

GenCLiP 2.0 使用手册

简介

GenCLiP 2.0 (<http://ci.smu.edu.cn>) 是一个基于文献挖掘的网络服务平台，主要有 4 大功能模块，包括基因功能注释、分子网络构建、GO 和 Pathway 分析和关键词相关基因搜索。

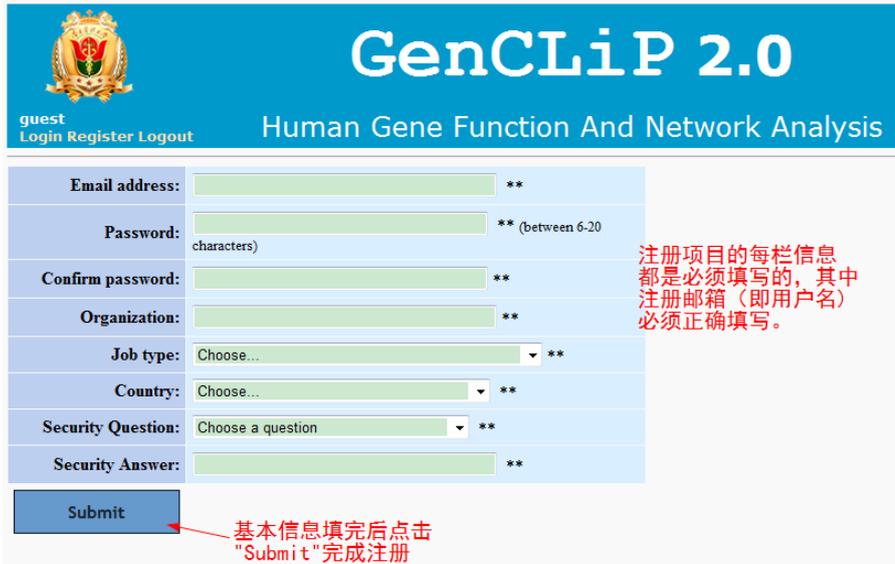
网络平台面向广大的生物医学工作者，包括国内外生物医药企业、科研机构、本专科院校、医疗机构、医药科研机构工作者和医疗服务工作者等，用户需适应全英文网页环境，具备良好的生物医学背景知识。

GenCLiP 2.0 兼容 IE、Safari、Chrome 等常用的浏览器，如浏览器不能显示基因网络图（由 Cytoscape Web 绘制），需从 <http://get.adobe.com/flashplayer/> 下载最新的 Flash 插件安装。

用户注册



进入填写注册基本信息的界面：



The registration form includes the following fields:

- Email address: **
- Password: ** (between 6-20 characters)
- Confirm password: **
- Organization: **
- Job type: Choose... **
- Country: Choose... **
- Security Question: Choose a question **
- Security Answer: **

Submit

注册项目的每栏信息都是必须填写的，其中注册邮箱（即用户名）必须正确填写。

基本信息填完后点击 "Submit" 完成注册

点击 “Login”进入注册用户登陆界面：



The login form includes the following fields:

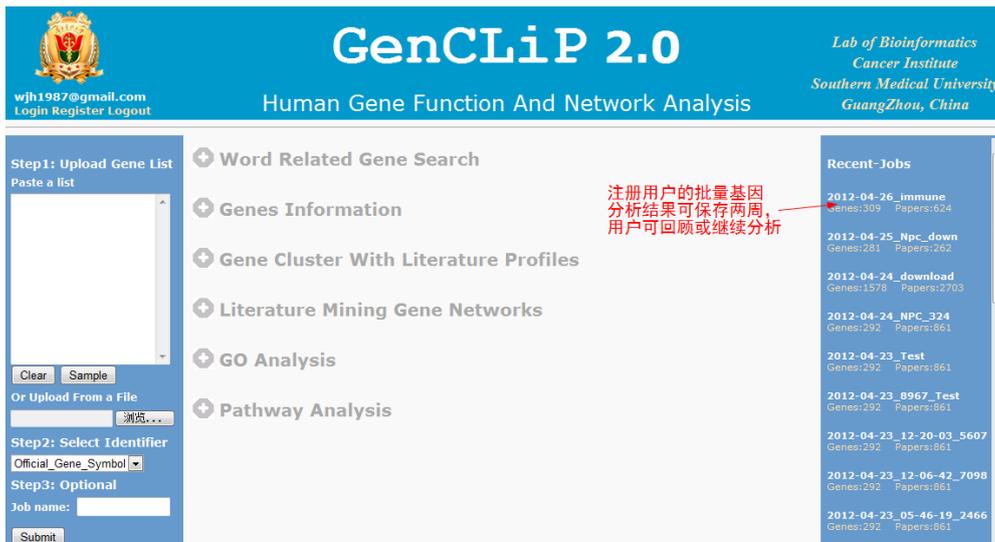
- Email address: wjh1987@gmail.com
- Password: ***** (Forgot your password?)

Login

填写注册邮箱、密码

点击 "Login" 进入注册用户界面

注册用户分析界面：



The dashboard includes the following sections:

- Step1: Upload Gene List (Paste a list, Clear, Sample, Or Upload From a File, Select Identifier, Official_Gene_Symbol, Job name, Submit)
- Word Related Gene Search
- Genes Information
- Gene Cluster With Literature Profiles
- Literature Mining Gene Networks
- GO Analysis
- Pathway Analysis
- Recent-Jobs (List of analysis jobs with Genes and Papers counts)

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

Word Related Gene Search

Genes information

Entered	Human Symbol	Papers
PTHLH	PTHLH	2852

Gene Cluster With Literature Profiles

Literature Mining Gene Networks

GO Analysis

pathway Analysis

模块可逐个点开查看

关键词：

Genes information

Entered	Human Symbol	Papers
PTHLH	PTHLH	2852

点击此按钮，显示基因关键词注释

Gene Cluster With Literature Profiles

Keyword	Hit Papers
PARATHYROID	2447
HYPERCALCEMIA	841
MALIGNANCY	605
HUMORAL	509
GROWTH FACTOR	360
RESORPTION	338
BONE RESORPTION	306
GENE EXPRESSION	261
PROTEIN KINASE	168
TRANSFORMING GROWTH FACTOR	139
CELL PROLIFERATION	125
SQUAMOUS CELL CARCINOMA	114
POLYMERASE CHAIN REACTION	114
ADENYLATE CYCLASE	112
CELL GROWTH	104
ALKALINE PHOSPHATASE	99
CHONDROCYTE DIFFERENTIATION	97

点击数字进入关键词与基因共同出现的摘要

Literature Mining Gene Networks

查阅文献：

Keyword : PARATHYROID

Genes: 1 Papers: 2447

Num	Gene	Hit	Total
1	PTHLH	2447	2852

Gene: PTHLH

Alias : parathyroid hormone-like related protein; PTHRP; BOE2; parathyroid hormone-like hormone; PLS; PTHLH; PTHR; Ith; 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, Collard 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 PTHrP1(-/-) 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.

相互作用的基因:

点击此按钮，显示相互作用的基因

Num	Gene	Record
1	PTH1R	42
2	PTH	35
3	TGFB1	16
4	CAMP	16
5	IHH	9
6	CASR	5
7	IL6	5
8	ETS1	5
9	VEGFA	4
10	RUNX2	4
11	SOX9	4
12	EGF	4
13	CCN1	4

点击查看描述两个基因有相互作用关系的文献

点击获取列表中的基因

点击 PTH1R 的记录数 “42”, 链接基因对的文献出处:

Gene: **PTH1R**
 Alias : parathyroid hormone-related protein; PTHRP; BDE2; parathyroid hormone-like hormone; PLP; PTHLH; 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/PTHr 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 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 (PTH1R) 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 和 Pathway 注释:

点击此按钮，显示基因的GO注释

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

点击注释可链接到GO官网，查看注释的信息

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。

Step 1: Upload Gene List

Paste a list

STAR
FCGR1B
CRLF3
STAT1
RACGAP1P
racgap1
hnrp11
CALD1
CD274
CDC7
fn1
slc39a14

Clear Sample

Or Upload From a File

浏览...

Step 2: Select Identifier

Official_Gene_Symbol

Step 3: Optional

Job name: Presentation

Submit

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

Word Related Gene S
Genes Information
Gene Cluster With Li
Literature Mining Ge
GO Analysis
Pathway Analysis

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
13	BCL2	BCL2	119	13	LOC653884	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	3	2	LOC732360	Not Found
293	RASSF4	RASSF4	9	3	FLJ45482	Not Found
294	GLS	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

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

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.

Modify

基因功能注释和聚类

点击“Gene Cluster With Literature Profiles”按钮，等待数秒后弹出聚类结果。



加载完后弹出基因关键词注释结果：

Gene Cluster With Literature Profiles

Map	Del	Keyword	Hit	Total	P-Value	Q-Value
<input checked="" type="checkbox"/>	<input type="checkbox"/>	cluster1 Enrichment Score : 48.11				
<input checked="" type="checkbox"/>	<input type="checkbox"/>	MITOSIS	37	254	1.439e-62	4.451e-59
<input checked="" type="checkbox"/>	<input type="checkbox"/>	CHROMOSOME SEGREGATION	38	342	1.553e-47	9.605e-45
<input checked="" type="checkbox"/>	<input type="checkbox"/>	M PHASE	44	469	3.583e-44	1.847e-41
<input checked="" type="checkbox"/>	<input type="checkbox"/>	CELL DIVISION	71	1119	4.516e-41	1.995e-38
<input checked="" type="checkbox"/>	<input type="checkbox"/>	cluster2 Enrichment Score : 28.55				
<input checked="" type="checkbox"/>	<input type="checkbox"/>	REPLICATION FORK	30	215	4.529e-48	3.502e-45
<input checked="" type="checkbox"/>	<input type="checkbox"/>	S PHASE	72	1155	1.485e-40	5.743e-38
<input checked="" type="checkbox"/>	<input type="checkbox"/>	DNA REPLICATION	57	911	3.02e-32	7.185e-30
<input checked="" type="checkbox"/>	<input type="checkbox"/>	DNA REPAIR	54	1048	1.936e-22	3.326e-20
<input checked="" type="checkbox"/>	<input type="checkbox"/>	G1 PHASE	30	459	1.602e-18	2.36e-16
<input checked="" type="checkbox"/>	<input type="checkbox"/>	CELL CYCLE ARREST	42	939	8.318e-14	7.35e-12
<input checked="" type="checkbox"/>	<input type="checkbox"/>	cluster3 Enrichment Score : 16.43				
<input checked="" type="checkbox"/>	<input type="checkbox"/>	CYCLIN DEPENDENT KINASE	48	803	2.207e-25	4.266e-23
<input checked="" type="checkbox"/>	<input type="checkbox"/>	SQUAMOUS CELL CARCINOMA	54	1341	2.072e-14	1.942e-12
<input checked="" type="checkbox"/>	<input type="checkbox"/>	BREAST CANCER CELL	57	1609	1.102e-11	7.747e-10

可更改默认参数对关键词结果筛选再聚类：

Filter:
 P-Value <= 1e-10 Hit >= 30 Total <= 3000

Add:
 Add keyword(s): (Keywords separated by comma)
 Assistant Term(optional): (Terms separated by comma)

Heat Map Type: Strict

1、选择需要改变的参数阈值

2、点击“Done”，重新聚类

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: Strict

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：

Cluster	Enrichment Score	Gene	Count	Score	P-Value
cluster2	28.55	REPLICATION FORK	30	215	4.529e-48
		S PHASE	72	1155	1.485e-40
		DNA REPLICATION	57	911	3.02e-32
		DNA REPAIR	54	1048	1.936e-22
		G1 PHASE	30	459	1.602e-18
		CELL CYCLE ARREST	42	939	8.318e-14
cluster3	16.43	CYCLIN DEPENDENT KINASE	48	803	2.207e-25
		SQUAMOUS CELL CARCINOMA	54	1341	2.072e-14
		BREAST CANCER CELL	57	1609	1.102e-11
cluster4	13.12	WOUND HEALING	37	652	3.151e-18
		TRANSFORMING GROWTH FACTOR	59	1652	2.742e-12
		EXTRACELLULAR MATRIX	64	1949	5.013e-11
nocluster					

Filter:
 P-Value <= 1e-10 Hit >= 30 Total <= 3000

Add:
 Add keyword(s): (Keywords separated by comma)
 Assistant Term(optional): (Terms separated by comma)

Buttons: Done Save Heat Map Type: Strict Heat Map

1、选择要删除的注释

2、点击“Done”，去除所选注释并重新聚类

选择关键词注释产生聚类分析热图:

Cluster	Enrichment Score	Gene	Count	Score	P-Value
cluster2	28.55	REPLICATION FORK	30	215	4.529e-48
		S PHASE	72	1155	1.485e-40
		DNA REPLICATION	57	911	3.02e-32
		DNA REPAIR	54	1048	1.936e-22
		G1 PHASE	30	459	1.602e-18
		CELL CYCLE ARREST	42	939	8.318e-14
cluster3	16.43	CYCLIN DEPENDENT KINASE	48	803	2.207e-25
		SQUAMOUS CELL CARCINOMA	54	1341	2.072e-14
		BREAST CANCER CELL	57	1609	1.102e-11
cluster4	13.12	WOUND HEALING	37	652	3.151e-18
		TRANSFORMING GROWTH FACTOR	59	1652	2.742e-12
		EXTRACELLULAR MATRIX	64	1949	5.013e-11
nocluster					
		RNA INTERFERENCE	78	1995	1.426e-19

Filter:
 P-Value <= 1e-10 Hit >= 30 Total <= 3000

Add:
 Add keyword(s): (Keywords separated by comma)
 Assistant Term(optional): (Terms separated by comma)

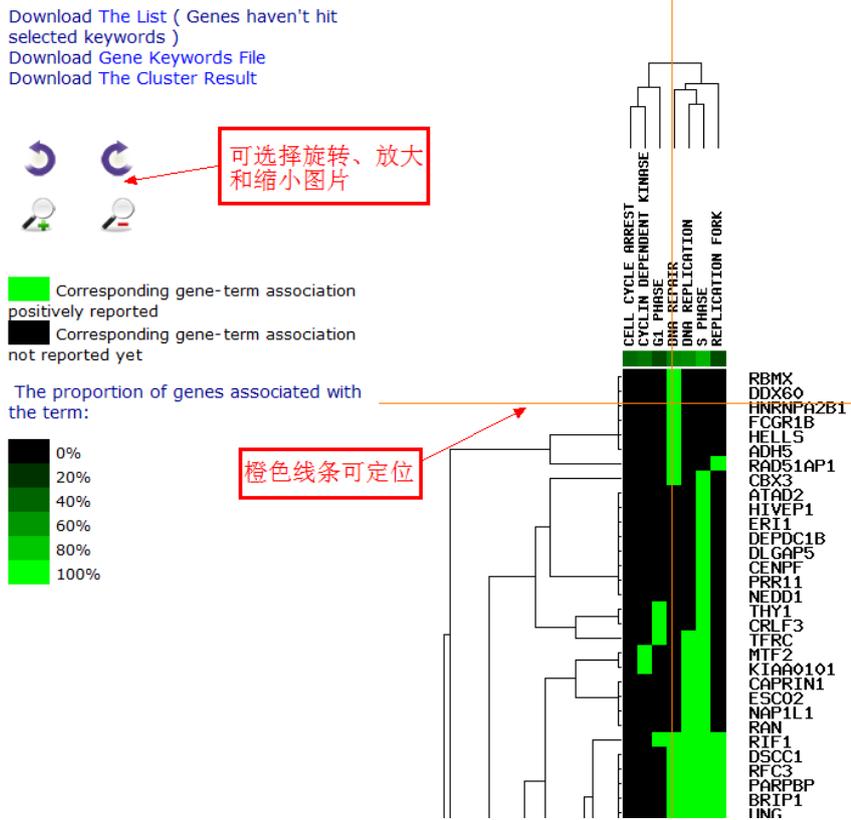
Buttons: Done Save Heat Map Type: Strict Heat Map

1、选择产生热图的注释

2、选择热图的类型

3、点击“Heat Map”产生聚类分析热图

聚类分析结果:



构建基因网络

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

Literature Mining Gene Networks

Network related with keyword(s): (Gene pairs related to the word(s) will be searched, and co-occurrence networks will be constructed.)

AND

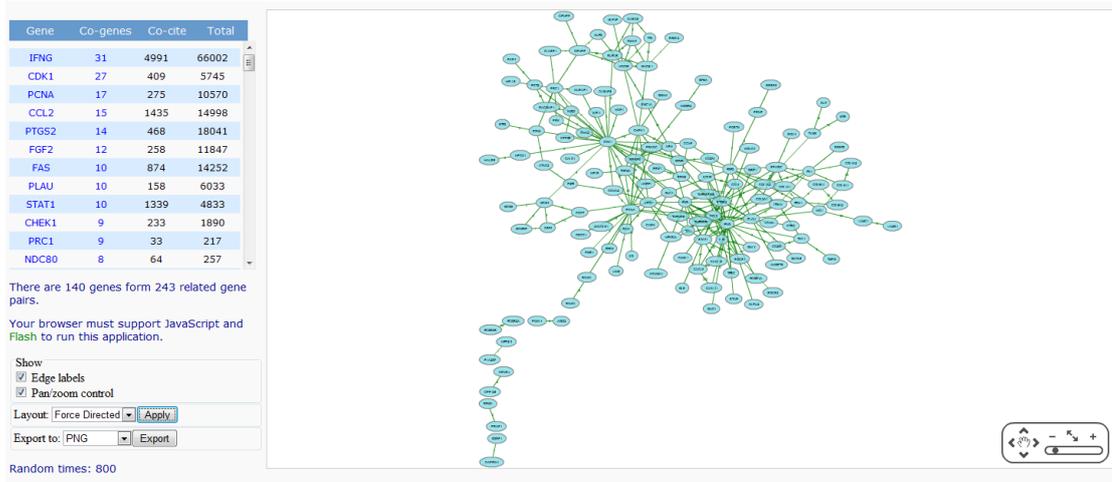
Co-occurrence of gene pair and keyword(s) in: sentence abstract

Gene(s) in the network related with keyword(s): (Related gene(s) will be shown in orange color, otherwise in blue.)

Gene network

点击“Gene network”生成网络图

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

Network related with keyword(s): (Gene pairs related to the word(s) will be searched, and co-occurrence networks will be constructed.)

1、输入搜索词，构建与之相关的网络

apoptosis,apoptotic AND

2、选择搜索词与基因共同出在的区域

Co-occurrence of gene pair and keyword(s) in: sentence abstract

Gene(s) in the network related with keyword(s): (Related gene(s) will be shown in orange color, otherwise in blue.)

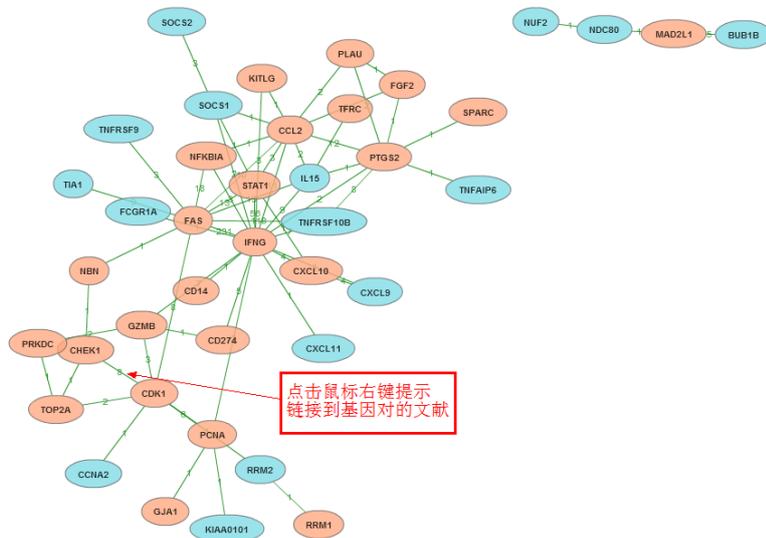
3、输入搜索词查找已知的相关基因

Nasopharyngeal Carcinoma,NPC

4、点击“Gene network”生成基因网络图

Gene network

生成与“apoptosis,apoptotic”（凋亡）相关的基因网络图，并在网络中显示与“Nasopharyngeal Carcinoma,NPC”（鼻咽癌）有关的基因（橙色）：



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 1;22(21):3852-36

[点击查看与"Known Genes"搜索词相关的已知基因的文章](#)

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 CHK1, 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

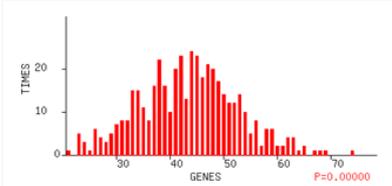
Nuclear volume and the number of nuclear pore complexes (NPCs) on the nucleus almost double during interphase in dividing cells. How these events are coordinated with the cell cycle is poorly understood, particularly in mammalian cells. **We report here, based on newly developed techniques for visualizing 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.

随机模拟

首次随机模拟结果与基因网络的结果同时给出，模拟次数限制在 1000 次以内，用户可以输入模拟次数（不超过首次次数的 10 倍）重新模拟，计算可能比较耗时，具体与基因数量和模拟次数有关，一般不超过 5 分钟。

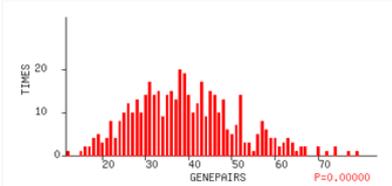
Random times: 451

Distribution of the number of related gene derived from the random genes:



Save

Distribution of the number of related gene pairs derived from the random genes:



Save

Simulate more times:

Times:

输入模拟次数
点击“Simulate”

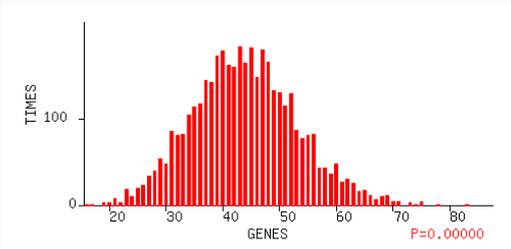
Simulate

结果在新的页面：

Analyzed Genes: 302 The Average Number of Papers: 936
Related Genes: 140 Related Gene Pairs: 243

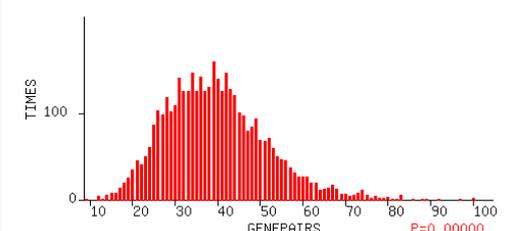
Random Times: 4000

Distribution of the number of related gene derived from the random genes:



Save

Distribution of the number of related gene pairs derived from the random genes:



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
18	IL3	11	11300

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; MCDR2

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 文献链接到PubMed

PLoS ONE. 2010;5(8):e12121.

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.

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

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	POU5F1	21	2013
12	SCLC1	20	3833
13	ABCG2	14	3048
14	ERBB2	14	11718
15	BMI1	13	550
16	ABC81	13	8752
17	IL3	13	9272

Click on the gene name to view other gene-related literature.

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

注册用户可查看近期的分析，或继续分析，分析档案保留两周。

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

Click on existing analysis to review or continue analysis.

回顾构建好的基因网络:

Literature Mining Gene Networks

Former Network:

- analysis
- analysis_nasopharyngeal_carcinoma_cell_cycle_sen
- analysis_nasopharyngeal_carcinoma_npc
- analysis_apoptosis-apoptotic_sen

Click on the former network to review the constructed gene network.

Network related with keyword(s): (Gene pairs related to the word(s) will be searched, and co-occurrence networks will be constructed.)

AND

Co-occurrence of gene pair and keyword(s) in: sentence abstract

Gene(s) in the network related with keyword(s): (Related gene(s) will be shown in orange color, otherwise in blue.)

Gene network