)针对编码AKR和/或CYP450的核苷酸序列的存在分析该样品。

[0027] 在一个另外的实施例中,本披露提供一种用于调节核酸序列在天然表达AKR和/或CYP450的细胞中的表达的方法,该方法包括:

(a)提供一种天然表达AKR和/或CYP450的细胞;

(b)诱变处理该细胞;

(c)使该细胞生长以获得多个细胞;并且

(d)确定该多个细胞是否包括一种包含调节水平的AKR和/或CYP450的细胞。

[0028] 在又另一个实施例中,本披露提供一种减少AKR和/或CYP450在细胞中的表达的方法,该方法包括:

(a)提供一种表达AKR和/或CYP450的细胞;并且

(b)使AKR和/或CYP450在该细胞中的表达沉默。

[0029] 本披露的其他特征和优点将从以下详细说明中变得清楚。然而,应该理解详细说明,在指示本披露的优选实施的同时,仅以说明的方式给出,因为在此披露内容的精神和范围内的不同变化和修改将由该详细说明而对本领域技术人员而言变得明显。

附图简要说明

[0030] 本披露在以下提供关于其附图描述的段落。在此提供的附图提供说明的目的并且不旨在限制本披露。

[0031] 图1描绘不同苄基异喹啉前体至(R)-网状番荔枝碱、(R)-网状番荔枝碱前体、吗啡以及萨卢它定的合成途径。包括所示化合物的化学结构。

[0032] 图2描绘一种用于由(S)-网状番荔枝碱及其合成中间体制造(R)-网状番荔枝碱的合成途径。包括这些合成中间体和能够催化这些合成中间体的化学转化的酶的化学结构。

[0033] 图3描绘本披露的一个实施例的一系列HPLC记录,该实施例提供如在实例1中进一步所述的(S)-网状番荔枝碱至(R)-网状番荔枝碱的转化。

[0034] 图4描绘本披露的一个实施例的一系列HPLC记录,该实施例提供如在实例2中进一步所述的(S)-网状番荔枝碱至1,2-脱氢网状番荔枝碱的转化。

[0035] 图5描绘本披露的一个实施例的一系列HPLC记录,该实施例示出如在实例3中进一步所述的1,2-脱氢网状番荔枝碱至(R)-网状番荔枝碱的转化。

[0036] 图6描绘本披露的一个实施例的一系列HPLC记录,该实施例示出如在实例4中进一步所述的(S)-N-甲基乌药碱至(R)-N-甲基乌药碱的转化。

[0037] 图7描绘关于如在实例5中进一步所述的基因沉默实验所获得的结果。靶向REPI基因中的两个不同区域(图7A;图7C)和COR1.3基因中的一个区域(图7B)。在图7A-7C的每个中,不同图表示以下:(图A)用于组装pTRV2构建体的REPI或COR1.3 cDNA的片段(灰色框)。黑色框表示编码区,而黑色线是侧翼非翻译区。箭头示出用于qRT-PCR分析的引物的退火位

点。(图B)示出使用总RNA通过RT-PCR检测pTRV2载体的溴化乙锭染色的琼脂糖凝胶，该总RNA从用具有pTRV2-REPI-a、pTRV2-REPI-5'、或pTRV2-COR1.3构建体、或pTRV2空载体对照的根瘤土壤杆菌浸润的单独的植物中提取。PCR引物(TRV2-MCS)被设计成退火至侧接pTRV2的多克隆位点(MCS)的区域。(图C)与对照(pTRV2)相比，在REPI-沉默(pTRV2-REPI-a；pRTV2-REPI-5')或COR1.3-沉默(pRTV2-COR1.3)植物茎和根中的相对REPI或COR1.3转录物水平。(图D)与对照(pTRV2)相比，示出REPI-沉默(pTRV2-REPI-a;pRTV2-REPI-5')或COR1.3-沉默(pRTV2-COR1.3)植物的主要生物碱分布的总离子色谱图。(图E)与对照(pTRV2)相比，示出REPI-沉默(pTRV2-REPI-a;pRTV2-REPI-5')植物或COR1.3-沉默(pRTV2-COR1.3)植物中的抑制水平的主要乳胶生物碱和其他生物碱的相对丰度。(图F)与对照(pTRV2)相比，REPI-沉默(pTRV2-REPI-a;pRTV2-REPI-5')植物或COR1.3-沉默(pRTV2-COR1.3)植物中的(S)-网状番荔枝碱与(R)-网状番荔枝碱的比率。星号指示使用一种不成对、双尾学生t检验确定的显著性差异($p<0.05$)。棒表示由6个单独浸润植物中的每个的3个技术重复获得的值的平均值±标准偏差。

[0038] 图8描绘如在实例6中进一步所述的在评估AKR多肽在还原剂和氧化剂存在下的活性时所获得的结果。图8A示出罂粟网状番荔枝碱表异构酶(REPI)的1,2-脱氢网状番荔枝碱还原酶(PsDRR)组分的活性。在NADH或NADPH的存在下，PsDRR将1,2-脱氢网状番荔枝碱[1]转化成(R)-网状番荔枝碱[2](图8A，图A)。在NAD^+或$NADP^+$的存在下，PsDRR将(R)-网状番荔枝碱[2]转化成1,2-脱氢网状番荔枝碱[1](图8A，图B)。图8B示出来自虞美人的1,2-脱氢网状番荔枝碱还原酶(PrDRR)的活性。在NADH或NADPH的存在下，PrDRR将1,2-脱氢网状番荔枝碱[1]转化成(R)-网状番荔枝碱[2](图8B，图A)。在NAD^+或$NADP^+$的存在下，PrDRR将(R)-网状番荔枝碱[2]转化成1,2-脱氢网状番荔枝碱[1](图8B，图B)。

[0039] 图9描绘如在实例7中进一步所述的在评估CYP450和AKR多肽的pH依赖性时所获得的结果。示出使用罂粟CYP450(PsDRS)和AKR在NADPH(PsDRS正向)存在下并且在$NADP^+$(PsDRS反向)存在下所获得的结果(图A)。进一步示出使用虞美人CYP450(PrDRS)和AKR在NADPH(PrDRS正向)存在下并且在$NADP^+$(PrDRS反向)存在下所获得的结果(图B)。

[0040] 图10描绘如在实例8中进一步所述的在经受病毒诱导性基因沉默(VIGS)的罂粟植物中的REPI和COR转录物水平的共抑制。其中COR的沉默被靶向的植物(pTRV2-COR1.3)示出COR的显著抑制(图10-底图)，并且另外地示出REPI的抑制(图10-顶图)。其中使用在REPI和COR两者中发现的保守区靶向的REPI的沉默的植物(pTRV2-REPIa)也示出COR的显著抑制(图10-底图)和REPI的显著抑制(图10-顶图)。其中使用REPI的独特区域(一个并未也在COR中发现的区域)靶向REPI的沉默的植物(pTRV2-REPIb)未示出COR的共沉默(图10-底图)。pTRV2是空载体对照。星号指示使用一种不成对、双尾学生t检验相比于对照显著不同的值($P<0.05$)。误差棒表示平均值±标准偏差。

披露详细说明

[0041] 将在以下描述不同的组合物和方法以提供每个要求保护的主题的实施例的实例。以下描述的实施例不限制任何要求保护的主题，并且任何要求保护的主题可以涵盖不同于以下描述的那些方法、过程、组合物或系统。该要求保护的主题不限于具有以下描述的任何一种组合物、方法、系统或过程的所有特征的组合物或方法，或不限于为以下描述的组合物、系统或方法中的多个或全部所共有的特征。以下描述的一种组合物、系统、方法或过程

不是任何要求保护的主题的一个实施例是可能的。在以下描述的一种组合物、系统、方法或过程中披露的、在本文件中未要求保护的任何主题可以是另一种保护工具(例如,一个继续专利申请)的主题,并且申请人、发明人或所有人不打算在本文件中通过其披露向公众放弃、否认或贡献任何这样的主题。

[0042] 应该注意,如在此使用的诸如“基本上”、“实质上”、“约”以及“大约”的程度术语意味着所修饰术语的合理偏差量,使得最终结果没有显著改变。如果此偏差不会否定它所修饰的术语的含义,那么这些程度术语应该被解释为包括所修饰术语的偏差。

[0043] 如在此所使用的,词语“和/或”旨在表示包含性的或者。也就是说,例如“X和/或Y”意思是指X或Y或两者。作为一个另外的实例,“X、Y、和/或Z”意思是指X或Y或Z或其任何组合。

[0044] 所有出版物、专利和专利申请以如同每个单独的公开的相同程度通过引用以其全文结合在此。

[0045] 如上文所提到的,本披露涉及次级代谢物(R)-网状番荔枝碱及其前体,以及涉及制备(R)-网状番荔枝碱及其前体的方法。当前披露进一步涉及能够催化导致转化(S)-网状番荔枝碱以形成(R)-网状番荔枝碱的反应的某些酶。在此提供的方法表示一种制造(R)-网状番荔枝碱及其前体的新颖和有效手段。在此提供的方法不依赖于化学合成并且可以在商业规模下进行。就本发明人所知的,当前披露首次提供一种使用通常不能合成(R)-网状番荔枝碱及其前体的活细胞来制造(R)-网状番荔枝碱及其前体的方法。此类细胞可被用作一种由此可经济地提取(R)-网状番荔枝碱及其前体的来源。根据本披露产生的(R)-网状番荔枝碱及其前体是有用的,尤其是在包含吗啡和可待因的药物组合物的制造中。

[0046] 因此,本披露在至少一个方面中提供一种制备(R)-网状番荔枝碱或其前体的方法的至少一个实施例,该方法包括:

(a)提供一种苄基异喹啉衍生物;

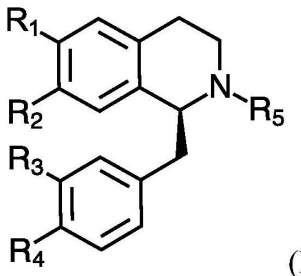
(b)使该苄基异喹啉衍生物与一种酶混合物接触,该酶混合物能够在允许将该苄基异喹啉衍生物转化成(R)-网状番荔枝碱或(R)-网状番荔枝碱前体的条件下将该苄基异喹啉衍生物转化成(R)-网状番荔枝碱或(R)-网状番荔枝碱前体。

[0047] 本披露进一步在至少一个方面中提供一种制备(R)-网状番荔枝碱或(R)-网状番荔枝碱前体的方法的至少一个实施例,该方法包括:

(a)提供一种苄基异喹啉衍生物;

(b)使该苄基异喹啉衍生物与一种酶混合物接触,该酶混合物能够在允许将该苄基异喹啉衍生物转化成(R)-网状番荔枝碱或(R)-网状番荔枝碱前体的条件下将该苄基异喹啉衍生物转化成(R)-网状番荔枝碱或(R)-网状番荔枝碱前体;

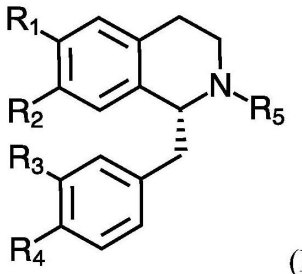
其中该苄基异喹啉衍生物具有化学式(I):



(I)

其中R_1、R_2、R_3以及R_4各自表示氢原子、羟基基团或甲氧基基团；并且其中R_5表示氢原子或甲基基团；并且

其中该(R)-网状番荔枝碱前体具有化学式：

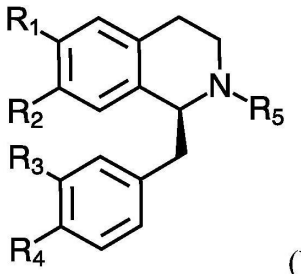


(II)

其中R_1、R_2、R_3以及R_4各自表示氢原子、羟基基团或甲氧基基团；并且其中R_5表示氢原子或甲基基团。

定义

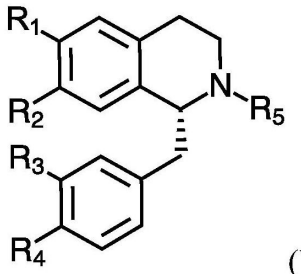
[0048] 如在此使用的术语“苄基异喹啉衍生物”是指具有化学式(VII)的化合物：



(VII)

其中R_1、R_2、R_3以及R_4各自独立地或同时地是氢原子、羟基基团、烷基基团(例如C_1-C_{10}-烷基)或烷氧基基团(例如C_1-C_{10}-烷氧基)，并且其中R_5表示氢原子或烷基基团(例如C_1-C_{10}-烷基)。

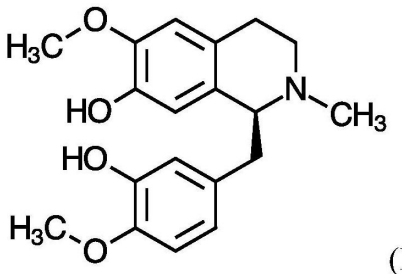
[0049] 如在此使用的术语“(R)-网状番荔枝碱前体”是指一种具有化学式(VIII)的化合物：



(VIII)

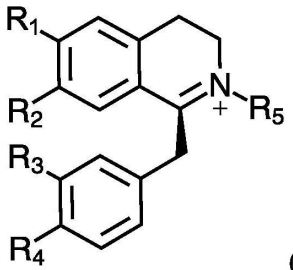
其中R_1、R_2、R_3以及R_4各自独立地或同时地是氢原子、羟基基团、烷基基团(例如C_1-C_{10}-烷基)或烷氧基基团(例如C_1-C_{10}-烷氧基)，并且其中R_5表示氢原子或烷基基团(例如C_1-C_{10}-烷基)，并且其中，在优选实施例中，R_5表示氢原子或烷基基团，其条件是化学式(VIII)将(R)-网状番荔枝碱除外，即确切地排除在如在此使用的术语(R)-网状番荔枝碱前体之外的是其中R_1是甲氧基基团；R_2是羟基基团，R_3是羟基基团，R_4是甲氧基基团并且R_5是甲基基团的化合物。

[0050] 如在此使用的术语“(S)-网状番荔枝碱”是指网状番荔枝碱的(S)-对映异构体和一种具有化学结构(III)的化合物：



(III)。

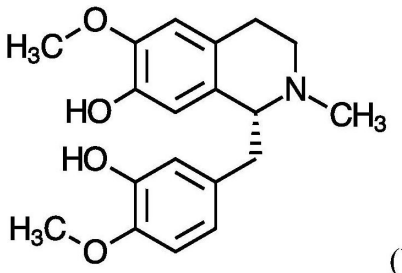
[0051] 术语“氧化苄基异喹啉衍生物”是指一种具有化学式(IX)的化合物：



(IX)

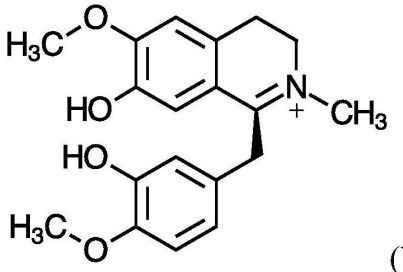
其中R_1、R_2、R_3以及R_4各自独立地或同时地是氢原子、羟基基团、烷基基团(例如C_1-C_{10}-烷基)或烷氧基基团(例如C_1-C_{10}-烷氧基)，并且其中R_5表示氢原子或烷基基团(例如C_1-C_{10}-烷基)。

[0052] 如在此使用的术语“(R)-网状番荔枝碱”是指网状番荔枝碱的(R)-对映异构体和一种具有化学结构(V)的化合物：



(V)。

[0053] 如在此使用的术语“1,2-脱氢网状番荔枝碱”是指一种具有化学式(VI)的化合物：



(VI)

[0054] 如在此可互换使用的术语“(R)-网状番荔枝碱途径”或“(R)-网状番荔枝碱合成途径”是指在图1中所描绘的用于合成(R)-网状番荔枝碱的代谢途径。当(R)-网状番荔枝碱途径中的第一化合物被表示为该途径中的第二化合物的“”时，其在此意味着该第一化合物的合成先于该第二化合物的合成。相反地，当第一化合物被表示为该(R)-网状番荔枝碱途径中的第二化合物的“下游”时，其在此意味着该第二化合物的合成先于该第一化合物的合成。

[0055] 如在此使用的术语“酶混合物”是指一种包含一种或两种或更多种酶的混合物。应

该注意，在含有两种或更多种酶的混合物中，这些酶可能是独立地生物活性的，不具有相互作用或协调以形成混合物。在一个实施例中，包含在该酶混合物中的这些酶可以作为独立的非连续的多肽链缔合或相互作用。在另一个实施例中，该酶混合物可以被制备成一种两个多肽之间的融合多肽。

[0056] 在此可互换使用的术语“细胞色素P450”、“CYP450”或“P450”是指包含以下氨基酸残基序列的任何和所有的酶：(i)与构成在此列出的任何CYP450多肽的氨基酸序列基本上一致，包括例如，SEQ.ID NO:219至SEQ.ID NO:321；SEQ.ID NO:325；以及SEQ.ID NO:338，或(ii)由一种能够在至少适度严格的条件下杂交至编码在此列出的任何CYP450多肽的任何核酸序列的核酸序列编码，但对于使用同义密码子。

[0057] 在此可互换使用的术语“醛-酮还原酶”或“AKR”指的是包含以下氨基酸残基序列的任何和所有的酶：(i)与构成在此列出的任何AKR多肽的氨基酸序列基本上一致，包括例如，SEQ.ID NO:59至SEQ.ID NO:115；SEQ.ID NO:327；SEQ.ID NO:329；SEQ.ID NO:330；以及SEQ.ID NO:340，或(ii)由一种能够在至少适度严格的条件下杂交至编码在此列出的任何AKR多肽的任何核酸序列的核酸序列编码，但对于使用同义密码子。

[0058] 如在此使用的术语“核酸序列”是指一种由天然存在的碱基、糖和糖间(主链)键组成的核苷或核苷酸单体的序列。该术语还包括包含非天然存在的单体或其部分的修饰或取代序列。本披露的核酸序列可以是脱氧核糖核酸序列(DNA)或核糖核酸序列(RNA)并且可以包含包括腺嘌呤、鸟嘌呤、胞嘧啶、胸苷以及尿嘧啶的天然存在的碱基。这些序列还可以含有修饰碱基。此类修饰碱基的实例包括氮杂和脱氮的腺嘌呤、鸟嘌呤、胞嘧啶、胸苷和尿嘧啶、以及黄嘌呤和次黄嘌呤。

[0059] 在此可互换使用的术语“编码CYP450的核酸序列”和“编码CYP450多肽的核酸序列”是指编码CYP450多肽的任何和所有的核酸序列，包括例如，SEQ.ID NO:116至SEQ.ID NO:218；SEQ.ID NO:324；以及SEQ.ID NO:337。编码CYP450多肽的核酸序列进一步包括以下的任何和所有的核酸序列：(i)编码与在此列出的CYP450多肽序列基本上一致的多肽；或(ii)在至少适度严格的杂交条件下，杂交至在此列出的任何CYP450核酸序列，或将在至少适度严格的条件下杂交至其上的核酸序列，但对于使用同义密码子。

[0060] 在此可互换使用的术语“编码AKR的核酸序列”和“编码AKR多肽的核酸序列”是指编码AKR多肽的任何和所有的核酸序列，包括例如，SEQ.ID NO:1至SEQ.ID NO:58；SEQ.ID NO:326；SEQ.ID NO:328；以及SEQ.ID NO:339。编码AKR多肽的核酸序列进一步包括以下的任何和所有的核酸序列：(i)编码与在此列出的AKR多肽序列基本上一致的多肽；或(ii)在至少适度严格的杂交条件下，杂交至在此列出的任何AKR核酸序列，或将在至少适度严格的条件下杂交至其上的核酸序列，但对于使用同义密码子。

[0061] 通过术语“基本上一致”其意味着两种多肽序列优选地是至少70％一致，并且更优选地是至少85％一致，并且最优选地至少95％一致，例如96％、97％、98％或99％一致。为了确定两种多肽序列之间的一致性百分比，使用例如由史密斯(Smith)和沃特曼(Waterman)(应用数学进展(Adv.Appl.Math.)，1981，2:482)修订的尼德尔曼(Needleman)和温施(Wunsch)(分子生物学杂志(J.Mol.Biol.)，1970，48:443)比对方法将此类两种序列的氨基酸序列进行比对，从而获得这两种序列之间的最高级匹配并且确定这两种序列之间的一致氨基酸的数目。计算两种氨基酸序列之间的百分比一致性的方法通常是本领域认可的并且

包括，例如，由卡里略(Carillo)和李普顿(Lipton)(工业和应用数学学会杂志(SIAM J.Applied Math.)，1988，48:1073)描述的那些方法和在计算分子生物学(Computational Molecular Biology)，莱斯克(Lesk)编著，牛津大学出版社(Oxford University Press)，纽约，1988，生物计算：信息学和基因组学项目(Biocomputing:Informatics and Genomics Projects)中描述的那些方法。通常，计算机程序将被用于此类计算。在此方面可使用的计算机程序包括但不限于GCG(德弗罗(Devereux)等人，核酸研究(Nucleic Acids Res)，1984，12:387)BLASTP、BLASTN以及FASTA(阿特休尔(Altschul)等人，分子生物学杂志(J.Molec.Biol)，1990:215:403)。一种用于确定两种多肽之间的百分比一致性的特别优选方法涉及Clustal W算法(汤普森(Thompson)J D、希金斯(Higgines)D G和吉普森(Gibson)T J，1994，核算研究(Nucleic Acid Res)22(22):4673-4680)连同使用10空位开放罚分和0.1空位延伸罚分的BLOSUM 62评分矩阵(海尼科夫(Henikoff)S和海尼科夫J G，1992，美国国家科学院院刊(Proc.Natl.Acad.Sci.USA)89:10915-10919)，从而在两种序列之间获得最高级匹配，其中这两种序列中的一种的全长的至少50％涉及比对。

[0062] 通过“至少适度严格的杂交条件”其意味着选择促进在溶液中的两种互补核酸分子之间的选择性杂交的条件。杂交可发生于核酸序列分子的全部或一部分中。该杂交部分典型地是至少15(例如20、25、30、40或50)个核苷酸长度。本领域的技术人员将认识到核酸双链体或杂交体的稳定性是由Tm确定的，在含钠缓冲液中的该稳定性是钠离子浓度和温度的函数(Tm＝81.5℃-16.6(Log10[Na+])+0.41(％(G+C)-600/l)，或类似的方程)。因此，在洗涤条件中确定杂交体稳定性的参数是钠离子浓度和温度。为了鉴定与一种已知核酸分子类似但不一致的分子，1％的不匹配可被认为导致Tm下降约1℃，例如如果寻求具有>95％一致性的核酸分子，那么最终洗涤温度将下降约5℃。基于这些考虑，本领域的技术人员将能够容易地选择适当的杂交条件。在优选实施例中，选择严格杂交条件。通过实例，可采用以下条件以实现严格杂交：在-5℃的Tm(基于上述方程)下在5×氯化钠/柠檬酸钠(SSC)/5×邓哈特溶液/1.0％SDS下杂交，随后用60℃的0.2×SSC/0.1％SDS洗涤。适度严格的杂交条件包括一个在42℃下的3×SSC中的洗涤步骤。然而应该理解，可使用替代的缓冲液、盐和温度来实现等效严格性。关于杂交条件的附加指导可在以下找到：分子生物学实验指南(Current Protocols in Molecular Biology)，约翰威利(John Wiley)和圣思(Sons)，N.Y.，1989，6.3.1.-6.3.6和萨姆布鲁克(Sambrook)等人，分子克隆(Molecular Cloning)，实验手册(Laboratory Manual)，冷泉港实验室出版社(Cold Spring Harbor Laboratory Press)，1989，第3卷。

[0063] 如在此使用的术语“嵌合”在核酸序列的语境中是指并非天然连接的至少两个连接的核酸序列。嵌合核酸序列包括不同天然来源的连接的核酸序列。例如一种构成连接至编码COR蛋白的核酸序列上的酵母启动子的核酸序列被认为是嵌合的。嵌合核酸序列还可包含相同天然来源的核酸序列，条件是它们不是天然连接的。例如一种构成由特定细胞类型获得的启动子的核酸序列可以连接至一种编码由相同细胞类型获得的多肽的核酸序列上，但是通常不连接至构成该启动子的该核酸序列上。嵌合核酸序列还包括包含连接至任何非天然存在的核酸序列上的任何天然存在的核酸序列的核酸序列。

[0064] 如在此可互换使用的术语“基本上纯的”和“分离的”描述一种已经从与其天然共存的组分分离的化合物，例如，一种途径合成中间体或一种多肽。典型地，当一个样品中的

总材料的至少60％、更优选至少75％、更优选至少90％、95％、96％、97％、或98％、并且最优选至少99％(以体积、湿重或干重、或者摩尔百分比或摩尔分数计)是感兴趣的化合物时，该化合物是基本上纯的。可以通过任何适当的方法，例如在多肽的情况下，通过色谱法、凝胶电泳或HPLC分析来测量纯度。

[0065] 如在此使用的与一种酶或蛋白质相关联的术语“回收”是指该酶或蛋白质的或多或少纯的形式。

[0066] 如在此使用的、用于描述制备(R)-网状番荔枝碱或(R)-网状番荔枝碱前体的方法的术语“体内”是指在一个活细胞(包括例如，一个微生物细胞或一个植物细胞)内使一种苄基异喹啉衍生物与一种能够催化转化该苄基异喹啉衍生物的酶接触以形成(R)-网状番荔枝碱或(R)-网状番荔枝碱前体。

[0067] 如在此使用的、用于描述制备(R)-网状番荔枝碱或(R)-网状番荔枝碱前体的方法的术语“体外”是指在一个活细胞外部环境(包括但不限于，例如在微孔板、试管、烧瓶、烧杯、罐、反应器等)中使一种苄基异喹啉衍生物与一种能够催化转化该苄基异喹啉衍生物的酶接触以形成(R)-网状番荔枝碱或(R)-网状番荔枝碱前体。

一般实施方式

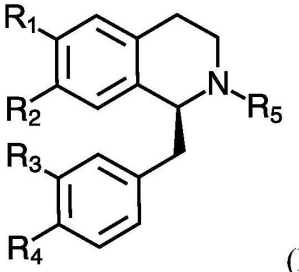
合成(R)-网状番荔枝碱和(R)-网状番荔枝碱前体

[0068] 本披露在至少一个方面中提供制备(R)-网状番荔枝碱或(R)-网状番荔枝碱前体的至少一个实施例，该至少一个实施例包括：

(a)提供一种苄基异喹啉衍生物；

(b)使该苄基异喹啉衍生物与一种酶混合物接触，该酶混合物能够在允许将该苄基异喹啉衍生物转化成(R)-网状番荔枝碱或(R)-网状番荔枝碱前体的条件下将该苄基异喹啉衍生物转化成(R)-网状番荔枝碱或(R)-网状番荔枝碱前体；

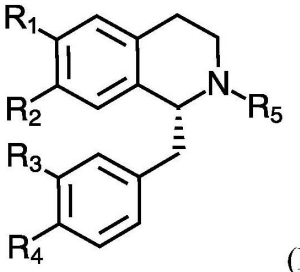
其中该苄基异喹啉衍生物具有化学式(I)：



(I)

其中R_1、R_2、R_3以及R_4各自表示氢原子、羟基基团或甲氧基基团；并且其中R_5表示氢原子或甲基基团；并且

其中该(R)-网状番荔枝碱前体具有化学式(II)：



(II)

其中R_1、R_2、R_3以及R_4各自表示氢原子、羟基基团或甲氧基基团；

并且其中R_5表示氢原子或甲基基团，其条件是化学式(II)将(R)-网状番荔枝碱除外。

[0069] 在一个优选实施例中，该苄基异喹啉衍生物(I)是一种其中R_1是甲氧基基团、R_2是羟基基团、R_3是氢原子或羟基基团、R_4是羟基基团或甲氧基基团、并且R_5是氢原子或甲基基团的衍生物。

[0070] 在一个另外的优选实施例中，该苄基异喹啉衍生物(I)是一种其中R_1是甲氧基基团、R_2是羟基基团、R_3是氢原子、R_4是羟基基团并且R_5是氢原子的衍生物。此化合物又称为(S)-乌药碱(参见：图1)。

[0071] 在一个另外的优选实施例中，该苄基异喹啉衍生物(I)是一种其中R_1是甲氧基基团、R_2是羟基基团、R_3是氢原子、R_4是羟基基团并且R_5是甲基基团的衍生物。此化合物又称为(S)-N-甲基-乌药碱(参见：图1)。

[0072] 在一个另外的优选实施例中，该苄基异喹啉衍生物(I)是一种其中R_1是甲氧基基团、R_2是羟基基团、R_3是羟基基团、R_4是羟基基团并且R_5是甲基基团的衍生物。此化合物又称为(S)-3'-羟基-N-甲基乌药碱(参见：图1)。

[0073] 在一个另外的优选实施例中，该苄基异喹啉衍生物(I)是一种其中R_1是甲氧基基团、R_2是羟基基团、R_3是羟基基团、R_4是甲氧基基团并且R_5是甲基基团的衍生物。此化合物又称为(S)-网状番荔枝碱(参见：图1；化合物(III))。

[0074] 在一个另外的优选实施例中，该(R)-网状番荔枝碱衍生物(II)是一种其中R_1是甲氧基基团、R_2是羟基基团、R_3是氢原子或羟基基团、R_4是羟基基团并且R_5是甲基基团的衍生物。

[0075] 在一个另外的优选实施例中，该(R)-网状番荔枝碱衍生物(II)是一种其中R_1是甲氧基基团、R_2是羟基基团、R_3是氢原子、R_4是羟基基团并且R_5是甲基基团的衍生物。此化合物又称为(R)-N-甲基乌药碱(参见：图1)。

[0076] 在一个另外的优选实施例中，该(R)-网状番荔枝碱衍生物(II)是一种其中R_1是甲氧基基团、R_2是羟基基团、R_3是羟基基团、R_4是羟基基团并且R_5是甲基基团的衍生物。此化合物又称为(R)-3'-羟基-N-甲基乌药碱(参见：图1)。

[0077] 在一个另外的优选实施例中，该苄基异喹啉衍生物(I)是一种其中R_1是甲氧基基团、R_2是羟基基团、R_3是氢原子、R_4是羟基基团并且R_5是甲基基团的衍生物；并且该(R)-网状番荔枝碱衍生物(II)是一种其中R_1是甲氧基基团、R_2是羟基基团、R_3是氢原子、R_4是羟基基团并且R_5是甲基基团的衍生物。

[0078] 在一个另外的优选实施例中，该苄基异喹啉衍生物(I)是一种其中R_1是甲氧基基团、R_2是羟基基团、R_3是羟基基团、R_4是羟基基团并且R_5是甲基基团的衍生物；并且(R)-网状番荔枝碱衍生物(II)是一种其中R_1是甲氧基基团、R_2是羟基基团、R_3是羟基基团、R_4是羟基基团并且R_5是甲基基团的衍生物。

[0079] 在本披露的一个优选实施例中，提供一种制备(R)-网状番荔枝碱的方法，该方法包括：

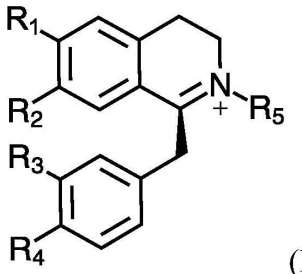
(a)提供(S)-网状番荔枝碱；并且

(b)使(S)-网状番荔枝碱与一种酶混合物接触，该酶混合物能够在允许将(S)-网状番荔枝碱转化成(R)-网状番荔枝碱的条件下将(S)-网状番荔枝碱转化成(R)-网状番荔

枝碱。

[0080] 在优选实施例中，该酶混合物包含一种能够将(S)-网状番荔枝碱氧化以形成1,2-脱氢网状番荔枝碱的第一多肽和一种能够将1,2-脱氢网状番荔枝碱还原以形成(R)-网状番荔枝碱的第二多肽(参见:图2)。

[0081] 在优选实施例中，该酶混合物包含一种第一多肽，该第一多肽能够将该苄基异喹啉衍生物(I)氧化以形成一种具有化学式(IV)的氧化苄基异喹啉衍生物：



(IV)

其中，在优选实施例中，R_1、R_2、R_3以及R_4各自表示氢原子、羟基基团或甲氧基基团；并且其中，在优选实施例中，R_5表示氢原子或甲基基团；以及一种第二多肽，该第二多肽能够将具有化学式(IV)的该氧化苄基异喹啉衍生物还原以形成具有化学式(II)的(R)-网状番荔枝碱或(R)-网状番荔枝碱衍生物，其中R_1、R_2、R_3以及R_4各自表示氢原子、羟基基团或甲氧基基团；并且其中R_5表示氢原子或甲基基团，其条件是化学式(II)将(R)-网状番荔枝碱除外。

[0082] 在优选实施例中，能够将该苄基异喹啉衍生物(I)氧化以形成该氧化苄基异喹啉衍生物(IV)的该第一多肽是一种细胞色素P450，并且能够将氧化苄基异喹啉衍生物还原以形成(R)-网状番荔枝碱或(R)-网状番荔枝碱衍生物的该第二多肽是一种醛-酮还原酶(AKR)。在特别优选的实施例中，该AKR多肽获得自或可获得自罂粟、大红罂粟以及虞美人。

[0083] 在某些实施例中，该第一多肽和该第二多肽以两个分离的多肽(即，不通过共价化学键连接的多肽)的形式被提供。在某些优选实施例中，该第一多肽和该第二多肽被制备成一种包含编码CYP450多肽的第一部分和编码AKR多肽的第二部分的融合多肽。这种融合多肽可被重组制备或者它可以是一种可以使用的天然存在的融合多肽，诸如在SEQ.ID NO:323中列出的罂粟多肽。

[0084] 根据本披露可使用的CYP450多肽的实例包括在SEQ.ID NO:219至SEQ.ID NO:321；SEQ.ID NO:325；和SEQ.ID NO:338中列出的多肽。根据本披露可使用的AKR多肽的实例包括在SEQ.ID NO:59至SEQ.ID NO:115；SEQ.ID NO:327；SEQ.ID NO:329；SEQ.ID NO:330以及SEQ.ID NO:340中列出的多肽。

[0085] 使前述反应在允许将该苄基异喹啉前体转化成(R)-网状番荔枝碱或(R)-网状番荔枝碱前体的条件下进行。这些条件包括体内或体外条件，如以下进一步详述。这些条件进一步典型地包括水和缓冲剂的存在。进一步典型地包括一种还原剂以便允许进行一种导致将该氧化苄基异喹啉前体转化成(R)-网状番荔枝碱或转化成(R)-网状番荔枝碱前体的还原反应。该还原剂可以是烟酰胺腺嘌呤二核苷酸(NADH)，并且在其他实施例中，该还原剂是烟酰胺腺嘌呤二核苷酸磷酸(NADPH)。进一步典型地包括在该反应中的是一种还原酶和一种还原剂，该还原酶能够还原将该苄基异喹啉衍生物转化成该氧化苄基异喹啉的酶。在优选实施例中，该还原酶是一种能够还原CYP450的细胞色素P450还原酶(诸如例如罂粟细胞

色素P450还原酶)，并且该还原剂是NADH、或者更优选是NADPH。应该进一步注意，这些反应可以在不同的pH(例如在大约pH 3、pH 4、pH 5、pH 6、pH 7、pH 8、pH 9或pH 10)下进行。本领域技术人员应该清楚，可如在此实例7中所示的通过在不同pH范围下进行一个反应并且评估该反应速率来鉴定用于该反应的最佳pH。该最佳pH可取决于例如据此选择的底物和酶而变化。因此，仅通过实例，实例7记录了用于将(S)-网状番荔枝碱转化成1,2-脱氢网状番荔枝碱的大约pH 8的最佳pH，用于将1,2-脱氢网状番荔枝碱转化成(R)-网状番荔枝碱的大约pH 7的最佳pH，以及用于将(R)-网状番荔枝碱转化成1,2-脱氢网状番荔枝碱的大约pH9的最佳pH。

[0086] 据此应该指出，取决于所选择的反应条件，涉及将1,2-脱氢网状番荔枝碱转化成(R)-网状番荔枝碱的反应可以反向或部分反向实现。因此，如实例6中所记录，(R)-网状番荔枝碱可被转化成1,2-脱氢网状番荔枝碱。因此，本披露进一步提供一种制备1,2-脱氢网状番荔枝碱的方法，该方法包括：

(a)提供(R)-网状番荔枝碱；并且

(b)使(R)-网状番荔枝碱与一种AKR多肽接触，该AKR多肽能够在允许将(R)-网状番荔枝碱转化成1,2-脱氢网状番荔枝碱的条件下将(R)-网状番荔枝碱转化成1,2-脱氢网状番荔枝碱。可用于进行前述反应的AKR多肽包括在SEQ.ID NO:59至SEQ.ID NO:115；SEQ.ID NO:327；SEQ.ID NO:329；SEQ.ID NO:330以及SEQ.ID NO:340中列出的任何多肽。允许该转化的反应条件包括在反应混合物中存在一种氧化剂，优选NAD^+或$NADP^+$。如以上所指出，用于该反应的pH可以被优化。进一步在图2中示出前述反应的可逆性。

[0087] 在优选实施例中，能够将该苄基异喹啉衍生物氧化以形成该氧化苄基异喹啉衍生物的该第一多肽是一种细胞色素P450，并且能够将该氧化苄基异喹啉衍生物还原以形成(R)-网状番荔枝碱或(R)-网状番荔枝碱衍生物的该第二多肽是一种醛-酮还原酶(AKR)。在特别优选的实施例中，该AKR获得自或可获得自罂粟、大红罂粟以及虞美人。

[0088] 在某些实施例中，该第一多肽和该第二多肽以两个分离的多肽(即，不通过共价化学键连接的多肽)的形式被提供。在某些优选实施例中，该第一多肽和该第二多肽被制备成一种包含编码CYP450多肽的第一部分和编码AKR多肽的第二部分的融合多肽。这种融合多肽可被重组制备或者它可以是一种可以使用的天然存在的融合多肽，诸如在SEQ.ID NO:323中列出的罂粟多肽。

[0089] 根据本披露可使用的CYP450多肽的实例包括可获得自不同的罂粟物种的CYP450多肽，包括：罂粟、虞美人和大红罂粟；蓟罂粟物种，包括蓟罂粟(Argemone mexicana)；小檗属物种，包括小檗黑松(Berberis thunbergii)；紫堇属物种，包括地柏枝(Corydalis chelantifolia)；白屈菜属物种，包括白屈菜(Chelidonium majus)；锡生藤属物种，包括棘状锡生藤(Cissampelos mucronata)；木防己属物种，包括木防己(Cocculus trilobus)；紫堇属物种，包括地柏枝(Corydalis chelantifolia)；海罂粟属物种，包括黄花海罂粟(Glaucium flavum)；北美黄连属物种，包括加拿大黄连(Hydrastis canadensis)；鲜黄莲属物种，包括二叶鲜黄莲(Jeffersonia diphylla)；十大功劳属物种，包括冬青叶十大功劳(Mahonia aquifolium)；蝙蝠葛属物种，包括蝙蝠葛(Menispermum canadense)；南天竹属物种，包括南天竹(Nandina domestica)；黑种草属物种，包括黑种草(Nigella sativa)；血根属物种，包括血根草(Sanguinaria canadensis)；金罂粟属物种，包括金罂粟

(Stylophorum diphyllum)；唐松草属物种，包括黄唐松草(Thalictrum flavum)；青牛胆属物种，包括心叶青牛胆(Tinospora cordifolia)；以及姜黄物种，包括黄根草(Xanthoriza simplicissima)。前述内容特定地包括来自在此于SEQ.ID NO:219至SEQ.ID NO:321；SEQ.ID NO:325；和SEQ.ID NO:338中列出的上述物种的多肽。根据本披露可使用的AKR多肽的实例包括可获得自不同的罂粟物种的AKR多肽，包括：罂粟、虞美人和大红罂粟；蓟罂粟物种，包括蓟罂粟；小檗属物种，包括小檗黑松；紫堇属物种，包括地柏枝；白屈菜物种，包括白屈菜；锡生藤属物种，包括棘状锡生藤；木防己属物种，包括木防己；紫堇属物种，包括地柏枝；海罂粟属物种，包括黄花海罂粟；北美黄连属物种，包括加拿大黄连；鲜黄莲属物种，包括二叶鲜黄莲；十大功劳属物种，包括冬青叶十大功劳；蝙蝠葛属物种，包括蝙蝠葛；南天竹属物种，包括南天竹；黑种草属物种，包括黑种草；血根属物种，包括血根草；金罂粟属物种、金罂粟；唐松草属物种，包括黄唐松草；青牛胆属物种，包括心叶青牛胆；以及姜黄物种，包括黄根草。前述内容特定地包括来自在此于SEQ.ID NO:59至SEQ.ID NO:115；SEQ.ID NO:327；SEQ.ID NO:329；SEQ.ID NO:330；以及SEQ.ID NO:340中列出的上述物种的多肽。

[0090] 将前述反应在允许将该苄基异喹啉前体转化成(R)-网状番荔枝碱或(R)-网状番荔枝碱前体的条件下进行。这些条件包括体内或体外条件，如以下进一步详述。这些条件进一步典型地包括水和缓冲剂的存在。进一步典型地包括一种还原剂以便允许进行一种导致将该氧化苄基异喹啉前体转化成(R)-网状番荔枝碱或转化成(R)-网状番荔枝碱前体的还原反应。该还原剂可以是烟酰胺腺嘌呤二核苷酸(NADH)，并且在其他实施例中，该还原剂是烟酰胺腺嘌呤二核苷酸磷酸(NADPH)。进一步典型地包括在该反应中的是一种还原酶和一种还原剂，该还原酶能够还原将该苄基异喹啉衍生物转化成该氧化苄基异喹啉的酶。在优选实施例中，该还原酶是一种能够还原CYP450的细胞色素P450还原酶，并且该还原剂是NADH、或者更优选是NADPH。

体外合成(R)-网状番荔枝碱或(R)-网状番荔枝碱衍生物

[0091] 根据本披露的某些方面，在体外反应条件下在允许一种酶催化的化学转化一种苄基异喹啉衍生物的反应条件下，使该苄基异喹啉衍生物与催化量的酶CYP450和AKR接触。在此类体外反应条件下，以或多或少纯的形式提供初始反应成分并且在允许必要的化学反应充分进行的条件下混合。可购买基本上纯的形式的初始苄基异喹啉衍生物。(S)-网状番荔枝碱，例如，可作为一种基本上纯的化合物被购买(例如购自圣克鲁斯生物技术公司(Santa Cruz Biotechnology Inc.))、由前体化合物化学合成、或从天然来源分离，这些天然来源包括罂粟和包含如所希望的此类化合物的植物的罂粟科、樟科、番荔枝科、大戟科或桑科家族的其他成员。适合的罂粟科成员包括，但不限于属于罂粟属；紫堇属；白屈菜属；以及卢默龙属的物种。此类物种可以能够制备(S)-网状番荔枝碱，包括但不限于选自以下物种的植物物种：白屈菜属；延胡索；延胡索静脉；黄紫堇；蛇果黄堇；异果黄堇；块茎紫堇；安纳托利亚罂粟；大红罂粟；柱形罂粟；德凯纳罂粟；杏黄罂粟；鬼罂粟；东方罂粟；罂粟花；波斯罂粟；伪东方罂粟；虞美人；维也纳罂粟；渥美罂粟；罂粟；tauricolum罂粟；三叶罂粟；以及卢默龙属番木瓜。可使用如例如在S.泰特尔(Teitel)和A.布罗斯(Bross)，杂环化学杂志(Journal of Heterocyclic Chemistry)5,825-829,1968中描述的标准方法进行(S)-网状番荔枝碱的化学合成。

[0092] 据此，或多或少纯的形式的酶可从包括但不限于罂粟、大红罂粟以及虞美人的天

然来源分离，或者它们可以重组制备或合成。因此，在此进一步提供一种用于制备选自由CYP450和AKR或其混合物组成的组的酶的方法，该方法包括：

(a)提供一种嵌合核酸序列，该嵌合核酸序列包含作为可操作地连接部件的以下各项：

(i)编码选自由CYP450和AKR组成的组的一种或多种多肽的一种或两种核酸序列；以及

(ii)能够控制在宿主细胞中的表达的一种或多种核酸序列；

(b)将该嵌合核酸序列引入一个宿主细胞中并且使该宿主细胞生长以产生选自由CYP450和AKR组成的组的该多肽；并且

(c)从该宿主细胞中回收选自由CYP450和AKR组成的组的多肽。

[0093] 该核酸序列可由含有此类序列的任何天然来源(例如，一个植物来源)获得。优选的植物来源包括罂粟物种，包括罂粟、虞美人和大红罂粟；蓟罂粟物种，包括蓟罂粟；小檗属物种，包括小檗黑松；紫堇属物种，包括地柏枝；白屈菜属物种，包括白屈菜；锡生藤属物种，包括棘状锡生藤；木防己属物种，包括木防己；紫堇属物种，包括地柏枝；海罂粟属物种，包括黄花海罂粟；北美黄连属物种，包括加拿大黄连；鲜黄莲属物种，包括二叶鲜黄莲；十大功劳属物种，包括冬青叶十大功劳；蝙蝠葛属物种，包括蝙蝠葛；南天竹属物种，包括南天竹；黑种草属物种，包括黑种草；血根属物种，包括血根草；金罂粟属物种、金罂粟；唐松草属物种，包括黄唐松草；青牛胆属物种，包括心叶青牛胆；以及姜黄物种，包括黄根草。关于CYP450，可获得自或获得自前述植物物种的核酸序列包括在SEQ.ID NO:116至SEQ.ID NO:218；SEQ.ID NO:324；以及SEQ.ID NO:337中列出的核酸序列。关于AKR，可获得自或获得自前述植物物种的核酸序列包括在此处列出为SEQ.ID NO:1至SEQ.ID NO:58；SEQ.ID NO:326；SEQ.ID NO:328；以及SEQ.ID NO:339的核酸序列。在另外的优选实施例中，可使用一种编码所阐述的CYP450与AKR之间的天然融合多肽的核酸序列，包括在此于SEQ.ID NO:322中列出的核酸序列。

[0094] 宿主细胞的生长导致CYP450和/或AKR多肽的产生。随后可通过各种不同的蛋白质纯化技术将这些多肽从其他宿主细胞组分中回收、离析和分离，这些蛋白质纯化技术包括例如离子交换色谱法、尺寸排阻色谱法、亲和色谱法、疏水相互作用色谱法、反相色谱法、凝胶过滤等。关于蛋白质纯化的另外的一般指导可例如在卡特勒(Cutler)P.蛋白质纯化操作(Protein Purification Protocols)，Humana Press出版社，2004，第二版中找到。因此可获得基本上纯的CYP450和/或AKR多肽的制剂。

[0095] 据此，在允许一种酶催化的化学转化一种苄基异喹啉衍生物的反应条件下，使该苄基异喹啉衍生物与催化量的酶CYP450和AKR中的一种或多种接触。在优选实施例中，使这些试剂彼此接触并且混合以形成一种混合物。在优选实施例中，该混合物是一种包含水和用于促进酶催化的另外任选的额外试剂(包括缓冲剂、盐、pH改性剂)的水性混合物。如上文所述，特别优选的是，该反应混合物包含NADPH和一种还原酶。可以在不同温度范围下进行该反应。在优选实施例中，在约18℃与约37℃之间的温度下进行该反应。在完成体外反应后，可获得以或多或少纯的形式的(R)-网状番荔枝碱或(R)-网状番荔枝碱前体。

体内合成(R)-网状番荔枝碱或(R)-网状番荔枝碱前体

[0096] 根据本披露的某些方面，在体内反应条件下在允许一种酶催化的化学转化一种苄

基异喹啉衍生物的反应条件下，使该苄基异喹啉衍生物与催化量的酶CYP450和AKR中的一种或多种接触。在此类体内反应条件下，以使得活细胞产生(R)-网状番荔枝碱或(R)-网状番荔枝碱前体的方式来修饰它们。在某些实施例中，这些活细胞是微生物，包括细菌细胞和真菌细胞。在其他实施例中，这些活细胞是多细胞生物，包括植物和植物细胞培养物。

[0097] 在一个实施例中，这些活细胞被选择为不能天然产生一种苄基异喹啉衍生物((S)-网状番荔枝碱)、(R)-网状番荔枝碱前体或(R)-网状番荔枝碱的宿主细胞。在另一个实施例中，这些宿主细胞能够天然产生(S)-网状番荔枝碱或苄基异喹啉衍生物但不能产生(R)-网状番荔枝碱或(R)-网状番荔枝碱前体，即，这些细胞不能天然从(S)-对映异构体进行差向异构化反应至(R)-对映异构体。在另一个实施例中，这些细胞能够产生一种苄基异喹啉衍生物或(S)-网状番荔枝碱和(R)-网状番荔枝碱或(R)-网状番荔枝碱前体，但(R)-网状番荔枝碱或(R)-网状番荔枝碱前体的水平低于所希望的水平，并且相对于未修饰细胞中的水平调节(R)-网状番荔枝碱或(R)-网状番荔枝碱前体的水平。此类细胞包括但不限于：细菌、酵母、其他真菌细胞、植物细胞、或动物细胞。

[0098] 为了产生(R)-网状番荔枝碱或(R)-网状番荔枝碱前体，在此进一步提供一种用于制备(R)-网状番荔枝碱或(R)-网状番荔枝碱前体的方法，该方法包括：

(a)提供一种嵌合核酸序列，该嵌合核酸序列包含作为可操作地连接部件的以下各项：

(i)一种编码CYP450多肽的第一核酸序列；

(ii)一种编码AKR多肽的第二核酸序列；以及

(iii)能够控制在宿主细胞中的表达的一种或多种核酸序列；

(b)将该嵌合核酸序列引入一个宿主细胞中并且使该宿主细胞生长以产生CYP450和AKR，并且产生(R)-网状番荔枝碱或(R)-网状番荔枝碱前体；并且

(c)回收(R)-网状番荔枝碱或(R)-网状番荔枝碱前体。

[0099] 在优选实施例中，该第一核酸序列和该第二核酸序列被可操作地连接以便产生一种包含CYP450和AKR的融合多肽。

[0100] 进一步提供一种用于制备(R)-网状番荔枝碱或(R)-网状番荔枝碱前体的方法，该方法包括：

(b)提供一种第一嵌合核酸序列，该第一嵌合核酸序列包含作为可操作地连接部件的一种编码CYP450多肽的第一核酸序列和一种控制该第一核酸序列在细胞中的表达的第一核酸序列；

(c)提供一种第二嵌合核酸序列，该第二嵌合核酸序列包含作为可操作地连接部件的一种编码AKR多肽的第二核酸序列和一种控制该第二核酸序列在细胞中的表达的第二核酸序列；

(c)将该第一嵌合核酸序列和该第二嵌合核酸序列引入一个宿主细胞中并且使该宿主细胞生长以产生CYP450和AKR，并且产生(R)-网状番荔枝碱或(R)-网状番荔枝碱前体；并且

(d)回收(R)-网状番荔枝碱或(R)-网状番荔枝碱前体。

[0101] 在优选实施例中，编码CYP450和AKR的核酸序列选自可获得自或获得自罂粟和包含如所希望的此类化合物的植物的罂粟科、樟科、番荔枝科、大戟科或桑科家族的其他成员

的编码CYP450和AKR的核酸序列。适合的罂粟科成员包括，但不限于属于罂粟属；紫堇属；白屈菜属；以及卢默龙属的物种。此类物种可以能够制备(R)-网状番荔枝碱，包括但不限于选自以下物种的植物物种：白屈菜属；延胡索；延胡索静脉；黄紫堇；蛇果黄堇；异果黄堇；块茎紫堇；安纳托利亚罂粟；大红罂粟；柱形罂粟；德凯纳罂粟；杏黄罂粟；鬼罂粟；东方罂粟；罂粟花；波斯罂粟；伪东方罂粟；虞美人；维也纳罂粟；渥美罂粟；罂粟；tauricolum罂粟；三叶罂粟；以及卢默龙属番木瓜。在特别优选的实施例中，编码CYP450和AKR的核酸序列是选自可获得自或获得自罂粟、大红罂粟以及虞美人的编码CYP450和AKR的核酸序列的核酸序列。在另外的优选实施例中，编码CYP450的核酸序列中的一种在此被列出为SEQ.ID NO:116至SEQ.ID NO:218；SEQ.ID NO:324；和SEQ.ID NO:337。在优选实施例中，编码AKR的核酸序列是在此被列出为SEQ.ID NO:1至SEQ.ID NO:58；SEQ.ID NO:326；SEQ.ID NO:328以及SEQ.ID NO:339的编码AKR的核酸序列中的一种。在另外的特别优选的实施例中，编码CYP450和AKR的核酸序列是能够产生一种CYP450-AKR融合多肽的核酸序列，包括但不限于在SEQ.ID NO:322中列出的序列。

[0102] 据此，编码CYP450和AKR的核酸序列被连接至一种能够控制CYP450和AKR在宿主细胞中的表达的核酸序列上。因此，本披露还提供一种连接至能够控制在宿主细胞中的表达的启动子上的编码CYP450和AKR的核酸序列。可在此使用的能够控制在宿主细胞中的表达的核酸序列包括能够控制多肽在宿主细胞中的表达的任何转录启动子。通常，当据此选择一种细菌宿主时，使用由细菌细胞获得的启动子，而当选择一种真菌宿主时，将使用一种真菌启动子，当选择一种植物细胞时，将使用一种植物启动子等等。能够控制在宿主细胞中的表达的另外的核酸元件包括转录终止子、增强子等，所有这些核酸元件可包括在本披露的嵌合核酸序列中。本领域技术人员应该理解的是，核酸序列的可操作连接包括在转录的5'至3'方向上能够控制表达的启动子和序列与编码序列的连接。

[0103] 根据本披露，包含一种能够控制在宿主细胞中的表达的启动子的连接至编码CYP450和AKR的核酸序列上的嵌合核酸序列可被整合入一种确保在宿主细胞中良好表达的重组表达载体中。因此，本披露包括一种重组表达载体，包含作为可操作地连接部件的以下各项：

(i)一种能够控制在宿主细胞中的表达的核酸序列；以及

(ii)一种编码CYP450的核酸序列，

其中该表达载体适合于在宿主细胞中的表达。

[0104] 本披露包括一种重组表达载体，包含作为可操作地连接部件的以下各项：

(i)一种能够控制在宿主细胞中的表达的核酸序列；以及

(ii)一种编码AKR的核酸序列，

其中该表达载体适合于在宿主细胞中的表达。

[0105] 本披露进一步包括一种重组表达载体，包含作为可操作地连接部件的以下各项：

(i)一种能够控制在宿主细胞中的表达的核酸序列；以及

(ii)一种编码CYP450和AKR的核酸序列，

其中该表达载体适合于在宿主细胞中的表达。术语“适合于在宿主细胞中的表达”意指该重组表达载体包含连接至实现在宿主细胞中的表达所需的遗传元件上的本披露嵌合核酸序列。在这点上，可包含在该表达载体中的遗传元件包括转录终止子区，编码标记基

因的一个或多个核酸序列、一个或多个复制起点等。在优选实施例中，该表达载体进一步包含在宿主细胞的基因组中整合该载体或其一部分所需的遗传元件，例如如果使用一种植物宿主细胞，则为有助于整合入该植物的核基因组中的T-DNA左边界序列和右边界序列。

[0106] 根据本披露，该表达载体可进一步含有一个标记基因。根据本披露可使用的标记基因包括允许区分转化细胞与非转化细胞的所有基因，包括所有可选择和可筛选的标记基因。标记基因可以是一种抗性标记物，诸如一种抵抗例如卡那霉素或氨比西林的抗生素抗性标记物。S可用于通过目测来鉴定转化体的可筛选标记物包括β-葡糖醛酸糖苷酶(GUS)(美国专利号5,268,463和5,599,670)和绿色荧光蛋白(GFP)(尼特斯(Niedz)等人，1995，植物细胞(Plant Cell Rep.)，14:403)。

[0107] 可以特别方便地使用的一种宿主细胞是大肠杆菌。可使用诸如限制性酶切消化、连接、凝胶电泳、DNA测序、聚合酶链式反应(PCR)以及其他方法的通常已知技术来完成大肠杆菌载体的制备。各种克隆载体可用于进行制备一种重组表达载体所需的必要步骤。在具有大肠杆菌中的复制系统功能的载体中的是诸如pBR322的载体、pUC系列载体、M13 mp系列载体、pBluescript等。典型地，这些克隆载体含有一种允许选择转化细胞的标记物。可将核酸序列引入这些载体，并且可通过制备感受态细胞、电穿孔或使用本领域技术人员熟知的其他方法来将载体引入大肠杆菌。大肠杆菌可在包括但不限于LB(Luria-Broth)培养基的适当培养基中生长并且收获。重组表达载体可在细胞收获和溶解时易于从细胞回收。另外，关于重组载体的制备和重组生物体的生长的一般指导可在例如：萨姆布鲁克等人，分子克隆，实验手册，冷泉港实验室出版社，2001，第三版中找到。

[0108] 本披露进一步包括一种宿主细胞，其中该宿主细胞包含一种嵌合核酸序列，该嵌合核酸序列包含作为可操作地连接部件的编码选自由CYP450和AKR组成的组的一种或两种多肽的一种或多种核酸序列。如上文所提到的，该宿主细胞优选地是一种不能天然产生一种苄基异喹啉衍生物((S)-网状番荔枝碱)或(R)-网状番荔枝碱或(R)-网状番荔枝碱前体的宿主细胞。在另一个实施例中，该宿主细胞能够天然产生(S)-网状番荔枝碱(一种苄基异喹啉衍生物)，但不能天然产生(R)-网状番荔枝碱或(R)-网状番荔枝碱前体。在另一个实施例中，该宿主细胞能够产生一种苄基异喹啉衍生物((S)-网状番荔枝碱)或(R)-网状番荔枝碱或(R)-网状番荔枝碱前体，但(R)-网状番荔枝碱或(R)-网状番荔枝碱前体的水平低于所希望的水平，并且相对于天然的未修饰细胞中的(R)-网状番荔枝碱或(R)-网状番荔枝碱前体的水平调节(R)-网状番荔枝碱或(R)-网状番荔枝碱前体的水平。在其中细胞不能天然产生(S)-网状番荔枝碱或一种苄基异喹啉衍生物的实施例中，可向这些细胞提供(S)-网状番荔枝碱或该苄基异喹啉衍生物作为这些细胞的生长培养基的一部分。在其中细胞不能天然产生(S)-网状番荔枝碱或一种苄基异喹啉衍生物的其他实施例中，可提供一种能够通过这些细胞分别转化成(S)-网状番荔枝碱或一种苄基异喹啉衍生物的(S)-网状番荔枝碱或一种苄基异喹啉衍生物的前体化合物。可向这些细胞提供作为细胞生长培养基的一部分的可替代底物包括但不限于：(S)-去甲基乌药碱、(S)-N-甲基去甲基乌药碱、(S)-全去甲劳丹碱、(S)-N-甲基全去甲劳丹碱、(S)-乌药碱、(S)-N-甲基乌药碱、(S)-3’-羟基乌药碱、(S)-3’-羟基-N-甲基乌药碱、(S)-去甲乌药碱、(S)-N-甲基去甲乌药碱、(S)-劳丹灵、(S)-去甲网脉番荔枝碱、(S)-Colletine、以及(S)-东罂粟灵。据此可使用的细胞包括但不限于细菌、酵母、或其他真菌细胞、植物细胞、动物细胞、或合成细胞。

[0109] 本披露进一步包括用于将一种(S)-对映异构体差向异构化成一种(R)-对映异构体的组合物，这些组合物包含一种酶混合物，该酶混合物包含一种能够将一种苄基异喹啉衍生物氧化成一种氧化苄基异喹啉衍生物的第一多肽和一种能够将该氧化苄基异喹啉衍生物还原成(R)-网状番荔枝碱前体的第二多肽，并且进一步包含一种酶混合物，该酶混合物包含一种能够将(S)-网状番荔枝碱氧化以形成1,2-脱氢网状番荔枝碱的第一多肽和一种能够将1,2-脱氢网状番荔枝碱还原以形成(R)-网状番荔枝碱的第二多肽。在优选实施例中，该第一多肽是一种细胞色素P450并且该第二多肽是一种AKR。

[0110] 在一些实施例中，AKR和CYP450多肽被可操作地连接以形成一种融合多肽。因此，本披露进一步包括一种多肽，该多肽包含或由SEQ.ID NO:323组成。

[0111] 本发明进一步包括包含编码能够将一种(S)-对映异构体差向异构化成一种(R)-对映异构体的多肽的核酸序列的组合物。在优选实施例中，这些核酸序列是一种如下的核酸序列：编码CYP450和AKR，能够一起将一种(S)-对映异构体差向异构化成一种(R)-对映异构体，并且优选地能够将一种苄基异喹啉衍生物氧化成一种氧化苄基异喹啉衍生物且将该苄基异喹啉衍生物还原成(R)-网状番荔枝碱前体，并且更优选能够将(S)-网状番荔枝碱氧化以形成1,2-脱氢网状番荔枝碱、将1,2-脱氢网状番荔枝碱还原以形成(R)-网状番荔枝碱。在优选实施例中，编码AKR和CYP450的核酸序列被可操作地连接以便产生一种CYP450-AKR融合多肽。因此，本披露进一步包括SEQ.ID NO:322。

[0112] 在宿主细胞中累积的(R)-网状番荔枝碱的量可改变。在本披露的其中宿主细胞天然产生(R)-网状番荔枝碱和(S)-网状番荔枝碱(例如罂粟细胞)的实施例中，通过被制备成包含根据本披露的嵌合核酸序列的此类细胞而在体内合成的(R)-网状番荔枝碱与(S)-网状番荔枝碱的比率，超过存在于天然宿主细胞(即，不包含这些嵌合核酸序列的细胞)或宿主细胞提取物中的(R)-网状番荔枝碱与(S)-网状番荔枝碱的比率。优选地，宿主细胞或宿主细胞提取物中的(R)-网状番荔枝碱与(S)-网状番荔枝碱的比率大于21:79，例如至少0.3:1、至少0.4:1、至少0.5:1、至少1:1、至少2:1、至少3:1、或至少4:1。

(R)-网状番荔枝碱和(R)-网状番荔枝碱前体的使用

[0113] 根据本披露获得的(R)-网状番荔枝碱可被配制用作一种药物、治疗剂或医疗试剂。因此本披露进一步包括一种包含根据本披露方法制备的(R)-网状番荔枝碱的药物组合物。包含根据本披露的(R)-网状番荔枝碱的药物制剂优选地进一步包含媒介物、赋形剂、稀释剂、以及诸如润湿剂或乳化剂、pH缓冲物质等的辅助物质。这些媒介物、赋形剂和辅助物质通常是可以被给予但没有过分毒性的药物试剂。药学上可接受的赋形剂包括但不限于诸如水、盐水、聚乙二醇、透明质酸、甘油以及乙醇的液体。在此还可以包括药学上可接受的盐，例如，诸如盐酸盐、磷酸盐、硫酸盐等的无机酸盐；以及诸如醋酸盐、丙酸盐、苯甲酸盐等的有机酸盐。同样优选地，尽管不是必要的，该制剂将含有一种作为稳定剂的药学上可接受的赋形剂。也用作肽的稳定剂的适合的载体实例包括但不限于，药物级右旋糖、蔗糖、乳糖、山梨糖醇、肌醇、右旋糖酐等。其他适合的载体包括，也不限于淀粉、纤维素、磷酸钠或磷酸钙、柠檬酸、甘氨酸、聚乙二醇(PEG)及其组合。该药物组合物可以被配制用于口服和静脉内给予以及所希望的其他给予途径。给药可改变并且可使用常规实验来优化。包含(R)-网状番荔枝碱的药物组合物可用于治疗秃顶或肌肉紧张。

[0114] 在另外的实施例中，本披露提供用于使用一种包含根据本披露制备的(R)-网状番

荔枝碱的药物组合物来治疗患者的方法。因此，本披露进一步提供一种用于使用根据本披露的方法制备的(R)-网状番荔枝碱来治疗患者的方法，所述方法包括向该患者给予一种包含(R)-网状番荔枝碱的组合物，其中(R)-网状番荔枝碱以足以改善该患者医学病状的量被给予。在优选实施例中，该医学病状选自由秃顶和肌肉张力释放组成的组。

[0115] 此外，在此提供的(R)-网状番荔枝碱可用作一种制造其他次级代谢物或医学组合物的试剂，包括但不限于萨卢它定、可待因和吗啡，并且进一步包括蒂巴因、罂粟碱、那可丁、可旦民碱、劳丹碱以及劳丹素(+)-深山黄堇碱、(-)-异波尔定碱、以及(-)-紫堇块茎碱。

[0116] 在此提供的(R)-网状番荔枝碱前体可用作一种制造其他次级代谢物，特别是(R)-网状番荔枝碱的试剂。如图1所示，(R)-N-甲基乌药碱可用作一种制造(R)-3'-羟基-N-甲基乌药碱的试剂。(R)-3'-羟基-N-甲基乌药碱可用作一种制造(R)-网状番荔枝碱的试剂。

编码AKR和CYP450多肽的核苷酸序列的可替代使用

[0117] 在另一个方面中，编码AKR和/或CYP450的核酸序列可用于检测一个样品中这些基因的存在或不存在。因此在本披露的一个实施例中，提供一种检测编码AKR和/或CYP450的核酸序列的存在或不存在的方法，该方法包括：

(a)提供一种怀疑包含编码AKR和/或CYP450的核酸序列的样品；并且

(b)针对编码AKR和/或CYP450的核苷酸序列的存在分析该样品。

[0118] 在一个优选实施例中，该样品包含含基因组DNA的细胞。因此在一个优选实施例中，提供一种检测一个细胞中编码AKR和/或CYP450的核酸序列的存在或不存在的方法，该方法包括：

(a)提供一种细胞；

(b)从该细胞提取基因组DNA；并且

(c)针对编码AKR和/或CYP450的核酸序列的存在分析该基因组DNA。

[0119] 分析基因组DNA的方法通常是本领域已知的，并且包括，例如使用聚合酶链式反应(PCR)和特定的多核苷酸引物以便扩增编码AKR和/或CYP450的核苷酸序列的特定部分。可使用另外的限制性酶切消化和DNA印迹分析。该分析可进一步涉及编码AKR和/或CYP450的核酸序列的内含子、外显子或上游区域或下游区域。该分析可进一步涉及鉴定一种包含编码AKR和/或CYP450的核酸序列的基因组基因座，其中这种基因座与AKR和/或CYP450表达的调节水平有关。

[0120] 在优选实施例中，该细胞是一种植物细胞。在另外的优选实施例中，该细胞是由一种属于植物家族罂粟科、樟科、番荔枝科、大戟科或桑科的植物获得的植物细胞，并且更优选地，该植物属于物种罂粟、大红罂粟或虞美人。

[0121] 在优选实施例中，为了进行前述分析而使用的CYP450和/或AKR序列在SEQ.ID NO:116至SEQ.ID NO:218；SEQ.ID NO:324；以及SEQ.ID NO:337中列出；或在SEQ.ID NO:1至SEQ.ID NO:58；SEQ.ID NO:326；SEQ.ID NO:328；以及SEQ.ID NO:339中的列出的那些序列；或在SEQ.ID NO:322中列出的序列。

[0122] 在另外的方面中，编码AKR和/或CYP450的核酸序列可用于产生一种具有调节水平的AKR和/或CYP450表达的细胞。这样的细胞优选是一种天然表达AKR和/或CYP450的植物细胞，并且更优选地一种由一种属于植物家族罂粟科、樟科、番荔枝科、大戟科或桑科的植物获得的植物细胞，并且最优选地，该植物属于物种罂粟、大红罂粟或虞美人。因此本披露进

一步提供一种用于调节核酸序列在天然表达AKR和/或CYP450的细胞中的表达的方法，该方法包括：

(a)提供一种天然表达AKR和/或CYP450的细胞；

(b)诱变处理该细胞；

(c)使该细胞生长以获得多个细胞；并且

(d)确定该多个细胞是否包括一种包含调节水平的AKR和/或CYP450的细胞。

[0123] 在优选实施例中，该方法进一步包括一个如下步骤(e)：

(e)选择一种包含调节水平的AKR和/或CYP450的细胞并且使这种细胞生长以获得多个细胞。

[0124] 在另外的优选实施例中，植物种子细胞可用于进行该诱变。可使用的诱变剂是化学试剂，包括但不限于，碱基类似物、脱氨剂、烷化剂、嵌入剂、转座子、溴、叠氮化钠、甲磺酸乙酯(EMS)以及物理试剂，包括但不限于，诸如电离辐射和UV辐射的辐射物。因此本披露进一步提供一种用于产生结籽植物的方法，该结籽植物包含核酸序列在天然表达AKR和/或CYP450的细胞中的调节表达，该方法包括：

(a)提供一种天然表达AKR和/或CYP450的结籽植物；

(b)诱变该植物的种子以获得诱变的种子；

(c)使该诱变的种子生长成能够结籽下一代种子的下一代诱变植物；并且

(d)获得这些诱变植物的下一代种子或另一个部分，并且分析这些下一代植物或下一代种子是否表现出调节的AKR和/或CYP450表达。

[0125] 在优选实施例中，可获得植物和/或种子的多个代，并且可分析任何和所有此类代中的植物和/或种子的部分。典型地通过比较在非诱变(野生型)植物或种子中的表达水平(例如RNA水平或蛋白质水平)与在诱变植物或种子中的表达来进行分析。在另外的优选实施例中，可通过分析野生型DNA与突变DNA之间的异源双链体形成来进行步骤(d)中的分析。因此在优选实施例中，步骤(d)中的分析包括：

i.从突变植物提取DNA；

ii.扩增包含一种编码AKR和/或CYP450的核酸序列的DNA的一部分以便获得扩增的突变DNA；

iii.从野生型植物提取DNA；

iv.将来自野生型植物的该DNA与该扩增的突变DNA混合并且形成一种异源双链多核苷酸；

v.将该异源双链多核苷酸与一种单链限制性内切核酸酶孵育，该单链限制性内切核酸酶能够限制在错配的该异源双链多核苷酸的一个区域处；并且

vi.确定该异源双链体多核苷酸中的错配位点。

[0126] 在优选实施例中，所使用的编码AKR和/或CYP450的核酸序列在SEQ.ID NO:116至SEQ.ID NO:218；SEQ.ID NO:324；以及SEQ.ID NO:337中列出；或在SEQ.ID NO:1至SEQ.ID NO:58；SEQ.ID NO:326；SEQ.ID NO:328；以及SEQ.ID NO:339中的列出的那些序列；或在SEQ.ID NO:322中列出的序列。

[0127] 在另外的方面中，编码AKR和/或CYP450的核酸序列可用于通过基因沉默产生一种具有调节水平的AKR和/或CYP450表达的细胞。因此，本披露进一步包括一种减少AKR和/或

CYP450在细胞中的表达的方法，该方法包括：

(a)提供一种表达AKR和/或CYP450的细胞；并且

(b)使AKR和/或CYP450在该细胞中的表达沉默。

[0128] 在优选实施例中，该细胞是一种植物细胞。优选地，该植物是一个属于植物家族罂粟科、樟科、番荔枝科、大戟科或桑科的成员，并且更优选地，该植物属于物种罂粟、大红罂粟或虞美人。所使用的一种使AKR和/或CYP450沉默的优选方法是病毒诱导性基因沉默(本领域已知为VIGS)。通常，在感染未修饰病毒的植物中，该病毒基因组被靶向。然而，当病毒载体已被修饰成携带来源于宿主基因的插入(例如，编码AKR和/或CYP45的序列的部分)时，该方法另外地靶向对应的mRNA。因此，本披露进一步包括一种产生表达降低水平的AKR和/或CYP450的植物的方法，该方法包括：

(a)提供一种表达AKR和/或CYP450的植物；并且

(b)使用病毒诱导性基因沉默降低AKR和/或CYP450在该植物中的表达。

[0129] 在实例5中进一步详述本披露的此方面。

[0130] 上文所提到的调节AKR和/或CYP450表达水平的方法可能导致调节植物中的植物碱的水平，这些植物碱包括但不限于：吗啡、可待因、蒂巴因、罂粟碱、那可丁、(S)-网状番荔枝碱、(R)-网状番荔枝碱、可旦民碱、劳丹碱以及劳丹素。这些方法可进一步导致调节(S)-网状番荔枝碱、(R)-网状番荔枝碱的比率。优选地这种调节导致植物细胞或植物细胞提取物中的(R)-网状番荔枝碱与(S)-网状番荔枝碱的比率小于21:79、更优选小于0.1、更优选小于0.05、更优选小于0.025并且更优选小于0.01。在实例5中示出这种调节。因此本披露包括使用这些方法以便在能够天然产生植物碱的植物中调节植物碱的水平。优选地，此类植物属于植物家族罂粟科、樟科、番荔枝科、大戟科或桑科，并且更优选地，该植物属于物种罂粟、大红罂粟或虞美人。

[0131] 在本披露的又另外的方面中，编码AKR和/或CYP450的核酸序列可用于基因型植物。优选地，该植物是一个属于植物家族罂粟科、樟科、番荔枝科、大戟科或桑科的成员，并且更优选地，该植物属于物种罂粟、大红罂粟或虞美人。通常，基因分型提供一种区别染色体对同系物的手段并且可用于鉴定植物群体的后续代中的分离子。分子标记方法可用于系统发生研究、表征植物品种之间的遗传关系、鉴定杂交或体细胞杂种、定位影响单基因性状的染色体片段、基于作图的克隆以及数量遗传的研究。参见，例如，植物分子生物学(Plant Molecular Biology)：实验手册，第7章，克拉克(Clark)编辑，柏林施普林格(Springer-Verlag,Berlin)(1997)。对于分子标记方法，通常参见，通过在以下中的安德鲁(Andrew)H.帕特森(Paterson)1996(第2章)的DNA改革：基因组作图植物(安德鲁H.帕特森编著)通过德克萨斯州奥斯汀市(Austin,Tex.)的学术出版社(Academic Press)/R.G.兰迪斯公司(Landis Company)，第7-21页。根据本披露的基因分型的具体方法可涉及采用任何分子标记分析技术，包括但不限于限制性片段长度多态性(RFLP)。RFLP反映由核苷酸序列变异性导致的DNA限制性片段之间的等位基因差异。如本领域的技术人员已知的，RFLP典型地通过植物基因组DNA的提取和用一种或多种限制性内切酶消化基因组DNA来检测。典型地，根据大小将所得片段分离并且用一种核酸探针杂交。揭示来自同源染色体的限制性片段。等位基因中的片段大小的差异表示RFLP。因此，本披露进一步提供一种遵循分离一部分或编码AKR和/或CYP450的基因组DNA，以及使用此类技术作为RFLP分析来遗传连接至这些AKR和/

或CYP450编码核酸序列上的染色体核酸序列的手段。连接的染色体核酸序列在一个编码AKR和/或CYP450的基因组核酸序列的50厘摩(cM)内，经常在40或30cM内、优选在20或10cM内、更优选在5、3、2、或1cM内。因此，根据本披露，本披露的AKR和/或CYP450编码序列可用作标记物评估植物群体中遗传连接至其上的核酸序列的分离。优选地，该植物群体包括或由属于植物家族罂粟科、樟科、番荔枝科、大戟科或桑科的植物组成，并且更优选地，该植物群体包括或由属于物种罂粟、大红罂粟或虞美人的植物组成。

[0132] 根据本披露，用于分子标记作图植物核基因组的核酸探针在选择性杂交条件下选择性杂交至一种编码AKR和/或CYP450的基因组序列。在优选实施例中，这些探针选自由本披露提供的编码AKR和/或CYP450的核酸序列。典型地，这些探针是cDNA探针。典型地这些探针是至少15个碱基长度、更优选至少20、25、30、35、40、或50个碱基长度。然而，通常，这些探针小于约1千碱基长度。优选地，这些探针是杂交单倍体植物染色体补体中的独特基因座的单拷贝探针。用于RFLP作图的一些示例性限制性内切酶是EcoRI、EcoRv、和SstI。如在此使用的术语“限制性内切酶”包括提及一种单独或与另一种组合物结合来识别并且裂解一个特定核苷酸序列处的多核苷酸的组合物。

[0133] 区别本披露核酸序列的多态(等位基因)变体的其他方法可以通过利用本领域技术人员熟知的分子标记技术来使用，这些分子标记技术包括但不限于：1)单链构象分析(SSCP)；2)变性梯度凝胶电泳(DGGE)；

3)RNA酶保护测定；4)等位基因特异性寡核苷酸(ASO)；5)识别核苷酸错配的蛋白质(诸如大肠杆菌mutS蛋白)的使用；以及6)等位基因特异性PCR。基于检测两个互补DNA链之间的错配的其他方法包括但不限于，夹固的变性凝胶电泳(CDGE)；异源双链分析(HA)以及化学错配裂解法(CMC)。因此，本披露进一步提供一种基因分型的方法，该方法包括以下步骤：在严格的杂交条件下，使一种怀疑包含编码AKR和CYP450的核酸的样品与一种能够杂交至其上的核酸探针接触。通常，该样品是一种植物样品；优选地，一种怀疑包含编码AKR和/或CYP450的罂粟核酸序列(例如，基因、mRNA)的样品。该核酸探针在严格条件下选择性地杂交至包含一种多态性标记物的编码AKR和/或CYP450的核酸序列的子序列。该核酸探针至该多态性标记物核酸序列的选择性杂交产生一种杂交复合物。该杂交复合物的检测指示了该多态性标记物在该样品中的存在。在优选实施例中，该核酸探针包含一种编码AKR和/或CYP450的核酸序列的一部分。

实例

[0134] 以下提供用于进行本披露方法的具体实施例、以及表示本披露组合物的实施例的实例。这些实例仅出于说明性目的提供，而非旨在以任何方式限制本披露的范围。

实例1-(S)-网状番荔枝碱至(R)-网状番荔枝碱的转化

[0135] 此实例示出使用一种酶混合物的(S)-网状番荔枝碱至(R)-网状番荔枝碱的体外转化，该酶混合物呈一种包含CYP450和AKR部分的罂粟的融合多肽(SEQ.ID:NO 323)的形式。

[0136] 使具有pESC-leu2d::PsCPR/PsREPI的酿酒酵母菌株YPH499生长并且如下所述进行微粒体纯化。简言之，将该酵母菌株在使用2%葡萄糖增补的缺乏亮氨酸的合成完全(SC)培养基中在30℃和250rpm下生长16小时。将一毫升培养物添加到50mL使用1.8%半乳糖、0.2%葡萄糖和1%棉子糖增补的缺乏亮氨酸的SC培养基中，并且在30℃和250rpm下生长72

小时。然后将培养物在4,000g下离心5分钟并且用5mL TEK缓冲液(50mM Tris-HCl pH 8，1mM EDTA,100mM KCl)进行洗涤。使沉淀在1mL TESB缓冲液(50mM Tris-HCl pH 8,1mM EDTA,0.6M山梨糖醇)中再悬浮并且添加相等体积的0.5mm玻璃珠。在10℃下手动地摇动试管4分钟。用TESB洗涤这些珠子，并且收集洗涤液且在14,000g下离心10min。将上清液在125,000g下超速离心1小时并且废弃该上清液。然后使微粒体在pH 7.5的50mM HEPES中再悬浮。

[0137] 酶测定物含有500μM NADPH和50μM的在HEPES缓冲液(pH 7.5)中的(S)-网状番荔枝碱以及如上所述制备的微粒体。将测定物在30℃下孵育过夜。在该反应后，将测定样品以0.2ml/min的流速在安捷伦(Agilent)1260HLPC上运行，并且使用LUX纤维素-1手性柱(150mm×2.1mm内径;Phenomenex)、使用增补有0.1％二乙胺的75％碳酸氢铵(溶剂A)和具有0.1％二乙胺的25％乙腈(溶剂B)来分离化合物。在284nm波长处监测(R)-网状番荔枝碱和(S)-网状番荔枝碱。

[0138] 结果在图3中示出。如在图3中可以看出，在该手性柱上的可信标准对照(R)-网状番荔枝碱和(S)-网状番荔枝碱的保留时间分别是大约13.5分钟(顶图)；和15分钟(从顶部的第二个图)。底图示出其中没有酶存在于混合物中的测定的结果，并且证实在些反应条件下没有(S)-网状番荔枝碱被差向异构化成(R)-网状番荔枝碱。从顶部的第三个图示出，在该酶混合物的存在下，(S)-网状番荔枝碱被差向异构化成(R)-网状番荔枝碱(参见箭头，以及在大约15min的保留时间处的峰的外观)。

实例2-(S)-网状番荔枝碱至1,2-脱氢网状番荔枝碱的转化

[0139] 此实例示出使用虞美人的CYP450(SEQ.ID:NO 325)，在酵母中的(S)-网状番荔枝碱至1,2-脱氢网状番荔枝碱的体外转化。使具有pESC-leu2d::PsCPR/PrDRS的酿酒酵母菌株YPH499生长并且如下所述进行微粒体纯化。简言之，将该酵母菌株在使用2％葡萄糖增补的缺乏亮氨酸的合成完全(SC)培养基中在30℃和250rpm下生长16小时。将一毫升此培养物添加到50mL使用1.8％半乳糖、0.2％葡萄糖和1％棉子糖增补的缺乏亮氨酸的SC培养基中，在30℃和250rpm下生长72小时。然后将培养物在4,000g下离心5分钟并且用5mL TEK缓冲液(50mM Tris-HCl pH 8,1mM EDTA,100mM KCl)进行洗涤。然后使沉淀在1mL TESB缓冲液(50mM Tris-HCl pH 8,1mM EDTA,0.6M山梨糖醇)中再悬浮并且添加相等体积的0.5mm玻璃珠。在10℃下手动地摇动试管4min。用TESB洗涤这些珠子，并且收集洗涤液且在14,000g下离心10min。然后将上清液在125,000g下超速离心1小时并且废弃该上清液。然后使微粒体在pH 7.5的50mM HEPES中再悬浮。

[0140] 酶测定物含有500μM NADPH和50μM的在HEPES缓冲液(pH 7.5)中的(S)-网状番荔枝碱以及如上所述制备的微粒体。将测定物在30℃下孵育过夜。在该反应后，将测定样品在结合6400B质谱仪的安捷伦1260HLPC上运行，该质谱仪具有以阳性模式操作的一个电喷雾离子源。该质谱仪从200-400m/z进行扫描。对于先前描述的酶测定物使用HLPC方法来分离化合物(法罗(Farrow)SC和法基尼(Facchini)PJ，(2013)，生物化学杂志(J.Biol.Chem.)(288)第28,997-29,012页;双加氧酶催化在罂粟中的苄基异喹啉生物碱新陈代谢中具有广泛作用的O-脱甲基作用和O,O-脱甲基作用)。

[0141] 结果在图4中示出。如在图4(顶图)中可以看出，在一个不包含该酶的对照样品中的HPLC柱上观察到一个具有大约3.1分钟的保留时间的峰。此峰对应于针对(S)-网状番荔

枝碱的碰撞诱导解离谱在m/z 330处的最大片段的3.13分钟的预测保留时间(参见:表1)。从顶部的第二个图示出,在相同对照样品的m/z 328处没有观察到峰,因此表明1,2-脱氢网状番荔枝碱不存在于该对照样品中。从顶部的第三个图示出,在包含该酶的样品的m/z 330处、在大约3.1分钟的保留时间处观察到一个峰,因此表明(S)-网状番荔枝碱存在于该测定样品中。底图示出,在测定样品的m/z 328处观察到一个具有大约3.0的保留时间的峰。此峰对应于针对1,2-脱氢网状番荔枝碱的碰撞诱导解离谱在m/z 328处的最大片段的3.02分钟的预测保留时间(参见:表1),表明了1,2-脱氢网状番荔枝碱在该酶的存在下存在于该测定样品中。

实例3-1,2-脱氢网状番荔枝碱至(R)-网状番荔枝碱的转化

[0142] 此实例示出使用虞美人的AKR(SEQ.ID:NO 327),在酵母中的1,2-脱氢网状番荔枝碱至(R)-网状番荔枝碱的体外转化。

[0143] 将增补有具有pET47b::PrDRR的大肠杆菌菌株Rosetta(DE3)的50μg/mL硫酸卡那霉素和35μg/mL氯霉素培养物的16小时、50mL LB添加到1L相同培养基中,并且在37℃、180rpm下生长直到OD600为0.6。然后添加IPTG至1mM的最终浓度,并且允许在25℃、180rpm下生长4h,并且通过离心收集细胞沉淀。使用一种弗氏压碎器将细胞溶解于增补有2mM苯甲基磺酰氟(PMSF)的缓冲液A(100mM磷酸钠缓冲液pH 7.0,300mM NaCl,10%(v/v)甘油)中。通过在14,000g下离心15分钟来去除细胞碎片。将总可溶性蛋白质提取物与缓冲液A平衡的TALON(Clonetech)树脂在4℃、65rpm下合并45分钟。使用缓冲液A将该树脂洗涤两次,并且使用缓冲液A中的咪唑梯度(2.5、10、100、200mM)逐步洗脱蛋白质。将纯化的蛋白质在100mM咪唑中洗脱。

[0144] 酶测定物含有500μM NADPH、50μM的在磷酸钠缓冲液(pH 7.0)中的1,2-脱氢网状番荔枝碱以及如上所述制备的蛋白质。将测定物在30℃下过夜。在该反应后,将测定样品在结合6400B质谱仪的安捷伦1260HLPC上运行,该质谱仪具有以阳性模式操作的一个电喷雾离子源。该质谱仪从200-400m/z进行扫描。对于先前描述的酶测定物使用HLPC方法来分离化合物(法罗SC和法基尼PJ,(2013),生物化学杂志(288)第28,997-29,012页;双加氧酶催化在罂粟中的苄基异喹啉生物碱新陈代谢中具有广泛作用的O-脱甲基作用和O,O-脱甲基作用)。

[0145] 结果在图5中示出。如在图5(顶图)中可以看出,在一个不包含该酶的对照样品中的HPLC柱上观察到一个具有大约3.0分钟的保留时间的峰。此峰对应于针对1,2-脱氢网状番荔枝碱的碰撞诱导解离谱在m/z328处的最大片段的3.02分钟的预测保留时间(参见:表1)。从顶部的第二个图示出,在大约3.1分钟的保留时间处没有观察到峰,因此(R)-网状番荔枝碱不存在于该样品中。在相同对照样品中在大约3.0分钟处观察到一个小峰。此峰表示底物1,2-脱氢网状番荔枝碱的一个同位素形式。从顶部的第三个图示出,在含有该酶的样品的m/z 328处观察到一个具有大约3.0分钟的保留时间的峰,因此表明少量未耗尽的1,2-脱氢网状番荔枝碱存在于该测定样品中。底图示出,在测定样品的m/z 330处观察到一个具有大约3.1的保留时间的峰。此峰对应于针对(R)-网状番荔枝碱的碰撞诱导解离谱在m/z 330处的最大片段的3.13分钟的预测保留时间(参见:表1),表明了(R)-网状番荔枝碱在该酶的存在下存在于该测定样品中。实例4-(S)-N-甲基乌药碱至(R)-N-甲基乌药碱的转化

[0146] 此实例示出使用一种酶混合物,在酵母中的(S)-N-甲基乌药碱至(R)-N-甲基乌药

碱的体外转化，该酶混合物呈一种包含CYP450和AKR部分组成的罂粟的融合多肽(SEQ.ID: NO 2)的形式。

[0147] 使具有pESC-leu2d::PsCPR/PsREPI的酿酒酵母菌株YPH499生长并且如下所述进行微粒体纯化。简言之，将该酵母菌株在使用2％葡萄糖增补的缺乏亮氨酸的合成完全(SC)培养基中在30℃和250rpm下生长16小时。将一毫升培养物添加到50mL使用1.8％半乳糖、0.2％葡萄糖和1％棉子糖增补的缺乏亮氨酸的SC培养基中，并且在30℃和250rpm下生长72小时。然后将培养物在4,000g下离心5分钟并且用5mL TEK缓冲液(50mM Tris-HCl pH 8，1mM EDTA，100mM KCl)进行洗涤。使沉淀在1mL TESB缓冲液(50mM Tris-HCl pH 8，1mM EDTA，0.6M山梨糖醇)中再悬浮并且添加相等体积的0.5mm玻璃珠。在10℃下手动地摇动试管4分钟。用TESB洗涤这些珠子，并且收集洗涤液且在14,000g下离心10min。将上清液在125,000g下超速离心1小时并且废弃该上清液。然后使微粒体在pH 7.5的50mM HEPES中再悬浮。

[0148] 酶测定物含有500μM NADPH和50μM的在HEPES缓冲液(pH7.5)中的(S)-N-甲基乌药碱以及如上所述制备的微粒体。将测定物在30℃下孵育过夜。在该反应后，将测定样品以0.2ml/min的流速在安捷伦1260HLPC上运行，并且使用LUX纤维素-1手性柱(150mm×2.1mm内径;Phenomenex)、使用增补有0.1％二乙胺的75％碳酸氢铵(溶剂A)和具有0.1％二乙胺的25％乙腈(溶剂B)来分离化合物。在230nm波长处监测(R)-N-甲基乌药碱和(S)-N-甲基乌药碱。

[0149] 结果在图6中示出。如在图6中可以看出，在该手性柱上的可信标准对照(S)-N-甲基乌药碱的保留时间是大约13.9分钟(顶图)。底图示出其中没有酶存在于混合物中的测定的结果，并且证实在些反应条件下没有(S)-N-甲基乌药碱被差向异构化成(R)-N-甲基乌药碱。中间图示出，在酶混合物的存在下，(S)-N-甲基乌药碱被差向异构化成(R)-N-甲基乌药碱。(参见箭头，以及在大约16.3min的保留时间处的峰的外观)

实例5-AKR和AKR-CYP450融合基因的基因沉默

[0150] 此实例示出使用病毒诱导性基因沉默(VIGS)来使编码AKR和/或CYP450的基因沉默。

[0151] 使用烟草脆裂病毒(TRV)载体系统来抑制来自罂粟(罂粟)的REPI和/或COR1.3(编码可待因酮还原酶)在罂粟(罂粟)的Bea的选择化学型中的转录物水平(分别由SEQ.ID.NO: 322和SEQ.ID NO:328转录)。使用以下引物对来扩增REPI cDNA的两个区域(REPI-a(图7A;图A)和REPI-5’(图7C;图A))以及COR1.3 cDNA的一个区域(图7B;图A)：

pTRV2-COR1.3

COR1.3-F，ggatccCATCAGTTCCATGCTCTGGT

COR1.3-R，ggtaccGGGCTCATCTCCACTTGATT

pTRV2-REPI-a

REPI-a-F，ggatccCATCACTTCCAAGCTCTGGT

REPI-a-R，ggtaccGGGCTCATCTCCACTTGAT

pTRV2-REPI-5’

REPI-5’-F，gaattcCCTACATACTGTATTGGGTTGAATCATG

REPI-5’-R，ggtaccTAACGGGATAGGACGGTTT

[0152] REPI-a区域和COR1.3区域表现相当大的相似性，在每种情况下导致REPI和COR1.3的相互共沉默。相比之下，REPI-5’区域是独特的并且仅导致REPI而没有COR1.3的沉默。

[0153] 如前所述地将扩增子单独地克隆到pTRV2中，并且将载体转移在根瘤土壤杆菌中。用一种具有pTRV1的根瘤土壤杆菌与含有基因特异性片段的构建pTRV2的1:1混合物来浸润两至三周龄的幼苗的顶端分生组织。空pTRV2被用作阴性对照，并且编码八氢番茄红素去饱和酶的pTRV2-PDS构建体被用作阳性浸润对照。将浸润的植物在温室中培养8-10周。如前所述地进行用根瘤土壤杆菌的浸润、和针对生物碱的乳胶、茎和根样品的收集与处理、以及转录物分析。典型地，用具有pTRV1的根瘤土壤杆菌和一种pTRV2构建体来浸润20-30个植物。在大约70％-80％的浸润植物中，通过RT-PCR检测出该pTRV2构建体的一个移动片段(图7A(图B)；图7B(图B)；图7C，图B)，这说明这些植物成功地被感染。使用甲醇从冻干乳胶提取生物碱。通过qRT-PCR来确定相对转录物丰度(图7A(图C)；图7B(图C)；图7C，图C)。从6个单独浸润的植物得出生物碱含量和相对转录物丰度的数据，并且在每个样品上进行三个技术复制。通过LC-MS/MS分析浸润植物的乳胶样品。使用总离子色谱图(图7A(图D)；图7B(图D)；图7C，图D)并且通过确定9种不同生物碱(吗啡、可待因、蒂巴因、罂粟碱、那可丁、可旦民碱、劳丹碱和劳丹素)在乳胶和根中的相对丰度(图7A(图E)；图7B(图E)；图7C，图E)来评估对于用具有pTRV1的根瘤土壤杆菌和分离pTRV2构建体中REPI或COR1.3两个区域中的每个浸润的罂粟植物生物碱含量的影响。除了吗啡含量更低之外，REPI或COR1.3的沉默导致可待因和蒂巴因水平的显著降低。REPI(即，AKR-CYP450基因)的沉默以及COR1.3(即，AKR基因)的沉默导致网状番荔枝碱、可旦民碱、劳丹碱、劳丹素累积的显著增加，并且罂粟碱和那可丁一致地更少。对照(pTRV2)植物的乳胶中的(R)-网状番荔枝碱与(S)-网状番荔枝碱的比率是大约21:79，但是pTRV2-REPI-a植物(图7A(图F)和pTRV2-COR1.3植物(图7B(图F))的乳胶中的(R)-网状番荔枝碱与(S)-网状番荔枝碱的比率降低至大约2:98；并且在乳胶和根中在pTRV2-REPI-5’植物的乳胶中降低至大约5:95(图7C，图F)。

实例6-AKR在NADPH/NADH和$NADP^+$/NAD^+存在下的催化活性

[0154] 此实例示出在还原剂NADH或NADPH的存在下，由AKR多肽将1,2-脱氢网状番荔枝碱转化成(R)-网状番荔枝碱。此实例进一步示出前述反应在氧化剂NAD^+或$NADP^+$存在下的可逆性。

[0155] 基本上如以上实例3所述地进行实验，除了使用从罂粟和虞美人获得的AKR进行这些反应，以及在相反的反应中，将(R)-网状番荔枝碱提供为底物，并且将NAD^+或$NADP^+$用作氧化剂以进行酶促反应。在pH9下进行最后提到的反应。如图8所示，在NADH和NADPH两者的存在下，使用催化量的来自罂粟(PsDRR)(图8A，图A)和虞美人(PrDRR)(图8B，图A)两者的AKR多肽将1,2-脱氢网状番荔枝碱转化成(R)-网状番荔枝碱。如图8进一步所示，使用罂粟AKR多肽PsDRR(图8A，图B)和虞美人多肽PrDRR(图8B，图B)两者，该反应可以被逆转，并且在NAD^+或$NADP^+$存在下，(R)-网状番荔枝碱被转化成1,2-脱氢网状番荔枝碱。

实例7-AKR活性的pH依赖性

[0156] 此实例示出AKR多肽在还原剂和氧化剂两者存在下的pH依赖性。

[0157] 检查罂粟和虞美人CYP450和AKR多肽两者的pH依赖性。基本上如实例3和实例6所述地进行酶促反应，除了将每个反应中的pH从pH 3.5逐步增加至pH 10。通过在结合6400B质谱仪的安捷伦1260HLPC上分析样品来定量每个评估pH下的酶活性，该质谱仪具有以阳性

模式操作的一个电喷雾离子源。该质谱仪从200-400m/z进行扫描。对于先前描述的酶测定物使用HLPC方法来分离化合物(法罗SC和法基尼PJ,(2013),生物化学杂志(288)第28,997-29,012页;双加氧酶催化在罂粟中的苄基异喹啉生物碱新陈代谢中具有广泛作用的O-脱甲基作用和O,O-脱甲基作用)。

[0158] 在图9中提供这些结果。在图A中示出的是示出使用罂粟CYP450(PsDRS)和AKR在NADPH(PsDRS正向)存在下并且在$NADP^+$(PsDRS反向)存在下作为pH函数的酶促活性的图。在图B中示出的是示出使用虞美人CYP450(PsDRS)和AKR在NADPH(PrDRS正向)存在下并且在$NADP^+$(PrDRS正向)存在下作为pH函数的酶促活性的图。如在图9中可看到的,PsDRS和PrDRS在大约pH 8的最佳条件下将(S)-网状番荔枝碱转化成1,2-脱氢网状番荔枝碱。在NADPH的存在下,PsDRR和PrDRR在大约pH 7的最佳条件下将1,2-脱氢网状番荔枝碱转化成(R)-网状番荔枝碱。在$NADP^+$的存在下,PsDRR和PrDRR在大约pH 9的最佳条件下将(R)-网状番荔枝碱转化成1,2-脱氢网状番荔枝碱。实例8-AKR和AKR-CYP450融合基因的基因沉默

[0159] 此实例进一步示出使用病毒诱导性基因沉默(VIGS)来使编码AKR和/或CYP450的基因沉默。

[0160] 基本上如实例5所述地进行基因沉默实验,除了使用以下构建体来靶向COR(AKR)和REPI(CYP450)基因:REPIa、REPIb和COR.1.3。REPIa表示一种靶向保存在COR基因和REPI基因两者中的序列的构建体。相比之下,REPIb靶向REPI独有的区域。COR 1.3靶向COR独有的区域。如实例5所述地确定REPI和COR的转录物水平。将一个空载体用作对照(PTRV2)。如在图10中可看到的,其中REPI通过REPIb独特靶向的植物相对于对照表现出降低水平的REPI转录物(图10-顶图),而COR转录物水平基本上保持相同(图10-底图)。其中REPI和COR两者均通过REPIa靶向的植物表现出降低转录物水平的REPI(图10-顶图)和COR(图10-底图)。当使用COR1.3靶向COR时,COR转录物水平减小(图10-底图)。此外,通过COR1.3响应于COR转录物水平的沉默,REPI转录物水平相对于对照也降低(图10-顶图)。

化合物(HPLC柱)	保留时间(min)	碰撞诱导解离谱	碰撞能量(eV)	λ_{max} (nm)
(R)-网状番荔枝碱(手性柱)	13.5	NA	NA	284
(S)-网状番荔枝碱(手性柱)	15.0	NA	NA	284
(S)-网状番荔枝碱(C18柱)	3.13	330.2 (10), 210.1 (6), 192.1 (100) 177.1 (4), 175.1 (14), 151.2 (4) 143.1 (16), 137.1 (38)	25	NA
(R)-网状番荔枝碱(C18柱)	3.13	330.1 (30), 210.1 (31), 192.1 (100) 175.1 (16), 142.9 (17), 136.9 (28)	25	NA
脱氢网状番荔枝碱(C18柱)	3.02	328.3 (100), 313.2 (83), 312.2 (80) 296.4 (6), 284.2 (26), 252.1 (5) 190.2 (4), 162.4 (7)	25	NA

表1

其他实施方式

实施方式1、一种制备(R)-网状番荔枝碱或(R)-网状番荔枝碱前体的方法，该方法包括：

(a)提供一种苄基异喹啉衍生物；

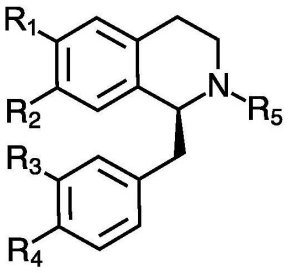
(b)使该苄基异喹啉衍生物与一种酶混合物接触，该酶混合物能够在允许将该苄基异喹啉衍生物转化成(R)-网状番荔枝碱或(R)-网状番荔枝碱前体的条件下将该苄基异喹啉衍生物转化成(R)-网状番荔枝碱或(R)-网状番荔枝碱前体。

实施方式2、一种制备(R)-网状番荔枝碱或(R)-网状番荔枝碱前体的方法，该方法包括：

(a)提供一种苄基异喹啉衍生物；

(b)使该苄基异喹啉衍生物与一种酶混合物接触，该酶混合物能够在允许将该苄基异喹啉衍生物转化成(R)-网状番荔枝碱或(R)-网状番荔枝碱前体的条件下将该苄基异喹啉衍生物转化成(R)-网状番荔枝碱或(R)-网状番荔枝碱前体；

其中该苄基异喹啉衍生物具有化学式：

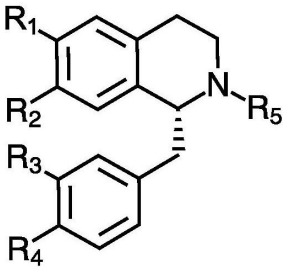


；

其中R_1、R_2、R_3以及R_4各自表示氢原子、羟基基团或甲氧基基团；

并且其中R_5表示氢原子或甲基基团；并且

其中该(R)-网状番荔枝碱前体具有化学式：



；

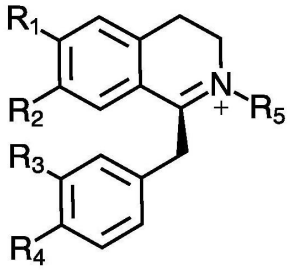
其中R_1、R_2、R_3以及R_4各自表示氢原子、羟基基团或甲氧基基团；

并且其中R_5表示氢原子或甲基基团，其条件是(R)-网状番荔枝碱被排除在该化学式之外。

实施方式3、根据实施方式2所述的方法，其中该苄基异喹啉衍生物选自下组，该组由以下各项组成：(S)-N-甲基乌药碱、(S)-3'-羟基-N-甲基乌药碱和(S)-网状番荔枝碱，并且其中该(R)-网状番荔枝碱前体选自(R)-N-甲基乌药碱、(R)-3'-羟基-N-甲基乌药碱。

实施方式4、根据实施方式2所述的方法，其中该酶混合物包含一种能够将该苄基异喹啉前体氧化以形成氧化苄基异喹啉前体的第一多肽和一种能够将该氧化苄基异喹啉前体还原以形成(R)-网状番荔枝碱或(R)-网状番荔枝碱前体的第二多肽，其中该氧化苄基

异喹啉前体具有化学式：



；

其中R_1、R_2、R_3以及R_4各自表示氢原子、羟基或甲氧基基团；

并且其中R_5表示氢原子或甲基基团。

实施方式5、根据实施方式4所述的方法，其中能够将该苄基异喹啉前体氧化成该氧化苄基异喹啉前体的该第一多肽是一种细胞色素P450，并且能够将该苄基异喹啉前体还原以形成(R)-网状番荔枝碱或(R)-网状番荔枝碱前体的该第二多肽是一种醛-酮还原酶。

实施方式6、根据实施方式4或5所述的方法，其中该第一多肽是一种选自下组的多肽，该组由以下各项组成：NO:219至SEQ.ID NO:321；SEQ.ID NO:325；以及SEQ.ID NO:338，并且其中该第二多肽是一种选自下组的多肽，该组由以下各项组成：SEQ.ID NO:59至SEQ.ID NO:115；SEQ.ID NO:327；SEQ.ID NO:329；SEQ.ID NO:330以及SEQ.ID NO:340。

实施方式7、根据实施方式4或5所述的方法，其中该第一多肽和该第二多肽是一种融合多肽。

实施方式8、根据实施方式7所述的方法，其中该融合多肽是在SEQ.ID NO:323中列出的该多肽。

实施方式9、根据实施方式1-8所述的方法，其中该方法在体内或体外进行。

实施方式10、根据实施方式5-9所述的方法，其中该细胞色素P450和该醛-酮还原酶可获得自以下植物家族的组中的一个成员，该组由以下各项组成：罂粟科、樟科、番荔枝科、大戟科以及桑科。

实施方式11、根据实施方式10所述的方法，其中植物家族的该成员选自以下植物物种的组，该组由以下各项组成：罂粟、大红罂粟以及虞美人。

实施方式12、一种用于制备(R)-网状番荔枝碱或(R)-网状番荔枝碱前体的方法，该方法包括：

(a)提供一种嵌合核酸序列，该嵌合核酸序列包含作为可操作地连接部件的以下各项：

(i)一种编码CYP450多肽的第一核酸序列；

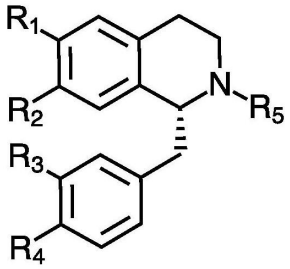
(ii)一种编码AKR多肽的第二核酸序列；以及

(iii)能够控制在宿主细胞中的表达的一种或多种核酸序列；

(b)将该嵌合核酸序列引入一个宿主细胞中并且使该宿主细胞生长以产生CYP450和AKR，并且产生(R)-网状番荔枝碱或该(R)-网状番荔枝碱前体；并且

(c)回收(R)-网状番荔枝碱或该(R)-网状番荔枝碱前体。

实施方式13、根据实施方式12所述的方法，其中该(R)-网状番荔枝碱前体具有化学式：



;

其中R_1、R_2、R_3以及R_4各自表示氢原子、羟基基团或甲氧基基团；

并且其中R_5表示氢原子或甲基基团，其条件是(R)-网状番荔枝碱被排除在该化学式之外。

实施方式14、根据实施方式12或13所述的方法，其中该第一核酸序列和该第二核酸序列被可操作地连接以便产生一种包含CYP450和AKR的融合多肽。

实施方式15、根据实施方式12-14所述的方法，其中编码CYP450的该核酸序列选自下组，该组由以下各项组成：SEQ.ID NO:116至SEQ.ID NO:218；SEQ.ID NO:324；以及SEQ.ID NO:337，并且其中编码AKR的该核酸序列选自下组，该组由以下各项组成：SEQ.ID NO:1至SEQ.ID NO:58；SEQ.ID NO:326；SEQ.ID NO:328；以及SEQ.ID NO:339。

实施方式16、根据实施方式12-14所述的方法，其中该CYP450和该AKR可获得自以下植物家族的组中的一个成员，该组由以下各项组成：罂粟科、樟科、番荔枝科、大戟科以及桑科。

实施方式17、根据实施方式16所述的方法，其中植物家族的该成员选自以下植物物种的组，该组由以下各项组成：罂粟、大红罂粟以及虞美人。

实施方式18、一种用于制备(R)-网状番荔枝碱或(R)-网状番荔枝碱前体的方法，该方法包括：

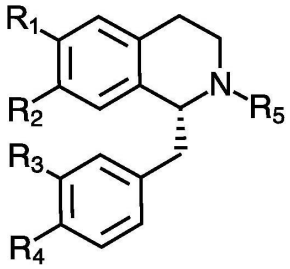
(a)提供一种第一嵌合核酸序列，该第一嵌合核酸序列包含作为可操作地连接部件的一种编码CYP450多肽的第一核酸序列和一种控制该第一核酸序列在细胞中的表达的第一核酸序列；

(b)提供一种第二嵌合核酸序列，该第二嵌合核酸序列包含作为可操作地连接部件的一种编码AKR多肽的第二核酸序列和一种控制该第二核酸序列在细胞中的表达的第二核酸序列；

(c)将该第一嵌合核酸序列和该第二嵌合核酸序列引入一个宿主细胞中并且使该宿主细胞生长以产生CYP450和AKR，并且产生(R)-网状番荔枝碱或(R)-网状番荔枝碱前体；并且

(d)回收(R)-网状番荔枝碱或(R)-网状番荔枝碱前体。

实施方式19、根据实施方式18所述的方法，其中该(R)-网状番荔枝碱前体具有化学式：



;

其中R_1、R_2、R_3以及R_4各自表示氢原子、羟基基团或甲氧基基团；

并且其中R_5表示氢原子或甲基基团，其条件是(R)-网状番荔枝碱被排除在该化学式之外。

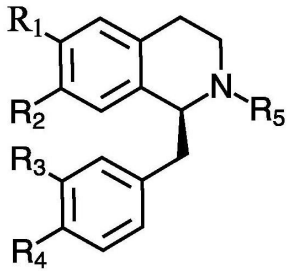
实施方式20、根据实施方式19所述的方法，其中编码CYP450的该核酸序列选自下组，该组由以下各项组成：SEQ.ID NO:116至SEQ.ID NO:218；SEQ.ID NO:324以及SEQ.ID NO:337，并且其中编码AKR的该核酸序列选自下组，该组由以下各项组成：SEQ.ID NO:1至SEQ.ID NO:58；SEQ.ID NO:326；SEQ.ID NO:328；以及SEQ.ID NO:339。

实施方式21、根据实施方式18或19所述的方法，其中该CYP450和该AKR可获得自以下植物家族的组中的一个成员，该组由以下各项组成：罂粟科、樟科、番荔枝科、大戟科以及桑科。

实施方式22、根据实施方式21所述的方法，其中植物家族的该成员选自以下植物物种的组，该组由以下各项组成：罂粟、大红罂粟以及虞美人。

实施方式23、一种用于制备(R)-网状番荔枝碱或(R)-网状番荔枝碱前体的组合物，该组合物包含一种酶混合物，该酶混合物包含一种能够将一种苄基异喹啉衍生物氧化以形成一种氧化苄基异喹啉衍生物的第一多肽和一种能够将该氧化苄基异喹啉衍生物还原以形成(R)-网状番荔枝碱或(R)-网状番荔枝碱前体的第二多肽；

其中该苄基异喹啉类生物碱衍生物具有化学式

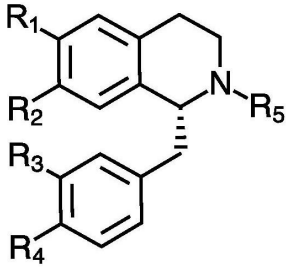


;

其中R_1、R_2、R_3以及R_4各自表示氢原子、羟基基团或甲氧基基团；

并且其中R_5表示氢原子或甲基基团；并且

其中该(R)-网状番荔枝碱前体具有化学式：



;

其中R_1、R_2、R_3以及R_4各自表示氢原子、羟基基团或甲氧基基团；

并且其中R_5表示氢原子或甲基基团，其条件是(R)-网状番荔枝碱被排除在该化学式之外。

实施方式24、根据实施方式23所述的组合物，其中该第一多肽是一种细胞色素P450并且该第二多肽是一种醛-酮还原酶。

实施方式25、根据实施方式23或24所述的组合物，其中该第一多肽是一种选自下组的多肽，该组由以下各项组成：NO:219至SEQ.ID NO:321；SEQ.ID NO:325；以及SEQ.ID NO:338，并且其中该第二多肽是一种选自下组的多肽，该组由以下各项组成：SEQ.ID NO:59至SEQ.ID NO:115；SEQ.ID NO:327；SEQ.ID NO:329；SEQ.ID NO:330以及SEQ.ID.NO:340。

实施方式26、根据实施方式23-25所述的组合物，其中该第一多肽和该第二多肽是一种融合多肽。

实施方式27、根据实施方式23至24或实施方式26所述的组合物，其中该细胞色素P450和该醛-酮还原酶可获得自以下植物家族的组中的一个成员，该组由以下各项组成：罂粟科、樟科、番荔枝科、大戟科以及桑科。

实施方式28、根据实施方式27所述的组合物，其中植物家族的该成员选自以下植物物种的组，该组由以下各项组成：罂粟、大红罂粟以及虞美人。

实施方式29、一种重组表达载体，包含作为可操作地连接部件的以下各项：

(i)一种能够控制在宿主细胞中的表达的核酸序列；以及

(ii)一种编码CYP450的核酸序列，

其中该表达载体适合于在宿主细胞中的表达。

实施方式30、根据实施方式29所述的重组表达载体，其中编码CYP450的该核酸序列是一种选自下组的核酸序列，该组由以下各项组成：SEQ.ID NO:116至SEQ.ID NO:218；SEQ.ID NO:324；以及SEQ.ID NO:337。

实施方式31、根据实施方式29所述的重组表达载体，其中该CYP450可获得自罂粟科、樟科、番荔枝科、大戟科以及桑科组成的植物家族的一个成员。

实施方式32、根据实施方式31所述的方法，其中植物家族的该成员选自由罂粟、大红罂粟以及虞美人组成的植物物种。

实施方式33、一种重组表达载体，包含作为可操作地连接部件的以下各项：

(i)一种能够控制在宿主细胞中的表达的核酸序列；以及

(ii)一种编码AKR的核酸序列，

其中该表达载体适合于在宿主细胞中的表达。

实施方式34、根据实施方式34所述的重组表达载体，其中编码AKR的该核酸序列选自下组，该组由以下各项组成：SEQ.ID NO:1至SEQ.ID NO:58；SEQ.ID NO:326；SEQ.ID NO:328；以及SEQ.ID NO:339。

实施方式35、根据实施方式33所述的重组表达载体，其中该AKR可获得自罂粟科、樟科、番荔枝科、大戟科以及桑科组成的植物家族的一个成员。

实施方式36、根据实施方式35所述的方法，其中植物家族的该成员选自由罂粟、大红罂粟以及虞美人组成的植物物种。

实施方式37、一种重组表达载体，包含作为可操作地连接部件的以下各项：

(i)一种能够控制在宿主细胞中的表达的核酸序列；以及

(ii)一种编码CYP450和AKR的核酸序列，

其中该表达载体适合于在宿主细胞中的表达。

实施方式38、根据实施方式37所述的重组表达载体，其中编码CYP450的该核酸序列是一种选自下组的核酸序列，该组由以下各项组成：SEQ.ID NO:116至SEQ.ID NO:218；SEQ.ID NO:324以及SEQ.ID NO:337，并且其中编码AKR的该核酸序列是一种选自下组的核酸序列，该组由以下各项组成：SEQ.ID NO:1至SEQ.ID NO:58；SEQ.ID NO:326；SEQ.ID NO:328；以及SEQ.ID NO:339。

实施方式39、根据实施方式37所述的重组表达载体，其中该AKR和该CYPR可获得自罂粟科、樟科、番荔枝科、大戟科以及桑科组成的植物家族的一个成员。

实施方式40、根据实施方式39所述的方法，其中植物家族的该成员选自由罂粟、大红罂粟以及虞美人组成的植物物种。

实施方式41、一种制备(R)-网状番荔枝碱的方法，该方法包括：

(a)提供(S)-网状番荔枝碱；并且

(b)使(S)-网状番荔枝碱与一种酶混合物接触，该酶混合物能够在允许将(S)-网状番荔枝碱转化成(R)-网状番荔枝碱的条件下将(S)-网状番荔枝碱转化成(R)-网状番荔枝碱。

实施方式42、根据实施方式41所述的方法，其中该酶混合物包含一种能够将(S)-网状番荔枝碱氧化以形成1,2-脱氢网状番荔枝碱的第一多肽和一种能够将1,2-脱氢网状番荔枝碱还原以形成(R)-网状番荔枝碱的第二多肽。

实施方式43、根据实施方式41所述的方法，其中能够将(S)-网状番荔枝碱氧化以形成1,2-脱氢网状番荔枝碱的该第一多肽是一种细胞色素P450，并且能够将1,2-脱氢网状番荔枝碱还原以形成(R)-网状番荔枝碱的该第二多肽是一种醛-酮还原酶。

实施方式44、根据实施方式41-42所述的方法，其中该第一多肽选自下组，该组由以下各项组成：NO:219至SEQ.ID NO:321；SEQ.ID NO:325；以及SEQ.ID NO:338，并且其中该第二多肽选自下组，该组由以下各项组成：SEQ.ID NO:59至SEQ.ID NO:115；SEQ.ID NO:327；SEQ.ID NO:329；SEQ.ID NO:330以及SEQ.ID NO:340。

实施方式45、根据实施方式42-44所述的方法，其中该第一多肽和该第二多肽是一种融合多肽。

实施方式46、根据实施方式41-45所述的方法，其中该方法在体内或体外进行。

实施方式47、根据实施方式43或45-46所述的方法，其中该细胞色素P450和该醛-酮还原酶可获得自罂粟科、樟科、番荔枝科、大戟科以及桑科组成的植物家族的一个成员。

实施方式48、根据实施方式47所述的方法，其中植物家族的该成员选自由罂粟、大红罂粟以及虞美人组成的植物物种。

实施方式49、一种用于制备(R)-网状番荔枝碱的方法，该方法包括：

(a)提供一种嵌合核酸序列，该嵌合核酸序列包含作为可操作地连接部件的以下各项：

(i)一种编码CYP450多肽的第一核酸序列；

(ii)一种编码AKR多肽的第二核酸序列；以及

(iii)能够控制在宿主细胞中的表达的一种或多种核酸序列；

(b)将该嵌合核酸序列引入一个宿主细胞中并且使该宿主细胞生长以产生CYP450和AKR,并且产生(R)-网状番荔枝碱;并且

(c)回收(R)-网状番荔枝碱。

实施方式50、根据实施方式51所述的方法,其中该第一核酸序列和该第二核酸序列被可操作地连接以便产生一种包含CYP450和AKR的融合多肽。

实施方式51、根据实施方式49或50所述的方法,其中编码CYP450的该核酸序列选自下组,该组由以下各项组成:SEQ.ID NO:116至SEQ.ID NO:218;SEQ.ID NO:324;以及SEQ.ID NO:337,并且其中编码AKR的该核酸序列选自下组,该组由以下各项组成:SEQ.ID NO:1至SEQ.ID NO:58;SEQ.ID NO:326;SEQ.ID NO:328;SEQ.ID NO:339。

实施方式52、根据实施方式49或50所述的方法,其中该CYP450和该AKR可获得自罂粟科、樟科、番荔枝科、大戟科以及桑科组成的植物家族的一个成员。

实施方式53、根据实施方式52所述的方法,其中植物家族的该成员选自由罂粟、大红罂粟以及虞美人组成的植物物种。

实施方式54、一种用于制备(R)-网状番荔枝碱的方法,该方法包括:

(a)提供一种第一嵌合核酸序列,该第一嵌合核酸序列包含作为可操作地连接部件的一种编码CYP450多肽的第一核酸序列和一种控制该第一核酸序列在细胞中的表达的第一核酸序列;

(b)提供一种第二嵌合核酸序列,该第二嵌合核酸序列包含作为可操作地连接部件的一种编码AKR多肽的第二核酸序列和一种控制该第二核酸序列在细胞中的表达的第二核酸序列;

(c)将该第一嵌合核酸序列和该第二嵌合核酸序列引入一个宿主细胞中并且使该宿主细胞生长以产生CYP450和AKR,并且产生(R)-网状番荔枝碱;并且

(d)回收(R)-网状番荔枝碱。

实施方式55、根据实施方式54所述的方法,其中编码CYP450的该核酸序列是一种选自下组的核酸序列,该组由以下各项组成:SEQ.ID NO:116至SEQ.ID NO:218;SEQ.ID NO:324以及SEQ.ID NO:337,并且其中编码AKR的该核酸序列是一种选自下组的核酸序列,该组由以下各项组成:SEQ.ID NO:1至SEQ.ID NO:58;SEQ.ID NO:326;SEQ.ID NO:328;以及SEQ.ID NO:339。

实施方式56、根据实施方式54所述的方法,其中该CYP450和该AKR可获得自罂粟科、樟科、番荔枝科、大戟科以及桑科组成的植物家族的一个成员。

实施方式57、根据实施方式56所述的方法,其中植物家族的该成员选自由罂粟、大红罂粟以及虞美人组成的植物物种。

实施方式58、一种用于制备(R)-网状番荔枝碱的组合物,该组合物包含一种酶混合物,该酶混合物包含一种能够将(S)-网状番荔枝碱氧化以形成1,2-脱氢网状番荔枝碱的第一多肽和一种能够将1,2-脱氢网状番荔枝碱还原以形成(R)-网状番荔枝碱的第二多肽。

实施方式59、根据实施方式58所述的组合物,其中该酶混合物包含一种能够将(S)-网状番荔枝碱氧化以形成1,2-脱氢网状番荔枝碱的第一多肽和一种能够将1,2-脱氢网状番荔枝碱还原以形成(R)-网状番荔枝碱的第二多肽。

实施方式60、根据实施方式59所述的组合物,其中能够将(S)-网状番荔枝碱氧化

以形成1,2-脱氢网状番荔枝碱的该第一多肽是一种细胞色素P450,并且能够将1,2-脱氢网状番荔枝碱还原以形成(R)-网状番荔枝碱的该第二多肽是一种醛-酮还原酶。

实施方式61、根据实施方式58-60所述的组合物,其中该第一多肽选自下组,该组由以下各项组成:NO:219至SEQ.ID NO:321;SEQ.ID NO:325;以及SEQ.ID NO:338,并且其中该第二多肽选自下组,该组由以下各项组成:SEQ.ID NO:59至SEQ.ID NO:115;SEQ.ID NO:327;SEQ.ID NO:329;SEQ.ID NO:330以及SEQ.ID NO:340。

实施方式62、根据实施方式58-61所述的组合物,其中该第一多肽和该第二多肽是一种融合多肽。

实施方式63、根据实施方式58-60和61所述的组合物,其中该细胞色素P450和该醛-酮还原酶可获得自罂粟科、樟科、番荔枝科、大戟科以及桑科组成的植物家族的一个成员。

实施方式64、根据实施方式63所述的组合物,其中植物家族的该成员选自由罂粟、大红罂粟以及虞美人组成的植物物种。

实施方式65、一种检测编码AKR和/或CYP450的核酸序列在细胞中的存在或不存在的方法,该方法包括:

(a)提供一种细胞;

(b)从该细胞提取基因组DNA;并且

(c)针对编码AKR和/或CYP450的核酸序列的存在分析该基因组DNA。

实施方式66、根据实施方式65所述的方法,其中该细胞是一种可获得自一种植物的植物细胞,该植物属于由罂粟科、樟科、番荔枝科、大戟科以及桑科组成的植物家族。

实施方式67、根据实施方式65所述的方法,其中该植物细胞可获得自一种植物,该植物属于由罂粟、大红罂粟以及虞美人组成的植物家族。

实施方式68、一种用于调节核酸序列在天然表达AKR和/或CYP450的细胞中的表达的方法,该方法包括:

(a)提供一种天然表达AKR和/或CYP450的细胞;

(b)诱变处理该细胞;

(c)使细胞生长以获得多个细胞;并且

(d)确定该多个细胞是否包括一种包含调节水平的AKR和/或CYP450的细胞。

实施方式69、根据实施方式68所述的方法,其中该细胞是一种可获得自一种植物的植物细胞,该植物属于由罂粟科、樟科、番荔枝科、大戟科以及桑科组成的植物家族。

实施方式70、根据实施方式68所述的方法,其中该植物细胞可获得自一种植物,该植物属于由罂粟、大红罂粟以及虞美人组成的植物家族。

实施方式71、一种用于产生结籽植物的方法,该结籽植物包含核酸序列在天然表达AKR和/或CYP450的细胞中的调节表达,该方法包括:

(a)提供一种天然表达AKR和/或CYP450的结籽植物;

(b)诱变该植物的种子以获得诱变的种子;

(c)使该诱变的种子生长成能够结籽下一代种子的下一代诱变植物;并且

(d)获得这些诱变植物的下一代种子或另一个部分,并且分析这些下一代植物或下一代种子是否表现出调节的AKR和/或CYP450表达。

实施方式72、根据实施方式71所述的方法，其中该植物属于由罂粟科、樟科、番荔枝科、大戟科以及桑科组成的植物家族。

实施方式73、根据实施方式71所述的方法，其中该植物属于由罂粟、大红罂粟以及虞美人组成的植物家族。

实施方式74、一种产生表达降低水平的AKR和/或CYP450的植物的方法，该方法包括：

(a)提供一种表达AKR和/或CYP450的植物；并且

(b)使用病毒诱导性基因沉默降低AKR和/或CYP450在该植物中的表达。

实施方式75、根据实施方式74所述的方法，其中该植物属于由罂粟科、樟科、番荔枝科、大戟科以及桑科组成的植物家族。

实施方式76、根据实施方式74所述的方法，其中该植物属于由罂粟、大红罂粟以及虞美人组成的植物家族。

实施方式77、根据实施方式69-76所述的方法，其中这些方法提供在能够天然产生生物碱的植物中的生物碱产生水平的调节。

实施方式78、根据实施方式77所述的方法，其中该生物碱选自以下生物碱的组，该组由以下各项组成：吗啡、可待因、蒂巴因、罂粟碱、那可丁、(S)-网状番荔枝碱、(R)-网状番荔枝碱、可旦民碱、劳丹碱以及劳丹素。

实施方式79、一种编码AKR或CYP450的核酸序列对植物进行基因分型的用途。

实施方式80、根据实施方式79所述的用途，其中该植物是由罂粟科、樟科、番荔枝科、大戟科以及桑科组成的植物家族的一个成员。

实施方式81、根据实施方式79所述的用途，其中该植物选自由罂粟、大红罂粟以及虞美人组成的植物家族。

实施方式82、一种编码AKR或CYP450的核酸序列作为标记物评估植物群体中遗传连接至其上的核酸序列的分离的用途。

实施方式83、根据实施方式82所述的用途，其中该植物群体包括属于由罂粟科、樟科、番荔枝科、大戟科以及桑科组成的植物家族的植物。

实施方式84、根据实施方式82所述的用途，其中该植物群体包括属于由罂粟、大红罂粟以及虞美人组成的植物家族的植物。

Sequence Listing

[0001]

1	**Sequence Listing Information**	
1-1	File Name	079690-8003CN03.xml
1-2	DTD Version	V1_3
1-3	Software Name	WIPO Sequence
1-4	Software Version	2.1.2
1-5	Production Date	2022-08-10
1-6	Original free text language code	
1-7	Non English free text language code	
2	**General Information**	
2-1	Current application: IP Office	
2-2	Current application: Application number	
2-3	Current application: Filing date	
2-4	Current application: Applicant file reference	079690-8003CN03
2-5	Earliest priority application: IP Office	US
2-6	Earliest priority application: Application number	US 61/911,759
2-7	Earliest priority application: Filing date	2013-12-04
2-8zh	Applicant name	安思雅公司
2-8	Applicant name: Name Latin	Antheia, Inc.
2-9	Inventor name	
2-9	Inventor name: Name Latin	
2-10zh	Invention title	用于制备(R)-网状番荔枝碱及其前体的组合物和方法
2-11	Sequence Total Quantity	340
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[0002]

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[0003]

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3-7-4-1	Features Location/Qualifiers	**source** 1..975 mol_type= genomic DNA organism= Corydalis chelantifolia
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3-7-5	Residues	atgatggtga gtgttcctga ggtgacactg cagagtagtt ccagtgataa aaagatgcct 60 attatgggca tgggcactgc agcctatcct ttcgccgaat cagatgaagc aaaggctgca 120 ctcttaactt caatcaagct tggttacaga cattttgata cagcttcact gtaccacaat 180 gagaagtctg taggtaaagc tatatctgag gctcttaaac tcggactcgt caaatctcga 240 gatgaattct acatcaactc caagctatgg tgctctgatt ctcacccaga ccgagtcatc 300 cctgcccttc aagagtcact caagaagctt gggttggagt accttgatat gtatcttatt 360 cattggccat tgagcttgaa gaaagggagt tatgagttcc ctataccaac ggacgaggaa 420 atactaccta tggacttcaa ggcagtatgg gcagccatgg aggagtgcca aaagcttggc 480 ctcactaagt ccattggtgt cagcaacttt tcttgtaaga agcttgaaac aattctctct 540 acggccaaga tacctcctgt tgttaatcag gtggagttga acacactttg gcaacagacg 600 aaactaaaca aattttgtaa ggacaatggt atcgttctta tggcattttc ccctttggga 660 gctcacggaa gtccttgggg aacaaaccgt gttatggaat gcgagttact tcatgagatt 720 gcaaaggcaa aaggaaagac tcttgctcag gtttgtctga gatggatata tgagcaaggt 780 gctggtatat tagtaaagag ctacaatgaa gtgcggatga aggaaaacct ggagatattc 840 gattgggaat tgagtgcaga agagttgaaa agtatcagtg aacttccaca gcatagaggc 900 ttcccagctg attctctcct ctcagctaaa gggccattta gaactgaaga agagctctgg 960 gatggagaga tctga 975
3-8	**Sequences**	
3-8-1	Sequence Number [ID]	8

[0004]

[0005]

3-8-2	Molecule Type	DNA
3-8-3	Length	1020
3-8-4-1	Features Location/Qualifiers	**source** 1..1020 mol_type= genomic DNA organism= Corydalis chelantifolia
	NonEnglishQualifier Value	
3-8-5	Residues	atggagagtg ttgcttgtga gcctggagta atcgagcagc agcagtactt tattcccgag 60 gtgacctgcg gtggaggcag cagcaccacc aggatgagga tgcctgttgt aggcatgggt 120 acagcctcgt acccgtttgc tggatcagaa ggtgtaaagc aagctctctt acatgcaatc 180 aagcttggtt actggcattt tgatacagct tctttttacc agaccgagca atctctgggt 240 gaagctatct ctgaggcaat ccaacttggg ctgatcaaat ctagagatga actcttcatc 300 acttctaagc tgtggtgcac tgatgcacac aaagatcttg tcctccctgc ccttcaaaac 360 accctcagga atcttcaatt ggagtacctt gacctttacc ttatacattt tccgataagc 420 ttgaagccag ggagatatga tttccctgta caatcaaagg aggacctcct tccaatggac 480 tttaaatcta tatgggcaaa aatggaagag tgtcagggac ttgggctcac taaatccatt 540 ggtgtcagca atttttcatg caagaaactt gaaaatttac ttgccacagc caagattcct 600 cctgctgtta atcaggtaga gatgaatcca ctttggcaac aaaagaaact aagggagttc 660 tgtaaagcta atggtatcac tattacggcc cactcccctt taggagccaa aggaactaat 720 tggggaacca accgtgtagt agaatgtgaa gtgttgcacc agattgccaa ggctaaagga 780 aaatctcatg ctcaggtttg tttgagatgg gtatatgagc aaggagtgag tctgttggtg 840 aagagcttca acaaagaaag gatgaaagag aacctgggga tatttgactg ggaattgaat 900 gctgaagatt taaagaagat cagtgagatt ccacagggta gaggactacc tgttgatggt 960 tttctttcac caaatggtcc tttcaagtct gaagaagaat tttgggatgg agagatttga 1020
3-9	**Sequences**	
3-9-1	Sequence Number [ID]	9
3-9-2	Molecule Type	DNA
3-9-3	Length	906
3-9-4-1	Features Location/Qualifiers	**source** 1..906 mol_type= genomic DNA organism= Corydalis chelantifolia
	NonEnglishQualifier Value	
3-9-5	Residues	atgcctgtag taggctttgg cacggctaaa tttccctttg gtgatgatga agcgattaaa 60 ttggcagttc ttgaaggaat caagcttggt tacagacact tcgacactgc tactaaatat 120 aaatcagaga agcctctcgg tgaaaccatt gttgaagcta ttaaccttgg tttaatcaaa 180 tctcgtgatg aattattcat cacgtccaaa ttatggtgtg gaagcactga gcgcagcctc 240 atcgtacctt cactcaagac gagtttacag aatctccaat tggactacct agatctttat 300 ctcatacatt ggcccctgag gtttagcacc gacgaaactc caacaccagt cccaaaggaa 360 caacttcttc cctttgacac caagtcagtt tggcaagcaa tggaagaatg ccaaaatctc 420 gggctcacga aatcgattgg tgtgagtaat ttctcatgca aaaaacttga agaattacta 480 tccactgcga agatcactcc ggcagttaat caagtggagt tgaacacatc ttggcaacag 540 acgaagatga gagagttctg taaaggaaaa ggtatacata taactggtta ttcacctcta 600 ggttcctatg gaacaaaatg gggagacaac agagttgttg agaatcaagt gttggaggag 660 attggcaagc ctagaggaaa aactgctgtt caggtttgct tgagatggat atatgagcag 720 ggagcaagta tggttgtcaa aagctttaac aaagagagga tgaaggctaa ccttgacatt 780 tttgattgga agttaactga ggaagagttg aagaggatca gtcagcttcc acagcataaa 840 gcatccctac ctactgcctc ctttggcgac catgatgaag ttagggagct tgactatgag 900 atctga 906
3-10	**Sequences**	
3-10-1	Sequence Number [ID]	10
3-10-2	Molecule Type	DNA
3-10-3	Length	984
3-10-4-1	Features Location/Qualifiers	**source** 1..984 mol_type= genomic DNA organism= Chelidonium majus

[0006]

	NonEnglishQualifier Value	
3-10-5	Residues	atggagagtg atagtgcagc agcagcagta gtagttccag taacgactct gagctcaggc 60 attgagatgc cgatgttagg tatgggaact gttgaaaact ttcttccagg ttccgaaaca 120 gtgaagttgg ctcttctgaa tgcaataaaa ttagggtaca ggcacttcga cacagctgct 180 atataccaaa ctgaggagtg tcttggtgaa gctgtagctg aagcacttca acttggtctg 240 atcaaatcta gagaccaact cttcatcact tccaagcttt ggtgttctga cgctcatcct 300 gatcttgtca tccctgctct tcagaactct ctcaggaagc tgaagttgga gtatcttgat 360 ttatatctgg tacattggcc gttaagctca aagccaggga actgtgtttt tccaatactc 420 aaggaggacc tccttccttt ggacttcaag tctgtgtggg cagccatgga agaatgtcaa 480 aagcttggcc tcacaaagtc aattggtgtt agcaacttct cttgtaagaa gcttcaagat 540 ttattgactt cggctatcat ccctcccgtt gttaatcaag tggagatgaa cccacgttgg 600 caacaaaaga aactgagaga gttttgtaag gccagagata ttgtggttac cgcctactcg 660 cctctgggag ccaaaggcac cgtgtatgga tccggtgcag ttatggactg cgaggtgttg 720 caccagattg ccaagattag agggaagtct gttgctcagg tttctctaag atgggtatac 780 cagcaaggtg tgacaccgtt agtgaagagt ttcaatgaag aaaggatgaa ggagaacatg 840 aagatattcg attgggaatt gtacgaagaa gacttaaaaa tgatcgacga gatcccacaa 900 agtagagtca accttgttta ttttttcctc tcagaaaacg gacccttcaa gactgtagaa 960 gaattctggg atggagaagt ctaa 984
3-11	**Sequences**	
3-11-1	Sequence Number [ID]	11
3-11-2	Molecule Type	DNA
3-11-3	Length	984
3-11-4-1	Features Location/Qualifiers	**source** 1..984 mol_type= genomic DNA organism= Chelidonium majus
	NonEnglishQualifier Value	
3-11-5	Residues	atggagagta gtaataatgc agtattagtt ccagtaataa ctctgaactc aggcagggag 60 atgccaattg ttggtatggg aacagctgaa aacctttttc aaggttcaga aagagtgaag 120 ttggctcttt tgactgcaat aaaggtgggt tatagacact ttgatacagc tgctgtttac 180 cagactgagg agtctcttgg tgaagctata gctgaagcac ttcaacttgg actgatcaaa 240 tctagagatg aactcttcat cacttccaag ctgtggttgc ctgattgtca ccatgatctt 300 gtcctccctg ctcttcagaa ttctctcagg aagcttaagt tggagtacct tgacctatat 360 ttgatacatt ggccggtaag ctcgaagcca ggagagatca agcatgttat accaaaggaa 420 gagctcctcc caatggattt caagtctgtg tgggcagcca tggaagaatg tcacaagctt 480 ggcctcgcca agtcaattgg agtcagcaac ttctcttgca agaagcttca agatttatta 540 gtcactgcca acatccctcc tgatgttaac caagtggaga tgaacccact ttggcagcag 600 acgaaactga gggaattttg taaggctcac ggcatcctcg ttgcagctta ctcgccttta 660 ggagccaaag gcactgcatg gggaagaacc aacggagtta tggactctga ggtgctacaa 720 cagattgcca aggctagagg aaagtctatt gcgcaggttt ctctacgatg ggtatatgaa 780 caaggggtgg ttttgttggt gaagagtttc aacgaggaaa ggatgaagga aaacctgaag 840 atattcgatt gggaattaag tggagaagac ttgaaaaaga tcagcgagat cctcccacag 900 cgtagaggac tccctagtca tgtttttgtc tccgatgacg ggccattcaa gtctgaggaa 960 gaactctggg atggagaagt gtga 984
3-12	**Sequences**	
3-12-1	Sequence Number [ID]	12
3-12-2	Molecule Type	DNA
3-12-3	Length	984
3-12-4-1	Features Location/Qualifiers	**source** 1..984 mol_type= genomic DNA organism= Chelidonium majus
	NonEnglishQualifier Value	
3-12-5	Residues	atggagagta gtaataatgc agtattagtt ccagtaataa ctctgaactc aggcagggag 60 atgccaattg ttggtatggg aacagctgaa aacctttttc aaggttcaga aagagtgaag 120 ttggctcttt tgactgcaat aaaggtgggt tatagacact ttgatacagc tgctgtttac 180 cagactgagg agtctcttgg tgaagctata gctgaagcac ttcaacttgg actgatcaaa 240 tccagagatg aactcttcgt cacttccaag ttgtggattc ctgattgtca ccatgatctt 300 gtcctccctg ctcttcaaaa ttctctcagg aagcttaagt tggagtacct tgacctctat 360

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		ttgatacatt ggccagtaag ctctaagcca ggggagctca ggtcacttat accaaaggag 420 gagctccttc caatggattt caagtctgtg tgggtggcca tggaagaatg tcacaagctt 480 ggcctcacaa agtcaattgg tgttagcaac ttctcttgca agaagcttcg agatttattg 540 ctcactgcca acatccctcc tgctgttaac caagtggaga tgaacccgct ttggcaacag 600 aagaaactga gggagttttg taaggccaac ggtatcgtca ttgcagctta ctcgccttta 660 ggagccaaag gcactgcatg gggaagaacc aacgacggag ttatggactc tgagttgcta 720 caaaagattg ccaaggctag aggaaagtct acggcgcagg tttctctacg atggggatat 780 gaacaagggg tgattttgtt ggtgaagagt ttcaatgaag agaggatgaa ggaaaacctg 840 aagacattcg attgggaatt aagtggagaa gacttgaaac agatcaacga gatcctccca 900 cagcgtagag gacatagcca tgaatttatc tcagataacg ggccattcaa gtctgaggaa 960 gagctatggg atggagaagt gtga 984
3-13	**Sequences**	
3-13-1	Sequence Number [ID]	13
3-13-2	Molecule Type	DNA
3-13-3	Length	987
3-13-4-1	Features Location/Qualifiers	**source** 1..987 mol_type= genomic DNA organism= Chelidonium majus
	NonEnglishQualifier Value	
3-13-5	Residues	atgggtgagg aaatgatcaa gacgagtagt gttgaaattc cagtagcgac tctaagcact 60 gggaggacga tgccgttgtt aggtatgggg acagcagcat acccatttgt ggggtcagat 120 ggagtggtga aagcgattct gcacgcgatt aagctagggt acaggcactt tgatacagct 180 gctctatact ttacagagga atgtcttggt gatgctgtag ctgaagcact tcgccttgga 240 ttgatcaaat ctcgagatga actcttcatc acctcaaagt tatattgctg tgatgctcat 300 cctgatcgcg tcgtccctgc tcttcagaac tctctcagga agctgaaaat ggagtacctt 360 gatctatatt tgatacattg gccggcaagc acacacgaag ggaacttcga atttccttta 420 caaaagcagg atatccttcc tttggatttc aagtctgtgt gggcagctat ggaagaatgt 480 caaaagcttg gcctcaccaa gtcaattggt gtcagcaact tctcttgcaa gaaacttcaa 540 gatttactag cctcggctaa gatccctccc gctgttaatc aagtggagat gaacccaatt 600 tggcaacaga ataaattgag ggaattctgc aaggcaaatg atatccacat tacagcgtac 660 tcgcctttgg gggccaatgg aactccttgg ggctctagtg gagttgccga aactcaagtg 720 ctgcacgaca ttgctaaggc tagagggaag actcatgctc aggtttgttt gcgatgggta 780 tatgagcaag gtgtgagtgt gttggttaag agttacaatg aagagaggat gaaggagaat 840 ctggctgtat tggattggga attgagcgaa gagaacttga agaagattag tgaaatccca 900 caacgtagag gacttcctgg tgatatcttc gtctcagata acgggccttt caaaactgta 960 gaagagctct gggatggaga agtatga 987
3-14	**Sequences**	
3-14-1	Sequence Number [ID]	14
3-14-2	Molecule Type	DNA
3-14-3	Length	921
3-14-4-1	Features Location/Qualifiers	**source** 1..921 mol_type= genomic DNA organism= Cocculus trilobus
	NonEnglishQualifier Value	
3-14-5	Residues	atgccagtgg tggggatggg gttggcagcc tatccatttc aagaatcaga ggtagtgaag 60 ttggcaatgc taagggccat tgagatgggt tacaggcatt tcgacacggc tgcgctgtac 120 cagacagagc agtcacttgg tctagccatt gcagaagcgc ttgagcttgg cttgatcaag 180 tcccgtgatg agctcttcat cacttccaag ctctggtgca gtgatgctca tcctcacctt 240 gtcattcctg ctcttcaaag gactctcaag aatcttgggt tggactatgt tgatctctat 300 ctcatacact ggccagtgag ctcaaacaaa ccaggaaagt atgattttcc agtaccaaag 360 gaagaactag ttcaaatgga ttatgaatct gtatgggcag ccatggaaga gggacatagg 420 cttggcctca caaagtccat tggtgtaagc aacttttctt gtaagaagct tgagaattta 480 ctcacaatag caaaggtccc tcctactgtc aatcaagtgg agatgaaccc cttttggcga 540 caatataaac tgaaagagtt ctgcaaggaa aagggaatta ttatcactgc ttactcacca 600 ttgggagcca aaggaactat ttggggcacc aacaaagtta tggaatctaa agtgcttgaa 660 gacattggaa ttgctagtgg aaagactctt gctcaggtct gtctgagatg ggtgtatgag 720 caaggagtga ctcttttggt aaaaagcttc aatgaggaga ggatgaaggg gaacctagac 780 atatttgatt gggaattaag tgagaaagag ctgaaaaaga tcaatgagat tccacagagc 840

		agaggactcc ctggtgacat ctttgtgtca gatgatggac ccttcaagtc tgaagcagag 900 ctctgggatg gagaagtttg a 921
3-15	**Sequences**	
3-15-1	Sequence Number [ID]	15
3-15-2	Molecule Type	DNA
3-15-3	Length	966
3-15-4-1	Features Location/Qualifiers	**source** 1..966 mol_type= genomic DNA organism= Eschscholzia californica
	NonEnglishQualifier Value	
3-15-5	Residues	atggggagtt gtagtatacc agtgaagagt ctgagctcag gaagggagat gcctgtaata 60 ggtatgggaa ctgctgacag caatctagca ggctctgatg cttcaaggat agcactagtg 120 aaagctatag aggttggtta tagacacttt gatacagctt caatttacca gagtgagcaa 180 aaccttggag atgccattgc tcaagcactt gaacttggtc tcatcaaatc tagagatgaa 240 ctattcatta cttccaagct atggtcttca gattctcacc ccgatcgtgt cgtccctgct 300 cttcaagaat ccctcaggaa gcttaaattg gagtatcttg atctatatct aatacattgg 360 ccggcaagtt cgacaccagg gatttatgag ttccctatac caaaagatga gatctttcca 420 ttggagtatg agactatttg ggcagccatg gaagaatgtc agaggcttgg gcttacaaaa 480 tctattggtg ttagcaactt ttcttccaag aagctccaaa ctatattgaa caccgccacc 540 atccctccgg ctgccaatca agtggagatg aacccagttt ggcaacagaa gaaattgaaa 600 gagttttgtg acgccaacaa tatcctgctt actgcatatt cgcctttggg tgctaaagga 660 acctcgtggg gaagcaataa agttatggag tctgaggttc tgaaacaaat tgctatggcg 720 aacgggaagt ctgttgctca ggttagtctg agatggttat accaaatagg tgcaactatg 780 gtagtgaaaa gttacaatgc agaaaggatg aaggagaacc tgaagatatt cgattgggag 840 ttgagtgatg aagacatgaa agcaatcagc gagattcctc agcgtcgaaa ttttgctggt 900 gatattctga tttcaagtaa cgggcccttc aaatccgaag acgaactctg ggatggagaa 960 gtatga 966
3-16	**Sequences**	
3-16-1	Sequence Number [ID]	16
3-16-2	Molecule Type	DNA
3-16-3	Length	972
3-16-4-1	Features Location/Qualifiers	**source** 1..972 mol_type= genomic DNA organism= Eschscholzia californica
	NonEnglishQualifier Value	
3-16-5	Residues	atgagtagtt atggtagtgt accaatgaag tcactaaact caggaagtaa aattcatgtt 60 ttagggtttg gaacagctgc ttacccattt gtgggatcag atggtgtgaa gaatgccatt 120 cttaatgcta taaagttagg ttataggcat tttgacacag ctgctctcta cttcactgag 180 gagtctcttg gtgaagctgt ttctgaagca cttcaacttg gtctcatcaa atctagagat 240 gaactcttca tcacttccaa gctttggatt tctgatgctt atcctgatcg tgtcctcccc 300 gccattcaaa aaacacttcg gaaccttaaa atggagtacc ttgatctata cctgatacac 360 tggcccatta gtgggaaaga ggggaatttt gatcttcctg tacctaaaga ttgtctccag 420 gaattggact acaagccagt gtgggcagcc atggaagaat gtcaaaagct tggactcact 480 aaatccattg gtgttagcaa tttctcttgt aagaaacttc aaatcattct ctcctcagct 540 accatccctc ctgctgttaa tcaggtggag atgaacccaa tttggcacca gaagaagttg 600 agagaatttt gtaaggccaa taatatcatg attgctgctt attcgccgtt aggagctgct 660 gggaccccat ggggatcctc cggtgtcgtc gagaccgaag tgctacacga gatagccaga 720 agtagaggca aaactcatgc tcaggtttgt ttgagatggg tatatgagca aggggtgatt 780 gtgttggtga agagctttaa tgaagagagg atgaaggaaa acctatctgt gtttgactgg 840 gagttgacgg acgaagactt gaagaaaatc agtcaaattc ctcaacgtag aggacttcct 900 agtggtgata tttgggtctc gacagaagga cctttcagat ctgaagaaga gctttgggat 960 ggagaaatct aa 972
3-17	**Sequences**	
3-17-1	Sequence Number [ID]	17
3-	Molecule Type	DNA

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[0009]

17-2		
3-17-3	Length	975
3-17-4-1	Features Location/Qualifiers	**source** 1..975 mol_type= genomic DNA organism= Glaucium Flavum
	NonEnglishQualifier Value	
3-17-5	Residues	atggagatga gtagtgcaca agtagttcca ctaatgactc taaactcagg caaggagata 60 cctgtattgg gcatgggtac tgctgaaaac catttccaag ggtctgatgg aacaaaagat 120 gcacttgtta atgcaataaa aattggttac agacactttg acacagctgc tatatataac 180 gttgaggagt gtcttggtga tgctatagct gaagcacttc aacatggtct catcaaatcc 240 cgtgacgaac ttttcatcac ttcaaagcta tggatatctg attcccaccc tgaccgtgtc 300 ctctttgctc ttcaaaattc tctccggaag cttaagttgg agtaccttga tctatatctg 360 atacattggc cgttaagctc aacgccaggg aaatcggtgt ttccggtacc caaggaggac 420 ttcctacctt tggacttcaa atctgtgtgg gcagccatgg aagaatgcca aaaacttggc 480 ctcaccaagt caattggtgt cagcaacttc tcttgcaaga agctccaaga tttattggac 540 attgccaaca tccctcctgc agttaatcaa gtggagatga gcccactttg gcaacagaag 600 aaacttaggg agttttgtaa ggtcaatggt atacttgtta cagcttactc gcctttagga 660 gccaaaggca ccttctgggg ctctaatgaa attatggact ctcatgtgtt acaagagatt 720 gctaaggcta gagggaagtc tgttgctcag gttactctca gatgggtata tgagcaagga 780 gtgattttgt tggtgaagag ttttaatgaa aatagaatga aggagaatat ggcgatattt 840 gattgggatt tgagcatcga cgacttgaaa aaattcgatg agatctcaca gcgcagagga 900 aaccttggcg atttttttgt ttcagaaaac gggcccttca agtctgtaga catggtttgg 960 gatggagagg tctaa 975
3-18	**Sequences**	
3-18-1	Sequence Number [ID]	18
3-18-2	Molecule Type	DNA
3-18-3	Length	981
3-18-4-1	Features Location/Qualifiers	**source** 1..981 mol_type= genomic DNA organism= Glaucium Flavum
	NonEnglishQualifier Value	
3-18-5	Residues	atggagagta gtagtagtag tgcagtagta gttccagtaa tgactctgaa ctcaggcaag 60 gagatgcctg tattaggtat gggaactgct gaaaacaatc ttcaagggtc tgagaaaaca 120 aaattggctc ttttgactgc tataaaagcc ggttacagac actttgacac agcttctgca 180 tacaatactg aggaggcact aggtgaggct gtggctgaag cacttcaact tggtctcatt 240 aaatctcgag acgaactctt catcacttcc aagctatggt gctctgatgc tcaccctgga 300 cttgttgtcc ctgctcttca aaattcacta cggaatctaa agttggagta tcttgatcta 360 tatctgatac attggccagt aagtttaaag ccgggaaaat tcgtgattcc tttttccaag 420 gaggacatcc ttcctttgga cttcaaaaat gtctgggcag ctatggaaga atgtcaaaag 480 cttggccttg ccaagtcaat tggtgtcagc aacttctctt gcaagaaact ccaagactta 540 ttggcaattg ccaacatccc tcctgctgtt aatcaagtgg agatgagccc actttggcaa 600 cagaagaaac tgagggagtt ttgtaaggtc aatggtatac ttgttacagc ttactcgcct 660 ttaggagcca aaggcacctt ctggggctct aatgaaatta tggactctga tgtgctaaac 720 caaattgcta aggctagagg aaagtctgtt gctcaggttt ctctcagatg ggtacacgag 780 caaggggtga ttttgttagt gaagagtttt aatgaaaata gaatgaagga gaatatggcc 840 atatttgact gggaattgag caacgacgac ttgaaaaaga tggatgagat ctcacagcgt 900 agaggacccc ttgctgatat ttttgtttca gaaaacgggc ccttcaagtc tgtagacatg 960 ctttgggatg gagggttctg a 981
3-19	**Sequences**	
3-19-1	Sequence Number [ID]	19
3-19-2	Molecule Type	DNA
3-19-3	Length	981
3-19-4-1	Features Location/Qualifiers	**source** 1..981 mol_type= genomic DNA organism= Glaucium Flavum

[0010]

3-19-5	NonEnglishQualifier Value	
	Residues	atggggagta gtgatgcagt agtagttcca gtaaagactt tgagctcggg gaggaagatg 60 cctgtaatag gcatgggaac tgctgaaatc cttcttgtgg acgggtccga aaaagtgaag 120 ttggctcttc taaatgctat taaaattggt tacagacact ttgatacagc tgctgtgtac 180 cgaactgaag aggctttggg tgaggttgtg gctgaagcaa ttcaacttgg tctcatcaaa 240 tctagagacg aactattcat cacttcaaag ttatggttat ctgattctca ccctgatctt 300 gttctccctg ctcttcagaa ctctctaagg aagcttaagt tcgagtatct tgacctatat 360 ttgatacatt ggccattaag ctcaaagcca ggggagctga aggttcttat accgaaggag 420 gaactccttc ctttggactt caaatctgtg tgggcagcca tggaagaatg tcaaaaactt 480 ggtctgacaa agtcaattgg agtcagcaac ttctcttgca agaagcttca agatttattg 540 gacattgcca acatcccacc cgcggttaac caagtggaga tgaacccact ttggcaacag 600 aaaaaattga atgagttttg taaagccaat gatatcgtca ttacagctta ctcgcctttg 660 ggagccaaag gcacccccttg gggatccaat agagttatgg actctgaggt attaaaccag 720 attgccaagg ctagaggaaa gtctgttgca caggttgctc ttagatgggt atatgaacaa 780 ggtgtgagtc tagtggtaaa aagttttaac gaagagcgga tgaaggaaaa cgtgacgaag 840 atatttgatt gggaattaag cgcagaagac ttgaaaaaga tcgaggaaat cccacaatgt 900 agaggagtcc ctagccatgt ttttgtctca gttaacgggc ctttcaaatc tgaagaagag 960 ctgtgggatg gtgaaatcta a 981
3-20	**Sequences**	
3-20-1	Sequence Number [ID]	20
3-20-2	Molecule Type	DNA
3-20-3	Length	984
3-20-4-1	Features Location/Qualifiers	**source** 1..984 mol_type= genomic DNA organism= Glaucium Flavum
	NonEnglishQualifier Value	
3-20-5	Residues	atgggtgagg aaatgaagat caagagtgtt gaaattccag tagtgacact aagctctgga 60 aggaccatgc ctgtgtttgg tatgggtacc gcagcattcc catttgtagg gtcagatgga 120 gtggtgaaag ccattactca tgctataaag cttgggtata ggcactttga tacggctgca 180 ctctacttca ctgaggagtc tcttggtgat gctatagctg aagcacttcg acttggactg 240 atcaaatctc gagatgaact attcatcact tctaagctat ggtgctgtga tgctcatcct 300 gatcgtgtcc tccctgctct gcgcaactct ttgaggaatc tgaaaataga gtatctagat 360 ctatacttga tacattggcc ggcaagcaca cacgaaggga acttggaatt tccaatacaa 420 aagcaggaca tccatccttt ggattacaat tctgtatggg cagccatgga ggagtgtcaa 480 acgcttggcc tcaccaagtc aattggagtc agcaacttct cttgcaagaa gcttcaacat 540 atattagcca ttgccaagat ccctcctgct gttaatcaag tggagatgaa cccaatttgg 600 caacagaaga aattaagaga attctgcaag gccaatgata tccatattac agcttactcg 660 cctttaggag ctaatgggac cccttggggg tctagtggag ttgttgagac tcaagtacta 720 catgacattg ctaaggctag agggaagact catgctcagg tttgtctaag atgggtatac 780 gagcaagggg tgattgtatt ggtgaagagc tacaatgaag aaaggatgaa agagaatctg 840 actgtattcg attgggaatt gagcgcagag gactcgatga agatcagtga gatcccacag 900 catagaggac ttcctggtga tattttcgtt tcagacagtg ggcctttcaa gtctgaagag 960 gagctttggg atggagaagt ctga 984
3-21	**Sequences**	
3-21-1	Sequence Number [ID]	21
3-21-2	Molecule Type	DNA
3-21-3	Length	960
3-21-4-1	Features Location/Qualifiers	**source** 1..960 mol_type= genomic DNA organism= Hydrastis canadensis
	NonEnglishQualifier Value	
3-21-5	Residues	atgggtagtg ttcctaatgt aattcttagc tctggtcatc caatgcctct tgttggcttt 60 ggcactgcgg gttttccatt tggaacatca gaaggtataa agtcagcaat actctgtggg 120 atcaagaatg gttacagaca cttcgatacg gcttccgtgt accaaacaga acagatactt 180 ggtgaagcta tagctgaagc acttgagcta ggcctcatta aatctagaga tgaactcttt 240 ttaacctcca agctatggtg cagtgatgct catcaacaac atgttctccc tgcccttcag 300 aagactctaa ggactcttca gctggattat cttgatcttt atctagtaca ctggccactg 360

[0011]

		agctcaaaac cagggaagta tgagtaccca ataccaaagg aagagcttct tcccatggat 420 ttcaaatctg tctgggctgc aatggaagag tgccaggctc ttggcctcac aaagtccatt 480 ggggtcagca atttctcttg taagaaactt gaacaattac tctccacttc aaacatccct 540 cctgctgtca atcaagtgga ggtcaaccca atttggcaac aaaataagct gagagagttt 600 tgtaaggcca aaggtataat tgttgctgct ttttctcctt tgggtgctaa aggaacatct 660 tggggaacta ataaagttat ggattctgag gtgctgaatg agattgccca ggctagagga 720 aagactactg ctcagaattg tcttagatgg ttacatgagc aaggtgtgtg tgtggtggtg 780 aagagcttca atgaggagag gatgaagggg aacctgaaat tatttgattg ggaattgagt 840 aaggaagagt ctaagaagat cagccagtta ccgcagagta aaggacatac cggagatgac 900 atggtctcgg ccaatgggcc atttaagtct ttagaggagc tatgggatgg agagatttga 960
3-22	**Sequences**	
3-22-1	Sequence Number [ID]	22
3-22-2	Molecule Type	DNA
3-22-3	Length	960
3-22-4-1	Features Location/Qualifiers NonEnglishQualifier Value	**source** 1..960 mol_type= genomic DNA organism= Hydrastis canadensis
3-22-5	Residues	atgacaagaa ttccagagat tgtgttgaac tcaggatgga ggatgccagt tttggggatg 60 ggaacagcaa cctttcctat ccaatcccca gaagtcattg agtcttccat tgttaacgcc 120 atcgaattgg gttatcgaca cttcgacaca gctagtgtat atcagtctga gtcacctcta 180 ggccgtgcca tatcagaagc tatacgtcga ggcctcattg agagtcgaaa agaggtcttc 240 atcacctcga agctatggtg cactgatgca caccatgacc ttgttatccc agctctccac 300 aaaactctcc agaatctggg gttggagtac ttggacttgt acctgattca tttcccagtg 360 agactgaaag gagacatatc ctttgacatt aagaaggcag accttatacc ctttgatgta 420 aagggtacat gggaggccat ggagaagtgt caagagctgg gacttaccag atctattggt 480 gttagcaact tttcatctaa gaagctttcc gagcttttaa cccatgctac catttctccc 540 gctgtgaatc aggtggaaat gcacccattt tggcaacaga aggaattgag agctttctgt 600 gcagacaaag gtatacatgt aagtgcttat tctcctttgg gaggaaaggg tgctttatgg 660 ggctccgaca tattactcaa ctccaaagag atcgaacgga tcgctcaagc taaaggaaag 720 agcatcgcgc aggtatgctt gagatgggca tatgaacaag gggtgagtta cttaccaaaa 780 agctacaata agggaaggat gaaagagaac atggaaattt ttgactggca attgagtgaa 840 gatgagttac aaaagatcag tcacctgcca caaggaaaga tatacacagg acatcatttt 900 atatcagatg atggggaata taaatctcct attgatttat gggattgtga gatatgttag 960
3-23	**Sequences**	
3-23-1	Sequence Number [ID]	23
3-23-2	Molecule Type	DNA
3-23-3	Length	963
3-23-4-1	Features Location/Qualifiers NonEnglishQualifier Value	**source** 1..963 mol_type= genomic DNA organism= Hydrastis canadensis
3-23-5	Residues	atgggtatag ttcgtgaggt agtgttgaat tctggggaaa gaatgccatt gctaggaatg 60 ggaacagcaa catacccagt tgctccattt gaactagttg agtcttcagt aattgctgcc 120 attgaacttg gttataggca ttttgacaca gcaagtgtgt atgagacaga gcaacctcta 180 ggcctagcca tatctgaagc cgtccggcaa ggccttatcg ctagtcgtga tgaaatcttc 240 ataaccacta agctttggtg tggtcatgca cattatgatc ttgttctacc agctcttcgg 300 gactcactag aaacgatggg gttggattat gttgatctgt acttgattca ttttcctgca 360 agattcaaca tgaaagagaa gagcttaaat gtgaataaga aagatcttct tcctttggat 420 ataagaggga catggaaagc tatggaggaa tgttatgaac ttggcttagc aaagtcaatt 480 ggtgtcagca acttcagttg caaaaagcta tctcaacttt tgtctgttgc taacattccg 540 cctgcagtga atcaggtgga gatgcatcct ctttggcaac aacagaagtt gagagagttt 600 tgtgaagaaa aaggtataca tgtgagtgct tattctcctt taggaggaaa agggaccata 660 tggggctcca acgcagtttt ggactcagat caaatcaaac aaatagctaa ggctaaaggg 720 aagagtattg ctcagatttg tttgagatgg ggatttgaac atggagtgag cattttacca 780 aagagcttca acaaagaaag gttgaaagaa aatatggaga tatttgattg ggagctaagc 840 aaggaagagt tacaaaagat gaataccttt cctcaaaata gaatttttca agctgagcat 900 ttagtctcac ctgatgaggg actgtttaaa tctgttgctg atttgtggga tggtgaaatc 960 taa 963

[0012]

3-24	**Sequences**	
3-24-1	Sequence Number [ID]	24
3-24-2	Molecule Type	DNA
3-24-3	Length	954
3-24-4-1	Features Location/Qualifiers	**source** 1..954 mol_type= genomic DNA organism= Jeffersonia diphylla
	NonEnglishQualifier Value	
3-24-5	Residues	atggggattg ttcctgaggt gacattgaac tctggccatc agatgcctct tgtaggcttt 60 ggaacagcac agtttccttt tccagagggg gatgaagcaa aacaaattat agctccaata 120 ctatgtggaa tcaagagtgg ttacagacac ttcgacacag cttccctgta caaaactgag 180 gaagcacttg gagaagctat aaaagaggca cttcgtcttg gccttatcaa atctcgagac 240 gagctattca ttacctcgaa gctttggtgt actgattctc atcaagatct tgttcttcct 300 gcccttaaga agactctcca gaatcttcag atggactacc ttgatctata ccttgtacat 360 tttccagtaa gctcaaagcc gggaaagcca gagttcccac cacagaaaga ggaccttctt 420 cctatggatt ttggatcggt atgggcagca atggaagagt gccagaggct cggtctaacc 480 aaatcaattg gagtcagtaa tttctcttgc aaaaagttag agcaactact cacaacagca 540 aagattattc ccgcggttaa cgaagtggag atgagcccag tttgccaaca gaataagctg 600 agagagtttt gtaaggtaaa aaacattgtt gtgactgctt actctcctct aggtggagga 660 agcaatgcag ttaaggacaa taaggtgctg aaagaaattg ccaaggctaa aggaaaaaca 720 tgtgctcagg tcactctgag atgggtatac gagcaaggtg ttgctctggt gcctaagagc 780 ttcaatgagg ggaggatgaa ggaaaacctg gatatattta attggacaat aagtgaagaa 840 gagttcaaac agatcagcca gttaccacag ggtagagtgg caactggaga atggtttgtg 900 tcggttgaag ggccattcaa gtctctagag gaactatggg atgaagtgat ctga 954
3-25	**Sequences**	
3-25-1	Sequence Number [ID]	25
3-25-2	Molecule Type	DNA
3-25-3	Length	966
3-25-4-1	Features Location/Qualifiers	**source** 1..966 mol_type= genomic DNA organism= Mahonia aquifolium
	NonEnglishQualifier Value	
3-25-5	Residues	atgggtgttg tacctgtggt aaccctgaac tctggtcatg agatgccact agtaggcttt 60 ggaacagcag tgcctgcctt cgggggatca gacgccataa agcaagcaat actatgtgga 120 atcaagaatg gttacagaca cttcgacact gcttctgtat accaaacaga gaagtcgctt 180 ggagaagcta tagtggaagc gcttcgcctt ggcctcatca aatctcgaga tgaactcttc 240 attacctcca agttatggtg tacagatgct catcaagatg gcgttctccc tgcccttagg 300 gagactctca agaatcttca gttggattac cttgatcttt accttataca ttggccgcta 360 agcgcaaagc cagggaagca tgagtaccaa ataccaaagg atgagcttct tcctatggac 420 tatgaatccg tatggggagc aatggaagaa tgccagaggc ttgacctctc taagtccatt 480 ggagtcagca acttctctat caagaagctt gaagagctac tcaaaactgc aaagattatt 540 cctgcagtta atgaagtgga agtgaaccct gtttggcatc aaaataagct aatagagttc 600 tgtaaggcca aaggtattgt tgtgactggt tactctcctt taggtgccaa aggaacaact 660 tggggaacca atagagtcat ggacaatgag gtcctgaaag agattgctaa gactagagga 720 aagacccatg ctcaggtttg tctgagatgg atatacgagc aaggagttgg cctggtggcg 780 aagagcttta atgaagagag gatgaaggag aatttagaga tatttgattg ggcattgact 840 gaagaagagt ctaaacagat cagccagtta ccacaatata aagggcaaaa tggagaaacg 900 tttctctcag ctgaagggcc tttcaagacc ttagaggagc tatgggatga agagatagca 960 gcttga 966
3-26	**Sequences**	
3-26-1	Sequence Number [ID]	26
3-26-2	Molecule Type	DNA
3-26-3	Length	963

[0013]

3-26-4-1	Features Location/Qualifiers	**source** 1..963 mol_type= genomic DNA organism= Menispermum canadense
	NonEnglishQualifier Value	
3-26-5	Residues	atggcgagtg ttccagaggt gacactgagc tctggccatc caatgcctct ctttggcttc 60 ggcaccgcag cctggccttt tgtgtcttca gaaggagcta agtctgcaat attgtgtggg 120 atggagctcg gttacagaca cttcgacact gcttccattt acggcacaga gagctctctc 180 ggcgaagcca tagccgaagc tcttaagctc ggcatcatca agtctcgcga cgagctcttc 240 atcacctcta agctctggtg ctgcgacggg caccatgacc gagtcttgcc tgcccttcaa 300 atgactctaa agaatcttca attggactac attgatctgt atctcgaaca ctggccattg 360 agctcagtcc ctaaaggtga gcttgagtac ccaataccaa aagaaaaact gtttcctatg 420 gatttgaagg ctgtgtggga agccatggaa gagtgccaga ggcttggcct caccaagtcc 480 attggagtca gcaacttctc ttgcaagaag cttgaagatt tactcgcctt cgcgaagatc 540 cctccggccg tcaatgaagt ggagatgaac ccagtttggc aacagaagaa actgagggac 600 ttctgtaagg ctaaaggtat tgttttgacg gcttactcag tgttaggagc caaaggaacc 660 ctttggggca ctaacaaagt tatggactct gaggtgctag gaaagattgc caaggcaaga 720 ggcaagactg ttggtcaggt ttgtttgaga tgggcatatg agcaaggtgc gtgtgtgttg 780 gtgaagagct tcaatgagga aagaatgaaa gagaacttag agacatttaa ctgggagtta 840 ggagaggaag acttgaagat gattagtgaa ataccacaat ataaaggact tcgtggtgag 900 gatatggtgg ctcctaatgg gccttacaag actttagagg aactttggga tggagagata 960 tga 963
3-27	**Sequences**	
3-27-1	Sequence Number [ID]	27
3-27-2	Molecule Type	DNA
3-27-3	Length	1026
3-27-4-1	Features Location/Qualifiers	**source** 1..1026 mol_type= genomic DNA organism= Menispermum canadense
	NonEnglishQualifier Value	
3-27-5	Residues	atgggagttg ataagacaaa cgagttctct aatggcaacg cagcgagccc agtactgatc 60 aaagaggcta acctctttaa gattgccgag gtgacgttga actccggtca ccatatgccg 120 gttctgggaa ctgggacggc ttcgtttccg tttcctccgt tgaaggagct gaagaaggcg 180 atcgtggaag ccatggaagt gggctatcgc cacttcgact cggccgcgct gtaccagagc 240 gaggaagggc tcggtgcagc catagctgag gctttggaga agggacttgt gaagaagaga 300 gaagaactat tcatcaccac caagctatgg tgcaataatg cccactctga tcgtgtcctg 360 cccgccattc gtgaatctct caggaaacta agactagact atgtagattt gtatttgatt 420 catttcccag taaggctgaa ggaagattta ttggatatga attgtaagaa gggtgggatt 480 tttgaacttg acctcaaatc agtatgggca gcaatggagc agatacaaca cctaggtctt 540 gcaaagtcaa ttggagtcag caacttcact tgtaagaagc ttactgacct tctttcttat 600 gcaaagatcc ctcctgcagt taatcaggta gaaatgcatc cagtgtggca acaaaagaag 660 cttagagact tctgcaagga gaaaggcatc catgttagtg catattctcc tctaggagca 720 aagcaatggg gatttgatgt tgttctcggt aacaaaatct tgaaagagat tgcacaagac 780 aaaggaaaga caattgctca gattgcttta agatggggat atgagcaagg agtgattttg 840 atcccaaaga gctttaacaa gggaaggttg actgaaaatc ttcgcatatt tgactggaag 900 ctaactgaag atgaattaaa gaagatttca tcaattcaac agagccgagt agctataatg 960 cctgaatttg tgtttcctga aagtccattc aagacctttg aagatttctg ggatggggaa 1020 atgtga 1026
3-28	**Sequences**	
3-28-1	Sequence Number [ID]	28
3-28-2	Molecule Type	DNA
3-28-3	Length	969
3-28-4-1	Features Location/Qualifiers	**source** 1..969 mol_type= genomic DNA organism= Menispermum canadense
	NonEnglishQualifier Value	

[0014]

3-28-5	Residues	atggaaggag gaggagttcc taagatactc ttgaattcag ggcataggat gcctgtgctt 60 ggaatgggca cagcttcctt cccaatctca ccacaacacc tcgtcaagtc ttccatacta 120 accgctatcg aacttggcta cacccacttc gacaccgcaa gcgtctatga gactgagcct 180 acactcagcc gggctatccg ccaagccctc gagggtagac acattgcgag ccgagaccag 240 ctcttcatca ccaccaagct ctggtgcggc caagcacaaa gcgatctcgt cgtcccagct 300 cttcgcgaat cacttcagga acttgggttg gactatgttg atctgtactt gattcatttt 360 ccagctagat ttaagtgtgt ggagaagaca tttaatgtca ccaaagagga tcttcttcct 420 ttggacatga aggggacatg gcaggccatg gaggagtgtt gtaaacttgg cctggccaag 480 tccattggtg tcagcaactt cagctgcaag aagctctctc agattctcac ctttgccacc 540 atccctcctg cagtcaatca ggtggaaatg cacccattat ggcagcaaag gaaactgaga 600 gagttctgta aggagaaagg catccatgtg agtgcctact ctcctttagg tgggaaaggt 660 gccaagtggg gttccaatgc agtgtttgaa tgtgaagaaa tcaaacagat tgctgaagct 720 aaagggaaga gtttggctca gatttgtctg aggtgggctt ttgagcaagg tgtgagtttt 780 gtgccaaaga gctttaacaa ggaaaggttg aaagagaaca tggagatata tggttgggag 840 ctgagcaagg aggaattgca aaagttaagt gttctgccac agtgcaggat cttcaaagga 900 gaatggctag tgtcagctga tcatggagtg ttcaaatcag ttgaagattt gtgggatgga 960 gaaatataa 969
3-29	**Sequences**	
3-29-1	Sequence Number [ID]	29
3-29-2	Molecule Type	DNA
3-29-3	Length	960
3-29-4-1	Features Location/Qualifiers	**source** 1..960 mol_type= genomic DNA organism= Nandina domestica
	NonEnglishQualifier Value	
3-29-5	Residues	atggtgagtg ttccagaggt aaccctgaac tccggtcacc ggatgcctct tgtgggtatg 60 ggcacggcat gctttcctct tccaggatca gaagtggtga agtcggcgat ggtaacggca 120 atcaagcttg gttatcgcca cttcgatacc gctgcgcttt accagagcga gcagcctcta 180 ggtgaagcta tagctgaagc acttcacctt ggcctcataa tatctaggga tgaacttttt 240 atcacctcca agctatggtg tactgatgct caccaagatc ttgttctccc tgctcttaag 300 acaagtctcc gaaatcttca gttggattac cttgatcttt accttataca ttttccggtg 360 agtttgaagc cagggaagat acagctgccg gtaccaaagg aagagcttct tccaatggat 420 ttcaagtctg tgtgggcagc catggaggaa tgtcagaagc ttggcctcac aaagtccatt 480 ggagtaagca atttctcttg caagaaactc gaacacatac tttcattggc aaagattcct 540 cctgcagtta atcaagtgga gctgaaccca atttggcgac aaaaaaagct catcgagttt 600 tgtaaggcca aaggtattgt tgttacggca tattctcctt tgggagctgt agcacccggt 660 caaggcagca atagagtcat ggaatgtgaa gtgctgagcg agattgcaaa agctcgagga 720 aaaactcatg cgcaggtttg tcttagatgg ataattgagc aaggggtcag tttagttgtg 780 aaaagcttca atgaggacag gaagaagaag aacttggaga tattcgactg ggaattgagc 840 gaagaagatt ccaaaaaaat cagccagata ccagagacta gaggaaaccc cggagatttt 900 gtcatctctg ttgatggtcc ttataagtct agagaggagc tttgggatgg agaaatctga 960
3-30	**Sequences**	
3-30-1	Sequence Number [ID]	30
3-30-2	Molecule Type	DNA
3-30-3	Length	960
3-30-4-1	Features Location/Qualifiers	**source** 1..960 mol_type= genomic DNA organism= Nandina domestica
	NonEnglishQualifier Value	
3-30-5	Residues	atgggaagag ttcctgagac taccttgagt tctgggcata acatgccatt gttggggatg 60 ggaacagcaa ccttccctct ccctccatct gaattgatag aatcttatat tcttgctgcc 120 attgaaatgg ggtatagaca ctttgacact gctagtgttt acgacacaga agtacccctt 180 ggtcgagcca tatctgaagc cctccggaga ggtcttgtgg caaatcgtga tgaactcttc 240 attaccacca aactctggtg tggtcatgca catccagatc tcgttgttcc agctcttcac 300 caatctctca tggaaatggg attggaatat gtggatttgt atttgattca ttttccagct 360 aggtttaaca aaaaggaaaa gaactttgat gtgaagaaag aggaagtcat tcccttggac 420 atgaagggaa catgggaagc catggaagag tgtagcaaac ttggacttgc aaagtccatt 480 ggtgtaagca acttcagctg caaaaagctc tctcaactcc tcacctatgc cactatccct 540 cctgcagtga atcaggtaga aatgcaccct ctttggcaac aatggaaatt gagagaattt 600

[0015]

		tgcgtagcaa atgatataca tgtgactgcc tattctcctc taggggggaa aggagcattg 660 tggggttcga attcagtgct cgattcaaaa gaaatccaac aaatggctga agcaaaagga 720 aagagtatcg ctcagatatg tttgagatgg gcatttgaac aaggagtaag cttcataccg 780 aaaagcttca atgtcgaaag gctaaaagaa aatatggaaa tatttgattg ggaaatgaac 840 aagaatgagt tgttgaaaat gagtttgctt ccacaaaaaa ggactttcac tgcagaatat 900 ttggtatcac ctgatggggc gtttaaatcg gttgacgatt tatgggatgg ggagatataa 960
3-31	**Sequences**	
3-31-1	Sequence Number [ID]	31
3-31-2	Molecule Type	DNA
3-31-3	Length	960
3-31-4-1	Features Location/Qualifiers	**source** 1..960 mol_type= genomic DNA organism= Nigella sativa
	NonEnglishQualifier Value	
3-31-5	Residues	atggcaagag tacctgagat aaccttaaac tccggccacc ggatgcctct cttgggtatg 60 ggaactgcag tagttccctt taaagaacca gaaccagtga agtcagcaat actcactgca 120 atcaagaatg gttacaggca cttcgataca gcttctctgt accgaactga gccagccctt 180 ggagatgcta tagctgaagc acttcaactt ggcctcatca actccaggga cgacctttc 240 atcacctcca agctctggtg cactgacaac caccctgatc tggtcctccc tgcactgcac 300 acaacacttc gaaatctgaa gttggactac cttgatctat atctaataca ttggccagta 360 agcatgactc cagggagaat tcggttccct gggccggatg agaagatact tccaatggat 420 tacaagtctg tatgggcagc catggaagag tgtcaaaagc ttggcctcac aaaatcaatt 480 ggagtcagca attttacctg caagaagctt gaattgttac tggcatcagc tactatccct 540 cctgctgtta atcaagtgga ggtgaaccct atgtggcaac aggaaaagct gatagagttt 600 tgtaggacta aaggtattgt tgtaacagct tacgctccct tggggactgt tggaacattt 660 ataggtaaca acgatattat gaactgtgag ttactgaaag aaattgccca agctaaagga 720 aagacaaatg gtcagatttg tctcagatgg gtacatgaac aaggagtggg tctgctagta 780 aagagcttca ctgaggtgag aatgaaacag aatcttgaga tatttgattg ggaactaagt 840 gaagaagaat caatgaaaat taaacaactg ccacaaagaa agagtcatca agggaagggc 900 tttgttactg ctgatggacc attcaaatcg ttgacagagc tttgggatgg agagatgtga 960
3-32	**Sequences**	
3-32-1	Sequence Number [ID]	32
3-32-2	Molecule Type	DNA
3-32-3	Length	954
3-32-4-1	Features Location/Qualifiers	**source** 1..954 mol_type= genomic DNA organism= Nigella sativa
	NonEnglishQualifier Value	
3-32-5	Residues	atggtttatg agatcatgtt gaactctgga tacagaattc cattgctggg aatgggaaca 60 gcagcctatc cagtgcctcc accagagcta gtggagtctt ctgttcttgc tgcaattgaa 120 ctcggttata ggcactttga cactgcccat atttatggaa cggaagcacc tttgggaaga 180 gccatatcag aagccttgag gaagggattg atcaaaagtc gagatgaact cttcataact 240 actaagctct ggcctggcca tgcacgccct gatcttgttc tacaagcttt gcatcaatct 300 ttagaagctt tgaggattga ttacgttgat ctgttcctaa ttcattttcc agcacggtac 360 aacacaacag aaataagaat ggatataaag aaggaagaca tccttccttt ggatatcaag 420 ggaacatggc aggccatgga agagtgttgt aaacttggct tggccaagtc catcggtgtc 480 agcaacttcg gttgcaagaa gctatcccaa ctattggatt cagccactat cccacctgca 540 gttaatcagg tggaaatgca tcctctctgg caacaagcaa aactgagaga gttttgtgca 600 gaaaggggta tccatgtcag tgcctattct cctttaggag gaaaggggac tctctgggga 660 tccaatgcag tgcttgattc tgagcaaatc aaacagattg cacttgctaa ggggaagagt 720 gtagcgcaga tatgcttgag atggggtttt caacaaggag taagcatcat agcaaagagc 780 ttcaacagag aaagactcaa agaaaatatg gaaatatttg attgggaatt gaacaaggaa 840 gaactataca agctaagcat ccttcctcaa aataggattt caacccttga atatttagtg 900 tcaccggatg cagttttcaa atcaattaac gatttgtggg atgaagaagt ttga 954
3-33	**Sequences**	
3-33-1	Sequence Number [ID]	33

[0016]

3-33-2	Molecule Type	DNA
3-33-3	Length	957
3-33-4-1	Features Location/Qualifiers	**source** 1..957 mol_type= genomic DNA organism= Nigella sativa
	NonEnglishQualifier Value	
3-33-5	Residues	atggataaca gtgtagtagt gctgaattct ggacatagaa tgccattgtt agggatggga 60 acagcagcca ctcctttacc tcccaatgaa gttgtccagt cttcagttct tgctgcaatc 120 gaactgggtt acaggcattt tgatacagca agtgtgtatg gctcagaagt gattttaggt 180 agagccatat ctgaagcttt aaggagaggt ttggttgcta gtagagatga gcttttcata 240 actactaagc tttggtgtgg taatggacac cctgatcttg ttcttggtgc tcttcaagaa 300 tctttaagaa ttatggagct ggattatgtg gacttgtact tgattcattt tcctgtgaga 360 ttcaatataa cagagaagct cttaaatatg aagaatgttc ctcttcttcc ttttgacatg 420 gaagggacat ggcaagctat ggaggagtgt tgtagactgg gtttagccaa gtccattggt 480 gttagcaatt ttagttgcaa aaggctatct gaacttctac tttccgcttc catccctcct 540 gctgtgaatc aggtggaaat gcatccgctt tggcagcaaa gaaatatgag agagttttgt 600 agaaaagaag gaattcatgt gagtgcttat tctcctttag gaggaaaagg agcagcttgg 660 gggtcgaatg cagtgctaga ttctgaagat atccaacaaa tagctcaaca taaagaaaag 720 agtgttgctc aggtatgctt gagatgggcg tttgagcaag gagtgagcat tatagtaaag 780 agtttcaata aagaaaggct taaagaaaat acacaaattt tcgactggga gctcaacaaa 840 caagagttgc agagaatcaa tactcttcca caaaataaga tttttaaagc ttcaaatttg 900 atttcagcag atggaccata taaaacattt gaggaattgt gggatggaga ggtatga 957
3-34	**Sequences**	
3-34-1	Sequence Number [ID]	34
3-34-2	Molecule Type	DNA
3-34-3	Length	960
3-34-4-1	Features Location/Qualifiers	**source** 1..960 mol_type= genomic DNA organism= Papaver Bracteatum
	NonEnglishQualifier Value	
3-34-5	Residues	atggagagta atggtgtacc tatgatcact ctcagttccg gcattcggat gcctgcttta 60 ggtatgggaa cagttgaaac aatggaaaag ggaacagaaa gagagaaatt ggcgtttttg 120 aaagcgatag aggtcggtta cagacacttc gatgcagctg ctgcatatca aactgaagag 180 tgtcttggtg aagctatagc tgaagcactt caacttggtc taattaaatc tcgagatgaa 240 ctcttcatca cttccaagct ctggtgcact gatgctcacg ctgatctcgt cctccctgct 300 cttcagaatt ctctgaggaa tcttaaattg gagtatctgg atctatattt gatacacttt 360 ccgctaagct tgaaaccagg gaagattgtt aacgaaatac caaaggatca aatgcttcca 420 atggactaca aatctgtgtg ggcagccatg gaagagtgtc agacccttgg cttcactagg 480 gcaatcggtg tcagcaattt ctcatgcaaa aagcttcaag agttgatggc gacagccaac 540 agccctccag ttgtaaatga agtggagatg agcccgattt tccaacaaaa aaaattgaga 600 gcatattgca aggccaataa tatcatgatc actgcatact cggttttggg atccagagga 660 gccgcatggg gcagcaatgc agttatggat tctaaggtgc ttcacgagat tgctgtgtcc 720 agaggaaaat ctgttgctca ggttagtatg agatgggttt accagcaagg cgcgtgtctt 780 gtggtgaaaa gtttcaatga agagagaatg aaggaaaacc ttaagatatt cgattgggag 840 ctatcggcag aagacatgga aaagatcagt gagattccgc aatgtagaac aagctctgtt 900 gatttcttgt tatcaccgac tgggcctttc aaaactgaag aagagttctg ggatgagtag 960
3-35	**Sequences**	
3-35-1	Sequence Number [ID]	35
3-35-2	Molecule Type	DNA
3-35-3	Length	966
3-35-4-1	Features Location/Qualifiers	**source** 1..966 mol_type= genomic DNA organism= Papaver Bracteatum
	NonEnglishQualifier	

[0017]

3-35-5	Value	
	Residues	atggagatta atggtgtacc agtgatcagt ctaagctcgg gcgttcggat gcctgcttta 60 ggtatgggaa cagctgaaac aatggaaaaa ggaaccgaca gagagagatc agcgtttttg 120 aaagcgattg aggtcggtta caggcacttc gatacagctg ctgcttatca aactgaagag 180 tgtcttggtg aagctatagc tgaagcactt caacttggtc taattaaatc tcgagatgaa 240 ctcttcatca cttccaagct ctggtgcact gatgctcacg ctgatctcgt cctccctgct 300 cttcagaatt ctctgaggaa tctcaaattg gagtatcttg atctatattt gatacacgct 360 ccggtaagct tgaagccagg gaagattctt aacgaaatac caaaggatca aatgcttcca 420 atggactaca aatctgtgtg ggcagccatg gaagagtgtc agacccttgg cttcactagg 480 gcaatcggtg tcagcaattt ctcatgcaaa aagcttcaag agttgatggc gacagctaat 540 agccctccag tggtaaatga agtggagatg agccccactt tacatcaaaa aaatctgaga 600 gaatattgca aggccaataa tatcatgatc attgcatact cggttttggg agccagagga 660 accggatggg gcagcaacgc agttatggat tctaaggtgc ttcaccagat tgctgtggcc 720 agaggaaaat ctgttgctca ggttagcatg agatgggttt accagcaagg tgcgtgtctt 780 gtggtaaaaa gtttcaatga agagaggatg aaggaaaacc ttaaaatatt cgattgggaa 840 ctaacggaag aagacatgga taagatcagt gagattccgc aatccagaac actatctgct 900 gatttcttgt tatcaccgac tggacctttc aaaactgaag aagagttctg ggatgaaatg 960 gtttga 966
3-36	**Sequences**	
3-36-1	Sequence Number [ID]	36
3-36-2	Molecule Type	DNA
3-36-3	Length	972
3-36-4-1	Features Location/Qualifiers	**source** 1..972 mol_type= genomic DNA organism= Papaver Bracteatum
	NonEnglishQualifier Value	
3-36-5	Residues	atgaggaata ctggtgtacc tgtaatcact ctgagctcgg ggaaggggat acctgtttta 60 ggtatgggaa catttgaaac agttggtaaa gggggtgaac gagagaggtt ggcgtttttg 120 aaagcgatag aggtgggtta cagacacttc gatactgctg cgtgctacca aactgaagag 180 tgtcttggtg aagctataga ggaagcactt caacttggcc taatcaaatc tcgagatgaa 240 ctctttatca cttctaagct ctggtgcacc gacgctcacc ctgaccgtgt cctgttggct 300 cttcagaatt ctctgaggaa tcttaagttg gagtatctgg atctatacct gatacacttt 360 ccagtaagct tgaagccagg gaatgaggtt actatggatg cagcaggggg cgaaattttt 420 ctaatggact acaagtctgt atgggcagcc atggaagagt gtcagaacct tggcttcact 480 aagtcaatcg gtgtcagcaa tttctcctgc aaaaagcttc aggaattatt ggcgacagca 540 aacatccctc cagttgtaaa tcaagtggag atgagcccag ttttccacca aaagaatctg 600 agagagtatt gcaaggccaa taatatactg gtggctgcat actcgatttt gggaggcaag 660 ggaaccgcat ggggctccaa ttcagttttg ggttccgagg ggcttaacca gattgctatc 720 gccagaggaa agtctattgc tcaggttagc atgagatggg tatacgagca aggcgcgatt 780 cttgtggtga aaagtttcag tgaaaagaat atgagggaaa acttgaacat attcgattgg 840 gaactgacta aggaagacct ggaaaggatt ggtgagattc ctcagcgcag attaataatt 900 caggaattta tggtatcatc taatggacct ttcaaatctc tagaagagtt ctgggatgaa 960 aaagctgatt ga 972
3-37	**Sequences**	
3-37-1	Sequence Number [ID]	37
3-37-2	Molecule Type	DNA
3-37-3	Length	966
3-37-4-1	Features Location/Qualifiers	**source** 1..966 mol_type= genomic DNA organism= Papaver Bracteatum
	NonEnglishQualifier Value	
3-37-5	Residues	atggagaatg taatacctgc agtgacatta agttctggaa gtgtgatgcc tatattaggt 60 atgggcactg ctgcataccc attagttgaa ccagaagaag cgaaattggc gtttttgaat 120 gctatcaaga ttggttacag acattttgat acagctgctt cttaccattg tgaaggattt 180 cttggtgaag ctatagctga agcacttcaa cttggtttga taaaatctcg agacgaactg 240 tttatcactt ctaagctctg gccctgtgat gctcaccctg accttgtcat ccccgcaatt 300 cagaactctc taaggaatct aaagttggag taccttgatc tatatctgat acattttcca 360 ataagcacga aaccagctgc agggcttgtt tttccgccac caaaggatgc tttgcttcca 420

[0018]

		atggattaca agtctgtatg ggcagctatg gaagagtgtc aaaaacttgg tcttacaaag 480 tcaattggtg tcagcaactt ctcttgtaag aagcttcaaa ccattttgga cattgctaac 540 atccctccag ctgttaacca agtggagatg aacccagttt ggcagaactt gaaattgagg 600 gacttctgca aggctaacaa tatcgttctc actgcctact cacctttagg agccagggga 660 accccgtggg ggtctaatgc agtctatgag gagcgagttc tgcatgaaat tgctgaggct 720 aaagggaaaa ctcatgcaca ggtgtgtcta agatgggtat acgagcaagg agtgagtctt 780 atagtcaaga gcttcaatga gttgaggatg aaggagaata tgatgatttt cgactgggaa 840 ctgactgaag atgaactgca aaagataggc aaaatcccac agaggagagg actcccaggt 900 gatttttttg tctcggaagc agcgcctttc aagactgtcg aagaattttg ggacggagaa 960 atttga 966
3-38	**Sequences**	
3-38-1	Sequence Number [ID]	38
3-38-2	Molecule Type	DNA
3-38-3	Length	969
3-38-4-1	Features Location/Qualifiers	**source** 1..969 mol_type= genomic DNA organism= Papaver Bracteatum
	NonEnglishQualifier Value	
3-38-5	Residues	atggaggttg taatccctaa agtggcactg agttctggta gagtgatgcc tgtgctagga 60 atgggcacat catcattccc gccagttggt ccggaagatg gaaaagccgc cattttgaat 120 gctatcaaga ttggttatag acactttgat acagcttctg tttacaagtc tgaagacttc 180 ctcggtgaag ctatagctga agcacttcta cttggattga tccaatctcg agaccagctt 240 ttcattactt ccaagttata ttgcaatgat gctcaccctg atcttgttgt ccctgcttta 300 cagaactctc tcaggaatct gaggctggag taccttgatc tatatctgat acactttccg 360 gtaagctcaa agccagtcaa gtacgagtat catctaaaaa aggagcatct cctccctatg 420 gactacgaat ctgtgtgggc agccatggaa aagtgtcaaa agcttggact tacaaagtca 480 attggagtca gcaatttctc ttgcaagaag cttcaaacta ttttggacac tgctaacatc 540 tctcctgctg ttaatcaagt ggagatgaat ccagtttggc aaaacttgaa actgagggat 600 ttctgcaaag ctaaaggtat cgttgtcact gcctactcac ctttgggagc cagcggaacc 660 ccctggggat ctaatgcagt caaagaagca caggaattgc acgaaatcgc aaaagctaga 720 gggaaaactc atgctcaggt ttgtcttaga tgggtatacg agcaaggagt gagcttgcta 780 gtcaagagct tcaaagaaga acggatgaaa gagaacctaa tgatctttga ttgggagttg 840 actaaagatg atttgttcaa aatcagcaaa attacacaac gcagaggact accaggttat 900 aggttcatct cgaaacttga agggtcaccc ttcaagacgg tcgaagaatt ctgggatgga 960 gaagtttaa 969
3-39	**Sequences**	
3-39-1	Sequence Number [ID]	39
3-39-2	Molecule Type	DNA
3-39-3	Length	966
3-39-4-1	Features Location/Qualifiers	**source** 1..966 mol_type= genomic DNA organism= Papaver Bracteatum
	NonEnglishQualifier Value	
3-39-5	Residues	atggagagta gtggtgtacc agtaatcact ctgagatcgg gcaaggtgat gcctgtttta 60 ggcatgggaa catttgagaa agctggtaaa gggtctgaaa gagagaggtt ggcgatatta 120 aaagcgatag aggtgggtta cagatacttc gacacagctg ctgcatacga aactgaagag 180 gttcttggag aagctattgc tgaagcactt caacttggcc taatcaaatc tcgagatgaa 240 cttttcatca gttccatgct ctggtgcact gatgctcacc ctgatcgtgt cctcctcgct 300 cttcagaatt ctctgaggaa tcttaaattg gagtatgtgg atctatatat gttacccttc 360 ccggcaagct tgaagccagg gaagataacg atggacatac cagaggaaga tatttgtcca 420 atggactaca ggtctgtatg gtcagccatg gaagagtgtc aaaaccttgg cctcactaaa 480 tcaatcggtg ttagcaattt ctcctgcaaa aaacttgagg aattgatggc gaccgccaac 540 atccctccag ccgtgaatca agtggagatg agcccggctt tccaacaaaa gaagctgaga 600 gagtattgca acgcaaataa tatattagtc agcgcagtct ctatactggg atcaaacgga 660 accccatggg gctccaatgc agttttgggt tctgaggtgc ttaagaaaat tgctatggcc 720 aaaggaaaat ctgttgctca ggttagtatg agatgggttt acgagcaagg cgcgagtctt 780 gtggtaaaaa gtttcagtga agagagattg agggaaaact tgaacatatt cgactggcaa 840 ctcaccaagg aagacaatga aaagatcggt gagattccac agtgcagaat cttgagtgct 900

[0019]

		tatttttttgg tctcacctaa agggcctttc aaatctcaag aagagttgtg ggatgacaaa 960 gcttga 966
3-40	**Sequences**	
3-40-1	Sequence Number [ID]	40
3-40-2	Molecule Type	DNA
3-40-3	Length	972
3-40-4-1	Features Location/Qualifiers	**source** 1..972 mol_type= genomic DNA organism= Papaver Bracteatum
	NonEnglishQualifier Value	
3-40-5	Residues	atgggaagta gttgtattcc tgttctcact ttgaactcgg gcaataagat gcctgtttta 60 ggtatgggaa catttgaaac atttgctaaa gggggtgaaa gagaaagatt ggcgtatttg 120 aaagcgatta aagtgggtta cagatacttc gatacaggcg ctgcatacgg aacggaagag 180 gttcttggcc aagctatagc tgaagcactt caacttggcc taataaaatc tcgagatgaa 240 ctcttcatca gtaccatgat ctgggccact gatgctcacc ctgatggtgt cctccccgct 300 gttcagagat ctttaaggaa tcttaaattg gactatgtgg atctctacct gataccattt 360 ccggcaagct tgaacccaga aggggagata cctaattaca taccagagaa cgaaactttt 420 ttaaaaatgg actacaagtc tgtatgggca gctatggaag agtgtcaaac ccttggcttt 480 accaagtcta tcggtgtcag caatttctcc tgcaaaaagc ttcaggaagt gatggagacc 540 gcaaatatcc ctccggctgt caacatggtg gaaatgaacc ctactttcca acaaaaatat 600 ctgagagagt actgcaaggc caataatata ttagtcaatg cgtactctgt tttgggatcc 660 acgggaactt catggggctc caatgcagtt atgggttctg aggtgcttaa gcaaattgct 720 acggacatag gaaaatctat tgctcaggtt agtatgagat gggtttacga gcaaggtgcg 780 ggttttgtgg taaaaagttt cagtgaagag aggatgaggg aaaacttgaa catattcgac 840 tgggagctga ctaaggaaga cttggagaag atcagtcaga ttccacaatg cagagtacta 900 cctatggatt ttttggtatc atctgatgga gctttcaaat ctttggaaga cttgtgggat 960 ggtgaagctt ga 972
3-41	**Sequences**	
3-41-1	Sequence Number [ID]	41
3-41-2	Molecule Type	DNA
3-41-3	Length	912
3-41-4-1	Features Location/Qualifiers	**source** 1..912 mol_type= genomic DNA organism= Papaver Bracteatum
	NonEnglishQualifier Value	
3-41-5	Residues	atgccgatct taggttttgg aacagctgaa aaccttttg aagggggtga taaagtgaag 60 ttggcgattt tgaaagcgat agaggtgggt tacagataca ttgatacagc tgccgtgtac 120 cgaactgaag agtctgttgg tgaagctgta gcagaagcac ttcaacttgg cttgataaaa 180 tctcgagacg agctattcat aacctccaag ctatggggtg tcgatgctca tcctgatctt 240 gtcctcccag ctcttcagaa ctcattgagg aaacttaaat tggagtattt ggatctgtat 300 ctgatacact atccggtaag cttgaagcca ggggagatgg tcgatgatat accgaaggac 360 gaaatatttc cactggacta caagtctgta tgggcagcca tggaagagtg tcagaagctt 420 ggctacacta agtcaatcgg ggtcagtaat ttctcttgca aaaagcttca acagcttatg 480 gccacagcta acatacctcc agctgtaaat caagtggaga tgaacccaac ttggcaacaa 540 aagaatctaa gggaatactg taaggccaac aatatcttca ttacagcata ctcgactttg 600 ggagctaaag acctttatg gggctccaat gcagttttag gctctaaagt gttgaaccag 660 attgccgtgg ccagaggaaa atcagttgcc caggttagtc tgagatgggt ttacgaacaa 720 ggtgtgagtc ttgtggtgaa aagttttaac gaggagagga tgaaggagaa cttgaagata 780 tttgattggg aactgaccac agaagacttg aaaatgatca gtgagatccc tcaacgcaga 840 gtagcaactg cggatttttt tgtgtcagat attggaccct tcaaatcttt agaagagctg 900 tgggatgaat aa 912
3-42	**Sequences**	
3-42-1	Sequence Number [ID]	42
3-42-2	Molecule Type	DNA

[0020]

3-42-3	Length	921
3-42-4-1	Features Location/Qualifiers	**source** 1..921 mol_type= genomic DNA organism= Papaver Bracteatum
	NonEnglishQualifier Value	
3-42-5	Residues	atgccggttt taggactggg aacagctgaa aaccttacta aaggttctga aagagagatg 60 ctggcgattt tgaaggcgat agaggtgggt tacagacact ttgatacagc tttcatatac 120 caaactcaag agtgtgttgg tgaagctata gctgaagcac ttcaactagg tatcatcaaa 180 tctcgggatg aactctttat cacttccaag ctctggggtt ctgatgctca ccctgattgc 240 gtcctcctgg ctcttcagaa ttctctaagg aatcttaaac tgcagtatct ggatctatat 300 ctgatacact atccagtaag cttgaagcca gggacaactt tgaaagattt ggggaataag 360 gacaacttcc ttccaatgga ctacaagtct gtatgggcag ctatggaaga gtgtcagaag 420 cttggcctca ctaagtcgat aggtgtcagc aacttctcct ccaaaaagat tcaagagcta 480 atgagcacag acagcatccc tcctgccgta aatcaagtag agatgaaccc cacatggcaa 540 caaaagaaac tgagagaata ttgtcaggcc aacaatatct tagttactgc atactctcct 600 ttgggagcta aaggaaccac atggggatcc aatgcggtta tgggatctga ggtactgaac 660 cagattgccc ttgccagagg gaaatctgtt gctcagatta gtctaagatg ggtttacgag 720 caaggtgtga gtctcgtggt gaaaagcttc aatgaagaga ggatgaggga gaacctgaaa 780 atatttgact gggagctaac tgccgaagac ttgaaaaaga tagatgagct tccacagagc 840 agagtggcaa ctgctgaatt tgttgtatca gagaatgggc ccttcaagtc tttagaagaa 900 ttttgggatg acgagtcctg a 921
3-43	**Sequences**	
3-43-1	Sequence Number [ID]	43
3-43-2	Molecule Type	DNA
3-43-3	Length	966
3-43-4-1	Features Location/Qualifiers	**source** 1..966 mol_type= genomic DNA organism= Papaver Bracteatum
	NonEnglishQualifier Value	
3-43-5	Residues	atggagaatg caatacccgc ggtaacattg aattctggaa gtgtgatgcc tgtattaggt 60 atgggaactg ctgcataccc atttgtcgaa tcagaagaag cgaaattggc gattttgaat 120 gctatcaaga ctggttacag acatttagat actgctgctc tttaccagtc tgaagaatca 180 cttggtgaag ctgtatctga agcaattcaa cttggtttga taaaatctcg agacgaactg 240 tttatcactt ctaagctctg gccctgtgat gctcaccctg accttgtcat ccccgcaatt 300 cagaactctc taaggaatct aaagttggag taccttgatc tatatctgat acattttcca 360 ataagcacga aaccagctgc agggcttgtt tttccgccac caaaggatgc tttgcttcca 420 atggattaca agtctgtatg ggcagctatg gaagagtgtc aaaaacttgg tcttacaaag 480 tcaattggtg tcagcaactt ctcttgtaag aagcttcaaa ccattttgga cattgctaac 540 atccctccag ctgttaacca agtggagatg aacccagttt ggcagaactt gcaattgagg 600 gacttctgca aggataagag tatcattctc actgcctact caccattaga agggaaggga 660 accccgtggg ggtctaatgc agtctacgga gcacaagttt tgcatgaaat tgctgaggct 720 aaaggcaaaa ctcacgcaca ggtttgtctg agatgggtat atgagcaagg agtgagtctg 780 ctagtgaaga gcttcaatga tcagaggatg aaggaaaaca tgatgatttt cgattgggaa 840 ctgaccgagg atgaactgga aaagataagc agaatcccac agaggagagg actcccaggt 900 gatttttttg tctcggaagc agcgcctttc aagactgtcg aagaattttg ggacggagaa 960 atttga 966
3-44	**Sequences**	
3-44-1	Sequence Number [ID]	44
3-44-2	Molecule Type	DNA
3-44-3	Length	966
3-44-4-1	Features Location/Qualifiers	**source** 1..966 mol_type= genomic DNA organism= Papaver Bracteatum
	NonEnglishQualifier Value	

[0021]

3-44-5	Residues	atggagaatg caatacccgc ggtaacattg aattctggaa gtgtgatgcc tgtattaggt 60 atgggaactg ctgcataccc atttgtcgaa tcagaagaag cgaaattggc gattttgaat 120 gctatcaaga ctggttacag acatttagat actgctgctc tttaccagtc tgaagaatca 180 cttggtgaag ctgtagctga agcaattcaa cttggtttaa taaaatctcg agacgaactt 240 tttatcactt ctaagctatg gccttgtgat gcacaccctg accgtgtcgt ccctactctt 300 cagaactctc taaggaagtt aaagttggag taccttgatc tatatctaat acattggcca 360 gtaagctcga acccagtggc agggcatgtg ttatcgctgc caaaggattc tttggttaca 420 atggattacg agtctgtatg ggcagctatg gaagagtgtc aaaaacttgg tcttacaaag 480 tcaattggtg tcagcaactt ctcttgtaag aagcttcaaa ccattttgga cattgctaac 540 atccctccag ctgttaacca agtggagatg aacccagttt ggcagaactt gaaattgagg 600 gacttctgca aggctaacaa tatcgttctc actgcctact cacctttagg agccagggga 660 accccgtggg ggtctaatgc agtctatgag gagcgagttc tgcatgaaat tgctgaggct 720 aaagggaaaa ctcatgcaca ggtgtgtcta agatgggtat acgagcaagg agtgagtctt 780 atagtcaaga gcttcaatga gttgaggatg aaggagaata tgatgatttt cgactgggaa 840 ctgactgaag atgaactgca aaagataggc aaaatcccac agaggagagg actcccaggt 900 gatttttttg tctcggaagc agcgcctttc aagactgtcg aagaattttg ggacggagaa 960 atttga 966
3-45	**Sequences**	
3-45-1	Sequence Number [ID]	45
3-45-2	Molecule Type	DNA
3-45-3	Length	972
3-45-4-1	Features Location/Qualifiers	**source** 1..972 mol_type= genomic DNA organism= Papaver Bracteatum
	NonEnglishQualifier Value	
3-45-5	Residues	atggagaatg taatacctgc agtgacatta agttctggaa gtgtgatgcc tatattggct 60 atgggcactg ctgcataccc attagttgaa ccagaagaag cgaaattggc gtttttgaat 120 gctatcaaga ttggttacag acattttgat acagctgctt cttaccattg tgaaggattt 180 cttggtgaag ctatagctga agcacttcaa cttggtttga taaaatctcg agacgaactg 240 tttatcactt ctaagctctg gccctgtgat gctcaccctg accttgtcat ccccgcaatt 300 cagaactctc taaggaatct aaagttggag taccttgatc tatatctgat acattttcca 360 ataagcacga aaccagctgc agggcttgtt tttccgccac caaaggatgc tttgcttcca 420 atggattaca agtctgtatg ggcagctatg gaagagtgtc aaaaacttgg tcttacaaag 480 tcaattggtg tcagcaactt ctcttgtaag aagcttcaaa ccattttgga cattgctaac 540 atccctccag ctgttaacca agtggagatg aacccagttt ggcagaactt gcaattgagg 600 gacttctgca aggataagag tatcattctc actgcctact caccattaga agggaaggga 660 accccgtggg ggtctaatgc agtctacgga gcacaagttt tgcatgaaat tgctgaggct 720 aaaggcaaaa ctcacgcaca ggtttgtctg agatgggtat atgagcaagg agtgagtctg 780 ctagtgaaga gcttcaatga tcagaggatg aaagaaaaca tgatgatttt cgattgggaa 840 ctcactgaag atgaactgga aaagataggc aaaatcccac agagtagagg actcccaggt 900 gatgtttttg tctcggaact tgaagctgcc cctttcaaga ctgtcgaaga attctgggac 960 ggagaggttt ga 972
3-46	**Sequences**	
3-46-1	Sequence Number [ID]	46
3-46-2	Molecule Type	DNA
3-46-3	Length	960
3-46-4-1	Features Location/Qualifiers	**source** 1..960 mol_type= genomic DNA organism= Sanguinaria canadensis
	NonEnglishQualifier Value	
3-46-5	Residues	atggagaacg tctctgtagt gactttgaac tcaggaagag agatgccaat tctaggtatg 60 ggcaccgctg catacccttc tgttggctca gaagaagcca aattggcgat tcttcttgcg 120 ataaaggtcg gctacagaca ctttgacaca gctgctgctt accagattga gtcttctctt 180 ggcgaagctg tagctgaagc acttcaactt ggactgctca aatctcgaga tgaactcttc 240 atcacctcca agttatggtg ctctgattct caccctgaac gtgtcctccc cgctcttcag 300 aactccctcc ggaatcttaa gttggagtat cttgatctat atctgataca ttggccggta 360 agcttgaagc cagggaactt tgatctgact atacccaaag aggatttgct ccctatggac 420 tacaagtctg tgtgggcagc catggaagaa tgtcagaaac ttggcctcac aaagtcgatt 480 ggtgtcagca atttctcttg caagaagctt caagatttat tggccaccgc caacatccct 540

[0022]

		cccgctgtta atcaagtgga gatgaaccca atttggcaac agaagaaatt gagggagttc 600 tgcaaggcca acggtatcct tattacagcc tactcaccgt tgggagccaa tggaactcct 660 tggggatcca gcggagtcgc caatactgag gtgctacacc aaattgctaa ggctagaggg 720 aagactcatg ctcaggtttg tctaaggtgg gtatacgagc aaggagtgag tttgttagta 780 aagagcttca atgaagagag gatgaaggag aacctgaaga tattcgattg ggaactgact 840 gcagaagatt tgaaacagat cagcgagatc ccacagcatc gaggactccc tgctgatatt 900 ttcgtctcag ttaacgggcc cttcaagact gtcgaagagt tctgggatgg cgaggtttga 960
3-47	**Sequences**	
3-47-1	Sequence Number [ID]	47
3-47-2	Molecule Type	DNA
3-47-3	Length	966
3-47-4-1	Features Location/Qualifiers	**source** 1..966 mol_type= genomic DNA organism= Sanguinaria canadensis
	NonEnglishQualifier Value	
3-47-5	Residues	atggagatta gtgttccaat aacgactctg agctccggga gggagatgcc aatcttaggt 60 atgggaactg ctgaaaatct attcaatgga tccgaaaaag tgaaattggc aattctagat 120 gcgataaaag tgggatacag acactttgat acagctgctg tgtaccaaac tgagtcgtct 180 ttgggtgaag cagtagctga agcacttcaa catggactgc tcaaatctcg agacgaactc 240 ttcatcacct ccaaattatg gtgctctgat tctcaccctg atcgtgtcct ccctgctctt 300 caaacctctc tcaggaagct taagttggag tatcttgatc tatatctgat acattggccg 360 ttaagctcta agcctgggag ccatgattat cctataccca aggaggattt gctccctttg 420 gactacaagt ctgtgtgggc agccatggaa gaatgtcaga agcttggcct cacaaagtcg 480 attggtgtca gcaatttctc ttgcaagaag cttcaagatt tattggacac agccaacatc 540 cctcccgctg ttaatcaagt ggagatgaac ccgctttggc aacagaagaa actgctggag 600 ttttgtaagg ggaacggtat tatcatcact gccttttcgc cgttgggtgc caaaggcacc 660 tcctggggcg ccaccaacgg agttatggac tctgaggtgc tacaccagat tgcccaggct 720 agaggaaagt ctattgctca ggtttctctg aggtggttat acgagcaagg tgtgagtctg 780 gttgtgaaga gtttcaatgt agagaggatg aaggagaacc tgaagatatt cgattgggaa 840 ttaagcgcag aagacttaaa aaagatcaac gagatcccac agcgtagagg actccctagt 900 ggtagtttca tctcagctaa cgggccattc aagtctgaag aagagctctg ggacggagaa 960 gtctga 966
3-48	**Sequences**	
3-48-1	Sequence Number [ID]	48
3-48-2	Molecule Type	DNA
3-48-3	Length	957
3-48-4-1	Features Location/Qualifiers	**source** 1..957 mol_type= genomic DNA organism= Sanguinaria canadensis
	NonEnglishQualifier Value	
3-48-5	Residues	atggccatgg aaaccgttcc taagctaccc ttaagctccg gtgacaattc catcccggta 60 ataggtttcg gcaccgccgc gtttccactc cccgatgacg aaactttaaa atcggcgttt 120 ctcaatggga ttgaagccgg ttaccgtcac tttgacacgg cggctgccta tggttcggag 180 aaggctctcg gcgaagctat aaccgaagct ttacgtctcg gtctgctaaa atctcgagaa 240 gaagttttca tcaccactaa gctttggtgt agcagttgtg aacgcagcct cgtggttcct 300 tcactcaaga atagcctccg gaatctacaa atggagtacg tagatctttt cctcatacat 360 tggcctgtaa gattaagtat tgatgcacag cgacctccaa ttccaaggga acaaattctt 420 actttcgata ctaaatcagt ttgggaagga atggaagaat gtcacgaact tggcctcgcc 480 aaaaatatcg gacttagtaa tttttatccc aagaagatcg atgaattgct cgccaccgca 540 aaaattcccc cggccgtcct tcaagtggaa ttgagcccaa cttggcaaca gaagaatttg 600 atcgaatatt gtagggaaaa gggtatcctt gtcacggctt attctgcttt aggagccaac 660 ggcacgcatt ggggagacaa tagagtggtg gagagcgatg tattaggaga catcgccaag 720 gctagaggaa aaaccactgc tcagattgcg ttgagatggg tgtatgaaca aggggtgtgt 780 atggtggtga agagcttcaa caaggaaagg atgaaactaa acctccagat ctttgatttt 840 gagttgaccg aggaagagtc aaacaagatc agtcaacttc cacaaatcaa aggagttaaa 900 ctatctccca tgtttgggaa ccatgatgta ctcaaggagc ttgaggatca actctga 957
3-49	**Sequences**	

[0023]

3-49-1	Sequence Number [ID]	49
3-49-2	Molecule Type	DNA
3-49-3	Length	987
3-49-4-1	Features Location/Qualifiers	**source** 1..987 mol_type= genomic DNA organism= Sanguinaria canadensis
	NonEnglishQualifier Value	
3-49-5	Residues	atgggtgagg aaatgaagtg tggtagggtt gttccagtgg cgactctgaa ctccggaagg 60 acgatgccgc tcttaggtat gggaacagcc gcatatccat ttgtcgggtc ggaaaaggta 120 aagtctgcga ttcttcatgc gataaagctg gggtaccggc actttgatac cgctgcgctg 180 taccaaactg aggagtgtct tggtgaagtt gtagctgaag cacttcaact tggactgctc 240 aaatctcgag acgaactctt catcacttcc aagctatggt gctctgattc tcaccctgac 300 cgtgtcctcc ctgctcttca gacctccctt cggaagctta agttggagta ccttgatcta 360 tatctgatac attggccgct aagtttgaag cctgggaact acggatttcc catacccaaa 420 gaggacatgc tccctatgga ctacaagtct gtgtgggcag ccatggaaga atgtcaaaag 480 cttggcctca caaagtcgat cggtgtcagc aatttctctt gcaagaagct tcaagattta 540 ttggccacag ccaacatccc tcccgctgtt aatcaagtgg agatgaaccc aatttggcaa 600 caaaagaaac tgagagagtt ttgcgaggcc aatggtatcc ttattacagc ctactcgcct 660 ttaggagcca atggaacccc ttggggctcc agcggagtcg cccagactca ggtgctgcac 720 gacattgcta aggctagagg gaagactcat gctcaggttt gtgtgagatg ggtatacgag 780 caaggggtga gtgtgttggt gaaaagctac aatgaagaga ggatgaagga gaacctgacg 840 gtattcgatt gggaattgga cgtagaggac ctgaagaaga tcagtactga aatcccacag 900 cgtagaggac ttcctagtga cattttcgtt tcagtactta ctggaccctt caagtctgca 960 gaagagctct gggatggaga gctctga 987
3-50	**Sequences**	
3-50-1	Sequence Number [ID]	50
3-50-2	Molecule Type	DNA
3-50-3	Length	981
3-50-4-1	Features Location/Qualifiers	**source** 1..981 mol_type= genomic DNA organism= Stylophorum diphyllum
	NonEnglishQualifier Value	
3-50-5	Residues	atggagagtg atagtacagc agtagcagtt ccagttacga ctctgagctc aggtattgag 60 atgccaatgt taggtctggg aactgctgat gaaaaacttc ttccaagttc cgaaacagtg 120 aagttggctt ttctgactgc gataaaacta gggtacaggc acttcgacac agctgctgtg 180 taccaaactg aggagtgtct tggtgaagct gtagctgaag cacttcaact tggtctgatc 240 aaatctagag acgaactctt catcacttcc aagctgtggt gctctgatgc tcaccctgat 300 cttgtcatcc ctgctcttca gaactctctc cggaagctga agttggagta tcttgattta 360 tatctgatac attggccgtt aagctcaaag ccagggaact gtgtttttcc aatacccaag 420 gaggacctcc ttcctttgga cttcaagtct gtgtgggcag ccatggaaga atgtcaaaag 480 cttggcctca caaagtcaat tggtgttagc aacttctctt gcaagaagct tcaagattta 540 ctggccatgg ctatcatccc gcccgctgtt aatcaagtgg agatgaaccc acattggcaa 600 cagaagaaac tgagggagtt ttgtaaggtc aaagatattg tcgttacagc ctactcgcct 660 ctgggagcca aaggcacccc atggggctcc aacgcagtta tggactccaa ggtgctacat 720 cagattgcca aggctagagg gaagtctgtt gctcaggttt ctcttagatg ggtataccag 780 caaggtgtgg ttttgttggt gaagagtttc aatgaagaaa ggatgaagga gaacatgaag 840 atattcaatt gggaactgaa cgaagaagac ttaaaaatga tcgacgagat cccacaatgt 900 agaggcaacc ctagtcatta ttacgtctca gaaaacggac cattcaagac tgttgaagaa 960 ttctgggatg gagaagtcta a 981
3-51	**Sequences**	
3-51-1	Sequence Number [ID]	51
3-51-2	Molecule Type	DNA
3-51-3	Length	924

[0024]

3-51-4-1	Features Location/Qualifiers	**source** 1..924 mol_type= genomic DNA organism= Stylophorum diphyllum
	NonEnglishQualifier Value	
3-51-5	Residues	atgccaattg ttggtatggg aacagctgaa aaccttttg aaggttcaga aagagtgaag 60 ttggctcttc tgactgcaat aaaggtgggt tatagacact ttgatacagc tgctgtttac 120 cagactgagg ggtctcttgg tgaagctata gctgaagcac ttcaacttgg actgatcaaa 180 tctagagacg aactctttat aacttccaag ctgtggattc atgattgtca ccatgatctt 240 gtcctccctg ctcttcagaa ttctcttagg aagcttaagt tggagtacct tgacctctat 300 ttgatacatt ggccagtaag ctcgaagcca ggggagctca ggtctcttat accaaaggag 360 gagctcctcc caatggattt caagtctgtg tgggtagcca tggaagaatg tcacaagatt 420 ggcctcacaa agtcaattgg tgttagcaac ttctcttgca agaagcttca agatttattg 480 ctcactgcca acatccctcc tgctgttaac caaaaggtgg agatgaaccc actttggcaa 540 cagaagaaac tgagggagtt ttgtaaggcc aacggtatcg tcattgcagc ttactcgcct 600 ttaggagcca aaggaacctt gtggggaacc aacggtgtta tggactctga ggtgctacaa 660 cagattgcca aggcaagacg aaagtctatt gcgcaggttt ctctacgatg ggtatatgaa 720 caaggggtgg ttttgttggt gaagagtttt aatgaaggga ggatgaagga aaacctgaag 780 atattcgatt gggaattaag tagagaagac ttgaaacaaa tcaacgagat cctcccacag 840 cgtagaggac tccctagtca tgtttttgtc tccgatgacg ggccattcaa gtctgaggaa 900 gaactgtggg atggagaagt gtga 924
3-52	**Sequences**	
3-52-1	Sequence Number [ID]	52
3-52-2	Molecule Type	DNA
3-52-3	Length	957
3-52-4-1	Features Location/Qualifiers	**source** 1..957 mol_type= genomic DNA organism= Stylophorum diphyllum
	NonEnglishQualifier Value	
3-52-5	Residues	atgaccatgg aagctgttcc aaaggtaacc ttaagcacca gtggcaaatc catgcccata 60 attggtttcg gcaccgcctt gtttccgact ggcaatgacg aagccgtgaa atcagcggtt 120 ctaagtggga ttgaagctgg ttatcgtcac ttcgacacag cagtcgccta cagatccgaa 180 aagggtctcg gtgaaggtat agcagaagct ctacgtctag gtctgatctt atctcgagac 240 gaagttttca tcaccaccaa gctttggtgt actagttgcg agcgcagcct cgttgtacct 300 tcactcaaga acagcctccg aaatctacaa atggaatacg tagatctttt tctcatacat 360 tggcctttac gactaagtgc cgatgcacaa cgacctccga ttcgaaacga tcagatactt 420 catttcgata cgaaatcagt ttgggaagga atggaagaat gttatgaact aggcctcgcc 480 aaaaatatag gagttagtaa cttctatccc aagaagattg atgagttact cgccactgca 540 aaaattcctc cagcaatcaa tcaagtggaa ttaaacccag cttggaacca gaaggatctg 600 atcaagtatt gtaagtcaaa gggtattctt atcacggctt actctgcttt aggagccaac 660 ggaacgcatt ggggagataa ccgagttgtg gacagcgatg tgctgaagga catcgcgaaa 720 gctcgaggaa aatccacagc tcaggttgca ttgagatggg tatatgagca aggggtgagt 780 atggtggtca agagctttaa caaggaaagg atgaaacaga accttcagat cttcgatttt 840 gagttgacgg aggaagagtc aaacaagatc agtcaacttc cacaacacaa aggtgttaaa 900 cttactccag tgtatggcga ccatgatgcc atgaagaaga ttgacaatga gatctga 957
3-53	**Sequences**	
3-53-1	Sequence Number [ID]	53
3-53-2	Molecule Type	DNA
3-53-3	Length	960
3-53-4-1	Features Location/Qualifiers	**source** 1..960 mol_type= genomic DNA organism= Tinospora cordifolia
	NonEnglishQualifier Value	
3-53-5	Residues	atggtgagtg tacctgaggt ggttctgagc aacgggcacc tcatgcctgt ggttggtatg 60 ggcatggcgg cctacccatt ccaagaatct gaaacagtga agcaggcaat gatcagggca 120 attaagatgg gctacaggca ttttgacaca gctgccttgt accaaacaga gaagtccctt 180 ggagatgcaa ttgtagaagc actaaagctt ggcctcatta aatctcgtga cgagcttttc 240

[0025]

		atcacttcca agctgtggtg cagtgatgct catccccatc acgtcattcc ggctcttcaa 300 agaactctga ggaatcttgg gttggagtac cttgatctct atctcataca ctggccagta 360 agctcagaac ctggcaaata cgagttccca gtacgaaagg aagagctaat tctgatggat 420 tttgaaaatg tatgggcaga tatggaagaa ggatataggc ttggcctcac aaagtcaatt 480 ggtgtaagca acttctcttg taagaagctc gaaagtttac tcactatggc aaagatccct 540 cctgcagtga atcaagtgga gatgaatccc ctctggagac agaataaact actaaggttt 600 tgtaaggaca agggcattgc tatcactgct tactcaccac tgggagccaa aggaactata 660 tggggcacta acagagtgat ggaaagcgag gtgctaaacg atactgccaa tgctagagaa 720 aagactcttg ctcaggtttg tctaagatgg gtttatgagc aagaagtatc catattggtc 780 aaaagcttca acgaagagag gatgaaggag aacttagaca tttttgattg gaaattaagt 840 gacgaggact tggaaaagat caatgagatt ccacaatgca gaggacttcc aggtgatatc 900 tttgtatcag atgatgggcc cttcaaatct gaagcagagc tctgggatgg agaaatctga 960
3-54	**Sequences**	
3-54-1	Sequence Number [ID]	54
3-54-2	Molecule Type	DNA
3-54-3	Length	990
3-54-4-1	Features Location/Qualifiers	**source** 1..990 mol_type= genomic DNA organism= Tinospora cordifolia
	NonEnglishQualifier Value	
3-54-5	Residues	atggtgggag ttaacaagga gaacgtggtt tcatcagtag caacggtgcc ggtggtgacg 60 ctgaactccg gtcataaaat gccagtgctg ggaacgggca cagcttcgtt tcctgttcct 120 ccattagagg aactgaagaa ggtgatcatg gaagccatgg aagtgggcta ccgccacttt 180 gatacagcag ccatgtatca aagcgaggaa gggctcggtg cggccattaa agaggcctta 240 gagaagggtc taattaagag cagagatgag cttttcatca ctaccaaact ttggtgcaat 300 aatgcccaac cccatcttgt gctccctgcc atccgcgact ctctcaggag gctaaggttg 360 gaatatgtgg acttatattt gattcattat ccagtaaggc tgaaggaaga tttattgagt 420 atggactgca aggaggatga aatatttccc attgacataa aatcagtatg gtcggcaatg 480 gaggaaatac acaatcttgg tcttgcaaaa tccattggag tcagcaactt cacttgcaag 540 aagctcactg atctacttgc tcatgcaaag atccctcctg cggttaatca ggtggaattg 600 cacccagcat ggcaacaaaa aaaattaaga gaattctgcc aggagaaagg catccaagtc 660 agtgcatatt ctcctcttgg agctaagcaa tggggatttg atgttgttct tagcaataag 720 atcatcaaag agattgccca tcacaaagga aaaacggttg ctcagattgc tttaaggtgg 780 ggacatgagc aaggaataat tttaatccca aagagcttca acaaggaaag attgattcag 840 aatctcctca tatttgattg ggagctaact caagatgaac tgaagaagat ggcatcaatt 900 caacagtcta gaatagccat agcccctgag tttgtgttcc ctggcagccc tttcaaatcc 960 tttgaagagt tctgggatgg agaaatgtga 990
3-55	**Sequences**	
3-55-1	Sequence Number [ID]	55
3-55-2	Molecule Type	DNA
3-55-3	Length	966
3-55-4-1	Features Location/Qualifiers	**source** 1..966 mol_type= genomic DNA organism= Tinospora cordifolia
	NonEnglishQualifier Value	
3-55-5	Residues	atgggaatta gcatgcctga cgcaaccctt aattccggcc atcggattcc tctcatcgga 60 ttcggaaccg cgagtttccc cttccctctt gaaggatcag aaactgctac acgggcaata 120 ctggaagcca tcaagattgg ttaccggcac tttgacacgg ctgccttgta ccagacagag 180 gttggacttg gtgaagcaat agaagaagct cttcatcttg gtctcatcga gtcccgtgat 240 gagctcttca ttacctccaa gctttggtgc actcatggcc gccctgagcg cgtccttcct 300 gcaattcgag aatctcttaa gaatctgaag ctggactacc ttgatcttta tctgatacac 360 atgccaatga gcttcaagtc agaaaagcca tggttcccat tacctggaga gtttgaagcc 420 atggatttca agtctgtatg ggaacagatg gaagcatgcc agaggcttgg ccttgcaaga 480 tccattggag ttagcaactt ctcctgcaaa aagctccaac tcatcctcac tactgcaaat 540 attcctcctg ctgtgaatca agtggagatg aacgcccttt ggcaacagaa taagctgaga 600 gagttttgca agagtgaagg cattgttatc actgcttact ctcccttggg aggcaaagga 660 accagttggg gttcaaatag agttatggaa tgtgaagtga taaaagagat tgccacggaa 720 aaaggaaaaa cacacgctca ggtttgtctt agatggctgt acgagcaagg cgtgagcatg 780 gtggtgaaga gcttcaacaa agagagaatg aaagagaact tggagatatt cgactgggag 840

		ctcacaagta aagagtgtga gcagatcaag aagctaccgc aaagcagagg atttactgca 900 caagggttgg tctcagaaga tgggcctttc aagtctatag aagatatatg ggatggagag 960 atttga 966
3-56	**Sequences**	
3-56-1	Sequence Number [ID]	56
3-56-2	Molecule Type	DNA
3-56-3	Length	1002
3-56-4-1	Features Location/Qualifiers	**source** 1..1002 mol_type= genomic DNA organism= Thalictrum flavum
	NonEnglishQualifier Value	
3-56-5	Residues	atgaggaggc cacacagcag actagctagt actagagata tgagtagtat tgttcctgat 60 gtggttctta gctctggcca taaaatgcct cttattggct tcggcacagt tgcgtatcct 120 atcgcagcat cagactccat aaagacagct atagtcaatg gaattaagca tggttacaga 180 cactttgata ctgcttcagt ttaccaaaca gaacaactac ttggtgaagc tatagctgaa 240 gcacttcaat ttggtcttat taaatctaga caagaacttt tcataacttc taagctatgg 300 tgcagtgatt ctcatcatga tcgtgttctc cctgctctgc agaatactct caagactctt 360 cagctagatt accttgatct gtatctcgta cattggccaa taagctctaa accagggaag 420 cacgagttcc caataccgaa agaggaactt cttcccctgc attttgagtc tgtatggaca 480 gccatggaag agtgtcaggc tgttggcctt acaaaatcga ttggtgtcag taacttttct 540 tccaagaagc ttgagcagct actctccact tccaagattc cacctgcggt taatcaagtg 600 gagatgaatc caatttggca acaatataag ttgcgagagt tttgtaaatc caaaggtata 660 gttattactg ccttttctcc attgggtgcc aaaggaacgt cttggggaac taataaagtt 720 atggactcgg aggtgttgaa tgagattgct caggctaaag gaaagactca tgctcaggtt 780 tgtcttcgat ggttgcatga acaaggcata tgtgtggtag tgaaaagctt caatgaagaa 840 aggatgaagg agaacctgga gatattcgac tgggaattga gcccagagga gtccgcatta 900 atccagcaat taccgcagag tagaggaaat actggagagg actttatctc agtcgacggg 960 ccattcaagt ccttagaaga gctatgggat ggagagattt ga 1002
3-57	**Sequences**	
3-57-1	Sequence Number [ID]	57
3-57-2	Molecule Type	DNA
3-57-3	Length	963
3-57-4-1	Features Location/Qualifiers	**source** 1..963 mol_type= genomic DNA organism= Thalictrum flavum
	NonEnglishQualifier Value	
3-57-5	Residues	atgggaagta tacctgaggt aagcttaaac tccggtcacc ggatgccact cataggcatg 60 ggcacagcat catacccttt tgcaggatca gaagtagtaa agtcagctat actcagtgca 120 atcaaacttg gtaacagaca ctttgacact gctgctttat acaaaacaga gcaaattatt 180 ggagaagcta tagctgaagc acttcaactt ggtcttatca aatctagaga agagcttttc 240 attactacca agctatgggt gaatgatggt cacaaagatt gcatcctccc tgctcttcaa 300 acatctctca aaaacctgca gctggactac gttgatctat atcttataca ttggccagta 360 tgcatcccac caggggagtt gcgaatgcct ggaccaaatg aaaaggttct tcccatagat 420 tatgcatctg tatgggaagc aatggaagag tgtcaaaggc atggccttac aaaatcaatt 480 ggagtcagca atttcacctg taagaaactt gaattgatac tggcctcagc aaagatccca 540 ccggctgtta atcaggtgga ggtgaatcca ctatggagac aagaaaaagt gataaggttt 600 tgcaaggaca gaggcattgc tgtcacagct tactctcctt tgggcactgc tggatcagat 660 tttatgggca acagaaacgt ggtgcaaagt gagttactga aagagattgc caaagctaca 720 ggaaagacgc atgctcaggt ttgtataaga tgggtttttg agcaaggagt aggggtaata 780 gttaagagct tcaaggagat gagactggag gagaacattg acatatttga ttgggaacta 840 agcaaagaag actctctgaa aattagccga ttaccagaga gtaaaggcta tcccggacat 900 ggcttcatta gagttgaagg gccattcaaa tctcttgagg agctttggga tggagagatc 960 tga 963
3-58	**Sequences**	
3-58-1	Sequence Number [ID]	58

[0026]

[0027]

3-58-2	Molecule Type	DNA
3-58-3	Length	963
3-58-4-1	Features Location/Qualifiers	**source** 1..963 mol_type= genomic DNA organism= Xanthoriza simplicissima
	NonEnglishQualifier Value	
3-58-5	Residues	atgggtagtg ttccagagat aaccttgaac tccggccaca gtatgcctgt cttaggcttg 60 ggtaccgcat ctgttccctt tgctggatat gaagtagtga agtcagcgat actcagtgcg 120 attaagcttg gttatagaca ctttgataca gcagcgttat acagaacaga gcagcctcta 180 ggagatgcta tagctgaagc aattcgcctt ggcatcatca aatccagaga agagcttttt 240 attacctcca gaccatggct caatgatact caccacgatc gaatcctccc cgctcttcag 300 acgactctcc aaaatctcca actggattac cttgatcttt atcttataca ttggccactg 360 agcataaaac cagggaatat acgattccct ggaccagacg aaaagattct tccaatggat 420 ttcgagtctg tatgggcagc catggaagag tgccaaaggc ttggtctcac aaggtcgatt 480 ggagtcagta atttctcctg caagaaactt gagaagattc ttgcctcagc aacgatccct 540 cctgctgtta atcaagtgga ggtgaaccca ctatggcgac aagagaaact gatacagttt 600 tgcaagtcta aaggtattgt tataacagct tattctcctt tgggaactgt tggttcaagt 660 tttcaaggta acaacaatat catggaatgt gaggttctga aagagattgc agggaacaga 720 ggaaagactc atgctcaggt ttgtcttaga tgggtatatg agcaaggggt ttgtttgctg 780 gtaaagagct tcaatgaggc gaggctgaag gaaaacatgg aaatatttgg ctgggcattg 840 agtgaggaag aagcaaacca gatcaatcag ctgccacagg gtagaggata tcctggacat 900 aatttcatta cgcctgatgg gcctttcaaa tctgaagagg agctttggga tggagagata 960 taa 963
3-59	**Sequences**	
3-59-1	Sequence Number [ID]	59
3-59-2	Molecule Type	AA
3-59-3	Length	325
3-59-4-1	Features Location/Qualifiers	**source** 1..325 mol_type= protein organism= Argemone Mexicana
	NonEnglishQualifier Value	
3-59-5	Residues	MEEVIGLETV VPKVTLSSSS GDNSMPVIGF GTAASPMADH EITKAAVLVG IENGYRHFDT 60 AAAYGTEKAV GEAIAEALRL GLIKSRAEVF ITTKLWCRSC ERDLVVPSLK NSLQDLQTDY 120 VDLFLIHWPV RLRHDAGRPP ISRDQILTFD TKSVWEGMEE CHELGLAKNI GVSNFSIKKL 180 EELLATAKIP PVLDQVELSP TWHQKNLIEY CKEKGIHVTA YSALGANNTH WGNNRVVESD 240 VLGEIAKARG KTTAQIALRW VYEQGVSMVV KSFNQERMKQ NLQIFDFELT EEESNKISQF 300 PQHKGVSLSA VYGDHDILKE MEAEL 325
3-60	**Sequences**	
3-60-1	Sequence Number [ID]	60
3-60-2	Molecule Type	AA
3-60-3	Length	322
3-60-4-1	Features Location/Qualifiers	**source** 1..322 mol_type= protein organism= Argemone Mexicana
	NonEnglishQualifier Value	
3-60-5	Residues	MENVIPRVTL SSGSVMPILG MGTASYPFVS SEEGKLAILN AIKVGYRHFD TASTYMFEEF 60 LGEAIAEAIQ LGLIKSRKEL FITSKLWCCD AHPDLVVPSL RNSLRNLKLE YLDLYLIHFP 120 VSLKAGRYEY PPLKEALVLM DYKSVWAAME ECQNLGLTKS IGVSNFSCKK LQTILDYAKI 180 PPSVNQVEMN PVWQQKKLRE FCKANDIVIT AYSPLGASGT PWGSSRVLDA QVLHEIARAK 240 GKTHAQVCLR WVYEQGVSLL VKTFNEERMK ENLRIFDWEL TEEDKQKISK IPQHRGLTGD 300 AFVSEHEGAP FKTAEELWDG EV 322

[0028]

3-61	**Sequences**	
3-61-1	Sequence Number [ID]	61
3-61-2	Molecule Type	AA
3-61-3	Length	322
3-61-4-1	Features Location/Qualifiers	**source** 1..322 mol_type= protein organism= Argemone Mexicana
	NonEnglishQualifier Value	
3-61-5	Residues	MDMNKHAVVY VPTKVIMGIP VIGFGTSADP PVDFDTTRLA IMQAIENGYR HFDTAALYNS 60 EQPLGEAINE AISRGLIKSR DELFITSKLW CSDTHPQHIL PAIQKTLRNL NMEYLDLYLI 120 HWPVSSRHEN FEYPIKKEDF LPMDFKKVWA AMEECHKQGL AKFIGVSNFS CKKLDNIMAS 180 ATISPSVLQV EVNPCWQQKR LIDFCKANGI FVVAYAPLGA VGTIYGTNRV MESDVLKQIA 240 KKRGKSVAQV CLRWAYEQGI GVVVKSFNKE RMKQNLEIFD WKLSEEDTKK ISEIQQDRAC 300 LGMDYTSPYG PYKTIKQLWD EE 322
3-62	**Sequences**	
3-62-1	Sequence Number [ID]	62
3-62-2	Molecule Type	AA
3-62-3	Length	322
3-62-4-1	Features Location/Qualifiers	**source** 1..322 mol_type= protein organism= Berberis thunbergii
	NonEnglishQualifier Value	
3-62-5	Residues	MEIVPKVTLN SGYQMPLLGF GTAENWPFTK SEAAKRAILC AIKNGYRHFD TASMYQSEES 60 LGEAIVEALH LGLIKSRNEL FITSKLWCSD CHQDRVLPAL RETLKNLHLD YLDLYLIHWP 120 LSAKPGKHEY PILKDKLLPM DYESVWGAME ECQRLGLSKS IGVSNFSSKK LEQLLKTAKI 180 IPAVNEVEVN PVWHQNKLIE FCKAKGIVVT GYSPLGAKGT TWGTNKVMDS EVLKEIAKTR 240 GKTHAQVCLR WIYEQGVGLV AKSFNEERMK ENLEIFDWAL TEEESKQISQ LPQYKGQNGE 300 TFLSAEGPFK TLEELWDEEV AA 322
3-63	**Sequences**	
3-63-1	Sequence Number [ID]	63
3-63-2	Molecule Type	AA
3-63-3	Length	320
3-63-4-1	Features Location/Qualifiers	**source** 1..320 mol_type= protein organism= Berberis thunbergii
	NonEnglishQualifier Value	
3-63-5	Residues	MEIVPKVTLN SGYQMPLLGF GTAENWPFTK SEAAKRAILC AIKNGYRHFD TASMYQSEES 60 LGEAIVEALH LGLIKSRNEL FITSKLWCSD CHQDRVLPAL KNTLQNLQLD YLDLYLIHFP 120 LSSKRGKLEY PLQEDETYPM DFGSVWEEME KCQRVGLTKS IGVSNFSAKK IEHLLTTAKI 180 IPAVDQVEMN PLWQQRTLRE YCKTKGIVVT AYSPLGAKGA IWGSNIVMEN EVLAEIAKAK 240 GKTHAQVCLR SVYEKGVALV TRSYNEERMK QNLNIFDWNL SKEETKRIDN LPQKRVFLGE 300 GFLSPLGPFK SPEELWDGEM 320
3-64	**Sequences**	
3-64-1	Sequence Number [ID]	64
3-64-2	Molecule Type	AA

[0029]

3-64-3	Length	324
3-64-4-1	Features Location/Qualifiers	**source** 1..324 mol_type= protein organism= Corydalis chelantifolia
	NonEnglishQualifier Value	
3-64-5	Residues	MMVSVPEVTL QSSSSDKKMP IMGMGTAAYP FAESDEAKAA LLTSIKLGYR HFDTASLYHN 60 EKSVGKAISE ALKLGLVKSR DEFYINSKLW CSDSHPDRVI PALQESLKKL GLEYLDMYLI 120 HWPLSLKKGS YEFPIPTDEE ILPMDFKAVW AAMEECQKLG LTKSIGVSNF SCKKLETILS 180 TAKIPPVVNQ VELNTLWQQT KLNKFCKDNG IVLMAFSPLG AHGSPWGTNR VMECELLHEI 240 AKAKGKTLAQ VCLRWIYEQG AGILVKSYNE VRMKENLEIF DWELSAEELK SISELPQHRG 300 FPADSLLSAK GPFRTEEELW DGEI 324
3-65	**Sequences**	
3-65-1	Sequence Number [ID]	65
3-65-2	Molecule Type	AA
3-65-3	Length	339
3-65-4-1	Features Location/Qualifiers	**source** 1..339 mol_type= protein organism= Corydalis chelantifolia
	NonEnglishQualifier Value	
3-65-5	Residues	MESVACEPGV IEQQQYFIPE VTCGGGSSTT RMRMPVVGMG TASYPFAGSE GVKQALLHAI 60 KLGYWHFDTA SFYQTEQSLG EAISEAIQLG LIKSRDELFI TSKLWCTDAH KDLVLPALQN 120 TLRNLQLEYL DLYLIHFPIS LKPGRYDFPV QSKEDLLPMD FKSIWAKMEE CQGLGLTKSI 180 GVSNFSCKKL ENLLATAKIP PAVNQVEMNP LWQQKKLREF CKANGITITA HSPLGAKGTN 240 WGTNRVVECE VLHQIAKAKG KSHAQVCLRW VYEQGVSLLV KSFNKERMKE NLGIFDWELN 300 AEDLKKISEI PQGRGLPVDG FLSPNGPFKS EEEFWDGEI 339
3-66	**Sequences**	
3-66-1	Sequence Number [ID]	66
3-66-2	Molecule Type	AA
3-66-3	Length	301
3-66-4-1	Features Location/Qualifiers	**source** 1..301 mol_type= protein organism= Corydalis chelantifolia
	NonEnglishQualifier Value	
3-66-5	Residues	MPVVGFGTAK FPFGDDEAIK LAVLEGIKLG YRHFDTATKY KSEKPLGETI VEAINLGLIK 60 SRDELFITSK LWCGSTERSL IVPSLKTSLQ NLQLDYLDLY LIHWPLRFST DETPTPVPKE 120 QLLPFDTKSV WQAMEECQNL GLTKSIGVSN FSCKKLEELL STAKITPAVN QVELNTSWQQ 180 TKMREFCKGK GIHITGYSPL GSYGTKWGDN RVVENQVLEE IGKPRGKTAV QVCLRWIYEQ 240 GASMVVKSFN KERMKANLDI FDWKLTEEEL KRISQLPQHK ASLPTASFGD HDEVRELDYE 300 I 301
3-67	**Sequences**	
3-67-1	Sequence Number [ID]	67
3-67-2	Molecule Type	AA
3-67-3	Length	327
3-67-4-1	Features Location/Qualifiers	**source** 1..327 mol_type= protein organism= Chelidonium majus

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	NonEnglishQualifier Value	
3-67-5	Residues	MESDSAAAAV VVPVTTLSSG IEMPMLGMGT VENFLPGSET VKLALLNAIK LGYRHFDTAA 60 IYQTEECLGE AVAEALQLGL IKSRDQLFIT SKLWCSDAHP DLVIPALQNS LRKLKLEYLD 120 LYLVHWPLSS KPGNCVFPIL KEDLLPLDFK SVWAAMEECQ KLGLTKSIGV SNFSCKKLQD 180 LLTSAIIPPV VNQVEMNPRW QQKKLREFCK ARDIVVTAYS PLGAKGTVYG SGAVMDCEVL 240 HQIAKIRGKS VAQVSLRWVY QQGVTPLVKS FNEERMKENM KIFDWELYEE DLKMIDEIPQ 300 SRVNPCYFFL SENGPFKTVE EFWDGEV 327
3-68	**Sequences**	
3-68-1	Sequence Number [ID]	68
3-68-2	Molecule Type	AA
3-68-3	Length	327
3-68-4-1	Features Location/Qualifiers	**source** 1..327 mol_type= protein organism= Chelidonium majus
	NonEnglishQualifier Value	
3-68-5	Residues	MESSNNAVLV PVITLNSGRE MPIVGMGTAE NLFQGSERVK LALLTAIKVG YRHFDTAAVY 60 QTEESLGEAI AEALQLGLIK SRDELFITSK LWLPDCHHDL VLPALQNSLR KLKLEYLDLY 120 LIHWPVSSKP GEIKHVIPKE ELLPMDFKSV WAAMEECHKL GLAKSIGVSN FSCKKLQDLL 180 VTANIPPDVN QVEMNPLWQQ TKLREFCKAH GILVAAYSPL GAKGTAWGRT NGVMDSEVLQ 240 QIAKARGKSI AQVSLRWVYE QGVVLLVKSF NEERMKENLK IFDWELSGED LKKISEILPQ 300 RRGLPSHVFV SDDGPFKSEE ELWDGEV 327
3-69	**Sequences**	
3-69-1	Sequence Number [ID]	69
3-69-2	Molecule Type	AA
3-69-3	Length	327
3-69-4-1	Features Location/Qualifiers	**source** 1..327 mol_type= protein organism= Chelidonium majus
	NonEnglishQualifier Value	
3-69-5	Residues	MESSNNAVLV PVITLNSGRE MPIVGMGTAE NLFQGSERVK LALLTAIKVG YRHFDTAAVY 60 QTEESLGEAI AEALQLGLIK SRDELFVTSK LWIPDCHHDL VLPALQNSLR KLKLEYLDLY 120 LIHWPVSSKP GELRSLIPKE ELLPMDFKSV WVAMEECHKL GLTKSIGVSN FSCKKLRDLL 180 LTANIPPAVN QVEMNPLWQQ KKLREFCKAN GIVIAAYSPL GAKGTAWGRT NDGVMDSELL 240 QKIAKARGKS TAQVSLRWGY EQGVILLVKS FNEERMKENL KTFDWELSGE DLKQINEILP 300 QRRGHSHEFI SDNGPFKSEE ELWDGEV 327
3-70	**Sequences**	
3-70-1	Sequence Number [ID]	70
3-70-2	Molecule Type	AA
3-70-3	Length	328
3-70-4-1	Features Location/Qualifiers	**source** 1..328 mol_type= protein organism= Chelidonium majus
	NonEnglishQualifier Value	
3-70-5	Residues	MGEEMIKTSS VEIPVATLST GRTMPLLGMG TAAYPFVGSD GVVKAILHAI KLGYRHFDTA 60 ALYFTEECLG DAVAEALRLG LIKSRDELFI TSKLYCCDAH PDRVVPALQN SLRKLKMEYL 120 DLYLIHWPAS THEGNFEFPL QKQDILPLDF KSVWAAMEEC QKLGLTKSIG VSNFSCKKLQ 180 DLLASAKIPP AVNQVEMNPI WQQNKLREFC KANDIHITAY SPLGANGTPW GSSGVAETQV 240

[0031]

		LHDIAKARGK THAQVCLRWV YEQGVSVLVK SYNEERMKEN LAVLDWELSE ENLKKISEIP 300 QRRGLPGDIF VSDNGPFKTV EELWDGEV 328
3-71	**Sequences**	
3-71-1	Sequence Number [ID]	71
3-71-2	Molecule Type	AA
3-71-3	Length	306
3-71-4-1	Features Location/Qualifiers	**source** 1..306 mol_type= protein organism= Cocculus trilobus
	NonEnglishQualifier Value	
3-71-5	Residues	MPVVGMGLAA YPFQESEVVK LAMLRAIEMG YRHFDTAALY QTEQSLGLAI AEALELGLIK 60 SRDELFITSK LWCSDAHPHL VIPALQRTLK NLGLDYVDLY LIHWPVSSNK PGKYDFPVPK 120 EELVQMDYES VWAAMEEGHR LGLTKSIGVS NFSCKKLENL LTIAKVPPTV NQVEMNPFWR 180 QYKLKEFCKE KGIIITAYSP LGAKGTIWGT NKVMESKVLE DIGIASGKTL AQVCLRWVYE 240 QGVTLLVKSF NEERMKGNLD IFDWELSEKE LKKINEIPQS RGLPGDIFVS DDGPFKSEAE 300 LWDGEV 306
3-72	**Sequences**	
3-72-1	Sequence Number [ID]	72
3-72-2	Molecule Type	AA
3-72-3	Length	321
3-72-4-1	Features Location/Qualifiers	**source** 1..321 mol_type= protein organism= Eschscholzia californica
	NonEnglishQualifier Value	
3-72-5	Residues	MGSCSIPVKS LSSGREMPVI GMGTADSNLA GSDASRIALV KAIEVGYRHF DTASIYQSEQ 60 NLGDAIAQAL ELGLIKSRDE LFITSKLWSS DSHPDRVVPA LQESLRKLKL EYLDLYLIHW 120 PASSTPGIYE FPIPKDEIFP LEYETIWAAM EECQRLGLTK SIGVSNFSSK KLQTILNTAT 180 IPPAANQVEM NPVWQQKKLK EFCDANNILL TAYSPLGAKG TSWGSNKVME SEVLKQIAMA 240 NGKSVAQVSL RWLYQIGATM VVKSYNAERM KENLKIFDWE LSDEDMKAIS EIPQRRNFAG 300 DILISSNGPF KSEDELWDGE V 321
3-73	**Sequences**	
3-73-1	Sequence Number [ID]	73
3-73-2	Molecule Type	AA
3-73-3	Length	323
3-73-4-1	Features Location/Qualifiers	**source** 1..323 mol_type= protein organism= Eschscholzia californica
	NonEnglishQualifier Value	
3-73-5	Residues	MSSYGSVPMK SLNSGSKIHV LGFGTAAYPF VGSDGVKNAI LNAIKLGYRH FDTAALYFTE 60 ESLGEAVSEA LQLGLIKSRD ELFITSKLWI SDAYPDRVLP AIQKTLRNLK MEYLDLYLIH 120 WPISGKEGNF DLPVPKDCLQ ELDYKPVWAA MEECQKLGLT KSIGVSNFSC KKLQIILSSA 180 TIPPAVNQVE MNPIWHQKKL REFCKANNIM IAAYSPLGAA GTPWGSSGVV ETEVLHEIAR 240 SRGKTHAQVC LRWVYEQGVI VLVKSFNEER MKENLSVFDW ELTDEDLKKI SQIPQRRGLP 300 SGDIWVSTEG PFRSEEELWD GEI 323
3-74	**Sequences**	
3-74-1	Sequence Number [ID]	74

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3-74-2	Molecule Type	AA
3-74-3	Length	324
3-74-4-1	Features Location/Qualifiers	**source** 1..324 mol_type= protein organism= Glaucium flavum
	NonEnglishQualifier Value	
3-74-5	Residues	MEMSSAQVVP LMTLNSGKEI PVLGMGTAEN HFQGSDGTKD ALVNAIKIGY RHFDTAAIYN 60 VEECLGDAIA EALQHGLIKS RDELFITSKL WISDSHPDRV LFALQNSLRK LKLEYLDLYL 120 IHWPLSSTPG KSVFPVPKED FLPLDFKSVW AAMEECQKLG LTKSIGVSNF SCKKLQDLLD 180 IANIPPAVNQ VEMSPLWQQK KLREFCKVNG ILVTAYSPLG AKGTFWGSNE IMDSHVLQEI 240 AKARGKSVAQ VTLRWVYEQG VILLVKSFNE NRMKENMAIF DWDLSIDDLK KFDEISQRRG 300 NLGDFFVSEN GPFKSVDMVW DGEV 324
3-75	**Sequences**	
3-75-1	Sequence Number [ID]	75
3-75-2	Molecule Type	AA
3-75-3	Length	326
3-75-4-1	Features Location/Qualifiers	**source** 1..326 mol_type= protein organism= Glaucium flavum
	NonEnglishQualifier Value	
3-75-5	Residues	MESSSSSAVV VPVMTLNSGK EMPVLGMGTA ENNLQGSEKT KLALLTAIKA GYRHFDTASA 60 YNTEEALGEA VAEALQLGLI KSRDELFITS KLWCSDAHPG LVVPALQNSL RNLKLEYLDL 120 YLIHWPVSLK PGKFVIPFSK EDILPLDFKN VWAAMEECQK LGLAKSIGVS NFSCKKLQDL 180 LAIANIPPAV NQVEMSPLWQ QKKLREFCKV NGILVTAYSP LGAKGTFWGS NEIMDSDVLN 240 QIAKARGKSV AQVSLRWVHE QGVILLVKSF NENRMKENMA IFDWELSNDD LKKMDEISQR 300 RGPLADIFVS ENGPFKSVDM LWDGGF 326
3-76	**Sequences**	
3-76-1	Sequence Number [ID]	76
3-76-2	Molecule Type	AA
3-76-3	Length	326
3-76-4-1	Features Location/Qualifiers	**source** 1..326 mol_type= protein organism= Glaucium flavum
	NonEnglishQualifier Value	
3-76-5	Residues	MGSSDAVVVP VKTLSSGRKM PVIGMGTAEI LLVDGSEKVK LALLNAIKIG YRHFDTAAVY 60 RTEEALGEVV AEAIQLGLIK SRDELFITSK LWLSDSHPDL VLPALQNSLR KLKFEYLDLY 120 LIHWPLSSKP GELKVLIPKE ELLPLDFKSV WAAMEECQKL GLTKSIGVSN FSCKKLQDLL 180 DIANIPPAVN QVEMNPLWQQ KKLNEFCKAN DIVITAYSPL GAKGTPWGSN RVMDSEVLNQ 240 IAKARGKSVA QVALRWVYEQ GVSLVVKSFN EERMKENVTK IFDWELSAED LKKIEEIPQC 300 RGVPSHVFVS VNGPFKSEEE LWDGEI 326
3-77	**Sequences**	
3-77-1	Sequence Number [ID]	77
3-77-2	Molecule Type	AA
3-77-3	Length	327
3-	Features	**source** 1..327

[0033]

77-4-1	Location/Qualifiers	mol_type= protein organism= Glaucium flavum
	NonEnglishQualifier Value	
3-77-5	Residues	MGEEMKIKSV EIPVVTLSSG RTMPVFGMGT AAFPFVGSDG VVKAITHAIK LGYRHFDTAA 60 LYFTEESLGD AIAEALRLGL IKSRDELFIT SKLWCCDAHP DRVLPALRNS LRNLKIEYLD 120 LYLIHWPAST HEGNLEFPIQ KQDIHPLDYN SVWAAMEECQ TLGLTKSIGV SNFSCKKLQH 180 ILAIAKIPPA VNQVEMNPIW QQKKLREFCK ANDIHITAYS PLGANGTPWG SSGVVETQVL 240 HDIAKARGKT HAQVCLRWVY EQGVIVLVKS YNEERMKENL TVFDWELSAE DSMKISEIPQ 300 HRGLPGDIFV SDSGPFKSEE ELWDGEV 327
3-78	**Sequences**	
3-78-1	Sequence Number [ID]	78
3-78-2	Molecule Type	AA
3-78-3	Length	319
3-78-4-1	Features Location/Qualifiers	**source** 1..319 mol_type= protein organism= Hydrastis canadensis
	NonEnglishQualifier Value	
3-78-5	Residues	MGSVPNVILS SGHPMPLVGF GTAGFPFGTS EGIKSAILCG IKNGYRHFDT ASVYQTEQIL 60 GEAIAEALEL GLIKSRDELF LTSKLWCSDA HQQHVLPALQ KTLRTLQLDY LDLYLVHWPL 120 SSKPGKYEYP IPKEELLPMD FKSVWAAMEE CQALGLTKSI GVSNFSCKKL EQLLSTSNIP 180 PAVNQVEVNP IWQQNKLREF CKAKGIIVAA FSPLGAKGTS WGTNKVMDSE VLNEIAQARG 240 KTTAQNCLRW LHEQGVCVVV KSFNEERMKG NLKLFDWELS KEESKKISQL PQSKGHTGDD 300 MVSANGPFKS LEELWDGEI 319
3-79	**Sequences**	
3-79-1	Sequence Number [ID]	79
3-79-2	Molecule Type	AA
3-79-3	Length	319
3-79-4-1	Features Location/Qualifiers	**source** 1..319 mol_type= protein organism= Hydrastis canadensis
	NonEnglishQualifier Value	
3-79-5	Residues	MTRIPEIVLN SGWRMPVLGM GTATFPIQSP EVIESSIVNA IELGYRHFDT ASVYQSESPL 60 GRAISEAIRR GLIESRKEVF ITSKLWCTDA HHDLVIPALH KTLQNLGLEY LDLYLIHFPV 120 RLKGDISFDI KKADLIPFDV KGTWEAMEKC QELGLTRSIG VSNFSSKKLS ELLTHATISP 180 AVNQVEMHPF WQQKELRAFC ADKGIHVSAY SPLGGKGALW GSDILLNSKE IERIAQAKGK 240 SIAQVCLRWA YEQGVSYLPK SYNKGRMKEN MEIFDWQLSE DELQKISHLP QGKIYTGHHF 300 ISDDGEYKSP IDLWDCEIC 319
3-80	**Sequences**	
3-80-1	Sequence Number [ID]	80
3-80-2	Molecule Type	AA
3-80-3	Length	320
3-80-4-1	Features Location/Qualifiers	**source** 1..320 mol_type= protein organism= Hydrastis canadensis
	NonEnglishQualifier Value	
3-	Residues	MGIVREVVLN SGERMPLLGM GTATYPVAPF ELVESSVIAA IELGYRHFDT ASVYETEQPL 60

[0034]

80-5		GLAISEAVRQ GLIASRDEIF ITTKLWCGHA HYDLVLPALR DSLETMGLDY VDLYLIHFPA 120 RFNMKEKSLN VNKKDLLPLD IRGTWKAMEE CYELGLAKSI GVSNFSCKKL SQLLSVANIP 180 PAVNQVEMHP LWQQQKLREF CEEKGIHVSA YSPLGGKGTI WGSNAVLDSD QIKQIAKAKG 240 KSIAQICLRW GFEHGVSILP KSFNKERLKE NMEIFDWELS KEELQKMNTF PQNRIFQAEH 300 LVSPDEGLFK SVADLWDGEI 320
3-81	**Sequences**	
3-81-1	Sequence Number [ID]	81
3-81-2	Molecule Type	AA
3-81-3	Length	328
3-81-4-1	Features Location/Qualifiers	**source** 1..328 mol_type= protein organism= Jeffersonia diphylla
	NonEnglishQualifier Value	
3-81-5	Residues	MCFCVLVTKR AMGIVPEVTL NSGHQMPLVG FGTAQFPFPE GDEAKQIIAP ILCGIKSGYR 60 HFDTASLYKT EEALGEAIKE ALRLGLIKSR DELFITSKLW CTDSHQDLVL PALKKTLQNL 120 QMDYLDLYLV HFPVSSKPGK PEFPPQKEDL LPMDFGSVWA AMEECQRLGL TKSIGVSNFS 180 CKKLEQLLTT AKIIPAVNEV EMSPVCQQNK LREFCKVKNI VVTAYSPLGG GSNAVKDNKV 240 LKEIAKAKGK TCAQVTLRWV YEQGVALVPK SFNEGRMKEN LDIFNWTISE EEFKQISQLP 300 QGRVATGEWF VSVEGPFKSL EELWDEVI 328
3-82	**Sequences**	
3-82-1	Sequence Number [ID]	82
3-82-2	Molecule Type	AA
3-82-3	Length	321
3-82-4-1	Features Location/Qualifiers	**source** 1..321 mol_type= protein organism= Mahonia aquifolium
	NonEnglishQualifier Value	
3-82-5	Residues	MGVVPVVTLN SGHEMPLVGF GTAVPAFGGS DAIKQAILCG IKNGYRHFDT ASVYQTEKSL 60 GEAIVEALRL GLIKSRDELF ITSKLWCTDA HQDGVLPALR ETLKNLQLDY LDLYLIHWPL 120 SAKPGKHEYQ IPKDELLPMD YESVWGAMEE CQRLDLSKSI GVSNFSIKKL EELLKTAKII 180 PAVNEVEVNP VWHQNKLIEF CKAKGIVVTG YSPLGAKGTT WGTNRVMDNE VLKEIAKTRG 240 KTHAQVCLRW IYEQGVGLVA KSFNEERMKE NLEIFDWALT EEESKQISQL PQYKGQNGET 300 FLSAEGPFKT LEELWDEEIA A 321
3-83	**Sequences**	
3-83-1	Sequence Number [ID]	83
3-83-2	Molecule Type	AA
3-83-3	Length	320
3-83-4-1	Features Location/Qualifiers	**source** 1..320 mol_type= protein organism= Menispermum canadense
	NonEnglishQualifier Value	
3-83-5	Residues	MASVPEVTLS SGHPMPLFGF GTAAWPFVSS EGAKSAILCG MELGYRHFDT ASIYGTESSL 60 GEAIAEALKL GIIKSRDELF ITSKLWCCDG HHDRVLPALQ MTLKNLQLDY IDLYLEHWPL 120 SSVPKGELEY PIPKEKLFPM DLKAVWEAME ECQRLGLTKS IGVSNFSCKK LEDLLAFAKI 180 PPAVNEVEMN PVWQQKKLRD FCKAKGIVLT AYSVLGAKGT LWGTNKVMDS EVLGKIAKAR 240 GKTVGQVCLR WAYEQGACVL VKSFNEERMK ENLETFNWEL GEEDLKMISE IPQYKGLRGE 300 DMVAPNGPYK TLEELWDGEI 320
3-84	**Sequences**	

[0035]

3-84-1	Sequence Number [ID]	84
3-84-2	Molecule Type	AA
3-84-3	Length	341
3-84-4-1	Features Location/Qualifiers	**source** 1..341 mol_type= protein organism= Menispermum canadense
	NonEnglishQualifier Value	
3-84-5	Residues	MGVDKTNEFS NGNAASPVLI KEANLFKIAE VTLNSGHHMP VLGTGTASFP FPPLKELKKA 60 IVEAMEVGYR HFDSAALYQS EEGLGAAIAE ALEKGLVKKR EELFITTKLW CNNAHSDRVL 120 PAIRESLRKL RLDYVDLYLI HFPVRLKEDL LDMNCKKGGI FELDLKSVWA AMEQIQHLGL 180 AKSIGVSNFT CKKLTDLLSY AKIPPAVNQV EMHPVWQQKK LRDFCKEKGI HVSAYSPLGA 240 KQWGFDVVLG NKILKEIAQD KGKTIAQIAL RWGYEQGVIL IPKSFNKGRL TENLRIFDWK 300 LTEDELKKIS SIQQSRVAIM PEFVFPESPF KTFEDFWDGE M 341
3-85	**Sequences**	
3-85-1	Sequence Number [ID]	85
3-85-2	Molecule Type	AA
3-85-3	Length	322
3-85-4-1	Features Location/Qualifiers	**source** 1..322 mol_type= protein organism= Menispermum canadense
	NonEnglishQualifier Value	
3-85-5	Residues	MEGGGVPKIL LNSGHRMPVL GMGTASFPIS PQHLVKSSIL TAIELGYTHF DTASVYETEP 60 TLSRAIRQAL EGRHIASRDQ LFITTKLWCG QAQSDLVVPA LRESLQELGL DYVDLYLIHF 120 PARFKCVEKT FNVTKEDLLP LDMKGTWQAM EECCKLGLAK SIGVSNFSCK KLSQILTFAT 180 IPPAVNQVEM HPLWQQRKLR EFCKEKGIHV SAYSPLGGKG AKWGSNAVFE CEEIKQIAEA 240 KGKSLAQICL RWAFEQGVSF VPKSFNKERL KENMEIYGWE LSKEELQKLS VLPQCRIFKG 300 EWLVSADHGV FKSVEDLWDG EI 322
3-86	**Sequences**	
3-86-1	Sequence Number [ID]	86
3-86-2	Molecule Type	AA
3-86-3	Length	319
3-86-4-1	Features Location/Qualifiers	**source** 1..319 mol_type= protein organism= Nandina domestica
	NonEnglishQualifier Value	
3-86-5	Residues	MVSVPEVTLN SGHRMPLVGM GTACFPLPGS EVVKSAMVTA IKLGYRHFDT AALYQSEQPL 60 GEAIAEALHL GLIISRDELF ITSKLWCTDA HQDLVLPALK TSLRNLQLDY LDLYLIHFPV 120 SLKPGKIQLP VPKEELLPMD FKSVWAAMEE CQKLGLTKSI GVSNFSCKKL EHILSLAKIP 180 PAVNQVELNP IWRQKKLIEF CKAKGIVVTA YSPLGAVAPG QGSNRVMECE VLSEIAKARG 240 KTHAQVCLRW IIEQGVSLVV KSFNEDRKKK NLEIFDWELS EEDSKKISQI PETRGNPGDF 300 VISVDGPYKS REELWDGEI 319
3-87	**Sequences**	
3-87-1	Sequence Number [ID]	87
3-87-2	Molecule Type	AA
3-	Length	319

[0036]

87-3		
3-87-4-1	Features Location/Qualifiers	**source** 1..319 mol_type= protein organism= Nandina domestica
	NonEnglishQualifier Value	
3-87-5	Residues	MGRVPETTLS SGHNMPLLGM GTATFPLPPS ELIESYILAA IEMGYRHFDT ASVYDTEVPL 60 GRAISEALRR GLVANRDELF ITTKLWCGHA HPDLVVPALH QSLMEMGLEY VDLYLIHFPA 120 RFNKKEKNFD VKKEEVIPLD MKGTWEAMEE CSKLGLAKSI GVSNFSCKKL SQLLTYATIP 180 PAVNQVEMHP LWQQWKLREF CVANDIHVTA YSPLGGKGAL WGSNSVLDSK EIQQMAEAKG 240 KSIAQICLRW AFEQGVSFIP KSFNVERLKE NMEIFDWEMN KNELLKMSLL PQKRTFTAEY 300 LVSPDGAFKS VDDLWDGEI 319
3-88	**Sequences**	
3-88-1	Sequence Number [ID]	88
3-88-2	Molecule Type	AA
3-88-3	Length	319
3-88-4-1	Features Location/Qualifiers	**source** 1..319 mol_type= protein organism= Nigella sativa
	NonEnglishQualifier Value	
3-88-5	Residues	MARVPEITLN SGHRMPLLGM GTAVVPFKEP EPVKSAILTA IKNGYRHFDT ASLYRTEPAL 60 GDAIAEALQL GLINSRDDLF ITSKLWCTDN HPDLVLPALH TTLRNLKLDY LDLYLIHWPV 120 SMTPGRIRFP GPDEKILPMD YKSVWAAMEE CQKLGLTKSI GVSNFTCKKL ELLLASATIP 180 PAVNQVEVNP MWQQEKLIEF CRTKGIVVTA YAPLGTVGTF IGNNDIMNCE LLKEIAQAKG 240 KTNGQICLRW VHEQGVGLLV KSFTEVRMKQ NLEIFDWELS EEESMKIKQL PQRKSHQGKG 300 FVTADGPFKS LTELWDGEM 319
3-89	**Sequences**	
3-89-1	Sequence Number [ID]	89
3-89-2	Molecule Type	AA
3-89-3	Length	317
3-89-4-1	Features Location/Qualifiers	**source** 1..317 mol_type= protein organism= Nigella sativa
	NonEnglishQualifier Value	
3-89-5	Residues	MVYEIMLNSG YRIPLLGMGT AAYPVPPPEL VESSVLAAIE LGYRHFDTAH IYGTEAPLGR 60 AISEALRKGL IKSRDELFIT TKLWPGHARP DLVLQALHQS LEALRIDYVD LFLIHFPARY 120 NTTEIRMDIK KEDILPLDIK GTWQAMEECC KLGLAKSIGV SNFGCKKLSQ LLDSATIPPA 180 VNQVEMHPLW QQAKLREFCA ERGIHVSAYS PLGGKGTLWG SNAVLDSEQI KQIALAKGKS 240 VAQICLRWGF QQGVSIIAKS FNRERLKENM EIFDWELNKE ELYKLSILPQ NRISTLEYLV 300 SPDAVFKSIN DLWDEEV 317
3-90	**Sequences**	
3-90-1	Sequence Number [ID]	90
3-90-2	Molecule Type	AA
3-90-3	Length	318
3-90-4-1	Features Location/Qualifiers	**source** 1..318 mol_type= protein organism= Nigella sativa
	NonEnglishQualifier	

[0037]

	Value	
3-90-5	Residues	MDNSVVVLNS GHRMPLLGMG TAATPLPPNE VVQSSVLAAI ELGYRHFDTA SVYGSEVILG 60 RAISEALRRG LVASRDELFI TTKLWCGNGH PDLVLGALQE SLRIMELDYV DLYLIHFPVR 120 FNITEKLLNM KNVPLLPFDM EGTWQAMEEC CRLGLAKSIG VSNFSCKRLS ELLLSASIPP 180 AVNQVEMHPL WQQRNMREFC RKEGIHVSAY SPLGGKGAAW GSNAVLDSED IQQIAQHKEK 240 SVAQVCLRWA FEQGVSIIVK SFNKERLKEN TQIFDWELNK QELQRINTLP QNKIFKASNL 300 ISADGPYKTF EELWDGEV 318
3-91	**Sequences**	
3-91-1	Sequence Number [ID]	91
3-91-2	Molecule Type	AA
3-91-3	Length	321
3-91-4-1	Features Location/Qualifiers	**source** 1..321 mol_type= protein organism= Papaver bracteatum
	NonEnglishQualifier Value	
3-91-5	Residues	MESNGVPMIT LSSGIRMPAL GMGTVETMEK GTEREKLAFL KAIEVGYRHF DAAAAYQTEE 60 CLGEAIAEAL QLGLIKSREE LFITSKLWCT DAHADLVLPA LQNSLRNLKL EYLDLYLIHF 120 PVSLKPGKIV SDIPKDQMLP MDYKSVWAAM EECQTLGFTR AIGVSNFSCK KLQELMATAN 180 SPPVVNEVEM SPIFQQKKLR AYCKANNIMI TAYSVLGARG AAWGSNAVMD SKVLHEIAVS 240 RGKSVAQVSM RWVYQQGACL VVKSFNEERM KENLKIFDWE LSAEDMEKIS EIPQSRTSSA 300 DFLLSPTGPF KTEEEFWDEK D 321
3-92	**Sequences**	
3-92-1	Sequence Number [ID]	92
3-92-2	Molecule Type	AA
3-92-3	Length	321
3-92-4-1	Features Location/Qualifiers	**source** 1..321 mol_type= protein organism= Papaver bracteatum
	NonEnglishQualifier Value	
3-92-5	Residues	MEINGVPVIS LSSGVRMPAL GMGTAETMEK GTDRERSAFL KAIEVGYRHF DTAAAYQTEE 60 CLGEAIAEAL QLGLIKSRDE LFITSKLWCT DAHADLVLPA LQNSLRNLKL EYLDLYLIHA 120 PVSLKPGKIL NEIPKDQMLP MDYKSVWAAM EECQTLGFTR AIGVSNFSCK KLQELMATAN 180 SPPVVNEVEM SPTLHQKNLR EYCKANNIMI IAYSVLGARG TGWGSNAVMD SKVLHQIAVA 240 RGKSVAQVSM RWVYQQGACL VVKSFNEERM KENLKIFDWE LTEEDMDKIS EIPQSRTLSA 300 DFLLSPTGPF KTEEEFWDEM V 321
3-93	**Sequences**	
3-93-1	Sequence Number [ID]	93
3-93-2	Molecule Type	AA
3-93-3	Length	323
3-93-4-1	Features Location/Qualifiers	**source** 1..323 mol_type= protein organism= Papaver bracteatum
	NonEnglishQualifier Value	
3-93-5	Residues	MRNTGVPVIT LSSGKGIPVL GMGTFETVGK GGERERLAFL KAIEVGYRHF DTAACYQTEE 60 CLGEAIEEAL QLGLIKSRDE LFITSKLWCT DAHPDRVLLA LQNSLRNLKL EYLDLYLIHF 120 PVSLKPGNEV TMDAAGGEIF LMDYKSVWAA MEECQNLGFT KSIGVSNFSC KKLQELLATA 180 NIPPVVNQVE MSPVFHQKNL REYCKANNIL VAAYSILGGK GTAWGSNSVL GSEGLNQIAI 240

[0038]

		ARGKSIAQVS MRWVYEQGAI LVVKSFSEKN MRENLNIFDW ELTKEDLERI GEIPQRRLII 300 QEFMVSSNGP FKSLEEFWDE KAD 323
3-94	**Sequences**	
3-94-1	Sequence Number [ID]	94
3-94-2	Molecule Type	AA
3-94-3	Length	321
3-94-4-1	Features Location/Qualifiers	**source** 1..321 mol_type= protein organism= Papaver bracteatum
	NonEnglishQualifier Value	
3-94-5	Residues	MENVIPAVTL SSGSVMPILG MGTAAYPLVE PEEAKLAFLN AIKIGYRHFD TAASYHCEGF 60 LGEAIAEALQ LGLIKSRDEL FITSKLWPCD AHPDLVIPAI QNSLRNLKLE YLDLYLIHFP 120 ISTKPAAGLV FPPPKDALLP MDYKSVWAAM EECQKLGLTK SIGVSNFSCK KLQTILDIAN 180 IPPAVNQVEM NPVWQNLKLR DFCKANNIVL TAYSPLGARG TPWGSNAVYE ERVLHEIAEA 240 KGKTHAQVCL RWVYEQGVSL IVKSFNELRM KENMMIFDWE LTEDELQKIG KIPQRRGLPG 300 DFFVSEAAPF KTVEEFWDGE I 321
3-95	**Sequences**	
3-95-1	Sequence Number [ID]	95
3-95-2	Molecule Type	AA
3-95-3	Length	322
3-95-4-1	Features Location/Qualifiers	**source** 1..322 mol_type= protein organism= Papaver bracteatum
	NonEnglishQualifier Value	
3-95-5	Residues	MEVVIPKVAL SSGRVMPVLG MGTSSFPPVG PEDGKAAILN AIKIGYRHFD TASVYKSEDF 60 LGEAIAEALL LGLIQSRDQL FITSKLYCND AHPDLVVPAL QNSLRNLRLE YLDLYLIHFP 120 VSSKPVKYEY HLKKEHLLPM DYESVWAAME KCQKLGLTKS IGVSNFSCKK LQTILDTANI 180 SPAVNQVEMN PVWQNLKLRD FCKAKGIVVT AYSPLGASGT PWGSNAVKEA QELHEIAKAR 240 GKTHAQVCLR WVYEQGVSLL VKSFKEERMK ENLMIFDWEL TKDDLFKISK ITQRRGLPGY 300 RFISKLEGSP FKTVEEFWDG EV 322
3-96	**Sequences**	
3-96-1	Sequence Number [ID]	96
3-96-2	Molecule Type	AA
3-96-3	Length	321
3-96-4-1	Features Location/Qualifiers	**source** 1..321 mol_type= protein organism= Papaver bracteatum
	NonEnglishQualifier Value	
3-96-5	Residues	MESSGVPVIT LRSGKVMPVL GMGTFEKAGK GSERERLAIL KAIEVGYRYF DTAAAYETEE 60 VLGEAIAEAL QLGLIKSRDE LFISSMLWCT DAHPDRVLLA LQNSLRNLKL EYVDLYMLPF 120 PASLKPGKIT MDIPEEDICP MDYRSVWSAM EECQNLGLTK SIGVSNFSCK KLEELMATAN 180 IPPAVNQVEM SPAFQQKKLR EYCNANNILV SAVSILGSNG TPWGSNAVLG SEVLKKIAMA 240 KGKSVAQVSM RWVYEQGASL VVKSFSEERL RENLNIFDWQ LTKEDNEKIG EIPQCRILSA 300 YFLVSPKGPF KSQEELWDDK A 321
3-97	**Sequences**	
3-97-1	Sequence Number [ID]	97

[0039]

3-97-2	Molecule Type	AA
3-97-3	Length	323
3-97-4-1	Features Location/Qualifiers	**source** 1..323 mol_type= protein organism= Papaver bracteatum
	NonEnglishQualifier Value	
3-97-5	Residues	MGSSCIPVLT LNSGNKMPVL GMGTFETFAK GGERERLAYL KAIKVGYRYF DTGAAYGTEE 60 VLGQAIAEAL QLGLIKSRDE LFISTMIWAT DAHPDGVLPA VQRSLRNLKL DYVDLYLIPF 120 PASLNPEGEI PNYIPENETF LKMDYKSVWA AMEECQTLGF TKSIGVSNFS CKKLQEVMET 180 ANIPPAVNMV EMNPTFQQKY LREYCKANNI LVNAYSVLGS TGTSWGSNAV MGSEVLKQIA 240 TDIGKSIAQV SMRWVYEQGA GFVVKSFSEE RMRENLNIFD WELTKEDLEK ISQIPQCRVL 300 PMDFLVSSDG AFKSLEDLWD GEA 323
3-98	**Sequences**	
3-98-1	Sequence Number [ID]	98
3-98-2	Molecule Type	AA
3-98-3	Length	303
3-98-4-1	Features Location/Qualifiers	**source** 1..303 mol_type= protein organism= Papaver bracteatum
	NonEnglishQualifier Value	
3-98-5	Residues	MPILGFGTAE NLFEGGDKVK LAILKAIEVG YRYIDTAAVY RTEESVGEAV AEALQLGLIK 60 SRDELFITSK LWGVDAHPDL VLPALQNSLR KLKLEYLDLY LIHYPVSLKP GEMVDDIPKD 120 EIFPLDYKSV WAAMEECQKL GYTKSIGVSN FSCKKLQQLM ATANIPPAVN QVEMNPTWQQ 180 KNLREYCKAN NIFITAYSTL GAKDLLWGSN AVLGSKVLNQ IAVARGKSVA QVSLRWVYEQ 240 GVSLVVKSFN EERMKENLKI FDWELTTEDL KMISEIPQRR VATADFFVSD IGPFKSLEEL 300 WDE 303
3-99	**Sequences**	
3-99-1	Sequence Number [ID]	99
3-99-2	Molecule Type	AA
3-99-3	Length	306
3-99-4-1	Features Location/Qualifiers	**source** 1..306 mol_type= protein organism= Papaver bracteatum
	NonEnglishQualifier Value	
3-99-5	Residues	MPVLGLGTAE NLTKGSEREM LAILKAIEVG YRHFDTAFIY QTQECVGEAI AEALQLGIIK 60 SRDELFITSK LWGSDAHPDC VLLALQNSLR NLKLQYLDLY LIHYPVSLKP GTTLKDLGNK 120 DNFLPMDYKS VWAAMEECQK LGLTKSIGVS NFSSKKIQEL MSTDSIPPAV NQVEMNPTWQ 180 QKKLREYCQA NNILVTAYSP LGAKGTTWGS NAVMGSEVLN QIALARGKSV AQISLRWVYE 240 QGVSLVVKSF NEERMRENLK IFDWELTAED LKKIDELPQS RVATAEFVVS ENGPFKSLEE 300 FWDDES 306
3-100	**Sequences**	
3-100-1	Sequence Number [ID]	100
3-100-2	Molecule Type	AA

[0040]

3-100-3	Length	321
3-100-4-1	Features Location/Qualifiers	**source** 1..321 mol_type= protein organism= Papaver bracteatum
	NonEnglishQualifier Value	
3-100-5	Residues	MENAIPAVTL NSGSVMPVLG MGTAAYPFVE SEEAKLAILN AIKTGYRHLD TAALYQSEES 60 LGEAVSEAIQ LGLIKSRDEL FITSKLWPCD AHPDLVIPAI QNSLRNLKLE YLDLYLIHFP 120 ISTKPAAGLV FPPPKDALLP MDYKSVWAAM EECQKLGLTK SIGVSNFSCK KLQTILDIAN 180 IPPAVNQVEM NPVWQNLQLR DFCKDKSIIL TAYSPLEGKG TPWGSNAVYG AQVLHEIAEA 240 KGKTHAQVCL RWVYEQGVSL LVKSFNDQRM KENMMIFDWE LTEDELEKIS RIPQRRGLPG 300 DFFVSEAAPF KTVEEFWDGE I 321
3-101	**Sequences**	
3-101-1	Sequence Number [ID]	101
3-101-2	Molecule Type	AA
3-101-3	Length	321
3-101-4-1	Features Location/Qualifiers	**source** 1..321 mol_type= protein organism= Papaver bracteatum
	NonEnglishQualifier Value	
3-101-5	Residues	MENAIPAVTL NSGSVMPVLG MGTAAYPFVE SEEAKLAILN AIKTGYRHLD TAALYQSEES 60 LGEAVAEAIQ LGLIKSRDEL FITSKLWPCD AHPDRVVPTL QNSLRKLKLE YLDLYLIHWP 120 VSSNPVAGHV LSLPKDSLVT MDYESVWAAM EECQKLGLTK SIGVSNFSCK KLQTILDIAN 180 IPPAVNQVEM NPVWQNLKLR DFCKANNIVL TAYSPLGARG TPWGSNAVYE ERVLHEIAEA 240 KGKTHAQVCL RWVYEQGVSL IVKSFNELRM KENMMIFDWE LTEDELQKIG KIPQRRGLPG 300 DFFVSEAAPF KTVEEFWDGE I 321
3-102	**Sequences**	
3-102-1	Sequence Number [ID]	102
3-102-2	Molecule Type	AA
3-102-3	Length	323
3-102-4-1	Features Location/Qualifiers	**source** 1..323 mol_type= protein organism= Papaver bracteatum
	NonEnglishQualifier Value	
3-102-5	Residues	MENVIPAVTL SSGSVMPILA MGTAAYPLVE PEEAKLAFLN AIKIGYRHFD TAASYHCEGF 60 LGEAIAEALQ LGLIKSRDEL FITSKLWPCD AHPDLVIPAI QNSLRNLKLE YLDLYLIHFP 120 ISTKPAAGLV FPPPKDALLP MDYKSVWAAM EECQKLGLTK SIGVSNFSCK KLQTILDIAN 180 IPPAVNQVEM NPVWQNLQLR DFCKDKSIIL TAYSPLEGKG TPWGSNAVYG AQVLHEIAEA 240 KGKTHAQVCL RWVYEQGVSL LVKSFNDQRM KENMMIFDWE LTEDELEKIG KIPQSRGLPG 300 DVFVSELEAA PFKTVEEFWD GEV 323
3-103	**Sequences**	
3-	Sequence Number	103

[0041]

103-1	[ID]	
3-103-2	Molecule Type	AA
3-103-3	Length	319
3-103-4-1	Features Location/Qualifiers	**source** 1..319 mol_type= protein organism= Sanguinaria canadensis
	NonEnglishQualifier Value	
3-103-5	Residues	MENVSVVTLN SGREMPILGM GTAAYPSVGS EEAKLAILLA IKVGYRHFDT AAAYQIESSL 60 GEAVAEALQL GLLKSRDELF ITSKLWCSDS HPERVLPALQ NSLRNLKLEY LDLYLIHWPV 120 SLKPGNFDLT IPKEDLLPMD YKSVWAAMEE CQKLGLTKSI GVSNFSCKKL QDLLATANIP 180 PAVNQVEMNP IWQQKKLREF CKANGILITA YSPLGANGTP WGSSGVANTE VLHQIAKARG 240 KTHAQVCLRW VYEQGVSLLV KSFNEERMKE NLKIFDWELT AEDLKQISEI PQHRGLPADI 300 FVSVNGPFKT VEEFWDGEV 319
3-104	**Sequences**	
3-104-1	Sequence Number [ID]	104
3-104-2	Molecule Type	AA
3-104-3	Length	321
3-104-4-1	Features Location/Qualifiers	**source** 1..321 mol_type= protein organism= Sanguinaria canadensis
	NonEnglishQualifier Value	
3-104-5	Residues	MEISVPITTL SSGREMPILG MGTAENLFNG SEKVKLAILD AIKVGYRHFD TAAVYQTESS 60 LGEAVAEALQ HGLLKSRDEL FITSKLWCSD SHPDRVLPAL QTSLRKLKLE YLDLYLIHWP 120 LSSKPGSHDY PIPKEDLLPL DYKSVWAAME ECQKLGLTKS IGVSNFSCKK LQDLLDTANI 180 PPAVNQVEMN PLWQQKKLLE FCKGNGIIIT AFSPLGAKGT SWGATNGVMD SEVLHQIAQA 240 RGKSIAQVSL RWLYEQGVSL VVKSFNVERM KENLKIFDWE LSAEDLKKIN EIPQRRGLPS 300 GSFISANGPF KSEEELWDGE V 321
3-105	**Sequences**	
3-105-1	Sequence Number [ID]	105
3-105-2	Molecule Type	AA
3-105-3	Length	318
3-105-4-1	Features Location/Qualifiers	**source** 1..318 mol_type= protein organism= Sanguinaria canadensis
	NonEnglishQualifier Value	
3-105-5	Residues	MAMETVPKLP LSSGDNSIPV IGFGTAAFPL PDDETLKSAF LNGIEAGYRH FDTAAAYGSE 60 KALGEAITEA LRLGLLKSRE EVFITTKLWC SSCERSLVVP SLKNSLRNLQ MEYVDLFLIH 120 WPVRLSIDAQ RPPIPREQIL TFDTKSVWEG MEECHELGLA KNIGLSNFYP KKIDELLATA 180

		KIPPAVLQVE LSPTWQQKNL IEYCREKGIL VTAYSALGAN GTHWGDNRVV ESDVLGDIAK 240 ARGKTTAQIA LRWVYEQGVC MVVKSFNKER MKLNLQIFDF ELTEEESNKI SQLPQIKGVK 300 LSPMFGNHDV LKELEDQL 318
3-106	**Sequences**	
3-106-1	Sequence Number [ID]	106
3-106-2	Molecule Type	AA
3-106-3	Length	328
3-106-4-1	Features Location/Qualifiers	**source** 1..328 mol_type= protein organism= Sanguinaria canadensis
	NonEnglishQualifier Value	
3-106-5	Residues	MGEEMKCGRV VPVATLNSGR TMPLLGMGTA AYPFVGSEKV KSAILHAIKL GYRHFDTAAL 60 YQTEECLGEV VAEALQLGLL KSRDELFITS KLWCSDSHPD RVLPALQTSL RKLKLEYLDL 120 YLIHWPLSLK PGNYGFPIPK EDMLPMDYKS VWAAMEECQK LGLTKSIGVS NFSCKKLQDL 180 LATANIPPAV NQVEMNPIWQ QKKLREFCEA NGILITAYSP LGANGTPWGS SGVAQTQVLH 240 DIAKARGKTH AQVCVRWVYE QGVSVLVKSY NEERMKENLT VFDWELDVED LKKISTEIPQ 300 RRGLPSDIFV SVLTGPFKSA EELWDGEL 328
3-107	**Sequences**	
3-107-1	Sequence Number [ID]	107
3-107-2	Molecule Type	AA
3-107-3	Length	326
3-107-4-1	Features Location/Qualifiers	**source** 1..326 mol_type= protein organism= Stylophorum diphyllum
	NonEnglishQualifier Value	
3-107-5	Residues	MESDSTAVAV PVTTLSSGIE MPMLGLGTAD EKLLPSSETV KLAFLTAIKL GYRHFDTAAV 60 YQTEECLGEA VAEALQLGLI KSRDELFITS KLWCSDAHPD LVIPALQNSL RKLKLEYLDL 120 YLIHWPLSSK PGNCVFPIPK EDLLPLDFKS VWAAMEECQK LGLTKSIGVS NFSCKKLQDL 180 LAMAIIPPAV NQVEMNPHWQ QKKLREFCKV KDIVVTAYSP LGAKGTPWGS NAVMDSKVLH 240 QIAKARGKSV AQVSLRWVYQ QGVVLLVKSF NEERMKENMK IFNWELNEED LKMIDEIPQC 300 RGNPSHYYVS ENGPFKTVEE FWDGEV 326
3-108	**Sequences**	
3-108-1	Sequence Number [ID]	108
3-108-2	Molecule Type	AA
3-108-3	Length	307
3-108-	Features Location/Qualifiers	**source** 1..307 mol_type= protein

[0042]

[0043]

4-1	NonEnglishQualifier Value	organism= Stylophorum diphyllum
3-108-5	Residues	MPIVGMGTAE NLFEGSERVK LALLTAIKVG YRHFDTAAVY QTEGSLGEAI AEALQLGLIK 60 SRDELFITSK LWIHDCHHDL VLPALQNSLR KLKLEYLDLY LIHWPVSSKP GELRSLIPKE 120 ELLPMDFKSV WVAMEECHKI GLTKSIGVSN FSCKKLQDLL LTANIPPAVN QKVEMNPLWQ 180 QKKLREFCKA NGIVIAAYSP LGAKGTLWGT NGVMDSEVLQ QIAKARRKSI AQVSLRWVYE 240 QGVVLLVKSF NEGRMKENLK IFDWELSRED LKQINEILPQ RRGLPSHVFV SDDGPFKSEE 300 ELWDGEV 307
3-109	**Sequences**	
3-109-1	Sequence Number [ID]	109
3-109-2	Molecule Type	AA
3-109-3	Length	318
3-109-4-1	Features Location/Qualifiers	**source** 1..318 mol_type= protein organism= Stylophorum diphyllum
	NonEnglishQualifier Value	
3-109-5	Residues	MTMEAVPKVT LSTSGKSMPI IGFGTALFPT GNDEAVKSAV LSGIEAGYRH FDTAVAYRSE 60 KGLGEGIAEA LRLGLILSRD EVFITTKLWC TSCERSLVVP SLKNSLRNLQ MEYVDLFLIH 120 WPLRLSADAQ RPPIRNDQIL HFDTKSVWEG MEECYELGLA KNIGVSNFYP KKIDELLATA 180 KIPPAINQVE LNPAWNQKDL IKYCKSKGIL ITAYSALGAN GTHWGDNRVV DSDVLKDIAK 240 ARGKSTAQVA LRWVYEQGVS MVVKSFNKER MKQNLQIFDF ELTEEESNKI SQLPQHKGVK 300 LTPVYGDHDA MKKIDNEI 318
3-110	**Sequences**	
3-110-1	Sequence Number [ID]	110
3-110-2	Molecule Type	AA
3-110-3	Length	319
3-110-4-1	Features Location/Qualifiers	**source** 1..319 mol_type= protein organism= Tinospora cordifolia
	NonEnglishQualifier Value	
3-110-5	Residues	MVSVPEVVLS NGHLMPVVGM GMAAYPFQES ETVKQAMIRA IKMGYRHFDT AALYQTEKSL 60 GDAIVEALKL GLIKSRDELF ITSKLWCSDA HPHHVIPALQ RTLRNLGLEY LDLYLIHWPV 120 SSEPGKYEFP VRKEELILMD FENVWADMEE GYRLGLTKSI GVSNFSCKKL ESLLTMAKIP 180 PAVNQVEMNP LWRQNKLLRF CKDKGIAITA YSPLGAKGTI WGTNRVMESE VLNDTANARE 240 KTLAQVCLRW VYEQEVSILV KSFNEERMKE NLDIFDWKLS DEDLEKINEI PQCRGLPGDI 300 FVSDDGPFKS EAELWDGEI 319
3-111	**Sequences**	
3-111-1	Sequence Number [ID]	111
3-111-2	Molecule Type	AA

[0044]

3-111-3	Length	329
3-111-4-1	Features Location/Qualifiers	**source** 1..329 mol_type= protein organism= Tinospora cordifolia
	NonEnglishQualifier Value	
3-111-5	Residues	MVGVNKENVV SSVATVPVVT LNSGHKMPVL GTGTASFPVP PLEELKKVIM EAMEVGYRHF 60 DTAAMYQSEE GLGAAIKEAL EKGLIKSRDE LFITTKLWCN NAQPHLVLPA IRDSLRRLRL 120 EYVDLYLIHY PVRLKEDLLS MDCKEDEIFP IDIKSVWSAM EEIHNLGLAK SIGVSNFTCK 180 KLTDLLAHAK IPPAVNQVEL HPAWQQKKLR EFCQEKGIQV SAYSPLGAKQ WGFDVVLSNK 240 IIKEIAHHKG KTVAQIALRW GHEQGIILIP KSFNKERLIQ NLLIFDWELT QDELKKMASI 300 QQSRIAIAPE FVFPGSPFKS FEEFWDGEM 329
3-112	**Sequences**	
3-112-1	Sequence Number [ID]	112
3-112-2	Molecule Type	AA
3-112-3	Length	321
3-112-4-1	Features Location/Qualifiers	**source** 1..321 mol_type= protein organism= Tinospora cordifolia
	NonEnglishQualifier Value	
3-112-5	Residues	MGISMPDATL NSGHRIPLIG FGTASFPFPL EGSETATRAI LEAIKIGYRH FDTAALYQTE 60 VGLGEAIEEA LHLGLIESRD ELFITSKLWC THGRPERVLP AIRESLKNLK LDYLDLYLIH 120 MPMSFKSEKP WFPLPGEFEA MDFKSVWEQM EACQRLGLAR SIGVSNFSCK KLQLILTTAN 180 IPPAVNQVEM NALWQQNKLR EFCKSEGIVI TAYSPLGGKG TSWGSNRVME CEVIKEIATE 240 KGKTHAQVCL RWLYEQGVSM VVKSFNKERM KENLEIFDWE LTSKECEQIK KLPQSRGFTA 300 QGLVSEDGPF KSIEDIWDGE I 321
3-113	**Sequences**	
3-113-1	Sequence Number [ID]	113
3-113-2	Molecule Type	AA
3-113-3	Length	333
3-113-4-1	Features Location/Qualifiers	**source** 1..333 mol_type= protein organism= Thalictrum flavum
	NonEnglishQualifier Value	
3-113-5	Residues	MRRPHSRLAS TRDMSSIVPD VVLSSGHKMP LIGFGTVAYP IAASDSIKTA IVNGIKHGYR 60 HFDTASVYQT EQLLGEAIAE ALQFGLIKSR QELFITSKLW CSDSHHDRVL PALQNTLKTL 120 QLDYLDLYLV HWPISSKPGK HEFPIPKEEL LPLHFESVWT AMEECQAVGL TKSIGVSNFS 180 SKKLEQLLST SKIPPAVNQV EMNPIWQQYK LREFCKSKGI VITAFSPLGA KGTSWGTNKV 240 MDSEVLNEIA QAKGKTHAQV CLRWLHEQGI CVVVKSFNEE RMKENLEIFD WELSPEESAL 300 IQQLPQSRGN TGEDFISVDG PFKSLEELWD GEI 333
3-114	**Sequences**	

[0045]

3-114-1	Sequence Number [ID]	114
3-114-2	Molecule Type	AA
3-114-3	Length	320
3-114-4-1	Features Location/Qualifiers	**source** 1..320 mol_type= protein organism= Thalictrum flavum
	NonEnglishQualifier Value	
3-114-5	Residues	MGSIPEVSLN SGHRMPLIGM GTASYPFAGS EVVKSAILSA IKLGNRHFDT AALYKTEQII 60 GEAIAEALQL GLIKSREELF ITTKLWVNDG HKDCILPALQ TSLKNLQLDY VDLYLIHWPV 120 CIPPGELRMP GPNEKVLPID YASVWEAMEE CQRHGLTKSI GVSNFTCKKL ELILASAKIP 180 PAVNQVEVNP LWRQEKVIRF CKDRGIAVTA YSPLGTAGSD FMGNRNVVQS ELLKEIAKAT 240 GKTHAQVCIR WVFEQGVGVI VKSFKEMRLE ENIDIFDWEL SKEDSLKISR LPESKGYPGH 300 GFIRVEGPFK SLEELWDGEI 320
3-115	**Sequences**	
3-115-1	Sequence Number [ID]	115
3-115-2	Molecule Type	AA
3-115-3	Length	320
3-115-4-1	Features Location/Qualifiers	**source** 1..320 mol_type= protein organism= Xanthoriza simplicissima
	NonEnglishQualifier Value	
3-115-5	Residues	MGSVPEITLN SGHSMPVLGL GTASVPFAGY EVVKSAILSA IKLGYRHFDT AALYRTEQPL 60 GDAIAEAIRL GIIKSREELF ITSRPWLNDT HHDRILPALQ TTLQNLQLDY LDLYLIHWPL 120 SIKPGNIRFP GPDEKILPMD FESVWAAMEE CQRLGLTRSI GVSNFSCKKL EKILASATIP 180 PAVNQVEVNP LWRQEKLIQF CKSKGIVITA YSPLGTVGSS FQGNNNIMEC EVLKEIAGNR 240 GKTHAQVCLR WVYEQGVCLL VKSFNEARLK ENMEIFGWAL SEEEANQINQ LPQGRGYPGH 300 NFITPDGPFK SEEELWDGEI 320
3-116	**Sequences**	
3-116-1	Sequence Number [ID]	116
3-116-2	Molecule Type	DNA
3-116-3	Length	1599
3-116-4-1	Features Location/Qualifiers	**source** 1..1599 mol_type= genomic DNA organism= Argemone mexicana
	NonEnglishQualifier Value	
3-116-	Residues	atggataatt ttcttctcca gttccaacca atttcaattg cagctttttt tgttgcccta 60 gtttttctgt attggagtta tggaagaaaa agcaacaaaa ccctaaaacc aagagcacca 120

[0046]

5		gaagcagcag gaggaagacc aataacaggt catcttcatc ttttttatgg agaagaatta 180 actcatcgaa aactaggttc catggctgat aaatatggac cagttttcaa tattagattt 240 ggttcacata aaaccctagt tgtaagtaat tgggaaatcg ttaaagaatg tttcactaca 300 aatgatcgat tattctcaaa tcgaccaggt actttagcta ttaaactaat gttttatgat 360 actgattcag taggttatgc accttatgga aattactgga gagaattaag aaaaatttca 420 actttaaaac ttctctctaa tcatagaata gaaaccctaa aacatttaag aacttctgaa 480 gttgaatcct gttttaaaca gctttataat caatgggaaa tgaaaaatga aaacagggta 540 gaagttgata aattagggtt tgcttcagta aggatggata attggtttgg ggatttaact 600 ttcaatgttg tagcaagaat tgttgctgga aaaaagaatt ttgcaggagg tgcagtaaat 660 ggtgatattg gagctcagag atataaagta gccatggatg aatcttttag attaatgcta 720 acatttgcat attcagatgt gattccatca ctgaaatggt tagacaaatt aagaggttta 780 attagagata tgaagcgttg tggatctgaa attgattcaa ttgttgctag ttgggtagaa 840 gaacatcgtt taaagagaaa ttcttctgaa aataataatt tagatcttga agaagatttt 900 attgatgttt gtttggatat tatagagagt tcttcattac ctggtgatga tccggatact 960 gtcatcaaat ctacttgtct ggatatgata ttgggtggga gtgataccac gacagtaacc 1020 ctaacatggg ccatctcctt aatattgaac aatcctcacg tgttgaaaag ggcaaaagag 1080 gaattaaatt ccgtagttgg aaaagatcga cgtgtagaag attcagacat ccctcatctt 1140 acatacatcc atgcaatcat caaagaaacc atgagactct accctgctgg accactgatc 1200 gaaaggagga caatggaaga ttgtgaagta ggtgggtacc acgttccagc tggcacacgt 1260 ttattggtta atgtatggaa gatgcaaaga gacggggatg tgtataaaga cgatccattg 1320 gtgtttagac ccgagagatt catgactagt aatgctgatg tggatctaaa gggtcagcat 1380 tttgaactga taccattcgg tgcgggtcgc aggatatgcc cgggtgtgtc atttgcggtt 1440 cagttgatgc atttggtatt ggctcgtctt ctacatgagt ttgaaattac tacaatacct 1500 tctgaaccaa aggtagatat gtctgaaagt ggaggattaa tctgtcataa gataaagcca 1560 ctagaagtgc taatcaaacc ccgactcgag ctgaactaa 1599
3-117	**Sequences**	
3-117-1	Sequence Number [ID]	117
3-117-2	Molecule Type	DNA
3-117-3	Length	1614
3-117-4-1	Features Location/Qualifiers NonEnglishQualifier Value	**source** 1..1614 mol_type= genomic DNA organism= Argemone mexicana
3-117-5	Residues	atggatttct catcaatact actacttctc aatattaatt gcttcacaac ttccttggtc 60 acccttcttg ttcttgtcat ggtttttctc tacaataata caagatttac taaacccaaa 120 ggtaataaaa agatgattaa accacccaga ctacccggtg cacgccctct tttaggtcac 180 ctccatctgt ttggaccagg tgagcttcct cacaaggttc tctcaaccat ggcagataaa 240 tacggtcctg cctttacaat taagttcggt aaacacacaa cattagttgt gagcgatatc 300 cataccataa aagaatgttt aactactaat gacatcctct tttctaaccg tccttcttct 360 atagcctttg atctcatgac ttacgctgat gactccgtag ctttcgcaca ttatagtcct 420 tattggcgtg agcttagaaa gatatctact ctcaaacttc tatctaataa ccgtcttcaa 480 tctatcaaac aacttcgact ctctgaggtg aacgtatgtt ttaaagaact atatagttta 540 tgcaacaata ataataaaag tggagctccg gttttgattg atatgaagaa atggttcaaa 600 gaggtcacga ctaatatagt cattagagtt attgttggta aacaaaattt tgggtctaag 660 attgtgcgag gcgaagatca agaagctgcc aattacaaga aaatcatgga tgaactttca 720 cgccttgcta aattgtctat gttctctgat tatgctcctt tacttagttt gtttgattac 780 ttccgaggaa acgtgagtgc tatgaaaaga aatggtaaag aattaaacgc gatgcttcag 840 aattggttgg aagagcataa gaggaagaag aactcatcaa tatcgaacga tgatgaacaa 900 gatttcatgg atcttatgtt gtcaattatt gacgaaacta agctatacgg acgtgacgct 960 gatactttca ttaaagctat ttccctttct atgatcgtgg gtggaataga caccgttgtc 1020 gtgactctaa catggattct cgccttaatt atgaagaatc cttttgcttt gaaaaaggct 1080 caagaagagt tagacttttt cgtcggaaag gaaagacaag tagaagattc agatctcaag 1140 aacttggtat acatgaatgc catcgttaaa gaaacgctgc gattataccc attaagttgt 1200 attcttgaac gtgatacgaa ggaagactgt gaagttggtg gctactacgt cgaaggtggc 1260 acacgtttac taataaacgc atggaagtta caacgggacc cgaatgtatg gacagaccct 1320 tcggaattta agccggagag atttctaaat gagaatgcag acatagatgt tggtggccaa 1380 cattacgaat taataccatt tggagctggt agaagagtgt gtcctggtgt atcttttgca 1440 ctccagttta tggatttggt tctggctcgt ctcatccatg ggtatgaatt gggaactcta 1500 aatggtgaag atgttgacct aactgaaaaa actgaaggac aaattaattt caaagcaacc 1560 cctctggatc tcatcgttac tcctcgtctc caccccaatc tttatgatta ttag 1614
3-118	**Sequences**	

[0047]

3-118-1	Sequence Number [ID]	118
3-118-2	Molecule Type	DNA
3-118-3	Length	1569
3-118-4-1	Features Location/Qualifiers	**source** 1..1569 mol_type= genomic DNA organism= Berberis thunbergii
	NonEnglishQualifier Value	
3-118-5	Residues	atggaatcaa ttgagtttct agtaactctg ctactcagcc tgcttgccct attttgtgct 60 tatgcatgga agaggaaaaa ccatacaaag gatagcaaaa tcaaagagcc accccaacca 120 gccggagcat ggccgataat cggccacctt catctaatat cccgcggcgg ccttcctcat 180 ataaacatgg gggccatggc ggacaagtac ggtccagttt tcatgatccg gctaggagta 240 aatcgagctg tgattgtgag taacacggag atcgtcaaag agtgcttcac aaccaacgat 300 aaattcctac taaaccgtcc agttgggtta gccttaaacc tcatgtgcta caacaacgcc 360 atgttcgggt tctgtcggta cggtccatat tggcgagaga tacacaaaat agtcatgctt 420 gagctcctct cgaacagccg gctcgagtcc ctgaagcacg tatgggactc ggaaatatcg 480 acatccatcg aagagttgta ccaattatgt caaacacaaa acaagaccca tgaaggccca 540 gttttggttg aaatgaagga ttggtttgca gatatggcac tcaatgtgtc ccttagaatg 600 attgctggga aaagatactt tggtgcaagt gccggtggta ataaagatga ggcaagaaag 660 tgtcaaaaga ccataagaga tttctttaga cttgttggct tgtttatagt gtctgatgca 720 cttccatttc ttaggtggct agacttggga gggcatcaga aggagatgaa gagaacattt 780 gaagatcttg actatatgct tcaaggatgg ttggatgagc ataaattgaa tagaaaatct 840 ggtgtgaatg gtgatcaaga tttcatggat gtgatgttat ctattcttga tgattcaaaa 900 tttccggatt acgacgttga caccgtcaac aaggctacgt gcttccaatt gatcatagga 960 ggaactgata ctacaacggt cactctaaca tgggcccttt ccttgatgtt aaaccaccca 1020 catgtattga aaaaggccca agatgagttg gacatccaag taggcaaaca cagacaagtg 1080 gaggaatcag acatcaagaa cctaaaatac cttgaagctg tgatcaaaga aaccttacgg 1140 atgcgcccag taggcccact gttaggccca cgagagacga tcgaggactg caccattggt 1200 ggatatcgag ttcgagcagg cacacgtgta atggtcaatg cttggaaggt gcatcgtgac 1260 ccatcggttt ggtcaaaccc tgatgacttc aaaccggaga ggtttctcaa gaaggatatt 1320 gacttcaggg accaaaactt tgaattcatc cctttcgggt ccggtagaag ggcctgccct 1380 ggaatatcat ttgccgtgga agtactgccc atggctttgg cccgtttact acatgggttt 1440 gagcttaaga ctcaattggg ttgcaaggtg gatatgacag agcatgccgg tttagttcat 1500 gctaaagcta cccctttgga agttcttgtc agcccacgcc tgtctcgaga gttgtatgta 1560 tcgtcttag 1569
3-119	**Sequences**	
3-119-1	Sequence Number [ID]	119
3-119-2	Molecule Type	DNA
3-119-3	Length	1543
3-119-4-1	Features Location/Qualifiers	**source** 1..1543 mol_type= genomic DNA organism= Berberis thunbergii
	NonEnglishQualifier Value	
3-119-5	Residues	gggatcactt gctctcattg ccattattat tctttccaac attgtcaaaa aatcttcgaa 60 atctctttcc agtaaaggtg gcaagagtgc acccgtggtt catggtgcgt ggccagtcat 120 cggtcacctg cacctactga tgggtaagga gttgcctcat catgcattag ccaaactggc 180 tgataagtac gggccagcct tcacactcaa cattggcgcg tatcaagaac tagtgatcag 240 tactcgggat cttgcaaaag aatgtttcac caccaaagac aagttcttcc taaatcgtcc 300 aagcaataag gccatgaaga tcctgacata tggtgaagca tcagttgggt tcgcaccata 360 tagcccactt tgggtcgaaa tgcgcaaggt tacgaaatct aatctcttat ctcaccaaag 420 ggtcttgatg caaaatcgtt cacgagcatc agaaattgat gcaagtttta aacaactata 480 tgaacaatgc aatgggaaga gtggagcttc ggtggaaatg aaaaactggt ttgaagaagt 540 gatgttgaat gtggttacta ggaatgtttc tgggaaaaga agttttggta ccaaggcaag 600

[0048]

		acttggtgat gcagaggccg tgaagtataa aagggttatt gatgagaccg cacggtttat 660 ggggaacctt gtgatctcag atatggttcc aagtctttgg tggttggata acatgttggg 720 tgctgagagt gctatgaaga aacttgccat agaattggat tctctacttg gtggttgggt 780 ggaggaacat agagggaaga agttgagtga cgacgaggag ggggacttta tcagtcttac 840 atgggagatg atcgatcaga ttcagcttca tggtcttgcc cctgagacgt tcatcaagtc 900 tatgtgtgtc ggcgtgctgt tgggtgggag tgataccaca tcagtagccc taacatgggc 960 actctcgcta atgttgaaca atcgcgaggt gttgaagaag gcccaagaag aattggactt 1020 ccacgtagga aaggaccgca aagtggacga ctcggacctc aagaatcttg tttacttaca 1080 agccattatg aaggaaacaa tgaggatata ccaagtaggt cctctaattg aacgagaggc 1140 cgttgaggac tgtgaagtgg gtggattcca aatcaagaag gggaaccgta tactagtgaa 1200 cctgtggaag ttgcaacgtg accctgaagt gtggtcagat ccgtccgaat ttcgacctga 1260 aagatttctt gaggataagt ctaaggtgga cttgaagggc caaaatgctg aactaatgcc 1320 gtttggcagt ggtcgacgta tgtgtccagg agtttggttt ggggtgcact ccacttcttt 1380 ggtacttgct cgtctcatcc aagggtttga aatagagaca ccactggatg caaaagttga 1440 catgacggag acatcaagtg tgaccaatta taagggaagt cctcttgaag ttattgctcg 1500 actccccggc tcgaacctaa gctttatgat ttgtagttat gta 1543
3-120	**Sequences**	
3-120-1	Sequence Number [ID]	120
3-120-2	Molecule Type	DNA
3-120-3	Length	1638
3-120-4-1	Features Location/Qualifiers	**source** 1..1638 mol_type= genomic DNA organism= Corydalis chelantifolia
	NonEnglishQualifier Value	
3-120-5	Residues	atgactccct caatttcaca acctttgag cttcttcttc ttctgatgac aatggagtct 60 cttcttctcc aatggcaacc aacttccatt gctgttcttc ttctcgccat cacaattttc 120 ctctacacct tcacaaaatc acccccctaaa acccacaaaa aactagcccc agacgcaaca 180 ggaggacggc cattaatggg tcatcttcat ctcttcaatt caaacgaatt aacacatcga 240 actctaggat ccatggctga taaatatggt ccagctttca acattcgatt cggttcacac 300 aaaaccctag ttgtatctac ttgggaaatc gtcaaagaat gtttcaccac caacgatcga 360 tcattctcaa atcgcccagg aactctatac atcaaactca tgttctataa cgaagattca 420 gtagggtatg caccttatgg agcttactgg agagatcttc gtaagctatc aacactgaaa 480 ctactctcaa accatcgatt ggaatcattg aaacatttga gggtttctga aatgaatgaa 540 tgtttcaaac agctttatga gatttgtaac aaaggaagta aatctgttgc tgttagaatg 600 gataattggt ttggtgattt gacttttaat gttgttgcaa ggattgttgc agggaaaagg 660 aattttgctt caattagtaa tgatgttgga gctatgagat ataagaatgc aatggatgaa 720 gcttttagat tgatgactgt tttttcattt tctgatgtga ttccatcact tggttggttg 780 gataatttga gaggattagt gggtgatatg aaaaaagctg ggaaagaaat tgattcagtg 840 gtttcaggtt ggattgaaga acatcgtgag aagagaaaga gaagatcatc tggtggtaat 900 aacagagatg gagaattaga agaggaggat ttcattgata ttactttgtc tatcttggaa 960 acttcaagtc tccctggtga tgatcctgac atgactatca aatctacttg cttggatatg 1020 atcttgggtg gtagcgacac tacaacggtg actatgactt gggctctctc cttgctatta 1080 aacaatgctc acgctttgaa aagagcaaga gaagaactgg acttgcacgt cgggagagat 1140 agacaagtgg aagattcaga tatcaacaat ttggtctaca tccaagcaat catcaaagaa 1200 acaatgagac tatacccagc tggacccctc attgaacgga tgacaaagga agattgtgag 1260 gtaggtggat tccacatccc agccggaaca cgtttgttag ttaatctctg gaagatgcaa 1320 cgagacccaa atgtgtggga ggatcctttg gaatttcgac ctgaaagatt ccttaccaac 1380 aatgcagaaa tagatctaaa gggtcagcat ttcgaactca tcccatttgg gacgggtaga 1440 aggatatgcc caggtgtttc atttgcctta caattgatgc atttggctct cgctcgttta 1500 cttcacagtt ttgaagttgc atcccccatg gatgccaaga ttgatatgac tgaaaccgca 1560 ggccttataa gccacaaggt aattccgcta gaagtcctca tgactccacg ccttgactct 1620 aagctttatg attattag 1638
3-121	**Sequences**	
3-121-1	Sequence Number [ID]	121
3-121-2	Molecule Type	DNA

3-121-3	Length	1572
3-121-4-1	Features Location/Qualifiers	**source** 1..1572 mol_type= genomic DNA organism= Corydalis chelantifolia
	NonEnglishQualifier Value	
3-121-5	Residues	acacacacaa ccgaaaagaa tttaccaccg gaagtgcctg gtgcattgcc tgtcatcggt 60 cacctccaca agttaggtgg tcggaaaggt cttctaccat atcatgttct tggagccatg 120 gctgataagt acggacctgc cttcacattc cagtttggtt ctaaccgaac ccttgtgatt 180 agtaattggg aaatggtaaa agaatgtttc acgtctacca acgataagtt attcgcttat 240 cgtccaacag cattgttcaa taaggaagta ttctgtagtg accattcttt tggattcgga 300 ccttatggcc cgttctggag ggagatgcgt aaggtttgtt cgcttcatct tctctccaat 360 tatcgcctcg agctcttaaa acactctcga aaatccgaga tggatgagtg tttcaaggag 420 ttgtaccaac tatggagtgc ttcaaatatt agcaaagaca agcaacctgc tgttttggtg 480 gtggaaatga agaaatggtt cgaagatgcg atgttcaatg ttgcttcgag agttgtggtg 540 ggaaaaggaa gtttgaaatc tcatgagaag gctggaggga gtgataatga agtagcgagg 600 aacaaatata agaaaggcat ggatgaggct agacgacata tgggaacatt tgttatatcg 660 gataggatcc cgtttctttg gtggattgat tatttacggg gtatccatag ttctatgaag 720 cgaacggcga aagaccttca tgccattgta gagacgtggt tagaggaaca ccgtcttcat 780 tgtcacaaac ggagagtatt gcaactcgat gccaaccatg aggttgaaga tatggcgaaa 840 gaggaagaaa aagattttat ggatgtttta ttgacgatgg cggacgaggg agccatcaaa 900 atctttgacc atgatcttga taccgttatc aaagctaatt gtctggatat ggttatcgct 960 ggaaccgata caccaaccgt aatgcttaca tggacccttt cactattact aaacaatcca 1020 gatgttttga aaagagttcg agatgaactg gatttacatg ttggaaaaga aagacaagta 1080 gaagaatctg atgtcaagaa tttggtctat ctccaagcag ttttcaaaga aaccctgcgt 1140 ttatacccag ctgtacctct aaatgaacgt ttgacaatgg aggattgcaa tgttgggggt 1200 tacgatatcc cagccggtac ccgtctatta atcaacattt ggaaggttca aagagaccca 1260 aatgtgtggc aggatccctc agaattccgt cctgaaagat tcttgagtaa ggaaaaatcc 1320 accatagatg tgaggggtct agattttgaa ctcattccat tcgggacagg tagacggatg 1380 tgcccaggga tttcattttc cctccagctc atgcatttgg gactcgctcg cctcattcac 1440 ggctttgaat tagcaactcc gatggatttg gatgtcgaca tgtctgcaaa tcctggagct 1500 ttcaactata aatcaaccga tcttcaagtt cttgttagcc cacggtttca ttctaagttc 1560 tacggttgtt aa 1572

[0049]

3-122	**Sequences**	
3-122-1	Sequence Number [ID]	122
3-122-2	Molecule Type	DNA
3-122-3	Length	1611
3-122-4-1	Features Location/Qualifiers	**source** 1..1611 mol_type= genomic DNA organism= Corydalis chelantifolia
	NonEnglishQualifier Value	
3-122-5	Residues	atggatttcc ttgctcttca atggttccca gcttccttga ctgcccttct tgccttggct 60 gtcctttaca acttctggac caagcaaagg acttacaaga atggaaagac gagtactaaa 120 caggcacctg tagctgccgg tgcatggcca gttcttggtc accttcactt gtttggtgga 180 ggtgaactgc ctcacaagat gcttgctact atggctgata aatatggacc tgccttcaca 240 atgaagtttg gtacacatca aacactagta gtcagtaaca ccaagattgt aaaagaatgt 300 ttcacaacca atgatacttt gtttgcaaac cgtccatcca ccacagcctt tcacctcatg 360 acctacgata acgagtcggt agccttcaca ccatatggtc cattctggcg tgagctgaga 420 aaaatctcaa cactcaagct tctttctaac caccgtctcc aagcaattaa ggatgtacgt 480 gcctcggaag tgaatgtgtg cttcagggag ttgtacagtc aatggaggat aaataaaagc 540 gagcctgaaa ccagtgatca tcagggtcca attctggttg atatgaagaa gtggttcgaa 600 gaagtctcag acaatgtggt gcttagagtg attgcaggga aacaaaactt tggctctaag 660 attgtgcatg gagacaaaga ggcccttcac tacaagaaaa tcatggacga gatactacgt 720 cttgcggcag tttccatgct ttcagatgtg gctcctttgc ttggttggtt agatatgttc 780 caagggcatt taagtgccat gaaacgaaat gcgaaagagg tagatactat gctatgtaac 840 tggttggagg agcatcgaac gaaaagactc tccagcgatc atgacggtgt agagcaggat 900 ttcatagatg tcatgctgtc aatcgtggag gagaacaagt tctctggcca cgacaatgat 960 accgtaatca aagctactgt cttggccatg atcatgggtg ggactgatac caccgctgtc 1020 agcttaactt ggattgtgtc cttgttgatg aacaaccgcc acgttttgag aagggcacaa 1080

[0050]

		gatgaacttg acttgcacgt ggggaaggat agacaagttg atgattcaga tctcaagaac 1140 ttggtttatc tcaatgctat agtcaaggaa accatgcgtt tgtacccatt aggtgctctt 1200 cttgaacgtg aaaccaagga ggattgtgag gttggtggtt tccatgtcaa aggtggaaca 1260 cgcctattag tgaatgtatg gaagctacaa cgagacccaa gcttttggac cgatccaaca 1320 gaatttaaac ctgaaagatt tttagcagac aaggcgaaca tagatgtcgg tggtcagcat 1380 tttgaactac tgccatttgg ggctggtaga agagtgtgcc caggagtctc gttcgcactg 1440 caattcatgc atttggtact tgctcgtcta cttcacggat ttgatttggc taccccctatg 1500 aatgcagatg tcgatctaac cgagagtact gaaggacatg tcaaccagaa agcatcccct 1560 ctcaatctac ttgtcactcc acgtctccat tctaagcttt atgaatacta g 1611
3-123	**Sequences**	
3-123-1	Sequence Number [ID]	123
3-123-2	Molecule Type	DNA
3-123-3	Length	1632
3-123-4-1	Features Location/Qualifiers	**source** 1..1632 mol_type= genomic DNA organism= Corydalis chelantifolia
	NonEnglishQualifier Value	
3-123-5	Residues	atggagtaca cattctcatc agcctcattg ttctcctcct cctcccttca acaatggctc 60 tcaacccttc tacttctaat ttcctccatc accatttctc tttaccttac tcgtcgcggt 120 aagtcatcac cgccaatggt ccctggagca tggccactca ttggtcacct acatttactt 180 ggtgggaacg atccacttca tatcgttctt ggaaccatgg ctgataagta tggacatacc 240 tttgccatgt tattcggtaa acatccatca cttgttgtta gtagtagtga cattgtaaag 300 gaatgtttca cttctacaaa cgataaattg ttttcgcatc gtcatgttcc taccggagtt 360 aaatacatgt tctacaataa tgactcgttt ggttttgcac cttacgggcc ttattggcgt 420 gaaatgcgta aaatgaattc actttctctt ttctcacacc atcgcgttga aatgcttaac 480 cgaattcgaa catctcaaat taacatttgg tttaaaaacc tatatgaaat gtgtaccaag 540 gagaagagta ctagtacaag tagtgatgga gttgtggttg aaatgaagtc atggtttgat 600 gaaatgtttt tcaatgtact tgtgaatatg attgttaaac ctattaatga tgatgaagag 660 ttggtgaaga aatacagaga agtggcgacc gaggcaggac gcctattgtc aagcatggct 720 gtttcggata tggttccatc tctaggatgg ttggatcatt tgtttgggat tgtgggtaaa 780 atgaagaaaa ctgcaaaaga tatggatgct atcctcacta cttggttaga acagcataag 840 atcaaatctc aacagctgag gagaagtaat ggaggagaag gtgctgctga tcaaacagag 900 gaggaggaga aggagggaaa agggctcatt ggtgatttgt tgtctatgca agagtctgct 960 cttttcggcc atgaccgaga cactgtcatc aaatctgctt gccaggcgtt gatcatggct 1020 gggagtgaca gtacatcagc cacattaaca tgggttctct ctttgttact gaaccatcgt 1080 gacgcactca gaaaggctcg agaagaactg gatcaagttg taggaaagga cagacaagta 1140 gatgattcag acattaagga tcttgtatat ctccaagcca ttttaaagga aacgatgcgg 1200 ttatatccag ctgcaccgat attagagcgc ttggcagtag aggactgcat tgtaggtgga 1260 tttcatgttc aagcaggcac aacactgttt gtgaatgtca gcaagctgca acgtgaccca 1320 aatttatgga cggatccttt agaatttaaa cccgagagat ttctcaccgg ctgtaacgcg 1380 gatgtggact tgaagggtca agattacgag ctcgtgcctt ttggttcggg tagacggtca 1440 tgtcccgcgg tatcgtttgc agttcgtgta atgcttttgg tacttgcacg cttcattcac 1500 tcatttgaag tgaagactcg tgaagaagat gggattttgg atatgactga gagttcaggt 1560 cacaccaatt gcaggtctag cccactggaa gtcctcatct caccacggtt ggattcgaag 1620 atctactgtt ga 1632
3-124	**Sequences**	
3-124-1	Sequence Number [ID]	124
3-124-2	Molecule Type	DNA
3-124-3	Length	1587
3-124-4-1	Features Location/Qualifiers	**source** 1..1587 mol_type= genomic DNA organism= Corydalis chelantifolia

[0051]

3-124-5	NonEnglishQualifier Value	
	Residues	atggagtact actcatcact accatttctt caacaatggc cactttcatc tatatcatca 60 tcaccaactt ctattgctac aacacttctc attgtagctt gtttcaccat tgttttcctc 120 tacataaaca ccagttctaa gtccaataac aacctgaaat caccaccgaa acttcccggt 180 gcatggccat tcatgggtca cctacattta ctaggtggaa accaaccagc tcatgtcagt 240 cttgcaaaca tagcagagaa gtacaaatcg actcccttca tgatccgaat gggtcaacat 300 tcaaccctcg ttgttagttc ggttgatctc gtaaaggaat gtttcaacaa tacaaatgat 360 aagctgtttt cgaatcgtag tatcgcaaga ggaattagag atatgtttta cgatatggaa 420 tcgtttgggt ttgcacctta tggttattac tggcgtgaac tacgaaaagt atctgccctt 480 actctgttct ctactcatcg tgttgattcg gttatccaaa ttaaaacacc tcaaatcgac 540 ggttggttta agaaacttta cgagcaatgt acgaatacga aaggcggaat tgttgaaata 600 aaatcatggt tggatgaaat gatgtttgat gttcttgtga agatgcttgt tgaacctaag 660 gatgaaggat ctgtggagaa atacagacat gtagcagggg aggctttgga agtgctgggg 720 aatatgagca tctatgattt agtacctagt cttggttggt tggatcactt cactgggctt 780 gtgaagaaat ataaggtaac tggtaagaaa atggacacta tcctcaacag ttggttagaa 840 gaccatcgag gtgagaaagt agctgaggaa cacaagggtt taattggtaa gttgttgtca 900 atgaaggaag gatcaaagct tcttggccat gatggagata ctgccatcaa atctactgtt 960 caggtgttga tcctaggtgc cggcgatagt gcaggagcaa ctttaacatg ggcaatctca 1020 ttattattga accatcctca cataatggag aagcttcgga aagaactgga tgcagccgta 1080 ggaaaggata gacaaatcga agactcggat gtgaaaaaat tcacttatct actagccata 1140 ttaaaagaaa caatgcgatt atacccggtg acaacgcttc tacaacggga aacgatggaa 1200 gattgtgcta taggtggata tcatgttgct gctggcacaa gactgatggt aaatgtttgg 1260 caggtgcaac gtgacccgaa tgcgtggtca gatcctttgg agtttaagcc tgagagattc 1320 ctaactgagt gcgcgcatgt ggatttctcg ggtcagtatt ctgagcttat tccattcgga 1380 acaggtcgac ggatatgccc agctcttacg ctatcggttc ggctcatgtt attgaccctt 1440 gcccgtatta tccattcgtt tgatgtgaaa attcctaatg gggcatcgag tgtggatatg 1500 gcaacaagcg taggttttgt taatctgagg ttgaccccac ttgaagtcga actctcacca 1560 cgcttggatt caaagatcta cggttga 1587
3-125	**Sequences**	
3-125-1	Sequence Number [ID]	125
3-125-2	Molecule Type	DNA
3-125-3	Length	1614
3-125-4-1	Features Location/Qualifiers	**source** 1..1614 mol_type= genomic DNA organism= Corydalis chelantifolia
	NonEnglishQualifier Value	
3-125-5	Residues	atggattcct ctcttcttca atggtacaca acagcttcaa tggctgccct tcttgcctta 60 gctttcttct acaaactctg gagtaagcca aggacttcta aaaatggaaa aagtactttg 120 caggcaccag tagcagctgg tgcatggcca gttcttggtc accttcatct gtttagtgga 180 ggtgagttac cacacaaaat gttggctgcc atggccgaca agtacggccc tgccttcaca 240 atgaagttcg gtacacaccg aacccttgtg gttagtgaca caaagattgt aaaggaatgt 300 ttcactacca atgatacgtt atttgctaac cgtccatcca ccatggcctt tcatctcatg 360 acctatgaca atgagtcggt agccttcaca ccatatggtc aattttggcg tgagttgaga 420 aagatctcca cactcaaact tctttctaac catcgccttc aggcaatcaa agatgtacgt 480 gcctcagagg tgaatttttg ctttaggacg ttgtacaacc aatggaggat aaataaaagt 540 gagactatcg gaaccggtga tcatcaagga ccaattttgg tggatatgaa gaagtggttc 600 gaagaagtgt caaacaatgt ggtgatcaga gtaattgtag gcaaacataa ctttggatct 660 aagatcgccc gcggaaaggg agaagccctt cactacaaga aagtcatgga cgaggtccta 720 cgtctagcgg cagtgtccat gctctcggat gtggcccctt tacttggttg gttcgatcat 780 ttgcaagggc atgtaagtgc aatgaaacga aatgcaaaag aagtagacac tttgctctgt 840 agttggatgg aggaacatcg aaaaaagaga acctccaacg gcagtaatgg tgtagagcaa 900 gatttcattg atgtcatgct gtccatcgtg gaggagaaca agttctctgg gcatgacagt 960 gacactgtca tcaaagctac cgtcttggcc atgatcatgg gtgggactga tacatcagcc 1020 gtgagcttaa cttggattgt ctccctgttg atgaacaatc gccacgtttt gagacgggca 1080 caagaagaac ttgacacaca tgtgggaaag gatagacaag ttgatgattc agatctcaag 1140 aacttggttt atctcaatgc tatcgtcaag gaaacaatgc gtttgtaccc actaggcgcc 1200 cttcttgaac gggaaactaa ggaggactgt gaggttggcg ggttccatgt taaggctggc 1260 acacgtctat tggtgaatgt atggaagcta caacgagacc caaacttttg gattgatcca 1320 acagaattta aaccagagag atttttaact gacaacgcaa acatagatgt tgggggtcag 1380 cattttgaac tgctaccatt tggtgccggt agaagagtgt gccccggagt ctcattcgca 1440 ttgcagttca tgcatttggt tcttgctcgg ctaattcatg ggttcgaatt ggataccccct 1500

[0052]

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3-126	**Sequences**	
3-126-1	Sequence Number [ID]	126
3-126-2	Molecule Type	DNA
3-126-3	Length	1716
3-126-4-1	Features Location/Qualifiers	**source** 1..1716 mol_type= genomic DNA organism= Corydalis chelantifolia
	NonEnglishQualifier Value	
3-126-5	Residues	atgttcaagt ctgttccaag tgcacaggca attttacwya arctttcatt catccaccag 60 tacttcctgc tctctcaaac aaatatggat tcccttcttt ttcaatggtt tccagcttca 120 atggctgccc ttgttgcctt tgcttttctt tataagcttt ggagtgcacc caaaattacc 180 aaaaatggaa agacaagtac taaacaggca cccatagcag ccggtgcatg gcctgttctt 240 ggtcacctcc atcttttcgg tggaggtgaa ttgcctcaca aaatgcttgc aggcatggct 300 gaaaaatatg gtcctgcctt cacaatgaaa tttggtatgc atcgcacact cgtggtcagt 360 gataccaaga tcgtaaagga atgtttcact acccacgata ctctctttgc taaccgtcca 420 tctaccacag cttttcacct tatgacctac gatcaagagt cggtggcctt cacccccttat 480 ggtcctttct ggcgtgaact acgaaagatc tccacgctca aattactttc taaccaccgg 540 ttacaagcaa tcaaggacgt tcgaacctct gaagtaaacg tttgctttag agggttatac 600 aacatatggc aaaccaacaa aaatgagcaa ggtggtactg ttagtgatca tccacgcccc 660 gttttgattg atatgaagaa atggttcgaa gaagtttcga ataatgtggt gattagggtg 720 attgccggta aacaaaactt tgggtctaaa attgtacgtg gtgaagagga ggcagtaaaa 780 tacaagaaaa tcatggatga agtcctacgc cttgcggcag tatctatgct ttctgatgta 840 gctcctttac ttggttggtt agatcttttc caagggaact tgagtgcaat gaaaagaaac 900 gcaaaagaag tagataatat gcttaatgct tgggtggagg agcatcgaag aaagaggctc 960 gcacatagtg ctaaagttga ggctactcat gtagaacaag actttgttga tgttatgttg 1020 tccatcatgg aggagaacaa gctttcatca gtccacgacg atgacactgt catcaaagcc 1080 actgtgttgg ccatgatcat gggtgggact gataccacag ctgtgagcct gacctggaca 1140 gtttccttgt taatgaacca tcgttatgtg ttgaagaagg ctcaagaaga aatcgatcaa 1200 catgtgggaa aagaaagaca agttgaagat tcagatctta agaacttggt ttatcttaat 1260 gccattgtca aagaaactat gcgtatgtac ccgttgggtg ctcttcttga acgtgaaacc 1320 aaggaggatt gtgaagttgg tgggttccat gtcaaaggtg gaacacgtct attggtgaat 1380 gtttggaagt tacaacggga tccaaatgtt tggattgatc caacagaatt taagccagag 1440 agatttttgg cagagaatgc caacatagat gttgggggtc agcattttga actgctacca 1500 tttggtgctg gcagaagggt gtgccctgga gtttcattcg cactccaatt catgcatttg 1560 gttcttgctc gcttaattca tggatttgaa ttggaaaccc caatgaatgc cgatgtcgat 1620 ctaactgaaa gtaccgaagg ccatgtcaac cacaaagcta gccctctcga tctgctcatc 1680 gccccacgac tcaactcgaa gctttatgaa ttgtag 1716
3-127	**Sequences**	
3-127-1	Sequence Number [ID]	127
3-127-2	Molecule Type	DNA
3-127-3	Length	1602
3-127-4-1	Features Location/Qualifiers	**source** 1..1602 mol_type= genomic DNA organism= Corydalis chelantifolia
	NonEnglishQualifier Value	
3-127-	Residues	atggattcct tgtttgttct tcttcaatgg ttctcagctt cattggctgc agttcttgct 60 ttggcttttc tttataacct atgggttaag ccaagaatta gtgatggtaa aggaaataaa 120

[0053]

5		gggagtacta aacaagcacc tgttgcagcc ggtgcgtggc ctgttctcgg tcaccttcat 180 ctctttggtg ggagtgaatt acctcacaaa atgcttgcag ccatggctga taagtatgga 240 cctgccttca caatgaagtt cggtacacat cgaacacttg tggtcagtaa cacccaaatc 300 gttaaggaat gttttactac caacgataca cacttttcca accgtccgtc caccacagct 360 tttcacctca tgacttatga caacgattcg gtagctttca caccttatgg tccattttgg 420 cgtgagttgc gtaagatctc taccctcaag cttttatcta accaccgtct tcaggcaatt 480 aaggatgtac gtgtttccga ggtgaatgtt tgcttcaagg atctatacaa tcaatggaag 540 acgaatcaaa accaacgtcc ggtcttggtg gacatgaaga aatggtttga agaagtatca 600 aacaatgtgg tgattagagt aattgtgggg aaacaaaact ttgggtctaa gattgtgcgc 660 ggtgaggagg aggctgtcaa atacaagaaa atcatggatg aaatcctacg ccttgcggca 720 gtgcctatgc tttcggatat ggcccctta cttggttggt tggatctttt ccaagctcac 780 aagagtgcaa tgaaacgcaa tgcgaaagaa gtagacaaca tgcttgaaag ctggctggag 840 gagcataaaa ggaaaagact atctggtgta aatggtgcag aggaggaaga tttcatggat 900 gttatgttgt caatcatgga agagaacaag ttcactggac gtgatagcaa tactgtagtc 960 aaatctactg tcctagccat gatcatgggt ggaaccgata ctacagccgt gagcttaact 1020 tggattttct ccttgttaat gaacaaccgt catgcactga aaaaggcaca agaagaattg 1080 gatatgcacg tcgggaaaga cagacaagtt gaagattcag acctgaaaaa cttagtttac 1140 ctcaatgcta tagtcaagga aaccatgcga atgtacccac taggtgcact tcttgaacgt 1200 gaaaccaaag aggattgtga ggtaggtgga taccacgtcc gcgcaggcac acggttgttg 1260 gtgaatgtat ggaaactaca acgagaccca agcttttgga ctgatcctac agaattcaaa 1320 ccagagagat ttttaaccga gaacgcaaag acagatgttg gtggtcaaca tttcgagcta 1380 ctaccatttg gagcaggtag aagggtatgt ccaggagtct catttgcact tcaattcatg 1440 catttggtta ttgctcgttt gattcacggt tttgaattgg gtactccaat ggatgccgat 1500 gttgacttaa ccgaaagtac tgaagggcat gtcaaccaca aagcaactcc actcgatctc 1560 ctcattgccc cacgcctcga ctcaaaagtt tatgattact aa 1602
3-128	**Sequences**	
3-128-1	Sequence Number [ID]	128
3-128-2	Molecule Type	DNA
3-128-3	Length	1593
3-128-4-1	Features Location/Qualifiers NonEnglishQualifier Value	**source** 1..1593 mol_type= genomic DNA organism= Chelidonium majus
3-128-5	Residues	atgaggagta attacttaaa gccgacgacg acgacgatcg aggataaaag taagaacaag 60 ataagcagga agaagccaat agcagcaaaa ccaccacctg aagcattggg cgcatggcca 120 gtgatcggtc actttcttct atttacaggg aaagggttga ctcatgtgac tctaggagac 180 atggcggata aatacggacc agcatttctt attcggttcg gtagccatag aacacttgtg 240 gtgagtagtt gggagatgat gaaggagtgt ttttcggccc ctaacgataa gatcttttca 300 aaccgtgaat ccaacttatt atggattaag tcaatgttct acggttccaa ttcatatggg 360 ttctcacctt atgggccata ctggaaggag ctacgcaaga tatcgaccca aaagcttctc 420 tcccaccacc gacttgatgc gatgaagcac ttgcagatgg tagaagttga tgcctcattt 480 aaacagattt acaatttatg caacaaaaat ggaggttcac catcacctag tagtattaat 540 actactgctc tggtgaacat ggacgaatgg ttgtcacacc tgatgttcaa cgtgatagca 600 agaatggtca gtggatacca atccgatgat gtcgggacag gtgctacgag tactggggaa 660 agattcaagg tttccatgga tgagacgatg cgtcttatgg ccattttcgc tgtttcagat 720 ttggttccat ggcttgcatg tgtggatcga ttaagaggcc ttacgagaaa aatgaaccgt 780 tgtggtaagg atttggactc gataattggg agactaatcg aagagcatcg tcaaaagaga 840 cgattatgca gaaataataa aggatcaaaa aatgaagatg gcggtcatga tgatgatcaa 900 gacttcattg acatttgctt gtcaattatg gagcaatctc agcttcctgg cgataaccct 960 gaaattgcca tcaaatccat tgtgctagac atgatatttg ctggaagtca caccacgact 1020 ctggcaatga cgtggaccct ctccttattg ttgaaccatc gccacatgtt gaaaaaagcc 1080 aaggaagaaa tagatgcaca cgtgggtaat gaaaggcagg tggatgactc agacatccat 1140 aatcttgtgt acattcaagc catcatcaaa gaatccatgc ggttgtaccc gcccagccca 1200 ctgttcgaac ggatgacaat ggaggattgt gaggtaggtg ggttccacat tccagctggc 1260 acacgcttat ttgtcaatgt atggaagatg caacgagacc caactgtgtg ggaggatcca 1320 ttagagtttc gacccgaaag attcttgacg agcaagagag agatagatgt gaaaggccag 1380 cattatgaac tcataccgtt tggtgcgggt aggcggatat gcccgggcgc gtcatttacc 1440 ttgcaggtgt tgcatttggt gcttgctcgc cttatccatg gcttcgaaat gacgacgccc 1500 atggatgtaa aagtggacat ggcgtcaagt gcagggctat tcagtaacaa gatgacgcct 1560 ttggaagtgc tgatcacacc acgtacagcc tag 1593
3-129	**Sequences**	

[0054]

3-129-1	Sequence Number [ID]	129
3-129-2	Molecule Type	DNA
3-129-3	Length	1674
3-129-4-1	Features Location/Qualifiers	**source** 1..1674 mol_type= genomic DNA organism= Chelidonium majus
	NonEnglishQualifier Value	
3-129-5	Residues	atgaagatat tgcaggagtt tcatcaactc accatttcca atattgttct tcttctactt 60 atttctttca tctttttctc tcttagtgca tggttcattg agagtactaa ttattattac 120 agtagtaaga agaagaagag caaaaagaca ccaccacctg aggcatcggg tgcatggcca 180 gtgataggac accttcatca atttaaaccg gacgatttac ctcatgaggc tcttggagac 240 atggcggata agtacggtcc tgtttttatt gttcgattcg gtagttatag aaaacttgtg 300 gtgagtaatt cggagatggt taaggagtgt ttcacggccg caaacgatag gtccttttcg 360 aaccgtccgg ccgtcttagg gattaggatc atgctctata acaccataac gtatgcgttc 420 gcaccttatg gaccgtactg gagggagttg cgtaggatat cgtcgcagaa tctcctctct 480 aaccatcgag ttgatatggt aaagcacttg catgtcgatg aagttaatac cttgtttaaa 540 caactttacg agttatgcaa caaaaatgga ggtcgacccc ctactggtac taatactagt 600 actagtgctg ctctagtgaa catggatgac tggttgtcaa acataatgtt caacgtgata 660 gcaagaattg tcaatggaaa caacaaatcc attaataatg agaggacagg tgccataaat 720 gagaaaagat acaaaacagc tatggatgag gcgaggcgtc ttgtggcaat ttttgcagtt 780 tcagattcag ttccatggct tggatggttg gatcgagtga gaggccttat aagaggaatg 840 aacctttgtg gaaaggaact agactcaatt attgaagata taatcgacga gcatcgtcaa 900 aagagacgat tatgcacaag taaattagga tcatcaggag atgatgatgc tgataatagt 960 aatcttgagg aagaagataa cttcattgat gcgtgcttgt cgatcgagga gcaatcgcag 1020 ttacctggcg aaaatcctga aatcgtcatc aaagctttga tcctggacat gtttgctggt 1080 ggaagtgatg gcccacattt tgtgttgacg tggaccctcg ccttattatt gaaccacccc 1140 cacgtgttga aaaaggcaag agaggaagtt gatgcacacg tggcaaacga tagacacgtg 1200 gatgtctctg atatctctaa tctcgtctac atacaagcaa tcctcaaaga gtcaatgagg 1260 ttgtacccgc ccaacgcact cattgagcga atgacaacag aagattgtga ggtaggtggg 1320 taccacattc cagctggcac atacctattg gttaacgtat ggaaggtaca aagggacccg 1380 accgtgtggc aggatccctc tgagtttcga cccgaaagat tcttattaac aaacacaaaa 1440 acggagatgg agtatgaaca tataccgttt ggtgcgggta ggcgaagatg cccaggaatg 1500 aggtttgcat tgcaggtgat gcatttggtg cttgctcgac ttattcatga attcgaaatc 1560 acgacacccg tggatgtaat aaaagtcgac atgacggcaa ctaatgggtt attcaatcac 1620 aaggccgtgc ctttggaagt gctactcaca ccacgtactc ttatccgagg ttag 1674
3-130	**Sequences**	
3-130-1	Sequence Number [ID]	130
3-130-2	Molecule Type	DNA
3-130-3	Length	1626
3-130-4-1	Features Location/Qualifiers	**source** 1..1626 mol_type= genomic DNA organism= Chelidonium majus
	NonEnglishQualifier Value	
3-130-5	Residues	atggattatt cagtccttct ccagtacggc tggtttgctc cttccatggc tgcccttctt 60 gccttagctt tcctttacaa tctctttttg gcttcatctc cgaaagctac tagcaagaga 120 acaataagta caaagaaacc gcccatggca gccggtgcat ggccaattct tggtcatctc 180 catctgttta aagagggtga gttgcctcac caaatgctta aatccatggc tgacaagtat 240 ggtcccgcct tcctcatgaa gttcggccaa caccgatccc tagttgtgag tgactaccgc 300 atcgtaaaag aatgttttac tactaatgat acccactttt gcaaccgtcc atccactaca 360 gctttcgatg tcatgactta cgctaatgaa tcggtagctt tcacagaata cagtccttac 420 tggcgcgagc ttagaaagat atccactctc aaacttctct ctaacaaccg tctccaggcc 480 atcaagaacc tccgagaaga ggaggtgaat gttagcttca aggggttgta tgattcatgg 540

[0055]

		aagaataaga acaacaagag taccggcagt gttggtgatg aacgagctcc ggttttggtc 600 gacatgaaga aatggtttga agaggtgtca aacaatgtgg tgattagggt aatcgtgggc 660 aaatgtaatt ttgggactaa gatcgtgcaa ggtgagaagg agggtgtaga gtacaagaca 720 atcatggatg agcttttacg acttgctagt ttgtctttgt tatccgattt tgcccctata 780 cttggtttgt tggatttctt ccaaggtcat gtccgtacca tgaaacgaaa tggcaagaaa 840 ctagacgtgt tacttcagag gtggttggag gagcataaga ggaagaagag cacaccagag 900 gatgagcaag acttcatgga cgttatgctg tcggttattg aggagagcaa gctttctggc 960 tatgacgctg ataccgtcat taaagctact tgtctggcca tgatcatggg tggaacagac 1020 acatccgcag tgagtctaac atggatcgtc tctttactga tgaacaatcg tcatgcacta 1080 aaaaaggctc gagaagaatt ggacgcgcag gtggggaagg atagacaagt tgaagattca 1140 gatctaaaga acttggttta cttgaatgcc atcgttaagg aaacaatgcg attatatcca 1200 ctaggtactc ttcttgaacg cgaaaccaag gaggactgtg aggttggtgg gtttcacctc 1260 gaaggtggta cacgtttact agtgaacgta tggatggtac aacgagaccc aagcgtgtgg 1320 actgatccga caaagttcac accagagagg tttcttacgg agaaggcaga catagatgtt 1380 tggggtggga attttgaact tataccattc ggagcgggta gaagggtgtg ccccggagtg 1440 tcctttgcac ttcaattcct aaatttggta ctagctcgtc tcattcatgg atatgaattg 1500 ggaactccag atgacgcgga tgtggatcta acggagagcc cagaaggaca tctcaatcac 1560 aaagcatcac ctctcgagct tctcctcacc ccacgcctca gtaaccctaa gctctatgat 1620 tattag 1626
3-131	**Sequences**	
3-131-1	Sequence Number [ID]	131
3-131-2	Molecule Type	DNA
3-131-3	Length	1614
3-131-4-1	Features Location/Qualifiers	**source** 1..1614 mol_type= genomic DNA organism= Chelidonium majus
	NonEnglishQualifier Value	
3-131-5	Residues	atggagtttc tctctctaga accccaacta atttccattt ttgttcttct tcttgcttca 60 tccatattcc tctacaatct cttgaagaat catggaagga aatccaagac ctcaaaacca 120 ccagcacctg tagcatcagg tggatggcca atcatgggtc atctccatct tttcaatgga 180 agcgagttaa ctcatcaaac tctaggttcc atggctgaca aatatggtcc agctttcaat 240 atccaactcg gttctcatca aacactcgtt gtgagtagtt gggagattgt taaagaatgt 300 ttcactacaa acgaccgatt cttttcgaat cggcctggat cgttagcgat taaactcatg 360 ttctacgacg ctgattcagt tggttacgca ccgtacggtg cttactggag agatcttaga 420 aaaatctcta cgttaaaact cctttcgaat catcgagtgg aaaccctaaa acatttgaga 480 acttctgaag ctgaatcatg ttttaaacaa ctgtataatc agtggaagaa caacaaagtt 540 ggcggcgacg acgatgaatt tgctatagtg aggatggata attggtttgg agacttgaca 600 tttaacgttg tggcgagaat tgtcgccgga aaaaagaatt ttgctggagg tgcgacgagt 660 ggcgacgtcg gagctaagag atataaggaa gctatggatg aagcgttccg gttaatgacg 720 attttcgcgt tctcagatgt ggttccgtcg ttaggatggt tggataaatt gagaggtttg 780 gttggaggga tgaagcgttg tggtgcggaa attgattcca ttgttggggg ttgggtggat 840 gaacatagat tgaagagagc ttctagaaag ggaggagatc ataatgatct cgatcttgaa 900 caagatttta tagatgtttg cttggagatt atggaacatt ctactttgcc tggtgatgat 960 cctgaaattg tcatcaaatc tacttgtctg gacatgattt tgggtgggag tgacacaaca 1020 acggtgaccc taacatgggc actctcctta ctattgaaca atcctcacgt attgaaaagg 1080 gctagggagg aattggacac acacgtcgga aaggacagac aagtagacga ctccgatatg 1140 tctaatcttg tgtacatcca agcgatcatc aaagagacga tgagattgta cccagcagga 1200 ccactgatcg agcgaaggac atcggaggat tgtgaggtca gtgggttcca tgtaccggcg 1260 ggcacacgct taatggtgaa cttatggaag atgcaacgag atgggagcgt gtataaggag 1320 gatccattgg agtttagacc agagagattc ttgactagca atgctgatgt tgacctaaag 1380 ggacagaatt atgaactgat accatttggt gcgggtagga ggatatgtcc tggtgtgtcg 1440 ttcgcagtgc agttgatgca tttggtgctt gctcgtcttg ttcatggctt tgaaatgaag 1500 acggccggag gtgcaaaggt tgacatgaca gaaagtgcag gactaattag ccacaaggtt 1560 acaccgctac aagtgctgct caaaccacgc cttgcgatcc aacaagcttt ataa 1614
3-132	**Sequences**	
3-132-1	Sequence Number [ID]	132
3-132-	Molecule Type	DNA

[0056]

2		
3-132-3	Length	1653
3-132-4-1	Features Location/Qualifiers	**source** 1..1653 mol_type= genomic DNA organism= Chelidonium majus
	NonEnglishQualifier Value	
3-132-5	Residues	atggattcga tgaacctgtt tcaacaagcg attgcagtag gtacccttgt catcttcctc 60 tactatctat ggaagtggac atcaataata ttcactcgaa ctcaccaggc ggcgccacca 120 gaacctgccg gagcatggcc tattatagga cacctccatc tcctagcagg aggagcaaac 180 caactcgtat atcacatact tggatccatg gctgacaagt acggcccaat tttcacggtc 240 cgactcggca tgcgacgagc cttaatagtg agcaactccg agttagcaaa agagtgtttc 300 accaccaacg acagaatctt ttccactcgc cctagttcag tagctataaa attgatgggc 360 tacgattcag ccatgtttgg cttcgcacca tacgggcctt actggcggga gatgcgcaag 420 atagcagtaa ctgagcttct ctctaatagg cgcctcgaga tacttaaaaa tattaggatc 480 tccgagatca acatgtctat aaaagattta tatcaactct gggttgagaa taagaacagt 540 ggtgttgatg gcggcggtga cggtggtgag gtggtggtgg gatcaccggt tttggtggag 600 atgaagaggt ggtttgaaga tgtgtcgttc aacgtggtgg ttaggatggt agctgggaaa 660 agatatttcg ggagaagggt tgaaagtgat gatcgtgaag aggaggaggc gaggaggtgg 720 cagaaggcga tgaatgattt tatgcatttg gtggggattt tcgtggtgtc ggatgccatt 780 ccatttttag ggtttttgga tttccaagga tatgagaagg agatgaagaa gacggcggtt 840 gagattgatt atgttatggg aagatgggtt gaggagcacc aacggcggaa gctggagagg 900 gtggcggggg gatctgatga tcaacaggaa gatttcatag atgtgatgtt gtcgatctta 960 aaagatggtg atcagttcta tggttatgat cctgatacgg ttattaagtc ttcatgcctg 1020 tctcttgttt taggtggtag cgacacaata tcagtaacac taacatggac ggtctcctta 1080 ctgctaaaca atcgcaatgt gttagaaaaa gctcaaagtg agttggacat ccacgtaggc 1140 aggggaagac aagtggacga atcagatatc aacaatctta aatatctcca agccatcgtc 1200 aaagaaacca tgcgtttata cccagctgga ccactatcag caccaagaga ggctatggaa 1260 gactgcacca tagctggatt ccatgtccct aaaggcacac agttgatgct caatctatgg 1320 aaattgcatc gagaccctcg cgtttggtcg gatcctttgg agttcaaacc ggagaggttt 1380 cttactactg gcacccatgg agatgttgat gttaaaggac aacatttcga attattaccg 1440 tttggagctg gtaggcggat atgcccaggg atatcttacg cccttcaagt cttgcatttg 1500 acccttgctc gtcttcttca tagttttcat ttatcaacgc catatgatat ccccgtcgat 1560 atgactgaat cttctggact ttcttgccca aaagcaactc ccttggatgt cctccttaca 1620 cctcgtctcc cttcagagct ttatgtgtct taa 1653
3-133	**Sequences**	
3-133-1	Sequence Number [ID]	133
3-133-2	Molecule Type	DNA
3-133-3	Length	1686
3-133-4-1	Features Location/Qualifiers	**source** 1..1686 mol_type= genomic DNA organism= Chelidonium majus
	NonEnglishQualifier Value	
3-133-5	Residues	atggatttgt tcatcttctt cagccggttc caatatattg taggattatt agctttcctg 60 accttcttct attatctatg gcgggtttca attacaggaa caaggatcaa aaccaaccaa 120 aacatcatga acggcaccaa tatgatggca ccggaagctg ccggtgcgtg gcccatagtt 180 ggtcatcttc ctcagctagt aggccctcag ccactcttca agattcttgg agacatggcc 240 gacaagtacg gttcgatatt catggttcgg ttcgggatgc acccaacctt ggttgtgagc 300 agttgggaaa tggcaaagga gtgcttcact accaatgaca agttccttgc tagtcgtcca 360 actagtgctg gaggcaagta cctcacctac gactttgcta tgtttggctt ctcattttat 420 ggcccctatt ggcgtgagat ccgtaagatc tccacgctcg aactactatc ccatcgtcgc 480 gttgagttgc tcaaacatgt cccttacact gagatcggcg gctctatcaa acaactttac 540 aaactttgga tggaaacaca aaaccaaaat aagcaacggg atgatcatca ggtaaaggtc 600 gacatgagcc aagtgttcgg atatctaaca ttgaatacag tgttaaagct agtggtagga 660 aagggtctat tcaacaacaa tgacatgaat catgaacagg aagaaggtcg aaagctccac 720 gagacagtac ttgaattctt caaactggca ggggtctcag ttgcatcgga tgctcttcca 780 ttccttggct ggctggatgt agatggacag aagagaagca tgaagaggat agccaaagaa 840 atggatttaa tcgctgaaag atggcttcaa gagcatcgac agaaaagact aacatcaaac 900

[0057]

		aacaaggcta gcagcggcca tgacgacttc atgagcgtgt tgctatccat ccttgacgac 960 gattccaatt tcttcaatta caatcgtgat actgtcatta aagccacctc tctgaacctg 1020 atattagcag cttcagacac tacatcagtg tccctgactt gggttctctc gttattagtc 1080 accaaccccg gtgccttgaa aaaggtccaa gatgaactgg atactaaggt gggcaggaac 1140 agacatgtcg aagaacgaga catcgagaaa ctggtctacc tccaagccac agtcaaggaa 1200 actctacgga tgtacccagc tggtccacta tcagtacccc acgaagctac ccaagactgc 1260 accgttggtg ggtatcaggt aacagcaggc acacgtttgg tggtgaacgt gtggaaattg 1320 caacgcgacc cgcgtgtgtg gccaaaccca tctgagttca agccggagag atttctacca 1380 gacgggtgtg aggttggttg tggtgaagca gcaaatatgg atttcagagg acaacatttt 1440 gaatacatac catttgggtc aggaagaagg atgtgtccag ggatcgactt tgccatacag 1500 atcatacaca tgacactggc ctgcctactc catgcattcg agttccaggt gccctcatca 1560 ctagataaac atcttgtacc tgcagtaatc gacatgagcg aaggttcagg actcaccatg 1620 cccaaagtaa ccccacttga agtcctcctt aacccacgcc tacctcttcc gctttatgag 1680 ttataa 1686
3-134	**Sequences**	
3-134-1	Sequence Number [ID]	134
3-134-2	Molecule Type	DNA
3-134-3	Length	1569
3-134-4-1	Features Location/Qualifiers	**source** 1..1569 mol_type= genomic DNA organism= Cissampelos mucronata
	NonEnglishQualifier Value	
3-134-5	Residues	atggaggcca tgggtgaata ttttcagctt atttcatgga ctgtgttttc ggctttgatc 60 accatctact ttatattcag taggaagact aatggaaaaa agaaggcacc ggaaccaggt 120 ggtgcatggc cgattattgg tcacctccat ctttttggag ctcatgacct gttgtaccga 180 aagcttgggg ccatggccga caaactcggc ccagtattca tgatccgttt tggcatgcat 240 cgagccgtcg tcgtaagtaa ctatgaagta gcaaaagaat gcttcactgt caacgataag 300 atactcgcaa gtcgcccacg gattattgct tcaaaactca tgggctacaa ccatgcggcc 360 gttggattaa gcccttatgg cccttattgg cgagaggcac gtaagatagc caccttggaa 420 cttctgtcta accatcgact ccaactactc aagcacatca ggatatcaga gattgatatg 480 tggataaaag agctaaaaga attttgtatg aaaagcagta gcgatggtcc agttcttgtt 540 caattagatg gatggttcaa tgctttgaca cttaatataa tggttaggaa tatagccggc 600 aagcgatatt gtggcggtgc tgaagccttt gaagatgaag agtcgcagcg atggaagaaa 660 gtttctagag aacttatgtt cttgttcgga gtctttatgg tacccgatgc atttcctgta 720 ctggaaggca tagatgtgca gggtttcgag cgagccatga aaagggttgg taaggaaatg 780 gatttcttct tgagtcgatg gttggaagag catagaagga agaaaataga actctccgag 840 aaaggaaacg aagttaatga tcaaggagct caagatttca tagacgtgat gctgaacaca 900 atcaaggatg ccaagatctt tgagcatgac gctgatacga tgatcaaagc cacttgtatg 960 gctctagttg tagcagggaa cgacacgaca atgatcactc tatcatgggc agtttcattg 1020 ttgctgaata atcgtggagt tttagagaaa gcccaggagg aattgagcaa ccagatagga 1080 aaaaacaggc atgttgagga aggagacatc gagagcttgc cttaccttca cgcaattgtg 1140 aaagagacct tccggctata ccctgctgca ccactttcat taccacatga agctatggaa 1200 gattgcacca ttgccggctt tcatgttcct gcaggaacac gcttgattac taatatttgg 1260 aagctgcata aagatcctaa tatttggcct gacccattgg agttcaagcc agagagattc 1320 ctcactactc atgcccatgt cgattttaaa ggtcaacact tcgaattcat ccctttcgga 1380 tcaggaagaa ggatgtgccc tggatcgtcg ctagcaatca gtgttttgca cctcaccctt 1440 gcacgtttgc tccatgaatt cgagcttaaa actccggatg atgcaccggt ggacatgacc 1500 gaaggtccgg gtatcacact catgagagca aaccccccttc acgtgctcat taatccaaga 1560 catgactga 1569
3-135	**Sequences**	
3-135-1	Sequence Number [ID]	135
3-135-2	Molecule Type	DNA
3-135-3	Length	1605

3-135-4-1	Features Location/Qualifiers	**source** 1..1605 mol_type= genomic DNA organism= Cissampelos mucronata
	NonEnglishQualifier Value	
3-135-5	Residues	atgtcctcgc ccatccaaca actactcctc tccttgacct ccattaatgg cggaaccatc 60 atctcagccg tcataatatc actccttctc atcctcaccc ttcatcgcct cctaaaaccc 120 attaattcca acaaaaccaa acaccctcca agagcatccg gggcatggcc cgtcatgggc 180 cacctccaca agctccgcgg gccggacctc ccccaccgca ccctctcatc catggccgac 240 cagtacggcc caatcttcac aatcaatctg ggccccacca ccgccctcgt catcagcgac 300 ccagccgtcg caaaagagtg cttcaccacc aacgacctca ccttctcctc tcgaccgacc 360 actctcgcca ccactctcat gtgctacaac aacaccatgt tcgggttcgc cccgtacggc 420 ccgtactggc gcgaagtccg caaggtcgtc atggcccaac tcttatcaac ccgtaggctc 480 gagtcactca aaaacatttg ggcctcggag attgaccgct gggttaaggg cctggcccaa 540 aaggcccaaa gtgggtcgca tggtgtggtt gaggtggaga tgggtgattg gctggcgagg 600 ttgactatga acattgggct aaggttggtc gtggggaaga gttgtggtga gatggggagt 660 gaggagtcgg agaggtgctt gggtgctatg cgggagtatc cggagttgct gggtcggttc 720 gcgttggagg acgcgttgcc gtggttgggt cggtttgatt tgcaagggca tcagagggag 780 atgaggaggg ctgcgagggt cttggatgag attcttgatg ggtggttgga tgagcataag 840 cgaaatagat cggggttaag tggtggtgat gatcataggg atcaggattt tatggatgtg 900 atgttgtctg ttcttgaaca agatcaagat tcgagtctta gcgaccatga tgctgatatg 960 atcaacaagt ccacttgcct gaatctaatc ttaggcatgg ctgataccac aatggtggcc 1020 ttaacatggg ccatttctct tctcctcaac aacaaaacgt ccctcaagaa ggcccaagaa 1080 gaattacaag cccaagttgg caatgaaaga cacgtggacg aatctgatgt caagaaccta 1140 gtctacctcc aatccatcat aaaagaagtg ttgaggcttt acccaccaga gccactatcg 1200 ggcccacgag aggcccttga agactgcgag gtggcaggat accatgtccc gcgaggcact 1260 cggcttatcg cgaatttgtg gaagatccat cgtgactcgt ccacgtggca ggattctatg 1320 gagtttcgac cggaaaggtt tctgacggcc cacgaacacg tggatgtgtg gggccagcac 1380 ttcgagttca tgcctttcgg gtcgggtcga aggtcgtgtc cgggagtctc gtttgaggtt 1440 cgggtgttgc cattgatact ggctcgtttg atacacgcat tcgagatgac gacacgtgga 1500 gatgtgccgg tggatatgag tgaaagaccg ggccttgtta tctcaaaagc aagcccactt 1560 gaagttatga tttctccgcg cttgcccctt cacttgtttg aataa 1605

[0058]

3-136	**Sequences**	
3-136-1	Sequence Number [ID]	136
3-136-2	Molecule Type	DNA
3-136-3	Length	1611
3-136-4-1	Features Location/Qualifiers	**source** 1..1611 mol_type= genomic DNA organism= Cissampelos mucronata
	NonEnglishQualifier Value	
3-136-5	Residues	atggagtttc atttgcttct ccaagcagtt gcagcaactc tagtgacctt cttcctttat 60 gagctatggg ctctaaggaa gaagttcagc aggcttacca aaactccctc atcaaaggct 120 ttgctcaaag caaagtgcgc accagagccg cccggtgcgt ggccgatcat cggtcacctt 180 cctttgctgg tttcagccaa gcagcctcat cgggcatttg ctgcacttgc tgagaagtat 240 ggtccagctt tcatgctccg catgggcatg agtcctatgc tgattgtgag taccaaagag 300 gttgccaaag aatgttacac cgccaatgat catgtgtttg ctactaggcc tgtcaccacc 360 gctgggaagc tcatggctta tgatcactcg gtcatgggct tcactccttt tggaacctac 420 tggagagaaa tacgaaagat cgcgacggtg gagctgttct cggctcgcag gatcgggatg 480 ttgaagccgg taagacagtc tgaggtctcg ttgtggatga agggattgca tgagaagtgg 540 gtgcataatg gaaatagctc ggtctccgtg gagctgaaga gtcaactgga agaactcact 600 ttcaatttgc ttacacaaat ggttgccgga aagcgttact acggaagtaa cgttgcaaag 660 gtggatgaga agatggcggg gctatttcgc cacgccgtcc aacaattcaa ttatcacctt 720 gggaactcgg agatgtatga tgccttgcca ttcatggcat ggttggactt caagggcgac 780 gccaaggcca tgaaaaagac acaaaaggac ttggatttta ttatgcagac ttggttggac 840 gagcaccgcc taaaagcgga tcaaatgcgc ggggacgcca tcaacaacac cagagacttc 900 ctcgacgtgc tggtgatgat ggagaagacc ggccaatttt catcggcaat taaagacaga 960 gacactacaa ttaaggcctt ggctctgacc caactagtag ccggagtgga cagcatggcc 1020 aacacaatgg tgtgggtgtt ggctctccta atgaacaacc cagaaatgct agccaaagca 1080 caagacgagc tcgacaacaa cgttggcaaa gacagactcg tggaggagtc agatatccct 1140 aatttgaagt acttacaagc cctcctaaag gagaccctcc gaatgtaccc cgtggggcct 1200 ttgttggtgc cgcacgaggc aacggaggat tgccacgtgg ccgggtattt tgttccacgt 1260 ggaactggcc tgttcatcaa cgcttggacc atacaacgtg acccaaatgt atgggctgag 1320

[0059]

		ccgaactgtt ttaatccaga gaggttctta accactcatg cagagatgga cgtgaagggt 1380 caaaatcatg agctgttgcc attcgggtcg ggtaggcgat cgtgcccagg tgtgggactg 1440 gccctccaag tgatgcacct caccttggct cgaatattac aagcgtttga gttgaagact 1500 caatcgggtg ttggaattga cttggaagag tgctccggca tactgctttc catgatgcac 1560 ccattgcaag tgatgatggc acctcgcctt ccttccgaac tctatgattg a 1611
3-137	**Sequences**	
3-137-1	Sequence Number [ID]	137
3-137-2	Molecule Type	DNA
3-137-3	Length	1575
3-137-4-1	Features Location/Qualifiers	**source** 1..1575 mol_type= genomic DNA organism= Eschscholzia californica
	NonEnglishQualifier Value	
3-137-5	Residues	atggattcct taatccttac caattggttt ccaatatcaa ttgcttctgt tttaacccta 60 gttttccttt acaaagtctt actttcctca agaactctta aagataagaa gattaagact 120 tcacccatgg caaatggtgc atggccaatt cttggtcatc tccatctctt tggttcaggt 180 gaattacctc ataaaatgct agctaccatg gctgacaagt atggctcagc cttcaggatg 240 aagttcggta aacacacaac actagttgtg agtgataccc gtatcgttaa agaatgtttc 300 actaccaacg ataccctctt ctctaaccgt ccttccacta aagcttttca actcatgact 360 tacgataatg agtcggttgc ctttacacct tacggtcctt actggcgtga gcttagaaag 420 atatccactc ttaaacttct atccaaccat cgtctccaag ccatcaagga cgttagagcc 480 tcggaggtaa acgtatgctt caaaagctta tacgatcagt gtaaaaatcc aagtggagct 540 cctattttga ttgatatgaa gaaatggttc gaagaggtgt cgaacaacgt ggtgatgagg 600 gtaattgtgg ggagacaaaa ctttgggtct aagattgtgc aaggtgagga ggaagctatc 660 cattacaaga aggtcatgga tgagctctta cgtctcgcta gcttgtctat gttctcggat 720 tttgctcctt tacttggttt cttggacatc tttcaaggga acttgagtgc catgaaacaa 780 aacgccaaga aggtagacgc aatccttgag aactggttgg aagagcatcg gaagaagaag 840 aactcagttg ctgaaagcga gcaagatttc atggatgtta tgttgtcaat tgccaacgag 900 agcaagttgt ctggtcacga tgccgatact gtcattaaag ctacttgcct agcaatgatt 960 atgggtggaa cagacactac tgctgtaagt ctaacatgga tcatttcttt attaatgaac 1020 aatcgccatg ctttgaagaa agctcgagaa gaattagatg cactagtagg aaaggacaga 1080 caagttgaag attcagattt aaagaattta gtatacatga atgctatcgt taaggaaacg 1140 atgagaatgt acccgttagg tactcttctc gaacgcgata ctaaggagga ctgtgagatc 1200 ggcgggttcc atgtcaaagg tgggacgagg ttgctagtga atgtgtggaa gttgcaacga 1260 gacccaaatg tatgggttga tccaacagaa tttagacctg aaagatttct aaccgagaat 1320 gcggatatag atgttggagg tcagcatttt gagttgctac catttggagc aggacgaagg 1380 gtgtgtcctg gggtgtcgtt tgcactacaa tttatgcatt tagtacttgc tcgtctcatc 1440 catggatacg atttgaatac tctaaacgaa gaaaatgtgg atctgacgga gagcccagaa 1500 ggacatgtga accacaaagc atcgcctctt gatctcatcc tcacccctcg tctacattac 1560 aagttgtacg aatag 1575
3-138	**Sequences**	
3-138-1	Sequence Number [ID]	138
3-138-2	Molecule Type	DNA
3-138-3	Length	1599
3-138-4-1	Features Location/Qualifiers	**source** 1..1599 mol_type= genomic DNA organism= Eschscholzia californica
	NonEnglishQualifier Value	
3-	Residues	atggatactg cttcatcaat ttcccttctc ctcccttggg cagtagtagt tccctccata 60

[0060]

138-5		gctacccttc ttgctttgct acttttcctc ttcatcactt caccaaaaac acccaagagg 120 aaaacaagtt caaaaccacc acccactgtt cttccaggtg cctggccaat tctaggtcat 180 ctccatctct ttaaagaagg agaatcacct caccacatgc ttaagaactt agctgataaa 240 tatggacctg ctttcgtcat gaaattcgga caacatcgtt ccctagttgt aagcaacact 300 aaaattgtta aagaatgttt tactactaat gacaccctct tttccaaccg tccatctact 360 actgcctttg atctcatgac ttatgctcat gactcggtag ctttcacacc ttatagtcct 420 tactggcgcg agctaagaaa gatatcgacc ctcaaacttc tatctaacaa ccgtctcaaa 480 gcaattaaga agctccgagg agaggaagtg gacgtttgtt ttcgtgggtt gtacggttta 540 tggaagaata aaactaaaaa tggtgctcca gtcttggttg acatgaaaaa atggtttgaa 600 gaggttgcaa ataatgtggt gattagagtg attgtgggga aacttagttt tgggaccaag 660 attgttgatg gtgaagaaga agccgttgaa tataaaacag tcatggatga actcttacgt 720 cttgctagtt tgtctttgtt atccgatatg gctcctatac tcggttggtt ggatttcttc 780 caaggaagtg ttcgtaaaat gaaacaaacc ggtaaaagac tagacgtttt acttgagaaa 840 tggttggggg agcaccgaga gaagaagaac ttggttgggg aagatgagca agatttcatg 900 gatgtcatgt tgtcgatcgt ggaagaaagt aagctatctg gccatgaagc tgatgccgta 960 attaaagcta catgcttggc catgattatg ggtggaacag acacaacagc agtaactctg 1020 acatggatca tctccttatt gatgaacaat cgtcacgcac tagaaaaagc tagagaagag 1080 ttggagacgc acgtcggaaa agatagacaa gtggaagata cggatttgca gaacttggtc 1140 tacttgagtg ctattgttaa ggaaacaatg cgattgtacc ctttgggtac tcttctcgaa 1200 cgagaaacta aagaagactg cgaggttgga gggttccaca tccaaggtgg aacgcgttta 1260 ttggtgaata tatggatggt acaacgagac cccaccgtat ggaatgaccc gtcggcattt 1320 aaaccagaga ggttcttaac agataaatcg gaaatagatg ttgggggtca acatttcgaa 1380 ctgataccat ttggggctgg tagaagagtg tgtcctgccg tgtcgtttgc tcttcaattc 1440 ttgcatttgg ttctcgctcg actcatccat ggatatgact tgggcactcc aagcaacgtg 1500 gaagtagact tgactgagag cctggaagga cacgttaatc ataaagcatc tcccctcgaa 1560 ctcctcctca ctccacgcct caacccgaag ctttattaa 1599
3-139	**Sequences**	
3-139-1	Sequence Number [ID]	139
3-139-2	Molecule Type	DNA
3-139-3	Length	1647
3-139-4-1	Features Location/Qualifiers NonEnglishQualifier Value	**source** 1..1647 mol_type= genomic DNA organism= Eschscholzia californica
3-139-5	Residues	atggaatctg agatccaata tcaaactgca acaatggctt ccattcttag tactaatttg 60 attctaagca gtatttttac tgcttttctt ctctatttct tactaaagat gagtccattt 120 aggtcatcaa aaaacaagtc aagaaagcaa gcaccaaaac caactggttc atggcccatt 180 ataggtcatc tccttcatct ccaaggacca aaccttcctc acataaactt agcagctttg 240 gctgataagt atggatcagt gttcagcttc cgtattggtc tccgtccagc cctcgttgtc 300 agttcttggg agatagctaa agagtgtcta actacaaatg atagagtctt cgtctctcgc 360 ccgccgttaa tagctatgaa acacatgggt tatgaccacg ccttgttcgg attctcccct 420 tatggtccat actggcgcga actccgtaaa ctagtgaacc aagaacttct ttcgaacact 480 aggattgagt tgataaaaca tgtttgggat actgaaataa atacattcat taatgacctt 540 tatgaagttt gggctatgaa aagtaatgaa ggtgggggtg atgttgtggt tgaaatgaag 600 caatgcttgt acgattttac tctcaatctc acactaaaaa tacttaccgg aaaacggtat 660 ttcggtggtg gtggcagcga agagttaaga gaagaagcag gaagatgtca aaaagcagta 720 agaaactttc ttaggttagt gggtactttt acagctcaag atgtcattcc atttttggaa 780 ggttggttag acttgggtgg tcatgagaag gagatgaaaa ttacaggaaa agaactcgac 840 tccctacttc aaaaatggtt agaagaacat aaagtaaaga aatcgtcagc tggggaagaa 900 ggccaggaga atcgaggtgg tgatgaagaa gatttcatgg gggtgatgct tacaaaactt 960 cgtgatcacg agaagctttt aagttattac gatgctgata ctatcaacaa ggctacttgc 1020 ttgactgtaa tcctaggtgg gagcgacacc acgatgatga ctctagtatg ggctctcgct 1080 ttactagtaa atcatccgca tgtaatgaag aagctccaag atgagttgga tacccacgta 1140 agtaaagaaa gacaggtgga agaatcagat atcaagaacc tcgcgtatct tcagtctgtt 1200 atgaaggaaa caatgcgtcg ttacccaggg acccctctat atgttagaga atcgatcgag 1260 gattgcacta tagctgggta cgacgtccca acaggaaccc gtcttgtagt gaatgcgtgg 1320 aagatccaac atgacccaca agtatggtct aacccattcg agttcaatcc agagagattc 1380 cttacaaccc acaaggacat agatgttaga ggtcagaatt tcgaacttat cccatttgga 1440 gcaggcagga gaatgtgccc cggggcttca ctcggtcttc aagtggtgca cctgactctg 1500 gctcgtctag tacatggatt tgagtttaaa acaccagatg gcgaacccat ggatatgacg 1560 gagagtatag gactaactaa tcttaaagcc actccacttg aaattatgct cactccgcgc 1620 ctctcttcca aactatatgt gtgttga 1647
3-	**Sequences**	

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140		
3-140-1	Sequence Number [ID]	140
3-140-2	Molecule Type	DNA
3-140-3	Length	1665
3-140-4-1	Features Location/Qualifiers	**source** 1..1665 mol_type= genomic DNA organism= Eschscholzia californica
	NonEnglishQualifier Value	
3-140-5	Residues	atgggtcttt catttgatct ttcttctcat aactttcttc aattctcgaa ccccactatt 60 ctcattggcc tctttggttt actagtttac cttttactag taaatcttcg aaaacgaata 120 tcacgaaaaa atgaggcacc cgaagtggag ggtgggtggc ctatcatagg tcatcttcat 180 catttcatgg gtgggaaaaa caagctactc catgtagcat ttggagcttg ggctgataag 240 tatggaccag tctatactct gaggatgggt ctgaataaag tactagttgt gaatagtgca 300 gaagtagcaa aagagtgttc aaccactaat gacatgcttt ttatggctcg tccatatcga 360 atagcctctg agatcatggg ttatggatat gcgatgtttc ctatcgctcc ttatggacca 420 ttctatctca aaatgcgaaa aatggtcacc caagagcttc tctcaaatag tagggttgat 480 tctctaaaac atgtgtgggg ttctgagata aaaaatgcca ttcaagaact tcacaagaaa 540 gtattatcaa ctaaaggtgg tggtccaatt tcaatggaca tgaagggatg ggtttccaat 600 ttaacgttcc gaacggctat gaaggtgatt tgtggtggtg ttggtgttga tggtggtggt 660 ggtggtggtg gtgctacttc tcctgcaact agtattggag aacataatta tgatgaagtt 720 ggaagttttc aaaaagcatt gaaagaattc tttgttttac taggagaaat taggatttct 780 gatgtgatac cattcctagg gtggttagat atgcgaacag ggtacgtgga aaagatgaag 840 gacaatggaa aatttctaga caatttaatg gaggaaatgt tggaagaaca caaaaggaag 900 agaaggtcac taactgaaga agaggaaaaa gatggaggtt atgtggagca agatttcatg 960 gacgtaatga tatcgaaact taatgatcca aagcttctgt cctattatga cgctgatact 1020 atcaacaagt ctacttgcct gactctaatt ttaagtggga gtgagacaac gatggttagt 1080 atagtttggg ccttagcgtt actagtcagt catccacacg tgttaaagaa agcgcaagat 1140 gagttggata cgcttgttgg tcgggaaaga caggtagacg aatctgatat caaagatttg 1200 gtatacctcc aagctgtagt taaggaagca ttgagactat ttccaccggc tccactttca 1260 actccacgcg ttgcaacaga ggattgtgtc gtatcaggat atcatgtacc tgcagggacc 1320 caactttttg taaatacttg gaagattcaa cgtaacccgg aagtatggcc tgaaccatca 1380 gagtttagac ctgagagatt tttcacaacc cacaaggatt tcgacgttag aggtctacat 1440 tatgacctcc acccttttcgg gtctggtaga agagcatgtc caggtgctgg cttcgccctt 1500 caagtggtgc atctaaccct agcttctcta ttacatgggt tcgagattaa aaacccatcg 1560 gatgaaccca ttgatatgac tgagagtcca ggagtaacta acttgaaagc aaccccactg 1620 aaagtcctcc tgacccctcg cctcttctct aaagaagttt attaa 1665
3-141	**Sequences**	
3-141-1	Sequence Number [ID]	141
3-141-2	Molecule Type	DNA
3-141-3	Length	1686
3-141-4-1	Features Location/Qualifiers	**source** 1..1686 mol_type= genomic DNA organism= Eschscholzia californica
	NonEnglishQualifier Value	
3-141-5	Residues	atggagaagc ccatcctcct ccagctccaa cctggtattt taggcttatt agctttgatg 60 tgcttcttat attatgtaat aaaggtttca ttatctacaa ggaactgtaa ccagttggtg 120 aggcatccgc cggaagctgc aggttcatgg cctatagttg gtcatcttcc tcaactagta 180 ggctctggta agcctctgtt tagagttctc ggagacatgg ctgacaagtt tggaccaatt 240 ttcatggtgc gatttggagt acacccaacc ttggttgtga gcagttggga gatggcaaag 300 gaatgcttca cctccaacga caagttcctg gctagtcgcc cacctagtgc tgctagcatt 360 tacatggcat acgaccacgc tatgcttggc ttctcctctt atggcccata ttggcgtgag 420

[0062]

		attcgtaaaa tatcaaccct ccacctactc tcccatcggc gccttgagtt gcttaagcac 480 gtccctcact tagagatcca caattttatc aagggattgt acggaatttg gaaagatcat 540 caaaaacagc agcagcagcc tactgcgaga gatgatcaag attcggttat gctggagatg 600 agccaattat ttgggtactt gaccttgaac atcgtattga gcttagttgt aggaaagagg 660 gtttgcaact accacgctga tggtcatctt gatgatgggg aagaagctgg ccaaggtcaa 720 aagctccatc agacgataac tgatttcttt aaactgtcag gggtttcagt ggcttcggat 780 gctcttccgt tcttaggctt gtttgatttg gatggacaaa aaaagatcat gaagcgggta 840 gccaaggaga tggactttgt tgcagaaaga tggcttcaag ataagaaatc gagtttgttg 900 ctgtctagca aaagcaacaa caaacagaat gaggcagggg aaggcgatgt ggacgatttc 960 atggacgtat taatgtccac actcccagat gatgacgatt ccttttcac gaagtatagt 1020 cgagatactg ttattaaagc caactccctc tctatggtcg tagcaggctc agacacgaca 1080 tctgtttctt tgacatgggc tctttcctta ttactcaaca acatacaagt cctaagaaag 1140 gctcaagatg agctggacac gaaagtcggt agggacaggc atgtagaaga gaaagacatc 1200 gataacttgg tctatcttca agctatcgtc aaggaaacac tccgcatgta ccctgccggt 1260 ccactttcag taccacacga agccattgaa gactgtaatg ttggcggata ccacataaaa 1320 acaggaaccc gtctgctggt gaacatatgg aagttgcagc gcgacccacg agtgtggtca 1380 aatccatctg agttcaggcc agagagattt cttgacaacc aaagtaatgg aacactgctg 1440 gatttcaggg gtcaacattt tgagtacata ccatttgggt ctgggcggag gatgtgccca 1500 ggcgtgaacc ttgcaacccc gattcttcat atgacactag cacgcttact acaatcattc 1560 gacttgacca caccctcgtc atccccagta gacatgactg aaggttcagg attgacaatg 1620 cccaaagtaa ctccacttaa agtactactc accccacgcc tccctcttcc actttatgat 1680 tattag 1686
3-142	**Sequences**	
3-142-1	Sequence Number [ID]	142
3-142-2	Molecule Type	DNA
3-142-3	Length	1698
3-142-4-1	Features Location/Qualifiers NonEnglishQualifier Value	**source** 1..1698 mol_type= genomic DNA organism= Eschscholzia californica
3-142-5	Residues	atgaatttgt ctagcaaatt gatgggttca tttgatcttt tctctcttaa ctttctccag 60 ttctcaaaac ccgccagtat ggttattatt ggcatttgta gttttctagt ttacttttca 120 ctactaaatc ttgtaaggcg agtactagca ccgtcttgta cgatgaaaaa cggaaaaact 180 gagccaccgg aggtggaaaa cgggtggcct attataggtc atcttcacca tttcatgggt 240 aaaaagaata agctaatcca tgaaatattt ggagacatgg ctgataagta tggaccgacc 300 tttactttaa ggatgggtct gactaaagtt ctagtagtga gtagtgccga agtagcgaaa 360 gagtgtttaa ctacaaacga tttggtattc attggtcgtc cacctcgtgt agccaattca 420 ctccttggtt atagttttgc catgtttcct ttttcgcctt atggcacata ctatagccaa 480 atgcgaaaaa tagtcaccca tgagcttctc tcaactagta gggttgagtc tctaaaacat 540 gtgtggaatt ctgagataaa caaagccatt caagaacttc atcacaaagt agtatcagtt 600 ggaggtggta gtcctgtttt aatagaattt aagcgttggt tttcggattt aacgttaaga 660 actactgtta agttgatctg tgggaagcag tactttggta cggatggtgc tactcaggcg 720 agtatgacta ttaatggagg aggagatgat gatgaagctg ggaagtttca agaggccttg 780 agagagttct tttgtttact aggaaaattt agggtttctg atgtgatacc atttttaggg 840 tggttagatt ttggaacagg ttataaggaa aagaaaaata gaatgttcat tgatagttta 900 atggaggaat ggttggaaga acacaaaatg aagagaagat tactaaatga agcagataaa 960 aaagaaagtc gtatagagca agatttcatg gatgtaatga tctcgaaact tgatgatcct 1020 aaccttctat cccattacga tgctgatact atcaacaagg ctacttgctt gactttgatt 1080 ttagggggaa gtgacacaac aatggttagt ttggtttggg ccttaacatt gttaatgaat 1140 catccacatg tgttgaaaaa ggtccaagat gagcttgatt tccacgtagg tcgtgagaga 1200 caggtcgaag aatctgatat gaaaaactta gtatatctcc acgctgtaat gaaagaggca 1260 atgagactaa atccagcagg tacgttatcg gctccacgta tgtcaacaaa ggactgcacc 1320 gtatccgggt accacattcc tgcaggaacc catctattca tgaatacttg gaagattcaa 1380 cgcgacccta atgcatgggt tgaaccaaca gagttcagac cagagagatt tctcactacc 1440 cataaggatt tcgatcttag agggcagaac tttgaactcc tccctttcgg gtcgggtaga 1500 agatcatgtc ttggtgctaa ctttgctctt caagtgttgc gccagactct agctcgcttg 1560 ttacatggat tcgatctcaa aactccatca gatgagcccg tcgatatgac tgggtctgct 1620 ggactaatta atatgaaagc cactccactc gaagttctag tcaccccacg cctcttctct 1680 agtgaattat atgggtaa 1698
3-143	**Sequences**	
3-	Sequence Number	143

[0063]

143-1	[ID]	
3-143-2	Molecule Type	DNA
3-143-3	Length	1853
3-143-4-1	Features Location/Qualifiers	**source** 1..1853 mol_type= genomic DNA organism= Eschscholzia californica
	NonEnglishQualifier Value	
3-143-5	Residues	atgctcataa aacctctcgg gagcaagata acatctcctc ctccctccag tgtcaaagaa 60 aaaagagaaa tccgaagggt cgtcatgagg tatataagtg ggcttaaacg atgcaaaatc 120 agcaagataa agccaattcc aagatgtaac caaaacattc tcgcatttaa tatcaccatg 180 acaaacacca agtatcttcc aatgaatttg ctcatcttct tccaattcct cctccaattc 240 caagttcttg taggattatc agttttgcta gccttctcct attacctatg ggtttcaaaa 300 aatcccaaaa tcaacaaatt taagggtaag ggtgccttat tagcacccca agctgccggg 360 gcatggccta ttgttggtca tctccctcaa ctagtaggcc ccaagccgct cttcagaatt 420 cttggagcca tggctgacaa ctatggacct atcttcatgc tccgattcgg ggttcatcca 480 actgtcgtcg tgagcagttg ggagatgaca aaggaatgtt tcactaccaa cgataggcac 540 cttgctagtc gtccatctaa tgctgcttcc cagtacctta tctacgaagt ctatgctttg 600 ttcggcttct ccttatatgg tagctcatat tggcgtgatg ctcgtaagat tgctacgctc 660 gaactactct cccatcgtag gcttgagttg ctcaagcatg taccttatac ggagatagat 720 acatgtatca aacaattgca cagactttgg acaaaaaata acaaaaacca aaacaaccct 780 gagcttaaag tcgaaatgaa ccaatttttt actgatctaa ccatgaatgt gatattgaag 840 ttggttgtag gaaagcggtt tttcaacgtt gacgatgcag cggatcatga aaaagaagaa 900 gctcgaaaaa tccaggggac aatatttgag ttttttaaac ttacggaggg ttcagtttca 960 gcaggtgctc ttccattact aaattggctg gatctaaatg gacagaagag agccatgaag 1020 agaacagcca agaagatgga ctccatagct gaaaaattgc ttgacgagca ccgacaaaaa 1080 aggctatcaa aggaaggtgt gaaaggcact catgatcata atgacttcat ggacgtatta 1140 ttgtccattc ttgatgctga tcaaggagat tattcccatc atccattcaa ctacagtcgc 1200 gaccatgtca taaaagccac cactctgtca atgatcctct cttccatgag catatctgtt 1260 agtctttcat gggcactctc tttattactc aacaaccgcc atgtcttaaa aaaggcgcaa 1320 gatgagttag acatgaacgt tggcaaggac agacaagttg aagagggaga catcaagaac 1380 ctggtctatc tccaagccat tgtcaaggaa acattccgta tgtatcctgc aaatccactt 1440 cttctacccc atgaagctat tgaagactgc aaaattggtg ggtttaacgt accagcaggc 1500 acacgtgtgg tagtcaacgc atggaaacta caacacgacc cacgcgtgtg gtcgaaccca 1560 tccgagttta agccagagag gtttctcaat gaccaagcag caaaggtagt agatgtgaga 1620 ggtcaaaatt ttgagtactt accatttggg tctggacgaa gagtgtgtcc aggaatctcc 1680 ttctccctcc aaaccattca catgtcacta gctcgcctag ttcaggcatt cgagctagga 1740 acgccctcga atgagcgcat cgatatgact gagggttccg gcttaaccat gcccaaaaca 1800 accccgcttc atgtccttct taacccacgt cttcctcttc cactctatga atg 1853
3-144	**Sequences**	
3-144-1	Sequence Number [ID]	144
3-144-2	Molecule Type	DNA
3-144-3	Length	1599
3-144-4-1	Features Location/Qualifiers	**source** 1..1599 mol_type= genomic DNA organism= Eschscholzia californica
	NonEnglishQualifier Value	
3-144-5	Residues	atggagtttc attttcctct catggaacaa ttccaaccat ttttcatttt tgcccttctt 60 ctagcctcct tcatttttct ctacaaactc ttcaattttg gaaacagaat cactaaaaat 120 gggaaaccaa cagctccgga agcatcagga ggaagactaa ttatgggtca tcttcatcta 180 ttcaatggaa ctgagttaac tcaccggaca ctcggttcta tggctgataa atacggtcca 240 gctttcaata tccgattcgg ttcacataaa acacttgtag tgagtagttg gaaaattatt 300 aaagaatgtt ttactacaaa tgaccgattc ttttcgaatc ggcctggttc tttagcaatc 360 aaactcatgt tttatgatgc cgattcagtt gggtatgcac catatggatc gtactggaga 420

[0064]

		gaacttagaa aaatttcaac cttaaaactc ctttcgaacc atcgtttaga aaccctaaaa 480 catttgagaa cttctgaagt tgattcttgt tttaatcaac taatgaattc ttgggctgaa 540 aacaaaaaca ggggagactc tgattttgct ccggtgagga tggatgattg gtttggggat 600 ttgacgttta atgttgtagc aagaattgtt gccggaaaga agaatttcgc cggaggagca 660 gcgagaggtg atgccggagc tcagagatat aaatcagcca tggatgaagc ttttagactg 720 atgacaatat ttgcttattc agatgtgatt ccatctcttg ggtggttaga taaattgaga 780 ggactagttg gagatatgaa aagatgtggg tctgaaattg attcagtagt tgagagttgg 840 gtggatgaac atagattgaa aagaagggtt tctaagaaag gaggtgaatt agatcttgaa 900 caggatttca ttgatgtttg tttggatatc atggaacatt cttctttgcc tggtgatgat 960 cctgaaattg tcatcaaatc tacttgcttg gacatgatat tgggtggaag tgacacaaca 1020 acagtaaccc tgacatgggc cctatccttg cttttgaacc atccccaagt cctgaaaaga 1080 gccaaggaag aattagatag tcaagttgga aaggaaagac aagtagaaga ctctgacatt 1140 cccaaccttc ctctcatcca agctatcatc aaagaaacaa tgagactgta tccagccggc 1200 ccattgatcg aacgacgaac tatggaagat tgcgaggttg ctgggttcca cgtaccggct 1260 ggcacacgtc tattagtgaa tctatggaag atgcagagag acaaggaagt gtggagtgaa 1320 gaacctttag agtttagacc agagagattc ctaacgagca acacagaagt tgatctcaaa 1380 ggacaacatt atgaactgat accatttgga gcaggaagaa ggatatgccc tggtgtgtcc 1440 tttgcggtgc agttgatgca tttggtgctc gcacgtcttc ttcatgggtt cgaaatgaca 1500 acaccaatgg gtgagaaggt tgatatgaca gagagtgcag gattaattag tcacaaaatc 1560 acaccacttg aagttcttat caaaccactc agggtctaa 1599
3-145	**Sequences**	
3-145-1	Sequence Number [ID]	145
3-145-2	Molecule Type	DNA
3-145-3	Length	1533
3-145-4-1	Features Location/Qualifiers NonEnglishQualifier Value	**source** 1..1533 mol_type= genomic DNA organism= Eschscholzia californica
3-145-5	Residues	atggattcct tcttgcttgc ttattgggtt ccaatttcag ttgcttctat tattgctttt 60 gttttcctct acaatctctt ttcttcaaga actcttcaaa ataagaagat taggacagca 120 cccatggcaa cgggtgcttg gccgattctc ggtcatctcc atctctttgg ttctggtgaa 180 ttgcctcata aaatgctagc tgccatggct gacaagtatg gctcagcctt caggatgaag 240 tttggtaaac acacaacact agttgtgagt gatacccgta tcgttaaaga atgtttcact 300 accaacgata ccctcttctc taaccgtcct tccactaaag cttttcaact catgacttac 360 gataatgagt cggttgcctt tacaccttac ggtycttact ggcgtgagat tagaaagata 420 tccactctta aacttctatc caaccatcgt ctccaagcca tcaaggacgt aagagcctcg 480 gaggtaaacg tctgcttcaa aaccttatac gaccagtgta agaatccaag tggatcagct 540 cctattttga tcgatatgaa gaaatggttc gaagaggtgt cgaacaacgt ggtgatgagg 600 gtaattgtgg ggagacaaaa ctttgggtct aagattgtgc aaggtgagga ggaagctatc 660 cattacaaga aggtcatgga tgagctctta cgtctcgcta gcttgtctat gttctcggat 720 tttgctcctt tacttggttt cgtggacatc tttcaaggaa acttgagtgc catgaaacga 780 aacgccaaga aggtagatgc aatcctggag aactggttgg aagagcatcg caagaagaag 840 aactcagttg ctgaaagcca gcaagatttc atggatgtta tgttgtcgat tgttgaggag 900 agcaagttgt ctggtcacga tgctgatgcc gtaattaaag ctacttgtct agccatgatc 960 atgggcggaa cagataccac agcagtgagt ctaacatgga tcatttcttt attaatgaat 1020 aatcgtcacg ctttgaagaa agctcgagaa gagttagatg cactagtagg aaaggacaga 1080 caagttgaag attcggattt gaagaattta gtttacatga atgctattgt taaggaaaca 1140 atgagaatgt acccattagg tactcttctc gaacgtgaga ctaaggagga ttgtgagatc 1200 gacgggtttc atgtcaaagg tgggactagg ttgctagtga atgtgtggaa gttgcaacga 1260 gacccaaatg tatgggttga tccaacagaa tttagacccg aaagatttct aacggagaat 1320 gcagatatag atgttggagg tcagcatttt gagttgctac catttggagc aggacgaagg 1380 gtgtgccctg gggtgtcgtt tgcactacaa cttcatgcat ttagtacttg ctcgcctcat 1440 ccatggatac gatttgaata ctctaaacga agaaaatgtg gatctgacgg agagcccaga 1500 aggacatgtg aaccacaaag catcgcctct tga 1533
3-146	**Sequences**	
3-146-1	Sequence Number [ID]	146
3-146-	Molecule Type	DNA

[0065]

2		
3-146-3	Length	1605
3-146-4-1	Features Location/Qualifiers	**source** 1..1605 mol_type= genomic DNA organism= Glaucium flavum
	NonEnglishQualifier Value	
3-146-5	Residues	atggagtttc tctctctaca acttcaacca gtttccattt ttgctcttct tgttgcctcc 60 attttcctct acaatttctt aattcacgga aaaaaatcca acaacaagaa gaccacaaaa 120 ccaccagcac cagaagcatc aggtggatgg ccaattatgg gtcatctcca tctcttcaat 180 gaaaacgagt taactcaccg aacactcggt tccatggctg acaaatacgg tccagctttc 240 aacatccgat tcggttctca tcctacactc gttgttagca gttgggacat cgttaaagaa 300 tgtttcacaa caaacgaccg attcttctcg aatcggcctg gttcgttagc gattaaactc 360 atgttctacg atgccgattc agtcggttat gctccctatg gtgcttattg gagagacttg 420 agaaaaattt caactctgaa gcttctttcg aatcatcgat tggaaaccct aaaacatttg 480 agaacttctg aagttgaatc ctgttttaaa gaactttata atcagtggag gaacaacaaa 540 actggtggtg gtggagatgg ttttgctccg gtgaggatgg ataattggtt tggtgatttg 600 acgtttaatg ttgtggcgag aattgttgcc ggaaaaaaga attttgccgg tggtgcggcg 660 agtggtgatg ccggagctca gagatataag gaagctatgg atgaagcgtt taggttgatg 720 acgatttttg cgttttctga tgtggttccc gcgttggggt ggttggataa attgagaggt 780 ttagttggag gaatgaagcg ttgtggggcg gaaattgatt ctatagttgc ggggtgggtt 840 gatgaacatc ggttgaagag aagctctggc aagggaagtg atgctgatct tgaacaggat 900 tttattgatg tttgtttgga gattatggaa cattccacat tgcctggtga tgatcctgaa 960 gttgtcatca agtctacttg cctggacatg attttgggtg ggagtgacac cacaacagtg 1020 accctaacat gggccctttc cttactattg aacaatcccc atgtgttgaa aagggctagg 1080 gaggaattgg atacaaatgt tggaaaggat agacaagtag acgactcaga tatccctaat 1140 cttgtataca tccaagcgat catcaaagag actatgagat tatacccagc tggaccactg 1200 atcgagcgga ggacatcaga ggattgtgag gtaggtgggt tccatgtacc agctggtaca 1260 cgcttattgg taaacttatg gaagatgcaa agggacggga gtgtgtataa ggaggatcct 1320 ttggagttta gcccggagag attcctgact agcaacgcag atgtagattt aaagggacag 1380 aattatgaat tgataccatt tggggcaggt aggaggatat gtccaggtgt gtcatttgca 1440 gtccaattga tgcatttggt gctggctcgc ctcattcatg gcttcgaaat gaagacgcct 1500 gaaggtggaa aggttgacat gacagaaagt gcaggactaa ttagtcacaa ggtgacgcct 1560 ttggaagttc tgctcaaacc acgtctagca atccaacatt catag 1605
3-147	**Sequences**	
3-147-1	Sequence Number [ID]	147
3-147-2	Molecule Type	DNA
3-147-3	Length	1686
3-147-4-1	Features Location/Qualifiers	**source** 1..1686 mol_type= genomic DNA organism= Glaucium flavum
	NonEnglishQualifier Value	
3-147-5	Residues	atgcatgcga aactgacctt gattaagaaa atggagttca ccatcatcaa ctctctagaa 60 atccaaccaa taatctccac tttcgctctt cttactttct ccattcttct ctacaaaatt 120 ctcttgaacc atggaagaga aaacaagaac aataaaccaa aaacatcatc atcatcatca 180 tcaataccag aagtagcagg tgcatggccg ataatgggtc atctccatct cttcaacgga 240 gacgagttaa tgcaccataa actcggttcc atggccgaaa aatatggtca agctttctat 300 atccgatttg gttctcataa agcggttgtg gttagcaatt gggagatggt taaaacatgt 360 ttcactacaa ataaccaaat cttcttaaat aggcctccca tgttagctat taacctcttg 420 tttttcccca ccgattcgct tagttacata ccgtatggtg accactggag agagttgaga 480 aaattttcaa accaaaaact tctttccaat caccgcatcg aaacccagaa aaatttgaga 540 aaattagaag ttgattactg ttttaaacag ctttgtaatc agtcttctaa gtattttata 600 attaacaaca tggacgacca agacagcaag tttgctctag tgaggatgga tacttggttt 660 gatgatgtga cattgaatgt tctggcaaga attattgccg ggaaaaagaa gtttatatcc 720 ggcggagcaa cgagtagtgg tgatgatgat aatgctgaag ctcggagata catggaagct 780 ttagatgaag gacttcgtct gatgacgagt ttcactttct ccgatgtgct tccgtggttg 840 gggtggttgg ataatttgag aggtttggct ggaaagatga agcgttgtgg tgcagaactt 900 gattcggttt ttgcggggtg ggttgaagaa catcgtgtga agagaggctc tagaaaggat 960

[0066]

		ggtgatgatg ctgatcttga acaggatttt attgatcttt gctgggagag tttggaacag 1020 gtgcctggaa atgatcctgc aaaaatcatc aagttaattt gcatggaaat gattttgaac 1080 gggagtggcg ccacggcagt gaccctaaca tggaccgtct ctttactatt gaacaacccc 1140 gacgtgttaa aaagggcaag ggaggagttg gatacacacg tcggaagtca tcgacaagtg 1200 gacgaatcag acatccctaa tcttgtttac atccaagcaa tcatcaaaga gggaatgaga 1260 ttgtatccac ctggaccatt ccttgagcga agtacaactg aagattttga gatagatggg 1320 gttcatgtac cagctgggac tcggttatgg gtgaacttat ggaagatgca ccgagacgag 1380 agcatgtatc aggaaccact cgagtttaaa ccagagaggt tcttgaatag caattcagat 1440 gtagatctaa agggacagag ttaccaattg ctaccatttg gggcaggtag gaggatatgt 1500 cctggcgtgt cgtttgcgtt gccgttgatg catctgacat tggctcgtct cattcatggc 1560 ttcgaaatga agttgcccgt aggtgttgaa aaggttgaca tgacagaaaa tggaggtata 1620 attaaccgga aggcgacaca tttggatgtg ctgctcaaac cgcgcctcat cgctcaacaa 1680 gcttaa 1686
3-148	**Sequences**	
3-148-1	Sequence Number [ID]	148
3-148-2	Molecule Type	DNA
3-148-3	Length	1611
3-148-4-1	Features Location/Qualifiers NonEnglishQualifier Value	**source** 1..1611 mol_type= genomic DNA organism= Glaucium flavum
3-148-5	Residues	atggatacac tttcaattca atggattgta ccttccatag ccacccttct tgccttagtt 60 ttcctctaca atctcatttt tacttccaaa aaaactacca agactaacaa cactaggaag 120 gcaccaatgg catccggcgc atggccggtt cttggccacc tccatttatt tggaaccggt 180 gagctacctc acaaaatgct tgcaacaatg gctgaaaact acggtaccgc cttcacaatg 240 aagttcggta accacactac actagtcgtt agcgacactc gcatcgtaaa agaatgtttc 300 actaccaacg acacccttttt cgcgaaccgt ccgtccacca aagcattcga tctcatgact 360 tatgccaatg actccgtagc cttcacacct tatagcccgt attggcgtga gcttcgaaag 420 atatcgactc ttaaacttct ctcgaaccat cgtctccaat cgattaaaga cgttcgcgtc 480 gcggaggtga acgtatgttt tagaggctta cacgttctat gcaagagtaa aatctatgga 540 gctccggttt tagttgacat gaaaaaatgg tttgaagagg tctcgaacaa tatagtcatg 600 agagtgatcg tggggaaaca aaattttggg tctaggattg tgcaaggaca agaggaggct 660 gtctattaca agagtgtcat ggacgagctt ttacgtctag ctagtgtatc cgttttatcg 720 gattttgcac cgttatttgg ttggttggat ttctttcaag gaaacataag tgctatgaaa 780 cgaaatggga agaaactaga tgtgatactt gagagatgga tggaggagca tagacaaaag 840 aagataagct catcgtcgtc gatagccgcg tccggcgccg gtgaagatga tgagcaagac 900 tttatggatg ttatgttgtc tatcattgag gagactaagt tgtccggtcg cgacgccgat 960 accgttatta aagctacttg cttggccatg atcatgggag ggactgacac tacagcggta 1020 agcctaacat ggatagtctc cttattgatg aacaatcgac atgtactgaa aaaggctcga 1080 gaagaattgg actcactagt tggaaaggat agacaagtag aagattcaga tttgaagaat 1140 tttgtataca tgaatgctat tgtcaaggaa acgatgcgat tgtatccgtt tggtgctttg 1200 ctcgaacgcg acaccaagga ggactgtgag gttggtgggt tccatgtcga agccggcacc 1260 cgtttactag taaacgtatg gaagttacaa cgagacccta atgtatggaa agatccatta 1320 gagtttcgac cagaaagatt tctggtcgag aacgtcgata tcgacgtcgg cggtcaacat 1380 ttcgaactat tgccgttcgg ggccggtaga agggtgtgcc ccggcgtgtc gttcgcactt 1440 cagttcatgc atttggtact agctcgtctc atacatggat atgaattgga aacactaaat 1500 ggtgaagatg tggatttaac tgagagcaca gaaggacatg ttaaccataa agcatcccct 1560 cttgatctcc tcatcacccc tcgcctcgac tctaaggtct acaattacta g 1611
3-149	**Sequences**	
3-149-1	Sequence Number [ID]	149
3-149-2	Molecule Type	DNA
3-149-3	Length	1599

3-149-4-1	Features Location/Qualifiers	**source** 1..1599 mol_type= genomic DNA organism= Glaucium flavum
	NonEnglishQualifier Value	
3-149-5	Residues	atggatagta cccttgttct ccaatgtttt gtaggttcca tggcagctgt ttctgccttg 60 gttttcctat acaatctcat atttagctca tcgaaaacta ccaagggtaa ggttcttagg 120 aaggcaccta tggcagccgg ggcatggcca attcttggtc acctccattt gtttgggtca 180 ggtgagctgc ctcacaaaat gttatccaag atggctgaga agtatggccc tgcgtttaca 240 ttgaagttcg gtaagcacac gacactagtt gtgagtgaca cccgcgtcgt aaaagagtgt 300 ttcactacca atgatacact tttcgctaac cggccttcga ctaccgcatt tgatctcatg 360 acttatgcca atgactctgt agccttcaca ccttatagtc cttattggcg tgagcttaga 420 aagatatcta ctctcaagct tctctctaac caccgtctcc aatcgattaa ggaaatccgt 480 gtctcggagg tgaacgtatg ttttagggag ctatttgaga tgagcaagag caaaaccgat 540 ggagctgctc cggctttggt ggatatgaag aaatggttcg aagaggtgtc gaacaatata 600 gtcatgaggg taatcgttgg aagacaaaat tttgggtcta agattgtgca aggtgatgcg 660 gaggctgtca actacaagaa tgtcatggat gagctcctac gtctcgctag tttgtctatg 720 ttatcggatt tcgctccttt acttggttgg gtggatatgt tccaaggaaa caagaacgca 780 atgaaacgaa atgccaagaa agttgacacc atactagaag gctggttgga ggagcatagg 840 aagaagaaca agaagatgag ctcatcagaa aatgatgaac aagacttcat ggatgttatg 900 ctttcgatta ttgaagagac caagttatct ggccgtgacg ctgataccgt tattaaagct 960 actgtcttgg ccatgataat gggtggaaca gacaccacgg cggttagtct aacatggatt 1020 gtctccttat tgatgaacaa tcgtcatgta ttgaagaagg ctagagagga aatagacgcc 1080 attgttggga aggatagaca agtagaagat tcagatttga agaactttgt atacatgaac 1140 gctatcgtca aggaaacgat gcgattgtat ccacttggtg ctatgctcga acgcgacacc 1200 aaggaggact gtgaggttgg tgggttccaa gtacaagccg gcacacgatt actagtaaac 1260 gtatggaagt tacaacgaga cccaaatgtt tggagtgatc catcagagtt tagaccagag 1320 agatttttat cggagaacgc tgatatagac gtcggcggtc aacatttcga attactacca 1380 tttggtgcag gtagaagggt gtgtcccagg gtgtcgttcg cgctccaatt catgcatttg 1440 gtactggctc gtcttatcca tggatatgaa ttgggaactc aaaatgatga gcttgtggac 1500 ttaactgaga gcacagaagg tcatgttaac catatggctt cccctctaga tctcatcctc 1560 accccacgcc tcagcaaccc taagctctat gattattag 1599
3-150	**Sequences**	
3-150-1	Sequence Number [ID]	150
3-150-2	Molecule Type	DNA
3-150-3	Length	1557
3-150-4-1	Features Location/Qualifiers	**source** 1..1557 mol_type= genomic DNA organism= Glaucium flavum
	NonEnglishQualifier Value	
3-150-5	Residues	atgttcttta cttcatcttc aaaaaccaca aacaaaaaca caagtaagaa accacccatg 60 gctcccggtg catggccaat actaggtcat cttcatttgt ttaaagaagg tgagttacct 120 caccacatgc ttaaatccat ggctgataaa tacggccccg ccttcctcat gaagttcggc 180 caacaccggt ccctcgtcgt cagcgactac cgcattgtta aagaatgttt cactaccaat 240 gacaccttat tttccaatag accgtctaca actgcctttg ctgtcatgac ttacgctacg 300 gactccgtcg cgttcaccga atatagtcct tattggcgtg agcttcgaaa gatatccact 360 cttaagctac tctcgaacaa ccgtctccag gcgataaaaa aactccgaga aagcgaagtg 420 aacgtctgtt tccgaggttt atatgattcg tggaggaaga ataagagtga acagaatggt 480 gctggtaata gtattgatgg tggtaacgaa cgagcacgtc cggttctcgt cgacatgaaa 540 aaatggttcg aagaggtgtc gaacaactta gtcatgaggg taattgttgg taaacgtaat 600 tttgggacta agattgttga aggggagaag gaggctgttg agtataagac cattatggat 660 gaactcttac gtcttgctag tttgtctttg ttatccgatt ttgcacctat acttcgtttg 720 tttgatcact ttcaaggaca tattcgtact atgaaacgaa atggcaagaa actagacgta 780 ctacttcaac ggtggttgga ggagcatcgg agaaagatga gcacgccgga ggaggagcaa 840 gatttcatgg atgttatgtt gtccattgtt gatgagagca agttgtctgg tcacgacgct 900 gatacggtta ttaaagctac ttgcctggcc atgataatgg gtgggacgga cacatcggcg 960 gtgagtctaa catggatagt ctccttattg atgaacaatc gtcatgcact agcaaaggct 1020 agagaagaat tggacaagca cgtaggtaaa gatagacaag tagaagaatc agatttgaag 1080 aacttggttt acttgcatgc aatcgttaaa gaaacaatgc gattatatcc attgggacct 1140 cttctcgaac gcgaaacgaa gcaggattgc gaggttggag gattcgatat cgccggaggc 1200 actcgtatac tagtaaacat atggatggta caaagagatc cggccgtctg gaacgacgcg 1260 acggagttta taccggagcg gtttctaacg gagaaatcgg atgtagatgt ttggggtggt 1320

[0067]

[0068]

		agttttgagc ttataccatt tggagccggc cggagggtgt gccccggcgt gtcgtttgct 1380 ctacaattct tacatttagt attggctcgt cttatacatg gatatgaatt gaaaacgcca 1440 aatgatatgc cggtcgactt aacggagagt actgaagggc atgttaacca taaagcatca 1500 cctttggatc ttcttctcgt ccctcgcctt agcgacctga agctctatga ttactag 1557
3-151	**Sequences**	
3-151-1	Sequence Number [ID]	151
3-151-2	Molecule Type	DNA
3-151-3	Length	1614
3-151-4-1	Features Location/Qualifiers NonEnglishQualifier Value	**source** 1..1614 mol_type= genomic DNA organism= Glaucium flavum
3-151-5	Residues	atggattcca ttcttacaac cgttgttctc ctttccatac ttctctactt tctattctca 60 tggcagctaa acaaatactc tgctactaag aagaatacca aatcatcaaa acagctacca 120 ccagaaccgg ctggttcatg gcccgtcatt ggtcatctcc atcttctcgc caaaggatca 180 aacttgcccc atataaattt gggagccatg gctgacaagt atggaccaat cttcatgatc 240 cgtatcggct taaatccaac actggtggtt agtagttggg aggtagcaag agagatattc 300 acaaccaacg accaagtttt ctcctcccgt ccaattcaag tatccacgaa acacttgggt 360 ttcgacactg ctatgtacgg tttcgcacct tatggaccat actggcgtga aatcagcaaa 420 ttagtgaagc gtgaagttct atccaacact agactagagt tcctaaagcc tgtttggggc 480 tctgagatca acacatctat caaagaattg tatgatgtgt gtgtaatgaa aaacaaagaa 540 gaaggtggta ctggtccaat tattgtggaa atgaagcaat ggttctcaga tttagcatta 600 aacatgtcgg ttaagttggt agccggtaag agatattttg gtgcttctca actaggaaat 660 gaggaagctg cgaggtggca aaaggcactg agaaactgct ttaggttggt ggggctgttt 720 gttgtgtcgg acgcaatacc atttctaagg tggttggacg tgggtggtca cgaaaaagaa 780 atgaagaata ctgctaaaga gttggacgat ttgttggagg gatggctgga agaacataaa 840 atgaaaaaga agttatcatt aagtgaagtt gaagctgaga agaaggaaag ggatcgggtt 900 gacttcatgg acgttatgct gtccacactt gaacatgaaa aggcatctga ctatttcccg 960 gctgatacta tcaacaaggc tacttgcttg gctctaatcc ttggtgggac tgatactacc 1020 acagttgttt gggtttgggc cttggctcta ctagtgaata acccgaatgt gttaaagaag 1080 gcccaagatg agttggatgt ccatgtaggt aagaaaagac aagtggatga atcagacatc 1140 aaaaacctta catatctcca agccataatc aaggaatcaa tgcgtctcta cccagcagct 1200 acattaggta taagagaatc aacagaggat tgcactgtag ctggctacca catccctgca 1260 gggactagtt tgatagtgaa ttcttggaag attcaacatg acccacaagt atggactgac 1320 ccatttgaat ttcagccgga gagatttctc acaggccaca tggacgtcga tattagaggt 1380 cagagttgca aattcctccc ttttgggtcg ggtagaaggt catgtccagg gacatcactc 1440 gctcttcaaa tggtaacctt gacacttgct cgtttgatcc atgggttcga gttcaggact 1500 ccgtcagaag cacccactga tatgacagag agcgctggac taactaatgt taaggccacc 1560 ccacttgaag ttctagtctc accgcgcctt ccttcggagc tttatgtttg ttaa 1614
3-152	**Sequences**	
3-152-1	Sequence Number [ID]	152
3-152-2	Molecule Type	DNA
3-152-3	Length	1614
3-152-4-1	Features Location/Qualifiers NonEnglishQualifier Value	**source** 1..1614 mol_type= genomic DNA organism= Glaucium flavum
3-152-	Residues	atggagttga tcaactctct tgaaatccaa ccaattacaa tatccatttt agctcttctt 60 actgtgtcca ttcttcttta caaaattatt tggaatcatg gaagcagaaa aaataataag 120

[0069]

5		agcaacaaga acaacagaaa gacatcatca tcagctggag tagtagaaat accaggtgca 180 tggccaatca tcggtcatct ccatctcttc aatggaagcg agcaaatgtt ccataaactc 240 ggttccttgg ccgaccaata tggtccggcg ccattcttta ttcgatttgg ttcgcgtaaa 300 tatgtcgttg ttagcaattg ggagctcgtt aaaacatgtt tcaccgcaca aagccaaatc 360 tttgtaagcc ggccacccat gttagccatg aacatcttgt ttttcccgaa agattcgctt 420 agttatatac agcatggtga ccattggaga gaattgagaa aaatttcaag cacgaaacta 480 ctttccagtc accgcgtcga aacccaaaaa catttgatag catcagaagt tgattactgt 540 tttaaacagc tttataaact ttccaataat ggagagttta ccttggtgag gctgaatact 600 tggtgtgagg atatggcatt gaatgttcat gttagaatga ttgccgggat gaagaattat 660 gttgctgcac ctgggagtgg tgaatatggc ggtcaagctc ggagataccg gaaagcttta 720 gaagaagctc ttgatctact gaaccagttc actatcactg acgtggtgcc atggttgggg 780 tggttggatc attttaggga tgtggttgga aggatgaagc gttgtggtgc agaacttgat 840 tcgatttttg cgacgtgggt tgaagaacat cgtgtgaaga gagcctctgg aaagggaggt 900 gatgttgaac cggattttat tgatctttgc tgggagagta tggaacaatt gcctggcaat 960 gatcctgcaa ctgtcatcaa gttaatgtgt aaggaacata ttttcaacgg gagtggcacc 1020 tcgtcactga ccctagcatg gatcctttct ttaataatga ataatcccta cgtgataaaa 1080 aaggcaaggg aggaattgga aaaacacgtc ggaaatcatc gacaagtgga agaatcagat 1140 ctccctaatc tcttatacat ccaagcgatc atcaaagagg ggatgagatt gtacacacca 1200 ggaccattca ttgatcgaaa tacaactgaa gattatgaga taaatggtgt ccatatacca 1260 gctggtactt gcttatacgt aaacttatgg aagattcacc gagacccgaa tgtgtatgaa 1320 gatccactcg agtttaaacc agagaggttc ttgaagaaca attcagattt ggatctaaag 1380 ggacagaatt accaactcct accgttcggg gcaggtagga ggatatgtcc cggtgtgtcg 1440 ttagcgttgc cgttgatgta tctgacagtg tctcgactca ttcatggctt cgatatgaag 1500 ttgcccaaag gtgttgaaaa ggctgacatg acggcacatg gaggtgtaat taaccaaagg 1560 gcgtaccctt tggaggtgct gctcaaacca cgtctcacct ttcagcaagc ttaa 1614
3-153	**Sequences**	
3-153-1	Sequence Number [ID]	153
3-153-2	Molecule Type	DNA
3-153-3	Length	1716
3-153-4-1	Features Location/Qualifiers NonEnglishQualifier Value	**source** 1..1716 mol_type= genomic DNA organism= Glaucium flavum
3-153-5	Residues	atggatttac aaatcttctt ccacttccaa ggaattgtag gctcattagc tttactatca 60 ttcttctatt atctatggag acttttaact acgacgaaga cgagtatttg taacggtaca 120 acggctgcac cacctgaagt ttccggtggt tggccgatac tgggtcatct tttgcagcta 180 gtaggatcga aacagccgtt gttcaaggtt cttggagaca tggctgataa atatggacct 240 atttttgttg tccggtttgg gatgtaccca actcttgttg tgagcagttg ggagatggca 300 aaggagtgct tcagtaccaa cgatagagtc ctagctactc gtccaactag tgctgctagc 360 aagtacctta cttacaacta tgccatgttt gctttcacat tttatgggcc ttattggcgt 420 gagattcgta agatatcaac tatagaattg ttgtcccatc gacgtgttga gatgttcaag 480 catgttccgt tcatggaaat cgatacgtgt atagaacaac tatatcttct ttggatgcag 540 aaccagaacc agaaccagaa ccaaccgaac ggagatccgg ttcaggtaaa catgagtaaa 600 gtatttgaag aactaactat gaatgcggtg ttgaagttag tcgtcggaaa acgccttacc 660 gacgacaaag aaggcgaaaa gctgcacaag accattcaag aattctttaa actgttagag 720 gtatcagttg catcggatgt ttttccattc cttgggtggc tagatgtgga tggacaaaag 780 agaaaaatga aaagggtagc taaggagatg gacataatag ctgaaaaatg gcttgaagag 840 caccgccaaa agagaagtag taagttggag gaggaggagg aggaggagga ggacgacggc 900 ggcggcaaag gagacgcggc ggcggcagat aaggatttca tggacgtgtt gttatcctta 960 ttggaaggag atgaaggtga ttctgatcaa cccttcatga actatagtcg cgatacagtc 1020 atcaaagcca cctctctgaa tatactcgtg gctgctacag acactacatc acctacctta 1080 acatgggcta tctcattact actcaacaac ccccatgtct taagagaggc ccaaaatgaa 1140 ctagacatga aggtaggaag ggatagacaa gtcgaagagc aagacattga gaacctaatc 1200 tacctccaag caatcgtcaa agagacactc cgattgtacc cagctggtcc tctctctatc 1260 ccccatgagg ctattcaaga ttgtaaactt ggcggatatc atgtaagggc aggtacacgg 1320 ttgttgctga acatatggaa gctacatcgc gacccacgcg tgtggtcgaa cccacttgaa 1380 ttcaagccag agaggttttt aattctatcg gaggaggtgt gtggttgcag tcgtggaaca 1440 caaaattttg attttaaagg ccaatgtttt gagtacatac catttgggtc gggacgaagg 1500 atgtgcccag gatacaactt tggcatacaa atcattcaca tgacactagc acgcctactt 1560 cagtcattcg agatgcagcc tgcaaaagct aaatcgctaa atgatcaaga tgggcctgtc 1620 gacatgagag aaggttctgg cctaacactt ccaaagataa ccccattaaa agttctcctt 1680 acaccacgcc tctatggtca gctttataat cattag 1716
3-	**Sequences**	

[0070]

154		
3-154-1	Sequence Number [ID]	154
3-154-2	Molecule Type	DNA
3-154-3	Length	1605
3-154-4-1	Features Location/Qualifiers	**source** 1..1605 mol_type= genomic DNA organism= Hydrastis canadensis
	NonEnglishQualifier Value	
3-154-5	Residues	atggacttct ccatgctctt ccaatggcta ttggttacta tggctaccct tcttttcttg 60 aattctgttt acaatgtttg gtataaatct tcaaaaaaca ctagtattac tactacgact 120 agtaaaggaa agaaggcacc agtagctgct ggtgcacggc cgttcatggg tcaccttcat 180 atgttagtag ggggcaagca attgcctcac caggcacttg gaaagttggc cgatatatac 240 gggccagctt tcatcattca tattggccca aacccagaac ttgttgtaag tagttgggag 300 cttgcaaagg agtgtttcac tactaatgac aagtatttcg ctaaccgtcc tactaacaaa 360 gccatgaagt acttgacata cgacgaagca tccgttggct ttggacctta tgggccactc 420 tgggttgaaa tgcgaaaaat agctaaatct aatcttctct ctcaacaaag gctccaaatg 480 cataaacgtg tccgagtctt agaaatagac gcgtttttta aagaactcca tgagctatgg 540 tcgatgaaga aagaggatgg tccagtttct gtagacatga agcaatggtt tgaagaattg 600 acacttaatg ttatcaccag aatggtttct ggtaaacata aatatgcaac taaggcaaga 660 cggggtgata gtgaggcgaa gcaattcaaa agagtaatag gtgaggcagc acattttaca 720 ggaaatcttt tgctatcaga tatatttcca tctcttgggt tcttggataa catgcaaggt 780 cgtgtgaatt ccatgaagcg aacaggcaag gaacttgact ccatccttag ttcatgggtt 840 gaagagcatc gccaaaagaa actatcagga gagcagtcag aggatgaaga gaaagacttt 900 atcgatctta cgttgtccat gatggacgaa attcagctcc actcgactga ctcagagacc 960 ttcatcaaag ctatttgcgt gggtgtgatc ctaggtggga gcgacacaac atcagtggga 1020 ataacatgga tcctttctct actaatgaat catcgcgatg ttttgaagaa ggcccaagaa 1080 gaattggatc aacaagttgg aatggacaga aaagtagagg attcagatct gaataatttg 1140 gtatatctca gggcaatcgt aaaggaatca atgcgtttgt accaagttgg gccacttatt 1200 gaacgaaagg catcacaaga ttgcaccata ggcgggttcc atgtcaaagc aggaactcgc 1260 cttttggtga acctttccaa ggtacacaaa gacccaactg tgtggtcaga tcctttggaa 1320 tttcaaccgg agagatttct tacgacgcac tcaaacatgg accttaaggg acagcatttc 1380 gaactacttc cttttgggtc aggtagacga atgtgtccag ggtacttgtt tgccctcaat 1440 gaaatgtatt tggtgcttgc tcgtctcatt caaggctttg aactgggaac tcctatggat 1500 gcaaaggttg atatgacaga aacatcaagt gttaccaact acagagcaac acccttcaa 1560 gtattgctca ccccacgcct cagtcctaag ctatacgatt attaa 1605
3-155	**Sequences**	
3-155-1	Sequence Number [ID]	155
3-155-2	Molecule Type	DNA
3-155-3	Length	1587
3-155-4-1	Features Location/Qualifiers	**source** 1..1587 mol_type= genomic DNA organism= Hydrastis canadensis
	NonEnglishQualifier Value	
3-155-5	Residues	atggcctttg ttgctcttat tgttgtttac aatatctggt ttaaatctgc agcaagcaga 60 aataagacca gctataataa caaaacaatg agcaagacac cagtagttga tggtgcgaag 120 cccatcattg gtcacctcca tttgttaatg ggaggtgacc tgcctcatca tgcgctcgga 180 agattagccg ataagtatgg gccaatcttc cttatgcaca ttggcgcatt cccagaactc 240 gttgtgagta gctcggaact cgcaaaagag tgtttcacta ccaatgataa atatattatc 300 aaccgtccta ccaataaggc catgacgtat ttgagttacg aacaagcatc tgttggtttt 360 gcaccttatg ggccactttg gattgagatg agaaagatct ctaaatccaa tcttctctct 420 aaccaaagga ttcacatgca gaagcaagta cgagtggcag aactggacgc gttctttaaa 480

[0071]

		gaactgtacc agctgtgtcg ttcaaacgat gaaaacaaca acaacagtac tagtcatggt 540 aaagttttgg tggagatgaa taaatggttt gaagaactga cactcaatgt agtgactaga 600 atgatatgtg gtaaacaaaa aatgggtact aaggcaaggc ttggggatag cgatgcgaag 660 cattacaaaa aaaccattga tgaggcagca cattttatgg gaaaccttgt gatctcagac 720 gtagttccat gtctaggaat gttggacaat ttactaggtc atgtgagcgc catgaagcgc 780 acaggcaagg aacttgacac aatctttggt tcatgggttg aagaacatca acaaaagatc 840 agactctctg gttataaaga tgatgctgaa gaggaggagc atgactttat tgatcttaca 900 ttgtccatga tgaagggatc aactgacctc catggtcttg accctgcaac tttcatcaaa 960 tctatatgtg tgggtatgat ccttggcggc acggacacga catcggtggc cttaacatgg 1020 atcctctctc tactactaaa taatcgccat attttgaaga aggcccaaga agaattggac 1080 catcaagtag gaaaagagag aaaggttgaa gattcagatc tcaacaatct ggtctttata 1140 ggagccattg tgaaagaatc aatgcgttta tacccagttg ggcctcttat tgaacgtgag 1200 gcaatagaag attgtcagat tggtggtgtc catgttaaag ccggcacgcg attactaata 1260 aacatttgga aggttcaaca agatcctaaa atttggccta atccttcaga gtttcgacca 1320 gaaaggtttc tggattctaa catggatgtt aagggccagc atttcgaact cattcctttt 1380 gggtccggta ggcgaatgtg tccaggaatg tcgttcgcca ttaatgaatt gaatttggtg 1440 cttgctcgtc ttcttcaagg cttcgagttg gaaactccaa tgaatgcaaa ggtagacatg 1500 actgaaactt caagcgttac gaattataag ggaacccctc tccaagtact tctcacccca 1560 cgtctcagtt ctaagttata tatgtaa 1587
3-156	**Sequences**	
3-156-1	Sequence Number [ID]	156
3-156-2	Molecule Type	DNA
3-156-3	Length	1596
3-156-4-1	Features Location/Qualifiers	**source** 1..1596 mol_type= genomic DNA organism= Hydrastis canadensis
	NonEnglishQualifier Value	
3-156-5	Residues	atggagtatt cccatcttct cccatggcta gcaacttcaa tagctgccat ttttgctttc 60 atttttctct tttatgtccg gaggaggaaa aacaacaaag cctttattca taatcatgcc 120 aaaaaagcac ctgtggtacc gggtgctttg ccgtttcttg gtcacctccg cctatttact 180 ggaccgattt tacctcacaa agcgcttgga gcacttgcgg ataagtacgg tccggctttc 240 actatctatc tgggaagtca tcaaacactt gtggtcagtg gtcgagagtt ggtaaaagaa 300 tgcttcacta ctaatgatag attgttctct aatagaccca gaagtaaggc tgtcaagtac 360 ttgacttatg atgaagcctc agttggtttt gcaccttatg gcccactttg ggttgagatg 420 cgaaaggttt caaaactcaa ttttctttct aatcaacgga tccagatgca gaaacaggca 480 ctagcctcag aattgaattt ttgcttcaag gatgtgtatc aattgtggtt gaaaaataag 540 gaactccccg ttatggttga tatgaccaaa tggtttgaag aaatgacgtt aaatgtgata 600 acaagattga tttgtgggaa acaaaactat ggatctaagg ctaacagtgg tgaaagtgag 660 gccaaaaggt ataaacaagt tgtagaaaag gcagcacatc ttacatcaac tgttgtgatg 720 tcagatgtgt ttccttttct tgaatggttt gataagtttc aaggacagga gaaagtcatg 780 aaaaaagtag ctaatgaatt tgattcaatc cttggttcat gggtcgacga acatcgtcga 840 aagagacttc ttcgaggcaa caatgaggag gaggaggaag agcaggactt cattgatctt 900 tccttggcca tgatggagga aactcagctt catggtgttg atcctgatac cttcatcaag 960 tcaatgtgtt tgggcatgat ccttggagga ggtgacacta cgccggtggc cctaacatgg 1020 gccctttcgc tactattgaa taacccagat attatgaaga aagcccaaga agaaatagac 1080 caagtcatag gaaaagagag aaaattagac gggtcggata taagtaatct ggtctacctc 1140 caagccgttg tgaaagaatc aatgcggtta taccaagttg ggccattgat tgaacgcgaa 1200 acaactgagg attgtaagat tggtgacttc catgttgaag caggcacgcg tttactagta 1260 aacatttgga aagtacaaca agatccatgt gtgtggtcga accctacgga gtttcaaccg 1320 gagagatttc tttctagtaa gtcagatatg gatcttaagg gtcagcattt tgaactaatt 1380 ccttttgggt caggtagacg aatgtgtcca gcagttgctt cagctctcca aatgatgcat 1440 ttggtgcttg caaaactcat tcatggcttt gaattaggaa ctcccatgaa tgcaaaaatc 1500 gacatgacag aaacttcaag tataaccaac aacatggcaa ctcatcttca agtgctactc 1560 aacccacgtt taaatgctaa tctttatgat ttttag 1596
3-157	**Sequences**	
3-157-1	Sequence Number [ID]	157
3-157-	Molecule Type	DNA

[0072]

2		
3-157-3	Length	1632
3-157-4-1	Features Location/Qualifiers	**source** 1..1632 mol_type= genomic DNA organism= Hydrastis canadensis
	NonEnglishQualifier Value	
3-157-5	Residues	atggcggatt tcaccatgct cctccaatgg ttattgctta ccatggctac ccttcttttc 60 ttgaatgctg tttacaaaag tattaaatct tcaaaaaaca ctattaatga taccagtttt 120 aaaaaaggaa agaaggcacc agtagctgct ggtgcaagac cctttattgg tcacctccat 180 atgttagtag gaggcaaaca actacctcat caagctctcg ggaagttggc cgataagtat 240 gggcctgcct tcatcatcaa tattggtcca aacccagagc ttgtcgtaag tagttgggag 300 cttgcaaagg agtgtttcac tataaacgat cggtgtttca ctgatcgtcc cagtaacaaa 360 gccatgaagt acttgaccta cgacgaagcc tctgttgggt ttgcacctta tggccctctc 420 tgggttgaaa tgcgcaagat tgctaaatcc aattgcgcat ttcaacaaag gctccaagta 480 cagaaacgtg tacgtgtctt agaaattgac ttatttttta aagagctcca cgagctatgg 540 tcccacgctg gtgctggtgc taccggtact agtgtaattc ctctttccat agacatgaag 600 aaatggttcg aggaattgac actaaacgtg atcaccagga tggtgtctgg aaaacataat 660 tatgcaacta aggcaagaaa gggtgatact gaggcgaagc gattcaaaag agtgataagt 720 gaggcagcac attttacagg aagacttctg ctctcagata tatttccatc acttgggttc 780 ttggataaca tgcaaggtcg tgtgaactcc atgaagcgaa caggcaagga acttgattcg 840 gtccttagtt cctgggtgga agaacatcgc caaaagagag tctctggaaa taaagagcag 900 tcacctgagg atgatgatgt ggaacaagat tttatcgatc tcacgttgtc catgatggag 960 gaaattcagc ttcactggac tgacgctgac accttcatca aagctatctg cgtgggtgtg 1020 atccttgggg ggagcgacac gacatccgtg ggcataacat ggattctttc tctgctaatg 1080 aatcatcccg atgttttgaa aaaggccaga gaagaattgg accaacaggt aggactggaa 1140 agaaaagtgg acgattcaga tctcaataat ctggcctatc tcagagccat tgtaaaggaa 1200 tcaatgcgtt tgtaccaagt tggcccactg attgaacgta aggcaaaaca agattgcaac 1260 ataggtgggt tccatctcaa agcaggcaca cgcctacttg tgaacctttc caaggtgcac 1320 aaagacccga ctgtgtggtc tgatcctaat gagtttcgcc ccgagagatt tttcaccacc 1380 cacaccaaca tagatatcaa ggggcagaat tttgaactca ttccttttgg gtctggcaga 1440 cgtatgtgcc cagggtactt atttgctctt agtgaaatat atttggtgct tgctcgtctc 1500 attcatggct tcgaattgag aactcccaat gatgccaagc ttgatatgac agaaacttcc 1560 agtgttacca attacagggc aacacctctc caagtactac tcactccgcg cctcagttct 1620 aagctctact ga 1632
3-158	**Sequences**	
3-158-1	Sequence Number [ID]	158
3-158-2	Molecule Type	DNA
3-158-3	Length	1599
3-158-4-1	Features Location/Qualifiers	**source** 1..1599 mol_type= genomic DNA organism= Hydrastis canadensis
	NonEnglishQualifier Value	
3-158-5	Residues	atggactact tttccatgcc ttaccaatgg ttactaactt ccttagctac tcttattgtc 60 tttgttttta tctggtctat tactgctgga aaaacaagta ctacttctaa caaagcgaaa 120 aaggcaccgc caatagcggc tggtgcatgg cccattatcg gtcacctcca tttgataatg 180 gggggtgaac tccctcatcg attgctttcg aatttagccg ataaatatgg cccaatcttc 240 atgctcaact atggttcaca acctggatta gttgtgagta gcttgaagct tgctaaggaa 300 tgttttgttc ataatgatag agctgttttt aaacgtccta atagcaaagc catgaagtat 360 ttcacttatg atcaagcttc atttggtttt gcaccttatg gaccactttg ggttgaaatg 420 agaaaagtgt ctaaatcaaa tcttctttct aaccaaaggc ttcaattaca aaggaatcaa 480 cgtgcctcag aagttgatgc ttttataaaa gagctttacc aactatgtaa gaagtccaac 540 aatggtactc ttatggtaga aatgaataaa tggtttgaag aattgacact taacgttgtg 600 actagaatgg tttgtgggaa aaaaaacatt ggggctaaag caaggcatgg tggtgataat 660 gaggcaaaat attataagaa agttatagat gaagcaacaa tatttacagc taaattggtg 720 gcttcagatt tttttccttc tcttggatgg gtagattatt tgcatggtga tgagagtgct 780 ataaagcaga cagccaaaga acttgattcc atcattggtt cctgggtgga agagcatcgt 840 caaaagagac tactctcgct caataaagac gactacgcag agcaggattt tatcgatatt 900

[0073]

		acgttgtcca tgatcgacca aactcagcac cagggtattg atgctgatac cttcgtcaag 960 tctatgtgtg tgggtatgat ctttggtggg agtgacagca catcggtggc cctaaattgg 1020 gctctttcaa tactaatgaa taatcgacat gttttaaaga gggcccgaga agaaatcgac 1080 acacttgtag ggaaggacag aaaagtgaac gatgtggatg ttactaaatt ggtttatctc 1140 aaagccattg taaaagaatc aatgcgttta tgcctagttg gaccgcttct tgaacgtgtg 1200 accgtagaag attgcgagat aggtggtttt tatgtcaaag caggctcgcg catagtggta 1260 aacatatgga agttgcaaca tgacccagac ctgtggtctg atgatgttat ggaatttcga 1320 ccagagagat ttctcacaac caactcaaat gtggaactta ggggtcaaca ttttgaactc 1380 attccttttg ggtctggtag tcgaatgtgc ccaggtgtaa cattcgcact cgaactcatg 1440 cacttgacac ttgctcgtct cattcatgga tttgaacttg gtacccctat ggatgcaaag 1500 gttgacatga cagaaacttc aagtgttacc aattacaagg ccacacccct tgaaatcctt 1560 ctcaccccac gccttcatcc taagctttat gatttttag 1599
3-159	**Sequences**	
3-159-1	Sequence Number [ID]	159
3-159-2	Molecule Type	DNA
3-159-3	Length	1605
3-159-4-1	Features Location/Qualifiers NonEnglishQualifier Value	**source** 1..1605 mol_type= genomic DNA organism= Hydrastis canadensis
3-159-5	Residues	atgtttatat cgatcactca acaatccatg gattcatttc accaatatct agcaactata 60 atttttggtg tcttttcctt tgtattattc ttgatctatt atctaccatt gaagagaagt 120 agaagtgata aaaagagagc tgctcccaaa ccggtcgggg catggcctat cataggtcac 180 ttgcctatgt tatcccggca ccaaccaccg cacataacgt tgggaaatat tgctgataag 240 tacggaccag ctttcactct tcagcttggc gtgcatcgag cattggtggt gagtagttca 300 gaggttgcca aggagtgttt cactaccaat gacaaggcct tagcttcccg cccaagctct 360 gtggctttaa agctaatggg ttataacaat gctatgtttg gcttcggccc ttatggttca 420 tattggcgac aaatgcgcaa aatagttgta cttgagcttc tctcaaacca tcggctccaa 480 ttgctaaaac acgttcgtat atctgaggtt agcacatctt taaaagaatt gtaccaggtt 540 tgggcatcat gtactaataa gaacgacaaa ggacaagttt tggtggatat gcagcaatgg 600 tttggtgact tgacactaaa cgtctccgtt aggatgattg ctgggaagcg atactttggt 660 gccagtgcag catgcgacga agatgaagcg aggaggtttc agaaggcgat taaagatttc 720 ctccatttag taggcttgtt tgtggtgtca gacgcgcttc cctttctaga atggctagat 780 attcagggtc atcagaaagc catgaagaga actttcaaag aattagatag aatacttggg 840 aaatgggtgg aagaacatcg acgaaataaa ttagacggtg gaacgaatgt gggacgagac 900 ttcatggatg tgatgtcttc gatacttgac gatgcaaata tctctgatta tgatgctgat 960 accattaaca aggctacttg cctgagtctg atcttgggtg ggactgacac cacaatggtc 1020 actctaacat gggctttatc cttattaatg aacaatcaac acatattgaa gaaggcccaa 1080 gatgaaattg acatctatgt tgggaaagat aaaaacgttg atgaatcaga tatagagaaa 1140 ctggtgtacc tccaagccat tgttaaggaa acattgcgtt tgtacccagc cggtccacta 1200 tctgggccac atgaggccat agaggactgc actgtagctg gttatcatgt accaagaggc 1260 acacgcttga taacaaatct ctggaagatt caacgagatc cacggatatg gtcgagccct 1320 tgtgagttcc aaccagagag atttctcacc actcaagcaa atgtggatgt taggggccag 1380 cattttgagt ttcttccatt cgggtctgga agacgttcgt gccctgcgac ctcatttgca 1440 cttcaagttg tgcacttagc attagcacgt gtattacaag gcttcgagtt tgaaactcaa 1500 tcaaatgcac ctgtggatat gaccgagagc gcgggactta caaatgtcaa agccaccccg 1560 cttgaagttc taatcacccc gcgcctccct ttgaatctat attaa 1605
3-160	**Sequences**	
3-160-1	Sequence Number [ID]	160
3-160-2	Molecule Type	DNA
3-160-3	Length	1590
3-	Features	**source** 1..1590

[0074]

160-4-1	Location/Qualifiers	mol_type= genomic DNA organism= Hydrastis canadensis
	NonEnglishQualifier Value	
3-160-5	Residues	atggagtcgc ttcaccaata tctagcagca gtcatgagtt gtatctttgc cttgttactc 60 ttcctctatt atttcccatg gaagatcaga agaagtagct ctgataataa catgagaagt 120 gcacctgaag cagctggtgc atggcctatc ataggtcact tgcccatgct gggagggcac 180 caactacccc acataacgtt gggaaacttg gccgataggt acggaccagc cttcactatc 240 cggcttggtg tatgccgggc actggtggta agtagttcag aggtcgcaaa ggagtgtttc 300 actaccaatg acaaggcctt tgccacccgc ccaagctctg tggccgtaaa gctaatgggc 360 tataactatg cactctttgg cttagcccct tatacttctt attggcgtga agtgcgcaaa 420 atagtaatac tggagcttct ctccaatcgt cggctagagt tgctaaaaca tgttcggatc 480 tctgaggtca acacatctat aaaagaattg ttccaagttt gggcatcatc aaataataag 540 aatgagaaag gacaagtttt ggtagagatg cagcgatggt ttggtgactt gacaataaac 600 gtagctgtta ggatggttgc tgggaaacga tacttcggtg ctagtgttaa tacgtgcgat 660 gatgaggagg aggcgaggag gtttcaaaag gcgattaaaa atttctttca tcttgtaggg 720 ttgtatgtgt tatcggattc tcttccattt ttggagtggt tggactttga gggtcatcaa 780 aaggctatga aaagaacttt caaagatgtg gactgtatac ttcaaagatg gttggaagaa 840 catcgacgag ataaagagaa tggtgcaatg aaggaggagc gagacttcat ggatgtgatg 900 ttgtcgatcc ttaaagatgc aaatctcttt ggttacgaag ctgatactgt taacaaggcc 960 actagtctga atataatatt gggtgcaaca gacactacaa tggttactct aacatgggcc 1020 ctatcgttat tattgaacaa tcgacacata ttaaagaagg ctgaagatga aattgacatc 1080 catgttggga aagataaagc tgttgatgaa tcagatatag agaaactagt atatctccaa 1140 gccattgtta aggaaacatt acgtctgtac ccagttgctc cactgttagc agcacatgaa 1200 gccatagaag actgcattgt agctggttat catgtaccaa gaggcacacg cttgatacca 1260 aatatttgga agattcaacg agatccacgc atatggtcta gtccttgtga tttccaacca 1320 gagagattcc tcacaaccca agcaaatgtg gacgttaggg gtcagcattt cgagttgttt 1380 ccttttgggt ctgggagaag aatgtgccca gggatctcat ttgggcttca agtagtgcac 1440 ttggcactag cgcgtgtatt acaaggcttc gagtttgata ctccatcaaa taaagctata 1500 gatatgactg aaagcgcagg acttaccaac ctcaaggcca cccctcttca agttctaatc 1560 accccgtgcc tccctttgaa tctgtattaa 1590
3-161	**Sequences**	
3-161-1	Sequence Number [ID]	161
3-161-2	Molecule Type	DNA
3-161-3	Length	1593
3-161-4-1	Features Location/Qualifiers	**source** 1..1593 mol_type= genomic DNA organism= Hydrastis canadensis
	NonEnglishQualifier Value	
3-161-5	Residues	atggattcaa ttttactacc aactccatta atggtcagtc tctttgcctt actattatgt 60 ctttactatt taatcatatc gaggccaagg tctagtcata atactagtac taaggaggca 120 cccgaagccg ctggagcatt gcctattatc gggcacctcc atttgttagg tgggcgaata 180 ttgcctcaca taacattagg agccatggct gataaacatg gaccagcctt catgattcgc 240 attggtgtac atagagcatt ggtggtaagt tcttcagaag ttgcaaagga gtgtttcaca 300 accaatgaca aggctttcgc ttctcgtcct aagcatacag cagcggaact catgggttat 360 aattatgcca tgtttggatt tgcaccttac ggtccttttt ggagcgaaat gcgcaagata 420 atcatggctg aactcctctc caatcgtcgg cttgagttgc ttaaatacat ccgggatttc 480 gaattaaaag catctatcaa agaactatac atgacatggg agaaccacag tgttactaat 540 aaaggtcagg tagtagtaga aatgaagaaa tggtttggag acttaactct aaatgtgatt 600 ctaaggatga ttgctgggaa aagatacttt ggttcaaatt ctacttgtga tgaaagtgaa 660 gcaaagatat gtcaaaaggg tatgagagat ttctttaggt tattgggaga gttccttgtt 720 gaggatgcaa ttccttattt ggggtggttg gacttgcaag gttttaaaaa agagatgaag 780 aatacagcta aagaacttga tattcttctt caaggatggt tggaagagca caaaaaaaag 840 agggagttct ctaaggatgt taaggaagag caagacttca tggacgtgat gatgaccata 900 cttgaagatg caaacttctc tgattttgat gctgatacta tcaataaggc tacgtgtttg 960 actataatct caggaggaag cgacactaca atgcttactc taacatgggc cctatcctta 1020 ctactgaaca atcaacatgt gttgaagaag gcccaagatg agttggacac ccacgtcggt 1080 agggatagac gcgtggacga atcagacatc aagaacctcg tctaccttaa cgccatagtg 1140 aaggaaacat tgcgcttata cccagctagt ccactactgg gtattcgggt gtccacagaa 1200 gactgcactg tagctgggta ccatgtccca tcagggaccc gtttaatggt aaatgcttgg 1260 aagattcaac gagacccgtt agtgtggtcc gacccatttg aatttcgccc agaaagattt 1320 ctcacaaccc atgtaaatgt ggatgttaag ggtcaaaatt ttaatttaat cccatttgca 1380

[0075]

		tcaggtagac gtgtgtgccc aggagttgca tttgcccttc aaatgctgcc actagttcta 1440 gctcatttgc tacatgggtt caaactcatg actcagttgg gtggacctgt cgatatgact 1500 gaatccactg ggttaactaa tatcaaagca actccattgg aagtagttat cagcccacgt 1560 cttcgtccag aactgtatga aatgtacaca tag 1593
3-162	**Sequences**	
3-162-1	Sequence Number [ID]	162
3-162-2	Molecule Type	DNA
3-162-3	Length	1578
3-162-4-1	Features Location/Qualifiers NonEnglishQualifier Value	**source** 1..1578 mol_type= genomic DNA organism= Hydrastis canadensis
3-162-5	Residues	atggagtcgc ttcaccaata tctagcaaca attttgagtt gtatctttgc ctttttactc 60 ttcctctatt atttcccatg gaagggaaga agaagctttg ataataactt aagaactgca 120 cctgaagcag ctggcgcatg gcctatcata ggccacttgc ctatgttaaa ccaacgtgat 180 ttaccccacg taacgttggg aaacttggcg gataggtacg ggccagcctt cactatccgg 240 cttggtgtac gccgagcact ggtggtgagt agttcagagg tcgcaaagga gtgtttcact 300 accaatgaca aggcctttgc cacccgccca agctctgtgg ctgtaaagct aatggcctat 360 aactatgcag tctttggctt tggcccttat ggttcttatt ggcgtgaaat gcgcaaaata 420 gtaatacttg agcttctctc taatcgtcgg ctagagttgc taaaacatgt tcggatctct 480 gaggtcaaca catctataaa agaattgtac caagtttggg catcaaataa taagaatgag 540 aaaggacaag ttttggtgga gatgcaacga tggtttggtg acttgacaat gaacgtagtt 600 gttaggatgg ttgctgggaa acgatacttc ggtgctagtg ttacgtgcga tgaggaggaa 660 gcgagaaggt ttcaaaaggc gattagagat tttagtcatc ttgctggttt gtatgtgttg 720 tcggatgctc ttccaaatat agagtggttg gactttgagg gtcatcacaa ggccatgaaa 780 aaaactttca aagatttgga ctgtatactt cagagatggt tggaagaaca tcgacgagat 840 agagagaatg gtgcaacgaa gggagagcga gacttcatgg atgtgatgtt gtcgattctt 900 aaagatgcaa atccttttga tttcgaggct gataccgtta acaaggctac tagcctgaat 960 atggttttgg gcggaacaga gactacaact gttactctaa catgggccct atcgttacta 1020 ttaaacaacc aacacatatt gaagaaggcg caagatgaaa ttaacatccg tgttgggaaa 1080 gacaaacctg ttgatgaatc agatatagag aaattggtgt acctccaagc cattgtcaag 1140 gaaacattgc ggttgtaccc tgtccttcca ttatccgtac cccacgaggc catagaagac 1200 tgcaccattg ctggttatca tgtaccaaga ggcacacgct tgataacaaa tctatggaag 1260 attcaacgag atccacacat atggtctagt ccttgtgagt tccaaccaga gagattcctc 1320 acaacccaag caaatgtgga cgttaggggt cagcatttcg agttgtttcc ttttgggtct 1380 gggagaagaa tgtgcccagg gatctcattt gggcttcaag tagtgcactt ggcactagcg 1440 cgtgtattac aaggcttcga gtttgaaact ccatcaaatg tacctatgga tatgactgaa 1500 agcgcaggac ttacgaattt caaaacaacc cctcttgaag ttctaatcac cccatgcctc 1560 cctttggacc aatattaa 1578
3-163	**Sequences**	
3-163-1	Sequence Number [ID]	163
3-163-2	Molecule Type	DNA
3-163-3	Length	1578
3-163-4-1	Features Location/Qualifiers NonEnglishQualifier Value	**source** 1..1578 mol_type= genomic DNA organism= Hydrastis canadensis
3-163-	Residues	atggattctc ttctccagtt acaaataatt ggagcacttg ctgccttaat attcacttac 60 aaactattga aagtgatatg tagaagtccc atgactgatg gcatggaagc cccggaacct 120

[0076]

5		ccgggagctt ggccgattat cggacacctc catctgctcg gtggccaaga cccaatagcc 180 cgtacacttg gagtcatgac tgataaatat gggccaattt taaaactccg gcttggtgta 240 catactgggc ttgttgttag taattgggaa ctggcaaagg agtgtttcac tacaaatgac 300 agagttttag cttcacgtcc tatgggtgca gcaggaaagt acttgggcta taattatgcg 360 atatttgggc tcgcgccgca tggaccatat tggagtgaag tacgtaagat agtattacgt 420 gaacttctct ctaatcagag tttagagaag cttaaacatg ttcgaatctc cgagattaat 480 acatgcttaa agaatttatt ttcattgaac aatgggaata ctccaataaa agttgacatg 540 aagcaatggt ttgaacgccc aatgttcaat gtggtcacta tgatgattgc agggaaacga 600 tattttagta tggagaatga caatgaggca atgaatttca ggaaagttgc cactgaattt 660 atgtacttaa ctggggtgtt tgtagtgtcg gatgcccttc catatctgga gtggttggat 720 ttgcaaggac atgtgagcgc catgaaacgc acggccaagg aattggacat ccatgttggg 780 aagtggcttg aggagcatcg tcgtgctaag cttctgggtg aaactaaaaa tgaagatgat 840 tttgttgatg tgctgctaac catcttgcca gaggacttga aggataatca aacgtatata 900 catgaccgcg ataccatcat caaggcaact gcactggctc tttttttagc tgcctcagat 960 actacagcta tcaccttgac atgggctcta tcgttgatac tcaacaatcc ggacgtcttg 1020 aaaagagcac aagatgagtt ggacaaacac gtcggtaaag aaaaactcgt caaagaatca 1080 gacatcataa atctagtgta cctccaagct atcatcaagg aaaccttacg cctgtatcca 1140 gctgcacccc tcttattgcc acatgaagcc atggaagatt gtacggtagg tggctatcat 1200 gttccaaaag ggactcgaat ttttgttaac atatggaagt tgcagcgtga tccgcgtgta 1260 tggtttgatc ctaacgagtt tcgaccagaa cgattcttaa ccactcatgc aaatgttgat 1320 tttaagggac agcattttga gtacatacct ttcagctctg gtagaagggt atgcccaggg 1380 atcacattta gtacccaaat catgcactta acacttgccc atctacttca tgaattcaac 1440 atagtgaccc ctacgaaatc aaatgcaggg gttgacatga ctgagagctt aggcatcaca 1500 atgcctaaag caactccact agaagtactt ctcactccac gtcttccatc taatctgtac 1560 aatcaataca gagactaa 1578
3-164	**Sequences**	
3-164-1	Sequence Number [ID]	164
3-164-2	Molecule Type	DNA
3-164-3	Length	1566
3-164-4-1	Features Location/Qualifiers NonEnglishQualifier Value	**source** 1..1566 mol_type= genomic DNA organism= Jeffersonia diphylla
3-164-5	Residues	atggattcac ttcaactcat agctagtgtt gtgtgtggat tgtttgcctt ccttcgtatc 60 tactacttac taaagaagtt gtctagtaac aaggaggcac cccaactcgg tggagcatgg 120 ccgattatcg gccacttaca tctattaggc cgagttgagc tcccccacat atttttagt 180 gccatggcag acaagtacgg tccagccttc atgattcagc ttggtatgcg acgagcacta 240 gtagtgagca gtgcggagat tgccaaagaa tgtttaacta caaatgataa ggccttagcc 300 actcgtccaa gttcaatagc agctgagatt atgggttatg actatgctat gttcgggtta 360 ggtccatacg gggactattg gcgtgaagtg cgcaaaatag tggtcttgga gtttctctct 420 aatcgtcggc ttgagttgct aaaacatgtt agggtgtctg aaatatccct gtctctgaaa 480 gagttgtacc aatcctggga aaaacaaaac aaagctgatg aaccagtttt agttcatctg 540 gaccaatggt ttggcgatat gacgctcaat ctttcagtta gaatggttgc tgggaaaagg 600 tactttggtg caactgctgc ttgtggtgaa gatgagtcta ggaaagttca aaaggcaaca 660 agggaattcg ataggctttt gggtctgttt gtagtgtcgg attatcttcc ttttctgcgg 720 tggctggact tggaaggtca ccagaagttg atgaagagca taggtagaga acttgattct 780 attctgcagg gatggttgga tgagcataaa actaggagga actctggtgg aggagctaag 840 ggagatcagg atttcataga cgtaatgctt tccgtccttg aagatggaaa cctttccaat 900 tacgatgctg ataagctcaa caaggctaca tcacttacga tgattgtagc tggaagcgaa 960 actacaatgg tcactctaac gtgggctgtc tgcttgttgc taaacaatcc ggaagtgtta 1020 aacaaagctc aagatgagtt ggacatgcac attggcaagg acagacaagt ggaagaatca 1080 gacatcaaga acctggcata cctccaagct gttatcaaag aaacgatgcg tttgtaccca 1140 gttgctccac tattaattcc ccatgaagcc atggaagact gcaccatagc tgggtatcat 1200 gttcgagcag gcacacgagt tatactaaat ggttggaagc ttcaacgaga cccatttatt 1260 tggtctgacc cttgtgagtt ccaacctgaa agatttctca acaacgatgt ggatgtgaga 1320 ggtcggcatt ttgagttatt gccatttggg tcaggtagac gtgcatgccc tgggatttca 1380 ttggccctta atgtggtgtc tttgacattg gctcgtttgt tacatgagtt caagttttcg 1440 aatccttcag aaggcaaggt tgatatgtct gagagtgcag gggtggttgt tgccaaggca 1500 acacctctgg aagtacttat cattccacgc ctaccttcaa agttttacga gtactataag 1560 ctatag 1566
3-165	**Sequences**	

[0077]

3-165-1	Sequence Number [ID]	165
3-165-2	Molecule Type	DNA
3-165-3	Length	1557
3-165-4-1	Features Location/Qualifiers	**source** 1..1557 mol_type= genomic DNA organism= Jeffersonia diphylla
	NonEnglishQualifier Value	
3-165-5	Residues	atgttttctc ttcagttgct atcaactcca ttgtttggct tctttaccct gctggccatt 60 tactatctct tatggactaa gagtaacaaa accaaggaag cacctcaacc tgctggagca 120 tggccaataa tcggccacct ccatctacta gccaggagtg aactccccca tataactttg 180 ggagccatgg ccgataagta cggtccagct ttcatgatcc gccttggtac acgccaagca 240 attgtagtga gtaattcaga gattgcaaag gagtgcttga ccatcaaaga taggatcttc 300 gctactcgtc caagcttagt agcatttaag ctcatgggct acaactctgc catggtcggg 360 ttaagccctt atggacctta ttggcgggag ttgcgtaaga taatcgcgtt aaaagtcctc 420 tcacaacgta ggctggagtc tctaaaggat gtgtgggact cagaaatatc ctcatcctta 480 aaccacttgc accaaatatg gtcacaccaa accgaaccca atggaaagat tttagttgaa 540 atggatcaat ggtttggtga tctaacacta aatgtggcag ttaagatggt tgcagggaag 600 agattcttta gtgctgatgc tgcttgtgat gaaaatgagt ctagaaggtg tcaaaaggca 660 ataagagagt tctttaggct tttgggtcaa tttgtagtat cagattctct tccatttcta 720 gggtggttgg acttggaagg ttatcagaaa gagatgaaga gtacagccaa ggaagttgat 780 tcaatacttc agaaatggtt ggatgaacat aaacagaaaa gacaatctgc aggagctgat 840 agagatcagg atttcatgga cgtgatgctt tctctcctag aagatgcaag cctctcccaa 900 tatgacactg ataccatcaa caaggctacc tgcttttcaa tgatcgtagg tggaagtgat 960 actacgaaga tcacactgac atgggctctc accttactac taaataatcc agatgtaatg 1020 aaaaagagcc aagacgagtt ggatatccag gttggaaaag ataggcatgt cgaagaatca 1080 gatatcaaga atctagtata cctggaagct atagtgaagg aaactttgcg tttgtatcca 1140 gctgctccac tattagctcc ccacgaggcc acagaagatt gtattgtagc tgggtataat 1200 gttcgcgcag gcacacgctt aatagtgaac gcttggaaga ttcaacgaga ccccttgatt 1260 tggccgaacc cttctgagtt tctaccagag agatatctta acaaagatgt cgacgttaaa 1320 ggacaacatt ttgaattaat cccatttggg tcaggtagac gtgcttgccc tggaatcaca 1380 tttggacttc aagtggtatc cttgaccttg gctcgtctcc tccatgagtt tgagatttcc 1440 attgcatcag gaattaaagt ggatatgacg gagagcggag gtctagttac tgccaaggcc 1500 acccctttga aagcacttat cgccccacgc tttctttatt ctcatcatca catttag 1557
3-166	**Sequences**	
3-166-1	Sequence Number [ID]	166
3-166-2	Molecule Type	DNA
3-166-3	Length	1578
3-166-4-1	Features Location/Qualifiers	**source** 1..1578 mol_type= genomic DNA organism= Mahonia aquifolium
	NonEnglishQualifier Value	
3-166-5	Residues	atgaattcac ttcagttcct agcaactcca ttgcttactc tcattgcatt actatgtgtt 60 tactgcatag tatggagaaa atcattctct agaaacggaa gcaaaataaa gcaggcgccc 120 tgggcaggtg gagcatggcc gatcatgggt cacctgcatc tactagcctg gggtgacctc 180 ccgcatataa cgttgggagc cttggccgat aagtacggcc cagtcttcat gatgcagctt 240 ggcatgcgcc aagcaatagt tgtaagcagt gcagagattg caagagagtg tttcaccact 300 aatgatagga tcttagcaac tcgcccaagc tctatagcag ttaagctcat ggcctacaac 360 tacgccatgt ttgcatttgc cccgtatggg cctaattggc gtgaaatacg caagacagtc 420 atgcttgagc tcctctccac ccctcgcctc gagtcactca agcatgtctg ggaggatgaa 480 atatccacga gtgtcaaaga gttgtatgaa ttatgtgcca gcaaaaccaa aacccatggc 540 catgtttcag tagacatgaa gcaacggttt ggtgatctga cactcaatgt gttagtgaag 600 ttggttaatg ggaagagata ctttggtgca aatactgatt atactgaaca tgaatcaagg 660

[0078]

		aggtgccaga aggcagtgag ggatttttc agtcttatgg ggttgtttgt ggtatcagat 720 tttcttccat ttcttgagcg gttggacttg cagggttatg agaaagagat gaaaagggta 780 gctagagaag ttgatggtat agttcaaggg tggttggacg agcataaaag gaagcgagag 840 tccagtgaaa ccacccacga tcaggacttc atggacgtga tgctttcgat acttaaagac 900 tcaaaattct ctaactctga ttatgatgcc gataccatca acaaggctac atgttttaac 960 atgatcttag gtggaagtga cacaacaatg agcacaatga cctgggcttt atcggcactg 1020 ctaaataatc cacatatgtt gaagaaggcc caagatgagt tggaattcca tgtcggaaag 1080 ggtagacagg tggaggaatc ggacatcaag aagctaacat acctacaagc tataatcaaa 1140 gaaactttgc gtttataccc gtcggctccc ctgttagctc cacgtgaagc cacagaagac 1200 tgcaaaatag cggggtatca tgttccagca ggcacacgcc taatcgtgaa tgtctggaag 1260 attcatagag acccatttgt ttggcccaac cctaacgagt tccaacctga aagattccta 1320 aataaagatg tggatgttaa gggtcagcat ttcgaattga tcccatttgg gtcagggaga 1380 cgtgcttgcc ctggggtatc attaggactt caagtggtgt cactgggctt ggcgcgcctc 1440 ctacacggat ttgagctttc gatcccatct ggaagcaagg tagacatgac tgaaactgca 1500 agtctagtta ctttcaaggc aacgcctctg gaagtattta tcactccacg cctatctcca 1560 catatgtatg tggagtag 1578
3-167	**Sequences**	
3-167-1	Sequence Number [ID]	167
3-167-2	Molecule Type	DNA
3-167-3	Length	1511
3-167-4-1	Features Location/Qualifiers	**source** 1..1511 mol_type= genomic DNA organism= Mahonia aquifolium
	NonEnglishQualifier Value	
3-167-5	Residues	cttatgcatg gaagaggaaa aaccatacaa aggatagcaa aatcaaagag ccaccccaac 60 cagccggagc atggccgata atcggccacc ttcatctaat atcccgcggc ggcctccccc 120 atataaacat gggggccatg gcggacaagt acggtccagt tttcatgatc cggctaggag 180 taaatcgagc cgtgattgtg agtaactcgg agatcgtaaa agagtgcttc acaacaaacg 240 ataaattcct actaaaccgt ccagttgggt tggccttaaa cctcatgagt tacaacaacg 300 ccatgttcgg gttctctcgg tacggtccat attggcgtga gatacacaaa atagtcatgc 360 ttgagctcct ctcgagcagc cggctcgagt ccctgaagca cgtatgggac tcggaaatat 420 tgacatccat cgaagagttg taccaattat gtcaaacaca aaacaaggct catgaaggcc 480 cagttttggt tgaaatgaag gattggtttg cagatatggc actcaatgtg tcctttagaa 540 tggttgctgg gaaaagatac tttggtgcaa gtgctggtgg taataaagat gaggcaagaa 600 ggtgtcaaaa gaccatgaga gatttcttta gacttgttgg cttgtttata gtgtctgatg 660 cacttccatt tcttaggtgg ctagacttgg gagggcatca gaaggagatg aagagaacat 720 ttgaagatct tgactatgtg cttcaaggat ggttggatga gcataaattg aatagaaaat 780 ctggtgggaa tggtgatcaa gatttcatgg atgtgatgtt atctactctt tatgattcaa 840 aatttaccga ttacgacgtt gacaccatca acaaggctac gtgctttcaa ttgatcctag 900 gaggaactga tactacaacg gtcactctaa catgggccct ttccttgatg ttaaaccacc 960 cacatgtatt gaaaaaggcc caagatgagt tggacatcca agtaggcaaa cacagacaag 1020 tggaggaatc agacatcaag aacctaaaat accttgaagc tgtgatcaaa gaaaccttac 1080 ggatgcgccc agtaggccca cttttaggcc cacgagaggc gatcgaggac tgcaccattg 1140 gtggatatcg agttcgagca ggcacacgcg taatggtcaa tgcttggaag gtgcaacgtg 1200 acccatcggt ttggccaaac cctgatgact tcaaaccgga gaggtttctc aagaaggata 1260 ttgacttcag ggaccaaaac tttgaattca tccctttcgg gtccggtaga agggcctgcc 1320 ctggaatatc atttgccgtg gaactaytgc ccatggcttt ggcccgttta ctacatgggt 1380 ttgagcttaa gactcaattg ggttgcaagg tggatatgac agagcatgcc ggtttagttc 1440 atgctaaggc taccccttg gaagttcttg tcagcccacg cctgtctcga gagttgtatg 1500 tatcgtctta g 1511
3-168	**Sequences**	
3-168-1	Sequence Number [ID]	168
3-168-2	Molecule Type	DNA
3-168-	Length	1590

[0079]

3		
3-168-4-1	Features Location/Qualifiers	**source** 1..1590 mol_type= genomic DNA organism= Menispermum canadense
	NonEnglishQualifier Value	
3-168-5	Residues	atggattcaa ctgatcatca cctggccctt gtaataccca ctcttctagc taccccctgtc 60 ttattgttct ccttctactg tctcctcttg agaccaagga gtctcaaaaa acctcgtact 120 aacaaaccac ctgaaccttc tggttcatgg cccatcatcg gccatctcca tctcttaagc 180 caaggcctac ctcacataac actgggagcc atggccgaca agctcggacc agccttctca 240 atccgcctcg gcacgcgccg agcactagtg gtcagcagct gggaggttgc taaggagtgt 300 tacaccacca acgaccgagc cttcgcgagc cgtcccagca gcatagcagt caagctcatg 360 agctacaaca actccatatt ggggttcgct ccgtacggac agtactggcg cgagctgcgg 420 aagatagtgg tgctccagct tctctcgaac cggaggctcg agtcgctgaa gaacgtttgg 480 gaatctgaga ttgatttgtc tataaaggag ttgtacgata catgggcaag taatagagga 540 ggagaagcgt taatggtgga catgaagcag tggtttggag accttacgat gaacatagtg 600 gtgaggttgg tggtggagaa gcgttgtttt gggagaagcg tgggtgacga tgagactgag 660 gcgaggaggg gccagagagc gctgaaagag tttttaaaac tggtgggttt gtttttggtg 720 gaagacgcgt ttccattttt gagttggttg gatgttcagg ggcatcagag agagatgaag 780 agaatagcga gagaactgga ctcgctgttt caggggtggt tggaggaaca taagaggaag 840 agaagcataa aaggtgaggc caaaggagat caggacttca tggacgtgat gttgtctgta 900 ctcgaggatt ctaccatcag cactgatata gaagatgaca cagttatcaa gtccacatgc 960 ttgactgttg tcttgggagg gagcgacagc acagtgggaa ctctcacttg ggccctctcc 1020 ctactcctaa acaacagaca cgaattgaaa aaggcccaag atgaattgga cgcctatgtg 1080 ggtaaggaaa gacaagtgga cgaatcagac atcaagaacc tcgtgtacct acaggccata 1140 gtcaaagagg ttctgcgact ctacccagcg ggcccactat caggcccacg agagtccgtt 1200 gaggacactg tggtagcagg ttaccatgtt cccaaaggca cacagctcat agtgaacctc 1260 tggaagattc aacgtgagcc gtccatctgg gccgaccctc tagagtttca accagagaga 1320 tttctcacga cccacaaagg catggacgtg tggggccagc acttcgaatt aatccctttt 1380 gggtccggga gacggtcgtg cccgggcaca gcgttcgccc ttcaagtgat tcacctcaca 1440 ttggctcgtt tgctacatgg gttcgagctc accacaccat gtggtgcacc tgtggatatg 1500 agtgagagcg ctggtctcat taatgtcaag accacgccag ttgaggttca cgtcgctcca 1560 cgcctccctc tcaagctata taaatcataa 1590
3-169	**Sequences**	
3-169-1	Sequence Number [ID]	169
3-169-2	Molecule Type	DNA
3-169-3	Length	1590
3-169-4-1	Features Location/Qualifiers	**source** 1..1590 mol_type= genomic DNA organism= Menispermum canadense
	NonEnglishQualifier Value	
3-169-5	Residues	atgattttaa ttgcaatggg caaccacatt gaactgcaag atatcatact gtattccctt 60 ggatttttg ctgctactat tttatggaga atttttagta cctatgtcct tagaaggaac 120 agttgctcca gaccaccaga agcagccgga aaattgccgt taattggtca ccttcatctt 180 ctaggagcga acaagatatt acatcataca cttggagaca tggccgatcg acacgggcca 240 atcttttctt tgaatttggg aattaaaaga actcttgtga tcactagttg ggaagtagca 300 aaagaatgtt ttacaacaca ggacagggtt ttcgccactc gtccgaaatc tttagttgga 360 aaagtagtag gatataatag cacagttatg atatttcagc agtatggacc atactggcgc 420 gagatacgca agctagcaat gattgagctt ctgtcaaatc gtcgactgga aatgctcaaa 480 catgttcggg aatcagaggt taatcttttc atcaaggagc tatatgagca atggtcaagc 540 aatgagaatg gaagcaaggt tgtggtggaa atgaaggaaa ggtttggaga tctgacaaca 600 aatattgtgg tcaggacagt ggcaggtaaa aaatattctg gtactggtgt gcatggtaat 660 gaagagtcga ggcgatttca gaaggcaatg acagatttta tgcacttagc ggggctgttt 720 atggtttctg atgcacttcc cttgctcggt tggattgata cattcaaagg atacagggga 780 aaaatgaaca agacagcaga agagattgat catgtacttg gaagctggtt gaaggagcat 840 cagcagaaaa gaaaaaatat cagcattaat catttagacg aagactttat ccatgtcatg 900 ctctctgcca tggacgggaa ccagtttcct gacatcgaca ccgaaactgc catcaagggc 960 acttgtttaa gtcttatctt aggtggttat gatacaacat ccgccacact tacgtgggca 1020 ctctccctaa tcgtcaacaa ccatcatgtg ttgaagaaag cacaagatga aatggacaag 1080 tacgtaggaa gagatcgcca agtaaaggaa tcagatgtga agaatttaac ttatttgcaa 1140 gccattgtca aggaaacact gcgattatat ccagcagcac cactatcagt ccaacacgaa 1200

[0080]

		gcaatggaag attgcacggt ggcaggatgt aacattccag ctggcacgcg gttagttgtg 1260 aacctctgga agatgcatcg tgacccgaaa gtttggtctg accctctaga gtttcaacca 1320 gacaggttcc tgcaaaaaca tgttaatgtg gacatttggg gtcagaattt tgagctttta 1380 ccatttggat caggacggag gtcatgccct ggtatcacat ttgcgatcca ggtcctgcac 1440 ttgacacttg ctcaattgct tcatgcgttt caactgggaa ctgtctttgc ctcgcccatt 1500 gatatgactg aaagttcggg tgttactaac ccaaaagcaa ctccactgca agtaactctt 1560 accccacgac tgcctcctga agtctactaa 1590
3-170	**Sequences**	
3-170-1	Sequence Number [ID]	170
3-170-2	Molecule Type	DNA
3-170-3	Length	1542
3-170-4-1	Features Location/Qualifiers	**source** 1..1542 mol_type= genomic DNA organism= Menispermum canadense
	NonEnglishQualifier Value	
3-170-5	Residues	atggattcaa cctaccaact tctctctgcc ctattgttca tcctctgcct ttactatctc 60 gtctgtaaac caatcaccaa aacaaaaaac gacgaagctc ctgtaccagc cggagcatgg 120 cccatcatgg gccacctcca catgctccgc ggcccaaacc tccctcacat aaccctttca 180 tccatggccg acaaacacgg cccggccttc acaatccgac tcggtacgcg ccgagccctc 240 gtagtcagca actctgatct cgcgaaggag tgcttcacag taaacgacaa ggccttctca 300 acccgcccga gcaccgtagc cacgaagctc atgggctaca acaacaccat gttcgggttc 360 gccccgtacg ggccgtactg gcgcgagttg cggaagatag tgatgaccga gcttctgtcg 420 agccgaagac tcgagtcgct cgcgagcgtt tgggcctctg agattgagtc ctcggttaaa 480 gagttgttcg cggaatgggc tgaaaacagg gcgaagggtc cagtggtggt ggagatggga 540 gagtggtttg gaaacttgac gctcaacata gcgcttcgaa tggtggtggg gaagaggtat 600 ttgagagaag agtcgcggaa atgcttgaaa gcgatgaggg attatccgga gctgtttggg 660 aggtttttgg tggaagacgc ggttccgttt cttgggtggt tggacttgat tcaggggtat 720 cagagagaaa tgaagaaaac agcgagagaa ctggactctg ttcttgaaaa atggctagtg 780 gaacataaag ataagagagg ttctggggag gggaaaggag agcatcagga cttcatggac 840 gtgatgatat cggtacttga agattcaaag ctcagttacg gagaggctga tacggtcaat 900 aagtcaactt gcctgaatct aatcttaggt gcaactgaca caacaatggt ggctctcaca 960 tgggccctct cacttctact caacaataaa caagtcctca aaagagccca acaagaacta 1020 aaatcccaaa tcggcaataa caaacaagtg tcccaatccg acatcaagaa cctactttat 1080 ctccaagcca cagtaaaaga agcactgcga ctttacccac cagagccgct atctggcccg 1140 cgagaggccc tcgaagactg taccgtcgcc ggctaccgtg tccgagccgg cacacggctg 1200 atagtgaacc tgtggaagat tcatcgagac ccgtcgatat ggcaggtccc tctcgagttc 1260 cggccggaga ggtttctcac ggcccacaaa gatgttgatg tgtggggcca gcacttcgag 1320 ctgatgccgt tcgggtcggg cagaaggtcg tgcccgggca tctcgtttgt tcttcaagtg 1380 gttccgttga tattggctcg tttgctacac gggttcgaac tcacaacgcc tggcgaggct 1440 ttagtggaca tgagcgagag cgcaggtctt gtgaacgcca aagtgacacc ccttgaagtt 1500 gttatttctc cacgcctccc gctcgagctc tttgcgggtt aa 1542
3-171	**Sequences**	
3-171-1	Sequence Number [ID]	171
3-171-2	Molecule Type	DNA
3-171-3	Length	1605
3-171-4-1	Features Location/Qualifiers	**source** 1..1605 mol_type= genomic DNA organism= Menispermum canadense
	NonEnglishQualifier Value	

[0081]

3-171-5	Residues	atgattatga tgttcatcga ctactactcc tcatggcttc cccaaactct actacttcaa 60 tcaattttac tagctgtttc cctagtcatc ttcatcaatc tctttctcac gaggaggagg 120 agctactcct ccaaatccca caccaatatc atacaccctc ccaaggccgc cggagccctg 180 ccggtaatag gccacctcta caccctcttt cgaggcctct ccgccggcgt tcctctctac 240 cggcaactgg atgccatggc cgaccgttac ggccccgcgt tcatcatcca ccttggcgtc 300 taccctaccc tcgtagtcac gtgccgagaa ctcgccaagg aatgtttcac tacaaacgac 360 caaacctttg ccacgcgccc cagcacgtgc gccggcaagt acatcggcta caactacgcg 420 ttcttcggct tcgcgcccta cggcccgtac tggcgcgaag ctcgcaagat cgccaccgtc 480 gagctgctct ccaactaccg cctcgactcg ctgcgccacg tgcgagaagc tgaggtgggg 540 cgcaacgtgg acgagctcta cgccctccac gcgtcgtcat caacgaataa gcaaaacatg 600 atgaagattg atatgaagca gtggttcgat caggtgacgc tgaacgtgat tttgatgatg 660 gtggtgggga agcggtgcgt gaccactggt gggaatgaag aggaggtgag agtggtgaag 720 gtgttgcacg agtttttcaa gcacctaggg actttgtcgg tatcggacgt ggtgccgtac 780 gtggagtgga tggatctgga cgggaatata gggaggatga agagcacagc caaggaatta 840 gattgtatat tagggagatg gttggaagag caccgccgtg agaggaggag tgatttcatg 900 gacgctatgt tggcgatggt ggaggggatt aagatacctt attatgacag cgacaccgtt 960 attaaagcca tttgcctgaa tctcctcaac gctggatccg ataccccttgg catcacgatg 1020 acctgggcac tgtcattact ccttaacaac cgccacgtgt tgaagaaagt caaagatgag 1080 ctggacgtcc acgtgggcaa aaaccgacaa gtggaagagt tagacgtcaa gaacttggtg 1140 tacctccacg ctgtcgtcaa ggaaacgctg cgcctcttcc ctcccgcgcc acttggcgtg 1200 ccacacgagg ccatggaaga ctgtgtcgtg ggaggcttcc acgtggcaaa aggtacacgt 1260 ctcgtcgtga acgtgtggaa gctgcataga gatcctagcg tctggtccga ccctctggcg 1320 ttcaagcccg agaggttctt ggacaacaac acggttgacg ttagaggtca gcacttccag 1380 ttattgccat tcgggtcggg caggcggggc tgcccgggaa tcacgttcgc gcttcaggtg 1440 gcgcacctga cgctcgctcg attgctgcat ggattcgagt gggacacacc ggatggtgcg 1500 ccggtggaca tgagcgaggt ctcggtattg accacggcaa aaaagaaccc tgttgaggtt 1560 ttgttcactc ctcgtcttcc ggcagaggtc tacacgcaaa attag 1605
3-172	**Sequences**	
3-172-1	Sequence Number [ID]	172
3-172-2	Molecule Type	DNA
3-172-3	Length	1572
3-172-4-1	Features Location/Qualifiers NonEnglishQualifier Value	**source** 1..1572 mol_type= genomic DNA organism= Menispermum canadense
3-172-5	Residues	taccaattat tattccttca aaccgccatt gcaggcctac tgttcgcctt agcactacta 60 gtgcgccttc gcttctcgag gcgtaacaat ggcaagaaga agcaagcacc accagaacca 120 gccggagcac ggctcatcat gggccacatc cacatgctca acagtggcga gcagcctcac 180 aagaccctcg ctgcactggc cgaccaatac ggcccagtca tcaagctccg cctcggccta 240 cgcgacgcca tagtagtaag caattgggag atggccaagg agtgtttcac cactaatgac 300 aaaatcttcc ttagccgtcc ccagaccgtc gtgtcaaagt tcatgagcta caacctcaaa 360 atgctcggct tcgctcctta cggcccgtac tggcgtgaga ttcgcaagat agtggtgtct 420 gagctgctct cgaaccgccg gctcgagctg ctgaagaacg cgtggacctc tgagatcagc 480 tcgtgggtga aagagttgtt tgacgagtgg ggtgcgaagg aggcgagagg gcctgttgtg 540 gtggacatga ggcattggtt cgggaacttg gcgttcaata tagggatgaa tatggtggct 600 gggaagaggt tttttgggcc gagagtggtg tctgacgagg acgggttgcg gcgagtccag 660 caaggcctca cggatttctt taggctaata ggcgcgttct tgttggagga tgcggtgccg 720 tttctaagct ggtgggacag tcaggggtat cagaaggaga tgaaggacac tgcgagagag 780 atggatacac tgattcaagg attgttggac gagcataaac gtaggagatc atcaagctct 840 ggtgaggcca aaggggagaa ggacttcatg gacgttatgc ttaatattct tgaaggttca 900 aagttcccca gtggagacgc tgataatatc aacaagtcta cttgcttgtc tctaatgctc 960 ggcttgacgg acacaacaac ggcgaccctc acatgggctc tctccttgct acttaacgac 1020 ccgcgtgtct taaagaaggc tcgagaagag ctggatttcc acgtcggaaa gaacagactg 1080 gtggacacat cggacttaat gaacctccca tacatccacg ccatagtcaa agaagtgttg 1140 cgtctccacc caccggcgcc tctctccggc caccgtgaat ccttggagga cagtgtggtg 1200 ggcggctacc atgtccccaa gggcacccgc tttatggtga acgtctggaa gatccaccat 1260 gacccgaata agtggcccga ccctattgag ttccgacccg agaggtttct gaccacccac 1320 aaagatgtgg aagtgtgggg ccagaacttt gaactgattc cgttcagttc aggaagacga 1380 gtgtgtcccg gggcttcgtt gtctctacaa gtgcttccgt tcacactggc tcgagtgttg 1440 caagggttcg aagttgcaac accaggaggt gcgccggtgg atgtcacgga gagcaaaggc 1500 ctctcaactg ctaaagagac tccgcttgac gtcgtgatca ctccgcgtct ccctgaaaag 1560 ttctaccatt ga 1572
3-	**Sequences**	

[0082]

173		
3-173-1	Sequence Number [ID]	173
3-173-2	Molecule Type	DNA
3-173-3	Length	1587
3-173-4-1	Features Location/Qualifiers	**source** 1..1587 mol_type= genomic DNA organism= Nandina domestica
	NonEnglishQualifier Value	
3-173-5	Residues	atggattcac tcatttcatt tcaagcaata gttgggcttt tcatcttgat cctagtttcc 60 tatcaatggc ttggaaggtc tagaagtatt aagactaaca agcataacga agcaccggaa 120 ccagccggca gatggcccat catcggtcat ctacatttac tcggagggtc ggaccaatta 180 ctctatcgaa cgctagggtc catggccgat aaacttgggc cggcattcaa tatccggctt 240 ggtagccgtc gggcctttgt cgttaacagt tgggaggtgg ccaaggagtg tttcaccatc 300 aatgacaagg cccttgctag tagacccatc actgtggctg caaagctcat gggctataac 360 tatgcagtct ttgggtttgc accatacagc ccattttggc gagcaatgcg aaaaatagcc 420 acacttgagc ttctttctaa tcgtaggctc gagatgctca aacatgttcg gatctcggag 480 gtggacatgg gcttgaaaga aatttatggg ctttggtcca agaacaagga ttcaggccct 540 ttaatgattg aactaaacag gtggtttgag aacttgactc taaatatggt tgtgagaatg 600 gtggctggca agagatattt tggtgctgat gcatcatgtg atgagaacga agcgcagcgc 660 tgccagaagg caatcagtga attcttccgt ctcattggga tatttgtagt atccgacgcg 720 attccttctc tatggtggtt ggatttgcag gggcatgaga aggccatgaa aagaactgcc 780 aaggacctgg attctatact aggaggctgg ttggagcagc atcggtcgcg gagagtcaat 840 ggtaaggtcc caaccgaggg ggaacaagac ttcatcgatg tgatgttatc gctacaagag 900 ggcgatcatc tctctgattt tgagtatgat gctgatattg ccatcaaatc aacttgcctg 960 gcacttatcc taggtggcag tgacaccact gcaggtaccc taacttgggc tatctcattg 1020 ctactaaacc atccctatgc tttgaaaaaa gcccaagagg aattggacct ccatgttggc 1080 aaggacagac aagtctatga tcaagacatc aagaatctgg tatatcttca agccatcatc 1140 aaagaaacac tgcgcctata cccagctggt ccactattgg gcccaaggga ggccatggaa 1200 gactgcacca tatcagggtt cgatgttcga gctgggacgc gcttggtggt aaatgtttgg 1260 aagattcaac gagacccaaa cgtgtggtcg aacccatctg agttttcacc tgaacggttt 1320 ttgacaagcc atgtggatgt cgatgttagg ggacaaaatt tcgagctcat gccatttgga 1380 tcaggccgac ggtcttgtcc aggcgcttca tttgccctcc aggtcctgca tttgacatta 1440 gcccgttttc ttcatgggtt tgggttggca aacccattgg gaaaacctgt agacatgaat 1500 gagagcccag gactaactat cccaaaagca acacccctaa atgtgctgct cactccacgt 1560 cttgattcag agctatatgg ttgctag 1587
3-174	**Sequences**	
3-174-1	Sequence Number [ID]	174
3-174-2	Molecule Type	DNA
3-174-3	Length	1563
3-174-4-1	Features Location/Qualifiers	**source** 1..1563 mol_type= genomic DNA organism= Nandina domestica
	NonEnglishQualifier Value	
3-174-5	Residues	atggaaacct ttcagttcct tggaattcca ttgtttggct tctttgcctt attatgcact 60 tactacctag tattgaggaa gccatcatcc actaagatca gggagccacc tcggccagcc 120 ggagcatggc caatcatcgg ccatctccat ttacttgccc ggggtgacct cccccacgta 180 actttgggga agatggctga taaatatggc ccagtcttca agttaaagct tggtgtccga 240 caagcaattg tggtaagtga ttgggaggtc gcaaaggagt gttacaccac caatgatcgt 300 gccttagcca atcgtccaag tggcctagga gcaaaaatca tgggctacaa ctatgctttg 360 attgggtctg ccccctatgg cccatattgg cgtgatttac gcaaaattat cacgcttgaa 420 gttctctcga gccgtcggct tgaatcactc aagcatgtat gggactctga aatatccaca 480

[0083]

		tctgtaaaag aattgtacca aatatgggca gatcaaaaca aagctcaagg ccaagtttct 540 gttgaaatga aacaatggtt tagtgatatg acactaaatg tggcagttag gttggctgtc 600 ggaaagaagt acttaggtgc aactgccgat tgtgaaaaga ataaggcagt gcaatgtcaa 660 aaggccatca ggaatttttt cagactcgct ggtttgtttg tggtggcaga ttaccttcca 720 tttctgggct ggttggactt gggagggcac gaaaaagaga tgaagcacac agcaaaagaa 780 ctcgattata tagctcaaga atggttggat gatcataaaa agaagagaac ctccaatcgg 840 acagtggacg agccacagga tttcatggat gtgatgctct cgatcttgga agaatcgact 900 ttcacgggtt atgatgttga tatcatcaac aagtccacat gttttgcatt gatcctaggt 960 ggaacagaca ctgtggcagt tactctgaca tgggctctct gtttattact gaacaatcca 1020 catgtactga aaaaggccca agatgagttg gacatccacg tcggcaagga tcgacacgtc 1080 aatgaatcag atatcaagaa cctcgtttac ctccaagcta tgatcaagga aacattgcgc 1140 ttatatccag ctggtccgct actaggtccc cgtcaggtca ttgaggactg caccatagct 1200 gggtaccacg tacgagcagg gacacgtgtg atagtcaatg cttggaagtt tcaacgagac 1260 ccgtcgatct ggtcaaaccc ttgtgagttc caaccggaga gatttctgga caaagacatc 1320 gatgtgaagg gtcaacactt cgaattgatc cccttcggag caggcagaag ggcatgcccc 1380 ggaatctcct ttgctcttca agtattacca ttggcattgg ctcgtttact acatggtttt 1440 gagcttaaaa acccatcgga aagccaagtg gatatgactg agacccccgg tatggttcat 1500 gccaagacaa ccccttttgga agtacttatc acaccgcgct tgtctccaaa attttatgta 1560 taa 1563
3-175	**Sequences**	
3-175-1	Sequence Number [ID]	175
3-175-2	Molecule Type	DNA
3-175-3	Length	1488
3-175-4-1	Features Location/Qualifiers	**source** 1..1488 mol_type= genomic DNA organism= Nandina domestica
	NonEnglishQualifier Value	
3-175-5	Residues	tggaagaggc caacctctgt taagtacagg gaggcacccc aaccagctgg cgcatggcct 60 atcatcggtc atctccattt actggcccgt ggagacctac accacataac tcttggagcc 120 atggccgaca agtacggccc agctttcatg atgcggcttg gtgtgcacca agcaatggtg 180 gtgagcgatt cggagtctgc gaaggagtgt tccaccacca acgatagggt cttggccact 240 cgaccaagta gcgtagctgt aaaacttatg ggctacaact atgccatgtt tgggttcggc 300 ccctatggat catattggcg tgaaatacgt aaaatagtta ttcttgaggt cctgtcaaac 360 catcggcttg agtcactaaa acatgtatgg aagtctgaaa tatccatgtc caccaaagag 420 ttgtaccaat tatggataaa ccaaaacaag gatgaaggcc cgactttggt tgaattgaag 480 caatggcttt gtaacatgac actaaatata ggagttagga ctgttgctgg gaaaagatac 540 tttggcgcaa gttcttgtga tgcaaatgaa tcaaacagga ttcaaagggc aatcagagat 600 ttctttagat ttgtaggttt gtttgttgtg tcagattttc ttccttttct agggtggttg 660 gacttggaag gttatcagaa ggagatgaag agtattgcta gggaacttga ttctatcctt 720 cagggatggt tggatgaaca cacaaggaaa agacaatctg gtgggaccaa cgaaaatcag 780 gattttatgg acataatgct ttcagttctt gaacattcga atgcattgac tcactatgat 840 gcagatacaa tcaacaaagc gacatgcttt acaatgatct taggtggaag tgatactaca 900 atggtcactc taacatgggc cctctccttg ttactgaaca atccacatgt cttgaaaaag 960 gcccaagatg aaatagatat ccaagtaggc aaggacagac ttgtggacga atcagatatc 1020 aagaacctag tatacctcca agctatagtc aaggaaactt tgcgtctgta cccagctgtt 1080 ccaataataa ctccacatga ggccatagaa gactgcacca tagctgggta tcatgttcca 1140 gcaggcacac gcctcattgt gaacgcttgg aagatacaaa gagacccatt gatttgggat 1200 aaccctggtg agttccaacc agagagattt ctctacaaag atgtggatgt gaaaggtaaa 1260 catttcgaat taatcccttt cgggtccggt agaagggtgt gccctgggat ctcgttggcc 1320 ctccaagtgg tgtcattggc catggcccat ctcctacatg agttcgacct tgcgaaacca 1380 tcagaaggca atgtggacat gactgagagt gttggtttgg ttaatgctaa ggcaacccct 1440 ttggaagtac ttatcactcc gcgcctatcc ccaaagtttt atgaatag 1488
3-176	**Sequences**	
3-176-1	Sequence Number [ID]	176
3-176-2	Molecule Type	DNA

3-176-3	Length	1578
3-176-4-1	Features Location/Qualifiers	**source** 1..1578 mol_type= genomic DNA organism= Nigella sativa
	NonEnglishQualifier Value	
3-176-5	Residues	atgggttcct tcaaccaaat aaatccatct gttgtatact ttgctgcctt taccatcttc 60 ttcttcttct ttctctataa aatattatac aagagaagaa ccagtgcgaa gaccagagtt 120 gctcctgaac ctgctggtgc gtggcctttc ataggtcact tacccttgct atcccagcaa 180 aacttgcccc atgtaacatt gggggtgttg gctgacaaat acggaccagc tttcactgtc 240 caactcggct tacacaaagc tgttgtggtg agtagttggg aggttgcaaa ggagtgcttc 300 actgtcaatg acaaagtgct cgctactcgc cctagctcag ttgcagtgaa gattatgtgc 360 tataactatg ctgtgtttgg ctttggacca tatggttcct attggcgtga agctcgcaag 420 atagttgtac gggagcttct ctcaaaccat cggcttaatt tgctaaaaca tgttctggtc 480 actgaaatta gcatgtctat gaatgaattg tacacagttt ggcaaaagaa tgctaataat 540 gttagtggaa aagctttggt ggagatgaag caatggtttg gtgacttgtc attgaacatg 600 attgtcaaga tagttgctgg aaagcgatac ttccaagcta gtgcaaattc agatgaaagg 660 gatcagttga aaaggggagt gcaagatctc ttccatttgg ttgggctgtt tctggtgtca 720 gatgcacttc catttcttag ctggttagac attggtgggc atgagaaagc catgaggaga 780 actgccaagg agcttgacaa catactgggg agttggttgg atgaacataa acaggctaaa 840 ttggcagggg cgacaaaggg agagcaagac tttatggatg tgttgatgtc catactagag 900 gataacaata atctccctga gtatgaacca gatgttgtca gtaaagctat ttgcttgggt 960 atgattttgg gtggagctga taccacaaca attactctga cgtggattgt gtccttacta 1020 ctcaacaatc aacacatttt gaagaaagcc caagatgaaa ttgacagcaa agttggaaaa 1080 gatagacaag taaatgaatc agacatagaa aaactggtat acctccaagc aattgtgaag 1140 gagacattgc gtctgtaccc acctgctcct ctgtcaacac aacatgaagc catggaggac 1200 tgcaccatag ctgggtatca tgtccaagct ggtacaagat tgataacaaa tatatggaag 1260 attcaaagag atccaggggt atggccgaat ccttgcgagt tccagccaga gaggtttctc 1320 actacccatg ccaatgtgga gtcaaatgga aagcattttg agtttattcc atttggatct 1380 ggtcgacggg cgtgcccagg tatgtcactt gggcttcagg tggtgcacct gacattagca 1440 cgtctgctac aaggttttga attggaaact ccgttgagtg tggaagtaga catgactgaa 1500 agtgctggac ttacaaatct caaagtaacg ccccttgaag ttttaatcaa tccgcgtcta 1560 ccttcaaatc tatactag 1578

[0084]

3-177	**Sequences**	
3-177-1	Sequence Number [ID]	177
3-177-2	Molecule Type	DNA
3-177-3	Length	1554
3-177-4-1	Features Location/Qualifiers	**source** 1..1554 mol_type= genomic DNA organism= Nigella sativa
	NonEnglishQualifier Value	
3-177-5	Residues	atggatttga caagcatctt gatttgtatc tttcttttca tcatttctat ctgctttctg 60 tcatggaagc gatcaaggag tctttccgga accagagcag ctccggaacc agttggtgca 120 tggcctgtca taggccatct aaggctgcta atggggtcca aaacacctca tatgacctta 180 ggaaacttgg ctgacaacta tgggccggca ttcaccatcc ggcttggtac gaagaaaaca 240 ctggttgtaa gtagctggga ggtggccaag gagtgtctca ctaccaacga caaagccttc 300 gctggccgcc acagcactat ggcggtggag ataatggggt acaactatgc cttcttcagc 360 ttaggtccta gtggtcaata ttggcgtgaa attcgcaaaa taacagtttc tgaacttctt 420 tcaaatcgtc ggttggagtt acttaaacac atatggagct cagagattaa gacttctatc 480 aaagaattgt atgaaatttg tgcagcacaa agtcaatatg ggaaaaaaca gtctcctatg 540 gtagaaatgc agcaatggtt tagtcatttg aacttgaatt tatcagcaag aatggttgtt 600 ggaaaacgat attttgctga cggtgttgaa gaaaatgaag gcgatatcag acgatttcaa 660 aatgcaatca aggagttctt ttactgggct ggagcgttta taatagctga tacaattcca 720 tatctaaggt ggatggattt cttaaatgag cggtcaatga aaagaacagc aaaagaaaca 780 gaccatgtac ttgaaggatg gttgcaggaa cacaaacgaa acaggctgaa cggtgtaacg 840 aaggagcaag atttcatgga tgtgctgctg acagaacttg gtgacaaaga tctgtgtggt 900 tacacagctg atgttgtgaa caaggccact tgcctgaaca tgatttttgg aggaacagat 960 accacaaaaa cgggcatgat atggacttta tcattaattc tcaacaatcc acaagtacta 1020 aagaagttac aaaatgaaat tgacatccaa gttgggaaag acagacaggt tgatgattct 1080

[0085]

		gacataggga atctcgtgta cctacaagcc actgtcaagg aagcgatgcg cctgtatcca 1140 cctgctacca tatttggacg tgaatccatc gaggactgca ctgtggctgg gtaccacatc 1200 caagctggga cacgtttgat tgtgaatgca tggaaaattc aaagagatcc aaatgtatgg 1260 cccaatcctg acgaatttca gcctgagaga tttctgacaa accaagcaga tgtggacttc 1320 aggggtcaag attttgagct cattcctttt ggggctggga gaagggcgtg tcctggtatt 1380 tcattgacag ttcgggttac acatttgaca ctggcatgtt tgctacaagg cttcaacttt 1440 gaaacccccct tgaatgaacc tgtagatatg tccgagaaat atggtttaac caactcaaag 1500 gcaacccctc tgaatgttat actcacacca agactccctt ccaatttgta ctag 1554
3-178	**Sequences**	
3-178-1	Sequence Number [ID]	178
3-178-2	Molecule Type	DNA
3-178-3	Length	1593
3-178-4-1	Features Location/Qualifiers	**source** 1..1593 mol_type= genomic DNA organism= Nigella sativa
	NonEnglishQualifier Value	
3-178-5	Residues	atggattcaa tatttcatat gtatgcacca attaatatcc ttgctgctac ctttgttttt 60 attgtcattt ctgtgtggtt tctgttatgg atgaagagat cgagaaagaa tagcaagagc 120 agaagagctc ctgaaccggt agggggatgg cccttgatag gtcatttgcg cttgttagtc 180 ggccctgagt tgccccatgt aatattggga agcttggctg acaagtatgg accagctctc 240 tccatccggc ttgggatgcg tcaagcattg gtggtcagta attgcgaggt agttaaagag 300 tgtctcacca ccaatgacag atgcttctcc actcgcccta gctctgtcgc agtagagtta 360 atgggatata actatgcgtc gtttggttta ggtccttacg ggggcttctg gcgtgaagtt 420 cgcaaaatcg caattcttga gctcctctca aatcatcgtt tgaagtctct taaacatgta 480 tggatatctg agattagtgg ttttgtcaaa gaactgtacc aattatgtgt agctaatggc 540 aatacaggaa ggcaatctgc tttggtggaa atgcgacagt ggttaaatga tttgacacta 600 aatgtgtctg tcagaatggt tgttggaaag cgatactttg gctctggtag tgaacatggt 660 ggtgaagatg tcaagcggtt tcaaaaggca attaaagatt tctttcgttt ggcaggaaaa 720 ttcacgctgg cagatgcaat accattccta aggtggttgg actttggtca tgaaagagcc 780 atgaagaaaa ctgccaaaga gttggactat gtacttgcaa gatggttgga tcaacatcaa 840 aagaacaaac tcaattgcga aacaaagcag gtggatcaag atttcatgga tgtcatgttg 900 actgtccttg gtgataaaga tctgtatggt ttcaaggctg atgttgtcaa taaggccact 960 tgccttaatt tgatcttagg tggggttgac acgacgtcag tgaccctaac atgggcattg 1020 tcattgctac taaacaatcc aaacattcta aacaaggcac aagaagaaat tgatgtccag 1080 attggaaaag atagacaagt tgatgacaat gacttgggaa aactagtgta cctagaggca 1140 attgtaaagg aaacaatgcg gttatatcca gcaggtccac tgtcaggtgc acgagctgcg 1200 atagaggact gcatggttgc gggatatcat gtaccaaaag gaacacgact gattgtgaat 1260 acatggaaga tacagagaga tccagagaaa tgggacaacc ctagtgagtt tcggccggag 1320 agatttctga tcaccaccac caatggccat gtggaagtgt ggggtcaaca ttttgagtac 1380 attccttttg gatcagggag aagaatttgt cctgccatct cattttcact tcagttggtg 1440 catttgacat tggcccgatt gctacaagcc ttcagctttc aaacaccatc aaatgcagca 1500 gtagacatga ctgagacccc tggcctggtc aatttcaaag ccaccccgct ccaaatttta 1560 ctcactcctc gacttccttc cagtttatac taa 1593
3-179	**Sequences**	
3-179-1	Sequence Number [ID]	179
3-179-2	Molecule Type	DNA
3-179-3	Length	1584
3-179-4-1	Features Location/Qualifiers	**source** 1..1584 mol_type= genomic DNA organism= Nigella sativa
	NonEnglishQualifier	

[0086]

3-179-5	Value	
	Residues	atgctcagta ttcatgattc aaccatggtt tttctccaac tacaagctat ttgtggcatt 60 tttggcttca ttttcattat tacatggtgg acaagatgga aaagttccaa caaaatgaaa 120 gcaccagaag tagctggtgc atggcctgta attgggcacc tgcatctgct tgggggcggc 180 cgtcccttat accagctcct tggagacatg tctgataagt atggaccagc ttttaccctc 240 cgaatgggaa tccaaaaggc acttgtagtg agcagctggg aagttgcaaa agagtgtcta 300 accaccaatg acagagctct tgctacccgc ccatcttcgg ctggagggaa gtacatgggt 360 tacaacaacg cacttatccc cttcagccct tatgggccat actggcgaga catgcgcaag 420 attgctacac ttgagctttt atctaatcat agactagagg agttgaagca tgtccgagaa 480 atggaaatca acacttgtat cagtgacatg tacaaacttt gtcaggttga ggatggagtt 540 gaaattaaac caatttctgt agatctgagt caatggtttg cagatcttac cttcaatgta 600 gtggtgatga tgataacagg aaagagatat attgggtcaa ctgatgcagg tgacatgaat 660 gaaataagac attttcaggc agcactggtt aaatttatga ggctattgag aatctctctt 720 ctggtagatg tatttccagt tctacagtgg attaattatg ggggattcaa aggagtcatg 780 aaatcaactg ctagagatat tgattccgta cttgaaaatt ggctgcagga gcatcagagg 840 aaaagacttt cccctgattt caatggaaac catgatttta ttgacgtgat gatatctacc 900 ttagaaggca cagaattctc tgattatgac cacaatacta tcataaaggc aatatccatg 960 gctatggtcg tgggcggcac tgatactaca actacaacac ttatatgggc tatttccctt 1020 ctattgaata atcctaatgc gatgaaaaaa gttcaagaag agttggagat acatgtaggc 1080 aaggaaagaa acgtagacgg atccgacata caacatttgg tatacctcca agctgttgtg 1140 aaggaaactc tcaggctata tcctcccgtt ccactctcag taatgcacca ggccatggaa 1200 gactgtgtta tcggaagtta caacattcaa gcaggtacgc gtgtactttt caatctctgg 1260 aagctacacc gtgactcgtc agtgtggtct gatcctttag aatttcgacc agagagattt 1320 cttactagcc atgttgatgt agacgtcagg ggtcaacatt ttgaactgat acctttttggg 1380 tctggaagaa ggtcatgccc tgggatttca tttgctcttc aggtcataca cttgacaata 1440 gctcgcttat ttcatggatt caatctgaca acacctggga attcatcagt tgatatgagt 1500 gagatttctg gagctacatt atcaaaagtt actccattag aagtactagt tactccacgg 1560 ctgtcttcca agctttacaa ttga 1584
3-180	**Sequences**	
3-180-1	Sequence Number [ID]	180
3-180-2	Molecule Type	DNA
3-180-3	Length	1566
3-180-4-1	Features Location/Qualifiers	**source** 1..1566 mol_type= genomic DNA organism= Nigella sativa
	NonEnglishQualifier Value	
3-180-5	Residues	atggatttct tgatctacgt tgctgccttt gccgccgcct tcttcttctt attgttctac 60 aacatattat ccaagagaat aaccggtaca aagagaagaa ttgctcctga acctgctggt 120 gcatggcctt ttattggtca cttgcccatg ctcttcgggc ccaacttacc ccatgtaacg 180 ttgggtgcct tggctgacaa gtatggacca gctttcacta tccagctggg cttacacaaa 240 gctcttgtgg tgagtagttg ggaggttgcc aaggactgct tcactgtcaa tgacaaagcc 300 ctcgccactc gccctacctc tgctgcagtg aagattatgg cctacaactg tgccgtgttc 360 agtttctcac catatggttc atactggcgt gaagcacgca aaatagctat acttgagctt 420 ctttcacacc ataggcttga tttgttaaaa catgttcgga aatctgaagt aagcacatct 480 ataagagaac tgtaccaatt ttggcaaaaa aatgctacgg aagttactaa atttgctcag 540 ctggaaatga agcaatggtt tggtgatttg acaatgaacc tgattgtcag gatggttgct 600 ggaaaaagat atgctagtgt tcaatcagat gatgatggtg aggggaaaag gctacaaaag 660 gccgttaatg atttcttcca tctagtaggg ttgtttgtgg tatccgacgc acttcccttc 720 cttggttggt tagatattgg gggcaacttg aaaaccatga agaaaactgc cagggaactt 780 gacagcataa tggagtgttg gttgaaggam catcaagctc ggagatcaaa tggggagcaa 840 gatttcttgg atgtgatgtt gtccatactg cgtgaagata ataagctgca agagtatgat 900 ggtgatgttg ttgtcaaagc tatgtgcttg aatatgattt tgggtggagc tgatagcaca 960 acaatcactc taacatggac catctcctta ctacttaaca acagacacat tttgcagaaa 1020 gcccaagacg aaattgacag caaagtgggg aaagatagac aagtgaatga atctgacata 1080 gagaaactag tataccttca agcaattgtr aaggagactt tgcgtctgta cccacctgct 1140 cccctatctt cacaacatga agccatagag gactgcacaa tagctggcta ccacatccca 1200 gctggtacaa gattaataac aaatctatgg aaaatccaac atgatccaag tgtatggcac 1260 aatccttccg agtttcagcc agagaggttc ctcactaccc aggcgaatgt ggactttaga 1320 ggtcagaatt tcgagtttat tccatttgga tttgggcgac ggtcatgccc aggtacctca 1380 cttggtcttc aaatggtgca cctgccatta gcacgtttgc tacaaggctt tacatttgaa 1440 acaccatcaa atgcagctgt ggacatgact gaaagtgctg ggcttacaaa tcacaaagta 1500 acaccacttg aggttctaat atcaccacgt ctccgtttcg atctttatca agaatctccc 1560 ccttga 1566

[0087]

3-181	**Sequences**	
3-181-1	Sequence Number [ID]	181
3-181-2	Molecule Type	DNA
3-181-3	Length	1580
3-181-4-1	Features Location/Qualifiers	**source** 1..1580 mol_type= genomic DNA organism= Nigella sativa
	NonEnglishQualifier Value	
3-181-5	Residues	attccttcaa ccaaacatat actggtttta tctgcttatc tgtctttgcc tccttcttct 60 tcttcttcct ttacagcgtg cagcagaaga ggagaacagg tagaaaggcc agatacgctc 120 ctgaacctac tggtgcatgg cctttaatag gtcacttgcc aatcttgttc gaacctaact 180 taccccatat acagttggga gccttagctg acaagtatgg accagtgttc tctatcaaac 240 ttggcttacg gaaggctctt gtggtaagca gctgggaagt tgtcaaggag tgcttcactg 300 tcaaagacaa agtccttgcc tcccgcccta gctcagttgc tgtgaagata atgggctatg 360 attatgccgt atatgcattc ggaccatatg gatcatattg gcgtgaagct cgcaagttaa 420 ctatacttga acttctctca gaccatcggc ttgatttgct aaaacatgtt cgggtctctg 480 aagttagcat gtctatgaaa gaactactca aattctgcca aaagaatgcc aataatgtca 540 gtggaaaagc tttattagta gatatgaagc aatggttcgg tgacttgaca ttaaatgtta 600 ttgttaggat ggttgctgga aagagctact tgggtgctag tgcaaaattg gaagacggcg 660 aacagaaacg gttacaaaac gcaattcatg agtttttccg tttggcgggg ctatttgtgg 720 tgtcagatgc acttccaatt cttagctggt tagacattgg ggggcatgag aaagccatga 780 ggagaaatgc cagggagatt gacaagataa tgagcagttg gttggatgaa catcgacgca 840 ataaattggc cggggtaaca aatggagagc aagactttat ggatgtattg ttgtccaaat 900 ttgagaatag taatctccct ggatatgaac ctgatgttgc aatcaaggct atttgcttga 960 atatgatttt aggtgcagct gataccacaa tcgtcactct aacatgggtt gtgtctttaa 1020 tacttaacaa ccgccaaatt ttgaagaagg cacgagagga aattgagaat aaagttggaa 1080 aagataggca agtgaatgaa tctgatatag agaaactagt atacctccaa gcaattgtga 1140 aagagacgtt gcgtttatac ccagctgctc ctctatcagc acaccatgaa tccatggagg 1200 actgcaccat tgctggctac cacgtcccag ccggtacaca attaataaca aatttgtgga 1260 agatccaaag ggatccacga gtatggccta atccttgcga gttcctacca gagaggttcc 1320 tcaccacgca tgcaaacgta aactataagg gtcagaattt tgaattcatt ccatttggat 1380 atggtcgaag gtcgtgccca ggtatgtcat ttggacttca aatggtgcac ttagtattgg 1440 catctcttct acaaggcttt gaattggaaa ctccattgaa tgaggcggta gacatgactg 1500 agagcgctgg acttacaaat ctcaaagcaa cgcctcttga agttctaatt actccacgta 1560 tgcctttgaa tctatactga 1580
3-182	**Sequences**	
3-182-1	Sequence Number [ID]	182
3-182-2	Molecule Type	DNA
3-182-3	Length	1530
3-182-4-1	Features Location/Qualifiers	**source** 1..1530 mol_type= genomic DNA organism= Nigella sativa
	NonEnglishQualifier Value	
3-182-5	Residues	gtaactgtta tctacttatt tacatttgcc atcttcttct acctctacag catattatgg 60 aagaacccaa gaaagagtgc aaagaccaga gttgctcctg aaccagctgg tgcatggcct 120 ttcatgggtc acttgcctat gctattggaa cccaacttgc cccatataaa gttgggagcc 180 ttagctgaca agtacggacc agccttcact gtccaactcg gcctccacaa ggctctagtg 240 gtgagcagtt gggaggttgc caaggagtgc ttcactgtca atgacaaagt cctcgcagat 300 cgccctagct cagttgcagt gaagataatg ggctatgata atgctgtttt cgcctttgga 360 ccatatggtt cttactggcg tgaagctcga aagatatcta cagttgagct tctctcgaac 420

[0088]

		catcgtctta gtttactgca acactttcga atttccgaag ctagcatgtc tatgaaggag 480 ctatatcaac tttgtgccaa taacgggaag gctttggtgg aaatgaagaa atggtttggt 540 gacttgtcat tgaatgtaat tgtcaggatg gttgccggaa agaggtatgc caaagctagt 600 gaagatgatg aacggagaca gttacagaag gggcttaaag atttctttta tttggtagga 660 ttgtttgtag tgtcggatgc acttccaatt ctaagttggt tagacattgg gggccatgag 720 aaagccatga ggagaaccgc caaggagctt gacaccataa tggagaggtg gttagatgaa 780 catagacggg ctaaattggc tggggtgaca aagggagaac aagacttcat ggatgtgttg 840 ttgtccatac ttgaagatgg caagcttcct cactatgaat ctaatacagt taacaaagct 900 atttgcttga ctatgatttt gggtgcagct cataccacaa cagtcactct aatttggaca 960 ttatcgttac tacttaacaa tcgacatatt ttaaacaagg ctcaagatga aattgattcc 1020 gaagttggga aggatagagc agtgactgaa tctgatataa agaatctagt atacctccaa 1080 gcaattgtga aggagacgtt gcgtttatat cctgctgcac ctctacctgc ccaccgtgaa 1140 gtcatggagg actgcatcat agctggttac cacgttccag ttggtacaag aataataaca 1200 aatttatgga agattcaacg agatcctcgt gtatggtcta atccttgtgc cttccaacca 1260 gagaggtttc ttactactca ttcaaatgtg gactttaggg gtcagaattt tgagttcatt 1320 ccatttggat ctggtcgaag atcatgccca ggtatctcac ttgggcttca aatggtgcac 1380 ttggcattag cgcgtctgct gcaaggattt gagttagaaa ctcctttgaa tctgggaata 1440 gacatgactg aaagttctgg acttacaaat cttaaagtaa caccgcttga agttgtgatc 1500 acaccacgac taccttcaaa tctatactga 1530
3-183	**Sequences**	
3-183-1	Sequence Number [ID]	183
3-183-2	Molecule Type	DNA
3-183-3	Length	1689
3-183-4-1	Features Location/Qualifiers NonEnglishQualifier Value	**source** 1..1689 mol_type= genomic DNA organism= Papaver bracteatum
3-183-5	Residues	atggcgtatt tgatgatcaa gaaatctttc cacttgtttt ccgatcaacc aacttcagtt 60 tccactctta tagtacttgc ttttctactg acactttcac ctgttattat ttactatgaa 120 cagaagaaga ggggtttgag gcgaaatcgg acctcatcgt catgtaccgc aattacaacg 180 actccgttac cagaggcatc aggtgcgtgg ccagtgatag gtcatcttct tcttttcatg 240 aacgaaaacg atttaaatca tgcaactctc ggtaacatgg ctgataaata tggacctatt 300 ttcagcttaa gattcggtag tcatagaact ctagttgtta gtagttggga gatggtaaag 360 gagtgtttta caggtgccaa tgacaagttt ttttcaaatc gtccttcctc cttggcggtt 420 aaacttatgt tttatgacac tgagtcttat ggctttgcac cgtatgggaa gtactggaga 480 gagttgcgga agatatctac acataaactc ctctctaatc agcaattaga caagttcaaa 540 cacttgcgga tttctgaagt ggacaactcc tttaaaaagc ttcacgactt atgcagcaac 600 aacaaactgg gaggagaaac tacatctgtg gctaatcttg tgagaatgga tgattggttc 660 gcttacttga cattcaacgt aataggacgg attgtcagcg gattccaatc aaatgcagtg 720 tcaggtgcca caagcagcca ggaaaaatac aagcttgcaa tcgatgaagt gtcaaatctt 780 atggcaacat ttgccgtttc agatgtggtt ccatgccttg ggtggattga ccgattgact 840 ggtcttacag gaaagatgaa gaaatgcgga aagaaattag atgcagtagt tggggatgca 900 gtggaggttc atcgccaaaa gaaactcaaa atttctagaa ataccgcagg agaacttacg 960 gagcatgaag aagaagactt catcgatgtt tgcttgtcga ttatggagca atcacagatt 1020 ccgggaaaca accccgaaat ctctgtcaaa tctattgcct tggacatgtt atcgggtggg 1080 agtgacacta caaagttgat aatgacatgg acccttttctt tgctgttgaa ccatccagac 1140 atattggaca aggctaaaga agaagtagat acatacttca ggaagaaaaa gatatcggat 1200 aacacacctg tggttgatgc tgccgatgtt cctaacctcg tctacatcca agctatcatc 1260 aaagaatcaa tgcggttata ccccgccagc acattgatgg agcggatgac cagtgatgat 1320 tgtgaggttg gtggcttcca cgttccagct ggaacccgac tatgggttaa cgtatggaag 1380 atgcaacgag acccaagggt ttggaatgat ccattggtat ttcgacctga gagattcttg 1440 agcaatgaca aagggatggt agatgtgaag ggtcagaatt atgaactgat accattcgga 1500 acaggcaggc ggatatgtcc cggtgcatct tttgccttag aagtcttgca tttggtcctc 1560 actcgtctta ttcttgagtt cgagatgaag gcaccagagg gggaaattga catgagggca 1620 agaccaggtt ttttcaacaa caaggtagtg ccactagatg ttctactcac cccacgcaca 1680 ctagattaa 1689
3-184	**Sequences**	
3-184-1	Sequence Number [ID]	184

[0089]

3-184-2	Molecule Type	DNA
3-184-3	Length	2561
3-184-4-1	Features Location/Qualifiers	**source** 1..2561 mol_type= genomic DNA organism= Papaver bracteatum
	NonEnglishQualifier Value	
3-184-5	Residues	atgaataact actcatcatc acctgcatca tcaacagaaa cagcggtact ttgtcatcag 60 cggcagcagt cgtgtgcatt gccaatttcc ggtcttcttc acattttcat gaataaaaac 120 ggcttaattc atgtaactct tggaaatatg gcggataaat acggaccgat tttcagtttc 180 ccaacaggta gccatagaat tctcgttgtg agcagttggg agatggtaaa agagtgtttt 240 acaggcaaca atgacactgc tttctcaaac cgtcctatcc cgttagcttt taagactata 300 ttctatgcat gccgtggcat agactcatac ggtctttcga gtgtacctta tggaaaatat 360 tggagggagc tacgaaaggt ctgtgtgcat aacctcctct ctaatcaaca actactcaag 420 ttcagacact tgataatttc tcaagtcgat acgtctttca ataagctgta tgagttatgc 480 aaaaactctg aagacaacca gggaatggtg agaatggatg attggctcgc ccaattatcg 540 ttcagtgtga taggaagaat agtctgcgga ttccaatcag accctaagac aggtgctcca 600 agcagggtgg aacaatttaa agaagcaatt aatgaagcat cttattttat gtcgacatct 660 ccagtgtcag ataacgttcc gatgctaggg tggattgacc aattgactgg tcttacgaga 720 aatatgacgc actgcggaaa gaaattagac ttggtggtag agagcataat taatgatcat 780 cgtcaaaaga gacgattctc tagaactaaa ggaggagatg agaaggacga tgaacaagat 840 gacttcatcg acatttgctt gtcaataatg gagcaaccac agcttcctgg caacaataac 900 cctcctaaga tacctatcaa atctattgtc ctggacatga taggtgcggg gactgacacc 960 acaaaactga ccatcatttg gaccctttcc ttgctgctga acaaccccaa tgtgttggcc 1020 aaggcaaaac aagaagtgga tgcacacttt gaaacgaaaa agagatcaac aaacgaagca 1080 tcagtcgtgg tggatttcga tgatattggg aaccttgtct acatccaggc aatcatcaaa 1140 gaatcaatga ggttgtatcc ggtcagccca gttgtggagc gactgagcag cgaagattgt 1200 gtggtcggtg ggtttcatgt accagcaggg acgagattat gggctaacgt atggaagatg 1260 caacgagacc ctaaagtatg ggatgatcca ttggtgtttc gaccagagag atttttgagc 1320 gatgaacaga agatggttga tgtaaggggt caaaattatg agctgttacc atttggagcc 1380 ggtcgacgta tatgtccagg tgtatccttc tctctggatc taatgcaact ggttctgact 1440 cgtcttattc ttgagtttga aatgaagtct cctagcggga aagtggacat gacagcaaca 1500 ccaggattaa tgagttacaa ggtggtccct cttgacattc tgctcaccca tcgtcgcata 1560 aagtcgtgtg tgcagttagc atcctctgag agagacatgg agagtagtgg tgtaccagta 1620 atcactctga gatcgggcaa ggtgatgcct gttttaggca tgggaacatt tgagaaagct 1680 ggtaaagggt ctgaaagaga gaggttggcg atattaaaag cgatagaggt gggttacaga 1740 tacttcgaca cagctgctgc atacgaaact gaagaggttc ttggagaagc tattgctgaa 1800 gcacttcaac ttggcctaat caaatctcga gatgaacttt tcatcagttc catgctctgg 1860 tgcactgatg ctcaccctga tcgtgtcctc ctcgctcttc agaattctct gaggaatctt 1920 aaattggagt atgtggatct atatatgtta cccttcccgg caagcttgaa gccagggaag 1980 ataacgatgg acataccaga ggaagatatt tgtccaatgg actacaggtc tgtatggtca 2040 gccatggaag agtgtcaaaa ccttggcctc actaaatcaa tcggtgttag caatttctcc 2100 tgcaaaaaac ttgaggaatt gatggcgacc gccaacatcc ctccagccgt gaatcaagtg 2160 gagatgagcc cggctttcca acaaaagaag ctgagagagt attgcaacgc aaataatata 2220 ttagtcagcg cagtctctat actgggatca aacggaaccc catggggctc caatgcagtt 2280 ttgggttctg aggtgcttaa gaaaattgct atggccaaag gaaaatctgt tgctcaggtt 2340 agtatgagat gggtttacga gcaaggcgcg agtcttgtgg taaaaagttt cagtgaagag 2400 agattgaggg aaaacttgaa catattcgac tggcaactca ccaaggaaga caatgaaaag 2460 atcggtgaga ttccacagtg cagaatcttg agtgcttatt ttttggtctc acctaaaggg 2520 cctttcaaat ctcaagaaga gttgtgggat gacaaagctt g 2561
3-185	**Sequences**	
3-185-1	Sequence Number [ID]	185
3-185-2	Molecule Type	DNA
3-185-3	Length	1623
3-185-4-1	Features Location/Qualifiers	**source** 1..1623 mol_type= genomic DNA organism= Papaver bracteatum
	NonEnglishQualifier	

[0090]

3-185-5	Value	
	Residues	atggagttct tgatgaagtt attattgtta cttgaaccaa tcacttttag tatttttctt 60 ggtataggtt ctattgttct tctatacaat gtcttcttct tggttattaa caagaaaaag 120 aagaagaaag caccaaatgc atcaggggca tggccgttga taggccatct caatcttttc 180 atgaatgata aggaagcgtt gtataaaaca ctaggaacca tggccgacaa gtacggacct 240 gcattcaacg ttcgattagg caaccaagaa atccttgtgg tgagtaattg gaagatggta 300 aaagaatgtt ttaacactca aaatgataag ctattttcga atcgtcgaac tacattgggt 360 gtgaaataca tgcttaacaa gaagacctct gttgcctttt caccatatgg aacatattgg 420 agggagctac gaaagctaac ggtgcaacaa ttgctctcta agcaacgttt agattcgtgg 480 aaacatttga aaatcaaaga aatagatgct tcatttggta gacttaacga tttatgcagc 540 aacaacaagg gtactggagc agctacccca attaggatgg acagttggtt tgccgagttg 600 acgttcaacg tgttcgcaag aattgtcttt ggctaccaaa gtggagaaag gttgatgcta 660 tcaggtgata cggcatccaa cggggagagg tacaagaaaa cattagaaga agcatttctc 720 cttatgtcaa gctttgcggt ttctgacgta ttcccatgct tagagtgggt agacagatca 780 agaggccttg taaggagcat gaaacgcttt ggagatcagc taaattcaat tgcagggtgt 840 cttattgagg agcatcgcca aaagagatca caatccgtat cagcatcaaa ttctacaaat 900 gataaaggag ttggtgatga acaagacttc attgatgttc tcttatcggt tgctgaacta 960 tcacaaattc ctggagatga ccctgatttg gtcatcaagt ctatgatttt ggaagcctta 1020 gcaggtggga gtgacacaac aacatcaacc ctaacttggg ttctttcact gctattgaac 1080 caccccaaag tgttaaagac ggcaaaagag gaaatagata tgcacgtcgg acgtaatcga 1140 tgcgtagaag agtcagatat tcccaagctc gtttatgtca atgcaattat caaagaatca 1200 atgagattgt atccaaatgg gtcattggtt gatcgattga cgttggaaga gtgtgaagtt 1260 ggtggattcc atgtcccagc tgagggacac ttattcgtaa acgtttggaa gatccataga 1320 gatccgagtg tgtgggagaa tcctctggag ttcaagccag agagattttt gagtaatgat 1380 tgcaaggtgg atatggattt cataagtcaa aaatatgaat tcataccatt cgggataggt 1440 cggaggatat gtcctggtat gctttcagca ttacaggtga tgcattttgt ggtagcccgt 1500 cttattcatg ggtttgatat ggaagcagca agtgccgatg ggaaagtgga tatggcagaa 1560 aagccaggca tgacttgcta taagatgaca cctcttgaag ttatgctcac ggctcgacag 1620 tag 1623
3-186	**Sequences**	
3-186-1	Sequence Number [ID]	186
3-186-2	Molecule Type	DNA
3-186-3	Length	1647
3-186-4-1	Features Location/Qualifiers	**source** 1..1647 mol_type= genomic DNA organism= Papaver bracteatum
	NonEnglishQualifier Value	
3-186-5	Residues	atgtatccgg taaaccagtt gcagagtcaa gcaattgctg tgctatgtgc cgtaattgtc 60 ttcatcttct atttggggag aaagttgttt aacagtaccc atattcataa gcctggaaag 120 acagcaccag aaccagcagg cgcatggccg attataggtc atcttcacct ccttgggga 180 gcaaaactca tgtaccgaac cctaggttct ttggcggacg aatacggacc agttttcatg 240 gttcgacttg gtatgcgacg ggttcttgta attagtaaca cggcgtcagc tagagagtgt 300 ttcactacaa atgataaggt ttttgctacc cgcccaacca cagttgctat aaagttgctg 360 acttacaatc acaccatgtt tggttttgca ccttatggac cttactggcg cgagatacgc 420 aagatagcaa caacggagct cctatcggat agacgtctag ccatgctcaa aaacgtgtgg 480 atctctgaga ttaatttgtg cataaatgaa ttacatcaac tcttgatgga caagaatagt 540 agaaaagtag atcatcatca acatgtttac aaccaaaata tggacccaat ttcggtggag 600 atgaacggat ggtttgcaga tttgtctttc aatgttgtgg ccagaatgat agctgggaaa 660 agatatttcg gaaagaacac cgatggtggc gaagaagaaa ccaggaggta tcgggaagca 720 atgaatgatt ttatgcactt ggtagtgata ttattggtgt ctgatgctgt tccattttta 780 gggggtttag acttccaggg atataagaaa aggatgaaga aaactgccaa ggaaattgat 840 tattttctgg gtaaatgggt tgatgaacat cgacagcgtt tgaaatataa aaacatatcc 900 aaggttgatc aacaagatga tttcattgat gtgttactgc tgaatttaaa tgatcaaccg 960 atctatggtc gcgatactga tacaatcatc aagtctactt gcctgtctct tatcgcaggt 1020 ggtagtgaca ccacagcagt taccctaact tgggcactat cgttactgct gaacaaccaa 1080 cacgtgttaa gaaaggctca ggacgagttg gacatacacg taggcaggga aagacaactg 1140 gaagaatcag atatcaagaa cctcgtttat ctccaggcca tagtgaagga aacattgcgt 1200 ttatatccag ctgcaccgtt atcagcacca aggatggcaa tggaagattg tacggttgcg 1260 ggattccaag ttagtaaagg cacacagctg atgcttaatg tatggaaact acatcgagac 1320 ccgcattttt ggggacctga tcctctggag tttaggccag agagatttct tactgctgat 1380 ggtagtagca cgggaagtgg tcattgcatt gatattgatg ttaagggtcg gcattatgag 1440 ttactaccat ttggatctgg tagacggatg tgcccaggag tttcatttgc catgcaagtc 1500 gttcatctga cgctcgctac tttacttcac ggatttcatt tatcgacgcc aacagatggt 1560

[0091]

		ccagttgata tgactgaaac ttcaggactt agttgcccca aagcaacccc attagaagtt 1620 ttgctcactc cacgtctgcc ctgttag 1647
3-187	**Sequences**	
3-187-1	Sequence Number [ID]	187
3-187-2	Molecule Type	DNA
3-187-3	Length	1704
3-187-4-1	Features Location/Qualifiers	**source** 1..1704 mol_type= genomic DNA organism= Papaver bracteatum
	NonEnglishQualifier Value	
3-187-5	Residues	atggatgtgg caatcatcgt cgatcaccac tacttgcagc cgttcgtgag tattgcaggc 60 ttattagctt tgctatcctt cttctattgt atttgggtct ttattataag gccaaggatt 120 atcaaaagca acttagacga gcgcaaatta tcaccatcat ctccacctga agttgcaggt 180 gcatggccga tagtagggca tcttcctcag ctaataggat ctacacctct attcaagatc 240 cttgcggata tgtctaacaa gtacggacct attttcatgg tcagatttgg tatgtatccg 300 accctagtag tgagcagttg ggagatgtca aaagaatgct tcactaccaa cgataggtta 360 ttcgctactc gtccacctag tgcggccgga aagtacctca ctaaagcctt gtttgccttt 420 tctgtgtatg gtccttactg gcgggagatc cgtaagatct ctacaatcca tttactctca 480 cttaggcgcc tcgagttact taagcatgga cggtacttag agatcgacaa atgcatgaaa 540 agattatttg aatattggat ggaacatcat aagaacatca taagcacaac tagttcagtt 600 aaggtcaaca tgagccaagt gtttgcagaa ctatccttaa atgtggtttt gaagataata 660 gttggaaaga cccttttat taaaaatggt aatgaagatt acaccaaaga ggaagaagaa 720 ggccaaaagc tccacaagac tatcctaaaa ttcatggaac tagcgggggt atcagttgca 780 tctgatgttc ttccattcct tgggtggttg gatgtggatg ggcaaaagaa acaaatgaag 840 agggtctaca aggagatgaa cttgattgct tcaaagtggc ttggagaaca tcgagagaga 900 aaaagactgc aaataataca aaaacgcgga gcagcaagag gcagtaatta tgatgatggg 960 aatgacttca tggatgtgtt gatgtcaatt cttgatgaag aaaacgatga tctcttcttt 1020 ggttacagtc gagatactgt catcaaatct acatgtctgc aacttatagt ggccgcttcg 1080 gatacaacgt cacttgcaat gacatgggct ctctcactgc tgctcaccaa tcctaatgtc 1140 ttacagaagg ctcaggatga gcttgatacc aaagttggca gggacagaat aatagaggaa 1200 cacgatatcg agtgtctcgt ctacctccaa gcaattgtca aggaaacact ccgattgtac 1260 cctcccgctc cactctccct accccatgag gctatggaag actgcactgt tggtgggtac 1320 caagtgaaag caggcacacg cttagtagtt aacctgtgga aactgcagcg tgatcctcga 1380 gtgtggtcaa acccgttgga gtttaagcca gagaggtttc ttccacagtc agatggtggt 1440 tttggtggtg aagaagcaag aatggacttc aggggacaac attttgagta cacgccattt 1500 ggatcaggga gaaggatatg cccaggtatc gactttttcc tccagacagt tcacatggca 1560 ctagctcgtc ttcttcaggc atttgatttc aacacagctg gaggactagt tatagacatg 1620 gtggaaggtc caggtctaac catgcccaaa gtaaccccac ttgaagttca cctaaaccca 1680 cgtctgccgg tcacacttta ctag 1704
3-188	**Sequences**	
3-188-1	Sequence Number [ID]	188
3-188-2	Molecule Type	DNA
3-188-3	Length	1677
3-188-4-1	Features Location/Qualifiers	**source** 1..1677 mol_type= genomic DNA organism= Papaver bracteatum
	NonEnglishQualifier Value	
3-188-	Residues	atgcaggtgg attggccaaa catcttacag aagtactacc caataataac atgttcatta 60 ttaactttgc tatccttcta ttatatatgg gtctccatca caaaaccaag caggaattca 120

[0092]

5		aaaaccaaat taccgccacc tgaagttgca ggttcatggc ctatagtagg tcatcttcca 180 cagctagtag gatctacacc tttgttcaaa atccttgcta acatgtctga caaatatgga 240 cctatcttca tggtccggtt tggtatgcac ccaaccttag ttgtgagtag ttgggagatg 300 tctaaggaat gcttcaccac caatgacaag ttcctcgcca gtcgtccacc tagtgcttca 360 gccaagtacc tcggttatga taacgccatg tttgttttct cagattatgg tccttattgg 420 cgtgagatac ggaagatctc tactctccaa ttactcacac acaagagact cgattcgctg 480 aagaatatcc cttacttaga gatcaacagc tgcgtgaaaa cgttatatac ccgttgggcg 540 aaaacccaaa gccagataaa gcaaaatgtt ggaggtgcag ctgacgattt tgttaaagtc 600 gacatgacag aaatgtttgg acatctaaac ttaaatgtgg tgttgaggct tgttgtagga 660 aagcctattt ttatccagaa agacaatgct gatgaagact acacaaagga tggccataac 720 aaagaggaat taggtcaaaa gcttcacaag actatcatag agttctttga attagcaggt 780 gcttcagtcg catctgatgt tcttccatat cttgggtggc ttgatgtaga tggacaaaag 840 aaacgcatga agaagatagc catggagatg gacttatttg ctcaaaaatg gcttgaagag 900 caccgacaaa aaggaatcaa tcatgataat gagaatgact tcatggccgt gttgatatca 960 gttcttggtg aaggaaagga tgaccacatc ttcggttaca gtcgggacac tgtcataaaa 1020 gccacatgtt tgacacttat cgtagcggct acagacacca ctttagtgtc attgacatgg 1080 gctctctcac tactactcac caatcctaga gtcttaagca aggcgcaaga tgagcttgac 1140 acagtagtcg gcaaggaacg aaacgtagaa gatcgagacg tcaatcacct ggtctacctc 1200 caagcagtca tcaaggaaac tctccggttg taccctccta gcccactcgc cgtaccccat 1260 gaggctattg aaaactgtaa tgtgggcggg tatgaagtga aagcaaggac acgtttattg 1320 gttaacttgt ggaaaattca tcgtgatcct agagtatggt caaacccgtt ggagtttaag 1380 ccagaaaggt ttctcccaaa actggatgga ggtactggtg aagcttctaa gttggacttc 1440 aaaggtcaag attttgtgta tacaccattc ggttcgggac gaaggatgtg cccagggatc 1500 aactttgcca gtcagacgct tcacatgacg ctagctcgcc tactccatgc attcgatttt 1560 gacattgagt caaatggact agtaatagac atgacggaag gttcaggttt aaccatgccc 1620 aaagtaaccc cactccaagt tcaccttcgc ccacgtctcc ctgccacact ttactag 1677
3-189	**Sequences**	
3-189-1	Sequence Number [ID]	189
3-189-2	Molecule Type	DNA
3-189-3	Length	1716
3-189-4-1	Features Location/Qualifiers NonEnglishQualifier Value	**source** 1..1716 mol_type= genomic DNA organism= Papaver bracteatum
3-189-5	Residues	atgatggatc tagcaatgtt catcgatcaa tacttctcat tagctaaaat tgcaggctta 60 ttagctttgt tatctttctt ctattatcta tggatctcaa ctttgtggtc gccaaggaat 120 cccaaactat catcagtatc accacctgaa gttgctggtg catggcctat attaggccat 180 cttcctcagc tactaggatc aagacctcta ttcaaaatcc tagcagacat gtctgacaat 240 tatggtccga tcttcatggt ccggtttggt atgcatccga ccttggtggt aagcagttgg 300 gagatggcta aagagtgctt caccaccaac gacaggttcc tcgctggccg cccatcgggt 360 gctgccaaca agtacctcac gttcgccctg tttgggtttt ccacatacgg cccttactgg 420 cgagagatcc gtaagatcgc taccctccat ttactctcac ataggcgtct cgagcttctc 480 aagcatgttc ctgacttgga ggtcaccaac tgcatgaaac acttgcatcg acgctggata 540 gacagtcaaa accaaataaa acaaaatgac gctgcagctg gttcagtaaa agttgacatg 600 ggcagagtat ttggcgagct aaccttgaat gtggtgttga agttagttgc tggaaaatca 660 attttttca agaacgacaa cactcgtcaa tatgactcca aggatggtca taacaaagag 720 gaggaagaag gtaaaaagct ccataagacc atcatagatt tctactcatt agcaggagct 780 tcggttgcat ctgatgttct tccatttctt gggtggttgg atgtggatgg acaaaagaaa 840 cgcatgaaaa gggtagccaa ggatatggat ttcatcgctg caaagtggct tgaagagcac 900 cggcatcaaa aaagacaaac agtactatca agctcagcaa cactaggcag cagtaatcat 960 gacgatgcga aagatttcat ggacgtgttg atgtcaattc ttgatgggga aaatgatgat 1020 ctcttctttg gttacagccg tgacactgta atcaaaacca catgtctgca acttatagca 1080 gctgccgcag ataccacatc agttacgatg acatgggctc tcgcactact aattactaat 1140 ccgaccatat taagaaaggc tcaggatgag cttgatacca aagtaggcaa ggacagaaac 1200 atagaggaac gcgacatcaa tgatcttgtc tacctccaag caattgttaa ggagacactc 1260 cggatgtacc ctgctggccc actcaacgta ccccacgagg ctatcgcaga ctgcaatatt 1320 ggtgggtatg aagtgagagc aggcacccgt ttgttggtaa acctatggaa aatgcaccgc 1380 gatcctcgag tatggtcaaa tccgtcagag ttcaagccag agaggttcct tccacaactg 1440 gatggtggat ctggtggtga ggcggcaaac ttggacttca ggggtcaaga ctttgagtat 1500 ctacctttta gtgcaggaag gaggatgtgt ccagggatcg acttttccct ccaaacgctt 1560 catatgactc ttgcgcgcct gcttcatggg ttcgatttca acaatgactc ggcaggaata 1620 ataatagaca tggaggaagg ttcaggttta actatgccca agttaacacc actagagatt 1680 tacctctgcc cacgccttcc agccaaactc tactag 1716

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3-190	**Sequences**	
3-190-1	Sequence Number [ID]	190
3-190-2	Molecule Type	DNA
3-190-3	Length	1632
3-190-4-1	Features Location/Qualifiers	**source** 1..1632 mol_type= genomic DNA organism= Sanguinaria canadensis
	NonEnglishQualifier Value	
3-190-5	Residues	atggagtttc tttctctaca attccaaccg attaccattt ttgcccttct tcttgccact 60 cccatttttc tgtacaatct ctggaattat ggaaggaaac tcaacaacaa gaacaagaag 120 agcagaaaac caccagcacc tgaagcatca ggtggatggc cgatcatggg tcattttcat 180 cttttcaatg gaaccgaggt gactcaccga gctctcggtt ccatggcgga caaatacggt 240 ccagctttca atatccgaat cggttctcat ccaacacttg ttgtgagtag ttgggagatc 300 gctaaggaat gtttcaccac aaacgaccga ctcttctcaa ataggccagg ttctttagcg 360 attaaactca tgttctacga tgccgattcg gttggttatg caccgtacgg aacttactgg 420 agagagttga gaaagatttc aactctaaaa cttctttcaa atcacagatt ggaaacgctt 480 aaacatttga gaacatctga agttgaatcc tgttttaagc agcttcatga tttgtggcgg 540 atgaacaata aaaagggggg gagcgatgat ggatcagatt ttgctctggt gaggatagat 600 aattggtttg gtgatttgac ttttaatgtt gtggcgagaa ttgttgccgg gaaaaagaat 660 tttgcgggag gtgcggcgag tggtgatgcc ggagctcaaa gatataagga agccatggat 720 gaagcgtttc gtttgatgac gaggtttgcg ttctcagatg ttgttccatc gcttggatgg 780 ttagataaat tgacaggact tgttggagga atgaaacgtt gtggatctga aattgattcg 840 atcgttgcaa gttgggtgga tgaacatcgg ttgaaaagaa tttctggaaa agaaggggat 900 gatcttgaac aggatttcat cgatgtttgc ttagagattt tggagcattc tactttgcct 960 ggcgatgatc ctgaagttgt catcaaatct acttgcctgg acatgatatt gggtgggagt 1020 gacaccacaa cagtgaccct aacatgggcc ctctccttac tattggacca tccccacgtg 1080 tggaaaaggg cgaaggagga agtggatgca cacgtgggaa aggagagaca ggtggaggac 1140 tcagatatcc ctaatcttgt gttcatccaa gcaatcgtca aagagacgat gagattgtac 1200 ccagctggac cactgatcga gcggaggaca atggatgatt gtgaggtagg tgggttccac 1260 ataccaggtg gcacacgttt aattgtgaat ttatggaaga ttcaaagaga cgggagcgtg 1320 tacaaggagg atccattgga gtttagacca gagaggttcc tgacgagcaa cgcggaggtg 1380 gatctaaagg gacagaatta cgaactgata ccatttggtg ctggaaggag gatatgtcct 1440 ggagtgtcgt tcgcagtgca attgatgcat ttggtactgg ctcgtctcat tcacgacttc 1500 gaaataacga tgcccatggg tgcgaaagta gacatgactg agagtggagg actaatcagc 1560 cacaaggtga cgccgctgga agtgctgctc aaaccacgcc tcccctcgct ccaacaagca 1620 gctttatatt aa 1632
3-191	**Sequences**	
3-191-1	Sequence Number [ID]	191
3-191-2	Molecule Type	DNA
3-191-3	Length	1578
3-191-4-1	Features Location/Qualifiers	**source** 1..1578 mol_type= genomic DNA organism= Sanguinaria canadensis
	NonEnglishQualifier Value	
3-191-5	Residues	atggaatatt cctcagtact tctccattgg ttccctgctt ccatggctgc ccttcttgcc 60 ttggtttttc tgtacaatct catctttaat tccccaaaaa ccggtaataa gaagattata 120 aggagggcac ccaaagcagc cggtgcatgg ccagtccttg gtcacctcca tttgtttgga 180 tcaggtgagc tgcctcacaa aatgctcgca gccatggcag aaaaatacgg ccccgccttc 240 acaatgaaat tcggtaagca cacgacacta gttgtgagtg acacccgcgt cgtaaaagaa 300 tgtttcacca ccaatgacac cctctttgcc aaccgtccat ccaccaaagc ctttgatctc 360

[0094]

		atgacttacg ccaacgactc ggtagccttc acaccttaca gtccttattg gcgcgagctt 420 agaaagatat ccactctcaa acttctctct aaccaccgcc tccaatcgat caaggaagtc 480 cgagtctccg aggtgagcgt atgttttagg gagctatacg atatatgcaa aaatgatgga 540 ggaggagctc ctccagtttt ggtggatatg aagaaatggt tcgaagaggt ctcgaacaac 600 atagtgatga gggtaatcgt agggaaacaa aattttgggt cgaagattgt ttgtggcgaa 660 gaggaagccg tcaattacaa gaacgtcatg gatgagctcc tacgtcttgc tagtgtgtct 720 atgttatcgg atgtggcacc tttacttggt tggttggata tgttccaagg acacatgagc 780 gccatgagac gaaatgggaa aaaactagac accatacttg agaggtggtt ggaggagcat 840 cggaagaaga agagtgagga tgagcaagat ttcatggatg ttatgttgtc gatcgttgag 900 gagactaagt tgtctggccg cgacgctgat accgtcatta aagctacttg tctggccatg 960 atcatgggtg ggacagacac cacggctgtg agtctaacat ggatcgtttc cttattgatg 1020 aacaatcgct atgcattgaa aaaggctcga gaagaattgg acgcgctcgt ggggaaagat 1080 agacaagttg aagattcaga tttgaagaat ttggtgtact tgaatgccgt cgtcaaggaa 1140 acgatgcgat tatacccgtt gggtactctt cttgaacgtg acaccaaaga agattgtgag 1200 gttggtgggt tccatgtgga aggcggtacg cgtttactag tgaatgtatg gaagttacaa 1260 cgagacccaa acgtgtggaa tgatccatta gaatttagac cagagagatt tctaacagag 1320 aatgcggata tagatgtcgg aggccaacat ttcgaattac taccatttgg ggcagggaga 1380 agggtgtgcc caggagtgtc gttcgcactc caattcatgc atttggtatt ggctcgtctc 1440 atccatggct atgaattggg aacccaaaat gatgaggatg tggatctaac tgagagcaca 1500 gaaggacatg ttaaccacaa agcctccccg ctcgatctcc tcatcacccc acgcctccac 1560 cctaaacttt atgaataa 1578
3-192	**Sequences**	
3-192-1	Sequence Number [ID]	192
3-192-2	Molecule Type	DNA
3-192-3	Length	1584
3-192-4-1	Features Location/Qualifiers NonEnglishQualifier Value	**source** 1..1584 mol_type= genomic DNA organism= Sanguinaria canadensis
3-192-5	Residues	atggattatt catcccattt gaaccagttc tacggggtag ctccatacat ggctgcccta 60 ctaattgcct tagtgtttct ctacaatatt ctttgggctt ccccaaaaac caccaacaag 120 aaaccaatca tggcagccgg ggcatggcca attctaggcc acctccatct gtttaaagat 180 ggggaattgc ctcaccacat gcttaaatcc atgtctgata aatacggccc tgccttcctc 240 atgaagttcg gccaacaccg aacactcgtt gtgagcaact accgcatggt aaaagaatgt 300 ttcactacta atgacaccca cttttgcaac cgtccatcca ccacagcctt cgatgtcatg 360 acttacgcta atgactccgt cgctttcaca gcttacagcc cttactggcg tgagcttaga 420 aagatttcca ctctcaaact tctctctaac aaccgtctcc aggccatcaa gaacctccga 480 gaagccgagg tgaacgtatc tttcaggggg ttgtatgatt tatggaagaa taatagtgat 540 cgagctgcgt cggttttggt cgatatgaag aaatggtttg aagaggtctc aaacaacgtc 600 gtgattaggg tgatcgtggg gaaacataat tttgggacta agattgtgaa gggtgagaag 660 gaggctgtgg aatacaagac gatcatggat gagctcttac gtcttgctag tttgtctttg 720 ttatctgatt ttgctcctat acttggttgg gtggacttct ttcaaggaaa cgttcgaaaa 780 atgaaacgaa atggcaagaa actagacgtg gtacttcaga ggtggttgga gacgcatcgg 840 aggaagaaga actcaccaga ggatgaacaa gacttcatgg atgttatgtt gtcgatcgtt 900 gaggagggcg acaagttgtc tggccaccac gctgatactg tcattaaagc tacttgcttg 960 gccatgataa tgggtgggac agacacgtcc gcagtgagtc taacatggat cgtctcctta 1020 ctgatgaaca atcgtcatgc attgaaaaag gctcgtgaag aattggatat gtacgttggg 1080 aaggataggc aagtagagga ttcagattta aaggacttgg tttacttgca tgcaatcgtt 1140 aaagaaacca tgcgactgta cccactgggt actcttcttg aacgcgagac caaagaagat 1200 tgtaaggttg gtgggttcca cgtcgaagcc ggtacgcgtt tactagtgaa catatggatg 1260 gtacaacgag acccaaccgt gtggagtgat ccaacaaaat ttataccaga gaggtttcta 1320 acagagaagg cggacataga tgttgggggt cagcatttcg aactcatacc attcggggcc 1380 ggtagacggg tgtgccctgc cgtgtccttt gcactccaat ttcttcactt gatactggct 1440 cgtctcatcc atggatatga attaggaacc ccaaatgacg cggatgtcga cttaaccgag 1500 agcccggaag gacatgttaa ccacaaagca tcccctctcg aactcctcct cacccacgc 1560 ctcgacccta agctctatat atga 1584
3-193	**Sequences**	
3-193-1	Sequence Number [ID]	193

[0095]

3-193-2	Molecule Type	DNA
3-193-3	Length	1608
3-193-4-1	Features Location/Qualifiers	**source** 1..1608 mol_type= genomic DNA organism= Sanguinaria canadensis
	NonEnglishQualifier Value	
3-193-5	Residues	atgaattcaa tcgcagtcgt cggtgttctt cttttcttcc tctactatct atggaggaca 60 ctattcacca ctcacaaagc ggcgccacca ccacaaccag ccggagcaag gcctattata 120 ggtcacctac atctcctcgg tggagcgaat caactagtcc atcaaacact cggttccatg 180 gcagacaagt acggatcaat tttcatgatc cgactcggga tgcgacgagt cctcgtggtg 240 agtagctccg agttagctaa agaatgtttc actacgaacg acaaggtttt cctcaaccgc 300 ccaagttcat tagctttaaa gctgatggcc tacaacaacg ccatctttgg ttttgcacct 360 tttggtcctt actggcgtaa gatgcgcaag atagcagtca ccgaacttct atccaacaga 420 cgcctcgaga tactaaaaaa catcaggatc tccgagatca acatgtctat aaaagaatta 480 catcaactat gggtagatat gaacagtggt gatgatcaag tggggggccc accaattgtg 540 gtggaaatga gaaagtggtt tggggattta tcgttcaacg tggtgggtag aatgatagct 600 gggaaaagat attttgggag gaattgtgat tgtgatgaag aagaaacgag gaggtatcag 660 aaggcgatgg gtgattttat gcatttagtg ggggtttttg tggtgtcgga tgcgattccg 720 ttattagggt ttttggattt acagggatat gagaagaaga tgaaaaggac ggccatggac 780 attgattgtg ttttagggag atgggttgat gaacatcgac gacgacgaca agaccacgat 840 gagaagagga ttatggtctc cgatgatgat catcaaggac aagatttcat tgatgtgatg 900 ctatcgatct taaatgatga tgatcagttc tacggttacg atgctgatac agttatcaag 960 tctacctgcc tgtctcttat cgcaggcggc cacgagacca cggcggtcac actaacatgg 1020 gccctctctt tactactaaa caatcgacac gtgttacaaa acgcgcaaga tgagttggac 1080 atccacatca gcaaggaaag acaagtggac gaatcagata tcaagaacct gaaatacctc 1140 caagccatag tcaaggaagc attgcgttta tacccagctt taccactttc agcactaaga 1200 ttggccatgg aggactgcac catagctgga tttcatgtcc ctaaaggcac agaattgatg 1260 cttaatctat ggaaattaca tcgagaccct cacgtttggt ctgacccttt ggagttcaag 1320 ccagaaaggt ttcttactaa tagcacccat gaagaagttg acgttggggg tcaacattac 1380 gaattactac catttgggtc tggtagacgg atgtgccctg gggtatcgtt tgctcttcaa 1440 gtcctgcact tgacgcttgc tcgtctactt catggatttc atttgtcgac tccgtccggt 1500 gtacctgtgg atatgactca aagttttggc cttagttgcc caaaagcaac tcccttggat 1560 gtcctcctta caccacgtct cccttcaaag ctatattatg tagcataa 1608
3-194	**Sequences**	
3-194-1	Sequence Number [ID]	194
3-194-2	Molecule Type	DNA
3-194-3	Length	1806
3-194-4-1	Features Location/Qualifiers	**source** 1..1806 mol_type= genomic DNA organism= Sanguinaria canadensis
	NonEnglishQualifier Value	
3-194-5	Residues	atgatttcaa ctacgccgga cgtactagct acctcatcat attcatcatc taacaagcat 60 atggattcag atcatcttta ccggttctca actagtacta gtatagttat tggcctcttt 120 attttactat tcttccttgt gctcctatgg aaaccaaaga agcagtctgc tacttctaag 180 actaacaaac caactagaga gcagcgggca ccggaacctt ctagttcatg gcccataatc 240 ggtcatctcc gtctcttcgg aggaccaaat agccttcccc acataacatt gggagctatg 300 gctgataagt atggaccagt cttcaccatc cgaatgggtt cgcgtccagt gcttgttgtg 360 agtagttggg agacggcgaa agaatgtttc accaccaacg acagggtctt cgcctctcgt 420 ccacgcacta tagccattaa acatatgtgt tatgaacatg tcatgcttgg gttcgcccct 480 tacggatcat actggcggga attgcgcaag atagtgaacc gagagcttct ttcgaataat 540 cggctagagt tgttaaaaca tgtatgggga tctgagatta acacatccat taaagaactg 600 tatgagttgt ggttggtgaa caaaaacaac attgaagcag aaggtgaaaa tgaaggtaca 660 agtgataggg ttttggtgga gatggagaga tggtttgcgg atttgactct aaacatgtct 720 attaagattg ttgttgggaa gcgatacccc tccggtgtta ctgccggtgg tagttctggt 780 tgtgatgatg atgaagctca gaggtgccgg aaggccctga gagatttctt taagctggtg 840

[0096]

		ggtctgtttt tggtgtcgga tgcgatcccc tttctaaggt ggttggactt gggtggttat 900 gaaagagaga tgaagactac tgcaagagag ttggactgtt taatggagga atggttggaa 960 gaacataaaa tgaagaggag attattaatt tcaccgtcgg caggtgatca tcatgaagct 1020 gcagagatca tgatcaataa gcagaaggaa gcagagctac aggaatatga cttcatggac 1080 gtgatgctat ccatacttga tgacgatatt gagggtaaaa acctttcaga ttacgacgtc 1140 aatgccgaca ctatcaacaa gtctacttgc ctgaatctaa tcctaggtgg gagcgacaca 1200 acaatggtta ctttaacatg ggccctcgct ttactactaa ataatccaca cgtgttacaa 1260 aaggcccaag atgagttgga tatccacgta ggcagcaaga gacaagtgga cgattcagat 1320 atgaagaacc tcatatacct ccaagctata gttaaggaaa caatgcgcct atacccagca 1380 ggtccactat cagtaccaca cgaatcaact gaagactgca ccgtagctgg ctaccacgtc 1440 cctgcaggga cccgtcttat tgtaaatacc tggaagatcc aacgtgaccc acgggtatgg 1500 tccaacccat cagaattcaa accagagaga tttctcacag acagtcacgt ggacatagat 1560 gttagaggtc ggaattttga attgatccct tttgggtcgg gcaggaggtc gtgcccgggt 1620 acctcatttg cactccaagt ggtgcacctg gtactggccc gtttgataca tgggttcgag 1680 tttaaaacac cgtcggaagc acccattgat atgacggaga gcgtaggcct aagtaatttt 1740 aaagccaccc cacttgatgt tctgctcacc ccacgtctcc cttctcagct ttattatgtt 1800 tcttag 1806
3-195	**Sequences**	
3-195-1	Sequence Number [ID]	195
3-195-2	Molecule Type	DNA
3-195-3	Length	1578
3-195-4-1	Features Location/Qualifiers	**source** 1..1578 mol_type= genomic DNA organism= Sanguinaria canadensis
	NonEnglishQualifier Value	
3-195-5	Residues	atggattcta ctttggtttt cattggcctc tttgctttac tactagtcta cccccttacta 60 ctaagaagat cagtattgaa gtctacttca aatactaata agactactta taaatcgaaa 120 aaccaagcac cggaggcggc cggggcgtgg ccgataatcg gtaatcttca tcaactcgcg 180 ggtggaggaa actgtctcca taaaacgttg ggagccatgg ctgacaagca cggaccggct 240 ttcaccatcc ggatgggtct acataaagca cttgtggtga gtagttggga gctagcgaaa 300 gagtgtttca ctaccaacga cgtggttttc atgtcccggc cgcatcaagt agccattaaa 360 cacatgggtt acagcaccgc catgtttgga atcgctcctt atggcccata ctatcgcgaa 420 atgagaaaga tagtgactca agagcttctc tctaaccgcc gcctagagtt gctaaaacat 480 gtatgggcct ctgaaatcaa caactccatt aaacaactct acgagaaagt cgaaggcgga 540 ccagttttga tcgaaatgaa gcgatggttt gcggatttaa cgctaagaac gacggttaag 600 gtgatttgtg gacagcaaca atttggagga gatgatgatg atgatgaagc tggaaggttt 660 caaacggcgc tgagagactt ctttaggttg ttaggtcact ttcgagtggc ggatgtgata 720 cctgttctag agtggctcga ttttcaggga tacaagaaag agatggagaa taatggaaga 780 gtgcttgata atttaatgaa taaatggttg gaagaacata aaaggaagag gaagaacggt 840 ggcaccgaag aggacttcat gaacgtgatg atatccaaac tgcttgatga tacaaagatg 900 ctttcctatt acgacgccga tactatcaac aaatctactt gcctgacact aatcctgggt 960 gggagtgaca caaccatggt tagtttaacg tgggcccttt ctttactagt gaatcatcca 1020 catgtgttga aaaaggccca agaagagttg gatgtccacg taggcaaaga aagacaggta 1080 gacgattcag atctctggag cctcacatac cttcaggcta ttatcaagga aacattgcga 1140 ctatacccac ctggtccact ctcagctcca cgcgaatcaa cggacaactg caccatagct 1200 ggctaccacg tccctgcagg aacccgtcta atagtgaata cctggaagat tcaacgtgac 1260 ccacgggtat ggcccgaccc attagagttc aagccagaga gatttctcac cacccatgtg 1320 gacgtggacg ttaaaggtca gaatttcgaa ctcctaccat tcgggtcggg tagaagagca 1380 tgcccaggtg cctcattcgc gcttcgggtg ctgcgcctgt cactggctcg tttgatacat 1440 gggttcgact ttaaaacacc attggacgac tcacccattg atatggtgga gagtggagga 1500 ataactaatg ttaaagacac cccacttgaa gtactagtca ccccacgcct cccttctagt 1560 ctttatgttt gcaaatag 1578
3-196	**Sequences**	
3-196-1	Sequence Number [ID]	196
3-196-2	Molecule Type	DNA

3-196-3	Length	1599
3-196-4-1	Features Location/Qualifiers	**source** 1..1599 mol_type= genomic DNA organism= Sanguinaria canadensis
	NonEnglishQualifier Value	
3-196-5	Residues	atggattttg atctttacca attctcaaaa cctactatct tcattggagg cctctttgct 60 atacttctct actttgtact caaaaaatct agtactccca aatccaaatc aaaattagaa 120 caaccacccg aaccggctgg cgcgtggccg atcatcggtc atcttcctct cctcggagga 180 cccgatctcc ctcacataac attaggaaaa ttggctgata aatatggacc agccttcacc 240 atccgaatcg gtgttcataa agcggtggtt attaatagtt gggaggtggc gaaagagtgt 300 ttcaccacca acgacaaggc gttttcttcc cgtccgcgtc aagtagccat gaaacacatg 360 ggttacgatt acgccatgtt tgggttcgcc ccttacggaa attactggcg tgaactccgt 420 aaaattgtga accgagaggt tctgtctcat agtcggatcg agtctttata tcacgtatgg 480 ggtactgaga tcaacacgtc cgttaaagaa ctgtacgagt tgtgggggaa gaaaagcacc 540 ggcagcggcg gtgcaccggt cttggtggaa atgaaacgat ggttctccga catgacactc 600 aacatgtctg ttatgatggt tgcaggtaag agatacaact ttagtggcaa caaagctgac 660 gatgaagctg ggaggtgcca agatgggctg aggaacttct ttcggttagt cggtctgttc 720 gtgccatccg acgcgttgcc gtttttggcg tggttggaca ttggtgggta cgagaaagaa 780 atgaagaaag tagcgaaaga gcttgatgtt ttagtgcagg aatggttgga agaacacaaa 840 gagaagaggt tggcattgac ggccgcgggg aagaaaggaa gcgaaaacga tttcatggac 900 gtgatgatga atatacttga agatcaaaaa ctatcagaat tcgatgcaga tactatcaac 960 aaggctactt gtctgacttt aatcctcggt ggaaccgata caaatatggt taacttagtg 1020 tgggccctga ctttactggt taacaatcaa gatgcgttga agaaagctca tgatgagttg 1080 gacttccacg taggcaaaga tagacaagtt gaagaatcag atgtaaagaa cctcgtgtac 1140 atccaggcta taatgaagga aacactgcgt ctatactcgg gcccactgtc gggcttacgc 1200 gaatctacgg aggactgcac cgtagctggt tactacgtcc cagcagggac ccgtttgatt 1260 attaatgcag cgaagattca tcgtgaccca cgggtatggt ctgacccaac agctttcaaa 1320 ccggatagat tcctcacgga acagaaagaa atggatgtta gaggtcagga tttcgaaatc 1380 cttccattcg gggcgggtag aagaatatgc ccgggtgtgt cattcgcact tcaagtattg 1440 ccattggcac tggctcgatt aatacatggg ttcgacttta aaacacccac ggatgcaccc 1500 attgatatga cagaaagtcc aggactaact aatgctaaat ccaccccact cgaagttcta 1560 gtctcacccc gcctcacttc taaactttat ggttgttaa 1599

[0097]

3-197	**Sequences**	
3-197-1	Sequence Number [ID]	197
3-197-2	Molecule Type	DNA
3-197-3	Length	1668
3-197-4-1	Features Location/Qualifiers	**source** 1..1668 mol_type= genomic DNA organism= Sanguinaria canadensis
	NonEnglishQualifier Value	
3-197-5	Residues	atggattcta ttctaaacca gttcatctca aaacctacta tggttatttg cagcctcttt 60 gctttactat ccctctactt tctactgatc aaaaggtcta ccactaaatc aaaattacaa 120 ctgccacccg agccggcggg tgcgtggcct gtcatcggtc atctccatca gttgggtgga 180 cctaacttac cccacataac attagcagcc atggctgata agtatggacc aatcttcacc 240 atgaaaattg gtacgtatcg agcactcgta gtgagtagtc cggaggtagc gaaagagatt 300 ttcaccaccc acgataggat atgggcaacc cgaccaaatc aagcagccat gaaacacttg 360 ggttacgact cggccatgtt tgggttcgca ccttatggac catactggcg tgaacttcgc 420 aagttagtga accgagaact tctctctaat actcggctcg atttgctaca tcatgtgtgg 480 gattctgaga ttaacacttc cattaaagaa ctgtacgatt cgttagcgac caaaaacaat 540 gcaaaaggcc gtggtactgg cggcgccggt agtactggtc ctgttttggt ggaaatgaaa 600 cggtggttcg cggatttgac gctaaacata actgttagga tggttgctgg gaaacgatac 660 tttggtgcta ataaaacttc tagtactagt actgatcaat gtgataatga aaaaggagat 720 agtaaagcat ggaagtgcca aagggagctg agaaacttct ttaggttggt aggtctgttt 780 gtagtgtcgg acgcgttacc gtttcttggg tggttggatt tgggtggtca cgagagagag 840 atgaagaata ctgcaagaga gttggatgtt ttagttcaag gatggttgga tgaacataag 900 aggaagagat cattatccgt ggctgaaggc ggggagaaga tcaacggcga acaggacttc 960 atggacatga tgctgtccac aatcgacgac gctaagttat ctggttattt cgacgctgat 1020 actatcaaca agtctacttg tctgaatcta atcctgggtg ggagtgacac aatgatggtt 1080

[0098]

		aatctaattt ggcccctcac gttactggtg aactatccag acgagttgaa gaaggtttat 1140 gatgagctgg acacccacgt aggcagagat agacaagtgg acgaatcaga tatcaagaat 1200 ctcgtgcacc tcaaggctgt aatcaaggaa acaatgcgtc tatacacggg tcggatcaca 1260 ggcctccgcc aatcatcaga ggattgtacc gtggcagggt accacgtacc agcaggtacc 1320 cgcctgattg taaacacgtg gaagattagc cgagacccac ggtactggtc cgacccgtta 1380 gagttcaagc cagagagatt tctcacgacc catgcggata tcgagcttac aggtcagaat 1440 tttgaactaa tcccgtttgg gtcgggcaga agatcatgcc cgggtgcctc atttgcaatt 1500 caattgctgc acctggcact ggctcgtctg gtacatgggt tctggtttga aaggccgtcg 1560 gatgcaccca ttgatacatc agagtgtcct ggactaacta attttaaagc caccccactt 1620 gaagttctgg ccaccccacg cctccctttct aaactctatg ttggttaa 1668
3-198	**Sequences**	
3-198-1	Sequence Number [ID]	198
3-198-2	Molecule Type	DNA
3-198-3	Length	1617
3-198-4-1	Features Location/Qualifiers	**source** 1..1617 mol_type= genomic DNA organism= Sanguinaria canadensis
	NonEnglishQualifier Value	
3-198-5	Residues	atggatttta ttctgaacca gttcatctca aaacctacta tggttcttgg caccctcttt 60 gcattactat ccctctactt tctactgatc aaaaggtcta ccactaaatc aaaattacaa 120 ctaccacccg aaccggctgg tgcgttgccc atcatcggtc atctccatct cctcggtgga 180 ccaaaccccgc cccatataac attagcaaac atggctgaga agtacggacc gatcttcagt 240 atcaagatgg gtttaaaacg agcactcata gtgagtagtt cggaagtaac caaggagtgt 300 ttcactaccc atgacttgaa tttcgtctct cgaccacgtc atgcggctat gaaactcatg 360 ggttataatt tcgctacgtt tgggttcgcg ccttatggac cttattggcg cgaacttcgt 420 atgataatta accgagaact tctctctcaa actcggatct tgtcgttaga acatgtatgg 480 ggttctgaga tcaatgaatc cattaaggaa ctgtatgatt tgttgacgag aaaaggtggt 540 ggtggtggtg gtccggtggt ggtggaaatg aagcgatggt ttgcggattt gaccttaaat 600 atagccgtta agatggtgtg tgggaagcga tacttcggtg ttaattctcc tagcactagt 660 acgactcgtg atgttcaaga agatgatgaa gctcggaggt gccaaaaggg gatgagaaat 720 ttctttaggt tgcttggtca gtttgtggtg tccgactcga taccgtttct ggggtggttg 780 gatttgggtg gttaccagag ggagatgaag aataccgcca gagagctcga cgatttaatg 840 cagggatggc tggaagaaca taagaagaag agattggaaa ggaagacggc cgcaggggaa 900 caagacttca tggacgtgat gctgaacata cttgaagatg gaaagctatc tcaatatttc 960 gacactgata ctatcaacaa gtctacttgc ctgagtctaa tcctgggcgg gagtgacaca 1020 acgatggtta atttagtgtg ggccttcagt ttactggtga aacatcaaga tgcgttgaag 1080 aaaactcgtg atgagttgga catccacgta ggcagagaaa gacaagtgga ggaatcagat 1140 atcaagaatc tggtattcct ccaggctgta gtcaaggaaa catttcgtct atacgctggc 1200 ccaatctcag gagtacggga agcagcggag gactgcacca tagcaggcta ccacgtccca 1260 gcagggaccc gtctacttat aaatagctgg aagattcacc gtgacccacg ggtatggtcc 1320 gacccattag agttccaccc agaaagatat ctcgaggcga ggcatgcgga cattgacgtt 1380 aaaggtcaga atttcgaact cgccccattc ggaatgggtc gaagagtttg cccgggttcc 1440 gcatttggac tgcaagtatt gcacctgaca ctggcccgtt tgatacatgg gttcgagttt 1500 aaaacaccgt cagacgcacc cgtggatatg acggagagtg taggaatgag tattattaaa 1560 gccaccccac ttgaagttct cgtcacacca cgcctccctt ctgaactata cgtctaa 1617
3-199	**Sequences**	
3-199-1	Sequence Number [ID]	199
3-199-2	Molecule Type	DNA
3-199-3	Length	1602
3-199-4-1	Features Location/Qualifiers	**source** 1..1602 mol_type= genomic DNA organism= Sanguinaria canadensis

[0099]

3-199-5	NonEnglishQualifier Value	
	Residues	atggatattt ctaatcttta cgagttatac tatttctcca cacctactct gtttgtcgga 60 ggcctctttg ttttattact catctactct ctattctcat ccaggcctgg aattaaatca 120 aaattacaac agccacctga accggccggt gcatggcctc tcatcggtca tcttcctgtc 180 ttaagtggac cggaactacc ccatgtcgca ttgggaaagt tggctgacaa gtacggacca 240 gtcttcacca ttcgtatggg tgttcataaa tcacttgttg ttagtgattg ggaggtaatt 300 aaagagtgtt tcactaccca cgacaaggtc ttctcgtctc gtccttgtca agttgctatg 360 aaactcatgg gtacggccat gtttggcttc tccccttacg gaaattattg gcgtgaactt 420 cgcaagatca tgaacagaga ggttctatct catggtcgga tcgaatctct ttaccatgta 480 tggggttctg agatcaatac gtccgttaaa gaactttacg atttgtgggc gaagaaaaac 540 aatggtggtg gtccaatttt ggtggaaatg aagcgatggt tctccgattt aacgcttaac 600 atgtcggtta tgatggccgc tggaaagcga tataattttg gtgatgattc ttctactact 660 aatgatgaag cggcgaggtg ccaacatgcg ctgagagagt tttttaggtt ggtgggtttg 720 tttgtgccat cggacgcctt accgtatctt gggtggttgg acataggtgg gtaccaaaaa 780 caaatgaaga aagtagcaag agaattggat gatttaatgc aggtatggtt ggatgaacat 840 aaaaagaaga ggttagcagc gaaagccgaa gggaagaagg gaggcgaaca agacttcatg 900 gacgtgatga tgactatact tgaggacgga aagctatctg attattacga cgctgatact 960 atcaacaagg ctacttgctt gactctaatc ctgggtggga ccgacacaaa catgcttagt 1020 ttagtgtgga ccctggcttt actgatgaat aatcgacaag ccttaaagaa ggttcatgaa 1080 gagttggata tccacgtagg cagggaaaga caagtggaag aatcagatat caagaacctc 1140 gtatacctcc aggctgtaat caaggaagaa atgcgtctat actcgggccc actttcaggt 1200 ctacgcgaaa caacggagga ctgcaccata gctgggtacc acatcccagc ggggacccgt 1260 ttgattataa atgcatcgaa gctccaccgt gatcctaagg tatggtccga cccgttagag 1320 ttcaagccag agagatttct tacggaaaac gtgggcgtgg atgttagagg tcagaatttg 1380 gaactccaac cattcggggc gggtagaaga atctgcccgg gtgtctcatt tgcacttcaa 1440 gttttgcccc tgacgttggc ccgtttgata catgggttcg agttgaatac acctggggat 1500 gcacccattg atatgacgga gtctccagga ctacaaaatg ctaaactcac cccacttgaa 1560 gttttaatca caccccgact cccttctaaa ctatatgttt aa 1602
3-200	**Sequences**	
3-200-1	Sequence Number [ID]	200
3-200-2	Molecule Type	DNA
3-200-3	Length	1608
3-200-4-1	Features Location/Qualifiers	**source** 1..1608 mol_type= genomic DNA organism= Sanguinaria canadensis
	NonEnglishQualifier Value	
3-200-5	Residues	atgattgtta ttggcgcctt ccttgcttta gtggtactag tggtctacta taatctacta 60 ctaagaaggc cagcattatt gaaatttaaa aacatgaagc agcaggcacc agaagcggcc 120 agtgcgtggc caataattgg tcatctccat aatctcgcgg gtggcatagg cggaaacggc 180 ctactccacg aaaagttggg agcaatggct gacaagcacg gaccggcttt catcattcgc 240 ttggggctgc ataaagcact ggtggttagt agttgggagg tagtgaaaga gtgtttcact 300 acaaacgacg ttgccctcat ttcccgcccg catcaagtag cttctaaaca catgggttac 360 ggcatggcca tgtttgcgtt cgcctcgcct tatggaccat actggcgcga attgcgtaag 420 attgtgaagc aagaacttct ctctaatagc cggcttgagt tgctaaaaca tgtatgggcg 480 tccgagatca acacctctat taaacaactc tacgagaaag ttaaagaagg tggtggtttg 540 ccggttttgg ttgaaatgaa gggatggttc gcggatttaa ccctaaaaat gacggtaaag 600 gtgatttgtg ggaagcgaca ctttcgagtt gcgggtaatg taggagatca tgttgatgct 660 gatgacgatg atgaagtaat tggtgggcga tttgaaaagg cgctgagaga ctttttagg 720 ttgttaggag atattcgagt ggtggacgtg ttaccgtttc ttcggtggtt ggattttggc 780 gttggttata agaaagagat ggagaataat ggaagagtgc tggatatttt aatggaggaa 840 tggttgcaag aacataaaag gaagaggatg aacggcggca ccgaagagga cttcatgaac 900 gtgatgatat ccaaattact taatgataca aagctgcttt cctattacga tgctgatact 960 atcaacaaat ctacttgcct gactttaatc ctgggtgcca gcgacacaac tatggttact 1020 ttaacgtggg ccctctcttt actagtgaat catccacaag tgctaaaaag ggcccaggac 1080 gagttggatg tccacgtagg cagggaaaga caggtggaag attcagatat ccagaacctc 1140 acataccttc aggctataat caaggaaaca ttgcgaatat gcccaccggg tccgattcaa 1200 gctccacacg aagccaagga cgactgcacc gtagctggct accacgtccc tgcagggacc 1260 cgtcttatag taaatacctg gaagatccaa cgtgacccac gggtatggcc caacccgtca 1320 gagttcaagc cagagagatt tctcacgacc catgtgggcg tggacgttag aggtcataat 1380 ttcgaactca tacctttcgg gtcgggtaga agatcgtgcc cagggacctc gttcgcactc 1440 caagttgtgc atctgacact ggctcgtttc atacatggat ttgagtttaa aacaccgtcg 1500

[0100]

		gacgcaccca ttgatatgac ggagagtgga cgaataacta atgttaaagc caccccactt 1560 gaagttctag tcaccccacg catcccgccg tctggtcttt atgtttaa 1608
3-201	**Sequences**	
3-201-1	Sequence Number [ID]	201
3-201-2	Molecule Type	DNA
3-201-3	Length	1719
3-201-4-1	Features Location/Qualifiers	**source** 1..1719 mol_type= genomic DNA organism= Sanguinaria canadensis
	NonEnglishQualifier Value	
3-201-5	Residues	atggatttgc tgatcttctc cagccagttg caaggtactg tggggttatt agctttacta 60 acctttttcct attatgtatg gattttaatt ataaagagga tcaaaacaac caacaccttg 120 aaggtcatga ataaagtggc ggccgcggcg gcaccggaag ttgccggtgc atggcccata 180 gtgggtcatc ttcctcagct agttggccct caacagcttt acaggattct tggagacatg 240 gccgacgagt atggaccgat cttcatggtc cggtttggga tgtacccaac tctggttgtg 300 agcagttggg agatgataaa ggagtgcttc actaccaacg acaggttcct cgctagtcgt 360 ccctctagtg ctgctgggaa gtacctcact tacgacttcg ctatgttcgg cttctccttt 420 tatggtccct attggcgtga gatccgtaag atctctactc tcgaactact ctcccatcga 480 cgccttgagt tgtttaagaa cgtccctttc actgagatcg acacctgcat caaaagattg 540 taccaacttt ggcgggttaa aaataatgat catccagctg ctgctccggt aattaaggtc 600 gacatgagcc aattgttgag agatctaacc ttaaatacaa tattgaagtt ggtggtagga 660 aagaatttat tcaacgagaa ggatcatggt gaacaggaag agggtcgaaa gctccacctc 720 cacaagacga tagttgaatt ctttaaactg gcaggggttt cagttgcatc ggatgctctt 780 ccgttcctag ggtggctgga tctggatgga cagaagaaaa agatgaagag gatagccaag 840 gaaatagact taatcgctga aagatggctt caagagcatc aagagaagaa atcactatca 900 aacaagaagc tgctggctgc tggcggcggc aaagtagacg gtcatgacga cttcatggac 960 gtgttgttat tcattcttga cgatgattcc cagttcttca atttcagtcg cgacactgtc 1020 attaaagcca cctcttgggc aatgatccta acagccgcgg acaccacatc cgtgtctatg 1080 acatgggctc tgacgctact actcaccaat ccccgtgtct taagaaaggc ccaagatgag 1140 ctggatatga aagtcggcag agacagacac gtggaagaac gagatatcga gaacctgatc 1200 tacctccaag ccatcgtcaa ggaaacattg cgtttgtacc cggctgctcc acttggagta 1260 cctcacgagg ctatccaaga ctgcaccgta gctgggtatc aggtaagagc aggcacacgt 1320 gtgttagtga acctatggaa gctgcatcgc gacccacgtg tgtggtcgaa cccatccgaa 1380 ttcaggccgg agaggtttct aatcgacgat attgacgagc aaggtggtgg tggtggtggt 1440 ggtggcggtg aatcaacagc taaggatttc agaggtcaac attttgagta cataccattt 1500 gggtcaggac gaaggatgtg tcccgggatc aacttcgccc ttcagatcgt tcacatgaca 1560 ctggcacgcc tacttcatgc attcgagttg aggactacta cgtccgcatc actaatggac 1620 atgaccgaag aatcaggcct caccatgccc aagaaaaccc cacttgtagt cctcctccaa 1680 ccacgcctcc ctcttccact ttatgatcac catgagtga 1719
3-202	**Sequences**	
3-202-1	Sequence Number [ID]	202
3-202-2	Molecule Type	DNA
3-202-3	Length	1602
3-202-4-1	Features Location/Qualifiers	**source** 1..1602 mol_type= genomic DNA organism= Stylophorum diphyllum
	NonEnglishQualifier Value	
3-202-	Residues	atggagtttc tctctctaca acaccaacta atttccattt ttgctcttct tcttgcttcc 60 atattcctct acaatctctt gaagaatcat ggaaggaaat ccaagacctc aaaaccacca 120

[0101]

5		gcacctgaag catcaggtgg atggccaatc atgggtcatc tcaatctctt caatggaagc 180 gaattaactc accaagctct aggttccatg gctgacaaat acggtccagc tttcaatatc 240 cgattcggtt ctcatcaaac actcgttgtc agtagctcgg agattgttaa agaatgtttc 300 actacaaacg atcgattctt ttcaaatcgg ccgggatcgt tagcgattaa actcatgttc 360 tacaacgctg attcagttgg ttacgcaccg tacggtgctt attggagaga tctcagaaaa 420 atctcaacct taaaactcct ttcgaatcat cgactggaaa ccctaaaaca tttgagaact 480 tctgaagttg agtcctgttt taaacaactt tataatcaat ggaagaacaa caaagttggc 540 ggcgaccatg attttgctct ggtgaggatg gataattggt ttggagactt gacatttaac 600 gttgtggcaa gaattgtcgc tggaaaaaag aattttgctg gaggtgcgac gaatggcgac 660 gtcggagctc agagatataa ggaagctatg gatgaagcgt tccggttgat gacgattttt 720 gcgttctcag atgtggttcc gtctttggga tggttggata aattgagagg tttggttgga 780 gggatgaagc gttgtggtgc ggaaattgat tccattgttg cgggttgggt ggatgaacat 840 agattgaaga gagcttctgg aaagggagga ggtcatactg atcttgaaca agattttatt 900 gatgtttgct tggagattat ggaacattct actttgcctg gtgatgatcc tgaaattgtc 960 atcaaatcta cttgtctgga catgattttg ggtgggagtg acacaacaac ggtgacccta 1020 acatgggcac tctccttact attgaacaat cctcacgtgt tgaaaagggc tagggaggaa 1080 ttggatacac atgtgggaaa ggacagacaa gtagacgact ccgatatgtc taatcttgtg 1140 tacatccagg cgatcatcaa agagacgatg agattgtacc cagcaggacc actgatcgag 1200 cgaaggacat cggaggattg tgaggtaggt gggttccatg taccggcggg cacacgctta 1260 ttggtgaact tatggaagat gcaacgagat gggagtgtgt ataaggagga tccattagag 1320 tttagaccag agagattctt gactagcaat gctgatgttg atctaaaggg acagaattat 1380 gaactgatac catttggtgc gggtaggagg atatgtcccg gtgtgtcgtt tgcggtgcag 1440 ttaatgcatt tggtgctggc tcgtctcgtt catggctttg aaatgaagac ggccggagat 1500 gcgaaggttg acatgacaga aagtgcagga ctaattagcc acaaggttac accgctagaa 1560 gtgctgctca aaccatgcct tgcgattcaa caagctttat aa 1602
3-203	**Sequences**	
3-203-1	Sequence Number [ID]	203
3-203-2	Molecule Type	DNA
3-203-3	Length	1602
3-203-4-1	Features Location/Qualifiers NonEnglishQualifier Value	**source** 1..1602 mol_type= genomic DNA organism= Stylophorum diphyllum
3-203-5	Residues	atggattctt ttcttctaat ccagtggttt gcagcttcca tggctgctct acttgctttt 60 gtttttctct acaatcttgt ctggagttct tcaagaacta caaagggtaa gaatattaga 120 aaggcaccca tggcggccgg tgcatggccg attcttggtc acctacatct gtttggatcc 180 ggtgagctgc ctcacaaaat gctctctacc atggctgaga agtacggtcc cgctttcacc 240 atgaagtttg gtaagcacac aacactagtt gtgagtgaca cccgtatcgt aaaagaatgt 300 tttactaccc acgataccct ctttgctaac cgtccttcga ctactgcatt tgatctcatg 360 acttatgcta atgactcggt agccttcaca ccttatggtc cttattggag ggaacttagg 420 aagatatcca ccctcaagct tctctctaac caccgcctcc aatctatcaa ggaaattcga 480 gtatcagagg tgaacgtatg ttttagggag ctatatgaat catgcaagag taaaactgat 540 gcaactccgg ttttggtgga tatgaagaaa tggttcgaag aggtctcgaa caacatagtc 600 atgagggtaa tagtggggag acagaatttt ggttctaaga ttgtgcaagg cgaagacgag 660 gccgtcaatt acaagaaagt aatggatgaa ctcttacgtc tcgctagttt gtctatgtta 720 tccgatgtgg cccctgtact tggctggttg gatatgttcc aaggaaacaa gagcgccatg 780 aaacgaaatg ccaaaaaagt agacaccata cttgagggct ggttggagga gcataggatg 840 aagaagagcg catcaggaat ctcttctgct ggtgagaatg accaggactt catggatgtt 900 atgttgtcca tcattgagga gaccaagttg tctggccgcg atgcggatac cgttattaaa 960 gctacttgct tggccatgat catgggtggt acagacacca ctgccgtgag tctaacatgg 1020 attgtctctt tactaatgaa ccatcgccat gtactgaaga aggcccgaga agaattggac 1080 gccctcgttg gtaaggatag acaagttgaa gattcagatt tgaagaactt ggtatacatg 1140 aatgccatag tcaaagaaac gatgcgaatg tacccactgg gtgctatgct cgagcgagaa 1200 accaaggagg attgtgaggt tggtgggttc caagtccaag gcggcacacg attactagtg 1260 aatgtgtgga agctacaacg agacccaaac gtttggaccg atccaacaga attcaaacca 1320 gagagatttc taaacgaaaa tgcggatata gacgttgggg gtcaacattt cgagctacta 1380 ccatttggag ctggtaggag ggcgtgcccg ggtgtgtcgt tcgcactcca attcatgcat 1440 ttggtactgg ctcgtctcat ccatggatat gaattgggaa ctcagaatga tgcggacgtt 1500 gacttaactg agagcacaga aggacatgtt aaccacaaag cttcccctct cgatctcctc 1560 cttaccccac gcctcaacaa ccctaatctg tatgattatt ag 1602
3-204	**Sequences**	

[0102]

3-204-1	Sequence Number [ID]	204
3-204-2	Molecule Type	DNA
3-204-3	Length	1707
3-204-4-1	Features Location/Qualifiers	**source** 1..1707 mol_type= genomic DNA organism= Stylophorum diphyllum
	NonEnglishQualifier Value	
3-204-5	Residues	atgactatag gggctctagc tttactatct ttcatctatt ttttacgggt ttcagttatt 60 aagaggacca aatacaccaa caccgcggtc accgccacca acaagttgga aaatgatgaa 120 gatgaggcca atcatagtaa gcgagtggtt gcaccacccg aagtcgccgg tgcatggcca 180 atattgggtc atcttcctca gctagtggga ctaaagcagc cactgttcag ggtactagga 240 gacatggccg acaagtatgg acctatcttc attgtccgat ttgggatgta ccctacccta 300 gttgtgagca gttgggagat ggcaaaggag tgcttcacca ccaacgacag ggtcctcgct 360 agtcgtccag ctagtgcttc tggcaagtac ctcacctaca attatgccat gttcggcttc 420 actaatggcc cttattggcg tgagatccgt aagatctcta tgctcgaact gctatcccat 480 cgtcgcgtag agttgctcaa gcacgtacct tccactgaga ttgacagctc tatcaaacag 540 ttgtaccatc tttgggtgga aaaccaaaac caaaataagc aaggggatca tcaggtaaag 600 gttgacatga gccaactact cagagatctg accttgaata tagtattgaa gttggtggta 660 ggaaagcgtc ttttcaacaa caacgacatg gatcatgaac aggatgaagc agctcgtaag 720 ctccagaaga caatggttga actcattaaa gtggcagggg cttcagttgc atcggatgcc 780 cttccattcc ttggttggtt ggatgtagat ggactaaaga gaaccatgaa gaggatagcc 840 aaggaaatag atgtaatcgc tgaaagatgg cttcaagagc atcgacaaaa aaaactaaca 900 tcaaacgaca agggtggcag caacaacatt caaggtggcg gtggcgataa cgacttcatg 960 gacgtgatgc tatccatcct tgacgatgat tccaatttct tcatcaatta caaccgcgat 1020 actgtcatta aagccacctc tctgacaatg atattagcag gttcggacac cacaactctg 1080 tccttgacat gggctctaac gctattagcc accaaccccg gtgccttgag aaaggctcaa 1140 gatgaacttg atactaaggt gggcagggat agacaagtag atgagcgaga catcaagaac 1200 ctggtctacc tccaagccat tgtcaaggaa acactacgga tgtacccagc tgctccacta 1260 gcaatacccc acgaggctac ccaagattgt attgttggcg ggtatcacgt aacagcaggc 1320 acacgtgtgt gggtgaatct gtggaagttg caacgggatc cacacgcgtg gccaaaccca 1380 tcggagttca ggccagagag gtttctagcc gttgagaacg attgcaagca acagggtact 1440 tgtgatggtg aagcagcaaa catggatttc agaggtcaac actttgagta catgcctttt 1500 gggtcaggaa gacggatgtg tccaggaatc aactttgcga tccagatcat tcacatgaca 1560 ctggcacggc tacttcattc attcgagttg cgggtgccag aagaagaagt aatcgacatg 1620 gctgaagatt caggtctaac catatccaaa gtaacaccac ttgaactcct acttacccca 1680 cgcctccctc ttccacttta tatatga 1707
3-205	**Sequences**	
3-205-1	Sequence Number [ID]	205
3-205-2	Molecule Type	DNA
3-205-3	Length	1584
3-205-4-1	Features Location/Qualifiers	**source** 1..1584 mol_type= genomic DNA organism= Stylophorum diphyllum
	NonEnglishQualifier Value	
3-205-5	Residues	atggctgccc ttcttccctt agctttcctc tacaatatct ttttggcttc atcttcgaaa 60 gctactagca agagaacaat aagtactaag aaaccgccca tggtagccgg tgcatggcca 120 attcttggtc atctccatct gtttaaagag ggtgagttgc ctcaccaaat gcttaaatcc 180 atggctgaca agtatggtcc agccttcctc atgaagttcg gtcaacacca atccctagtt 240 gtgagtgact accgcatcgt aaaagaatgc tttactacta atgataccct cttctgcaac 300 cgtccatcca ctacagcttt cgatgtcatg acttacgcta atgaatcggt agctttcaca 360 gaatacagtc cttactggcg cgagcttaga aagatatcca ctctcaagct tctctctaac 420 aaccgtctcc aggccatcaa gaacctccga gaagaggagg tggatgtgag cttcaagggg 480

[0103]

		ttgtatgatt catggaagaa taagaacaac aagagtactg ctggcagtgt tggtgatgaa 540 cgagctccgg ttttggtcga catgaagaaa tggtttgaag aagtgtcaaa caacgtggtg 600 attagggtaa tcgtgggcaa atgtaatttt gggactaaga tcgtgcaagg tgagaaggag 660 ggtgtggagt acaagacaat catggatgag cttttacgac ttgctagttt gtctttgtta 720 tccgatttcg cccctatact tggtttgttg gatttcttcc aaggccatgt ccgtaccatg 780 aaacgaaatg gcaagaaact agacgtgtta cttcagaggt ggttggagga gcataagagg 840 aagaagagca caccagagga tgagcaagac ttcatggatg ttatgctgtc gattattgag 900 gagagcaagc tgtctggcta tgacgctgat accgtcatta aagctacttg tctggccatg 960 atcatgggtg gaacagacac atccgcagtg agtctaacat ggatcgtctc tttactgatg 1020 aacaatcgtc aagcactaaa aaaggctcga gaagaattgg acgcgcaggt ggggaaggat 1080 agacaagttg aagattcaga tttaaagaac ttggtttact tgaatgccat cgttaaggaa 1140 acaatgcgat tatacccact aggtactctt cttgaacgcg aaactaagga ggactgtgaa 1200 gttggtgggt ttcacctcga aggtggtact cgtttactag tgaacgtatg gatggtacag 1260 cgagacccag acgtgtggac tgatccgaca aagttcatac cagagaggtt tcttacggag 1320 aaggcagaca tagatgttgg gggtgggaat tttgaactta taccattcgg agccggtaga 1380 agggtgtgcc ccggagtgtc ctttgcactt caattcctaa atttggtact agctcgtctc 1440 attcatggat atgaattggg aactccagaa gatgcggatg tggatctaac tgagagccca 1500 gaaggacatg tcaaccacaa agcatcccct ctcgagcttc tcctcacccc acgcctcagt 1560 aaccctaagc tctatgatta ttag 1584
3-206	**Sequences**	
3-206-1	Sequence Number [ID]	206
3-206-2	Molecule Type	DNA
3-206-3	Length	1644
3-206-4-1	Features Location/Qualifiers NonEnglishQualifier Value	**source** 1..1644 mol_type= genomic DNA organism= Stylophorum diphyllum
3-206-5	Residues	atggattctg atcatcaact tctcagttac cagttctctg caagtaatat gtttatcagc 60 ctctttgctt ttgttctcta ctatctacta gtatggaggc caacaaaatc taatcttaag 120 atgaaaacca tatcatctga agacaagcaa gcacccgaac tcgccggttc atggccagtt 180 atcggtcatc ttcatctcct tcatggacct aacccactcc atgtagcttt gggagccatg 240 gcggacaagt acggaccagc tttcaccgtt cgagttggtg tccatcggac acttgttgtg 300 agtagttggg aggtagcgaa agaatgtttc actaccaatg acaaggtctt tgtatctcgt 360 ccacgtcaag cagcaggaaa acacatgggt tacaacaacg ccatgttgcg attcgcctcc 420 gatacaccat actggaccca aatccgtaaa atgttgaaac gagacctcct ctctaacaac 480 cggattgagt tgctaaacca tgcatggcat tccgagatta acacatccat taaagaactg 540 tacgagatga attggtcatc aggcgaagga cgtcgtggcg gcattagacc gccggtctcg 600 gtggacatga agcaatggct tggtgattta accctaaaca tgtctgttaa aatgattgct 660 gggaagagat gttttggcag tggtgtttct gcttgtgatg aaggagaagc tagaaggtgt 720 caaaaggggt tgaaagactt cgttaggttg atgggtcaga ttgtggtgtc ggatgcaata 780 ccatttcttg gatggttgga tttggatggc tacgaggggg aaatgaagcg agccggaaaa 840 gagctcgacc gtttactagg aggatggttg gaagagcata aaatgaagag atcaccaggt 900 gatgaagctt cagcccagaa ggactggatg gacttgatgc tgtccgtact tggggatgga 960 aagcttgacg gctattacga cgctgatacg atcaacaaag ctacttgtct ggctctattg 1020 cagggtggta gcatctggac gatgcttact ttattatggg catttgcctt actagtgaat 1080 catccacatg tgatgaaaaa ggcccatgat gagctggaca accatgtagg cagagaaaga 1140 caagttgagg aatcagacat caagaacctc acttaccttc aagccatagt caaggaagca 1200 atgcgtcttt actcggtgtc gatgcgacta ctcgaatcca ccgcagactg cactgtttct 1260 ggctacgatg tcccagctgg gactcgtcta atcgtaaata cttggaagat tcagcgtgac 1320 cctcgggtat ggtccgaccc atctgaattc catccagaga gattcctcac acaccgccat 1380 agggacatgg acttgtatgg tcagaatttt gaaatcacac cttttgggtc gggcagaaga 1440 tcatgcccag gttcctcatt gggtcttcaa atggtgcaac tgacaatagc tcgtttgcta 1500 catgggtttg agtttaaaac accttcggac gcccccattg atatgactga gagtgttggg 1560 gtagaaaata tggttaaagc aacaccaatt gaagttctgc tcaccccgcg cctcctcgat 1620 gaggtttatg ctttctataa ttag 1644
3-207	**Sequences**	
3-207-1	Sequence Number [ID]	207
3-	Molecule Type	DNA

[0104]

207-2		
3-207-3	Length	1687
3-207-4-1	Features Location/Qualifiers	**source** 1..1687 mol_type= genomic DNA organism= Stylophorum diphyllum
	NonEnglishQualifier Value	
3-207-5	Residues	ctttgccag ttccaaggta ttgtaggaat cttattagct ttcctaacct tcttatatta 60 tctatggcgg gcttcaatta caggattaag gactaaaccc aaacacaacg actttaaagt 120 cactaaggca gcacctgaag ctgatggtgc atggcccata gttggtcatt ttgctcagtt 180 cataggccct cggccacttt tcaggattct tggagatatg gccgacaagt acggttcgat 240 cttcatggtc cgatttggga tgtacccaac cttggttgtg agcagttggg agatggcaaa 300 ggagtgcttc actaccaacg acaggttcct tgctagtcgt ccagctagcg ctgctggcaa 360 gtaccttacc tacgactttg ctatgttaag tttctccttt tatggcccttt attggcgtga 420 gatccgtaag atctctatgc tcgaactgct atcccatcgt cgcgtagagt tgctcaagca 480 cgtaccttcc actgagattg acagctctat caaacagttg taccatcttt gggtggaaaa 540 ccaaaaccaa aataagcaag gggatcatca ggtaaaggtt gacatgagcc aactactcag 600 agatctgacc ttgaatatag tattgaagtt ggtggtagga aagcgtcttt tcaacaacaa 660 cgacatggat catgaacagg atgaagcagc tcgtaagctc cagaagacaa tggttgaact 720 cattaaagtg gcaggggctt cagttgcatc ggatgccctt ccattccttg gttggttgga 780 tgtagatgga ctaaagagaa ccatgaagag gatagccaag gaaatagatg taatcgctga 840 aagatggctt caagagcatc gacaaaaaaa actaacatca aacgacaagg gtggcagcaa 900 caacattcaa ggtggcggtg gcgataacga cttcatggac gtgatgctat ccatccttga 960 cgatgattcc aatttcttca tcaattacaa ccgcgatact gtcattaaag ccacctctct 1020 gacaatgata ttagcaggtt cggacaccac aactctgtcc ttgacatggg ctctaacgct 1080 attagccacc tawcccctgt gtgccttgag aaaggctcaa gatgaacttg atactaaggt 1140 gggcagggat agacaagtag atgagcgaga catcaagaac ctggtctacc tccaagccat 1200 tgtcaaggaa acactacgga tgtacccagc tgctccacta gcaatacccc acgaggctac 1260 ccaagattgt attgttggcg ggtatcacgt aacagcaggc acacgtgtgt gggtgaatct 1320 gtggaagttg caacgggatc cacacgcgtg gccaaaccca tcggagttca ggccagagag 1380 gtttctagcc gttgagaacg attgcaagca acagggtact tgtgatggtg aagcagcaaa 1440 catggatttc agaggtcaac actttgagta catgcctttt gggtcaggaa gacggatgtg 1500 tccaggaatc aactttgcga tccagatcat tcacatgaca ctggcacggc tacttcattc 1560 attcgagttg cgggtgccag aagaagaagt aatcgacatg gctgaagatt caggtctaac 1620 catatccaaa gtaacaccac ttgaactcct acttacccca cgcctccctc ttccacttta 1680 tatatga 1687
3-208	**Sequences**	
3-208-1	Sequence Number [ID]	208
3-208-2	Molecule Type	DNA
3-208-3	Length	1569
3-208-4-1	Features Location/Qualifiers	**source** 1..1569 mol_type= genomic DNA organism= Tinospora cordifolia
	NonEnglishQualifier Value	
3-208-5	Residues	atggatttac cacaaccgac catatcaacc acacttctag ctttttcag catcttatta 60 ttcatcatat gctatcgtct cttgagcact aaatctgaca agagatcatc atcttccaga 120 aacaaacctc ttgacgctcc tggagcatgg cccgtcatcg gtcacctaca ccttctaaac 180 ggcgtcatac aacacgaaat tctgggaacc atggcggaca aatacggacc ggcgttcacc 240 atctggctcg gcacgcgtcc ggcactagtg gtaagcaact gggaagtggc taaggagtgc 300 ttcaccacct gcgataaggc cttagcaagc cgtcccccaa gcttagcttt gaagatcatg 360 ggctacaacg acgcgttatt cgcgttcgct ccttacgggc aatactggcg tgagttgcgc 420 aaaatagtga tgattgagct tctttctagt cggcagcttg attcgctgaa gcatgtttgg 480 gattctgaaa ttgattcatg catcgaagat ttgtatgaaa aatgtaaggg tcatcgtgaa 540 acagtactgg tgaatatgaa gcagtggttt gcggatttga tgatgaacgt agtggtgaga 600 atggtggttg ggaagctgaa ttttgggaaa acgaaagaag gtgatgatga ggtcgcgaag 660 gcgcaccaag ggcagttgaa ggcgatgaga gagttcttca agtgggtgga tgtgtttatg 720 atagaagacg cgtttccgat tctgacttgg ttggatcctc aagggtatca aagaaaaatg 780

[0105]

		aagaatatag cgaaagatct ggactcgctg gttcaggggt ggttagatga gcataagttg 840 aagcaaaaaa ctggcgataa tgggaagaaa gacttcatgg atatcatgct gtcggcggtc 900 aaagatgcta gtatatctga cagagacgat gagacaatct gcaaggcgac gtgcttgaat 960 ataattcttg gggcgagtga taccacaacg gtgaccctca catggaccct ttctttgtta 1020 ctaaataatc gacatgtctt gaggaaggcc caagaagaat tacaagcaca agttggcaaa 1080 cacagatgcg tggaagaatc agacgtcaag aaccttgttt atctacatgc catcatcaaa 1140 gaagtgctaa gactttaccc agctgttccg cttttaggcc cacgagagag tgtagccgat 1200 actgtggtgg caggctacca tatacccgca ggcacacggc taatcgtgaa cctttggaag 1260 attcatcgag acccgcttaa ctggcctgac ccgcttgagt ttcgacccga gagattcctt 1320 acgacccaca aagacacaga tgtgtggggt cagaattttg agttgactcc ttttggatcc 1380 ggaagaagga tatgcccagg tatttcgttt gcgcttcaag taattcctct cacactggct 1440 cgattgctcc atgggtttga gctcaccaca ccaggtagtg caccggtgga catgactgaa 1500 agcactgggc tcaccaactt gaaagccaca cctttagatg ttttcatcag tccacggctt 1560 gttctttga 1569
3-209	**Sequences**	
3-209-1	Sequence Number [ID]	209
3-209-2	Molecule Type	DNA
3-209-3	Length	1581
3-209-4-1	Features Location/Qualifiers	**source** 1..1581 mol_type= genomic DNA organism= Tinospora cordifolia
	NonEnglishQualifier Value	
3-209-5	Residues	atggagtcca ttcccacagc aattaatgtg cttcttgcct tcgtctccat ctactatctt 60 ctgaagttcc ggaaaaagat catcacaacg actagagata tcaagaagat caaagcacca 120 gaactaaagg gtgcatggcc gatcataggt caccttcatc tattcagatc cgatgatctt 180 ctgcatcgaa agctcggtgc catggccgac gagttggggc cagcgtttat gatccggcta 240 ggtatgcgcc ctgctcttgt agtgagtaac tggcaaacag ccaaggagtg ctttactacc 300 aaagacagga tcttcgcaac ccgtcccgat tcggttgctg cgaagcacat gggctacgaa 360 aatttaatat tgggcttcac tcgttacgga ccttactggc gtgaggttcg caagattgtc 420 acgctcgagc ttctctccag ccatcggcta cacctgctca ggcatgtcag gatatcagag 480 attgacatgt ccattaagaa actccatcag ctttgtacca gtaacgacaa caaatattca 540 tcagttgtgg tcgacctgaa tcaatggttt aaagctttaa ctcttaatat aatcgtgaga 600 ataatagcgg gcaagcggta ttacggtgga gacctcgagg acgatgagga gtcgcggcgg 660 tggaagaaag ctcttaacga atttatgcat ctctttggaa tattttcggt gtcggatgcg 720 attcctcagt tgcagggtat ggacgtgcag ggacatgagc gtgtcatgaa gaggactggt 780 aaggatattg atgtgattct gagcaaatgg ttggaagagc acagaaggaa gaagatcagg 840 gttaacaggg aaggagctga gaaagatttc atagatataa tgcttgacct aatcaaagaa 900 aacgtcaata tctccggtca tgatgctgat aacgtcgtta aagccacttg tttggccctt 960 gtatcagcag gaagtgatac tacaatgatc actctaacat gggctgtgtc gttacttctg 1020 aataatcatc gagtcttgga gaaagctcaa gccgagttgg ataatcaaat tggaataaac 1080 agagtacatg tagaagaaga ggacatcaag aatctaccat accttcaagc aattgtgaag 1140 gagactcttc gcttatatcc tgctgctcca ttttcattgc cacatgaggc catggaggaa 1200 tgtactgttg caggcttcca tgttccgaaa gggacacgct taatcacaaa tatctggaag 1260 ctgcaacgag atccccaagt ctgggaggat cctttggagt tcaggccaga gagattcctc 1320 acaagtgatc gtcgtcatgt ggattttaga gggcaacatt ttgaattaat accatttgga 1380 tcaggaagaa ggatgtgccc tggcatttca tttgccattg gtgtcttgca cctgacgctt 1440 gcgcgtttac ttcatgaatt ccaccttgga actccgacca acgcacccat agacatgaat 1500 gaaaatccag gaattaccct cgagaaagca gatcctcttc atccactcgt ctctccaaga 1560 cttacttcca tcaactactg a 1581
3-210	**Sequences**	
3-210-1	Sequence Number [ID]	210
3-210-2	Molecule Type	DNA
3-210-3	Length	1617

3-210-4-1	Features Location/Qualifiers	**source** 1..1617 mol_type= genomic DNA organism= Tinospora cordifolia
	NonEnglishQualifier Value	
3-210-5	Residues	atggattccc agttaacttc gtttcaatcc aagcccagtg catatctaat tgctgcactt 60 cttgccttag tttctgcata ctatctcatc atcaagaaga aaagcagagc aacttaccaa 120 gataactacg gcaagattag ggcaccggaa ccaaagggtg cgtggccaat catcggtcac 180 cttctcctgt tcaaacccaa cgatgtgctg tatcaaaagc ttagctcgct cgcagacgag 240 ttaggaccag cgttcatgat acggctgggc atgcgctcag ctctcgtaat aagtaactgg 300 gaaatagcca aagaatgctt caccaccaac gacaggatct tcgcgacccg tccaaagttg 360 atggcctcaa agcacatggg ctacggtggc gcagaagtcg gcgtcgcgcc ctacggtccc 420 tactggcgtg aggttcgcaa aatcatcacg gtagagcttg tctccaacca ccggctcaac 480 ttgctcaagg acgtcaggat atcggagatc gatatgtcct taaaagagct ctatgatctt 540 tgtatgaaga agaagaagaa cggcagtgga gaagaatcat cgcgggttga attggacctg 600 taccaatggt tcaaggacat gtcgctcaac atattggtca agctcatcgc gggcaagcgg 660 tattacgggg tggccgctgc cgccaacgaa gatgaggaat cgcggcggtg gaagaaagca 720 acggaggaat cggttttcct gtttggacaa tttgtggtgg gggatgcgat tcctttgttg 780 gagggtgtgg atgtgcaagg gcttgagcgt gccatgaaga agactggtaa ggaaattgat 840 gcagttttga gtaaatgggt ggaagagcat agaatgaaga agcagcagct taatggggca 900 agagatgagc aagatttcat agatgtgatg cttaacataa taaaggatgg caagatctct 960 gatcatgatg ctgatactat cgttaaagcc acttgtatgt ctcttgtaca agccggaagt 1020 gacaccacaa tgcttaccct gacttgggct gtgtgcttgc tactaaacaa ttgcaatgtt 1080 ttagagaaag ctcaagcaga gttggatgat caaattggaa gaagcaaagg acgtattgta 1140 gaggaagatg acatcaagaa actgccttat ctccaagcaa ttgtgaagga gacttggcgc 1200 ttgtaccctc ctgctccact tgctgtacca cgtgaagcca tggaggactg tactgtagct 1260 ggcttccatg ttccaaaggg tacacgctta atgacaaaca tatggaaact gcatcgagat 1320 cccaaagtgt gggacgattc tttaaagttt aggccagaaa gattcctctc cagtgaacat 1380 gcacatgtgg attttagagg gcaacagcat gagtttatgc cctttggatc cgggagaagg 1440 atgtgccttg gaatgccatt agctattggt gtggtacacc ttacacttgc ccgtttactt 1500 catgaattcg agcttgcaac tccgtcaaat gcaccagtag atatgagtga aaaagctggt 1560 cttactttgg ttaaagcgac gcctctaaat gttcttatcg ccccacgcct ttgctaa 1617

[0106]

3-211	**Sequences**	
3-211-1	Sequence Number [ID]	211
3-211-2	Molecule Type	DNA
3-211-3	Length	1596
3-211-4-1	Features Location/Qualifiers	**source** 1..1596 mol_type= genomic DNA organism= Tinospora cordifolia
	NonEnglishQualifier Value	
3-211-5	Residues	atggattcaa taatactcca gagtaacctt cttaccactg ttataataat aacatccttt 60 ggcctctttg tcctttcctt ttactatgtt ctctggaagg caattagaac tggcaacaag 120 agaaattgca gcaaccctaa ggctcctgaa gctgctggag gatggcccat tctcggtcat 180 cttcatttat tcagaggcca aggcctatta ctgcacaaaa tttttggagc catggccgaa 240 aaacacggac cagcattcac cattcggctc ggaatgcgtc cggcactagt tgtgagcaac 300 tgggaagtgg ctaaggagtg tttcaccgca aatgatcggg cccttgcgag ccgccctacg 360 agcttagcct tgaagattat gggctacaac aacagcttgt tcgcgttcgc tccatacggg 420 caatattggc gtgagttgcg caagatagtg atgcatcagc ttctctctag ccgtaggctc 480 gagttactca agaacgtttg gctttctgaa attgatatat ggatcaaagg cttgtacgag 540 aattccttgg ttaataaagt ggtggatatg aagcagtggt ttggggaatt gatgatgaac 600 atagtggtga gattggtagc aggaaagcga agttttggga aaatcagaga aggcgatagt 660 gaggaagcga aggcgcatca gcggcaaatt aaggcactgc gagatttctt caggttggtg 720 gaggttttta tgatagaaga tgcgtttcct tttctaactt ggttggatcc tcgagggtat 780 caaaaagaaa tgaagaatat agcaaaagaa ctggattatc ttcttgagga gtggttagaa 840 gagcataaac tgaagcaaca agctgcatgt gatgatcaga gcaaggactt catggatgtt 900 atgctgtcgg aggtcaagga ttctactatc actgaaagag atgcaaacac aatctgcaaa 960 gcgacttgcc tgaatgtaat tttaggtgcg agtgatacca caactctgac tctcacatgg 1020 gccctttccc tactactgaa caacagacac gtattgaaga aggcccagga agaattaaat 1080 gcccaagttg gcaaggataa acaagtggaa gaatcagaca tgaagaacct tgtgtaccta 1140 catgccataa tcaaagaagt tctaagactc tacccagctg ctcctttgtc agtggcacat 1200 gagtctttag aagacaccgt ggtggctggt taccatgtct ccaagggcac acaggtcata 1260 ttcaaccttt ggaaaattca acgtgatcca tctgtatggt ccaacccgct agaattccaa 1320

[0107]

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3-212	**Sequences**	
3-212-1	Sequence Number [ID]	212
3-212-2	Molecule Type	DNA
3-212-3	Length	1575
3-212-4-1	Features Location/Qualifiers NonEnglishQualifier Value	**source** 1..1575 mol_type= genomic DNA organism= Thalictrum flavum
3-212-5	Residues	atgccaagcc aaaccataca aattataatg gatttctttc atcaatgtgt tgcaactata 60 ttattttgtg tcttagcttc acctttttc ttttattatc tactcccatg gtggaaaaat 120 gctaatgatc atgatcttgc caagagcaga ggaaagcctg ttcctgaagt agatggtgca 180 tggcctatta tcggtcatat gcatatgctg caaccatcag atagctttta ctcatctttg 240 gcggaaaagt atggaccaat tttcacactt cgaattggtt tatgcaaaac aattgtgatt 300 aatagttggg agctagctaa ggaatgttgt accactcatg atagagtgtt tgcaagctcg 360 cctgaagcta cagcggcaaa gatattggga tatgattatg ctatgtttgg acgaaaccct 420 tatgggcctt actggcgtga aatgcgcaaa ataattataa ctgaacttgt gtcaaatcgg 480 agactggagc tactaaaaca tattagagta acggagatca gtacatccat acaagaattg 540 taccagttgt gggaagcaag gagtagtaag aatgtaaaag aaagagttgt ggtggatatg 600 caaaaatggt ttggtgactt gatgctaaat attggtgtcg agatggttgc tggaaagaga 660 tattttggtg caagttcgaa tgaagataaa gaggaagcaa gacagttgca taagacattt 720 aaagatttct cgaacctatt tggagtgcct gtgctatctg atgcaattcc atttcttagg 780 tggttagact ataaaggaca tattaaagcc atgaagagat gtgcaaaaca agtagattgt 840 atcttgcata gatggttgga ggaacataaa caaaacaaga caacaattgc tggggatttc 900 atggatattt tgttgtcagt acttcaggat aaagagatct ttggtaggga tgcagacacc 960 gtaatcaagg ctacatgtct gaatatgatg ctgggtgttg tagaaaccaa taaggtcact 1020 gtaacaatgg cactcatctc attgttgaac aatcgtcgca ttttgaagaa ggcacaagaa 1080 gaaatagaca ttcatgttgg gagcgataaa caagttgaag aatcagatat agagaaactt 1140 gtatatctcc aagccattgt caaggaaacg ttgcgcttgt actcacctgg tctaggaaca 1200 cgtgagccct cagaggactg caccatatca ggtttccatg ttccaaaagg cacagaggta 1260 atggtaaatg ttcagcagat tcatcgagat ccaagcattt ggtctaaccc tcttgaattt 1320 caaccagaga gattcctcac cacacaagca aatatagact ttgggggtca acatcatgaa 1380 tacattcctt tcggggcagg ccgtagatta tgccctgcaa tctcattcgc agttctggtg 1440 gtgcacttga cactagcacg tttgctgcaa gggtttgatt ttgcaacacc aaaggatgca 1500 cctgtggaaa tgaatgagag tgtggaaact ctggaagttt taatcacccc acgactccct 1560 ttgcatatgt attaa 1575
3-213	**Sequences**	
3-213-1	Sequence Number [ID]	213
3-213-2	Molecule Type	DNA
3-213-3	Length	1605
3-213-4-1	Features Location/Qualifiers NonEnglishQualifier Value	**source** 1..1605 mol_type= genomic DNA organism= Xanthoriza simplicissima
3-	Residues	atgcacaatc ccataccaaa ccaatggcta ccaagttcaa ctcttctgac gcctatcatt 60

[0108]

213-5		gttagtttcc tcgttatcgt tctcttctat atctataaga agagaagtag taacacgatc 120 aggaccaaga aggcgcctga agtagtagga gcatggcctg taattggaca tctaaattta 180 tttagttgtc ctaaaccggg tcatatagtg ctgggcgaac tagctgatca atatggcccc 240 gcatttacta tccattttgg tatgcatcca acactggtgg ttagtagttc ggagctggtg 300 agggactgtt tcactacgaa tgacaaatta ttttccagcc gtctagttaa caaagccatc 360 aagtacatgt tctacgatca ggacactatt tcattcgcac cttatgggcc ttattggcgt 420 gagcttcgta agatgattgc tcttaatctt ttaaataatg aacgcatcaa aatgctccag 480 cagcaaagga tttcagagat ggatgcttgt ttaaaaaagc tgtacgattt atcagcaaaa 540 agaaaagacg agaacgcagg ggtattggtg gatatgagta aatggtttgc cgaaatttcc 600 tttaatgtgg ttaccagaat tgttgctgga aaacatattt ttgggcctaa agttgaaaga 660 tacaagaatg tgatggaaga ggcacgccgt cttatggacg tcatggtttt ctccgacatg 720 gtaccttatt taggatggtt ggatagattg cgaggagtgg acagtgctat aaagcggaca 780 gccaaagaat tggactctgt tcttgagagc tgggtggagg aacatcgtcg aaagagcgtg 840 tcaatctcag ctggaacggg aggcattttc aacataaaag aagaggagga attggatttt 900 atagacatta tgttgtcgat tatagccaag aacaatttac caggtgacga tcctgatact 960 ttaatcaagg ctattgtcca ggaaacgtac cttgctgcgt gggacaacac aacggtaact 1020 cttacatggg tcttgtgttt gttattaaac aataagcaag ttctgaaaag agctcaaaat 1080 gaattagacg ctcaagttgg gaaggagagg caagtagaag attcagacat taataatctt 1140 ccctatgtac aagccattgt taaagaatca ttgagattat atccaccagg accgataatt 1200 gaacgggcga ctactgagga ttgtaacgtt ggtggcttcc gcgtcccggc aggtacacgg 1260 ctttgggtaa acttatggaa gttacaacga gacccaaaag tatggcctaa tgatccgcta 1320 gaatttcgac cagaaagatt tctcaatgac aatgcagaca ttgatttgag gggtcagaat 1380 tctgaattaa taccatttgg atcagggagg cgcatgtgtc ccggtgtctc attttctctt 1440 caagtcatac atctggtgat tgctcgaata attcagggat ttgagttaaa ggccccaaca 1500 gatgcagata tcgacatgtc tacaacgcta ggaatgataa gctggaaagc aacaccactt 1560 gaagtactca tgaatccacg cttcccaccc gtgttttaca agtga 1605
3-214	**Sequences**	
3-214-1	Sequence Number [ID]	214
3-214-2	Molecule Type	DNA
3-214-3	Length	1653
3-214-4-1	Features Location/Qualifiers NonEnglishQualifier Value	**source** 1..1653 mol_type= genomic DNA organism= Xanthoriza simplicissima
3-214-5	Residues	atgtctacat tacaaattag cattttaaca gttaaatccc cgtattcaca aatgcattat 60 tatccccttc ttcaccaatg gctaccagct tcaatggcgc tagtcagttt gctcgttatc 120 attctcttct ctatcttcaa gaagagaagt agtaagatga tcaaggccaa gaaggcgcct 180 gaagtagcag gtgcatggcc tctaatcgga catctcaatc tatttagtgg tcctaagcta 240 cttcatttag tacttggaga actcaccgat caatatggac cggcctttat gatccatctt 300 ggtatgtatc caactttggt ggtgagtaat tgggagcttc taaaggactg tttcactaca 360 aatgacatat tcttctcaaa tcgtccagtt aacaaagcga tcaagcacat gttctacaat 420 aaagagtcta ttggattcac accttatgga tcctattggc gtgagcttcg taagatgact 480 actctcaaac ttctatcaaa ccaccgcctt gatctgctca agcccttgag aatttcagag 540 atggacgctt gttttagaaa cctttatgag ttgtggacga aagataaaga cgggaatgca 600 tggctgttgg tggatatgag taaatggttt ggcgagatct cgtttaatgt ggttgcaaga 660 attgtagctg gaaaaaagaa ttttgggtcc aaaggtgata ggtataagac agttatggaa 720 gaggtggtcc gtcttatggg tctcagagct ttgtcggacg cggtaccata tttaggatgg 780 ttggatcagt tgcgaggact ggacagtgct atgaagcggg cggccaagga attggattct 840 gtgcttgaga gctgggtgga ggaacaccgc ctaaagaggg tgtcagtttc agctggaact 900 ggaagcactg taaagacagc aaaagaggag gaggaggagg aggacttcat agacattaca 960 ttgtcgattt tggcggagaa ccaattacca ggtgatgatc ctgataccgg catcaagtct 1020 cttatcctgg acatgatcct gggtgggagc gacacttcaa cggtgacact aatatgggca 1080 atgtgtctgc tattaaacaa tgtgcatgtg ttgaaaaggg ctcaatatga attggacgca 1140 cagattggga aggaaagaca agtagaggat tcagacataa agaatctgcc ctacatccaa 1200 gccattatta aagaaacaat gagattatac ccagcaggac cgattatcga acgccaggct 1260 aatgaggact gcgacgtggg tggcttccat gtcccagcag gtacacggct atgggtaaac 1320 ttatggaagt tacaacgaga cccaaatgta tggaaggacg acgcattaga gtttcgacct 1380 gaaagatttc tcactgatca tgcagacatt gatttgaagg gtcagcatct ggaattaatt 1440 ccatttggat caggtaggcg tatatgtcct ggtatctcat ttgctcttca agtcatgcat 1500 ttggcacttg ctcgaattat tcatggattt gagttgaaga ccccaaatga ttcaaatatc 1560 gacatgtctg gaactcctgg acttttatgc tgcaaagcaa caccactcca agtactcctg 1620 actccacgtt ttaaccccat gttttataag tga 1653
3-	**Sequences**	

[0109]

215		
3-215-1	Sequence Number [ID]	215
3-215-2	Molecule Type	DNA
3-215-3	Length	1563
3-215-4-1	Features Location/Qualifiers	**source** 1..1563 mol_type= genomic DNA organism= Xanthoriza simplicissima
	NonEnglishQualifier Value	
3-215-5	Residues	atggattcac ttcgacattg tttaggaggt attcttgcct tactaatctt tcttggttat 60 ctgcaatgga agagaggaac aagtaacaag tgcatagaag ctcctcaacc ggatggggca 120 tggcctatca taggccattt gcctaggttg atgaaacccc aaataatgca tagaacgttg 180 agcaccatgg ctgataaaca cggcccagcg tttactctcc ggcttggcgt acataaaaca 240 ttggtggtga gtagttggga ggtagccaag gagtgtttca ctaccaacga cagagtcttc 300 gctacccgcc caacctctat cgccgtggag atattgggct acaactacgc cttatttgcc 360 tttggtcctt atggctcata ttggcgtgaa gcccgcaaga tagcaatact tgagcttctc 420 tcaaaccata ggctcgagtt gctgaaacat gttcggatct ctgaggtgag cacatctata 480 agagaattgt accaagtgtg gaaagaaaat tgtgatatag caaatggatc tgctttggtg 540 gatatgaaac catggtttgg tgacttgaca ctaaacgtgg ttgttagaat ggttgctgga 600 aaacggtaca tgggtggcag tgttaaatcg gatgatgttg agggaaggcg atttcagaag 660 gccactaaag atctctttga tttatttgga ctgtttatat tgtcagacgc gcttccattt 720 atgggttggt tagacctcca tggccataag aaagccatga aaaaaactgc caaggagctg 780 gactccatta tgcagagatg gttggaagaa catcgacaaa gtttattgga tgatggaaca 840 aaggaggaga agaaggactt catgtatgta atgttatcta tccttgagga taaaaagcta 900 tttcaatatg atgccgacat cgttaacaaa gctatttgca tgaatatgat tatggcaggt 960 actgatactc aaatgatcac tctaacatgg gtcctttctt tactactcaa caatcgacac 1020 attttaaaga aggcccaaga tgaaatcgac tccagtgttg gaaaagatag acaagtcgag 1080 gagtcagaca tagtgaaact agtgtacctc caagcaattg tgaaggaagc attgcgtctc 1140 tacccacccg ctcctctatc cgcacaacat gaggccatgg aggactgcac tgtggctggc 1200 tactatgtcc cagctggcac acgcctaata acgaacatac ggaagattca acgagatcca 1260 cgcgtatggt ctgacccttt tgagttccat ccagagagat ttctcacaaa ccaagcaaat 1320 gtggacttta gaggtcaatc ttttgagttc attccttttg gatctggaag acgaatgtgc 1380 ccaggcattt catttgcgct tcaagtggtg catttgacat tagcacgtat cctacaaggt 1440 tttgattttg aaacaccaat gaatgcttct gtggacatga ctgaggcacc aggtctgaca 1500 aatgttaaat caacccctct tcaagttcta atcacccccc gtctccaccc aaacctatat 1560 taa 1563
3-216	**Sequences**	
3-216-1	Sequence Number [ID]	216
3-216-2	Molecule Type	DNA
3-216-3	Length	1572
3-216-4-1	Features Location/Qualifiers	**source** 1..1572 mol_type= genomic DNA organism= Xanthoriza simplicissima
	NonEnglishQualifier Value	
3-216-5	Residues	atggatttac ttaacccata ttttgcaact atctttggtg gtttctttgc gttactaatt 60 tttcttttta tcatttcaca gaagagaagt aggattccca agatcagagc agctccagaa 120 ccagttgggg catggcctat cgtaggacac ttgcctatgt tacttggacc cagattaccc 180 cattttgtgt tgggagacct tggagagaag tacggatcag catttactct ccggcttggc 240 atacataaaa cattagtggt gagtagttgg gaggttgcca aggagtgttt tactacaaat 300 gaccaagtat tcgccacccg ccctagcttc atggcagcga agataatggg ctataattat 360 gctctatttg gcttagcacc ttacgggtca tattggcgtg aactccgtaa aatatctatt 420 attgagcttc tttcaagtca taggcttgaa ttgctgaagc atgttcgagt ctctgaggtt 480

[0110]

		agtacatcaa tgaaagaatt gtacgaggtg tgggcagaaa actgtagtaa tggaaacgga 540 tctgttttgg tggagatgca gcgatggttt ggtgacttga cactaaatat aagtgttagg 600 atggttgctg gtaagcgata ctttggtact agtgctagtt tggatgacga cgaggcaagg 660 cgaatatcaa aggccacaaa agatttcttc cgtttgacag ggatgtttgt ggtgtcggac 720 tcggttcctt tcctttggtg gctagatttt cagggccacg agaaagccat gaagagaacc 780 gccaaggaaa tggacgatat atttgggggа tggttggagg atcatcgacg aaataaactt 840 gctggtggaa caaaggtgca gcaagacttc atggatgtga tgttgtctat ccttgaggac 900 gaaaagttct ttggttataa tgccgatgtt gtcacaaagg ctacttgcct gaatatgttg 960 ttgggtggga cggataccac aatggtcacc ttgacatggg ccctctcatt actactgaac 1020 aaccgtcata ttttgaagaa ggcccaaact gaaattaaca ctcatgttgg aaaagataca 1080 caagttgatg aatcagatat agtgaaactt gtgtacctcc aagcaattgt caaggaaaca 1140 ttgcgtctct acccagctgc tccactatcc acaccacacg aggccactaa ggactgcacc 1200 atcgctggct accacgtcac tgcagggacg cgcttgataa caaatatatg gaagattcaa 1260 cgagacccac gcgtatggtc caaccctagt gagtttcaac cagaaaggtt tctcactgat 1320 caagcaaatg tggacgttag gggccaacat tttgaattca ttccttttgg gtccggtaga 1380 cgatcctgcc caggaatctc gcttgggcta cttgtggtgc agttggcatt agcacgtttg 1440 ctacaaggct ttgatttcga aacaccatcg gatgcattgg tggacatgac tgagagcgct 1500 ggattaacta atctcaaagc aacacctctt catgtcctaa ttacaccgcg tctccattca 1560 agcctgtatt aa 1572
3-217	**Sequences**	
3-217-1	Sequence Number [ID]	217
3-217-2	Molecule Type	DNA
3-217-3	Length	1593
3-217-4-1	Features Location/Qualifiers NonEnglishQualifier Value	**source** 1..1593 mol_type= genomic DNA organism= Xanthoriza simplicissima
3-217-5	Residues	atggactcag ttcaccaagg ccaataccta ccaactccga tggtcagtgt ctttgtgttt 60 tttatcagtc tttactttct aattgtgtgg aagacaaggt ctagttccaa gactaacact 120 tgcaacgaag tacccgaagc gcctggggcg tggcctatta tcgggcacct ccatttgtta 180 ggtgggagtg aattacccca caagacatta ggagccatgg ctgataagta cggcccaatc 240 tttaagattc gtattggtgt gcatcaagca ttggtggtga gtagttcgga tattgtaaag 300 gagtgtttca ctactaatga taaggttttt gcttctcgtc ctacctcgac agcatcaaag 360 atcctgggct atgattatgt catgtttggt ttctctcctt acggaccgta ttggattgaa 420 ctacgcaaaa taattatgtc ggaacttctc tcaaaccgca ggctggaact actaaaacat 480 gttagggact ctgaaatcga tatatctatc caagaactat acaaggtgtg gaagaatcat 540 gataagtcaa aaggtccaat cttagtagac atgaagcaat ggtttggaga cttggcactc 600 aatgtgattc taaggatgat tgccggaaag agatactctg gttcaatctt ttcttctgat 660 gagacagaag caaggagatg tcaaaaggga gcgagagatt tctttaggct gttggggcta 720 ttcatcattg aagatgcact tccgtatcta agttggttcg acttacaagg ttacaagaaa 780 gagatgaaga acacggcaaa agaacttgat tctgtttttc agagatggct ggaagagcat 840 aaacgaacga gagaaaccgg tgaactgaat cgggagcagg acttcatgga tatcttaatg 900 tccacactgg aagagacaaa gatatctgaa tacgacaatg acactatcat caagtctact 960 tgcctgagca ttgtaacagg tggaaatgac actacaatgg ttactctcac ttggatccta 1020 tccttacttc taaacaataa acatgcactg aagaaggttc aagatgagct ggacagccac 1080 gttggaaagc atagacacgt ggaagagtca gatatcaaga acctcatcta cctccaagct 1140 ataatgaagg aagccttgcg gttgtaccct gcaggtccac tatcaggtcc tcgggtggca 1200 gacgctgact gcaccttagc aggctaccac atcccagcag gcacccgctt acttgtgaat 1260 acctacaaga ttcaaagaga tccattggtg tggtctgagc catctgagtt ccgaccagag 1320 agattcctca ctagccatgt aaacatggat gttaagggtc tgcaatatga attaatacct 1380 tttgggacag gtaggcgtgc gtgtccaggg atgttatttg cgcttcaagt ggtgccacta 1440 gtcctggctc ggtttctaca tgagttcgag ccaaagactg aaatggatat gccagtggat 1500 atgacggaga ctgcgggact aagtaacgcc aaagcaacgc cactagaagt agtaatcacc 1560 ccacgccttc agcccgagct ttatagttta taa 1593
3-218	**Sequences**	
3-218-1	Sequence Number [ID]	218
3-218-	Molecule Type	DNA

[0111]

2		
3-218-3	Length	1587
3-218-4-1	Features Location/Qualifiers	**source** 1..1587 mol_type= genomic DNA organism= Xanthoriza simplicissima
	NonEnglishQualifier Value	
3-218-5	Residues	atggacttca ccatgatcat ccaatggctt ctcacatcct ttgctattct tgttgcattt 60 gttctaatct ggtctagtgc aacaagatct agtactagga aaagaaacaa aacagcacct 120 gtagctgctg gtgctttgcc cattgtagga cacctacata tgctaatggg acgagaactg 180 cctcatcgat tgctttcaaa tatggctgac aagtatggtc ctgccttcat gatgaagtat 240 ggcttacaac ctgcacttgt ggtgagcagt ttgaagctca ctaaagagtg ttttgttcac 300 aacgatagag ctgtttttaa acgtccaaga agcaaagcat tgaaaaacttt gacctatgat 360 caagcttctt tgggttttgc gccatatgga ccactttggg tggagatgcg aaaagtatct 420 aaaactaatc tcctctctaa ccaaaggctt caaatgcaaa gacatgtaag agcctcagaa 480 gtcgacgctt tcatcaaaga gctttacgat ctatggtctt ccaaatccaa caacatcaaa 540 ggcgcgccac ttttggttga aatgaataaa tggtttgaag aactggcact taacgtagtg 600 accaggatgc tgagtggaaa aagacacatt ggctttaagg caaggcgtgg tgaagatagt 660 gaatctatgc attataagaa agttgtagtt gatgctactc ttttaactgc aaagcttgtt 720 gtgtcagatt tctttccttc tcttggattg gtggactact tgcaaggtga cgagagctct 780 ataaagggga caagcaaaga actagacgcg atcctcgcca cttgggtgga agagcatcgc 840 cataagaagg tttcaggctc agaggatgat gagaaagact tcattgatct cactttgtcc 900 atgatagatc aaactcagca ccaaggtgca gatgtcgaca ccttcatcaa gtctatgtgt 960 gtgggcatga tctttggtgg gagtgatagc acatcagtgg ccttagcatg ggctctttcc 1020 atactgatga ataatcgtcc tgttttgaag aaagcccgag aagaaatcga tcgacaagta 1080 ggtagagata ggaaagtgaa cgatttggat gtcctcaaat tggattatct caaggcaatc 1140 gtaaaggaat cgatgcgatt atgcctagtc ggaccgcttc ttgaacgcgt cgccgtagaa 1200 gattgtgaga taggcgggta tcatgttaaa gcaggctcgc gcgtagtagt gaatatttgg 1260 aaaatgcaac atgatccaaa cttatggtct gatcctttgg aattccaacc agagagattt 1320 ctcactacaa acgcaaatgt tgaacttaga ggccagcatt tcgaactcct tccatttgga 1380 gctggtagtc gtatttgtcc tggaattaca tttgccctcg aacttattca gttaacactt 1440 gctcgtctaa ttcatggatt tgaactggga actccgatgg atgcagacgt cgacatgaca 1500 gaaacatcaa gtgttaccaa ctatagggca acacctcttg aaatattact aacaccacgc 1560 ctggatccaa agctttacaa ttattag 1587
3-219	**Sequences**	
3-219-1	Sequence Number [ID]	219
3-219-2	Molecule Type	AA
3-219-3	Length	532
3-219-4-1	Features Location/Qualifiers	**source** 1..532 mol_type= protein organism= Argemone mexicana
	NonEnglishQualifier Value	
3-219-5	Residues	MDNFLLQFQP ISIAAFFVAL VFLYWSYGRK SNKTLKPRAP EAAGGRPITG HLHLFYGEEL 60 THRKLGSMAD KYGPVFNIRF GSHKTLVVSN WEIVKECFTT NDRLFSNRPG TLAIKLMFYD 120 TDSVGYAPYG NYWRELRKIS TLKLLSNHRI ETLKHLRTSE VESCFKQLYN QWEMKNENRV 180 EVDKLGFASV RMDNWFGDLT FNVVARIVAG KKNFAGGAVN GDIGAQRYKV AMDESFRLML 240 TFAYSDVIPS LKWLDKLRGL IRDMKRCGSE IDSIVASWVE EHRLKRNSSE NNNLDLEEDF 300 IDVCLDIIES SSLPGDDPDT VIKSTCLDMI LGGSDTTTVT LTWAISLILN NPHVLKRAKE 360 ELNSVVGKDR RVEDSDIPHL TYIHAIIKET MRLYPAGPLI ERRTMEDCEV GGYHVPAGTR 420 LLVNVWKMQR DGDVYKDDPL VFRPERFMTS NADVDLKGQH FELIPFGAGR RICPGVSFAV 480 QLMHLVLARL LHEFEITTIP SEPKVDMSES GGLICHKIKP LEVLIKPRLE LN 532
3-220	**Sequences**	
3-220-1	Sequence Number [ID]	220

[0112]

3-220-2	Molecule Type	AA
3-220-3	Length	537
3-220-4-1	Features Location/Qualifiers	**source** 1..537 mol_type= protein organism= Argemone mexicana
	NonEnglishQualifier Value	
3-220-5	Residues	MDFSSILLLL NINCFTTSLV TLLVLVMVFL YNNTRFTKPK GNKKMIKPPR LPGARPLLGH 60 LHLFGPGELP HKVLSTMADK YGPAFTIKFG KHTTLVVSDI HTIKECLTTN DILFSNRPSS 120 IAFDLMTYAD DSVAFAHYSP YWRELRKIST LKLLSNNRLQ SIKQLRLSEV NVCFKELYSL 180 CNNNNKSGAP VLIDMKKWFK EVTTNIVIRV IVGKQNFGSK IVRGEDQEAA NYKKIMDELS 240 RLAKLSMFSD YAPLLSLFDY FRGNVSAMKR NGKELNAMLQ NWLEEHKRKK NSSISNDDEQ 300 DFMDLMLSII DETKLYGRDA DTFIKAISLS MIVGGIDTVV VTLTWILALI MKNPFALKKA 360 QEELDFFVGK ERQVEDSDLK NLVYMNAIVK ETLRLYPLSC ILERDTKEDC EVGGYYVEGG 420 TRLLINAWKL QRDPNVWTDP SEFKPERFLN ENADIDVGGQ HYELIPFGAG RRVCPGVSFA 480 LQFMDLVLAR LIHGYELGTL NGEDVDLTEK TEGQINFKAT PLDLIVTPRL HPNLYDY 537
3-221	**Sequences**	
3-221-1	Sequence Number [ID]	221
3-221-2	Molecule Type	AA
3-221-3	Length	522
3-221-4-1	Features Location/Qualifiers	**source** 1..522 mol_type= protein organism= Berberis thunbergii
	NonEnglishQualifier Value	
3-221-5	Residues	MESIEFLVTL LLSLLALFCA YAWKRKNHTK DSKIKEPPQP AGAWPIIGHL HLISRGGLPH 60 INMGAMADKY GPVFMIRLGV NRAVIVSNTE IVKECFTTND KFLLNRPVGL ALNLMCYNNA 120 MFGFCRYGPY WREIHKIVML ELLSNSRLES LKHVWDSEIS TSIEELYQLC QTQNKTHEGP 180 VLVEMKDWFA DMALNVSLRM IAGKRYFGAS AGGNKDEARK CQKTIRDFFR LVGLFIVSDA 240 LPFLRWLDLG GHQKEMKRTF EDLDYMLQGW LDEHKLNRKS GVNGDQDFMD VMLSILDDSK 300 FPDYDVDTVN KATCFQLIIG GTDTTTVTLT WALSLMLNHP HVLKKAQDEL DIQVGKHRQV 360 EESDIKNLKY LEAVIKETLR MRPVGPLLGP RETIEDCTIG GYRVRAGTRV MVNAWKVHRD 420 PSVWSNPDDF KPERFLKKDI DFRDQNFEFI PFGSGRRACP GISFAVEVLP MALARLLHGF 480 ELKTQLGCKV DMTEHAGLVH AKATPLEVLV SPRLSRELYV SS 522
3-222	**Sequences**	
3-222-1	Sequence Number [ID]	222
3-222-2	Molecule Type	AA
3-222-3	Length	514
3-222-4-1	Features Location/Qualifiers	**source** 1..514 mol_type= protein organism= Berberis thunbergii
	NonEnglishQualifier Value	

[0113]

3-222-5	Residues	GSLALIAIII LSNIVKKSSK SLSSKGGKSA PVVHGAWPVI GHLHLLMGKE LPHHALAKLA 60 DKYGPAFTLN IGAYQELVIS TRDLAKECFT TKDKFFLNRP SNKAMKILTY GEASVGFAPY 120 SPLWVEMRKV TKSNLLSHQR VLMQNRSRAS EIDASFKQLY EQCNGKSGAS VEMKNWFEEV 180 MLNVVTRNVS GKRSFGTKAR LGDAEAVKYK RVIDETARFM GNLVISDMVP SLWWLDNMLG 240 AESAMKKLAI ELDSLLGGWV EEHRGKKLSD DEEGDFISLT WEMIDQIQLH GLAPETFIKS 300 MCVGVLLGGS DTTSVALTWA LSLMLNNREV LKKAQEELDF HVGKDRKVDD SDLKNLVYLQ 360 AIMKETMRIY QVGPLIEREA VEDCEVGGFQ IKKGNRILVN LWKLQRDPEV WSDPSEFRPE 420 RFLEDKSKVD LKGQNAELMP FGSGRRMCPG VWFGVHSTSL VLARLIQGFE IETPLDAKVD 480 MTETSSVTNY KGSPLEVIAR LPGSNLSFMI CSYV 514
3-223	**Sequences**	
3-223-1	Sequence Number [ID]	223
3-223-2	Molecule Type	AA
3-223-3	Length	545
3-223-4-1	Features Location/Qualifiers	**source** 1..545 mol_type= protein organism= Corydalis chelanthofolia
	NonEnglishQualifier Value	
3-223-5	Residues	MTPSISQPFE LLLLLMTMES LLLQWQPTSI AVLLLAITIF LYTFTKSPPK THKKLAPDAT 60 GGRPLMGHLH LFNSNELTHR TLGSMADKYG PAFNIRFGSH KTLVVSTWEI VKECFTTNDR 120 SFSNRPGTLY IKLMFYNEDS VGYAPYGAYW RDLRKLSTLK LLSNHRLESL KHLRVSEMNE 180 CFKQLYEICN KGSKSVAVRM DNWFGDLTFN VVARIVAGKR NFASISNDVG AMRYKNAMDE 240 AFRLMTVFSF SDVIPSLGWL DNLRGLVGDM KKAGKEIDSV VSGWIEEHRE KRKRRSSGGN 300 NRDGELEEED FIDITLSILE TSSLPGDDPD MTIKSTCLDM ILGGSDTTTV TMTWALSLLL 360 NNAHALKRAR EELDLHVGRD RQVEDSDINN LVYIQAIIKE TMRLYPAGPL IERMTKEDCE 420 VGGFHIPAGT RLLVNLWKMQ RDPNVWEDPL EFRPERFLTN NAEIDLKGQH FELIPFGTGR 480 RICPGVSFAL QLMHLALARL LHSFEVASPM DAKIDMTETA GLISHKVIPL EVLMTPRLDS 540 KLYDY 545
3-224	**Sequences**	
3-224-1	Sequence Number [ID]	224
3-224-2	Molecule Type	AA
3-224-3	Length	523
3-224-4-1	Features Location/Qualifiers	**source** 1..523 mol_type= protein organism= Corydalis chelanthofolia
	NonEnglishQualifier Value	
3-224-5	Residues	THTTEKNLPP EVPGALPVIG HLHKLGGRKG LLPYHVLGAM ADKYGPAFTF QFGSNRTLVI 60 SNWEMVKECF TSTNDKLFAY RPTALFNKEV FCSDHSFGFG PYGPFWREMR KVCSLHLLSN 120 YRLELLKHSR KSEMDECFKE LYQLWSASNI SKDKQPAVLV VEMKKWFEDA MFNVASRVVV 180 GKGSLKSHEK AGGSDNEVAR NKYKKGMDEA RRHMGTFVIS DRIPFLWWID YLRGIHSSMK 240 RTAKDLHAIV ETWLEEHRLH CHKRRVLQLD ANHEVEDMAK EEEKDFMDVL LTMADEGAIK 300 IFDHDLDTVI KANCLDMVIA GTDTPTVMLT WTLSLLLNNP DVLKRVRDEL DLHVGKERQV 360 EESDVKNLVY LQAVFKETLR LYPAVPLNER LTMEDCNVGG YDIPAGTRLL INIWKVQRDP 420 NVWQDPSEFR PERFLSKEKS TIDVRGLDFE LIPFGTGRRM CPGISFSLQL MHLGLARLIH 480 GFELATPMDL DVDMSANPGA FNYKSTDLQV LVSPRFHSKF YGC 523
3-225	**Sequences**	
3-225-	Sequence Number [ID]	225

[0114]

1		
3-225-2	Molecule Type	AA
3-225-3	Length	536
3-225-4-1	Features Location/Qualifiers	**source** 1..536 mol_type= protein organism= Corydalis chelanthofolia
	NonEnglishQualifier Value	
3-225-5	Residues	MDFLALQWFP ASLTALLALA VLYNFWTKQR TYKNGKTSTK QAPVAAGAWP VLGHLHLFGG 60 GELPHKMLAT MADKYGPAFT MKFGTHQTLV VSNTKIVKEC FTTNDTLFAN RPSTTAFHLM 120 TYDNESVAFT PYGPFWRELR KISTLKLLSN HRLQAIKDVR ASEVNVCFRE LYSQWRINKS 180 EPETSDHQGP ILVDMKKWFE EVSDNVVLRV IAGKQNFGSK IVHGDKEALH YKKIMDEILR 240 LAAVSMLSDV APLLGWLDMF QGHLSAMKRN AKEVDTMLCN WLEEHRTKRL SSDHDGVEQD 300 FIDVMLSIVE ENKFSGHDND TVIKATVLAM IMGGTDTTAV SLTWIVSLLM NNRHVLRRAQ 360 DELDLHVGKD RQVDDSDLKN LVYLNAIVKE TMRLYPLGAL LERETKEDCE VGGFHVKGGT 420 RLLVNVWKLQ RDPSFWTDPT EFKPERFLAD KANIDVGGQH FELLPFGAGR RVCPGVSFAL 480 QFMHLVLARL LHGFDLATPM NADVDLTEST EGHVNQKASP LNLLVTPRLH SKLYEY 536
3-226	**Sequences**	
3-226-1	Sequence Number [ID]	226
3-226-2	Molecule Type	AA
3-226-3	Length	543
3-226-4-1	Features Location/Qualifiers	**source** 1..543 mol_type= protein organism= Corydalis chelanthofolia
	NonEnglishQualifier Value	
3-226-5	Residues	MEYTFSSASL FSSSSLQQWL STLLLLISSI TISLYLTRRG KSSPPMVPGA WPLIGHLHLL 60 GGNDPLHIVL GTMADKYGHT FAMLFGKHPS LVVSSSDIVK ECFTSTNDKL FSHRHVPTGV 120 KYMFYNNDSF GFAPYGPYWR EMRKMNSLSL FSHHRVEMLN RIRTSQINIW FKNLYEMCTK 180 EKSTSTSSDG VVVEMKSWFD EMFFNVLVNM IVKPINDDEE LVKKYREVAT EAGRLLSSMA 240 VSDMVPSLGW LDHLFGIVGK MKKTAKDMDA ILTTWLEQHK IKSQQLRRSN GGEGAADQTE 300 EEEKEGKGLI GDLLSMQESA LFGHDRDTVI KSACQALIMA GSDSTSATLT WVLSLLLNHR 360 DALRKAREEL DQVVGKDRQV DDSDIKDLVY LQAILKETMR LYPAAPILER LAVEDCIVGG 420 FHVQAGTTLF VNVSKLQRDP NLWTDPLEFK PERFLTGCNA DVDLKGQDYE LVPFGSGRRS 480 CPAVSFAVRV MLLVLARFIH SFEVKTREED GILDMTESSG HTNCRSSPLE VLISPRLDSK 540 IYC 543
3-227	**Sequences**	
3-227-1	Sequence Number [ID]	227
3-227-2	Molecule Type	AA
3-227-3	Length	528
3-227-4-1	Features Location/Qualifiers	**source** 1..528 mol_type= protein organism= Corydalis chelanthofolia

[0115]

3-227-5	NonEnglishQualifier Value	
	Residues	MEYYSSLPFL QQWPLSSISS SPTSIATTLL IVACFTIVFL YINTSSKSNN NLKSPPKLPG 60 AWPFMGHLHL LGGNQPAHVS LANIAEKYKS TPFMIRMGQH STLVVSSVDL VKECFNNTND 120 KLFSNRSIAR GIRDMFYDME SFGFAPYGYY WRELRKVSAL TLFSTHRVDS VIQIKTPQID 180 GWFKKLYEQC TNTKGGIVEI KSWLDEMMFD VLVKMLVEPK DEGSVEKYRH VAGEALEVLG 240 NMSIYDLVPS LGWLDHFTGL VKKYKVTGKK MDTILNSWLE DHRGEKVAEE HKGLIGKLLS 300 MKEGSKLLGH DGDTAIKSTV QVLILGAGDS AGATLTWAIS LLLNHPHIME KLRKELDAAV 360 GKDRQIEDSD VKKFTYLLAI LKETMRLYPV TTLLQRETME DCAIGGYHVA AGTRLMVNVW 420 QVQRDPNAWS DPLEFKPERF LTECAHVDFS GQYSELIPFG TGRRICPALT LSVRLMLLTL 480 ARIIHSFDVK IPNGASSVDM ATSVGFVNLR LTPLEVELSP RLDSKIYG 528
3-228	**Sequences**	
3-228-1	Sequence Number [ID]	228
3-228-2	Molecule Type	AA
3-228-3	Length	537
3-228-4-1	Features Location/Qualifiers	**source** 1..537 mol_type= protein organism= Corydalis chelanthofolia
	NonEnglishQualifier Value	
3-228-5	Residues	MDSSLLQWYT TASMAALLAL AFFYKLWSKP RTSKNGKSTL QAPVAAGAWP VLGHLHLFSG 60 GELPHKMLAA MADKYGPAFT MKFGTHRTLV VSDTKIVKEC FTTNDTLFAN RPSTMAFHLM 120 TYDNESVAFT PYGQFWRELR KISTLKLLSN HRLQAIKDVR ASEVNFCFRT LYNQWRINKS 180 ETIGTGDHQG PILVDMKKWF EEVSNNVVIR VIVGKHNFGS KIARGKGEAL HYKKVMDEVL 240 RLAAVSMLSD VAPLLGWFDH LQGHVSAMKR NAKEVDTLLC SWMEEHRKKR TSNGSNGVEQ 300 DFIDVMLSIV EENKFSGHDS DTVIKATVLA MIMGGTDTSA VSLTWIVSLL MNNRHVLRRA 360 QEELDTHVGK DRQVDDSDLK NLVYLNAIVK ETMRLYPLGA LLERETKEDC EVGGFHVKAG 420 TRLLVNVWKL QRDPNFWIDP TEFKPERFLT DNANIDVGGQ HFELLPFGAG RRVCPGVSFA 480 LQFMHLVLAR LIHGFELDTP MNANVDMTES TEGHVNHKAS ALDLLITPRL RSTLYDY 537
3-229	**Sequences**	
3-229-1	Sequence Number [ID]	229
3-229-2	Molecule Type	AA
3-229-3	Length	571
3-229-4-1	Features Location/Qualifiers	**source** 1..571 mol_type= protein organism= Corydalis chelanthofolia
	NonEnglishQualifier Value	
3-229-5	Residues	MFKSVPSAQA ILHKLSFIHQ YFLLSQTNMD SLLFQWFPAS MAALVAFAFL YKLWSAPKIT 60 KNGKTSTKQA PIAAGAWPVL GHLHLFGGGE LPHKMLAGMA EKYGPAFTMK FGMHRTLVVS 120 DTKIVKECFT THDTLFANRP STTAFHLMTY DQESVAFTPY GPFWRELRKI STLKLLSNHR 180 LQAIKDVRTS EVNVCFRGLY NIWQTNKNEQ GGTVSDHPRP VLIDMKKWFE EVSNNVVIRV 240 IAGKQNFGSK IVRGEEEAVK YKKIMDEVLR LAAVSMLSDV APLLGWLDLF QGNLSAMKRN 300 AKEVDNMLNA WVEEHRRKRL AHSAKVEATH VEQDFVDVML SIMEENKLSS VHDDDTVIKA 360 TVLAMIMGGT DTTAVSLTWT VSLLMNHRYV LKKAQEEIDQ HVGKERQVED SDLKNLVYLN 420 AIVKETMRMY PLGALLERET KEDCEVGGFH VKGGTRLLVN VWKLQRDPNV WIDPTEFKPE 480 RFLAENANID VGGQHFELLP FGAGRRVCPG VSFALQFMHL VLARLIHGFE LETPMNADVD 540 LTESTEGHVN HKASPLDLLI APRLNSKLYE L 571
3-230	**Sequences**	

[0116]

3-230-1	Sequence Number [ID]	230
3-230-2	Molecule Type	AA
3-230-3	Length	533
3-230-4-1	Features Location/Qualifiers	**source** 1..533 mol_type= protein organism= Corydalis chelanthofolia
	NonEnglishQualifier Value	
3-230-5	Residues	MDSLFVLLQW FSASLAAVLA LAFLYNLWVK PRISDGKGNK GSTKQAPVAA GAWPVLGHLH 60 LFGGSELPHK MLAAMADKYG PAFTMKFGTH RTLVVSNTQI VKECFTTNDT HFSNRPSTTA 120 FHLMTYDNDS VAFTPYGPFW RELRKISTLK LLSNHRLQAI KDVRVSEVNV CFKDLYNQWK 180 TNQNQRPVLV DMKKWFEEVS NNVVIRVIVG KQNFGSKIVR GEEEAVKYKK IMDEILRLAA 240 VPMLSDMAPL LGWLDLFQAH KSAMKRNAKE VDNMLESWLE EHKRKRLSGV NGAEEEDFMD 300 VMLSIMEENK FTGRDSNTVV KSTVLAMIMG GTDTTAVSLT WIFSLLMNNR HALKKAQEEL 360 DMHVGKDRQV EDSDLKNLVY LNAIVKETMR MYPLGALLER ETKEDCEVGG YHVRAGTRLL 420 VNVWKLQRDP SFWTDPTEFK PERFLTENAK TDVGGQHFEL LPFGAGRRVC PGVSFALQFM 480 HLVIARLIHG FELGTPMDAD VDLTESTEGH VNHKATPLDL LIAPRLDSKV YDY 533
3-231	**Sequences**	
3-231-1	Sequence Number [ID]	231
3-231-2	Molecule Type	AA
3-231-3	Length	530
3-231-4-1	Features Location/Qualifiers	**source** 1..530 mol_type= protein organism= Chelidonium majus
	NonEnglishQualifier Value	
3-231-5	Residues	MRSNYLKPTT TTIEDKSKNK ISRKKPIAAK PPPEALGAWP VIGHFLLFTG KGLTHVTLGD 60 MADKYGPAFL IRFGSHRTLV VSSWEMMKEC FSAPNDKIFS NRESNLLWIK SMFYGSNSYG 120 FSPYGPYWKE LRKISTQKLL SHHRLDAMKH LQMVEVDASF KQIYNLCNKN GGSPSPSSIN 180 TTALVNMDEW LSHLMFNVIA RMVSGYQSDD VGTGATSTGE RFKVSMDETM RLMAIFAVSD 240 LVPWLACVDR LRGLTRKMNR CGKDLDSIIG RLIEEHRQKR RLCRNNKGSK NEDGGHDDDQ 300 DFIDICLSIM EQSQLPGDNP EIAIKSIVLD MIFAGSHTTT LAMTWTLSLL LNHRHMLKKA 360 KEEIDAHVGN ERQVDDSDIH NLVYIQAIIK ESMRLYPPSP LFERMTMEDC EVGGFHIPAG 420 TRLFVNVWKM QRDPTVWEDP LEFRPERFLT SKREIDVKGQ HYELIPFGAG RRICPGASFT 480 LQVLHLVLAR LIHGFEMTTP MDVKVDMASS AGLFSNKMTP LEVLITPRTA 530
3-232	**Sequences**	
3-232-1	Sequence Number [ID]	232
3-232-2	Molecule Type	AA
3-232-3	Length	557
3-232-	Features Location/Qualifiers	**source** 1..557 mol_type= protein

[0117]

4-1	NonEnglishQualifier Value	organism= Chelidonium majus
3-232-5	Residues	MKILQEFHQL TISNIVLLLL ISFIFFSLSA WFIESTNYYY SSKKKKSKKT PPPEASGAWP 60 VIGHLHQFKP DDLPHEALGD MADKYGPVFI VRFGSYRKLV VSNSEMVKEC FTAANDRSFS 120 NRPAVLGIRI MLYNTITYAF APYGPYWREL RRISSQNLLS NHRVDMVKHL HVDEVNTLFK 180 QLYELCNKNG GRPPTGTNTS TSAALVNMDD WLSNIMFNVI ARIVNGNNKS INNERTGAIN 240 EKRYKTAMDE ARRLVAIFAV SDSVPWLGWL DRVRGLIRGM NLCGKELDSI IEDIIDEHRQ 300 KRRLCTSKLG SSGDDDADNS NLEEEDNFID ACLSIEEQSQ LPGENPEIVI KALILDMFAG 360 GSDGPHFVLT WTLALLLNHP HVLKKAREEV DAHVANDRHV DVSDISNLVY IQAILKESMR 420 LYPPNALIER MTTEDCEVGG YHIPAGTYLL VNVWKVQRDP TVWQDPSEFR PERFLLTNTK 480 TEMEYEHIPF GAGRRRCPGM RFALQVMHLV LARLIHEFEI TTPVDVIKVD MTATNGLFNH 540 KAVPLEVLLT PRTLIRG 557
3-233	**Sequences**	
3-233-1	Sequence Number [ID]	233
3-233-2	Molecule Type	AA
3-233-3	Length	541
3-233-4-1	Features Location/Qualifiers	**source** 1..541 mol_type= protein organism= Chelidonium majus
	NonEnglishQualifier Value	
3-233-5	Residues	MDYSVLLQYG WFAPSMAALL ALAFLYNLFL ASSPKATSKR TISTKKPPMA AGAWPILGHL 60 HLFKEGELPH QMLKSMADKY GPAFLMKFGQ HRSLVVSDYR IVKECFTTND THFCNRPSTT 120 AFDVMTYANE SVAFTEYSPY WRELRKISTL KLLSNNRLQA IKNLREEEVN VSFKGLYDSW 180 KNKNNKSTGS VGDERAPVLV DMKKWFEEVS NNVVIRVIVG KCNFGTKIVQ GEKEGVEYKT 240 IMDELLRLAS LSLLSDFAPI LGLLDFFQGH VRTMKRNGKK LDVLLQRWLE EHKRKKSTPE 300 DEQDFMDVML SVIEESKLSG YDADTVIKAT CLAMIMGGTD TSAVSLTWIV SLLMNNRHAL 360 KKAREELDAQ VGKDRQVEDS DLKNLVYLNA IVKETMRLYP LGTLLERETK EDCEVGGFHL 420 EGGTRLLVNV WMVQRDPSVW TDPTKFTPER FLTEKADIDV WGGNFELIPF GAGRRVCPGV 480 SFALQFLNLV LARLIHGYEL GTPDDADVDL TESPEGHLNH KASPLELLLT PRLSNPKLYD 540 Y 541
3-234	**Sequences**	
3-234-1	Sequence Number [ID]	234
3-234-2	Molecule Type	AA
3-234-3	Length	537
3-234-4-1	Features Location/Qualifiers	**source** 1..537 mol_type= protein organism= Chelidonium majus
	NonEnglishQualifier Value	
3-234-5	Residues	MEFLSLEPQL ISIFVLLLAS SIFLYNLLKN HGRKSKTSKP PAPVASGGWP IMGHLHLFNG 60 SELTHQTLGS MADKYGPAFN IQLGSHQTLV VSSWEIVKEC FTTNDRFFSN RPGSLAIKLM 120 FYDADSVGYA PYGAYWRDLR KISTLKLLSN HRVETLKHLR TSEAESCFKQ LYNQWKNNKV 180 GGDDDEFAIV RMDNWFGDLT FNVVARIVAG KKNFAGGATS GDVGAKRYKE AMDEAFRLMT 240 IFAFSDVVPS LGWLDKLRGL VGGMKRCGAE IDSIVGGWVD EHRLKRASRK GGDHNDLDLE 300 QDFIDVCLEI MEHSTLPGDD PEIVIKSTCL DMILGGSDTT TVTLTWALSL LLNNPHVLKR 360 AREELDTHVG KDRQVDDSDM SNLVYIQAII KETMRLYPAG PLIERRTSED CEVSGFHVPA 420 GTRLMVNLWK MQRDGSVYKE DPLEFRPERF LTSNADVDLK GQNYELIPFG AGRRICPGVS 480 FAVQLMHLVL ARLVHGFEMK TAGGAKVDMT ESAGLISHKV TPLQVLLKPR LAIQQAL 537

[0118]

3-235	**Sequences**	
3-235-1	Sequence Number [ID]	235
3-235-2	Molecule Type	AA
3-235-3	Length	550
3-235-4-1	Features Location/Qualifiers	**source** 1..550 mol_type= protein organism= Chelidonium majus
	NonEnglishQualifier Value	
3-235-5	Residues	MDSMNLFQQA IAVGTLVIFL YYLWKWTSII FTRTHQAAPP EPAGAWPIIG HLHLLAGGAN 60 QLVYHILGSM ADKYGPIFTV RLGMRRALIV SNSELAKECF TTNDRIFSTR PSSVAIKLMG 120 YDSAMFGFAP YGPYWREMRK IAVTELLSNR RLEILKNIRI SEINMSIKDL YQLWVENKNS 180 GVDGGGDGGE VVVGSPVLVE MKRWFEDVSF NVVVRMVAGK RYFGRRVESD DREEEEARRW 240 QKAMNDFMHL VGIFVVSDAI PFLGFLDFQG YEKEMKKTAV EIDYVMGRWV EEHQRRKLER 300 VAGGSDDQQE DFIDVMLSIL KDGDQFYGYD PDTVIKSSCL SLVLGGSDTI SVTLTWTVSL 360 LLNNRNVLEK AQSELDIHVG RGRQVDESDI NNLKYLQAIV KETMRLYPAG PLSAPREAME 420 DCTIAGFHVP KGTQLMLNLW KLHRDPRVWS DPLEFKPERF LTTGTHGDVD VKGQHFELLP 480 FGAGRRICPG ISYALQVLHL TLARLLHSFH LSTPYDIPVD MTESSGLSCP KATPLDVLLT 540 PRLPSELYVS 550
3-236	**Sequences**	
3-236-1	Sequence Number [ID]	236
3-236-2	Molecule Type	AA
3-236-3	Length	561
3-236-4-1	Features Location/Qualifiers	**source** 1..561 mol_type= protein organism= Chelidonium majus
	NonEnglishQualifier Value	
3-236-5	Residues	MDLFIFFSRF QYIVGLLAFL TFFYYLWRVS ITGTRIKTNQ NIMNGTNMMA PEAAGAWPIV 60 GHLPQLVGPQ PLFKILGDMA DKYGSIFMVR FGMHPTLVVS SWEMAKECFT TNDKFLASRP 120 TSAGGKYLTY DFAMFGFSFY GPYWREIRKI STLELLSHRR VELLKHVPYT EIGGSIKQLY 180 KLWMETQNQN KQRDDHQVKV DMSQVFGYLT LNTVLKLVVG KGLFNNNDMN HEQEEGRKLH 240 ETVLEFFKLA GVSVASDALP FLGWLDVDGQ KRSMKRIAKE MDLIAERWLQ EHRQKRLTSN 300 NKASSGHDDF MSVLLSILDD DSNFFNYNRD TVIKATSLNL ILAASDTTSV SLTWVLSLLV 360 TNPGALKKVQ DELDTKVGRN RHVEERDIEK LVYLQATVKE TLRMYPAGPL SVPHEATQDC 420 TVGGYQVTAG TRLVVNVWKL QRDPRVWPNP SEFKPERFLP DGCEVGCGEA ANMDFRGQHF 480 EYIPFGSGRR MCPGIDFAIQ IIHMTLACLL HAFEFQVPSS LDKHLVPAVI DMSEGSGLTM 540 PKVTPLEVLL NPRLPLPLYE L 561
3-237	**Sequences**	
3-237-1	Sequence Number [ID]	237
3-237-2	Molecule Type	AA
3-237-	Length	522

[0119]

3		
3-237-4-1	Features Location/Qualifiers	**source** 1..522 mol_type= protein organism= Cissampleos mucronata
	NonEnglishQualifier Value	
3-237-5	Residues	MEAMGEYFQL ISWTVFSALI TIYFIFSRKT NGKKKAPEPG GAWPIIGHLH LFGAHDLLYR 60 KLGAMADKLG PVFMIRFGMH RAVVVSNYEV AKECFTVNDK ILASRPRIIA SKLMGYNHAA 120 VGLSPYGPYW REARKIATLE LLSNHRLQLL KHIRISEIDM WIKELKEFCM KSSSDGPVLV 180 QLDGWFNALT LNIMVRNIAG KRYCGGAEAF EDEESQRWKK VSRELMFLFG VFMVPDAFPV 240 LEGIDVQGFE RAMKRVGKEM DFFLSRWLEE HRRKKIELSE KGNEVNDQGA QDFIDVMLNT 300 IKDAKIFEHD ADTMIKATCM ALVVAGNDTT MITLSWAVSL LLNNRGVLEK AQEELSNQIG 360 KNRHVEEGDI ESLPYLHAIV KETFRLYPAA PLSLPHEAME DCTIAGFHVP AGTRLITNIW 420 KLHKDPNIWP DPLEFKPERF LTTHAHVDFK GQHFEFIPFG SGRRMCPGSS LAISVLHLTL 480 ARLLHEFELK TPDDAPVDMT EGPGITLMRA NPLHVLINPR HD 522
3-238	**Sequences**	
3-238-1	Sequence Number [ID]	238
3-238-2	Molecule Type	AA
3-238-3	Length	534
3-238-4-1	Features Location/Qualifiers	**source** 1..534 mol_type= protein organism= Cissampleos mucronata
	NonEnglishQualifier Value	
3-238-5	Residues	MSSPIQQLLL SLTSINGGTI ISAVIISLLL ILTLHRLLKP INSNKTKHPP RASGAWPVMG 60 HLHKLRGPDL PHRTLSSMAD QYGPIFTINL GPTTALVISD PAVAKECFTT NDLTFSSRPT 120 TLATTLMCYN NTMFGFAPYG PYWREVRKVV MAQLLSTRRL ESLKNIWASE IDRWVKGLAQ 180 KAQSGSHGVV EVEMGDWLAR LTMNIGLRLV VGKSCGEMGS EESERCLGAM REYPELLGRF 240 ALEDALPWLG RFDLQGHQRE MRRAARVLDE ILDGWLDEHK RNRSGLSGGD DHRDQDFMDV 300 MLSVLEQDQD SSLSDHDADM INKSTCLNLI LGMADTTMVA LTWAISLLLN NKTSLKKAQE 360 ELQAQVGNER HVDESDVKNL VYLQSIIKEV LRLYPPEPLS GPREALEDCE VAGYHVPRGT 420 RLIANLWKIH RDSSTWQDSM EFRPERFLTA HEHVDVWGQH FEFMPFGSGR RSCPGVSFEV 480 RVLPLILARL IHAFEMTTRG DVPVDMSERP GLVISKASPL EVMISPRLPL HLFE 534
3-239	**Sequences**	
3-239-1	Sequence Number [ID]	239
3-239-2	Molecule Type	AA
3-239-3	Length	536
3-239-4-1	Features Location/Qualifiers	**source** 1..536 mol_type= protein organism= Cissampleos mucronata
	NonEnglishQualifier Value	
3-239-5	Residues	MEFHLLLQAV AATLVTFFLY ELWALRKKFS RLTKTPSSKA LLKAKCAPEP PGAWPIIGHL 60 PLLVSAKQPH RAFAALAEKY GPAFMLRMGM SPMLIVSTKE VAKECYTAND HVFATRPVTT 120 AGKLMAYDHS VMGFTPFGTY WREIRKIATV ELFSARRIGM LKPVRQSEVS LWMKGLHEKW 180 VHNGNSSVSV ELKSQLEELT FNLLTQMVAG KRYYGSNVAK VDEKMAGLFR HAVQQFNYHL 240 GNSEMYDALP FMAWLDFKGD AKAMKKTQKD LDFIMQTWLD EHRLKADQMR GDAINNTRDF 300 LDVLVMMEKT GQFSSAIKDR DTTIKALALT QLVAGVDSMA NTMVWVLALL MNNPEMLAKA 360 QDELDNNVGK DRLVEESDIP NLKYLQALLK ETLRMYPVGP LLVPHEATED CHVAGYFVPR 420

[0120]

		GTGLFINAWT IQRDPNVWAE PNCFNPERFL TTHAEMDVKG QNHELLPFGS GRRSCPGVGL 480 ALQVMHLTLA RILQAFELKT QSGVGIDLEE CSGILLSMMH PLQVMMAPRL PSELYD 536
3-240	**Sequences**	
3-240-1	Sequence Number [ID]	240
3-240-2	Molecule Type	AA
3-240-3	Length	524
3-240-4-1	Features Location/Qualifiers	**source** 1..524 mol_type= protein organism= Eschscholzia californica
	NonEnglishQualifier Value	
3-240-5	Residues	MDSLILTNWF PISIASVLTL VFLYKVLLSS RTLKDKKIKT SPMANGAWPI LGHLHLFGSG 60 ELPHKMLATM ADKYGSAFRM KFGKHTTLVV SDTRIVKECF TTNDTLFSNR PSTKAFQLMT 120 YDNESVAFTP YGPYWRELRK ISTLKLLSNH RLQAIKDVRA SEVNVCFKSL YDQCKNPSGA 180 PILIDMKKWF EEVSNNVVMR VIVGRQNFGS KIVQGEEEAI HYKKVMDELL RLASLSMFSD 240 FAPLLGFLDI FQGNLSAMKQ NAKKVDAILE NWLEEHRKKK NSVAESEQDF MDVMLSIANE 300 SKLSGHDADT VIKATCLAMI MGGTDTTAVS LTWIISLLMN NRHALKKARE ELDALVGKDR 360 QVEDSDLKNL VYMNAIVKET MRMYPLGTLL ERDTKEDCEI GGFHVKGGTR LLVNVWKLQR 420 DPNVWVDPTE FRPERFLTEN ADIDVGGQHF ELLPFGAGRR VCPGVSFALQ FMHLVLARLI 480 HGYDLNTLNE ENVDLTESPE GHVNHKASPL DLILTPRLHY KLYE 524
3-241	**Sequences**	
3-241-1	Sequence Number [ID]	241
3-241-2	Molecule Type	AA
3-241-3	Length	532
3-241-4-1	Features Location/Qualifiers	**source** 1..532 mol_type= protein organism= Eschscholzia californica
	NonEnglishQualifier Value	
3-241-5	Residues	MDTASSISLL LPWAVVVPSI ATLLALLLFL FITSPKTPKR KTSSKPPPTV LPGAWPILGH 60 LHLFKEGESP HHMLKNLADK YGPAFVMKFG QHRSLVVSNT KIVKECFTTN DTLFSNRPST 120 TAFDLMTYAH DSVAFTPYSP YWRELRKIST LKLLSNNRLK AIKKLRGEEV DVCFRGLYGL 180 WKNKTKNGAP VLVDMKKWFE EVANNVVIRV IVGKLSFGTK IVDGEEEAVE YKTVMDELLR 240 LASLSLLSDM APILGWLDFF QGSVRKMKQT GKRLDVLLEK WLGEHREKKN LVGEDEQDFM 300 DVMLSIVEES KLSGHEADAV IKATCLAMIM GGTDTTAVTL TWIISLLMNN RHALEKAREE 360 LETHVGKDRQ VEDTDLQNLV YLSAIVKETM RLYPLGTLLE RETKEDCEVG GFHIQGGTRL 420 LVNIWMVQRD PTVWNDPSAF KPERFLTDKS EIDVGGQHFE LIPFGAGRRV CPAVSFALQF 480 LHLVLARLIH GYDLGTPSNV EVDLTESLEG HVNHKASPLE LLLTPRLNPK LY 532
3-242	**Sequences**	
3-242-1	Sequence Number [ID]	242
3-242-2	Molecule Type	AA
3-	Length	548

[0121]

242-3		
3-242-4-1	Features Location/Qualifiers	**source** 1..548 mol_type= protein organism= Eschscholzia californica
	NonEnglishQualifier Value	
3-242-5	Residues	MESEIQYQTA TMASILSTNL ILSSIFTAFL LYFLLKMSPF RSSKNKSRKQ APKPTGSWPI 60 IGHLLHLQGP NLPHINLAAL ADKYGSVFSF RIGLRPALVV SSWEIAKECL TTNDRVFVSR 120 PPLIAMKHMG YDHALFGFSP YGPYWRELRK LVNQELLSNT RIELIKHVWD TEINTFINDL 180 YEVWAMKSNE GGGDVVVEMK QCLYDFTLNL TLKILTGKRY FGGGGSEELR EEAGRCQKAV 240 RNFLRLVGTF TAQDVIPFLE GWLDLGGHEK EMKITGKELD SLLQKWLEEH KVKKSSAGEE 300 GQENRGGDEE DFMGVMLTKL RDHEKLLSYY DADTINKATC LTVILGGSDT TMMTLVWALA 360 LLVNHPHVMK KLQDELDTHV SKERQVEESD IKNLAYLQSV MKETMRRYPG TPLYVRESIE 420 DCTIAGYDVP TGTRLVVNAW KIQHDPQVWS NPFEFNPERF LTTHKDIDVR GQNFELIPFG 480 AGRRMCPGAS LGLQVVHLTL ARLVHGFEFK TPDGEPMDMT ESIGLTNLKA TPLEIMLTPR 540 LSSKLYVC 548
3-243	**Sequences**	
3-243-1	Sequence Number [ID]	243
3-243-2	Molecule Type	AA
3-243-3	Length	554
3-243-4-1	Features Location/Qualifiers	**source** 1..554 mol_type= protein organism= Eschscholzia californica
	NonEnglishQualifier Value	
3-243-5	Residues	MGLSFDLSSH NFLQFSNPTI LIGLFGLLVY LLLVNLRKRI SRKNEAPEVE GGWPIIGHLH 60 HFMGGKNKLL HVAFGAWADK YGPVYTLRMG LNKVLVVNSA EVAKECSTTN DMLFMARPYR 120 IASEIMGYGY AMFPIAPYGP FYLKMRKMVT QELLSNSRVD SLKHVWGSEI KNAIQELHKK 180 VLSTKGGGPI SMDMKGWVSN LTFRTAMKVI CGGVGVDGGG GGGGATSPAT SIGEHNYDEV 240 GSFQKALKEF FVLLGEIRIS DVIPFLGWLD MRTGYVEKMK DNGKFLDNLM EEMLEEHKRK 300 RRSLTEEEEK DGGYVEQDFM DVMISKLNDP KLLSYYDADT INKSTCLTLI LSGSETTMVS 360 IVWALALLVS HPHVLKKAQD ELDTLVGRER QVDESDIKDL VYLQAVVKEA LRLFPPAPLS 420 TPRVATEDCV VSGYHVPAGT QLFVNTWKIQ RNPEVWPEPS EFRPERFFTT HKDFDVRGLH 480 YDLHPFGSGR RACPGAGFAL QVVHLTLASL LHGFEIKNPS DEPIDMTESP GVTNLKATPL 540 KVLLTPRLFS KEVY 554
3-244	**Sequences**	
3-244-1	Sequence Number [ID]	244
3-244-2	Molecule Type	AA
3-244-3	Length	561
3-244-4-1	Features Location/Qualifiers	**source** 1..561 mol_type= protein organism= Eschscholzia californica
	NonEnglishQualifier Value	
3-244-5	Residues	MEKPILLQLQ PGILGLLALM CFLYYVIKVS LSTRNCNQLV RHPPEAAGSW PIVGHLPQLV 60 GSGKPLFRVL GDMADKFGPI FMVRFGVHPT LVVSSWEMAK ECFTSNDKFL ASRPPSAASI 120 YMAYDHAMLG FSSYGPYWRE IRKISTLHLL SHRRLELLKH VPHLEIHNFI KGLYGIWKDH 180 QKQQQQPTAR DDQDSVMLEM SQLFGYLTLN IVLSLVVGKR VCNYHADGHL DDGEEAGQGQ 240

		KLHQTITDFF KLSGVSVASD ALPFLGLFDL DGQKKIMKRV AKEMDFVAER WLQDKKSSLL 300 LSSKSNNKQN EAGEGDVDDF MDVLMSTLPD DDDSFFTKYS RDTVIKANSL SMVVAGSDTT 360 SVSLTWALSL LLNNIQVLRK AQDELDTKVG RDRHVEEKDI DNLVYLQAIV KETLRMYPAG 420 PLSVPHEAIE DCNVGGYHIK TGTRLLVNIW KLQRDPRVWS NPSEFRPERF LDNQSNGTLL 480 DFRGQHFEYI PFGSGRRMCP GVNLATPILH MTLARLLQSF DLTTPSSSPV DMTEGSGLTM 540 PKVTPLKVLL TPRLPLPLYD Y 561
3-245	**Sequences**	
3-245-1	Sequence Number [ID]	245
3-245-2	Molecule Type	AA
3-245-3	Length	565
3-245-4-1	Features Location/Qualifiers	**source** 1..565 mol_type= protein organism= Eschscholzia californica
	NonEnglishQualifier Value	
3-245-5	Residues	MNLSSKLMGS FDLFSLNFLQ FSKPASMVII GICSFLVYFS LLNLVRRVLA PSCTMKNGKT 60 EPPEVENGWP IIGHLHHFMG KKNKLIHEIF GDMADKYGPT FTLRMGLTKV LVVSSAEVAK 120 ECLTTNDLVF IGRPPRVANS LLGYSFAMFP FSPYGTYYSQ MRKIVTHELL STSRVESLKH 180 VWNSEINKAI QELHHKVVSV GGGSPVLIEF KRWFSDLTLR TTVKLICGKQ YFGTDGATQA 240 SMTINGGGDD DEAGKFQEAL REFFCLLGKF RVSDVIPFLG WLDFGTGYKE KKNRMFIDSL 300 MEEWLEEHKM KRRLLNEADK KESRIEQDFM DVMISKLDDP NLLSHYDADT INKATCLTLI 360 LGGSDTTMVS LVWALTLLMN HPHVLKKVQD ELDFHVGRER QVEESDMKNL VYLHAVMKEA 420 MRLNPAGTLS APRMSTKDCT VSGYHIPAGT HLFMNTWKIQ RDPNAWVEPT EFRPERFLTT 480 HKDFDLRGQN FELLPFGSGR RSCLGANFAL QVLRQTLARL LHGFDLKTPS DEPVDMTGSA 540 GLINMKATPL EVLVTPRLFS SELYG 565
[0122] **3-246**	**Sequences**	
3-246-1	Sequence Number [ID]	246
3-246-2	Molecule Type	AA
3-246-3	Length	550
3-246-4-1	Features Location/Qualifiers	**source** 1..550 mol_type= protein organism= Eschscholzia californica
	NonEnglishQualifier Value	
3-246-5	Residues	MNLLIFFQFL LQFQVLVGLS VLLAFSYYLW VSKNPKINKF KGKGALLAPQ AAGAWPIVGH 60 LPQLVGPKPL FRILGAMADN YGPIFMLRFG VHPTVVVSSW EMTKECFTTN DRHLASRPSN 120 AASQYLIYEV YALFGFSLYG SSYWRDARKI ATLELLSHRR LELLKHVPYT EIDTCIKQLH 180 RLWTKNNKNQ NNPELKVEMN QFFTDLTMNV ILKLVVGKRF FNVDDAADHE KEEARKIQGT 240 IFEFFKLTEG SVSAGALPLL NWLDLNGQKR AMKRTAKKMD SIAEKLLDEH RQKRLSKEGV 300 KGTHDHNDFM DVLLSILDAD QGDYSHHPFN YSRDHVIKAT TLSMILSSMS ISVSLSWALS 360 LLLNNRHVLK KAQDELDMNV GKDRQVEEGD IKNLVYLQAI VKETFRMYPA NPLLLPHEAI 420 EDCKIGGFNV PAGTRVVVNA WKLQHDPRVW SNPSEFKPER FLNDQAAKVV DVRGQNFEYL 480 PFGSGRRVCP GISFSLQTIH MSLARLVQAF ELGTPSNERI DMTEGSGLTM PKTTPLHVLL 540 NPRLPLPLYE 550
3-247	**Sequences**	
3-247-1	Sequence Number [ID]	247

[0123]

3-247-2	Molecule Type	AA
3-247-3	Length	532
3-247-4-1	Features Location/Qualifiers	**source** 1..532 mol_type= protein organism= Eschscholzia californica
	NonEnglishQualifier Value	
3-247-5	Residues	MEFHFPLMEQ FQPFFIFALL LASFIFLYKL FNFGNRITKN GKPTAPEASG GRLIMGHLHL 60 FNGTELTHRT LGSMADKYGP AFNIRFGSHK TLVVSSWKII KECFTTNDRF FSNRPGSLAI 120 KLMFYDADSV GYAPYGSYWR ELRKISTLKL LSNHRLETLK HLRTSEVDSC FNQLMNSWAE 180 NKNRGDSDFA PVRMDDWFGD LTFNVVARIV AGKKNFAGGA ARGDAGAQRY KSAMDEAFRL 240 MTIFAYSDVI PSLGWLDKLR GLVGDMKRCG SEIDSVVESW VDEHRLKRRV SKKGGELDLE 300 QDFIDVCLDI MEHSSLPGDD PEIVIKSTCL DMILGGSDTT TVTLTWALSL LLNHPQVLKR 360 AKEELDSQVG KERQVEDSDI PNLPLIQAII KETMRLYPAG PLIERRTMED CEVAGFHVPA 420 GTRLLVNLWK MQRDKEVWSE EPLEFRPERF LTSNTEVDLK GQHYELIPFG AGRRICPGVS 480 FAVQLMHLVL ARLLHGFEMT TPMGEKVDMT ESAGLISHKI TPLEVLIKPL RV 532
3-248	**Sequences**	
3-248-1	Sequence Number [ID]	248
3-248-2	Molecule Type	AA
3-248-3	Length	510
3-248-4-1	Features Location/Qualifiers	**source** 1..510 mol_type= protein organism= Eschscholzia californica
	NonEnglishQualifier Value	
3-248-5	Residues	MDSFLLAYWV PISVASIIAF VFLYNLFSSR TLQNKKIRTA PMATGAWPIL GHLHLFGSGE 60 LPHKMLAAMA DKYGSAFRMK FGKHTTLVVS DTRIVKECFT TNDTLFSNRP STKAFQLMTY 120 DNESVAFTPY GPYWREIRKI STLKLLSNHR LQAIKDVRAS EVNVCFKTLY DQCKNPSGSA 180 PILIDMKKWF EEVSNNVVMR VIVGRQNFGS KIVQGEEEAI HYKKVMDELL RLASLSMFSD 240 FAPLLGFVDI FQGNLSAMKR NAKKVDAILE NWLEEHRKKK NSVAESQQDF MDVMLSIVEE 300 SKLSGHDADA VIKATCLAMI MGGTDTTAVS LTWIISLLMN NRHALKKARE ELDALVGKDR 360 QVEDSDLKNL VYMNAIVKET MRMYPLGTLL ERETKEDCEI DGFHVKGGTR LLVNVWKLQR 420 DPNVWVDPTE FRPERFLTEN ADIDVGGQHF ELLPFGAGRR VCPGVSFALQ LHAFSTCSPH 480 PWIRFEYSKR RKCGSDGEPR RTCEPQSIAS 510
3-249	**Sequences**	
3-249-1	Sequence Number [ID]	249
3-249-2	Molecule Type	AA
3-249-3	Length	534
3-249-4-1	Features Location/Qualifiers	**source** 1..534 mol_type= protein organism= Glaucium flavum
	NonEnglishQualifier Value	

[0124]

3-249-5	Residues	MEFLSLQLQP VSIFALLVAS IFLYNFLIHG KKSNNKKTTK PPAPEASGGW PIMGHLHLFN 60 ENELTHRTLG SMADKYGPAF NIRFGSHPTL VVSSWDIVKE CFTTNDRFFS NRPGSLAIKL 120 MFYDADSVGY APYGAYWRDL RKISTLKLLS NHRLETLKHL RTSEVESCFK ELYNQWRNNK 180 TGGGGDGFAP VRMDNWFGDL TFNVVARIVA GKKNFAGGAA SGDAGAQRYK EAMDEAFRLM 240 TIFAFSDVVP ALGWLDKLRG LVGGMKRCGA EIDSIVAGWV DEHRLKRSSG KGSDADLEQD 300 FIDVCLEIME HSTLPGDDPE VVIKSTCLDM ILGGSDTTTV TLTWALSLLL NNPHVLKRAR 360 EELDTNVGKD RQVDDSDIPN LVYIQAIIKE TMRLYPAGPL IERRTSEDCE VGGFHVPAGT 420 RLLVNLWKMQ RDGSVYKEDP LEFSPERFLT SNADVDLKGQ NYELIPFGAG RRICPGVSFA 480 VQLMHLVLAR LIHGFEMKTP EGGKVDMTES AGLISHKVTP LEVLLKPRLA IQHS 534
3-250	**Sequences**	
3-250-1	Sequence Number [ID]	250
3-250-2	Molecule Type	AA
3-250-3	Length	561
3-250-4-1	Features Location/Qualifiers	**source** 1..561 mol_type= protein organism= Glaucium flavum
	NonEnglishQualifier Value	
3-250-5	Residues	MHAKLTLIKK MEFTIINSLE IQPIISTFAL LTFSILLYKI LLNHGRENKN NKPKTSSSSS 60 SIPEVAGAWP IMGHLHLFNG DELMHHKLGS MAEKYGQAFY IRFGSHKAVV VSNWEMVKTC 120 FTTNNQIFLN RPPMLAINLL FFPTDSLSYI PYGDHWRELR KFSNQKLLSN HRIETQKNLR 180 KLEVDYCFKQ LCNQSSKYFI INNMDDQDSK FALVRMDTWF DDVTLNVLAR IIAGKKKFIS 240 GGATSSGDDD NAEARRYMEA LDEGLRLMTS FTFSDVLPWL GWLDNLRGLA GKMKRCGAEL 300 DSVFAGWVEE HRVKRGSRKD GDDADLEQDF IDLCWESLEQ VPGNDPAKII KLICMEMILN 360 GSGATAVTLT WTVSLLLNNP DVLKRAREEL DTHVGSHRQV DESDIPNLVY IQAIIKEGMR 420 LYPPGPFLER STTEDFEIDG VHVPAGTRLW VNLWKMHRDE SMYQEPLEFK PERFLNSNSD 480 VDLKGQSYQL LPFGAGRRIC PGVSFALPLM HLTLARLIHG FEMKLPVGVE KVDMTENGGI 540 INRKATHLDV LLKPRLIAQQ A 561
3-251	**Sequences**	
3-251-1	Sequence Number [ID]	251
3-251-2	Molecule Type	AA
3-251-3	Length	536
3-251-4-1	Features Location/Qualifiers	**source** 1..536 mol_type= protein organism= Glaucium flavum
	NonEnglishQualifier Value	
3-251-5	Residues	MDTLSIQWIV PSIATLLALV FLYNLIFTSK KTTKTNNTRK APMASGAWPV LGHLHLFGTG 60 ELPHKMLATM AENYGTAFTM KFGNHTTLVV SDTRIVKECF TTNDTLFANR PSTKAFDLMT 120 YANDSVAFTP YSPYWRELRK ISTLKLLSNH RLQSIKDVRV AEVNVCFRGL HVLCKSKIYG 180 APVLVDMKKW FEEVSNNIVM RVIVGKQNFG SRIVQGQEEA VYYKSVMDEL LRLASVSVLS 240 DFAPLFGWLD FFQGNISAMK RNGKKLDVIL ERWMEEHRQK KISSSSSIAA SGAGEDDEQD 300 FMDVMLSIIE ETKLSGRDAD TVIKATCLAM IMGGTDTTAV SLTWIVSLLM NNRHVLKKAR 360 EELDSLVGKD RQVEDSDLKN FVYMNAIVKE TMRLYPFGAL LERDTKEDCE VGGFHVEAGT 420 RLLVNVWKLQ RDPNVWKDPL EFRPERFLVE NVDIDVGGQH FELLPFGAGR RVCPGVSFAL 480 QFMHLVLARL IHGYELETLN GEDVDLTEST EGHVNHKASP LDLLITPRLD SKVYNY 536
3-252	**Sequences**	
3-252-	Sequence Number [ID]	252

[0125]

1		
3-252-2	Molecule Type	AA
3-252-3	Length	532
3-252-4-1	Features Location/Qualifiers	**source** 1..532 mol_type= protein organism= Glaucium flavum
	NonEnglishQualifier Value	
3-252-5	Residues	MDSTLVLQCF VGSMAAVSAL VFLYNLIFSS SKTTKGKVLR KAPMAAGAWP ILGHLHLFGS 60 GELPHKMLSK MAEKYGPAFT LKFGKHTTLV VSDTRVVKEC FTTNDTLFAN RPSTTAFDLM 120 TYANDSVAFT PYSPYWRELR KISTLKLLSN HRLQSIKEIR VSEVNVCFRE LFEMSKSKTD 180 GAAPALVDMK KWFEEVSNNI VMRVIVGRQN FGSKIVQGDA EAVNYKNVMD ELLRLASLSM 240 LSDFAPLLGW VDMFQGNKNA MKRNAKKVDT ILEGWLEEHR KKNKKMSSSE NDEQDFMDVM 300 LSIIEETKLS GRDADTVIKA TVLAMIMGGT DTTAVSLTWI VSLLMNNRHV LKKAREEIDA 360 IVGKDRQVED SDLKNFVYMN AIVKETMRLY PLGAMLERDT KEDCEVGGFQ VQAGTRLLVN 420 VWKLQRDPNV WSDPSEFRPE RFLSENADID VGGQHFELLP FGAGRRVCPR VSFALQFMHL 480 VLARLIHGYE LGTQNDELVD LTESTEGHVN HMASPLDLIL TPRLSNPKLY DY 532
3-253	**Sequences**	
3-253-1	Sequence Number [ID]	253
3-253-2	Molecule Type	AA
3-253-3	Length	518
3-253-4-1	Features Location/Qualifiers	**source** 1..518 mol_type= protein organism= Glaucium flavum
	NonEnglishQualifier Value	
3-253-5	Residues	MFFTSSSKTT NKNTSKKPPM APGAWPILGH LHLFKEGELP HHMLKSMADK YGPAFLMKFG 60 QHRSLVVSDY RIVKECFTTN DTLFSNRPST TAFAVMTYAT DSVAFTEYSP YWRELRKIST 120 LKLLSNNRLQ AIKKLRESEV NVCFRGLYDS WRKNKSEQNG AGNSIDGGNE RARPVLVDMK 180 KWFEEVSNNL VMRVIVGKRN FGTKIVEGEK EAVEYKTIMD ELLRLASLSL LSDFAPILRL 240 FDHFQGHIRT MKRNGKKLDV LLQRWLEEHR RKMSTPEEEQ DFMDVMLSIV DESKLSGHDA 300 DTVIKATCLA MIMGGTDTSA VSLTWIVSLL MNNRHALAKA REELDKHVGK DRQVEESDLK 360 NLVYLHAIVK ETMRLYPLGP LLERETKQDC EVGGFDIAGG TRILVNIWMV QRDPAVWNDA 420 TEFIPERFLT EKSDVDVWGG SFELIPFGAG RRVCPGVSFA LQFLHLVLAR LIHGYELKTP 480 NDMPVDLTES TEGHVNHKAS PLDLLLVPRL SDLKLYDY 518
3-254	**Sequences**	
3-254-1	Sequence Number [ID]	254
3-254-2	Molecule Type	AA
3-254-3	Length	537
3-254-4-1	Features Location/Qualifiers	**source** 1..537 mol_type= protein organism= Glaucium flavum
	NonEnglishQualifier	

[0126]

3-254-5	Value Residues	MDSILTTVVL LSILLYFLFS WQLNKYSATK KNTKSSKQLP PEPAGSWPVI GHLHLLAKGS 60 NLPHINLGAM ADKYGPIFMI RIGLNPTLVV SSWEVAREIF TTNDQVFSSR PIQVSTKHLG 120 FDTAMYGFAP YGPYWREISK LVKREVLSNT RLEFLKPVWG SEINTSIKEL YDVCVMKNKE 180 EGGTGPIIVE MKQWFSDLAL NMSVKLVAGK RYFGASQLGN EEAARWQKAL RNCFRLVGLF 240 VVSDAIPFLR WLDVGGHEKE MKNTAKELDD LLEGWLEEHK MKKKLSLSEV EAEKKERDRV 300 DFMDVMLSTL EHEKASDYFP ADTINKATCL ALILGGTDTT TVVWVWALAL LVNNPNVLKK 360 AQDELDVHVG KKRQVDESDI KNLTYLQAII KESMRLYPAA TLGIRESTED CTVAGYHIPA 420 GTSLIVNSWK IQHDPQVWTD PFEFQPERFL TGHMDVDIRG QSCKFLPFGS GRRSCPGTSL 480 ALQMVTLTLA RLIHGFEFRT PSEAPTDMTE SAGLTNVKAT PLEVLVSPRL PSELYVC 537
3-255	**Sequences**	
3-255-1	Sequence Number [ID]	255
3-255-2	Molecule Type	AA
3-255-3	Length	537
3-255-4-1	Features Location/Qualifiers NonEnglishQualifier Value	**source** 1..537 mol_type= protein organism= Glaucium flavum
3-255-5	Residues	MELINSLEIQ PITISILALL TVSILLYKII WNHGSRKNNK SNKNNRKTSS SAGVVEIPGA 60 WPIIGHLHLF NGSEQMFHKL GSLADQYGPA PFFIRFGSRK YVVVSNWELV KTCFTAQSQI 120 FVSRPPMLAM NILFFPKDSL SYIQHGDHWR ELRKISSTKL LSSHRVETQK HLIASEVDYC 180 FKQLYKLSNN GEFTLVRLNT WCEDMALNVH VRMIAGMKNY VAAPGSGEYG GQARRYRKAL 240 EEALDLLNQF TITDVVPWLG WLDHFRDVVG RMKRCGAELD SIFATWVEEH RVKRASGKGG 300 DVEPDFIDLC WESMEQLPGN DPATVIKLMC KEHIFNGSGT SSLTLAWILS LIMNNPYVIK 360 KAREELEKHV GNHRQVEESD LPNLLYIQAI IKEGMRLYTP GPFIDRNTTE DYEINGVHIP 420 AGTCLYVNLW KIHRDPNVYE DPLEFKPERF LKNNSDLDLK GQNYQLLPFG AGRRICPGVS 480 LALPLMYLTV SRLIHGFDMK LPKGVEKADM TAHGGVINQR AYPLEVLLKP RLTFQQA 537
3-256	**Sequences**	
3-256-1	Sequence Number [ID]	256
3-256-2	Molecule Type	AA
3-256-3	Length	571
3-256-4-1	Features Location/Qualifiers NonEnglishQualifier Value	**source** 1..571 mol_type= protein organism= Glaucium flavum
3-256-5	Residues	MDLQIFFHFQ GIVGSLALLS FFYYLWRLLT TTKTSICNGT TAAPPEVSGG WPILGHLLQL 60 VGSKQPLFKV LGDMADKYGP IFVVRFGMYP TLVVSSWEMA KECFSTNDRV LATRPTSAAS 120 KYLTYNYAMF AFTFYGPYWR EIRKISTIEL LSHRRVEMFK HVPFMEIDTC IEQLYLLWMQ 180 NQNQNQNQPN GDPVQVNMSK VFEELTMNAV LKLVVGKRLT DDKEGEKLHK TIQEFFKLLE 240 VSVASDVFPF LGWLDVDGQK RKMKRVAKEM DIIAEKWLEE HRQKRSSKLE EEEEEEEDDG 300 GGKGDAAAAD KDFMDVLLSL LEGDEGDSDQ PFMNYSRDTV IKATSLNILV AATDTTSPTL 360 TWAISLLLNN PHVLREAQNE LDMKVGRDRQ VEEQDIENLI YLQAIVKETL RLYPAGPLSI 420 PHEAIQDCKL GGYHVRAGTR LLLNIWKLHR DPRVWSNPLE FKPERFLILS EEVCGCSRGT 480 QNFDFKGQCF EYIPFGSGRR MCPGYNFGIQ IIHMTLARLL QSFEMQPAKA KSLNDQDGPV 540 DMREGSGLTL PKITPLKVLL TPRLYGQLYN H 571
3-257	**Sequences**	

[0127]

3-257-1	Sequence Number [ID]	257
3-257-2	Molecule Type	AA
3-257-3	Length	534
3-257-4-1	Features Location/Qualifiers	**source** 1..534 mol_type= protein organism= Hydrastis canadensis
	NonEnglishQualifier Value	
3-257-5	Residues	MDFSMLFQWL LVTMATLLFL NSVYNVWYKS SKNTSITTTT SKGKKAPVAA GARPFMGHLH 60 MLVGGKQLPH QALGKLADIY GPAFIIHIGP NPELVVSSWE LAKECFTTND KYFANRPTNK 120 AMKYLTYDEA SVGFGPYGPL WVEMRKIAKS NLLSQQRLQM HKRVRVLEID AFFKELHELW 180 SMKKEDGPVS VDMKQWFEEL TLNVITRMVS GKHKYATKAR RGDSEAKQFK RVIGEAAHFT 240 GNLLLSDIFP SLGFLDNMQG RVNSMKRTGK ELDSILSSWV EEHRQKKLSG EQSEDEEKDF 300 IDLTLSMMDE IQLHSTDSET FIKAICVGVI LGGSDTTSVG ITWILSLLMN HRDVLKKAQE 360 ELDQQVGMDR KVEDSDLNNL VYLRAIVKES MRLYQVGPLI ERKASQDCTI GGFHVKAGTR 420 LLVNLSKVHK DPTVWSDPLE FQPERFLTTH SNMDLKGQHF ELLPFGSGRR MCPGYLFALN 480 EMYLVLARLI QGFELGTPMD AKVDMTETSS VTNYRATPLQ VLLTPRLSPK LYDY 534
3-258	**Sequences**	
3-258-1	Sequence Number [ID]	258
3-258-2	Molecule Type	AA
3-258-3	Length	528
3-258-4-1	Features Location/Qualifiers	**source** 1..528 mol_type= protein organism= Hydrastis canadensis
	NonEnglishQualifier Value	
3-258-5	Residues	MAFVALIVVY NIWFKSAASR NKTSYNNKTM SKTPVVDGAK PIIGHLHLLM GGDLPHHALG 60 RLADKYGPIF LMHIGAFPEL VVSSSELAKE CFTTNDKYII NRPTNKAMTY LSYEQASVGF 120 APYGPLWIEM RKISKSNLLS NQRIHMQKQV RVAELDAFFK ELYQLCRSND ENNNNSTSHG 180 KVLVEMNKWF EELTLNVVTR MICGKQKMGT KARLGDSDAK HYKKTIDEAA HFMGNLVISD 240 VVPCLGMLDN LLGHVSAMKR TGKELDTIFG SWVEEHQQKI RLSGYKDDAE EEEHDFIDLT 300 LSMMKGSTDL HGLDPATFIK SICVGMILGG TDTTSVALTW ILSLLLNNRH ILKKAQEELD 360 HQVGKERKVE DSDLNNLVFI GAIVKESMRL YPVGPLIERE AIEDCQIGGV HVKAGTRLLI 420 NIWKVQQDPK IWPNPSEFRP ERFLDSNMDV KGQHFELIPF GSGRRMCPGM SFAINELNLV 480 LARLLQGFEL ETPMNAKVDM TETSSVTNYK GTPLQVLLTP RLSSKLYM 528
3-259	**Sequences**	
3-259-1	Sequence Number [ID]	259
3-259-2	Molecule Type	AA
3-259-3	Length	531
3-259-4-1	Features Location/Qualifiers	**source** 1..531 mol_type= protein organism= Hydrastis canadensis

[0128]

	NonEnglishQualifier Value	
3-259-5	Residues	MEYSHLLPWL ATSIAAIFAF IFLFYVRRRK NNKAFIHNHA KKAPVVPGAL PFLGHLRLFT 60 GPILPHKALG ALADKYGPAF TIYLGSHQTL VVSGRELVKE CFTTNDRLFS NRPRSKAVKY 120 LTYDEASVGF APYGPLWVEM RKVSKLNFLS NQRIQMQKQA LASELNFCFK DVYQLWLKNK 180 ELPVMVDMTK WFEEMTLNVI TRLICGKQNY GSKANSGESE AKRYKQVVEK AAHLTSTVVM 240 SDVFPFLEWF DKFQGQEKVM KKVANEFDSI LGSWVDEHRR KRLLRGNNEE EEEEQDFIDL 300 SLAMMEETQL HGVDPDTFIK SMCLGMILGG GDTTPVALTW ALSLLLNNPD IMKKAQEEID 360 QVIGKERKLD GSDISNLVYL QAVVKESMRL YQVGPLIERE TTEDCKIGDF HVEAGTRLLV 420 NIWKVQQDPC VWSNPTEFQP ERFLSSKSDM DLKGQHFELI PFGSGRRMCP AVASALQMMH 480 LVLAKLIHGF ELGTPMNAKI DMTETSSITN NMATHLQVLL NPRLNANLYD F 531
3-260	**Sequences**	
3-260-1	Sequence Number [ID]	260
3-260-2	Molecule Type	AA
3-260-3	Length	543
3-260-4-1	Features Location/Qualifiers	**source** 1..543 mol_type= protein organism= Hydrastis canadensis
	NonEnglishQualifier Value	
3-260-5	Residues	MADFTMLLQW LLLTMATLLF LNAVYKSIKS SKNTINDTSF KKGKKAPVAA GARPFIGHLH 60 MLVGGKQLPH QALGKLADKY GPAFIINIGP NPELVVSSWE LAKECFTIND RCFTDRPSNK 120 AMKYLTYDEA SVGFAPYGPL WVEMRKIAKS NCAFQQRLQV QKRVRVLEID LFFKELHELW 180 SHAGAGATGT SVIPLSIDMK KWFEELTLNV ITRMVSGKHN YATKARKGDT EAKRFKRVIS 240 EAAHFTGRLL LSDIFPSLGF LDNMQGRVNS MKRTGKELDS VLSSWVEEHR QKRVSGNKEQ 300 SPEDDDVEQD FIDLTLSMME EIQLHWTDAD TFIKAICVGV ILGGSDTTSV GITWILSLLM 360 NHPDVLKKAR EELDQQVGLE RKVDDSDLNN LAYLRAIVKE SMRLYQVGPL IERKAKQDCN 420 IGGFHLKAGT RLLVNLSKVH KDPTVWSDPN EFRPERFFTT HTNIDIKGQN FELIPFGSGR 480 RMCPGYLFAL SEIYLVLARL IHGFELRTPN DAKLDMTETS SVTNYRATPL QVLLTPRLSS 540 KLY 543
3-261	**Sequences**	
3-261-1	Sequence Number [ID]	261
3-261-2	Molecule Type	AA
3-261-3	Length	532
3-261-4-1	Features Location/Qualifiers	**source** 1..532 mol_type= protein organism= Hydrastis canadensis
	NonEnglishQualifier Value	
3-261-5	Residues	MDYFSMPYQW LLTSLATLIV FVFIWSITAG KTSTTSNKAK KAPPIAAGAW PIIGHLHLIM 60 GGELPHRLLS NLADKYGPIF MLNYGSQPGL VVSSLKLAKE CFVHNDRAVF KRPNSKAMKY 120 FTYDQASFGF APYGPLWVEM RKVSKSNLLS NQRLQLQRNQ RASEVDAFIK ELYQLCKKSN 180 NGTLMVEMNK WFEELTLNVV TRMVCGKKNI GAKARHGGDN EAKYYKKVID EATIFTAKLV 240 ASDFFPSLGW VDYLHGDESA IKQTAKELDS IIGSWVEEHR QKRLLSLNKD DYAEQDFIDI 300 TLSMIDQTQH QGIDADTFVK SMCVGMIFGG SDSTSVALNW ALSILMNNRH VLKRAREEID 360 TLVGKDRKVN DVDVTKLVYL KAIVKESMRL CLVGPLLERV TVEDCEIGGF YVKAGSRIVV 420 NIWKLQHDPD LWSDDVMEFR PERFLTTNSN VELRGQHFEL IPFGSGSRMC PGVTFALELM 480 HLTLARLIHG FELGTPMDAK VDMTETSSVT NYKATPLEIL LTPRLHPKLY DF 532
3-	**Sequences**	

[0129]

262		
3-262-1	Sequence Number [ID]	262
3-262-2	Molecule Type	AA
3-262-3	Length	534
3-262-4-1	Features Location/Qualifiers	**source** 1..534 mol_type= protein organism= Hydrastis canadensis
	NonEnglishQualifier Value	
3-262-5	Residues	MFISITQQSM DSFHQYLATI IFGVFSFVLF LIYYLPLKRS RSDKKRAAPK PVGAWPIIGH 60 LPMLSRHQPP HITLGNIADK YGPAFTLQLG VHRALVVSSS EVAKECFTTN DKALASRPSS 120 VALKLMGYNN AMFGFGPYGS YWRQMRKIVV LELLSNHRLQ LLKHVRISEV STSLKELYQV 180 WASCTNKNDK GQVLVDMQQW FGDLTLNVSV RMIAGKRYFG ASAACDEDEA RRFQKAIKDF 240 LHLVGLFVVS DALPFLEWLD IQGHQKAMKR TFKELDRILG KWVEEHRRNK LDGGTNVGRD 300 FMDVMSSILD DANISDYDAD TINKATCLSL ILGGTDTTMV TLTWALSLLM NNQHILKKAQ 360 DEIDIYVGKD KNVDESDIEK LVYLQAIVKE TLRLYPAGPL SGPHEAIEDC TVAGYHVPRG 420 TRLITNLWKI QRDPRIWSSP CEFQPERFLT TQANVDVRGQ HFEFLPFGSG RRSCPATSFA 480 LQVVHLALAR VLQGFEFETQ SNAPVDMTES AGLTNVKATP LEVLITPRLP LNLY 534
3-263	**Sequences**	
3-263-1	Sequence Number [ID]	263
3-263-2	Molecule Type	AA
3-263-3	Length	529
3-263-4-1	Features Location/Qualifiers	**source** 1..529 mol_type= protein organism= Hydrastis canadensis
	NonEnglishQualifier Value	
3-263-5	Residues	MESLHQYLAA VMSCIFALLL FLYYFPWKIR RSSSDNNMRS APEAAGAWPI IGHLPMLGGH 60 QLPHITLGNL ADRYGPAFTI RLGVCRALVV SSSEVAKECF TTNDKAFATR PSSVAVKLMG 120 YNYALFGLAP YTSYWREVRK IVILELLSNR RLELLKHVRI SEVNTSIKEL FQVWASSNNK 180 NEKGQVLVEM QRWFGDLTIN VAVRMVAGKR YFGASVNTCD DEEEARRFQK AIKNFFHLVG 240 LYVLSDSLPF LEWLDFEGHQ KAMKRTFKDV DCILQRWLEE HRRDKENGAM KEERDFMDVM 300 LSILKDANLF GYEADTVNKA TSLNIILGAT DTTMVTLTWA LSLLLNNRHI LKKAEDEIDI 360 HVGKDKAVDE SDIEKLVYLQ AIVKETLRLY PVAPLLAAHE AIEDCIVAGY HVPRGTRLIP 420 NIWKIQRDPR IWSSPCDFQP ERFLTTQANV DVRGQHFELF PFGSGRRMCP GISFGLQVVH 480 LALARVLQGF EFDTPSNKAI DMTESAGLTN LKATPLQVLI TPCLPLNLY 529
3-264	**Sequences**	
3-264-1	Sequence Number [ID]	264
3-264-2	Molecule Type	AA
3-264-3	Length	530
3-	Features	**source** 1..530

[0130]

264-4-1	Location/Qualifiers	mol_type= protein organism= Hydrastis canadensis
	NonEnglishQualifier Value	
3-264-5	Residues	MDSILLPTPL MVSLFALLLC LYYLIISRPR SSHNTSTKEA PEAAGALPII GHLHLLGGRI 60 LPHITLGAMA DKHGPAFMIR IGVHRALVVS SSEVAKECFT TNDKAFASRP KHTAAELMGY 120 NYAMFGFAPY GPFWSEMRKI IMAELLSNRR LELLKYIRDF ELKASIKELY MTWENHSVTN 180 KGQVVVEMKK WFGDLTLNVI LRMIAGKRYF GSNSTCDESE AKICQKGMRD FFRLLGEFLV 240 EDAIPYLGWL DLQGFKKEMK NTAKELDILL QGWLEEHKKK REFSKDVKEE QDFMDVMMTI 300 LEDANFSDFD ADTINKATCL TIISGGSDTT MLTLTWALSL LLNNQHVLKK AQDELDTHVG 360 RDRRVDESDI KNLVYLNAIV KETLRLYPAS PLLGIRVSTE DCTVAGYHVP SGTRLMVNAW 420 KIQRDPLVWS DPFEFRPERF LTTHVNVDVK GQNFNLIPFA SGRRVCPGVA FALQMLPLVL 480 AHLLHGFKLM TQLGGPVDMT ESTGLTNIKA TPLEVVISPR LRPELYEMYT 530
3-265	**Sequences**	
3-265-1	Sequence Number [ID]	265
3-265-2	Molecule Type	AA
3-265-3	Length	525
3-265-4-1	Features Location/Qualifiers	**source** 1..525 mol_type= protein organism= Hydrastis canadensis
	NonEnglishQualifier Value	
3-265-5	Residues	MESLHQYLAT ILSCIFAFLL FLYYFPWKGR RSFDNNLRTA PEAAGAWPII GHLPMLNQRD 60 LPHVTLGNLA DRYGPAFTIR LGVRRALVVS SSEVAKECFT TNDKAFATRP SSVAVKLMAY 120 NYAVFGFGPY GSYWREMRKI VILELLSNRR LELLKHVRIS EVNTSIKELY QVWASNNKNE 180 KGQVLVEMQR WFGDLTMNVV VRMVAGKRYF GASVTCDEEE ARRFQKAIRD FSHLAGLYVL 240 SDALPNIEWL DFEGHHKAMK KTFKDLDCIL QRWLEEHRRD RENGATKGER DFMDVMLSIL 300 KDANPFDFEA DTVNKATSLN MVLGGTETTT VTLTWALSLL LNNQHILKKA QDEINIRVGK 360 DKPVDESDIE KLVYLQAIVK ETLRLYPVLP LSVPHEAIED CTIAGYHVPR GTRLITNLWK 420 IQRDPHIWSS PCEFQPERFL TTQANVDVRG QHFELFPFGS GRRMCPGISF GLQVVHLALA 480 RVLQGFEFET PSNVPMDMTE SAGLTNFKTT PLEVLITPCL PLDQY 525
3-266	**Sequences**	
3-266-1	Sequence Number [ID]	266
3-266-2	Molecule Type	AA
3-266-3	Length	525
3-266-4-1	Features Location/Qualifiers	**source** 1..525 mol_type= protein organism= Hydrastis canadensis
	NonEnglishQualifier Value	
3-266-5	Residues	MDSLLQLQII GALAALIFTY KLLKVICRSP MTDGMEAPEP PGAWPIIGHL HLLGGQDPIA 60 RTLGVMTDKY GPILKLRLGV HTGLVVSNWE LAKECFTTND RVLASRPMGA AGKYLGYNYA 120 IFGLAPHGPY WSEVRKIVLR ELLSNQSLEK LKHVRISEIN TCLKNLFSLN NGNTPIKVDM 180 KQWFERPMFN VVTMMIAGKR YFSMENDNEA MNFRKVATEF MYLTGVFVVS DALPYLEWLD 240 LQGHVSAMKR TAKELDIHVG KWLEEHRRAK LLGETKNEDD FVDVLLTILP EDLKDNQTYI 300 HDRDTIIKAT ALALFLAASD TTAITLTWAL SLILNNPDVL KRAQDELDKH VGKEKLVKES 360 DIINLVYLQA IIKETLRLYP AAPLLLPHEA MEDCTVGGYH VPKGTRIFVN IWKLQRDPRV 420 WFDPNEFRPE RFLTTHANVD FKGQHFEYIP FSSGRRVCPG ITFSTQIMHL TLAHLLHEFN 480 IVTPTKSNAG VDMTESLGIT MPKATPLEVL LTPRLPSNLY NQYRD 525

[0131]

3-267	**Sequences**	
3-267-1	Sequence Number [ID]	267
3-267-2	Molecule Type	AA
3-267-3	Length	521
3-267-4-1	Features Location/Qualifiers	**source** 1..521 mol_type= protein organism= Jeffersonia diphylla
	NonEnglishQualifier Value	
3-267-5	Residues	MDSLQLIASV VCGLFAFLRI YYLLKKLSSN KEAPQLGGAW PIIGHLHLLG RVELPHIFFS 60 AMADKYGPAF MIQLGMRRAL VVSSAEIAKE CLTTNDKALA TRPSSIAAEI MGYDYAMFGL 120 GPYGDYWREV RKIVVLEFLS NRRLELLKHV RVSEISLSLK ELYQSWEKQN KADEPVLVHL 180 DQWFGDMTLN LSVRMVAGKR YFGATAACGE DESRKVQKAT REFDRLLGLF VVSDYLPFLR 240 WLDLEGHQKL MKSIGRELDS ILQGWLDEHK TRRNSGGGAK GDQDFIDVML SVLEDGNLSN 300 YDADKLNKAT SLTMIVAGSE TTMVTLTWAV CLLLNNPEVL NKAQDELDMH IGKDRQVEES 360 DIKNLAYLQA VIKETMRLYP VAPLLIPHEA MEDCTIAGYH VRAGTRVILN GWKLQRDPFI 420 WSDPCEFQPE RFLNNDVDVR GRHFELLPFG SGRRACPGIS LALNVVSLTL ARLLHEFKFS 480 NPSEGKVDMS ESAGVVVAKA TPLEVLIIPR LPSKFYEYYK L 521
3-268	**Sequences**	
3-268-1	Sequence Number [ID]	268
3-268-2	Molecule Type	AA
3-268-3	Length	518
3-268-4-1	Features Location/Qualifiers	**source** 1..518 mol_type= protein organism= Hydrastis canadensis
	NonEnglishQualifier Value	
3-268-5	Residues	MFSLQLLSTP LFGFFTLLAI YYLLWTKSNK TKEAPQPAGA WPIIGHLHLL ARSELPHITL 60 GAMADKYGPA FMIRLGTRQA IVVSNSEIAK ECLTIKDRIF ATRPSLVAFK LMGYNSAMVG 120 LSPYGPYWRE LRKIIALKVL SQRRLESLKD VWDSEISSSL NHLHQIWSHQ TEPNGKILVE 180 MDQWFGDLTL NVAVKMVAGK RFFSADAACD ENESRRCQKA IREFFRLLGQ FVVSDSLPFL 240 GWLDLEGYQK EMKSTAKEVD SILQKWLDEH KQKRQSAGAD RDQDFMDVML SLLEDASLSQ 300 YDTDTINKAT CFSMIVGGSD TTKITLTWAL TLLLNNPDVM KKSQDELDIQ VGKDRHVEES 360 DIKNLVYLEA IVKETLRLYP AAPLLAPHEA TEDCIVAGYN VRAGTRLIVN AWKIQRDPLI 420 WPNPSEFLPE RYLNKDVDVK GQHFELIPFG SGRRACPGIT FGLQVVSLTL ARLLHEFEIS 480 IASGIKVDMT ESGGLVTAKA TPLKALIAPR FLYSHHHI 518
3-269	**Sequences**	
3-269-1	Sequence Number [ID]	269
3-269-2	Molecule Type	AA
3-269-3	Length	525

[0132]

3-269-4-1	Features Location/Qualifiers	**source** 1..525 mol_type= protein organism= Mahonia aquifolium
	NonEnglishQualifier Value	
3-269-5	Residues	MNSLQFLATP LLTLIALLCV YCIVWRKSFS RNGSKIKQAP WAGGAWPIMG HLHLLAWGDL 60 PHITLGALAD KYGPVFMMQL GMRQAIVVSS AEIARECFTT NDRILATRPS SIAVKLMAYN 120 YAMFAFAPYG PNWREIRKTV MLELLSTPRL ESLKHVWEDE ISTSVKELYE LCASKTKTHG 180 HVSVDMKQRF GDLTLNVLVK LVNGKRYFGA NTDYTEHESR RCQKAVRDFF SLMGLFVVSD 240 FLPFLERLDL QGYEKEMKRV AREVDGIVQG WLDEHKRKRE SSETTHDQDF MDVMLSILKD 300 SKFSNSDYDA DTINKATCFN MILGGSDTTM STMTWALSAL LNNPHMLKKA QDELEFHVGK 360 GRQVEESDIK KLTYLQAIIK ETLRLYPSAP LLAPREATED CKIAGYHVPA GTRLIVNVWK 420 IHRDPFVWPN PNEFQPERFL NKDVDVKGQH FELIPFGSGR RACPGVSLGL QVVSLGLARL 480 LHGFELSIPS GSKVDMTETA SLVTFKATPL EVFITPRLSP HMYVE 525
3-270	**Sequences**	
3-270-1	Sequence Number [ID]	270
3-270-2	Molecule Type	AA
3-270-3	Length	502
3-270-4-1	Features Location/Qualifiers	**source** 1..502 mol_type= protein organism= Mahonia aquifolium
	NonEnglishQualifier Value	
3-270-5	Residues	YAWKRKNHTK DSKIKEPPQP AGAWPIIGHL HLISRGGLPH INMGAMADKY GPVFMIRLGV 60 NRAVIVSNSE IVKECFTTND KFLLNRPVGL ALNLMSYNNA MFGFSRYGPY WREIHKIVML 120 ELLSSSRLES LKHVWDSEIL TSIEELYQLC QTQNKAHEGP VLVEMKDWFA DMALNVSFRM 180 VAGKRYFGAS AGGNKDEARR CQKTMRDFFR LVGLFIVSDA LPFLRWLDLG GHQKEMKRTF 240 EDLDYVLQGW LDEHKLNRKS GGNGDQDFMD VMLSTLYDSK FTDYDVDTIN KATCFQLILG 300 GTDTTTVTLT WALSLMLNHP HVLKKAQDEL DIQVGKHRQV EESDIKNLKY LEAVIKETLR 360 MRPVGPLLGP REAIEDCTIG GYRVRAGTRV MVNAWKVQRD PSVWPNPDDF KPERFLKKDI 420 DFRDQNFEFI PFGSGRRACP GISFAVELLP MALARLLHGF ELKTQLGCKV DMTEHAGLVH 480 AKATPLEVLV SPRLSRELYV SS 502
3-271	**Sequences**	
3-271-1	Sequence Number [ID]	271
3-271-2	Molecule Type	AA
3-271-3	Length	529
3-271-4-1	Features Location/Qualifiers	**source** 1..529 mol_type= protein organism= Menispermum canadense
	NonEnglishQualifier Value	
3-271-5	Residues	MDSTDHHLAL VIPTLLATPV LLFSFYCLLL RPRSLKKPRT NKPPEPSGSW PIIGHLHLLS 60 QGLPHITLGA MADKLGPAFS IRLGTRRALV VSSWEVAKEC YTTNDRAFAS RPSSIAVKLM 120 SYNNSILGFA PYGQYWRELR KIVVLQLLSN RRLESLKNVW ESEIDLSIKE LYDTWASNRG 180 GEALMVDMKQ WFGDLTMNIV VRLVVEKRCF GRSVGDDETE ARRGQRALKE FLKLVGLFLV 240 EDAFPFLSWL DVQGHQREMK RIARELDSLF QGWLEEHKRK RSIKGEAKGD QDFMDVMLSV 300 LEDSTISTDI EDDTVIKSTC LTVVLGGSDS TVGTLTWALS LLLNNRHELK KAQDELDAYV 360 GKERQVDESD IKNLVYLQAI VKEVLRLYPA GPLSGPRESV EDTVVAGYHV PKGTQLIVNL 420

		WKIQREPSIW ADPLEFQPER FLTTHKGMDV WGQHFELIPF GSGRRSCPGT AFALQVIHLT 480 LARLLHGFEL TTPCGAPVDM SESAGLINVK TTPVEVHVAP RLPLKLYKS 529
3-272	**Sequences**	
3-272-1	Sequence Number [ID]	272
3-272-2	Molecule Type	AA
3-272-3	Length	529
3-272-4-1	Features Location/Qualifiers	**source** 1..529 mol_type= protein organism= Menispermum canadense
	NonEnglishQualifier Value	
3-272-5	Residues	MILIAMGNHI ELQDIILYSL GFFAATILWR IFSTYVLRRN SCSRPPEAAG KLPLIGHLHL 60 LGANKILHHT LGDMADRHGP IFSLNLGIKR TLVITSWEVA KECFTTQDRV FATRPKSLVG 120 KVVGYNSTVM IFQQYGPYWR EIRKLAMIEL LSNRRLEMLK HVRESEVNLF IKELYEQWSS 180 NENGSKVVVE MKERFGDLTT NIVVRTVAGK KYSGTGVHGN EESRRFQKAM TDFMHLAGLF 240 MVSDALPLLG WIDTFKGYRG KMNKTAEEID HVLGSWLKEH QQKRKNISIN HLDEDFIHVM 300 LSAMDGNQFP DIDTETAIKG TCLSLILGGY DTTSATLTWA LSLIVNNHHV LKKAQDEMDK 360 YVGRDRQVKE SDVKNLTYLQ AIVKETLRLY PAAPLSVQHE AMEDCTVAGC NIPAGTRLVV 420 NLWKMHRDPK VWSDPLEFQP DRFLQKHVNV DIWGQNFELL PFGSGRRSCP GITFAIQVLH 480 LTLAQLLHAF QLGTVFASPI DMTESSGVTN PKATPLQVTL TPRLPPEVY 529
3-273	**Sequences**	
3-273-1	Sequence Number [ID]	273
3-273-2	Molecule Type	AA
3-273-3	Length	513
3-273-4-1	Features Location/Qualifiers	**source** 1..513 mol_type= protein organism= Menispermum canadense
	NonEnglishQualifier Value	
3-273-5	Residues	MDSTYQLLSA LLFILCLYYL VCKPITKTKN DEAPVPAGAW PIMGHLHMLR GPNLPHITLS 60 SMADKHGPAF TIRLGTRRAL VVSNSDLAKE CFTVNDKAFS TRPSTVATKL MGYNNTMFGF 120 APYGPYWREL RKIVMTELLS SRRLESLASV WASEIESSVK ELFAEWAENR AKGPVVVEMG 180 EWFGNLTLNI ALRMVVGKRY LREESRKCLK AMRDYPELFG RFLVEDAVPF LGWLDLIQGY 240 QREMKKTARE LDSVLEKWLV EHKDKRGSGE GKGEHQDFMD VMISVLEDSK LSYGEADTVN 300 KSTCLNLILG ATDTTMVALT WALSLLLNNK QVLKRAQQEL KSQIGNNKQV SQSDIKNLLY 360 LQATVKEALR LYPPEPLSGP REALEDCTVA GYRVRAGTRL IVNLWKIHRD PSIWQVPLEF 420 RPERFLTAHK DVDVWGQHFE LMPFGSGRRS CPGISFVLQV VPLILARLLH GFELTTPGEA 480 LVDMSESAGL VNAKVTPLEV VISPRLPLEL FAG 513
3-274	**Sequences**	
3-274-1	Sequence Number [ID]	274
3-274-2	Molecule Type	AA
3-	Length	534

[0133]

[0134]

274-3		
3-274-4-1	Features Location/Qualifiers	**source** 1..534 mol_type= protein organism= Menispermum canadense
	NonEnglishQualifier Value	
3-274-5	Residues	MIMMFIDYYS SWLPQTLLLQ SILLAVSLVI FINLFLTRRR SYSSKSHTNI IHPPKAAGAL 60 PVIGHLYTLF RGLSAGVPLY RQLDAMADRY GPAFIIHLGV YPTLVVTCRE LAKECFTTND 120 QTFATRPSTC AGKYIGYNYA FFGFAPYGPY WREARKIATV ELLSNYRLDS LRHVREAEVG 180 RNVDELYALH ASSSTNKQNM MKIDMKQWFD QVTLNVILMM VVGKRCVTTG GNEEEVRVVK 240 VLHEFFKHLG TLSVSDVVPY VEWMDLDGNI GRMKSTAKEL DCILGRWLEE HRRERRSDFM 300 DAMLAMVEGI KIPYYDSDTV IKAICLNLLN AGSDTLGITM TWALSLLLNN RHVLKKVKDE 360 LDVHVGKNRQ VEELDVKNLV YLHAVVKETL RLFPPAPLGV PHEAMEDCVV GGFHVAKGTR 420 LVVNVWKLHR DPSVWSDPLA FKPERFLDNN TVDVRGQHFQ LLPFGSGRRG CPGITFALQV 480 AHLTLARLLH GFEWDTPDGA PVDMSEVSVL TTAKKNPVEV LFTPRLPAEV YTQN 534
3-275	**Sequences**	
3-275-1	Sequence Number [ID]	275
3-275-2	Molecule Type	AA
3-275-3	Length	523
3-275-4-1	Features Location/Qualifiers	**source** 1..523 mol_type= protein organism= Menispermum canadense
	NonEnglishQualifier Value	
3-275-5	Residues	YQLLFLQTAI AGLLFALALL VRLRFSRRNN GKKKQAPPEP AGARLIMGHI HMLNSGEQPH 60 KTLAALADQY GPVIKLRLGL RDAIVVSNWE MAKECFTTND KIFLSRPQTV VSKFMSYNLK 120 MLGFAPYGPY WREIRKIVVS ELLSNRRLEL LKNAWTSEIS SWVKELFDEW GAKEARGPVV 180 VDMRHWFGNL AFNIGMNMVA GKRFFGPRVV SDEDGLRRVQ QGLTDFFRLI GAFLLEDAVP 240 FLSWWDSQGY QKEMKDTARE MDTLIQGLLD EHKRRRSSSS GEAKGEKDFM DVMLNILEGS 300 KFPSGDADNI NKSTCLSLML GLTDTTTATL TWALSLLLND PRVLKKAREE LDFHVGKNRL 360 VDTSDLMNLP YIHAIVKEVL RLHPPAPLSG HRESLEDSVV GGYHVPKGTR FMVNVWKIHH 420 DPNKWPDPIE FRPERFLTTH KDVEVWGQNF ELIPFSSGRR VCPGASLSLQ VLPFTLARVL 480 QGFEVATPGG APVDVTESKG LSTAKETPLD VVITPRLPEK FYH 523
3-276	**Sequences**	
3-276-1	Sequence Number [ID]	276
3-276-2	Molecule Type	AA
3-276-3	Length	528
3-276-4-1	Features Location/Qualifiers	**source** 1..528 mol_type= protein organism= Nandina domestica
	NonEnglishQualifier Value	
3-276-5	Residues	MDSLISFQAI VGLFILILVS YQWLGRSRSI KTNKHNEAPE PAGRWPIIGH LHLLGGSDQL 60 LYRTLGSMAD KLGPAFNIRL GSRRAFVVNS WEVAKECFTI NDKALASRPI TVAAKLMGYN 120 YAVFGFAPYS PFWRAMRKIA TLELLSNRRL EMLKHVRISE VDMGLKEIYG LWSKNKDSGP 180 LMIELNRWFE NLTLNMVVRM VAGKRYFGAD ASCDENEAQR CQKAISEFFR LIGIFVVSDA 240 IPSLWWLDLQ GHEKAMKRTA KDLDSILGGW LEQHRSRRVN GKVPTEGEQD FIDVMLSLQE 300 GDHLSDFEYD ADIAIKSTCL ALILGGSDTT AGTLTWAISL LLNHPYALKK AQEELDLHVG 360

		KDRQVYDQDI KNLVYLQAII KETLRLYPAG PLLGPREAME DCTISGFDVR AGTRLVVNVW 420 KIQRDPNVWS NPSEFSPERF LTSHVDVDVR GQNFELMPFG SGRRSCPGAS FALQVLHLTL 480 ARFLHGFGLA NPLGKPVDMN ESPGLTIPKA TPLNVLLTPR LDSELYGC 528
3-277	**Sequences**	
3-277-1	Sequence Number [ID]	277
3-277-2	Molecule Type	AA
3-277-3	Length	520
3-277-4-1	Features Location/Qualifiers	**source** 1..520 mol_type= protein organism= Nandina domestica
	NonEnglishQualifier Value	
3-277-5	Residues	METFQFLGIP LFGFFALLCT YYLVLRKPSS TKIREPPRPA GAWPIIGHLH LLARGDLPHV 60 TLGKMADKYG PVFKLKLGVR QAIVVSDWEV AKECYTTNDR ALANRPSGLG AKIMGYNYAL 120 IGSAPYGPYW RDLRKIITLE VLSSRRLESL KHVWDSEIST SVKELYQIWA DQNKAQGQVS 180 VEMKQWFSDM TLNVAVRLAV GKKYLGATAD CEKNKAVQCQ KAIRNFFRLA GLFVVADYLP 240 FLGWLDLGGH EKEMKHTAKE LDYIAQEWLD DHKKKRTSNR TVDEPQDFMD VMLSILEEST 300 FTGYDVDIIN KSTCFALILG GTDTVAVTLT WALCLLLNNP HVLKKAQDEL DIHVGKDRHV 360 NESDIKNLVY LQAMIKETLR LYPAGPLLGP RQVIEDCTIA GYHVRAGTRV IVNAWKFQRD 420 PSIWSNPCEF QPERFLDKDI DVKGQHFELI PFGAGRRACP GISFALQVLP LALARLLHGF 480 ELKNPSESQV DMTETPGMVH AKTTPLEVLI TPRLSPKFYV 520
3-278	**Sequences**	
3-278-1	Sequence Number [ID]	278
3-278-2	Molecule Type	AA
3-278-3	Length	495
3-278-4-1	Features Location/Qualifiers	**source** 1..495 mol_type= protein organism= Nandina domestica
	NonEnglishQualifier Value	
3-278-5	Residues	WKRPTSVKYR EAPQPAGAWP IIGHLHLLAR GDLHHITLGA MADKYGPAFM MRLGVHQAMV 60 VSDSESAKEC STTNDRVLAT RPSSVAVKLM GYNYAMFGFG PYGSYWREIR KIVILEVLSN 120 HRLESLKHVW KSEISMSTKE LYQLWINQNK DEGPTLVELK QWLCNMTLNI GVRTVAGKRY 180 FGASSCDANE SNRIQRAIRD FFRFVGLFVV SDFLPFLGWL DLEGYQKEMK SIARELDSIL 240 QGWLDEHTRK RQSGGTNENQ DFMDIMLSVL EHSNALTHYD ADTINKATCF TMILGGSDTT 300 MVTLTWALSL LLNNPHVLKK AQDEIDIQVG KDRLVDESDI KNLVYLQAIV KETLRLYPAV 360 PIITPHEAIE DCTIAGYHVP AGTRLIVNAW KIQRDPLIWD NPGEFQPERF LYKDVDVKGK 420 HFELIPFGSG RRVCPGISLA LQVVSLAMAH LLHEFDLAKP SEGNVDMTES VGLVNAKATP 480 LEVLITPRLS PKFYE 495
3-279	**Sequences**	
3-279-1	Sequence Number [ID]	279
3-279-2	Molecule Type	AA
3-	Length	525

[0135]

[0136]

279-3		
3-279-4-1	Features Location/Qualifiers	**source** 1..525 mol_type= protein organism= Nigella sativa
	NonEnglishQualifier Value	
3-279-5	Residues	MGSFNQINPS VVYFAAFTIF FFFFLYKILY KRRTSAKTRV APEPAGAWPF IGHLPLLSQQ 60 NLPHVTLGVL ADKYGPAFTV QLGLHKAVVV SSWEVAKECF TVNDKVLATR PSSVAVKIMC 120 YNYAVFGFGP YGSYWREARK IVVRELLSNH RLNLLKHVLV TEISMSMNEL YTVWQKNANN 180 VSGKALVEMK QWFGDLSLNM IVKIVAGKRY FQASANSDER DQLKRGVQDL FHLVGLFLVS 240 DALPFLSWLD IGGHEKAMRR TAKELDNILG SWLDEHKQAK LAGATKGEQD FMDVLMSILE 300 DNNNLPEYEP DVVSKAICLG MILGGADTTT ITLTWIVSLL LNNQHILKKA QDEIDSKVGK 360 DRQVNESDIE KLVYLQAIVK ETLRLYPPAP LSTQHEAMED CTIAGYHVQA GTRLITNIWK 420 IQRDPGVWPN PCEFQPERFL TTHANVESNG KHFEFIPFGS GRRACPGMSL GLQVVHLTLA 480 RLLQGFELET PLSVEVDMTE SAGLTNLKVT PLEVLINPRL PSNLY 525
3-280	**Sequences**	
3-280-1	Sequence Number [ID]	280
3-280-2	Molecule Type	AA
3-280-3	Length	517
3-280-4-1	Features Location/Qualifiers	**source** 1..517 mol_type= protein organism= Nigella sativa
	NonEnglishQualifier Value	
3-280-5	Residues	MDLTSILICI FLFIISICFL SWKRSRSLSG TRAAPEPVGA WPVIGHLRLL MGSKTPHMTL 60 GNLADNYGPA FTIRLGTKKT LVVSSWEVAK ECLTTNDKAF AGRHSTMAVE IMGYNYAFFS 120 LGPSGQYWRE IRKITVSELL SNRRLELLKH IWSSEIKTSI KELYEICAAQ SQYGKKQSPM 180 VEMQQWFSHL NLNLSARMVV GKRYFADGVE ENEGDIRRFQ NAIKEFFYWA GAFIIADTIP 240 YLRWMDFLNE RSMKRTAKET DHVLEGWLQE HKRNRLNGVT KEQDFMDVLL TELGDKDLCG 300 YTADVVNKAT CLNMIFGGTD TTKTGMIWTL SLILNNPQVL KKLQNEIDIQ VGKDRQVDDS 360 DIGNLVYLQA TVKEAMRLYP PATIFGRESI EDCTVAGYHI QAGTRLIVNA WKIQRDPNVW 420 PNPDEFQPER FLTNQADVDF RGQDFELIPF GAGRRACPGI SLTVRVTHLT LACLLQGFNF 480 ETPLNEPVDM SEKYGLTNSK ATPLNVILTP RLPSNLY 517
3-281	**Sequences**	
3-281-1	Sequence Number [ID]	281
3-281-2	Molecule Type	AA
3-281-3	Length	530
3-281-4-1	Features Location/Qualifiers	**source** 1..530 mol_type= protein organism= Nigella sativa
	NonEnglishQualifier Value	
3-281-5	Residues	MDSIFHMYAP INILAATFVF IVISVWFLLW MKRSRKNSKS RRAPEPVGGW PLIGHLRLLV 60 GPELPHVILG SLADKYGPAL SIRLGMRQAL VVSNCEVVKE CLTTNDRCFS TRPSSVAVEL 120 MGYNYASFGL GPYGGFWREV RKIAILELLS NHRLKSLKHV WISEISGFVK ELYQLCVANG 180 NTGRQSALVE MRQWLNDLTL NVSVRMVVGK RYFGSGSEHG GEDVKRFQKA IKDFFRLAGK 240 FTLADAIPFL RWLDFGHERA MKKTAKELDY VLARWLDQHQ KNKLNCETKQ VDQDFMDVML 300 TVLGDKDLYG FKADVVNKAT CLNLILGGVD TTSVTLTWAL SLLLNNPNIL NKAQEEIDVQ 360

		IGKDRQVDDN DLGKLVYLEA IVKETMRLYP AGPLSGARAA IEDCMVAGYH VPKGTRLIVN 420 TWKIQRDPEK WDNPSEFRPE RFLITTTNGH VEVWGQHFEY IPFGSGRRIC PAISFSLQLV 480 HLTLARLLQA FSFQTPSNAA VDMTETPGLV NFKATPLQIL LTPRLPSSLY 530
3-282	**Sequences**	
3-282-1	Sequence Number [ID]	282
3-282-2	Molecule Type	AA
3-282-3	Length	527
3-282-4-1	Features Location/Qualifiers NonEnglishQualifier Value	**source** 1..527 mol_type= protein organism= Nigella sativa
3-282-5	Residues	MLSIHDSTMV FLQLQAICGI FGFIFIITWW TRWKSSNKMK APEVAGAWPV IGHLHLLGGG 60 RPLYQLLGDM SDKYGPAFTL RMGIQKALVV SSWEVAKECL TTNDRALATR PSSAGGKYMG 120 YNNALIPFSP YGPYWRDMRK IATLELLSNH RLEELKHVRE MEINTCISDM YKLCQVEDGV 180 EIKPISVDLS QWFADLTFNV VVMMITGKRY IGSTDAGDMN EIRHFQAALV KFMRLLRISL 240 LVDVFPVLQW INYGGFKGVM KSTARDIDSV LENWLQEHQR KRLSPDFNGN HDFIDVMIST 300 LEGTEFSDYD HNTIIKAISM AMVVGGTDTT TTTLIWAISL LLNNPNAMKK VQEELEIHVG 360 KERNVDGSDI QHLVYLQAVV KETLRLYPPV PLSVMHQAME DCVIGSYNIQ AGTRVLFNLW 420 KLHRDSSVWS DPLEFRPERF LTSHVDVDVR GQHFELIPFG SGRRSCPGIS FALQVIHLTI 480 ARLFHGFNLT TPGNSSVDMS EISGATLSKV TPLEVLVTPR LSSKLYN 527
3-283	**Sequences**	
3-283-1	Sequence Number [ID]	283
3-283-2	Molecule Type	AA
3-283-3	Length	520
3-283-4-1	Features Location/Qualifiers NonEnglishQualifier Value	**source** 1..520 mol_type= protein organism= Nigella sativa
3-283-5	Residues	MDFLIYVAAF AAAFFFLLFY NILSKRITGT KRRIAPEPAG AWPFIGHLPM LFGPNLPHVT 60 LGALADKYGP AFTIQLGLHK ALVVSSWEVA KDCFTVNDKA LATRPTSAAV KIMAYNCAVF 120 SFSPYGSYWR EARKIAILEL LSHHRLDLLK HVRKSEVSTS IRELYQFWQK NATEVTKFAQ 180 LEMKQWFGDL TMNLIVRMVA GKRYASVQSD DDGEGKRLQK AVNDFFHLVG LFVVSDALPF 240 LGWLDIGGNL KTMKKTAREL DSIMECWLKH QARRSNGEQD FLDVMLSILR EDNKLQEYDG 300 DVVVKAMCLN MILGGADSTT ITLTWTISLL LNNRHILQKA QDEIDSKVGK DRQVNESDIE 360 KLVYLQAIVK ETLRLYPPAP LSSQHEAIED CTIAGYHIPA GTRLITNLWK IQHDPSVWHN 420 PSEFQPERFL TTQANVDFRG QNFEFIPFGF GRRSCPGTSL GLQMVHLPLA RLLQGFTFET 480 PSNAAVDMTE SAGLTNHKVT PLEVLISPRL RFDLYQESPP 520
3-284	**Sequences**	
3-284-1	Sequence Number [ID]	284
3-284-2	Molecule Type	AA
3-	Length	525

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284-3		
3-284-4-1	Features Location/Qualifiers	**source** 1..525 mol_type= protein organism= Nigella sativa
	NonEnglishQualifier Value	
3-284-5	Residues	SFNQTYTGFI CLSVFASFFF FFLYSVQQKR RTGRKARYAP EPTGAWPLIG HLPILFEPNL 60 PHIQLGALAD KYGPVFSIKL GLRKALVVSS WEVVKECFTV KDKVLASRPS SVAVKIMGYD 120 YAVYAFGPYG SYWREARKLT ILELLSDHRL DLLKHVRVSE VSMSMKELLK FCQKNANNVS 180 GKALLVDMKQ WFGDLTLNVI VRMVAGKSYL GASAKLEDGE QKRLQNAIHE FFRLAGLFVV 240 SDALPILSWL DIGGHEKAMR RNAREIDKIM SSWLDEHRRN KLAGVTNGEQ DFMDVLLSKF 300 ENSNLPGYEP DVAIKAICLN MILGAADTTI VTLTWVVSLI LNNRQILKKA REEIENKVGK 360 DRQVNESDIE KLVYLQAIVK ETLRLYPAAP LSAHHESMED CTIAGYHVPA GTQLITNLWK 420 IQRDPRVWPN PCEFLPERFL TTHANVNYKG QNFEFIPFGY GRRSCPGMSF GLQMVHLVLA 480 SLLQGFELET PLNEAVDMTE SAGLTNLKAT PLEVLITPRM PLNLY 525
3-285	**Sequences**	
3-285-1	Sequence Number [ID]	285
3-285-2	Molecule Type	AA
3-285-3	Length	509
3-285-4-1	Features Location/Qualifiers	**source** 1..509 mol_type= protein organism= Nigella sativa
	NonEnglishQualifier Value	
3-285-5	Residues	VTVIYLFTFA IFFYLYSILW KNPRKSAKTR VAPEPAGAWP FMGHLPMLLE PNLPHIKLGA 60 LADKYGPAFT VQLGLHKALV VSSWEVAKEC FTVNDKVLAD RPSSVAVKIM GYDNAVFAFG 120 PYGSYWREAR KISTVELLSN HRLSLLQHFR ISEASMSMKE LYQLCANNGK ALVEMKKWFG 180 DLSLNVIVRM VAGKRYAKAS EDDERRQLQK GLKDFFYLVG LFVVSDALPI LSWLDIGGHE 240 KAMRRTAKEL DTIMERWLDE HRRAKLAGVT KGEQDFMDVL LSILEDGKLP HYESNTVNKA 300 ICLTMILGAA HTTTVTLIWT LSLLLNNRHI LNKAQDEIDS EVGKDRAVTE SDIKNLVYLQ 360 AIVKETLRLY PAAPLPAHRE VMEDCIIAGY HVPVGTRIIT NLWKIQRDPR VWSNPCAFQP 420 ERFLTTHSNV DFRGQNFEFI PFGSGRRSCP GISLGLQMVH LALARLLQGF ELETPLNLGI 480 DMTESSGLTN LKVTPLEVVI TPRLPSNLY 509
3-286	**Sequences**	
3-286-1	Sequence Number [ID]	286
3-286-2	Molecule Type	AA
3-286-3	Length	562
3-286-4-1	Features Location/Qualifiers	**source** 1..562 mol_type= protein organism= Papaver bracteatum
	NonEnglishQualifier Value	
3-286-5	Residues	MAYLMIKKSF HLFSDQPTSV STLIVLAFLL TLSPVIIYYE QKKRGLRRNR TSSSCTAITT 60 TPLPEASGAW PVIGHLLLFM NENDLNHATL GNMADKYGPI FSLRFGSHRT LVVSSWEMVK 120 ECFTGANDKF FSNRPSSLAV KLMFYDTESY GFAPYGKYWR ELRKISTHKL LSNQQLDKFK 180 HLRISEVDNS FKKLHDLCSN NKLGGETTSV ANLVRMDDWF AYLTFNVIGR IVSGFQSNAV 240 SGATSSQEKY KLAIDEVSNL MATFAVSDVV PCLGWIDRLT GLTGKMKKCG KKLDAVVGDA 300 VEVHRQKKLK ISRNTAGELT EHEEEDFIDV CLSIMEQSQI PGNNPEISVK SIALDMLSGG 360

		SDTTKLIMTW TLSLLLNHPD ILDKAKEEVD TYFRKKKISD NTPVVDAADV PNLVYIQAII 420 KESMRLYPAS TLMERMTSDD CEVGGFHVPA GTRLWVNVWK MQRDPRVWND PLVFRPERFL 480 SNDKGMVDVK GQNYELIPFG TGRRICPGAS FALEVLHLVL TRLILEFEMK APEGEIDMRA 540 RPGFFNNKVV PLDVLLTPRT LD 562
3-287	**Sequences**	
3-287-1	Sequence Number [ID]	287
3-287-2	Molecule Type	AA
3-287-3	Length	519
3-287-4-1	Features Location/Qualifiers	**source** 1..519 mol_type= protein organism= Papaver bracteatum
	NonEnglishQualifier Value	
3-287-5	Residues	MNNYSSSPAS STETAVLCHQ RQQSCALPIS GLLHIFMNKN GLIHVTLGNM ADKYGPIFSF 60 PTGSHRILVV SSWEMVKECF TGNNDTFFSN RPIPLAFKII FYAGGVDSYG LALVPYGKYW 120 RELRKICVHN LLSNQQLLKF RHLIISQVDT SFNKLYELCK NSEDNQGMVR MDDWLAQLSF 180 SVIGRIVCGF QSDPKTGAPS RVEQFKEAIN EASYFMSTSP VSDNVPMLGW IDQLTGLTRN 240 MTHCGKKLDL VVESIINDHR QKRRFSRTKG GDEKDDEQDD FIDICLSIME QPQLPGNNNP 300 PKIPIKSIVL DMIGGGTDTT KLTTIWTLSL LLNNPHVLDK AKQEVDAHFL TKRRSTNDAA 360 VVDFDDIRNL VYIQAIIKES MRLYPASPVV ERLSGEDCVV GGFHVPAGTR LWVNVWKMQR 420 DPNVWADPMV FRPERFLSDE QKMVDVRGQN YELLPFGAGR RICPGVSFSL DLMQLVLTRL 480 ILEFEMKSPG GEVDMTATPG LMSYKVLPLD VLLTHLSAS 519
3-288	**Sequences**	
3-288-1	Sequence Number [ID]	288
3-288-2	Molecule Type	AA
3-288-3	Length	540
3-288-4-1	Features Location/Qualifiers	**source** 1..540 mol_type= protein organism= Papaver bracteatum
	NonEnglishQualifier Value	
3-288-5	Residues	MEFLMKLLLL LEPITFSIFL GIGSIVLLYN VFFLVINKKK KKKAPNASGA WPLIGHLNLF 60 MNDKEALYKT LGTMADKYGP AFNVRLGNQE ILVVSNWKMV KECFNTQNDK LFSNRRTTLG 120 VKYMLNKKTS VAFSPYGTYW RELRKLTVQQ LLSKQRLDSW KHLKIKEIDA SFGRLNDLCS 180 NNKGTGAATP IRMDSWFAEL TFNVFARIVF GYQSGERLML SGDTASNGER YKKTLEEAFL 240 LMSSFAVSDV FPCLEWVDRS RGLVRSMKRF GDQLNSIAGC LIEEHRQKRS QSVSASNSTN 300 DKGVGDEQDF IDVLLSVAEL SQIPGDDPDL VIKSMILEAL AGGSDTTTST LTWVLSLLLN 360 HPKVLKTAKE EIDMHVGRNR CVEESDIPKL VYVNAIIKES MRLYPNGSLV DRLTLEECEV 420 GGFHVPAEGH LFVNVWKIHR DPSVWENPLE FKPERFLSND CKVDMDFISQ KYEFIPFGIG 480 RRICPGMLSA LQVMHFVVAR LIHGFDMEAA SADGKVDMAE KPGMTCYKMT PLEVMLTARQ 540
3-289	**Sequences**	
3-289-1	Sequence Number [ID]	289
3-289-2	Molecule Type	AA

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3-289-3	Length	548
3-289-4-1	Features Location/Qualifiers	**source** 1..548 mol_type= protein organism= Papaver bracteatum
	NonEnglishQualifier Value	
3-289-5	Residues	MYPVNQLQSQ AIAVLCAVIV FIFYLGRKLF NSTHIHKPGK TAPEPAGAWP IIGHLHLLGG 60 AKLMYRTLGS LADEYGPVFM VRLGMRRVLV ISNTASAREC FTTNDKVFAT RPTTVAIKLL 120 TYNHTMFGFA PYGPYWREIR KIATTELLSD RRLAMLKNVW ISEINLCINE LHQLLMDKNS 180 RKVDHHQHVY NQNMDPISVE MNGWFADLSF NVVARMIAGK RYFGKNTDGG EEETRRYREA 240 MNDFMHLVVI LLVSDAVPFL GGLDFQGYKK RMKKTAKEID YFLGKWVDEH RQRLKYKNIS 300 KVDQQDDFID VLLLNLNDQP IYGRDTDTII KSTCLSLIAG GSDTTAVTLT WALSLLLNNQ 360 HVLRKAQDEL DIHVGRERQL EESDIKNLVY LQAIVKETLR LYPAAPLSAP RMAMEDCTVA 420 GFQVSKGTQL MLNVWKLHRD PHFWGPDPLE FRPERFLTAD GSSTGSGHCI DIDVKGRHYE 480 LLPFGSGRRM CPGVSFAMQV VHLTLATLLH GFHLSTPTDG PVDMTETSGL SCPKATPLEV 540 LLTPRLPC 548
3-290	**Sequences**	
3-290-1	Sequence Number [ID]	290
3-290-2	Molecule Type	AA
3-290-3	Length	567
3-290-4-1	Features Location/Qualifiers	**source** 1..567 mol_type= protein organism= Papaver bracteatum
	NonEnglishQualifier Value	
3-290-5	Residues	MDVAIIVDHH YLQPFVSIAG LLALLSFFYC IWVFIIRPRI IKSNLDERKL SPSSPPEVAG 60 AWPIVGHLPQ LIGSTPLFKI LADMSNKYGP IFMVRFGMYP TLVVSSWEMS KECFTTNDRL 120 FATRPPSAAG KYLTKALFAF SVYGPYWREI RKISTIHLLS LRRLELLKHG RYLEIDKCMK 180 RLFEYWMEHH KNIISTTSSV KVNMSQVFAE LSLNVVLKII VGKTLFIKNG NEDYTKEEEE 240 GQKLHKTILK FMELAGVSVA SDVLPFLGWL DVDGQKKQMK RVYKEMNLIA SKWLGEHRER 300 KRLQIIQKRG AARGSNYDDG NDFMDVLMSI LDEENDDLFF GYSRDTVIKS TCLQLIVAAS 360 DTTSLAMTWA LSLLLTNPNV LQKAQDELDT KVGRDRIIEE HDIECLVYLQ AIVKETLRLY 420 PPAPLSLPHE AMEDCTVGGY QVKAGTRLVV NLWKLQRDPR VWSNPLEFKP ERFLPQSDGG 480 FGGEEARMDF RGQHFEYTPF GSGRRICPGI DFFLQTVHMA LARLLQAFDF NTAGGLVIDM 540 VEGPGLTMPK VTPLEVHLNP RLPVTLY 567
3-291	**Sequences**	
3-291-1	Sequence Number [ID]	291
3-291-2	Molecule Type	AA
3-291-3	Length	558
3-291-4-1	Features Location/Qualifiers	**source** 1..558 mol_type= protein organism= Papaver bracteatum
	NonEnglishQualifier Value	
3-291-	Residues	MQVDWPNILQ KYYPIITCSL LTLLSFYYIW VSITKPSRNS KTKLPPPEVA GSWPIVGHLP 60 QLVGSTPLFK ILANMSDKYG PIFMVRFGMH PTLVVSSWEM SKECFTTNDK FLASRPPSAS 120

[0141]

5		AKYLGYDNAM FVFSDYGPYW REIRKISTLQ LLTHKRLDSL KNIPYLEINS CVKTLYTRWA 180 KTQSQIKQNV GGAADDFVKV DMTEMFGHLN LNVVLRLVVG KPIFIQKDNA DEDYTKDGHN 240 KEELGQKLHK TIIEFFELAG ASVASDVLPY LGWLDVDGQK KRMKKIAMEM DLFAQKWLEE 300 HRQKGINHDN ENDFMAVLIS VLGEGKDDHI FGYSRDTVIK ATCLTLIVAA TDTTLVSLTW 360 ALSLLLTNPR VLSKAQDELD TVVGKERNVE DRDVNHLVYL QAVIKETLRL YPPSPLAVPH 420 EAIENCNVGG YEVKARTRLL VNLWKIHRDP RVWSNPLEFK PERFLPKLDG GTGEASKLDF 480 KGQDFVYTPF GSGRRMCPGI NFASQTLHMT LARLLHAFDF DIESNGLVID MTEGSGLTMP 540 KVTPLQVHLR PRLPATLY 558
3-292	**Sequences**	
3-292-1	Sequence Number [ID]	292
3-292-2	Molecule Type	AA
3-292-3	Length	571
3-292-4-1	Features Location/Qualifiers	**source** 1..571 mol_type= protein organism= Papaver bracteatum
	NonEnglishQualifier Value	
3-292-5	Residues	MMDLAMFIDQ YFSLAKIAGL LALLSFFYYL WISTLWSPRN PKLSSVSPPE VAGAWPILGH 60 LPQLLGSRPL FKILADMSDN YGPIFMVRFG MHPTLVVSSW EMAKECFTTN DRFLAGRPSG 120 AANKYLTFAL FGFSTYGPYW REIRKIATLH LLSHRRLELL KHVPDLEVTN CMKHLHRRWI 180 DSQNQIKQND AAAGSVKVDM GRVFGELTLN VVLKLVAGKS IFFKNDNTRQ YDSKDGHNKE 240 EEEGKKLHKT IIDFYSLAGA SVASDVLPFL GWLDVDGQKK RMKRVAKDMD FIAAKWLEEH 300 RHQKRQTVLS SSATLGSSNH DDAKDFMDVL MSILDGENDD LFFGYSRDTV IKTTCLQLIA 360 AAADTTSVTM TWALALLITN PTILRKAQDE LDTKVGKDRN IEERDINDLV YLQAIVKETL 420 RMYPAGPLNV PHEAIADCNI GGYEVRAGTR LLVNLWKMHR DPRVWSNPSE FKPERFLPQL 480 DGGSGGEAAN LDFRGQDFEY LPFSAGRRMC PGIDFSLQTL HMTLARLLHG FDFNNDSAGI 540 IIDMEEGSGL TMPKLTPLEI YLCPRLPAKL Y 571
3-293	**Sequences**	
3-293-1	Sequence Number [ID]	293
3-293-2	Molecule Type	AA
3-293-3	Length	543
3-293-4-1	Features Location/Qualifiers	**source** 1..543 mol_type= protein organism= Sanguinaria canadensis
	NonEnglishQualifier Value	
3-293-5	Residues	MEFLSLQFQP ITIFALLLAT PIFLYNLWNY GRKLNNKNKK SRKPPAPEAS GGWPIMGHFH 60 LFNGTEVTHR ALGSMADKYG PAFNIRIGSH PTLVVSSWEI AKECFTTNDR LFSNRPGSLA 120 IKLMFYDADS VGYAPYGTYW RELRKISTLK LLSNHRLETL KHLRTSEVES CFKQLHDLWR 180 MNNKKGGSDD GSDFALVRID NWFGDLTFNV VARIVAGKKN FAGGAASGDA GAQRYKEAMD 240 EAFRLMTRFA FSDVVPSLGW LDKLTGLVGG MKRCGSEIDS IVASWVDEHR LKRISGKEGD 300 DLEQDFIDVC LEILEHSTLP GDDPEVVIKS TCLDMILGGS DTTTVTLTWA LSLLLDHPHV 360 WKRAKEEVDA HVGKERQVED SDIPNLVFIQ AIVKETMRLY PAGPLIERRT MDDCEVGGFH 420 IPGGTRLIVN LWKIQRDGSV YKEDPLEFRP ERFLTSNAEV DLKGQNYELI PFGAGRRICP 480 GVSFAVQLMH LVLARLIHDF EITMPMGAKV DMTESGGLIS HKVTPLEVLL KPRLPSLQQA 540 ALY 543
3-294	**Sequences**	
3-294-	Sequence Number [ID]	294

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1		
3-294-2	Molecule Type	AA
3-294-3	Length	525
3-294-4-1	Features Location/Qualifiers	**source** 1..525 mol_type= protein organism= Sanguinaria canadensis
	NonEnglishQualifier Value	
3-294-5	Residues	MEYSSVLLHW FPASMAALLA LVFLYNLIFN SPKTGNKKII RRAPKAAGAW PVLGHLHLFG 60 SGELPHKMLA AMAEKYGPAF TMKFGKHTTL VVSDTRVVKE CFTTNDTLFA NRPSTKAFDL 120 MTYANDSVAF TPYSPYWREL RKISTLKLLS NHRLQSIKEV RVSEVSVCFR ELYDICKNDG 180 GGAPPVLVDM KKWFEEVSNN IVMRVIVGKQ NFGSKIVCGE EEAVNYKNVM DELLRLASVS 240 MLSDVAPLLG WLDMFQGHMS AMRRNGKKLD TILERWLEEH RKKKSEDEQD FMDVMLSIVE 300 ETKLSGRDAD TVIKATCLAM IMGGTDTTAV SLTWIVSLLM NNRYALKKAR EELDALVGKD 360 RQVEDSDLKN LVYLNAVVKE TMRLYPLGTL LERDTKEDCE VGGFHVEGGT RLLVNVWKLQ 420 RDPNVWNDPL EFRPERFLTE NADIDVGGQH FELLPFGAGR RVCPGVSFAL QFMHLVLARL 480 IHGYELGTQN DEDVDLTEST EGHVNHKASP LDLLITPRLH PKLYE 525
3-295	**Sequences**	
3-295-1	Sequence Number [ID]	295
3-295-2	Molecule Type	AA
3-295-3	Length	527
3-295-4-1	Features Location/Qualifiers	**source** 1..527 mol_type= protein organism= Sanguinaria canadensis
	NonEnglishQualifier Value	
3-295-5	Residues	MDYSSHLNQF YGVAPYMAAL LIALVFLYNI LWASPKTTNK KPIMAAGAWP ILGHLHLFKD 60 GELPHHMLKS MSDKYGPAFL MKFGQHRTLV VSNYRMVKEC FTTNDTHFCN RPSTTAFDVM 120 TYANDSVAFT AYSPYWRELR KISTLKLLSN NRLQAIKNLR EAEVNVSFRG LYDLWKNNSD 180 RAASVLVDMK KWFEEVSNNV VIRVIVGKHN FGTKIVKGEK EAVEYKTIMD ELLRLASLSL 240 LSDFAPILGW VDFFQGNVRK MKRNGKKLDV VLQRWLETHR RKKNSPEDEQ DFMDVMLSIV 300 EEGDKLSGHH ADTVIKATCL AMIMGGTDTS AVSLTWIVSL LMNNRHALKK AREELDMYVG 360 KDRQVEDSDL KDLVYLHAIV KETMRLYPLG TLLERETKED CKVGGFHVEA GTRLLVNIWM 420 VQRDPTVWSD PTKFIPERFL TEKADIDVGG QHFELIPFGA GRRVCPAVSF ALQFLHLILA 480 RLIHGYELGT PNDADVDLTE SPEGHVNHKA SPLELLLTPR LDPKLYI 527
3-296	**Sequences**	
3-296-1	Sequence Number [ID]	296
3-296-2	Molecule Type	AA
3-296-3	Length	535
3-296-4-1	Features Location/Qualifiers	**source** 1..535 mol_type= protein organism= Sanguinaria canadensis
	NonEnglishQualifier	

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3-296-5	Value	
	Residues	MNSIAVVGVL LFFLYYLWRT LFTTHKAAPP PQPAGARPII GHLHLLGGAN QLVHQTLGSM 60 ADKYGSIFMI RLGMRRVLVV SSSELAKECF TTNDKVFLNR PSSLALKLMA YNNAIFGFAP 120 FGPYWRKMRK IAVTELLSNR RLEILKNIRI SEINMSIKEL HQLWVDMNSG DDQVGGPPIV 180 VEMRKWFGDL SFNVVGRMIA GKRYFGRNCD CDEEETRRYQ KAMGDFMHLV GVFVVSDAIP 240 LLGFLDLQGY EKKMKRTAMD IDCVLGRWVD EHRRRRQDHD EKRIMVSDDD HQGQDFIDVM 300 LSILNDDDQF YGYDADTVIK STCLSLIAGG HETTAVTLTW ALSLLLNNRH VLQNAQDELD 360 IHISKERQVD ESDIKNLKYL QAIVKEALRL YPALPLSALR LAMEDCTIAG FHVPKGTELM 420 LNLWKLHRDP HVWSDPLEFK PERFLTNSTH EEVDVGGQHY ELLPFGSGRR MCPGVSFALQ 480 VLHLTLARLL HGFHLSTPSG VPVDMTQSFG LSCPKATPLD VLLTPRLPSK LYYVA 535
3-297	**Sequences**	
3-297-1	Sequence Number [ID]	297
3-297-2	Molecule Type	AA
3-297-3	Length	601
3-297-4-1	Features Location/Qualifiers	**source** 1..601 mol_type= protein organism= Sanguinaria canadensis
	NonEnglishQualifier Value	
3-297-5	Residues	MISTTPDVLA TSSYSSSNKH MDSDHLYRFS TSTSIVIGLF ILLFFLVLLW KPKKQSATSK 60 TNKPTREQRA PEPSSSWPII GHLRLFGGPN SLPHITLGAM ADKYGPVFTI RMGSRPVLVV 120 SSWETAKECF TTNDRVFASR PRTIAIKHMC YEHVMLGFAP YGSYWRELRK IVNRELLSNN 180 RLELLKHVWG SEINTSIKEL YELWLVNKNN IEAEGENEGT SDRVLVEMER WFADLTLNMS 240 IKIVVGKRYP SGVTAGGSSG CDDDEAQRCR KALRDFFKLV GLFLVSDAIP FLRWLDLGGY 300 EREMKTTARE LDCLMEEWLE EHKMKRRLLI SPSAGDHHEA AEIMINKQKE AELQEYDFMD 360 VMLSILDDDI EGKNLSDYDV NADTINKSTC LNLILGGSDT TMVTLTWALA LLLNNPHVLQ 420 KAQDELDIHV GSKRQVDDSD MKNLIYLQAI VKETMRLYPA GPLSVPHEST EDCTVAGYHV 480 PAGTRLIVNT WKIQRDPRVW SNPSEFKPER FLTDSHVDID VRGRNFELIP FGSGRRSCPG 540 TSFALQVVHL VLARLIHGFE FKTPSEAPID MTESVGLSNF KATPLDVLLT PRLPSQLYYV 600 S 601
3-298	**Sequences**	
3-298-1	Sequence Number [ID]	298
3-298-2	Molecule Type	AA
3-298-3	Length	525
3-298-4-1	Features Location/Qualifiers	**source** 1..525 mol_type= protein organism= Sanguinaria canadensis
	NonEnglishQualifier Value	
3-298-5	Residues	MDSTLVFIGL FALLLVYPLL LRRSVLKSTS NTNKTTYKSK NQAPEAAGAW PIIGNLHQLA 60 GGGNCLHKTL GAMADKHGPA FTIRMGLHKA LVVSSWELAK ECFTTNDVVF MSRPHQVAIK 120 HMGYSTAMFG IAPYGPYYRE MRKIVTQELL SNRRLELLKH VWASEINNSI KQLYEKVEGG 180 PVLIEMKRWF ADLTLRTTVK VICGQQQFGG DDDDDEAGRF QTALRDFFRL LGHFRVADVI 240 PVLEWLDFQG YKKEMENNGR VLDNLMNKWL EEHKRKRKNG GTEEDFMNVM ISKLLDDTKM 300 LSYYDADTIN KSTCLTLILG GSDTTMVSLT WALSLLVNHP HVLKKAQEEL DVHVGKERQV 360 DDSDLWSLTY LQAIIKETLR LYPPGPLSAP RESTDNCTIA GYHVPAGTRL IVNTWKIQRD 420 PRVWPDPLEF KPERFLTTHV DVDVKGQNFE LLPFGSGRRA CPGASFALRV LRLSLARLIH 480 GFDFKTPLDD SPIDMVESGG ITNVKDTPLE VLVTPRLPSS LYVCK 525
3-299	**Sequences**	

[0144]

3-299-1	Sequence Number [ID]	299
3-299-2	Molecule Type	AA
3-299-3	Length	532
3-299-4-1	Features Location/Qualifiers	**source** 1..532 mol_type= protein organism= Sanguinaria canadensis
	NonEnglishQualifier Value	
3-299-5	Residues	MDFDLYQFSK PTIFIGGLFA ILLYFVLKKS STPKSKSKLE QPPEPAGAWP IIGHLPLLGG 60 PDLPHITLGK LADKYGPAFT IRIGVHKAVV INSWEVAKEC FTTNDKAFSS RPRQVAMKHM 120 GYDYAMFGFA PYGNYWRELR KIVNREVLSH SRIESLYHVW GTEINTSVKE LYELWGKKST 180 GSGGAPVLVE MKRWFSDMTL NMSVMMVAGK RYNFSGNKAD DEAGRCQDGL RNFFRLVGLF 240 VPSDALPFLA WLDIGGYEKE MKKVAKELDV LVQEWLEEHK EKRLALTAAG KKGSENDFMD 300 VMMNILEDQK LSEFDADTIN KATCLTLILG GTDTNMVNLV WALTLLVNNQ DALKKAHDEL 360 DFHVGKDRQV EESDVKNLVY IQAIMKETLR LYSGPLSGLR ESTEDCTVAG YYVPAGTRLI 420 INAAKIHRDP RVWSDPTAFK PDRFLTEQKE MDVRGQDFEI LPFGAGRRIC PGVSFALQVL 480 PLALARLIHG FDFKTPTDAP IDMTESPGLT NAKSTPLEVL VSPRLTSKLY GC 532
3-300	**Sequences**	
3-300-1	Sequence Number [ID]	300
3-300-2	Molecule Type	AA
3-300-3	Length	555
3-300-4-1	Features Location/Qualifiers	**source** 1..555 mol_type= protein organism= Sanguinaria canadensis
	NonEnglishQualifier Value	
3-300-5	Residues	MDSILNQFIS KPTMVICSLF ALLSLYFLLI KRSTTKSKLQ LPPEPAGAWP VIGHLHQLGG 60 PNLPHITLAA MADKYGPIFT MKIGTYRALV VSSPEVAKEI FTTHDRIWAT RPNQAAMKHL 120 GYDSAMFGFA PYGPYWRELR KLVNRELLSN TRLDLLHHVW DSEINTSIKE LYDSLATKNN 180 AKGRGTGGAG STGPVLVEMK RWFADLTLNI TVRMVAGKRY FGANKTSSTS TDQCDNEKGD 240 SKAWKCQREL RNFFRLVGLF VVSDALPFLG WLDLGGHERE MKNTARELDV LVQGWLDEHK 300 RKRSLSVAEG GEKINGEQDF MDMMLSTIDD AKLSGYFDAD TINKSTCLNL ILGGSDTMMV 360 NLIWPLTLLV NYPDELKKVY DELDTHVGRD RQVDESDIKN LVHLKAVIKE TMRLYTGRIT 420 GLRQSSEDCT VAGYHVPAGT RLIVNTWKIS RDPRYWSDPL EFKPERFLTT HADIELTGQN 480 FELIPFGSGR RSCPGASFAI QLLHLALARL VHGFWFERPS DAPIDTSECP GLTNFKATPL 540 EVLATPRLPS KLYVG 555
3-301	**Sequences**	
3-301-1	Sequence Number [ID]	301
3-301-2	Molecule Type	AA
3-301-3	Length	538
3-301-	Features Location/Qualifiers	**source** 1..538 mol_type= protein

[0145]

4-1		organism= Sanguinaria canadensis
	NonEnglishQualifier Value	
3-301-5	Residues	MDFILNQFIS KPTMVLGTLF ALLSLYFLLI KRSTTKSKLQ LPPEPAGALP IIGHLHLLGG 60 PNPPHITLAN MAEKYGPIFS IKMGLKRALI VSSSEVTKEC FTTHDLNFVS RPRHAAMKLM 120 GYNFATFGFA PYGPYWRELR MIINRELLSQ TRILSLEHVW GSEINESIKE LYDLLTRKGG 180 GGGGPVVVEM KRWFADLTLN IAVKMVCGKR YFGVNSPSTS TTRDVQEDDE ARRCQKGMRN 240 FFRLLGQFVV SDSIPFLGWL DLGGYQREMK NTARELDDLM QGWLEEHKKK RLERKTAAGE 300 QDFMDVMLNI LEDGKLSQYF DTDTINKSTC LSLILGGSDT TMVNLVWAFS LLVKHQDALK 360 KTRDELDIHV GRERQVEESD IKNLVFLQAV VKETFRLYAG PISGVREAAE DCTIAGYHVP 420 AGTRLLINSW KIHRDPRVWS DPLEFHPERY LEARHADIDV KGQNFELAPF GMGRRVCPGS 480 AFGLQVLHLT LARLIHGFEF KTPSDAPVDM TESVGMSIIK ATPLEVLVTP RLPSELYV 538
3-302	**Sequences**	
3-302-1	Sequence Number [ID]	302
3-302-2	Molecule Type	AA
3-302-3	Length	533
3-302-4-1	Features Location/Qualifiers	**source** 1..533 mol_type= protein organism= Sanguinaria canadensis
	NonEnglishQualifier Value	
3-302-5	Residues	MDISNLYELY YFSTPTLFVG GLFVLLLIYS LFSSRPGIKS KLQQPPEPAG AWPLIGHLPV 60 LSGPELPHVA LGKLADKYGP VFTIRMGVHK SLVVSDWEVI KECFTTHDKV FSSRPCQVAM 120 KLMGTAMFGF SPYGNYWREL RKIMNREVLS HGRIESLYHV WGSEINTSVK ELYDLWAKKN 180 NGGGPILVEM KRWFSDLTLN MSVMMAAGKR YNFGDDSSTT NDEAARCQHA LREFFRLVGL 240 FVPSDALPYL GWLDIGGYQK QMKKVARELD DLMQVWLDEH KKKRLAAKAE GKKGGEQDFM 300 DVMMTILEDG KLSDYYDADT INKATCLTLI LGGTDTNMLS LVWTLALLMN NRQALKKVHE 360 ELDIHVGRER QVEESDIKNL VYLQAVIKEE MRLYSGPLSG LRETTEDCTI AGYHIPAGTR 420 LIINASKLHR DPKVWSDPLE FKPERFLTEN VGVDVRGQNL ELQPFGAGRR ICPGVSFALQ 480 VLPLTLARLI HGFELNTPGD APIDMTESPG LQNAKLTPLE VLITPRLPSK LYV 533
3-303	**Sequences**	
3-303-1	Sequence Number [ID]	303
3-303-2	Molecule Type	AA
3-303-3	Length	535
3-303-4-1	Features Location/Qualifiers	**source** 1..535 mol_type= protein organism= Sanguinaria canadensis
	NonEnglishQualifier Value	
3-303-5	Residues	MIVIGAFLAL VVLVVYYNLL LRRPALLKFK NMKQQAPEAA SAWPIIGHLH NLAGGIGGNG 60 LLHEKLGAMA DKHGPAFIIR LGLHKALVVS SWEVVKECFT TNDVALISRP HQVASKHMGY 120 GMAMFAFASP YGPYWRELRK IVKQELLSNS RLELLKHVWA SEINTSIKQL YEKVKEGGGL 180 PVLVEMKGWF ADLTLKMTVK VICGKRHFRV AGNVGDHVDA DDDDEVIGGR FEKALRDFFR 240 LLGDIRVVDV LPFLRWLDFG VGYKKEMENN GRVLDILMEE WLQEHKRKRM NGGTEEDFMN 300 VMISKLLNDT KLLSYYDADT INKSTCLTLI LGASDTTMVT LTWALSLLVN HPQVLKRAQD 360 ELDVHVGRER QVEDSDIQNL TYLQAIIKET LRICPPGPIQ APHEAKDDCT VAGYHVPAGT 420 RLIVNTWKIQ RDPRVWPNPS EFKPERFLTT HVGVDVRGHN FELIPFGSGR RSCPGTSFAL 480 QVVHLTLARF IHGFEFKTPS DAPIDMTESG RITNVKATPL EVLVTPRIPP SGLYV 535
3-	**Sequences**	

[0146]

304		
3-304-1	Sequence Number [ID]	304
3-304-2	Molecule Type	AA
3-304-3	Length	572
3-304-4-1	Features Location/Qualifiers	**source** 1..572 mol_type= protein organism= Sanguinaria canadensis
	NonEnglishQualifier Value	
3-304-5	Residues	MDLLIFSSQL QGTVGLLALL TFSYYVWILI IKRIKTTNTL KVMNKVAAAA APEVAGAWPI 60 VGHLPQLVGP QQLYRILGDM ADEYGPIFMV RFGMYPTLVV SSWEMIKECF TTNDRFLASR 120 PSSAAGKYLT YDFAMFGFSF YGPYWREIRK ISTLELLSHR RLELFKNVPF TEIDTCIKRL 180 YQLWRVKNND HPAAAPVIKV DMSQLLRDLT LNTILKLVVG KNLFNEKDHG EQEEGRKLHL 240 HKTIVEFFKL AGVSVASDAL PFLGWLDLDG QKKKMKRIAK EIDLIAERWL QEHQEKKSLS 300 NKKLLAAGGG KVDGHDDFMD VLLFILDDDS QFFNFSRDTV IKATSWAMIL TAADTTSVSM 360 TWALTLLLTN PRVLRKAQDE LDMKVGRDRH VEERDIENLI YLQAIVKETL RLYPAAPLGV 420 PHEAIQDCTV AGYQVRAGTR VLVNLWKLHR DPRVWSNPSE FRPERFLIDD IDEQGGGGGG 480 GGGESTAKDF RGQHFEYIPF GSGRRMCPGI NFALQIVHMT LARLLHAFEL RTTTSASLMD 540 MTEESGLTMP KKTPLVVLLQ PRLPLPLYDH HE 572
3-305	**Sequences**	
3-305-1	Sequence Number [ID]	305
3-305-2	Molecule Type	AA
3-305-3	Length	533
3-305-4-1	Features Location/Qualifiers	**source** 1..533 mol_type= protein organism= Stylophorum diphyllum
	NonEnglishQualifier Value	
3-305-5	Residues	MEFLSLQHQL ISIFALLLAS IFLYNLLKNH GRKSKTSKPP APEASGGWPI MGHLNLFNGS 60 ELTHQALGSM ADKYGPAFNI RFGSHQTLVV SSSEIVKECF TTNDRFFSNR PGSLAIKLMF 120 YNADSVGYAP YGAYWRDLRK ISTLKLLSNH RLETLKHLRT SEVESCFKQL YNQWKNNKVG 180 GDHDFALVRM DNWFGDLTFN VVARIVAGKK NFAGGATNGD VGAQRYKEAM DEAFRLMTIF 240 AFSDVVPSLG WLDKLRGLVG GMKRCGAEID SIVAGWVDEH RLKRASGKGG GHTDLEQDFI 300 DVCLEIMEHS TLPGDDPEIV IKSTCLDMIL GGSDTTTVTL TWALSLLLNN PHVLKRAREE 360 LDTHVGKDRQ VDDSDMSNLV YIQAIIKETM RLYPAGPLIE RRTSEDCEVG GFHVPAGTRL 420 LVNLWKMQRD GSVYKEDPLE FRPERFLTSN ADVDLKGQNY ELIPFGAGRR ICPGVSFAVQ 480 LMHLVLARLV HGFEMKTAGD AKVDMTESAG LISHKVTPLE VLLKPCLAIQ QAL 533
3-306	**Sequences**	
3-306-1	Sequence Number [ID]	306
3-306-2	Molecule Type	AA
3-306-3	Length	533

[0147]

3-306-4-1	Features Location/Qualifiers	**source** 1..533 mol_type= protein organism= Stylophorum diphyllum
	NonEnglishQualifier Value	
3-306-5	Residues	MDSFLLIQWF AASMAALLAF VFLYNLVWSS SRTTKGKNIR KAPMAAGAWP ILGHLHLFGS 60 GELPHKMLST MAEKYGPAFT MKFGKHTTLV VSDTRIVKEC FTTHDTLFAN RPSTTAFDLM 120 TYANDSVAFT PYGPYWRELR KISTLKLLSN HRLQSIKEIR VSEVNVCFRE LYESCKSKTD 180 ATPVLVDMKK WFEEVSNNIV MRVIVGRQNF GSKIVQGEDE AVNYKKVMDE LLRLASLSML 240 SDVAPVLGWL DMFQGNKSAM KRNAKKVDTI LEGWLEEHRM KKSASGISSA GENDQDFMDV 300 MLSIIEETKL SGRDADTVIK ATCLAMIMGG TDTTAVSLTW IVSLLMNHRH VLKKAREELD 360 ALVGKDRQVE DSDLKNLVYM NAIVKETMRM YPLGAMLERE TKEDCEVGGF QVQGGTRLLV 420 NVWKLQRDPN VWTDPTEFKP ERFLNENADI DVGGQHFELL PFGAGRRACP GVSFALQFMH 480 LVLARLIHGY ELGTQNDADV DLTESTEGHV NHKASPLDLL LTPRLNNPNL YDY 533
3-307	**Sequences**	
3-307-1	Sequence Number [ID]	307
3-307-2	Molecule Type	AA
3-307-3	Length	568
3-307-4-1	Features Location/Qualifiers	**source** 1..568 mol_type= protein organism= Stylophorum diphyllum
	NonEnglishQualifier Value	
3-307-5	Residues	MTIGALALLS FIYFLRVSVI KRTKYTNTAV TATNKLENDE DEANHSKRVV APPEVAGAWP 60 ILGHLPQLVG LKQPLFRVLG DMADKYGPIF IVRFGMYPTL VVSSWEMAKE CFTTNDRVLA 120 SRPASASGKY LTYNYAMFGF TNGPYWREIR KISMLELLSH RRVELLKHVP STEIDSSIKQ 180 LYHLWVENQN QNKQGDHQVK VDMSQLLRDL TLNIVLKLVV GKRLFNNNDM DHEQDEAARK 240 LQKTMVELIK VAGASVASDA LPFLGWLDVD GLKRTMKRIA KEIDVIAERW LQEHRQKKLT 300 SNDKGGSNNI QGGGGDNDFM DVMLSILDDD SNFFINYNRD TVIKATSLTM ILAGSDTTTL 360 SLTWALTLLA TNPGALRKAQ DELDTKVGRD RQVDERDIKN LVYLQAIVKE TLRMYPAAPL 420 AIPHEATQDC IVGGYHVTAG TRVWVNLWKL QRDPHAWPNP SEFRPERFLA VENDCKQQGT 480 CDGEAANMDF RGQHFEYMPF GSGRRMCPGI NFAIQIIHMT LARLLHSFEL RVPEEEVIDM 540 AEDSGLTISK VTPLELLLTP RLPLPLYI 568
3-308	**Sequences**	
3-308-1	Sequence Number [ID]	308
3-308-2	Molecule Type	AA
3-308-3	Length	527
3-308-4-1	Features Location/Qualifiers	**source** 1..527 mol_type= protein organism= Stylophorum diphyllum
	NonEnglishQualifier Value	
3-308-5	Residues	MAALLPLAFL YNIFLASSSK ATSKRTISTK KPPMVAGAWP ILGHLHLFKE GELPHQMLKS 60 MADKYGPAFL MKFGQHQSLV VSDYRIVKEC FTTNDTLFCN RPSTTAFDVM TYANESVAFT 120 EYSPYWRELR KISTLKLLSN NRLQAIKNLR EEEVDVSFKG LYDSWKNKNN KSTAGSVGDE 180 RAPVLVDMKK WFEEVSNNVV IRVIVGKCNF GTKIVQGEKE GVEYKTIMDE LLRLASLSLL 240 SDFAPILGLL DFFQGHVRTM KRNGKKLDVL LQRWLEEHKR KKSTPEDEQD FMDVMLSIIE 300 ESKLSGYDAD TVIKATCLAM IMGGTDTSAV SLTWIVSLLM NNRQALKKAR EELDAQVGKD 360 RQVEDSDLKN LVYLNAIVKE TMRLYPLGTL LERETKEDCE VGGFHLEGGT RLLVNVWMVQ 420

[0148]

		RDPDVWTDPT KFIPERFLTE KADIDVGGGN FELIPFGAGR RVCPGVSFAL QFLNLVLARL 480 IHGYELGTPE DADVDLTESP EGHVNHKASP LELLLTPRLS NPKLYDY 527
3-309	**Sequences**	
3-309-1	Sequence Number [ID]	309
3-309-2	Molecule Type	AA
3-309-3	Length	547
3-309-4-1	Features Location/Qualifiers	**source** 1..547 mol_type= protein organism= Stylophorum diphyllum
	NonEnglishQualifier Value	
3-309-5	Residues	MDSDHQLLSY QFSASNMFIS LFAFVLYYLL VWRPTKSNLK MKTISSEDKQ APELAGSWPV 60 IGHLHLLHGP NPLHVALGAM ADKYGPAFTV RVGVHRTLVV SSWEVAKECF TTNDKVFVSR 120 PRQAAGKHMG YNNAMLRFAS DTPYWTQIRK MLKRDLLSNN RIELLNHAWH SEINTSIKEL 180 YEMNWSSGEG RRGGIRPPVS VDMKQWLGDL TLNMSVKMIA GKRCFGSGVS ACDEGEARRC 240 QKGLKDFVRL MGQIVVSDAI PFLGWLDLDG YEGEMKRAGK ELDRLLGGWL EEHKMKRSPG 300 DEASAQKDWM DLMLSVLGDG KLDGYYDADT INKATCLALL QGGSIWTMLT LLWAFALLVN 360 HPHVMKKAHD ELDNHVGRER QVEESDIKNL TYLQAIVKEA MRLYSVSMRL LESTADCTVS 420 GYDVPAGTRL IVNTWKIQRD PRVWSDPSEF HPERFLTHRH RDMDLYGQNF EITPFGSGRR 480 SCPGSSLGLQ MVQLTIARLL HGFEFKTPSD APIDMTESVG VENMVKATPI EVLLTPRLLD 540 EVYAFYN 547
3-310	**Sequences**	
3-310-1	Sequence Number [ID]	310
3-310-2	Molecule Type	AA
3-310-3	Length	561
3-310-4-1	Features Location/Qualifiers	**source** 1..561 mol_type= protein organism= Stylophorum diphyllum
	NonEnglishQualifier Value	
3-310-5	Residues	FCQFQGIVGI LLAFLTFLYY LWRASITGLR TKPKHNDFKV TKAAPEADGA WPIVGHFAQF 60 IGPRPLFRIL GDMADKYGSI FMVRFGMYPT LVVSSWEMAK ECFTTNDRFL ASRPASAAGK 120 YLTYDFAMLS FSFYGPYWRE IRKISMLELL SHRRVELLKH VPSTEIDSSI KQLYHLWVEN 180 QNQNKQGDHQ VKVDMSQLLR DLTLNIVLKL VVGKRLFNNN DMDHEQDEAA RKLQKTMVEL 240 IKVAGASVAS DALPFLGWLD VDGLKRTMKR IAKEIDVIAE RWLQEHRQKK LTSNDKGGSN 300 NIQGGGGDND FMDVMLSILD DDSNFFINYN RDTVIKATSL TMILAGSDTT TLSLTWALTL 360 LATYPLCALR KAQDELDTKV GRDRQVDERD IKNLVYLQAI VKETLRMYPA APLAIPHEAT 420 QDCIVGGYHV TAGTRVWVNL WKLQRDPHAW PNPSEFRPER FLAVENDCKQ QGTCDGEAAN 480 MDFRGQHFEY MPFGSGRRMC PGINFAIQII HMTLARLLHS FELRVPEEEV IDMAEDSGLT 540 ISKVTPLELL LTPRLPLPLY I 561
3-311	**Sequences**	
3-311-1	Sequence Number [ID]	311
3-311-2	Molecule Type	AA

[0149]

3-311-3	Length	522
3-311-4-1	Features Location/Qualifiers	**source** 1..522 mol_type= protein organism= Tinosporia cardofolia
	NonEnglishQualifier Value	
3-311-5	Residues	MDLPQPTIST TLLAFFSILL FIICYRLLST KSDKRSSSSR NKPLDAPGAW PVIGHLHLLN 60 GVIQHEILGT MADKYGPAFT IWLGTRPALV VSNWEVAKEC FTTCDKALAS RPPSLALKIM 120 GYNDALFAFA PYGQYWRELR KIVMIELLSS RQLDSLKHVW DSEIDSCIED LYEKCKGHRE 180 TVLVNMKQWF ADLMMNVVVR MVVGKLNFGK TKEGDDEVAK AHQGQLKAMR EFFKWVDVFM 240 IEDAFPILTW LDPQGYQRKM KNIAKDLDSL VQGWLDEHKL KQKTGDNGKK DFMDIMLSAV 300 KDASISDRDD ETICKATCLN IILGASDTTT VTLTWTLSLL LNNRHVLRKA QEELQAQVGK 360 HRCVEESDVK NLVYLHAIIK EVLRLYPAVP LLGPRESVAD TVVAGYHIPA GTRLIVNLWK 420 IHRDPLNWPD PLEFRPERFL TTHKDTDVWG QNFELTPFGS GRRICPGISF ALQVIPLTLA 480 RLLHGFELTT PGSAPVDMTE STGLTNLKAT PLDVFISPRL VL 522
3-312	**Sequences**	
3-312-1	Sequence Number [ID]	312
3-312-2	Molecule Type	AA
3-312-3	Length	526
3-312-4-1	Features Location/Qualifiers	**source** 1..526 mol_type= protein organism= Tinosporia cardofolia
	NonEnglishQualifier Value	
3-312-5	Residues	MESIPTAINV LLAFVSIYYL LKFRKKIITT TRDIKKIKAP ELKGAWPIIG HLHLFRSDDL 60 LHRKLGAMAD ELGPAFMIRL GMRPALVVSN WQTAKECFTT KDRIFATRPD SVAAKHMGYE 120 NLILGFTRYG PYWREVRKIV TLELLSSHRL HLLRHVRISE IDMSIKKLHQ LCTSNDNKYS 180 SVVVDLNQWF KALTLNIIVR IIAGKRYYGG DLEDDEESRR WKKALNEFMH LFGIFSVSDA 240 IPQLQGMDVQ GHERVMKRTG KDIDVILSKW LEEHRRKKIR VNREGAEKDF IDIMLDLIKE 300 NVNISGHDAD NVVKATCLAL VSAGSDTTMI TLTWAVSLLL NNHRVLEKAQ AELDNQIGIN 360 RVHVEEEDIK NLPYLQAIVK ETLRLYPAAP FSLPHEAMEE CTVAGFHVPK GTRLITNIWK 420 LQRDPQVWED PLEFRPERFL TSDRRHVDFR GQHFELIPFG SGRRMCPGIS FAIGVLHLTL 480 ARLLHEFHLG TPTNAPIDMN ENPGITLEKA DPLHPLVSPR LTSINY 526
3-313	**Sequences**	
3-313-1	Sequence Number [ID]	313
3-313-2	Molecule Type	AA
3-313-3	Length	538
3-313-4-1	Features Location/Qualifiers	**source** 1..538 mol_type= protein organism= Tinosporia cardofolia
	NonEnglishQualifier Value	
3-313-5	Residues	MDSQLTSFQS KPSAYLIAAL LALVSAYYLI IKKKSRATYQ DNYGKIRAPE PKGAWPIIGH 60 LLLFKPNDVL YQKLSSLADE LGPAFMIRLG MRSALVISNW EIAKECFTTN DRIFATRPKL 120 MASKHMGYGG AEVGVAPYGP YWREVRKIIT VELVSNHRLN LLKDVRISEI DMSLKELYDL 180 CMKKKKNGSG EESSRVELDL YQWFKDMSLN ILVKLIAGKR YYGVAAAANE DEESRRWKKA 240

		TEESVFLFGQ FVVGDAIPLL EGVDVQGLER AMKKTGKEID AVLSKWVEEH RMKKQQLNGA 300 RDEQDFIDVM LNIIKDGKIS DHDADTIVKA TCMSLVQAGS DTTMLTLTWA VCLLLNNCNV 360 LEKAQAELDD QIGRSKGRIV EEDDIKKLPY LQAIVKETWR LYPPAPLAVP REAMEDCTVA 420 GFHVPKGTRL MTNIWKLHRD PKVWDDSLKF RPERFLSSEH AHVDFRGQQH EFMPFGSGRR 480 MCLGMPLAIG VVHLTLARLL HEFELATPSN APVDMSEKAG LTLVKATPLN VLIAPRLC 538
3-314	**Sequences**	
3-314-1	Sequence Number [ID]	314
3-314-2	Molecule Type	AA
3-314-3	Length	531
3-314-4-1	Features Location/Qualifiers	**source** 1..531 mol_type= protein organism= Tinosporia cardofolia
	NonEnglishQualifier Value	
3-314-5	Residues	MDSIILQSNL LTTVIIITSF GLFVLSFYYV LWKAIRTGNK RNCSNPKAPE AAGGWPILGH 60 LHLFRGQGLL LHKIFGAMAE KHGPAFTIRL GMRPALVVSN WEVAKECFTA NDRALASRPT 120 SLALKIMGYN NSLFAFAPYG QYWRELRKIV MHQLLSSRRL ELLKNVWLSE IDIWIKGLYE 180 NSLVNKVVDM KQWFGELMMN IVVRLVAGKR SFGKIREGDS EEAKAHQRQI KALRDFFRLV 240 EVFMIEDAFP FLTWLDPRGY QKEMKNIAKE LDYLLEEWLE EHKLKQQAAC DDQSKDFMDV 300 MLSEVKDSTI TERDANTICK ATCLNVILGA SDTTTLTLTW ALSLLLNNRH VLKKAQEELN 360 AQVGKDKQVE ESDMKNLVYL HAIIKEVLRL YPAAPLSVAH ESLEDTVVAG YHVSKGTQVI 420 FNLWKIQRDP SVWSNPLEFQ PERFLTTHKH VDIWGQNFEL IPFGSGRRMC PGVPFALQVV 480 SLTLARLLHG FELTTPGGAA VDMTETPGLT NMKATPVEVF LRPDLPHQLY A 531
3-315	**Sequences**	
3-315-1	Sequence Number [ID]	315
3-315-2	Molecule Type	AA
3-315-3	Length	524
3-315-4-1	Features Location/Qualifiers	**source** 1..524 mol_type= protein organism= Thalictrum flavum
	NonEnglishQualifier Value	
3-315-5	Residues	MPSQTIQIIM DFFHQCVATI LFCVLASPFF FYYLLPWWKN ANDHDLAKSR GKPVPEVDGA 60 WPIIGHMHML QPSDSFYSSL AEKYGPIFTL RIGLCKTIVI NSWELAKECC TTHDRVFASS 120 PEATAAKILG YDYAMFGRNP YGPYWREMRK IIITELVSNR RLELLKHIRV TEISTSIQEL 180 YQLWEARSSK NVKERVVVDM QKWFGDLMLN IGVEMVAGKR YFGASSNEDK EEARQLHKTF 240 KDFSNLFGVP VLSDAIPFLR WLDYKGHIKA MKRCAKQVDC ILHRWLEEHK QNKTTIAGDF 300 MDILLSVLQD KEIFGRDADT VIKATCLNMM LGVVETNKVT VTMALISLLN NRRILKKAQE 360 EIDIHVGSDK QVEESDIEKL VYLQAIVKET LRLYSPGLGT REPSEDCTIS GFHVPKGTEV 420 MVNVQQIHRD PSIWSNPLEF QPERFLTTQA NIDFGGQHHE YIPFGAGRRL CPAISFAVLV 480 VHLTLARLLQ GFDFATPKDA PVEMNESVET LEVLITPRLP LHMY 524
3-316	**Sequences**	
3-316-1	Sequence Number [ID]	316
3-316-	Molecule Type	AA

[0150]

[0151]

2		
3-316-3	Length	534
3-316-4-1	Features Location/Qualifiers	**source** 1..534 mol_type= protein organism= Xanthoriza simplicissima
	NonEnglishQualifier Value	
3-316-5	Residues	MHNPIPNQWL PSSTLLTPII VSFLVIVLFY IYKKRSSNTI RTKKAPEVVG AWPVIGHLNL 60 FSCPKPGHIV LGELADQYGP AFTIHFGMHP TLVVSSSELV RDCFTTNDKL FSSRLVNKAI 120 KYMFYDQDTI SFAPYGPYWR ELRKMIALNL LNNERIKMLQ QQRISEMDAC LKKLYDLSAK 180 RKDENAGVLV DMSKWFAEIS FNVVTRIVAG KHIFGPKVER YKNVMEEARR LMDVMVFSDM 240 VPYLGWLDRL RGVDSAIKRT AKELDSVLES WVEEHRRKSV SISAGTGGIF NIKEEEELDF 300 IDIMLSIIAK NNLPGDDPDT LIKAIVQETY LAAWDNTTVT LTWVLCLLLN NKQVLKRAQN 360 ELDAQVGKER QVEDSDINNL PYVQAIVKES LRLYPPGPII ERATTEDCNV GGFRVPAGTR 420 LWVNLWKLQR DPKVWPNDPL EFRPERFLND NADIDLRGQN SELIPFGSGR RMCPGVSFSL 480 QVIHLVIARI IQGFELKAPT DADIDMSTTL GMISWKATPL EVLMNPRFPP VFYK 534
3-317	**Sequences**	
3-317-1	Sequence Number [ID]	317
3-317-2	Molecule Type	AA
3-317-3	Length	550
3-317-4-1	Features Location/Qualifiers	**source** 1..550 mol_type= protein organism= Xanthoriza simplicissima
	NonEnglishQualifier Value	
3-317-5	Residues	MSTLQISILT VKSPYSQMHY YPLLHQWLPA SMALVSLLVI ILFSIFKKRS SKMIKAKKAP 60 EVAGAWPLIG HLNLFSGPKL LHLVLGELTD QYGPAFMIHL GMYPTLVVSN WELLKDCFTT 120 NDIFFSNRPV NKAIKHMFYN KESIGFTPYG SYWRELRKMT TLKLLSNHRL DLLKPLRISE 180 MDACFRNLYE LWTKDKDGNA WLLVDMSKWF GEISFNVVAR IVAGKKNFGS KGDRYKTVME 240 EVVRLMGLRA LSDAVPYLGW LDQLRGLDSA MKRAAKELDS VLESWVEEHR LKRVSVSAGT 300 GSTVKTAKEE EEEEDFIDIT LSILAENQLP GDDPDTGIKS LILDMILGGS DTSTVTLIWA 360 MCLLLNNVHV LKRAQYELDA QIGKERQVED SDIKNLPYIQ AIIKETMRLY PAGPIIERQA 420 NEDCDVGGFH VPAGTRLWVN LWKLQRDPNV WKDDALEFRP ERFLTDHADI DLKGQHLELI 480 PFGSGRRICP GISFALQVMH LALARIIHGF ELKTPNDSNI DMSGTPGLLC CKATPLQVLL 540 TPRFNPMFYK 550
3-318	**Sequences**	
3-318-1	Sequence Number [ID]	318
3-318-2	Molecule Type	AA
3-318-3	Length	520
3-318-4-1	Features Location/Qualifiers	**source** 1..520 mol_type= protein organism= Xanthoriza simplicissima
	NonEnglishQualifier Value	
3-	Residues	MDSLRHCLGG ILALLIFLGY LQWKRGTSNK CIEAPQPDGA WPIIGHLPRL MKPQIMHRTL 60 STMADKHGPA FTLRLGVHKT LVVSSWEVAK ECFTTNDRVF ATRPTSIAVE ILGYNYALFA 120

318-5		FGPYGSYWRE ARKIAILELL SNHRLELLKH VRISEVSTSI RELYQVWKEN CDIANGSALV 180 DMKPWFGDLT LNVVVRMVAG KRYMGGSVKS DDVEGRRFQK ATKDLFDLFG LFILSDALPF 240 MGWLDLHGHK KAMKKTAKEL DSIMQRWLEE HRQSLLDDGT KEEKKDFMYV MLSILEDKKL 300 FQYDADIVNK AICMNMIMAG TDTQMITLTW VLSLLLNNRH ILKKAQDEID SSVGKDRQVE 360 ESDIVKLVYL QAIVKEALRL YPPAPLSAQH EAMEDCTVAG YYVPAGTRLI TNIRKIQRDP 420 RVWSDPFEFH PERFLTNQAN VDFRGQSFEF IPFGSGRRMC PGISFALQVV HLTLARILQG 480 FDFETPMNAS VDMTEAPGLT NVKSTPLQVL ITPRLHPNLY 520
3-319	**Sequences**	
3-319-1	Sequence Number [ID]	319
3-319-2	Molecule Type	AA
3-319-3	Length	523
3-319-4-1	Features Location/Qualifiers	**source** 1..523 mol_type= protein organism= Xanthoriza simplicissima
	NonEnglishQualifier Value	
3-319-5	Residues	MDLLNPYFAT IFGGFFALLI FLFIISQKRS RIPKIRAAPE PVGAWPIVGH LPMLLGPRLP 60 HFVLGDLGEK YGSAFTLRLG IHKTLVVSSW EVAKECFTTN DQVFATRPSF MAAKIMGYNY 120 ALFGLAPYGS YWRELRKISI IELLSSHRLE LLKHVRVSEV STSMKELYEV WAENCSNGNG 180 SVLVEMQRWF GDLTLNISVR MVAGKRYFGT SASLDDDEAR RISKATKDFF RLTGMFVVSD 240 SVPFLWWLDF QGHEKAMKRT AKEMDDIFGG WLEDHRRNKL AGGTKVQQDF MDVMLSILED 300 EKFFGYNADV VTKATCLNML LGGTDTTMVT LTWALSLLLN NRHILKKAQT EINTHVGKDT 360 QVDESDIVKL VYLQAIVKET LRLYPAAPLS TPHEATKDCT IAGYHVTAGT RLITNIWKIQ 420 RDPRVWSNPS EFQPERFLTD QANVDVRGQH FEFIPFGSGR RSCPGISLGL LVVQLALARL 480 LQGFDFETPS DALVDMTESA GLTNLKATPL HVLITPRLHS SLY 523

[0152]

3-320	**Sequences**	
3-320-1	Sequence Number [ID]	320
3-320-2	Molecule Type	AA
3-320-3	Length	530
3-320-4-1	Features Location/Qualifiers	**source** 1..530 mol_type= protein organism= Xanthoriza simplicissima
	NonEnglishQualifier Value	
3-320-5	Residues	MDSVHQGQYL PTPMVSVFVF FISLYFLIVW KTRSSSKTNT CNEVPEAPGA WPIIGHLHLL 60 GGSELPHKTL GAMADKYGPI FKIRIGVHQA LVVSSSDIVK ECFTTNDKVF ASRPTSTASK 120 ILGYDYVMFG FSPYGPYWIE LRKIIMSELL SNRRLELLKH VRDSEIDISI QELYKVWKNH 180 DKSKGPILVD MKQWFGDLAL NVILRMIAGK RYSGSIFSSD ETEARRCQKG ARDFFRLLGL 240 FIIEDALPYL SWFDLQGYKK EMKNTAKELD SVFQRWLEEH KRTRETGELN REQDFMDILM 300 STLEETKISE YDNDTIIKST CLSIVTGGND TTMVTLTWIL SLLLNNKHAL KKVQDELDSH 360 VGKHRHVEES DIKNLIYLQA IMKEALRLYP AGPLSGPRVA DADCTLAGYH IPAGTRLLVN 420 TYKIQRDPLV WSEPSEFRPE RFLTSHVNMD VKGLQYELIP FGTGRRACPG MLFALQVVPL 480 VLARFLHEFE PKTEMDMPVD MTETAGLSNA KATPLEVVIT PRLQPELYSL 530
3-321	**Sequences**	
3-321-1	Sequence Number [ID]	321
3-	Molecule Type	AA

	321-2		
	3-321-3	Length	528
	3-321-4-1	Features Location/Qualifiers	**source** 1..528 mol_type= protein organism= Xanthoriza simplicissima
		NonEnglishQualifier Value	
	3-321-5	Residues	MDFTMIIQWL LTSFAILVAF VLIWSSATRS STRKRNKTAP VAAGALPIVG HLHMLMGREL 60 PHRLLSNMAD KYGPAFMMKY GLQPALVVSS LKLTKECFVH NDRAVFKRPR SKALKNLTYD 120 QASLGFAPYG PLWVEMRKVS KTNLLSNQRL QMQRHVRASE VDAFIKELYD LWSSKSNNIK 180 GAPLLVEMNK WFEELALNVV TRMLSGKRHI GFKARRGEDS ESMHYKKVVV DATLLTAKLV 240 VSDFFPSLGL VDYLQGDESS IKGTSKELDA ILATWVEEHR HKKVSGSEDD EKDFIDLTLS 300 MIDQTQHQGA DVDTFIKSMC VGMIFGGSDS TSVALAWALS ILMNNRPVLK KAREEIDRQV 360 GRDRKVNDLD VLKLDYLKAI VKESMRLCLV GPLLERVAVE DCEIGGYHVK AGSRVVVNIW 420 KMQHDPNLWS DPLEFQPERF LTTNANVELR GQHFELLPFG AGSRICPGIT FALELIQLTL 480 ARLIHGFELG TPMDADVDMT ETSSVTNYRA TPLEILLTPR LDPKLYNY 528
	3-322	**Sequences**	
	3-322-1	Sequence Number [ID]	322
	3-322-2	Molecule Type	DNA
	3-322-3	Length	2703
[0153]	3-322-4-1	Features Location/Qualifiers	**source** 1..2703 mol_type= genomic DNA organism= Papaver somniferum
		NonEnglishQualifier Value	
	3-322-5	Residues	atggagctcc aatatatttc ttattttcaa ccaacttcct ccgttgttgc tcttctactt 60 gctcttgtat ccatcttatc cagtgtcgtt gttttgagga agacattttt gaataactac 120 tcatcatcac ctgcatcatc cacaaaaaca gcggtacttt ctcatcagcg gcagcagtcg 180 tgtgcattgc caatttccgg tctcctccat attttcatga ataaaaacgg cttaattcat 240 gtaactcttg gaaatatggc tgataaatac ggtccgattt tcagtttccc aacaggtagc 300 catagaactc tcgttgtgag cagttgggag atggtaaaag agtgttttac tggcaacaat 360 gacactgctt tctcaaaccg tcctatcccg ttagctttta agactatatt ctatgcatgc 420 ggtggcatag actcatacgg tctttcgagt gtaccttatg gaaaatattg gagggagctt 480 cgaaaggtct gtgtgcataa cctcctgtct aatcaacaac tactcaagtt cagacacttg 540 ataatttctc aagtcgatac gtctttcaat aagctgtatg agttatgcaa aaactctgaa 600 gacaaccagg gaaactatcc tactactact accgcagctg gcatggtgag aatcgatgat 660 tggctcgccg aattatcgtt caatgtgata ggaagaatag tctgcggatt ccaatcaggc 720 cctaagacag gtgctccaag cagggtggaa caatttaaag aagcaattaa tgaagcatct 780 tattttatgt cgacatctcc agtgtcagat aatgttccaa tgctagggtg gattgaccaa 840 ttgacaggtc ttacgagaaa tatgaagcac tgcggaaaga aattagactt ggtggtcgag 900 agcataatta atgatcatcg tcaaaagaga cgattctcta gaactaaagg aggagatgag 960 aaggacgatg aacaagatga cttcatcgac atttgtttgt caataatgga gcaaccacag 1020 cttcctggca acaataatcc ttctcagata cctatcaaat ctattgtcct ggacatgata 1080 ggtgggggca ctgacaccac aaaactgacc accatctgga ccctttcctt gctgctgaac 1140 aacccccatg tgttggacaa ggcaaaacaa gaagtggatg cacactttcg aaccaaaagg 1200 agatcaacaa atgatgcagc agcagccgtg gtggattttg atgatattcg taaccttgtc 1260 tacatccagg caatcatcaa agaatcaatg cggttgtatc cagccagccc cgtggtggag 1320 cgactgagcg gcgaagattg tgtggtcggt gggtttcatg taccagcagg gacgagatta 1380 tgggctaacg tatggaagat gcaacgagac cctaaagtat gggatgatcc attggtgttt 1440 cgaccagaca gatttttgag cgatgaacag aagatggttg atgtaagggg tcaaaattat 1500 gagctgttac catttggagc cggtcgacgt gtatgtccag gtgtatcctt ctctttggat 1560 ctaatgcaac tggtactgac tcgtcttatt ctcgagtttg aaatgaagtc tcctagcggg 1620 aaagtggaca tgacagcaac accaggatta atgagttaca aggtgatccc ccttgacatt 1680 ctgctcaccc atcgtcgcat aaagccgtgt gtgcagtcag cagcctctga gagagacatg 1740 gagagtagtg gtgtaccagt aatcactctg ggctcgggca aggtgatgcc tgttctgggc 1800 atgggaacat ttgagaaagt tggtaaaggg tccgaaagag agaggttggc gattttaaaa 1860 gcgatagagg tgggttacag atacttcgat acagctgctg catacgaaac tgaagaggtt 1920 cttggagaag ctattgctga agcacttcaa cttggcctag tcaaatctcg agatgaactt 1980

[0154]

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3-323	**Sequences**	
3-323-1	Sequence Number [ID]	323
3-323-2	Molecule Type	AA
3-323-3	Length	900
3-323-4-1	Features Location/Qualifiers	**source** 1..900 mol_type= protein organism= Papaver somniferum
	NonEnglishQualifier Value	
3-323-5	Residues	MELQYISYFQ PTSSVVALLL ALVSILSSVV VLRKTFLNNY SSSPASSTKT AVLSHQRQQS 60 CALPISGLLH IFMNKNGLIH VTLGNMADKY GPIFSFPTGS HRTLVVSSWE MVKECFTGNN 120 DTAFSNRPIP LAFKTIFYAC GGIDSYGLSS VPYGKYWREL RKVCVHNLLS NQQLLKFRHL 180 IISQVDTSFN KLYELCKNSE DNQGNYPTTT TAAGMVRIDD WLAELSFNVI GRIVCGFQSG 240 PKTGAPSRVE QFKEAINEAS YFMSTSPVSD NVPMLGWIDQ LTGLTRNMKH CGKKLDLVVE 300 SIINDHRQKR RFSRTKGGDE KDDEQDDFID ICLSIMEQPQ LPGNNNPSQI PIKSIVLDMI 360 GGGTDTTKLT TIWTLSLLLN NPHVLDKAKQ EVDAHFRTKR RSTNDAAAAV VDFDDIRNLV 420 YIQAIIKESM RLYPASPVVE RLSGEDCVVG GFHVPAGTRL WANVWKMQRD PKVWDDPLVF 480 RPDRFLSDEQ KMVDVRGQNY ELLPFGAGRR VCPGVSFSLD LMQLVLTRLI LEFEMKSPSG 540 KVDMTATPGL MSYKVIPLDI LLTHRRIKPC VQSAASERDM ESSGVPVITL GSGKVMPVLG 600 MGTFEKVGKG SERERLAILK AIEVGYRYFD TAAAYETEEV LGEAIAEALQ LGLVKSRDEL 660 FISSMLWCTD AHADRVLLAL QNSLRNLKLE YVDLYMLPFP ASLKPGKITM DIPEEDICRM 720 DYRSVWAAME ECQNLGFTKS IGVSNFSCKK LQELMATANI PPAVNQVEMS PAFQQKKLRE 780 YCNANNILVS AISVLGSNGT PWGSNAVLGS EVLKKIAMAK GKSVAQVSMR WVYEQGASLV 840 VKSFSEERLR ENLNIFDWEL TKEDHEKIGE IPQCRILSAY FLVSPNGPFK SQEELWDDEA 900
3-324	**Sequences**	
3-324-1	Sequence Number [ID]	324
3-324-2	Molecule Type	DNA
3-324-3	Length	1473
3-324-4-1	Features Location/Qualifiers	**source** 1..1473 mol_type= genomic DNA organism= Papaver rhoeas
	NonEnglishQualifier Value	
3-324-5	Residues	atgatcggtc tttatcatgt tttcatgaat aaaaccggct taattcatgt aactcttgga 60 aacatggctg ataaatacgg acccattttc agtttcccaa caggtggcca tagggctcta 120 gttgtgagta gttgggagat ggcaaaagag tgttttacag gcgacaatga cattgttttt 180 tcaaatcgtc ctatgccgtt atcgtttaag attatattca atgcaggtgg tatagactca 240 gccggtctta cacaagtacc gtatggaaaa tattggaggg agttacgaaa gatctgtgtg 300

[0155]

		cacaaccttc tctcaaatca acaattactc aagttcaggc acttgataaa ttctcaagtt 360 gatacctctt tcactaaact gtacgagtca tgcaacaagg gaaattctgg catggtgaga 420 atggatgatt ggcttggaga attatcattc aacgtgatag gaagaatagt ctgcggattc 480 cgatcagaca ctgagacaag tgctacaagc agtgcggaac gatttacagt agcaattgat 540 gaagcatcgc gttttatgtc catacctgca gtgtcagata cctttccgtg gctaggatgg 600 attgatcgat taactggtct tataaaagat atgaagcacc atgcagaaaa attagactta 660 gtggttgaaa gcataattga agatcatcgt caaaagagac gattttctag aactaaaaaa 720 ggagatgaga ataacaccga ggatgaacaa gatgacttca ttgacatttg tttgtcaatt 780 atggagcaac cagagcttcc tggaaacaac tacgctcgtc aaatgcctat caaatctatc 840 atcgtggaca tgataggcgg ggcgactgac accacaaaac tgaccacaat ctggaccctt 900 tccttgctgc tgaataaccc acatgtgtta ggcaaggcaa aagaagaagt ggatgcacac 960 tttggaaaga aaaggagttc aaccaatggg gaagtcatgg tggattttga tgatattcgt 1020 agccttgtct acatccaggc aatcatcaaa gaatcaatgc ggttgtaccc agccagtcca 1080 gtggtggagc gactgagcag tgaagattgt gtggttggtg ggtttcatgt atcagcaggg 1140 acgcgattat gggttaacgt atggaaggtt caacgagacc cagaagtatg ggatgatccg 1200 tcggtgtttc gaccagagag atttttgagt aatgagcaga agatggttga tgtaaggggt 1260 caagattatg agttgttacc atttggagcc ggtcgacgga tatgtccagg tgtatcgttc 1320 tctttggatc taatgcacct ggtacttact cgtcttattc ttgagtttga aattaagtct 1380 cctggtgggg aagtggacat gacagcaaca caaggtttaa tgagttacaa ggtagtcccc 1440 cttgacattc tgctcacccg tcgcatgctt tag 1473
3-325	**Sequences**	
3-325-1	Sequence Number [ID]	325
3-325-2	Molecule Type	AA
3-325-3	Length	490
3-325-4-1	Features Location/Qualifiers NonEnglishQualifier Value	**source** 1..490 mol_type= protein organism= Papaver rhoeas
3-325-5	Residues	MIGLYHVFMN KTGLIHVTLG NMADKYGPIF SFPTGGHRAL VVSSWEMAKE CFTGDNDIVF 60 SNRPMPLSFK IIFNAGGIDS AGLTQVPYGK YWRELRKICV HNLLSNQQLL KFRHLINSQV 120 DTSFTKLYES CNKGNSGMVR MDDWLGELSF NVIGRIVCGF RSDTETSATS SAERFTVAID 180 EASRFMSIPA VSDTFPWLGW IDRLTGLIKD MKHHAEKLDL VVESIIEDHR QKRRFSRTKK 240 GDENNTEDEQ DDFIDICLSI MEQPELPGNN YARQMPIKSI IVDMIGGATD TTKLTTIWTL 300 SLLLNNPHVL GKAKEEVDAH FGKKRSSTNG EVMVDFDDIR SLVYIQAIIK ESMRLYPASP 360 VVERLSSEDC VVGGFHVSAG TRLWVNVWKV QRDPEVWDDP SVFRPERFLS NEQKMVDVRG 420 QDYELLPFGA GRRICPGVSF SLDLMHLVLT RLILEFEIKS PGGEVDMTAT QGLMSYKVVP 480 LDILLTRRML 490
3-326	**Sequences**	
3-326-1	Sequence Number [ID]	326
3-326-2	Molecule Type	DNA
3-326-3	Length	981
3-326-4-1	Features Location/Qualifiers NonEnglishQualifier Value	**source** 1..981 mol_type= genomic DNA organism= Papaver rhoeas
3-326-5	Residues	atggatagta gtggtgtacc tgtaatccct ctgagctccg gtaaagggat gcctgcttta 60 gctctaggaa catttgaaac atttggtaaa ggatcgtccg aaagacagag atcggcgttt 120 ttgaaagcga tagaggtggg ttacagatac tttgacacag gtgcttcata cggaaccgaa 180 gaggtccttg gcgaagctat agatgaagca cttcaacttg gccttatcga atctcgagag 240

[0156]

		gaactgttta tcagttccaa tctctggtgt actgatgctc accctgatcg tgtcctcctt 300 gctcttcaga attctctaag gaatcttaaa ttggagtatc tggatctata catgataccc 360 tttccgataa gcttgaagcc tgggaagata atggaggaga taactatgga cataccagag 420 gatgaaatgt tacctatgga ctacaagtct gtatgggcag ccatggaaga gtgtcaggac 480 cttggcttca ctaagtcgat cggtgtcagc aatttctcct gcaaaaagct tcaggagttg 540 atggcgaccg ccaatatccc accagctgtg aatcaagtgg agatgagccc cgttttccaa 600 caaaagaaac tgagagagta ttgcaaggcc aataatatat tagtcagcgc agtctcggtt 660 ttgggatcga acggaaccgc atggggctcc aatcaagtta tgggttctga ggtgttgaaa 720 caaattgcta ctgacagagg aaaatctgtt gctcagatta gtatgagatg ggtttatgag 780 caaggtgcga gtcttgtggt aaaaagtttc aatgaagtga ggatgaggga aaatttgaac 840 atattcaact ggcaacttac taaggaagat ttggaaaaga tcagcgagat tccacaatgc 900 aggatattaa ctggtgattt tttagtttca gctaatggac ctttcaaatc tctacaagag 960 ttatgggatg accaagtttg a 981
3-327	**Sequences**	
3-327-1	Sequence Number [ID]	327
3-327-2	Molecule Type	AA
3-327-3	Length	326
3-327-4-1	Features Location/Qualifiers	**source** 1..326 mol_type= protein organism= Papaver rhoeas
	NonEnglishQualifier Value	
3-327-5	Residues	MDSSGVPVIP LSSGKGMPAL ALGTFETFGK GSSERQRSAF LKAIEVGYRY FDTGASYGTE 60 EVLGEAIDEA LQLGLIESRE ELFISSNLWC TDAHPDRVLL ALQNSLRNLK LEYLDLYMIP 120 FPISLKPGKI MEEITMDIPE DEMLPMDYKS VWAAMEECQD LGFTKSIGVS NFSCKKLQEL 180 MATANIPPAV NQVEMSPVFQ QKKLREYCKA NNILVSAVSV LGSNGTAWGS NQVMGSEVLK 240 QIATDRGKSV AQISMRWVYE QGASLVVKSF NEVRMRENLN IFNWQLTKED LEKISEIPQC 300 RILTGDFLVS ANGPFKSLQE LWDDQV 326
3-328	**Sequences**	
3-328-1	Sequence Number [ID]	328
3-328-2	Molecule Type	DNA
3-328-3	Length	966
3-328-4-1	Features Location/Qualifiers	**source** 1..966 mol_type= genomic DNA organism= Papaver somniferum
	NonEnglishQualifier Value	
3-328-5	Residues	atggagagta atggtgtacc tatgatcact ctcagttccg gcattcggat gcctgcttta 60 ggtatgggaa cagctgaaac aatggtaaaa ggaacagaaa gagagaaatt ggcgtttttg 120 aaagcgatag aggtcggtta cagacacttc gatacagctg ctgcatacca aagtgaagag 180 tgtcttggtg aagctatagc tgaagcactt caacttggtc taataaaatc tcgagatgaa 240 ctcttcatca cttccaagct ctggtgcgct gatgctcacg ctgatcttgt cctccctgct 300 cttcagaatt ctctgaggaa tcttaaattg gactatcttg atctatattt gatacaccat 360 ccggtaagct tgaagccagg gaagtttgtt aacgaaatac caaaggatca tatccttcca 420 atggactaca aatctgtatg ggcagccatg gaagagtgtc agacccttgg cttcactagg 480 gcaatcgggg tctgtaattt ctcatgcaaa aagcttcaag agttgatggc agcagccaag 540 atccctccag ttgtgaatca agtggagatg agcccgactt tacatcaaaa aaatctgagg 600 gaatattgca aggccaataa tatcatgatc actgcacact cggttttggg agccatatgt 660 gctccatggg gcagcaatgc agttatggat tctaaggtgc ttcaccagat tgctgtggca 720 agaggaaaat ctgttgccca ggttagtatg agatgggttt accagcaagg cgcgagtcta 780 gtggtgaaaa gtttcaatga agggaggatg aaggaaaacc ttaagatatt tgattgggaa 840

[0157]

		ctaacggcag agaatatgga aaagatcagt gagattccgc aatctagaac aagctctgct 900 gatttcttgt tatcaccgac tggacctttc aaaactgaag aagagttctg ggatgagaag 960 gattga 966
3-329	**Sequences**	
3-329-1	Sequence Number [ID]	329
3-329-2	Molecule Type	AA
3-329-3	Length	321
3-329-4-1	Features Location/Qualifiers	**source** 1..321 mol_type= protein organism= Papaver somniferum
	NonEnglishQualifier Value	
3-329-5	Residues	MESNGVPMIT LSSGIRMPAL GMGTAETMVK GTEREKLAFL KAIEVGYRHF DTAAAYQSEE 60 CLGEAIAEAL QLGLIKSRDE LFITSKLWCA DAHADLVLPA LQNSLRNLKL DYLDLYLIHH 120 PVSLKPGKFV NEIPKDHILP MDYKSVWAAM EECQTLGFTR AIGVCNFSCK KLQELMAAAK 180 IPPVVNQVEM SPTLHQKNLR EYCKANNIMI TAHSVLGAIC APWGSNAVMD SKVLHQIAVA 240 RGKSVAQVSM RWVYQQGASL VVKSFNEGRM KENLKIFDWE LTAENMEKIS EIPQSRTSSA 300 DFLLSPTGPF KTEEEFWDEK D 321
3-330	**Sequences**	
3-330-1	Sequence Number [ID]	330
3-330-2	Molecule Type	AA
3-330-3	Length	321
3-330-4-1	Features Location/Qualifiers	**source** 1..321 mol_type= protein organism= Papaver somniferum
	NonEnglishQualifier Value	
3-330-5	Residues	MESSGVPVIT LGSGKVMPVL GMGTFEKVGK GSERERLAIL KAIEVGYRYF DTAAAYETEE 60 VLGEAIAEAL QLGLVKSRDE LFISSMLWCT DAHADRVLLA LQNSLRNLKL EYVDLYMLPF 120 PASLKPGKIT MDIPEEDICR MDYRSVWAAM EECQNLGFTK SIGVSNFSCK KLQELMATAN 180 IPPAVNQVEM SPAFQQKKLR EYCNANNILV SAISVLGSNG TPWGSNAVLG SEVLKKIAMA 240 KGKSVAQVSM RWVYEQGASL VVKSFSEERL RENLNIFDWE LTKEDHEKIG EIPQCRILSA 300 YFLVSPNGPF KSQEELWDDE A 321
3-331	**Sequences**	
3-331-1	Sequence Number [ID]	331
3-331-2	Molecule Type	DNA
3-331-3	Length	26
3-331-	Features Location/Qualifiers	**source** 1..26 mol_type= genomic DNA

[0158]

4-1		organism= Papaver somniferum
	NonEnglishQualifier Value	
3-331-5	Residues	ggatcccatc agttccatgc tctggt 26
3-332	**Sequences**	
3-332-1	Sequence Number [ID]	332
3-332-2	Molecule Type	DNA
3-332-3	Length	26
3-332-4-1	Features Location/Qualifiers	**source** 1..26 mol_type= genomic DNA organism= Papaver somniferum
	NonEnglishQualifier Value	
3-332-5	Residues	ggtaccgggc tcatctccac ttgatt 26
3-333	**Sequences**	
3-333-1	Sequence Number [ID]	333
3-333-2	Molecule Type	DNA
3-333-3	Length	26
3-333-4-1	Features Location/Qualifiers	**source** 1..26 mol_type= genomic DNA organism= Papaver somniferum
	NonEnglishQualifier Value	
3-333-5	Residues	ggatcccatc acttccaagc tctggt 26
3-334	**Sequences**	
3-334-1	Sequence Number [ID]	334
3-334-2	Molecule Type	DNA
3-334-3	Length	25
3-334-	Features Location/Qualifiers	**source** 1..25 mol_type= genomic DNA

[0159]

4-1		organism= Papaver somniferum
	NonEnglishQualifier Value	
3-334-5	Residues	ggtaccgggc tcatctccac ttgat 25
3-335	**Sequences**	
3-335-1	Sequence Number [ID]	335
3-335-2	Molecule Type	DNA
3-335-3	Length	34
3-335-4-1	Features Location/Qualifiers	**source** 1..34 mol_type= genomic DNA organism= Papaver somniferum
	NonEnglishQualifier Value	
3-335-5	Residues	gaattcccta catactgtat tgggttgaat catg 34
3-336	**Sequences**	
3-336-1	Sequence Number [ID]	336
3-336-2	Molecule Type	DNA
3-336-3	Length	25
3-336-4-1	Features Location/Qualifiers	**source** 1..25 mol_type= genomic DNA organism= Papaver somniferum
	NonEnglishQualifier Value	
3-336-5	Residues	ggtacctaac gggataggac ggttt 25
3-337	**Sequences**	
3-337-1	Sequence Number [ID]	337
3-337-2	Molecule Type	DNA
3-337-3	Length	1704
3-337-	Features Location/Qualifiers	**source** 1..1704 mol_type= genomic DNA

[0160]

4-1	NonEnglishQualifier Value	organism= Papaver somniferum
3-337-5	Residues	atggagctcc aatatatttc ttattttcaa ccaacttcct ccgttgttgc tcttctactt 60 gctcttgtat ccatcttatc cagtgtcgtt gttttgagga agacattttt gaataactac 120 tcatcatcac ctgcatcatc cacaaaaaca gcggtacttt ctcatcagcg gcagcagtcg 180 tgtgcattgc caatttccgg tctcctccat attttcatga ataaaaacgg cttaattcat 240 gtaactcttg gaaatatggc tgataaatac ggtccgattt tcagtttccc aacaggtagc 300 catagaactc tcgttgtgag cagttgggag atggtaaaag agtgttttac tggcaacaat 360 gacactgctt tctcaaaccg tcctatcccg ttagctttta agactatatt ctatgcatgc 420 ggtggcatag actcatacgg tctttcgagt gtaccttatg gaaaatattg gagggagctt 480 cgaaaggtct gtgtgcataa cctcctgtct aatcaacaac tactcaagtt cagacacttg 540 ataatttctc aagtcgatac gtctttcaat aagctgtatg agttatgcaa aaactctgaa 600 gacaaccagg gaaactatcc tactactact accgcagctg gcatggtgag aatcgatgat 660 tggctcgccg aattatcgtt caatgtgata ggaagaatag tctgcggatt ccaatcaggc 720 cctaagacag gtgctccaag cagggtggaa caatttaaag aagcaattaa tgaagcatct 780 tattttatgt cgacatctcc agtgtcagat aatgttccaa tgctagggtg gattgaccaa 840 ttgacaggtc ttacgagaaa tatgaagcac tgcggaaaga aattagactt ggtggtcgag 900 agcataatta atgatcatcg tcaaaagaga cgattctcta gaactaaagg aggagatgag 960 aaggacgatg aacaagatga cttcatcgac atttgtttgt caataatgga gcaaccacag 1020 cttcctggca acaataatcc ttctcagata cctatcaaat ctattgtcct ggacatgata 1080 ggtgggggca ctgacaccac aaaactgacc accatctgga ccctttcctt gctgctgaac 1140 aacccccatg tgttggacaa ggcaaaacaa gaagtggatg cacactttcg aaccaaaagg 1200 agatcaacaa atgatgcagc agcagccgtg gtggattttg atgatattcg taaccttgtc 1260 tacatccagg caatcatcaa agaatcaatg cggttgtatc cagccagccc cgtggtggag 1320 cgactgagcg gcgaagattg tgtggtcggt gggtttcatg taccagcagg gacgagatta 1380 tgggctaacg tatggaagat gcaacgagac cctaaagtat gggatgatcc attggtgttt 1440 cgaccagaca gatttttgag cgatgaacag aagatggttg atgtaaggggg tcaaaattat 1500 gagctgttac catttggagc cggtcgacgt gtatgtccag gtgtatcctt ctctttggat 1560 ctaatgcaac tggtactgac tcgtcttatt ctcgagtttg aaatgaagtc tcctagcggg 1620 aaagtggaca tgacagcaac accaggatta atgagttaca aggtgatccc ccttgacatt 1680 ctgctcaccc atcgtcgcat aaag 1704
3-338	**Sequences**	
3-338-1	Sequence Number [ID]	338
3-338-2	Molecule Type	AA
3-338-3	Length	568
3-338-4-1	Features Location/Qualifiers	**source** 1..568 mol_type= protein organism= Papaver somniferum
	NonEnglishQualifier Value	
3-338-5	Residues	MELQYISYFQ PTSSVVALLL ALVSILSSVV VLRKTFLNNY SSSPASSTKT AVLSHQRQQS 60 CALPISGLLH IFMNKNGLIH VTLGNMADKY GPIFSFPTGS HRTLVVSSWE MVKECFTGNN 120 DTAFSNRPIP LAFKTIFYAC GGIDSYGLSS VPYGKYWREL RKVCVHNLLS NQQLLKFRHL 180 IISQVDTSFN KLYELCKNSE DNQGNYPTTT TAAGMVRIDD WLAELSFNVI GRIVCGFQSG 240 PKTGAPSRVE QFKEAINEAS YFMSTSPVSD NVPMLGWIDQ LTGLTRNMKH CGKKLDLVVE 300 SIINDHRQKR RFSRTKGGDE KDDEQDDFID ICLSIMEQPQ LPGNNNPSQI PIKSIVLDMI 360 GGGTDTTKLT TIWTLSLLLN NPHVLDKAKQ EVDAHFRTKR RSTNDAAAAV VDFDDIRNLV 420 YIQAIIKESM RLYPASPVVE RLSGEDCVVG GFHVPAGTRL WANVWKMQRD PKVWDDPLVF 480 RPDRFLSDEQ KMVDVRGQNY ELLPFGAGRR VCPGVSFSLD LMQLVLTRLI LEFEMKSPSG 540 KVDMTATPGL MSYKVIPLDI LLTHRRIK 568
3-339	**Sequences**	
3-339-1	Sequence Number [ID]	339
3-339-2	Molecule Type	DNA
3-	Length	966

339-3		
3-339-4-1	Features Location/Qualifiers	**source** 1..966 mol_type= genomic DNA organism= Papaver somniferum
	NonEnglishQualifier Value	
3-339-5	Residues	atggagagta atggtgtacc tatgatcact ctcagttccg gcattcggat gcctgcttta 60 ggtatgggaa cagctgaaac aatggtaaaa ggaacagaaa gagagaaatt ggcgtttttg 120 aaagcgatag aggtcggtta cagacacttc gatacagctg ctgcatacca aactgaagag 180 tgtcttggtg aagctatagc tgaagcactt caacttggtc taataaaatc tcgagatgaa 240 ctcttcatca cttccaagct ctggtgcgct gatgctcacg ctgatcttgt cctccctgct 300 cttcagaatt ctctgaggaa tcttaaattg gactatcttg atctatattt gatacaccat 360 ccggtaagct tgaagccagg gaagtttgtt aacgaaatac caaaggatca tatccttcca 420 atggactaca aatctgtatg ggcagccatg gaagagtgtc agacccttgg cttcactagg 480 gcaatcgggg tctgtaattt ctcatgcaaa aggcttcaag agttgatgga aacagccaac 540 agccctccag ttgtgaatca agtggagatg agcccgactt tacatcaaaa aaatctgagg 600 gaatattgca aggccaataa tatcatgatc accgcacact cagttttggg agccgtaggt 660 gccgcctggg gcaccaatgc agttatgcat tctaaggtgc ttcaccagat tgctgtggcc 720 agaggaaaat ctgttgccca ggttagtatg agatgggttt accagcaagg cgcgagtctt 780 gtggtgaaaa gtttcaatga agcgaggatg aaggaaaacc ttaagatatt tgattgggaa 840 ctaacggcag aagacatgga aaagatcagt gagattccac aatctagaac aagctctgct 900 gctttcttgt tatcaccgac tggacctttc aaaactgaag aagagttctg ggatgagaag 960 gattga 966

[0161]

3-340	**Sequences**	
3-340-1	Sequence Number [ID]	340
3-340-2	Molecule Type	AA
3-340-3	Length	321
3-340-4-1	Features Location/Qualifiers	**source** 1..321 mol_type= protein organism= Papaver somniferum
	NonEnglishQualifier Value	
3-340-5	Residues	MESSGVPVIT LGSGKVMPVL GMGTFEKVGK GSERERLAIL KAIEVGYRYF DTAAAYETEE 60 VLGEAIAEAL QLGLVKSRDE LFISSMLWCT DAHADRVLLA LQNSLRNLKL EYVDLYMLPF 120 PASLKPGKIT MDIPEEDICR MDYRSVWAAM EECQNLGFTK SIGVSNFSCK KLQELMATAN 180 IPPAVNQVEM SPAFQQKKLR EYCNANNILV SAISVLGSNG TPWGSNAVLG SEVLKKIAMA 240 KGKSVAQVSM RWVYEQGASL VVKSFSEERL RENLNIFDWE LTKEDHEKIG EIPQCRILSA 300 YFLVSPNGPF KSQEELWDDE A 321

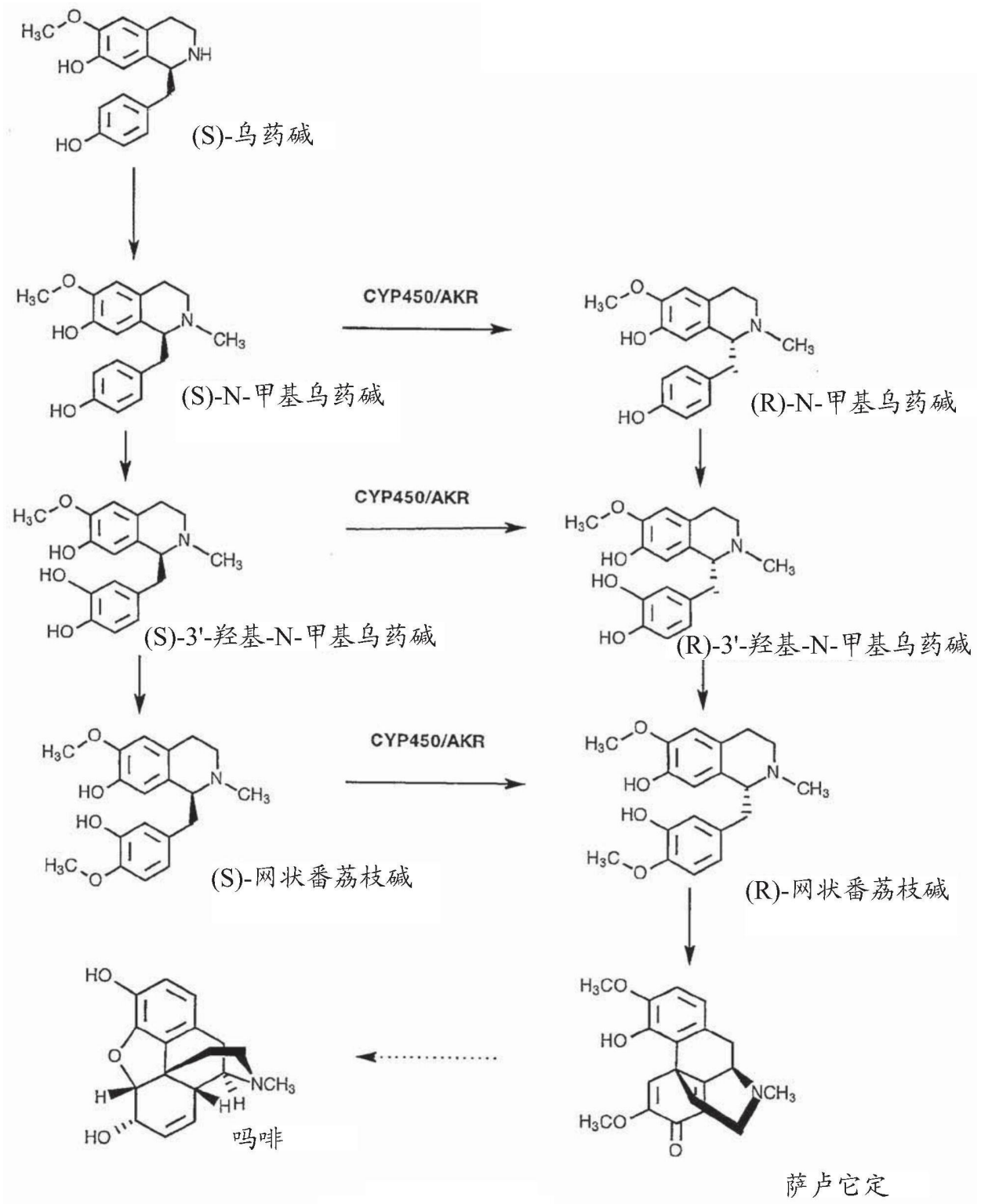
(S)-乌药碱
CYP450/AKR
(S)-N-甲基乌药碱
(R)-N-甲基乌药碱
CYP450/AKR
(S)-3'-羟基-N-甲基乌药碱
(R)-3'-羟基-N-甲基乌药碱
CYP450/AKR
(S)-网状番荔枝碱
(R)-网状番荔枝碱
吗啡
萨卢它定

图1

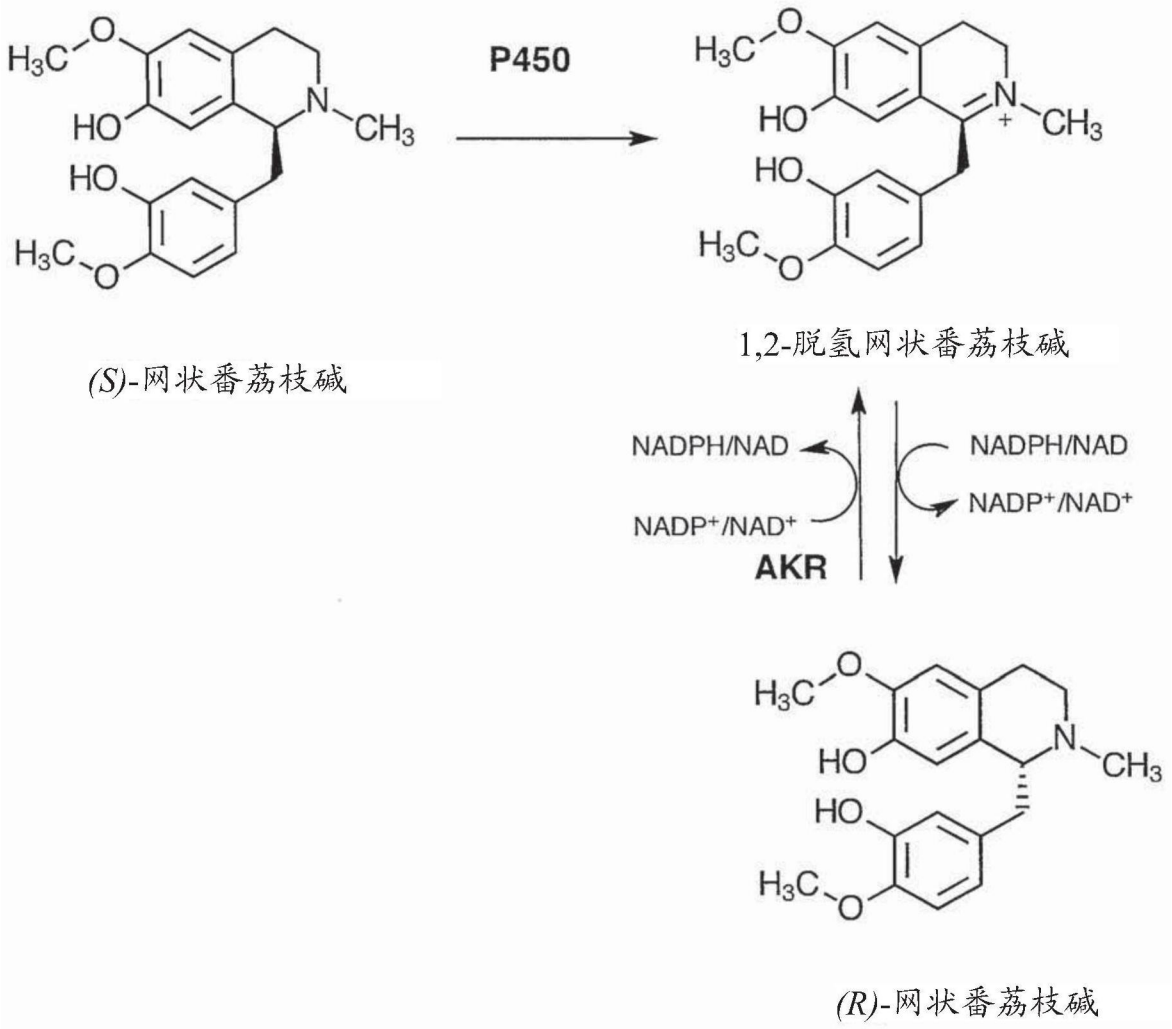
P450
(S)-网状番荔枝碱
1,2-脱氢网状番荔枝碱
NADPH/NAD
NADP+/NAD+
NADPH/NAD
NADP+/NAD+
AKR
(R)-网状番荔枝碱

图2

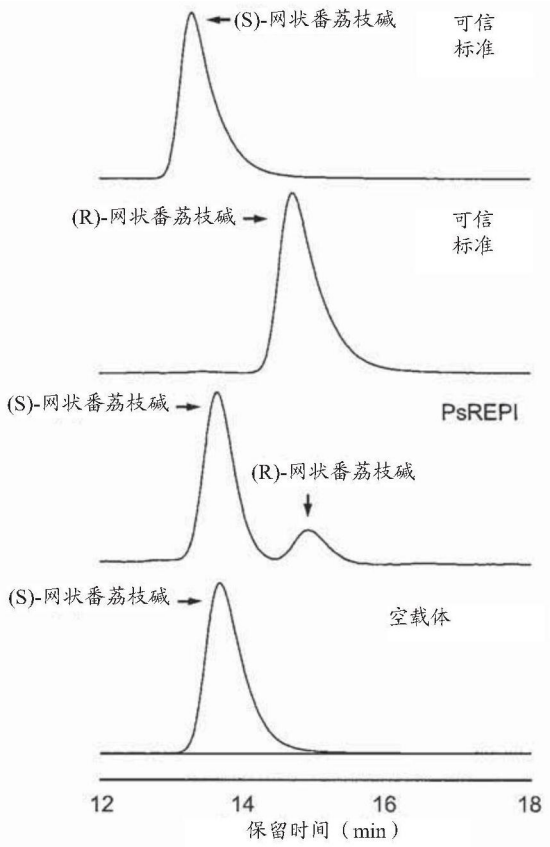
(S)-网状番荔枝碱
可信
标准
(R)-网状番荔枝碱
可信
标准
(S)-网状番荔枝碱
PsREPI
(R)-网状番荔枝碱
(S)-网状番荔枝碱
空载体
12
14
16
18
保留时间（min）

图3

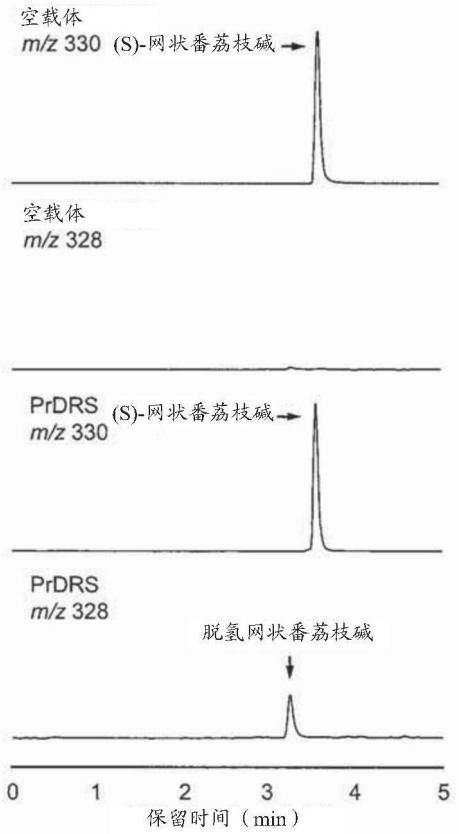
空载体
m/z 330
(S)-网状番荔枝碱
空载体
m/z 328
PrDRS
m/z 330
(S)-网状番荔枝碱
PrDRS
m/z 328
脱氢网状番荔枝碱
0
1
2
3
4
5
保留时间（min）

图4

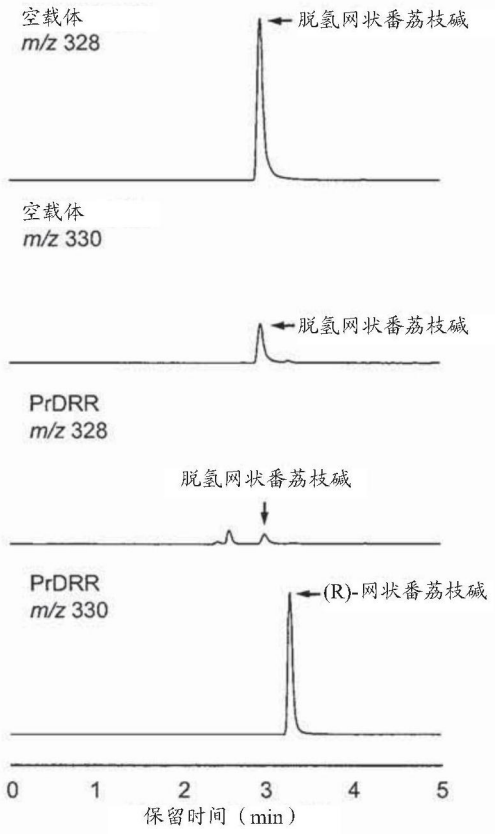
空载体
m/z 328
脱氢网状番荔枝碱
空载体
m/z 330
脱氢网状番荔枝碱
PrDRR
m/z 328
脱氢网状番荔枝碱
PrDRR
m/z 330
(R)-网状番荔枝碱
0
1
2
3
4
5
保留时间（min）

图5

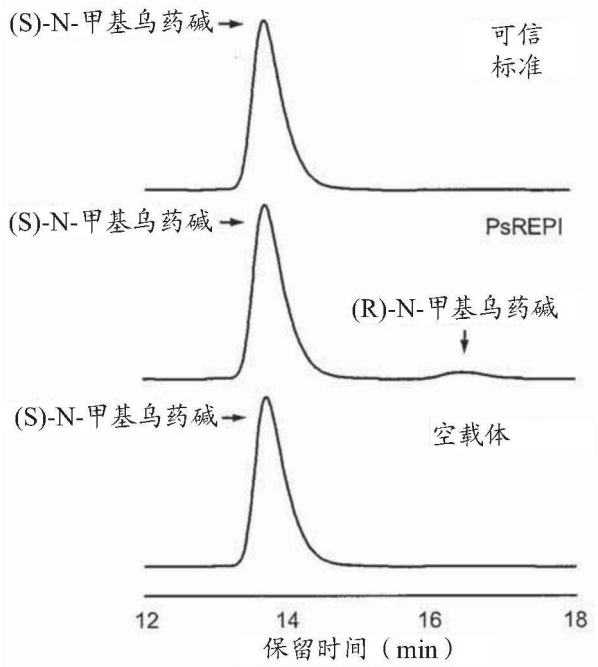
(S)-N-甲基乌药碱
可信
标准
(S)-N-甲基乌药碱
PsREPI
(R)-N-甲基乌药碱
(S)-N-甲基乌药碱
空载体
12
14
16
18
保留时间（min）

图6

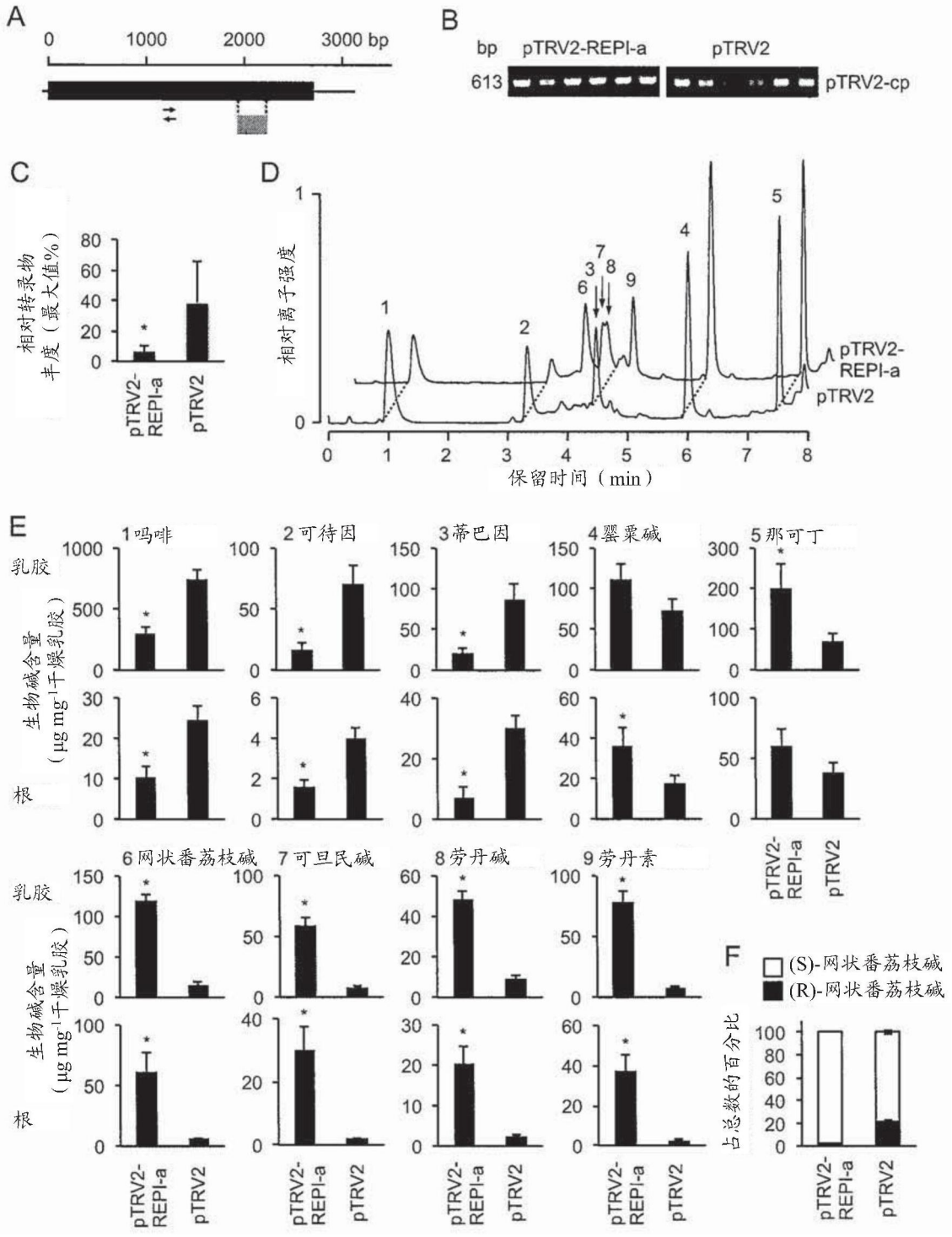
A
0
1000
2000
3000 bp
B
bp
pTRV2-REPI-a
pTRV2
613
pTRV2-cp
C
相对转录物丰度（最大值%）
pTRV2-REPI-a
pTRV2
D
相对离子强度
保留时间（min）
pTRV2-REPI-a
pTRV2
E
1吗啡
2可待因
3蒂巴因
4罂粟碱
5那可丁
6网状番荔枝碱
7可旦民碱
8劳丹碱
9劳丹素
乳胶
根
生物碱含量（μg mg-1干燥乳胶）
F
(S)-网状番荔枝碱
(R)-网状番荔枝碱
占总数的百分比

图7A

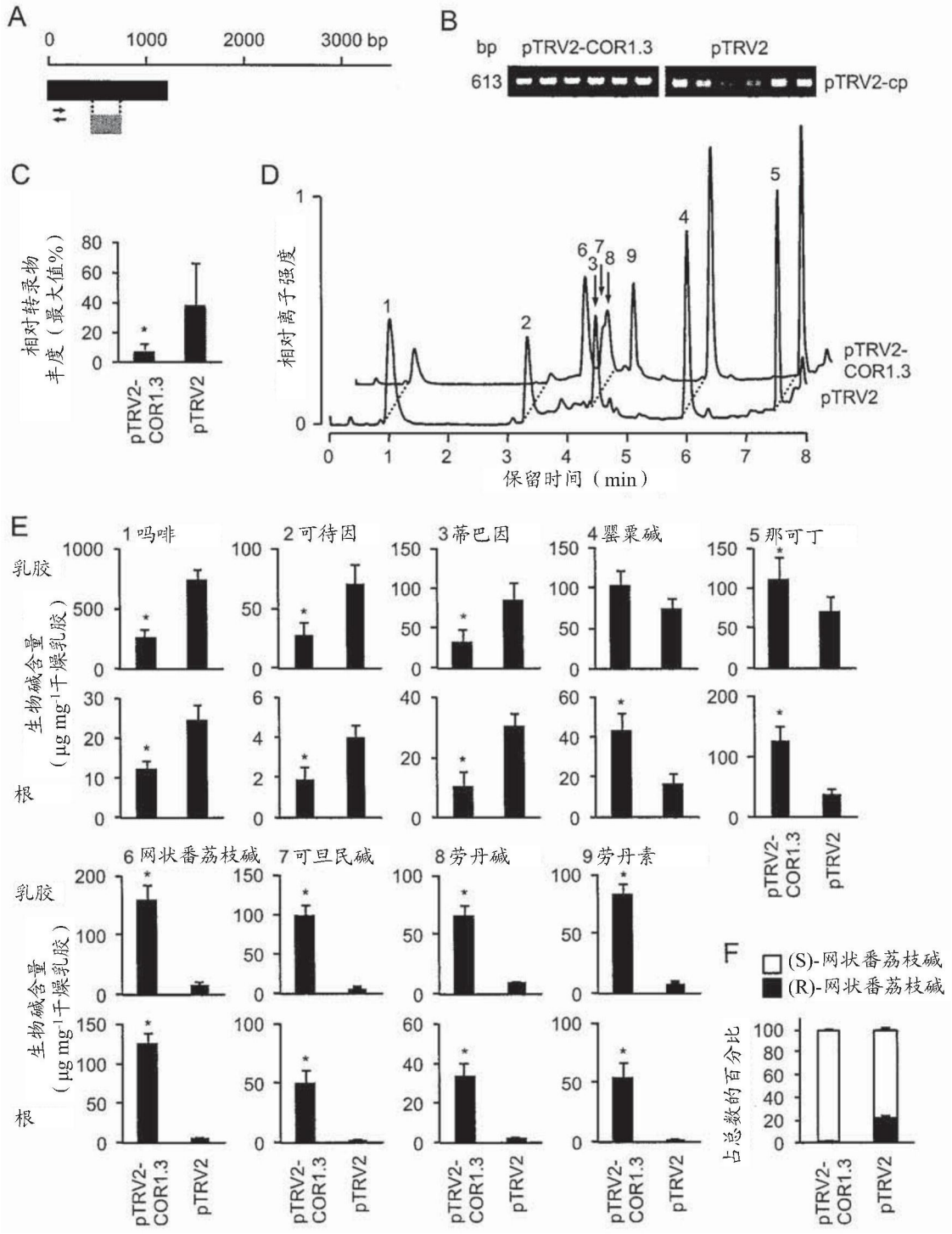
A
0
1000
2000
3000 bp
B
bp
pTRV2-COR1.3
pTRV2
613
pTRV2-cp
C
相对转录物丰度（最大值%）
pTRV2-COR1.3
pTRV2
D
相对离子强度
保留时间（min）
pTRV2-COR1.3
pTRV2
E
1 吗啡
2 可待因
3 蒂巴因
4 罂粟碱
5 那可丁
6 网状番荔枝碱
7 可旦民碱
8 劳丹碱
9 劳丹素
乳胶
根
生物碱含量（μg mg-1干燥乳胶）
F
(S)-网状番荔枝碱
(R)-网状番荔枝碱
占总数的百分比

图7B

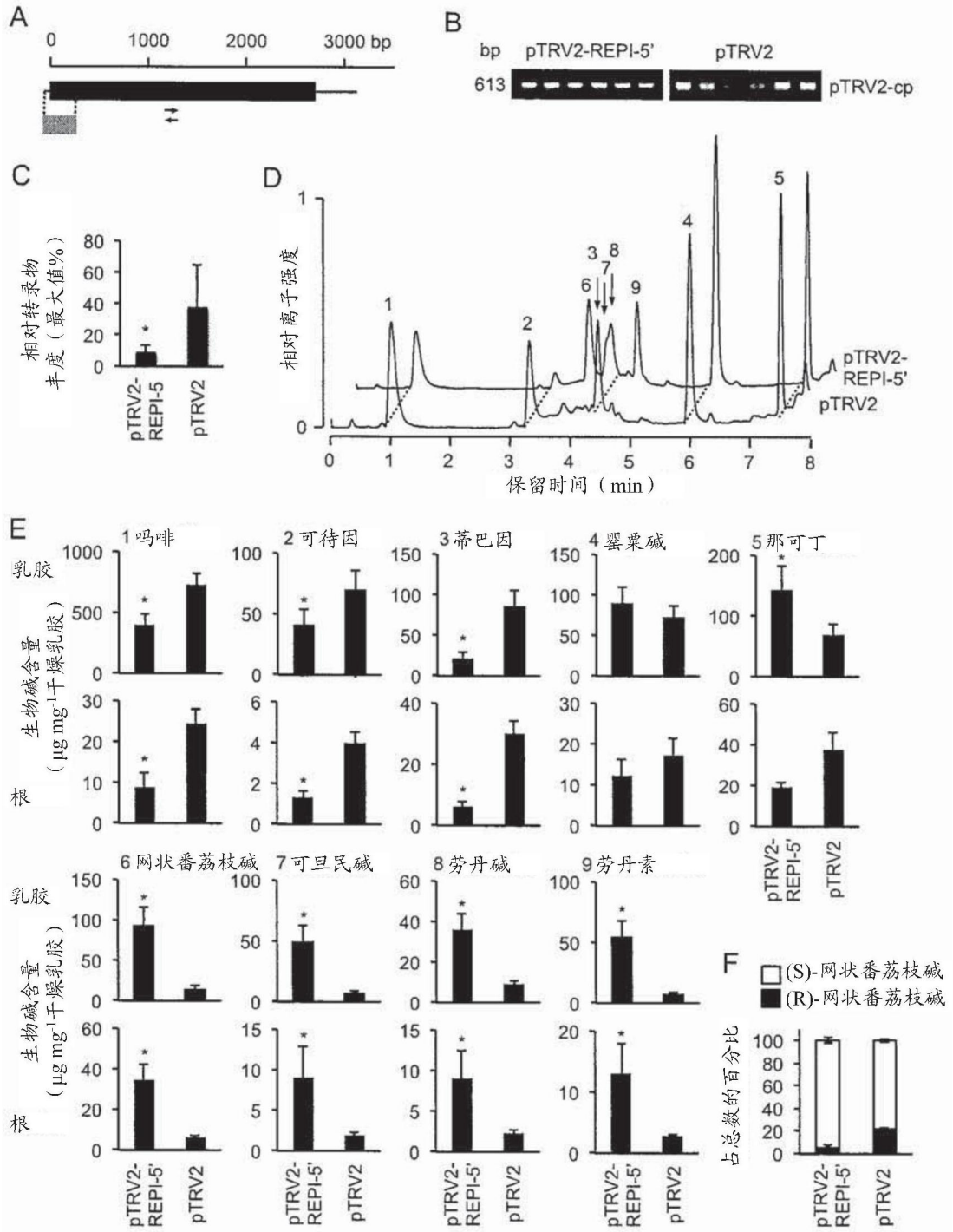
A
0
1000
2000
3000 bp
B
bp
pTRV2-REPI-5'
pTRV2
613
pTRV2-cp
C
相对转录物丰度（最大值%）
pTRV2-REPI-5
pTRV2
D
相对离子强度
保留时间（min）
pTRV2-REPI-5'
pTRV2
E
1 吗啡
2 可待因
3 蒂巴因
4 罂粟碱
5 那可丁
6 网状番荔枝碱
7 可旦民碱
8 劳丹碱
9 劳丹素
乳胶
根
生物碱含量（μg mg-1干燥乳胶）
F
(S)-网状番荔枝碱
(R)-网状番荔枝碱
占总数的百分比

图7C

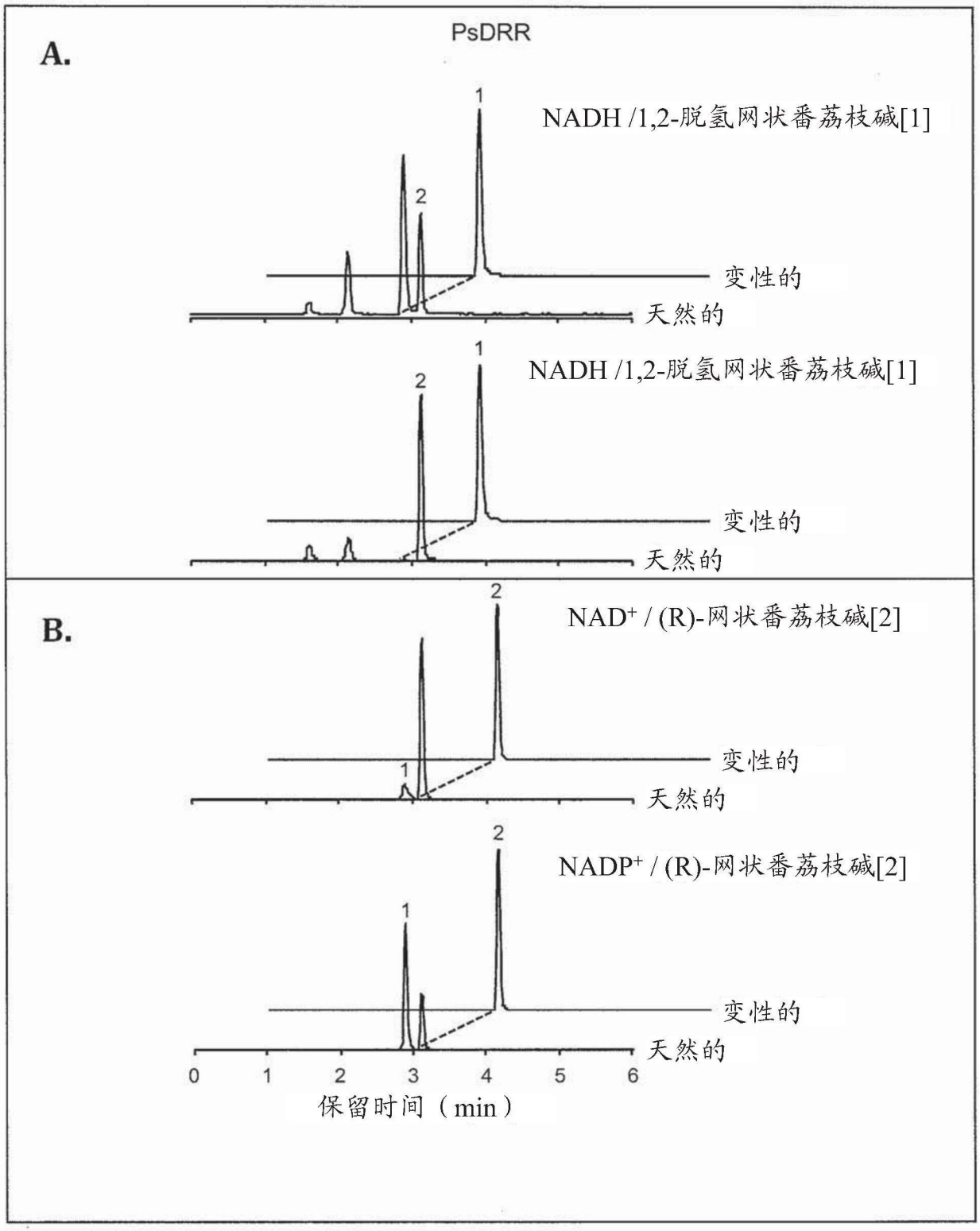
PsDRR
A.
NADH /1,2-脱氢网状番荔枝碱[1]
变性的
天然的
NADH /1,2-脱氢网状番荔枝碱[1]
变性的
天然的
B.
NAD+ / (R)-网状番荔枝碱[2]
变性的
天然的
NADP+ / (R)-网状番荔枝碱[2]
变性的
天然的
0 1 2 3 4 5 6
保留时间（min）

图8A

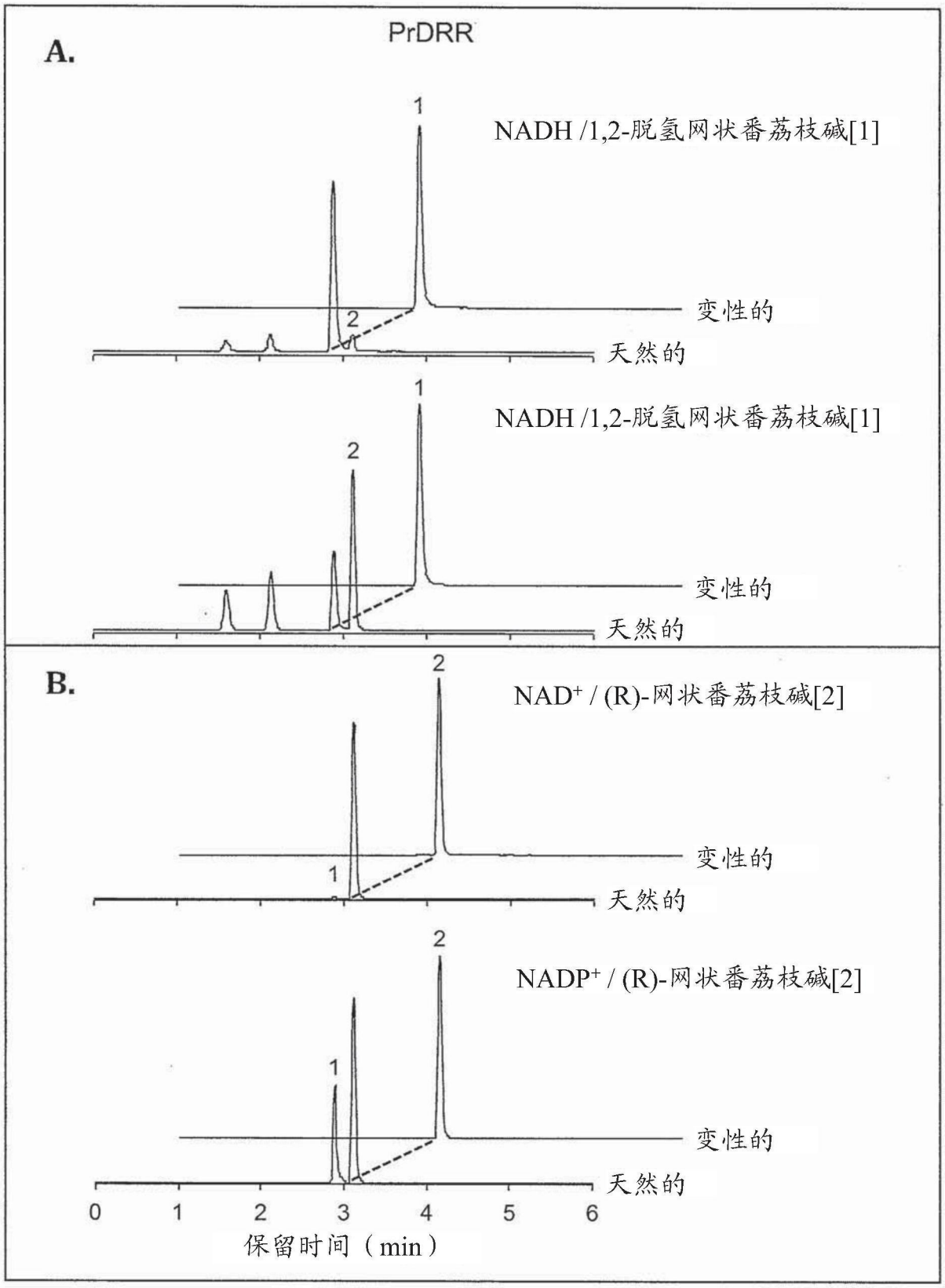
PrDRR
A.
1
NADH /1,2-脱氢网状番荔枝碱[1]
2
变性的
天然的
1
NADH /1,2-脱氢网状番荔枝碱[1]
2
变性的
天然的
B.
2
NAD+ / (R)-网状番荔枝碱[2]
1
变性的
天然的
2
NADP+ / (R)-网状番荔枝碱[2]
1
变性的
天然的
0 1 2 3 4 5 6
保留时间（min）

图8B

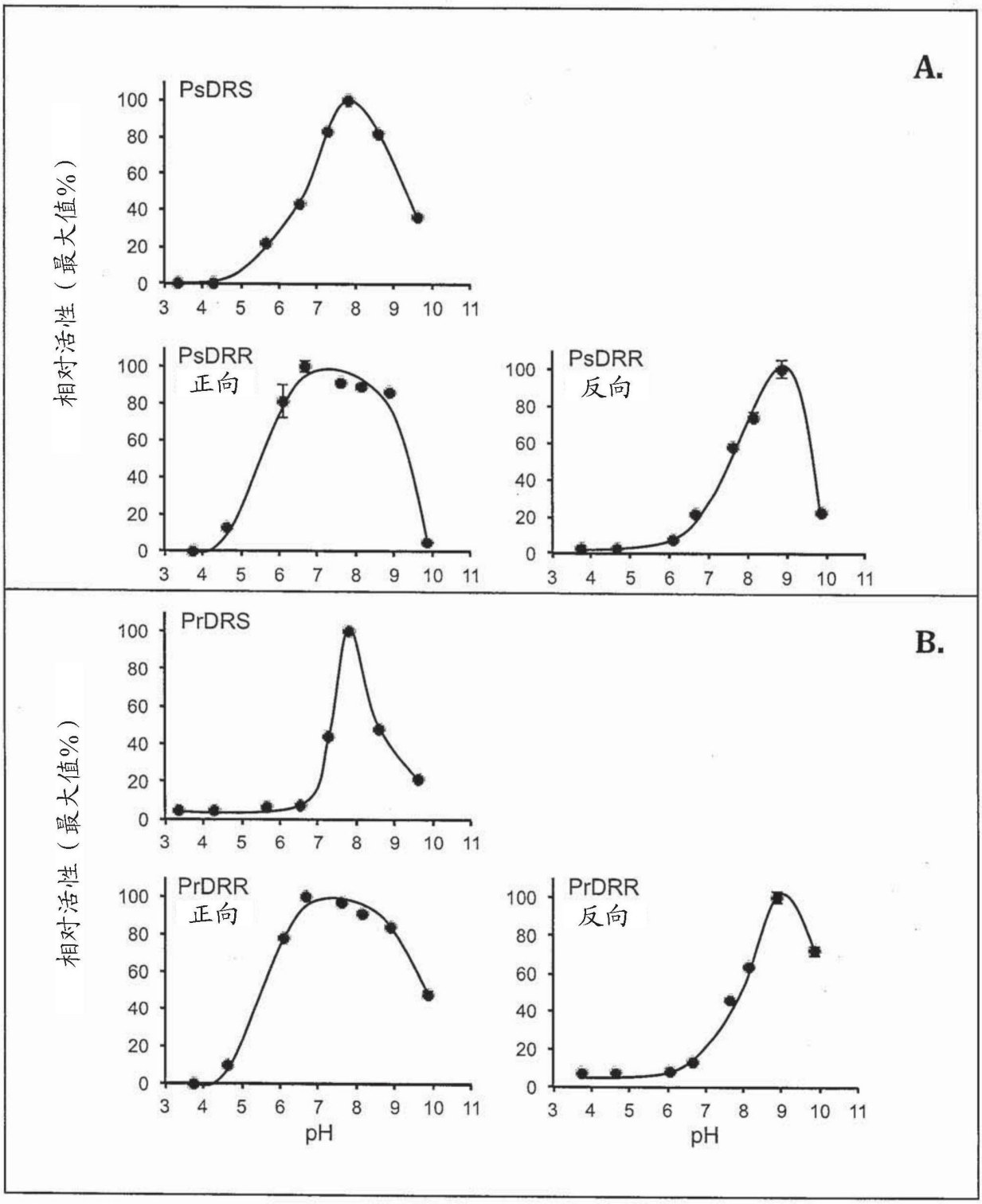
A.
PsDRS
PsDRR
正向
PsDRR
反向
相对活性（最大值%）
B.
PrDRS
PrDRR
正向
PrDRR
反向
相对活性（最大值%）
pH
pH

图9

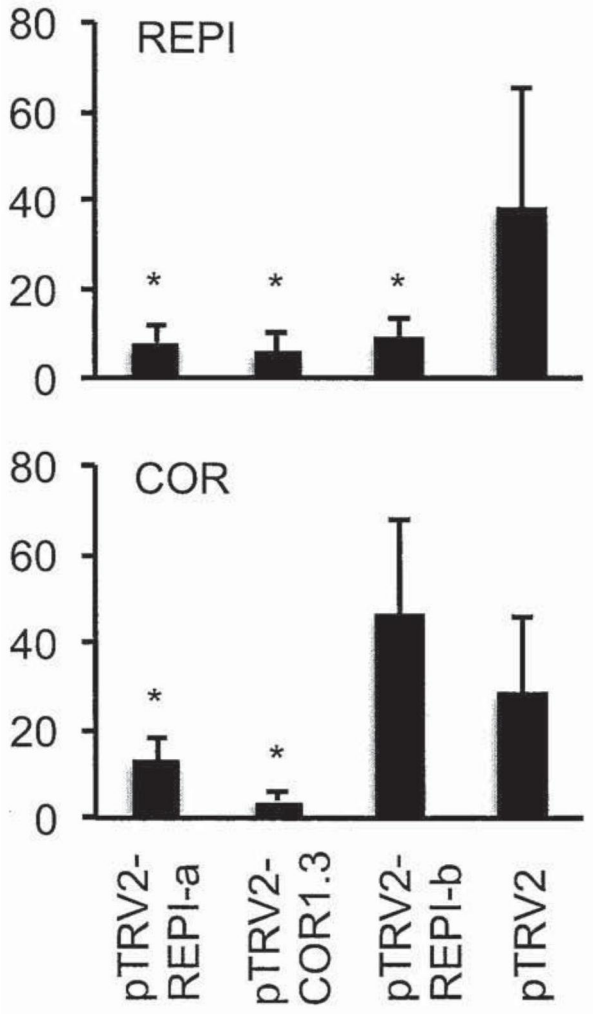
REPI
80
60
40
20
0
*
*
*
COR
80
60
40
20
0
*
*
pTRV2-REPI-a
pTRV2-COR1.3
pTRV2-REPI-b
pTRV2

图10