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(54)发明名称

嵌合抗原受体

(57)摘要

提供包含双唾液酸神经节苷脂(GD2)结合域的嵌合抗原受体(CAR),所述GD2结合域包含a)具有互补决定区(CDR)的重链可变区(VH),所述CDRs具有以下序列;b)具有CDR的轻链可变区(VL),所述CDR具有以下序列:表达此类CAR的T细胞在一些癌症的治疗中有用。

1. 包含双唾液酸神经节苷脂(GD2)结合域的嵌合抗原受体(CAR),所述GD2结合域包含
 - a) 重链可变区(VH),其包含具有如SEQ ID No:10所示的序列的VH域;和
 - b) 轻链可变区(VL),其包含具有如SEQ ID No:12所示的序列的VL域。
2. 根据权利要求1的CAR,其中所述GD2结合域包含如SEQ ID No.8所示的序列。
3. 根据前述权利要求任一项的CAR,其包含跨膜域,所述跨膜域包含如SEQ ID No.13所示的序列。
4. 根据前述权利要求任一项的CAR,其中GD2结合域和所述跨膜域通过间隔区连接。
5. 根据权利要求4的CAR,其中所述间隔区包含以下的一种:人IgG1 Fc域;IgG1铰链;IgG1铰链-CD8茎部;或CD8茎部。
6. 根据权利要求5的CAR,其中所述间隔区包含IgG1铰链-CD8茎部或CD8茎部。
7. 根据权利要求5的CAR,其中所述间隔区包含IgG1 Fc域。
8. 根据权利要求7的CAR,其中所述间隔区包含IgG1 Fc域,其包含如SEQ ID No.23或SEQ ID No.24所示的序列。
9. 前述权利要求任一项的CAR,其还包含细胞内T细胞信号传导域。
10. 根据权利要求9的CAR,其中所述细胞内T细胞信号传导域包含一个或多个以下胞内域:CD28胞内域;OX40和CD3-Zeta胞内域。
11. 根据权利要求10的CAR,其中所述细胞内T细胞信号传导域包含所有以下胞内域:CD28胞内域;OX40和CD3-Zeta胞内域。
12. 根据前述权利要求任一项的CAR,其包含如SEQ ID No.27至35任一项所示的序列。
13. 编码根据前述权利要求任一项的CAR的核酸序列。
14. 根据权利要求13的核酸序列,其为密码子优化的。
15. 根据权利要求13或14的核酸序列,其包含如SEQ ID No.25所示的序列。
16. 根据权利要求13至15任一项的核酸,其还编码自杀基因。
17. 包含根据权利要求13至16任一项的核酸序列的载体。
18. 表达根据权利要求1至12任一项的CAR的T细胞。
19. T细胞,其共表达根据权利要求1至12任一项的CAR和自杀基因。
20. 根据权利要求19的T细胞,其中所述自杀基因是iCasp9或RQR8。
21. 用于制造根据权利要求18至20任一项的T细胞的方法,其包括将根据权利要求13至16任一项的核酸导入T细胞的步骤。
22. 药物组合物,其包含根据权利要求18至20任一项的T细胞以及药学上可接受的载体,稀释剂或赋形剂。
23. 根据权利要求18至20任一项的T细胞在制造用于治疗癌症的药物中的用途。
24. 根据权利要求23的用途,其中所述癌症为神经母细胞瘤。

嵌合抗原受体

发明领域

[0001] 本发明涉及嵌合抗原受体 (CAR) , 其结合癌抗原双唾液酸神经节苷脂 (disialoganglioside) (GD2)。表达此类CAR的T细胞在癌症疾病, 例如神经母细胞瘤的治疗中是有用的。

[0002] 发明背景

[0003] 双唾液酸神经节苷脂 (GD2, pubchem:6450346) 是一种含唾液酸的鞘糖脂, 主要在细胞表面上表达。该碳水化合物抗原的功能尚未完全理解; 然而, 认为其在肿瘤细胞对细胞外基质蛋白的附着中发挥重要作用。GD2在神经母细胞瘤 (neuroblastoma) 上密集, 同质且几乎普遍表达的。在正常组织中, GD2的表达很大程度上限制在皮肤黑色素细胞, 和外周疼痛纤维髓鞘。在CNS中, GD2似乎是胚胎抗原, 但发现在分散的少突胶质细胞中和在垂体后叶中暗淡地表达。这使得GD2非常适合用于靶向抗肿瘤疗法。

[0004] 抗GD2抗体已经在神经母细胞瘤的治疗中广泛地测试。两个克隆和它们的衍生物是目前临床使用的: 3F814和3F8。在同种型转换为IgG2a (14g2a) 和最终与人IgG1嵌合以形成ch4.18后, 已经测试了作为小鼠IgG3的另一个克隆14.187。后者抗体在随机化研究中已经产生了明确的效力: US Children's Oncology Group报道了在具有高风险神经母细胞瘤的儿童中ch14:18的随机化III期研究, 所述儿童在最初治疗后已经实现了放射学缓解 (radiological remission)。在这些患者中, 在ch14:18组 (arm) 中, EFS中存在20%的改善, 其中平均随访2.1年。重要地, 神经毒性是这些试剂的主要剂量限制毒性, 所述神经毒性最常见作为慢性疼痛诱导神经病, 而不太常见作为眼肌麻痹 (ophthalmoplegia)。

[0005] 这些治疗性mAb继续被完善: 已经描述了衍生于ch14.18的IL-2免疫细胞因子。这是相当毒性的试剂, 对微量残存疾病具有一些效果, 但无一针对大体积的疾病 (bulky disease)。Ch14.18已经完全人源化且其Fc经突变以抑制补体活化。Ch14.18的这一人源化版本在临床研究中但仅非常有限的数据是可用的。也描述了3F8抗体的人源化。尽管来自GD2血清疗法的临床数据是令人鼓舞的, 但是持续的完全缓解仍然有限, 且除了在最小程度疾病背景中外, 对于抗体在临床上有用的作用没有证据。

[0006] 因此, 对于治疗神经母细胞瘤和其它表达GD2的癌症的改进的治疗方法存在需要。

[0007] 嵌合抗原受体 (CAR)

[0008] 嵌合抗原受体是常见形式为将单克隆抗体 (mAb) 的特异性移植到T细胞的效应功能的蛋白质。它们通常的形式是I型跨膜域蛋白的修饰, 具有抗原识别氨基末端, 间隔区, 跨膜域、与它们全部连接的复合胞内域 (endodomain), 其传输T细胞存活和活化信号 (见图1a)。

[0009] 这些分子的最常见形式是识别靶抗原的来源于单克隆抗体的单链可变片段 (scFv) 通过间隔区和跨膜域融合至信号传导胞内域的融合物。响应scFv对其靶标的识别, 此类分子导致T细胞的活化。当T细胞表达此类CAR时, 它们识别并杀伤表达所述靶抗原的靶细胞。针对肿瘤相关抗原已经开发了几种CAR, 且使用此类表达CAR的T细胞的过继转移方法目前在临床试验中用于多种癌症的治疗。

[0010] 已经描述了针对GD2的嵌合抗原受体,其抗原结合域基于scFv14g2a (WO 2013/040371和Yvon等人 (2009,Clin Cancer Res 15:5852-5860))。

[0011] 表达14g2a-CD28-OX40- ζ CAR的人T细胞被证明具有一些抗肿瘤活性,但不能完全地根除该疾病(Yvon等人 (2009) 如上文)。

[0012] 本发明人寻求制造具有改进的特性的备选GD2-靶向CAR。

[0013] 附图简述

[0014] 图1-嵌合抗原受体 (CAR) 设计。

[0015] (a) CAR的一般性架构:结合域识别抗原;间隔区将结合域从细胞表面升高;跨膜域将蛋白锚定到膜上而胞内域传输信号。(b) 至 (d) :CAR胞内域的不同代和排列:(b) 初始设计通过Fc ϵ R1- γ 或CD3胞内域仅传输ITAM信号,而后来的设计以顺式 (in cis) 传输额外的(c) 一种或 (d) 两种共刺激信号。

[0016] 图2-构建的抗GD2CARs的变体:(a) 使用小鼠KM666抗体作为scFv与人IgG1间隔区和CD28-OX40-Zeta胞内域的抗GD2CAR; (b) 使用Nakamura人源化的抗体huKM666与(a) 为相同形式的抗GD2CAR; (c) 与 (b) 相同的形式,除了Fc域经修饰以去除Fc受体识别基序; (d) 与 (c) 相同的形式,除了间隔区为IgG1铰链-CD8茎部; (e) 与 (c) 相同的形式,除了间隔区为仅CD8茎部; (f) 与 (c) 相同的形式,除了间隔区为仅IgG1铰链。

[0017] 图3-基于muKM666和huKM666的CAR的比较。(a) 来自3个正常供体的外周血T细胞上的表达; (b) 这些facs图的平均荧光强度示作柱状图; (c) 使用非转导的,经muKM666和经huKM666转导的T细胞作为效应细胞针对A204 (GD2阴性), 和LAN-1 (GD2阳性) 靶标的铬释放测定; (d) 来自相同激发 (challenge) 的IL-2产生; (e) 来自相同激发的干扰素-gamma产生; 和(f) 来自相同激发的倍数增殖 (fold-proliferation)。

[0018] 图4. (a) 允许CD34标志物基因与CAR的1:1共表达的逆转录病毒构建体; (b) 相对于CD34标志物基因的CAR表达 (HA标签) 的流式细胞分析; (c) 非转导的T细胞和使用3种不同CAR变体转导的T细胞针对GD2阳性靶标 (LAN-1), 和GD2阴性靶标 (A204) 的铬释放测定; (d) 干扰素-gamma释放; (e) IL-2释放; 和 (f) 相同靶标和效应细胞的增殖。

[0019] 图5-将FcR结合破坏突变引入Fc间隔区:(a) 引入的突变; (b) 通过抗Fc染色确认的CAR表达:非转导的,wt 和突变的; (c) 使用非转导的,wt Fc 和突变的Fc抗GD2CAR T细胞对GD2阴性和GD2阳性靶标的杀伤; (d) 使用表达FcR的细胞系THP-1对非转导的,wt Fc 和突变的Fc抗GD2T细胞的活化;响应非转导的,wt Fc 和突变的Fc CAR T细胞由THP-1细胞系的IL-1Beta释放。

[0020] 图6-表达基因盒的优化

[0021] (a) 引入以下盒中的图谱优化:SAR或CHS4; (b) 具有使用wt或密码子优化的开放读码框的不同修饰的CAR的代表性表达.SAR构建体给出表达的紧密峰 (tight peak), 其为所需的。(c) 来自3个正常供体的该FACS数据的条形图表示。

[0022] 图7-不同胞内域的比较

[0023] 比较了三种不同的嵌合抗原受体。受体都由huK666scFv,突变以去除FcR结合的IgG1的Fc域和CD8跨膜域构成.CAR“28tmZ”具有CD3Zeta胞内域;“28Z”具有复合CD28-CD3Zeta胞内域;“280XZ”具有包含CD28,OX40和CD3Zeta的复合胞内域。使用这些构建体用相似滴度的逆转录病毒载体转导来正常供体的外周血T细胞。比较了这些不同T细胞系,连

同非转导的T细胞作为对照。使用A204细胞(GD2阴性的横纹肌肉瘤细胞系),和LAN-1细胞(GD2阳性的神经母细胞瘤细胞系)激发T细胞。增殖和细胞因子释放表明受体活性为 $28\text{tmZ} < 28\text{Z} < 280\text{XZ}$ 。

[0024] 图8-与iCasp9自杀基因共表达

[0025] (a) 使用FMD-2A序列,iCasp9与抗GD2CAR的共表达;(b)单独和使用CID处理后的NT T细胞,经GD2CAR转导的T细胞和经iCasp9-2A-GD2CART细胞中的CAR表达;(c)使用或不使用CID处理的未转导的,经GD2CAR转导的和经iCasp9-2A-GD2CAR转导的T细胞对GD2阳性(LAN-1)和阴性(A204)靶标的杀伤。5位正常供体T细胞的平均值。

[0026] 图9-与RQR8自杀基因的共表达

[0027] (a) 将CAR huK666Fc与RQR8分选自杀基因(sort-suicide gene)在逆转录病毒载体中共表达。(b) 使用该逆转录病毒载体转导T细胞并通过使用多克隆抗Fc和单克隆抗体QBend10染色转导的细胞确认CAR和RQR8的共表达。(c) 在利妥昔单抗(Rituximab)和补体的存在下,可以将来自这些T细胞的CAR阳性群体耗竭。(d) 使用利妥昔单抗耗竭的T细胞不再识别表达GD2的靶标。

[0028] 图10-(a) 表达GM3合酶和GD2合酶的双顺反子载体。(b) 使用该载体转导的SupT1细胞成为GD2阳性(非转导的空心图;转导的灰色图)。

[0029] 图11-在以下群体(cohort)中小鼠中的单个肿瘤的生长曲线:左上:具有表达GD2的CT26肿瘤的小鼠,接受抗GD2CAR脾细胞;右上:表达GD2的CT26肿瘤,接受假(mock)转导的脾细胞;左下:GD2阴性(wt)CD26肿瘤与抗GD2CAR脾细胞;和右下:表达GD2的CT26肿瘤,不接受脾细胞。

[0030] 图12-氨基酸序列

[0031] A.图2中示作(a)的抗GD2CAR(muKM666-HCH2CH3-CD280XZ-SEQ ID No.26)

[0032] B.图2中示作(b)的抗GD2CAR(huKM666-HCH2CH3-CD280XZ-SEQ ID No.27)

[0033] C.图2中示作(c)的抗GD2CAR(huKM666-HCH2CH3pvaa-CD280XZ-SEQ ID No.28)

[0034] D.图2中示作(d)的抗GD2CAR(huKM666-HSTK-CD280XZ-SEQ ID No.29)

[0035] E.图2中示作(e)的抗GD2CAR(huKM666-STK-CD28X0XZ-SEQ ID No.30)

[0036] F.图2中示作(e)的抗GD2CAR(huKM666-HNG-CD280XZ-SEQ ID No.31)

[0037] G.图2(c)中所示的抗GD2CAR但具有第1代胞内域(huKM666-HCH2CH3pvaa-CD28tmZ-SEQ ID No.32)

[0038] H.图2(c)中所示的抗GD2CAR但具有第2代胞内域(huMK666-HCH2CH3pvaa-CD28Z-SEQ ID No.33)

[0039] I.与iCasp9自杀基因共表达的抗GD2CAR-SEQ ID No.34

[0040] J.与RQR8自杀基因共表达的抗GD2CAR-SEQ ID No.35

[0041] 图13-GD2的结构

[0042] 图14-huK666和14g2a CARs的比较。(a)构建体的图谱

[0043] 测试:在原代T细胞中测试了两种构建体。两种都是编码与FMD-2A样序列共表达的RQR8和第2代GD2CAR的逆转录病毒载体。构建体之间仅有的差异为在一个中,scFv为huK666而在另一个中为14g2a。使用这些构建体转导的T细胞使用A204(GD2阴性横纹肌肉瘤细胞系),和LAN-1(GD2阳性细胞系)之任一以1:1激发。(b)在24小时,从上清测量干扰素-gamma。

huK666CAR T细胞产生更多的IFN- γ 。(c)一周后对T细胞计数,huK666表现出更多增殖。

[0044] 图15-基于huK666或14g2a的第2代CAR与神经母细胞瘤细胞系LAN1之间共培养的流式细胞分析。(a)实验的设置。共培养一周后,收获细胞并通过流式细胞术分析。CD45表达允许区分淋巴样细胞和非淋巴样细胞,其中CD45+细胞为LAN-1细胞。使用CD3/QBEND/10进一步染色允许对CAR T细胞的计数。(b)单独T细胞;(c)NT T细胞和LAN-1细胞;(d)huK666-28-Z CAR T细胞和LAN-1细胞;(e)14g2a-28-Z CAR T细胞和LAN-1细胞。在14g2a CAR T细胞共培养中看到了LAN-1残留物。

[0045] 发明简述

[0046] 本发明人已经构建了靶向GD2的新的嵌合抗原受体(CAR),其包含基于K666抗体的GD2结合域。

[0047] 抗GD2抗体14g2a可以视为黄金标准,因为其用作治疗性抗体且是CAR研究中迄今测试的唯一scFv (PMID:18978797)。本发明人比较了基于14g2a和huK666的第二代形式的CAR,因为这是在临床研究中最广泛使用的CAR形式。我们发现huK666CAR T细胞比14g2a等同物释放更多IFN- γ ,增殖更好且杀伤更完全。

[0048] 因此,在本发明的第一个方面中提供包含双唾液酸神经节苷脂(GD2)结合域的嵌合抗原受体(CAR),其包含

[0049] a)具有互补决定区(CDRs)的重链可变区(VH),所述CDR具有以下序列:

[0050] CDR1-SYNIH (SEQ ID No.1);

[0051] CDR2-VIWAGGSTNYNSALMS (SEQ ID No.2)

[0052] CDR3-RSDDYSWFAY (SEQ ID No.3);和

[0053] b)具有CDRs的轻链可变区(VL),所述CDR具有以下序列:

[0054] CDR1-RASSSVSSSYLH (SEQ ID No.4);

[0055] CDR2-STSNLAS (SEQ ID No.5)

[0056] CDR3-QQYSGYPIT (SEQ ID No.6)

[0057] GD2结合域可以包含具有如SEQ ID No.9或SEQ ID NO 10所示序列的VH域;或具有如SEQ ID No 11或SEQ ID No.12所示序列或具有至少90%序列同一性的其变体的VL域,,所述变体保留了i)结合GD2和ii)诱导T细胞信号传导的能力。

[0058] GD2结合域可以包含如SEQ ID No 7或SEQ ID No.8所示的序列,或具有至少90%序列同一性的其变体,其保留了i)结合GD2和ii)诱导T细胞信号传导的能力。

[0059] 跨膜域可以包含如SEQ ID No.13所示的序列或具有至少90%序列同一性的其变体,其保留了i)结合GD2和ii)诱导T细胞信号传导的能力。

[0060] GD2结合域和所述跨膜域可以通过间隔区连接。

[0061] 间隔区可以包含以下之一:人IgG1Fc域;IgG1铰链;IgG1铰链-CD8茎部;或CD8茎部。

[0062] 间隔区可以包含IgG1铰链-CD8茎部;或CD8茎部。

[0063] 间隔区可以包含IgG1Fc域或其变体。

[0064] 间隔区可以包含IgG1Fc域,其包括如SEQ ID No.23或SEQ ID No.24所示的序列或具有至少80%序列同一性的其变体。

[0065] CAR可以包含细胞内T细胞信号传导域或与细胞内T细胞信号传导域相关。

[0066] 细胞内T细胞信号传导域可以包含一个或多个以下胞内域:CD28胞内域;OX40和CD3-Zeta胞内域。

[0067] 细胞内T细胞信号传导域可以包含所有以下胞内域:CD28胞内域;OX40和CD3-Zeta胞内域。

[0068] CAR可以包含SEQ ID No.26至35任一项所示的序列,或具有至少80%序列同一性但保留了i)结合GD2和ii)诱导T细胞信号传导的能力的其变体。

[0069] 在第二个方面中,本发明提供核酸序列,其编码根据本发明的第一个方面的CAR。

[0070] 核酸序列可以是密码子优化的。

[0071] 核酸序列可以包含如SEQ ID No 25所示的序列或具有至少90%序列同一性的其变体。

[0072] 核酸可以也编码自杀基因。

[0073] 在第三个方面中,本发明提供载体,其包含根据本发明的第二个方面的核酸序列。

[0074] 在第四个方面中,本发明提供细胞,其表达根据本发明的第一个方面的CAR。所述细胞可以是细胞溶解性免疫细胞,如T细胞或天然杀伤(NK)细胞。

[0075] 细胞可以共表达根据本发明的第一个方面的CAR和自杀基因。

[0076] 自杀基因可以是,例如iCasp9或RQR8。

[0077] 在第五个方面中,本发明提供用于制造根据本发明的第四个方面的细胞的方法,其包括将根据本发明的第二个方面的核酸导入细胞中。

[0078] 在第六个方面中,本发明提供药物组合物,其包含根据本发明的第三个方面的载体,或根据本发明的第二个方面的细胞,连同药学上可接受的载体,稀释剂或赋形剂。

[0079] 在第七个方面中,本发明提供用于治疗癌症的方法,其包括向受试者施用根据本发明的第三个方面的载体或根据本发明的第四个方面的细胞的步骤。

[0080] 癌症可以是神经母细胞瘤。

[0081] 在第八个方面中,本发明提供根据本发明的第三个方面的载体或根据本发明的第四个方面的细胞,用于治疗癌症中的用途。

[0082] 在第九个方面中,本发明提供根据本发明的第三个方面的载体或根据本发明的第四个方面的细胞在制造用于治疗癌症的药物中的用途。

[0083] 在第十个方面中,本发明提供用于制造表达GD2的细胞的方法,其包括将编码GM3合酶的核酸和编码GD2合酶的核酸导入细胞中。

[0084] 在第十一个方面中,本发明提供表达GD2的细胞,其包含编码GM3合酶的异源性核酸和编码GD2合酶的异源性核酸。

[0085] 在第十二个方面中,本发明提供用于体外刺激根据本发明的第四个方面的细胞的方法,其包括使得所述细胞与根据本发明的第十一个方面的表达GD2的细胞接触的步骤。

[0086] 在第十三个方面,本发明提供表达CAR的表达基因盒,所述CAR包括支架附着区(scaffold attachment region) (SAR)。

[0087] 表达基因盒可以表达根据本发明的第一个方面的CAR。

[0088] 发明详述

[0089] 嵌合抗原受体(CAR)

[0090] 嵌合抗原受体,也称为嵌合T细胞受体,人工T细胞受体和嵌合免疫受体,是工程化

的受体，其将任意特异性嫁接到免疫效应细胞上。在经典的CAR中，将单克隆抗体嫁接到T细胞上。可以使用例如逆转录病毒将编码CAR的核酸转移到T细胞中。以这种方式，可以产生大量癌症特异性的T细胞用于过继细胞转移。该方法的I期临床研究表现出效力。

[0091] CAR的靶抗原结合域通常经由间隔区和跨膜域融合至信号传导胞内域。当所述CAR结合靶抗原时，这导致活化信号传输至它在上面表达的T细胞。

[0092] 本发明的CAR包含GD2结合域，其基于KM666单克隆抗体 (Nakamura等人，(2001) *Cancer Immunol. Immunother.* 50:275-284)。

[0093] 本发明的CAR包含GD2结合域，其包含

[0094] a) 具有互补决定区 (CDRs) 的重链可变区 (VH)，所述CDR具有以下序列：

[0095] CDR1-SYNIH (SEQ ID No.1)；

[0096] CDR2-VIWAGGSTNYNSALMS (SEQ ID No.2)

[0097] CDR3-RSDDYSWFAY (SEQ ID No.3)；和

[0098] b) 具有CDRs的轻链可变区 (VL)，所述CDR具有以下序列：

[0099] CDR1-RASSSVSSSYLH (SEQ ID No.4)；

[0100] CDR2-STSNLAS (SEQ ID No.5)

[0101] CDR3-QQYSGYPIT (SEQ ID No.6)。

[0102] 将一个或多个突变(取代，添加或缺失)引入所述或每个CDR而不负面影响GD2结合活性可以是可能的。每个CDR可以例如具有一个，两个或三个氨基酸突变。

[0103] 本发明的CAR可以包含以下氨基酸序列之一：

[0104] SEQ ID No.7 (鼠KM666序列)

[0105] QVQLKESGPVLVAPSQTLSITCTVSGFSLASYNIHWVRQPPGKGLEWLGVIWAGGSTNYNSALMSRLSI SKDNSKSQVFLQMNSLQTDDTAMYCAKRSDDYSWFAYWGQGTLTVVSASGGGSGGGSGGGSENVLTQSPAIMS ASPGEKVTMTCRASSSVSSSYLHWYQQKSGASPKVWIYSTSNLASGVPGRFSGSGSTSYSLTISSVEAEDAATYYC QQYSGYPITFGAGTKVEVKR

[0106] SEQ ID No.8 (人源化的KM666序列)

[0107] QVQLQESGPGLVKPSQTLSITCTVSGFSLASYNIHWVRQPPGKGLEWLGVIWAGGSTNYNSALMSRLTI SKDNSKNQVFLKMSSLTAADTAVYYCAKRSDDYSWFAYWGQGTLTVSSGGGSGGGSGGGSENVMTQSPSSLSA SVGDRVMTCRASSSVSSSYLHWYQQKSGKAPKVWIYSTSNLASGVPSRFSGSGSTDYTLTISSLQPEDFATYYCQ QYSGYPITFGQGTKVEIKR

[0108] 本发明的CAR可以包含以下VH序列之一：

[0109] SEQ ID No.9 (鼠KM666VH序列)

[0110] QVQLKESGPVLVAPSQTLSITCTVSGFSLASYNIHWVRQPPGKGLEWLGVIWAGGSTNYNSALMSRLSI SKDNSKSQVFLQMNSLQTDDTAMYCAKRSDDYSWFAYWGQGTLTVSA

[0111] SEQ ID No.10 (人源化的KM666VH序列)

[0112] QVQLQESGPGLVKPSQTLSITCTVSGFSLASYNIHWVRQPPGKGLEWLGVIWAGGSTNYNSALMSRLTI SKDNSKNQVFLKMSSLTAADTAVYYCAKRSDDYSWFAYWGQGTLTVSS

[0113] 本发明的CAR可以包含以下VL序列之一：

[0114] SEQ ID No.11 (鼠KM666VL序列)

[0115] ENVLTQSPAIMSASPGEKVTMTCRASSSVSSSYLHWYQQKSGASPKVWIYSTSNLASGVPGRFSGSGSG

TSYSLTISSVEAEDAATYYCQQYSGYPITFGAGTKVEVK

[0116] SEQ ID No.12(人源化的KM666VH序列)

[0117] ENQMTQSPSSLASVGDRVTMTCRASSSVSSSYLHWYQQKSGKAPKVWIYSTSNLASGVPSRFSGSGSGTDYTLTISSLQPEDFATYYCQQYSGYPITFGQGTKVEIK

[0118] 本发明的CAR可以包含如SEQ ID No.7,8,9,10,11或12所示的序列的变体,具有至少80,85,90,95,98或99%序列同一性,只要所述变体序列保留了结合GD2的能力(当与互补VL或VH域结合时,若适当的话)。

[0119] 两个多肽序列之间的百分比同一性可以通过例如BLAST的程序容易地确定,其在<http://blast.ncbi.nlm.nih.gov>免费可用。

[0120] 跨膜域

[0121] 本发明的CAR还可以包含跨越膜的跨膜域。其可以包含疏水alpha螺旋。跨膜域可以来源于CD28,其给予良好的受体稳定性。

[0122] 跨膜域可以包含如SEQ ID No.13所示的序列。

[0123] SEQ ID No.13

[0124] FWVLVVVGVLACYSLLVTVAFIIFWV

[0125] 细胞内T细胞信号传导域(胞内域)

[0126] 胞内域是CAR的信号传输部分。抗原识别后,受体簇集且信号传输至细胞。最普遍使用的胞内域组分是CD3-zeta的,其含有3个ITAMs。在抗原结合后,其传输活化信号至T细胞。CD3-zeta可以不提供完全有能力的活化信号,可以需要另外的共刺激信号。例如,嵌合CD28和OX40可以与CD3-Zeta一起使用以传输增殖/存活信号,或所有三种可以一起使用。

[0127] 本发明的CAR的胞内域可以包含CD28胞内域和OX40及CD3-Zeta胞内域。

[0128] 本发明的CAR的跨膜和细胞内T细胞信号传导域(胞内域)可以包含如SEQ ID No.14,15,16,17或18所示的序列,或具有至少80%序列同一性的其变体。

[0129] SEQ ID No.14(CD28胞内域)

[0130] RSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAY

[0131] SEQ ID No.15(CD40胞内域)

[0132] RSRDQRLPPDAHKPPGGSFRTPIQEEQADAHSTLAKI

[0133] SEQ ID No.16(CD3zeta胞内域)

[0134] RSRVKFSRSADAPAYQQGQNQLYNELNLGRREYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQDKM
AEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQLPPR

[0135] SEQ ID No.17(CD28Z)

[0136] RSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGR
REYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALH
MQALPPR

[0137] SEQ ID No.18(CD280XZ)

[0138] RSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRDQRLPPDAHKPPGGSFRTPIQEEQAD
AHSTLAKIRVKFSRSADAPAYQQGQNQLYNELNLGRREYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQDKMAE
AYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQLPPR

[0139] 变体序列可以与SEQ ID No.13,14,15,16,17或18具有至少80%,85%,90%,

95%, 98%或99%序列同一性,只要所述序列提供有效的跨膜域/细胞内T细胞信号传导域。

[0140] 信号肽

[0141] 本发明的CAR可以包含信号肽,使得当CAR表达在细胞如T细胞内时,初生蛋白被引导至内质网和随后到细胞表面,在那里其被表达。

[0142] 信号肽的核心可以含有一长段疏水性氨基酸,其具有形成单个 α 螺旋的倾向。信号肽可以以短的,带正电的氨基酸段开始,其帮助转位期间执行多肽的正确拓扑结构。在信号肽的末端,通常是由信号肽酶识别并切割的氨基酸段。信号肽可以在转位期间或转位完成后切割,以生成游离的信号肽和成熟蛋白。接着,游离的信号肽被特定蛋白酶消化。

[0143] 信号肽可以在分子的氨基末端。

[0144] 本发明的CAR可以具有以下通式:

[0145] 信号肽-GD2结合域-间隔域-跨膜域-细胞内T细胞信号传导域

[0146] 信号肽可以包含SEQ ID No.19或具有5,4,3,2或1个氨基酸突变(插入,取代或添加)的其变体,只要信号肽仍然发挥功能以引起CAR的细胞表面表达。

[0147] SEQ ID No.19:METDTLLWVLLLWVPGSTG

[0148] SEQ ID No.19的信号肽是紧密并高度有效的。预测它在末端甘氨酸之后产生约95%的切割,产生由信号肽酶的有效移除。

[0149] 间隔区

[0150] 本发明的CAR可以包含间隔区序列以连接GD2结合域与跨膜域并在空间上分开GD2结合域与胞内域。柔性间隔区允许GD2结合域在不同方向定向使得能够进行GD2结合。

[0151] 间隔区序列可以例如包含IgG1Fc区,IgG1铰链或CD8茎部,或其组合。或者该接头可以包含备选序列,其具有与IgG1Fc区,IgG1铰链或CD8茎部相似的长度和/或结构域间隔特性。

[0152] 可以改变人IgG1间隔区以去除Fc结合基序。

[0153] 这些间隔区的氨基酸序列的例子在以下给出:

[0154] SEQ ID No.20(人IgG1铰链-CH2CH3)

[0155] AEPKSPDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMIAARTPEVTCVVVDVSHEDEPEVKFNWYVDGVEV
HNAKTKPREEQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKN
QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCVMHEALHNHYTQ
KSLSLSPGKKD

[0156] SEQ ID No.21(人CD8茎部):

[0157] TTTPAPRPPPTPAPTIASQPLSLRPEACRPAAGGAHVTRGLDFACDI

[0158] SEQ ID No.22(人IgG1铰链):

[0159] AEPKSPDKTHTCPPCPKDPK

[0160] SEQ ID No.23(IgG1铰链-Fc)

[0161] AEPKSPDKTHTCPPCPAPEELLGGPSVLFPPKPKDTLMISRTPEVTCVVVDVSHEDEPEVKFNWYVDGVE
VHNNAKTKPREEQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK
NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCVMHEALHNHYT
QKSLSLSPGKKDPK

[0162] SEQ ID No.24(IgG1铰链-Fc经修饰以去除Fc结合基序)

[0163] AEPKSPDKTHTCPPCPAPPVA*GPSVFLFPPKPKDTLMIARTPEVTCVVVDVSHEDPEVKFNWYVDGV
EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPVYTLPPSRDELT
KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY
TQKSLSLSPGKKDPK

[0164] 修饰的残基用下划线标出;*表示缺失。

[0165] GD2

[0166] GD2是在神经外胚层来源的肿瘤(包括人神经母细胞瘤和黑素瘤)上表达的双唾液酸神经节苷脂,在正常组织上具有高度限制的表达,主要在人的小脑和外周神经上。

[0167] GD2的相对肿瘤特异性表达使得其为用于免疫疗法的合适靶标。

[0168] 核酸序列

[0169] 本发明的第二个方面涉及核酸序列,其编码本发明的第一个方面的CAR。

[0170] 核酸序列可以能够编码具有如SEQ ID No.26-35任一项所示的氨基酸序列的CAR。

[0171] 核酸序列可以包含以下序列:

[0172] SEQ ID No.25逆转录病毒基因盒的DNA序列,包括与RQR8自杀基因共表达的抗GD2CAR,具有密码子优化的框和SAR区以增强表达

```

1  tgaaagaccc cacctgttagg tttggcaagc tagcttaagt aacgccattt tgcaaggcat gaaaaaatac
>>.....LTR.....>

71  ataactgaga atagaaaagt tcagatcaag gtcaggaaca gatggaacag ctgaatatgg gccaaacagg
>.....LTR.....>

141  atatctgtgg taagcagttc ctgcggcgcc tcagggccaa gaacagatgg aacagctgaa tatggccaa
>.....LTR.....>

211  acaggatatac tgtggtaagc agttctgtcc ccggctcagg gccaagaaca gatggcccc agatgeggc
>.....LTR.....>

281  cagccctcag cagttcttag agaaccatca gatgttcca gggtgccccca aggacctgaa atgacacctgt
>.....LTR.....>

351  gccttatttg aactaaccaa tcagtttgt ttcgtttct gttagcgcgc ttatgtccc cgagctcaat
>.....LTR.....>

[0173] 421  aaaagagccc acaacccttc actggggcg ccagtctcc gattgactga gtgcggggg taccctgtta
>.....LTR.....>

491  tccaataaac cctcttgcag ttgcattccga cttgtggctc cgctgttct tgggagggtc tcctctgagt
>.....LTR.....>

561  gattgactac ccgtcagccg gggctttca ttgggggct cgtccggat cgggagaccc ctgcccagg
>.....LTR.....>>

631  accaccgacc caccacccggg aggttaagctg gccagcaact tatctgtgtc tgtccgattt tctatgttct

701  atgactgatt ttatgcgcct gctcggtac tagtagcta actagctctg tatctggcg accccgtggtg

          Eco52I
          -----
771  gaactgacga gttcggaaaca cccggccgca accctggag acgtcccagg gacttcgggg gccgttttg

          PshAI
          -----
841  tggcccgacc tgagtcccaa aatcccgata gtttaggact ctttggtgca cccccccttag aggaggata

```

911 tgggttctg gtaggagacg agaacataaa acagttcccg ctcgtctg aattttgtt ttcgtttgg
981 gaccaagcc ggcgcgcgcg tctgtctgc tgcagcatcg ttctgtgtg tctgtctg actgtgttc

SrfI

1051 tgtatttgc tgaaaatatg gccccggct acgttgcac cactccctta agtttgcac taggtcactg
1121 gaaagatgtc gagcgatcg ctcacaacca gtccgtatgt tcagaaga gacgttggt tacctctgc
1191 tctgcagaat ggccaacctt taacgtcggg tggccgcgg acggcacctt taaccgagac ctcatcaccc
1261 aggttaagat caaggcttt tcaacgtggcc cgcatggaca cccagaccag gtgggttaca tctgtacactg
1331 ggaaggcttg gctttgacc cccctccctg ggtcaagccc tttgtacacc ctaagcctcc gcctcccttt
1401 cctccatccg ccccgatctt ccccttggaa ctcctctgtt cgacccggcc tgcatactcc ctttatccag

BglII

1471 ccctcaactcc ttctcttaggc gcccccataat gcccataatga gatcttatat ggggcacccc cgccctttgt
1541 aaactccctt gaccctgaca tgacaagagt tactaacagc ccctcttcc aagctcaactt acaggctctc

AgeI

1611 tacttagtcc agcacgaagt ctggagaccc ctggccggcag cctaccaaga acaactggac cgaccgggtgg
1681 tacccatccc ttaccgatgc ggcacacacag tgggggtccg ccgcacacacg actaagaacc tagaacatcg

AccI

1751 ctggaaagga ctttacacag tcctgtgtac caccccccacc gcccctaaag tagacggcat cgccagttgg

PmlI

1821 atacacgcgg cccacgtgaa ggctgcccac cccgggggtg gaccatccctc tagactgcca acatggcac
[0174] >..... orf>
RQR8>

1891 cagcctgtg tgctggatgg ccctgtgcct gctggggccg gaccacgcgg atgcctgccc ctacaccaac
>..... orf>
RQR8>

1961 cccagcctgt gcagcgagg cggccggcgcg gagctgccc cccaggccac ctttcacac gtgtccacca
>..... orf>
RQR8>

2031 acgtgagccc agccaagccc accaccaccc cctgtccctt ttccaatctt tccctgtgtt gcccgggggg
>..... orf>
RQR8>

2101 aggcaagccc gccccagac ctccccaccc accaccaccc atgcgcagcc agccctctgag cctgagaccc
>..... orf>
RQR8>

SgrAI

2171 gaggcctgcc gcccaggccgc cggccggccgc gtgcacaccca gaggcctggta ttccgtctgc gatatctaca
>..... orf>
RQR8>

BclI

2241 tctggggccc actggccggc acctgtggcg tgctgtgtt gaggcctgggt atcaccctgt actgcaacca
>..... orf>
RQR8>

2311 ccgcaaccgc aggccgtgt gcaagtgcgg caggccgtg gtgagagccg agggcagagg cagccgtgt

```

>..... orf .....>
>..... RQR8 .....>>
>>..... FMD-2A .....>

NcoI
-----
2381 acctgcggcg acgtggagga gaacccaggc cccatggaga ccgacacccat gctgctgtgg gtgctgtgc
>..... orf .....>
>..... FMD-2A .....>>
>>..... CAR .....>

2451 tgtgggtgcc aggcagcacc gccagggtgc agctgcagga gtctggcca ggcctggta agccaggca
>..... orf .....>
>..... CAR .....>

2521 gaccctgagc atcacctgca ccgtgagcgg cttagccgtg gccagctaca acatccactg ggtgcggcag
>..... orf .....>
>..... CAR .....>

2591 cccccaggca agggcttgg a tggctggc gtatctgg ctggccgca caccaactac aacagcggcc
>..... orf .....>
>..... CAR .....>

2661 tgatgagccg gtcgaccatc agcaaggaca acagcaagaa ccaggtgttc ctgaagatga gcagcgtac
>..... orf .....>
>..... CAR .....>

2731 agccgcgcac accgcgtgt actactgcgc caagcggagc gacgactaca gtcgggtcgc ctactgggc
>..... orf .....>
>..... CAR .....>

2801 cagggcaccc tgggacccgt gagctctggc ggaggcggct ctggcggagg cggctctggc ggaggcggca
>..... orf .....>
>..... CAR .....>

2871 gcgagaacca gatgacccag agccccagca gttgagcgc cagcgtggc gaccgggtga ccatgacctg
>..... orf .....>
>..... CAR .....>

[0175] 2941 cagagccagc agcagcgtga gcagcagcta cttgcactgg taccaggaga agagcggcaa ggcccaaag
>..... orf .....>
>..... CAR .....>

3011 gtgtggatct acagcaccag caacctggcc acggcgtgc ccagccgtt cagcggcagc ggcagcggca
>..... orf .....>
>..... CAR .....>

3081 ccgactacac cttgaccatc agcagcgtgc agcccgagga cttcgccacc tactactgcc agcagtacag
>..... orf .....>
>..... CAR .....>

BamHI
-----
3151 cggctacccc atcaccttgc gcccggcac caaggtggag atcaagcgtt cggatccgc cgagccaaa
>..... orf .....>
>..... CAR .....>

FseI
-----
3221 tctcctgaca aaactcacac atgcccaccc tgcccagcac ctcccggtgc cggcccgatca gtcttcctct
>..... orf .....>
>..... CAR .....>

3291 tccccccaaa acccaaggac accctcatga tcgcccggac ccctgaggc acatgcgtgg tggggacgt
>..... orf .....>
>..... CAR .....>

3361 gagccacaa gaccctgagg tcaagttca cttgtacgtg gacggcgtgg aggtgcataa tgccaaagaca
>..... orf .....>
>..... CAR .....>

SacII
-----
3431 aaggcgggg aggaggagta caacagcagc taccgtgtgg tcagegtcct caccgtctg caccaggact
>..... orf .....>
>..... CAR .....>

```

3501 ggctaatgg caaggatgc aagtgcagg ttcacacaa agccctccca gccccatcg agaaaaccat
>..... orf>
>..... CAR>

3571 ctccaaagcc aaagggcgc cccgagaacc acagggtgtac accctgccc catccggga tgagctgacc
>..... orf>
>..... CAR>

3641 aagaaccagg tcagcgtac ctgcgttgc aaaggcttct atccagcga catcgccgt gaggggaga
>..... orf>
>..... CAR>

3711 gcaatggca accggagaac aactacaaga ccacgcctcc cgtgctggac tccgacggct ctttcttct
>..... orf>
>..... CAR>

Ppu10I

NsiI

BfrBI

3781 ctacagcaag ctcacccgtgg acaagagcag gtggcagcag gggAACgtct ttcatgttc cgtatgtcat
>..... orf>
>..... CAR>

Van91I

3851 gaggccctgc acaatcacta tacccagaaa tctctgagtc tgagccagg caagaaggac cccaaggttct
>..... orf>
>..... CAR>

3921 gggtocttgtt ggtggggaa ggcgtgtgg cctgttactt ttcctgttg accgtggct tcatcatctt
>..... orf>
>..... CAR>

3991 ctgggtgcgc tccaagagga gcaggctctt gcacagtgtac tacatgaaca tgactccccg ccggccggg
>..... orf>
[0176] >..... CAR>

4061 cccaccggca agcattacca gccttatgcc ccaccacgcg acttcgcagc ctatcgctcc cgggtgaagt
>..... orf>
>..... CAR>

4131 tctctcgctc tgccgatgcc ccaggctatc agcaggccca gaatcagctg tacaatgaac tgaacctgg
>..... orf>
>..... CAR>

4201 caggcgggag gatcagcagc tgctggataa gcggagaggc agagaccccg agatggccgg caaaccacgg
>..... orf>
>..... CAR>

4271 cgcaaaaatc cccaggaggg actctataac gagctgcaga aggacaaaat ggccgaggcc tattccgaga
>..... orf>
>..... CAR>

4341 tcggcatgaa gggagagaga agacgcggaa agggccacga cggcctgtat cagggattgt ccaccgtac
>..... orf>
>..... CAR>

MluI Clal

4411 aaaagataca tatgtgccc tgacatgca ggcctgcca cccagatgac gcttatcgat actgttctca
>..... orf>>
>..... CAR>>
 >>..SAR..>

4481 tcacatcata tcaaggatatacatttgcata gatgttactt agcctttaa tatttctcta
>..... SAR>

4551 atttagtta tatgaatga tagttctgtt atttctgaga ttgagttctt catgttaat gattatttag
>..... SAR>

4621 agtttcttctt tcatgttgc aaatttttgtt ctatgttataat tttttactga ttgttaagac ttcttttat
>..... SAR>

```

4691 aatctgcata ttacaattot cttaactggg gtgttgc当地 tattttctgt catttatgg octgactttt
>.....SAR.....>

4761 cttaatggtt ttttaatttt aaaaataagt cttaatattc atgcaatcta attaacaatc ttttctttgt
>.....SAR.....>

SphI
-----
4831 ggtaggact ttgagtcata agaaattttt ctctacactg aagtcatgat ggcatttc tatattttt
>.....SAR.....>

4901 tctaaaagat ttaaagttt gccttctcca ttttagactta taattcactg gaattttttt gtgtgtatgg
>.....SAR.....>

4971 tatgacatat gggttccctt ttattttta catataaata tatttccctg ttttctaaa aaagaaaaag
>.....SAR.....>

5041 atcatcattt tccatttgta aaatgccata ttttttcat aggtcaacta catastatcaa tgggtctgtt
>.....SAR.....>

5111 tctgagctct actctatattt atcagcctca ctgtctatcc ccacacatct catgcttgc tctaaatctt
>.....SAR.....>

5181 gatatttagt ggaacattctt tcccattttt gtttacaag aatatttttgg tatttgttctt tgggttttctt
>.....SAR.....>

5251 atatacattt tgaaatgagg ttgacaagg ttgatttagtc caatttggta aagacaggat atcagtggtc
>.....SAR.....>>

[0177] 5321 caggctctag ttttgcactca acaatatcac cagctgaagc ctatagacta cgagccatag ataaaataaa
5391 agattttatt tagtctccag aaaaaggggg gaatgaaaga ccccacctgt aggtttggca agctagctta
>.....LTR.....>

5461 agtaacgcca ttttgc当地 agtggaaaaa tacataactg agaatagaga agttcagatc aaggtcagga
>.....LTR.....>

5531 acagatggaa cagctgaata tggccaaac aggatatctg tggtaagcag ttctgcccc ggctcaggcc
>.....LTR.....>

5601 caagaacaga tggaaacagct gaatatggcc caaacaggat atctgtggta agcagttctt gccccggctc
>.....LTR.....>

5671 agggccaaaga acagatggtc cccagatgog gtc当地ccctt cagoagttt tagagaacca tcagatgttt
>.....LTR.....>

5741 ccagggtgcc ccaaggaccc gaaatgaccc tgc当地ctt tggactaac caatcagttc gcttctcgat
>.....LTR.....>

5811 tctgttagcg cgcttctgtc ccccgagctc aataaaagag cccacaaccc ctcactoggg gggccagtc
>.....LTR.....>

5881 tccgattgac ttagtgc当地 gggtaaccgt gtatccaata aaccctctt cagttgc当地 cgacttgg
>.....LTR.....>

5951 tctcgctgtt ccttggagg gtc当地cttctg agtattgac tacccgtcag cgggggtt tcac
>.....LTR.....>>

```

[0178] 传密码子的简并性可以具有不同的核酸序列。核酸序列可以与如SEQ ID No.25所示的序列具有至少80,85,90,95,98或99%同一性,只要其编码如本发明的第一个方面所定义的CAR。

[0179] 自杀基因

[0180] 由于T细胞嫁接且是自主的,在抗GD2CAR T细胞的接受体中选择性删除CAR T细胞的方式是理想的。自杀基因是遗传上可编码的机制,其导致面对不可接受的毒性时对输注的T细胞的选择性破坏。对于自杀基因,最早的临床经验是用疱疹病毒胸昔激酶(HSV-TK),其使得T细胞对于更昔洛韦(Ganciclovir)易感。HSV-TK是高度有效的自杀基因。然而,预先形成的免疫应答可以将其限于具有相当大的免疫抑制的临床环境,如单倍相合造血干细胞(haploididentical stem cell)移植。可诱导半胱天冬酶(caspase)9(iCasp9)是一种通过使用经修饰的FKBP12置换半胱天冬酶9的活化域构建的自杀基因。iCasp9由在其它方面为惰

性的小分子二聚化化学诱导子(CID)活化。最近,在单倍相合HSCT的环境中测试了iCasp9并可以终止GvHD。iCasp9的最大限制依赖于临床级别的专有CID的可用性。iCasp9和HSV-TK两者都是细胞内蛋白,所以当用作单独的转基因时,它们已经与标志物基因共表达以允许对转导细胞的选择。

[0181] iCasp9可以包含如SEQ ID No.36所示的序列或具有至少80,90,95或98%序列同一性的变体。

[0182] SEQ ID No.36

[0183] MLEGVQVETISPGDGRTPKRGQTCVVHYTGMLEDGKKVDSSRDRNPKFKMLGKQEVRGWEEGVAQM
SVGQRALKTISPDYAYGATGHPGIIPPHATLVFDVELLKLESGGSGVDGFGDVGAELESLRGNADLAYILSMEPCGH
CLIINNVNFCRESLRTRTGSNIDCEKLRRRFSSLHFMVEVKGDLTAKMVLALLELAQQDHGALDCCVVVILSHGC
QASHLQFPGAVYGTGCPVSVEKIVNIFNGTSCPSLGGPKLFFIQACGGEQKDHGFEVASTSPEDESPGSNEPDAT
TPFQEGLRTFDQLDAISSLPTPSDIFVSYSTFPGFVSWRDPKSGSWYVETLDDIFEQWAHSEDLQSLLRVANAVSV
KGIYKQMPGCFNFLRKKLFFKTSAS

[0184] 本发明人最近描述了称为RQR8的新的标志物/自杀基因,其可以使用抗体QBEnd10检测且表达细胞被治疗性抗体利妥昔单抗(Rituximab)裂解。

[0185] RQR8可以包含如SEQ ID No.37所示的序列或具有至少80,90,95或98%序列同一性的变体。

[0186] SEQ ID No.37

[0187] MGTSLLCWMALCLLGADHADACPYSNPSLCGGGGSELPTQGTFSNVSTNVSPAKPTTACPYSNPSLC
SGGGGSPAPRPPTPAPTIASQPLSLRPEACRPAAGGAHVTRGLDFACDIYIWAPLAGTCGVLLSLVITLYCNHRNR
RRVCKCPRPVV

[0188] 自杀基因可以与CAR作为单个多肽表达,例如通过使用两个序列之间的自剪切肽。

[0189] 载体

[0190] 本发明还提供载体,其包含根据本发明的核酸序列。此类载体可以用于将核酸序列引入宿主细胞中使得其表达并产生根据本发明的第一个方面的分子。

[0191] 载体可以是例如质粒或病毒载体,如逆转录病毒载体或慢病毒载体。

[0192] 载体可以能够转染或转导T细胞。

[0193] 载体可以包含编码自杀基因如iCasp9或RQR8的核酸序列。

[0194] 宿主细胞

[0195] 本发明还提供宿主细胞,其包含根据本发明的核酸。宿主细胞可以能够表达根据本发明的第一个方面的CAR。

[0196] 宿主细胞可以是溶细胞性免疫细胞,如人T细胞或自然杀伤(NK)细胞。

[0197] 可以通过使用编码CAR的核酸转导或转染T细胞制成能够表达根据本发明的CAR的T细胞。

[0198] 可以离体生成CAR T细胞。T细胞可以来自患者或供体的外周血单核细胞(PBMC)。在使用编码CAR的核酸转导前,可以活化和/或扩增T细胞,例如通过使用抗CD3单克隆抗体处理。

[0199] 药物组合物

[0200] 本发明还涉及药物组合物,其含有本发明的载体或表达CAR的T细胞连同药学上可

接受的载体,稀释剂或赋形剂,以及可选地一种或多种另外的药学上活性的多肽和/或化合物。此类配制剂可以是例如为适合用于静脉内输注的形式。

[0201] 治疗方法

[0202] 表达本发明的CAR分子的T细胞能够杀伤癌细胞,例如神经母细胞瘤细胞。可以离体或从患者自身的外周血(第一方),或在来自供体外周血的造血干细胞移植植物(第二方)的背景中,或来自无关联供体的外周血(第三方)中创建表达CAR的T细胞。或者,CAR T细胞可以来源于可诱导祖细胞或胚胎祖细胞离体向T细胞的分化。在这些情况下,通过许多方法的一种引入编码CAR的DNA或RNA生成CAR T细胞,所述方法包括使用病毒载体转导,使用DNA或RNA转染。

[0203] 表达本发明的CAR分子的T细胞可以用于癌症疾病的治疗,特别是GD2表达相关的癌症疾病。

[0204] 癌症可以是外胚层肿瘤(ectodermal tumour)。

[0205] 与升高的GD2表达水平相关的癌症的例子为:神经母细胞瘤,黑色瘤,成神经管细胞瘤,软组织肉瘤,骨肉瘤,和小细胞肺癌例如NSCLC。

[0206] 用于疾病的治疗的方法涉及本发明的载体或T细胞的治疗性用途。在这方面,可以将载体或T细胞施用至患有存在的疾病或状况的受试者,以减轻,降低或改善与疾病相关的至少一种症状和/或减慢,降低或阻断疾病的进展。本发明的方法可以导致或促进T细胞介导的对表达GD2细胞,如癌细胞的杀伤。

[0207] 表达GD2的细胞

[0208] 本发明还提供用于制造表达GD2的细胞的方法,其包括将编码GM3合酶的核酸和编码GD2合酶的核酸引入细胞中的步骤。

[0209] 例如,可以通过使用载体,如质粒或病毒载体转染或转导引入核酸。

[0210] 本发明还涉及表达GD2的细胞,其包含编码GM3合酶的异源性核酸和编码GD2合酶的异源性核酸。

[0211] 核酸可以是“异源性”,就其通常不存在于细胞中而言。其为人工引入的重组核酸序列。

[0212] 细胞可以来自细胞系。

[0213] 细胞可以用于刺激培养中的GD2CAR T细胞,如本发明的T细胞。

[0214] 本发明将通过实施例的方式进一步描述,其是为了起到帮助本领域的普通技术人员实施本发明,而不意图以任何方式限制本发明的范围。

实施例

[0215] 实施例1-使用人源化的抗体huK666作为结合物

[0216] 使用如Nakamura等人(2001-如上文)所描述的来自小鼠抗体KM666或其人源化版本hu666的序列,使用scFv构建了CAR(以上图2中变体(a)和(b))。比较这些受体的表达/稳定性并发现对于两种受体相等。接着,测试了当由不表达或表达GD2的靶细胞激发时,使用这些受体转导的T细胞的杀伤,细胞因子分泌和增殖。得出的结论是两种受体的杀伤是相似的,但基于人源化scFc的受体导致更好的IL2产生和增殖(图3)。

[0217] 实施例2-测试不同间隔区形式对表达和功能的影响

[0218] 生成了具有Fc间隔区,铰链,铰链-CD8茎部和CD8茎部的抗GD2CAR(分别为图2(b), (d), (e) 和 (f))。将这些CARs与标志物基因,截短的CD34共表达与2A口蹄疫自剪切肽强制1:1的形式以允许精确比较(图4a)。此外,使用氨基末端HA标签标记huK666scFv以允许转基因相对于CAR表达的比较。

[0219] 对使用这些构建体转导的正常供体T细胞的流式细胞分析表明了以下顺序的较明亮的CAR表达:Fc>铰链-茎部=茎部>铰链(图4b)。

[0220] 使用铬释放测定比较了对GD2阳性靶标相对于GD2阴性靶标的杀伤。这允许以下顺序的杀伤效率:Fc>铰链-茎部=茎部>铰链(图4c)。

[0221] 比较了当使用GD2阳性或阴性靶标激发CAR T细胞时,干扰素-gamma释放和IL-2释放。在具有Fc,铰链-茎部和茎部的CARs中,干扰素-gamma释放相似,但在铰链变体中较少。检测到IL2释放为以下顺序:Fc,茎部,铰链-茎部,铰链(图4d和e)。

[0222] 实施例3-FcR突变消除了非特异性活性

[0223] 来自以上实施例的整体数据提示Fc间隔区总体表现最好。然而,Fc域在体内可以引起来自表达Fc受体的细胞的非特异性活性。为了消除该效果,如图5(a)中所示将突变引入Fc区中。这些突变对CAR表达没有不利影响,如图5(b)中所示。

[0224] 另外,证明了这些突变对CAR杀伤功能没有影响(图5(c))。最后,证明了在对表达FcR的靶标(称为THP1的单核细胞样系)的非特异性杀伤,和由这些单核细胞的IL-1Beta释放方面,这些突变具有期望的效果(图5e)。

[0225] 实施例4-表达基因盒的优化

[0226] 考虑到受体表达的优化,测试了以下项:(a) 将支架附接区(SAR)纳入盒中;(b) 将鸡beta血红蛋白染色质绝缘子(CHS4)纳入3'LTR中和(c) 对开放阅读框的密码子优化(图6a)。表明了SAR的纳入改善表达的性质,密码子优化亦然,而CHS4影响不大(图6b)。将SAR和密码子优化组合叠加地改进了表达(图6c)。

[0227] 实施例5-不同胞内域的比较

[0228] 生成了具有三种不同胞内域的构建体:具有CD3-zeta胞内域的CD28跨膜域(CD28tmZ);具有CD28胞内域和CD3-zeta胞内域的CD28跨膜域(CD28Z),和CD28跨膜域,CD28胞内域,OX30胞内域以及CD3-zeta胞内域(CD280XZ),其中CAR以Fc间隔区的形式。注意到增殖,IFN γ 释放和IL2释放以CD28tmZ<CD28Z<CD280XZ的顺序增加(图7)。

[0229] 实施例6-与iCasp9自杀基因共表达

[0230] 将iCasp9自杀基因与抗GD2CAR共表达(图8a-CAR以Fc间隔区的形式,随意选择CD280XZ以证明功能)。尽管与iCasp9共表达,CAR可以良好表达(图8b)。使用小分子二聚化剂(dimerizer)活化iCasp9导致CAR阳性T细胞的删除(图8b)。暴露于该二聚化剂的iCasp9-GD2CAR T细胞当暴露于二聚化剂时,失去了它们的GD2特异性(图8c)。

[0231] 实施例7-与RQR8自杀基因共表达

[0232] 将抗GD2CAR与RQR8分选自杀基因(sort-suicide gene)共表达(图9a-CAR以Fc间隔区的形式,随意选择CD28Z以证明功能)。共表达受体和CAR是可能的(图9b)。使用利妥昔单抗和补体对RQR8自杀基因功能的活化导致转导的T细胞的删除和GD2识别的丧失(图9c和d)。

[0233] 实施例8-GD2合酶和GM3合酶的表达导致任意细胞系中GD2表达

[0234] 为了刺激培养中的GD2CAR T细胞,为了具有理想的GD2-或GD2+靶标,且为了能够生成同基因细胞用于小动物模型,期望的是能够在细胞系上转基因表达GD2。GD2不是蛋白质,并且需要由一组复杂的酶合成。这里表明了仅两种酶:GM3合酶和GM2合酶的转基因表达导致在至今转导的所有细胞系中明亮的GD2表达(图10)。

[0235] 实施例9-抗GD2CAR的体内功能

[0236] 如上文所述CT26细胞系经工程化以表达GD2(命名为CT26克隆#7或缩写为CT25#7)。将 2×10^5 个野生型(wt)或GD2阳性细胞接种到C57BL/6小鼠(与CT26同基因)体侧。肿瘤攻击后10天,制备假转导的和抗GD2CAR转导的同基因脾细胞。将小鼠分为以下4个群体:具有表达GD2的CT26肿瘤的小鼠,接受抗GD2CAR脾细胞;表达GD2的CT26肿瘤,接受假转导的脾细胞;GD2阴性(wt)CD26肿瘤与抗GD2CAR脾细胞;和表达GD2的CT26肿瘤,不接受脾细胞。使用数显卡尺以3维测量肿瘤并以此估算体积。图11示出了肿瘤的生长曲线。仅接受抗GD2CAR T细胞小鼠中的GD2阳性肿瘤具有很少的生长或没有生长。

[0237] 实施例10-比较包含基于huK666和14g2a的抗原结合域的CAR的功能

[0238] CAR的抗原结合域可以影响其功能。在本研究中,与具有基于14g2a的抗原结合域的等同CAR比较具有基于huK666的抗原结合域的本发明的CAR的功能。

[0239] 抗体14g2a可以视为针对GD2的黄金标准抗体,因为其用作治疗性mAb且是在CAR研究中测试的唯一scFv。

[0240] 基于huK666或14g2a构建并表达了第二代CAR。它们的结构示于图14a中。

[0241] 通过使用编码GD2CAR、gag/pol和包膜蛋白RD114的质粒瞬时转染293T细胞产生了逆转录病毒。3天后收获上清并用于在Retronectin包被的平板上与相同滴度的逆转录病毒转导PHA/IL2活化的PBMCs。CAR仅在它们的抗原结合域中不同。在两种情况下,都使用IgG Fc片段将结合域连接到膜,并含有来自CD28和CD3-zeta的细胞内活化基序。转导后六天,通过流式细胞术确认CAR表达,并将PBMCs与GD2阳性Lan1细胞(GD2阳性细胞系)或GD2阴性A204细胞(GD2阴性横纹肌肉瘤细胞系)以1:1比率培养。一天后,来自这些共培养的上清通过ELISA测定干扰素- γ 水平,并在6天后通过流式细胞术评估T细胞增殖。

[0242] 结果示于图14和图15中。24小时后,从上清测量干扰素-gamma。证明了huK666CAR产生更多的IFN- γ (图14b)。一周后对T细胞计数,且证明了huK666CAR具有更多的增殖(图14c)。

[0243] 与神经母细胞瘤细胞系LAN1共培养一周后,收获细胞并通过流式细胞术分析。CD45表达允许区分淋巴样细胞和非淋巴样细胞,其中CD45-细胞为LAN-1细胞。使用CD3/QBEND/10进一步染色允许对CAR T细胞计数。发现huK666CAR T细胞比14g2a等同物增殖更好且杀伤更完全(图15)。

[0244] 以上说明书中提及的所有出版物通过提述并入本文。本发明描述的方法和系统的各种修改和变化对于本领域的技术人员将是显而易见的而不脱离本发明的范围和精神。尽管已经与特定的优选实施方案相关联描述本发明,应当理解作为要求保护的本发明不应当过度限于这些特定实施方案。实际上,对于实现本发明所描述的模式的各种修改对于分子生物学,细胞免疫学或相关领域的技术人员是显而易见的,并意图在所附权利要求书的范围内。

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Arg Ser Asp Asp Tyr Ser Trp Phe Ala Tyr
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Arg Ala Ser Ser Ser Val Ser Ser Ser Tyr Leu His
1 5 10

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1 5

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<223> 轻链可变区 CDR3

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Gln Gln Tyr Ser Gly Tyr Pro Ile Thr
1 5

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<223> 鼠KM666序列

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Gln Val Gln Leu Lys Glu Ser Gly Pro Val Leu Val Ala Pro Ser Gln
1 5 10 15

[0002] Thr Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Ala Ser Tyr
20 25 30

Asn Ile His Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn Ser Ala Leu Met
50 55 60

Ser Arg Leu Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Leu
65 70 75 80

Gln Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Met Tyr Tyr Cys Ala
85 90 95

Lys Arg Ser Asp Asp Tyr Ser Trp Phe Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ala Ser Gly Gly Gly Ser Gly Gly Gly
115 120 125

Ser Gly Gly Gly Ser Glu Asn Val Leu Thr Gln Ser Pro Ala Ile
130 135 140

Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
145 150 155 160

Ser Ser Val Ser Ser Ser Tyr Leu His Trp Tyr Gln Gln Lys Ser Gly
165 170 175

Ala Ser Pro Lys Val Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly
180 185 190

Val Pro Gly Arg Phe Ser Gly Ser Gly Ser Thr Ser Tyr Ser Leu
195 200 205

Thr Ile Ser Ser Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln
210 215 220

Gln Tyr Ser Gly Tyr Pro Ile Thr Phe Gly Ala Gly Thr Lys Val Glu
225 230 235 240

Val Lys Arg

<210> 8

<211> 242

<212> PRT

<213> 人工序列

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<223> 人源化的KM666序列

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Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Ala Ser Tyr
20 25 30

[0003]

Asn Ile His Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn Ser Ala Leu Met
50 55 60

Ser Arg Leu Thr Ile Ser Lys Asp Asn Ser Lys Asn Gln Val Phe Leu
65 70 75 80

Lys Met Ser Ser Leu Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Lys Arg Ser Asp Asp Tyr Ser Trp Phe Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Gly Gly Ser Gly Gly Gly Ser
115 120 125

Gly Gly Gly Ser Glu Asn Gln Met Thr Gln Ser Pro Ser Ser Leu
130 135 140

Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys Arg Ala Ser Ser
145 150 155 160

Ser Val Ser Ser Ser Tyr Leu His Trp Tyr Gln Gln Lys Ser Gly Lys
165 170 175

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

180

185

190

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr
 195 200 205

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
 210 215 220

Tyr Ser Gly Tyr Pro Ile Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
 225 230 235 240

Lys Arg

<210> 9

<211> 118

<212> PRT

<213> 人工序列

<220>

<223> 鼠KM666 VH (重链可变区) 序列

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Gln Val Gln Leu Lys Glu Ser Gly Pro Val Leu Val Ala Pro Ser Gln
 1 5 10 15

Thr Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Ala Ser Tyr
 20 25 30

[0004] Asn Ile His Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu
 35 40 45

Gly Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn Ser Ala Leu Met
 50 55 60

Ser Arg Leu Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Leu
 65 70 75 80

Gln Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Met Tyr Tyr Cys Ala
 85 90 95

Lys Arg Ser Asp Asp Tyr Ser Trp Phe Ala Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ala
 115

<210> 10

<211> 118

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<223> 人源化的 KM666 VH 序列

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Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
 1 5 10 15

Thr Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Ala Ser Tyr

20	25	30
----	----	----

Asn Ile His Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu	35 40 45	
---	--	--

Gly Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn Ser Ala Leu Met	50 55 60	
---	--	--

Ser Arg Leu Thr Ile Ser Lys Asp Asn Ser Lys Asn Gln Val Phe Leu	65 70 75	80
---	--	----

Lys Met Ser Ser Leu Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala	85 90 95	
---	--	--

Lys Arg Ser Asp Asp Tyr Ser Trp Phe Ala Tyr Trp Gly Gln Gly Thr	100 105 110	
---	---	--

Leu Val Thr Val Ser Ser	115	
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<210> 11

<211> 108

<212> PRT

<213> 人工序列

<220>

<223> 鼠 KM666 VL (轻链可变区) 序列

<400> 11

[0005] Glu Asn Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly
1 5 10 15

Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Ser Ser Ser	20 25 30	
---	--	--

Tyr Leu His Trp Tyr Gln Gln Lys Ser Gly Ala Ser Pro Lys Val Trp	35 40 45	
---	--	--

Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Gly Arg Phe Ser	50 55 60	
---	--	--

Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Val Glu	65 70 75	80
---	--	----

Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Gly Tyr Pro	85 90 95	
---	--	--

Ile Thr Phe Gly Ala Gly Thr Lys Val Glu Val Lys	100 105	
---	----------------------------------	--

<210> 12

<211> 108

<212> PRT

<213> 人工序列

<220>

<223> 人源化的 KM666 VL 序列

<400> 12

Glu Asn Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1	5	10	15
Asp Arg Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Ser Ser Ser			
20	25	30	

Tyr Leu His Trp Tyr Gln Gln Lys Ser Gly Lys Ala Pro Lys Val Trp			
35	40	45	

Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser			
50	55	60	

Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln			
65	70	75	80

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Gly Tyr Pro			
85	90	95	

Ile Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys			
100	105		

<210> 13

<211> 27

<212> PRT

<213> 人工序列

<220>

<223> 跨膜区

<400> 13

[0006] Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu
1 5 10 15

Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val			
20	25		

<210> 14

<211> 39

<212> PRT

<213> 人工序列

<220>

<223> CD28 胞内域

<400> 14

Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr			
1	5	10	15

Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro			
20	25	30	

Pro Arg Asp Phe Ala Ala Tyr			
35			

<210> 15

<211> 38

<212> PRT

<213> 人工序列

<220>

<223> CD40 胞内域

<400> 15

Arg Ser Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly
1 5 10 15

Gly Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His
20 25 30

Ser Thr Leu Ala Lys Ile
35

<210> 16
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<212> PRT
<213> 人工序列

<220>
<223> CD3 zeta 胞内域

<400> 16

Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln
1 5 10 15

Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu
20 25 30

Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly
35 40 45

Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
50 55 60

[0007]

Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
65 70 75 80

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
85 90 95

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

Pro Arg

<210> 17
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<212> PRT
<213> 人工序列

<220>
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<400> 17

Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr
1 5 10 15

Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
20 25 30

Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser
35 40 45

Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu
50 55 60

Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg
65 70 75 80

Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln
85 90 95

Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr
100 105 110

Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Gly Lys Gly His Asp
115 120 125

Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala
130 135 140

Leu His Met Gln Ala Leu Pro Pro Arg
145 150

<210> 18

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<213> 人工序列

<220>

<223> CD280XZ

<400> 18

[0008]

Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr
1 5 10 15

Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
20 25 30

Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Asp Gln Arg Leu Pro Pro
35 40 45

Asp Ala His Lys Pro Pro Gly Gly Ser Phe Arg Thr Pro Ile Gln
50 55 60

Glu Glu Gln Ala Asp Ala His Ser Thr Leu Ala Lys Ile Arg Val Lys
65 70 75 80

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln
85 90 95

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
100 105 110

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
115 120 125

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
130 135 140

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly

145	150	155	160
-----	-----	-----	-----

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
 165 170 175

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
 180 185

<210> 19
 <211> 20
 <212> PRT
 <213> 人工序列

<220>
 <223> 信号肽

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Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
 1 5 10 15

Gly Ser Thr Gly
 20

<210> 20
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 <213> 人工序列

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 <223> 人IgG1铰链-CH₂CH₃间隔区

[0009] <400> 20

Ala Glu Pro Lys Ser Pro Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 1 5 10 15

Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 20 25 30

Lys Asp Thr Leu Met Ile Ala Arg Thr Pro Glu Val Thr Cys Val Val
 35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
 100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
 130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

145	150	155	160
-----	-----	-----	-----

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr	165	170	175
---	-----	-----	-----

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr	180	185	190
---	-----	-----	-----

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe	195	200	205
---	-----	-----	-----

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys	210	215	220
---	-----	-----	-----

Ser Leu Ser Leu Ser Pro Gly Lys Lys Asp	225	230	
---	-----	-----	--

<210> 21

<211> 46

<212> PRT

<213> 人工序列

<220>

<223> 人CD8茎部间隔区

<400> 21

Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala	1	5	10	15
---	---	---	----	----

[0010] Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly

20	25	30	
----	----	----	--

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile	35	40	45
---	----	----	----

<210> 22

<211> 20

<212> PRT

<213> 人工序列

<220>

<223> 人IgG1铰链间隔区

<400> 22

Ala Glu Pro Lys Ser Pro Asp Lys Thr His Thr Cys Pro Pro Cys Pro	1	5	10	15
---	---	---	----	----

Lys Asp Pro Lys	20	
-----------------	----	--

<210> 23

<211> 237

<212> PRT

<213> 人工序列

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<223> IgG1 铰链-Fc间隔区

<400> 23

Ala Glu Pro Lys Ser Pro Asp Lys Thr His Thr Cys Pro Pro Cys Pro	1	5	10	15
---	---	---	----	----

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
20 25 30

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
35 40 45

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
50 55 60

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
65 70 75 80

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
85 90 95

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
100 105 110

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
115 120 125

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
130 135 140

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
145 150 155 160

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
[0011] 165 170 175

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
180 185 190

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
195 200 205

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
210 215 220

Lys Ser Leu Ser Leu Ser Pro Gly Lys Lys Asp Pro Lys
225 230 235

<210> 24

<211> 236

<212> PRT

<213> 人工序列

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<223> IgG1 铰链间隔区 - Fc经修饰以去除Fc受体识别基序

<400> 24

Ala Glu Pro Lys Ser Pro Asp Lys Thr His Thr Cys Pro Pro Cys Pro
1 5 10 15

Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ala Arg Thr Pro Glu Val Thr Cys Val Val

35	40	45
----	----	----

Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val
50					55				60						

Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln
65					70				75				80		

Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln
	85					90				95					

Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala
		100				105				110					

Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro
	115				120			125							

Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr
	130				135			140							

Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser
	145				150			155		160					

Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr
		165				170				175					

Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr
		180				185				190					

[0012]

Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe
	195				200			205							

Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys
	210				215			220							

Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys	Lys	Asp	Pro	Lys
225				230				235			

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<220>
<223> 逆转录病毒基因盒

<400> 25																
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gaaaaaaatac	ataactgaga	atagaaaagt	tcatatcaag	gtcaggaaca	gtatggaaacag									120		
ctgaatatatgg	gccaaacagg	atatctgtgg	taagcagttc	ctggccccgc	tcaggccaa									180		
gaacagatgg	aacagctgaa	tatggccaa	acaggatatac	tgtggtaagc	agttcctgcc									240		
ccggctcagg	gccaagaaca	gatggcccc	agatgcggtc	cagccctcag	cagtttctag									300		
agaaccatca	gatgtttcca	gggtgcccc	aggacctgaa	atgaccctgt	gccttatttg									360		
aactaaccaa	tcagttcgct	tctcgcttct	gttcgcgcgc	ttatgctccc	cgagctaat									420		
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[0013]	tacccgtgta tccaataaac cctcttgag ttgcattccga ctgtggct cgctgttct	540
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	cgtccggat cgggagaccc ctgcccgagg accaccgacc caccaccggg aggtaaatcg	660
	gccagcaact tatctgtgtc tgtccgattt ctatgtgtct atgactgatt ttatgcgct	720
	gcttcggta tagtagcta actagctctg tatctggccg acccgtggta gaactgacga	780
	gttcggaca cccggccgca accctggag acgtcccagg gacttcggg gccgttttg	840
	tggccgacc tgagtctaa aatccgatc gtttagact ctttggtgc acccccttag	900
	aggaggata tgtggttctg gtaggagacg agaacctaaa acagttcccg cctccgtctg	960
	aattttgtc ttcggttgg gaccgaagcc gcgcgcgcgc tcttgcgtc tgacgatcg	1020
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	agcctgttac cactccctta agtttgcacct taggtcactg gaaagatgtc gagcggatcg	1140
	ctcacaacca gtcggtagat gtcaagaaga gacgttgggt taccttgc tctgcagaat	1200
	ggccaaccc taacgtcgga tggccgcgag acggcaccc taaccgagac ctcatcaccc	1260
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	ctaagectcc gcctctctt cctccatccg cccctgtctt ccccttggaa cctcctcg	1440
	cgaccccgcc tcgatccctcc ctatccag ccctactcc ttctcttaggc gccccat	1500
	ggccatata gatcttatat gggcacccccc cgcccttgt aaactccctt gaccctgaca	1560
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	agcacgaagt ctggagaccc ctggcgccag cctaccaaga acaactggac cgaccgggt	1680
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	tagacggcat cgccagttgg atacacgccc cccacgtgaa ggctggcgc cccgggggt	1860
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	cggccgcagc gagctgccc cccagggcac ctctccaaac gtgtccacca acgtgagccc	2040
	agccaagccc accaccaccc cctgtccctt ttccaatccctt ccctgtgtaa gggggggg	2100
	aggcagccca gccccagac ctcccaaccc agccccacc atgcccggcc agccctgt	2160
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	gagccctggc atcaccctgt actgcaacca cggcaaccgc aggccgtgt gcaagtggcc	2340
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	ggtgccggcag ccccccaggca agggcctggaa gtggctggc gtgtatctgg ctggccgc	2640
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[0014]	caaggcggc gacgactaca gctggttcgc ctactgggc cagggcaccc tggtgaccgt	2820
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	gatgacccag agccccagca gcttgagcgc cagcgtggc gaccgggtga ccatgacctg	2940
	cagagccagc agcagcgtga gcagcagcta cctgcactgg taccagcaga agagcggcaa	3000
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	caaggtggag atcaagcggt cggtatccgc cgagccaaa ttcctgaca aaactcacac	3240
	atgcccaccc tgcccgac ccctcggtc cggccgtca gtttctct tcccccaaa	3300
	acccaaggac accctcatga tcgcccggac ccctgaggc acatgcgtgg tggtggacgt	3360
	gagccacgaa gaccctgagg tcaagttcaa ctggtaatc gacggcgtgg aggtgcataa	3420
	tgccaagaca aagccgcggg aggagcagta caacagcacg taccgtgtgg ttagcgtct	3480
	caccgtctcg caccaggact ggctaatgg caaggagtac aatgcgtgg ttcctcaacaa	3540
	agccctccca gcctccatcg agaaaaccat ctccaaagcc aaaggcggc cccgagaacc	3600
	acagggtgtac accctgcacc catcccgga tgagctgacc aagaaccagg tcaagctgac	3660
	ctgcctggc aaaggcttct atccacgcg catgcgtgt gagtgggaga gcaatggca	3720
	accggagaac aactacaaga ccacgcctcc cgtgctggc tccgacggct cttcttct	3780
	ctacagcaag ctcaccgtgg acaagagcag gtggcagcag gggacgtct tctcatgctc	3840
	cgtgatgcat gaggccctgc acaatacta taccctggaaa tctctgatc tgacccagg	3900
	caagaaggac cccaaatctt gggctctgtt ggtggggaa ggcgtgtgg cctgttactc	3960
	tctctgggtt accgtggct tcatcatctt ctgggtgcgc tccaaggagga gcaggctct	4020
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	gccctatgcc ccaccacgca acttcgcagc ctatgcctcc cgggtgaatg tctctcgctc	4140
	tgcgcgtgcc ccagecttac agcaggggca gaatcgtgtg tacaatgaac tgaacctggg	4200
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	cggcctgtat caggattgt ccaccgtac aaaagataca tatgtgccc tgcacatgca	4440
	ggccctgcca cccagatgac gcttatcgat actgttctca tcacatcata tcaaggttat	4500
	ataccatcaa tattccaca gatgttactt agcctttttaa tatttctcta atttagtga	4560
	tatgcaatga tagttcttg atttctgaga ttgagtttct catgtgtat gattatttg	4620
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	ttttttttt aatctgcata ttacaattct cttaactggg gtgttgcata tttttctgt	4740
	cattctatgg cctgactttt cttaatgggtt ttttaatttt aaaataagt cttaatattc	4800
	atgcaatcta attaacaatc ttttctttgtt ggtttagact ttgagtcata agaaatttt	4860
	ctctacactg aagtcatgtat ggcgtatcctc tatattttt tctaaaatgg tttttttttt	4920
	gccttctcca tttagactta taattcactg gaattttttt gtgtgtatgg tatgacatata	4980
	gggttccctt ttattttttta catataaata tattttccctg tttttctaaaa agaaaaaaag	5040

atcatcattt	tccattgtaaatgcata	ttttttcat	aggtaactta	cataatatcaa	5100
tgggtctgtt	tctgagctct	actctatttt	atcagcctca	ctgtctatcc	5160
catgetttgc	tctaaatctt	gatatttagt	ggaacattct	ttcccathtt	5220
aatatttttg	ttattgtctt	tgggcttctt	atatacattt	tgaatgagg	5280
cggattagtc	caatttgtta	aagacaggat	atcagtggc	caggctctag	5340
acaatatcac	cagctgaagc	ctatagagta	cgagccatag	ataaaataaa	5400
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atctgtgta	agcagttctt	gcccccggc	agggccaaga	acagatggc	5700
gtccagccct	cagcagttc	tagagaacca	ttagatgtt	ccagggtgcc	5760
gaaatgaccc	tgtgccttat	ttgaactaac	caatcagttc	gcttctcgct	5820
cgttctgct	ccccgagctc	aataaaagag	cccacaaccc	ctcaactcggg	5880
tccgattgac	tgagtcgccc	gggtaccctgt	gtatccaata	aaccctttg	5940
cgacttgtgg	tctcgtgtt	ccttgggagg	gtctcctctg	agtgattgac	6000
cgggggtctt	tcac				6014

[0015]

 <210> 26

 <211> 719

 <212> PRT

 <213> 人工序列

<220>

<223> 抗GD2 CAR, muKM666-HCH2CH3-CD280XZ

<400> 26

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
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Gly Ser Thr Gly Gln Val Gln Leu Lys Glu Ser Gly Pro Val Leu Val
 20 25 30

Ala Pro Ser Gln Thr Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser
 35 40 45

Leu Ala Ser Tyr Asn Ile His Trp Val Arg Gln Pro Pro Gly Lys Gly
 50 55 60

Leu Glu Trp Leu Gly Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn
 65 70 75 80

Ser Ala Leu Met Ser Arg Leu Ser Ile Ser Lys Asp Asn Ser Lys Ser
 85 90 95

Gln Val Phe Leu Gln Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Met
 100 105 110

Tyr Tyr Cys Ala Lys Arg Ser Asp Asp Tyr Ser Trp Phe Ala Tyr Trp
 115 120 125

Gly Gln Gly Thr Leu Val Thr Val Ser Ala Ser Gly Gly Gly Ser
 130 135 140

Gly Gly Gly Ser Gly Gly Gly Ser Glu Asn Val Leu Thr Gln
 145 150 155 160

Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr
 165 170 175

Cys Arg Ala Ser Ser Ser Val Ser Ser Ser Tyr Leu His Trp Tyr Gln
 180 185 190

Gln Lys Ser Gly Ala Ser Pro Lys Val Trp Ile Tyr Ser Thr Ser Asn
 195 200 205

Leu Ala Ser Gly Val Pro Gly Arg Phe Ser Gly Ser Gly Thr
 210 215 220

Ser Tyr Ser Leu Thr Ile Ser Ser Val Glu Ala Glu Asp Ala Ala Thr
 225 230 235 240

Tyr Tyr Cys Gln Gln Tyr Ser Gly Tyr Pro Ile Thr Phe Gly Ala Gly
 245 250 255

Thr Lys Val Glu Val Lys Arg Ser Asp Pro Ala Glu Pro Lys Ser Pro
 260 265 270

[0016] Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 275 280 285

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 290 295 300

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 305 310 315 320

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 325 330 335

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
 340 345 350

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 355 360 365

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
 370 375 380

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 385 390 395 400

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
 405 410 415

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 420 425 430

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 435 440 445

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 450 455 460

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 465 470 475 480

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 485 490 495

Pro Gly Lys Lys Asp Pro Lys Phe Trp Val Leu Val Val Val Gly Gly
 500 505 510

Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe
 515 520 525

Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn
 530 535 540

Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr
 545 550 555 560

Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Asp Gln Arg Leu
 565 570 575

Pro Pro Asp Ala His Lys Pro Pro Gly Gly Ser Phe Arg Thr Pro
 580 585 590

Ile Gln Glu Glu Gln Ala Asp Ala His Ser Thr Leu Ala Lys Ile Arg
 595 600 605

Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln
 610 615 620

Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp
 625 630 635 640

Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Lys Pro
 645 650 655

Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp
 660 665 670

Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg
 675 680 685

Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr
 690 695 700

Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
 705 710 715

<210> 27
 <211> 718
 <212> PRT

<213> 人工序列

<220>

<223> 抗GD2 CAR, huKM666-HCH2CH3-CD280XZ

<400> 27

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

Gly Ser Thr Gly Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val
20 25 30

Lys Pro Ser Gln Thr Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser
35 40 45

Leu Ala Ser Tyr Asn Ile His Trp Val Arg Gln Pro Pro Gly Lys Gly
50 55 60

Leu Glu Trp Leu Gly Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn
65 70 75 80

Ser Ala Leu Met Ser Arg Leu Thr Ile Ser Lys Asp Asn Ser Lys Asn
85 90 95

Gln Val Phe Leu Lys Met Ser Ser Leu Thr Ala Ala Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Lys Arg Ser Asp Asp Tyr Ser Trp Phe Ala Tyr Trp
115 120 125

[0018]

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly
130 135 140

Gly Gly Gly Ser Gly Gly Gly Ser Glu Asn Gln Met Thr Gln Ser
145 150 155 160

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys
165 170 175

Arg Ala Ser Ser Ser Val Ser Ser Tyr Leu His Trp Tyr Gln Gln
180 185 190

Lys Ser Gly Lys Ala Pro Lys Val Trp Ile Tyr Ser Thr Ser Asn Leu
195 200 205

Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
210 215 220

Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
225 230 235 240

Tyr Cys Gln Gln Tyr Ser Gly Tyr Pro Ile Thr Phe Gly Gln Gly Thr
245 250 255

Lys Val Glu Ile Lys Arg Ser Asp Pro Ala Glu Pro Lys Ser Pro Asp
260 265 270

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly

275	280	285
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Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile	290	295
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Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu	305	310
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Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His	325	330
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Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg	340	345
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Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys	355	360
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Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu	370	375
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Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr	385	390
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Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu	405	410
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Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp	420	425
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[0019]

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val	435	440
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Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp	450	455
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Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His	465	470
---	-----	-----

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro	485	490
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Gly Lys Lys Asp Pro Lys Phe Trp Val Leu Val Val Val Gly Gly Val	500	505
---	-----	-----

Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp	515	520
---	-----	-----

Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met	530	535
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Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala	545	550
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Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Asp Gln Arg Leu Pro	565	570
---	-----	-----

Pro Asp Ala His Lys Pro Pro Gly Gly Ser Phe Arg Thr Pro Ile		
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580 585 590

Gln Glu Glu Gln Ala Asp Ala His Ser Thr Leu Ala Lys Ile Arg Val
 595 600 605

Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn
 610 615 620

Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
 625 630 635 640

Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg
 645 650 655

Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
 660 665 670

Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
 675 680 685

Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
 690 695 700

Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
 705 710 715

<210> 28

<211> 717

<212> PRT

<213> 人工序列

<220>

<223> 抗GD2 CAR, huKM666-HCH2CH3pvaa-CD280XZ

<400> 28

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Trp Val Pro
 1 5 10 15

Gly Ser Thr Gly Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val
 20 25 30

Lys Pro Ser Gln Thr Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser
 35 40 45

Leu Ala Ser Tyr Asn Ile His Trp Val Arg Gln Pro Pro Gly Lys Gly
 50 55 60

Leu Glu Trp Leu Gly Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn
 65 70 75 80

Ser Ala Leu Met Ser Arg Leu Thr Ile Ser Lys Asp Asn Ser Lys Asn
 85 90 95

Gln Val Phe Leu Lys Met Ser Ser Leu Thr Ala Ala Asp Thr Ala Val
 100 105 110

Tyr Tyr Cys Ala Lys Arg Ser Asp Asp Tyr Ser Trp Phe Ala Tyr Trp
 115 120 125

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly
 130 135 140

Gly Gly Gly Ser Gly Gly Ser Glu Asn Gln Met Thr Gln Ser
 145 150 155 160

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys
 165 170 175

Arg Ala Ser Ser Ser Val Ser Ser Tyr Leu His Trp Tyr Gln Gln
 180 185 190

Lys Ser Gly Lys Ala Pro Lys Val Trp Ile Tyr Ser Thr Ser Asn Leu
 195 200 205

Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
 210 215 220

Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
 225 230 235 240

Tyr Cys Gln Gln Tyr Ser Gly Tyr Pro Ile Thr Phe Gly Gln Gly Thr
 245 250 255

Lys Val Glu Ile Lys Arg Ser Asp Pro Ala Glu Pro Lys Ser Pro Asp
 260 265 270

[0021] Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro
 275 280 285

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ala
 290 295 300

Arg Thr Pro Glu Val Thr Cys Val Val Asp Val Ser His Glu Asp
 305 310 315 320

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
 325 330 335

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
 340 345 350

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
 355 360 365

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
 370 375 380

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
 385 390 395 400

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
 405 410 415

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
 420 425 430

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
 435 440 445

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
 450 455 460

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
 465 470 475 480

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 485 490 495

Lys Lys Asp Pro Lys Phe Trp Val Leu Val Val Val Gly Gly Val Leu
 500 505 510

Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val
 515 520 525

Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr
 530 535 540

Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
 545 550 555 560

Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Asp Gln Arg Leu Pro Pro
 565 570 575

Asp Ala His Lys Pro Pro Gly Gly Ser Phe Arg Thr Pro Ile Gln
 580 585 590

[0022] Glu Glu Gln Ala Asp Ala His Ser Thr Leu Ala Lys Ile Arg Val Lys
 595 600 605

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln
 610 615 620

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
 625 630 635 640

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
 645 650 655

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
 660 665 670

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
 675 680 685

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
 690 695 700

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
 705 710 715

<210> 29
 <211> 527
 <212> PRT

<213> 人工序列

<220>

<223> 抗GD2 CAR, huKM666-HSTK-CD280XZ

<400> 29

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

Gly Ser Thr Gly Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val
20 25 30

Lys Pro Ser Gln Thr Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser
35 40 45

Leu Ala Ser Tyr Asn Ile His Trp Val Arg Gln Pro Pro Gly Lys Gly
50 55 60

Leu Glu Trp Leu Gly Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn
65 70 75 80

Ser Ala Leu Met Ser Arg Leu Thr Ile Ser Lys Asp Asn Ser Lys Asn
85 90 95

Gln Val Phe Leu Lys Met Ser Ser Leu Thr Ala Ala Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Lys Arg Ser Asp Asp Tyr Ser Trp Phe Ala Tyr Trp
115 120 125

[0023]

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly
130 135 140

Gly Gly Gly Ser Gly Gly Gly Ser Glu Asn Gln Met Thr Gln Ser
145 150 155 160

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys
165 170 175

Arg Ala Ser Ser Ser Val Ser Ser Tyr Leu His Trp Tyr Gln Gln
180 185 190

Lys Ser Gly Lys Ala Pro Lys Val Trp Ile Tyr Ser Thr Ser Asn Leu
195 200 205

Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
210 215 220

Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
225 230 235 240

Tyr Cys Gln Gln Tyr Ser Gly Tyr Pro Ile Thr Phe Gly Gln Gly Thr
245 250 255

Lys Val Glu Ile Lys Arg Ser Asp Pro Thr Thr Pro Ala Pro Arg
260 265 270

Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg

275	280	285
-----	-----	-----

Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly		
290	295	300

Leu Asp Phe Ala Cys Asp Ile Phe Trp Val Leu Val Val Val Gly Gly			
305	310	315	320

Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe		
325	330	335

Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn		
340	345	350

Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr		
355	360	365

Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Asp Gln Arg Leu		
370	375	380

Pro Pro Asp Ala His Lys Pro Pro Gly Gly Ser Phe Arg Thr Pro			
385	390	395	400

Ile Gln Glu Glu Gln Ala Asp Ala His Ser Thr Leu Ala Lys Ile Arg		
405	410	415

Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gln		
420	425	430

[0024]

Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp		
435	440	445

Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro		
450	455	460

Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp			
465	470	475	480

Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg		
485	490	495

Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr		
500	505	510

Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg		
515	520	525

<210> 30
 <211> 527
 <212> PRT
 <213> 人工序列

<220>
 <223> 抗GD2 CAR, huKM666-STK-CD28XOZ

<400> 30

Met Glu Thr Asp Thr Leu Leu Trp Val Leu Leu Leu Trp Val Pro			
1	5	10	15

Gly Ser Thr Gly Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val
 20 25 30

Lys Pro Ser Gln Thr Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser
 35 40 45

Leu Ala Ser Tyr Asn Ile His Trp Val Arg Gln Pro Pro Gly Lys Gly
 50 55 60

Leu Glu Trp Leu Gly Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn
 65 70 75 80

Ser Ala Leu Met Ser Arg Leu Thr Ile Ser Lys Asp Asn Ser Lys Asn
 85 90 95

Gln Val Phe Leu Lys Met Ser Ser Leu Thr Ala Ala Asp Thr Ala Val
 100 105 110

Tyr Tyr Cys Ala Lys Arg Ser Asp Asp Tyr Ser Trp Phe Ala Tyr Trp
 115 120 125

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly
 130 135 140

Gly Gly Gly Ser Gly Gly Ser Glu Asn Gln Met Thr Gln Ser
 145 150 155 160

[0025] Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys
 165 170 175

Arg Ala Ser Ser Ser Val Ser Ser Tyr Leu His Trp Tyr Gln Gln
 180 185 190

Lys Ser Gly Lys Ala Pro Lys Val Trp Ile Tyr Ser Thr Ser Asn Leu
 195 200 205

Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
 210 215 220

Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
 225 230 235 240

Tyr Cys Gln Gln Tyr Ser Gly Tyr Pro Ile Thr Phe Gly Gln Gly Thr
 245 250 255

Lys Val Glu Ile Lys Arg Ser Asp Pro Thr Thr Thr Pro Ala Pro Arg
 260 265 270

Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg
 275 280 285

Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly
 290 295 300

Leu Asp Phe Ala Cys Asp Ile Phe Trp Val Leu Val Val Val Gly Gly
 305 310 315 320

Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe
325 330 335

Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn
340 345 350

Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr
355 360 365

Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Asp Gln Arg Leu
370 375 380

Pro Pro Asp Ala His Lys Pro Pro Gly Gly Ser Phe Arg Thr Pro
385 390 395 400

Ile Gln Glu Glu Gln Ala Asp Ala His Ser Thr Leu Ala Lys Ile Arg
405 410 415

Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln
420 425 430

Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp
435 440 445

Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro
450 455 460

[0026] Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp
465 470 475 480

Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
485 490 495

Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr
500 505 510

Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
515 520 525

<210> 31

<211> 501

<212> PRT

<213> 人工序列

<220>

<223> 抗GD2 CAR, huKM666-HNG-CD280XZ

<400> 31

Met Glu Thr Asp Thr Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

Gly Ser Thr Gly Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val
20 25 30

Lys Pro Ser Gln Thr Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser
35 40 45

Leu Ala Ser Tyr Asn Ile His Trp Val Arg Gln Pro Pro Gly Lys Gly

50 55 60

Leu Glu Trp Leu Gly Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn
65 70 75 80

Ser Ala Leu Met Ser Arg Leu Thr Ile Ser Lys Asp Asn Ser Lys Asn
85 90 95

Gln Val Phe Leu Lys Met Ser Ser Leu Thr Ala Ala Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Lys Arg Ser Asp Asp Tyr Ser Trp Phe Ala Tyr Trp
115 120 125

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly
130 135 140

Gly Gly Gly Ser Gly Gly Ser Glu Asn Gln Met Thr Gln Ser
145 150 155 160

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys
165 170 175

Arg Ala Ser Ser Ser Val Ser Ser Tyr Leu His Trp Tyr Gln Gln
180 185 190

Lys Ser Gly Lys Ala Pro Lys Val Trp Ile Tyr Ser Thr Ser Asn Leu
195 200 205

[0027]

Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Thr Asp
210 215 220

Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
225 230 235 240

Tyr Cys Gln Gln Tyr Ser Gly Tyr Pro Ile Thr Phe Gly Gln Gly Thr
245 250 255

Lys Val Glu Ile Lys Arg Ser Asp Pro Ala Glu Pro Lys Ser Pro Asp
260 265 270

Lys Thr His Thr Cys Pro Pro Cys Pro Lys Asp Pro Lys Phe Trp Val
275 280 285

Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr
290 295 300

Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu
305 310 315 320

His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg
325 330 335

Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg
340 345 350

Ser Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly

355 360 365

Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser
370 375 380

Thr Leu Ala Lys Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro
385 390 395 400

Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly
405 410 415

Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
420 425 430

Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr
435 440 445

Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly
450 455 460

Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln
 465 470 475 480

Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
 485 490 495

Ala Leu Pro Pro Arg
500

[0028]

<210> 32
<211> 642

<212> PRT

〈213〉 人工

223

400 32

1 5 10 15

20 25 30

Lys Pro Ser Gln Thr Leu Ser Thr Thr Cys Thr Val Ser Gly The Ser
35 40 45

Lys Gly Pro Pro Gly Lys
50 55 60

Led Gln Ile Leu Gly Val Thr Ile Asp Gly Ser Thr Asp Tyr Asp
65 70 75 80

Ser Ala Leu Met Ser Arg Leu Thr Ile Ser Lys Asp Ash Ser Lys Ash
85 90 95

Gln Val Phe Leu Lys Met Ser Ser Leu Thr Ala Ala Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Lys Arg Ser Asp Asp Tyr Ser Trp Phe Ala Tyr Trp
 115 120 125

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly
 130 135 140

Gly Gly Ser Gly Gly Ser Gly Asn Gln Met Thr Gln Ser
 145 150 155 160

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys
 165 170 175

Arg Ala Ser Ser Ser Val Ser Ser Tyr Leu His Trp Tyr Gln Gln
 180 185 190

Lys Ser Gly Lys Ala Pro Lys Val Trp Ile Tyr Ser Thr Ser Asn Leu
 195 200 205

Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Thr Asp
 210 215 220

Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
 225 230 235 240

Tyr Cys Gln Gln Tyr Ser Gly Tyr Pro Ile Thr Phe Gly Gln Gly Thr
 245 250 255

[0029] Lys Val Glu Ile Lys Arg Ser Asp Pro Ala Glu Pro Lys Ser Pro Asp
 260 265 270

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro
 275 280 285

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ala
 290 295 300

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
 305 310 315 320

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
 325 330 335

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
 340 345 350

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
 355 360 365

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
 370 375 380

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
 385 390 395 400

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
 405 410 415

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
420 425 430

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
435 440 445

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
450 455 460

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
465 470 475 480

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
485 490 495

Lys Lys Asp Pro Lys Phe Trp Val Leu Val Val Val Gly Gly Val Leu
500 505 510

Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val
515 520 525

Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln
530 535 540

Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu
545 550 555 560

[0030] Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly
565 570 575

Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
580 585 590

Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
595 600 605

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
610 615 620

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
625 630 635 640

Pro Arg

<210> 33

<211> 681

<212> PRT

<213> 人工序列

<220>

<223> 抗GD2 CAR, huMK666-HCH2CH3pvaa-CD28Z

<400> 33

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

Gly Ser Thr Gly Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val

20	25	30
----	----	----

Lys Pro Ser Gln Thr Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser	35	40	45
---	----	----	----

Leu Ala Ser Tyr Asn Ile His Trp Val Arg Gln Pro Pro Gly Lys Gly	50	55	60
---	----	----	----

Leu Glu Trp Leu Gly Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn	65	70	75	80
---	----	----	----	----

Ser Ala Leu Met Ser Arg Leu Thr Ile Ser Lys Asp Asn Ser Lys Asn	85	90	95
---	----	----	----

Gln Val Phe Leu Lys Met Ser Ser Leu Thr Ala Ala Asp Thr Ala Val	100	105	110
---	-----	-----	-----

Tyr Tyr Cys Ala Lys Arg Ser Asp Asp Tyr Ser Trp Phe Ala Tyr Trp	115	120	125
---	-----	-----	-----

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly	130	135	140
---	-----	-----	-----

Gly Gly Gly Ser Gly Gly Ser Glu Asn Gln Met Thr Gln Ser	145	150	155	160
---	-----	-----	-----	-----

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys	165	170	175
---	-----	-----	-----

[0031]

Arg Ala Ser Ser Ser Val Ser Ser Tyr Leu His Trp Tyr Gln Gln	180	185	190
---	-----	-----	-----

Lys Ser Gly Lys Ala Pro Lys Val Trp Ile Tyr Ser Thr Ser Asn Leu	195	200	205
---	-----	-----	-----

Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp	210	215	220
---	-----	-----	-----

Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr	225	230	235	240
---	-----	-----	-----	-----

Tyr Cys Gln Gln Tyr Ser Gly Tyr Pro Ile Thr Phe Gly Gln Gly Thr	245	250	255
---	-----	-----	-----

Lys Val Glu Ile Lys Arg Ser Asp Pro Ala Glu Pro Lys Ser Pro Asp	260	265	270
---	-----	-----	-----

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro	275	280	285
---	-----	-----	-----

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ala	290	295	300
---	-----	-----	-----

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp	305	310	315	320
---	-----	-----	-----	-----

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn

325

330

335

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
 340 345 350

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
 355 360 365

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
 370 375 380

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
 385 390 395 400

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
 405 410 415

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
 420 425 430

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
 435 440 445

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
 450 455 460

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
 465 470 475 480

[0032]

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 485 490 495

Lys Lys Asp Pro Lys Phe Trp Val Leu Val Val Val Gly Gly Val Leu
 500 505 510

Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val
 515 520 525

Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr
 530 535 540

Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
 545 550 555 560

Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser
 565 570 575

Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu
 580 585 590

Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg
 595 600 605

Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln
 610 615 620

Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr

625	630	635	640
Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp			
645	650	655	
Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala			
660	665	670	
Leu His Met Gln Ala Leu Pro Pro Arg			
675	680		
<210> 34			
<211> 1103			
<212> PRT			
<213> 人工序列			
<220>			
<223> 与iCasp9自杀基因共表达的抗GD2 CAR			
<400> 34			
Met Leu Glu Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg			
1	5	10	15
Thr Phe Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met			
20	25	30	
Leu Glu Asp Gly Lys Lys Val Asp Ser Ser Arg Asp Arg Asn Lys Pro			
35	40	45	
[0033]	Phe Lys Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu		
50	55	60	
Gly Val Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser			
65	70	75	80
Pro Asp Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro			
85	90	95	
His Ala Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Ser Gly			
100	105	110	
Gly Gly Ser Gly Val Asp Gly Phe Gly Asp Val Gly Ala Leu Glu Ser			
115	120	125	
Leu Arg Gly Asn Ala Asp Leu Ala Tyr Ile Leu Ser Met Glu Pro Cys			
130	135	140	
Gly His Cys Leu Ile Ile Asn Asn Val Asn Phe Cys Arg Glu Ser Gly			
145	150	155	160
Leu Arg Thr Arg Thr Gly Ser Asn Ile Asp Cys Glu Lys Leu Arg Arg			
165	170	175	
Arg Phe Ser Ser Leu His Phe Met Val Glu Val Lys Gly Asp Leu Thr			
180	185	190	
Ala Lys Lys Met Val Leu Ala Leu Leu Glu Leu Ala Gln Gln Asp His			
195	200	205	

Gly Ala Leu Asp Cys Cys Val Val Val Ile Leu Ser His Gly Cys Gln
 210 215 220

Ala Ser His Leu Gln Phe Pro Gly Ala Val Tyr Gly Thr Asp Gly Cys
 225 230 235 240

Pro Val Ser Val Glu Lys Ile Val Asn Ile Phe Asn Gly Thr Ser Cys
 245 250 255

Pro Ser Leu Gly Gly Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Gly
 260 265 270

Gly Glu Gln Lys Asp His Gly Phe Glu Val Ala Ser Thr Ser Pro Glu
 275 280 285

Asp Glu Ser Pro Gly Ser Asn Pro Glu Pro Asp Ala Thr Pro Phe Gln
 290 295 300

Glu Gly Leu Arg Thr Phe Asp Gln Leu Asp Ala Ile Ser Ser Leu Pro
 305 310 315 320

Thr Pro Ser Asp Ile Phe Val Ser Tyr Ser Thr Phe Pro Gly Phe Val
 325 330 335

Ser Trp Arg Asp Pro Lys Ser Gly Ser Trp Tyr Val Glu Thr Leu Asp
 340 345 350

[0034] Asp Ile Phe Glu Gln Trp Ala His Ser Glu Asp Leu Gln Ser Leu Leu
 355 360 365

Leu Arg Val Ala Asn Ala Val Ser Val Lys Gly Ile Tyr Lys Gln Met
 370 375 380

Pro Gly Cys Phe Asn Phe Leu Arg Lys Lys Leu Phe Phe Lys Thr Ser
 385 390 395 400

Ala Ser Arg Ala Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val
 405 410 415

Glu Glu Asn Pro Gly Pro Met Glu Thr Asp Thr Leu Leu Trp Val
 420 425 430

Leu Leu Leu Trp Val Pro Gly Ser Thr Gly Gln Val Gln Leu Gln Glu
 435 440 445

Ser Gly Pro Gly Leu Val Lys Pro Ser Gln Thr Leu Ser Ile Thr Cys
 450 455 460

Thr Val Ser Gly Phe Ser Leu Ala Ser Tyr Asn Ile His Trp Val Arg
 465 470 475 480

Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Ala Gly
 485 490 495

Gly Ser Thr Asn Tyr Asn Ser Ala Leu Met Ser Arg Leu Thr Ile Ser
 500 505 510

Lys Asp Asn Ser Lys Asn Gln Val Phe Leu Lys Met Ser Ser Leu Thr
 515 520 525

Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Lys Arg Ser Asp Asp Tyr
 530 535 540

Ser Trp Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 545 550 555 560

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu
 565 570 575

Asn Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp
 580 585 590

Arg Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Ser Ser Tyr
 595 600 605

Leu His Trp Tyr Gln Gln Lys Ser Gly Lys Ala Pro Lys Val Trp Ile
 610 615 620

Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
 625 630 635 640

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
 645 650 655

[0035] Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Gly Tyr Pro Ile
 660 665 670

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ser Asp Pro Ala
 675 680 685

Glu Pro Lys Ser Pro Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 690 695 700

Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
 705 710 715 720

Asp Thr Leu Met Ile Ala Arg Thr Pro Glu Val Thr Cys Val Val Val
 725 730 735

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
 740 745 750

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
 755 760 765

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
 770 775 780

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
 785 790 795 800

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
 805 810 815

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
 820 825 830

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
 835 840 845

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
 850 855 860

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
 865 870 875 880

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
 885 890 895

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
 900 905 910

Leu Ser Leu Ser Pro Gly Lys Lys Asp Pro Lys Phe Trp Val Leu Val
 915 920 925

Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala
 930 935 940

Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser
 945 950 955 960

[0036] Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His
 965 970 975

Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg
 980 985 990

Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln
 995 1000 1005

Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
 1010 1015 1020

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
 1025 1030 1035

Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
 1040 1045 1050

Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
 1055 1060 1065

Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly
 1070 1075 1080

Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
 1085 1090 1095

Ala Leu Pro Pro Arg
 1100

<210> 35
 <211> 858
 <212> PRT
 <213> 人工序列

<220>
 <223> 与RQR8自杀基因共表达的抗GD2 CAR

<400> 35

Met Gly Thr Ser Leu Leu Cys Trp Met Ala Leu Cys Leu Leu Gly Ala
 1 5 10 15

Asp His Ala Asp Ala Cys Pro Tyr Ser Asn Pro Ser Leu Cys Ser Gly
 20 25 30

Gly Gly Gly Ser Glu Leu Pro Thr Gln Gly Thr Phe Ser Asn Val Ser
 35 40 45

Thr Asn Val Ser Pro Ala Lys Pro Thr Thr Ala Cys Pro Tyr Ser
 50 55 60

Asn Pro Ser Leu Cys Ser Gly Gly Ser Pro Ala Pro Arg Pro
 65 70 75 80

Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
 85 90 95

Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu
 100 105 110

[0037]

Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys
 115 120 125

Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn His Arg
 130 135 140

Asn Arg Arg Arg Val Cys Lys Cys Pro Arg Pro Val Val Arg Ala Glu
 145 150 155 160

Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly
 165 170 175

Pro Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val
 180 185 190

Pro Gly Ser Thr Gly Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu
 195 200 205

Val Lys Pro Ser Gln Thr Leu Ser Ile Thr Cys Thr Val Ser Gly Phe
 210 215 220

Ser Leu Ala Ser Tyr Asn Ile His Trp Val Arg Gln Pro Pro Gly Lys
 225 230 235 240

Gly Leu Glu Trp Leu Gly Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr
 245 250 255

Asn Ser Ala Leu Met Ser Arg Leu Thr Ile Ser Lys Asp Asn Ser Lys

260

265

270

Asn Gln Val Phe Leu Lys Met Ser Ser Leu Thr Ala Ala Asp Thr Ala
 275 280 285

Val Tyr Tyr Cys Ala Lys Arg Ser Asp Asp Tyr Ser Trp Phe Ala Tyr
 290 295 300

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser
 305 310 315 320

Gly Gly Gly Ser Gly Gly Ser Glu Asn Gln Met Thr Gln
 325 330 335

Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr
 340 345 350

Cys Arg Ala Ser Ser Ser Val Ser Ser Ser Tyr Leu His Trp Tyr Gln
 355 360 365

Gln Lys Ser Gly Lys Ala Pro Lys Val Trp Ile Tyr Ser Thr Ser Asn
 370 375 380

Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
 385 390 395 400

Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
 405 410 415

[0038]

Tyr Tyr Cys Gln Gln Tyr Ser Gly Tyr Pro Ile Thr Phe Gly Gln Gly
 420 425 430

Thr Lys Val Glu Ile Lys Arg Ser Asp Pro Ala Glu Pro Lys Ser Pro
 435 440 445

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly
 450 455 460

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
 465 470 475 480

Ala Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
 485 490 495

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 500 505 510

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 515 520 525

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 530 535 540

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
 545 550 555 560

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr

565 570 575

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
580 585 590

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
595 600 605

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
610 615 620

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
625 630 635 640

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
645 650 655

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
660 665 670

Gly Lys Lys Asp Pro Lys Phe Trp Val Leu Val Val Val Gly Gly Val
675 680 685

Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp
690 695 700

Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met
705 710 715 720

[0039]

Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala
725 730 735

Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg
740 745 750

Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn
 755 760 765

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
 770 775 780

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
785 790 795 800

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
805 810 815

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
 820 825 830

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
835 840 845

Ala Leu His Met Gln Ala Leu Pro Pro Arg
850 855

〈210〉 36

<211> 402

<212> PRT

<213> 人工序列

<220>

<223> 可诱导半胱天冬酶9 (iCasp9) 序列

<400> 36

Met	Leu	Glu	Gly	Val	Gln	Val	Glu	Thr	Ile	Ser	Pro	Gly	Asp	Gly	Arg
1				5				10				15			

Thr	Phe	Pro	Lys	Arg	Gly	Gln	Thr	Cys	Val	Val	His	Tyr	Thr	Gly	Met
							20		25			30			

Leu	Glu	Asp	Gly	Lys	Lys	Val	Asp	Ser	Ser	Arg	Asp	Arg	Asn	Lys	Pro
						35		40			45				

Phe	Lys	Phe	Met	Leu	Gly	Lys	Gln	Glu	Val	Ile	Arg	Gly	Trp	Glu	Glu
						50		55		60					

Gly	Val	Ala	Gln	Met	Ser	Val	Gly	Gln	Arg	Ala	Lys	Leu	Thr	Ile	Ser
65						70			75			80			

Pro	Asp	Tyr	Ala	Tyr	Gly	Ala	Thr	Gly	His	Pro	Gly	Ile	Ile	Pro	Pro
							85		90			95			

His	Ala	Thr	Leu	Val	Phe	Asp	Val	Glu	Leu	Leu	Lys	Leu	Glu	Ser	Gly
							100		105			110			

[0040] Gly Gly Ser Gly Val Asp Gly Phe Gly Asp Val Gly Ala Leu Glu Ser
115 120 125

Leu	Arg	Gly	Asn	Ala	Asp	Leu	Ala	Tyr	Ile	Leu	Ser	Met	Glu	Pro	Cys
130						135			140						

Gly	His	Cys	Leu	Ile	Ile	Asn	Asn	Val	Asn	Phe	Cys	Arg	Glu	Ser	Gly
145						150			155			160			

Leu	Arg	Thr	Arg	Thr	Gly	Ser	Asn	Ile	Asp	Cys	Glu	Lys	Leu	Arg	Arg
							165		170			175			

Arg	Phe	Ser	Ser	Leu	His	Phe	Met	Val	Glu	Val	Lys	Gly	Asp	Leu	Thr
							180		185			190			

Ala	Lys	Lys	Met	Val	Leu	Ala	Leu	Leu	Glu	Leu	Ala	Gln	Gln	Asp	His
						195		200			205				

Gly	Ala	Leu	Asp	Cys	Cys	Val	Val	Val	Ile	Leu	Ser	His	Gly	Cys	Gln
210						215			220						

Ala	Ser	His	Leu	Gln	Phe	Pro	Gly	Ala	Val	Tyr	Gly	Thr	Asp	Gly	Cys
225							230			235			240		

Pro	Val	Ser	Val	Glu	Lys	Ile	Val	Asn	Ile	Phe	Asn	Gly	Thr	Ser	Cys
							245		250			255			

Pro	Ser	Leu	Gly	Gly	Lys	Pro	Lys	Leu	Phe	Phe	Ile	Gln	Ala	Cys	Gly
							260		265			270			

Gly Glu Gln Lys Asp His Gly Phe Glu Val Ala Ser Thr Ser Pro Glu
275 280 285

Asp Glu Ser Pro Gly Ser Asn Pro Glu Pro Asp Ala Thr Pro Phe Gln
290 295 300

Glu Gly Leu Arg Thr Phe Asp Gln Leu Asp Ala Ile Ser Ser Leu Pro
305 310 315 320

Thr Pro Ser Asp Ile Phe Val Ser Tyr Ser Thr Phe Pro Gly Phe Val
325 330 335

Ser Trp Arg Asp Pro Lys Ser Gly Ser Trp Tyr Val Glu Thr Leu Asp
340 345 350

Asp Ile Phe Glu Gln Trp Ala His Ser Glu Asp Leu Gln Ser Leu Leu
355 360 365

Leu Arg Val Ala Asn Ala Val Ser Val Lys Gly Ile Tyr Lys Gln Met
370 375 380

Pro Gly Cys Phe Asn Phe Leu Arg Lys Lys Leu Phe Phe Lys Thr Ser
385 390 395 400

Ala Ser

[0041]

<210> 37

<211> 157

<212> PRT

<213> 人工序列

<220>

<223> 新的标志物/自杀基因RQR8序列

<400> 37

Met Gly Thr Ser Leu Leu Cys Trp Met Ala Leu Cys Leu Leu Gly Ala
1 5 10 15

Asp His Ala Asp Ala Cys Pro Tyr Ser Asn Pro Ser Leu Cys Ser Gly
20 25 30

Gly Gly Gly Ser Glu Leu Pro Thr Gln Gly Thr Phe Ser Asn Val Ser
35 40 45

Thr Asn Val Ser Pro Ala Lys Pro Thr Thr Thr Ala Cys Pro Tyr Ser
50 55 60

Asn Pro Ser Leu Cys Ser Gly Gly Ser Pro Ala Pro Arg Pro
65 70 75 80

Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
85 90 95

Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu
100 105 110

Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys

115 120 125

Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn His Arg
[0042] 130 135 140

Asn Arg Arg Arg Val Cys Lys Cys Pro Arg Pro Val Val
145 150 155

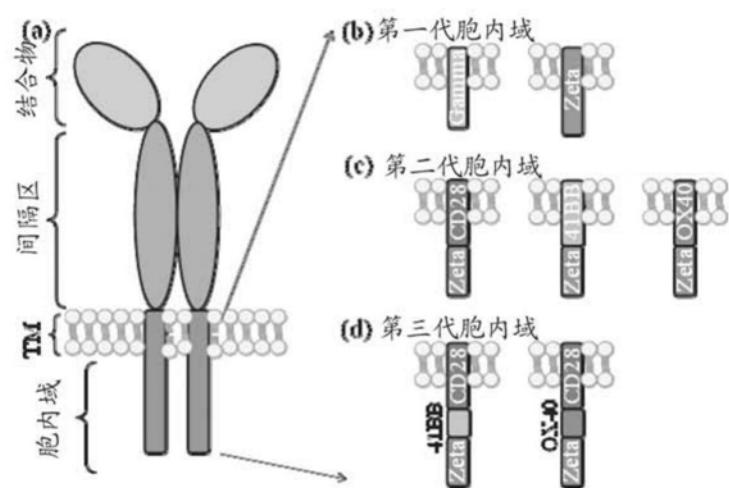


图1

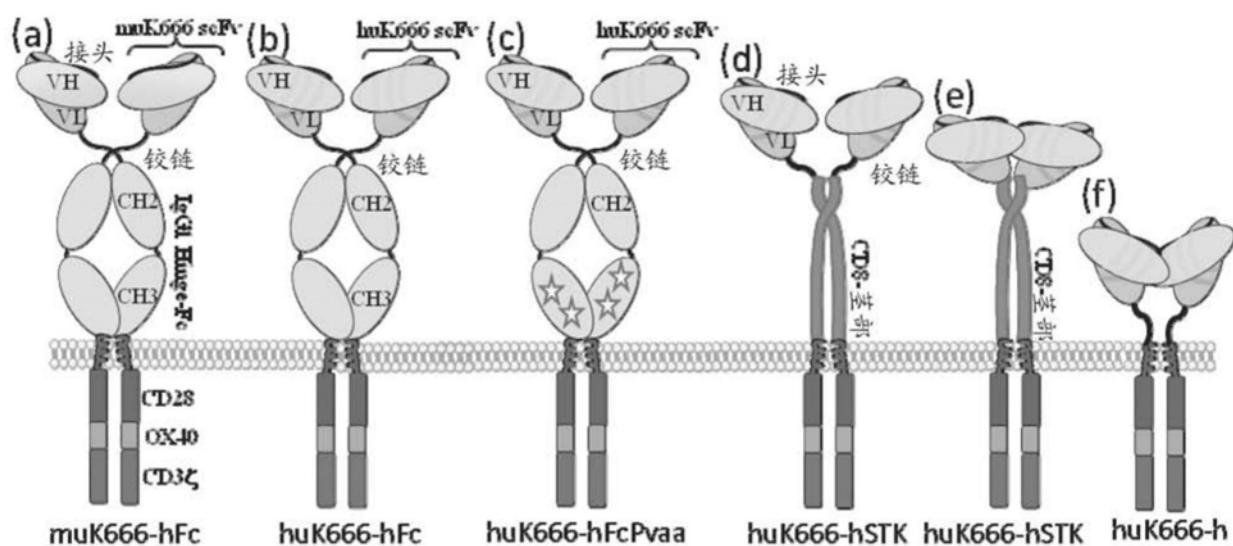


图2

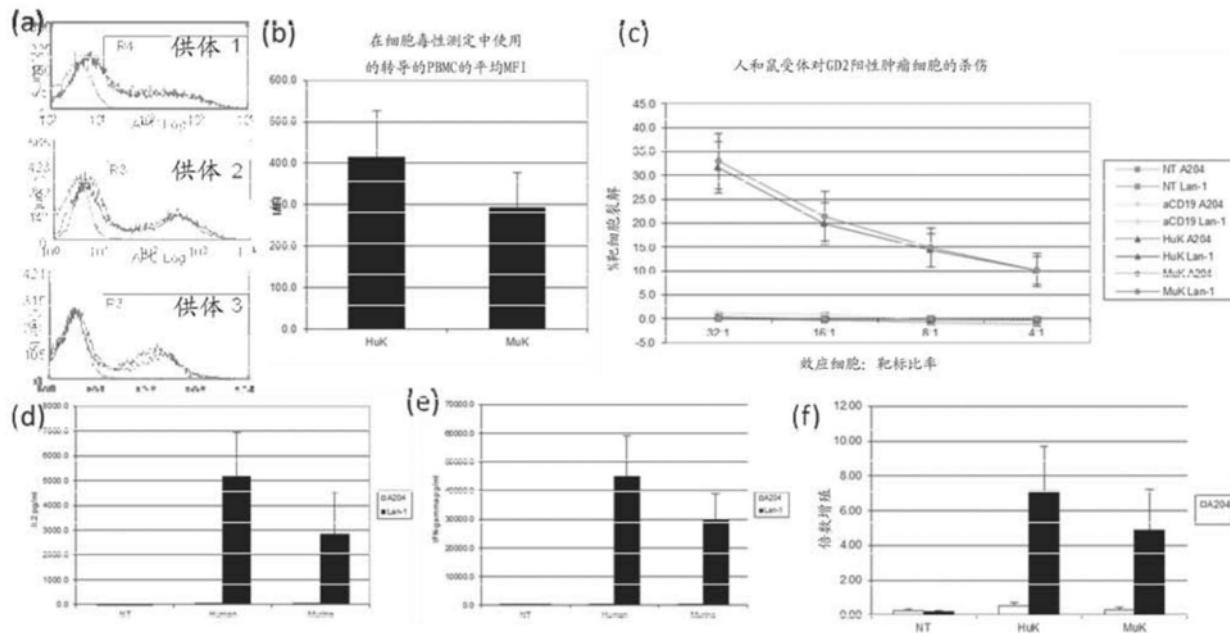


图3

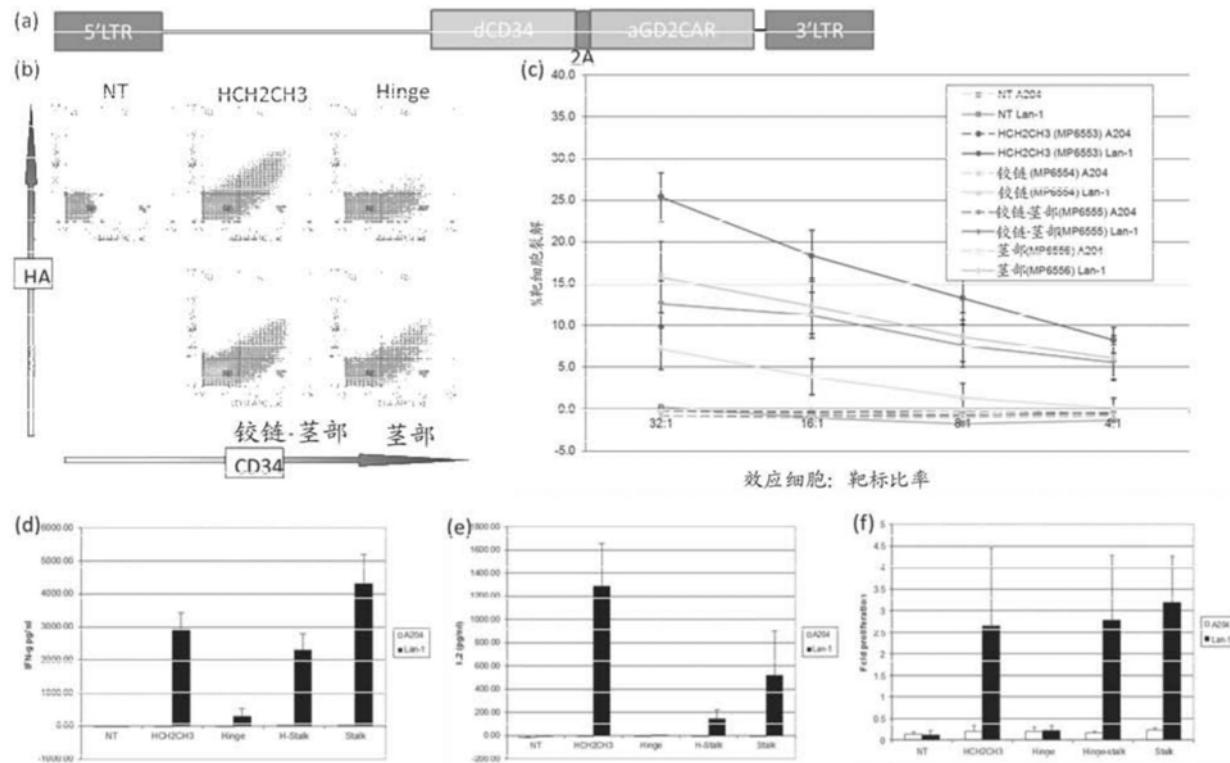


图4

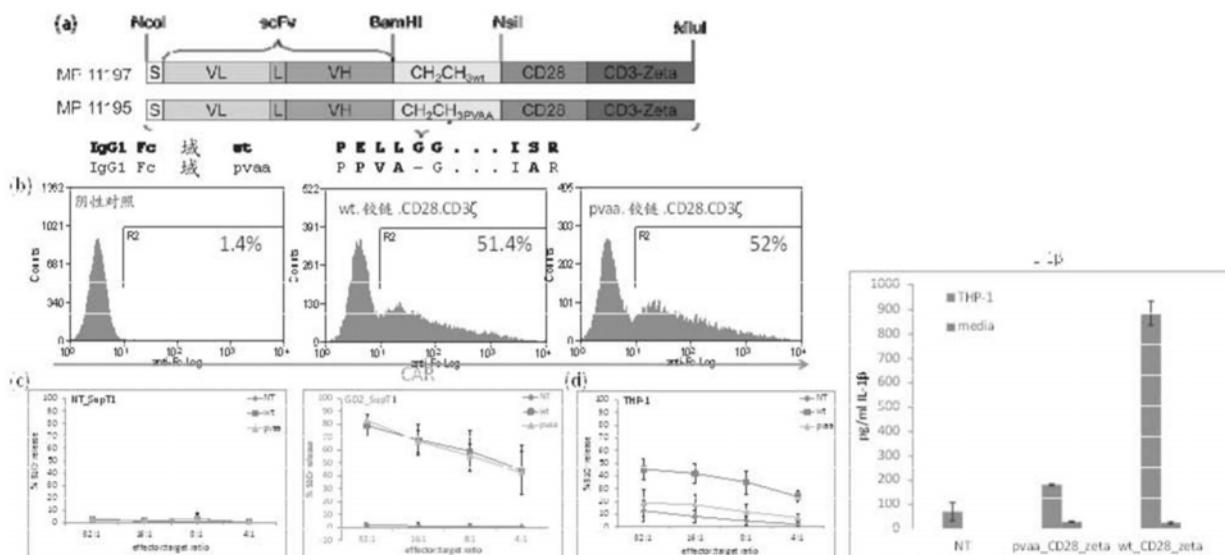


图5

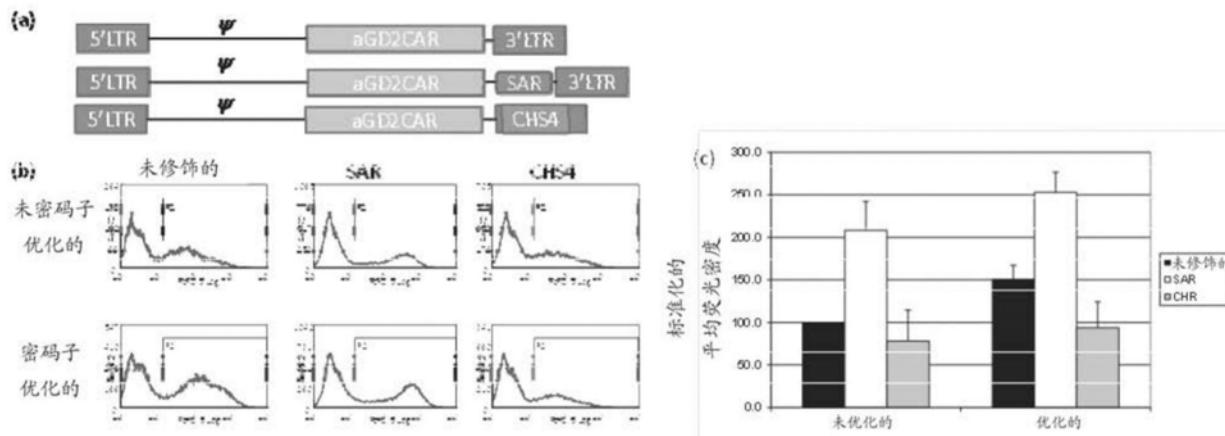


图6

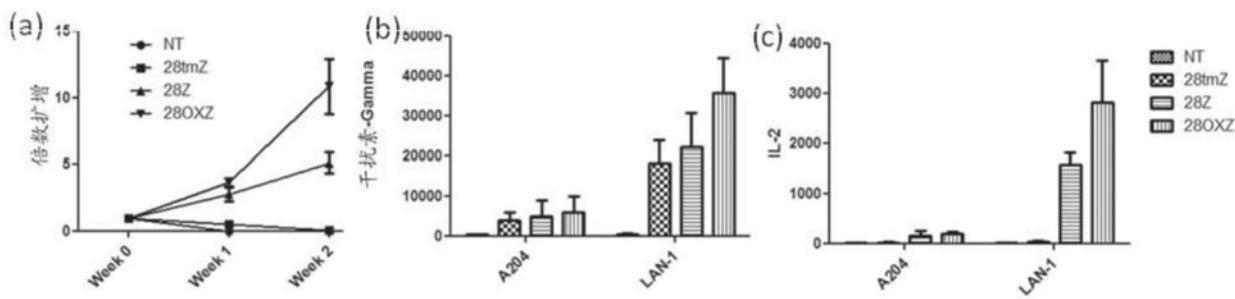


图7

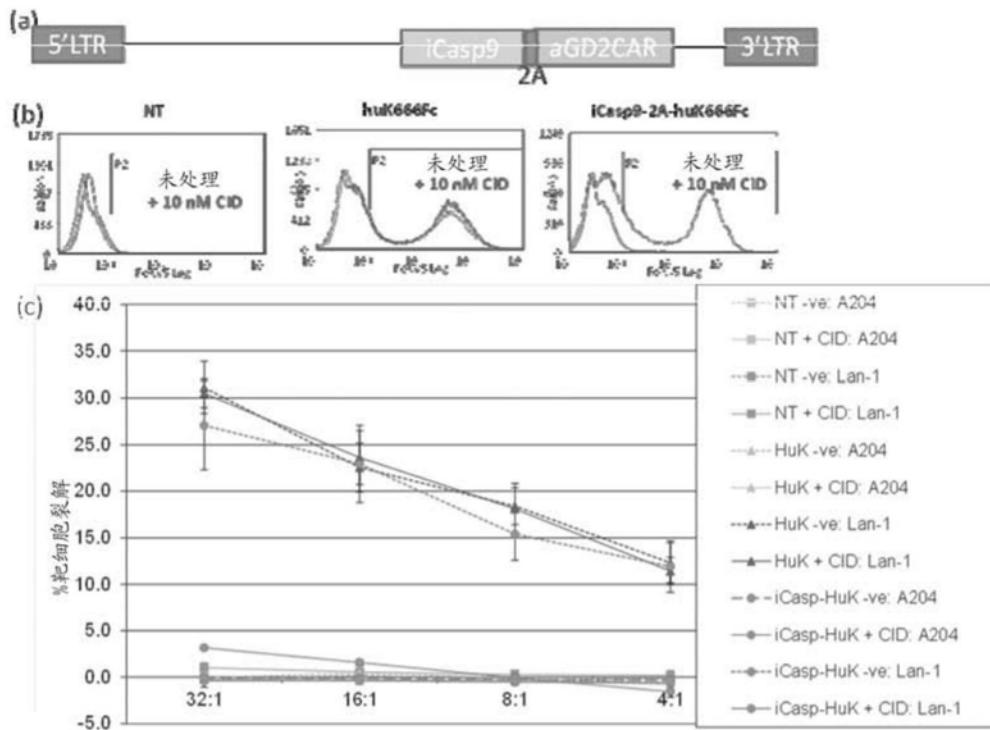


图8

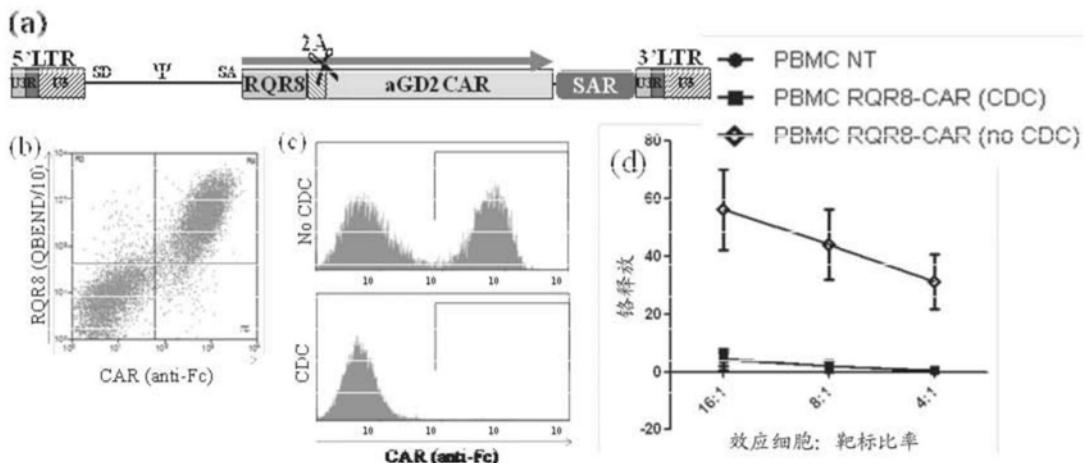


图9

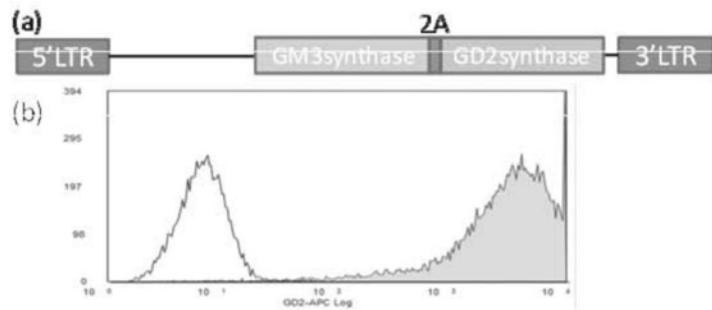


图10

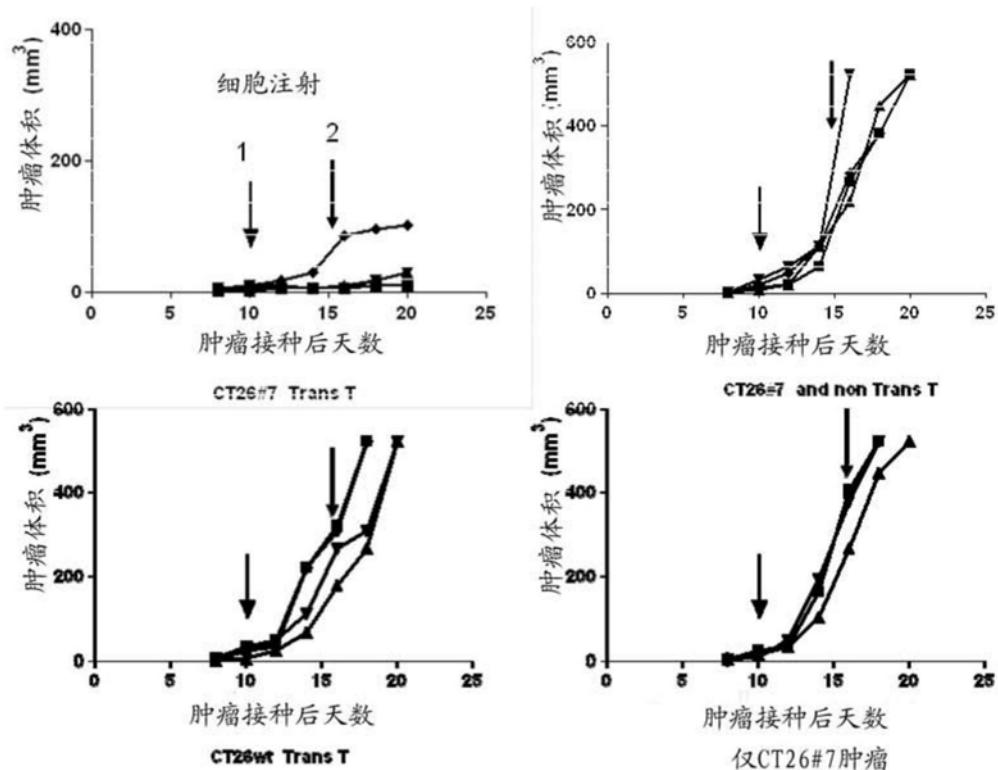


图11

A.

METDTLILIVVLLMVPGSTGQVOLKESGPVLVAPSQTLSTTCCTVSGFSLASVNIHWYRQPPGKGELEWLGVIWAGGS
THYNSALMERLSISKTNSKSQVFLQMNLSQTDDTAMYCYAKRSDDYEWFAWGQGTLLTVSAASGGGEGSGGGGGGGGG
GSENVLITQSPAIMSASPGEKVTMTCRASSVSSSYLHNYYQQKSGASEPKWVITYSTSNTLASGVPGRF3URGS3TSVEL
TISSVEAEDAATYYCOOYSGYIPITFGAGTKVEVKR **SDP**

FWVILVVUGGVIACKYSLLIVTVAFILIFWY-

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10. The following table shows the number of hours worked by each employee.

B.

METPTLLWVIIINVPGSTGQVQLQESGPGLVRPSQTLSTITCTVSGFSLASPYNIRHWRQPPGKGLRWLGVIWAGGS
TNYNSALMSRLTISKNSKNQVFLKMQSSLTAUTAVYYCAKKSDDYSWFAYWGQSTLTVTSSGGGGSGGGGSGGGGG
SENQMTQSFSELSAAGVGDRTMTCRASSSVSSSYLHNWYQKSGKAPKVWIYSTSMLA2GVPSERFSGB3E9GTDTLJ
ISSLOPEDFATYYCQOXSGLPITYMOGTRKVEIERSDP

FWVVLVVVGGVLACYSLLVTVAEIIIFWV

EXPLOITATION OF THE GROWTH OF PLANT DISEASES IN PESTICIDE RESISTANCE

10. The following table gives the number of hours of direct sunlight received by the sun at the equator during the year.

6

METDTILLWVLLLWVEGSTEGQVQLQESGFGLVKPFSQTLISITCTVSGFSLASYNIHIVVRQPFPGKGLEWLGVIWAGGS
TNYNSALMSRLTISKDN3KNQVFLKMSSLTAACTAVYYCAKRSDDYSWFAVW3QGTIVTVSSGGGSGGGGNGGGG
SENQMTQSPS3LSASVGDRVTMTCRASS9V3SSYLYHIVQOMSGKAFKVWIIYSTSNLASGPVPSFPGSG3CTDYITLT
LSS1QFEDFATYCCOXSSEYLTTEGOGTKVIEKRSDE

EWYLVVSYVACYSLLVTGELFIV

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19. The following table shows the number of hours worked by each of the 100 workers in the firm.

D

METDTLLEWVLLNVPGSTGQVOLQESGPGLVKPSQTLSTCTVSGFSIASYNIHWVRQPPGKLEWLGVIVAGGS
TWYNSALMSRLTISKINNSKNQVFLXKMSSLTAADTAVYYCAKRSDDYSWFAYWGQGTLVTVESGGGSGGGGGGG
SENQMTQEPSSLSASVGDRVTMTCRASSSVSSSYLHWWYQOKSGKAFKVWVIIYSTENLASGVPSRFSGSGSGGTDTYLT
T

DEPARTMENT OF THE NAVY - MARINE CORPS - AIR FORCE - COAST GUARD - NATIONAL GUARD

ANSWER The answer is 1000. The first two digits of the number are 10, so the number is 1000.

5

METDTLILWVILLMVGSTGQVQLQESGPGLVKPSQTLISITCTVSGFSLASYNIMHVRQPPGKGLEWLGVIWAGGS
TNYNSALMSPLTISKDNESKNQVFLKMSLTAADTAVYYCAKRSDDY3WFAYNGQGTFLTVSSGGGGSGGGCGGGGG
SENQWTQSPSSLGAAVGDRVTMTCRASSSVSSSYLHWYQOKSGKAPKVWIYSTSMLASGVPSRF3C9G3GUTDNTLT
ISSLQEDFDATYYCQJYSGYFIFTFGOGTKVEIKRSDP

FWVLVVGGVLACYSLIVTVAFIIFWV

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图 12

F.

METDTLLIIVVLLWVEGSTGQVQLQESGPGLVKPSQTLISITCTVSGFSLASYNIHWRQPPGKGLEWLGVVIWAGGS
 TNYNSALMGRLTISKDNISKNQVFLKMSSLTAAATAVYYCAKRSDDYSWFAYWGQGTIVTWSGGGGSGGGGGGGGG
 SENQMTQSPSSLASAVGDRVTMTCRASSSVSSSYLHWYQQKSGKAPKVWIYSTSMLASGVPSRFSGSGSGTDYTLT
 ISSLQPEDFATYYCQQYSGYPITFGQGTKEVIEKRS~~SDP~~

FWVLVVVGGVLACYSLV



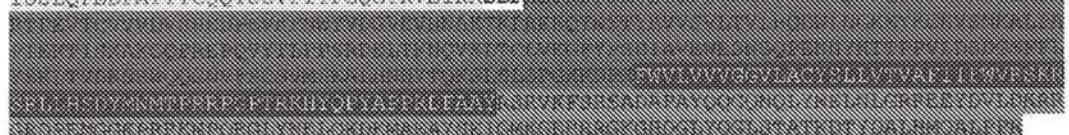
G.

METDTLLIIVVLLWVEGSTGQVQLQESGPGLVKPSQTLISITCTVSGFSLASYNIHWRQPPGKGLEWLGVVIWAGGS
 TNYNSALMGRLTISKDNISKNQVFLKMSSLTAAATAVYYCAKRSDDYSWFAYWGQGTIVTWSGGGGSGGGGGGGGG
 SENQMTQSPSSLASAVGDRVTMTCRASSSVSSSYLHWYQQKSGKAPKVWIYSTSMLASGVPSRFSGSGSGTDYTLT
 ISSLQPEDFATYYCQQYSGYPITFGQGTKEVIEKRS~~SDP~~



H.

METDTLLIIVVLLWVEGSTGQVQLQESGPGLVKPSQTLISITCTVSGFSLASYNIHWRQPPGKGLEWLGVVIWAGGS
 TNYNSALMGRLTISKDNISKNQVFLKMSSLTAAATAVYYCAKRSDDYSWFAYWGQGTIVTWSGGGGSGGGGGGGGG
 SENQMTQSPSSLASAVGDRVTMTCRASSSVSSSYLHWYQQKSGKAPKVWIYSTSMLASGVPSRFSGSGSGTDYTLT
 ISSLQPEDFATYYCQQYSGYPITFGQGTKEVIEKRS~~SDP~~



I.

METDTLLIIVVLLWVEGSTGQVQLQESGPGLVKPSQTLISITCTVSGFSLASYNIHWRQPPGKGLEWLGVVIWAGGS
 TNYNSALMGRLTISKDNISKNQVFLKMSSLTAAATAVYYCAKRSDDYSWFAYWGQGTIVTWSGGGGSGGGGGGGGG
 SENQMTQSPSSLASAVGDRVTMTCRASSSVSSSYLHWYQQKSGKAPKVWIYSTSMLASGVPSRFSGSGSGTDYTLT
 ISSLQPEDFATYYCQQYSGYPITFGQGTKEVIEKRS~~SDP~~

FWVLVVVGGVLACYSLV



J.

METDTLLIIVVLLWVEGSTGQVQLQESGPGLVKPSQTLISITCTVSGFSLAS
 YNIHWRQPPGKGLEWLGVVIWAGGSTNYNSALMGRLTISKDNISKNQVFLKMSSLTAAATAVYYCAKRSDDYSWFAY
 WGQGTIVTWSGGGGSGGGGGGGGGSENQMTQSPSSLASAVGDRVTMTCRASSSVSSSYLHWYQQKSGKAPKVWIY
 STSMLASGVPSRFSGSGSGTDYTLTISSLQPEDFATYYCQQYSGYPITFGQGTKEVIEKRS~~SDP~~

FWVLVV
VGGVLACYSLV

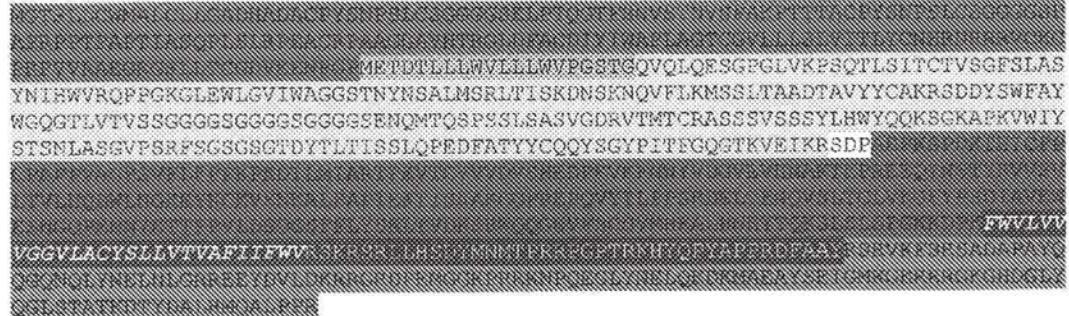


图12续

区域	描述
自杀基因	iCasp9或RQR8
FMD-2A	口蹄疫2A肽
信号	信号肽
scFv1	scFv (muKM666或huKM666)
SDP	接头和链断裂
间隔区	CD8alpha 茎部
CD28 TM	CD28 跨膜域
CD28 endo	CD28 胞内域
OX40 endo	OX40 胞内域
CD3Z endo	CD3 Zeta 胞内域

图12续

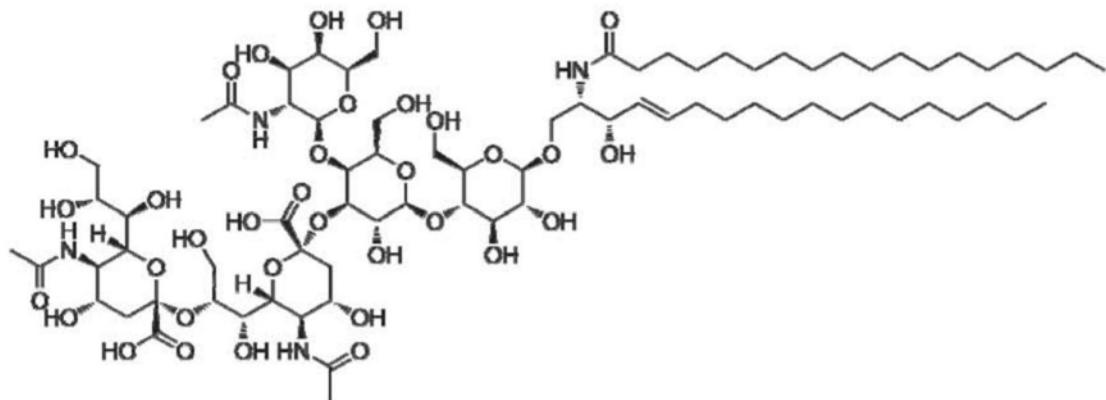


图13

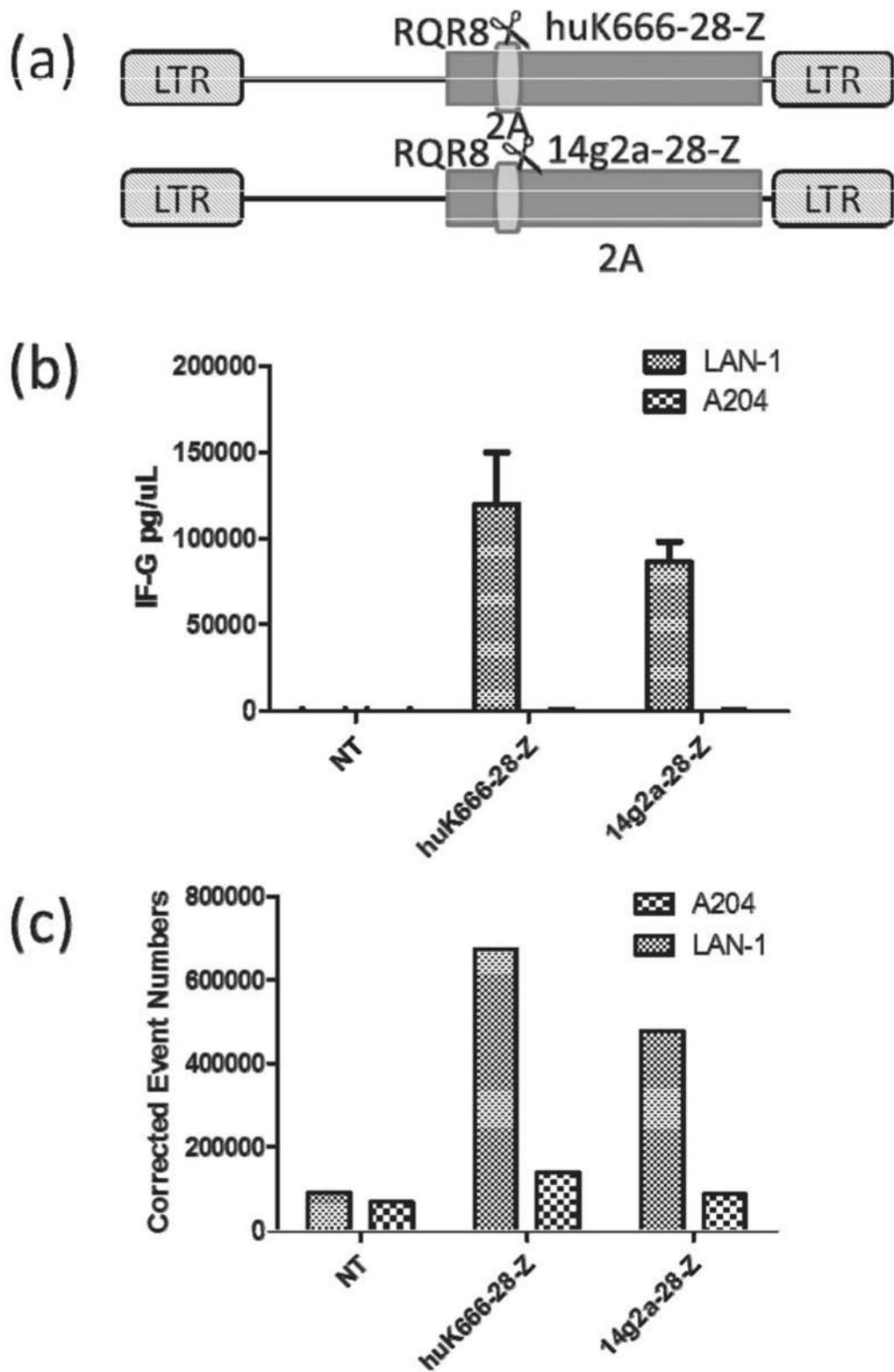


图14

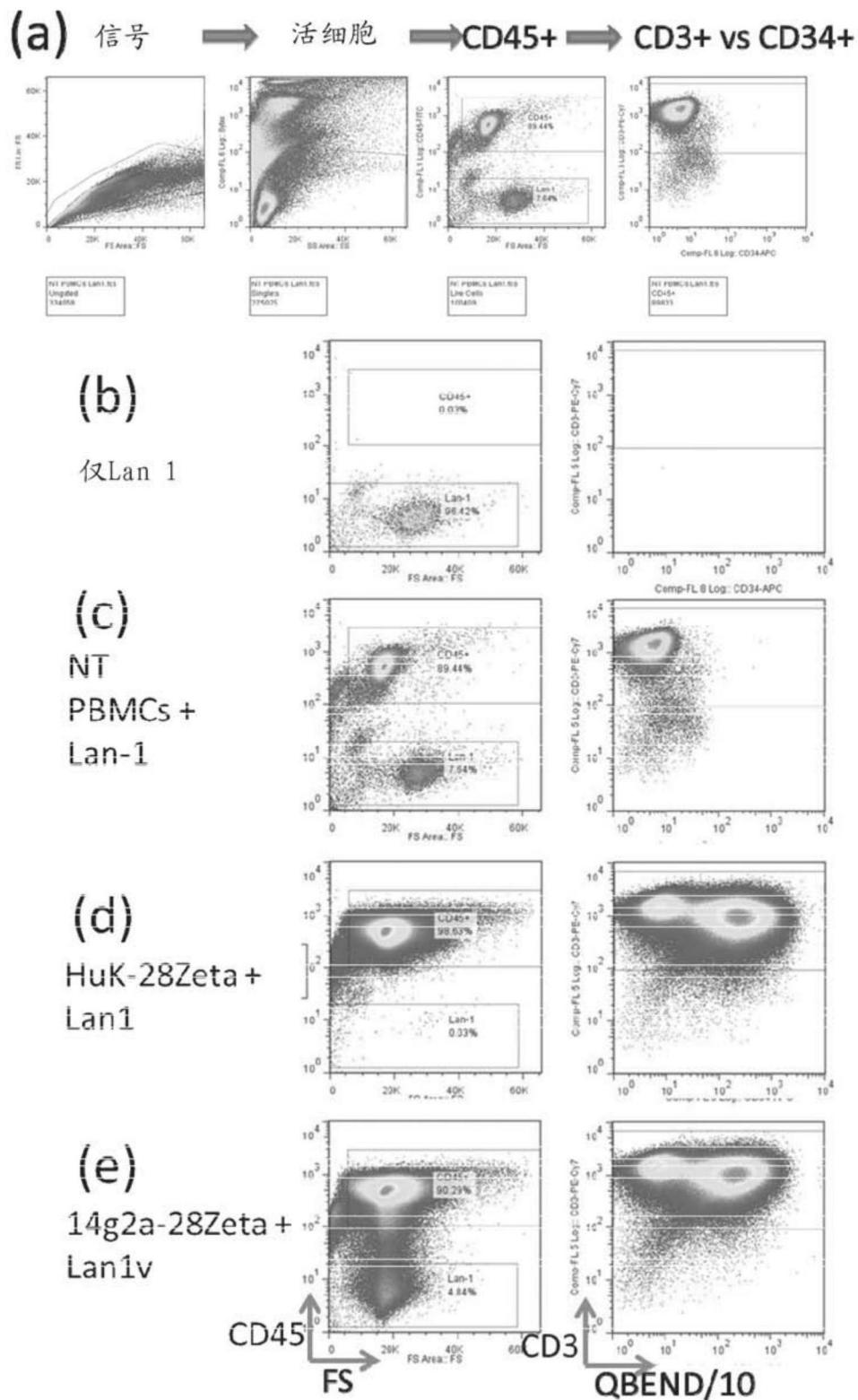


图15