

GenCLiP 2.0 使用手册

■ 用户注册



进入填写注册基本信息的界面：

点击“Login”进入注册用户登陆界面：

注册用户分析界面:

GenCLiP 2.0
Human Gene Function And Network Analysis

Lab of Bioinformatics
Cancer Institute
Southern Medical University
GuangZhou, China

wjh1987@gmail.com
Login Register Logout

Step1: Upload Gene List
Paste a list

Or Upload From a File

Step2: Select Identifier
Official_Gene_Symbol
Step3: Optional
Job name:

- Word Related Gene Search
- Genes Information
- Gene Cluster With Literature Profiles
- Literature Mining Gene Networks
- GO Analysis
- Pathway Analysis

Recent-Jobs

- 2012-04-26_immune
Genes:309 Papers:624
- 2012-04-25_Npc_down
Genes:281 Papers:262
- 2012-04-24_download
Genes:1578 Papers:2703
- 2012-04-24_NPC_324
Genes:292 Papers:861
- 2012-04-23_Test
Genes:292 Papers:861
- 2012-04-23_8967_Test
Genes:292 Papers:861
- 2012-04-23_12-20-03_5607
Genes:292 Papers:861
- 2012-04-23_12-06-42_7098
Genes:292 Papers:861
- 2012-04-23_05-46-19_2466
Genes:292 Papers:861

注册用户的批量基因
分析结果可保存两周,
用户可回顾或继续分析

■ 单个基因信息检索

1、输入基因，如"PTHLH"

2、选择基因符号的类型

3、点击"Submit"提交

模块可逐个点开查看

逐个模块点击弹开：

点击此按钮，显示基因关键词注释

点击数字进入关键词与基因共同出现的摘要

Keyword : PARATHYROID

Genes: 1 Papers: 2447

Num	Gene	Hit	Total
1	PTHLH	2447	2852

Gene: PTHLH

Alias : parathyroid hormone-like related protein; PTHrP; BDE2; parathyroid hormone-like hormone; PLP; PTHLH; PTHR; HHM; parathyroid hormone-related protein; osteostatin; PTH-rP; PTH-related protein

Summary : The protein encoded by this gene is a member of the parathyroid hormone family. This hormone regulates endochondral bone development and epithelial-mesenchymal interactions during the formation of the mammary glands and teeth. This hormone is involved in lactation possibly by regulating the mobilization and transfer of calcium to the milk. The receptor of this hormone, PTHR1, is responsible for most cases of humoral hypercalcemia of malignancy. Four alternatively spliced transcript variants encoding two distinct isoforms have been observed. There is also evidence for alternative translation initiation from non-AUG (CUG and GUG) start sites, in-frame and downstream of the initiator AUG codon, to give rise to nuclear forms of this hormone. [provided by RefSeq]

<<First <Prev Page 1 of 245 Next > Last>>

1. PMID: 20951345
Dev Cell. 2010 Oct 19;19(4):533-46.
Zfp521 is a target gene and key effector of parathyroid hormone-related peptide signaling in growth plate chondrocytes.
Correa D, Hesse E, Seriwatanachai D, Kiviranta R, Saito H, Yamana K, Neff L, Atfi A, Coillard L, Sitara D, Maeda Y, Warming S, Jenkins NA, Copeland NG, Horne WC, Lanske B, Baron R.
Department of Oral Medicine, Infection and Immunity, Harvard School of Dental Medicine, Boston, MA 02115, USA.
In the growth plate, the interplay between parathyroid hormone-related peptide (PTHrP) and Indian hedgehog (Ihh) signaling tightly regulates chondrocyte proliferation and differentiation during longitudinal bone growth. We found that PTHrP increases the expression of Zfp521, a zinc finger transcriptional coregulator, in prehypertrophic chondrocytes. Mice with chondrocyte-targeted deletion of Zfp521 resembled PTHrP(-/-) and chondrocyte-specific PTHR1(-/-) mice, with decreased chondrocyte proliferation, early hypertrophic transition, and reduced growth plate thickness. Deleting Zfp521 increased expression of Runx2 and Runx2 target genes, and decreased Cyclin D1 and Bcl-2 expression while increasing Caspase-3 activation and apoptosis. Zfp521 associated with Runx2 in chondrocytes, antagonizing its activity via an HDAC4-dependent mechanism. PTHrP failed to upregulate Cyclin D1 and to antagonize Runx2, Ihh, and collagen X expression when Zfp521 was absent. Thus, Zfp521 is an important PTHrP target gene that regulates growth plate chondrocyte proliferation and differentiation.
Journal Article. Research Support, N.I.H., Extramural. Research Support, Non-U.S. Gov't.

2. PMID: 20683010
Anticancer Res. 2010 Jul;30(7):2755-67.
PTHrP regulates angiogenesis and bone resorption via VEGF expression.

Genes information

Entered	Human Symbol	Papers
PTHLH	PTHLH	2852

Gene Cluster With Literature Profiles

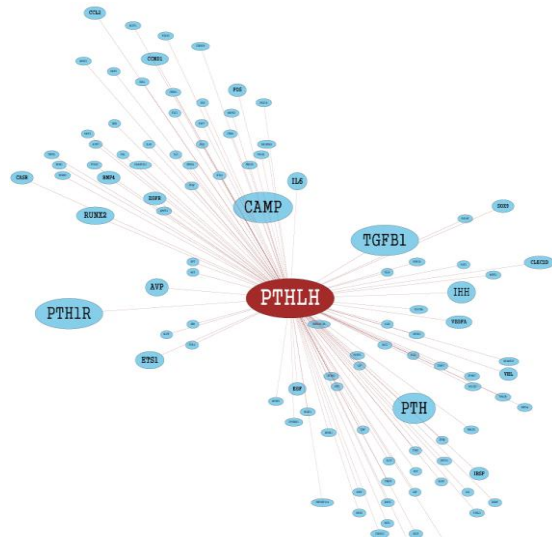
点击此按钮，显示相互作用的基因

Literature Mining Gene Networks

Num	Gene	Record
1	PTH1R	40
2	PTH	33
3	CAMP	19
4	TGFB1	15
5	IHH	8
6	IL6	5
7	ETS1	5
8	CASR	5
9	EGF	4
10	VEGFA	4
11	IBSP	3
12	EGFR	3
13	CCND1	2

点击数字查看确定两个基因有相互作用关系的文献

Generate Graph 点击生成基因网络图



点击 PTH1R 的记录数“40”，链接基因对的文献出处：

Gene: **PTHLH**
 Alias : parathyroid hormone-like related protein; PTHRP; BDE2; parathyroid hormone-like hormone; PLP; PTHLP; PTHR; HHM; parathyroid hormone-related protein; osteostatin; PTH-rP; PTH-related protein

Gene: **PTH1R**
 Alias : parathyroid hormone/parathyroid hormone-related peptide receptor; parathyroid hormone/parathyroid hormone-related protein receptor; parathyroid hormone receptor 1; PTH/PTHrP type 1 receptor; PTH1 receptor; PTH1R; seven transmembrane helix receptor; PTHR1; PTH/PTHrP receptor; parathyroid hormone 1 receptor; PTHR; PFE

31. PMID: 10912527
 Pediatr Nephrol. 2000 Jul;14(7):606-11.
Role of parathyroid hormone-related peptide and Indian hedgehog in skeletal development.
 J??ppner H.
 Department of Pediatrics, Massachusetts General Hospital and Harvard Medical School, Boston 02114, USA.

Parathyroid hormone-related peptide (PTHrP), which frequently causes the humoral hypercalcemia of malignancy syndrome, is an autocrine/paracrine regulator of chondrocyte proliferation and differentiation that acts through the PTH/PTHrP receptor (PTH1R). PTHrP is generated in response to Indian hedgehog (Ihh), which mediates its actions through the membrane receptor patched, but interacts also with hedgehog-interacting protein (Hip). Mice lacking PTHrP show accelerated chondrocyte differentiation, and thus premature ossification of those bones that are formed through an endochondral process, and similar but more-severe abnormalities are observed in PTH1R-ablated animals. The mirror image of these skeletal findings, i.e., a severe delay in chondrocyte differentiation and endochondral ossification, is observed in transgenic mice that overexpress PTHrP under the control of the alpha1(I) procollagen promoter. Severe abnormalities in chondrocyte proliferation and differentiation are also observed in two genetic disorders in humans that are most likely caused by mutations in the PTH1R. Heterozygous PTH1R mutations that lead to constitutively active were identified in Jansen metaphyseal chondrodysplasia, and homozygous or compound heterozygous mutations that lead to less-active or completely inactive receptors were identified in patients with Blomstrand lethal chondrodysplasia. Based on the growth plate abnormalities observed in these human disorders and in mice with abnormal expression of either PTHrP or the PTH1R, it appears plausible that impaired expression of PTHrP and/or its receptor contributes to the growth abnormalities in children with end-stage renal disease. In fact, mild-to-moderate renal failure leads in animals to a reduction in PTH1R expression in growth plates and impaired growth, but it remains uncertain whether this contributes to altered chondrocyte growth and differentiation.

Journal Article. Review.

32. PMID: 10875241
 Endocrinology. 2000 Jul;141(7):2410-21.
Dissection of differentially regulated (G+C)-rich promoters of the human parathyroid hormone (PTH)/PTH-related peptide receptor gene.
 Minagawa M, Kwan MY, Bettoun JD, Mansour FW, Dassa J, Hendy GN, Goltzman D, White JH.
 Department of Medicine, McGill University, Montr??al, Qu??bec, Canada.

The PTH/PTH-related peptide (PTHrP) receptor (PTHR) is required for normal skeletal development, and a wide array of physiological responses mediated by PTH and PTHrP. We have previously identified three promoters, P1-P3, which control human PTHR gene transcription. P2 and P3 are (G+C)-rich, function in a number of tissues, lie within the same CpG island, and display many hallmarks of housekeeping promoters. However, they are differentially regulated during development as P2, but not P3, functions in fetal tissues. Here, we have used both stably and transiently transfected

GO Analysis

点击此按钮，显示基因的GO注释

点击注释可链接到GO官网，查看注释的信息

GO Term
surfactant homeostasis
endochondral ossification
negative regulation of chondrocyte differentiation
positive regulation of cAMP biosynthetic process
activation of adenylate cyclase activity by G-protein signaling pathway
positive regulation of cAMP metabolic process
regulation of chondrocyte differentiation
activation of adenylate cyclase activity
nipple morphogenesis
positive regulation of cyclic nucleotide biosynthetic process
osteoblast development
negative regulation of sequence-specific DNA binding transcription factor activity
positive regulation of adenylate cyclase activity by G-protein signaling pathway
peptide hormone receptor binding
positive regulation of adenylate cyclase activity

pathway Analysis

点击此按钮，显示基因参与的Pathway

Pathway
REACTOME_CLASS_B2_SECRETIN_FAMILY_RECEPTORS
REACTOME_DOWNSTREAM_EVENTS_IN_GPCR_SIGNALING
REACTOME_G_ALPHA_S_SIGNALLING_EVENTS
REACTOME_GPCR_LIGAND_BINDING

■ 批量基因的分析流程

以网页上提供的样本基因，324 个鼻咽癌表达上调基因为例。

无论是在输入框输入还是以文本文件（txt 格式）上传一组分析基因，格式都为一个基因一行。

1、输入一组分析基因，点击“Sample”，以样本基因为例

2、选择基因符号的类型

3、将分析任务命名为：Presentation

4、点击“Submit”提交任务

提交后显示基因信息，其它按钮为灰色，表示尚未分析

■ 基因信息

2012-05-10_Presentation

Word Related Gene Search

Genes information

输入的基因符号 基因的官方名称

retrieve the Gene List(311/324)				Genes Ignored(13/324)		
Num	Entered	Human Symbol	Papers	Num	Entered	Status
1	ACER3	ACER3	5	1	LOC100130935	Not Found
2	ADH5P4	ADH5P4	1	2	LOC732360	Not Found
3	ANGPT2	ANGPT2	1029	3	FLJ45482	Not Found
4	ARNT2	ARNT2	61	4	LOC642132	Not Found
5	ASCC3	ASCC3	39	5	C20orf199	Not Found
6	ATAD2	ATAD2	20	6	LOC100133317	Not Found
7	ATP11C	ATP11C	2	7	LOC644101	Not Found
8	Akt3	AKT3	177	8	LOC728715	Not Found
9	Anln	ANLN	158	9	LOC100131735	Not Found
10	Apoc1	APOC1	186	10	LOC731751	Not Found
11	Arhgap8	ARHGAP8	12	11	LOC100129585	Not Found
12	B4GALT6	B4GALT6	6	12	LOC100129240	Not Found

文献数

点击链接到 NCBI

The average number of paper per gene(exclude no paper's): 861
Attention: There are 20 genes with multi-symbol (red). Please select a correct one.

被剔除的基因及原因

Modify

如有红字“Attention”提示有基因符号对应了多个基因，可进行修正：

Genes Information

retrieve the Gene List(311/324)				Genes Ignored(13/324)		
Num	Entered	Human Symbol	Papers	Num	Entered	Status
291	ankrd29	ANKRD29	0	1	LOC100130935	Not Found
292	TTF2	TTF2		2	LOC723360	Not Found
293	RASSF4	TTF2 FOXE1		3	LOC43482	Not Found
294	GL5	GLS	1350	4	LOC642132	Not Found
295	Fas	FAS	1239	5	C20orf199	Not Found
296	CSAG2	CSAG2	13	6	LOC100133317	Not Found
297	ADH5	ADH5	372	7	LOC644101	Not Found
298	FGF2	FGF2	1003	8	LOC728715	Not Found
299	dtl	DTL	39	9	LOC100131735	Not Found
300	Dleu2	DLEU2	69	10	LOC731751	Not Found
				11	LOC100129585	Not Found
				12	LOC100129240	Not Found
				13	LOC653884	Not Found

The average number of paper per gene(exclude no paper's): 861
 Attention: There are 20 genes with multi-symbol (red). Please select a correct one.

1、从下拉菜单中选择需要的基因

2、选择完需要修正的基因后点击“Modify”提交修改

■ 基因功能注释和聚类

点击“Gene Cluster With Literature Profiles”按钮，短暂的等待后弹出聚类结果。

2012-05-10_Presentation

- Word Related Gene Search
- Genes Information
- Gene Cluster With Literature Profiles**
- Literature Mining G
- GO Analysis
- Pathway Analysis

点击灰色按钮，分析并加载结果

Loading

加载完后弹出基因关键词注释结果，

Gene Cluster With Literature Profiles

<input checked="" type="checkbox"/>	Del	Keyword	Hit	Total	P-Value	Q-Value
<input checked="" type="checkbox"/>		cluster1				
<input checked="" type="checkbox"/>	<input type="checkbox"/>	CELL PROLIFERATION	142	4196	3.487e-26	6.062e-25
<input checked="" type="checkbox"/>	<input type="checkbox"/>	GROWTH FACTOR	134	5299	8.956e-11	5.47e-10
<input checked="" type="checkbox"/>	<input type="checkbox"/>	POLYMERASE CHAIN REACTION	132	5899	1.345e-06	3.495e-06
<input checked="" type="checkbox"/>	<input type="checkbox"/>	SIGNAL TRANSDUCTION	86	3563	1.178e-05	2.376e-05
<input checked="" type="checkbox"/>	<input type="checkbox"/>	CELL SURFACE	77	3695	0.0072	0.0088
<input checked="" type="checkbox"/>		cluster2				
<input checked="" type="checkbox"/>	<input type="checkbox"/>	PROTEIN KINASE	106	4725	3.037e-05	5.536e-05
<input checked="" type="checkbox"/>	<input type="checkbox"/>	CELL GROWTH	89	3097	3.664e-10	1.972e-09
<input checked="" type="checkbox"/>	<input type="checkbox"/>	CELL DEATH	86	2942	2.755e-10	1.519e-09
<input checked="" type="checkbox"/>		cluster3				
<input checked="" type="checkbox"/>	<input type="checkbox"/>	S PHASE	66	1026	2.559e-37	1.157e-35
<input checked="" type="checkbox"/>	<input type="checkbox"/>	KINASE ACTIVITY	49	1576	4.546e-07	1.269e-06
<input checked="" type="checkbox"/>	<input type="checkbox"/>	M PHASE	42	418	1.896e-44	1.428e-42

Add:

Add keyword(s): (Keywords separated by comma)

Assistant Term(optional): (Terms separated by comma)

Heat Map Type:

添加新的词进行注释，可同时输入多个词，以逗号隔开：

Add:

Add keyword(s): (Keywords separated by comma)

Assistant Term(optional): (Terms separated by comma)

Heat Map Type:

1、输入添加的词

2、点击"Done"，搜索、重新聚类

重新搜索、返回聚类结果：

Gene Cluster With Literature Profiles

<input checked="" type="checkbox"/>	Del	Keyword	Hit	Total	P-Value	Q-Value
<input checked="" type="checkbox"/>		nocluster				
<input checked="" type="checkbox"/>	<input type="checkbox"/>	CELL DIVISION	68	976	4.014e-43	2.057e-41
<input checked="" type="checkbox"/>	<input type="checkbox"/>	CELL CYCLE	142	4109	3.094e-27	5.286e-26
<input checked="" type="checkbox"/>	<input type="checkbox"/>	SISTER CHROMATID COHESION	11	82	4.659e-16	5.306e-15
<input checked="" type="checkbox"/>	<input type="checkbox"/>	RNA INTERFERENCE	65	1631	6.904e-16	7.077e-15
<input checked="" type="checkbox"/>	<input type="checkbox"/>	CENTROMERE	10	79	1.214e-13	9.57e-13
<input checked="" type="checkbox"/>	<input type="checkbox"/>	GENE EXPRESSION	216	9667	2.831e-13	2.001e-12
<input checked="" type="checkbox"/>	<input type="checkbox"/>	ELECTROPHORETIC MOBILITY SHIFT	32	741	1.538e-09	6.707e-09
<input checked="" type="checkbox"/>	<input type="checkbox"/>	DNA BINDING	75	2644	3.625e-08	1.161e-07
<input checked="" type="checkbox"/>	<input type="checkbox"/>	HELICASE	11	144	4.312e-08	1.339e-07
<input checked="" type="checkbox"/>	<input type="checkbox"/>	Nasopharyngeal Carcinoma	10	127	1.085e-07	3.176e-07
<input checked="" type="checkbox"/>	<input type="checkbox"/>	BREAST CANCER CELL	41	1245	7.295e-07	1.759e-06
<input checked="" type="checkbox"/>	<input type="checkbox"/>	PROTEIN COMPLEX	38	1148	1.665e-06	3.793e-06
<input checked="" type="checkbox"/>	<input type="checkbox"/>	MICROTUBULE ASSOCIATED PROTEIN	14	279	1.315e-05	2.386e-05

添加新的词并且需要辅助词进行注释：

Add:

Add keyword(s): (Keywords separated by comma)

Assistant Term(optional): (Terms separated by comma)

Heat Map Type:

1、输入要添加的词

2、输入辅助词

3、点击"Done"，搜索，重新聚类

重新搜索、返回聚类结果：

<input checked="" type="checkbox"/>	Del	Keyword	Hit	Total	P-Value	Q-Value
<input checked="" type="checkbox"/>	<input type="checkbox"/>	TUMOUR NECROSIS FACTOR	20	525	3.975e-05	6.429e-05
<input checked="" type="checkbox"/>	<input type="checkbox"/>	TH1(T Cell)	20	339	1.713e-10	8.647e-10
<input checked="" type="checkbox"/>	<input type="checkbox"/>	INDUCTION OF APOPTOSIS	20	481	5.46e-06	1.056e-05
<input checked="" type="checkbox"/>	<input type="checkbox"/>	EPSTEIN BARR VIRUS	19	479	2.696e-05	4.5e-05
<input checked="" type="checkbox"/>	<input type="checkbox"/>	PROTEIN BINDING	17	536	0.0031	0.0036
<input checked="" type="checkbox"/>	<input type="checkbox"/>	TH2(T Cell)	17	273	3.398e-09	1.353e-08
<input checked="" type="checkbox"/>	<input type="checkbox"/>	C REACTIVE PROTEIN	17	366	2.553e-06	5.231e-06
<input checked="" type="checkbox"/>	<input type="checkbox"/>	TYROSINE KINASE INHIBITOR	16	355	9.778e-06	1.823e-05

去除不需要的关键词注释：

<input checked="" type="checkbox"/>	Del	Keyword	Hit	Total	P-Value	Q-Value
<input checked="" type="checkbox"/>	<input type="checkbox"/>	cluster1				
<input checked="" type="checkbox"/>	<input type="checkbox"/>	CELL PROLIFERATION	142	4196	5.941e-26	9.46e-25
<input checked="" type="checkbox"/>	<input type="checkbox"/>	GROWTH FACTOR	134	5299	1.235e-10	6.907e-10
<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	POLYMERASE CHAIN REACTION	132	5899	1.718e-06	3.782e-06
<input checked="" type="checkbox"/>	<input type="checkbox"/>	SIGNAL TRANSDUCTION	86	3563	1.391e-05	2.482e-05
<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	CELL SURFACE	77	3695	0.008	0.0088
<input checked="" type="checkbox"/>	<input type="checkbox"/>	cluster2				
<input checked="" type="checkbox"/>	<input type="checkbox"/>	PROTEIN KINASE	106	4725	3.646e-05	5.943e-05
<input checked="" type="checkbox"/>	<input type="checkbox"/>	CELL GROWTH	89	3097	4.649e-10	2.187e-09
<input checked="" type="checkbox"/>	<input type="checkbox"/>	CELL DEATH	86	2942	3.485e-10	1.718e-09
<input checked="" type="checkbox"/>	<input type="checkbox"/>	cluster3				
<input checked="" type="checkbox"/>	<input type="checkbox"/>	S PHASE	66	1026	4.056e-37	1.679e-35
<input checked="" type="checkbox"/>	<input type="checkbox"/>	KINASE ACTIVITY	49	1576	5.224e-07	1.287e-06
<input checked="" type="checkbox"/>	<input type="checkbox"/>	M PHASE	42	418	2.996e-44	2.067e-42

Add:

Add keyword(s): (Keywords separated by comma)

Assistant Term(optional): (Terms separated by comma)

Heat Map Type:

1、选择要删除的注释

2、点击"Done"，去除所选注释并重新聚类

去除了所选注释，聚类结果随之发生变化

<input checked="" type="checkbox"/>	Del	Keyword	Hit	Total	P-Value	Q-Value
<input checked="" type="checkbox"/>		cluster1				
<input checked="" type="checkbox"/>	<input type="checkbox"/>	CELL PROLIFERATION	142	4196	5.941e-26	9.368e-25
<input checked="" type="checkbox"/>	<input type="checkbox"/>	GROWTH FACTOR	134	5299	1.235e-10	6.84e-10
<input checked="" type="checkbox"/>	<input type="checkbox"/>	PROTEIN KINASE	106	4725	3.646e-05	5.932e-05
<input checked="" type="checkbox"/>	<input type="checkbox"/>	CELL GROWTH	89	3097	4.649e-10	2.166e-09
<input checked="" type="checkbox"/>	<input type="checkbox"/>	SIGNAL TRANSDUCTION	86	3563	1.391e-05	2.479e-05
<input checked="" type="checkbox"/>		cluster2				
<input checked="" type="checkbox"/>	<input type="checkbox"/>	S PHASE	66	1026	4.056e-37	1.663e-35
<input checked="" type="checkbox"/>	<input type="checkbox"/>	KINASE ACTIVITY	49	1576	5.224e-07	1.275e-06
<input checked="" type="checkbox"/>	<input type="checkbox"/>	M PHASE	42	418	2.996e-44	2.047e-42
<input checked="" type="checkbox"/>	<input type="checkbox"/>	CYCLIN DEPENDENT KINASE	40	695	4.466e-19	5.385e-18
<input checked="" type="checkbox"/>	<input type="checkbox"/>	CELL CYCLE ARREST	40	786	1.332e-15	1.3e-14
<input checked="" type="checkbox"/>		cluster3				
<input checked="" type="checkbox"/>	<input type="checkbox"/>	EXTRACELLULAR MATRIX	62	1743	6.293e-12	4.031e-11

选择关键词注释产生聚类分析热图：

Gene Cluster With Literature Profiles

<input checked="" type="checkbox"/>	Del	Keyword	Hit	Total	P-Value	Q-Value
<input type="checkbox"/>	<input type="checkbox"/>	T CELL DIFFERENTIATION	10	144	1.511e-06	3.403e-06
<input checked="" type="checkbox"/>		cluster5				
<input checked="" type="checkbox"/>	<input type="checkbox"/>	DNA REPLICATION	53	822	6.448e-30	1.322e-28
<input checked="" type="checkbox"/>	<input type="checkbox"/>	DNA REPAIR	41	845	1.017e-14	9.066e-14
<input checked="" type="checkbox"/>	<input type="checkbox"/>	DOUBLE STRAND BREAK	24	370	3.285e-14	2.694e-13
<input checked="" type="checkbox"/>	<input type="checkbox"/>	REPLICATION FORK	23	177	1.865e-32	5.463e-31
<input checked="" type="checkbox"/>	<input type="checkbox"/>	DNA DAMAGE RESPONSE	18	297	2.535e-09	1.019e-08
<input checked="" type="checkbox"/>	<input type="checkbox"/>	DNA DAMAGE CHECKPOINT	16	137	7.979e-20	1.09e-18
<input checked="" type="checkbox"/>	<input type="checkbox"/>	CELL CYCLE CHECKPOINT	15	175	1.264e-12	8.356e-12
<input checked="" type="checkbox"/>	<input type="checkbox"/>	MISMATCH REPAIR	12	160	1.421e-08	4.777e-08
<input checked="" type="checkbox"/>	<input type="checkbox"/>	DNA HELICASE	10	111	4.27e-09	1.621e-08
<input type="checkbox"/>		cluster6				
<input type="checkbox"/>	<input type="checkbox"/>	CENTRAL NERVOUS SYSTEM	49	2374	0.0507	0.0507
<input type="checkbox"/>	<input type="checkbox"/>	SQUAMOUS CELL CARCINOMA	44	1063	9.023e-12	5.605e-11

Add: 1、选择产生热图的注释

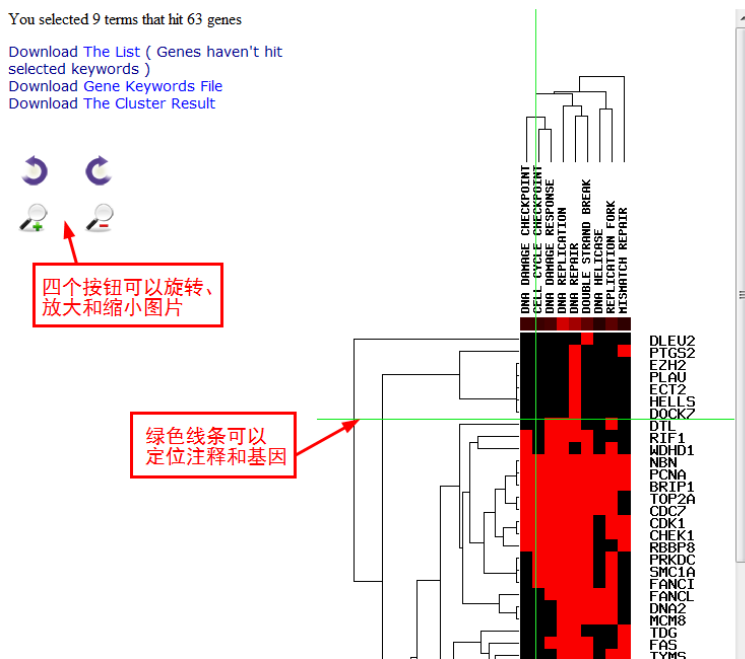
Add keyword(s): (Keywords separated by comma)

Assistant Term(optional): (Terms separated by comma)

Heat Map Type: 3、点击"Heat Map"产生聚类分析热图

2、选择热图的类型

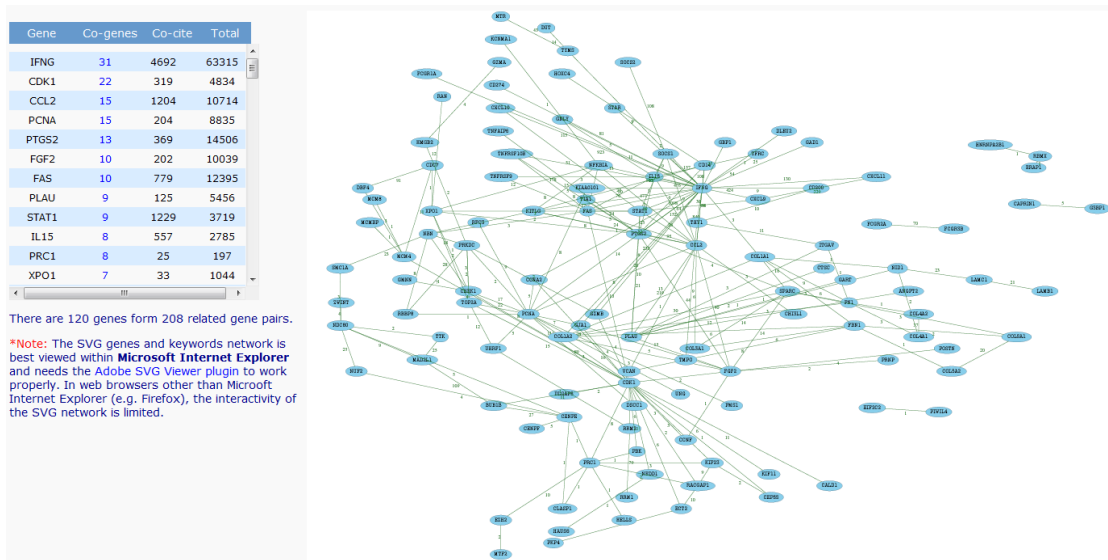
聚类分析结果:



■ 构建文献基因网络

点击“Literature Mining Gene Network”，打开基因网络构建的界面：

不加任何条件生成的网络图:



构建与自由词相关的基因网络，并且在网络中显示已知的基因，如果想用某个主题的多个词构建网络，以逗号将词隔开。

Literature Mining Gene Networks

Known Genes: (Gene(s) known related to the word(s) will be shown in orange color, otherwise in blue.)

Nasopharyngeal Carcinoma,NPC 1、输入搜索词，查找相关的已知基因

Network Keywords: (Genes related to the word(s) will be searched, and co-occurrence networks will be constructed.)

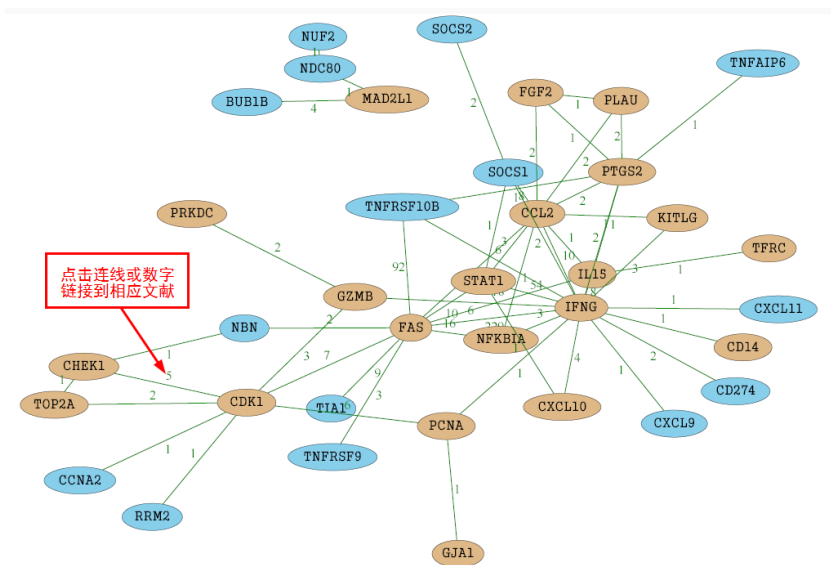
apoptosis,apoptotic AND 2、输入搜索词，构建与之相关的网络

Co-occurrence: Sentence Abstract

3、选择搜索词与基因共同出现在句子

点击"Gene network"生成基因网络图

生成与“apoptosis,apoptotic”（凋亡）相关的基因网络图:



CDK1 和 CHEK1 相互作用，并且搜索词与它们共同出现在一个句子的文献：

Source: Literature mining

点击查看此基因对的来源

Gene: **CDK1**

Alias : cell division cycle 2 G1 to S and G2 to M; P34CDC2; CDK1; cell division protein kinase 1; cell cycle controller CDC2; cell division cycle 2, G1 to S and G2 to M; CDC2; cyclin-dependent kinase 1; p34 protein kinase; cell division control protein 2 homolog; CDC28A

Gene: **CHEK1**

Alias : Checkpoint, S. pombe, homolog of, 1; serine/threonine-protein kinase Chk1; CHEK1; CHK1; CHK1 checkpoint homolog; CHK1 homolog

Search word(s): apoptosis,apoptotic

Click here to get abstracts about Nasopharyngeal Carcinoma,NPC and CDK1 CHEK1

1. PMID: 18981479

Genes Dev. 2008 Nov 11;22(23):3952-60

Differentiation of trophoblast stem cells into giant cells is triggered by p57/Kip2 inhibition of CDK1 activity.

Ullah Z, Kohn MJ, Yagi R, Vassilev LT, DePamphilis ML.

National Institute of Child Health and Human Development, National Institutes of Health, Bethesda, Maryland 20892, USA.

Genome endoreduplication during mammalian development is a rare event for which the mechanism is unknown. It first appears when fibroblast growth factor 4 (FGF4) deprivation induces differentiation of trophoblast stem (TS) cells into the nonproliferating trophoblast giant (TG) cells required for embryo implantation. Here we show that RO3306 inhibition of cyclin-dependent protein kinase 1 (CDK1), the enzyme required to enter mitosis, induced differentiation of TS cells into TG cells. In contrast, RO3306 induced abortive endoreduplication and apoptosis in embryonic stem cells, revealing that inactivation of CDK1 triggers endoreduplication only in cells programmed to differentiate into polyploid cells. Similarly, FGF4 deprivation resulted in CDK1 inhibition by overexpressing two CDK-specific inhibitors, p57/KIP2 and p21/CIP1. **TS cell mutants revealed that p57 was required to trigger endoreduplication by inhibiting CDK1, while p21 suppressed expression of the checkpoint protein kinase CHEK1, thereby preventing induction of apoptosis.** Furthermore, Cdk2(-/-) TS cells revealed that CDK2 is required for endoreduplication when CDK1 is inhibited. Expression of p57 in TG cells was restricted to G-phase nuclei to allow CDK activation of S phase. Thus, endoreduplication in TS cells is triggered by p57 inhibition of CDK1 with concomitant suppression of the DNA damage response by p21.

Journal Article.

点击“Literature mining”的结果：

Gene: **CDK1**

Alias : cell division cycle 2 G1 to S and G2 to M; P34CDC2; CDK1; cell division protein kinase 1; cell cycle controller CDC2; cell division cycle 2, G1 to S and G2 to M; CDC2; cyclin-dependent kinase 1; p34 protein kinase; cell division control protein 2 homolog; CDC28A

Gene: **CHEK1**

Alias : Checkpoint, S. pombe, homolog of, 1; serine/threonine-protein kinase Chk1; CHEK1; CHK1; CHK1 checkpoint homolog; CHK1 homolog

1. PMID: 16629900

Genes Cells. 2006 May;11(5):477-85.

Regulation of mitotic function of Chk1 through phosphorylation at novel sites by cyclin-dependent kinase 1 (Cdk1).

Shiromizu T, Goto H, Tomono Y, Bartek J, Totsukawa G, Inoko A, Nakanishi M, Matsumura F, Inagaki M.

Division of Biochemistry, Aichi Cancer Center Research Institute, Nagoya, Aichi 464-8681, Japan.

Chk1 is phosphorylated at Ser317 and Ser345 by ATR in response to stalled replication and genotoxic stresses. This Chk1 activation is thought to play critical roles in the prevention of premature mitosis. However, the behavior of Chk1 in mitosis remains largely unknown. Here we reported that Chk1 was phosphorylated in mitosis. The reduction of this phosphorylation was observed at the metaphase-anaphase transition. Two-dimensional phosphopeptide mapping revealed that Chk1 phosphorylation sites in vivo were completely overlapped with the in vitro sites by cyclin-dependent protein kinase (Cdk) 1 or by p38 MAP kinase. Ser286 and Ser301 were identified as novel phosphorylation sites on Chk1. Treatment with Cdk inhibitor butyrolactone I induced the reduction of Chk1-S301 phosphorylation, although treatment with p38-specific inhibitor SB203580 or siRNA did not. In addition, ionizing radiation (IR) or ultraviolet (UV) light did not induce Chk1 phosphorylation at Ser317 and Ser345 in nocodazole-arrested mitotic cells. **These observations imply the regulation of mitotic Chk1 function through Chk1 phosphorylation at novel sites by Cdk1.**

Journal Article. Research Support, Non-U.S. Gov't.

<<First <Prev Page 1 of 1 Next> Last>>

点击“Click here”的结果，这两个基因已知与鼻咽癌相关：

Search word(s) :
Nasopharyngeal
Carcinoma,NPC

Gene	Hit	Total
CDK1	13	4834
CHEK1	2	1276

Gene: **CDK1**

Alias : cell division cycle 2 G1 to S and G2 to M; P34CDC2; CDK1; cell division protein kinase 1; cell cycle controller CDC2; cell division cycle 2, G1 to S and G2 to M; CDC2; cyclin-dependent kinase 1; p34 protein kinase; cell division control protein 2 homolog; CDC28A

Summary : The protein encoded by this gene is a member of the Ser/Thr protein kinase family. This protein is a catalytic subunit of the highly conserved protein kinase complex known as M-phase promoting factor (MPF), which is essential for G1/S and G2/M phase transitions of eukaryotic cell cycle. Mitotic cyclins stably associate with this protein and function as regulatory subunits. The kinase activity of this protein is controlled by cyclin accumulation and destruction through the cell cycle. The phosphorylation and dephosphorylation of this protein also play important regulatory roles in cell cycle control. Alternatively spliced transcript variants encoding different isoforms have been found for this gene. [provided by RefSeq]

<<First <Prev Page 1 of 2 Next> Last>>

1. PMID: 20711190

Nat Struct Mol Biol. 2010 Sep;17(9):1065-71.

Nuclear pore formation but not nuclear growth is governed by cyclin-dependent kinases (Cdks) during interphase.

Maeshima K, Iino H, Hihara S, Funakoshi T, Watanabe A, Nishimura M, Nakatomi R, Yahata K, Imamoto F, Hashikawa T, Yokota H, Imamoto N.

Cellular Dynamics Laboratory, RIKEN Advanced Science Institute, Wako, Saitama, Japan. kmaeshim@lab.nig.ac.jp

Nuclear volume and the number of nuclear pore complexes (NPCs) on the nucleus almost double during interphase in dividing cells. How these events are coordinated with the cell cycle is poorly understood, particularly in mammalian cells. **We report here, based on newly developed techniques for visualizing NPC formation, that cyclin-dependent kinases (Cdks), especially Cdk1 and Cdk2, promote interphase NPC formation in human dividing cells.** Cdks seem to drive an early step of NPC formation because Cdk inhibition suppressed generation of 'nascent pores', which we argue are immature NPCs under the formation process. Consistent with this, Cdk inhibition disturbed proper expression and localization of some nucleoporins, including Elys/Mel-28, which triggers postmitotic NPC assembly. Strikingly, Cdk suppression did not notably affect nuclear growth.

■ GO 和 Pathway 分析

点击“GO Analysis”和“Pathway Analysis”，进行分析和自动加载结果：



GO 分析结果，选择注释产生聚类分析热图与关键词注释中的操作一致。

GO Analysis

<input checked="" type="checkbox"/>	GO Term	Hit	Total	P-Value	Q-Value
<input checked="" type="checkbox"/>	cluster1 Enrichment Score : 21.17				
<input checked="" type="checkbox"/>	condensed chromosome	20	144	1.038e-24	3.515e-23
<input checked="" type="checkbox"/>	microtubule cytoskeleton organization	19	200	2.049e-14	2.731e-13
<input checked="" type="checkbox"/>	chromosome, centromeric region	18	148	7.32e-19	1.288e-17
<input checked="" type="checkbox"/>	chromosome segregation	16	117	2.069e-19	4.138e-18
<input checked="" type="checkbox"/>	condensed chromosome, centromeric region	15	80	1.921e-26	7.686e-25
<input checked="" type="checkbox"/>	kinetochore	15	92	1.816e-22	4.439e-21
<input checked="" type="checkbox"/>	mitotic prometaphase	15	86	2.576e-24	7.555e-23
<input checked="" type="checkbox"/>	condensed chromosome kinetochore	14	75	1.579e-24	4.962e-23
<input checked="" type="checkbox"/>	cluster2 Enrichment Score : 19.49				
<input checked="" type="checkbox"/>	cellular component organization	108	3448	2.86e-09	2.517e-08
<input checked="" type="checkbox"/>	cellular component organization or biogenesis at cellular level	93	2791	1.353e-09	1.294e-08
<input checked="" type="checkbox"/>	cellular component organization at cellular level	92	2697	3.699e-10	3.876e-09

Heat Map Save

Pathway Analysis 结果，解释和其他操作与 GO 的一致。

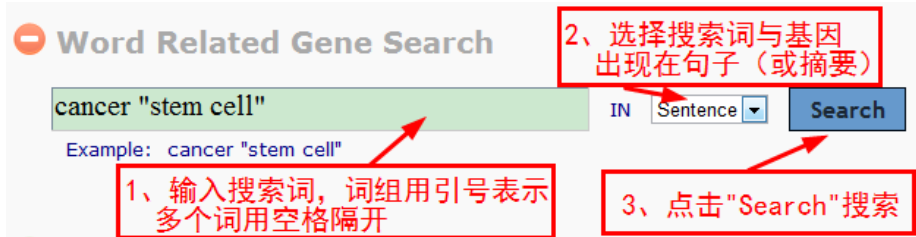
Pathway Analysis

<input checked="" type="checkbox"/>	Pathway	Hit	Total	P-Value	Q-Value
<input checked="" type="checkbox"/>	cluster1 Enrichment Score : 20.23				
<input checked="" type="checkbox"/>	REACTOME_CELL CYCLE MITOTIC	35	306	1.924e-27	9.043e-26
<input checked="" type="checkbox"/>	REACTOME_MITOTIC M M G1 PHASES	20	157	1.68e-17	2.632e-16
<input checked="" type="checkbox"/>	REACTOME_MITOTIC PROMETAPHASE	15	92	6.132e-18	1.441e-16
<input checked="" type="checkbox"/>	cluster2 Enrichment Score : 6.41				
<input checked="" type="checkbox"/>	KEGG_PATHWAYS IN CANCER	17	325	0.0003	0.0006
<input checked="" type="checkbox"/>	KEGG_SMALL CELL LUNG CANCER	11	84	4.309e-10	2.893e-09
<input checked="" type="checkbox"/>	cluster3 Enrichment Score : 6.29				
<input checked="" type="checkbox"/>	KEGG_FOCAL ADHESION	12	199	0.001	0.0016
<input checked="" type="checkbox"/>	KEGG_ECM RECEPTOR INTERACTION	11	84	4.309e-10	3.375e-09
<input checked="" type="checkbox"/>	REACTOME_AXON GUIDANCE	11	161	0.0003	0.0006
<input checked="" type="checkbox"/>	REACTOME_INTEGRIN CELL SURFACE INTERACTIONS	9	81	8.604e-07	4.044e-06
<input checked="" type="checkbox"/>	REACTOME_NCAM SIGNALING FOR NEURITE OUT GROWTH	8	69	2.07e-06	8.844e-06

Heat Map Save

词相关基因检索功能

查找与检索词相关的基因，可以限定检索词与基因共同出现在同一个句子或摘要，输入时不需要带除双引号外的其它标点符号，每个词之间用空格隔开，表示在同时出现这些词，词组用双引号表示。



Search word(s) : cancer "stem cell" Gene: PROM1

Genes: 333 Papers: 660

Num	Gene	Hit	Total
1	PROM1	84	1324
2	PSCA	68	133
3	KITLG	60	5427
4	CSF3	56	14020
5	CD44	53	7848
6	KIT	30	7613
7	CD24	28	682
8	CD34	22	13288
9	CSF2	22	19367
10	TP53	21	40587
11	POUSF1	21	2013
12	SCLC1	20	3833
13	ABCG2	14	3048
14	ERBB2	14	11718
15	BMI1	13	550
16	ABCB1	13	8752
17	IL3	13	9272

Alias : prominin-like 1; RP41; prominin 1; prominin-1; AC133; MSTP061; macular dystrophy retinal 2; hPROMININ; PROM1; Stargardt disease 4; CD133; prominin-like 1; prominin-like protein 1; hematopoietic stem cell antigen; antigen AC133; STGD4; PROM1; CORD12; MCDK2

Summary : This gene encodes a pentaspan transmembrane glycoprotein. The protein localizes to membrane protrusions and is often expressed on adult stem cells, where it is thought to function in maintaining stem cell properties by suppressing differentiation. Mutations in this gene have been shown to result in retinitis pigmentosa and Stargardt disease. Expression of this gene is also associated with several types of cancer. This gene is expressed from at least five alternative promoters that are expressed in a tissue-dependent manner. Multiple transcript variants encoding different isoforms have been found for this gene. [provided by RefSeq]

基因的别名 多文献时翻页 基因概述

1. PMID: 20711432
 PLoS ONE. 2010;5(8):e12121. 文献链接到PubMed

Prospectively isolated cancer-associated CD10(+) fibroblasts have stronger interactions with CD133(+) colon cancer cells than with CD133(-) cancer cells.
 Cui L, Ohuchida K, Mizumoto K, Moriyama T, Onimaru M, Nakata K, Nabae T, Ueki T, Sato N, Tominaga Y, Tanaka M.
 Department of Surgery and Oncology, Graduate School of Medical Sciences, Kyushu University, Fukuoka, Japan.

Although CD133 has been reported to be a promising colon cancer stem cell marker, the biological functions of CD133+ colon cancer cells remain controversial. In the present study, we investigated the biological differences between CD133+ and CD133- colon cancer cells, with a particular focus on their interactions with cancer-associated fibroblasts, especially CD10+ fibroblasts. We used 19 primary colon cancer tissues, 30 primary cultures of fibroblasts derived from colon cancer tissues and 6 colon cancer cell lines. We isolated CD133+ and CD133- subpopulations from the colon cancer tissues and cultured cells. In vitro analyses revealed that the two populations showed similar biological behaviors in their proliferation and chemosensitivity. In vivo analyses revealed that CD133+ cells showed significantly greater tumor growth than CD133- cells (P=0.007). Moreover, in cocultures with primary fibroblasts derived from colon cancer tissues, CD133+ cells exhibited significantly more invasive behaviors than CD133- cells (P<0.001), especially in cocultures with CD10+ fibroblasts (P<0.0001). Further in vivo analyses revealed that CD10+ fibroblasts enhanced the tumor growth of CD133+ cells significantly more than CD10- fibroblasts (P<0.05). These data demonstrate that the in vitro invasive properties and in vivo tumor growth of CD133+ colon cancer cells are enhanced in the presence of specific cancer-associated fibroblasts, CD10+ fibroblasts, suggesting that the interactions between these specific cell populations have important roles in cancer progression. Therefore, these specific interactions may be promising targets for new colon cancer therapies.

Click on gene or number to view other genes and literature related to the search term. 点击基因查看文献出处 基因与检索词相关的文献数

点击基因或数字查看其他基因与搜索词相关的文献：

Search word(s) : cancer "stem cell" Gene: PSCA

Genes: 333 Papers: 660

Num	Gene	Hit	Total
1	PROM1	84	1324
2	PSCA	68	133
3	KITLG	60	5427
4	CSF3	56	14020
5	CD44	53	7848
6	KIT	30	7613
7	CD24	28	682
8	CD34	22	13288
9	CSF2	22	19367
10	TP53	21	40587
11	POUSF1	21	2013
12	SCLC1	20	3833
13	ABCG2	14	3048
14	ERBB2	14	11718
15	BMI1	13	550
16	ABCB1	13	8752
17	IL3	13	9272

Alias : PSCA; highly expressed in the prostate; it is also expressed in the bladder, placenta, colon, kidney, and stomach. This gene is up-regulated in a large proportion of prostate cancers and is also detected in cancers of the bladder and pancreas. This gene includes a polymorphism that results in an upstream start codon in some individuals; this polymorphism is thought to be associated with a risk for certain gastric and bladder cancers. Alternative splicing results in multiple transcript variants. [provided by RefSeq]

Summary : This gene encodes a glycosylphosphatidylinositol-anchored cell membrane glycoprotein. In addition to being highly expressed in the prostate it is also expressed in the bladder, placenta, colon, kidney, and stomach. This gene is up-regulated in a large proportion of prostate cancers and is also detected in cancers of the bladder and pancreas. This gene includes a polymorphism that results in an upstream start codon in some individuals; this polymorphism is thought to be associated with a risk for certain gastric and bladder cancers. Alternative splicing results in multiple transcript variants. [provided by RefSeq]

Click on gene or number to view other genes and literature related to the search term. 点击基因查看其他基因的文献

Vaccine. 2010 Aug 31;28(38):6333-7.
Vaccination with a chaperone complex based on PSCA and GRP170 adjuvant enhances the CTL response and inhibits the tumor growth in mice.
 Huo W, Ye J, Liu R, Chen J, Li Q.
 Department of Urology, Institute of Surgery Research, Daping Hospital, Third Military Medical University, Chongqing 400042, China.

Increasing knowledge demonstrate that prostate stem cell antigen (PSCA) is a promising candidate for immunotherapy of advanced prostate cancer. However, tumor escape with down-regulation of target antigens may limit the susceptibility of tumor cells to the immune attack. Concomitant generation of T-cell responses against several immunodominant antigens may circumvent this potential drawback. In this study, we prepared the chaperone complex vaccine based on PSCA and GRP170, and utilized it to immunize the C57BL/6 mice. In addition, the T-cell response was monitored with ELISPOT and (51)Cr-release assays, and the tumor growth and the life span of tumor-bearing mice were assessed. The results demonstrated the chaperone complex based on PSCA and GRP170 could enhance the T-cell mediate immune responses, which significantly inhibited the tumor growth and prolonged the life span of tumor-bearing mice. In conclusion, our findings supported the strategy of chaperone complex, based on PSCA and GRP170, could be an effective treatment for prostate cancer therapy.

Journal Article.

2. PMID: 20507324
 Cancer Sci. 2010 Jul;101(7):1582-9.
Genome-wide germline analyses on cancer susceptibility and GeMDBJ database: Gastric cancer as an example.

■ 回顾分析

相同的一组基因可以不重新输入，可以回顾已有的分析，或者继续分析。

2012-05-10_Presentation

- Word Related Gene Search
- Genes Information
- Gene Cluster With Literature Profiles
- Literature Mining Gene Networks
- GO Analysis
- Pathway Analysis

Recent-Jobs

- 2012-05-10_Presentation
Genes:292 Papers:861
- 2012-04-26_immune
Genes:309 Papers:624
- 2012-04-25_Npc_down
Genes:281 Papers:262
- 2012-04-24_download
Genes:1578 Papers:2703
- 2012-04-24_NPC_324
Genes:292 Papers:861
- 2012-04-23_Test
Genes:292 Papers:861
- 2012-04-23_8967_Test
Genes:292 Papers:861
- 2012-04-23_12-20-03_5607
Genes:292 Papers:861
- 2012-04-23_12-06-42_7098
Genes:292 Papers:861

回顾构建好的基因网络：

2012-05-10_Presentation

- Word Related Gene Search
- Genes Information
- Gene Cluster With Literature Profiles
- Literature Mining Gene Networks

Former Network:

- analysis
- analysis_nasopharyngeal carcinoma-npc_apoptosis-apoptotic_sen

Known Genes: (Gene(s) known related to the word(s) will be shown in orange color, otherwise in blue.)

Network Keywords: (Genes related to the word(s) will be searched, and co-occurrence networks will be constructed.)

Co-occurrence: Sentence Abstract

Gene network