



中山大學
SUN YAT-SEN UNIVERSITY

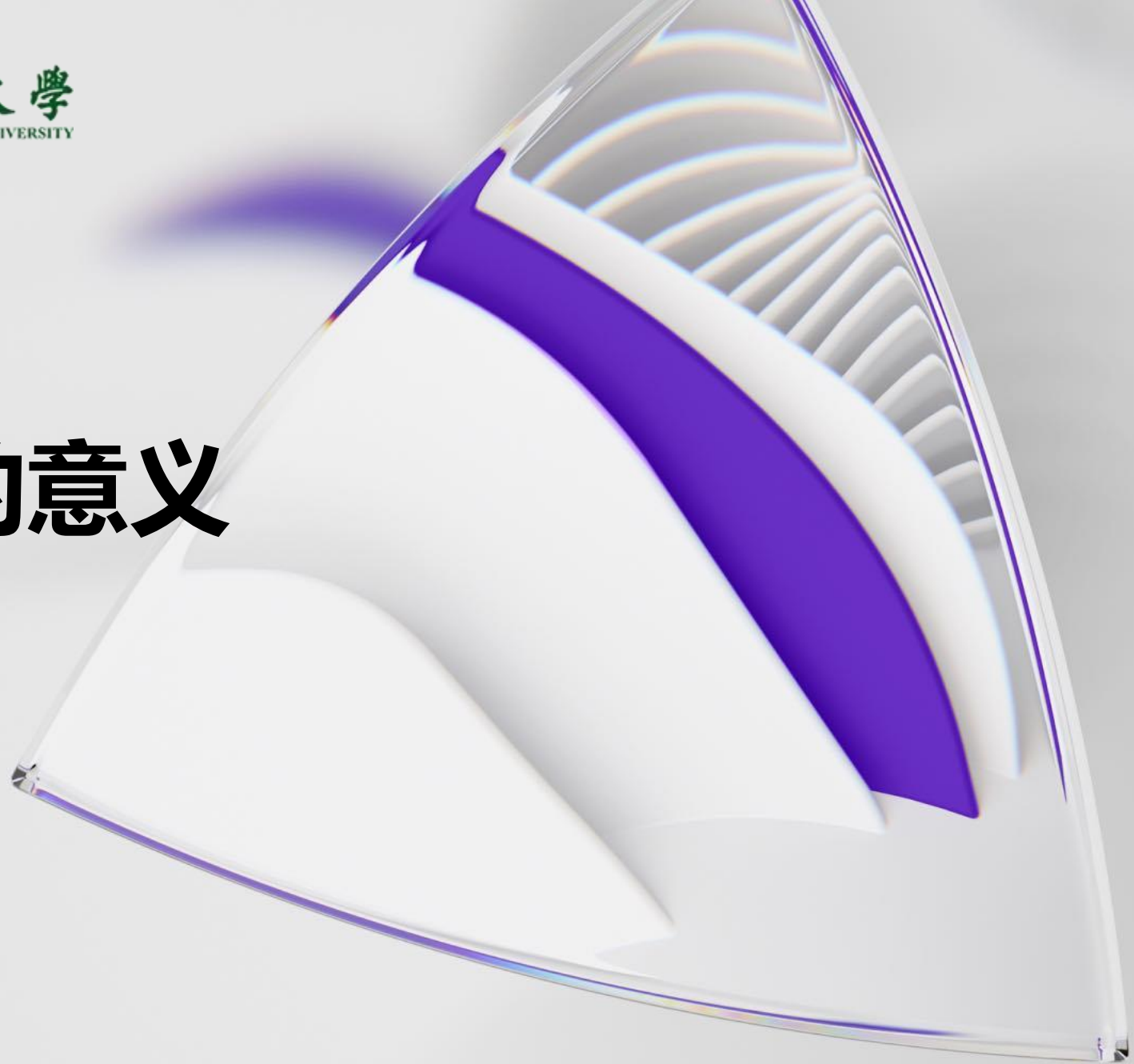
中山大学 探索数据背后的意义

MetaCore助力疾病通路研究

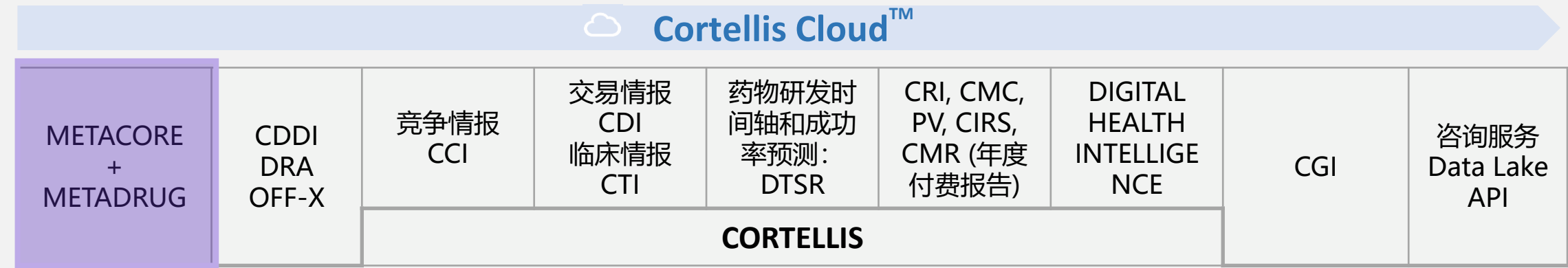
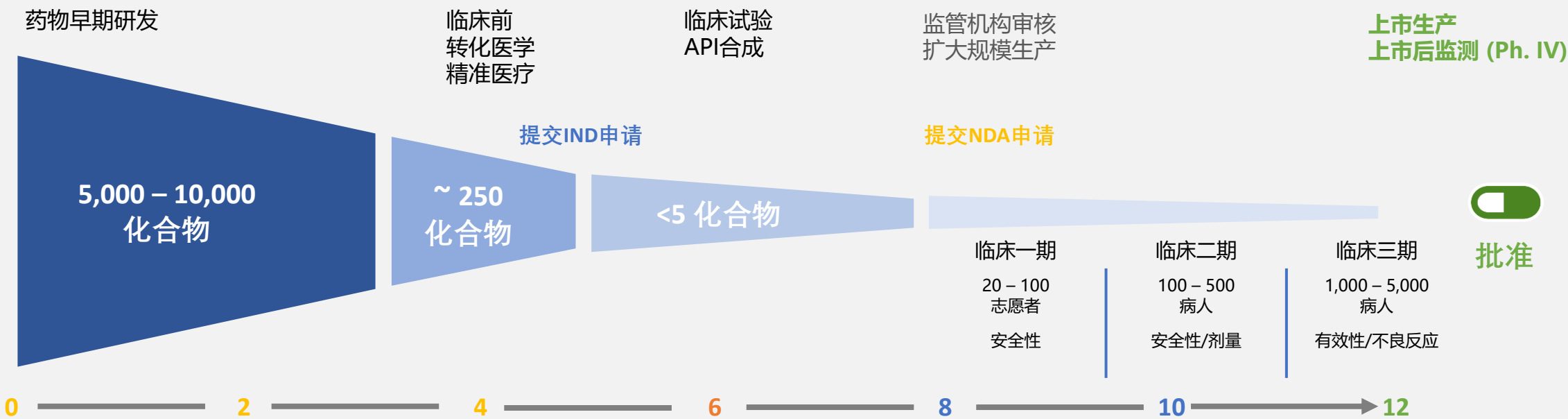
Rachel.Song@clarivate.com

130 8914 1107

2022-06-28



科睿唯安生命科学领域数据库：覆盖药物研发全流程



科睿唯安：专业信息服务提供商，致力于加快创新步伐

我们与180多个国家的

18,000

多家客户合作

总部位于**英国伦敦**

纽约证券交易所上市公司，代码：**CCC**



50/TOP50

国际制药企业及生物技术公司



17/TOP20

全球国际医疗器械企业



~200

中国领先的制药企业及生物技术公司



+600

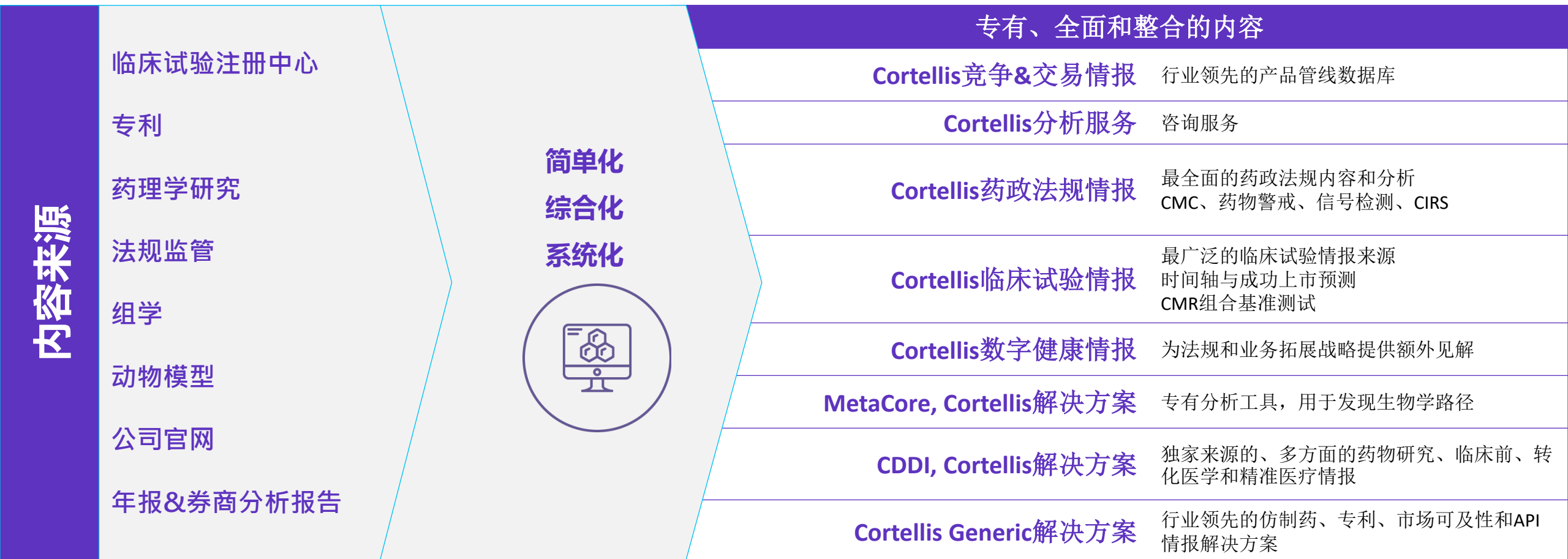
投资公司、政府基金



+7,000

领先的学术机构、非盈利组织及政府单位

内容覆盖全面



日程

第一部分：MetaCore数据平台简介

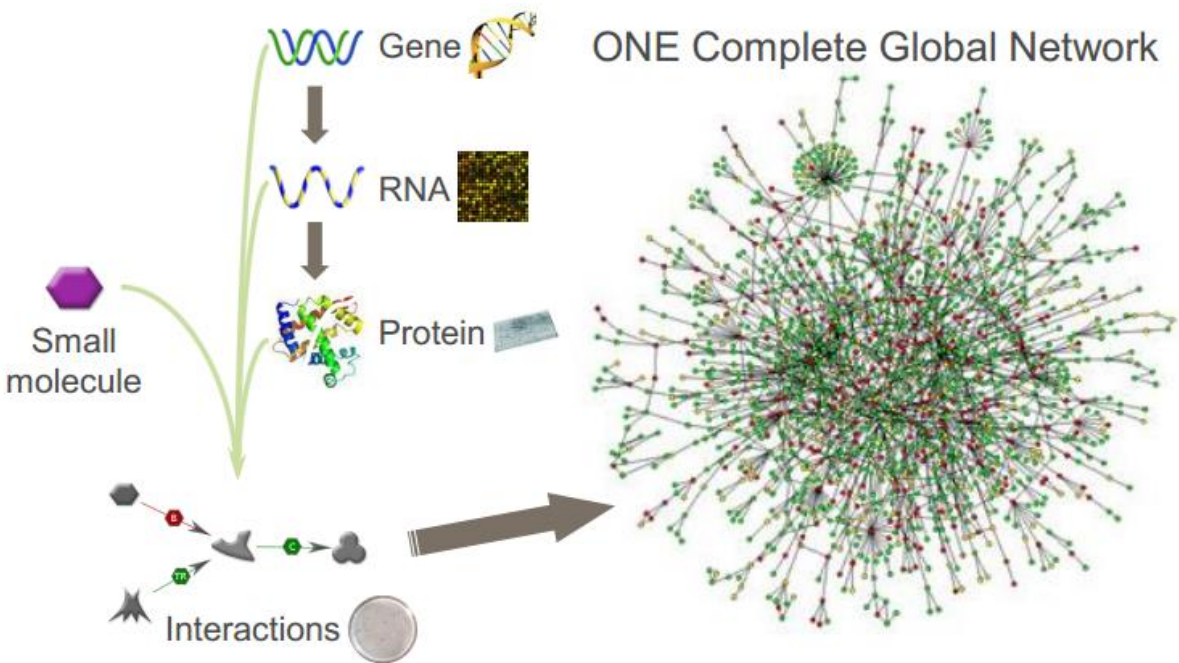
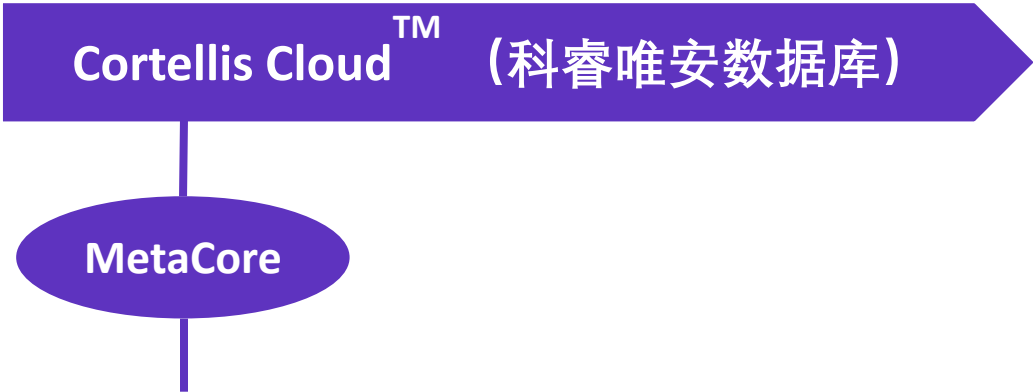
第二部分：MetaCore重点功能介绍

第三部分：系统生物学案例分享

第四部分：内容回顾与总结

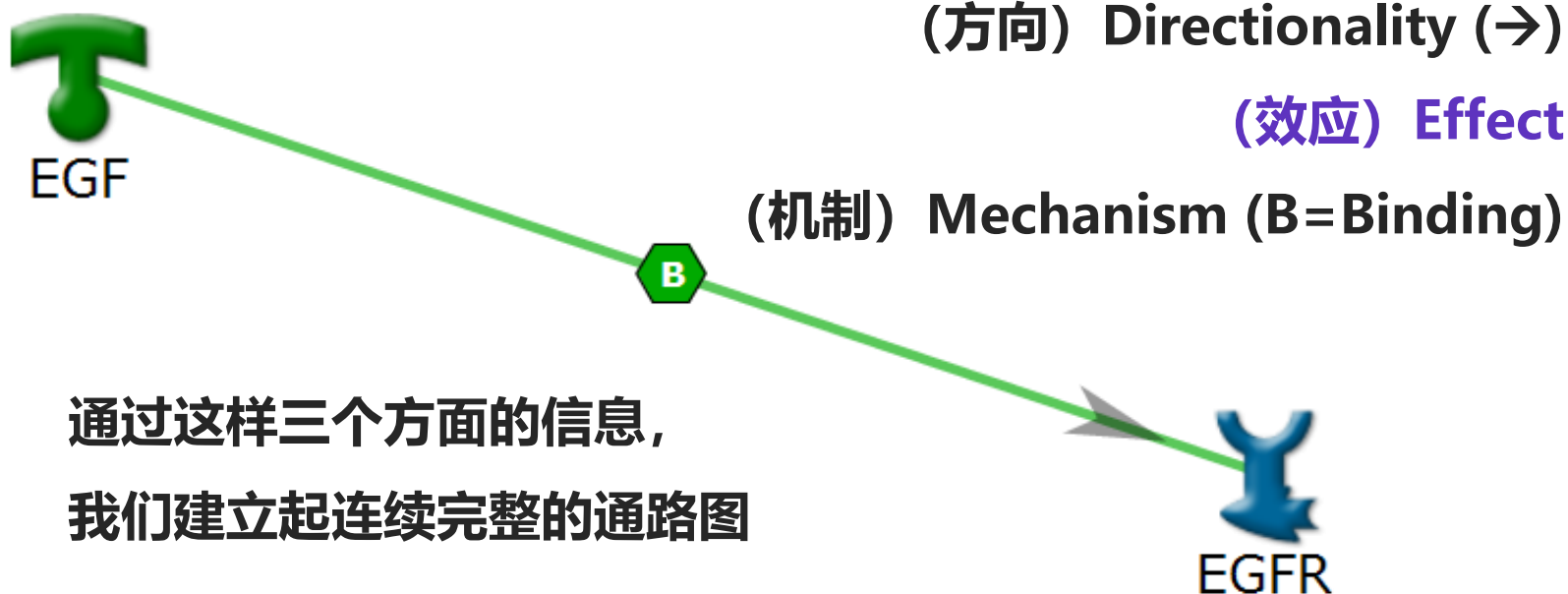
什么是MetaCore?

系统生物学简化复杂系统



Enrichment Analysis	Build Network	Interactome Analysis	Data mining
基因可以通过富集分析映射到已知的 pathway/network 上，并支持多组高通量数据分析	可根据实验数据或网络节点构建网络	分析互作关系，寻找重要的靶点/基因	通过快速检索或高级检索快速找到疾病/基因/蛋白等文献数据。

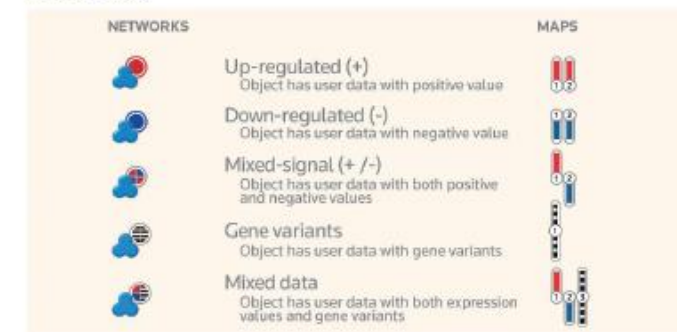
MetaCore 中的分子相互作用数据—— 包含：方向，效应，机制



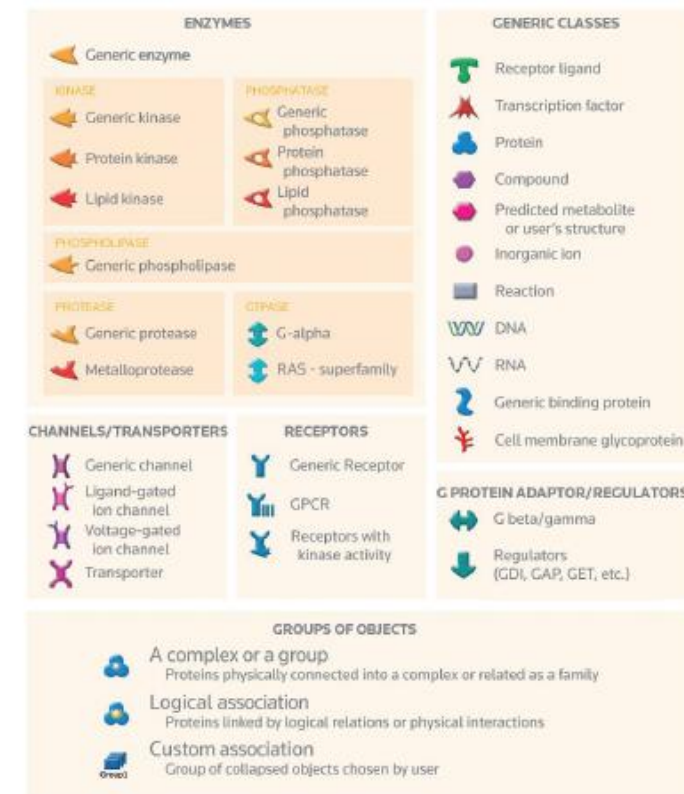
通过这样三个方面的信息，
我们建立起连续完整的通路图

Quick reference guide

User Data

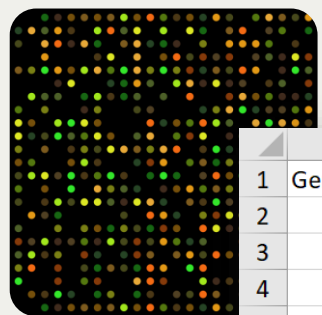


Network Objects



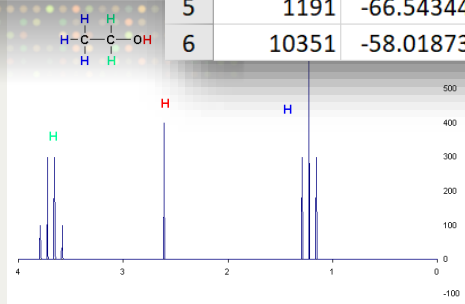


搜索/浏览

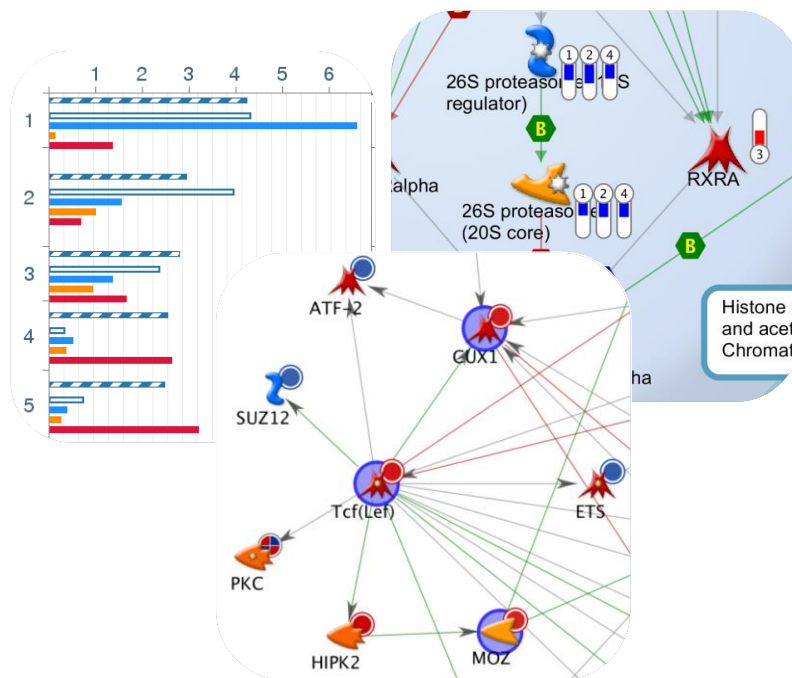


组学分析

	A	B	C
1	GeneID	Fold change	p-value
2	25890	-94.7858701	4.03E-07
3	7432	-94.6483041	0.00016
4	91851	-67.9404389	2.94E-06
5	1191	-66.5434408	4.90E-07
6	10351	-58.0187396	4.03E-07



MetaCore

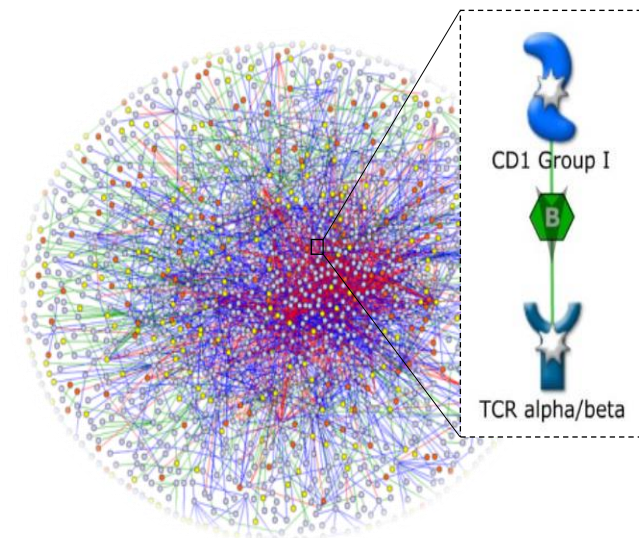


- 在经过验证的生物途径的背景了解实验数据
- 生成并确认新靶标和生物标志物的假设

MetaBase



3700 种期刊，由科学家手动策划



MetaCore / MetaBase的数据 载量

Content Overview

- 每季度更新
- 科学家手动上传

MetaBase	number
Human Genes	63885
Human SwissProt proteins	20385
Mouse genes	73080
Mouse SwissProt proteins	17082
Rat genes	43048
Rat SwissProt proteins	8135
Compounds	983111
Compounds with structure	966368
Endogenous compounds	5464
Nutritional compounds	127
Metabolites of xenobiotic	40335
Drugs	9117
- Biologics	1360
- Small Molecules	7757
- Approved drugs	2290
- Withdrawn drugs	261
- Clinical trial drugs	4993
- Discontinued drugs	1187
- Preclinical drugs	250
- Unknown	136
- Drug combination regimens	8445

MetaCore	number
Human genes in network	29503
Mouse genes in network	28505
Rat genes in network	18685
Chemical compounds	528016
Drugs	4944
Endogenous compounds	3602
Metabolic reactions	50304
Transport reactions	4591
Processing Reactions	4459
Pubmed journals	3765
Pubmed records	3584562
Pubmed articles (unique)	319065
Total amount of interactions	3181746
- Protein – Protein	1398912
- Compound – Protein	990222
- Compound – Compound	12180
- Metabolic enzyme -Reaction	61429
- Transporter – Reaction	5217
- Substrate, Product – Reaction	134335
- RNA – Protein	579451
Pathway maps	1590
- Human genes in maps	8132
- Mouse genes in maps	7409
- Rat genes in maps	7213
- Interactions in maps	35698

一、常用数据库 | 中山大学北校园图书馆

中山大学北校园图书馆——资源——常用数据库列表——页面底部



中山大学北校园图书馆 SUN YAT-SEN UNIVERSITY LIBRARY NORTH CAMPUS

概况 服务 资源 帮助中心 联系我们

中山大学北校园图书馆 > 资源 > 常用数据库

常用数据库

试用数据库

循证医学

专利资源

页面导航

中文数据库 外文数据库 外文全文电子期刊 工具类数据库

工具类数据库

NoteExpress ^①	Essential Science Indicators (基本科学指标) ^①
SciVal科研管理与全球前沿研究发现平台 ^②	InCites ^②
Journal Citation Reports (期刊引证报告) ^③	中科院JCR期刊分区表 (账号:sysu; 密码:84111666) ^④
MetaCore信号通路与组学研究数据库^⑤	

更多

<https://library.sysu.edu.cn/northcampus/commondatabase>

二、MetaCore信号通路与组学研究数据库 | 中山大学图书馆

中山大学图书馆——资源——数据库——医药卫生



中山大学图书馆 SUN YAT-SEN UNIVERSITY LIBRARY

概况 服务 资源 分馆 咨询台 联系我们

中山大学图书馆 > MetaCore信号通路与组学研究数据库

多媒体资源

学位论文

数据库

电子图书

电子期刊

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不得使用网络下载工具如迅雷、flashget、电驴等批量下载或多线程下载图书馆购买的电子资源; 不得连续、系统、集中、批量地进行下载、浏览、检索数据库等操作。

相关规定: 中山大学合理使用引进电子资源的规定 [中大图书 [2004] 1号文]

数据库公司/出版商: 科睿唯安

数据库名称: MetaCore信号通路

检索入口: <https://portal.gen>

检索指南

MetaCore_Advanced_Training_Manual_5.0.pdf

MetaCore_bio_manual_5.0.pdf

产品介绍_Metacore_系统生物学+作用机理.pdf

中山大学“MetaCore信号通路与组学研究数据库”账号申请表.docx

<https://library.sysu.edu.cn/eresource/1978>

Meta Core 支持的浏览器

考虑到如果使用不支持的浏览器，会遇到的问题，特此建议使用metacore推荐的以下四种。



TIP: Microsoft are withdrawing support for the Internet Explorer from August 17, 2021 and therefore, from October 1, **2021 Clarivate will no longer support IE**. You may continue to use IE for MetaCore, but over time you may encounter issues that our support team will not be able to help with. To ensure you continue to have the best experience with MetaCore we encourage you to upgrade to MS Edge or other supported browsers.

Meta Core 界面概览

Start PageApplications▼Help▼User: rsong▼

FileEditViewToolsHelp

Activate/Deactivate

HomeMy Data

Name	Type	Date
My Data		
STRUCTURES		08/28/2021 05:34:41
VARIANT EXPERIMENTS		10/08/2021 09:03:47
EXPERIMENTS		10/08/2021 12:13:40
SAVED NETWORKS		11/16/2021 05:53:30
NETWORK OBJECTS LISTS		12/20/2021 09:50:56
Lost&Found		15/01/2021 15:01:31
Active Data		

此区域为数据区，用户上传的数据会在这一区域的文件夹中体现。

HomeActive Data

Name	Type	Date
[...] Active Data		

此区域为数据激活区，在Metacore中，数据激活之后会出现在此区域，未激活的数据不能分析。

Genomic AnalysisMost Popular QuestionsUploadWorkflows & ReportsOne-click AnalysisBuild NetworkCustom ContentPredict Compound Activity (MetaDrug)Search & Browse Content

1Genomic Variant Analysis2Cohort Analysis3Somatic Mutation Detection4Trio Analysis5Genomic Variant Filter

此区域为常用工作区，分为9个子板块，如上方所示，点击子板块会进入相应的分析界面，可根据需要进入子版块进行分析。

Filter and Analyse Genomic Variants

The Genomic Analysis is designed to allow users to load genomic variant into MetaCore. Once loaded, variants can be filtered using a combinations of annotations, functional predictions and statistical analyses. As well as filtering, variant datasets can be combined with gene expression datasets for further downstream analysis using the enrichment, network building or interactome analysis.

Upload Genomic Variants: parse standard VCF or proprietary VX format files. VCF files will be converted to proprietary VX files for downstream analysis.

Cohort Analysis: Identify groups of variants based on a common annotation or functional prediction. This can be used to filter variants based on a specific group.

Somatic Mutation Detection: Compare tumour/normal pairs for somatic mutations in active dataset.

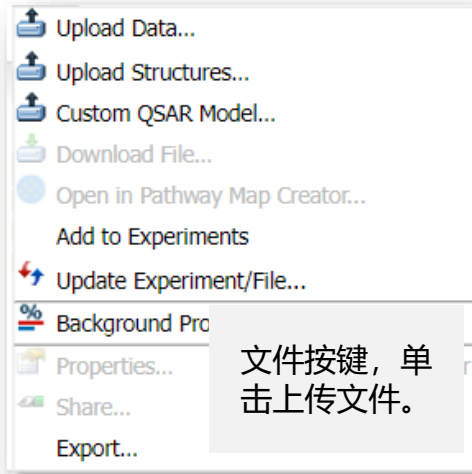
Trio Analysis: Analyse family trios for inherited variants, filter for autosomal recessive and sex linked variants in active dataset.

Genomic Variant Filter: Filter a single or multiple variant files according to all the annotations and functional predictors found in the Genomic Variant Database.

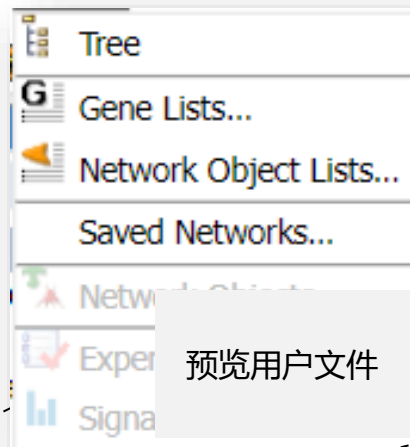
此区域为注释区，功能为对方所选择的模块功能进行备注。

Clarivate™

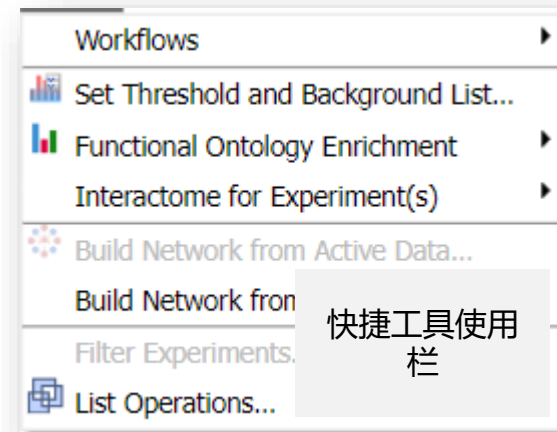
Insert footer12



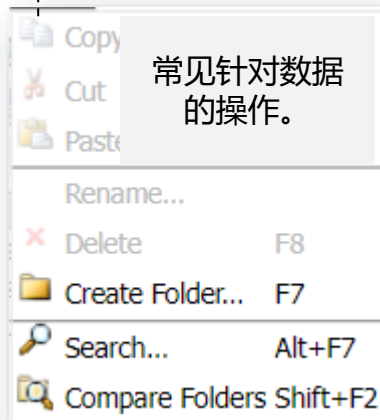
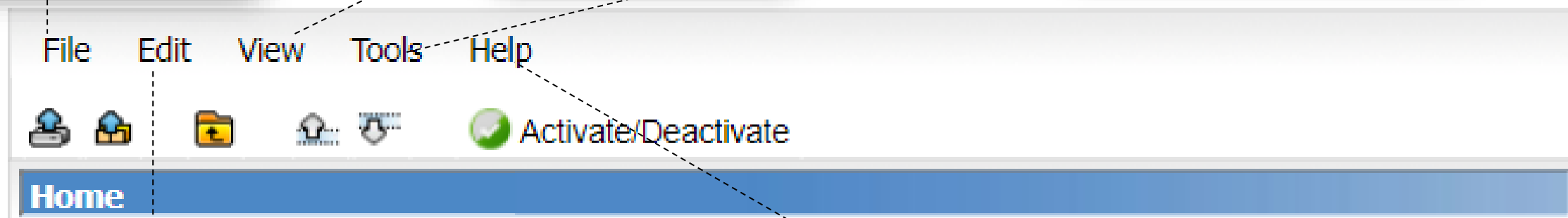
文件按键，单击上传文件。



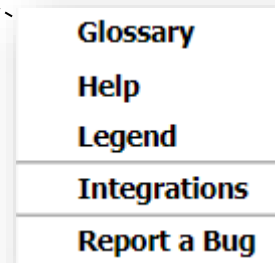
预览用户文件



快捷工具使用栏

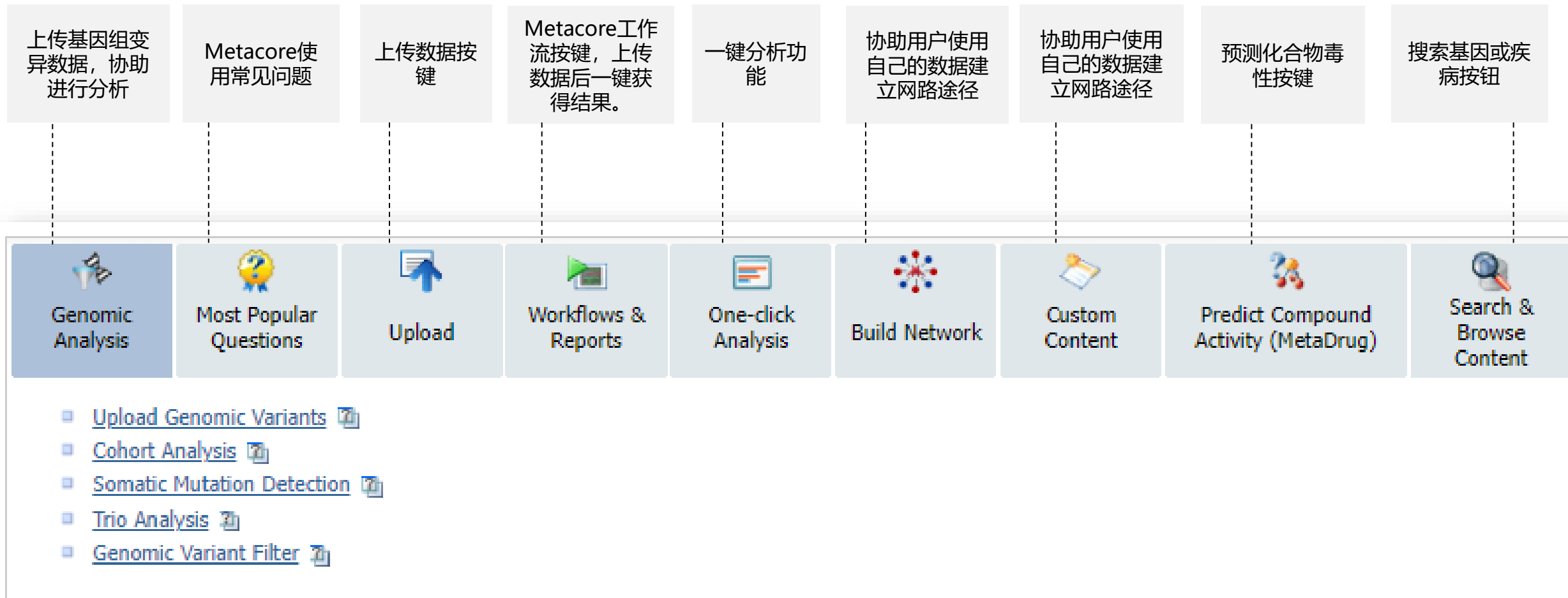


常见针对数据的操作。



常见线上文档或出现问题时报错。

Meta Core 界面功能介绍



日程

第一部分：MetaCore数据平台简介

第二部分：MetaCore重点功能介绍

第三部分：系统生物学案例分享

第四部分：内容回顾与总结

MetaCore, a Cortellis Solution

• 关键问题

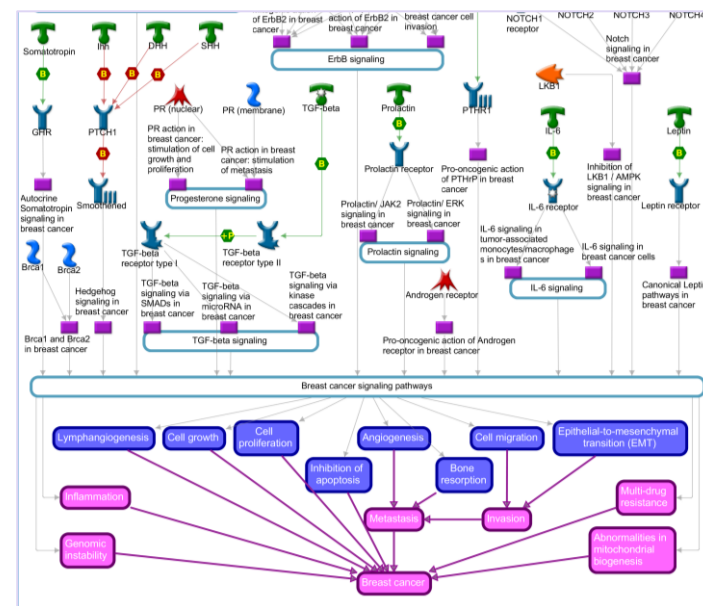
- 我的组学数据在健康和患病分子途径的背景下意味着什么?
- 在我的疾病领域已经做了什么研究，可以帮助我开发新的假设?
- 在我感兴趣的途径或网络中，每种分子相互作用的机制，方向性和作用是什么?

• 功能和数据源

- 一键式分析和节省时间的工作流程，如富集分析、实验比较、生物标志物评估等
- 来自同行评审文献的 1, 500 多种**手动策划的途径**
- 3M+分子相互作用的机制、方向性和效果

关键解决方案

- 模拟疾病途径并研究因果机制
- 发现药物靶点和生物标志物
- 可视化生物关系



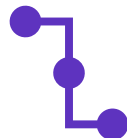
MetaCore 基础功能与应用价值-概述



EZ Search

功能

- 检索某对象的基因/突变/蛋白/药物/疾病等基本信息;
- 查看某对象参与的重要疾病过程及信号通路;
- 查看与该对象有直接相互作用关系的其他对象;
- 多种算法构建单个/多个对象的相互作用关系网络;
- 多组学数据同时分析, 富集相关性最高的通路;



Build Network



Enrichment Analysis

价值

- 帮助科研人员快速、全面、准确了解某个新的领域, 提供项目/课题所需的基本资料, 提高科研效率;
- 通过构建相互作用网络, 发现潜在的分子间相互作用关系, 为项目/课题顺利进行提供可能的方向;
- 通过上传数据富集分析, 挖掘实验数据中隐藏的逻辑关系, 帮助科研人员研究疾病机制、药物靶标、发现生物标记物及药物研发等;

查资料

指方向

定逻辑



日程

第一部分：MetaCore数据平台简介

第二部分：MetaCore重点功能介绍

第三部分：系统生物学案例分享

第四部分：内容回顾与总结

1-检索和靶点机制相关药物

- MetaCore具有丰富的检索功能，协助高效检索。



CASE-通过知识挖掘了解肿瘤免疫靶点PD-1

EZ search

EZ search

Advanced Search

Export to MetaCore

 **EZ Search**

Name

Objects Found

Genes (15)

Gene Aberrations (222)

Proteins (63)

RNA (56)

Compounds (2)

Network Objects (13)

Interactions (76)

Drugs (6)

Find **Network Objects** that regulate transcription or regulation of PD-1 ... with high trust only

Find:

that ▾

inter

 **PD-1**

Network object |  [Build Network](#)

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Gene Details

Protein Details

Thomson Reuters Integrity

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Pathways and Processes

Diseases

Interactions

Human	Mouse
▼ Gene Details	
<u>PDCD1</u>	
Symbols	PDCD1, CD279, hPD-1, H
Full Name	programmed cell death 1
Synonyms	protein PD-1, systemic lup programmed cell death pr
Description	This gene encodes a cell s superfamily. This protein i a role in their differentiat the thymus when anti-CD3

通过知识挖掘了解肿瘤免疫靶点PD-1



EZ Search

Name

☐ Exact match

[Search compounds by structure](#)

Objects Found

[Genes \(16\)](#)
[Gene Aberrations \(364\)](#)
[Proteins \(77\)](#)
[RNA \(71\)](#)
[Compounds \(2\)](#)
[Network Objects \(18\)](#)
[Interactions \(263\)](#)
[Drugs \(11\)](#)
 [Small Molecule Drugs \(1\)](#)
 [Biologics \(10\)](#)
[Adverse Effect Agents \(1\)](#)
[Maps \(37\)](#)
[Networks \(1\)](#)

Selected Proteins

Results

- ☐ **Y** [PDCD1](#) Programmed cell death protein 1 ([Mus musculus](#))
SwissProt ID: Q02242;
Synonyms: CD279, mPD-1, PDCD1_MOUSE, Programmed cell death protein 1, Protein **PD-1**
Genes: [Pdc1](#) (*Mus musculus*)
Clarivate Analytics Integrity: [Pdc1](#) (*Mus musculus*)
Description: Inhibitory receptor on antigen activated T-cells that plays a critical role in induction and maintenance of immune tolerance to self (PubMed:10485649, PubMed:11698646, PubMed:11209085, PubMed:21300912). Delivers
Associated with GO Processes: [adaptive immune response](#), [apoptotic process](#), [immune system process](#), [negative regulation of apoptotic process](#), [negative regulation of immune response](#), [negative regulation of tolerance induction](#), [positive regulation of T cell apoptotic process](#), [positive regulation of apoptotic process](#)
- ☐ **Y** [Pdc1 predicted](#) programmed cell death 1 (predicted) ([Rattus norvegicus](#))
Synonyms: programmed cell death 1 (predicted), programmed cell death protein 1-like
Genes: [Pdc1](#) (*Rattus norvegicus*)
Clarivate Analytics Integrity: [Pdc1](#) (*Rattus norvegicus*)
- ☐ **Y** [PDCD1](#) Programmed cell death protein 1 ([Homo sapiens](#))
SwissProt ID: Q15116;
Synonyms: CD279, hPD-1, PDCD1_HUMAN, Programmed cell death protein 1, Protein **PD-1**, SLEB2, systemic lupus erythematosus susceptibility 2
Genes: [PDCD1](#) (*Homo sapiens*)
Clarivate Analytics Integrity: [PDCD1](#) (*Homo sapiens*)
Description: Inhibitory receptor on antigen activated T-cells that plays a critical role in induction and maintenance of immune tolerance to self (PubMed:21276005). Delivers inhibitory signals upon binding to ligands CD274/PDCD1L1 and
Associated with Diseases: [Arthritis](#), [Rheumatoid](#), [Carcinoma](#), [Non-Small-Cell Lung](#), [Carcinoma](#), [Renal Cell](#), [Central Nervous System Neoplasms](#), [Cervical Intraepithelial Neoplasia](#), [Esophageal Squamous Cell Carcinoma](#), [HIV Infections](#),
Associated with GO Processes: [T cell costimulation](#), [adaptive immune response](#), [apoptotic process](#), [humoral immune response](#), [immune system process](#), [multicellular organism development](#), [negative regulation of apoptotic process](#),

通过知识挖掘了解肿瘤免疫靶点PD-1



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GO Processes

GO Molecular Functions

Diseases

Associated Diseases

Drug Target for

Interactions

General

Protein Details

PDCD1_HUMAN

Name	PDCD1_HUMAN / Programmed cell death protein 1
Synonyms	CD279, hPD-1, PDCD1_HUMAN, Programmed cell death protein 1, Protein PD-1, SLEB2, systemic lupus erythematosus susceptibility 2
Description	Inhibitory receptor on antigen activated T-cells that plays a critical role in induction and maintenance of immune tolerance to self (PubMed:21276005). Delivers inhibitory signals upon binding to ligands CD274/PDCD1L1 and CD273/PDCD1LG2 (PubMed:21276005). Following T-cell receptor (TCR) engagement, PDCD1 associates with CD3-TCR in the immunological synapse and directly inhibits T-cell activation (By similarity). Suppresses T-cell activation through the recruitment of PTPN11/SHP-2: following ligand-binding, PDCD1 is phosphorylated within the ITSM motif, leading to the recruitment of the protein tyrosine phosphatase PTPN11/SHP-2 that mediates dephosphorylation of key TCR proximal signaling molecules, such as ZAP70, PRKCQ/PKCtheta and CD247/CD3zeta (By similarity). The PDCD1-mediated inhibitory pathway is exploited by tumors to attenuate anti-tumor immunity and escape destruction by the immune system, thereby facilitating tumor survival (PubMed:28951311). The interaction with CD274/PDCD1L1 inhibits cytotoxic T lymphocytes (CTLs) effector function (PubMed:28951311). The blockage of the PDCD1-mediated pathway results in the reversal of the exhausted T-cell phenotype and the normalization of the anti-tumor response, providing a rationale for cancer immunotherapy (PubMed:22658127, PubMed:25034862, PubMed:25399552).
Molecular Weight	31647
Genes	PDCD1
Network objects	PD-1
Precursor	PDCD1 (HUMAN) transcript
Localization	external side of plasma membrane, integral component of membrane, plasma membrane
Organ/Tissue/Fluid Expression (RNA)	Adrenal Cortex; Adrenal Glands; Amniotic Fluid; Amygdala; Appendix; Atrioventricular Node; Blood; Bone Marrow; Brain; Caudate Nucleus; Cerebellum; Cerebral Cortex; Ciliary ganglion; Conjunctiva; Corpus Uterus; Fetal Brain; Fetal Liver; Fetal Lung; Fetal Thyroid; Frontal Lobe; Ganglia, Spinal; Globus Pallidus; Gyrus Cinguli; Heart; Hippocampus; Hypothalamus; Kidney; Lacrimal Apparatus; Lens, Crystalline; Leydig Cells; Liver; Lung; Lymph Nodes; Medulla Oblongata; Muscle, Skeletal; Muscle, Smooth; Myometrium; Occipital Lobe; Olfactory Bulb; Ovary; Palatine Tonsil; Pancreas; Parietal Lobe; Pituitary Gland; Placenta; Plasma; Pons; Prefrontal Cortex; Prostate; Respiratory Mucosa; Salivary Glands; Seminiferous Tubules; Spinal Cord; Superior Cervical Ganglion; Temporal Lobe; Testis; Thalamus; Thymus Gland; Thyroid Gland; Tongue; Trachea; Trigeminal Ganglion; Urinary Bladder; Urothelium; Uterus

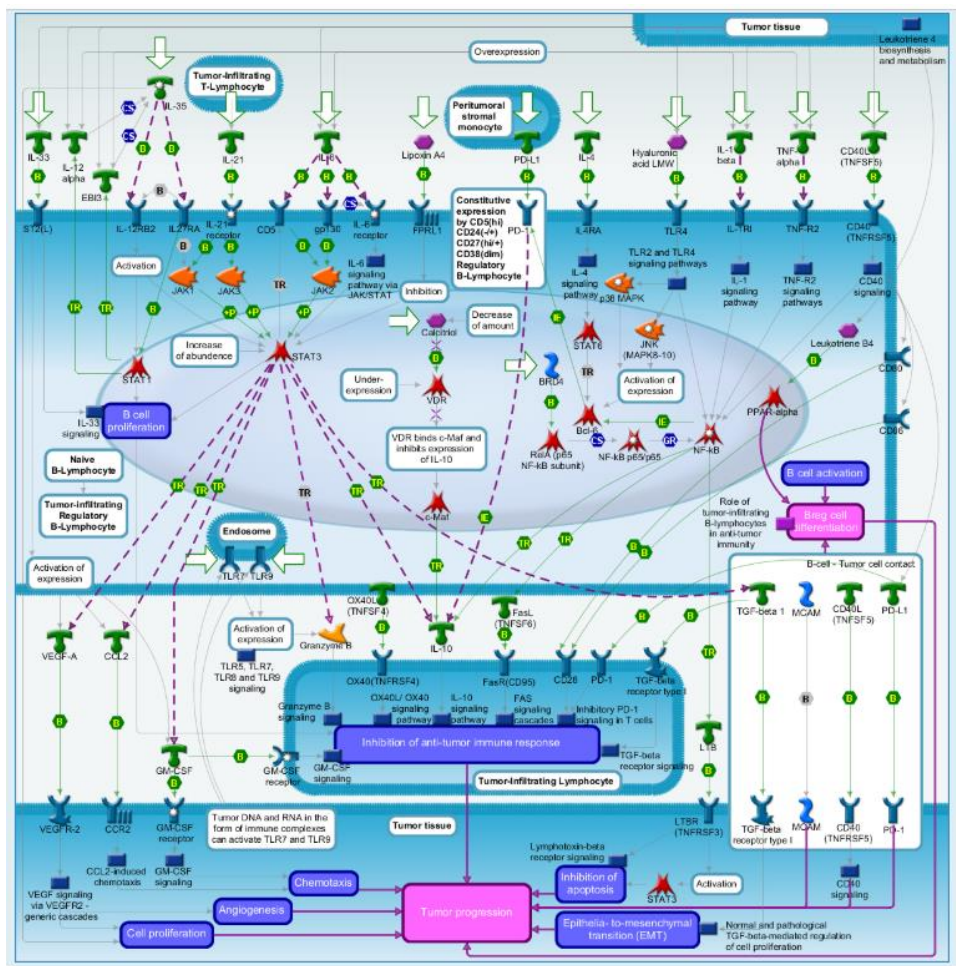
Clarivate Analytics Integrity

External Databases

Vendors

通过知识挖掘了解肿瘤免疫靶点PD-1

调节性B细胞与肿瘤细胞的相互作用



B-regulatory cells and tumor cells intercellular interaction

Abstract:

In neoplastic disorders, B-regulatory cells (Bregs) are generated in response to signals from the tumor microenvironment and in turn promote tumor growth through expression of number of mediators that can act directly and indirectly on the diversity of leukocyte subsets infiltrating developing tumors and evolving neoplastic cells. Bregs express a variety of cytokines and other immunosuppressive molecules including *IL-10*, *IL-35*, *TGF-beta 1*, *PD-L1*, *PD-1*, *FasL* (TNFSF6), *CD40L* (TNFSF5), *CD40* (TNFRSF5) and *OX40L* (TNFSF4). This cell subset may also express proteases, such as *Granzyme B*, that directly impair T cell function.

Details:

In neoplastic disorders, B-regulatory cells (Bregs) are generated in response to signals from the tumor microenvironment and in turn promote tumor growth through expression of number of mediators that can act directly and indirectly on the diversity of leukocyte subsets infiltrating developing tumors and evolving neoplastic cells [1], [2], [3], [4], [5]. In addition to secreting mediators, tumor cells can promote Breg cells generation via direct cell-to-cell contact [6], [7], [8].

Bregs infiltration has been identified in a many malignancies including ovarian, gastric, non-small cell lung cancer, pancreatic, esophageal, head and neck, tongue squamous cell carcinoma and hepatocellular carcinomas [9], [10], [11], [12], [13], [14], [15], [16], [17].

Bregs express a variety of suppressive cytokines and ligands which are implicated in the suppression of anti-tumor immunity including *IL-10*, *IL-35*, *TGF-beta 1*, *PD-L1*, *PD-1*, *FasL* (TNFSF6), *CD40L* (TNFSF5), *CD40* (TNFRSF5) and *OX40L* (TNFSF4). This cell subset may also express proteases, such as *Granzyme B*, which directly impair T cell function [3], [4], [5], [18], [19], [20].

Capability of tumor-infiltrating B cells to differentiate into Bregs subset is regulated by B cell antigen receptor (BCR), *IL-35*, *IL-21*, *IL-6*, *PD-L1*, *IL-4*, *TLR4*, *IL-1 beta*, *TNF-alpha*, *CD40L* (TNFSF5) and *Calcitriol* signaling pathways [15], [21], [22], [23], [24], [25].

IL-35, via *IL-12RB2* and *IL27RA*, activates *STAT1* and *STAT3*, thereby inducing Breg subset, and promotes the expression of *IL-35* subunits *IL-12 alpha* and *EBI3*, and *IL-10* expression [26], [27]. Breg-mediated production of *IL-35* can lead to tumor cell proliferation [19], [20]. Overexpression of *IL-12 alpha* and *EBI3* in tumor tissue can result in higher induction of Bregs subset, elevated production of *IL-35* and *IL-10*, which in turn promote tumor progression [28], [29], [30], [31], [32].

B cells stimulated with *IL-21* also respond with the development of a population of B cells expressing *IL-10*, *IL-21* via *IL-21 receptor* induces *JAK1* and *JAK3*-dependent *STAT3* pathway. Activated *STAT3* promotes the expression of suppressors of anti-tumor immune response *IL-10* and *Granzyme B* [5], [22], [33]. Moreover, tumor DNA and RNA in the form of immune complexes can activate *TLR7* and *TLR9* that elevate the expression levels of *Granzyme B* [22], [34], [35], [36].

IL-6 can induce the expression of *IL-10* via *CD5* and *IL-6 receptor*-dependent activation of *STAT3*. *IL-6* directly binds to *CD5* and *gp130* that leads to activation of *JAK2* and its downstream transcription factor *STAT3*. *STAT3* upregulates *CD5* expression, thereby forming a feed-forward loop in the B cells. In addition, *IL-6*, possibly via *STAT3* activation, promotes the expression of *VEGF-A*, *CCL2* and *GM-CSF*, by B cells, which leads to tumor cell population proliferation, angiogenesis and chemotaxis [23], [37], [38], [39], [40], [41], [42], [43], [44]. Overexpression of *IL-6* in tumor can lead to increased production of *IL-10* by Bregs [45], [46], [47].

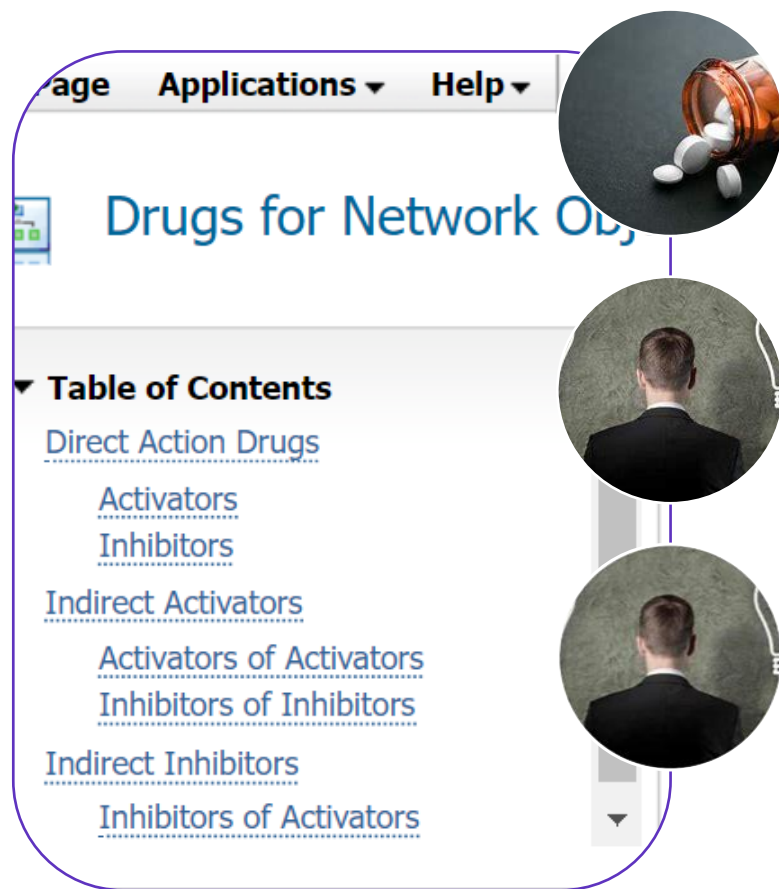
Name: Immune response_TCR signaling

File Show/Hide Network objects Interactions Network layout Expand/collapse Trace mode About network



查找网络对象的药物-Drugs for Network Object

MetaCore提供直接或间接地激活或抑制所选对象的药物。这些药物被安排在三个主要组别，每个组别有两个分组，说明如下：



Direct action drugs

- Activators: **直接激活**原始网络对象的药物。
- Inhibitors: **直接抑制**原始网络对象的药物。

Indirect activators

- Activators of activators: 激活原始网络对象的药物。
- Inhibitors of inhibitors: 抑制原始网络对象的药物

Indirect inhibitors

- Inhibitors of activators: 抑制网络对象的药物，能激活原有的网络对象。
- Activators of inhibitors: 激活网络对象的药物，抑制了原有的网络对象。

CASE: PD-1 网络对象的药物-Drugs for Network Object

▼ Indirect Activators

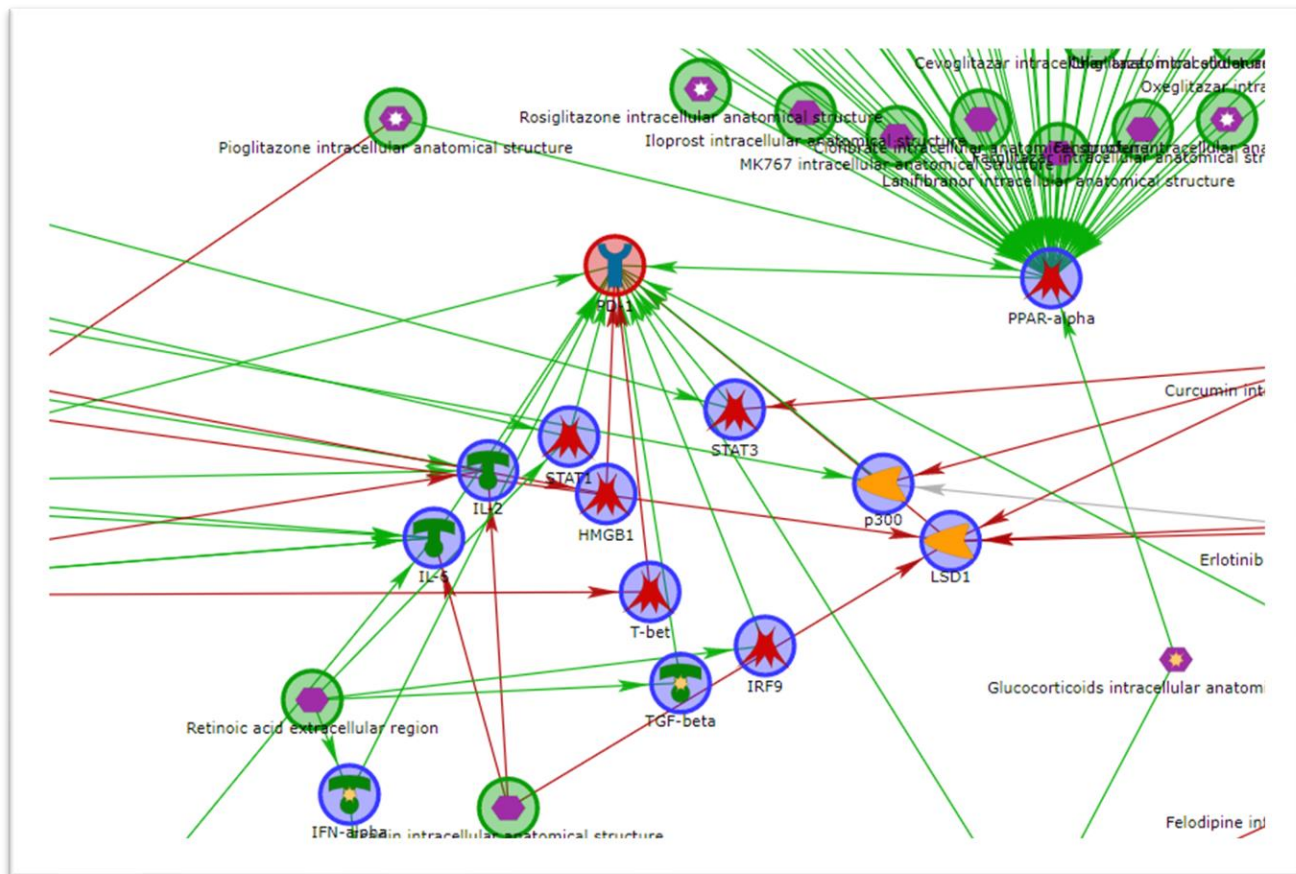
▼ Activators of Activators

Indirect Activators

NW Object	#	NW Object 2	Reference (NW Obj-NW Obj2)	Drug	Mechanism	Reference (NW Obj2-Drug)
PD-1	1.	PPAR-alpha		Imiglitzar intracellular anatomical structure	Binding	15219816
				Oleic acid intracellular anatomical structure	Binding	10198642,10529898,10691680,16731579,16731579,8611035,16731579
				Eicosapentaenoic acid intracellular anatomical structure	Binding	9113986,10198642,10529898
				Linolenic acid intracellular anatomical structure	Binding	16731579,10198642,16731579,9113986,16731579
				GW501516 intracellular anatomical structure	Binding	12699745,16797985,17512197,12699745
				Chiglitazar intracellular anatomical structure	Unspecified	
				Flufenamic acid intracellular anatomical structure	Unspecified	9013583
				Muraglitazar intracellular anatomical structure	Binding	15771468

CASE: PD-1 网络对象的药物-Drugs for Network Object

Indirect Activators



原始对象，红色圈。



药物，绿色圈。



中间物体，蓝色圈。

2-按细胞类型/组织或细胞定位确定基因的优先级

- 从筛选中了解候选基因列表，更有效地识别和优先处理有前途的靶标。



2.按细胞类型/组织或细胞定位确定基因的优先级

Filter Experiments

Filter by:

- ☐ Species
- ☐ Fluid
- ☒ Tissue
- ☐ Disease
- ☐ GO Process
- ☐ GO Molecular Function
- ☐ Toxic Pathology

liver

Click to check any individual term. Use Shift+Click to include child terms.

☐ Expand all ☐ Collapse all

☒ Liver

☐ Hemic and Immune Systems

☐ Blood

☐ Immune System

☐ Body Regions

☐ Breast

☐ Urogenital System

GO Localizations

Enrichment | Save Enrichment

Experiments

Experiment name: M1 - activated vs. M0 - unactivated_FF

Export Build Network

Network Objects

Export Build Network

highlight text... 0/0

Result pages: 1 2 3 15 (Showing results 1 to 20 of 285)

#	Name	
1	A630077B13Rik	2.817
2	ABCC5	5.070
3	ACSL1	30.025
4	Adenosine A2a receptor	3.043
5	cell periphery	5.195
6	plasma membrane	2.056
7	organelle	2.249
8	ALP	2.554
9	APS	2.159
10	Aquaporin 9	7.728
11	ASEF2	5.235
12	ASK1 (MAP3K5)	2.992
13	ATF-4	2.217
14	ATP6V0A	2.149
15	ATP6V0A2	2.149
16	ATR/TEM8	20.582
17	ATRAP	3.363
18	BAFF(TNFSF13B)	2.055
19	Bcl-3	2.357
20	BETA-1G-H3	5.532

Conditional Search

Find Network Objects that are expressed in Cell Lines HEK293 ...

Find: Network Objects that are expressed in Cell Lines HEK293

Background List

List Source: ☐ Array ☐ Gene list ☒ Network object list

List Name: Cell_line_HEK293

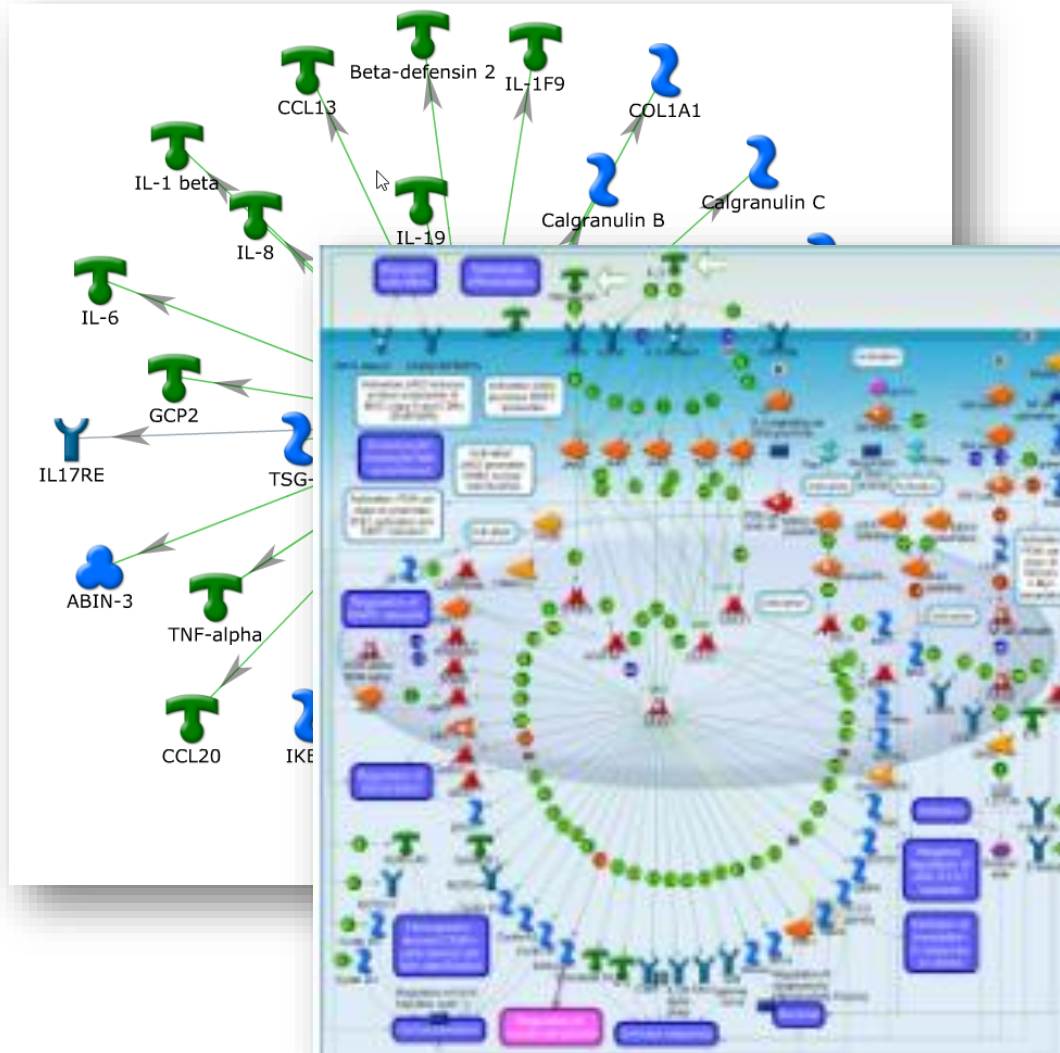
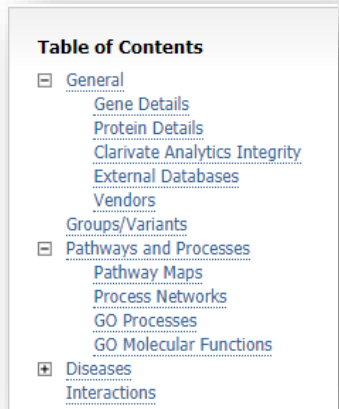
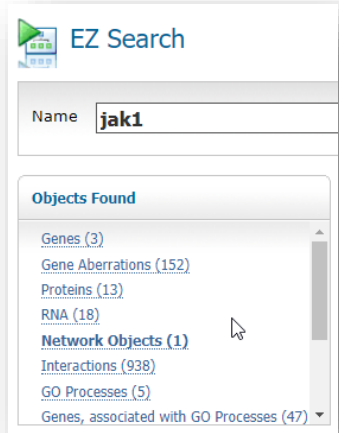
- 从候选基因列表中识别潜在靶标
- 优先考虑位于plasma membrane-细胞膜中的候选物或已知在特定细胞系或组织中表达的候选物，以专注于那些成功可能性较大的候选物。

3-了解靶点和疾病之间的关联

- 加速并简化查找文献证据,高效确定候选目标的过程。



3.靶点 - 疾病关联



- 加速并简化查找文献证据以确定候选目标的过程
- 建立基因- 疾病背后的生物学原理关联，以便更支持做出选择决策。

3.靶点 – 疾病关联

The screenshot shows a software interface with two tabs: 'Pathway Maps' and 'Network Objects'. Under 'Pathway Maps', there are buttons for 'Export', 'Export to image', and 'Reorder enrichment profile'. Below these is a list of maps:

#	Maps
1	Role of IL-23/ T17 pathogenic axis in psoriasis
2	Immune response IL-17 signaling pathways
3	Th17 cells in CF

A 'Link Info' pop-up window is open, displaying a link between 'IL-3' and 'IL-3 receptor'. The link is represented by a green arrow with a 'B' in a circle in the middle. Below the link, there is a 'References' section with buttons for 'Hide All Details', 'Show All Details', and 'Export to EndNote'.

- 加速并简化查找文献证据以确定候选目标的过程
- 每一条疾病通路都有专业编辑进行注释。

4-定义特殊的疾病机制

- 加速并简化查找文献证据以确定候选目标的过程。
- 通过建立自己的路径并使用metacore专有知识进行注释，以确保研究相关人员之间拥有清晰一致的沟通。



4. 建立研究特殊路径

Genes in Special pathway List

Export Build network Drug Look-up Delete Search Maps Search Networks

#	Genes Code	Species	Location
1	OCL2	Homo sapiens	17q12
2	CCR5	Homo sapiens	3p21.31
3	CCR5AS	Homo sapiens	3p21.31
4	CXCL8	Homo sapiens	4q13.3
5	DDX42	Homo sapiens	17q23.3

Network objects Pre-filters Additional options

Filter by:

- ☒ Tissues
- ☐ Cell lines
- ☐ Subcellular localizations
- ☒ Species
- ☒ Orthologs
- ☐ Object types
- ☐ Interaction types

highlight text...

Mechanisms:

- ☐ ? Unspecified
- ☐ CM Covalent modification
- ☐ +P Phosphorylation
- ☐ -P Dephosphorylation
- ☐ B Binding
- ☐ Cn Competition
- ☐ T Transformation
- ☐ C Cleavage
- ☐ TR Transcription regulation
- ☐ IE Influence on expression
- ☐ Z Catalysis
- ☐ Tn Transport
- ☐ cRE Co-regulation of transcription
- ☐ PE Pharmacological effect
- ☐ TE Toxic effect
- ☐ M miRNA binding
- ☐ Rg Regulation

Effects:

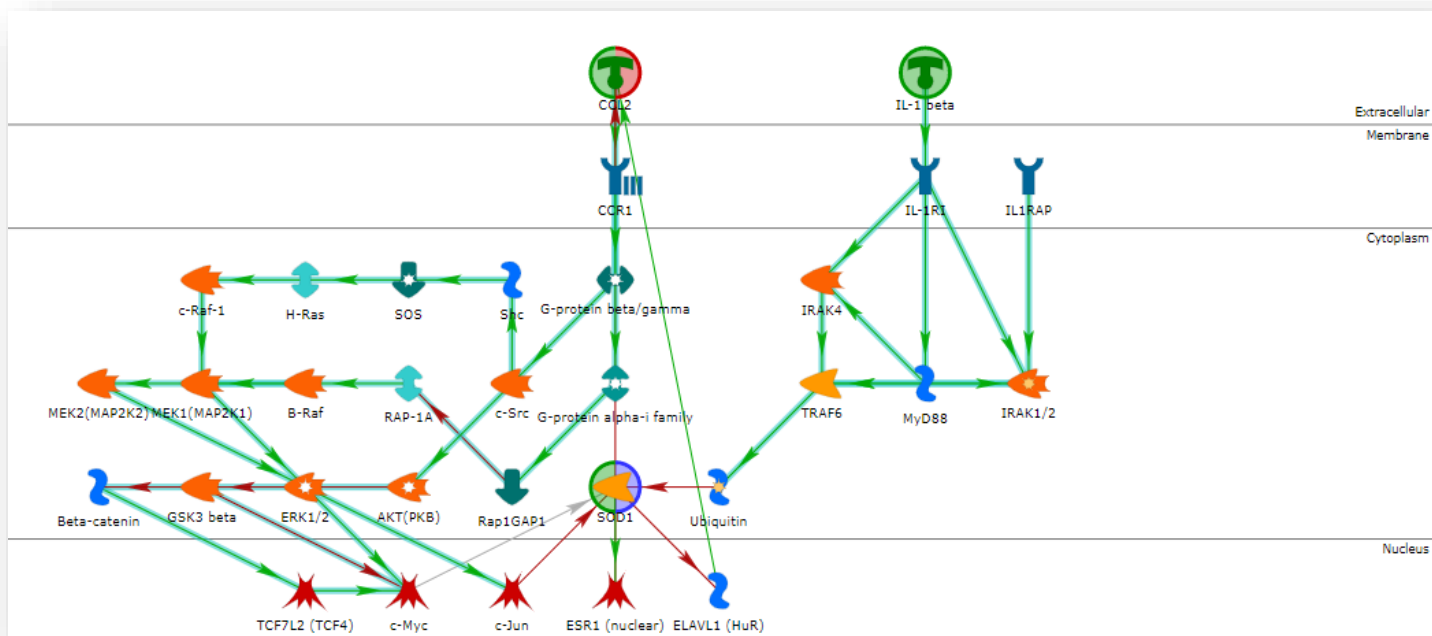
- ☐ Activation
- ☐ Inhibition
- ☐ Unspecified

Selected Items:

- Tissues[3]
Olfactory Mucosa; Respiratory Mucosa; Trachea
- Species[1]
Human *H. sapiens*
- Orthologs[1]
Human *H. sapiens*

- 分析特殊的基因列表。
- 过滤特殊研究偏好：组织（呼吸道黏膜，气管位置，）物种过滤等。

4. 建立研究特殊路径



- 可调节通路图
- 提供多种数据进行筛选。
- 建立研究路径，用 metacore 专有知识进行注释，确保研究相关人员之间拥有清晰一致的沟通。

4.通路图分析

The screenshot displays the Clarivate software interface. At the top, a menu bar includes 'File', 'Show/Hide', 'Network objects', 'Interactions', 'Network layout', 'Expand/collapse', and 'Trace mode'. Below this is a toolbar with various icons. A purple box highlights the 'About network' menu, which contains 'Network description', 'Network statistics', and 'Legend'. Another purple box highlights the 'Toxic Pathologies' table, which lists various toxic pathologies and their associated statistics.

#	Toxic Pathology	%	p-Value	Genes from Active Data
1	Small intestine, intestinal epithelium injury	48.39	3.100e-09	No such genes
2	Intestinal epithelium injury	74.19	5.786e-09	No such genes
3	Small intestine, mucosa injury	48.39	1.299e-08	No such genes
4	Intestine pathology	83.87	3.050e-08	No such genes
5	Small intestine injury	51.61	4.315e-08	No such genes
6	Bone-femur, osteoclast injury	25.81	7.895e-08	No such genes
7	Colon-dysplasia	29.03	8.497e-08	No such genes
8	Large intestine-dysplasia	29.03	8.497e-08	No such genes
9	Intestine-proliferation	45.16	1.880e-07	No such genes
10	Intestine-dysplasia	29.03	2.342e-07	No such genes
11	Lung-interstitial edema	32.26	2.849e-07	No such genes
12	Bone-osteoclast injury	25.81	3.973e-07	No such genes

- 一键获得关于通路图注解以及相关疾病网络。
- 快速进一步挖掘相关疾病机制。

5-对比研究 workflow

Compare Experiments Workflow

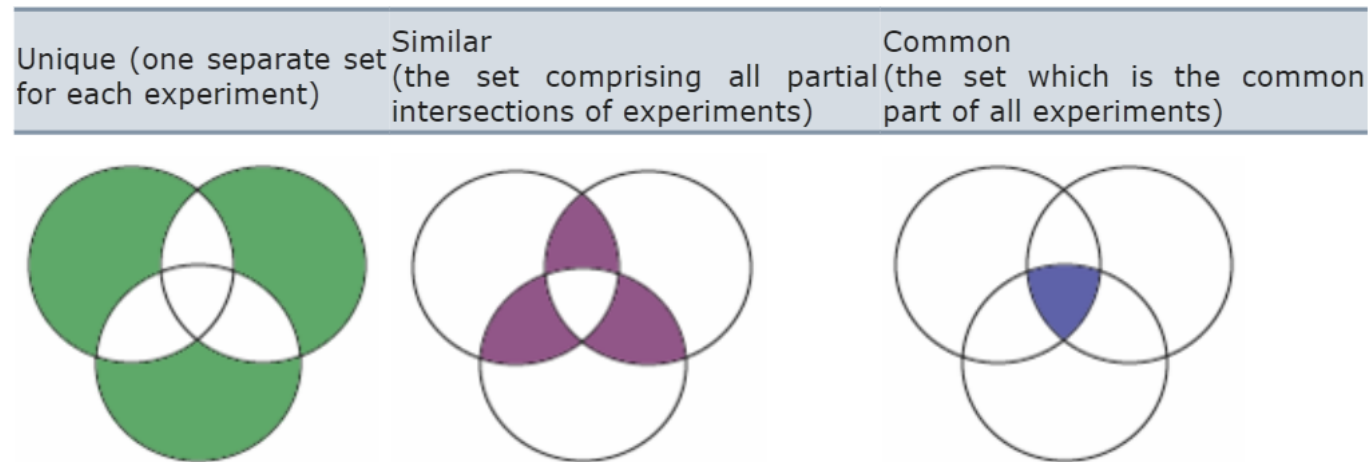
实用场景

- 多个数据集情况。
- 希望了解哪些过程（通路、网络、基因本体、疾病等）是独特的，哪些是数据集共有的。
- 例：已在组学数据中识别出两个患者亚组，并希望了解每个亚组独有的生物学过程

A large, stylized graphic of the letters 'VS' in a light beige color. The letters are bold and have a slight 3D effect with a dark shadow. They are set against a dark background with a diagonal line running from the top left to the bottom right, creating a sense of division or comparison.

5.数据集意义

Figure 2. Datasets



- “Unique” set: 每个单独的实验（由该实验特有的对象组成）。
- “Similar” set：由所有既不唯一，也不常见的对象组成）。
- ” Common “set:（由每个实验中发现的所有网络对象组成）。

分析后数据颜色

- Unique”set 着彩色
- “similar” set 不着色
- “common” set: 斑马纹

5. Compare Experiments Workflow-操作步骤

The screenshot displays the Clarivate software interface. The top navigation bar includes several icons and labels: Genomic Analysis, Most Popular Questions, Upload, Workflows & Reports (highlighted with a purple box), One-click Analysis, Build Network, Custom Content, Predict Generated, and Search & .

Below the navigation bar, the 'Data Analysis Workflows' section is visible. It contains a list of workflows: Enrichment Analysis, Analyze Single Experiment, Compare Experiments (highlighted with a purple box), Compare Compounds, Toxicity Analysis, Biomarker Assessment, and Interactome Analysis.

A dropdown menu for 'Experiments' is open, showing a table of experiments:

Experiment name	Species	Network Objects
PNC_453.2_genelist	Homo sapiens	7504
PNC_392.4_genelist	Homo sapiens	5094

Below the table, a list of comparison results is shown:

- Pathway Maps
- GO Processes
- Process Networks
- Diseases (by Biomarkers)
- Network Statistics

The 'Comparison Results' section is highlighted with a purple box.

5.Compare Experiments Workflow

▼ Experiments

Experiment name	Species	Network Objects
PNC_453.2_genelist	Homo sapiens	7504
PNC_392.4_genelist	Homo sapiens	5094

- Pathway Maps
- GO Processes
- Process Networks
- Diseases (by Biomarkers)
- Network Statistics

Settings

Threshold
0

P-value
1

Signals
☐ up
☐ down
☒ both

Apply

▼ Comparison Results

#	Unique	Similar	Common	Recalculate
1	2452	42	0	5052

back to top

▼ Pathway Maps

Export

Export to image

Filter by Map Categories

Filtered

Sorting method: Similarity by maps

#	Maps	0	0.3	0.6	0.9	1.2	1.5	1.8	2.1	-log(pValue)	pValue	err(-log(pValue)) [†]	FDR	Ratio
1	Cigarette smoke-induced proliferation, metaplasia and survival of airway epithelial cells										1.000e+0	0.850	1.000e+0	0/50
2	NF-κB-, AP-1- and MAPKs-mediated proinflammatory cytokine production by eosinophils in asthma										1.000e+0	1.000	1.000e+0	0/43
3	Role of type 2 innate lymphoid cells in asthma										1.000e+0	1.000	1.000e+0	0/38
4	Role of integrins in eosinophil degranulation in asthma										1.000e+0	1.000	1.000e+0	0/58

Compare Experiments Workflow-结果

Export

close

Name: VS

To: Excel

Select columns to export

Genes/Network object of

☒ Homo sa

☐ Mus mus

☐ Rattus ni

Exporting...

☐ Through:

Human (H. sapiens)

Show additional options

Export

Cancel

MetaCore Data								CDDI Data				PNC_392.4_genelist		PNC_453.2_genelist	
#	Input ID	Network Object Name	Gene Symbol	Unit (protein or chem)	Object Type	Description	Therapeutic Drugs	CDDI Biomarker	CDDI Biomarker Role	CDDI Biomarker Type	CDDI Genes & Targets	Sign ⁺	p-value	Sign ⁺	p-value
4	ENSG00000175793				Generic binding protein				Diagnosis; Predicting Drug Resistance; Predicting Treatment Efficacy	Genomic	C-X-C motif chemokine ligand 5; ENAH actin regulator; Kruppel like factor 5; MIB E3 ubiquitin protein ligase 1; S100 calcium binding protein A8; SMAD family member 8	1	0	1	0
5	ENSG00000175793				Generic binding protein				Predicting Treatment Efficacy	Genomic	G protein subunit gamma 7; H2B clustered histone 8; H2B clustered histone 7; ISG15 ubiquitin like modifier; RecQ like helicase; SEL1L subunit subunit of ERAD E3	1	0	1	0
6	ENSG00000175793				Generic binding protein				Predicting Treatment Efficacy	Genomic		1	0	1	0
7	ENSG00000175793				Generic binding protein				Diagnosis	Genomic		1	0	1	0
8	ENSG00000175793				Generic binding protein				Diagnosis	Genomic; Proteomic		1	0	1	0
9	ENSG00000175793				Generic binding protein				Prognosis	Genomic	2'-5'-oligoadenylate synthetase 3; 2'-5'-oligoadenylate synthetase like; 3-hydroxy-3-methylglutaryl-CoA synthase 1; 5'-nucleotidase, cytosolic; IIR; ADP absorption	1	0	1	0
10	ENSG00000175793				Generic binding protein				Differential Diagnosis	Genomic		1	0	1	0
11	ENSG00000175793				Generic binding protein				Diagnosis	Proteomic		1	0	1	0
12	ENSG00000175793				Generic binding protein				Prognosis - Risk Stratification	Genomic	Alv/REF export factor; H2A.J histone; H2A.Z variant histone 1; NADH:ubiquinone oxidoreductase subunit B10; eukaryotic translation initiation factor 5 beta	1	0	1	0
13	ENSG00000175793				Generic binding protein				Diagnosis; Differential Diagnosis; Disease Profiling; Monitoring Treatment Efficacy; Monitoring Treatment	Genomic; Proteomic		1	0	1	0

6. 多基因列表或多组学数据 通路分析

- 全面了解生物学背景，以帮助推动研究计划的下一步。
- 最大限度地提高生成多类型数据的投资回报。



多组学数据分析的小技巧

- 代谢物变化和转录变化可以帮助我们找到引起代谢变化的通道和酶
- **蛋白组和转录组学的分析**可以有助于找到与翻译水平相关的表达
- 代谢组和蛋白组学的分析可以有助于找到生物标志物.

TIPS:

比较不同的组学数据时，我们需要想一想他们是怎样相互关联的？

多组学方法已被证明是发现样本量有限的疾病表型的强大工具

You can upload your experimental data as well as list of genes/proteins/metabolites.

- ☐ [Upload Experiments with Gene or Protein IDs](#)
- ☐ [Upload Metabolites](#)
- ☐ [Upload Interactions](#)
- ☐ [Upload Structures](#)

Home ▸ Active Data

	Name		Type	Date
Active Data				
	T2D Genetic Variants		VX	07/22/2013 11:45:19
	pre diabetic metabolites		MX	11/07/2012 09:55:03
	Diabetes vs. Normal Gene Expression		GX	11/20/2012 15:24:43

☒	Experiment name	Species	Network Objects
☒	T2D Genetic Variants	Homo sapiens	1135
☒	pre diabetic metabolites		187
☒	Diabetes vs. Normal Gene Expression	Homo sapiens	1535

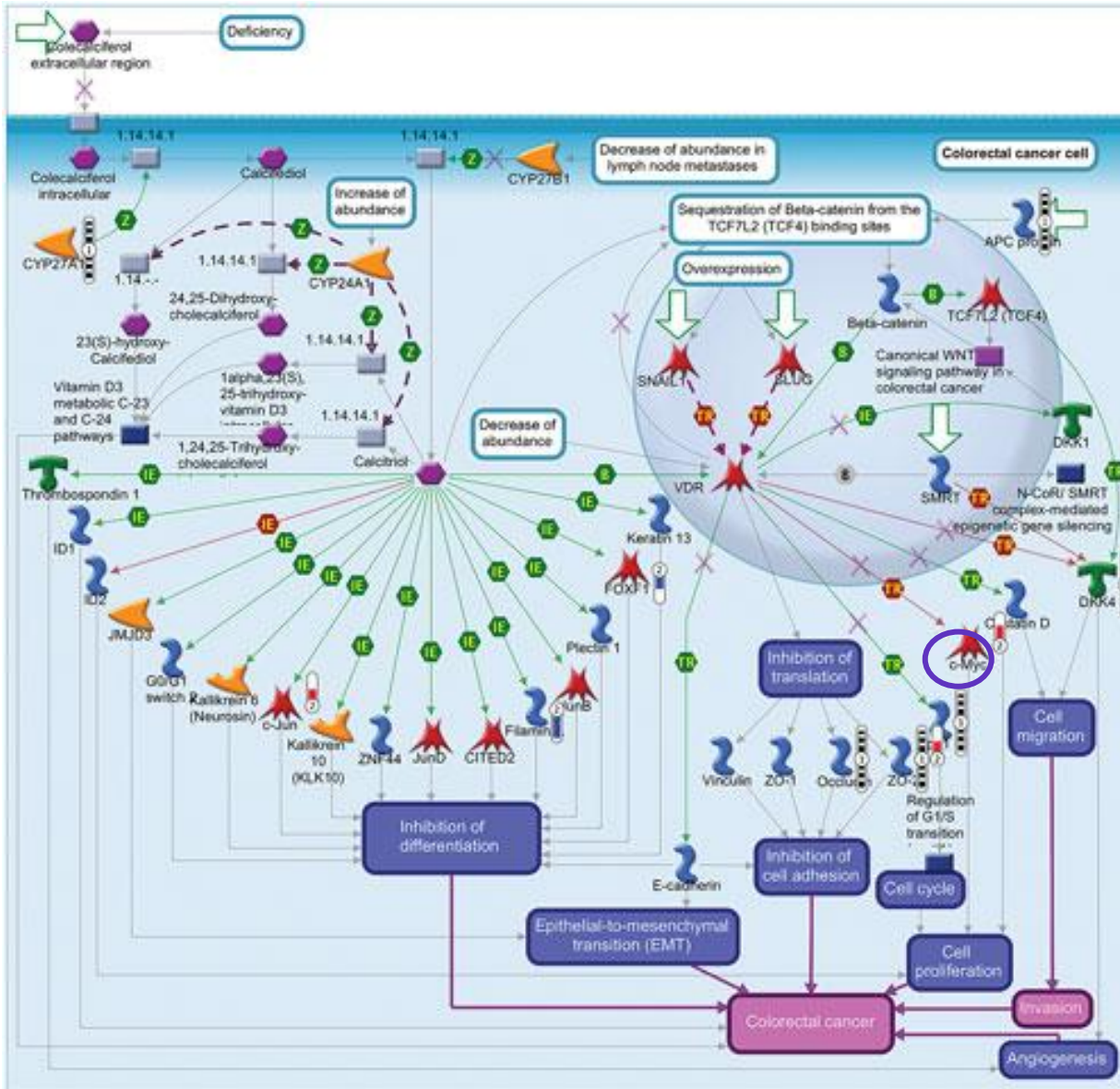
方法：过滤结直肠癌（CRC）.vcf文件，使用优先变体运行通路图富集以及整合来自MetaCore微阵列存储库的CRC转录组学数据。

案例说明：围绕CRC的机制提出了多个假设，使用MetaCore中可用的知识和数据驱动方法的组合。

结果解读

3. 这张图描述了细胞周期中的细胞增殖,对CRC表型有影响。数据显示细胞周期蛋白依赖性激酶抑制剂1A或p21中的两种变体（位置36651971 C>A和36652122 C>G），它们可能参与细胞周期的失调,导致细胞增殖的变化。

该图还显示了c-Myc在mRNA水平上的上调（折叠变化= +2.3和p值= .0009），这也可能有助于增加细胞增殖。因此，可以**假设基因组和转录组学变化的这种组合通过失调的细胞增殖来驱动CRC。**



日程

第一部分：MetaCore数据平台简介

第二部分：MetaCore重点功能介绍

第三部分：系统生物学案例分享

第四部分：内容回顾与总结

Meta Core 功能总结

MetaCore™ 是所有产品的Back Bone。它包含许多功能和工具，主要八项功能及作用如下所示：

Data Manager:

- 安全的个人数据存储平台。可存储实验,基因列表,进程列表和其他数据集;协作工作。

comparison tool

- 对比实验中的不同数据

Enrichment Analysis tool :

- 允许在多种ontologies 和 GO ontologies选择进行数据的富集分析。

Network Building engine:

- **数十种独家算法。**（专门为转录因子和受体分析而设计的算法。）允许根据所上传的数据自定义网络。

Interactome 工具:

- 显示网络对象与从的实验数据中获取/推断的对象之间的交互的统计数据。

向导及工作流程工具:

- 帮助运行连续的任务.
- 仅需数次点击便可获得说明性的报告。

搜索工具:

- 支持围绕整个MetaCore™ 数据库查找基因、网络中的对象、疾病、路径等。

数据过滤工具:

- 灵活方便（对于VCF文件等）

数据库特点总结:



数据挖掘

协助挖掘感兴趣的基因和靶点之间
关系



智能分析

多种算法，支持一键分析
无需编写代码



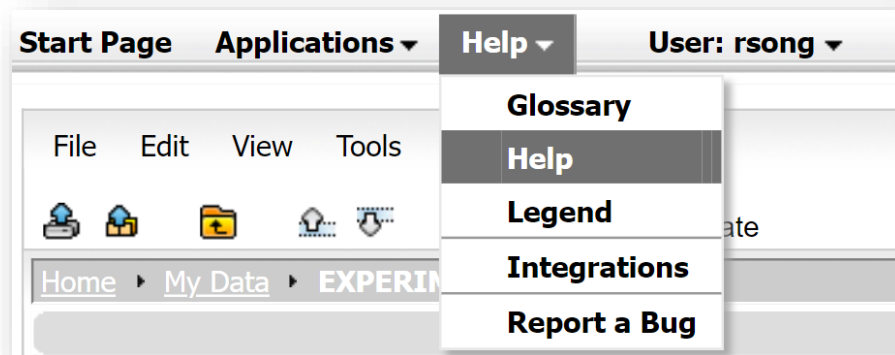
操作简便

团队新成员上手方便，点击即可分
析。

详实的线上帮助文档

关于数据库使用操作以及多种功能介绍。

系统生物学领域知识体系概况。



支持关键词检索查询
线下操作详细介绍
帮助文档互联

- EZ Start Help
- Discovery Platform
 - Welcome to MetaCore Online Help!
 - MetaCore™/MetaDrug™ Database
 - Microarray Data Repository (MAR)
 - Genomic Analysis Tools (GAT)
 - Data Management
 - Data Analysis
 - Compound Activity Prediction (MetaDrug™)
- Glossary



分子特征可预测 NAFLD 患者的癌症风险

由德克萨斯大学西南医学中心领导的研究揭示了一种蛋白质特征，可以可靠地预测非酒精性脂肪性肝病 (NAFLD) 患者是否可能患上肝细胞癌，这是最常见的肝癌形式。

治疗部分

癌症	内分泌代谢
心血管疾病	胃肠道疾病
中枢神经系统疾病	血液系统疾病
会议	免疫介导的疾病
皮肤病	感染和艾滋病
诊断和生物标志物	研发和商业新闻
耳、眼和口腔疾病	肾脏和泌尿系统疾病
	呼吸系统疾病

Brilacidin 在体外抑制 Omicron、Delta、Gamma 和 Alpha SARS-CoV-2 变体

东京理科大学公开 LXR 拮抗剂

SAN-903 抑制慢性肾病小鼠模型中的肾纤维化

施维雅为新型 MAT2A 抑制剂申请专利

住友制药披露 Chk1 抑制剂

抗 HER2 域特异性抗体药物放射性偶联物在乳腺癌模型中显示出前景

CXCR4/ACKR3 双重抑制剂与 ICT 联用可阻止 4T1 肿瘤生长和转移

Evaxion 将 EVX-03 推进 NSCLC 临床

Ginisortamab 在 CRC 细胞系中恢复 gremlin-1 消融的 BMP 信号

Voltron 在免疫肿瘤学模型中启动候选疫苗 VTX-067 的临床前研究

[89Zr]-靶向glypican-1的标记抗体被开发用于治疗胰腺癌

Soligenix 报告使用针对 MARV 和 SUDV 的二价疫苗对 NHP 提供 100% 保护

Silo 签署了用于自身免疫性疾病的下一代脂质体的商业评估许可协议

SAGE Therapeutics 描述了新的 GABA-A 受体调节剂

FDA 批准了 Fusion 的 FPI-2059 和成像模拟 FPI-2058 的 IND 申请

NR2F6 拮抗剂 TES-4207 的首个临床前数据

默克公司确定了新的 GLCT-1 抑制剂

分子特征可预测 NAFLD 患者的癌症风险

新型鼠模型可能为侵袭性胶质母细胞瘤的未来策略提供启示

罗氏合成新的 HBV HBsAg 和 HBeAg 抑制剂

Apellis 和 Affilogic 扩大研发合作，包括针对 TYR 的 Nanofitins

在 Chiesi 发现新的 P2X 嘌呤受体 3 拮抗剂

Mindset Pharma 与 CAMH 合作进行 MSP-1014 的临床前评估

[177Lu]rhPSMA-10.1 与 [177Lu]PSMA-I&T 在前列腺癌中的生物分布和疗效比较

丰富的新闻数据

- 专业记者现场访谈
- 24小时内成独家稿件
- 覆盖多种疾病领域

帮助科研老师在早期阶段获得支持关键药物研发决策的重要发现和临床前研究新闻。

售后服务支持

- 数据库培训：为订购客户提供免费培训交流活动；
- 在线培训：组织俱乐活动，定期在线解答大家的疑问，提供最新的检索技巧，分享检索经验；
- 技术支持：我们会为我们的客户提供400电话和Email咨询服务，保证您们在工作时间内有任何疑问都可以通过我们人工服务获得解答；TS技术支持团队：400 8424 896 ; ts.support.china@Clarivate.com
- 行业资讯：可访问科睿唯安在线学院或者官方微信：
<http://clarivate.com.cn/e-Clarivate/>

Thanks Very Much
The future is worth looking forward to



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