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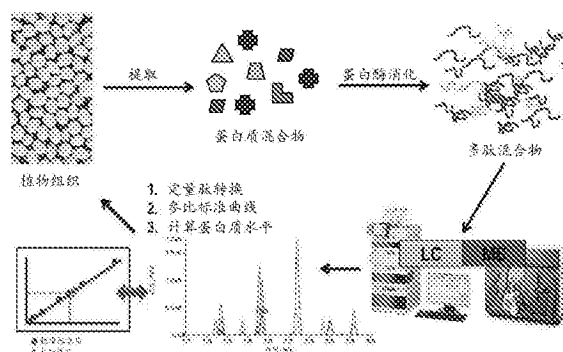
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(54)发明名称

用于变应原的选择性定量与检测的系统和
方法

(57)摘要

本发明涉及这样的方法和系统,其借助生物信息学研究来鉴定候选特征肽,以供利用质谱对来自植物、植物部分和/或食物产品的复杂蛋白质样品进行定量多路分析。提供了利用生物信息学手段选择用于定量的候选特征肽的用途和方法。还提供了包含色谱和质谱的系统,用于使用选定的特征肽。



1. 一种选择候选特征肽用于从基于植物的样品中定量已知的变应原及潜在变应原的方法,包括:

- (a) 基于与至少一种已知变应原蛋白质序列的同源性鉴定潜在变应原;
- (b) 进行所述至少一种已知变应原与步骤(a)中鉴定的潜在变应原的序列比对;
- (c) 基于所述序列比对选择共有序列或代表性序列;
- (d) 基于来自步骤(c)中选择的共有序列或代表性序列的序列比对和计算机消化数据的保守区域或结构域,确定多个候选特征肽;和
- (e) 基于所述特征肽的测量,定量所述基于植物的样品中的所述至少一种已知变应原和潜在变应原的量。

2. 权利要求1的方法,其中所述定量步骤使用柱色谱和质谱。

3. 权利要求1的方法,其中所述定量步骤包括使用高分辨率精确质量质谱(HRAM MS)测量所述多个候选特征肽。

4. 权利要求1的方法,其中所述定量步骤包括从质谱计算所述候选特征肽的相应峰高度或峰面积。

5. 权利要求1的方法,其中所述定量步骤包括将来自质谱的高碎裂模式和低碎裂模式的数据进行比较。

6. 权利要求1的方法,其中所述至少一种已知的变应原包括Gly m Bd 28K、Gly m Bd 30K、Kunitz胰蛋白酶抑制剂1、Kunitz胰蛋白酶抑制剂3、Gly m 8(2S白蛋白)、凝集素或脂加氧酶。

7. 权利要求1的方法,其中所述潜在的变应原包括选自下组的至少一种序列:

- (a) 对于Gly m Bd 28K为SEQ ID NO:21和29-33;
- (b) 对于Gly m Bd 30K为SEQ ID NO:22和43-44;
- (c) 对于Kunitz胰蛋白酶抑制剂1为SEQ ID NO:23和53-54;
- (d) 对于Kunitz胰蛋白酶抑制剂3为SEQ ID NO:24和62-63;
- (e) 对于Gly m 8(2S白蛋白)为SEQ ID NO:25和72-74;
- (f) 对于凝集素为SEQ ID NO:26和83-90;
- (g) 对于脂加氧酶为SEQ ID NO:27和96-104。

8. 权利要求1的方法,其中所述候选特征肽包含选自下组的至少一种序列:

- (a) 对于Gly m Bd 28K为SEQ ID NO:9和34-42;
- (b) 对于Gly m Bd 30K为SEQ ID NO:10和45-51;
- (c) 对于Kunitz胰蛋白酶抑制剂1为SEQ ID NO:7和55-60;
- (d) 对于Kunitz胰蛋白酶抑制剂3为SEQ ID NO:8和64-71;
- (e) 对于Gly m 8(2S白蛋白)为SEQ ID NO:11和75-81;
- (f) 对于凝集素为SEQ ID NO:91-94;和
- (g) 对于脂加氧酶为SEQ ID NO:105-120。

9. 权利要求1的方法,其中所述基于植物的样品包含大豆种子或大豆种子的部分。

10. 一种用于在基于植物的样品中定量一种或多种具有已知氨基酸序列的目标蛋白质的系统,所述系统包括:

- (a) 用于从基于植物的样品中提取蛋白质的高通量手段;

- (b) 用于以至少一种蛋白酶消化所提取的蛋白质的处理模块;
 - (c) 用于在单个步骤中分离肽的分离模块;
 - (d) 选择模块,用于为至少一种已知的变应原和潜在的变应原选择多个特征肽;和
 - (e) 用于测量多个特征肽的质谱法。
11. 权利要求10的系统,其中所述分离模块包括柱色谱。
12. 权利要求11的系统,其中所述柱色谱包括液相柱色谱。
13. 权利要求10的系统,其中所述质谱包括高分辨率精确质量质谱 (HRAM MS)。
14. 权利要求10的系统,其中所述选择模块使用根据权利要求1的方法。
15. 权利要求10的系统,其中所述至少一种已知的变应原包括Gly m Bd 28K、Gly m Bd 30K、Kunitz胰蛋白酶抑制剂1、Kunitz胰蛋白酶抑制剂3、Gly m 8 (2S白蛋白)、凝集素、或脂加氧酶。
16. 权利要求10的系统,其中所述潜在的变应原包括选自以下的至少一种序列:
- (a) 对于Gly m Bd 28K为SEQ ID NO:21和29-33;
 - (b) 对于Gly m Bd 30K为SEQ ID NO:22和43-44;
 - (c) 对于Kunitz胰蛋白酶抑制剂1为SEQ ID NO:23和53-54;
 - (d) 对于Kunitz胰蛋白酶抑制剂3为SEQ ID NO:24和62-63;
 - (e) 对于Gly m 8 (2S白蛋白) 为SEQ ID NO:25和72-74;
 - (f) 对于凝集素为SEQ ID NO:26和83-90;
 - (g) 对于脂加氧酶为SEQ ID NO:27和96-104。
17. 权利要求10的系统,其中所述特征肽包含选自下组的至少一种序列:
- (a) 对于Gly m Bd 28K为SEQ ID NO:9和34-42;
 - (b) 对于Gly m Bd 30K为SEQ ID NO:10和45-51;
 - (c) 对于Kunitz胰蛋白酶抑制剂1为SEQ ID NO:7和55-60;
 - (d) 对于Kunitz胰蛋白酶抑制剂3为SEQ ID NO:8和64-71;
 - (e) 对于Gly m 8 (2S白蛋白) 为SEQ ID NO:11和75-81;
 - (f) 对于凝集素为SEQ ID NO:91-94;和
 - (e) 对于脂加氧酶为SEQ ID NO:105-120。
18. 权利要求10的系统,其中所述基于植物的样品包括大豆种子或大豆种子的部分。
19. 一种在基于植物的样品中定量至少一种具有已知氨基酸序列的变应原及同源潜在变应原的高通量方法,包括使用权利要求10的系统。

用于变应原的选择性定量与检测的系统和方法

[0001] 优先权要求

[0002] 本申请要求下列美国临时专利申请的申请日的权益：系列号62/035,968,2014年8月11日提交,题为“Methods and Systems for Selective Quantitation and Detection of Allergens Including GLY M BD 28 K”；系列号62/035,981,2014年8月11日提交,题为“Methods and Systems for Selective Quantitation and Detection of Allergens Including GLY M BD 30 K”；系列号62/035,997,2014年8月11日提交,题为“Methods and Systems for Selective Quantitation and Detection of Allergens Including Kunitz Trypsin Inhibitor 1”；系列号62/036,007,2014年8月11日提交,题为“Methods and Systems for Selective Quantitation and Detection of Allergens Including Kunitz Trypsin Inhibitor 3”；系列号62/036,016,2014年8月11日提交,题为“Methods and Systems for Selective Quantitation and Detection of Allergens Including GLY M 8 (2S Albumin)”；系列号62/036,024,2014年8月11日提交,题为“Methods and Systems for Selective Quantitation and Detection of Allergens Including Lectin”；及系列号62/036,032,2014年8月11日提交,题为“Methods and Systems for Selective Quantitation and Detection of Allergens Including Lipoxxygenase,”,每一个申请的披露内容通过引用整体并入本文。

[0003] 背景

[0004] 本领域当前优选用于分析植物中基因表达的方法包括基于DNA的技术(例如PCR和/或RT-PCR)；使用报告基因；Southern印迹；和免疫化学。这些方法都有各种缺点。在植物、植物部分和/或食品中检测已知和潜在的变应原是公共安全的一个重要课题。

[0005] 质谱虽然先前已经公开,但是现有的手段是有限的,没有选择和灵敏的定量。仍然需要用于在植物、植物部分和/或食品中已知和/或潜在的变应原的选择的、灵敏的定量的高通量方法。

[0006] 公开

[0007] 本发明涉及利用生物信息学研究来鉴定候选特征肽,用于使用质谱法对来自植物、植物部分和/或食品的复杂蛋白质样品进行定量多重分析的方法和系统。提供了使用生物信息学方法选择候选特征肽用于定量的用途和方法。还提供了包括色谱和质谱的系统,用于利用所选出的特征肽。

[0008] 在一个方面,提供了选择候选特征肽用于从基于植物的样品中定量已知的变应原和潜在的变应原的方法。该方法包括：

[0009] (a) 基于与至少一种已知变应原蛋白质序列的同源性鉴定潜在变应原；

[0010] (b) 进行所述至少一种已知变应原与步骤(a)中鉴定的潜在变应原的序列比对；

[0011] (c) 基于所述序列比对选择共有序列或代表性序列；

[0012] (d) 基于来自在步骤(c)中选择的共有序列或代表性序列的序列比对和计算机消化数据的保守区域或结构域,确定多个候选特征肽；和

[0013] (e) 基于所述特征肽的测量(measurements),定量所述基于植物的样品中的所述

至少一种已知变应原和潜在变应原的量。

[0014] 在一个实施方案中,所述定量步骤使用柱色谱和质谱。在另一个实施方案中,定量步骤包括使用高分辨率精确质量质谱 (HRAM MS) 测量所述多个候选特征肽。在另一个实施方案中,定量步骤包括从质谱计算候选特征肽的相应峰高度或峰面积。在另一个实施方案中,定量步骤包括将来自质谱法高碎裂模式的数据和低碎裂模式的数据进行比较。

[0015] 在一个实施方案中,所述至少一种已知的变应原包含至少一种选自下组的变应原:Gly m 1,Gly m 3,Gly m 4,Gly m 5(β -伴大豆球蛋白),Gly m 6(大豆球蛋白)Gly m 6(大豆球蛋白)G2,Gly m 6(大豆球蛋白)G3,Gly m 6(大豆球蛋白)G4,Gly m 6(大豆球蛋白)前体,Kunitz胰蛋白酶抑制剂1,Kunitz胰蛋白酶抑制剂3,Gly m Bd 28 K,Gly m Bd 30 K,Gly m 8(2S白蛋白),凝集素和脂加氧酶。在另一个实施方案中,至少一种已知的变应原包括Gly m Bd 28 K、Gly m Bd 30 K、Kunitz胰蛋白酶抑制剂1、Kunitz胰蛋白酶抑制剂3、Gly m 8(2S白蛋白)、凝集素,或脂加氧酶。

[0016] 在另一个实施方案中,步骤(c)的共有序列或代表性序列对于Gly m Bd28 K而言包含SEQ ID NO:21,28,29,30,31,32或33。在一个进一步的实施方案中,对于Gly m Bd 28 K,步骤(c)的共有序列或代表性序列包含SEQ ID NO:21或28。在另一个实施方案中,对于Gly m Bd 30 K,步骤(c)的共有序列或代表性序列包含SEQ ID NO:22、43、或44。在一个进一步的实施方案中,对于Gly m Bd 30 K,步骤(c)的共有序列或代表性序列包含SEQ ID NO:22或43。在另一个实施方案中,对于Kunitz胰蛋白酶抑制剂1,步骤(c)的共有序列或代表性序列包含SEQ ID NO:23、52、53、或54。在一个进一步的实施方案中,对于Kunitz胰蛋白酶抑制剂1,步骤(c)的共有序列或代表性序列包含SEQ ID NO:23或52。在另一个实施方案中,对于Kunitz胰蛋白酶抑制剂3,步骤(c)的共有序列或代表性序列包含SEQ ID NO:24、61、62、或63。在一个进一步的实施方案中,对于Kunitz胰蛋白酶抑制剂3,步骤(c)的共有序列或代表性序列包含SEQ ID NO:24或61。在另一个实施方案中,对于Gly m 8(2S白蛋白),步骤(c)的共有序列或代表性序列包含SEQ ID NO:25、72、73、或74。在一个进一步的实施方案中,对于Gly m 8(2S白蛋白),步骤(c)的共有序列或代表性序列包含SEQ ID NO:25。在另一个实施方案中,对于凝集素,步骤(c)的共有序列或代表性序列包含SEQ ID NO:26、82、83、84、85、86、87、88、89、或90。在一个进一步的实施方案中,对于凝集素,步骤(c)的共有序列或代表性序列包含SEQ ID NO:26或82。在另一个实施方案中,对于脂加氧酶,步骤(c)的共有序列或代表性序列包含SEQ ID NO:27、95、96、97、98、99、100、101、102、103、或104。在一个进一步的实施方案中,对于脂加氧酶,步骤(c)的共有序列或代表性序列包含SEQ ID NO:27或95。

[0017] 在一个实施方案中,对于Gly m Bd 28 K,潜在的变应原包含选自SEQ ID NO:21和29-33的至少一个序列。在另一个实施方案中,对于Gly m Bd 30 K,潜在的变应原包含选自SEQ ID NOs:22和43-44的至少一个序列。在另一个实施方案中,对于Kunitz胰蛋白酶抑制剂1,潜在的变应原包含选自SEQ ID NO:23和53-54的至少一个序列。在另一个实施方案中,对于Kunitz胰蛋白酶抑制剂3,潜在的变应原包含选自SEQ ID NO:24和62-63的至少一个序列。在另一个实施方案中,对于Gly m 8(2S白蛋白),潜在的变应原包含选自SEQ ID NO:25和72-74的至少一个序列。在另一个实施方案中,对于凝集素,潜在的变应原包含选自SEQ ID NO:26和83-90的至少一个序列。在另一个实施方案中,对于脂加氧酶,潜在的变应原包

含选自SEQ ID NO:27和96-104的至少一个序列。

[0018] 在另一个实施方案中,对于Gly m Bd 28 K,候选特征肽包含选自SEQ ID NO:9和34-42的至少一个序列。在另一个实施方案中,对于Gly m Bd 28 K,候选特征肽包含SEQ ID NO:34-42。在另一个实施方案中,对于Gly m Bd 30 K,候选特征肽包含选自SEQ ID NO:10和45-51的至少一个序列。在另一个实施方案中,对于Gly m Bd 30 K,候选特征肽包含SEQ ID NO:45-51。在另一个实施方案中,对于Kunitz胰蛋白酶抑制剂1,候选特征肽包含选自SEQ ID NO:7和55-60的至少一个序列。在另一个实施方案中,对于Kunitz胰蛋白酶抑制剂1,候选特征肽包含SEQ ID NO:55-60。在另一个实施方案中,对于Kunitz胰蛋白酶抑制剂3,候选特征肽包含选自SEQ ID NO:8和64-71的至少一个序列。在另一个实施方案中,对于Kunitz胰蛋白酶抑制剂3,候选特征肽包含SEQ ID NO:64-71。在另一个实施方案中,对于Gly m 8 (2S白蛋白),候选特征肽包含选自SEQ ID NO:11和75-81的至少一个序列。在另一个实施方案中,对于Gly m 8 (2S白蛋白),候选特征肽包含SEQ ID NO:75-81。在另一个实施方案中,对于凝集素,候选特征肽包含选自SEQ ID NO:91-94的至少一个序列。在另一个实施方案中,对于凝集素,候选特征肽包含SEQ ID NO:91-94。在另一个实施方案中,对于脂加氧酶,候选特征肽包含选自SEQ ID NO:105-120的至少一个序列。在另一个实施方案中,对于脂加氧酶,候选特征肽包含SEQ ID NO:105-120。在另一个实施方案中,基于植物的样品包含选自大豆种子或大豆种子的部分。

[0019] 在另一方面,提供了用于在基于植物的样品中定量一种或多种具有已知氨基酸序列的目标蛋白质的系统。该系统包括:

[0020] (a) 用于从基于植物的样品中提取蛋白质的高通量手段;

[0021] (b) 用于以至少一种蛋白酶消化所提取的蛋白质的处理模块;

[0022] (c) 用于在单个步骤中分离肽的分离模块;

[0023] (d) 用于为至少一种已知的变应原和潜在的变应原选择多个特征肽的选择模块;
和

[0024] (e) 用于测量所述多个特征肽的质谱。

[0025] 在一个实施方案中,分离模块包括柱色谱。在另一个实施方案中,柱色谱法包括液相柱色谱。在另一个实施方案中,质谱包括高分辨率精确质量质谱 (HRAM MS)。在另一个实施方案中,选择模块使用本文提供的方法。

[0026] 在一个实施方案中,基于植物的样品中的具有已知氨基酸序列的一种或多种目的蛋白质包含潜在的变应原。在另一个实施方案中,对于Gly m Bd 28 K,潜在的变应原包含选自SEQ ID NO:21和29-33的至少一个序列。在另一个实施方案中,对于Gly m Bd 30 K,潜在的变应原包含选自SEQ ID NO:22和43-44的至少一个序列。在另一个实施方案中,对于Kunitz胰蛋白酶抑制剂1,潜在的变应原包含选自SEQ ID NO:23和53-54的至少一个序列。在另一个实施方案中,对于Kunitz胰蛋白酶抑制剂3,潜在的变应原包含选自SEQ ID NO:24和62-63的至少一个序列。在另一个实施方案中,对于Gly m 8 (2S白蛋白),潜在的变应原包含选自SEQ ID NO:25和72-74的至少一个序列。在另一个实施方案中,对于凝集素,潜在的变应原包含选自SEQ ID NO:26和83-90的至少一个序列。在另一个实施方案中,对于脂加氧酶,潜在的变应原包含选自SEQ ID NO:27和96-104的至少一个序列。

[0027] 在另一个实施方案中,对于Gly m Bd 28 K,候选特征肽包含选自SEQ ID NO:9和

34-42的至少一个序列。在另一个实施方案中,对于Gly m Bd 28 K,特征肽包含SEQ ID NO: 34-42。在另一个实施方案中,对于Gly m Bd 30 K,候选特征肽包含选自SEQ ID NO:10和45-51的至少一个序列。在另一个实施方案中,对于Gly m Bd 30 K,特征肽包含SEQ ID NO: 45-51。在另一个实施方案中,对于Kunitz胰蛋白酶抑制剂1,候选特征肽包含选自SEQ ID NO:7和55-60的至少一个序列。在另一个实施方案中,对于Kunitz胰蛋白酶抑制剂1,特征肽包含SEQ ID NO:55-60。在另一个实施方案中,对于Kunitz胰蛋白酶抑制剂3,候选特征肽包含选自SEQ ID NO:8和64-71的至少一个序列。在另一个实施方案中,对于Kunitz胰蛋白酶抑制剂3,特征肽包含SEQ ID NO:64-71。在另一个实施方案中,对于Gly m 8(2S白蛋白),候选特征肽包含选自SEQ ID NO:11和75-81的至少一个序列。在另一个实施方案中,对于Gly m 8(2S白蛋白),特征肽包含SEQ ID NO:75-81。在另一个实施方案中,对于凝集素,候选特征肽包含选自SEQ ID NO:91-94的至少一个序列。在另一个实施方案中,对于凝集素,特征肽包含SEQ ID NO:91-94。在另一个实施方案中,对于脂加氧酶,候选特征肽包含选自SEQ ID NO:105-120的至少一个序列。在另一个实施方案中,对于脂加氧酶,特征肽包含SEQ ID NO:105-120。在另一个实施方案中,基于植物的样品包含大豆种子或大豆种子的部分。

[0028] 在另一方面,提供了在基于植物的样品中定量至少一种具有已知氨基酸序列的变应原和同源的潜在变应原的高通量方法。该方法包括使用本文提供的系统。

附图说明

[0029] 图1示出了本文公开的方法和系统的代表性分析工作流程。

[0030] 图2A-2J显示了下列选定的特征肽:SEQ ID NO:9 NKPQFLAGAASLLR;SEQ ID NO:34 LGFIYDDELAER;SEQ ID NO:35 TVVEEIFSK;SEQ ID NO:36 MMQDQEEDEEEK;SEQ ID NO:37 NAYGWSK;SEQ ID NO:38 ALHGGEYPPLSEPDIGVLLVK;SEQ ID NO:39 QGDVFVVP;SEQ ID NO:40 YFPFCQVASR;SEQ ID NO:41 TLMGPELSAAGVSEDTLR;SEQ ID NO:42 SFANDVMDVVF的代表性SRM LC-MS/MS,来自Gly m Bd 28 K的胰蛋白酶消化大豆样品色谱图。

[0031] 图2K显示代表性SRM LC-MS/MS标准色谱图-500ng/mL合成肽SEQ ID NO:9 NKPQFLAGAASLLR天然丰度肽和重同位素标记肽转换。

[0032] 图2L显示Gly m Bd 28 K和Gly m Bd 28 K的潜在同源物之间的序列比对。

[0033] 图3A-3H显示下列选定的特征肽:SEQ ID NO:10 GVITQVK;SEQ ID NO:45 SILDLDTK;SEQ ID NO:46 FTTQK;SEQ ID NO:47 NNLNYIR;SEQ ID NO:48 FADITPQEFSK;SEQ ID NO:49 EQYSCDHPPASWDWR;SEQ ID NO:50 VTIDGYETLIMSDESTESETEQAFLSAILEQPISVSIDAK;和SEQ ID NO:51 NTGNLLGVCGMNYFASYPTK的代表性SRM LC-MS/MS,来自Gly m Bd 30 K的胰蛋白酶消化大豆样品色谱图。

[0034] 图3I显示代表性SRM LC-MS/MS标准色谱图-500ng/mL合成肽SEQ ID NO:10 GVITQVK天然丰度肽和重同位素标记肽转换。

[0035] 图3J显示Gly m Bd 30 K和Gly m Bd 30 K的潜在同源物之间的序列比对。

[0036] 图4A-4G显示下列选定的特征肽:SEQ ID NO:7 GGGIEVDSTGK;SEQ ID NO:55 EICPLTVVQSPNELDK;SEQ ID NO:56 EGLQAVK;SEQ ID NO:57 LVFCPQQAEDNK;SEQ ID NO:58 CEDIGIQIDDDGIR;SEQ ID NO:59 LVLSK;和SEQ ID NO:60 NKPLVVQFQK的代表性SRM LC-MS/MS,来自Kunitz胰蛋白酶抑制剂1的胰蛋白酶消化大豆样品色谱图。

[0037] 图4H显示代表性SRM LC-MS/MS标准色谱图-500ng/mL合成肽SEQ ID NO:7 GGGIEVDSTGK天然丰度肽和重同位素标记肽转换。

[0038] 图4I显示Kunitz胰蛋白酶抑制剂1与Kunitz胰蛋白酶抑制剂1的潜在同源物之间的序列比对。

[0039] 图5A-5I显示下列选定的特征肽:SEQ ID NO:8 GIGTISSPYR;SEQ ID NO:64 CPLTVVQSR;SEQ ID NO:65 NELDK;SEQ ID NO:66 IGENK;SEQ ID NO:67 DAMDGWFR;SEQ ID NO:68 LVFCPQQAEDDK;SEQ ID NO:69 CGDIGISIDHDDGTR;SEQ ID NO:70 LVVSK;和SEQ ID NO:71 NKPLVVQFQK的代表性SRM LC-MS/MS,来自Kunitz胰蛋白酶抑制剂3的胰蛋白酶消化大豆样品色谱图。

[0040] 图5J显示代表性SRM LC-MS/MS标准色谱图-500ng/mL合成肽SEQ ID NO:8 GIGTISSPYR天然丰度肽和重同位素标记肽转换。

[0041] 图5K显示Kunitz胰蛋白酶抑制剂3和Kunitz胰蛋白酶抑制剂3的潜在同源物之间的序列比对。

[0042] 图6A-6H显示下列选定的特征肽:SEQ ID NO:11 IMENQSEEELEEK;SEQ ID NO:75 WQHQQDSCR;SEQ ID NO:76 QLQGVNLTPCEK;SEQ ID NO:77 HIMEK;SEQ ID NO:78 DEDEEEEGHMQK;SEQ ID NO:79 CCTEMSELR;SEQ ID NO:80 ELINLATMCR;和SEQ ID NO:81 FGPMIQCDLSSDD的代表性SRM LC-MS/MS,来自Gly m 8(2S白蛋白)的胰蛋白酶消化大豆样品色谱图。

[0043] 图6I显示代表性SRM LC-MS/MS标准色谱图-500ng/mL合成肽SEQ ID NO:11 IMENQSEEELEEK天然丰度肽和重同位素标记肽转换。

[0044] 图6J显示Gly m 8(2S白蛋白)和Gly m 8的潜在同源物之间的序列比对。

[0045] 图7A-7D显示下列选定的特征肽:SEQ ID NO:91 VFSPNK;SEQ ID NO:92 ANSTNTVSFTVSK;SEQ ID NO:93 QQNLIFQGDAISP SGVLR;和SEQ ID NO:94 TADGLAFLAPVGSKPQSK的代表性SRM LC-MS/MS,来自凝集素的胰蛋白酶消化大豆样品色谱图。

[0046] 图7E显示代表性SRM LC-MS/MS标准色谱图-500ng/mL合成肽SEQ ID NO:91 VFSPNK天然丰度肽和重同位素标记肽转换。

[0047] FIG 7F显示凝集素和凝集素的潜在同源物之间的序列比对。

[0048] 图8A-8P显示下列选定的特征肽:SEQ ID NO:105 SSDFLTYGIK;SEQ ID NO:106 GTVVLMPK;SEQ ID NO:107 NVLDFNAITSIGK;SEQ ID NO:108 GGVIDTATGILGQGVSLVGGVIDTATSFLGR;SEQ ID NO:109 IFFVNDTYLPSATPAPLLK;SEQ ID NO:110 DENFGHLK;SEQ ID NO:111 SLSHDVIPLFK;SEQ ID NO:112 SLYEGGIK;SEQ ID NO:113 TDGENVLQFPPPHVAK;SEQ ID NO:114 INSLPTAK;SEQ ID NO:115 TILFLK;SEQ ID NO:116 HLSVLHPIYK;SEQ ID NO:117 QSLINADGIIK;SEQ ID NO:118 FIPAEGTPEYDEMVK;SEQ ID NO:119 ALEAFK;和SEQ ID NO:120 GIPNSISI的代表性SRM LC-MS/MS,来自胰蛋白酶消化大豆样品色谱图。

[0049] 图8Q显示代表性SRM LC-MS/MS标准色谱图-500ng/mL合成肽SEQ ID NO:105 SSDFLTYGIK天然丰度肽和重同位素标记肽转换。

[0050] 图8R显示脂加氧酶和脂加氧酶的潜在同源物之间的序列比对。

具体实施方式

[0051] 启用能够选择性地检测目标蛋白质和测量目标蛋白质水平的灵敏多重测定具有重要的意义。目前,相关的蛋白质表达检测的技术严重依赖于传统的免疫化学技术,如何应对该技术中每个样品要求产生的数据量成为了一项挑战。

[0052] 大豆是价值数以十亿美元计的贸易品,这是由于其平衡蛋白质、淀粉、油组成——按重量比2:2:1。许多种子,包括大豆,所含的某些蛋白质是变应原和抗营养因子。因此有人担忧,在遗传修饰的大豆品种中,与通过传统育种开发的品种相比,变应原水平潜在可能改变。迄今为止作物中的变应原水平几乎完全是通过免疫测定法,例如酶联免疫吸附测定(ELISA)或IgE-免疫印迹等来测量的;然而,这些方法的问题是灵敏度和特异性有限,且变化性高。

[0053] 最近,人们对开发基于LC-MS/MS的方法以在单一分析中定量几种植物表达的蛋白质产生了兴趣。使用这些“特征肽”进行的分析包括通过定量目标蛋白质的几个高度特异性消化片段来跟踪蛋白质表达水平。这通常可以使用与选择反应监测(SRM)串联质谱联用的液相色谱法来完成。本文提供了改进的多重LC-MS/MS方法和系统,其使得在转基因和非转基因大豆中同时定量几种变应原蛋白成为可能。本文提供的方法和系统就包括准确度、精确度、线性、检测限和定量限等在内的分析优值(analytical figures of merit),以及包括样品通量、可转移性和易用性在内的其他考虑因素得到了验证。可以使用复用型式(multiplexing format)来定量变应原,并且可以例如在一天(二十四小时)窗口(从田间到测量的数值)内从田间收获样品、处理和分析/定量。此外,所提供的方法和系统的样品制备可以完全规模放大以实现高通量,因此能够在单一批次中分析数百个样品。

[0054] 代表性的大豆变应原包括例如Gly m 1,Gly m 3,Gly m 4,Gly m 5(β -伴大豆球蛋白),Gly m 6(大豆球蛋白)G1,Gly m 6(大豆球蛋白)G2,Gly m 6)G3,Gly m 6(大豆球蛋白)G4,Gly m 6(大豆球蛋白)前体,Gly m 6(大豆球蛋白)G4前体,Kunitz胰蛋白酶抑制剂1,Kunitz胰蛋白酶抑制剂3,Gly m Bd 28 K,Gly m Bd 30 K,Gly m 8(2S白蛋白),凝集素和脂加氧酶。

[0055] 代表性的小麦变应原包括例如前纤维蛋白(Tri a12),小麦脂质转移蛋白1(Tri a14),凝集素同工凝集素1(Tri a18), ω -5麦醇溶蛋白-种子储存蛋白(Tri a19),麦醇溶蛋白(Tri a20;NCBI登录号M10092,M11073,M11074,M11075,M11076,K03074和K03075),硫氧还蛋白(Tri a25),高分子量麦谷蛋白(Tri a26),低分子量麦谷蛋白(Tri a36),和 α -噻吩硫堇(purothionin)(Tri a37)。

[0056] 代表性的玉米变应原包括例如玉米脂转移蛋白(LTP)(Zea m14)和硫氧还蛋白(Zea m25)。

[0057] 代表性的玉米变应原包括,例如,水稻前纤维蛋白A(Ory s12)。

[0058] 在一些实施方案中,所提供的方法和系统使用偶联于串联质谱的液相色谱(LC-MS/MS)检测来自大豆的十六种不同变应原的蛋白质表达水平。在一些实施方案中,所述方法和系统能够分析单独的变应原,或分析每种变应原与其它蛋白质的组合以进行多重测定,用于植物基质中的定性和定量分析。

[0059] 在一些实施方案中,用于定量研究的质谱检测可以通过在三重四极杆质谱仪上进

行选择反应监测来实现。使用这种类型的仪器设备,对在源中形成的目标离子(肽)的初始质量选择,随后在MS的碰撞区域中解离该前体离子,然后是特定产物(子)离子的质量选择和计数。在一些实施方案中,用于定量研究的质谱检测可以使用选择反应监测(SRM)来完成。使用特定类型的仪器设备,在源中形成的目标离子的初始质量选择,随后在质谱仪(MS)的碰撞区域中解离该前体(蛋白质)离子,然后是特定产物(肽)离子的质量选择和计数。在一些实施方案中,单位时间的计数可以提供可积分的峰面积,从中可以确定分析物的量或浓度。在一些实施方案中,在具有HRAM能力的质谱仪上进行的定量用高分辨率精确质量(HRAM)监测可以包括但不限于混合四极-飞行时间、四极-轨道阱、离子阱-轨道阱、或四极-离子阱-轨道阱(三栅)质谱仪。使用特定类型的仪器设备,肽不经历碎裂条件,而是作为完整肽使用全扫描或靶向扫描模式(例如选择性离子监测模式或SIM)测量。可以通过为每个特定分析物产生提取离子色谱图来确定可积分的峰面积,并且可以计算分析物的量或浓度。数据的高分辨率和精确质量性质使得目标分析物(蛋白质和/或肽)的高度特异性和灵敏的离子信号成为可能。

[0060] 除非另有说明,本申请中,包括说明书和权利要求书中使用的以下术语,具有下面给出的定义。必须注意,如说明书和所附权利要求中所使用的,单数形式“一”,“一个”和“该”包括复数指示物,除非上下文另有明确指示。

[0061] 如本文所用,术语“生物限制”是指限制遗传修饰的植物或其遗传物质运动到指定区域。该术语包括物理的、物理化学的、生物学的限制,以及其他形式的可防止遗传修饰的植物在自然环境或人工生长条件中的存活、扩散或繁殖的限制。

[0062] 如本文所用,术语“复杂蛋白质样品”用于区分样品与纯化的蛋白质样品。复杂蛋白样品含有多种蛋白质,并可另外含有其他污染物。

[0063] 如本文所用的,通用术语“质谱”或“MS”是指任何合适的质谱方法、装置或配置,包括例如电喷雾电离(ESI)、基质辅助激光解吸/电离(MALDI)MS、MALDI-飞行时间(TOF)MS、大气压(AP)MALDI MS、真空MALDI MS、或其组合。质谱装置通过测量分子通过一组磁场和电场的飞行路径来测量分子的分子量(作为分子的质荷比的函数)。质荷比是在带电粒子的电动力学中广泛使用的物理量。特定肽的质荷比可以由本领域技术人员先验地计算。具有不同质荷比的两个粒子当受到相同的电场和磁场时,在真空中不会在相同的路径中移动。

[0064] 质谱仪器由三个模块组成:离子源,其将样品分子分离成离子;质量分析器,其通过施加电磁场来按照质量对离子进行分类;和检测器,其测量指示物的量的值,并因此提供用于计算每种离子存在的丰度的数据。该技术可以应用于定性和定量。这些包括鉴定未知化合物,确定分子中元素的同位素组成,通过观察化合物碎裂来确定其结构,以及定量样品中化合物的量。

[0065] 质谱方法和装置的详细概述可以在以下参考文献中找到,这些通过引用并入本文:Can和Annan(1997) Overview of peptide and protein analysis by mass spectrometry的潜在同源物之间的序列比对。收录于Current Protocols in Molecular Biology, Ausubel等人编, New York:Wiley, p.10.21.1-10.21.27; Paterson和Aebersold(1995) Electrophoresis 16:1791-1814; Patterson(1998) Protein identification and characterization by mass spectrometry. 收录于Current Protocols in Molecular Biology, Ausubel等人编, New York:Wiley, p.10.22.1-10.22.24; 和Domon和Aebersold

(2006) Science 312 (5771):212-17。

[0066] 如本文所用的术语,当同一样品中存在两种或更多种目的蛋白质和/或肽时,蛋白质和/或肽是“多重的”。

[0067] 如本文所使用的,“植物性状”可以指植物的任何单一特征或可量化的度量。

[0068] 如本文所用,短语“肽”或“肽”可以指 α -氨基酸以确定的顺序连接而形成的短聚合物。肽也可以通过用蛋白酶消化多肽例如蛋白质产生。

[0069] 如本文所使用的,短语“蛋白质”可以指由排列在直链中并通过相邻氨基酸残基的羧基和氨基之间的肽键连接在一起的氨基酸构成的有机化合物。蛋白质中的氨基酸序列由基因的序列定义,基因的序列以遗传密码编码。通常,遗传密码指定20个标准氨基酸,然而在某些生物体中,遗传密码可包括硒代半胱氨酸,在某些古细菌中,可包括吡咯赖氨酸。通常观察到蛋白质中的残基通过翻译后修饰作用被化学修饰,翻译后修饰作用可以在该蛋白质被细胞使用之前发生,或作为控制机制的一部分发生。蛋白质残基也可以根据本领域技术人员熟悉的技术通过设计加以修饰。如本文所用的,术语“蛋白质”涵盖包含天然存在的氨基酸、合成氨基酸、修饰的氨基酸或任何或所有上述的组合的直链。

[0070] 如本文所使用的,术语“单次注射”是指MS或LC-MS装置操作中的初始步骤。当蛋白质样品在单次注射中被引入装置时,整个该样品是在单个步骤中引入的。

[0071] 如本文所用,短语“特征肽”是指特定蛋白质的标识(短肽)序列。任何蛋白质可以含有平均10至100种特征肽。通常特征肽具有以下标准中的至少一种:容易通过质谱法检测;可预测且稳定地从液相色谱(LC)柱洗脱;通过反相高效液相色谱(RP-HPLC)富集;良好电离;良好碎裂;或上述者的组合。容易通过质谱法定量的肽通常具有以下标准中的至少一种:易于合成,能够被高度纯化($>97\%$),可溶于 $\leq 20\%$ 乙腈,低非特异性结合,抗氧化,抗合成后修饰,疏水性或疏水性指数 ≥ 10 且 ≤ 40 。疏水性指数可以根据Krokhin, Molecular and Cellular Proteomics 3 (2004) 908计算,其通过引用并入本文。已知疏水性指数小于10或大于40的肽可能无法通过RP-HPLC柱可重复地分开或洗脱。

[0072] 如本文所用的,术语“堆叠”是指掺入到植物基因组中的多个异源多核苷酸的存在。

[0073] 串联质谱:在串联质谱中,从目标分子产生的母离子可以在质谱仪中被过滤,并且母离子随后被碎裂以产生一个或多个子离子,子离子随后在第二个质谱程序中被分析(检测和/或定量)。在一些实施方案中,排除串联质谱的使用。在这些实施方案中,在所提供的方法和系统中不使用串联质谱。因此,在这些实施方案中既不产生母离子也不产生子离子。

[0074] 如本文所用的,术语“转基因植物”可以指在其基因组内包含异源多核苷酸的植物。通常,异源多核苷酸稳定整合在基因组内,使得多核苷酸被传递给后续世代。异源多核苷酸可以单独地或作为重组表达盒的一部分整合到基因组中。“转基因”在本文中用于包括任何这样的细胞、细胞系、愈伤组织、组织、植物部分或植物,其基因型已被异源核酸的存在改变,包括最初如此改变的那些转基因植物、以及从最初的转基因植物通过有性杂交或无性繁殖而生成的转基因植物。

[0075] 在本发明的实施中可以处理任何可提供有用的植物部分的植物。实例包括提供花、水果、蔬菜和谷物的植物。

[0076] 如本文所用,短语“植物”包括双子叶植物和单子叶植物。双子叶植物的实例包括

烟草,拟南芥,大豆,番茄,木瓜,卡诺拉,向日葵,棉花,苜蓿,马铃薯,葡萄,木豆,豌豆,芸苔,鹰嘴豆,甜菜,油菜,西瓜,甜瓜,胡椒,花生,南瓜,萝卜,菠菜,倭瓜,西兰花,卷心菜,胡萝卜,花椰菜,芹菜,大白菜,黄瓜,茄子和莴苣。单子叶植物的实例包括玉米,水稻,小麦,甘蔗,大麦,黑麦,高粱,兰花,竹子,香蕉,香蒲,百合,燕麦,洋葱,小米和黑小麦。水果的实例包括香蕉,菠萝,橙子,葡萄,葡萄柚,西瓜,甜瓜,苹果,桃,梨,猕猴桃,芒果,油桃,番石榴,柿子,鳄梨,柠檬,无花果,和浆果。花的例子包括满天星,康乃馨,大丽花,水仙,天竺葵,非洲菊,百合,兰花,牡丹,野胡萝卜(Queen Anne's lace),玫瑰,金鱼草或其他插花或装饰花,盆花和花球。

[0077] 在质谱方法中从复杂样品中鉴定单个蛋白质所允许的特异性是独特的,因为鉴定目标蛋白质仅需要目标蛋白质的序列。与其他形式的多重化相比,质谱法的独特之处是能够利用蛋白质的一级氨基酸序列的全长来靶向蛋白质的一级氨基酸序列的唯一标识类型部分,从而几乎消除非特异性检出。在本发明的一些实施方案中,利用独特地标识目标蛋白质的蛋白水解片段或一组蛋白水解片段来检测复杂蛋白质样品中的目标蛋白质。

[0078] 在一些实施方案中,所公开的方法能够通过单次质谱分析来定量复杂蛋白质样品中的多种蛋白质或测定其比例,而不是分别多次测量每种目标蛋白质,再将单独的结果汇编成一个样品结果。

[0079] 在一些实施方案中,本公开内容还提供了可用于开发和利用转基因植物技术的方法。具体地,公开的方法可以用于维持转基因植物的基因型经历连续世代。此外,本文公开的方法的一些实施方案可用于提供对如下所述的非转基因植物的高通量分析:该非转基因植物处于被来自邻近植物的转基因污染(例如通过异花授粉)的风险中。通过这些实施方案,可以促进和/或完成转基因的生物限制。在其它实施方案中,本文公开的方法可用于以高通量方式筛选植物转化程序的结果,以鉴定表现出期望的表达特征的转化体。

[0080] 质荷比可以使用四极分析器来确定。例如,在“四极”或“四极离子阱”仪器中,振荡射频场中的离子受到与施加在电极之间的DC电势、RF信号的振幅、以及 m/z 成比例的力。可以选择电压和振幅,使得只有具有特定 m/z 的离子可以行进四极杆的全长,而所有其他离子被偏转。因此,四极仪器可以充当注入仪器中的离子的“质量过滤器”和“质量检测器”。

[0081] 碰撞诱导解离(“CID”)通常用于产生用于进一步检测的子离子。在CID中,母离子通过与惰性气体(例如氦气)碰撞而获得能量,并且随后通过称为“单分子分解”的过程而碎裂。母离子中必须储存足够的能量,使得离子内的某些键由于能量增加而断裂。

[0082] 质谱仪通常为用户提供离子扫描;即在给定范围(例如10至1200amu)内每个 m/z 的相对丰度。分析物测定的结果,即质谱,可以通过许多本领域已知的方法与原始样品中的分析物的量关联。例如,鉴于取样和分析参数是被仔细控制的,可以将给定离子的相对丰度与将该相对丰度转化为原始分子的绝对量的表进行比较。或者,可以与样品一起运行分子标准(例如,内标和外标),并基于从那些标准产生的离子构建标准曲线。使用这种标准曲线,给定离子的相对丰度可以转化为原始分子的绝对量。许多其它用于将离子的存在或量与原始分子的存在或量相关联的方法是本领域普通技术人员公知的。

[0083] 电离方法的选择可以基于待测量的分析物、样品类型、检测器类型、阳性对阴性模式的选择等来确定。离子可以使用多种方法产生,包括但不限于:电子电离,化学电离,快速原子轰击,场解吸和基质辅助激光解吸电离(MALDI),表面增强激光解吸电离(SELDI),解吸

电喷雾离子化 (DESI), 光子电离, 电喷雾离子化和电感耦合等离子体。电喷雾离子化是指这样的方法, 其中令溶液通过一段短的毛细管, 管的末端施加高的正或负电位。到达管末端的溶液在溶剂蒸气中被蒸发 (雾化) 成非常小的溶液液滴的射流或喷雾。这种液滴的雾流过蒸发室, 蒸发室被加热以防止冷凝并蒸发溶剂。随着液滴变小, 电表面电荷密度增加, 直到这样的时间到来: 相同电荷之间的自然排斥导致离子和中性分子被释放。

[0084] LC的流出物可以直接且自动地 (即, “在线”) 注入到电喷雾装置中。在一些实施方案中, LC流出物中包含的蛋白质首先通过电喷雾离子化成母离子。

[0085] 各种不同的质量分析器可用于液相色谱-质谱联用 (LC-MS)。示例性质量分析器包括但不限于单四极杆、三重四极杆、离子阱、TOF (飞行时间) 和四极杆飞行时间 (Q-TOF)。

[0086] 四极质量分析器可以由4个彼此平行设置的圆棒组成。在四极杆质谱仪 (QMS) 中, 四极杆是仪器中负责基于质荷比 (m/z) 过滤样品离子的组成部分。基于离子在施加到杆上的振荡电场中的轨迹的稳定性, 在四极中分离离子。

[0087] 离子阱是电场或磁场的组合, 可捕获真空系统或管的某个区域中的离子。在操作离子的量子态时, 可以在质谱中使用离子阱。

[0088] 飞行时间质谱法 (TOFMS) 是一种质谱方法, 其中通过时间测量来确定离子的质荷比。离子通过已知强度的电场加速。该加速导致离子具有与任何其它具有相同电荷的离子相同的动能。离子的速度取决于质荷比。测量粒子随后到达相距已知距离的检测器所花费的时间。这个时间将取决于粒子的质荷比 (越重的粒子达到的速度越低)。从这个时间和已知的实验参数, 可以求出离子的质荷比。

[0089] 在一些实施方案中, 由所提供的方法和/或系统使用的特定仪器可以包括高碎裂模式和低碎裂模式 (或可选地, 非碎裂模式)。这样的不同模式可以包括交替扫描高能量和低能量获取方法以产生高分辨率质量数据。在一些实施方案中, 高分辨率质量数据可以包括产物数据集 (例如在高碎裂模式下从产物离子 (碎片离子) 得到的数据) 和前体数据集 (例如在低碎裂或非碎裂模式下从前体离子 (未碎裂离子) 得到的数据)。

[0090] 在一些实施方案中, 所提供的方法和/或系统使用质谱仪, 质谱仪包括可用于选择步骤的过滤装置、可用于碎裂步骤的碎裂装置、和/或可用于获取和/或质谱创建步骤中的一个或多个质量分析器。

[0091] 过滤装置和/或质量分析器可以包括四极。选择步骤和/或获取步骤和/或质谱创建步骤可涉及使用分辨四极 (resolving quadrupole)。另外或替代地, 过滤装置可包括二维或三维离子阱或飞行时间 (ToF) 质量分析器。该一个或多个质量分析器可以包括、或可以进一步包括下述的一种或多种: 飞行时间质量分析器和/或离子回旋共振质量分析器和/或轨道阱质量分析器和/或二维或三维离子阱。

[0092] 借助于基于质荷比 (m/z) 的选择的过滤可以通过使用能够基于 m/z 选择离子的质量分析器 (例如四极杆) 来实现; 或传输宽的 m/z 范围, 根据离子的 m/z 分离离子, 然后通过离子的 m/z 值选择目标离子。后者的示例是与计时离子选择器组合的飞行时间质量分析器。所提供的方法和/或系统可包括使用色谱技术, 例如液相色谱 (LC), 分离和/或分开一种或多种目的蛋白质, 例如从多种蛋白质中的两种或多种中分离和/或分开。该方法可以进一步包括测量目标蛋白质的洗脱时间和/或将测量的洗脱时间与预期的洗脱时间进行比较。

[0093] 另外或可选地, 可以使用离子迁移率技术分离目标蛋白质, 其可以使用离子迁移

小室进行。另外,可以通过离子迁移率漂移的次序或时间来选择目标蛋白质。该方法还可以包括测量感兴趣蛋白质的漂移时间和/或将测量的漂移时间与预期漂移时间进行比较。

[0094] 在一些实施方案中,所提供的方法和/或系统是无标记的,其中定量可以通过比较注射之间和各样品之间的目标前体或产物 m/z 值的峰强度或质谱峰下面积来实现。在一些实施方案中,可以利用内标标准化来应对任何已知的相关分析误差。另一种无标记的定量方法,谱图计数(spectral counting),包括以非冗余或冗余方式对每个给定肽获得的碎片离子谱或扫描的数目求和。然后将每种蛋白质的相关肽质谱相加,从而提供每种蛋白质的扫描数的度量,其与该蛋白质的丰度成比例。然后可以在样品/注射之间进行比较。

[0095] 在一些实施方案中,离子源选自:(1)电喷雾离子化(“ESI”)离子源;(2)大气压光电离(“APPI”)离子源;(3)大气压化学电离(“APCI”)离子源;(4)基质辅助激光解吸电离(“MALDI”)离子源;(5)激光解吸电离(“LDI”)离子源;(6)大气压电离(“API”)离子源;(7)硅上的解吸电离(“DIOS”)离子源;(8)电子轰击(“EI”)离子源;(9)化学电离(“CI”)离子源;(10)场电离(“FI”)离子源;(11)场解吸(“FD”)离子源;(12)电感耦合等离子体(“ICP”)离子源;(13)快速原子轰击(“FAB”)离子源;(14)液体二次离子质谱(“LSIMS”)离子源;(15)解吸电喷雾离子化(“DESI”)离子源;(16)镍-63放射性离子源;(17)大气压基质辅助激光解吸电离离子源;和(18)热喷射离子源。

[0096] 在一些实施方案中,所提供的方法和/或系统包括被配置为执行计算机程序元件的装置和/或控制系统,所述计算机程序元件包括用于令处理器执行用于实现所述方法的过程的计算机可读程序代码手段。

[0097] 在一些实施方案中,所提供的方法和/或系统使用交替的低能量和高能量扫描功能与液相色谱分离植物提取物组合。可以提供目标蛋白质的信息列表,包括但不限于前体离子的 m/z ,产物离子的 m/z ,保留时间,离子迁移率漂移时间和迁移率变化率。在LC分离过程中,和当靶离子洗脱到质谱仪中时(以及当检测到低能前体离子或检测到高能量产物离子或者激活保留时间窗时),所以方法的质量分析器和/或系统可以选择窄的 m/z 范围(具有可变化和可改变的宽度),以将离子传递到气室。因此,可以显著增强信噪比以用于目标蛋白质的定量。

[0098] 在一些实施方案中,在目标靶蛋白即将洗脱到质谱仪离子源中时的色谱保留时间,所提供的方法和/或系统的质量分析器可以根据靶前体例子选择窄的 m/z 范围(具有可变化和可改变的宽度)。然后将这些选定的离子转移到能够通过高碎裂模式和低碎裂模式(或非碎裂模式)之间交替和重复切换来离解离子的仪器级,在所述高碎裂模式下样品前体离子基本上被碎裂成产物离子,在所述低碎裂模式下样品前体离子基本上不碎裂。通常在两种模式下均获得高分辨率的、准确的质谱,并且在实验结束时,通过其色谱洗脱时间和任选的其他物理化学性质的拟合紧密程度来识别相关的前体和产物离子。与目标靶蛋白相关的前体离子或产物离子的信号强度可用于确定植物提取物中蛋白质的量。

[0099] 本领域技术人员将理解,在所提供的公开的基础上可以存在某些变化。因此,给出以下实施例用于说明本发明的目的,而不应解释为对本发明或权利要求的范围的限制。

[0100] 实施例

[0101] 实施例1

[0102] 所提供的方法和系统用于测定大豆种子中的内源性大豆变应原蛋白,包括Gly m

1, Gly m 3, Gly m 4, Gly m 5 (β -伴大豆球蛋白), Gly m 6, Kunitz胰蛋白酶抑制剂1, Kunitz胰蛋白酶抑制剂3, Gly m Bd 28 K, Gly m Bd 30 K和Gly m 8(2S白蛋白)。

[0103]

表1. 特征肽校准标准品的制备				
起始浓度 (ng/mL)	标准品	稀释鸡尾酒的 体积(μ L)	标准品体积 (μ L)	最终浓度 (ng/mL)
5880.00	Std 12	-	-	500.00
500.00	Std 11	200	200	250.00
250.00	Std 10	200	200	125.00
125.00	Std 9	200	200	62.50
62.50	Std 8	200	200	31.25
31.25	Std 7	200	200	15.63
15.63	Std 6	200	200	7.81
7.81	Std 5	200	200	3.91
3.91	Std 4	200	200	1.95
1.95	Std 3	200	200	0.98
0.98	Std 2	200	200	0.49
0.49	Std 1	2000	2000	0.24

[0104] 将 100 ± 0.5 mg研磨的大豆种子样品用己烷脱脂两次并干燥,然后用含有5M尿素, 2M硫脲, 50mM Tris pH 8.0和65mM DTT的提取缓冲液提取。将样品在水浴中超声处理30分钟,涡旋1分钟,超声处理另外30分钟,并在4℃以 $>3,000$ rpm离心10分钟。

[0105] 收集水性上清液并用提取缓冲液稀释以使内源性大豆变应原蛋白浓度达到校准标准范围。将稀释的提取物在95℃下与外加的1M Tris pH 8.0, 0.5M DTT和去离子水一起变性20分钟,随后在4℃下冷藏10分钟。变性的提取物在37℃下与0.5mg/mL胰蛋白酶温育过夜(~15小时)。消化反应用甲酸水(50/50v/v)淬灭并在4℃以 $>3,000$ rpm离心分钟。将消化的提取物的一份等分试样转移到自动进样器小瓶中,并与校准标准品一起分析液相色谱连同正离子电喷雾(ESI)串联质谱(LC-MS/MS)进行分析。特征肽的校准标准品如表1所列制备。

[0106] 在该实施例中,内源性大豆变应原的检测限(LOD)和定量限(LOQ)列于表2,其中LOD和LOQ代表蛋白浓度(ng/mg)。

[0107]

表2. 针对实施例1中的内源大豆变应原的检测限(LOD)和定量限(LOQ) (LOD和LOQ代表蛋白质浓度)			
变应原	特征肽	LOD (ng/mg)	LOQ (ng/mg)
Gly m 1	SYPSNATCPR (SEQ ID NO: 1)	0.23	0.46
Gly m 3	YMVIQGEPGA VIR (SEQ ID NO: 2)	0.20	0.39
Gly m 5	NILEASYDTK (SEQ ID NO: 3)	1.22	2.44
大豆球蛋白 G2	VTAPAMR (SEQ ID NO: 4)	1.46	2.92
大豆球蛋白 G3	NNNPFSFLVPPK (SEQ ID NO: 5)	1.58	3.16
大豆球蛋白 前体	ADFYNPK (SEQ ID NO: 6)	-	-
Kunitz胰蛋白 酶抑制剂1	GGGIEVDSTGK (SEQ ID NO: 7)	-	-
Kunitz胰蛋白 酶抑制剂3	GIGTLLSSPYR (SEQ ID NO: 8)	-	-
Gly m Bd 28 K	NKPQFLAGAASLLR (SEQ ID NO: 9)	5.70	11.40
Gly m Bd 30 K	GVITQVK (SEQ ID NO: 10)	1.15	2.30
Gly m 8	IMENQSEELEEK (SEQ ID NO: 11)	0.25	0.50

[0108] 变应原的浓度从特征肽的定量(例如用于LC-MS/MS的Analyst Bioanalytical软件)计算,并通过包括酶联免疫吸附测定(ELISA)的其它方法验证。使用统计分析比较来自不同样品的变应原的计算浓度,结果显示了样品之间的良好一致性。

[0109] 实施例2

[0110] 从包括NCBI,Phytozome和UniProt在内的公共数据库中鉴定出几种Gly m Bd 28K的同源蛋白质序列。对鉴定的序列(SEQ ID NO: 21和29-33)使用生物信息学工具加以分析,以鉴定可用的蛋白质序列之间的序列同源性和共有序列组成(参见图2L)。具体地,这涉及使用Vector NTI Align X比对工具,该工具执行CLUSTAL W型比对。从该分析出发,可以确定共有序列和/或代表性序列。

[0111] 一旦选择或测定了共有序列和/或代表性序列,将其在计算机上(in silico)消化,产生待通过LC-MS检测和测量的候选特征肽片段。根据本文提供的独特方法,基于可用的蛋白质序列之间的保守程度来选择特征肽,使得所选出的特征肽可以用于在公共序列数据库中鉴定出的蛋白质序列中定量所有或尽可能多的蛋白质同种型。因此,所选择的特征肽的定量不仅可以测量Gly m Bd 28 K本身,还可以测量与Gly m Bd 28 K高度同源的潜在变应原。

[0112] 将大豆种子样品研磨成细粉,用己烷脱脂两次,并用合适的测定缓冲液(例如5M尿素,2M硫脲,50mM Tris(pH 8.0),65mM DTT)提取。将样品在缓冲液中超声处理以提取蛋白质。将提取的蛋白质稀释,变性,然后通过加入胰蛋白酶并在37℃下孵育15-20小时

进行蛋白水解消化。消化反应用甲酸 (pH=1-2) 酸化, 并使用LC-MS/MS分析。

[0113] 所选出的特征肽可以用于Gly m Bd 28 K(单独或在多重测定型式中与其它蛋白质组合)的定性和定量分析。在该实施例中, 从所有肽可能性中选择了数个特征肽 (SEQ ID NO:9 NKPQFLAGAASLLR; SEQ ID NO:34 LGFIYDDELAER; SEQ ID NO:35 TVVEEIFSK; SEQ ID NO:36 MMQDQEEDDEEEK; SEQ ID NO:37 NAYGWSK; SEQ ID NO:38 ALHGGEYPPLSEPDIGVLLVK; SEQ ID NO:39 QGDVFVVP; SEQ ID NO:40 YFPFCQVASR; SEQ ID NO:41 TLMGPELSAAGVSEDTLR; SEQ ID NO:42 SFANDVMDVF), 并且这些特征肽的代表性定量显示于图2A-2J中。为SEQ ID NO:9 NKPQFLAGAASLLR合成了肽标准品用于定量和定性分析 (参见图2K)。合成肽可以直接作为蛋白质定量的分析参考标准。

[0114] 实施例3

[0115] 从包括NCBI, Phytozome和UniProt在内的公共数据库中鉴定出Gly m Bd30 K的几个同源蛋白质序列。使用生物信息学工具分析鉴定出的序列 (SEQ ID NO:22和43-44) 以鉴定可用的蛋白质序列之间的序列同源性和共有序列组成 (参见图3J)。具体地, 这包括使用Vector NTI Align X比对工具, 该工具执行CLUSTAL W型比对。从该分析出发, 可以确定共有序列和/或代表性序列。

[0116] 一旦选择或测定了共有序列和/或代表性序列, 对其进行计算机上消化以产生待通过LC-MS检测和测量的候选特征肽片段。根据本文提供的独特方法, 基于可用的蛋白质序列之间的保守程度选择特征肽, 使得所选出的特征肽可以用于在公共序列数据库中鉴定出的蛋白质序列中定量所有或尽可能多的蛋白质同种型。因此, 选定的特征肽的定量不仅可以测量Gly m Bd 30 K本身, 而且可以测量与Gly m Bd 30 K高度同源的潜在变应原。

[0117] 将大豆种子样品研磨成细粉, 用己烷脱脂两次, 并用合适的测定缓冲液 (例如5M尿素, 2M硫脲, 50mM Tris (pH 8.0), 65mM DTT) 提取。将样品在缓冲液中超声处理以提取蛋白质。将提取的蛋白质稀释, 变性, 然后通过加入胰蛋白酶并在37°C下孵育15-20小时进行蛋白水解消化。消化反应用甲酸 (pH=1-2) 酸化, 并使用LC-MS/MS分析。

[0118] 所选出的特征肽可以用于Gly m Bd 30 K(单独或在多重测定型式中与其它蛋白质组合)的定性和定量分析。在该实施例中, 从所有肽可能性中选择了数个特征肽 (SEQ ID NO:10 GVITQVK; SEQ ID NO:45 SILDLTLK; SEQ ID NO:46 FTTQK; SEQ ID NO:47 NNLNYIR; SEQ ID NO:48 FADITPQEFSK; SEQ ID NO:49 EQYSCDHPPASWDWR; SEQ ID NO:50 VTIDGYETLIMSDESTESETEQAFLSAILEQPISVSIDAK; 和SEQ ID NO:51 NTGNLLGVCGMNYFASYPTK), 并且这些特征肽的代表性定量显示于图3A-3H中。为SEQ ID NO:10 GVITQVK合成了肽标准品用于定量和定性分析 (参见图3I)。合成肽可以直接作为蛋白质定量的分析参考标准。

[0119] 实施例4

[0120] 从包括NCBI, Phytozome和UniProt在内的公共数据库中鉴定出Kunitz胰蛋白酶抑制剂1的几个同源蛋白质序列。使用生物信息学工具分析鉴定出的序列 (SEQ ID NO:23和53-54) 以鉴定可用的蛋白质序列之间的序列同源性和共有序列组成 (参见图4I)。具体地, 这涉及使用Vector NTI Align X比对工具, 该工具执行CLUSTAL W型比对。从该分析出发, 可以确定共有序列和/或代表性序列。

[0121] 一旦选择或测定了共有序列和/或代表性序列, 对其进行计算机上消化以产生待

通过LC-MS检测和测量的候选特征肽片段。根据本文提供的独特方法,基于可用的蛋白质序列之间的保守程度选择特征肽,使得所选出的特征肽可以用于在公共序列数据库中鉴定出的蛋白质序列中定量所有或尽可能多的蛋白质同种型。因此,所选择的特征肽的定量不仅可以测量Kunitz胰蛋白酶抑制剂1本身,而且还可以测量与Kunitz胰蛋白酶抑制剂1高度同源的潜在变应原。

[0122] 将大豆种子样品研磨成细粉,用己烷脱脂两次,并用合适的测定缓冲液(例如5M尿素,2M硫脲,50mM Tris (pH 8.0),65mM DTT)提取。将样品在缓冲液中超声处理以提取蛋白质。将提取的蛋白质稀释,变性,然后通过加入胰蛋白酶并在37℃下孵育15-20小时进行蛋白水解消化。消化反应用甲酸(pH=1-2)酸化,并使用LC-MS/MS分析。

[0123] 所选出的特征肽可以用于Kunitz胰蛋白酶抑制剂1(单独或在多重测定型式中与其它蛋白质组合)的定性和定量分析。在该实施例中,从所有肽可能性中选择出几种特征肽(SEQ ID NO:7 GGGIEVDSTGK;SEQ ID NO:55 EICPLTVVQSPNELDK;SEQ ID NO:56 EGLQAVK;SEQ ID NO:57 LVFCPQQAEDNK;SEQ ID NO:58 CEDIGIQIDDDGIR;SEQ ID NO:59 LVLSK;和SEQ ID NO:60 NKPLVVQFQK),并且这些特征肽的代表性定量显示在图4A-4G中。为SEQ ID NO:7 GGGIEVDSTGK合成了肽标准品用于定量和定性分析(见图4H)。合成肽可以直接作为蛋白质定量的分析参考标准。

[0124] 实施例5

[0125] 从包括NCBI,Phytozome和UniProt在内的公共数据库中鉴定出Kunitz胰蛋白酶抑制剂3的几个同源蛋白质序列。使用生物信息学工具分析鉴定出的序列(SEQ ID NO:24和62-63)以鉴定可用的蛋白质序列之间的序列同源性和共有序列组成(参见图5K)。具体地,这涉及使用Vector NTI Align X比对工具,该工具执行CLUSTAL W型比对。从该分析出发,可以确定共有序列和/或代表性序列。

[0126] 一旦选择或测定了共有序列和/或代表性序列,对其进行计算机上消化以产生待通过LC-MS检测和测量的候选特征肽片段。根据本文提供的独特方法,基于可用的蛋白质序列之间的保守程度选择特征肽,使得所选出的特征肽可以用于在公共序列数据库中鉴定出的蛋白质序列中定量所有或尽可能多的蛋白质同种型。因此,所选择的特征肽的定量不仅可以测量Kunitz胰蛋白酶抑制剂3本身,还可以测量与Kunitz胰蛋白酶抑制剂3高度同源的潜在变应原。

[0127] 将大豆种子样品研磨成细粉,用己烷脱脂两次,并用合适的测定缓冲液(例如5M尿素,2M硫脲,50mM Tris (pH 8.0),65mM DTT)提取。将样品在缓冲液中超声处理以提取蛋白质。将提取的蛋白质稀释,变性,然后通过加入胰蛋白酶并在37℃下孵育15-20小时进行蛋白水解消化。消化反应用甲酸(pH=1-2)酸化,并使用LC-MS/MS分析。

[0128] 所选出的特征肽可以用于Kunitz胰蛋白酶抑制剂3(单独或在多重测定型式中与其它蛋白质组合)的定性和定量分析。在该实施例中,从所有肽可能性中选出了几种特征肽(SEQ ID NO:8 GIGTISSPYR;SEQ ID NO:64 CPLTVVQSR;SEQ ID NO:65 NELDK;SEQ ID NO:66 IGENK;SEQ ID NO:67 DAMDGWFR;SEQ ID 68 LVFCPQQAEDDK;SEQ ID NO:69 CGDIGISIDHDDGTR;SEQ ID NO:70 LVVSK;和SEQ ID NO:71 NKPLVVQFQK),这些特征肽的代表性定量显示在5A-5I中。为SEQ ID NO:8 GIGTISSPYR合成肽标准品用于定量和定性分析(参见图5J)。合成肽可以直接作为蛋白质定量的分析参考标准。

[0129] 实施例6

[0130] 从包括NCBI,Phytozome和UniProt在内的公共数据库鉴定了Gly m 8(2S白蛋白)的数个同源蛋白质序列。使用生物信息学工具分析鉴定出的序列(SEQ ID NO:25和72-74),以鉴定可用的蛋白质序列之间的序列同源性和共有序列组成(参见图6J)。具体地,这涉及使用Vector NTI Align X比对工具,该工具执行CLUSTAL W型比对。从该分析出发,可以确定共有序列和/或代表性序列。

[0131] 一旦选择或测定了共有序列和/或代表性序列,对其进行计算机上消化以产生待通过LC-MS检测和测量的候选特征肽片段。根据本文提供的独特方法,基于可用的蛋白质序列之间的保守程度选择特征肽,使得所选出的特征肽可以用于在公共序列数据库中鉴定出的蛋白质序列中定量所有或尽可能多的蛋白质同种型。因此,选定的特征肽的定量不仅可以测量Gly m 8(2S白蛋白)本身,而且还可以测量与Gly m 8(2S白蛋白)高度同源的潜在变应原。

[0132] 将大豆种子样品研磨成细粉,用己烷脱脂两次,并用合适的测定缓冲液(例如5M尿素,2M硫脲,50mM Tris(pH 8.0),65mM DTT)提取。将样品在缓冲液中超声处理以提取蛋白质。将提取的蛋白质稀释,变性,然后通过加入胰蛋白酶并在37℃下孵育15-20小时进行蛋白水解消化。消化反应用甲酸(pH=1-2)酸化,并使用LC-MS/MS分析。

[0133] 所选出的特征肽可以用于Gly m 8(2S白蛋白)(单独或在多重测定型式中与其它蛋白质组合)的定性和定量分析。在该实施例中,从所有肽可能性中选择了几个特征肽(SEQ ID NO:11 IMENQSEEELEEK;SEQ ID NO:75 WQHQQDSCR;SEQ ID NO:76 QLQGVNLTPECK;SEQ ID NO:77 HIMEK;SEQ ID NO:78 DEDEEEEGHMQK;SEQ ID NO:79 CCTEMSELR;SEQ ID NO:80 ELINLATMCR;和SEQ ID NO:81 FGPMIQCDSLSSDD),这些标志肽的代表性定量显示于6A-6H中。为SEQ ID NO:11 IMENQSEEELEEK合成肽标准品用于定量和定性分析(参见图6I)。合成肽可以直接作为蛋白质定量的分析参考标准。

[0134] 实施例7

[0135] 从包括NCBI,Phytozome和UniProt在内的公共数据库鉴定出凝集素的数个同源蛋白质序列。使用生物信息学工具分析鉴定出的序列(SEQ ID NO:26和83-90)以鉴定可用蛋白序列之间的序列同源性和共有序列组成(参见图7F)。具体地,这涉及使用Vector NTI Align X比对工具,该工具执行CLUSTAL W型比对。从该分析出发,可以确定共有序列和/或代表性序列。

[0136] 一旦选择或测定了共有序列和/或代表性序列,对其进行计算机上消化以产生待通过LC-MS检测和测量的候选特征肽片段。根据本文提供的独特方法,基于可用的蛋白质序列之间的保守程度选择特征肽,使得所选出的特征肽可以用于在公共序列数据库中鉴定出的蛋白质序列中定量所有或尽可能多的蛋白质同种型。因此,选定的特征肽的定量不仅可以测量凝集素本身,而且还可以测量与凝集素高度同源的潜在变应原。

[0137] 将大豆种子样品研磨成细粉,用己烷脱脂两次,并用合适的测定缓冲液(例如5M尿素,2M硫脲,50mM Tris(pH 8.0),65mM DTT)提取。将样品在缓冲液中超声处理以提取蛋白质。将提取的蛋白质稀释,变性,然后通过加入胰蛋白酶并在37℃下孵育15-20小时进行蛋白水解消化。消化反应用甲酸(pH=1-2)酸化,并使用LC-MS/MS分析。

[0138] 所选出的特征肽可以用于凝集素(单独或在多重测定型式中与其它蛋白质组合)

的定性和定量分析。在该实施例中,从所有肽可能性中选择了几个特征肽(SEQ ID NO:91 VFSPNK;SEQ ID NO:92 ANSTNTVSFTVSK;SEQ ID NO:93 QQNLIFQGDAIISPSGVLR;和SEQ ID NO:94 TADGLAFFLAPVGSKPQSK),并且这些特征肽的代表性定量显示在图7A-7D中。为SEQ ID NO:91 VFSPNK合成肽标准品用于定量和定性分析(参见图7E)。合成肽可以直接作为蛋白质定量的分析参考标准。

[0139] 实施例8

[0140] 从包括NCBI,Phytozome和UniProt在内的公共数据库鉴定出脂加氧酶的数个同源蛋白质序列。使用生物信息学工具分析鉴定出的序列(SEQ ID NO:27和96-104)以鉴定可用蛋白序列之间的序列同源性和共有序列组成(参见图8R)。具体地,这涉及使用Vector NTI Align X比对工具,该工具执行CLUSTAL W型比对。从该分析出发,可以确定共有序列和/或代表性序列。

[0141] 一旦选择或测定了共有序列和/或代表性序列,对其进行计算机上消化以产生待通过LC-MS检测和测量的候选特征肽片段。根据本文提供的独特方法,基于可用的蛋白质序列之间的保守程度选择特征肽,使得所选出的特征肽可以用于在公共序列数据库中鉴定出的蛋白质序列中定量所有或尽可能多的蛋白质同种型。因此,选定的特征肽的定量不仅可以测量脂加氧酶本身,而且还可以测量与脂加氧酶高度同源的潜在变应原。

[0142] 将大豆种子样品研磨成细粉,用己烷脱脂两次,并用合适的测定缓冲液(例如5M尿素,2M硫脲,50mM Tris(pH 8.0),65mM DTT)提取。将样品在缓冲液中超声处理以提取蛋白质。将提取的蛋白质稀释,变性,然后通过加入胰蛋白酶并在37℃下孵育15-20小时进行蛋白水解消化。消化反应用甲酸(pH=1-2)酸化,并使用LC-MS/MS分析。

[0143] 所选出的特征肽可以用于脂加氧酶(单独或在多重测定型式中与其它蛋白质组合)的定性和定量分析。在该实施例中,从所有肽可能性中选择了几个特征肽(SEQ ID NO:105 SSDFLTYGIK;SEQ ID NO:106 GTVVLMPK;SEQ ID NO:107 NVLDFNAITSIGK;SEQ ID NO:108 GGVIDTATGILGQGVSLVGGVIDTATSFLGR;SEQ ID NO:109 IFFVNDTYLPSATPAPLLK;SEQ ID NO:110 DENFGHLK;SEQ ID NO:111 SLSHDVIPLFK;SEQ ID NO:112 SLYEGGIK;SEQ ID NO:113 TDGENVLQFPPPHVAK;SEQ ID NO:114 INSLPTAK;SEQ ID NO:115 TILFLK;SEQ ID NO:116 HLSVLHPIYK;SEQ ID NO:117 QSLINADGIIEK;SEQ ID NO:118 FIPAEGTPEYDEMVK;SEQ ID NO:119 ALEAFK;和SEQ ID NO:120 GIPNSISI),并且这些特征肽的代表性定量显示在图8A-8P中。为SEQ ID NO:105 SSDFLTYGIK合成肽标准品用于定量和定性分析(参见图8Q)。合成肽可以直接作为蛋白质定量的分析参考标准。

[0144] 序列表

[0145] SEQ ID NO:1 Gly m 1的示例性特征肽

[0146] SYPSNATCPR

[0147] SEQ ID NO:2 Gly m 3的示例性特征肽

[0148] YMVIQGEPGA VIR

[0149] SEQ ID NO:3 Gly m 5(β -伴大豆球蛋白)的示例性特征肽

[0150] NILEASYDTK

[0151] SEQ ID NO:4 Gly m 6(大豆球蛋白)G2的示例性特征肽

[0152] VTAPAMR

- [0153] SEQ ID NO:5 Gly m 6 (大豆球蛋白)G3的示例性特征肽
- [0154] NNNPFSFLVPPK
- [0155] SEQ ID NO:6 Gly m 6 (大豆球蛋白)前体的示例性特征肽
- [0156] ADFYNPK
- [0157] SEQ ID NO:7 Kunitz胰蛋白酶抑制剂1的示例性特征肽
- [0158] GGGIEVDSTGK
- [0159] SEQ ID NO:8 Kunitz胰蛋白酶抑制剂3的示例性特征肽
- [0160] GIGTIISSPYR
- [0161] SEQ ID NO:9 Gly m Bd 28 K的示例性特征肽
- [0162] NKPQFLAGAASLLR
- [0163] SEQ ID NO:10 Gly m Bd 30 K的示例性特征肽
- [0164] GVITQVK
- [0165] SEQ ID NO:11 Gly m 8 (2S白蛋白)的示例性特征肽
- [0166] IMENQSEELEEK
- [0167] SEQ ID NO:12 Gly m 1 ABA54898.1 [MW=12482.64Da]
- [0168] MGSKVVASVALLLSINILFISMVSSSSHYDPQPQPSHTALITRPSCPDLISICLNILGGS LGTVDDCCA LIGGLGDIEAIVCLCIQLRALGILNLRNLQLILNSCGRSYPSNATCPRT
- [0169] SEQ ID NO:13 Gly m 3 CAA11755.1 [MW=14100.07Da]
- [0170] MSWQAYVDDHLLCGIEGNHLTHAAIIGQDGSVWLQSTDFPQFKPEEITAIMNDFNEPGSLAPTGLYLGG TKYMVIIQGEPAVIRGKKPGGVTVKKTGAALIIGIYDEPMTPGQCNMVVERLGDYLIDQGY
- [0171] SEQ ID NO:14 Gly m 4P26987 [MW=16771.81Da]
- [0172] MGVFTFEDEINSPVAPATLYKALVTDADNVIPKALDSFKSVENVEGNGGPGTIKKITFLEDGETKFLVH KIESIDEANLGYSYSVVGAALPDTAEKITFDSKLVAGPNGGSAGKLT VKYETKGDAEPNQDELKTGKAKADALFKA IEAYLLAHPDYN
- [0173] SEQ ID NO:15 Gly m 5 (β -伴大豆球蛋白) 121281 [MW=70293.13Da] MMRARFPLLLLGLVFLASVSVSFGIAYWEKENPKHNKCLQSCNSERDSYRNQACHARCNNLKVEKEECEGEI PRPR PRPQHPEREPQQPGEKEEDEDEQPRPIPFPRPQPRQEEHEQREEQEWPRKEEKRGEKGSEEEDEDEDEEQDERQFP FPRPPHQKEERNEEDEDDEEQRESESESESELRRHNKNPFLFGSNRFETLFKNQYGRIRVLQRFNQRSPQLQNL R DYRILEFNSKPNTLLLPNHADADYLIVILNGTAILSLVNDDRDSYRLQSGDALRVPSGTTYVVNPDNNENLRLIT LAIPVKNPGRFESFFLSSTEAAQSYLQGF SRNILEASYDTKFEEINKVLFSREEGQQQGEQRLQESVIVEISKEQIR ALSKRAKSSSRKTISSEDKPFNLRSRDPIYSNKLKGFFEITPEKNPQLRDLDFLSIVDMNEGALLLPHFN SKAIVI LVINEGDANIELVGLKEQQQEQQEEQPLEVRKYRAELSEQDIFVIPAGYPVVNATSNLNF FAIGINAENNQRNFL AGSQDNVISQIPSQVQELAFPGSAQAVEKLLKNQRESYFVDAQPKKKEEGNKGRKGPLSSILRAFY
- [0174] SEQ ID NO:16 Gly m 6大豆球蛋白G1 121276 [MW=55706.34Da]
- [0175] MAKLVFSLCFLLFSGCCFAFSSREQPQQNECQIQKLNALKPDNRIESEGGLIETWNPNNKPFQCAGVAL SRCTLNRNALRRPSYTNGPQEIIYIQQKGIFGMIYPGCPSTFEPPQQPQQRGQSSRPQDRHQKIYNFREGDLIAVPT GVAWWWYNNEDTPVVAVSIIDTNSLENQLDQMPRRFYLAGNQEQEFLKYQQEQGGHQSQKGKHQQEEENEGGSILSG FTLEFLEHAFSVDKQIAKNLQGENEGEDKGAIVTVKGGLSVIKPPTDEQQQRPQEEEEEEEEDEK PQCKGKDKHCQRP RGSQSKSRRNGIDETICTMRLRHNIGQTSSPD IYNPQAGSVTTATSLDFPALS WLRLSAEFGSLRKNAMFVPHYNLN

ANSIIYALNGRALIQVVNCNGERVFDGELQEGRVLIVPQNFVVAARSQSDNFEYVSFKTNDTPMIGTLAGANSLLNALPEEVIQHTFNLSQQARQIKNNNPFKFLVPPQESQKRAVA

[0176] SEQ ID NO:17 Gly m 6大豆球蛋白G2 121277 [MW=54390.76Da]

[0177] MAKLVLSLCFLLFSGCFALREQAQQNECQIQKLNALKPDNRIESEGGFIETWNPNNKPFQCAGVALSRC
TLNRNALRRPSYTNQPQEIYIQQGNGIFGMIFPGCPSTYQEPQESQQRGRSQRPDQRHVKVHRFREGDLIAVPTGVA
WWMYNNEDTPVVAVSIIDTNSLENQLDQMPRRFYLAGNQEQEFLKYQQQQQGGSSQSKGKQQEEENEGSNILSGFAP
EFLKEAFGVNMQIVRNLCGENEEEDSGAIVTVKGGRLVTAPAMRKPPQEEEDDDDEEEQPQCVETDKGCQRQSKRSRN
GIDETICTMRLRQNIQGNSSPDIYNPQAGSITTATSLDFPALWLLKLSAQYGLSRKNAMFVPHYTLNANSIIYALNG
RALVQVVNCNGERVFDGELQEGGVIVPQNFVAAKSQSDNFEYVSFKTNDRPSIGNLAGANSLLNALPEEVIQHTF
NLKSQQARQVKNNNPFSLVPPQESQRRRAVA

[0178] SEQ ID NO:18 Gly m 6大豆球蛋白G3 121278 [MW=54241.73Da]

[0179] MAKLVLSLCFLLFSGCCFAFSFREQPQQNECQIQRLNALKPDNRIESEGGFIETWNPNNKPFQCAGVAL
SRCTLNRNALRRPSYTNAPQEIYIQQSGIFGMIFPGCPSTFEPPQKQSSRPQDRHQKIYHFREGDLIAVPTGFA
YWMYNNEDTPVVAVSLIDTNSFQNLQDQMPRRFYLAGNQEQEFLQYQPKQQGGTQSQKGRQQEEENEGGSILSGF
APEFLEHAFVVDQRQIVRKLCGENEEEEKGAIVTVKGGLSVISPTTEEQQQRPEEEEEKPCDEKDKHCQSQRNGIDE
TICTMRLRHNIQTSSPDIFNPQAGSITTATSLDFPALSWLKLSAQFGSLRKNAMFVPHYNLNANSIIYALNGRALV
QVVNCNGERVFDGELQEGQVLIVPQNFVAAARSQSDNFEYVSFKTNDRPSIGNLAGANSLLNALPEEVIQQTFLNRR
QQARQVKNNNPFSLVPPKESQRRVVA

[0180] SEQ ID NO:19 Gly m 6大豆球蛋白G4 121279 [MW=63587.16Da]

[0181] MGKPFTLSLSSCLLLLSSACFAISSSKLNECQLNNLNALPDHRVESEGGLIQTWNSQHPCLKAGVT
VSKLTLNRNGLHSPSYSPYPRMIIIAQKGALGVAIPGCPETFEPPQEESNRRGSRSSQKQLQDSHQKIRHFNEGDV
LVIPPSVPYWTYNTGDEPVVAISLLDTSNFNQLDQTPRVFYLAGNPDIETPETMQQQQQQKSHGGRKQGQHQQEEE
EEGGSVLSGFSKHFLAQSFNTNEDIAEKLSPDDEKQIVTVEGGLSVISPKWQEQQDEDEDEDEDEDEQIPSHPP
RRPSHGKREQDEDEDEDEDEKPRPSRPSQGKRNTGQDEDEDEDEDEQPRKSREWRSKKTQPRRPRQEEPRERGCETRN
GVEENICTLKLHENIARPSRADFYNPAGRI STLNSLTLPALRQFQLSAQYVVLYKNGIYSPHWNLNANSVIYVTRG
QGKVRVVNCQGNVFDGELRRGQLLVVPQNFVVAEQAGEQGFYIVFKTHHNAVTSYLDKDFRAIPSEVLASYNLR
QSQVSELKYEGNWGPLVNPESQQGSPRVKVA

[0182] SEQ ID NO:20 Gly m 6大豆球蛋白前体75221455 [MW=63876.47Da]

MGKPFTLSLSSCLLLLSSACFAISSSKLNECQLNNLNALPDHRVEFEGGLIQTWNSQHPCLKAGVTVSKLTLNR
NGLHLPSPSYSPYPRMIIIAQKGALQCKPGCPETFEPPQEESNRRGSRSSQKQLQDSHQKIRHFNEGDVLIIPPGVPY
WTYNTGDEPVVAISLLDTSNFNQLDQTPRVFYLAGNPDIETPETMQQQQQQKSHGGRKQGQHQQEEEEEGGSVLSG
FSKHFLAQSFNTNEDIAEKLQSPDDEKQIVTVEGGLSVISPKWQEQQDEDEDEDEDEDEQIPSHPPRRPSHGKRE
QDEDEDEDEDEKPRPSRPSQGKREQDQDQDEDEDEDEDEQPRKSREWRSKKTQPRRPRQEEPRERGCETRNGVEENICT
LKLHENIARPSRADFYNPAGRI STLNSLTLPALRQFQLSAQYVVLYKNGIYSPHWNLNANSVIYVTRGQGKVRVVN
CQGNVFDGELRRGQLLVVPQNFVVAEQAGEQGFYIVFKTHHNAVTSYLDKDFRAIPSEVLASYNLRQSQVSELK
YEGNWGPLVNPESQQGSPRVKVA

[0183] SEQ ID NO:21 Gly m Bd 28K 12697782 [MW=52944.36Da]

[0184] MGKNTTLLLLLVLCCHGVATTTMAFHDDDEGGDKKSPKSLFLMSNSTRVFKTDAGEMRVLKSHGGRIFYR
HMHIGFISMEPKSLFVPQYLDNLIIIFIRRGEAKLGFYDDELAERRLKTGDLYMIPSGSAFYLVNIGEGQRLHVIC

SIDPSTSLGLETFQSFYIGGGANSHSVLSGFEPAILLETAFNESRTVVEEIFSKELDGPIMFVDDSHAPSLWTKFLQL
KKDDKEQQLKKMMQDQEEDEEEKQTSRQSWRKLLTVFGKVNKIKENKDTAGSPASYNLYDDKKADFKNAYGWSKALH
GGEYPPLSEPDIGVLLVKLSAGSMLAPHVNPISDEYTIIVLSGYGELHIGYPNGSRAMKTKIKQGDVFVVPYFPFCQ
VASRDGPLEFFGFSTSAKKNKQFLAGAASLLRTLMPGELSAAFVSEDTLRRAVDAQHEAVILPSAWAAPPENAGK
LKMEEEPNAIRSFANDVVMDF

[0185] SEQ ID NO:22 Gly m Bd 30K 84371705 [MW=42757.81Da]

[0186] MGFLVLLLFSLGLSSSSSISTHRSLDLTKFTTQKQVSSLFQLWKSEHGRVYHNHEEEAKRLEIFK
NNLNYIRDMNANRKSPHSHRLGLNKFADITPQEFSSKYLQAPKDVSSQIKMANKKMKKEQYSCDHPPASWDWRKKG
ITQVKYQGGCGSGWAFSATGAIEAAHAATGDLVSLSEQLVDCVEESEGCVNGWHYQSFVLEHGGIATDDDPY
RAKEGRCKANKIQDKVTIDGYETLIMSDESTESETEQAFLSAILEQPISVSIDAKDFHLYTGGIYDGENCTSPYGIN
HFVLLVGYSADGVYWIAKNSWGEDWGEDGYIWIQRNTGNLLGVCGMNYFASYPTKEESETLV SARVKGHRRVDHS
PL

[0187] SEQ ID NO:23 KTI 1 125722 [MW=22545.94Da]

[0188] MKSTIFFALFLVCAFTISYLP SATAQFVLDTDDPLQNGGTYMLPVMRGKGGGIEVDSTGKEICPLTV
VQSPNELDKGIGLVFTSPLHALFIAERYPLSIKFGSFAVITLCAGMPTEWAIVEREGLQAVKLAARDTVDGWFNIE
VSREYNDYKLVFCPQQAEDNKCEDIGIQIDDDGIRRLVLSKNKPLVVQFQKFRSSTA

[0189] SEQ ID NO:24 KTI 3 125020 [MW=24005.29Da]

[0190] MKSTIFFLFLCAFTTSYLP SAIADFVLDNEGNPLENGGTYIILSDITAFGGIRAAPTGNERCPLTVVQ
SRNELDKGIGITIISSPYRIRFIAEGHPLSLKFD SFAVIMLCVGIPTEWSVVEDLPEGPAVKIGENKDAMDGWFRLE
VSDDEFNNYKLVFCPQQAEDDKCGDIGISIDHDDGTRRLVVSKNKPLVVQFQKLDKESLAKKNHGLSRSE

[0191] SEQ ID NO:25 Gly m 8 (2S 白蛋白) NP_001238443 [MW=18459.97Da]
MTKFTILLISLLFCIAHTCSASKWQHQQDSCRKQLQGVNLTPEKHIMEKIQGRGDDDDDDDDNHILRTMRGRINY
IRRNEGKDEDEEEGHMKCCTEMSEL RSPKCQCKALQKIMENQSEELEEKQKKMEKELINLATMCRFGPMIQCDL
SSDD

[0192] SEQ ID NO:26 凝集素ADC94422 [MW=30186.22Da]

[0193] MATSNFSIVLSLSLAFFLVLLTKANSTNTVSFTVSKFSPRQQNLIFQGDAIISPSGVLRLTKVDSIDVP
TTGSLGRALYATPIQIWDSETGKVASWATSFKFKVFSNKTADGLAFLAPVGSKPQSKGGFLGLFNSDSKNKSVQT
VAVEFDTYNAKWDPANRHIGIDVNSIKSVKTASWGLANGQIAQILITYDADTSLLVASLIHPSRKTSYILSETVSL
KSNLPEWVNIGFSATTGLNKGFEVTHDVSWSFASKLSDGSTSDTLDLPSFLLNEAI

[0194] SEQ ID NO:27 脂氧合酶CAA39604 [MW=96817.14Da]

[0195] MFGIFDKGQKIKGTVVLMKPNVLDFAITSIGKGGVIDTATGILGQGVSLVGGVIDTATSFLGRNISMQ
LISATQTDGSGNGKVGKEVYLEKHLPTLPTLGARQDAFSIFFEWDASFGIPGAFYIKNFMTDEFFLVSVKLEDIPNH
GTIEFVCNSWVYNFRSYKKNRIFFVNDTYLP SATPAPLLKYRKEELEVLRGDGTGKRKDFDRIYDYDVYNDLGNPDG
GDPRPILGSSSIYPYPRRVRTGRERTRDPNSEKPGEVYVPRDENFGHLKSSDFLTGIKSLSHDVIPLFKSAIFQL
RVTSSFEFESFEDVRSLYEGGIKLPTDILSQISPLPALKEIFRTDGENVLQFPPPHVAKVSKSGWMTDEEFAREVIAG
VNPNVIRRLQEFPPKSTLDPTLYGDQTSTITKEQLEINMGVTVVEALSTQRLFILDYQDAFIPYLTRINSLPTAKA
YATRTILFLKDDGTLKPLAIELSKPHPDGDNLGPESIVVLPATEGV DSTI WLLAKAHVIVNDSGYHQLVSHWLNTHA
VMEPFAIATNRHLSVLHPIYKLLYPHYRDTININGLARQSLINADGII EKSF LPGKYSIEMSSSVYKNWVFTDQALP
ADLVKRGLAIEDPSAPHGLRLVIEDYPYAVDGLIWD A IKTWVHEYVSLYYPTDAAVQQDTELQAWWKEAVEKGHGD

LKEKPWWPKMQTTEDLIQSCSIIVWTASALHAAVNFGQYPYGGILNRP TLARRFIPAEGTPEYDEMVKNPQKAYLR
TITPKFETLIDLSVIEILSRHASDEIYLGERETPNWTTDKKALEAFKFRFGSKLTGIEGKINARNSDPSLRNRTGPVQ
LPYTLLHRSSEGLTFKGIPNSISI

[0196] SEQ ID NO:28 Gly m Bd 28 K共有序列

[0197] VLCHGVATTTMAFHDDDEGGDKKSPKSLFLMSNSTRVFKTDAGEMRVLKSHGGRIFYRHHIGFISMEPK
SLFVPQYLDNLIIIFIRRGAKLGFYDDELAERRLKTGDLYMIPSGSAFYLVNIGEGQRLHVICSIDPSTSLGLET
FQSFYIGGGANSHSVLSGFEPAILLETAFNESRTVVEE IFSKELDGPIMFVDDSHAPSLWTKFLQLKKDDKEQQLKKM
MQDQEEDEEEKQTSRSWRKLLTVFGKVNEK IENKDTAGSPASYNLYDDKKADFKNAYGWSKALHGGEYPPLSEPD I
GVLLVKLSAGSMLAPHVNPISDEYTIIVLSGYGELHIGYPNGSKAMKTKIKQGDVFVVPYRFPFCQVASRDGPLEFFG
FSTSARKNKPQFLAGAASLLRTLMPPELSAAGVSEDTLRRAVDAQHEAVILPSAWAAPPENAGKLMEEEEP

[0198] SEQ ID NO:29 Gly m Bd 28 K Eric BAB21619 473aa

[0199] KTTLLLLLVFLCHGVATTTMAFHDDDEGGDKKSPKSLFLMSNSTRVFKTDAGEMRVLKSHGGRIFYRHHI
IGFISMEPKSLFVPQYLDNLIIIFIRRGAKLGFYDDELAERRLKTGDLYMIPSGSAFYLVNIGEGQRLHVICSID
PSTSLGLET FQSFYIGGGANSHSVLSGFEPAILLETAFNESRTVVEE IFSKELDGPIMFVDDSHAPSLWTKFLQLKKD
DKEQQLKKMMQDQEEDEEEKQTSRSWRKLLTVFGKVNEK IENKDTAGSPASYNLYDDKKADFKNAYGWSKALHGGE
YPPLSEPDIGVLLVKLSAGSMLAPHVNPISDEYTIIVLSGYGELHIGYPNGSRAMKTKIKQGDVFVVPYRFPFCQVAS
RDGPLEFFGFSTSARKNKPQFLAGAASLLRTLMPPELSAAGVSEDTLRRAVDAQHEAVILPSAWAAPPENAGKLM
EEEPNAIRSFANDVVMDF

[0200] SEQ ID NO:30 Gly m Bd 28 K Ping ACD36978.1 455aa

[0201] VLCHGVATTTMAFHDDDEGGDKKSPKSLFLMSNSTRVFKTDAGEMRVLKSHGGRIFYRHHIGFISMEPK
SLFVPQYLDNLIIIFIRRGAKLGFYDDELAERRLKTGDLYMIPSGSAFYLVNIGEGQRLHVICSIDPSTSLGLET
FQSFYIGGGANSHSVLSGFEPAILLETAFNESRTVVEE IFSKELDGPIMFVDDSHAPSLWTKFLQLKKDDKEQQLKKM
MQDQEEDEEEKQTSRSWRKLLTVFGKVNEK IENKDTAGSPASYNLYDDKKADFKNAYGWSKALHGGEYPPLSEPD I
GVLLVKLSAGSMLAPHVNPISDEYTIIVLSGYGELHIGYPNGSKAMKTKIKQGDVFVVPYRFPFCQVASRDGPLEFFGF
STSARKNKPQFLAGAASLLRTLMPPELSAAGVSEDTLRRAVDAQHEAVILPSAWAAPRKMQEAEEMESQMLLKLCCQ

[0202] SEQ ID NO:31 Gly m Bd 28 K ACD36975.1 373aa

[0203] LDSNLIIIFIRRGAKLGFYDDELAERRLKTGDLYMIPSGSAFYLVNIGEGQRLHVICSIDPSTSLGLE
TFQSFYIGGGANSHSVLSGFEPAILLETAFNESRTVVEE IFSKELDGPIMFVDDSHAPSLWTKFLQLKKDDKEQQLKK
MMQDQEEDEEEKQTSRSWRKLLTVFGKVNEK IENKDTAGSPASYNLYDDKKADFKNAYGWSKALHGGEYPPLSEPD
IGVLLVKLSAGSMLAPHVNPISDEYTIIVLSGYGELHIGYPNGSKAMKTKIKQGDVFVVPYRFPFCQVASRDGPLEFF
GFSTSARKNKPQFLAGAASLLRTLMPPELSAAGVSEDTLRRAVDAQHEAVILPSAWAAPPENAGKLMEEEEP

[0204] SEQ ID NO:32 Gly m Bd 28 K Ping ACD36976.1 373aa

[0205] LDSNLIIIFIRRGAKLGFYDDELAERRLKTGDLYMIPSGSAFYLVNIGEGQRLHVICSIDPSTSLGLE
TFQSFNIGGGANSHSVLSGFEPAILLETAFNESRTVVEE IFSKELDGPIMFVDDSHAPSLWTKFLQLKKDDKEQQLKK
MMQDQEEDEEEKQTSRSWRKLLTVFGKVNEK IENKDTAGSPASYNLYDDKKADFKNAYGWSKALHGGEYPPLSEPD
IGVLLVKLSAGSMLAPHVNPISDEYTIIVLSGYGELHIGYPNGSKAMKTKIKQGDVFVVPYRFPFCQVASRDGPLEFF
GFSTSARKNKPQFLAGAASLLRTLMPPELSAAGVSEDTLRRAVDAQHAAVILPSAWAAPPENAGKLMEEEEP

[0206] SEQ ID NO:33 Gly m Bd 28 K Ping ACD36974.1 320aa

[0207] LDSNLIIIFIRRGAKLGFYDDELAERRLKTGDLYMIPSGSAFYLVNIGEGQRLHVICSIDPSTSLGLE

TFQSFYIGGGANSHSVLSGFEPAILLETAFNESRTVVEEIFSKELDGPIMFVDDSHVPSLWTKFLQLKKDDKEQQLKK
MMQDQEEDEEEKQTSRSWRKLLTETVFGKVNEKIENKDTAGSPASYNLYDDKKADFKNAYGWSKALHGGEYPPLSEPD
IGVLLVKLSAGSMLAPHVNPISDEYTTIVLSGYGELHIGYPNGSKAMKTKIKQGDVFVVPRYFPFCQVASRDGPLEFF
GFSTSARKNKPQFLAGAASL

[0208] SEQ ID NO:34 LGFIYDDELAER

[0209] SEQ ID NO:35 TVVEEIFSK

[0210] SEQ ID NO:36 MMQDQEEDEEEK

[0211] SEQ ID NO:37 NAYGWSK

[0212] SEQ ID NO:38 ALHGGEYPPLSEPDIGVLLVK

[0213] SEQ ID NO:39 QGDVFVVPR

[0214] SEQ ID NO:40 YFPFCQVASR

[0215] SEQ ID NO:41 TLMGPELSAAGVSEDTLR

[0216] SEQ ID NO:42 SFANDVVMDF

[0217] SEQ ID NO:43 Gly m Bd 30 K Ping AAB09252.1 379aa (也充当共有序列)
MGFLVLLLFSLGLSSSSSISTHRSILDLDLTKFTTQKQVSSLFQLWKSEHGRVYHNHEEEAKRLEIFKNNSNYIRD
MNANRKSPHSHRLGLNKFADITPQEFSKKYLQAPKDVSSQIKMANKMKKEQYSCDHPPASWDWRKKGVITQVKYQG
GCGRGWAFSATGAIEAAHAIAITGDLVSLSEQLVDCVEESEGSYNGWQYQSFVLEHGGIATDDDYPYRAKEGRCK
ANKIQDKVTIDGYETLIMSDESTESETEQAFLSAILEQPISVSIDAKDFHLYTGGIYDGENCTSPYGINHFVLLVGY
GSADGVYDVIWIAKNSWGEDWGEDGYIWIQRNTGNLLGVCGMNYFASYPTKEESETLV SARVKGHRRVDHSPL

[0218] SEQ ID NO:44 Gly m Bd 30 K Ping P22895.1 379aa

[0219] MGFLVLLLFSLGLSSSSSISTHRSILDLDLTKFTTQKQVSSLFQLWKSEHGRVYHNHEEEAKRLEIFK
NNSNYIRDMNANRKSPHSHRLGLNKFADITPQEFSKKYLQAPKDVSSQIKMANKMKKEQYSCDHPPASWDWRKKG
VITQVKYQGGCGRGWAFSATGAIEAAHAIAITGDLVSLSEQLVDCVEESEGSYNGWQYQSFVLEHGGIATDDDYPY
RAKEGRCKANKIQDKVTIDGYETLIMSDESTESETEQAFLSAILEQPISVSIDAKDFHLYTGGIYDGENCTSPYGIN
HFVLLVGYGSADGVYDVIWIAKNSWGFWDGEDGYIWIQRNTGNLLGVCGMNYFASYPTKEESETLV SARVKGHRRVDHS
PL

[0220] SEQ ID NO:45 SILDLDTK

[0221] SEQ ID NO:46 FTTQK

[0222] SEQ ID NO:47 NNLNYIR

[0223] SEQ ID NO:48 FADITPQEFSK

[0224] SEQ ID NO:49 EQYSCDHPPASWDWR

[0225] SEQ ID NO:50 VTIDGYETLIMSDESTESETEQAFLSAILEQPISVSIDAK

[0226] SEQ ID NO:51 NTGNLLGVCGMNYFASYPTK

[0227] SEQ ID NO:52 KTI 1共有序列

[0228] MKSTIFFALFLVCFTTISYLP SATAQFVLDTDDDP LQNGGTYMLPVMRGKGGGIEGASTGKEICPLTV
VQSPNELDKGIGLVFSSPLHALFIAERYPLSIKFGSFAVISLCGGMPTKWAIVEREGLQAVTLAARDTVDGWFNIER
VSREYNDYKLVFCPQNAEDNKCEDIGIQIDNDGIRRLVLSKNKPLVVQFQKFRSSTA

[0229] SEQ ID NO:53 KTI 1 AAB23483.1 204aa

[0230] MKSTIFFALFLVCFTTISYLP SATAQFVLDTDDDP LQNGGTYMLPVMRGKSGGIEGNSTGKEICPLTV

VQSPNKHNGIGLVFKSPLHALFIAERYPLSIKFDSSFAVIPLCGVMPTKWAIVEREGLQAVTLAARDTVDGWFNIER
VSREYNDYYKLVFCPQEAEDNKCEDIGIQIDNDGIRRLVLSKNKPLVVEFQKFRSSTA

[0231] SEQ ID NO:54 KTI 1 CAA56343.1 208aa

[0232] MKSTTSLALFLLCALTSSYQPSATADIVFDTEGNPIRNGGTYVLPVIRGKGGGIEFAKTETETCPLTV
VQSPFEGLQRGLPLTISSPFKILDITEGLILSLKFHLCTPLSLNSFSVDYRYSQGSARRTPCQTHWLQKHNRWCWFRIQ
RASSESNNYYKLVFCTSNDDSSCGDIVAPIDREGNRPLIVTHDQNHPLLVQFQKVEAYESSTA

[0233] SEQ ID NO:55 EICPLTVVQSPNELDK

[0234] SEQ ID NO:56 EGLQAVK

[0235] SEQ ID NO:57 LVFCPQQAEDNK

[0236] SEQ ID NO:58 CEDIGIQIDDDGIR

[0237] SEQ ID NO:59 LVLSK

[0238] SEQ ID NO:60 NKPLVVQFQK

[0239] SEQ ID NO:61 KTI 3共有序列

[0240] MKSTIFFALFLFCFTTSYLPSAIAADFVLNDEGNPLENGGTYIILSDITAFGGIRAAPTGNERCPLTVV
QSRNELDKGIGTISSPYRIRFIAEGHPLSLKFDSFAVIMLCVGIPTEWSVVEDLPEGPAVKIGENKDAMDGWFRLE
RVSDDEFNNYKLVFCPQQAEDDKCGDIGISIDHDDGTRRLVVSKNKPLVVQFQKLDKESLAKKNHGLSRSE

[0241] SEQ ID NO:62 KTI 3 CAA45777.1 217aa

[0242] MKSTIFFALFLFCFTTSYLPSAIAADFVLNDEGNPLENGGTYIILSDITAFGGIRAAPTGNERCPLTVV
QSRNELDKGIGTISSPYRIRFIAEGHPLSLKFDSFAVIMLCVGIPTEWSVVEDLPEGPAVKIGENKDAMDGWFRLE
RVSDDEFNNYKLVFCPQQAEDDKCGDIGISIDHDDGTRRLVVSKNKPLVVQFQKLDKESLAKKNHGLSRSE

[0243] SEQ ID NO:63 KTI 3 CAA45778.1 217aa

[0244] MKSTIFFALFLFCFTTSYLPSAIAADFVLNDEGNPLDSGGTYIILSDITAFGGIRAAPTGNERCPLTVV
QSRNELDKGIGTISSPFIRIRFIAEGNPLRLKFDSFAVIMLCVGIPTEWSVVEDLPEGPAVKIGENKDAVDGWFRLE
RVSDDEFNNYKLVFCTQQAEDDKCGDIGISIDHDDGTRRLVVSKNKPLVVQFQKVDKESLAKKNHGLSRSE

[0245] SEQ ID NO:64 CPLTVVQSR

[0246] SEQ ID NO:65 NELDK

[0247] SEQ ID NO:66 IGENK

[0248] SEQ ID NO:67 DAMDGWFR

[0249] SEQ ID NO:68 LVFCPQQAEDDK

[0250] SEQ ID NO:69 CGDIGISIDHDDGTR

[0251] SEQ ID NO:70 LVVSK

[0252] SEQ ID NO:71 NKPLVVQFQK

[0253] SEQ ID NO:72 2S白蛋白Glyma13g36400.1 BLAST 174aa

[0254] MPPPSLHFTSPINSKMTKFTILLISLLFCIAHTCSASKWQHQQDSCRKQLQGVNLTPCEKHIMEKIQGR
GDDDDDDDDNHILRTMRGRINYIRRNEGKDEDEEEEGHMQKCCTEMSELRSPPKCQCKALQKIMENQSEELEEKQKK
KMEKELINLATMCRFGPMIQCDSLSSDD

[0255] SEQ ID NO:73 2S白蛋白NP_001234950 BLAST 158aa

[0256] MTKFTILLISLLFCIAHTCSASEWQHQQDSCRKQLQGVNLTPCEKHIMEKIQGRGDDDDDDDDNHILR
TMRGRINYIRRNEGKDEDEEEEGHMQKCRTEMSELRSPPKCQCKALQKIMENQSEELEEKQKKKMEKELINLATMCRF

GPMIQCDLSSDD

[0257] SEQ ID NO:74 2S白蛋白Glyma12g34160.1 BLAST 156aa

[0258] MTKLTILLIALLFIAHTCCASKWQQHQEQESCRLKGINLNPCEHIMEKIQAGRRGEDGSDEDHILIRT
MPGRINYIRKKEGKEEEEEGHMQKCCSEMSELKSPICQCKALQKIMDNQSEQLEGKEKKQMERELMNLAIRCLGPM
IGCDLSSDD

[0259] SEQ ID NO:75 WQHQQDSCR

[0260] SEQ ID NO:76 QLQGVNLTPCEK

[0261] SEQ ID NO:77 HIMEK

[0262] SEQ ID NO:78 DEDEEEEGHMQK

[0263] SEQ ID NO:79 CCTEMSELR

[0264] SEQ ID NO:80 ELINLATMCR

[0265] SEQ ID NO:81 FGPMIQCDLSSDD

[0266] SEQ ID NO:82 凝集素共有序列

[0267] MATSNFSIVLSLSLAFFLVLLTKANSTNTVSFTFSKFSRQPNLILQGDAAISSSGVLRLTKVDSNGVP
TSGSLGRALYAAPIQIWDSETGKVASWATSFKFNVFAPNKTADGLAFFLAPVGSKPQSKGGFLGLFNDSKDKSLQT
VAVEFDITYSNKKWDPANRHIGIDVNSIKSVKTASWGLANGQVAQILITYDAATSLLVASLIHPSRKTSYILSETVSL
KSNLPEWVSIGFSATTGLNEGSVETHDVISWSFASKLSDGSTSDALDLPFLLNEAI

[0268] SEQ ID NO:83 凝集素XP_003535884BLAST 280aa

[0269] MATSNFSIVLSLSLALFLMLLTKANSTNTVSFTTSKFSRQQNLILQGDAAISSSGVLRLTKVDSYGV
TSRSLGRALYAAPIQIWDSETGKVASWATSFKFNVFSPDKTADGLAFFLAPVGSKPQYKAGFLGLFNDSKNSLQT
VAVEFDITYNQKWDPASRHIGIDVNSIKSVKTAPWGFANGQVAQILITYNADTSLLVASLVHPSRKTSYILSETVSL
KSNLPEWVNVGFSATTGANKGFAETHDVFSWSFASKLSDGSTSDTLDLASFLLNEAI

[0270] SEQ ID NO:84 凝集素Glyma10g15480.1 BLAST

[0271] MATSNFSIVLSLSLALFLMLLTKANSTNTVSFTTSKFSRQQNLILQGDAAISSSGVLRLTKVDSYGV
TSRSLGRALYAAPIQIWDSETGKVASWATSFKFNVFSPDKTADGLAFFLAPVGSKPQYKAGFLGLFNDSKNSLQT
VAWDPASRHIGIDVNSIKSVKTAPWGFANGQVAQILITYNADTSLLVASLVHPSRKTSYILSETVSLKSNLPEWVNV
GFSATTGANKGFAETHDVFSWSFASKLSDGSTSDTLDLASFLLNEAI

[0272] SEQ ID NO:85 凝集素NP_001237210 BLAST 282aa

[0273] MATSNFSIVLSVSLAFLVLLTKAHSTDVTSFTFNKFNVPQPNIMLQKDASISSSGVLQLTKVGSNGVP
TSGSLGRALYAAPIQIWDSETGKVASWATSFKFNIFAPNKSNSADGLAFFLAPVGSQPSDDGFLGLFN SPLKDKSL
QTVAIEFDTF SNKKWDPANRHIGIDVNSIKSVKTASWGLSNGQVAEILVTYNAATSLLVASLIHPSKKT SYILSDTV
NLKSNLPEWVSVGFSATTGLHEGSVETHDVISWSFASKLSDGSSNDALDLPFVLNEAI

[0274] SEQ ID NO:86 凝集素Glyma02g18090.1 BLAST

[0275] MKVLCIIFEFKQIKAMATSNFSIVLSVSLAFLVLLTKAHSTDVTSFTFNKFNVPQPNIMLQKDASISS
SGVLQLTKVGSNGVPTSGSLGRALYAAPIQIWDSETGKVASWATSFKFNIFAPNKSNSADGLAFFLAPVGSQPSDD
GFLGLFN SPLKDKSLQTVAIEFDTF SNKKWDPANRHIGIDVNSIKSVKTASWGLSNGQVAEILVTYNAATSLLVASL
IHPSKKT SYILSDTVNLKSNLPEWVSVGFSATTGLHEGSVETHDVISWSFASKLSDGSSNDALDLPFVLNEAI

[0276] SEQ ID NO:87 凝集素ACU23599BLAST 282aa

[0277] MATSNFSIVLSVSLAFLVLLTKAHPTDVTFTFNKFNVPQPNIMLQKDASISSSGVLQLTKVGSNGVP

TSGSLGRALYAAPIQIWDSETGKVASWATSFKFNIFAPNKSNSADGLAFFLAPVGSQPPQSDDGFLGLFNSPLKDKSL
QTVAIEFDTFSNKKWDPANRHIGIDVDSIKSIKTASWGLSNGQVAEILVTYNAATSLLVASLIHPSKKTSYILSDTV
NLKSNLPEWVSVGFSATTGLHEGVSVDHVISWSFASKLSDGSSNDALDLPFVLNEAI

[0278] SEQ ID NO:88 凝集素CAH60173BLAST 280aa

[0279] MASSKFSTVISFSLALFLVLLTQANSTNIFSFNFQTFDSPNLIFQGDASVSSSGQLRLTKVKGNGKPTA
ASLGRAFYSAPIQIWDSTTGNVASFATSFTFNILAPNKSNSADGLAFALVPVGSQPKSNGGFLGLFDNATYDSSAQT
VAVEFDTYSNPKWDPENRHIGIDVNSIESIRTASWGLANGQNAEILITYDSSTKLLVASLVHPSRRTSYIVSERVDL
KSVLPEWVSIGFSATTGLLEGSIEHVDLSWSFASKLSDDTTSEGLNLANFVLNKIL

[0280] SEQ ID NO:89 凝集素Glyma10g01620.2 BLAST 228aa

[0281] MATSKFHTQKPLFVVLSVVVLLTMTKVNSTKPFLSPGTSSCRTNRTLILQGDALVTSSRKSLGRALYS
TPIHIWDSEIGSVASFAASFNFYASDIANLADGLAFFLAPIDTQPQTRGGYLGLYNNPSNSSWGLANDQVTNVL
TYDASTNLLVASLVHPSQRSSYILSDVLDLKVALPEWVRIGFSATTGLNVASETHDVHSWSFSSNLPGSSNTNPSD
FAIFI

[0282] SEQ ID NO:90 凝集素Glyma02g01590.1 BLAST 285aa

[0283] MATSKLKTQNVVLSLTLTLVLVLLTSKANSATVFSWNKFVPKQPNMILQGDALVTSSGKLQLNKV
DENGTPKPSLGRALYSTPIHIWDKETGSVASFAASFNFYAPDTKRLADGLAFFLAPIDTKPQTHAGYLGLFNEN
ESGDQVVAVEFDTRNSWDPPNPHINGINVNSIRSIKTTSWDLANNKVAKVLITYDASTLLVASLVYPSQRTSNILS
DVVDLKTSLPEWVRIGFSAATGLDIPGESHDVLSWSFASNLPHASSNIDPLDLTSFVLHEAI

[0284] SEQ ID NO:91 VFSPNK

[0285] SEQ ID NO:92 ANSTNTVSFTVSK

[0286] SEQ ID NO:93 QQNLIFQGDAIISPSGVLR

[0287] SEQ ID NO:94 TADGLAFFLAPVGSKPQSK

[0288] SEQ ID NO:95脂加氧酶共有序列

[0289]

MGGIFDKGQKIKGTVVLMKPNVLDFAITSIGKGGVIDTATGILGAGVSLVGGVIDTATAFLGRNISMQLISATQTD
GSGNGKVGEVYLEKHLPTLPTLGARQDAFSIFFEWDASFGIPGAFYIKNFMTEFFLVSVKLEDIPNHGTIEFVCN
SWVYNFKSYKKNRIFVNDTYLPSATPAPLLKYRKEELEVLRGDGTGKRKDFDRIYDYDVYNDLGNPDGGDPRPILG
GSSIYPYPRRVRTGRERTRDPNSEKPGEVYVPRDENFGHLKSSDFLTGIKSLSHDVIPLFKSAIFQLRVTSSEFD
SFEDVRSLYEGGIKLPTDILSQISPLPALKEIFRTDGENVLQFPPPHVAKVSKSGWMTDEEFAREMIAGVNPVIRR
LQEFPPKSTLDPTLYGDQTSTITKEQLEINMGGVTVVEALSTQRLFILDYQDAFIPYLTRINSLPTAKAYATRTILF
LKDDGTLKPLAIELSKPHPDGDNLGPEISVVLPALEGVDSTIWLLAKAHVIVNDSGYHQLVSHWLNTHAVMEPFAIA
TNRHLSVLHPIYKLLYPHYRDTININGLARQSLINADGIEKSFLPGKYSIEMSSSVYKNWVFTDQALPADLVKRL
AIEDPSAPHGLRLVIEDYPYAVDGLIWDIAIKTWVHEYVSLYYPTDAAVQQDTELQAWWKEAVEKGHGLDKDPWWP
KMQTTEDLIQSCSIIWTASALHAAVNFGQYPYGGILNRPRLARRFIPEEGTPEYDEMVKNPQKAYLRTITPKFET
LIDL SVIEILSRHASDEIYLGERDTPNWTDDKKALEAFKKFGSKLTGIEGKINARNSDPSLRNRTGPV
QLPYTLLHRSSEEGLTFGKIPNSISI

[0290] SEQ ID NO:96脂加氧酶2IUUK_A BLAST 864aa

[0291] MGGIFDKGQKIKGTVVLMKPNVLDFAITSIGKGGVIDTATGILGQGVSLVGGVIDTATSFLGRNISMQ
LISATQTDGSGNGKVGEVYLEKHLPTLPTLGARQDAFSIFFEWDASFGIPGAFYIKNFMTEFFLVSVKLEDIPNH

GTIEFVCNSWVYNFRSYKKNRIFFVNDTYLPSATPAPLLKYRKEEFVLRGDTGKRKDFDRIYDYDVYNDLGNPDG
GDPRPILGGCSIYPYPLRVRTGRERTRDPNSEKPGEVYVPRDENFGHLKSSDFLTGIGKSLSHDVIPLFKSAIFQL
RVTSSFEFESFEDVRSLYEGGIKLPTDILSQISPLPALKEIFRTDGENVLQFPPPHVAKVSKSGVMTDEEFAREVIAG
VNPVIRRLQEFPPKSTLDPTLYGDQTSTITKEQLEINMGVTVVEALSTQRLFILDYQDAFIPYLTRINSLPTAKA
YATRTILFLKDDGTLKPLAIELSKPHPDGDNLGPESIVVLPATEGVDSTIWLLAKAHVIVNDSGYHQLVSHWLNTHA
VMEPFAIATNRHLSVLHPIYKLLYPHYRDTININGLARQSLINADGIEKSFLPGKYSIEMSSSVYKNWVFTHQALP
ADLVKRG LAIEDPSAPHGLRLVIEDYPYAVDGLIWD AIKTWVHEYVSLYYPTDAAVQQDTELQAWWKEAVEKGHGD
LKEKPWWPKKQTTEDLIQSCSIIVWTASALHAAVNFGQYPYGGILNRP TLARRFI PAEGTPEYDEMVKNPQKAYLR
TITPKFETLIDLSVIEILSRHASDEIYLGERETPNWTTDKKALEAFKRFGSKLTGIEGKINARNSDPSLRNRTGPVQ
LPYTLLHRSSEGLTFKGIPNSISI

[0292] SEQ ID NO:97脂加氧酶NP_001238676 BLAST 864aa

[0293] MFGIFDKGQKIKGTVVLM PKNVLD FNAITSIGKGGVIDTATGILGQGVSLVGGVIDTATSFLGRNISMQ
LISATQTDGSGNGKVGKEVYLEKHLPTLPTLGARQDAFSIFFEWDASFGIPGAFYIKNFM TDEFFLVSVKLEDIPNH
GTIEFVCNSWVYNFRSYKKNRIFFVNDTYLPSATPAPLLKYRKEELEVLRGDTGKRKDFDRIYDYDVYNDLGNPDG
GDPRPILGGCSIYPYPLRVRTGRERTRDPNSEKPGEVYVPRDENFGHLKSSDFLTGIGKSLSHDVIPLFKSAIFQL
RVTSSFEFESFEDVRSLYEGGIKLPTDILSQISPLPALKEIFRTDGENVLQFPPPHVAKVSKSGWMTDEEFAREVIAG
VNPVIRRLQEFPPKSTLDPTLYGDQTSTITKEQLEINMGVTVVEALSTQRLFILDYQDAFIPYLTRINSLPTAKA
YATRTILFLKDDGTLKPLAIELSKPHPDGDNLGPESIVVLPATEGVDSTIWLLAKAHVIVNDSGYHQLVSHWLNTHA
VMEPFAIATNRHLSVLHPIYKLLYPHYRDTININGLARQSLINADGIEKSFLPGKYSIEMSSSVYKNWVFTHQALP
ADLVKRG LAIEDPSAPHGLRLVIEDYPYAVDGLIWD AIKTWVHEYVSLYYPTDAAVQQDTELQAWWKEAVEKGHGD
LKEKPWWPKKQTTEDLIQSCSIIVWTASALHAAVNFGQYPYGGILNRP TLARRFI PAEGTPEYDEMVKNPQKAYLR
TITPKFETLIDLSVIEILSRHASDEIYLGERETPNWTTDKKALEAFKRFGSKLTGIEGKINARNSDPSLRNRTGPVQ
LPYTLLHRSSEGLTFKGIPNSISI

[0294] SEQ ID NO:98脂加氧酶Glyma08g20220.1 BLAST 867aa

[0295] MLGLFDKSHKIKGTVVLM PKSVLD INDLNSVKNGGVSGIFGAVADVTGQIVDTATAIFSRNVSFK
LISATSTDAGNGKVGNETFLEKHLPTLPTLGDRRDAYDIHF EWDANFGIPGAFYIRNYTYDEFFLVSVTLEDIPNH
GTIHFVCNSWVYNFKDYDKKDRIFFANKTYLPSATPGPLVKYREEELKILRGDTGERKEHERIYDYDVYNDLGNPD
EDVKLARPVLGGSSTYPYPRRVRTGRKATKKDPKSERPASELYMPRDEKFGHLKSSDFLTGIGKSLSQKLLPSLENV
FDSDLTWNEFDSFEFVRDLYEGGIKVPTGVLSDISPIPIFKEIFRTDGESVLQFPPPHVVQVTKSAWMTDDEFAREM
IAGVNPVIRLLKEFPPQSKLDPSLYGDQSSTITKEHLEINMDGVTVVEALNGQRLFILDYQDAFMPYLTRINALPS
AKAYATRTILLKDDGTLKPLAIELSKPHPSGDNLGAESKVLPADQGVESTIWLLAKAHVIVNDSGYHQLMSHWLN
THAVTEPFIIATNRRLSVLHPIYKLLYPHYRDTININGLARNALINAGGVIEESFLPGRYSIEMSSAVYKNWVFTDQ
ALPVDLIKRGMAVEDPSSPHGLRLAVEDYPYAVDGLIWD AIKSWVQEYVSLYYPTDLAIQQDTELQAWWKEVVEKG
HGDLDKDPWWPKMQTRQELIQSCSTIIWIASALHAAVNFGQYPYGGFILNRP TLRRIPEPGTKEYDEMVESPQTA
YLRTITPKRQTIIDLT VIEILSRHASDEIYLGERDNPNTSDSKALEAFKKFGSKLAEIEGKITARNKDSNKKNRYG
PVQLPYTLLPTSEGLTFRGIPNSISI

[0296] SEQ ID NO:99脂加氧酶P24095 BLAST 864aa

[0297] MFGIFDKGQKIKGTVVLM PKNVLD FNAITSIGKGGVIDTATGILGQGVSLVGGVIDTATSFLGRNISMQ
LISATQTDGSGNGKVGKEVYLEKHLPTLPTLGARQDAFSIFFEWDASFGIPGAFYIKNFM TDEFFLVSVKLEDIPNH

GTIEFVCNSWVYNFRSYKKNRIFFVNDTYLPSATPAPLLKYRKEELEVLRGDGTGKRKDFDRIYDYDVYNDLGNPDG
GDPRPILGGSSIYPYPRRVRTGRERTRTDPNSEKPGEVYVPRDENFGHLKSSDFLTGIGKSLSHDVIPLFKSAIFQL
RVTSSFESEFEDVRSLEYEGGIKLPTDILSQISPLPALKEIFRTDGENVLQFPPPHVAKVSKSGWMTDEEFAREVIAG
VNPVIRRLQEFPPKSTLDPTLYGDQTSTITKEQLEINMGVTVVEEALSTQRLFILDYQDAFIPYLTRINSLPTAKA
YATRTILFLKDDGTLKPLAIELSKPHPDGDNLGPESIVVLPATEGVDSTIWLLAKAHVIVNDSGYHQLVSHWLNTA
VMEPFAIATNRHLSVLHPIYKLLYPHYRDTININGLARQSLINADGIEKSFLPGKYSIEMSSSVYKNWVFTDQALP
ADLVKRGLAIEDPSAPHGLRLVIEDYPYAVDGLIEWDAIKTWVHEYVSLYYPTDAAVQQDTELQAWWKEAVEKGHD
LKEKPWWPKMQTTEDLIQSCSIIVWTASALHAAVNFGQYPYGGILNRP TLARRFIPAEGTPEYDEMVKNPQKAYLR
TITPKFETLIDLSVIEILSRHASDEIYLGERETPNWTTDKKALEAFKRFGSKLTGIEGKINARNSDPSLRNRTGPVQ
LPYTLLHRSSEGLTFKGIPNSISI

[0298] SEQ ID NO:100脂加氧酶Glyma07g00900.1 BLAST 866aa

[0299] MTGGMFGRKGQKIKGTVVLM PKNVDFNAITSVGKGS AKDTATDFLGKGLDALGHAVDALTAFA GHSIS
LQLISATQTDGSGKGKVGNEAYLEKHLPTLPTLGARQEAFDINFEDASFGIPGAFYIKNFMTDEFFLVSVKLEDIP
NHGTINFCNSWVYNFKSYKKNRIFFVNDTYLPSATPAPLLKYRKEELEVLRGDGTGKRKDFDRIYDYDVYNDLGNP
DGGDPRPILGGSSIYPYPRRVRTGRERTRTDPNSEKPGEVYVPRDENFGHLKSSDFLTGIGKSLSHDVIPLFKSAIF
QLRVTSSFESEFEDVRSLEYEGGIKLPTDILSQISPLPALKEIFRTDGENVLQFPPPHVAKVSKSGWMTDEEFAREVI
AGVNPVIRRLQEFPPKSTLDPTLYGDQTSTITKEQLEINMGVTVVEEALSTQRLFILDYQDAFIPYLTRINSLPTA
KAYATRTILFLKDDGTLKPLAIELSKPHPDGDNLGPESIVVLPATEGVDSTIWLLAKAHVIVNDSGYHQLVSHWLNT
HAVMEPFAIATNRHLSVLHPIYKLLYPHYRDTININGLARQSLINADGIEKSFLPGKYSIEMSSSVYKNWVFTDQA
LPADLVKRGLAIEDPSAPHGLRLVIEDYPYAVDGLIEWDAIKTWVHEYVSLYYPTDAAVQQDTELQAWWKEAVEKGH
GDLKEKPWWPKMQTTEDLIQSCSIIVWTASALHAAVNFGQYPYGGILNRP TLARRFIPAEGTPEYDEMVKNPQKAY
LRTITPKFETLIDLSVIEILSRHASDEIYLGERETPNWTTDKKALEAFKRFGSKLTGIEGKINARNSDPSLRNRTGP
VQLPYTLLHRSSEGLTFKGIPNSISI

[0300] SEQ ID NO:101脂加氧酶NP_001235189 BLAST 859aa

[0301] MTGGMFGRKGQKIKGTVVLM PKNVDFNAITSVGKGS AKDTATDFLGKGLDALGHAVDALTAFA GHSIS
LQLISATQTDGSGKGKVGNEAYLEKHLPTLPTLGARQEAFDINFEDASFGIPGAFYIKNFMTDEFFLVSVKLEDIP
NHGTINFCNSWVYNFKSYKKNRIFFVNDTYLPSATPGPLVKYRQEELEVLRGDGTGKRKDFDRIYDYDIYNDLGNP
DGGDPRPIIGGSSNYPYPRRVRTGREKTRKDPNSEKPGEIVVPRDENFGHLKSSDFLTGIGKSLSQNVIPLFKSII
NLRTVTSSEFDSFDEVRLFEFGGIKLPTNLSQISPLPVLKEIFRTDGENVLQFPPPHVIRVSKSGWMTDDEFAREMI
AGVNPVIRRLQEFPPKSTLDPATYGDQTSTITKQQLINLGGVTVVEEASAHRLFILDYHDAFFPYLTKINSLPIA
KAYATRTILFLKDDGSLKPLAIELSKPATVSKVVL PATEGVESTIWLLAKAHVIVNDSGYHQLISHWLNTHAVMEPF
AIATNRHLSVLHPIYKLLYPHYKDTININGLARQSLINAGGIEQTFLPGKYSIEMSSSVYKNWVFTDQALPADLVK
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WWPKLQTVEDLIQSCSIIITWASALHAAVNFGQYPYGGYIVNRPTLARRFIP EEGTKEYDEMVKDPQKAYLRTITPK
FETLIDISVIEILSRHASDEVYLGQRDNPNWTTDSKALEAFKKFGNKLAEIEGKITQRNNDPSLKS RHGPVQLPYTL
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[0302] SEQ ID NO:102脂加氧酶Glyma07g03910.1 BLAST 865aa

[0303] MFGILGGNGKHKIKGTVVLM SKNVDFNEIVSTTQGGVLGAATGIFGAATGIVGGVVDGATAIFSRNIA
IQLISATKTDGLGNGKVKGQTYLEKHLPSLPTLGDRQDAFSVYFEWDNDFGIPGAFYIKNFMQSEFFLVSVTLEDIP

NHGTIHFVCNSWVYNAKSYKRDRIF FANKTYLPNETPTPLVKYRKEELENLRGDGKGERKEYDRIYDYDVYNDLGNP
DKSNDLARPVLGSSAYPYPRRGRTGRKPTTKDSKSESPSSSTYIPRDENFGHLKSSDFLT YGIKSIAQT VLP TFQS
AFGLNAEFD RFDDVRGLFEGGIHLPTDALSKISPLPVLKEIFRTDGEQVLKFPPPHVIKVS KSAWMTDEEFGREMLA
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AVIEPFVIATNRHLSVLHPIYKLLLPHYRDTMNINGLARQSLINAGGIIIEQSFLPGPFAVEMSSAVYKGVFTDQAL
PADLIKRGMAVEDPSSPYGLRLVIDDYPYAVDGLEIWSAIQTWVKDYVSLYYATDDAVKKDSELQAWWKEAVEKGHG
DLKDKPWWPKLNTLQDLIHICCI I IWTASALHAAVNFGQYPYGGF ILNRPTLTRRLPEPGTKEYGELTSNHQKAYL
RTITGKTEALVDLTVIEILSRHASDEVYLGQRDNPNWTD DTKAIQAFKKFGNKLKEIEDKISGRNKNSSLRNNGPA
QMPYTVLLPTS GEGLTFRGIPNSISI

[0304] SEQ ID NO:103 脂加氧酶Glyma07g03920.2 BLAST 868aa

[0305] MLIGSLLNRRPKIKGT VVLMTKNVFDVNDFMATTRGGPAAVAGGIFGAAQDIVGGIVDGATAIFSRNIA
IQLISATKSENALGHGKVGKLTYLEKHLPSLPNLGDRQDAFDVYFEWDESGFIPGAFYIKNYMQSEFFLVSKLEDV
PNHGTILFACNSWVYNAKLYKKDRIF FANKAYLPNDTPTPLVKYRKEELENLRGDGRGERKELDRIYDYDVYNDLGN
PDENDDLARPILGSSSKHPYPRRGRTGRKPTKKDPRCERPTSDTYIPRDENFGHLKSSDFLT YAIKSLTQNVLPQFN
TAFGFNNEFDSFEDVRCLFDGGVYLPDVL SKISPIPVLKEIFRTDGEQALKFPPPHVIKVRESEWMTDEEFGREML
AGVNPGMIQRLQEFPKSKLDPTTEFGDQSTITKEHLEINLGGLTVEQALKGNKLFILDHHD AFIIPFMNLINGLPTA
KSYATRTILFLQDDGTLKPLAIELSLPHPRGHEFGADSRVLP PAAVNSAEGTIWLIAKAYVAVNDTGYHQLISHWL
NTHATIEPFVIATNRHLSVLHPIHKLLLPHYRDTMNINALARQSLINADGV IERSFLPGKYSLEMSSAVYKSWVFTD
QALPADLIKRGMAIEDPCAPHGLRLVIEDYPYAVDGLEIWD AITWVKNYVSLYYPTDDAIKKDSELQAWWKEAVET
GHGDLKDKPWWPKLNT PQDLVHICSI I IWIASALHAAVNFGQYPYGGF ILNRPTLTRRFLPEPGSKEYEELSTNYQK
AYLRTITRKIEALVDLSVIEILSRHASDEIYLGKRDSDDWTD DQKAIQAFEKFGTKLKEIEAKINSRNKDSSLRNRN
GPVQMPYTVLLPTSEGLTFRGIPNSISI

[0306] SEQ ID NO:104 脂加氧酶Glyma08g20190.1 BLAST 860aa

[0307] MYSGVKGLFNRSQKVKGTVVLMRKNVLDINSITSVRGLIGTG INIIGSTIDGLTSFLGRSVCLQLISAT
KADGNGNGVVGKTYLEGII TSIPTLGAGQSAFTIHFEWDADMGIPGAFLIKNYMQVELFLVSLTLEDIPNQGS MHF
VCNSWVYNSKVYEKDRIF FASETYVPSETPGPLVTYREAELQALRGNGTGKRKEWDRVYDYDVYNDLGNPDSENF A
RPVLGGS LTHPYPRRGRTGRKPTKKDPNSEKPG EAYIPRDENFGHLKSSDFLT YGLKSLTRSFLPALKTVFDINFTP
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TILFLKDDGTLKPLAIELSLPHPGQQQLGAYSKVILPANQGVESTIWLLAKAHVIVNDSCYHQLISHWLNTHAVIEP
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KRGMAIEDSSCPNGLRLVIEDYPYAVDGLEIWD AIKTWVQEYVSLYYATND AIKKDHELQAWWKEVVEKGHGDLKDK
PWWPKMQTLQELIQSCSTIIWIASALHAAVNFGQYPYGGF ILNRPTLSRRWIPEEGTPEYDEM TKNPQKAYLRTITP
KFQALVDLSVIEILSRHASDEVYLGQRDNPNWTSNPKAIEAFKKFGKKLAEIETKISERNHDPNLRNRTGPAQLPYT
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[0308] SEQ ID NO:105 SSDFLT YGIK

[0309] SEQ ID NO:106 GTVVLM PK

[0310] SEQ ID NO:107 NVLDFNAITSIGK

[0311] SEQ ID NO:108 GGVIDTATGILGQGVSLVGGVIDTATSFLGR
[0312] SEQ ID NO:109 IFFVNDTYLPSATPAPLLK
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[0314] SEQ ID NO:111 SLSHDVIPLFK
[0315] SEQ ID NO:112 SLYEGGIK
[0316] SEQ ID NO:113 TDGENVLQFPPPHVAK
[0317] SEQ ID NO:114 INSLPTAK
[0318] SEQ ID NO:115 TILFLK
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[0320] SEQ ID NO:117 QSLINADGIIEK
[0321] SEQ ID NO:118 FIPAEGTPEYDEMVK
[0322] SEQ ID NO:119 ALEAFK
[0323] SEQ ID NO:120 GIPNSISI

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<110> T·J·阿曼

B·W·谢弗

R·C·希尔

G·单

<120> 用于变应原的选择性定量与检测的系统和方法

<130> 2971-12526.1PC (76268-W0-PCT)

<160> 120

<170> PatentIn version 3.5

<210> 1

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<212> PRT

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<400> 1

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<210> 6

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<213> 人工序列

<220>

<223> Gly m 6 (大豆球蛋白) 前体的示例性特征肽

<400> 6

Ala Asp Phe Tyr Asn Pro Lys

1 5

<210> 7

<211> 11

<212> PRT

<213> 人工序列

<220>

<223> Kunitz胰蛋白酶抑制剂1的示例性特征肽

<400> 7

Gly Gly Gly Ile Glu Val Asp Ser Thr Gly Lys

1 5 10

<210> 8

<211> 11

<212> PRT

<213> 人工序列

<220>

<223> Kunitz胰蛋白酶抑制剂3的示例性特征肽

<400> 8

Gly Ile Gly Thr Ile Ile Ser Ser Pro Tyr Arg

1 5 10

<210> 9

<211> 14

<212> PRT

<213> 人工序列

<220>

<223> Gly m Bd 28 K的示例性特征肽

<400> 9

Asn Lys Pro Gln Phe Leu Ala Gly Ala Ala Ser Leu Leu Arg

1 5 10

<210> 10

<211> 7

<212> PRT

<213> 人工序列

<220>

<223> Gly m Bd 30 K的示例性特征肽

<400> 10

Gly Val Ile Thr Gln Val Lys

1 5

<210> 11

<211> 12

<212> PRT

<213> 人工序列

<220>

<223> Gly m 8 (2S albumin)的示例性特征肽

<400> 11

Ile Met Glu Asn Gln Ser Glu Glu Leu Glu Glu Lys

1 5 10

<210> 12

<211> 119

<212> PRT

<213> 人工序列

<220>

<223> Gly m 1 ABA54898.1 [MW= 12482.64 Da]

<400> 12

Met Gly Ser Lys Val Val Ala Ser Val Ala Leu Leu Leu Ser Ile Asn

1	5	10	15
Ile Leu Phe	Ile Ser Met Val Ser Ser Ser Ser	His Tyr Asp Pro	Gln
20	25	30	
Pro Gln Pro	Ser His Val Thr Ala Leu Ile Thr Arg Pro	Ser Cys Pro	
35	40	45	
Asp Leu Ser	Ile Cys Leu Asn Ile Leu Gly Gly Ser Leu Gly Thr Val		
50	55	60	
Asp Asp Cys Cys Ala Leu Ile Gly Gly Leu Gly Asp Ile Glu Ala Ile			
65	70	75	80
Val Cys Leu Cys Ile Gln Leu Arg Ala Leu Gly Ile Leu Asn Leu Asn			
85	90	95	
Arg Asn Leu Gln Leu Ile Leu Asn Ser Cys Gly Arg Ser Tyr Pro Ser			
100	105	110	
Asn Ala Thr Cys Pro Arg Thr			
115			
<210> 13			
<211> 131			
<212> PRT			
<213> 人工序列			
<220>			
<223> Gly m 3 CAA11755.1 [MW= 14100.07 Da]			
<400> 13			
Met Ser Trp Gln Ala Tyr Val Asp Asp His Leu Leu Cys Gly Ile Glu			
1	5	10	15
Gly Asn His Leu Thr His Ala Ala Ile Ile Gly Gln Asp Gly Ser Val			
20	25	30	
Trp Leu Gln Ser Thr Asp Phe Pro Gln Phe Lys Pro Glu Glu Ile Thr			
35	40	45	
Ala Ile Met Asn Asp Phe Asn Glu Pro Gly Ser Leu Ala Pro Thr Gly			
50	55	60	
Leu Tyr Leu Gly Gly Thr Lys Tyr Met Val Ile Gln Gly Glu Pro Gly			
65	70	75	80
Ala Val Ile Arg Gly Lys Lys Gly Pro Gly Gly Val Thr Val Lys Lys			
85	90	95	
Thr Gly Ala Ala Leu Ile Ile Gly Ile Tyr Asp Glu Pro Met Thr Pro			
100	105	110	
Gly Gln Cys Asn Met Val Val Glu Arg Leu Gly Asp Tyr Leu Ile Asp			
115	120	125	
Gln Gly Tyr			

130
 <210> 14
 <211> 158
 <212> PRT
 <213> 人工序列
 <220>
 <223> Gly m 4 P26987 [MW= 16771.81 Da]
 <400> 14
 Met Gly Val Phe Thr Phe Glu Asp Glu Ile Asn Ser Pro Val Ala Pro
 1 5 10 15
 Ala Thr Leu Tyr Lys Ala Leu Val Thr Asp Ala Asp Asn Val Ile Pro
 20 25 30
 Lys Ala Leu Asp Ser Phe Lys Ser Val Glu Asn Val Glu Gly Asn Gly
 35 40 45
 Gly Pro Gly Thr Ile Lys Lys Ile Thr Phe Leu Glu Asp Gly Glu Thr
 50 55 60
 Lys Phe Val Leu His Lys Ile Glu Ser Ile Asp Glu Ala Asn Leu Gly
 65 70 75 80
 Tyr Ser Tyr Ser Val Val Gly Gly Ala Ala Leu Pro Asp Thr Ala Glu
 85 90 95
 Lys Ile Thr Phe Asp Ser Lys Leu Val Ala Gly Pro Asn Gly Gly Ser
 100 105 110
 Ala Gly Lys Leu Thr Val Lys Tyr Glu Thr Lys Gly Asp Ala Glu Pro
 115 120 125
 Asn Gln Asp Glu Leu Lys Thr Gly Lys Ala Lys Ala Asp Ala Leu Phe
 130 135 140
 Lys Ala Ile Glu Ala Tyr Leu Leu Ala His Pro Asp Tyr Asn
 145 150 155

<210> 15
 <211> 605
 <212> PRT
 <213> 人工序列
 <220>
 <223> Gly m 5 (beta-伴大豆球蛋白) 121281 [MW= 70293.13 Da]
 <400> 15
 Met Met Arg Ala Arg Phe Pro Leu Leu Leu Leu Gly Leu Val Phe Leu
 1 5 10 15
 Ala Ser Val Ser Val Ser Phe Gly Ile Ala Tyr Trp Glu Lys Glu Asn
 20 25 30

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

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

<210> 16

<211> 495

<212> PRT

<213> 人工序列

<220>

<223> Gly m 6 大豆球蛋白 G1 121276 [MW= 55706.34 Da]

<400> 16

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

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

<210> 17

<211> 485

<212> PRT

<213> 人工序列

<220>

<223> Gly m 6 大豆球蛋白 G2 121277 [MW= 54390.76 Da]

<400> 17

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

Ala	Leu	Ser	Arg	Cys	Thr	Leu	Asn	Arg	Asn	Ala	Leu	Arg	Arg	Pro	Ser
65					70					75					80
Tyr	Thr	Asn	Gly	Pro	Gln	Glu	Ile	Tyr	Ile	Gln	Gln	Gly	Asn	Gly	Ile
			85						90					95	
Phe	Gly	Met	Ile	Phe	Pro	Gly	Cys	Pro	Ser	Thr	Tyr	Gln	Glu	Pro	Gln
			100						105					110	
Glu	Ser	Gln	Gln	Arg	Gly	Arg	Ser	Gln	Arg	Pro	Gln	Asp	Arg	His	Gln
			115						120					125	
Lys	Val	His	Arg	Phe	Arg	Glu	Gly	Asp	Leu	Ile	Ala	Val	Pro	Thr	Gly
			130						135					140	
Val	Ala	Trp	Trp	Met	Tyr	Asn	Asn	Glu	Asp	Thr	Pro	Val	Val	Ala	Val
145									150					155	
Ser	Ile	Ile	Asp	Thr	Asn	Ser	Leu	Glu	Asn	Gln	Leu	Asp	Gln	Met	Pro
									165					170	
Arg	Arg	Phe	Tyr	Leu	Ala	Gly	Asn	Gln	Glu	Gln	Glu	Phe	Leu	Lys	Tyr
									180					185	
Gln	Gln	Gln	Gln	Gln	Gly	Gly	Ser	Gln	Ser	Gln	Lys	Gly	Lys	Gln	Gln
									195					200	
Glu	Glu	Glu	Asn	Glu	Gly	Ser	Asn	Ile	Leu	Ser	Gly	Phe	Ala	Pro	Glu
									210					215	
Phe	Leu	Lys	Glu	Ala	Phe	Gly	Val	Asn	Met	Gln	Ile	Val	Arg	Asn	Leu
225									230					235	
Gln	Gly	Glu	Asn	Glu	Glu	Glu	Asp	Ser	Gly	Ala	Ile	Val	Thr	Val	Lys
									245					250	
Gly	Gly	Leu	Arg	Val	Thr	Ala	Pro	Ala	Met	Arg	Lys	Pro	Gln	Gln	Glu
									260					265	
Glu	Asp	Asp	Asp	Asp	Glu	Glu	Glu	Gln	Pro	Gln	Cys	Val	Glu	Thr	Asp
									275					280	
Lys	Gly	Cys	Gln	Arg	Gln	Ser	Lys	Arg	Ser	Arg	Asn	Gly	Ile	Asp	Glu
									290					295	
Thr	Ile	Cys	Thr	Met	Arg	Leu	Arg	Gln	Asn	Ile	Gly	Gln	Asn	Ser	Ser
305									310					315	
Pro	Asp	Ile	Tyr	Asn	Pro	Gln	Ala	Gly	Ser	Ile	Thr	Thr	Ala	Thr	Ser
									325					330	
Leu	Asp	Phe	Pro	Ala	Leu	Trp	Leu	Leu	Lys	Leu	Ser	Ala	Gln	Tyr	Gly
									340					345	
Ser	Leu	Arg	Lys	Asn	Ala	Met	Phe	Val	Pro	His	Tyr	Thr	Leu	Asn	Ala
									355					360	
Asn	Ser	Ile	Ile	Tyr	Ala	Leu	Asn	Gly	Arg	Ala	Leu	Val	Gln	Val	Val

370	375	380
Asn Cys Asn Gly Glu Arg Val Phe Asp Gly Glu Leu Gln Glu Gly Gly		
385	390	395
Val Leu Ile Val Pro Gln Asn Phe Ala Val Ala Ala Lys Ser Gln Ser		400
	405	410
Asp Asn Phe Glu Tyr Val Ser Phe Lys Thr Asn Asp Arg Pro Ser Ile		415
	420	425
Gly Asn Leu Ala Gly Ala Asn Ser Leu Leu Asn Ala Leu Pro Glu Glu		430
	435	440
Val Ile Gln His Thr Phe Asn Leu Lys Ser Gln Gln Ala Arg Gln Val		445
	450	455
Lys Asn Asn Asn Pro Phe Ser Phe Leu Val Pro Pro Gln Glu Ser Gln		460
465	470	475
Arg Arg Ala Val Ala		480
	485	
<210> 18		
<211> 481		
<212> PRT		
<213> 人工序列		
<220>		
<223> Gly m 6 大豆球蛋白 G3 121278 [MW= 54241.73 Da]		
<400> 18		
Met Ala Lys Leu Val Leu Ser Leu Cys Phe Leu Leu Phe Ser Gly Cys		
1	5	10
Cys Phe Ala Phe Ser Phe Arg Glu Gln Pro Gln Gln Asn Glu Cys Gln		15
	20	25
Ile Gln Arg Leu Asn Ala Leu Lys Pro Asp Asn Arg Ile Glu Ser Glu		30
	35	40
Gly Gly Phe Ile Glu Thr Trp Asn Pro Asn Asn Lys Pro Phe Gln Cys		45
	50	55
Ala Gly Val Ala Leu Ser Arg Cys Thr Leu Asn Arg Asn Ala Leu Arg		60
65	70	75
Arg Pro Ser Tyr Thr Asn Ala Pro Gln Glu Ile Tyr Ile Gln Gln Gly		80
	85	90
Ser Gly Ile Phe Gly Met Ile Phe Pro Gly Cys Pro Ser Thr Phe Glu		95
	100	105
Glu Pro Gln Gln Lys Gly Gln Ser Ser Arg Pro Gln Asp Arg His Gln		110
	115	120
Lys Ile Tyr His Phe Arg Glu Gly Asp Leu Ile Ala Val Pro Thr Gly		125

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

Thr Phe Asn Leu Arg Arg Gln Gln Ala Arg Gln Val Lys Asn Asn Asn
 450 455 460
 Pro Phe Ser Phe Leu Val Pro Pro Lys Glu Ser Gln Arg Arg Val Val
 465 470 475 480
 Ala
 <210> 19
 <211> 562
 <212> PRT
 <213> 人工序列
 <220>
 <223> Gly m 6 大豆球蛋白 G4 121279 [MW= 63587.16 Da]
 <400> 19
 Met Gly Lys Pro Phe Thr Leu Ser Leu Ser Ser Leu Cys Leu Leu Leu
 1 5 10 15
 Leu Ser Ser Ala Cys Phe Ala Ile Ser Ser Ser Lys Leu Asn Glu Cys
 20 25 30
 Gln Leu Asn Asn Leu Asn Ala Leu Glu Pro Asp His Arg Val Glu Ser
 35 40 45
 Glu Gly Gly Leu Ile Gln Thr Trp Asn Ser Gln His Pro Glu Leu Lys
 50 55 60
 Cys Ala Gly Val Thr Val Ser Lys Leu Thr Leu Asn Arg Asn Gly Leu
 65 70 75 80
 His Ser Pro Ser Tyr Ser Pro Tyr Pro Arg Met Ile Ile Ile Ala Gln
 85 90 95
 Gly Lys Gly Ala Leu Gly Val Ala Ile Pro Gly Cys Pro Glu Thr Phe
 100 105 110
 Glu Glu Pro Gln Glu Gln Ser Asn Arg Arg Gly Ser Arg Ser Gln Lys
 115 120 125
 Gln Gln Leu Gln Asp Ser His Gln Lys Ile Arg His Phe Asn Glu Gly
 130 135 140
 Asp Val Leu Val Ile Pro Pro Ser Val Pro Tyr Trp Thr Tyr Asn Thr
 145 150 155 160
 Gly Asp Glu Pro Val Val Ala Ile Ser Leu Leu Asp Thr Ser Asn Phe
 165 170 175
 Asn Asn Gln Leu Asp Gln Thr Pro Arg Val Phe Tyr Leu Ala Gly Asn
 180 185 190
 Pro Asp Ile Glu Tyr Pro Glu Thr Met Gln Gln Gln Gln Gln Gln Lys
 195 200 205
 Ser His Gly Gly Arg Lys Gln Gly Gln His Gln Gln Glu Glu Glu Glu

210	215	220
Glu Gly Gly Ser Val Leu Ser Gly Phe Ser Lys His Phe Leu Ala Gln		
225	230	235
Ser Phe Asn Thr Asn Glu Asp Ile Ala Glu Lys Leu Glu Ser Pro Asp		240
	245	250
Asp Glu Arg Lys Gln Ile Val Thr Val Glu Gly Gly Leu Ser Val Ile		255
	260	265
Ser Pro Lys Trp Gln Glu Gln Gln Asp Glu Asp Glu Asp Glu Asp Glu		270
	275	280
Asp Asp Glu Asp Glu Gln Ile Pro Ser His Pro Pro Arg Arg Pro Ser		285
	290	300
His Gly Lys Arg Glu Gln Asp Glu Asp Glu Asp Glu Asp Glu Asp Lys		
305	310	315
Pro Arg Pro Ser Arg Pro Ser Gln Gly Lys Arg Asn Lys Thr Gly Gln		320
	325	330
Asp Glu Asp Glu Asp Glu Asp Glu Asp Gln Pro Arg Lys Ser Arg Glu		335
	340	345
Trp Arg Ser Lys Lys Thr Gln Pro Arg Arg Pro Arg Gln Glu Glu Pro		350
	355	360
Arg Glu Arg Gly Cys Glu Thr Arg Asn Gly Val Glu Glu Asn Ile Cys		365
	370	375
Thr Leu Lys Leu His Glu Asn Ile Ala Arg Pro Ser Arg Ala Asp Phe		380
385	390	395
Tyr Asn Pro Lys Ala Gly Arg Ile Ser Thr Leu Asn Ser Leu Thr Leu		400
	405	410
Pro Ala Leu Arg Gln Phe Gln Leu Ser Ala Gln Tyr Val Val Leu Tyr		415
	420	425
Lys Asn Gly Ile Tyr Ser Pro His Trp Asn Leu Asn Ala Asn Ser Val		430
	435	440
Ile Tyr Val Thr Arg Gly Gln Gly Lys Val Arg Val Val Asn Cys Gln		445
	450	455
Gly Asn Ala Val Phe Asp Gly Glu Leu Arg Arg Gly Gln Leu Leu Val		460
465	470	475
Val Pro Gln Asn Phe Val Val Ala Glu Gln Ala Gly Glu Gln Gly Phe		480
	485	490
Glu Tyr Ile Val Phe Lys Thr His His Asn Ala Val Thr Ser Tyr Leu		495
	500	505
Lys Asp Val Phe Arg Ala Ile Pro Ser Glu Val Leu Ala His Ser Tyr		510
	515	520
		525

Asn Leu Arg Gln Ser Gln Val Ser Glu Leu Lys Tyr Glu Gly Asn Trp
 530 535 540
 Gly Pro Leu Val Asn Pro Glu Ser Gln Gln Gly Ser Pro Arg Val Lys
 545 550 555 560
 Val Ala
 <210> 20
 <211> 562
 <212> PRT
 <213> 人工序列
 <220>
 <223> Gly m 6 大豆球蛋白前体 75221455 [MW= 63876.47 Da]
 <400> 20
 Met Gly Lys Pro Phe Thr Leu Ser Leu Ser Ser Leu Cys Leu Leu Leu
 1 5 10 15
 Leu Ser Ser Ala Cys Phe Ala Ile Ser Ser Ser Lys Leu Asn Glu Cys
 20 25 30
 Gln Leu Asn Asn Leu Asn Ala Leu Glu Pro Asp His Arg Val Glu Phe
 35 40 45
 Glu Gly Gly Leu Ile Gln Thr Trp Asn Ser Gln His Pro Glu Leu Lys
 50 55 60
 Cys Ala Gly Val Thr Val Ser Lys Leu Thr Leu Asn Arg Asn Gly Leu
 65 70 75 80
 His Leu Pro Ser Tyr Ser Pro Tyr Pro Arg Met Ile Ile Ile Ala Gln
 85 90 95
 Gly Lys Gly Ala Leu Gln Cys Lys Pro Gly Cys Pro Glu Thr Phe Glu
 100 105 110
 Glu Pro Gln Glu Gln Ser Asn Arg Arg Gly Ser Arg Ser Gln Lys Gln
 115 120 125
 Gln Leu Gln Asp Ser His Gln Lys Ile Arg His Phe Asn Glu Gly Asp
 130 135 140
 Val Leu Val Ile Pro Pro Gly Val Pro Tyr Trp Thr Tyr Asn Thr Gly
 145 150 155 160
 Asp Glu Pro Val Val Ala Ile Ser Leu Leu Asp Thr Ser Asn Phe Asn
 165 170 175
 Asn Gln Leu Asp Gln Thr Pro Arg Val Phe Tyr Leu Ala Gly Asn Pro
 180 185 190
 Asp Ile Glu Tyr Pro Glu Thr Met Gln Gln Gln Gln Gln Gln Lys Ser
 195 200 205
 His Gly Gly Arg Lys Gln Gly Gln His Gln Gln Glu Glu Glu Glu Glu

210	215	220
Gly Gly Ser Val Leu Ser Gly Phe Ser Lys His Phe Leu Ala Gln Ser		
225	230	235
Phe Asn Thr Asn Glu Asp Ile Ala Glu Lys Leu Gln Ser Pro Asp Asp		240
	245	250
Glu Arg Lys Gln Ile Val Thr Val Glu Gly Gly Leu Ser Val Ile Ser		255
	260	265
Pro Lys Trp Gln Glu Gln Gln Asp Glu Asp Glu Asp Glu Asp Glu Asp		270
	275	280
Asp Glu Asp Glu Gln Ile Pro Ser His Pro Pro Arg Arg Pro Ser His		285
	290	295
Gly Lys Arg Glu Gln Asp Glu Asp Glu Asp Glu Asp Glu Asp Lys Pro		300
305	310	315
Arg Pro Ser Arg Pro Ser Gln Gly Lys Arg Glu Gln Asp Gln Asp Gln		320
	325	330
Asp Glu Asp Glu Asp Glu Asp Glu Asp Gln Pro Arg Lys Ser Arg Glu		335
	340	345
Trp Arg Ser Lys Lys Thr Gln Pro Arg Arg Pro Arg Gln Glu Glu Pro		350
	355	360
Arg Glu Arg Gly Cys Glu Thr Arg Asn Gly Val Glu Glu Asn Ile Cys		365
	370	375
Thr Leu Lys Leu His Glu Asn Ile Ala Arg Pro Ser Arg Ala Asp Phe		380
385	390	395
Tyr Asn Pro Lys Ala Gly Arg Ile Ser Thr Leu Asn Ser Leu Thr Leu		400
	405	410
Pro Ala Leu Arg Gln Phe Gln Leu Ser Ala Gln Tyr Val Val Leu Tyr		415
	420	425
Lys Asn Gly Ile Tyr Ser Pro His Trp Asn Leu Asn Ala Asn Ser Val		430
	435	440
Ile Tyr Val Thr Arg Gly Gln Gly Lys Val Arg Val Val Asn Cys Gln		445
	450	455
Gly Asn Ala Val Phe Asp Gly Glu Leu Arg Arg Gly Gln Leu Leu Val		460
465	470	475
Val Pro Gln Asn Phe Val Val Ala Glu Gln Ala Gly Glu Gln Gly Phe		480
	485	490
Glu Tyr Ile Val Phe Lys Thr His His Asn Ala Val Thr Ser Tyr Leu		495
	500	505
Lys Asp Val Phe Arg Ala Ile Pro Ser Glu Val Leu Ala His Ser Tyr		510
	515	520
		525

Asn Leu Arg Gln Ser Gln Val Ser Glu Leu Lys Tyr Glu Gly Asn Trp
 530 535 540
 Gly Pro Leu Val Asn Pro Glu Ser Gln Gln Gly Ser Pro Arg Val Lys
 545 550 555 560
 Val Ala
 <210> 21
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 <223> Gly m Bd 28K 12697782 [MW= 52944.36 Da]
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 Met Gly Asn Lys Thr Thr Leu Leu Leu Leu Leu Phe Val Leu Cys His
 1 5 10 15
 Gly Val Ala Thr Thr Thr Met Ala Phe His Asp Asp Glu Gly Gly Asp
 20 25 30
 Lys Lys Ser Pro Lys Ser Leu Phe Leu Met Ser Asn Ser Thr Arg Val
 35 40 45
 Phe Lys Thr Asp Ala Gly Glu Met Arg Val Leu Lys Ser His Gly Gly
 50 55 60
 Arg Ile Phe Tyr Arg His Met His Ile Gly Phe Ile Ser Met Glu Pro
 65 70 75 80
 Lys Ser Leu Phe Val Pro Gln Tyr Leu Asp Ser Asn Leu Ile Ile Phe
 85 90 95
 Ile Arg Arg Gly Glu Ala Lys Leu Gly Phe Ile Tyr Asp Asp Glu Leu
 100 105 110
 Ala Glu Arg Arg Leu Lys Thr Gly Asp Leu Tyr Met Ile Pro Ser Gly
 115 120 125
 Ser Ala Phe Tyr Leu Val Asn Ile Gly Glu Gly Gln Arg Leu His Val
 130 135 140
 Ile Cys Ser Ile Asp Pro Ser Thr Ser Leu Gly Leu Glu Thr Phe Gln
 145 150 155 160
 Ser Phe Tyr Ile Gly Gly Gly Ala Asn Ser His Ser Val Leu Ser Gly
 165 170 175
 Phe Glu Pro Ala Ile Leu Glu Thr Ala Phe Asn Glu Ser Arg Thr Val
 180 185 190
 Val Glu Glu Ile Phe Ser Lys Glu Leu Asp Gly Pro Ile Met Phe Val
 195 200 205
 Asp Asp Ser His Ala Pro Ser Leu Trp Thr Lys Phe Leu Gln Leu Lys

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

<210> 22

<211> 379

<212> PRT

<213> 人工序列

<220>

<223> Gly m Bd 30K 84371705 [MW= 42757.81 Da]

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

Leu Val Gly Tyr Gly Ser Ala Asp Gly Val Asp Tyr Trp Ile Ala Lys
 305 310 315 320
 Asn Ser Trp Gly Glu Asp Trp Gly Glu Asp Gly Tyr Ile Trp Ile Gln
 325 330 335
 Arg Asn Thr Gly Asn Leu Leu Gly Val Cys Gly Met Asn Tyr Phe Ala
 340 345 350
 Ser Tyr Pro Thr Lys Glu Glu Ser Glu Thr Leu Val Ser Ala Arg Val
 355 360 365
 Lys Gly His Arg Arg Val Asp His Ser Pro Leu
 370 375
 <210> 23
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 <223> KTI 1 125722 [MW= 22545.94 Da]
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 Met Lys Ser Thr Ile Phe Phe Ala Leu Phe Leu Val Cys Ala Phe Thr
 1 5 10 15
 Ile Ser Tyr Leu Pro Ser Ala Thr Ala Gln Phe Val Leu Asp Thr Asp
 20 25 30
 Asp Asp Pro Leu Gln Asn Gly Gly Thr Tyr Tyr Met Leu Pro Val Met
 35 40 45
 Arg Gly Lys Gly Gly Gly Ile Glu Val Asp Ser Thr Gly Lys Glu Ile
 50 55 60
 Cys Pro Leu Thr Val Val Gln Ser Pro Asn Glu Leu Asp Lys Gly Ile
 65 70 75 80
 Gly Leu Val Phe Thr Ser Pro Leu His Ala Leu Phe Ile Ala Glu Arg
 85 90 95
 Tyr Pro Leu Ser Ile Lys Phe Gly Ser Phe Ala Val Ile Thr Leu Cys
 100 105 110
 Ala Gly Met Pro Thr Glu Trp Ala Ile Val Glu Arg Glu Gly Leu Gln
 115 120 125
 Ala Val Lys Leu Ala Ala Arg Asp Thr Val Asp Gly Trp Phe Asn Ile
 130 135 140
 Glu Arg Val Ser Arg Glu Tyr Asn Asp Tyr Lys Leu Val Phe Cys Pro
 145 150 155 160
 Gln Gln Ala Glu Asp Asn Lys Cys Glu Asp Ile Gly Ile Gln Ile Asp
 165 170 175

Asp Asp Gly Ile Arg Arg Leu Val Leu Ser Lys Asn Lys Pro Leu Val
 180 185 190
 Val Gln Phe Gln Lys Phe Arg Ser Ser Thr Ala
 195 200
 <210> 24
 <211> 216
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 <223> KTI 3 125020 [MW= 24005.29 Da]
 <400> 24
 Met Lys Ser Thr Ile Phe Phe Leu Phe Leu Phe Cys Ala Phe Thr Thr
 1 5 10 15
 Ser Tyr Leu Pro Ser Ala Ile Ala Asp Phe Val Leu Asp Asn Glu Gly
 20 25 30
 Asn Pro Leu Glu Asn Gly Gly Thr Tyr Tyr Ile Leu Ser Asp Ile Thr
 35 40 45
 Ala Phe Gly Gly Ile Arg Ala Ala Pro Thr Gly Asn Glu Arg Cys Pro
 50 55 60
 Leu Thr Val Val Gln Ser Arg Asn Glu Leu Asp Lys Gly Ile Gly Thr
 65 70 75 80
 Ile Ile Ser Ser Pro Tyr Arg Ile Arg Phe Ile Ala Glu Gly His Pro
 85 90 95
 Leu Ser Leu Lys Phe Asp Ser Phe Ala Val Ile Met Leu Cys Val Gly
 100 105 110
 Ile Pro Thr Glu Trp Ser Val Val Glu Asp Leu Pro Glu Gly Pro Ala
 115 120 125
 Val Lys Ile Gly Glu Asn Lys Asp Ala Met Asp Gly Trp Phe Arg Leu
 130 135 140
 Glu Arg Val Ser Asp Asp Glu Phe Asn Asn Tyr Lys Leu Val Phe Cys
 145 150 155 160
 Pro Gln Gln Ala Glu Asp Asp Lys Cys Gly Asp Ile Gly Ile Ser Ile
 165 170 175
 Asp His Asp Asp Gly Thr Arg Arg Leu Val Val Ser Lys Asn Lys Pro
 180 185 190
 Leu Val Val Gln Phe Gln Lys Leu Asp Lys Glu Ser Leu Ala Lys Lys
 195 200 205
 Asn His Gly Leu Ser Arg Ser Glu
 210 215

<210> 25

<211> 158

<212> PRT

<213> 人工序列

<220>

<223> Gly m 8 (2S albumin) NP_001238443 [MW= 18459.97 Da]

<400> 25

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

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<210> 26

<211> 280

<212> PRT

<213> 人工序列

<220>

<223> 凝集素 ADC94422 [MW= 30186.22 Da]

<400> 26

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

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

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

625	630	635	640
Leu Glu Ile Trp Asp Ala Ile Lys Thr Trp Val His Glu Tyr Val Ser			
	645	650	655
Leu Tyr Tyr Pro Thr Asp Ala Ala Val Gln Gln Asp Thr Glu Leu Gln			
	660	665	670
Ala Trp Trp Lys Glu Ala Val Glu Lys Gly His Gly Asp Leu Lys Glu			
	675	680	685
Lys Pro Trp Trp Pro Lys Met Gln Thr Thr Glu Asp Leu Ile Gln Ser			
	690	695	700
Cys Ser Ile Ile Val Trp Thr Ala Ser Ala Leu His Ala Ala Val Asn			
705	710	715	720
Phe Gly Gln Tyr Pro Tyr Gly Gly Leu Ile Leu Asn Arg Pro Thr Leu			
	725	730	735
Ala Arg Arg Phe Ile Pro Ala Glu Gly Thr Pro Glu Tyr Asp Glu Met			
	740	745	750
Val Lys Asn Pro Gln Lys Ala Tyr Leu Arg Thr Ile Thr Pro Lys Phe			
	755	760	765
Glu Thr Leu Ile Asp Leu Ser Val Ile Glu Ile Leu Ser Arg His Ala			
	770	775	780
Ser Asp Glu Ile Tyr Leu Gly Glu Arg Glu Thr Pro Asn Trp Thr Thr			
785	790	795	800
Asp Lys Lys Ala Leu Glu Ala Phe Lys Arg Phe Gly Ser Lys Leu Thr			
	805	810	815
Gly Ile Glu Gly Lys Ile Asn Ala Arg Asn Ser Asp Pro Ser Leu Arg			
	820	825	830
Asn Arg Thr Gly Pro Val Gln Leu Pro Tyr Thr Leu Leu His Arg Ser			
	835	840	845
Ser Glu Glu Gly Leu Thr Phe Lys Gly Ile Pro Asn Ser Ile Ser Ile			
	850	855	860
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<400> 28			
Val Leu Cys His Gly Val Ala Thr Thr Thr Met Ala Phe His Asp Asp			
1	5	10	15
Glu Gly Gly Asp Lys Lys Ser Pro Lys Ser Leu Phe Leu Met Ser Asn			

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

Gly Tyr Pro Asn Gly Ser Lys Ala Met Lys Thr Lys Ile Lys Gln Gly
 340 345 350
 Asp Val Phe Val Val Pro Arg Tyr Phe Pro Phe Cys Gln Val Ala Ser
 355 360 365
 Arg Asp Gly Pro Leu Glu Phe Phe Gly Phe Ser Thr Ser Ala Arg Lys
 370 375 380
 Asn Lys Pro Gln Phe Leu Ala Gly Ala Ala Ser Leu Leu Arg Thr Leu
 385 390 395 400
 Met Gly Pro Glu Leu Ser Ala Ala Phe Gly Val Ser Glu Asp Thr Leu
 405 410 415
 Arg Arg Ala Val Asp Ala Gln His Glu Ala Val Ile Leu Pro Ser Ala
 420 425 430
 Trp Ala Ala Pro Pro Glu Asn Ala Gly Lys Leu Lys Met Glu Glu Glu
 435 440 445
 Pro
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 Thr Thr Thr Met Ala Phe His Asp Asp Glu Gly Gly Asp Lys Lys Ser
 20 25 30
 Pro Lys Ser Leu Phe Leu Met Ser Asn Ser Thr Arg Val Phe Lys Thr
 35 40 45
 Asp Ala Gly Glu Met Arg Val Leu Lys Ser His Gly Gly Arg Ile Phe
 50 55 60
 Tyr Arg His Met His Ile Gly Phe Ile Ser Met Glu Pro Lys Ser Leu
 65 70 75 80
 Phe Val Pro Gln Tyr Leu Asp Ser Asn Leu Ile Ile Phe Ile Arg Arg
 85 90 95
 Gly Glu Ala Lys Leu Gly Phe Ile Tyr Asp Asp Glu Leu Ala Glu Arg
 100 105 110
 Arg Leu Lys Thr Gly Asp Leu Tyr Met Ile Pro Ser Gly Ser Ala Phe
 115 120 125
 Tyr Leu Val Asn Ile Gly Glu Gly Gln Arg Leu His Val Ile Cys Ser

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

Ala Gly Lys Leu Lys Met Glu Glu Glu Pro Asn Ala Ile Arg Ser Phe
 450 455 460
 Ala Asn Asp Val Val Met Asp Val Phe
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 35 40 45
 Ser His Gly Gly Arg Ile Phe Tyr Arg His Met His Ile Gly Phe Ile
 50 55 60
 Ser Met Glu Pro Lys Ser Leu Phe Val Pro Gln Tyr Leu Asp Ser Asn
 65 70 75 80
 Leu Ile Ile Phe Ile Arg Arg Gly Glu Ala Lys Leu Gly Phe Ile Tyr
 85 90 95
 Asp Asp Glu Leu Ala Glu Arg Arg Leu Lys Thr Gly Asp Leu Tyr Met
 100 105 110
 Ile Pro Ser Gly Ser Ala Phe Tyr Leu Val Asn Ile Gly Glu Gly Gln
 115 120 125
 Arg Leu His Val Ile Cys Ser Ile Asp Pro Ser Thr Ser Leu Gly Leu
 130 135 140
 Glu Thr Phe Gln Ser Phe Tyr Ile Gly Gly Gly Ala Asn Ser His Ser
 145 150 155 160
 Val Leu Ser Gly Phe Glu Pro Ala Ile Leu Glu Thr Ala Phe Asn Glu
 165 170 175
 Ser Arg Thr Val Val Glu Glu Ile Phe Ser Lys Glu Leu Asp Gly Pro
 180 185 190
 Ile Met Phe Val Asp Asp Ser His Ala Pro Ser Leu Trp Thr Lys Phe
 195 200 205
 Leu Gln Leu Lys Lys Asp Asp Lys Glu Gln Gln Leu Lys Lys Met Met
 210 215 220

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

325	330	335
Glu Asp Thr Leu Arg Arg Ala Val Asp Ala Gln His Glu Ala Val Ile		
340	345	350
Leu Pro Ser Ala Trp Ala Ala Pro Pro Glu Asn Ala Gly Lys Leu Lys		
355	360	365
Met Glu Glu Glu Pro		
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Asp Leu Tyr Met Ile Pro Ser Gly Ser Ala Phe Tyr Leu Val Asn Ile		
35 40 45		
Gly Glu Gly Gln Arg Leu His Val Ile Cys Ser Ile Asp Pro Ser Thr		
50 55 60		
Ser Leu Gly Leu Glu Thr Phe Gln Ser Phe Asn Ile Gly Gly Gly Ala		
65 70 75 80		
Asn Ser His Ser Val Leu Ser Gly Phe Glu Pro Ala Ile Leu Glu Thr		
85 90 95		
Ala Phe Asn Glu Ser Arg Thr Val Val Glu Glu Thr Phe Ser Lys Glu		
100 105 110		
Leu Asp Gly Pro Ile Met Phe Val Asp Asp Ser His Ala Pro Ser Leu		
115 120 125		
Trp Thr Lys Phe Leu Gln Leu Lys Lys Asp Asp Lys Glu Gln Gln Leu		
130 135 140		
Lys Lys Met Met Gln Asp Gln Glu Glu Asp Glu Glu Glu Lys Gln Thr		
145 150 155 160		
Ser Arg Ser Trp Arg Lys Leu Leu Glu Thr Val Phe Gly Lys Val Asn		
165 170 175		
Glu Lys Ile Glu Asn Lys Asp Thr Ala Gly Ser Pro Ala Ser Tyr Asn		
180 185 190		
Leu Tyr Asp Asp Lys Lys Ala Asp Phe Lys Asn Ala Tyr Gly Trp Ser		

195	200	205
Lys Ala Leu His Gly Gly Glu Tyr Pro Pro Leu Ser Glu Pro Asp Ile		
210	215	220
Gly Val Leu Leu Val Lys Leu Ser Ala Gly Ser Met Leu Ala Pro His		
225	230	235
Val Asn Pro Ile Ser Asp Glu Tyr Thr Ile Val Leu Ser Gly Tyr Gly		240
245	250	255
Glu Leu His Ile Gly Tyr Pro Asn Gly Ser Lys Ala Met Lys Thr Lys		
260	265	270
Ile Lys Gln Gly Asp Val Phe Val Val Pro Arg Tyr Phe Pro Phe Cys		
275	280	285
Gln Val Ala Ser Arg Asp Gly Pro Leu Glu Phe Phe Gly Phe Ser Thr		
290	295	300
Ser Ala Arg Lys Asn Lys Pro Gln Phe Leu Ala Gly Ala Ala Ser Leu		
305	310	315
Leu Arg Thr Leu Met Gly Pro Glu Leu Ser Ala Ala Phe Gly Val Ser		
325	330	335
Glu Asp Thr Leu Arg Arg Ala Val Asp Ala Gln His Ala Ala Val Ile		
340	345	350
Leu Pro Ser Ala Trp Ala Ala Pro Pro Glu Asn Ala Gly Lys Leu Lys		
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Met Glu Glu Glu Pro		
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Asp Leu Tyr Met Ile Pro Ser Gly Ser Ala Phe Tyr Leu Val Asn Ile		
35	40	45
Gly Glu Gly Gln Arg Leu His Val Ile Cys Ser Ile Asp Pro Ser Thr		
50	55	60
Ser Leu Gly Leu Glu Thr Phe Gln Ser Phe Tyr Ile Gly Gly Gly Ala		

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

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<400> 39

Gln Gly Asp Val Phe Val Val Pro Arg

1 5

<210> 40

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Tyr Phe Pro Phe Cys Gln Val Ala Ser Arg

1 5 10

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Thr Leu Met Gly Pro Glu Leu Ser Ala Ala Phe Gly Val Ser Glu Asp

1 5 10 15

Thr Leu Arg

<210> 42

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Ser Phe Ala Asn Asp Val Val Met Asp Val Phe

1 5 10

<210> 43

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<400> 43

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

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260	265	270
Val Ser Ile Asp Ala Lys Asp Phe His Leu Tyr Thr Gly Gly Ile Tyr		
275	280	285
Asp Gly Glu Asn Cys Thr Ser Pro Tyr Gly Ile Asn His Phe Val Leu		
290	295	300
Leu Val Gly Tyr Gly Ser Ala Asp Gly Val Asp Tyr Trp Ile Ala Lys		
305	310	315
Asn Ser Trp Gly Glu Asp Trp Gly Glu Asp Gly Tyr Ile Trp Ile Gln		
325	330	335
Arg Asn Thr Gly Asn Leu Leu Gly Val Cys Gly Met Asn Tyr Phe Ala		
340	345	350
Ser Tyr Pro Thr Lys Glu Glu Ser Glu Thr Leu Val Ser Ala Arg Val		
355	360	365
Lys Gly His Arg Arg Val Asp His Ser Pro Leu		
370	375	
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20	25	30
Lys Phe Thr Thr Gln Lys Gln Val Ser Ser Leu Phe Gln Leu Trp Lys		
35	40	45
Ser Glu His Gly Arg Val Tyr His Asn His Glu Glu Glu Ala Lys Arg		
50	55	60
Leu Glu Ile Phe Lys Asn Asn Ser Asn Tyr Ile Arg Asp Met Asn Ala		
65	70	75
Asn Arg Lys Ser Pro His Ser His Arg Leu Gly Leu Asn Lys Phe Ala		
85	90	95
Asp Ile Thr Pro Gln Glu Phe Ser Lys Lys Tyr Leu Gln Ala Pro Lys		
100	105	110
Asp Val Ser Gln Gln Ile Lys Met Ala Asn Lys Lys Met Lys Lys Glu		
115	120	125
Gln Tyr Ser Cys Asp His Pro Pro Ala Ser Trp Asp Trp Arg Lys Lys		

130	135	140
Gly Val Ile Thr Gln Val Lys Tyr Gln Gly Gly Cys Gly Arg Gly Trp		
145	150	155
Ala Phe Ser Ala Thr Gly Ala Ile Glu Ala Ala His Ala Ile Ala Thr		
165	170	175
Gly Asp Leu Val Ser Leu Ser Glu Gln Glu Leu Val Asp Cys Val Glu		
180	185	190
Glu Ser Glu Gly Ser Tyr Asn Gly Trp Gln Tyr Gln Ser Phe Glu Trp		
195	200	205
Val Leu Glu His Gly Gly Ile Ala Thr Asp Asp Asp Tyr Pro Tyr Arg		
210	215	220
Ala Lys Glu Gly Arg Cys Lys Ala Asn Lys Ile Gln Asp Lys Val Thr		
225	230	235
Ile Asp Gly Tyr Glu Thr Leu Ile Met Ser Asp Glu Ser Thr Glu Ser		
245	250	255
Glu Thr Glu Gln Ala Phe Leu Ser Ala Ile Leu Glu Gln Pro Ile Ser		
260	265	270
Val Ser Ile Asp Ala Lys Asp Phe His Leu Tyr Thr Gly Gly Ile Tyr		
275	280	285
Asp Gly Glu Asn Cys Thr Ser Pro Tyr Gly Ile Asn His Phe Val Leu		
290	295	300
Leu Val Gly Tyr Gly Ser Ala Asp Gly Val Asp Tyr Trp Ile Ala Lys		
305	310	315
Asn Ser Trp Gly Phe Asp Trp Gly Glu Asp Gly Tyr Ile Trp Ile Gln		
325	330	335
Arg Asn Thr Gly Asn Leu Leu Gly Val Cys Gly Met Asn Tyr Phe Ala		
340	345	350
Ser Tyr Pro Thr Lys Glu Glu Ser Glu Thr Leu Val Ser Ala Arg Val		
355	360	365
Lys Gly His Arg Arg Val Asp His Ser Pro Leu		
370	375	
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1 5

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Phe Thr Thr Gln Lys

1 5

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Asn Asn Leu Asn Tyr Ile Arg

1 5

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<211> 11

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Phe Ala Asp Ile Thr Pro Gln Glu Phe Ser Lys

1 5 10

<210> 49

<211> 15

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<400> 49

Glu Gln Tyr Ser Cys Asp His Pro Pro Ala Ser Trp Asp Trp Arg

1 5 10 15

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<400> 50

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

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Asn	Thr	Gly	Asn	Leu	Leu	Gly	Val	Cys	Gly	Met	Asn	Tyr	Phe	Ala	Ser
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Tyr	Pro	Thr	Lys												
			20												

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<400> 52

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

Gly	Leu	Val	Phe	Ser	Ser	Pro	Leu	His	Ala	Leu	Phe	Ile	Ala	Glu	Arg
				85					90					95	
Tyr	Pro	Leu	Ser	Ile	Lys	Phe	Gly	Ser	Phe	Ala	Val	Ile	Ser	Leu	Cys
			100					105					110		
Gly	Gly	Met	Pro	Thr	Lys	Trp	Ala	Ile	Val	Glu	Arg	Glu	Gly	Leu	Gln
		115					120					125			
Ala	Val	Thr	Leu	Ala	Ala	Arg	Asp	Thr	Val	Asp	Gly	Trp	Phe	Asn	Ile
		130				135					140				
Glu	Arg	Val	Ser	Arg	Glu	Tyr	Asn	Asp	Tyr	Lys	Leu	Val	Phe	Cys	Pro
145					150					155				160	
Gln	Asn	Ala	Glu	Asp	Asn	Lys	Cys	Glu	Asp	Ile	Gly	Ile	Gln	Ile	Asp
				165					170				175		
Asn	Asp	Gly	Ile	Arg	Arg	Leu	Val	Leu	Ser	Lys	Asn	Lys	Pro	Leu	Val
			180					185					190		
Val	Gln	Phe	Gln	Lys	Phe	Arg	Ser	Ser	Thr	Ala					
			195					200							

<210> 53

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<213> 人工序列

<220>

<223> KTI 1 AAB23483.1 204aa

<400> 53

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

Ala Val Thr Leu Ala Ala Arg Asp Thr Val Asp Gly Trp Phe Asn Ile
 130 135 140
 Glu Arg Val Ser Arg Glu Tyr Asn Asp Tyr Tyr Lys Leu Val Phe Cys
 145 150 155 160
 Pro Gln Glu Ala Glu Asp Asn Lys Cys Glu Asp Ile Gly Ile Gln Ile
 165 170 175
 Asp Asn Asp Gly Ile Arg Arg Leu Val Leu Ser Lys Asn Lys Pro Leu
 180 185 190
 Val Val Glu Phe Gln Lys Phe Arg Ser Ser Thr Ala
 195 200

<210> 54

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

Arg Glu Gly Asn Arg Pro Leu Ile Val Thr His Asp Gln Asn His Pro
180 185 190
Leu Leu Val Gln Phe Gln Lys Val Glu Ala Tyr Glu Ser Ser Thr Ala
195 200 205

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

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

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

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

	165		170		175										
Ile	Asp	His	Asp	Asp	Gly	Thr	Arg	Arg	Leu	Val	Val	Ser	Lys	Asn	Lys
	180				185				190						
Pro	Leu	Val	Val	Gln	Phe	Gln	Lys	Val	Asp	Lys	Glu	Ser	Leu	Ala	Lys
	195					200					205				
Lys	Asn	His	Gly	Leu	Ser	Arg	Ser	Glu							
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1				5											
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1				5											
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<400> 67

Asp Ala Met Asp Gly Trp Phe Arg

1 5

<210> 68

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<400> 68

Leu Val Phe Cys Pro Gln Gln Ala Glu Asp Asp Lys

1 5 10

<210> 69

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Cys Gly Asp Ile Gly Ile Ser Ile Asp His Asp Asp Gly Thr Arg

1 5 10 15

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Leu Val Val Ser Lys

1 5

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<211> 10

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Asn Lys Pro Leu Val Val Gln Phe Gln Lys

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

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

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<223> 2S白蛋白Glyma12g34160.1 BLAST 156aa

<400> 74

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

Lys Ile Met Asp Asn Gln Ser Glu Gln Leu Glu Gly Lys Glu Lys Lys
115 120 125
Gln Met Glu Arg Glu Leu Met Asn Leu Ala Ile Arg Cys Arg Leu Gly
130 135 140
Pro Met Ile Gly Cys Asp Leu Ser Ser Asp Asp
145 150 155
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Trp Gln His Gln Gln Asp Ser Cys Arg
1 5
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Gln Leu Gln Gly Val Asn Leu Thr Pro Cys Glu Lys
1 5 10
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His Ile Met Glu Lys
1 5
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Asp Glu Asp Glu Glu Glu Glu Gly His Met Gln Lys

1 5 10

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Cys Cys Thr Glu Met Ser Glu Leu Arg

1 5

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Glu Leu Ile Asn Leu Ala Thr Met Cys Arg

1 5 10

<210> 81

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Phe Gly Pro Met Ile Gln Cys Asp Leu Ser Ser Asp Asp

1 5 10

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Met Ala Thr Ser Asn Phe Ser Ile Val Leu Ser Leu Ser Leu Ala Phe

1 5 10 15

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

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<223> 凝集素 XP_003535884 BLAST 280aa

<400> 83

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

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<223> 凝集素 Glyma10g15480.1 BLAST

<400> 84

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

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

	245		250		255
Ser Phe Ala Ser Lys Leu Ser Asp Gly Ser Ser Asn Asp Ala Leu Asp					
	260		265		270
Leu Pro Ser Phe Val Leu Asn Glu Ala Ile					
	275		280		
<210> 86					
<211> 297					
<212> PRT					
<213> 人工序列					
<220>					
<223> 凝集素 Glyma02g18090.1 BLAST					
<400> 86					
Met Lys Val Leu Cys Ile Ile Phe Glu Phe Lys Gln Ile Lys Ala Met					
1	5		10		15
Ala Thr Ser Asn Phe Ser Ile Val Leu Ser Val Ser Leu Ala Phe Phe					
	20		25		30
Leu Val Leu Leu Thr Lys Ala His Ser Thr Asp Thr Val Ser Phe Thr					
	35		40		45
Phe Asn Lys Phe Asn Pro Val Gln Pro Asn Ile Met Leu Gln Lys Asp					
50	55		60		
Ala Ser Ile Ser Ser Ser Gly Val Leu Gln Leu Thr Lys Val Gly Ser					
65	70		75		80
Asn Gly Val Pro Thr Ser Gly Ser Leu Gly Arg Ala Leu Tyr Ala Ala					
	85		90		95
Pro Ile Gln Ile Trp Asp Ser Glu Thr Gly Lys Val Ala Ser Trp Ala					
	100		105		110
Thr Ser Phe Lys Phe Asn Ile Phe Ala Pro Asn Lys Ser Asn Ser Ala					
	115		120		125
Asp Gly Leu Ala Phe Phe Leu Ala Pro Val Gly Ser Gln Pro Gln Ser					
130	135		140		
Asp Asp Gly Phe Leu Gly Leu Phe Asn Ser Pro Leu Lys Asp Lys Ser					
145	150		155		160
Leu Gln Thr Val Ala Ile Glu Phe Asp Thr Phe Ser Asn Lys Lys Trp					
	165		170		175
Asp Pro Ala Asn Arg His Ile Gly Ile Asp Val Asn Ser Ile Lys Ser					
	180		185		190
Val Lys Thr Ala Ser Trp Gly Leu Ser Asn Gly Gln Val Ala Glu Ile					
	195		200		205
Leu Val Thr Tyr Asn Ala Ala Thr Ser Leu Leu Val Ala Ser Leu Ile					

210	215	220
His Pro Ser Lys Lys Thr Ser Tyr Ile Leu Ser Asp Thr Val Asn Leu		
225	230	235
Lys Ser Asn Leu Pro Glu Trp Val Ser Val Gly Phe Ser Ala Thr Thr		240
	245	250
Gly Leu His Glu Gly Ser Val Glu Thr His Asp Val Ile Ser Trp Ser		255
	260	265
Phe Ala Ser Lys Leu Ser Asp Gly Ser Ser Asn Asp Ala Leu Asp Leu		270
	275	280
Pro Ser Phe Val Leu Asn Glu Ala Ile		285
290	295	
<210> 87		
<211> 282		
<212> PRT		
<213> 人工序列		
<220>		
<223> 凝集素 ACU23599 BLAST 282aa		
<400> 87		
Met Ala Thr Ser Asn Phe Ser Ile Val Leu Ser Val Ser Leu Ala Phe		
1	5	10
Phe Leu Val Leu Leu Thr Lys Ala His Pro Thr Asp Thr Val Ser Phe		15
	20	25
Thr Phe Asn Lys Phe Asn Pro Val Gln Pro Asn Ile Met Leu Gln Lys		30
	35	40
Asp Ala Ser Ile Ser Ser Ser Gly Val Leu Gln Leu Thr Lys Val Gly		45
	50	55
Ser Asn Gly Val Pro Thr Ser Gly Ser Leu Gly Arg Ala Leu Tyr Ala		60
65	70	75
Ala Pro Ile Gln Ile Trp Asp Ser Glu Thr Gly Lys Val Ala Ser Trp		80
	85	90
Ala Thr Ser Phe Lys Phe Asn Ile Phe Ala Pro Asn Lys Ser Asn Ser		95
	100	105
Ala Asp Gly Leu Ala Phe Phe Leu Ala Pro Val Gly Ser Gln Pro Gln		110
	115	120
Ser Asp Asp Gly Phe Leu Gly Leu Phe Asn Ser Pro Leu Lys Asp Lys		125
	130	135
Ser Leu Gln Thr Val Ala Ile Glu Phe Asp Thr Phe Ser Asn Lys Lys		140
145	150	155
Trp Asp Pro Ala Asn Arg His Ile Gly Ile Asp Val Asp Ser Ile Lys		160

	165		170		175										
Ser	Ile	Lys	Thr	Ala	Ser	Trp	Gly	Leu	Ser	Asn	Gly	Gln	Val	Ala	Glu
	180							185					190		
Ile	Leu	Val	Thr	Tyr	Asn	Ala	Ala	Thr	Ser	Leu	Leu	Val	Ala	Ser	Leu
	195							200					205		
Ile	His	Pro	Ser	Lys	Lys	Thr	Ser	Tyr	Ile	Leu	Ser	Asp	Thr	Val	Asn
	210							215					220		
Leu	Lys	Ser	Asn	Leu	Pro	Glu	Trp	Val	Ser	Val	Gly	Phe	Ser	Ala	Thr
225						230					235				240
Thr	Gly	Leu	His	Glu	Gly	Ser	Val	Glu	Thr	His	Asp	Val	Ile	Ser	Trp
				245						250					255
Ser	Phe	Ala	Ser	Lys	Leu	Ser	Asp	Gly	Ser	Ser	Asn	Asp	Ala	Leu	Asp
				260											270
Leu	Pro	Ser	Phe	Val	Leu	Asn	Glu	Ala	Ile						
				275											280

<210> 88

<211> 280

<212> PRT

<213> 人工序列

<220>

<223> 凝集素 CAH60173 BLAST 280aa

<400> 88

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

130				135				140							
Gln	Thr	Val	Ala	Val	Glu	Phe	Asp	Thr	Tyr	Ser	Asn	Pro	Lys	Trp	Asp
145				150				155				160			
Pro	Glu	Asn	Arg	His	Ile	Gly	Ile	Asp	Val	Asn	Ser	Ile	Glu	Ser	Ile
165				170				175							
Arg	Thr	Ala	Ser	Trp	Gly	Leu	Ala	Asn	Gly	Gln	Asn	Ala	Glu	Ile	Leu
180				185				190							
Ile	Thr	Tyr	Asp	Ser	Ser	Thr	Lys	Leu	Leu	Val	Ala	Ser	Leu	Val	His
195				200				205							
Pro	Ser	Arg	Arg	Thr	Ser	Tyr	Ile	Val	Ser	Glu	Arg	Val	Asp	Leu	Lys
210				215				220							
Ser	Val	Leu	Pro	Glu	Trp	Val	Ser	Ile	Gly	Phe	Ser	Ala	Thr	Thr	Gly
225				230				235				240			
Leu	Leu	Glu	Gly	Ser	Ile	Glu	Thr	His	Asp	Val	Leu	Ser	Trp	Ser	Phe
245				250				255							
Ala	Ser	Lys	Leu	Ser	Asp	Asp	Thr	Thr	Ser	Glu	Gly	Leu	Asn	Leu	Ala
260				265				270							
Asn	Phe	Val	Leu	Asn	Lys	Ile	Leu								
275				280											

<210> 89

<211> 228

<212> PRT

〈213〉 人工序列

 $\langle 220 \rangle$

<223> 凝集素 Glyma10g01620.2 BLAST 228aa

<400> 89

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

100	105	110
Asp Thr Gln Pro Gln Thr Arg Gly Gly Tyr Leu Gly Leu Tyr Asn Asn		
115	120	125
Pro Ser Asn Ser Ser Trp Gly Leu Ala Asn Asp Gln Val Thr Asn Val		
130	135	140
Leu Ile Thr Tyr Asp Ala Ser Thr Asn Leu Leu Val Ala Ser Leu Val		
145	150	155
His Pro Ser Gln Arg Ser Ser Tyr Ile Leu Ser Asp Val Leu Asp Leu		
165	170	175
Lys Val Ala Leu Pro Glu Trp Val Arg Ile Gly Phe Ser Ala Thr Thr		
180	185	190
Gly Leu Asn Val Ala Ser Glu Thr His Asp Val His Ser Trp Ser Phe		
195	200	205
Ser Ser Asn Leu Pro Phe Gly Ser Ser Asn Thr Asn Pro Ser Asp Phe		
210	215	220
Ala Ile Phe Ile		
225		
<210> 90		
<211> 285		
<212> PRT		
<213> 人工序列		
<220>		
<223> 凝集素 Glyma02g01590.1 BLAST 285aa		
<400> 90		
Met Ala Thr Ser Lys Leu Lys Thr Gln Asn Val Val Val Ser Leu Ser		
1	5	10
Leu Thr Leu Thr Leu Val Leu Val Leu Leu Thr Ser Lys Ala Asn Ser		
20	25	30
Ala Glu Thr Val Ser Phe Ser Trp Asn Lys Phe Val Pro Lys Gln Pro		
35	40	45
Asn Met Ile Leu Gln Gly Asp Ala Ile Val Thr Ser Ser Gly Lys Leu		
50	55	60
Gln Leu Asn Lys Val Asp Glu Asn Gly Thr Pro Lys Pro Ser Ser Leu		
65	70	75
Gly Arg Ala Leu Tyr Ser Thr Pro Ile His Ile Trp Asp Lys Glu Thr		
85	90	95
Gly Ser Val Ala Ser Phe Ala Ala Ser Phe Asn Phe Thr Phe Tyr Ala		
100	105	110
Pro Asp Thr Lys Arg Leu Ala Asp Gly Leu Ala Phe Phe Leu Ala Pro		

115	120	125
Ile Asp Thr Lys Pro Gln Thr His Ala Gly Tyr Leu Gly Leu Phe Asn		
130	135	140
Glu Asn Glu Ser Gly Asp Gln Val Val Ala Val Glu Phe Asp Thr Phe		
145	150	155
Arg Asn Ser Trp Asp Pro Pro Asn Pro His Ile Gly Ile Asn Val Asn		
165	170	175
Ser Ile Arg Ser Ile Lys Thr Thr Ser Trp Asp Leu Ala Asn Asn Lys		
180	185	190
Val Ala Lys Val Leu Ile Thr Tyr Asp Ala Ser Thr Ser Leu Leu Val		
195	200	205
Ala Ser Leu Val Tyr Pro Ser Gln Arg Thr Ser Asn Ile Leu Ser Asp		
210	215	220
Val Val Asp Leu Lys Thr Ser Leu Pro Glu Trp Val Arg Ile Gly Phe		
225	230	235
Ser Ala Ala Thr Gly Leu Asp Ile Pro Gly Glu Ser His Asp Val Leu		
245	250	255
Ser Trp Ser Phe Ala Ser Asn Leu Pro His Ala Ser Ser Asn Ile Asp		
260	265	270
Pro Leu Asp Leu Thr Ser Phe Val Leu His Glu Ala Ile		
275	280	285

<210> 91

<211> 6

<212> PRT

<213> 人工序列

<220>

<223> 人工序列

<400> 91

Val Phe Ser Pro Asn Lys

1

5

<210> 92

<211> 13

<212> PRT

<213> 人工序列

<220>

<223> 人工序列

<400> 92

Ala Asn Ser Thr Asn Thr Val Ser Phe Thr Val Ser Lys

1

5

10

<210> 93

<211> 19

<212> PRT

<213> 人工序列

<220>

<223> 人工序列

<400> 93

Gln Gln Asn Leu Ile Phe Gln Gly Asp Ala Ala Ile Ser Pro Ser Gly

1 5 10 15

Val Leu Arg

<210> 94

<211> 19

<212> PRT

<213> 人工序列

<220>

<223> 人工序列

<400> 94

Thr Ala Asp Gly Leu Ala Phe Phe Leu Ala Pro Val Gly Ser Lys Pro

1 5 10 15

Gln Ser Lys

<210> 95

<211> 864

<212> PRT

<213> 人工序列

<220>

<223> 脂加氧酶共有序列

<400> 95

Met Gly Gly Ile Phe Asp Lys Gly Gln Lys Ile Lys Gly Thr Val Val

1 5 10 15

Leu Met Pro Lys Asn Val Leu Asp Phe Asn Ala Ile Thr Ser Ile Gly

20 25 30

Lys Gly Gly Val Ile Asp Thr Ala Thr Gly Ile Leu Gly Ala Gly Val

35 40 45

Ser Leu Val Gly Gly Val Ile Asp Thr Ala Thr Ala Phe Leu Gly Arg

50 55 60

Asn Ile Ser Met Gln Leu Ile Ser Ala Thr Gln Thr Asp Gly Ser Gly

65 70 75 80

Asn Gly Lys Val Gly Lys Glu Val Tyr Leu Glu Lys His Leu Pro Thr

85 90 95

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

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

Phe Gly Gln Tyr Pro Tyr Gly Gly Leu Ile Leu Asn Arg Pro Thr Leu
 725 730 735
 Ala Arg Arg Phe Ile Pro Glu Glu Gly Thr Pro Glu Tyr Asp Glu Met
 740 745 750
 Val Lys Asn Pro Gln Lys Ala Tyr Leu Arg Thr Ile Thr Pro Lys Phe
 755 760 765
 Glu Thr Leu Ile Asp Leu Ser Val Ile Glu Ile Leu Ser Arg His Ala
 770 775 780
 Ser Asp Glu Ile Tyr Leu Gly Glu Arg Asp Thr Pro Asn Trp Thr Thr
 785 790 795 800
 Asp Lys Lys Ala Leu Glu Ala Phe Lys Lys Phe Gly Ser Lys Leu Thr
 805 810 815
 Gly Ile Glu Gly Lys Ile Asn Ala Arg Asn Ser Asp Pro Ser Leu Arg
 820 825 830
 Asn Arg Thr Gly Pro Val Gln Leu Pro Tyr Thr Leu Leu His Arg Ser
 835 840 845
 Ser Glu Glu Gly Leu Thr Phe Lys Gly Ile Pro Asn Ser Ile Ser Ile
 850 855 860

<210> 96

<211> 864

<212> PRT

<213> 人工序列

<220>

<223> 脂加氧酶 2IUK_A BLAST 864aa

<400> 96

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

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

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

Ala Arg Arg Phe Ile Pro Ala Glu Gly Thr Pro Glu Tyr Asp Glu Met		
740	745	750
Val Lys Asn Pro Gln Lys Ala Tyr Leu Arg Thr Ile Thr Pro Lys Phe		
755	760	765
Glu Thr Leu Ile Asp Leu Ser Val Ile Glu Ile Leu Ser Arg His Ala		
770	775	780
Ser Asp Glu Ile Tyr Leu Gly Glu Arg Glu Thr Pro Asn Trp Thr Thr		
785	790	795
Asp Lys Lys Ala Leu Glu Ala Phe Lys Arg Phe Gly Ser Lys Leu Thr		
805	810	815
Gly Ile Glu Gly Lys Ile Asn Ala Arg Asn Ser Asp Pro Ser Leu Arg		
820	825	830
Asn Arg Thr Gly Pro Val Gln Leu Pro Tyr Thr Leu Leu His Arg Ser		
835	840	845
Ser Glu Glu Gly Leu Thr Phe Lys Gly Ile Pro Asn Ser Ile Ser Ile		
850	855	860
<210> 97		
<211> 864		
<212> PRT		
<213> 人工序列		
<220>		
<223> 脂加氧酶 NP_001238676 BLAST 864aa		
<400> 97		
Met Phe Gly Ile Phe Asp Lys Gly Gln Lys Ile Lys Gly Thr Val Val		
1	5	10
Leu Met Pro Lys Asn Val Leu Asp Phe Asn Ala Ile Thr Ser Ile Gly		
20	25	30
Lys Gly Gly Val Ile Asp Thr Ala Thr Gly Ile Leu Gly Gln Gly Val		
35	40	45
Ser Leu Val Gly Gly Val Ile Asp Thr Ala Thr Ser Phe Leu Gly Arg		
50	55	60
Asn Ile Ser Met Gln Leu Ile Ser Ala Thr Gln Thr Asp Gly Ser Gly		
65	70	75
Asn Gly Lys Val Gly Lys Glu Val Tyr Leu Glu Lys His Leu Pro Thr		
85	90	95
Leu Pro Thr Leu Gly Ala Arg Gln Asp Ala Phe Ser Ile Phe Phe Glu		
100	105	110
Trp Asp Ala Ser Phe Gly Ile Pro Gly Ala Phe Tyr Ile Lys Asn Phe		
115	120	125

Met Thr Asp Glu Phe Phe Leu Val Ser Val Lys Leu Glu Asp Ile Pro		
130	135	140
Asn His Gly Thr Ile Glu Phe Val Cys Asn Ser Trp Val Tyr Asn Phe		
145	150	155 160
Arg Ser Tyr Lys Lys Asn Arg Ile Phe Phe Val Asn Asp Thr Tyr Leu		
	165	170 175
Pro Ser Ala Thr Pro Ala Pro Leu Leu Lys Tyr Arg Lys Glu Glu Leu		
	180	185 190
Glu Val Leu Arg Gly Asp Gly Thr Gly Lys Arg Lys Asp Phe Asp Arg		
	195	200 205
Ile Tyr Asp Tyr Asp Val Tyr Asn Asp Leu Gly Asn Pro Asp Gly Gly		
	210	215 220
Asp Pro Arg Pro Ile Leu Gly Gly Cys Ser Ile Tyr Pro Tyr Pro Leu		
225	230	235 240
Arg Val Arg Thr Gly Arg Glu Arg Thr Arg Thr Asp Pro Asn Ser Glu		
	245	250 255
Lys Pro Gly Glu Val Tyr Val Pro Arg Asp Glu Asn Phe Gly His Leu		
	260	265 270
Lys Ser Ser Asp Phe Leu Thr Tyr Gly Ile Lys Ser Leu Ser His Asp		
	275	280 285
Val Ile Pro Leu Phe Lys Ser Ala Ile Phe Gln Leu Arg Val Thr Ser		
	290	295 300
Ser Glu Phe Glu Ser Phe Glu Asp Val Arg Ser Leu Tyr Glu Gly Gly		
305	310	315 320
Ile Lys Leu Pro Thr Asp Ile Leu Ser Gln Ile Ser Pro Leu Pro Ala		
	325	330 335
Leu Lys Glu Ile Phe Arg Thr Asp Gly Glu Asn Val Leu Gln Phe Pro		
	340	345 350
Pro Pro His Val Ala Lys Val Ser Lys Ser Gly Trp Met Thr Asp Glu		
	355	360 365
Glu Phe Ala Arg Glu Val Ile Ala Gly Val Asn Pro Asn Val Ile Arg		
	370	375 380
Arg Leu Gln Glu Phe Pro Pro Lys Ser Thr Leu Asp Pro Thr Leu Tyr		
385	390	395 400
Gly Asp Gln Thr Ser Thr Ile Thr Lys Glu Gln Leu Glu Ile Asn Met		
	405	410 415
Gly Gly Val Thr Val Glu Glu Ala Leu Ser Thr Gln Arg Leu Phe Ile		
	420	425 430
Leu Asp Tyr Gln Asp Ala Phe Ile Pro Tyr Leu Thr Arg Ile Asn Ser		

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

Val Lys Asn Pro Gln Lys Ala Tyr Leu Arg Thr Ile Thr Pro Lys Phe		
755	760	765
Glu Thr Leu Ile Asp Leu Ser Val Ile Glu Ile Leu Ser Arg His Ala		
770	775	780
Ser Asp Glu Ile Tyr Leu Gly Glu Arg Glu Thr Pro Asn Trp Thr Thr		
785	790	795
800		
Asp Lys Lys Ala Leu Glu Ala Phe Lys Arg Phe Gly Ser Lys Leu Thr		
805	810	815
Gly Ile Glu Gly Lys Ile Asn Ala Arg Asn Ser Asp Pro Ser Leu Arg		
820	825	830
Asn Arg Thr Gly Pro Val Gln Leu Pro Tyr Thr Leu Leu His Arg Ser		
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Ser Glu Glu Gly Leu Thr Phe Lys Gly Ile Pro Asn Ser Ile Ser Ile		
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Asn Gly Gly Val Gly Gly Val Val Ser Gly Ile Phe Gly Ala Val Ala		
35	40	45
Asp Val Thr Gly Gln Ile Val Asp Thr Ala Thr Ala Ile Phe Ser Arg		
50	55	60
Asn Val Ser Phe Lys Leu Ile Ser Ala Thr Ser Thr Asp Ala Lys Gly		
65	70	75
80		
Asn Gly Lys Val Gly Asn Glu Thr Phe Leu Glu Lys His Leu Pro Thr		
85	90	95
Leu Pro Thr Leu Gly Asp Arg Arg Asp Ala Tyr Asp Ile His Phe Glu		
100	105	110
Trp Asp Ala Asn Phe Gly Ile Pro Gly Ala Phe Tyr Ile Arg Asn Tyr		
115	120	125
Thr Tyr Asp Glu Phe Phe Leu Val Ser Val Thr Leu Glu Asp Ile Pro		
130	135	140

Asn His Gly Thr Ile His Phe Val Cys Asn Ser Trp Val Tyr Asn Phe			
145	150	155	160
Lys Asp Tyr Asp Lys Lys Asp Arg Ile Phe Phe Ala Asn Lys Thr Tyr			
	165	170	175
Leu Pro Ser Ala Thr Pro Gly Pro Leu Val Lys Tyr Arg Glu Glu Glu			
	180	185	190
Leu Lys Ile Leu Arg Gly Asp Gly Thr Gly Glu Arg Lys Glu His Glu			
	195	200	205
Arg Ile Tyr Asp Tyr Asp Val Tyr Asn Asp Leu Gly Asn Pro Asp Glu			
	210	215	220
Asp Val Lys Leu Ala Arg Pro Val Leu Gly Gly Ser Ser Thr Tyr Pro			
	225	230	235
240			
Tyr Pro Arg Arg Val Arg Thr Gly Arg Lys Ala Thr Lys Lys Asp Pro			
	245	250	255
Lys Ser Glu Arg Pro Ala Ser Glu Leu Tyr Met Pro Arg Asp Glu Lys			
	260	265	270
Phe Gly His Leu Lys Ser Ser Asp Phe Leu Thr Tyr Gly Ile Lys Ser			
	275	280	285
Leu Ser Gln Lys Leu Leu Pro Ser Leu Glu Asn Val Phe Asp Ser Asp			
	290	295	300
Leu Thr Trp Asn Glu Phe Asp Ser Phe Glu Glu Val Arg Asp Leu Tyr			
	305	310	315
320			
Glu Gly Gly Ile Lys Val Pro Thr Gly Val Leu Ser Asp Ile Ser Pro			
	325	330	335
Ile Pro Ile Phe Lys Glu Ile Phe Arg Thr Asp Gly Glu Ser Val Leu			
	340	345	350
Gln Phe Pro Pro Pro His Val Val Gln Val Thr Lys Ser Ala Trp Met			
	355	360	365
Thr Asp Asp Glu Phe Ala Arg Glu Met Ile Ala Gly Val Asn Pro Asn			
	370	375	380
Val Ile Arg Leu Leu Lys Glu Phe Pro Pro Gln Ser Lys Leu Asp Pro			
	385	390	395
400			
Ser Leu Tyr Gly Asp Gln Ser Ser Thr Ile Thr Lys Glu His Leu Glu			
	405	410	415
Ile Asn Met Asp Gly Val Thr Val Glu Glu Ala Leu Asn Gly Gln Arg			
	420	425	430
Leu Phe Ile Leu Asp Tyr Gln Asp Ala Phe Met Pro Tyr Leu Thr Arg			
	435	440	445
Ile Asn Ala Leu Pro Ser Ala Lys Ala Tyr Ala Thr Arg Thr Ile Leu			

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

Pro Lys Arg Gln Thr Ile Ile Asp Leu Thr Val Ile Glu Ile Leu Ser
 770 775 780
 Arg His Ala Ser Asp Glu Ile Tyr Leu Gly Glu Arg Asp Asn Pro Asn
 785 790 795 800
 Trp Thr Ser Asp Ser Lys Ala Leu Glu Ala Phe Lys Lys Phe Gly Ser
 805 810 815
 Lys Leu Ala Glu Ile Glu Gly Lys Ile Thr Ala Arg Asn Lys Asp Ser
 820 825 830
 Asn Lys Lys Asn Arg Tyr Gly Pro Val Gln Leu Pro Tyr Thr Leu Leu
 835 840 845
 Leu Pro Thr Ser Glu Glu Gly Leu Thr Phe Arg Gly Ile Pro Asn Ser
 850 855 860
 Ile Ser Ile
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 35 40 45
 Ser Leu Val Gly Gly Val Ile Asp Thr Ala Thr Ser Phe Leu Gly Arg
 50 55 60
 Asn Ile Ser Met Gln Leu Ile Ser Ala Thr Gln Thr Asp Gly Ser Gly
 65 70 75 80
 Asn Gly Lys Val Gly Lys Glu Val Tyr Leu Glu Lys His Leu Pro Thr
 85 90 95
 Leu Pro Thr Leu Gly Ala Arg Gln Asp Ala Phe Ser Ile Phe Phe Glu
 100 105 110
 Trp Asp Ala Ser Phe Gly Ile Pro Gly Ala Phe Tyr Ile Lys Asn Phe
 115 120 125
 Met Thr Asp Glu Phe Phe Leu Val Ser Val Lys Leu Glu Asp Ile Pro
 130 135 140

Asn His Gly Thr Ile Glu Phe Val Cys Asn Ser Trp Val Tyr Asn Phe			
145	150	155	160
Arg Ser Tyr Lys Lys Asn Arg Ile Phe Phe Val Asn Asp Thr Tyr Leu			
	165	170	175
Pro Ser Ala Thr Pro Ala Pro Leu Leu Lys Tyr Arg Lys Glu Glu Leu			
	180	185	190
Glu Val Leu Arg Gly Asp Gly Thr Gly Lys Arg Lys Asp Phe Asp Arg			
	195	200	205
Ile Tyr Asp Tyr Asp Val Tyr Asn Asp Leu Gly Asn Pro Asp Gly Gly			
	210	215	220
Asp Pro Arg Pro Ile Leu Gly Gly Ser Ser Ile Tyr Pro Tyr Pro Arg			
225	230	235	240
Arg Val Arg Thr Gly Arg Glu Arg Thr Arg Thr Asp Pro Asn Ser Glu			
	245	250	255
Lys Pro Gly Glu Val Tyr Val Pro Arg Asp Glu Asn Phe Gly His Leu			
	260	265	270
Lys Ser Ser Asp Phe Leu Thr Tyr Gly Ile Lys Ser Leu Ser His Asp			
	275	280	285
Val Ile Pro Leu Phe Lys Ser Ala Ile Phe Gln Leu Arg Val Thr Ser			
	290	295	300
Ser Glu Phe Glu Ser Phe Glu Asp Val Arg Ser Leu Tyr Glu Gly Gly			
305	310	315	320
Ile Lys Leu Pro Thr Asp Ile Leu Ser Gln Ile Ser Pro Leu Pro Ala			
	325	330	335
Leu Lys Glu Ile Phe Arg Thr Asp Gly Glu Asn Val Leu Gln Phe Pro			
	340	345	350
Pro Pro His Val Ala Lys Val Ser Lys Ser Gly Trp Met Thr Asp Glu			
	355	360	365
Glu Phe Ala Arg Glu Val Ile Ala Gly Val Asn Pro Asn Val Ile Arg			
	370	375	380
Arg Leu Gln Glu Phe Pro Pro Lys Ser Thr Leu Asp Pro Thr Leu Tyr			
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Gly Asp Gln Thr Ser Thr Ile Thr Lys Glu Gln Leu Glu Ile Asn Met			
	405	410	415
Gly Gly Val Thr Val Glu Glu Ala Leu Ser Thr Gln Arg Leu Phe Ile			
	420	425	430
Leu Asp Tyr Gln Asp Ala Phe Ile Pro Tyr Leu Thr Arg Ile Asn Ser			
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Leu Pro Thr Ala Lys Ala Tyr Ala Thr Arg Thr Ile Leu Phe Leu Lys			

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Asp Asp Gly Thr Leu Lys Pro Leu Ala Ile Glu Leu Ser Lys Pro His		
465	470	475
Pro Asp Gly Asp Asn Leu Gly Pro Glu Ser Ile Val Val Leu Pro Ala		
485	490	495
Thr Glu Gly Val Asp Ser Thr Ile Trp Leu Leu Ala Lys Ala His Val		
500	505	510
Ile Val Asn Asp Ser Gly Tyr His Gln Leu Val Ser His Trp Leu Asn		
515	520	525
Thr His Ala Val Met Glu Pro Phe Ala Ile Ala Thr Asn Arg His Leu		
530	535	540
Ser Val Leu His Pro Ile Tyr Lys Leu Leu Tyr Pro His Tyr Arg Asp		
545	550	555
Thr Ile Asn Ile Asn Gly Leu Ala Arg Gln Ser Leu Ile Asn Ala Asp		
565	570	575
Gly Ile Ile Glu Lys Ser Phe Leu Pro Gly Lys Tyr Ser Ile Glu Met		
580	585	590
Ser Ser Ser Val Tyr Lys Asn Trp Val Phe Thr Asp Gln Ala Leu Pro		
595	600	605
Ala Asp Leu Val Lys Arg Gly Leu Ala Ile Glu Asp Pro Ser Ala Pro		
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His Gly Leu Arg Leu Val Ile Glu Asp Tyr Pro Tyr Ala Val Asp Gly		
625	630	635
Leu Glu Ile Trp Asp Ala Ile Lys Thr Trp Val His Glu Tyr Val Ser		
645	650	655
Leu Tyr Tyr Pro Thr Asp Ala Ala Val Gln Gln Asp Thr Glu Leu Gln		
660	665	670
Ala Trp Trp Lys Glu Ala Val Glu Lys Gly His Gly Asp Leu Lys Glu		
675	680	685
Lys Pro Trp Trp Pro Lys Met Gln Thr Thr Glu Asp Leu Ile Gln Ser		
690	695	700
Cys Ser Ile Ile Val Trp Thr Ala Ser Ala Leu His Ala Ala Val Asn		
705	710	715
Phe Gly Gln Tyr Pro Tyr Gly Gly Leu Ile Leu Asn Arg Pro Thr Leu		
725	730	735
Ala Arg Arg Phe Ile Pro Ala Glu Gly Thr Pro Glu Tyr Asp Glu Met		
740	745	750
Val Lys Asn Pro Gln Lys Ala Tyr Leu Arg Thr Ile Thr Pro Lys Phe		
755	760	765

Glu Thr Leu Ile Asp Leu Ser Val Ile Glu Ile Leu Ser Arg His Ala		
770	775	780
Ser Asp Glu Ile Tyr Leu Gly Glu Arg Glu Thr Pro Asn Trp Thr Thr		
785	790	795 800
Asp Lys Lys Ala Leu Glu Ala Phe Lys Arg Phe Gly Ser Lys Leu Thr		
	805	810 815
Gly Ile Glu Gly Lys Ile Asn Ala Arg Asn Ser Asp Pro Ser Leu Arg		
	820	825 830
Asn Arg Thr Gly Pro Val Gln Leu Pro Tyr Thr Leu Leu His Arg Ser		
	835	840 845
Ser Glu Glu Gly Leu Thr Phe Lys Gly Ile Pro Asn Ser Ile Ser Ile		
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Val Gly Lys Gly Ser Ala Lys Asp Thr Ala Thr Asp Phe Leu Gly Lys		
	35	40 45
Gly Leu Asp Ala Leu Gly His Ala Val Asp Ala Leu Thr Ala Phe Ala		
50	55	60
Gly His Ser Ile Ser Leu Gln Leu Ile Ser Ala Thr Gln Thr Asp Gly		
65	70	75 80
Ser Gly Lys Gly Lys Val Gly Asn Glu Ala Tyr Leu Glu Lys His Leu		
	85	90 95
Pro Thr Leu Pro Thr Leu Gly Ala Arg Gln Glu Ala Phe Asp Ile Asn		
	100	105 110
Phe Glu Trp Asp Ala Ser Phe Gly Ile Pro Gly Ala Phe Tyr Ile Lys		
	115	120 125
Asn Phe Met Thr Asp Glu Phe Phe Leu Val Ser Val Lys Leu Glu Asp		
	130	135 140
Ile Pro Asn His Gly Thr Ile Asn Phe Val Cys Asn Ser Trp Val Tyr		
145	150	155 160

Asn Phe Lys Ser Tyr Lys Lys Asn Arg Ile Phe Phe Val Asn Asp Thr		
165	170	175
Tyr Leu Pro Ser Ala Thr Pro Ala Pro Leu Leu Lys Tyr Arg Lys Glu		
180	185	190
Glu Leu Glu Val Leu Arg Gly Asp Gly Thr Gly Lys Arg Lys Asp Phe		
195	200	205
Asp Arg Ile Tyr Asp Tyr Asp Val Tyr Asn Asp Leu Gly Asn Pro Asp		
210	215	220
Gly Gly Asp Pro Arg Pro Ile Leu Gly Gly Ser Ser Ile Tyr Pro Tyr		
225	230	235
Pro Arg Arg Val Arg Thr Gly Arg Glu Arg Thr Arg Thr Asp Pro Asn		
245	250	255
Ser Glu Lys Pro Gly Glu Val Tyr Val Pro Arg Asp Glu Asn Phe Gly		
260	265	270
His Leu Lys Ser Ser Asp Phe Leu Thr Tyr Gly Ile Lys Ser Leu Ser		
275	280	285
His Asp Val Ile Pro Leu Phe Lys Ser Ala Ile Phe Gln Leu Arg Val		
290	295	300
Thr Ser Ser Glu Phe Glu Ser Phe Glu Asp Val Arg Ser Leu Tyr Glu		
305	310	315
Gly Gly Ile Lys Leu Pro Thr Asp Ile Leu Ser Gln Ile Ser Pro Leu		
325	330	335
Pro Ala Leu Lys Glu Ile Phe Arg Thr Asp Gly Glu Asn Val Leu Gln		
340	345	350
Phe Pro Pro Pro His Val Ala Lys Val Ser Lys Ser Gly Trp Met Thr		
355	360	365
Asp Glu Glu Phe Ala Arg Glu Val Ile Ala Gly Val Asn Pro Asn Val		
370	375	380
Ile Arg Arg Leu Gln Glu Phe Pro Pro Lys Ser Thr Leu Asp Pro Thr		
385	390	395
Leu Tyr Gly Asp Gln Thr Ser Thr Ile Thr Lys Glu Gln Leu Glu Ile		
405	410	415
Asn Met Gly Gly Val Thr Val Glu Glu Ala Leu Ser Thr Gln Arg Leu		
420	425	430
Phe Ile Leu Asp Tyr Gln Asp Ala Phe Ile Pro Tyr Leu Thr Arg Ile		
435	440	445
Asn Ser Leu Pro Thr Ala Lys Ala Tyr Ala Thr Arg Thr Ile Leu Phe		
450	455	460
Leu Lys Asp Asp Gly Thr Leu Lys Pro Leu Ala Ile Glu Leu Ser Lys		

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

His	Ala	Ser	Asp	Glu	Ile	Tyr	Leu	Gly	Glu	Arg	Glu	Thr	Pro	Asn	Trp
785					790					795					800
Thr	Thr	Asp	Lys	Lys	Ala	Leu	Glu	Ala	Phe	Lys	Arg	Phe	Gly	Ser	Lys
				805					810					815	
Leu	Thr	Gly	Ile	Glu	Gly	Lys	Ile	Asn	Ala	Arg	Asn	Ser	Asp	Pro	Ser
				820				825						830	
Leu	Arg	Asn	Arg	Thr	Gly	Pro	Val	Gln	Leu	Pro	Tyr	Thr	Leu	Leu	His
				835				840						845	
Arg	Ser	Ser	Glu	Glu	Gly	Leu	Thr	Phe	Lys	Gly	Ile	Pro	Asn	Ser	Ile
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Ser	Ile														
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Val	Val	Leu	Met	Pro	Lys	Asn	Val	Leu	Asp	Phe	Asn	Ala	Ile	Thr	Ser
				20					25					30	
Val	Gly	Lys	Gly	Ser	Ala	Lys	Asp	Thr	Ala	Thr	Asp	Phe	Leu	Gly	Lys
				35					40					45	
Gly	Leu	Asp	Ala	Leu	Gly	His	Ala	Val	Asp	Ala	Leu	Thr	Ala	Phe	Ala
				50				55						60	
Gly	His	Ser	Ile	Ser	Leu	Gln	Leu	Ile	Ser	Ala	Thr	Gln	Thr	Asp	Gly
65					70					75					80
Ser	Gly	Lys	Gly	Lys	Val	Gly	Asn	Glu	Ala	Tyr	Leu	Glu	Lys	His	Leu
					85					90					95
Pro	Thr	Leu	Pro	Thr	Leu	Gly	Ala	Arg	Gln	Glu	Ala	Phe	Asp	Ile	Asn
					100					105				110	
Phe	Glu	Trp	Asp	Ala	Ser	Phe	Gly	Ile	Pro	Gly	Ala	Phe	Tyr	Ile	Lys
					115					120				125	
Asn	Phe	Met	Thr	Asp	Glu	Phe	Phe	Leu	Val	Ser	Val	Lys	Leu	Glu	Asp
					130					135				140	
Ile	Pro	Asn	His	Gly	Thr	Ile	Asn	Phe	Val	Cys	Asn	Ser	Trp	Val	Tyr
145						150					155				160

Asn Phe Lys Ser Tyr Lys Lys Asn Arg Ile Phe Phe Val Asn Asp Thr		
165	170	175
Tyr Leu Pro Ser Ala Thr Pro Gly Pro Leu Val Lys Tyr Arg Gln Glu		
180	185	190
Glu Leu Glu Val Leu Arg Gly Asp Gly Thr Gly Lys Arg Arg Asp Phe		
195	200	205
Asp Arg Ile Tyr Asp Tyr Asp Ile Tyr Asn Asp Leu Gly Asn Pro Asp		
210	215	220
Gly Gly Asp Pro Arg Pro Ile Ile Gly Gly Ser Ser Asn Tyr Pro Tyr		
225	230	235
240		
Pro Arg Arg Val Arg Thr Gly Arg Glu Lys Thr Arg Lys Asp Pro Asn		
245	250	255
Ser Glu Lys Pro Gly Glu Ile Tyr Val Pro Arg Asp Glu Asn Phe Gly		
260	265	270
His Leu Lys Ser Ser Asp Phe Leu Thr Tyr Gly Ile Lys Ser Leu Ser		
275	280	285
Gln Asn Val Ile Pro Leu Phe Lys Ser Ile Ile Leu Asn Leu Arg Val		
290	295	300
Thr Ser Ser Glu Phe Asp Ser Phe Asp Glu Val Arg Gly Leu Phe Glu		
305	310	315
320		
Gly Gly Ile Lys Leu Pro Thr Asn Ile Leu Ser Gln Ile Ser Pro Leu		
325	330	335
Pro Val Leu Lys Glu Ile Phe Arg Thr Asp Gly Glu Asn Thr Leu Gln		
340	345	350
Phe Pro Pro Pro His Val Ile Arg Val Ser Lys Ser Gly Trp Met Thr		
355	360	365
Asp Asp Glu Phe Ala Arg Glu Met Ile Ala Gly Val Asn Pro Asn Val		
370	375	380
Ile Arg Arg Leu Gln Glu Phe Pro Pro Lys Ser Thr Leu Asp Pro Ala		
385	390	395
400		
Thr Tyr Gly Asp Gln Thr Ser Thr Ile Thr Lys Gln Gln Leu Glu Ile		
405	410	415
Asn Leu Gly Gly Val Thr Val Glu Glu Ala Ile Ser Ala His Arg Leu		
420	425	430
Phe Ile Leu Asp Tyr His Asp Ala Phe Phe Pro Tyr Leu Thr Lys Ile		
435	440	445
Asn Ser Leu Pro Ile Ala Lys Ala Tyr Ala Thr Arg Thr Ile Leu Phe		
450	455	460
Leu Lys Asp Asp Gly Ser Leu Lys Pro Leu Ala Ile Glu Leu Ser Lys		

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

Leu Gly Gln Arg Asp Asn Pro Asn Trp Thr Thr Asp Ser Lys Ala Leu
 785 790 795 800
 Glu Ala Phe Lys Lys Phe Gly Asn Lys Leu Ala Glu Ile Glu Gly Lys
 805 810 815
 Ile Thr Gln Arg Asn Asn Asp Pro Ser Leu Lys Ser Arg His Gly Pro
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 Ala Thr Gly Ile Val Gly Gly Val Val Asp Gly Ala Thr Ala Ile Phe
 50 55 60
 Ser Arg Asn Ile Ala Ile Gln Leu Ile Ser Ala Thr Lys Thr Asp Gly
 65 70 75 80
 Leu Gly Asn Gly Lys Val Gly Lys Gln Thr Tyr Leu Glu Lys His Leu
 85 90 95
 Pro Ser Leu Pro Thr Leu Gly Asp Arg Gln Asp Ala Phe Ser Val Tyr
 100 105 110
 Phe Glu Trp Asp Asn Asp Phe Gly Ile Pro Gly Ala Phe Tyr Ile Lys
 115 120 125
 Asn Phe Met Gln Ser Glu Phe Phe Leu Val Ser Val Thr Leu Glu Asp
 130 135 140
 Ile Pro Asn His Gly Thr Ile His Phe Val Cys Asn Ser Trp Val Tyr
 145 150 155 160
 Asn Ala Lys Ser Tyr Lys Arg Asp Arg Ile Phe Phe Ala Asn Lys Thr
 165 170 175

Tyr	Leu	Pro	Asn	Glu	Thr	Pro	Thr	Pro	Leu	Val	Lys	Tyr	Arg	Lys	Glu	
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Glu	Leu	Glu	Asn	Leu	Arg	Gly	Asp	Gly	Lys	Gly	Glu	Arg	Lys	Glu	Tyr	
			195				200						205			
Asp	Arg	Ile	Tyr	Asp	Tyr	Asp	Val	Tyr	Asn	Asp	Leu	Gly	Asn	Pro	Asp	
			210				215						220			
Lys	Ser	Asn	Asp	Leu	Ala	Arg	Pro	Val	Leu	Gly	Gly	Ser	Ser	Ala	Tyr	
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Pro	Tyr	Pro	Arg	Arg	Gly	Arg	Thr	Gly	Arg	Lys	Pro	Thr	Thr	Lys	Asp	
						245				250					255	
Ser	Lys	Ser	Glu	Ser	Pro	Ser	Ser	Ser	Thr	Tyr	Ile	Pro	Arg	Asp	Glu	
			260						265					270		
Asn	Phe	Gly	His	Leu	Lys	Ser	Ser	Asp	Phe	Leu	Thr	Tyr	Gly	Ile	Lys	
			275					280						285		
Ser	Ile	Ala	Gln	Thr	Val	Leu	Pro	Thr	Phe	Gln	Ser	Ala	Phe	Gly	Leu	
			290					295						300		
Asn	Ala	Glu	Phe	Asp	Arg	Phe	Asp	Asp	Val	Arg	Gly	Leu	Phe	Glu	Gly	
305						310					315				320	
Gly	Ile	His	Leu	Pro	Thr	Asp	Ala	Leu	Ser	Lys	Ile	Ser	Pro	Leu	Pro	
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Val	Leu	Lys	Glu	Ile	Phe	Arg	Thr	Asp	Gly	Glu	Gln	Val	Leu	Lys	Phe	
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Pro	Pro	Pro	His	Val	Ile	Lys	Val	Ser	Lys	Ser	Ala	Trp	Met	Thr	Asp	
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Glu	Glu	Phe	Gly	Arg	Glu	Met	Leu	Ala	Gly	Val	Asn	Pro	Cys	Leu	Ile	
			370						375					380		
Glu	Cys	Leu	Gln	Val	Phe	Pro	Pro	Lys	Ser	Lys	Leu	Asp	Pro	Thr	Val	
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Tyr	Gly	Asp	Gln	Thr	Ser	Thr	Ile	Thr	Lys	Glu	His	Leu	Glu	Ile	Asn	
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Leu	Gly	Gly	Leu	Ser	Val	Glu	Gln	Ala	Leu	Ser	Gly	Asn	Arg	Leu	Phe	
			420						425						430	
Ile	Leu	Asp	His	His	Asp	Ala	Phe	Ile	Ala	Tyr	Leu	Arg	Lys	Ile	Asn	
			435						440						445	
Asp	Leu	Pro	Thr	Ala	Lys	Ser	Tyr	Ala	Thr	Arg	Thr	Ile	Leu	Phe	Leu	
			450						455						460	
Lys	Asp	Asp	Gly	Thr	Leu	Lys	Pro	Leu	Ala	Ile	Glu	Leu	Ser	Leu	Pro	
465						470					475				480	
His	Pro	Arg	Gly	Asp	Glu	Phe	Gly	Ala	Val	Ser	Arg	Val	Val	Leu	Pro	

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

Asp Asp Thr Lys Ala Ile Gln Ala Phe Lys Lys Phe Gly Asn Lys Leu
 805 810 815
 Lys Glu Ile Glu Asp Lys Ile Ser Gly Arg Asn Lys Asn Ser Ser Leu
 820 825 830
 Arg Asn Arg Asn Gly Pro Ala Gln Met Pro Tyr Thr Val Leu Leu Pro
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 35 40 45
 Ala Gln Asp Ile Val Gly Gly Ile Val Asp Gly Ala Thr Ala Ile Phe
 50 55 60
 Ser Arg Asn Ile Ala Ile Gln Leu Ile Ser Ala Thr Lys Ser Glu Asn
 65 70 75 80
 Ala Leu Gly His Gly Lys Val Gly Lys Leu Thr Tyr Leu Glu Lys His
 85 90 95
 Leu Pro Ser Leu Pro Asn Leu Gly Asp Arg Gln Asp Ala Phe Asp Val
 100 105 110
 Tyr Phe Glu Trp Asp Glu Ser Phe Gly Ile Pro Gly Ala Phe Tyr Ile
 115 120 125
 Lys Asn Tyr Met Gln Ser Glu Phe Phe Leu Val Ser Phe Lys Leu Glu
 130 135 140
 Asp Val Pro Asn His Gly Thr Ile Leu Phe Ala Cys Asn Ser Trp Val
 145 150 155 160
 Tyr Asn Ala Lys Leu Tyr Lys Lys Asp Arg Ile Phe Phe Ala Asn Lys
 165 170 175

Ala Tyr Leu Pro Asn Asp Thr Pro Thr Pro Leu Val Lys Tyr Arg Lys		
180	185	190
Glu Glu Leu Glu Asn Leu Arg Gly Asp Gly Arg Gly Glu Arg Lys Glu		
195	200	205
Leu Asp Arg Ile Tyr Asp Tyr Asp Val Tyr Asn Asp Leu Gly Asn Pro		
210	215	220
Asp Glu Asn Asp Asp Leu Ala Arg Pro Ile Leu Gly Gly Ser Ser Lys		
225	230	235
His Pro Tyr Pro Arg Arg Gly Arg Thr Gly Arg Lys Pro Thr Lys Lys		
245	250	255
Asp Pro Arg Cys Glu Arg Pro Thr Ser Asp Thr Tyr Ile Pro Arg Asp		
260	265	270
Glu Asn Phe Gly His Leu Lys Ser Ser Asp Phe Leu Thr Tyr Ala Ile		
275	280	285
Lys Ser Leu Thr Gln Asn Val Leu Pro Gln Phe Asn Thr Ala Phe Gly		
290	295	300
Phe Asn Asn Glu Phe Asp Ser Phe Glu Asp Val Arg Cys Leu Phe Asp		
305	310	315
Gly Gly Val Tyr Leu Pro Thr Asp Val Leu Ser Lys Ile Ser Pro Ile		
325	330	335
Pro Val Leu Lys Glu Ile Phe Arg Thr Asp Gly Glu Gln Ala Leu Lys		
340	345	350
Phe Pro Pro Pro His Val Ile Lys Val Arg Glu Ser Glu Trp Met Thr		
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Asp Glu Glu Phe Gly Arg Glu Met Leu Ala Gly Val Asn Pro Gly Met		
370	375	380
Ile Gln Arg Leu Gln Glu Phe Pro Pro Lys Ser Lys Leu Asp Pro Thr		
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Glu Phe Gly Asp Gln Thr Ser Thr Ile Thr Lys Glu His Leu Glu Ile		
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Asn Leu Gly Gly Leu Thr Val Glu Gln Ala Leu Lys Gly Asn Lys Leu		
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Phe Ile Leu Asp His His Asp Ala Phe Ile Pro Phe Met Asn Leu Ile		
435	440	445
Asn Gly Leu Pro Thr Ala Lys Ser Tyr Ala Thr Arg Thr Ile Leu Phe		
450	455	460
Leu Gln Asp Asp Gly Thr Leu Lys Pro Leu Ala Ile Glu Leu Ser Leu		
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Pro His Pro Arg Gly His Glu Phe Gly Ala Asp Ser Arg Val Val Leu		

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Lys	Ala	Tyr	Val	Ala	Val	Asn	Asp	Thr	Gly	Tyr	His	Gln	Leu	Ile	Ser											
					515								520								525					
His	Trp	Leu	Asn	Thr	His	Ala	Thr	Ile	Glu	Pro	Phe	Val	Ile	Ala	Thr											
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Asn	Arg	His	Leu	Ser	Val	Leu	His	Pro	Ile	His	Lys	Leu	Leu	Leu	Pro											
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His	Tyr	Arg	Asp	Thr	Met	Asn	Ile	Asn	Ala	Leu	Ala	Arg	Gln	Ser	Leu											
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Ile	Asn	Ala	Asp	Gly	Val	Ile	Glu	Arg	Ser	Phe	Leu	Pro	Gly	Lys	Tyr											
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Ser	Leu	Glu	Met	Ser	Ser	Ala	Val	Tyr	Lys	Ser	Trp	Val	Phe	Thr	Asp											
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Gln	Ala	Leu	Pro	Ala	Asp	Leu	Ile	Lys	Arg	Gly	Met	Ala	Ile	Glu	Asp											
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Pro	Cys	Ala	Pro	His	Gly	Leu	Arg	Leu	Val	Ile	Glu	Asp	Tyr	Pro	Tyr											
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					645								650								655					
Asn	Tyr	Val	Ser	Leu	Tyr	Tyr	Pro	Thr	Asp	Asp	Ala	Ile	Lys	Lys	Asp											
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Arg	Pro	Thr	Leu	Thr	Arg	Arg	Phe	Leu	Pro	Glu	Pro	Gly	Ser	Lys	Glu											
					740								745								750					
Tyr	Glu	Glu	Leu	Ser	Thr	Asn	Tyr	Gln	Lys	Ala	Tyr	Leu	Arg	Thr	Ile											
					755								760								765					
Thr	Arg	Lys	Ile	Glu	Ala	Leu	Val	Asp	Leu	Ser	Val	Ile	Glu	Ile	Leu											
770								775								780										
Ser	Arg	His	Ala	Ser	Asp	Glu	Ile	Tyr	Leu	Gly	Lys	Arg	Asp	Ser	Asp											
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 Thr Lys Leu Lys Glu Ile Glu Ala Lys Ile Asn Ser Arg Asn Lys Asp
 820 825 830
 Ser Ser Leu Arg Asn Arg Asn Gly Pro Val Gln Met Pro Tyr Thr Val
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 50 55 60
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 65 70 75 80
 Lys Lys Thr Tyr Leu Glu Gly Ile Ile Thr Ser Ile Pro Thr Leu Gly
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 Ala Gly Gln Ser Ala Phe Thr Ile His Phe Glu Trp Asp Ala Asp Met
 100 105 110
 Gly Ile Pro Gly Ala Phe Leu Ile Lys Asn Tyr Met Gln Val Glu Leu
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 Phe Leu Val Ser Leu Thr Leu Glu Asp Ile Pro Asn Gln Gly Ser Met
 130 135 140
 His Phe Val Cys Asn Ser Trp Val Tyr Asn Ser Lys Val Tyr Glu Lys
 145 150 155 160
 Asp Arg Ile Phe Phe Ala Ser Glu Thr Tyr Val Pro Ser Glu Thr Pro
 165 170 175

Gly Pro Leu Val Thr Tyr Arg Glu Ala Glu Leu Gln Ala Leu Arg Gly		
180	185	190
Asn Gly Thr Gly Lys Arg Lys Glu Trp Asp Arg Val Tyr Asp Tyr Asp		
195	200	205
Val Tyr Asn Asp Leu Gly Asn Pro Asp Ser Gly Glu Asn Phe Ala Arg		
210	215	220
Pro Val Leu Gly Gly Ser Leu Thr His Pro Tyr Pro Arg Arg Gly Arg		
225	230	235
Thr Gly Arg Lys Pro Thr Lys Lys Asp Pro Asn Ser Glu Lys Pro Gly		
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Asp Phe Leu Thr Tyr Gly Leu Lys Ser Leu Thr Arg Ser Phe Leu Pro		
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Ala Leu Lys Thr Val Phe Asp Ile Asn Phe Thr Pro Asn Glu Phe Asp		
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Ser Phe Glu Glu Val Arg Ala Leu Cys Glu Gly Gly Ile Lys Leu Pro		
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Thr Asp Ile Leu Ser Lys Ile Ser Pro Leu Pro Val Leu Lys Glu Ile		
325	330	335
Phe Arg Thr Asp Gly Glu Ser Val Leu Lys Phe Ser Val Pro Asp Leu		
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Ile Lys Val Ser Lys Ser Ala Trp Met Thr Asp Glu Glu Phe Ala Arg		
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Glu Met Ile Ala Gly Val Asn Pro Cys Val Ile Arg Arg Leu Gln Glu		
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Phe Pro Pro Gln Ser Lys Leu Asp Pro Ser Val Tyr Gly Asp Gln Thr		
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Ser Cys Tyr His Gln Leu Ile Ser His Trp Leu Asn Thr His Ala Val					
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	530		535		540
Pro Ile Tyr Lys Leu Leu Phe Pro His Tyr Arg Asp Thr Met Asn Ile					
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Asn Ala Leu Ala Arg Gln Ser Leu Ile Asn Ala Asp Gly Phe Ile Glu					
	565		570		575
Lys Thr Phe Leu Gly Gly Lys Tyr Ala Val Glu Ile Ser Ser Ser Gly					
	580		585		590
Tyr Lys Asn Trp Val Phe Leu Asp Gln Ala Leu Pro Ala Asp Leu Ile					
	595		600		605
Lys Arg Gly Met Ala Ile Glu Asp Ser Ser Cys Pro Asn Gly Leu Arg					
610		615		620	
Leu Val Ile Glu Asp Tyr Pro Tyr Ala Val Asp Gly Leu Glu Ile Trp					
625		630		635	640
Asp Ala Ile Lys Thr Trp Val Gln Glu Tyr Val Ser Leu Tyr Tyr Ala					
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Thr Asn Asp Ala Ile Lys Lys Asp His Glu Leu Gln Ala Trp Trp Lys					
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Glu Val Val Glu Lys Gly His Gly Asp Leu Lys Asp Lys Pro Trp Trp					
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Pro Lys Met Gln Thr Leu Gln Glu Leu Ile Gln Ser Cys Ser Thr Ile					
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Ile Trp Ile Ala Ser Ala Leu His Ala Ala Val Asn Phe Gly Gln Tyr					
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Pro Tyr Gly Gly Phe Ile Leu Asn Arg Pro Thr Leu Ser Arg Arg Trp					
	725		730		735
Ile Pro Glu Glu Gly Thr Pro Glu Tyr Asp Glu Met Thr Lys Asn Pro					
	740		745		750
Gln Lys Ala Tyr Leu Arg Thr Ile Thr Pro Lys Phe Gln Ala Leu Val					
	755		760		765
Asp Leu Ser Val Ile Glu Ile Leu Ser Arg His Ala Ser Asp Glu Val					
	770		775		780
Tyr Leu Gly Gln Arg Asp Asn Pro Asn Trp Thr Ser Asn Pro Lys Ala					
785		790		795	800

Ile Glu Ala Phe Lys Lys Phe Gly Lys Lys Leu Ala Glu Ile Glu Thr
805 810 815
Lys Ile Ser Glu Arg Asn His Asp Pro Asn Leu Arg Asn Arg Thr Gly
820 825 830
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Ile Asn Ser Leu Pro Thr Ala Lys

1 5

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Thr Ile Leu Phe Leu Lys

1 5

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His Leu Ser Val Leu His Pro Ile Tyr Lys

1 5 10

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1 5 10

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Phe Ile Pro Ala Glu Gly Thr Pro Glu Tyr Asp Glu Met Val Lys

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1 5

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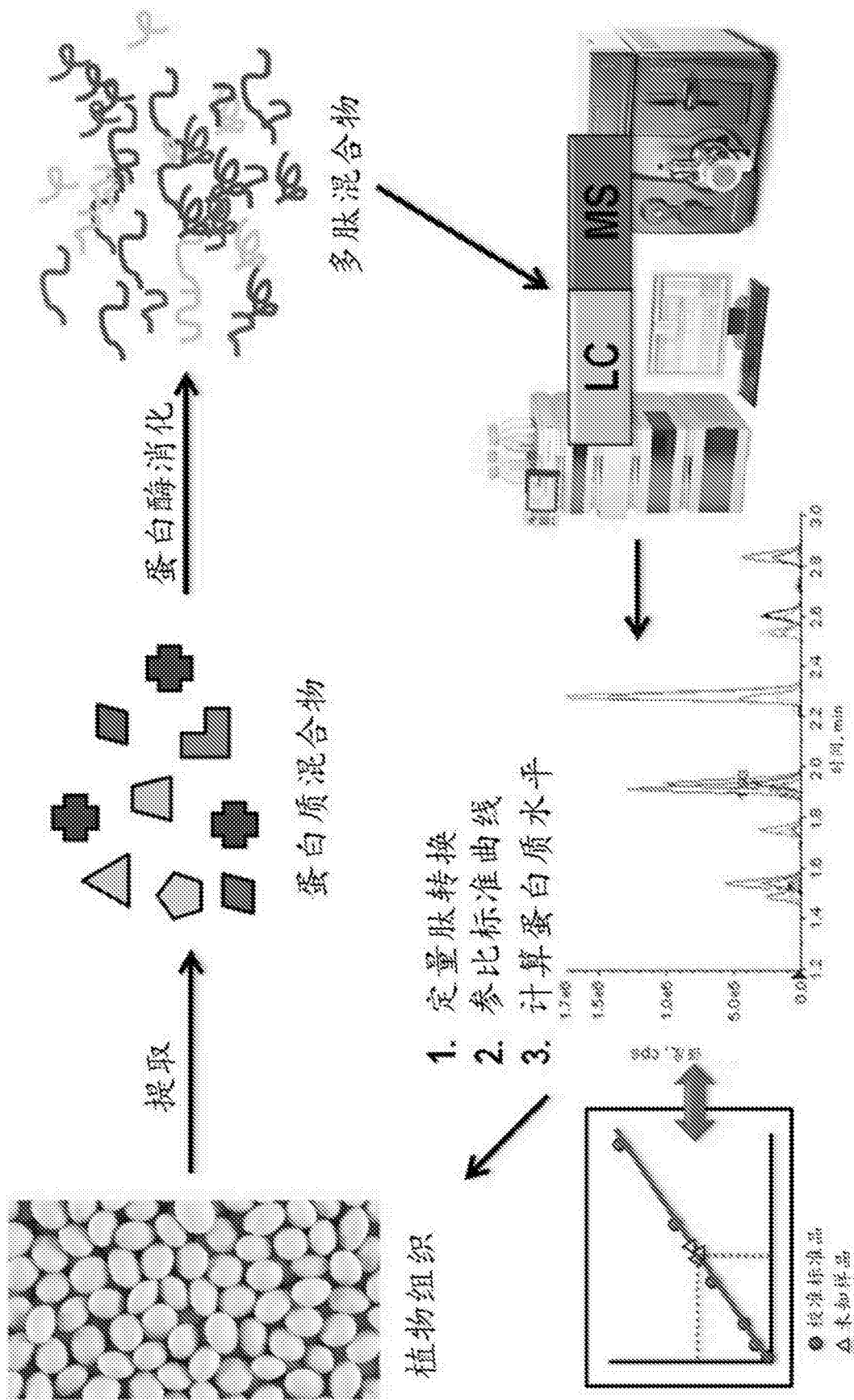


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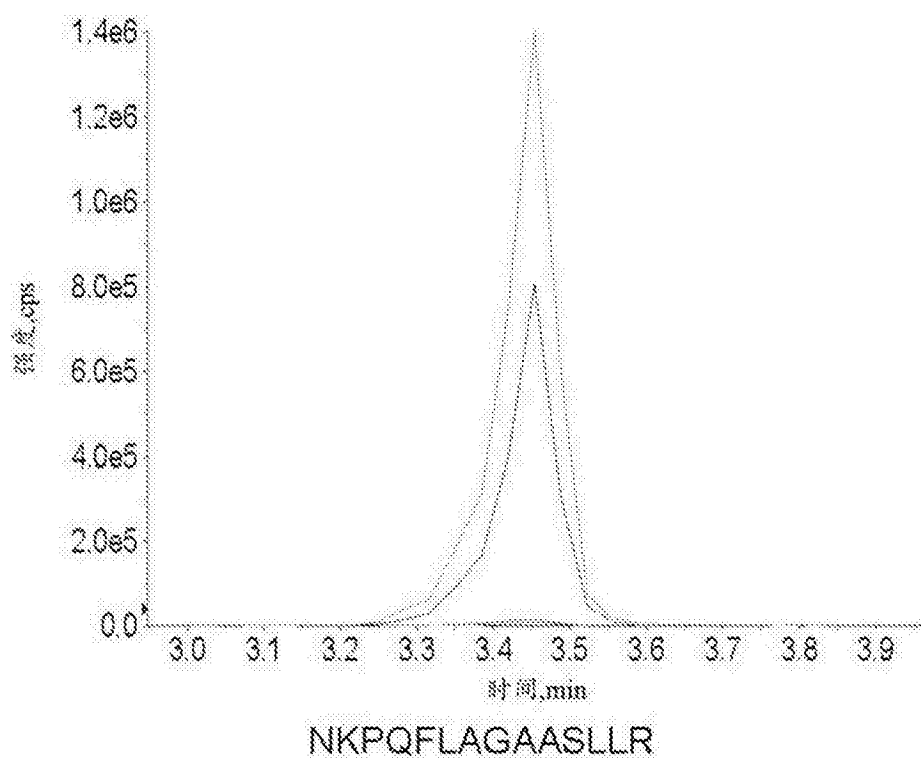


图2A

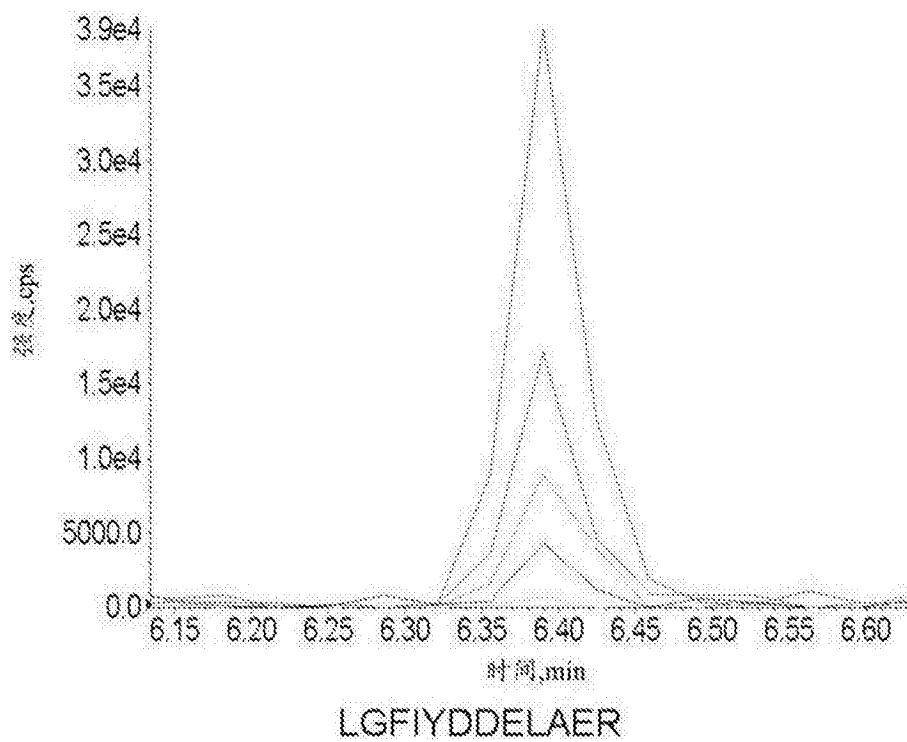


图2B

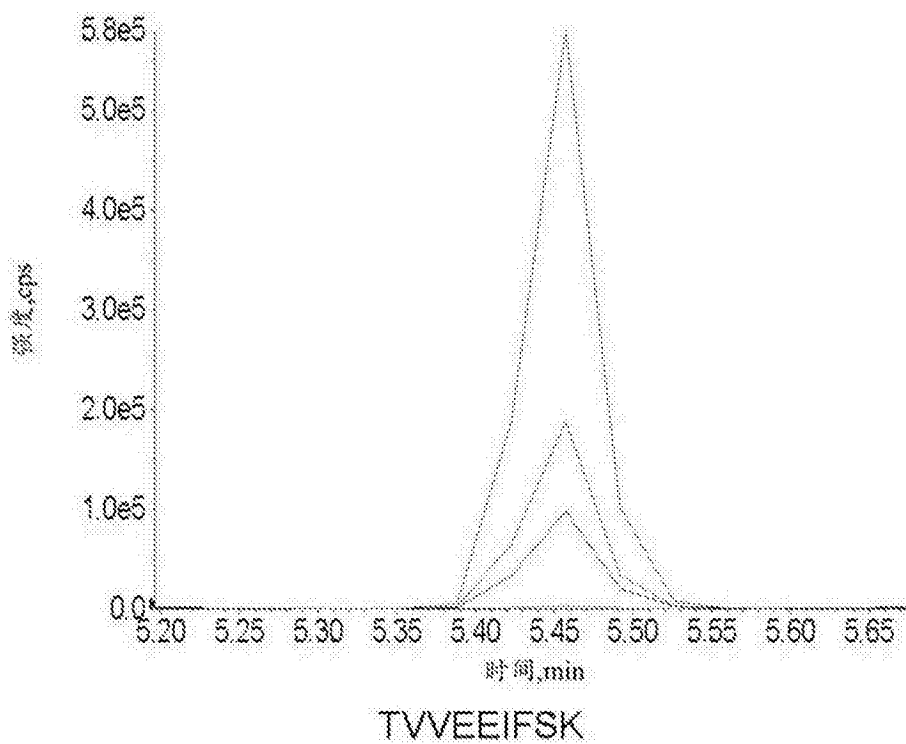


图2C

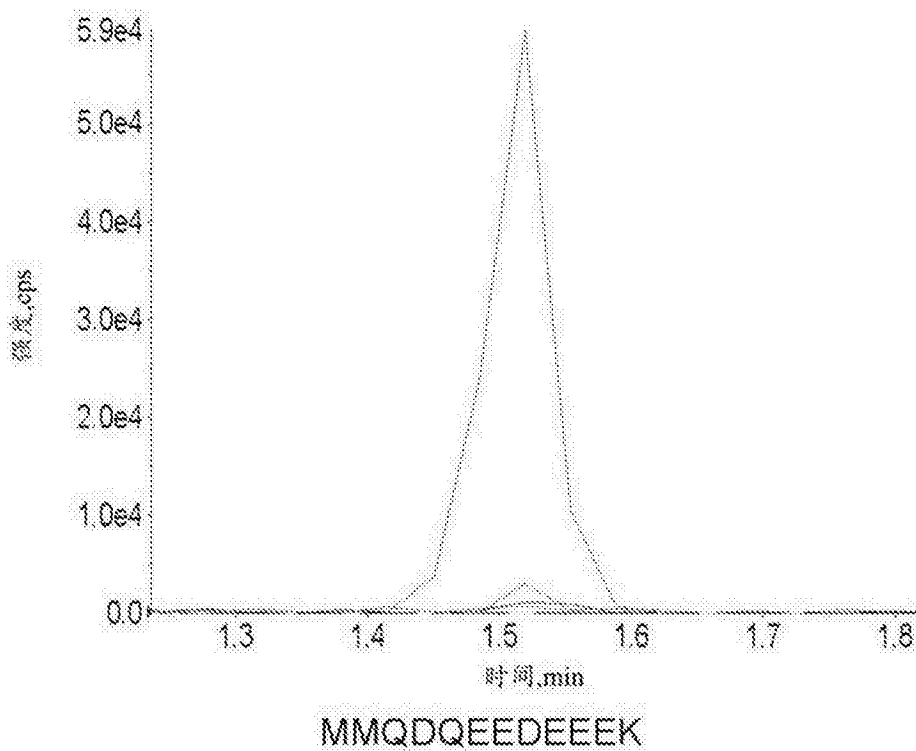


图2D

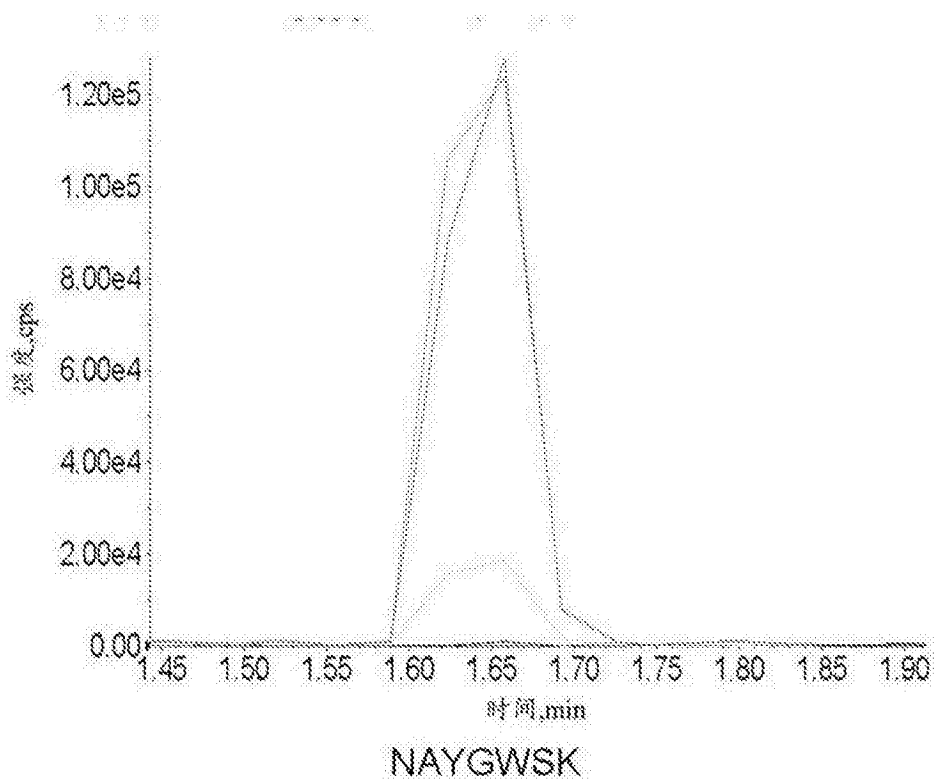


图2E

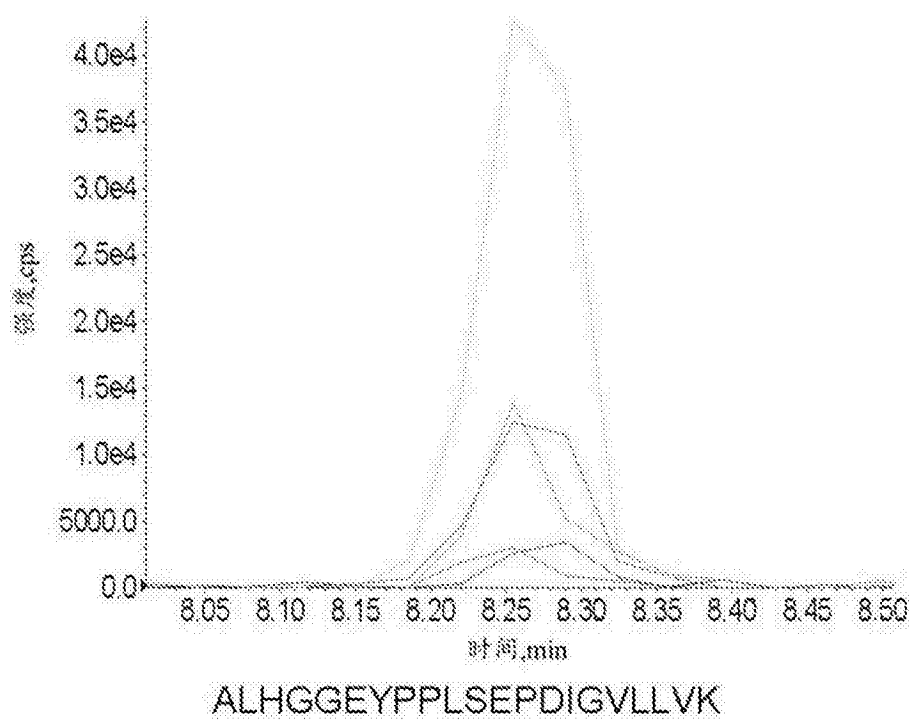
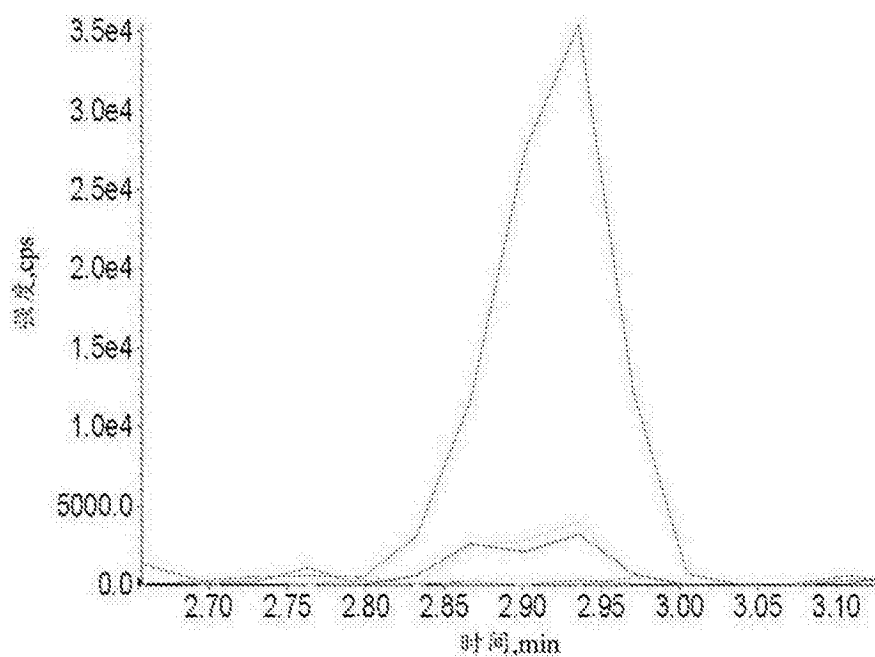
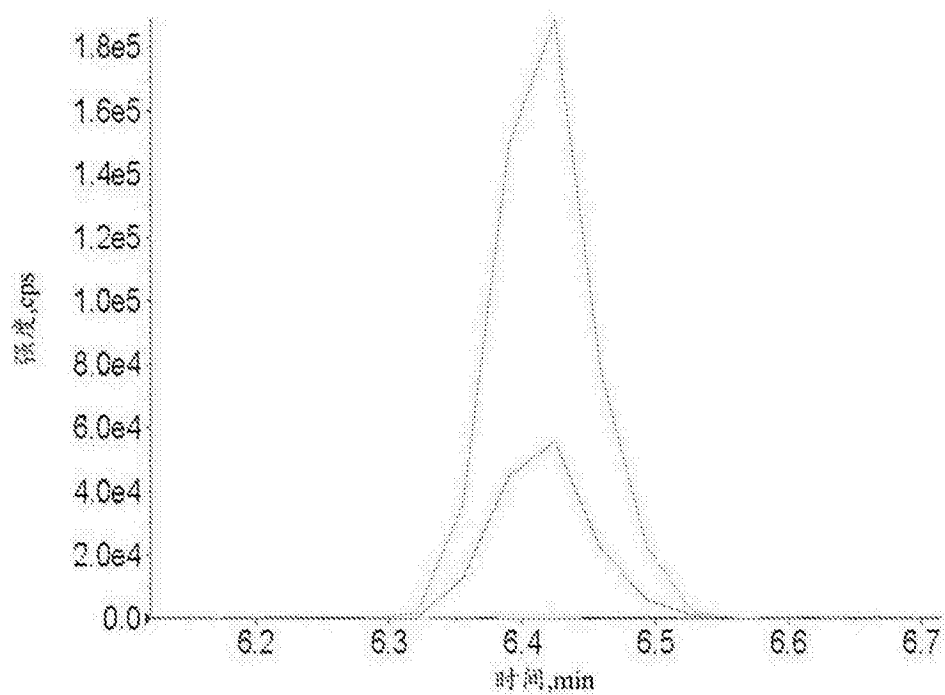


图2F



QGDVFVPR

图2G



YFPFCQVASR

图2H

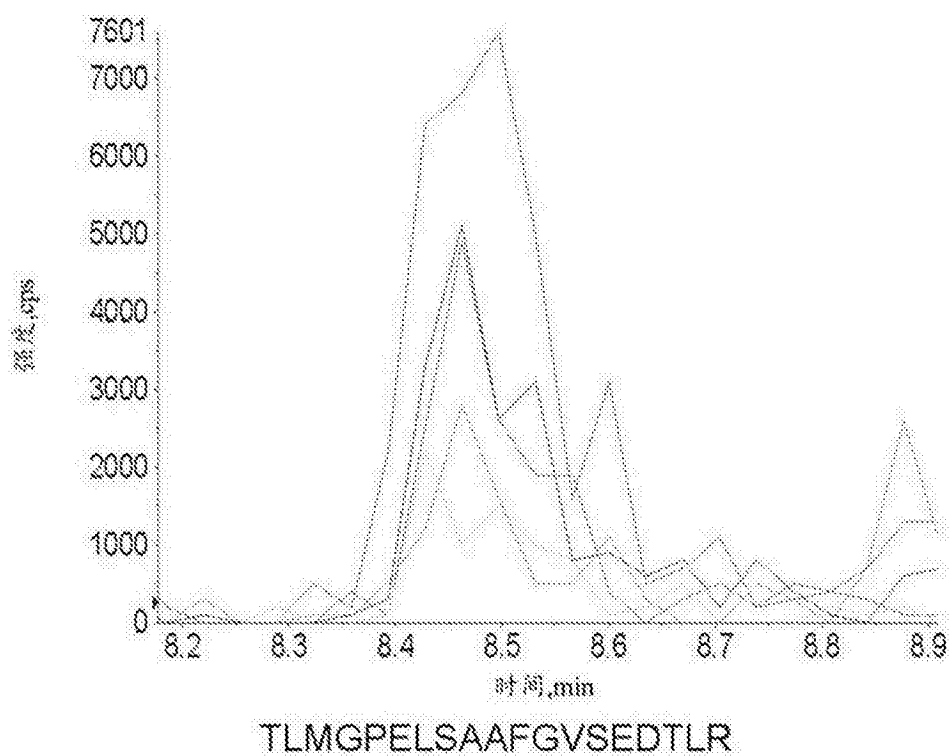


图2I

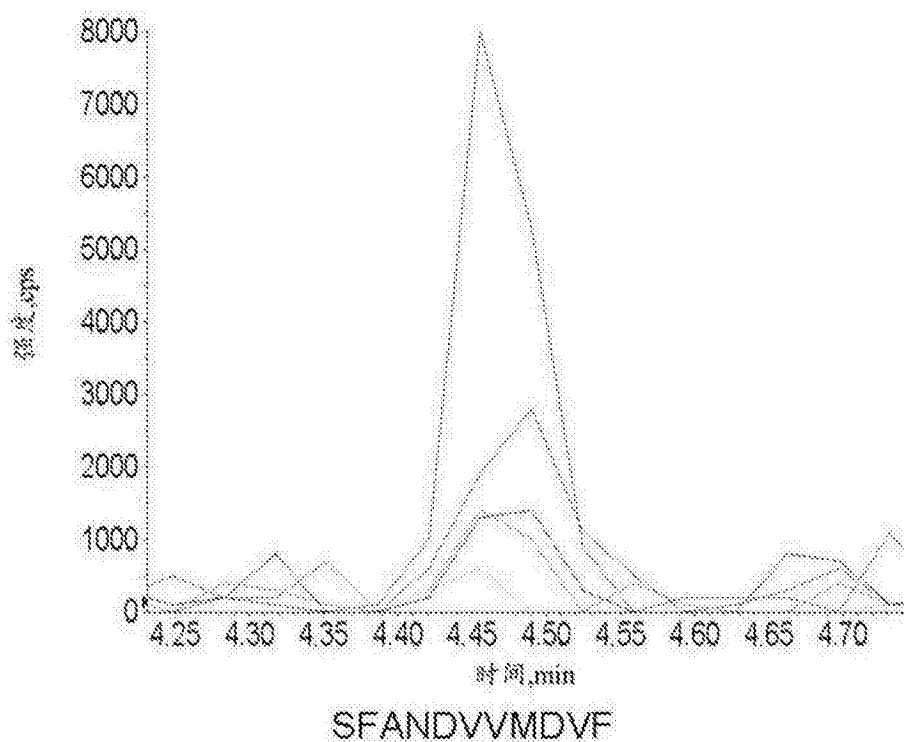


图2J

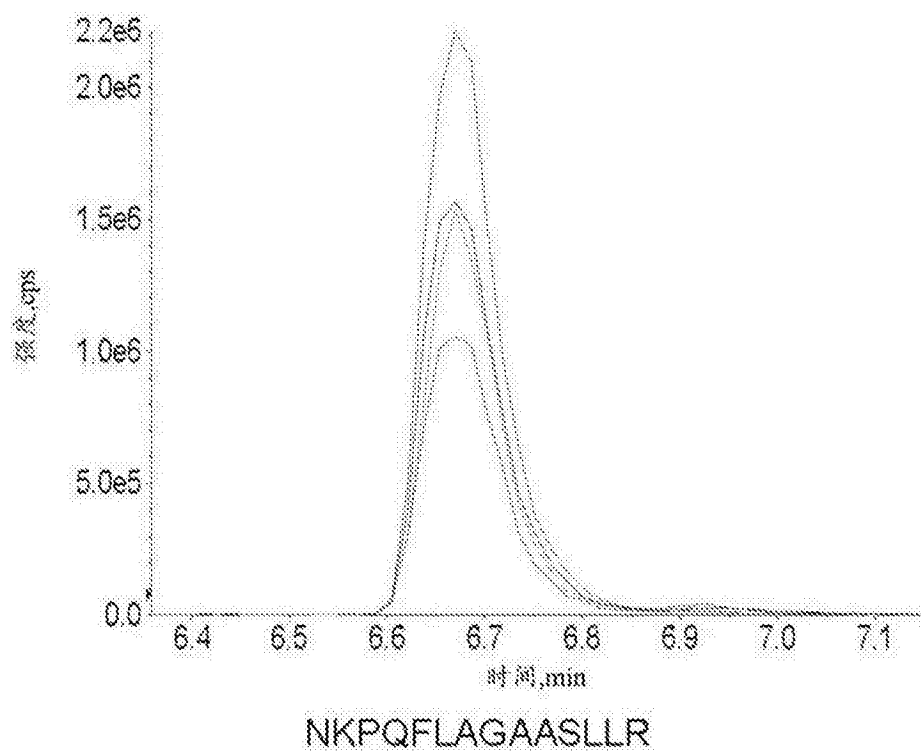


图2K

	1	50
28K Eric BAB21619	(1)	---NTTLNLLLVFLCHGVATTMTAFHDDEGGGKESPKSLFLMSNSTRVFK
28K ILSI 12697782	(1)	MGNKNTLNLNLLLVFLCHGVATTMTAFHDDEGGGKESPKSLFLMSNSTRVFK
28K Ping ACD36978.1	(1)	-----VLCHEGVATTMTAFHDDEGGGKESPKSLFLMSNSTRVFK
28K Ping ACD36975.1	(1)	-----
28K Ping ACD36976.1	(1)	-----
28K Ping ACD36974.1	(1)	-----
共有	(1)	VLCHEGVATTMTAFHDDEGGGKESPKSLFLMSNSTRVFK
	51	100
28K Eric BAB21619	(48)	TDAGEMVVLKSHGGRIFVYRHHIGFISMEPKSLFVFPQYLDNLIIIFIRRG
28K ILSI 12697782	(51)	TDAGEMVVLKSHGGRIFVYRHHIGFISMEPKSLFVFPQYLDNLIIIFIRRG
28K Ping ACD36978.1	(39)	TDAGEMVVLKSHGGRIFVYRHHIGFISMEPKSLFVFPQYLDNLIIIFIRRG
28K Ping ACD36975.1	(1)	-----LDNLIIIFIRRG
28K Ping ACD36976.1	(1)	-----LDNLIIIFIRRG
28K Ping ACD36974.1	(1)	-----LDNLIIIFIRRG
共有	(51)	TDAGEMVVLKSHGGRIFVYRHHIGFISMEPKSLFVFPQYLDNLIIIFIRRG
	101	150
28K Eric BAB21619	(98)	EAKLGFIYDDELAERRLKTGDLYMIPSGSAFYLVNIGEGQRLHVICSIDP
28K ILSI 12697782	(101)	EAKLGFIYDDELAERFLKTGDLYMIPSGSAFYLVNIGEGQRLHVICSIDP
28K Ping ACD36978.1	(89)	EAKLGFIYDDELAERFLKTGDLYMIPSGSAFYLVNIGEGQRLHVICSIDP
28K Ping ACD36975.1	(13)	EAKLGFIYDDELAERRLKTGDLYMIPSGSAFYLVNIGEGQRLHVICSIDP
28K Ping ACD36976.1	(13)	EAKLGFIYDDELAERFLKTGDLYMIPSGSAFYLVNIGEGQRLHVICSIDP
28K Ping ACD36974.1	(13)	EAKLGFIYDDELAERRLKTGDLYMIPSGSAFYLVNIGEGQRLHVICSIDP
共有	(101)	EAKLGFIYDDELAERRLKTGDLYMIPSGSAFYLVNIGEGQRLHVICSIDP
	151	200
28K Eric BAB21619	(148)	STSLGLETFQSFYIGGGANSHSVLSGFEPAILLETAFNESRTVVEEIFSKE
28K ILSI 12697782	(151)	STSLGLETFQSFYIGGGANSHSVLSGFEPAILLETAFNESRTVVEEIFSKE
28K Ping ACD36978.1	(139)	STSLGLETFQSFYIGGGANSHSVLSGFEPAILLETAFNESRTVVEEIFSKE
28K Ping ACD36975.1	(63)	STSLGLETFQSFYIGGGANSHSVLSGFEPAILLETAFNESRTVVEEIFSKE
28K Ping ACD36976.1	(63)	STSLGLETFQSFNIGGGANSHSVLSGFEPAILLETAFNESRTVVEEIFSKE
28K Ping ACD36974.1	(63)	STSLGLETFQSFYIGGGANSHSVLSGFEPAILLETAFNESRTVVEEIFSKE
共有	(151)	STSLGLETFQSFYIGGGANSHSVLSGFEPAILLETAFNESRTVVEEIFSKE

图2L

		201		250
28K Eric BAB21619	(198)	LDGPIMFVDDSHAPSLWTKFLQLKKDDKEQQLKXMMQDQEEDDEEEKQTSR		
28K ILST 12697782	(201)	LDGPIMFVDDSHAPSLWTKFLQLKKDDKEQQLKXMMQDQEEDDEEEKQTSR		
28K Ping ACD36978.1	(199)	LDGPIMFVDDSHAPSLWTKFLQLKKDDKEQQLKXMMQDQEEDDEEEKQTSR		
28K Ping ACD36975.1	(113)	LDGPIMFVDDSHAPSLWTKFLQLKKDDKEQQLKXMMQDQEEDDEEEKQTSR		
28K Ping ACD36976.1	(113)	LDGPIMFVDDSHAPSLWTKFLQLKKDDKEQQLKXMMQDQEEDDEEEKQTSR		
28K Ping ACD36974.1	(113)	LDGPIMFVDDSHVPSLWTKFLQLKKDDKEQQLKXMMQDQEEDDEEEKQTSR		
共有	(201)	LDGPIMFVDDSHAPSLWTKFLQLKKDDKEQQLKXMMQDQEEDDEEEKQTSR		
		251		300
28K Eric BAB21619	(240)	SWRKLLSTVFGKVNKIEKNEDTAGSPASYNLYDDKKADFFKNAYGWSKALH		
28K ILST 12697782	(251)	SWRKLLSTVFGKVNKIEKNEDTAGSPASYNLYDDKKADFFKNAYGWSKALH		
28K Ping ACD36978.1	(239)	SWRKLLSTVFGKVNKIEKNEDTAGSPASYNLYDDKKADFFKNAYGWSKALH		
28K Ping ACD36975.1	(163)	SWRKLLSTVFGKVNKIEKNEDTAGSPASYNLYDDKKADFFKNAYGWSKALH		
28K Ping ACD36976.1	(163)	SWRKLLSTVFGKVNKIEKNEDTAGSPASYNLYDDKKADFFKNAYGWSKALH		
28K Ping ACD36974.1	(163)	SWRKLLSTVFGKVNKIEKNEDTAGSPASYNLYDDKKADFFKNAYGWSKALH		
共有	(251)	SWRKLLSTVFGKVNKIEKNEDTAGSPASYNLYDDKKADFFKNAYGWSKALH		
		301		350
28K Eric BAB21619	(290)	GGEYFPLSEPDIGVLLVVKLSAGSMLAPHVNPISDEYTTIVLSGYGELHIGY		
28K ILST 12697782	(301)	GGEYFPLSEPDIGVLLVVKLSAGSMLAPHVNPISDEYTTIVLSGYGELHIGY		
28K Ping ACD36978.1	(269)	GGEYFPLSEPDIGVLLVVKLSAGSMLAPHVNPISDEYTTIVLSGYGELHIGY		
28K Ping ACD36975.1	(213)	GGEYFPLSEPDIGVLLVVKLSAGSMLAPHVNPISDEYTTIVLSGYGELHIGY		
28K Ping ACD36976.1	(213)	GGEYFPLSEPDIGVLLVVKLSAGSMLAPHVNPISDEYTTIVLSGYGELHIGY		
28K Ping ACD36974.1	(213)	GGEYFPLSEPDIGVLLVVKLSAGSMLAPHVNPISDEYTTIVLSGYGELHIGY		
共有	(301)	GGEYFPLSEPDIGVLLVVKLSAGSMLAPHVNPISDEYTTIVLSGYGELHIGY		
		351		400
28K Eric BAB21619	(349)	PNGSKAMTKIKQGQGVFVFRYFFFCQVASRDGPLEFFGFSTSAFENKPKQ		
28K ILST 12697782	(351)	PNGSKAMTKIKQGQGVFVFRYFFFCQVASRDGPLEFFGFSTSAFENKPKQ		
28K Ping ACD36978.1	(339)	PNGSKAMTKIKQGQGVFVFRYFFFCQVASRDGPLEFFGFSTSAFENKPKQ		
28K Ping ACD36975.1	(263)	PNGSKAMTKIKQGQGVFVFRYFFFCQVASRDGPLEFFGFSTSAFENKPKQ		
28K Ping ACD36976.1	(263)	PNGSKAMTKIKQGQGVFVFRYFFFCQVASRDGPLEFFGFSTSAFENKPKQ		
28K Ping ACD36974.1	(263)	PNGSKAMTKIKQGQGVFVFRYFFFCQVASRDGPLEFFGFSTSAFENKPKQ		
共有	(351)	PNGSKAMTKIKQGQGVFVFRYFFFCQVASRDGPLEFFGFSTSAFENKPKQ		

图2L续

		401	450
28K Eric BAB21619	(398)	FLAGAASLLRTLMGPFLSAAPFGVSEDTLRRAVDAQHEAVILPSAWAAPPE	
28K ILSI 12697782	(401)	FLAGAASLLRTLMGPFLSAAPFGVSEDTLRRAVDAQHEAVILPSAWAAPPE	
28K Ping ACD36978.1	(389)	FLAGAASLLRTLMGPFLSAAPFGVSEDTLRRAVDAQHEAVILPSAWAAP-R	
28K Ping ACD36975.1	(313)	FLAGAASLLRTLMGPFLSAAPFGVSEDTLRRAVDAQHEAVILPSAWAAPPE	
28K Ping ACD36976.1	(313)	FLAGAASLLRTLMGPFLSAAPFGVSEDTLRRAVDAQHEAVILPSAWAAPPE	
28K Ping ACD36974.1	(313)	FLAGAASL-----	
共有	(401)	FLAGAASLLRTLMGPFLSAAPFGVSEDTLRRAVDAQHEAVILPSAWAAPPE	
		451	476
28K Eric BAB21619	(448)	NAGKLNMEEEPNAIRSFANDVVMDF	
28K ILSI 12697782	(451)	NAGKLNMEEEPNAIRSFANDVVMDF	
28K Ping ACD36978.1	(438)	FMQEAEMEEESQMLLKLCQ-----	
28K Ping ACD36975.1	(363)	NAGKLNMEEEP-----	
28K Ping ACD36976.1	(363)	NAGKLNMEEEP-----	
28K Ping ACD36974.1	(321)	-----	
共有	(451)	NAGKLNMEEEP	

图2L续

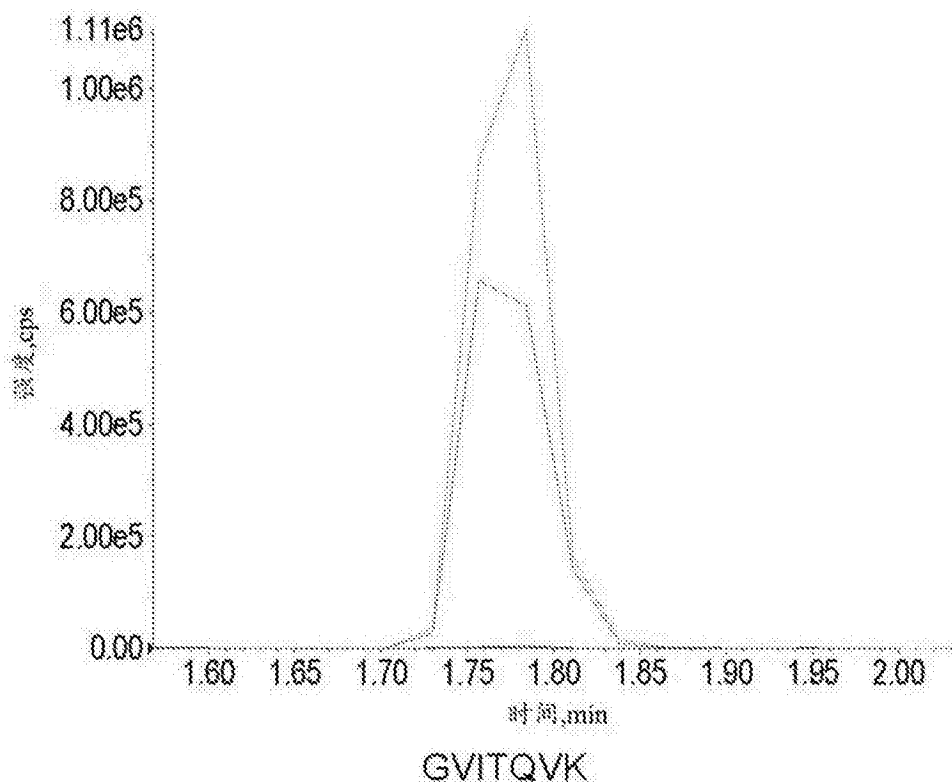


图3A

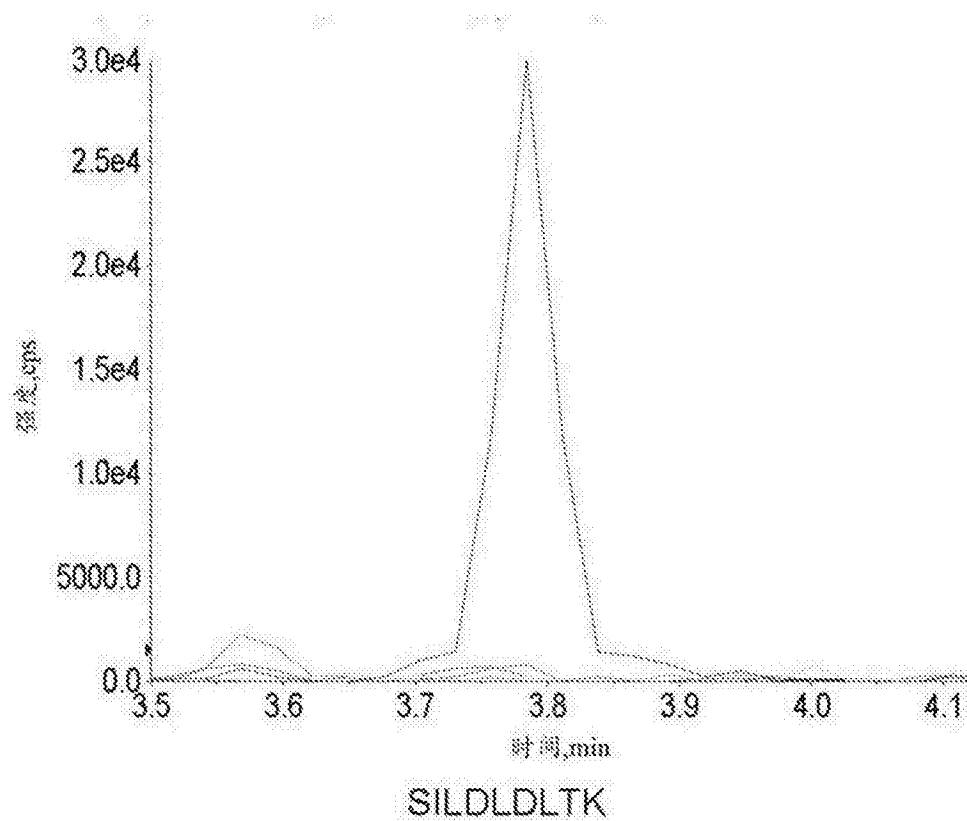


图3B

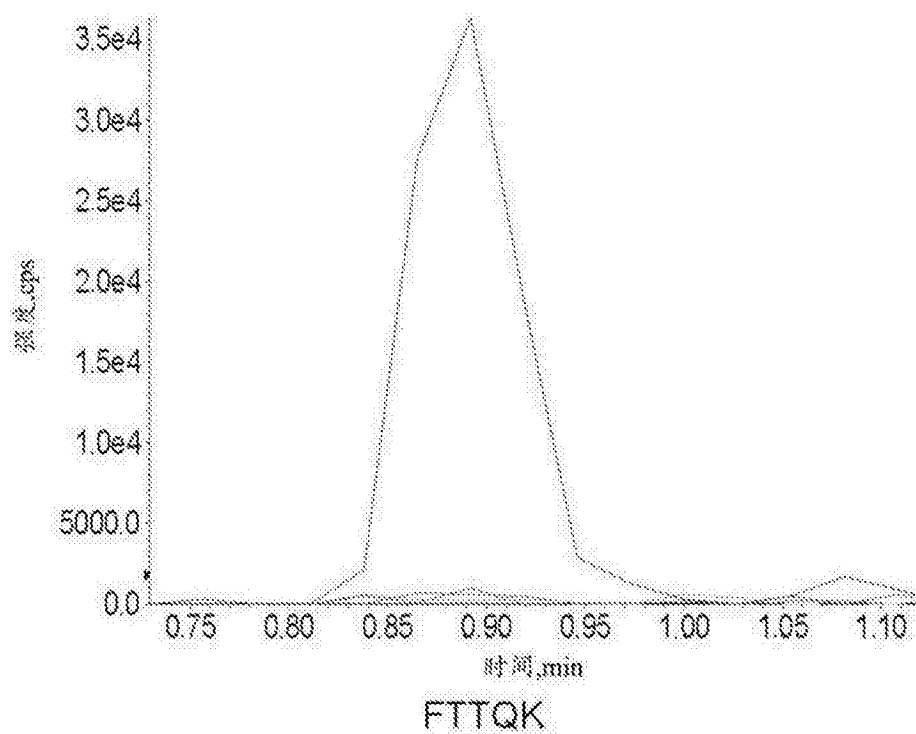


图3C

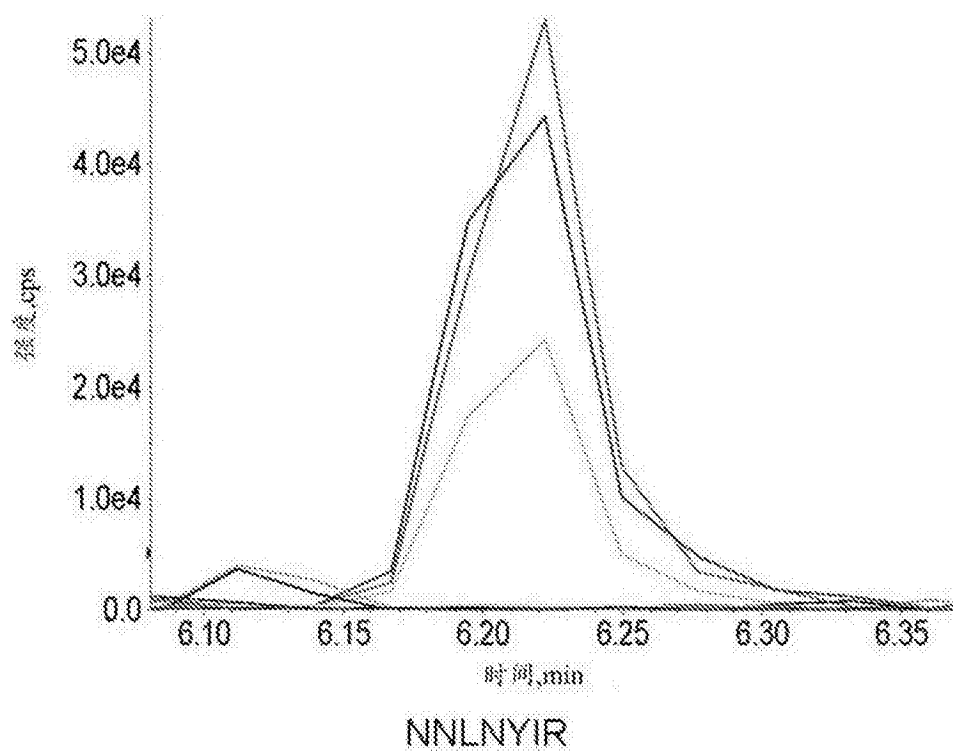


图3D

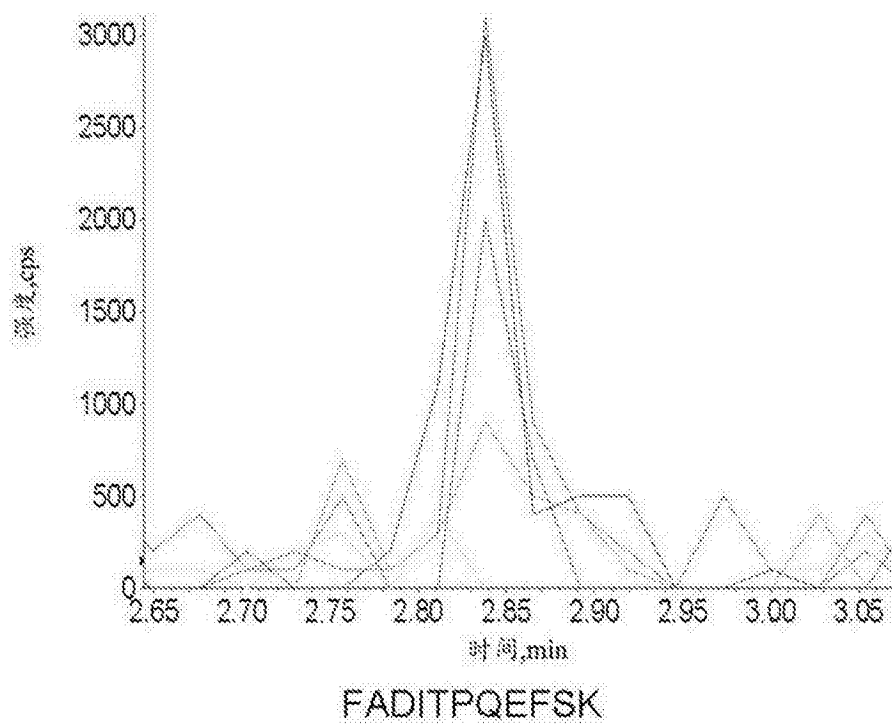


图3E

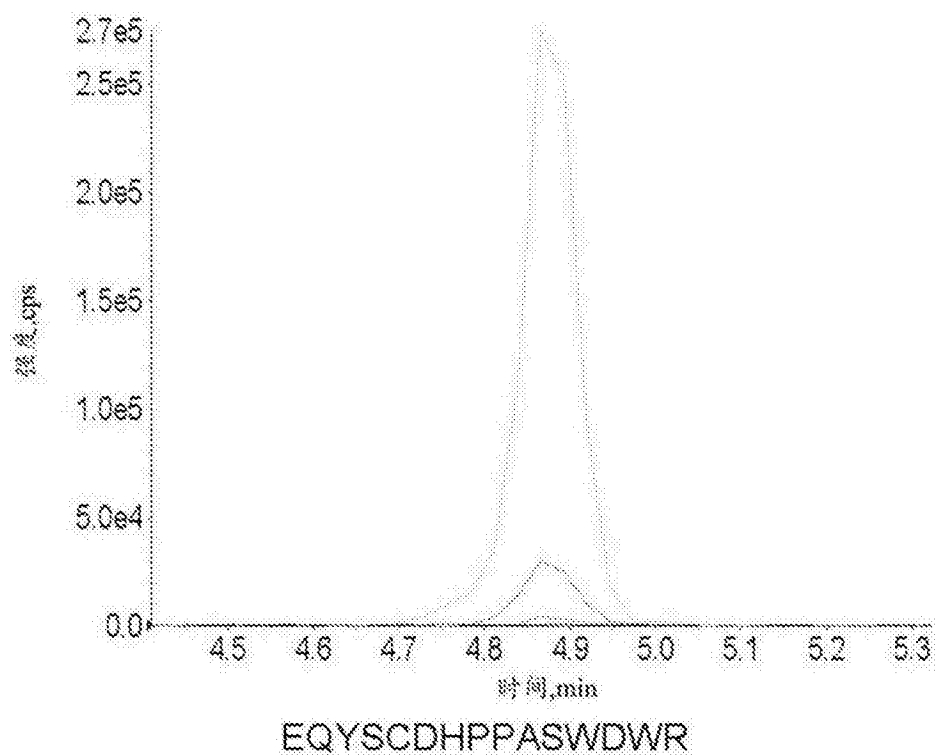


图3F

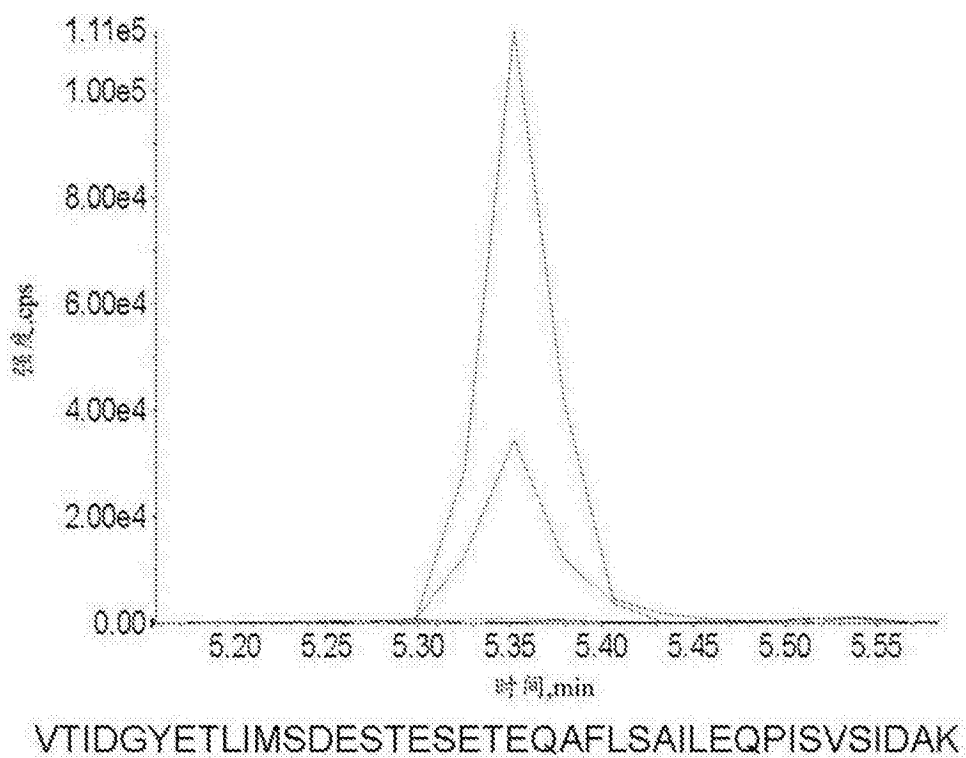


图3G

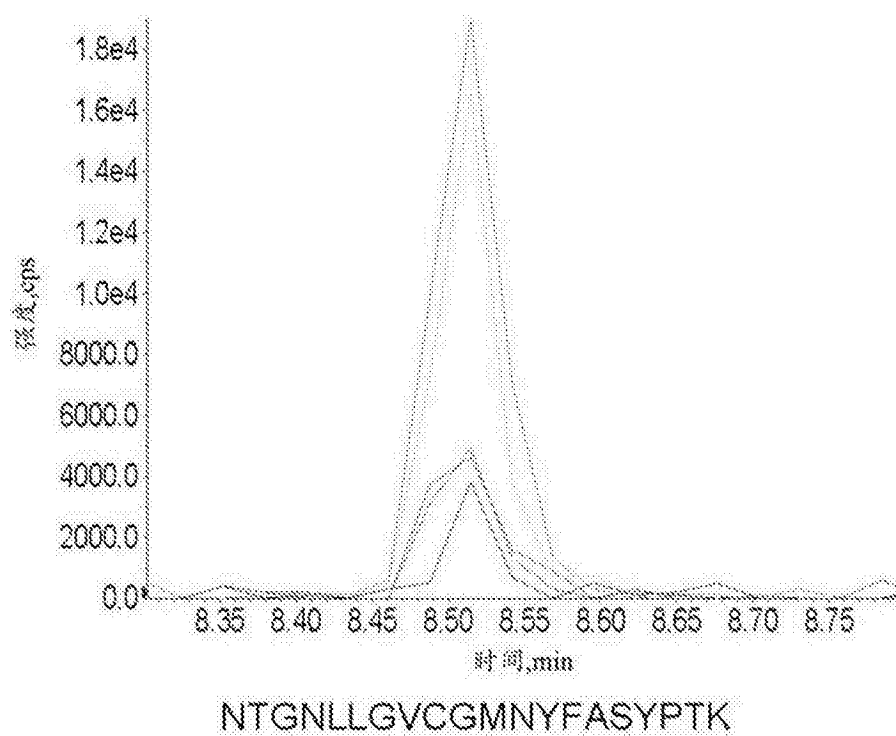


图3H

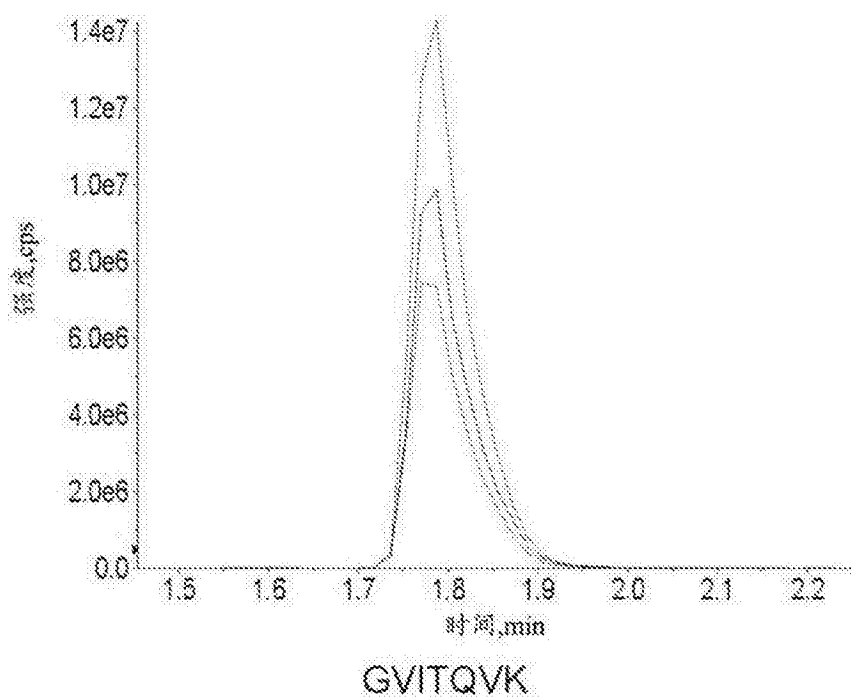


图3I

	1	50
30K ILSI 84371705	(1) MGFLVLLLPSLLGLSSSSSSISTHRSILDLDLTkFTTQKQVSSLPQLWKSE	
30K Ping AAB09252.1	(1) MGFLVLLLPSLLGLSSSSSSISTHRSILDLDLTkFTTQKQVSSLPQLWKSE	
30K Ping P22895.1	(1) MGFLVLLLPSLLGLSSSSSSISTHRSILDLDLTkFTTQKQVSSLPQLWKSE	
共有	(1) MGFLVLLLPSLLGLSSSSSSISTHRSILDLDLTkFTTQKQVSSLPQLWKSE	
	51	100
30K ILSI 84371705	(51) HGRVYHNHEEEAHPLEIFFQNNLNYIRDMNANRKSPPHSHRLGLNKFADITP	
30K Ping AAB09252.1	(51) HGRVYHNHEEEAHPLEIFFQNNLNYIRDMNANRKSPPHSHRLGLNKFADITP	
30K Ping P22895.1	(51) HGRVYHNHEEEAHPLEIFFQNNLNYIRDMNANRKSPPHSHRLGLNKFADITP	
共有	(51) HGRVYHNHEEEAHPLEIFFQNNLNYIRDMNANRKSPPHSHRLGLNKFADITP	
	101	150
30K ILSI 84371705	(101) QEFSSKRYLQAPKDV8QQIKMANKKMKKEQVSCDHPPASWDWREKKGVTQV	
30K Ping AAB09252.1	(101) QEFSSKRYLQAPKDV8QQIKMANKKMKKEQVSCDHPPASWDWREKKGVTQV	
30K Ping P22895.1	(101) QEFSSKRYLQAPKDV8QQIKMANKKMKKEQVSCDHPPASWDWREKKGVTQV	
共有	(101) QEFSSKRYLQAPKDV8QQIKMANKKMKKEQVSCDHPPASWDWREKKGVTQV	
	151	200
30K ILSI 84371705	(151) KYQGGCGSGWAFSATGAIEAAAHAIATGDLVSLSEQELVDVVEESEGGSYNG	
30K Ping AAB09252.1	(151) KYQGGCGSGWAFSATGAIEAAAHAIATGDLVSLSEQELVDVVEESEGGSYNG	
30K Ping P22895.1	(151) KYQGGCGSGWAFSATGAIEAAAHAIATGDLVSLSEQELVDVVEESEGGSYNG	
共有	(151) KYQGGCGSGWAFSATGAIEAAAHAIATGDLVSLSEQELVDVVEESEGGSYNG	
	201	250
30K ILSI 84371705	(201) WHYQSPFEWVLEHGGIATDDDYPIRAKEGRCKANKIQDKVTIDGYETLINS	
30K Ping AAB09252.1	(201) WHYQSPFEWVLEHGGIATDDDYPIRAKEGRCKANKIQDKVTIDGYETLINS	
30K Ping P22895.1	(201) WHYQSPFEWVLEHGGIATDDDYPIRAKEGRCKANKIQDKVTIDGYETLINS	
共有	(201) WHYQSPFEWVLEHGGIATDDDYPIRAKEGRCKANKIQDKVTIDGYETLINS	
	251	300
30K ILSI 84371705	(251) DESTESETEQAFLSAILEQPISVSIDAKDFHLYTGGIYDGENCTSPYGIN	
30K Ping AAB09252.1	(251) DESTESETEQAFLSAILEQPISVSIDAKDFHLYTGGIYDGENCTSPYGIN	
30K Ping P22895.1	(251) DESTESETEQAFLSAILEQPISVSIDAKDFHLYTGGIYDGENCTSPYGIN	
共有	(251) DESTESETEQAFLSAILEQPISVSIDAKDFHLYTGGIYDGENCTSPYGIN	
	301	350
30K ILSI 84371705	(301) HFVLLVGYGSADGVDYWIAPNSWGEDWGEDGYIWIQRNTGNLLGVOGMNY	
30K Ping AAB09252.1	(301) HFVLLVGYGSADGVDYWIAPNSWGEDWGEDGYIWIQRNTGNLLGVOGMNY	
30K Ping P22895.1	(301) HFVLLVGYGSADGVDYWIAPNSWGEDWGEDGYIWIQRNTGNLLGVOGMNY	
共有	(301) HFVLLVGYGSADGVDYWIAPNSWGEDWGEDGYIWIQRNTGNLLGVOGMNY	
	351	379
30K ILSI 84371705	(351) FASYPTKEESETLV SARVKGHRVVDHSPL	
30K Ping AAB09252.1	(351) FASYPTKEESETLV SARVKGHRVVDHSPL	
30K Ping P22895.1	(351) FASYPTKEESETLV SARVKGHRVVDHSPL	
共有	(351) FASYPTKEESETLV SARVKGHRVVDHSPL	

图3J

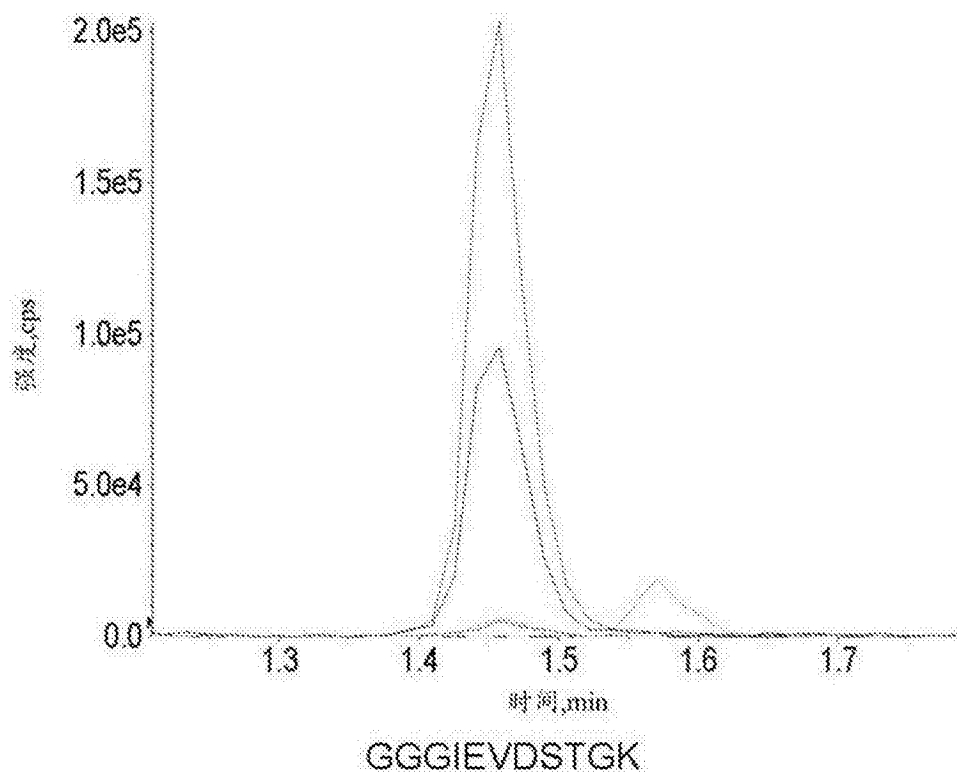


图4A

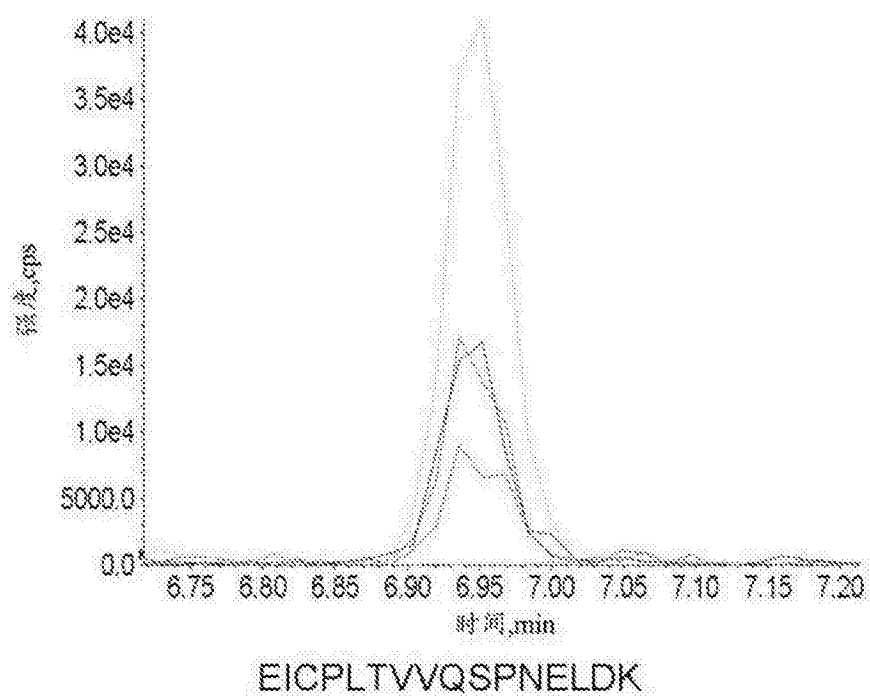


图4B

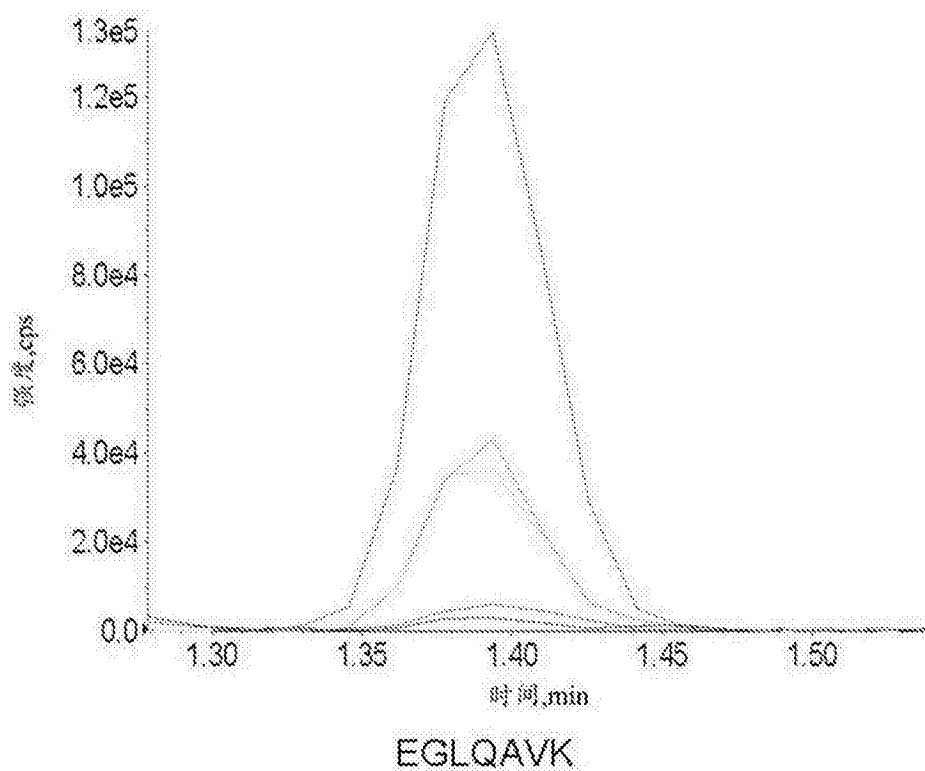


图4C

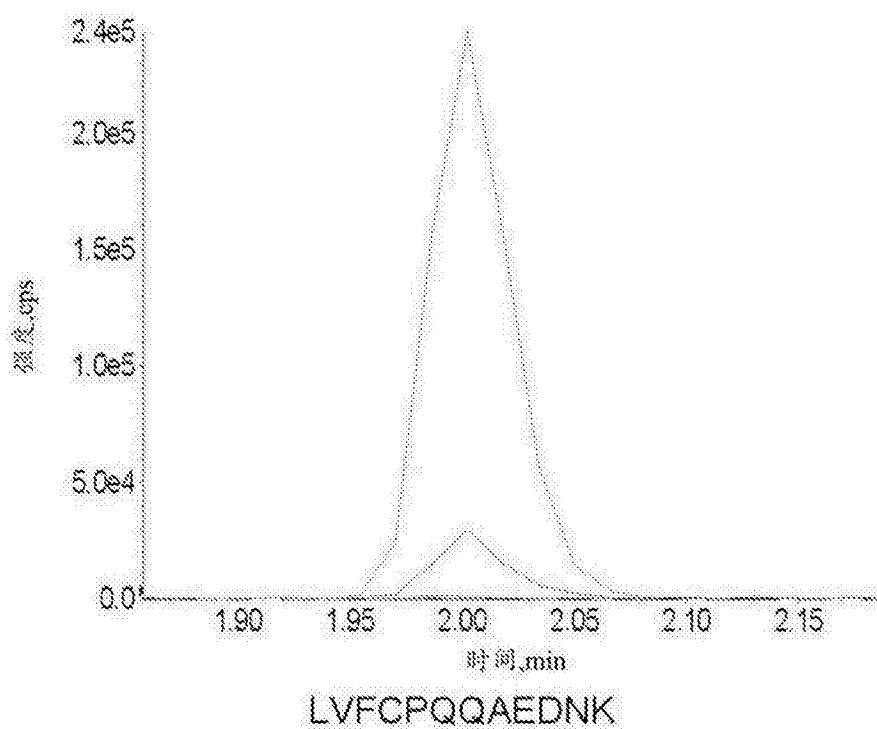


图4D

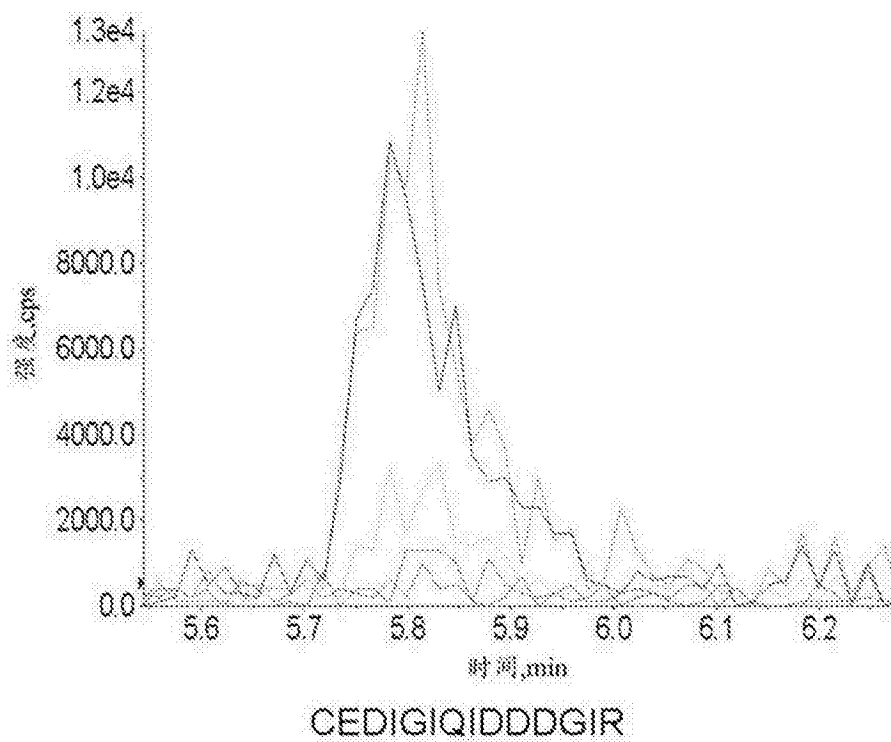


图4E

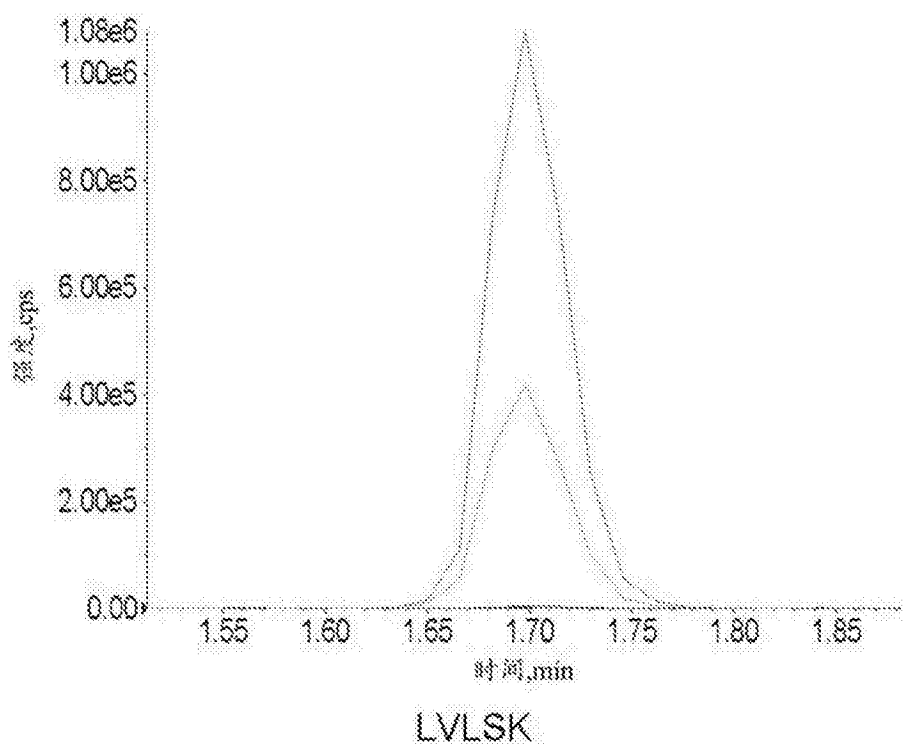


图4F

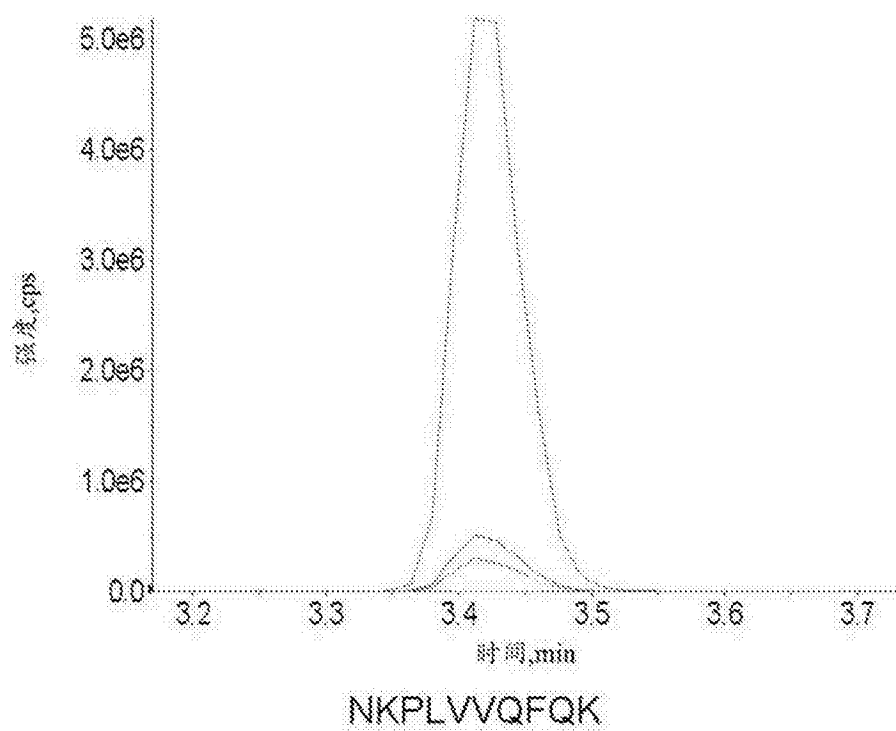


图4G

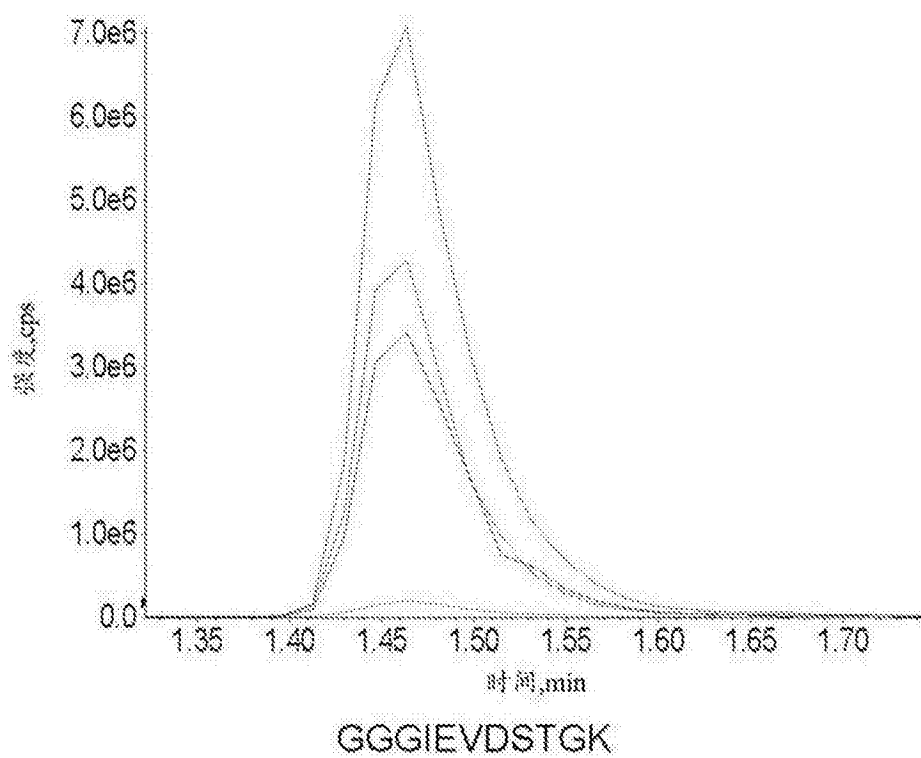


图4H

		1	50
KTI 1 AAB23482.1	(1)	MKSTIFFALFLVCFTISYLP SATAQFVLD TDD DPLQNGGTY YMLPV MRG	
KTI 1 AAB23483.1	(1)	MKSTIFFALFLVCFTISYLP SATAQFVLD TDD DPLQNGGTY YMLPV MRG	
KTI 1 CAA56343.1	(1)	MKSTTSLALFLLCALTSSYQPSATADIVFDTEGNPIRNGGTY YVLPVIRG	
共有	(1)	MKSTIFFALFLVCFTISYLP SATAQFVLD TDD DPLQNGGTY YMLPV MRG	
		51	100
KTI 1 AAB23482.1	(51)	KGGGIEVDSTGKEICPLTVVQSPNE-LDNGIGLVFTSPLHALFIAERYPL	
KTI 1 AAB23483.1	(51)	KSGGIEGNSTGKEICPLTVVQSPNK-HNNGIGLVFKSPLHALFIAERYPL	
KTI 1 CAA56343.1	(51)	KGGGIEFAKTETETCPLTVVQSPFEG LQRGLFLIISPPFKILDITEGLIL	
共有	(51)	KGGGIEGASTGKEICPLTVVQSPNE LDNGIGLVFSSPLHALFIAERYPL	
		101	150
KTI 1 AAB23482.1	(100)	SINFGSFAVITLCAGMPTENAIIVEREGLQAVKLAARDTVDGWFNIERVSR	
KTI 1 AAB23483.1	(100)	SINFDGFAVIFLOGVMPTKWAIVEREGLQAVTLAARDTVDGWFNIERVSR	
KTI 1 CAA56343.1	(101)	SLRFHLCTPLSLNSFSVDRYSQGSARRTPCQTHWLQKHNRQWFRIQRASS	
共有	(101)	SINFGSFAVISLOGGMPTKWAIVEREGLQAVTLAARDTVDGWFNIERVSR	
		151	200
KTI 1 AAB23482.1	(150)	EYND-YKLVFCPQQAEDNKCEDIGIQIDEDGIRRLVLS--KNNPLVVQFQ	
KTI 1 AAB23483.1	(150)	EYNDYKLVFCPQQAEDNKCEDIGIQIDNDGIRRLVLS--KNNPLVVEFQ	
KTI 1 CAA56343.1	(151)	ESNY-YKLVFCTSN-DDSSCGDIVAPIREGNRPLIVTHDQNHPLLVOFQ	
共有	(151)	EYND YKLVFCPQNAEDNKCEDIGIQIDNDGIRRLVLS KNNPLVVQFQ	
		201	
KTI 1 AAB23482.1	(197)	KFRSSTA----	
KTI 1 AAB23483.1	(198)	KFRSSTA----	
KTI 1 CAA56343.1	(199)	KVEAYESSTA	
共有	(201)	KFRSSTA	

图4I

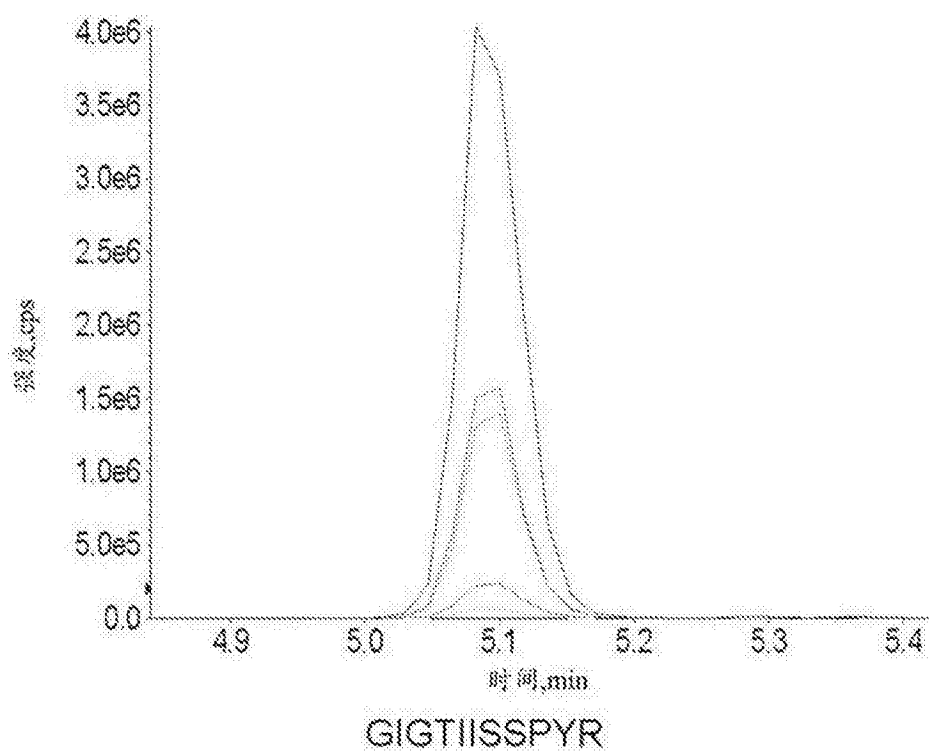


图5A

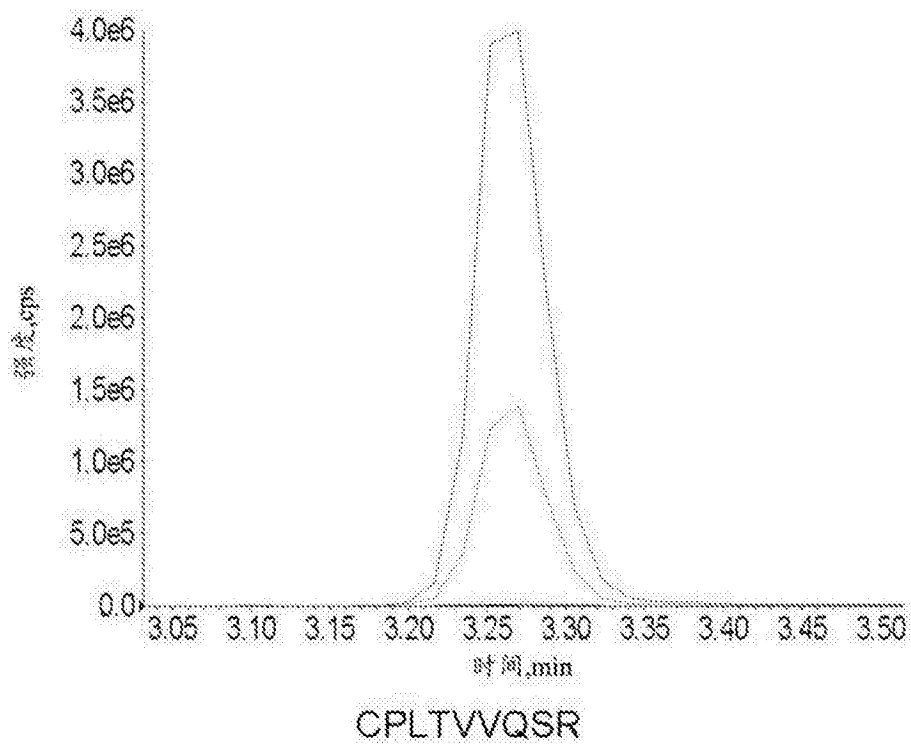


图5B

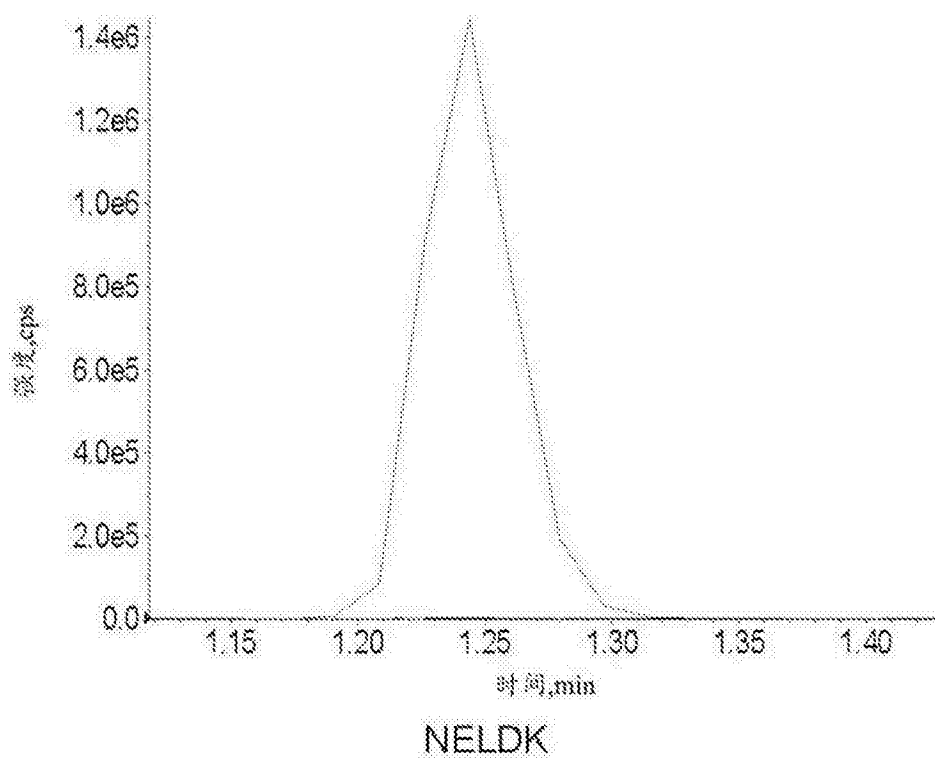


图5C

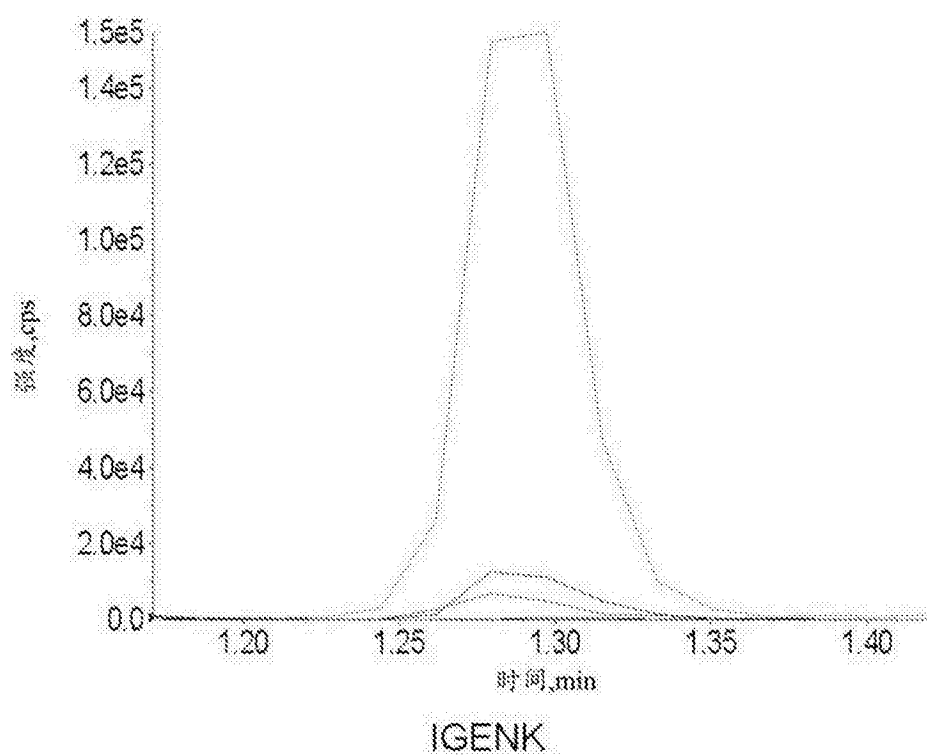


图5D

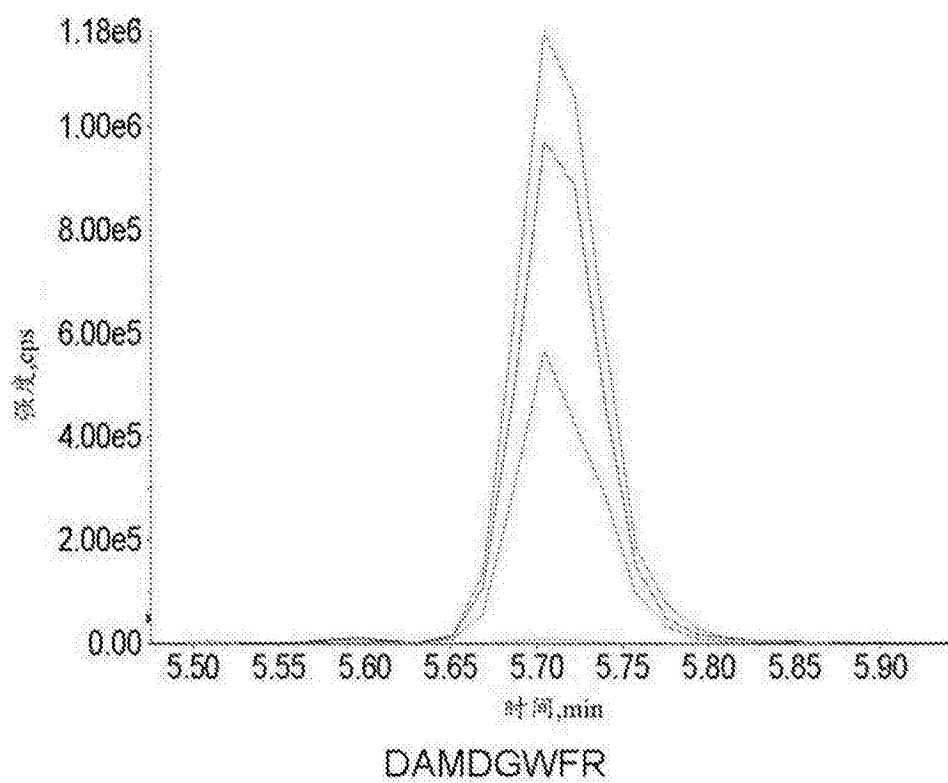


图5E

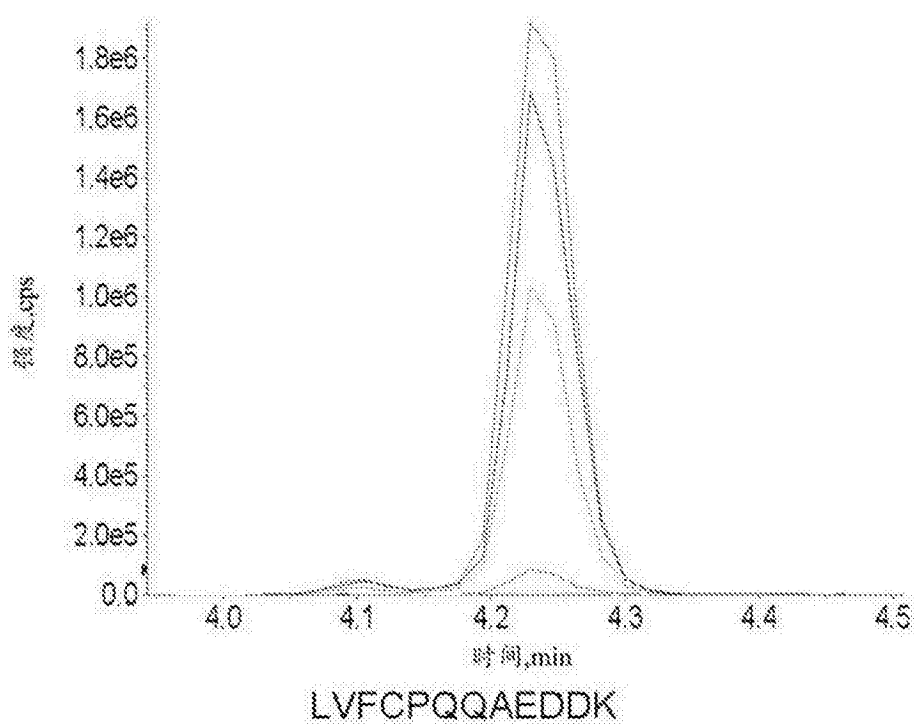


图5F

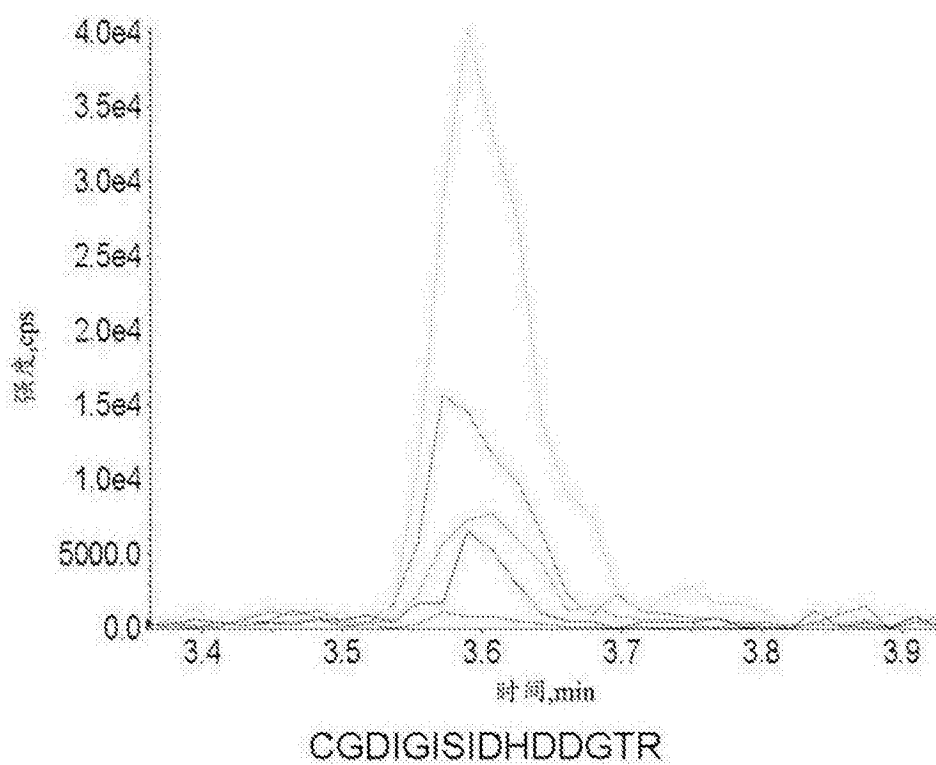


图5G

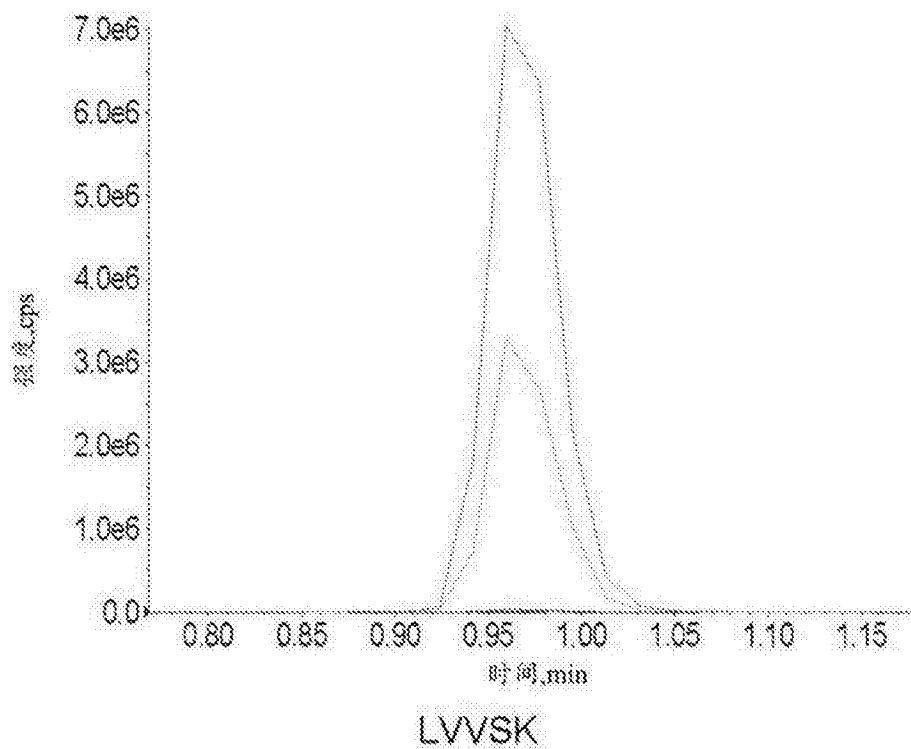


图5H

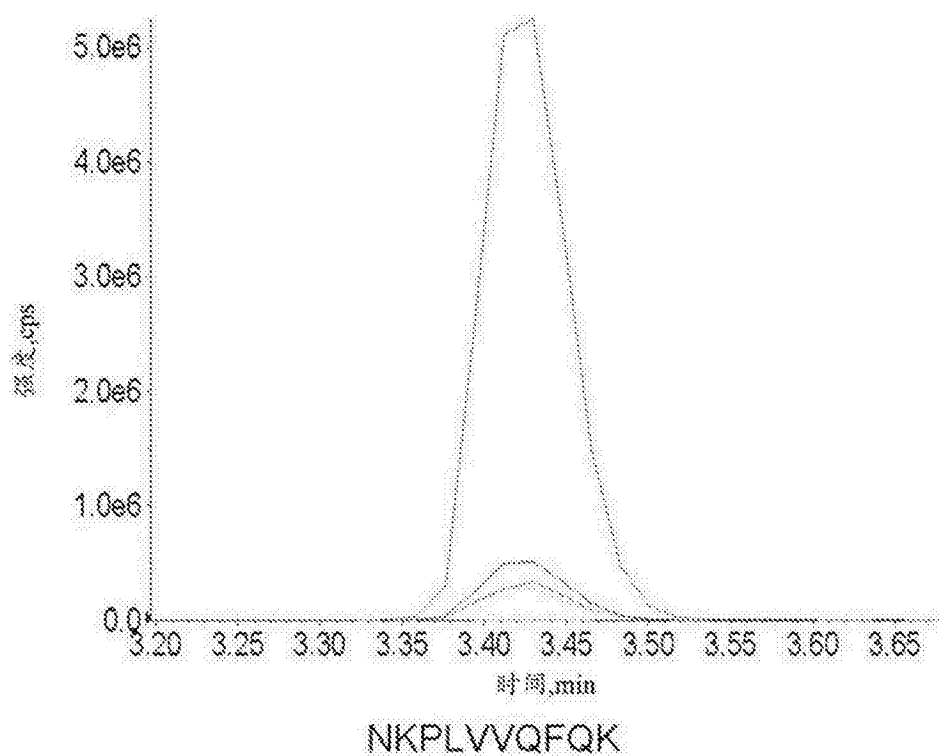


图5I

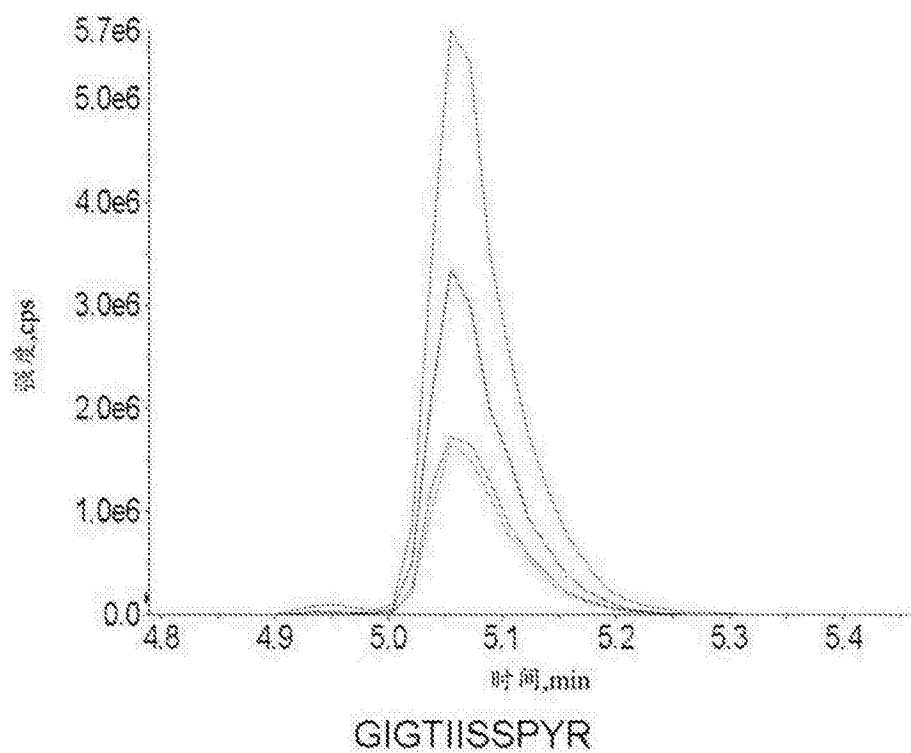


图5J

		1	50
KTI 3 AAB23464.1	(1)	MKSTIFF-LFLFCAPTTSYLPSAIADFVLONEGNPLENGGTYVILSDITA	
KTI 3 CAA45777.1	(1)	MKSTIFFALFLFCAPTTSYLPSAIADFVLONEGNPLENGGTYVILSDITA	
KTI 3 CAA45778.1	(1)	MKSTIFFALFLFCAPTTSYLPSAIADFVLONEGNFLDSGGTYVILSDITA	
共有	(1)	MKSTIFFALFLFCAPTTSYLPSAIADFVLONEGNPLENGGTYVILSDITA	
		51	100
KTI 3 AAB23464.1	(50)	FGGIRAAFTGNERCPLTVVQSRNELDKGIGTIISSPYRIRFIAEGHPLSL	
KTI 3 CAA45777.1	(51)	FGGIRAAFTGNERCPLTVVQSRNELDKGIGTIISSPYRIRFIAEGHPLSL	
KTI 3 CAA45778.1	(51)	FGGIRAAFTGNERCPLTVVQSRNELDKGIGTIISSPFIRIRFIAEGNPLRL	
共有	(51)	FGGIRAAFTGNERCPLTVVQSRNELDKGIGTIISSPYRIRFIAEGHPLSL	
		101	150
KTI 3 AAB23464.1	(100)	KFDSFAVIMLCVGIPTEWSVVEDLPEGPAVKIGENKDAWDGNFRLERVSD	
KTI 3 CAA45777.1	(101)	KFDSFAVIMLCVGIPTEWSVVEDLPEGPAVKIGENKDAWDGNFRLERVSD	
KTI 3 CAA45778.1	(101)	KFDSFAVIMLCVGIPTEWSVVEDLPEGPAVKIGENKDAVDGNFRIERVSD	
共有	(101)	KFDSFAVIMLCVGIPTEWSVVEDLPEGPAVKIGENKDAWDGNFRLERVSD	
		151	200
KTI 3 AAB23464.1	(150)	DEFNNYKLVFCPQQAEDDKCGDIGISIDHDDGTRRLVVSXNNKPLVVQFQK	
KTI 3 CAA45777.1	(151)	DEFNNYKLVFCPQQAEDDKCGDIGISIDHDDGTRRLVVSXNNKPLVVQFQK	
KTI 3 CAA45778.1	(151)	DEFNNYKLVFCTQQAEDDKCGDIGISIDHDDGTRRLVVSXNNKPLVVQFQK	
共有	(151)	DEFNNYKLVFCPQQAEDDKCGDIGISIDHDDGTRRLVVSXNNKPLVVQFQK	
		201	217
KTI 3 AAB23464.1	(200)	LDKESLAKXNHGLSRSE	
KTI 3 CAA45777.1	(201)	LDKESLAFENHGLSRSE	
KTI 3 CAA45778.1	(201)	VDKESLAKXNHGLSRSE	
共有	(201)	LDKESLAKXNHGLSRSE	

图5K

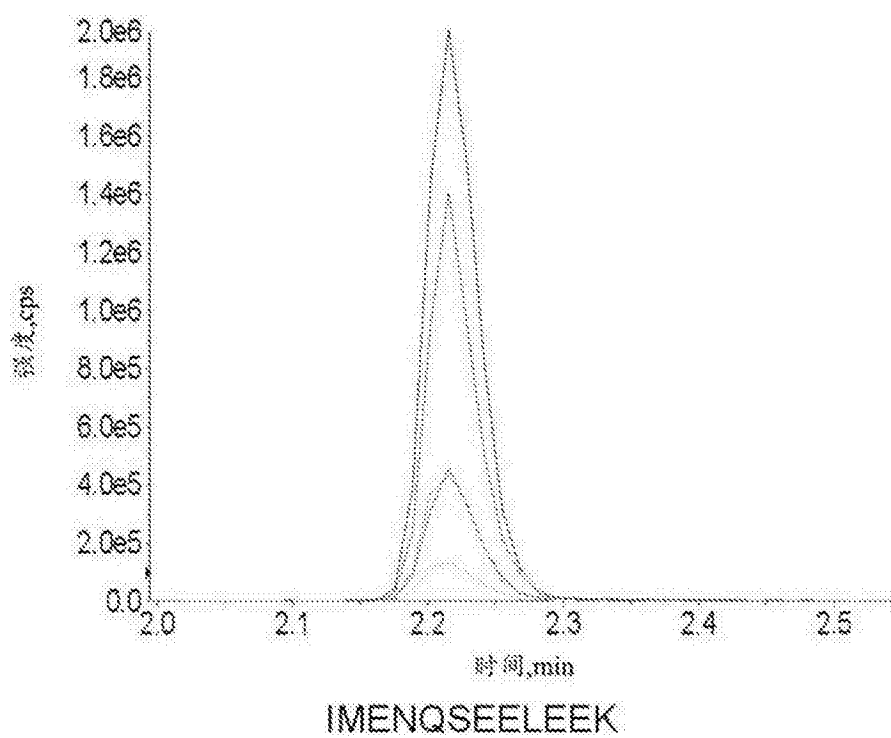


图6A

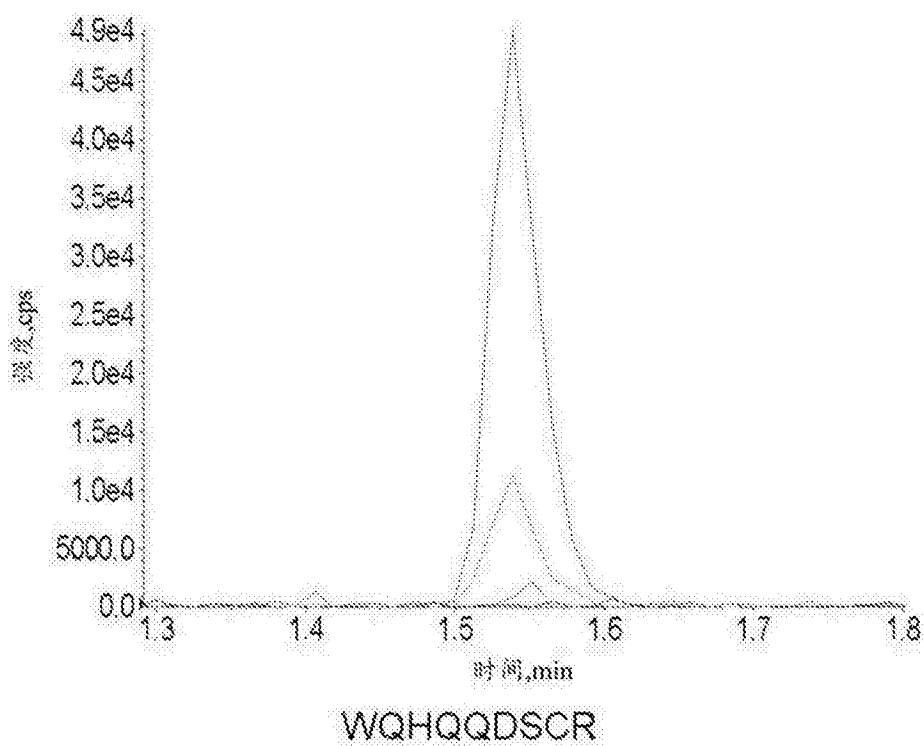


图6B

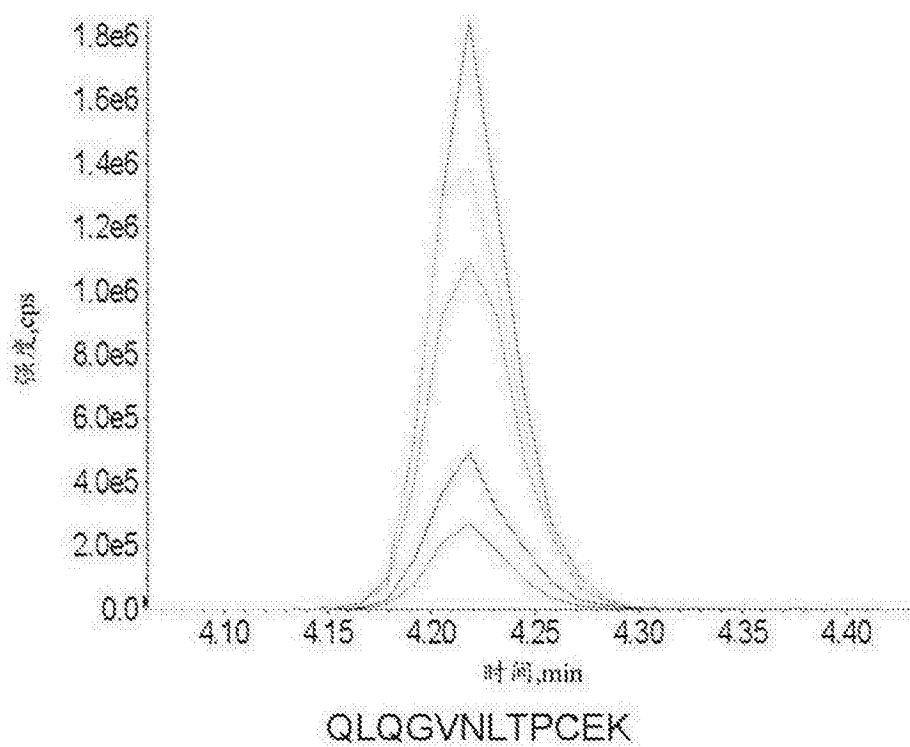


图6C

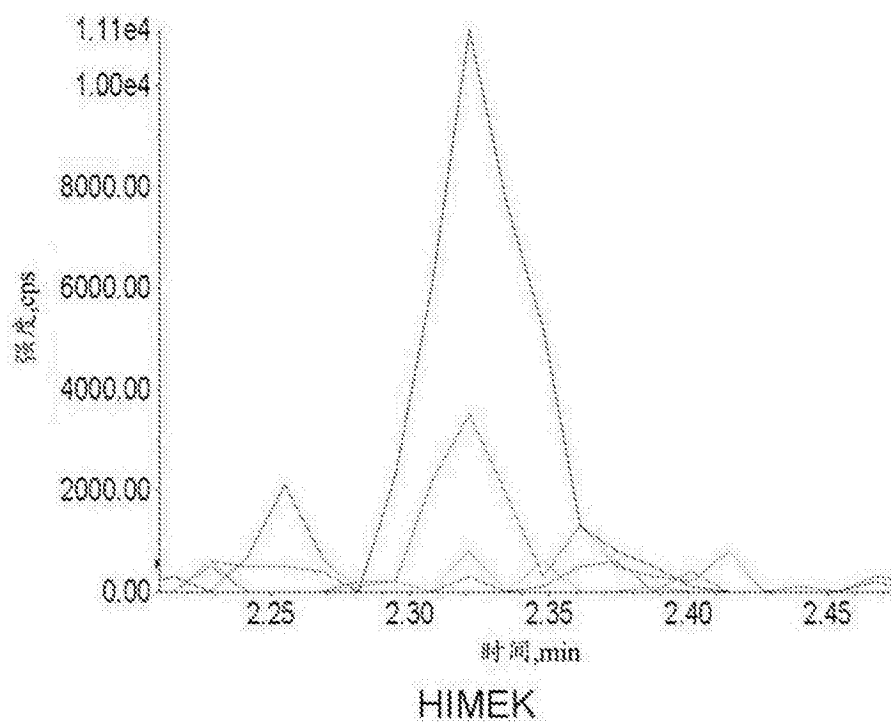


图6D

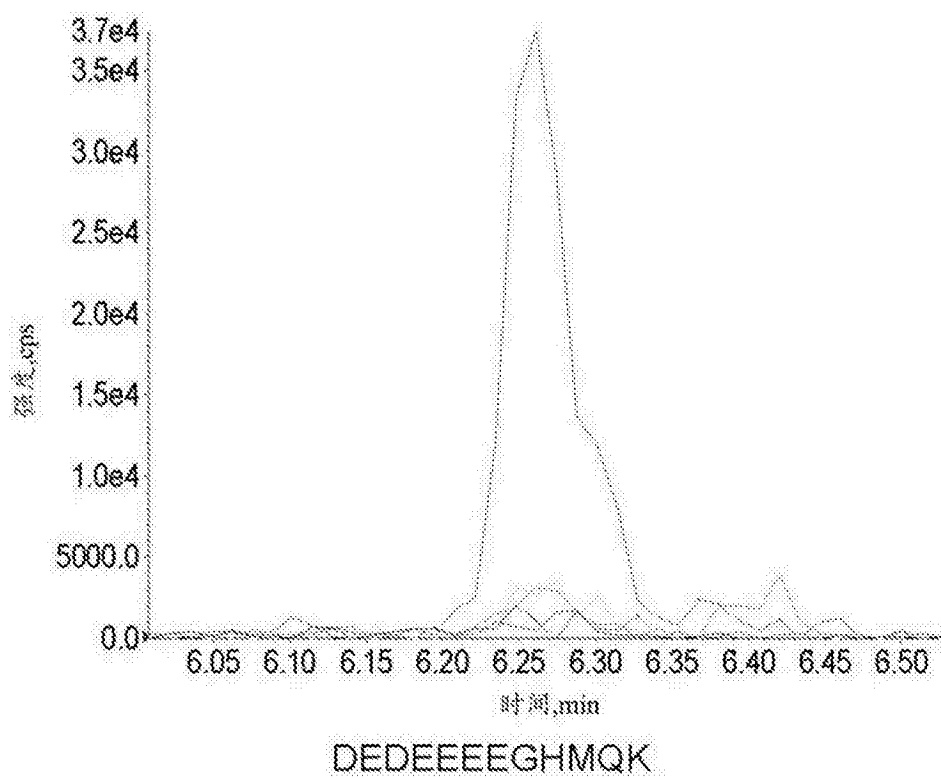


图6E

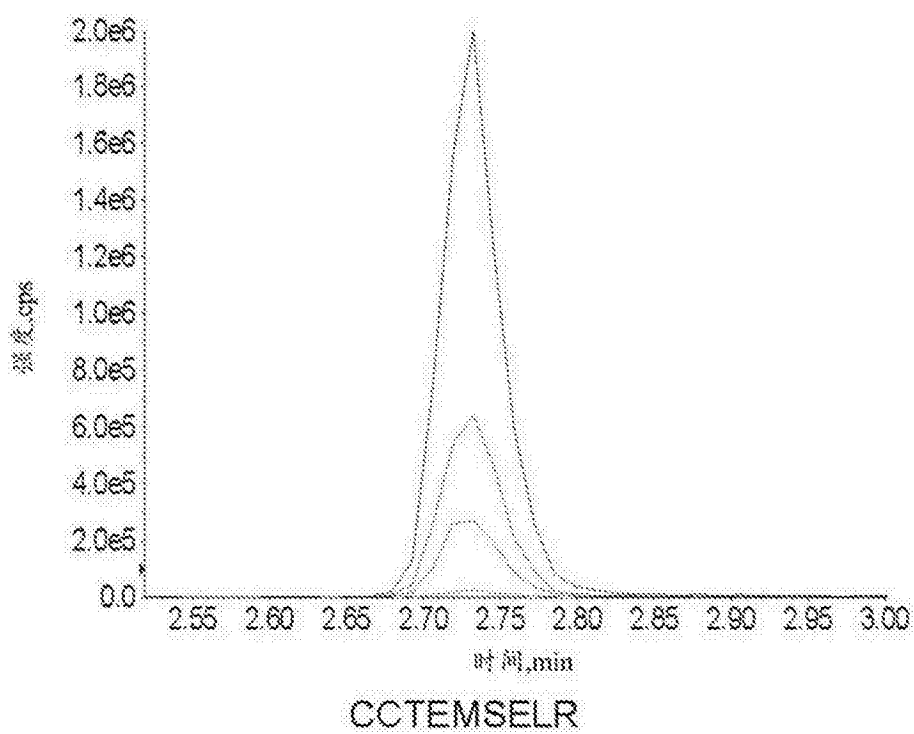


图6F

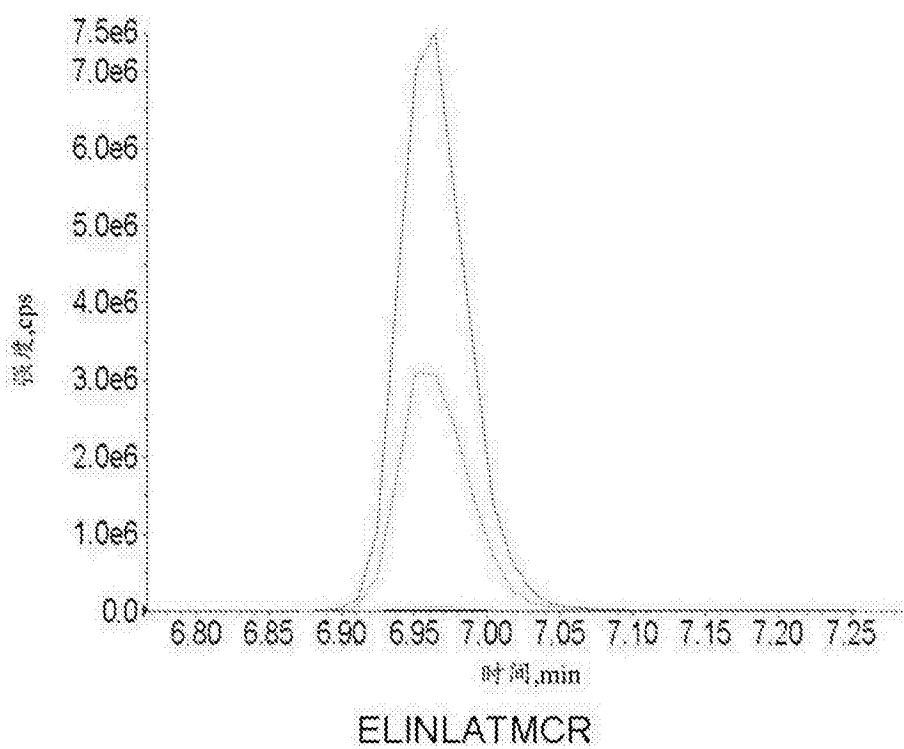


图6G

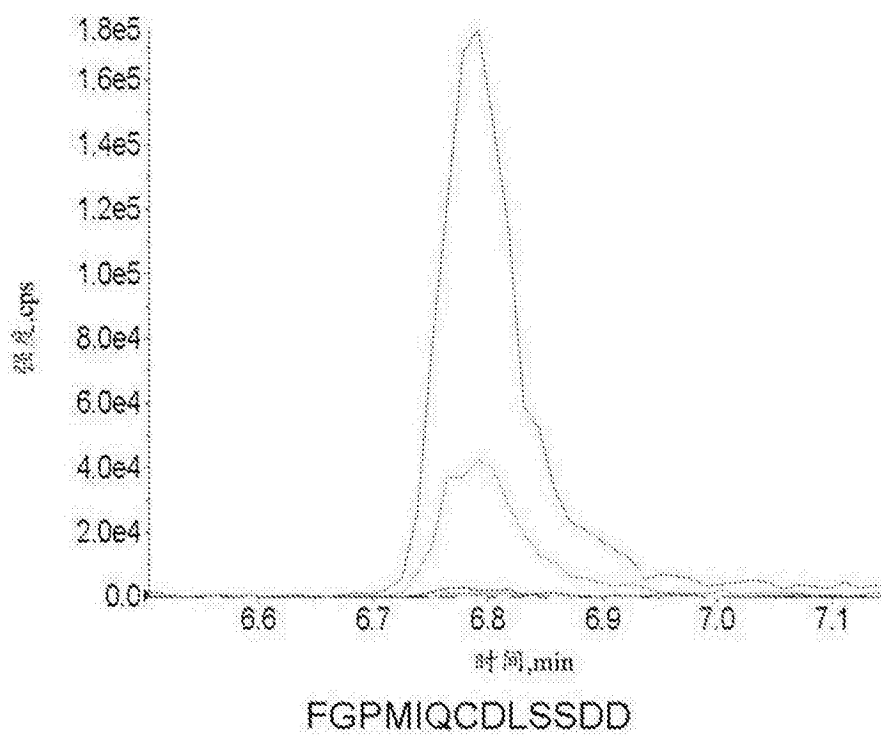


图6H

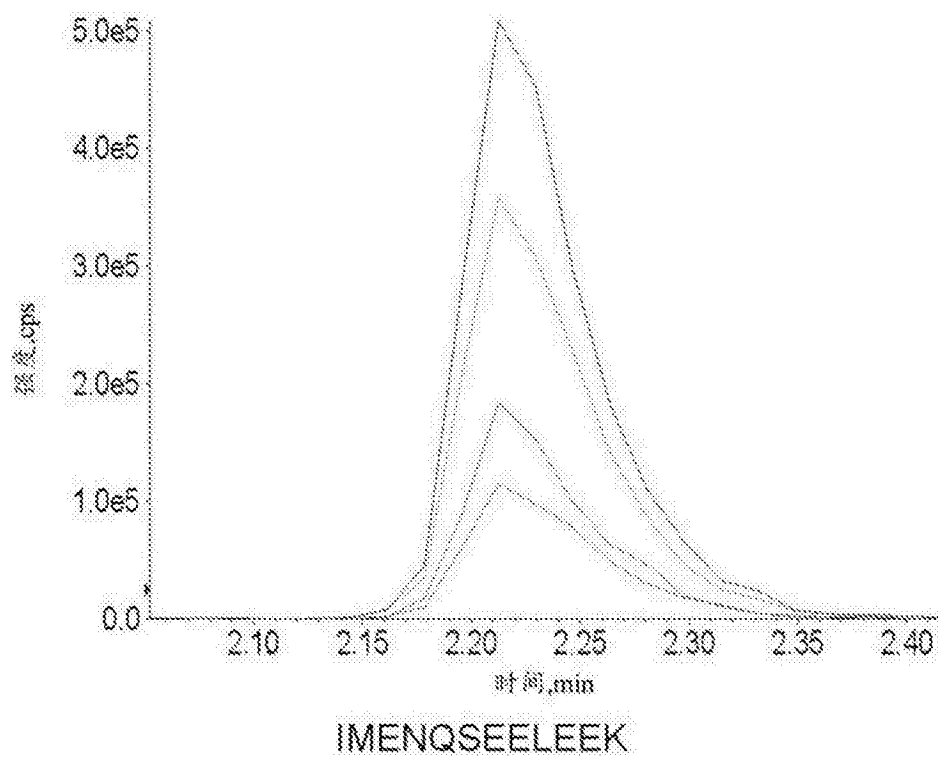


图6I

		1	50
2S 白蛋白 Eric NP_001238443	(1)	-----MTKFTILLISLLFCIAHTCSASKWQHQQDSCRKQL	
2S 白蛋白 Glyma13g36400.1 BLAST	(1)	MPPPSLHFTSPINSKMTKFTILLISLLFCIAHTCSASKWQHQQDSCRKQL	
2S 白蛋白 NP_001234950 BLAST	(1)	-----MTKFTILLISLLFCIAHTCSASEWQHQQDSCRKQL	
2S 白蛋白 Glyma12g34160.1 BLAST	(1)	-----MTKLTILLIALLFIAHTCCASKWQHQQDSCREQL	
共有	(1)	MTKFTILLISLLFCIAHTCSASKWQHQQDSCRKQL	
		51	100
2S 白蛋白 Eric NP_001238443	(36)	QGVNLTPECKHIMEKIQGRGDDDDDDDDNHILRTMRGRINYIRNEGKD	
2S 白蛋白 Glyma13g36400.1 BLAST	(51)	QGVNLTPECKHIMEKIQGRGDDDDDDDDNHILRTMRGRINYIRNEGKD	
2S 白蛋白 NP_001234950 BLAST	(36)	QGVNLTPECKHIMEKIQGRGDDDDDDDDNHILRTMRGRINYIRNEGKD	
2S 白蛋白 Glyma12g34160.1 BLAST	(36)	KGINLNPC-HIMEKIQAGRGEDGSDHILRTMPGRINYIRNEGKE	
共有	(51)	QGVNLTPECKHIMEKIQGRGDDDDDDDDNHILRTMRGRINYIRNEGKD	
		101	150
2S 白蛋白 Eric NP_001238443	(86)	EDDEEGEHQKCCTEMSELRSFKQCKALQKIMENQSELEEKQKKMEK	
2S 白蛋白 Glyma13g36400.1 BLAST	(101)	EDDEEGEHQKCCTEMSELRSFKQCKALQKIMENQSELEEKQKKMEK	
2S 白蛋白 NP_001234950 BLAST	(86)	EDDEEGEHQKCCTEMSELRSFKQCKALQKIMENQSELEEKQKKMEK	
2S 白蛋白 Glyma12g34160.1 BLAST	(85)	EDE--EGEHQKCCSESELKSPICQCKALQKIMENQSELEGKEKQMER	
共有	(101)	EDDEEGEHQKCCTEMSELRSFKQCKALQKIMENQSELEEKQKKMEK	
		151	174
2S 白蛋白 Eric NP_001238443	(136)	ELINLATMCRFGPMIQCDLSSDD-	
2S 白蛋白 Glyma13g36400.1 BLAST	(151)	ELINLATMCRFGPMIQCDLSSDD-	
2S 白蛋白 NP_001234950 BLAST	(136)	ELINLATMCRFGPMIQCDLSSDD-	
2S 白蛋白 Glyma12g34160.1 BLAST	(133)	ELMNLAIKRLGPMIGCDLSSDD-	
共有	(151)	ELINLATMCRFGPMIQCDLSSDD	

图6J

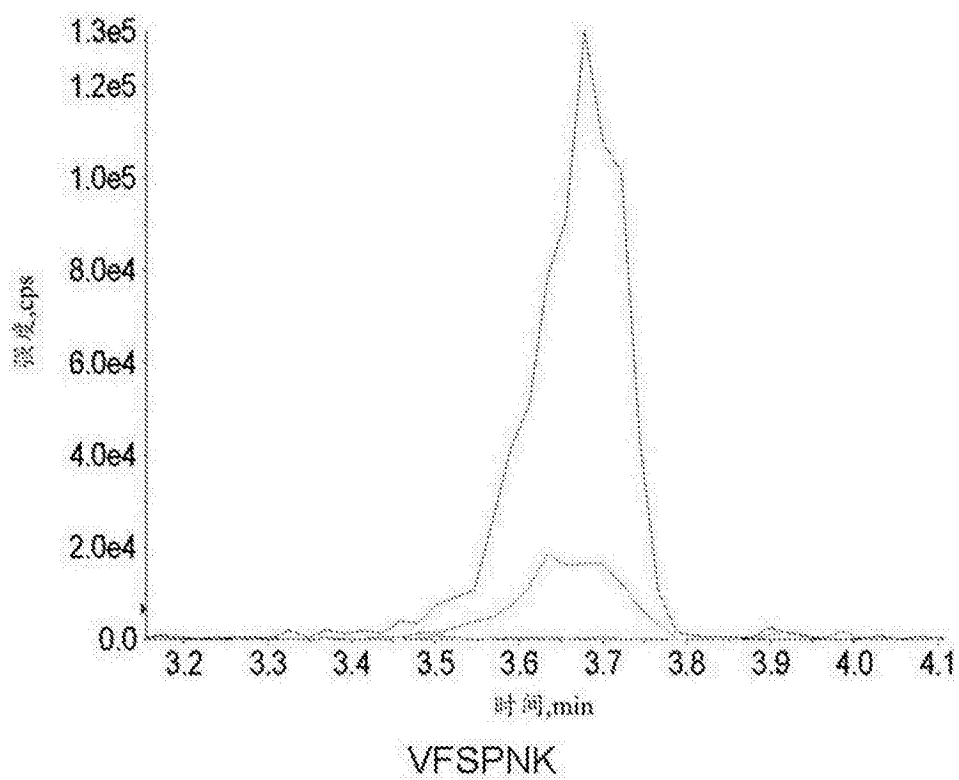


图7A

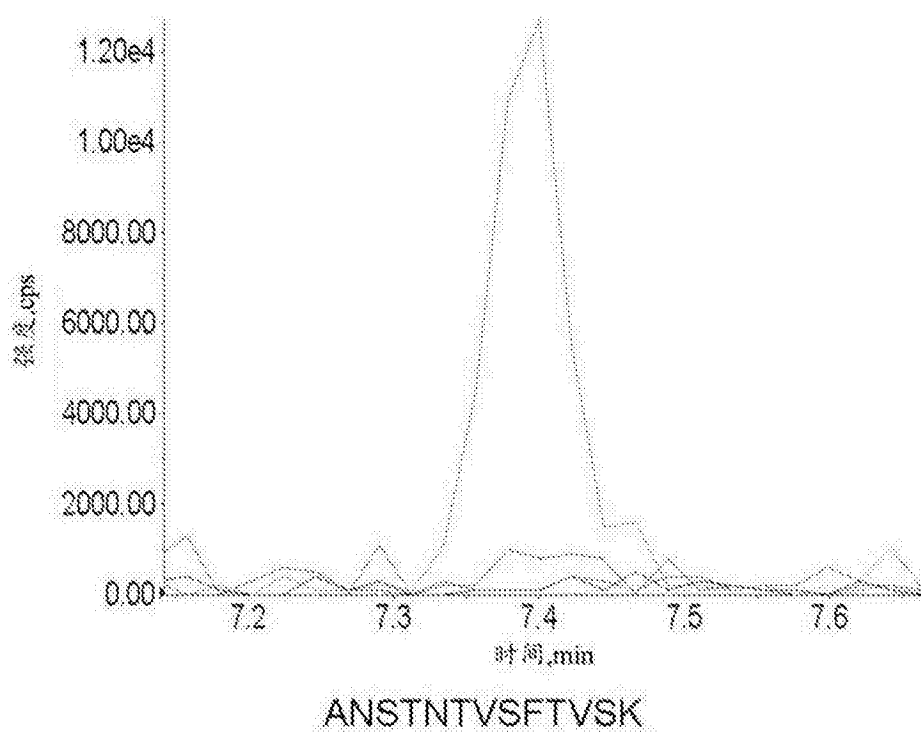


图7B

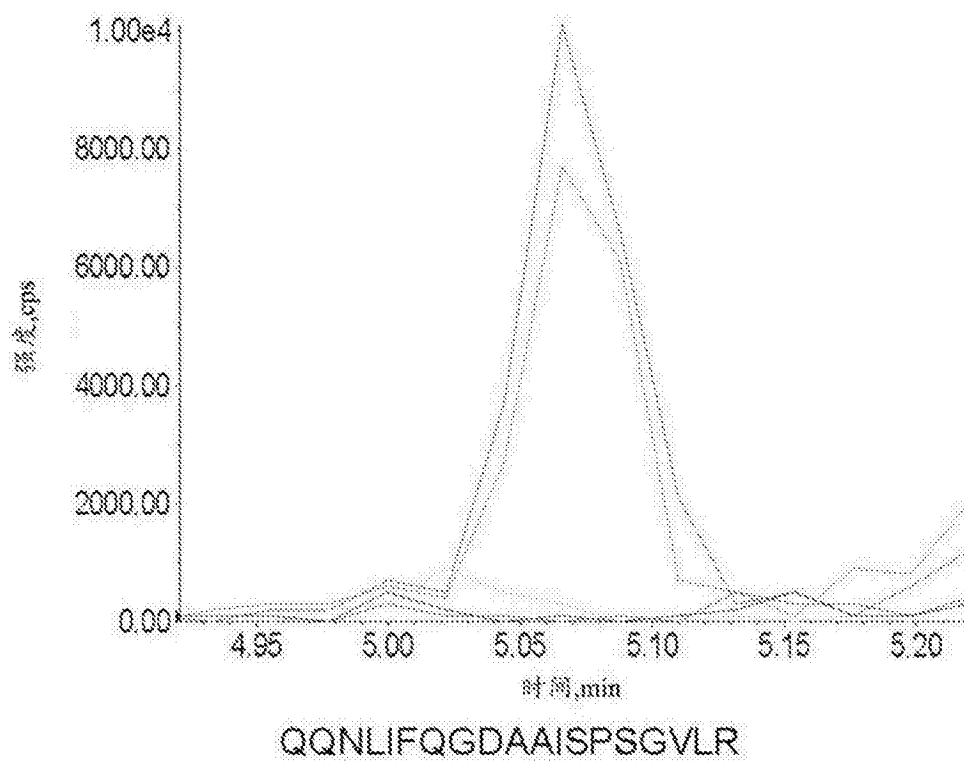


图7C

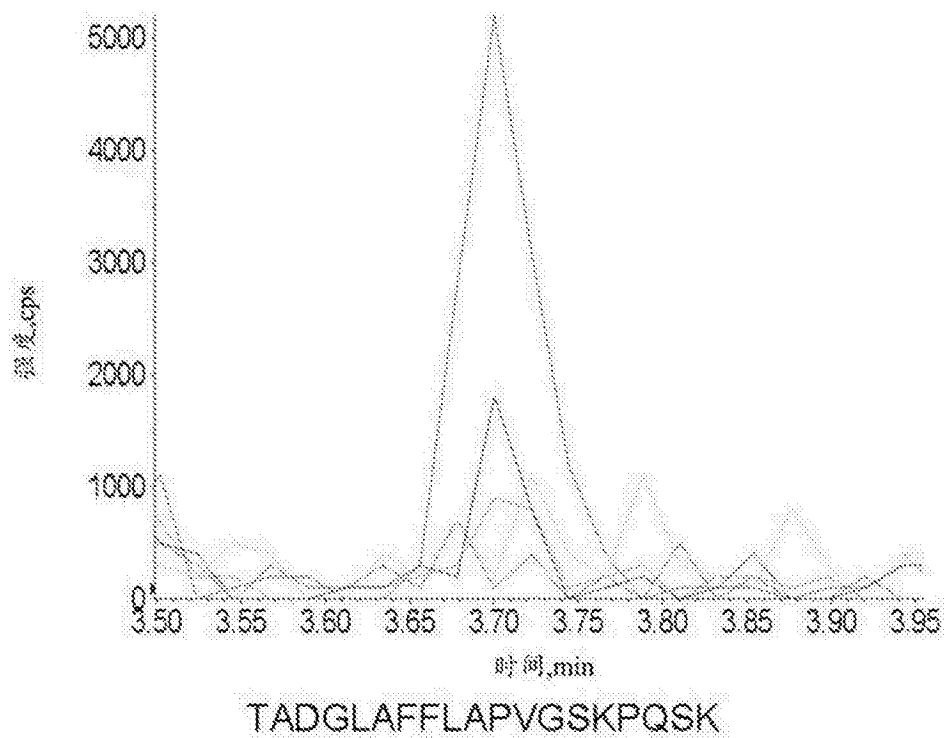


图7D

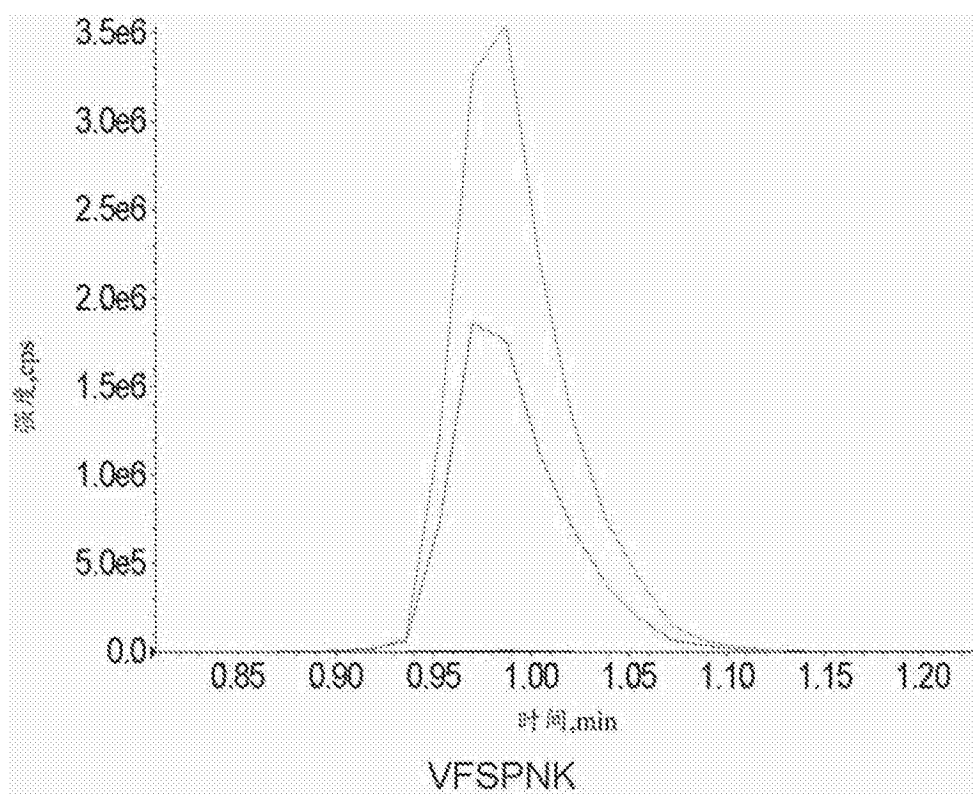


图7E

		1	50
凝集素 Eric ADC94422	(1)	-----MATSNFS-----IVLSLSLAFFLVILTKANSTNT	
凝集素 XP_003535884 BLAST	(1)	-----MATSNFS-----IVLSLSLSALFLMLTKANSTNT	
凝集素 Glyma10g15480.1 BLAST	(1)	-----MATSNFS-----IVLSLSLSALFLMLTKANSTNT	
凝集素 NF_001237210 BLAST	(1)	-----MATSNFS-----IVLSVSLAFFLVILTKANSTDT	
凝集素 Glyma02g18090.1 BLAST	(1)	MEVLCIIFEPFQIKAMATSNFS-----IVLSVSLAFFLVILTKANSTDT	
凝集素 ACU23399 BLAST	(1)	-----MATSNFS-----IVLSVSLAFFLVILTKANSTDT	
凝集素 CAH60173 BLAST	(1)	-----MATSNFS-----TVISPSLSALFLVILTKANSTNI	
凝集素 Glyma10g01620.2 BLAST	(1)	-----MATSEFHTQEPFLFTVLS--VVVVLLTKVWSTKP	
凝集素 Glyma02g01590.1 BLAST	(1)	-----MATSEKLTQNVVYVSLGLTLTLVLVILTKANSTNT	
共有	(1)	MATSNFS IVLSLSLAFFLVILTKANSTNT	
		81	100
凝集素 Eric ADC94422	(30)	VSFTTVSKFSFPCQNLIFQGDAAISPSGVRLTKVDSDIVFTTSGLGRALY	
凝集素 XP_003535884 BLAST	(30)	VSFTTSKFSFPCQNLILQGDAAISPSGVRLTKVDSDIVFTTSGLGRALY	
凝集素 Glyma10g15480.1 BLAST	(30)	VSFTTSKFSFPCQNLILQGDAAISPSGVRLTKVDSDIVFTTSGLGRALY	
凝集素 NF_001237210 BLAST	(30)	VSFTTNRKFMFVQPNIMLQKQASISISGVLLQTKVDSNGVFTSGGLGRALY	
凝集素 Glyma02g18090.1 BLAST	(45)	VSFTTNRKFMFVQPNIMLQKQASISISGVLLQTKVDSNGVFTSGGLGRALY	
凝集素 ACU23399 BLAST	(30)	VSFTTNRKFMFVQPNIMLQKQASISISGVLLQTKVDSNGVFTSGGLGRALY	
凝集素 CAH60173 BLAST	(30)	FSFNFOTFDS--FNLIFQGDASVSSIGQLRLTKVFGNGKFTAAQLGRAFY	
凝集素 Glyma10g01620.2 BLAST	(24)	FLSPGTSSRTWTLILQGDALVTISF-----KSLGRALY	
凝集素 Glyma02g01590.1 BLAST	(36)	VSFNWRKFPVKQPNMILQGDALVTISGKLLQTKVDSNGVFTSGGLGRALY	
共有	(51)	VSFTTSKFSFPCQNLILQGDAAISPSGVRLTKVDSDIVFTTSGLGRALY	
		101	150
凝集素 Eric ADC94422	(90)	ATPIQIWDSETGKVASWATSFKFNVFSPSK--TADGLAFFLAPVGSQPKS	
凝集素 XP_003535884 BLAST	(80)	AAPIQIWDSETGKVASWATSFKFNVFSPSK--TADGLAFFLAPVGSQPKS	
凝集素 Glyma10g15480.1 BLAST	(80)	AAPIQIWDSETGKVASWATSFKFNVFSPSK--TADGLAFFLAPVGSQPKS	
凝集素 NF_001237210 BLAST	(80)	AAPIQIWDSETGKVASWATSFKFNI FAPNKSNSADGLAFFLAPVGSQPKS	
凝集素 Glyma02g18090.1 BLAST	(95)	AAPIQIWDSETGKVASWATSFKFNI FAPNKSNSADGLAFFLAPVGSQPKS	
凝集素 ACU23399 BLAST	(80)	AAPIQIWDSETGKVASWATSFKFNI FAPNKSNSADGLAFFLAPVGSQPKS	
凝集素 CAH60173 BLAST	(78)	SAPIQIWDSETGKVASWATSFTFWILAPNKSNSADGLAFALVPGSQPKS	
凝集素 Glyma10g01620.2 BLAST	(69)	STPIHINDSEIGNVASTAASFNTTVYANDIANLADGLAFFLAPIDTKPQT	
凝集素 Glyma02g01590.1 BLAST	(94)	STPIHINDKETGKVASWATSFAASFNTFVAPDTKPLADGLAFFLAPIDTKPQT	
共有	(101)	AAPIQIWDSETGKVASWATSFKFNVFAPSK TADGLAFFLAPVGSQPKS	
		151	200
凝集素 Eric ADC94422	(128)	EGGFLGLFNSDSFNMKSLQTVAVEFDITYNKNWDPANRHIGIDVNSIKSVK	
凝集素 XP_003535884 BLAST	(128)	EAGFLGLFNSDSFNMKSLQTVAVEFDITYNKNWDPANRHIGIDVNSIKSVK	
凝集素 Glyma10g15480.1 BLAST	(128)	EAGFLGLFNSDSFNMKSLQTV-----NDPASEHIGIDVNSIKSVK	
凝集素 NF_001237210 BLAST	(130)	DDGFLGLFNSFLKDKSLQTVAIETDTFSNKNWDPANRHIGIDVNSIKSVK	
凝集素 Glyma02g18090.1 BLAST	(145)	DDGFLGLFNSFLKDKSLQTVAIETDTFSNKNWDPANRHIGIDVNSIKSVK	
凝集素 ACU23399 BLAST	(130)	DDGFLGLFNSFLKDKSLQTVAIETDTFSNKNWDPANRHIGIDVNSIKSVK	
凝集素 CAH60173 BLAST	(129)	NGGFLGLFDMATYSSAQTVAVEFDITYNKNWDPANRHIGIDVNSIKSVK	
凝集素 Glyma10g01620.2 BLAST	(119)	RGVYLGLYN-----N-----PSN-----	
凝集素 Glyma02g01590.1 BLAST	(134)	EAGVGLGFNSK--EAGGQTVAVEFDITF--RNSWDPANRHIGIDVNSIKSVK	
共有	(131)	EGGFLGLFNSDSFNMKSLQTVAVEFDITYNKNWDPANRHIGIDVNSIKSVK	

图7F

		201	250
凝集素 Eric ADC94422	(178)	TASWGLANGQVIAQILITYDAATSLIVASLIHFSPKNTSYILSETVSLKSNL	
凝集素 XF_003535884 BLAST	(178)	TAPWGFANGQVIAQILITYDAATSLIVASLIHFSPKNTSYILSETVSLKSNL	
凝集素 Glyma10g15480.1 BLAST	(168)	TAPWGFANGQVIAQILITYDAATSLIVASLIHFSPKNTSYILSETVSLKSNL	
凝集素 NF_001237210 BLAST	(180)	TASWGLANGQVIAQILITYDAATSLIVASLIHFSPKNTSYILSETVSLKSNL	
凝集素 Glyma02g19090.1 BLAST	(195)	TASWGLANGQVIAQILITYDAATSLIVASLIHFSPKNTSYILSETVSLKSNL	
凝集素 ACU23599 BLAST	(180)	TASWGLANGQVIAQILITYDAATSLIVASLIHFSPKNTSYILSETVSLKSNL	
凝集素 CAN60173 BLAST	(178)	TASWGLANGQVIAQILITYDAATSLIVASLIHFSPKNTSYILSETVSLKSNL	
凝集素 Glyma10g01620.2 BLAST	(132)	~SWWGLANDQVTVFLITYDAATSLIVASLIHFSPKNTSYILSETVSLKSNL	
凝集素 Glyma02g01590.1 BLAST	(189)	TTSWGLANNEVAVFLITYDAATSLIVASLIHFSPKNTSYILSETVSLKSNL	
共有	(201)	TASWGLANGQVIAQILITYDAATSLIVASLIHFSPKNTSYILSETVSLKSNL	
		251	300
凝集素 Eric ADC94422	(228)	FEWVNVGFSAITGLNEGSVETRDVFSWGFASKLSDGST~SDTLDLPSFLL	
凝集素 XF_003535884 BLAST	(228)	FEWVNVGFSAITGLNEGSVETRDVFSWGFASKLSDGST~SDTLDLPSFLL	
凝集素 Glyma10g15480.1 BLAST	(218)	FEWVNVGFSAITGLNEGSVETRDVFSWGFASKLSDGST~SDTLDLPSFLL	
凝集素 NF_001237210 BLAST	(230)	FEWVNVGFSAITGLNEGSVETRDVFSWGFASKLSDGST~SDTLDLPSFLL	
凝集素 Glyma02g19090.1 BLAST	(245)	FEWVNVGFSAITGLNEGSVETRDVFSWGFASKLSDGST~SDTLDLPSFLL	
凝集素 ACU23599 BLAST	(230)	FEWVNVGFSAITGLNEGSVETRDVFSWGFASKLSDGST~SDTLDLPSFLL	
凝集素 CAN60173 BLAST	(228)	FEWVNVGFSAITGLNEGSVETRDVFSWGFASKLSDGST~SDTLDLPSFLL	
凝集素 Glyma10g01620.2 BLAST	(181)	FEWVNVGFSAITGLNEGSVETRDVFSWGFASKLSDGST~SDTLDLPSFLL	
凝集素 Glyma02g01590.1 BLAST	(233)	FEWVNVGFSAITGLNEGSVETRDVFSWGFASKLSDGST~SDTLDLPSFLL	
共有	(251)	FEWVNVGFSAITGLNEGSVETRDVFSWGFASKLSDGST~SDTLDLPSFLL	
		301	
凝集素 Eric ADC94422	(277)	NEAI-	
凝集素 XF_003535884 BLAST	(277)	NEAI-	
凝集素 Glyma10g15480.1 BLAST	(267)	NEAI-	
凝集素 NF_001237210 BLAST	(278)	NEAI-	
凝集素 Glyma02g19090.1 BLAST	(294)	NEAI-	
凝集素 ACU23599 BLAST	(278)	NEAI-	
凝集素 CAN60173 BLAST	(277)	NRIL-	
凝集素 Glyma10g01620.2 BLAST	(229)	-----	
凝集素 Glyma02g01590.1 BLAST	(282)	NEAI-	
共有	(301)	NEAI-	

图7F续

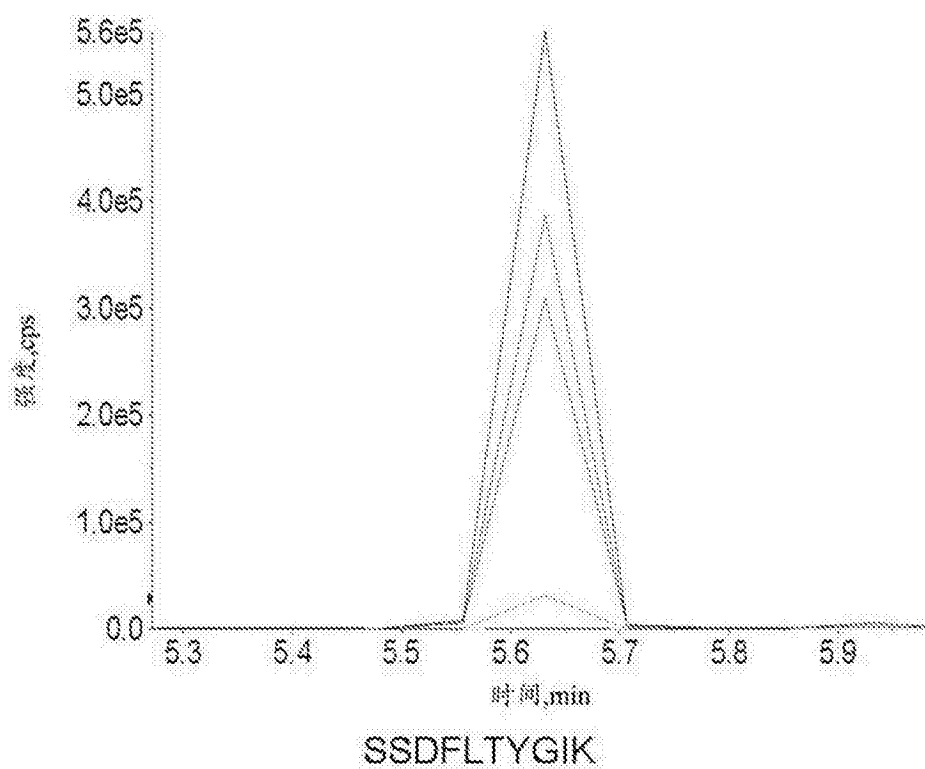


图8A

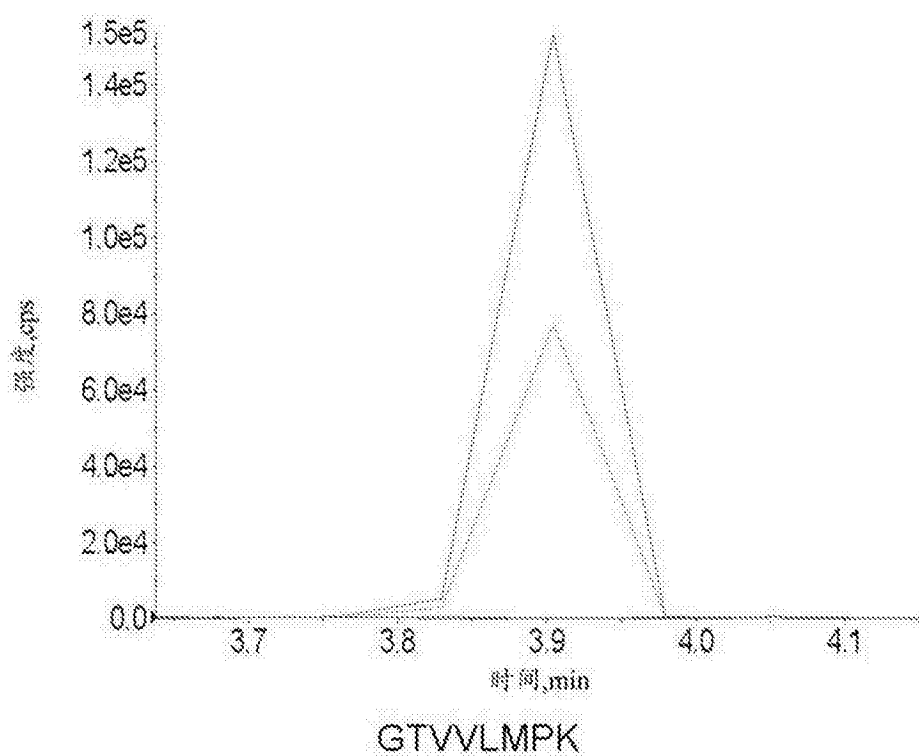


图8B

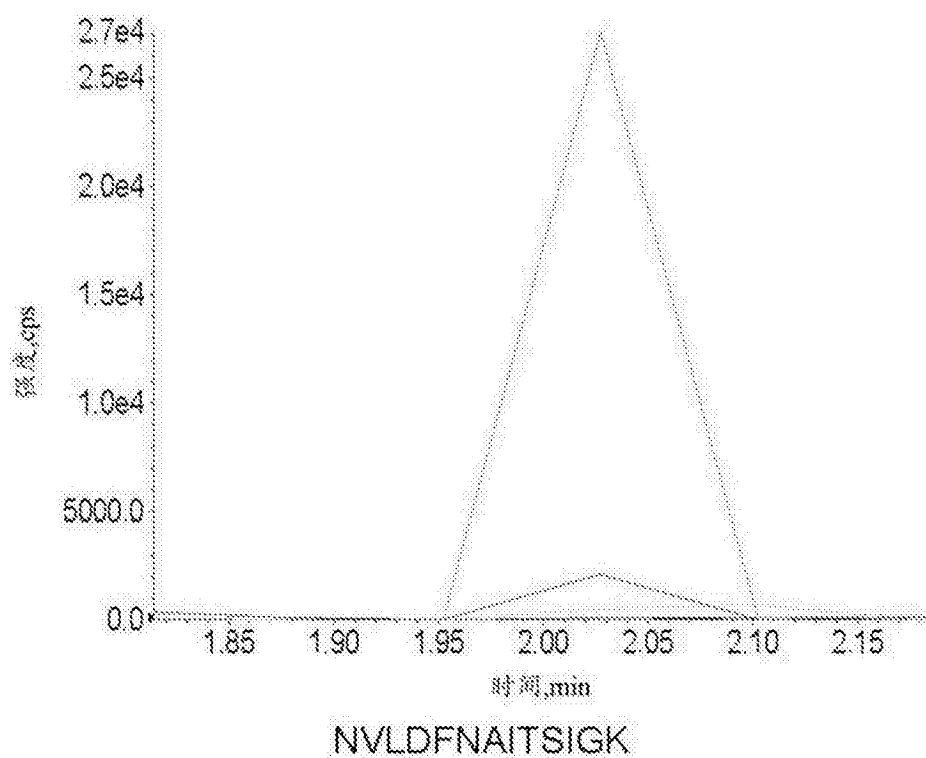


图8C

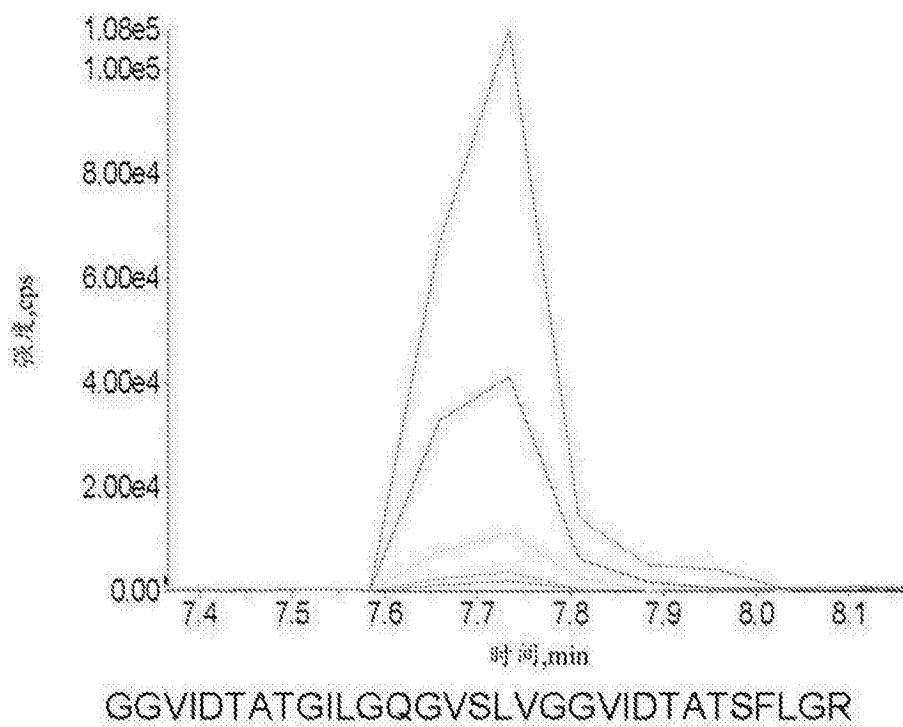


图8D

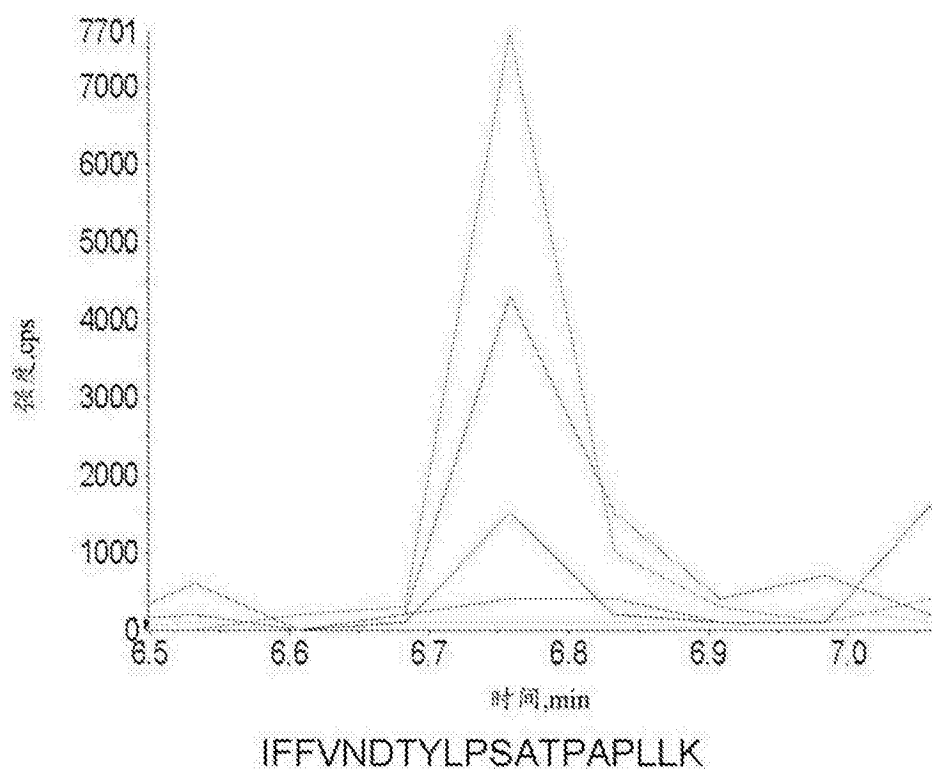


图8E

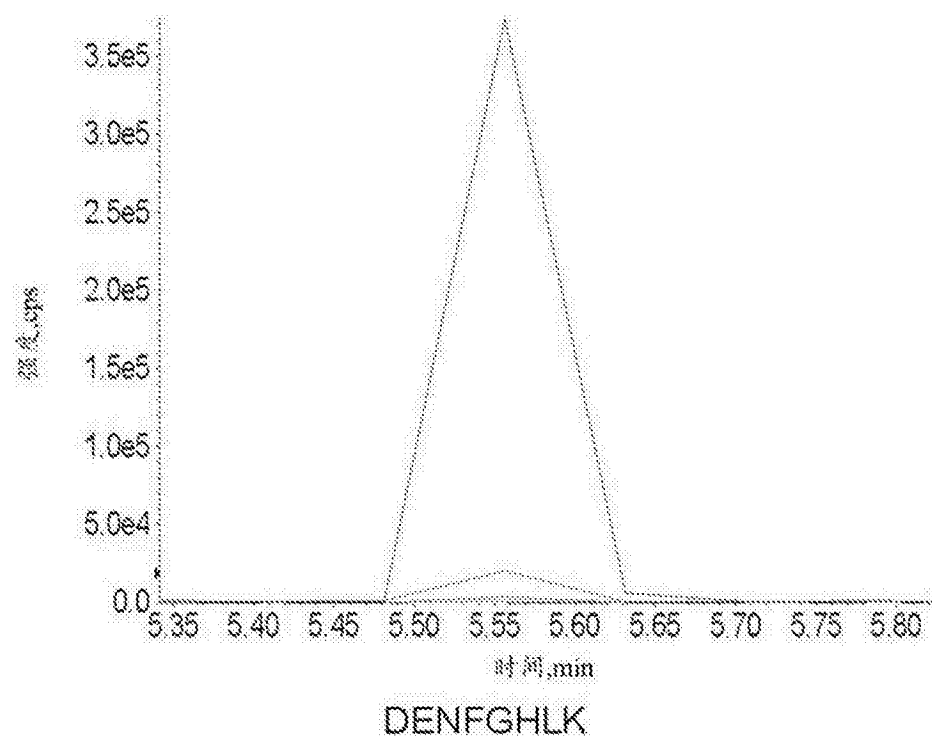


图8F

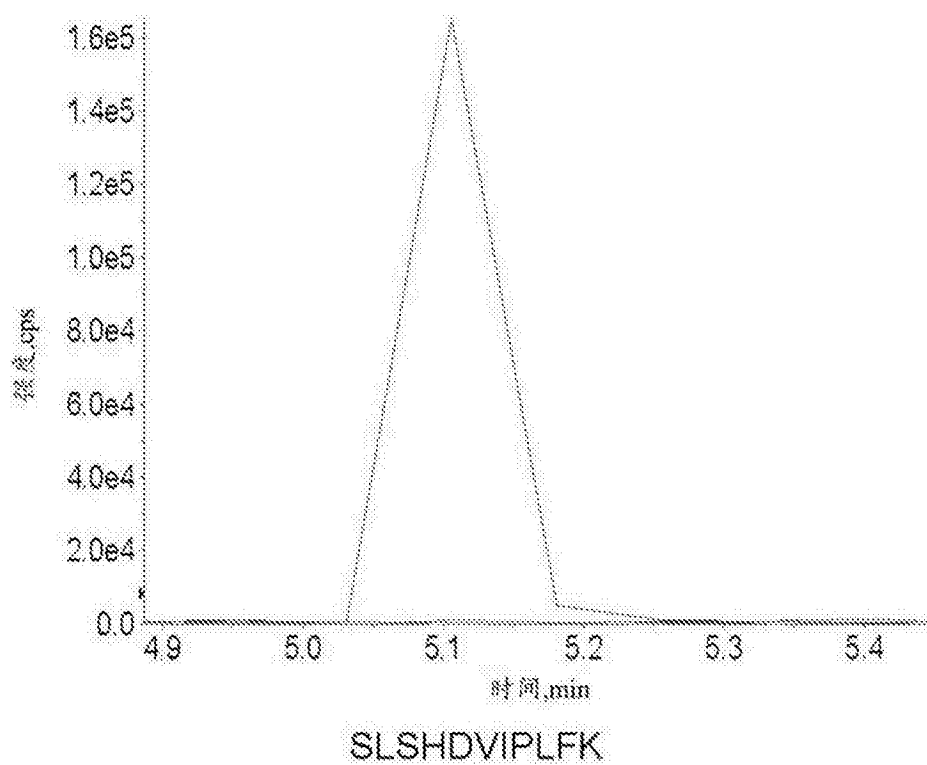


图8G

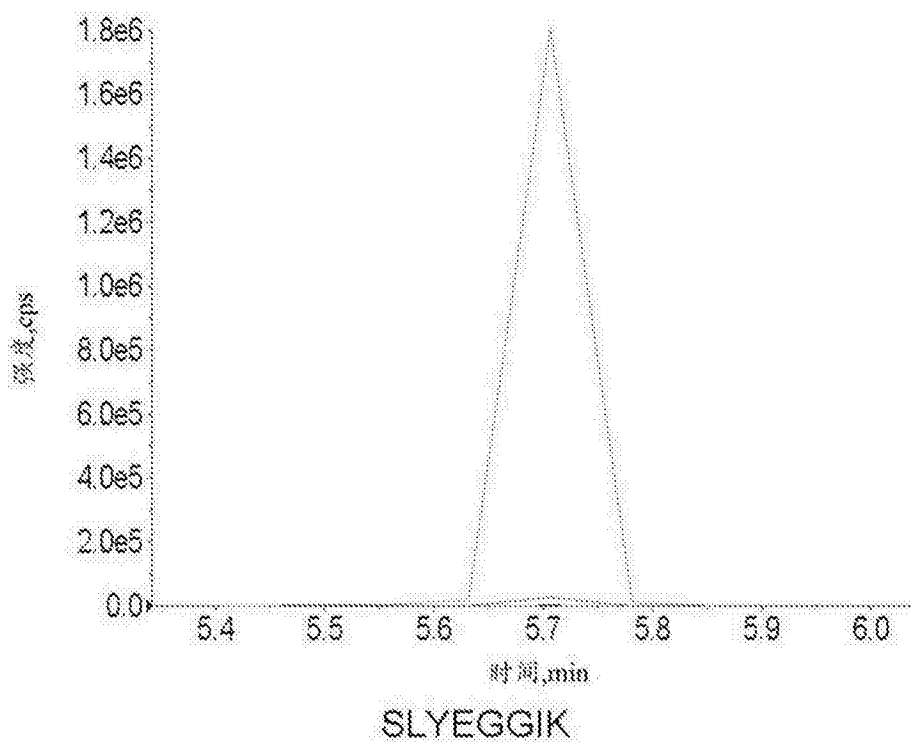


图8H

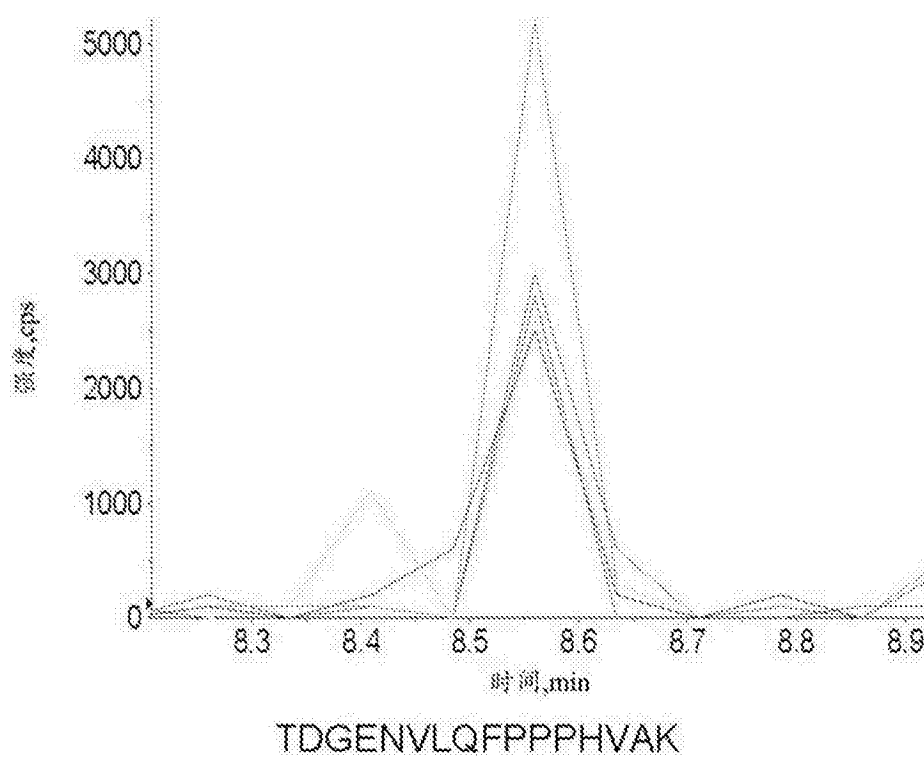


图8I

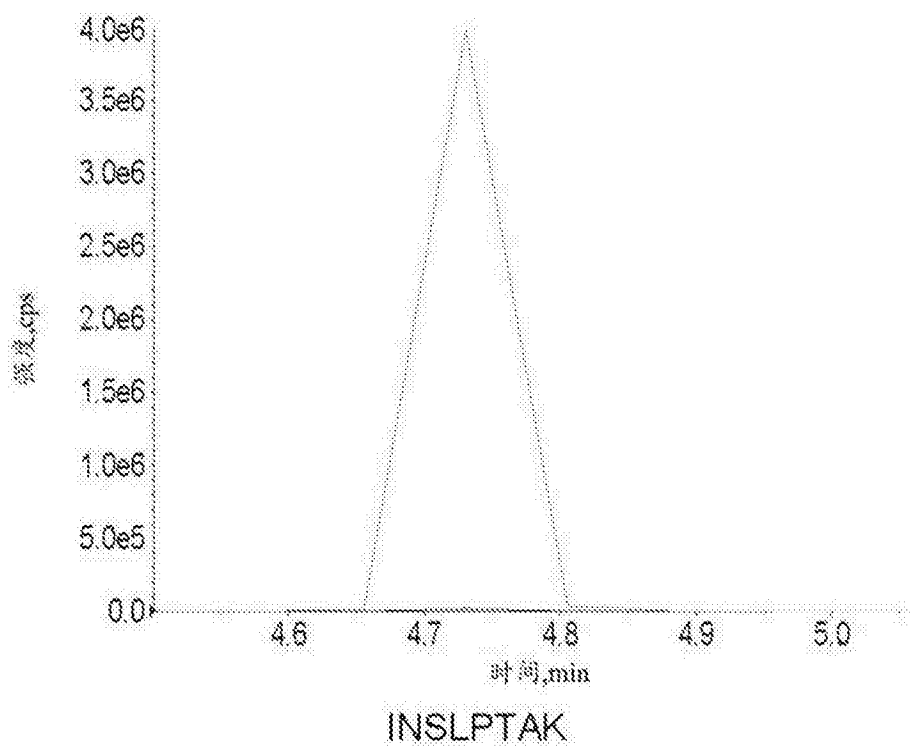


图8J

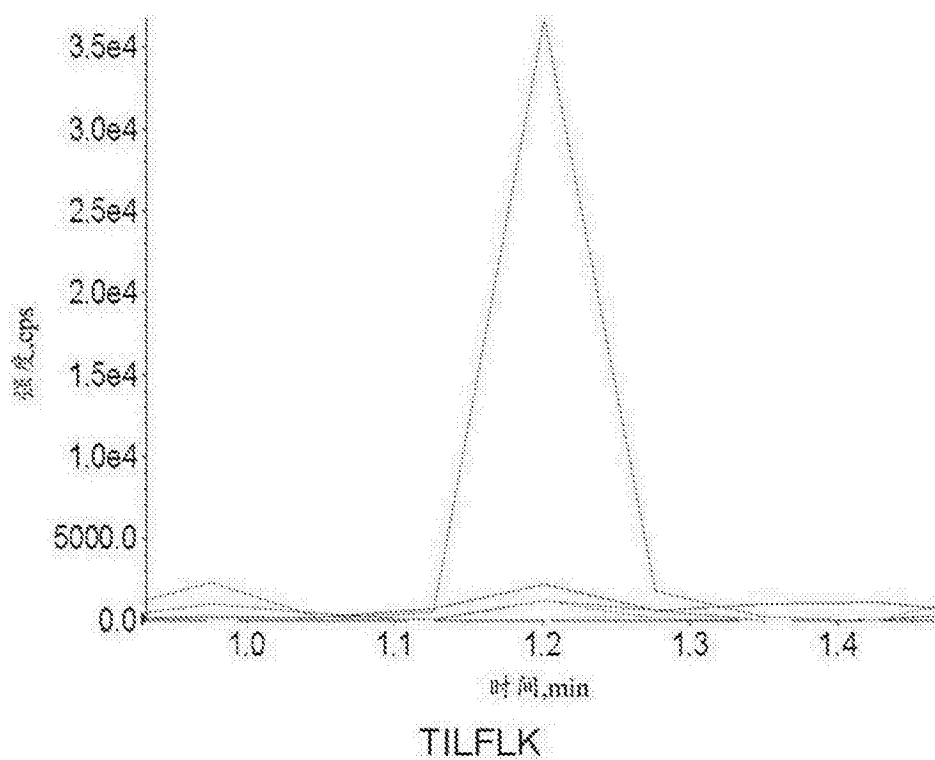


图8K

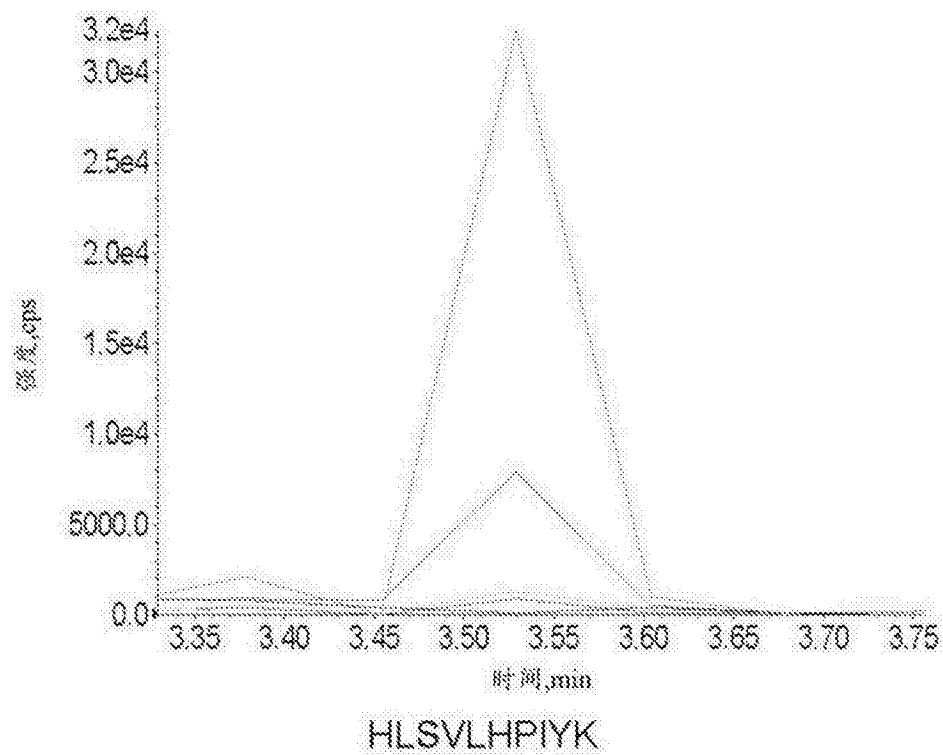


图8L

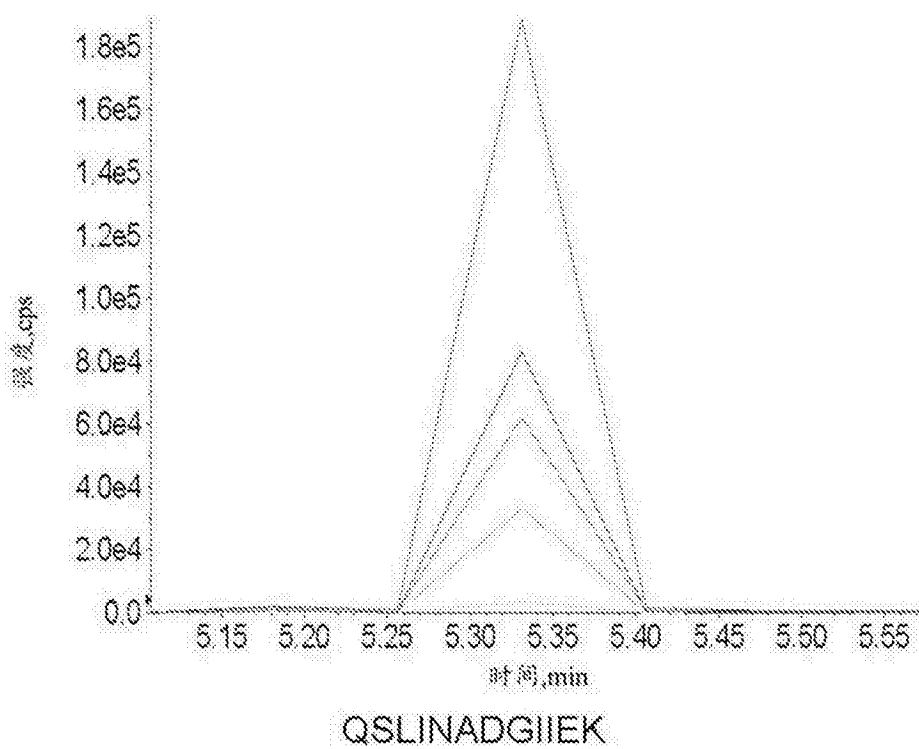


图8M

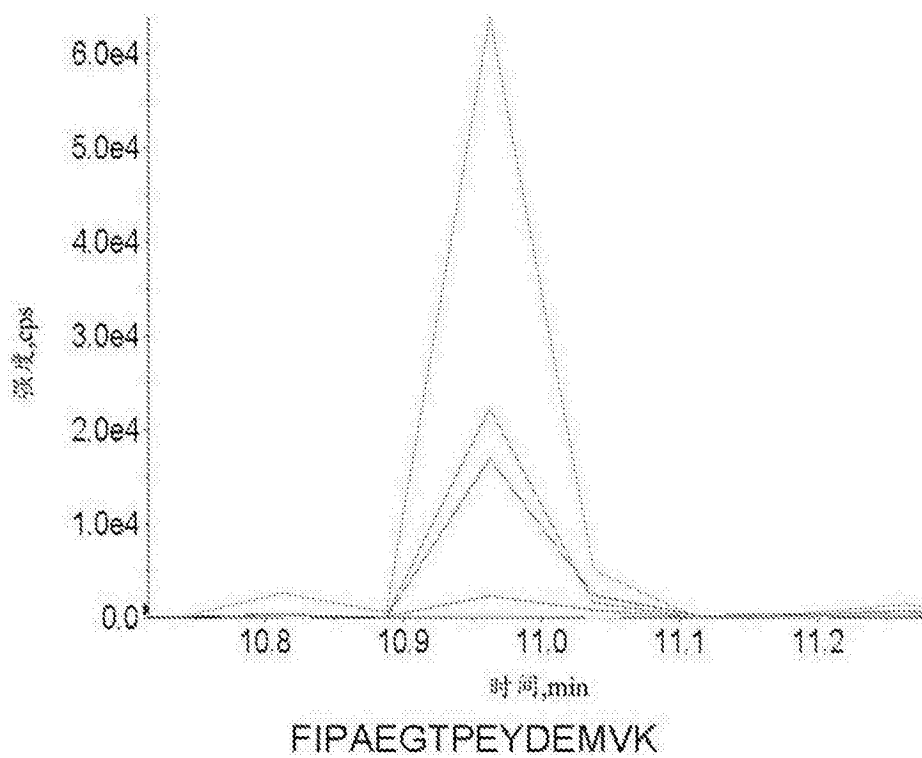


图8N

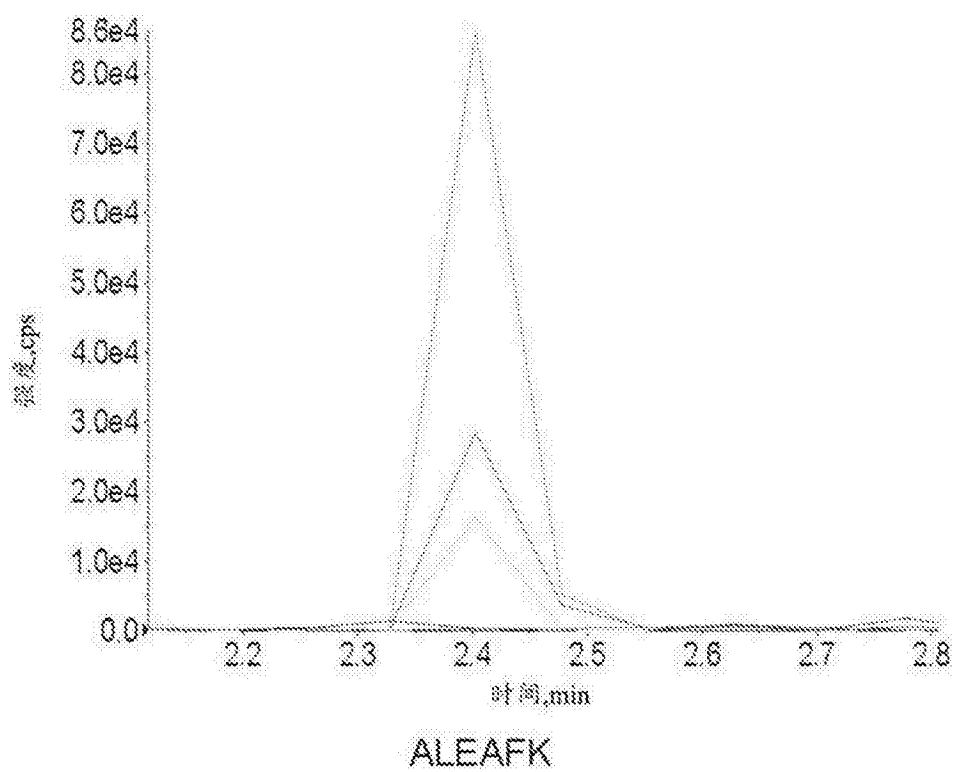


图80

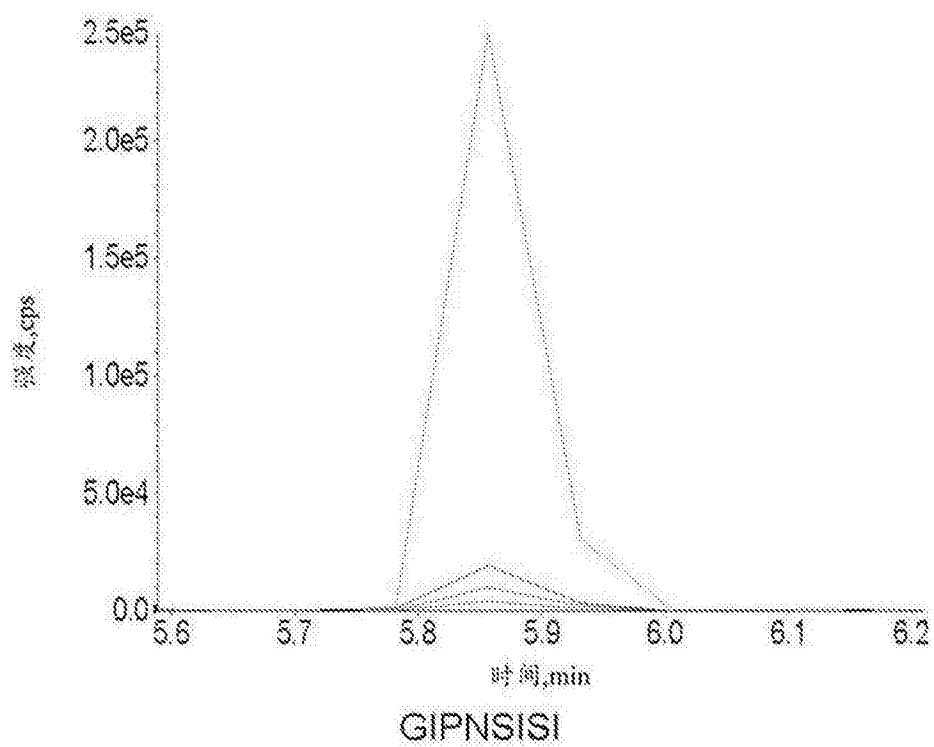


图8P

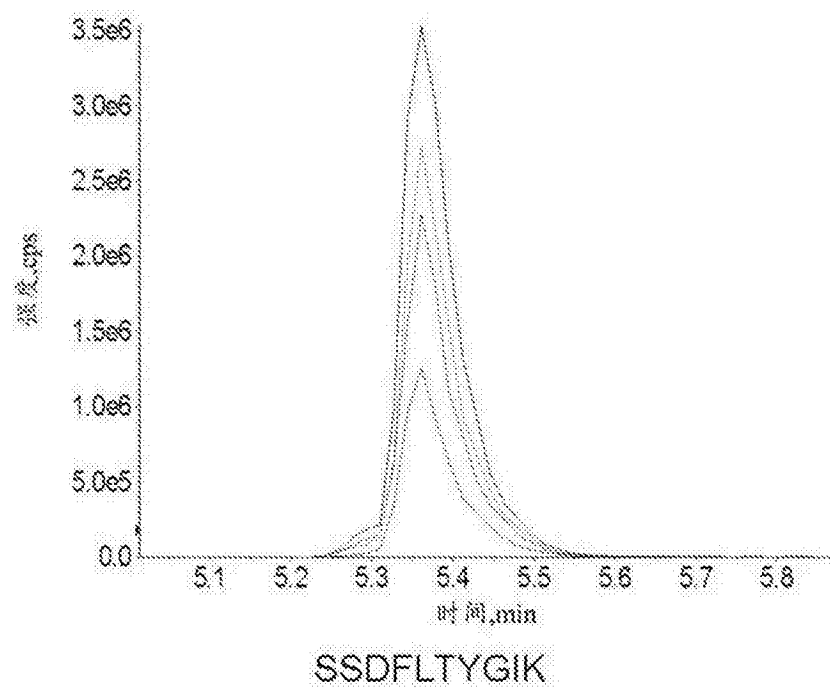


图8Q

	1	50
脂加氧酶 ZIUK_A BLAST	(1) ----MFGIFDK-GQKINGTVVLMFKNVLDFAITTSIGSGGVIDTATGILG	
脂加氧酶 NP_001238676 BLAST	(1) ----MFGIFDK-GQKINGTVVLMFKNVLDFAITTSIGSGGVIDTATGILG	
脂加氧酶 CAA39604	(1) ----MFGIFDK-GQKINGTVVLMFKNVLDFAITTSIGSGGVIDTATGILG	
脂加氧酶 Glyma08g20220.1 BLAST	(1) ----MLGLFDK-SHRINGTVVLMFKNVLDFAITTSIGSGGVIDTATGILG	
脂加氧酶 P24095 BLAST	(1) ----MFGIFDK-GQKINGTVVLMFKNVLDFAITTSIGSGGVIDTATGILG	
脂加氧酶 Glyma07g00900.1 BLAST	(1) ---MTGGMFGRKGGKINGTVVLMFKNVLDFAITTSIGSGGVIDTATGILG	
脂加氧酶 NP_001238189 BLAST	(1) ---MTGGMFGRKGGKINGTVVLMFKNVLDFAITTSIGSGGVIDTATGILG	
脂加氧酶 Glyma07g03910.1 BLAST	(1) ---MFGILGKNGKINGTVVLMFKNVLDFAITTSIGSGGVIDTATGILG	
脂加氧酶 Glyma07g03920.2 BLAST	(1) --MLIGLLNKR-PKINGTVVLMFKNVLDFAITTSIGSGGVIDTATGILG	
脂加氧酶 Glyma08g20190.1 BLAST	(1) MTSGVSLFNR-SQEVNGTVVLMFKNVLDFAITTSIGSGGVIDTATGILG	
共有	(1) MFGIFDK GQKINGTVVLMFKNVLDFAITTSIGSGGVIDTATGILG	
	51	100
脂加氧酶 ZIUK_A BLAST	(46) QGVSLVGGVIDTATSFLOGNISMQILSATQTD-QSGNGKVGWEVYLEKHL	
脂加氧酶 NP_001238676 BLAST	(46) QGVSLVGGVIDTATSFLOGNISMQILSATQTD-QSGNGKVGWEVYLEKHL	
脂加氧酶 CAA39604	(46) QGVSLVGGVIDTATSFLOGNISMQILSATQTD-QSGNGKVGWEVYLEKHL	
脂加氧酶 Glyma08g20220.1 BLAST	(46) AVADVTGGVIDTATSFLOGNISMQILSATQTD-QSGNGKVGWEVYLEKHL	
脂加氧酶 P24095 BLAST	(46) QGVSLVGGVIDTATSFLOGNISMQILSATQTD-QSGNGKVGWEVYLEKHL	
脂加氧酶 Glyma07g00900.1 BLAST	(46) KGLDALGNAVDALTAFAHGISLQLISATQTD-QSGNGKVGWEVYLEKHL	
脂加氧酶 NP_001238189 BLAST	(46) KGLDALGNAVDALTAFAHGISLQLISATQTD-QSGNGKVGWEVYLEKHL	
脂加氧酶 Glyma07g03910.1 BLAST	(46) AATGIVGGVIDGATAIFSRNIAIQLISATQTD-GLNGKVGWQTYLEKHL	
脂加氧酶 Glyma07g03920.2 BLAST	(46) AAQDIVGGVIDGATAIFSRNIAIQLISATQTD-GLNGKVGWQTYLEKHL	
脂加氧酶 Glyma08g20190.1 BLAST	(41) TGINIIGSTIDGLTSLGHSVCLQLISATQTD-GWNGVVGKTYLEKHL	
共有	(51) QGVSLVGGVIDTATSFLOGNISMQILSATQTD QSGNGKVGWEVYLEKHL	
	101	150
脂加氧酶 ZIUK_A BLAST	(95) PTLPTLGARQDAFPIFFENDASFGIPGAFYIKNFMTDEFFLVSVKLEDIF	
脂加氧酶 NP_001238676 BLAST	(95) PTLPTLGARQDAFPIFFENDASFGIPGAFYIKNFMTDEFFLVSVKLEDIF	
脂加氧酶 CAA39604	(95) PTLPTLGARQDAFPIFFENDASFGIPGAFYIKNFMTDEFFLVSVKLEDIF	
脂加氧酶 Glyma08g20220.1 BLAST	(95) PTLPTLGARQDAFPIFFENDASFGIPGAFYIKNFMTDEFFLVSVKLEDIF	
脂加氧酶 P24095 BLAST	(95) PTLPTLGARQDAFPIFFENDASFGIPGAFYIKNFMTDEFFLVSVKLEDIF	
脂加氧酶 Glyma07g00900.1 BLAST	(97) PTLPTLGARQDAFPIFFENDASFGIPGAFYIKNFMTDEFFLVSVKLEDIF	
脂加氧酶 NP_001238189 BLAST	(97) PTLPTLGARQDAFPIFFENDASFGIPGAFYIKNFMTDEFFLVSVKLEDIF	
脂加氧酶 Glyma07g03910.1 BLAST	(97) PSLPTLGARQDAFPIFFENDASFGIPGAFYIKNFMTDEFFLVSVKLEDIF	
脂加氧酶 Glyma07g03920.2 BLAST	(98) PSLPTLGARQDAFPIFFENDASFGIPGAFYIKNFMTDEFFLVSVKLEDIF	
脂加氧酶 Glyma08g20190.1 BLAST	(90) TSIPTLGARQDAFPIFFENDASFGIPGAFYIKNFMTDEFFLVSVKLEDIF	
共有	(101) PTLPTLGARQDAFPIFFENDASFGIPGAFYIKNFMTDEFFLVSVKLEDIF	
	151	200
脂加氧酶 ZIUK_A BLAST	(145) NHGTIEFVCHSWVYNFRSYKK-NRIFFVNDTVLPSATPAPLLKYRKEELE	
脂加氧酶 NP_001238676 BLAST	(145) NHGTIEFVCHSWVYNFRSYKK-NRIFFVNDTVLPSATPAPLLKYRKEELE	
脂加氧酶 CAA39604	(145) NHGTIEFVCHSWVYNFRSYKK-NRIFFVNDTVLPSATPAPLLKYRKEELE	
脂加氧酶 Glyma08g20220.1 BLAST	(145) NHGTIEFVCHSWVYNFRSYKK-NRIFFVNDTVLPSATPAPLLKYRKEELE	
脂加氧酶 P24095 BLAST	(145) NHGTIEFVCHSWVYNFRSYKK-NRIFFVNDTVLPSATPAPLLKYRKEELE	
脂加氧酶 Glyma07g00900.1 BLAST	(147) NHGTIEFVCHSWVYNFRSYKK-NRIFFVNDTVLPSATPAPLLKYRKEELE	
脂加氧酶 NP_001238189 BLAST	(147) NHGTIEFVCHSWVYNFRSYKK-NRIFFVNDTVLPSATPAPLLKYRKEELE	
脂加氧酶 Glyma07g03910.1 BLAST	(147) NHGTIEFVCHSWVYNFRSYKK-NRIFFVNDTVLPSATPAPLLKYRKEELE	
脂加氧酶 Glyma07g03920.2 BLAST	(149) NHGTIEFVCHSWVYNFRSYKK-NRIFFVNDTVLPSATPAPLLKYRKEELE	
脂加氧酶 Glyma08g20190.1 BLAST	(140) NQGMHFVCHSWVYNFRSYKK-NRIFFVNDTVLPSATPAPLLKYRKEELE	
共有	(151) NHGTIEFVCHSWVYNFRSYKK-NRIFFVNDTVLPSATPAPLLKYRKEELE	

图8R

脂加氧酶 ZIUK_A BLAST	(194)	VLRGGDTGKRRDFDRIVDYDVYNDLGNPDG--GDPRFILGGGSIYFYFLR	250
脂加氧酶 NP_001238678 BLAST	(194)	VLRGGDTGKRRDFDRIVDYDVYNDLGNPDG--GDPRFILGGGSIYFYFLR	
脂加氧酶 CAA39604	(194)	VLRGGDTGKRRDFDRIVDYDVYNDLGNPDG--GDPRFILGGGSIYFYFLR	
脂加氧酶 Glyma08g20120.1 BLAST	(195)	ILRGDTGKRRERERIVDYDVYNDLGNPDGDFVLARFVLRGGSTYFYFLR	
脂加氧酶 P24095 BLAST	(194)	VLRGGDTGKRRDFDRIVDYDVYNDLGNPDG--GDPRFILGGGSIYFYFLR	
脂加氧酶 Glyma07g00900.1 BLAST	(194)	VLRGGDTGKRRDFDRIVDYDVYNDLGNPDG--GDPRFILGGGSIYFYFLR	
脂加氧酶 NP_001238189 BLAST	(196)	VLRGGDTGKRRDFDRIVDYDVYNDLGNPDG--GDPRFILGGGSIYFYFLR	
脂加氧酶 Glyma07g03910.1 BLAST	(196)	NLRGGGRRERERIVDYDVYNDLGNPDGDKWDLARFVLRGGSIYFYFLR	
脂加氧酶 Glyma07g03920.2 BLAST	(197)	NLRGGGRRERERIVDYDVYNDLGNPDGDKWDLARFVLRGGSIYFYFLR	
脂加氧酶 Glyma08g20190.1 BLAST	(189)	ALRGDTGKRRERERIVDYDVYNDLGNPDGSGENFARFVLRGGSIYFYFLR	
共有	(201)	VLRGGDTGKRRDFDRIVDYDVYNDLGNPDG GDPRFILGGGSIYFYFLR	251
脂加氧酶 ZIUK_A BLAST	(242)	VRTGRERTITDENSEKPG-EVTVPRDENFGLKSSDPLTYGKSLSHDVI	300
脂加氧酶 NP_001238678 BLAST	(242)	VRTGRERTITDENSEKPG-EVTVPRDENFGLKSSDPLTYGKSLSHDVI	
脂加氧酶 CAA39604	(242)	VRTGRERTITDENSEKPG-EVTVPRDENFGLKSSDPLTYGKSLSHDVI	
脂加氧酶 Glyma08g20120.1 BLAST	(245)	VRTGRKATFDENSEKPGSELNMPDENFGLKSSDPLTYGKSLSQLL	
脂加氧酶 P24095 BLAST	(242)	VRTGRERTITDENSEKPG-EVTVPRDENFGLKSSDPLTYGKSLSHDVI	
脂加氧酶 Glyma07g00900.1 BLAST	(244)	VRTGRERTITDENSEKPG-EVTVPRDENFGLKSSDPLTYGKSLSHDVI	
脂加氧酶 NP_001238189 BLAST	(244)	VRTGRERTITDENSEKPG-EVTVPRDENFGLKSSDPLTYGKSLSHDVI	
脂加氧酶 Glyma07g03910.1 BLAST	(246)	GRTGRKPTFDENSEKPGSTSTYIPDENFGLKSSDPLTYGKSLAQTVL	
脂加氧酶 Glyma07g03920.2 BLAST	(247)	GRTGRKPTFDENSEKPGSTSTYIPDENFGLKSSDPLTYGKSLAQTVL	
脂加氧酶 Glyma08g20190.1 BLAST	(239)	GRTGRKPTFDENSEKPG-EAYIPDENFGLKSSDPLTYGKSLTRSL	
共有	(251)	VRTGRERTITDENSEKPG EVTVPRDENFGLKSSDPLTYGKSLSHDVI	301
脂加氧酶 ZIUK_A BLAST	(291)	PLFKSAIFQLVTSSEFESEFEDVRSLYEGGKILPTDILSQISPLPALKEI	350
脂加氧酶 NP_001238678 BLAST	(291)	PLFKSAIFQLVTSSEFESEFEDVRSLYEGGKILPTDILSQISPLPALKEI	
脂加氧酶 CAA39604	(291)	PLFKSAIFQLVTSSEFESEFEDVRSLYEGGKILPTDILSQISPLPALKEI	
脂加氧酶 Glyma08g20120.1 BLAST	(295)	SELEN-VFSDLTWNEFDSEFEVSLYEGGKILPTDILSQISPLPALKEI	
脂加氧酶 P24095 BLAST	(291)	PLFKSAIFQLVTSSEFESEFEDVRSLYEGGKILPTDILSQISPLPALKEI	
脂加氧酶 Glyma07g00900.1 BLAST	(293)	PLFKSAIFQLVTSSEFESEFEDVRSLYEGGKILPTDILSQISPLPALKEI	
脂加氧酶 NP_001238189 BLAST	(293)	PLFKSAIFQLVTSSEFESEFEDVRSLYEGGKILPTDILSQISPLPALKEI	
脂加氧酶 Glyma07g03910.1 BLAST	(296)	STFQS---AF-GLNAEFDAFDVRLFGGKILPTDILSKISPLPALKEI	
脂加氧酶 Glyma07g03920.2 BLAST	(297)	EQFNT---AF-GFNNEFDSEFDVRLFGGKILPTDILSKISPLPALKEI	
脂加氧酶 Glyma08g20190.1 BLAST	(298)	PALET-VFDINFTSEFDSEFEVRLCEGGKILPTDILSKISPLPALKEI	
共有	(301)	PLFKSAIFQLVTSSEFESEFEDVRSLYEGGKILPTDILSQISPLPALKEI	351
脂加氧酶 ZIUK_A BLAST	(341)	FRIDGENVLQFPFPHVAVVRSGWMTDEEFAREVILAGVNPVIRLQEFF	400
脂加氧酶 NP_001238678 BLAST	(341)	FRIDGENVLQFPFPHVAVVRSGWMTDEEFAREVILAGVNPVIRLQEFF	
脂加氧酶 CAA39604	(341)	FRIDGENVLQFPFPHVAVVRSGWMTDEEFAREVILAGVNPVIRLQEFF	
脂加氧酶 Glyma08g20120.1 BLAST	(344)	FRIDGENVLQFPFPHVAVVRSGWMTDEEFAREVILAGVNPVIRLQEFF	
脂加氧酶 P24095 BLAST	(341)	FRIDGENVLQFPFPHVAVVRSGWMTDEEFAREVILAGVNPVIRLQEFF	
脂加氧酶 Glyma07g00900.1 BLAST	(343)	FRIDGENVLQFPFPHVAVVRSGWMTDEEFAREVILAGVNPVIRLQEFF	
脂加氧酶 NP_001238189 BLAST	(343)	FRIDGENVLQFPFPHVAVVRSGWMTDEEFAREVILAGVNPVIRLQEFF	
脂加氧酶 Glyma07g03910.1 BLAST	(342)	FRIDGENVLQFPFPHVAVVRSGWMTDEEFAREVILAGVNPVIRLQEFF	
脂加氧酶 Glyma07g03920.2 BLAST	(343)	FRIDGENVLQFPFPHVAVVRSGWMTDEEFAREVILAGVNPVIRLQEFF	
脂加氧酶 Glyma08g20190.1 BLAST	(337)	FRIDGENVLQFPFPHVAVVRSGWMTDEEFAREVILAGVNPVIRLQEFF	
共有	(351)	FRIDGENVLQFPFPHVAVVRSGWMTDEEFAREVILAGVNPVIRLQEFF	

图8R续

脂加氧酶 GIUK_A BLAST	401	450
脂加氧酶 NF_001238676 BLAST	(391) FNSITLSEPTLYSGDQTSTITFEQLEINMGQVTVVEEALSTQRLFILDYQDAFI	
脂加氧酶 CAA39604	(391) FNSITLSEPTLYSGDQTSTITFEQLEINMGQVTVVEEALSTQRLFILDYQDAFI	
脂加氧酶 Glyma08g20120.1 BLAST	(394) FNSITLSEPTLYSGDQTSTITFEQLEINMGQVTVVEEALSTQRLFILDYQDAFI	
脂加氧酶 F24093 BLAST	(391) FNSITLSEPTLYSGDQTSTITFEQLEINMGQVTVVEEALSTQRLFILDYQDAFI	
脂加氧酶 Glyma07g00990.1 BLAST	(393) FNSITLSEPTLYSGDQTSTITFEQLEINMGQVTVVEEALSTQRLFILDYQDAFI	
脂加氧酶 NF_001238189 BLAST	(393) FNSITLSEPTLYSGDQTSTITFEQLEINMGQVTVVEEALSTQRLFILDYQDAFI	
脂加氧酶 Glyma07g00990.1 BLAST	(392) FNSITLSEPTLYSGDQTSTITFEQLEINMGQVTVVEEALSTQRLFILDYQDAFI	
脂加氧酶 Glyma07g00990.2 BLAST	(393) FNSITLSEPTLYSGDQTSTITFEQLEINMGQVTVVEEALSTQRLFILDYQDAFI	
脂加氧酶 Glyma08g20190.1 BLAST	(397) FNSITLSEPTLYSGDQTSTITFEQLEINMGQVTVVEEALSTQRLFILDYQDAFI	
共有	(401) FNSITLSEPTLYSGDQTSTITFEQLEINMGQVTVVEEALSTQRLFILDYQDAFI	
脂加氧酶 GIUK_A BLAST	451	500
脂加氧酶 NF_001238676 BLAST	(441) FYLTRINSILPTAKAYATATILFLNDDGSLKFLAIELSKPHFDGDNLPES	
脂加氧酶 CAA39604	(441) FYLTRINSILPTAKAYATATILFLNDDGSLKFLAIELSKPHFDGDNLPES	
脂加氧酶 Glyma08g20120.1 BLAST	(444) FYLTRINSILPTAKAYATATILFLNDDGSLKFLAIELSKPHFDGDNLPES	
脂加氧酶 F24093 BLAST	(441) FYLTRINSILPTAKAYATATILFLNDDGSLKFLAIELSKPHFDGDNLPES	
脂加氧酶 Glyma07g00990.1 BLAST	(443) FYLTRINSILPTAKAYATATILFLNDDGSLKFLAIELSKPHFDGDNLPES	
脂加氧酶 NF_001238189 BLAST	(443) FYLTRINSILPTAKAYATATILFLNDDGSLKFLAIELSKPHFDGDNLPES	
脂加氧酶 Glyma07g00990.1 BLAST	(442) FYLTRINSILPTAKAYATATILFLNDDGSLKFLAIELSKPHFDGDNLPES	
脂加氧酶 Glyma07g00990.2 BLAST	(443) FYLTRINSILPTAKAYATATILFLNDDGSLKFLAIELSKPHFDGDNLPES	
脂加氧酶 Glyma08g20190.1 BLAST	(437) FYLTRINSILPTAKAYATATILFLNDDGSLKFLAIELSKPHFDGDNLPES	
共有	(451) FYLTRINSILPTAKAYATATILFLNDDGSLKFLAIELSKPHFDGDNLPES	
脂加氧酶 GIUK_A BLAST	501	550
脂加氧酶 NF_001238676 BLAST	(491) IVVLP--ATEGVSDSTINLLAKARVIVNDGGYHQLVSHWLNTHAVNEFFAI	
脂加氧酶 CAA39604	(491) IVVLP--ATEGVSDSTINLLAKARVIVNDGGYHQLVSHWLNTHAVNEFFAI	
脂加氧酶 Glyma08g20120.1 BLAST	(494) IVVLP--ATEGVSDSTINLLAKARVIVNDGGYHQLVSHWLNTHAVNEFFAI	
脂加氧酶 F24093 BLAST	(491) IVVLP--ATEGVSDSTINLLAKARVIVNDGGYHQLVSHWLNTHAVNEFFAI	
脂加氧酶 Glyma07g00990.1 BLAST	(493) IVVLP--ATEGVSDSTINLLAKARVIVNDGGYHQLVSHWLNTHAVNEFFAI	
脂加氧酶 NF_001238189 BLAST	(496) IVVLP--ATEGVSDSTINLLAKARVIVNDGGYHQLVSHWLNTHAVNEFFAI	
脂加氧酶 Glyma07g00990.1 BLAST	(492) IVVLP--ATEGVSDSTINLLAKARVIVNDGGYHQLVSHWLNTHAVNEFFAI	
脂加氧酶 Glyma07g00990.2 BLAST	(493) IVVLP--ATEGVSDSTINLLAKARVIVNDGGYHQLVSHWLNTHAVNEFFAI	
脂加氧酶 Glyma08g20190.1 BLAST	(497) IVVLP--ATEGVSDSTINLLAKARVIVNDGGYHQLVSHWLNTHAVNEFFAI	
共有	(501) IVVLP--ATEGVSDSTINLLAKARVIVNDGGYHQLVSHWLNTHAVNEFFAI	
脂加氧酶 GIUK_A BLAST	551	600
脂加氧酶 NF_001238676 BLAST	(539) ATNRRLSVLMFIYKLLYPHYRDTININGLARQSLINAGGIIKSFLEPKY	
脂加氧酶 CAA39604	(539) ATNRRLSVLMFIYKLLYPHYRDTININGLARQSLINAGGIIKSFLEPKY	
脂加氧酶 Glyma08g20120.1 BLAST	(542) ATNRRLSVLMFIYKLLYPHYRDTININGLARQSLINAGGIIKSFLEPKY	
脂加氧酶 F24093 BLAST	(539) ATNRRLSVLMFIYKLLYPHYRDTININGLARQSLINAGGIIKSFLEPKY	
脂加氧酶 Glyma07g00990.1 BLAST	(541) ATNRRLSVLMFIYKLLYPHYRDTININGLARQSLINAGGIIKSFLEPKY	
脂加氧酶 NF_001238189 BLAST	(534) ATNRRLSVLMFIYKLLYPHYRDTININGLARQSLINAGGIIKSFLEPKY	
脂加氧酶 Glyma07g00990.1 BLAST	(540) ATNRRLSVLMFIYKLLYPHYRDTININGLARQSLINAGGIIKSFLEPKY	
脂加氧酶 Glyma07g00990.2 BLAST	(543) ATNRRLSVLMFIYKLLYPHYRDTININGLARQSLINAGGIIKSFLEPKY	
脂加氧酶 Glyma08g20190.1 BLAST	(535) ATNRRLSVLMFIYKLLYPHYRDTININGLARQSLINAGGIIKSFLEPKY	
共有	(551) ATNRRLSVLMFIYKLLYPHYRDTININGLARQSLINAGGIIKSFLEPKY	

图8R续

脂加氧酶 ZIUK_A BLAST	(589)	SIEMSSSVYKHWVFTDQALPADLVKGLAIEDPSAPHGSLRLVIEDYPTAY	650
脂加氧酶 NP_001238676 BLAST	(589)	SIEMSSSVYKHWVFTDQALPADLVKGLAIEDPSAPHGSLRLVIEDYPTAY	
脂加氧酶 CAA39404	(589)	SIEMSSSVYKHWVFTDQALPADLVKGLAIEDPSAPHGSLRLVIEDYPTAY	
脂加氧酶 Glyma08g20220.1 BLAST	(592)	SIEMSSSVYKHWVFTDQALPADLVKGLAIEDPSAPHGSLRLVIEDYPTAY	
脂加氧酶 P24093 BLAST	(599)	SIEMSSSVYKHWVFTDQALPADLVKGLAIEDPSAPHGSLRLVIEDYPTAY	
脂加氧酶 Glyma07g00900.1 BLAST	(591)	SIEMSSSVYKHWVFTDQALPADLVKGLAIEDPSAPHGSLRLVIEDYPTAY	
脂加氧酶 NP_001235139 BLAST	(594)	SIEMSSSVYKHWVFTDQALPADLVKGLAIEDPSAPHGSLRLVIEDYPTAY	
脂加氧酶 Glyma07g00910.1 BLAST	(590)	AVEMSSSVYKHWVFTDQALPADLVKGLAIEDPSAPHGSLRLVIEDYPTAY	
脂加氧酶 Glyma07g00920.2 BLAST	(593)	SIEMSSSVYKHWVFTDQALPADLVKGLAIEDPSAPHGSLRLVIEDYPTAY	
脂加氧酶 Glyma08g20190.1 BLAST	(585)	AVE1SSSVYKHWVFTDQALPADLVKGLAIEDPSAPHGSLRLVIEDYPTAY	
共有	(601)	SIEMSSSVYKHWVFTDQALPADLVKGLAIEDPSAPHGSLRLVIEDYPTAY	
脂加氧酶 ZIUK_A BLAST	(639)	DGLEIWDIAIKTWVHEVSLYYFTDAAVQQDTQLQAWWKEAVFKHGGLKE	700
脂加氧酶 NP_001238676 BLAST	(639)	DGLEIWDIAIKTWVHEVSLYYFTDAAVQQDTQLQAWWKEAVFKHGGLKE	
脂加氧酶 CAA39404	(639)	DGLEIWDIAIKTWVHEVSLYYFTDAAVQQDTQLQAWWKEAVFKHGGLKE	
脂加氧酶 Glyma08g20220.1 BLAST	(643)	DGLEIWDIAIKTWVHEVSLYYFTDAAVQQDTQLQAWWKEAVFKHGGLKE	
脂加氧酶 P24093 BLAST	(639)	DGLEIWDIAIKTWVHEVSLYYFTDAAVQQDTQLQAWWKEAVFKHGGLKE	
脂加氧酶 Glyma07g00900.1 BLAST	(641)	DGLEIWDIAIKTWVHEVSLYYFTDAAVQQDTQLQAWWKEAVFKHGGLKE	
脂加氧酶 NP_001235139 BLAST	(634)	DGLEIWDIAIKTWVHEVSLYYFTDAAVQQDTQLQAWWKEAVFKHGGLKE	
脂加氧酶 Glyma07g00910.1 BLAST	(640)	DGLEIWDIAIKTWVHEVSLYYFTDAAVQQDTQLQAWWKEAVFKHGGLKE	
脂加氧酶 Glyma07g00920.2 BLAST	(643)	DGLEIWDIAIKTWVHEVSLYYFTDAAVQQDTQLQAWWKEAVFKHGGLKE	
脂加氧酶 Glyma08g20190.1 BLAST	(635)	DGLEIWDIAIKTWVHEVSLYYFTDAAVQQDTQLQAWWKEAVFKHGGLKE	
共有	(651)	DGLEIWDIAIKTWVHEVSLYYFTDAAVQQDTQLQAWWKEAVFKHGGLKE	
脂加氧酶 ZIUK_A BLAST	(689)	EFWPFPMQTTEDLIQSCSTIIVWTASALHAAVNFQCYFYGGILNRPFTLAR	750
脂加氧酶 NP_001238676 BLAST	(689)	EFWPFPMQTTEDLIQSCSTIIVWTASALHAAVNFQCYFYGGILNRPFTLAR	
脂加氧酶 CAA39404	(689)	EFWPFPMQTTEDLIQSCSTIIVWTASALHAAVNFQCYFYGGILNRPFTLAR	
脂加氧酶 Glyma08g20220.1 BLAST	(692)	EFWPFPMQTTEDLIQSCSTIIVWTASALHAAVNFQCYFYGGILNRPFTLAR	
脂加氧酶 P24093 BLAST	(689)	EFWPFPMQTTEDLIQSCSTIIVWTASALHAAVNFQCYFYGGILNRPFTLAR	
脂加氧酶 Glyma07g00900.1 BLAST	(691)	EFWPFPMQTTEDLIQSCSTIIVWTASALHAAVNFQCYFYGGILNRPFTLAR	
脂加氧酶 NP_001235139 BLAST	(694)	EFWPFPMQTTEDLIQSCSTIIVWTASALHAAVNFQCYFYGGILNRPFTLAR	
脂加氧酶 Glyma07g00910.1 BLAST	(690)	EFWPFPMQTTEDLIQSCSTIIVWTASALHAAVNFQCYFYGGILNRPFTLAR	
脂加氧酶 Glyma07g00920.2 BLAST	(693)	EFWPFPMQTTEDLIQSCSTIIVWTASALHAAVNFQCYFYGGILNRPFTLAR	
脂加氧酶 Glyma08g20190.1 BLAST	(685)	EFWPFPMQTTEDLIQSCSTIIVWTASALHAAVNFQCYFYGGILNRPFTLAR	
共有	(701)	EFWPFPMQTTEDLIQSCSTIIVWTASALHAAVNFQCYFYGGILNRPFTLAR	
脂加氧酶 ZIUK_A BLAST	(739)	RFIFAEETPEYDEMVKNFQKAYLRTITTFEFETLIDLSVIEILSRHASDEI	800
脂加氧酶 NP_001238676 BLAST	(739)	RFIFAEETPEYDEMVKNFQKAYLRTITTFEFETLIDLSVIEILSRHASDEI	
脂加氧酶 CAA39404	(739)	RFIFAEETPEYDEMVKNFQKAYLRTITTFEFETLIDLSVIEILSRHASDEI	
脂加氧酶 Glyma08g20220.1 BLAST	(742)	RFIFAEETPEYDEMVKNFQKAYLRTITTFEFETLIDLSVIEILSRHASDEI	
脂加氧酶 P24093 BLAST	(739)	RFIFAEETPEYDEMVKNFQKAYLRTITTFEFETLIDLSVIEILSRHASDEI	
脂加氧酶 Glyma07g00900.1 BLAST	(741)	RFIFAEETPEYDEMVKNFQKAYLRTITTFEFETLIDLSVIEILSRHASDEI	
脂加氧酶 NP_001235139 BLAST	(734)	RFIFAEETPEYDEMVKNFQKAYLRTITTFEFETLIDLSVIEILSRHASDEI	
脂加氧酶 Glyma07g00910.1 BLAST	(740)	RFIFAEETPEYDEMVKNFQKAYLRTITTFEFETLIDLSVIEILSRHASDEI	
脂加氧酶 Glyma07g00920.2 BLAST	(743)	RFIFAEETPEYDEMVKNFQKAYLRTITTFEFETLIDLSVIEILSRHASDEI	
脂加氧酶 Glyma08g20190.1 BLAST	(735)	RFIFAEETPEYDEMVKNFQKAYLRTITTFEFETLIDLSVIEILSRHASDEI	
共有	(751)	RFIFAEETPEYDEMVKNFQKAYLRTITTFEFETLIDLSVIEILSRHASDEI	

图8R续

		801	850
脂加氧酶 Z1UK_A BLAST	(789)	YLGERETPNWTTDXXKALEAFKRFSGSKLTGIEGKINARNSDPSLKNRTGKV	
脂加氧酶 NP_001238676 BLAST	(789)	YLGERETPNWTTDXXKALEAFKRFSGSKLTGIEGKINARNSDPSLKNRTGKV	
脂加氧酶 CAA39604	(789)	YLGERETPNWTTDXXKALEAFKRFSGSKLTGIEGKINARNSDPSLKNRTGKV	
脂加氧酶 Glyma08g20220.1 BLAST	(792)	YLGERDNPWTTSDSKALEAFKRFSGSKLAEIEGKITARNKDSNKKKNTGKV	
脂加氧酶 P24095 BLAST	(789)	YLGERETPNWTTDXXKALEAFKRFSGSKLTGIEGKINARNSDPSLKNRTGKV	
脂加氧酶 Glyma07g00900.1 BLAST	(791)	YLGERETPNWTTDXXKALEAFKRFSGSKLTGIEGKINARNSDPSLKNRTGKV	
脂加氧酶 NP_001238189 BLAST	(784)	YLGQRDNFWTTDXXKALEAFKRFSGSKLAEIEGKITQRNNDPSLKNRTGKV	
脂加氧酶 Glyma07g03910.1 BLAST	(790)	YLGQRDNFWTTDQTKAIQAFKKFSGNKLAEIEGKITQRNNDPSLKNRTGKV	
脂加氧酶 Glyma07g03920.2 BLAST	(793)	YLGKRDSDQWTDQTKAIQAFKKFSGNKLAEIEGKITQRNNDPSLKNRTGKV	
脂加氧酶 Glyma08g20190.1 BLAST	(785)	YLGQRDNFWTTSDNFKALEAFKRFSGSKLAEIEGKITQRNNDPSLKNRTGKV	
Conserved	(801)	YLGERDTPWTTDXXKALEAFKRFSGSKLTGIEGKINARNSDPSLKNRTGKV	
		851	876
脂加氧酶 Z1UK_A BLAST	(839)	QLPYTLLHRSSSEGLTFNGIFNSISI	
脂加氧酶 NP_001238676 BLAST	(839)	QLPYTLLHRSSSEGLTFNGIFNSISI	
脂加氧酶 CAA39604	(839)	QLPYTLLHRSSSEGLTFNGIFNSISI	
脂加氧酶 Glyma08g20220.1 BLAST	(842)	QLPYTLLIPTSEEGLTFRGIFNSISI	
脂加氧酶 P24095 BLAST	(839)	QLPYTLLHRSSSEGLTFNGIFNSISI	
脂加氧酶 Glyma07g00900.1 BLAST	(841)	QLPYTLLHRSSSEGLTFNGIFNSISI	
脂加氧酶 NP_001238189 BLAST	(834)	QLPYTLLHRSSSEGMSTFGIFNSISI	
脂加氧酶 Glyma07g03910.1 BLAST	(840)	QMPYTVLLPT36EGLTFRGIFNSISI	
脂加氧酶 Glyma07g03920.2 BLAST	(843)	QMPYTVLLPTSEGLTFNGIFNSISI	
脂加氧酶 Glyma08g20190.1 BLAST	(835)	QLPYTVLLPTSETGLTFNGIFNSISI	
共有	(851)	QLPYTLLHRSSSEGLTFNGIFNSISI	

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