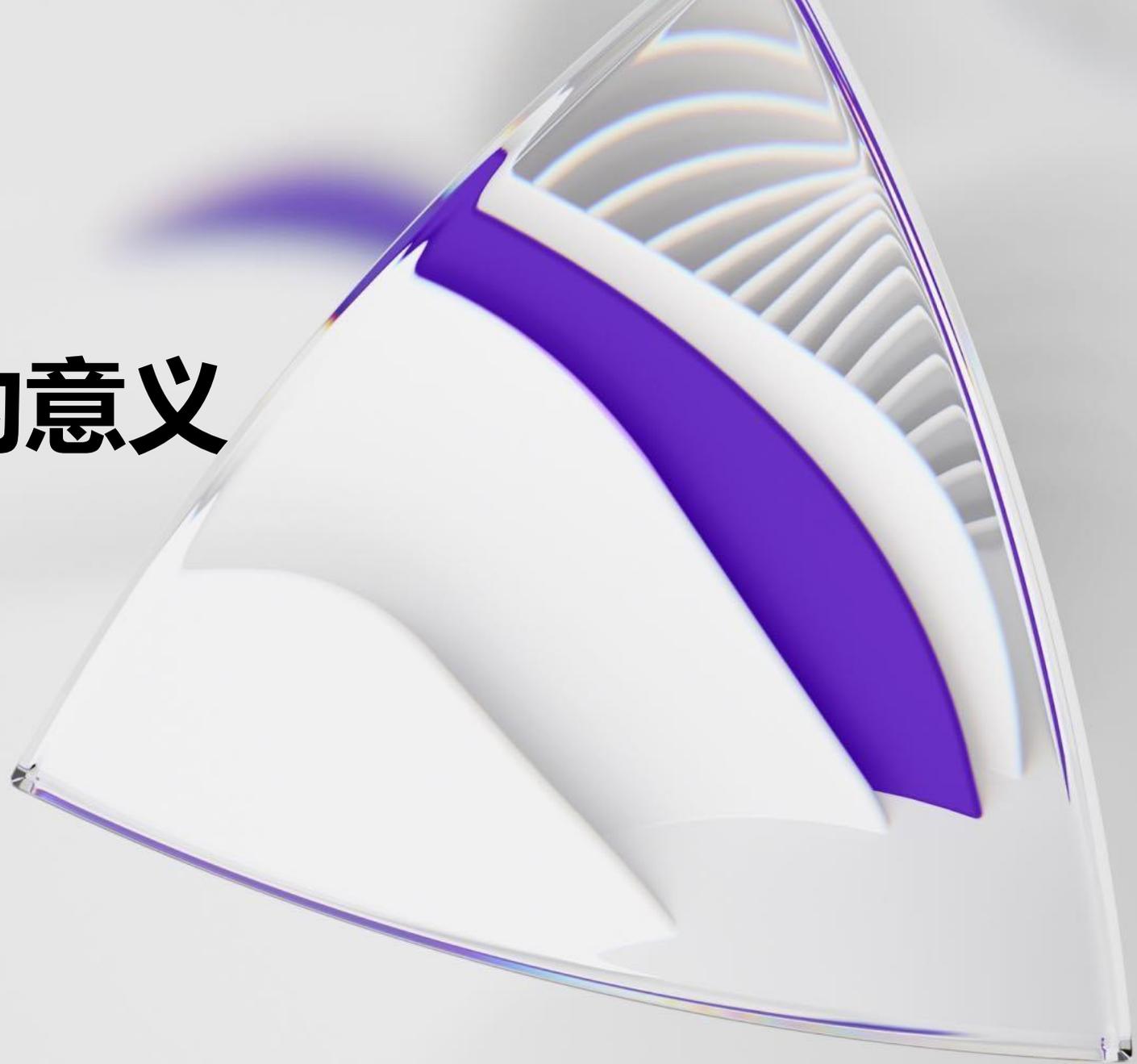




探索数据背后的意义

MetaCore助力疾病通路研究



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

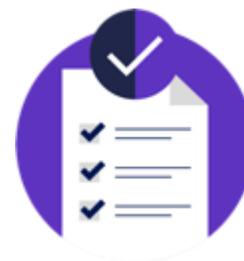
总部位于英国伦敦

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



+600

投资公司、政府基金



17/TOP20

全球国际医疗器械企业



+7,000

领先的学术机构、非盈利组织及政府单位

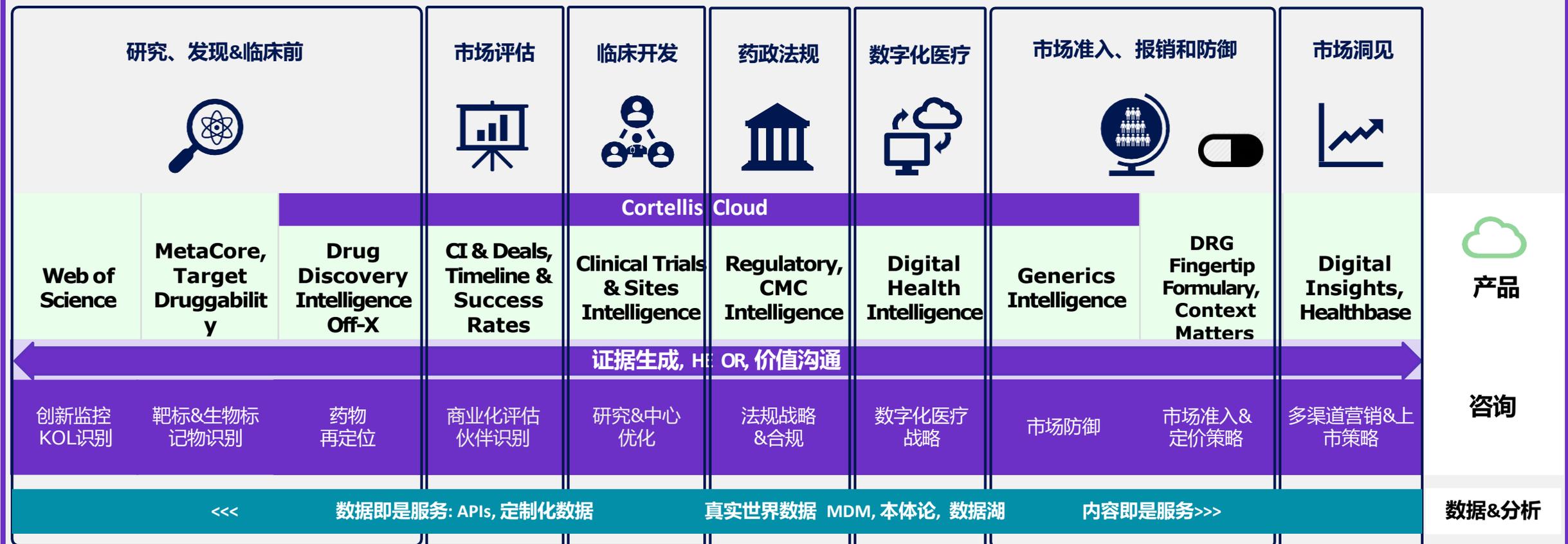


~200

中国领先的制药企业及生物技术公司

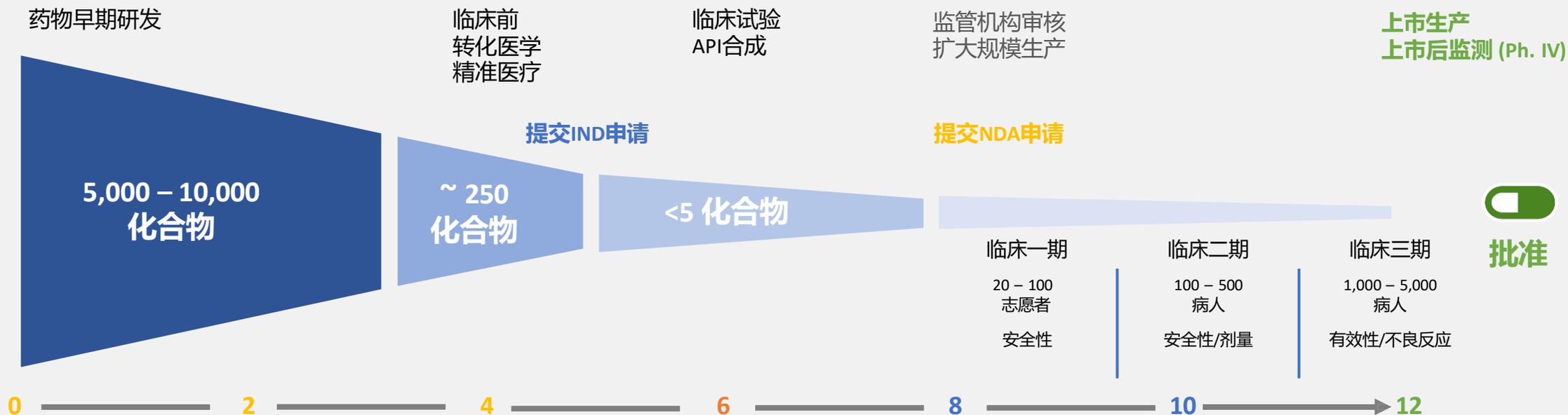
科睿唯安生命科学与医疗健康提供药品全生命周期解决方案

端到端系列解决方案



整合专业知识、数据和技术，为您提供最解决方案

科睿唯安生命科学领域数据库：覆盖药物研发全流程



Cortellis Cloud™

METACORE + METADRUG	CDDI DRA OFF-X	竞争情报 CCI	交易情报 CDI 临床情报 CTI	药物研发时 间轴和成功 率预测： DTSR	CRI, CMC, PV, CIRS, CMR (年度 付费报告)	DIGITAL HEALTH INTELLIGE NCE	CGI	咨询服务 Data Lake API
		CORTELLIS						

内容覆盖全面



Cortellis Drug Discovery Intelligence

早期研发情报数据库, 含Biomarker

(已订购)



Cortellis 药物早期研发情报提供

For Scientists, By Scientists



700000+
药物 (含大分子药物、
 疫苗细胞治疗、基因治疗)



47000+
靶点及基因



19w+
动物实验模型



3200000+
药理学数据



1380000+
药代动力学数据



36000+
药物药物相互作用



530000+
专利



3020000+
文献



50000+
药物代谢

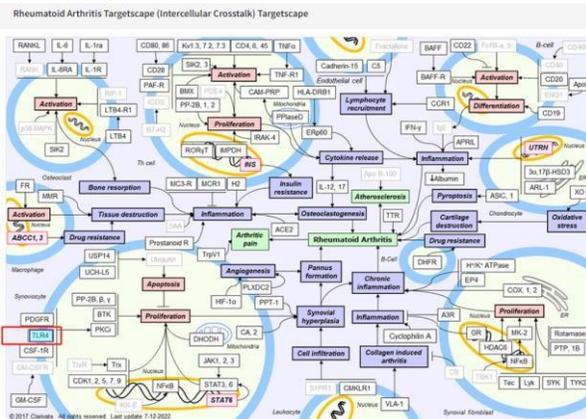
Rheumatoid Arthritis

- Facts about Rheumatoid Arthritis
- Pathophysiology
- Risk Factors
- Epidemiology
- Morbidity and Mortality
- Cost
- Diagnosis
- Prevention
- Treatment
- Targets for Therapeutic Intervention
- Latest Headlines
- Links to Related Websites
- Links to Selected Publications
- Links to Guidelines
- Multimedia

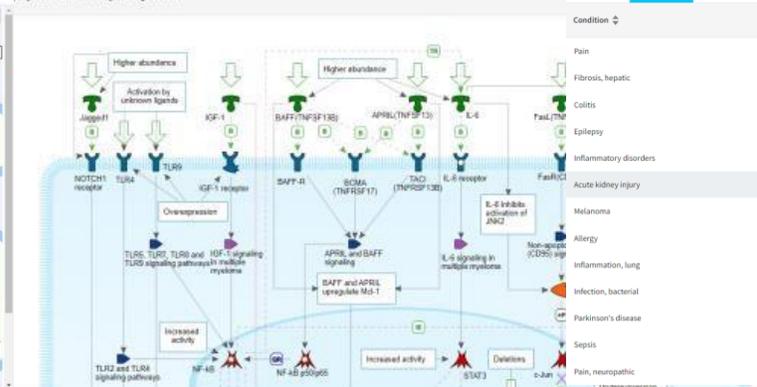
Facts about Rheumatoid Arthritis

Rheumatoid arthritis (RA) is a chronic, debilitating systemic inflammatory disorder characterized by intense autoimmune activity, symmetrical joint pain and inflammation, local destruction of bone and articular pannus formation. Inflammation of the synovial membranes lining the joints causes pain, stiffness and swelling which affects the distal small joints of the hands, wrists and feet. Extraarticular manifestations of the disease may involve the vascular, metabolic, bone and psychological domain associated interstitial lung disease causing significant morbidity (Kaduna, S. and Raghui, G., 2021; F. et al., 2021; Dai, Y. et al., 2021). Various specific and nonspecific skin manifestations are also associated (Noug, T.P. et al., 2021). Widespread pain manifests even during the early stages of the disease (Bib 2018; Lin, X.J. et al., 2020; Iyer, P. and Lee, X.C., 2021). RA is a chronic condition, although some patients experience specific flares separated by periods of remission (Hamden, K. et al., 2016; McInnes, I.B., G., 2017; Dai, Y. et al., 2021).

Systemic inflammation and autoimmunity in RA begin before the onset of detectable joint inflammation. It is suspected that autoimmunity may be initiated at a mucosal site years before the onset of joint inflammation (Petrovská, N. et al., 2021). Synovial proliferation results in a dramatic increase in the population of lining cells and lymphocytes. Synovial fluid is frequently inflammatory, releasing enzymes that invade and damage bone and cartilage. Pathological analysis indicates that synovial alterations occur first in the synovial lining is thinnest. Joint involvement typically includes small joints, although larger affected in 50-75% of all patients. Affected joints may lose their shape and alignment, causing pain and movement (Iyer, P. and Lee, X.C., 2021). Cervical spine involvement is not uncommon, but other sites may indicate a disorder other than RA. The individual pattern of joint involvement usually becomes



apoptosis in multiple myeloma

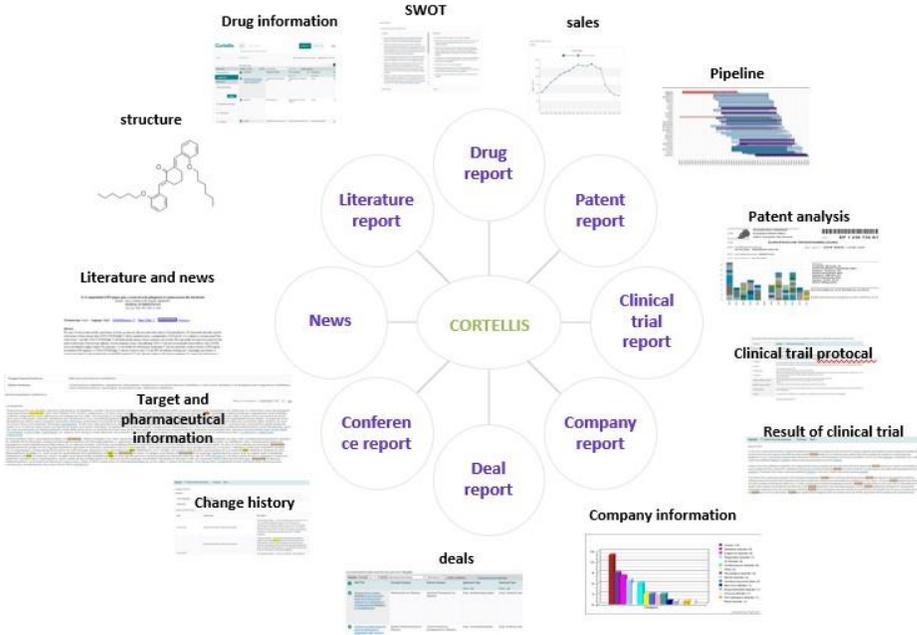


Condition	Drug Score	Gene Variant Score	Experimental Model Score	Biomarker Use Score
Pain				
Fibrosis, hepatic				
Colitis				
Epilepsy				
Inflammatory disorders				
Acute kidney injury				
Melanoma				
Allergy				
Inflammation, lung				
Infection, bacterial				
Parkinson's disease				
Sepsis				
Pain, neuropathic				
Immunosuppression				

Cortellis Competitive Intelligence 竞争情报数据库



Cortellis: a comprehensive collection of innovative drugs information



Data for innovation:

- ✓ **Drugs: 90,000+**
- ✓ **Clinical trials: 600,000+***
- ✓ **Deals: 140,000+***
- ✓ **Patents: 5,700,000+**
- ✓ **Disease briefing: 169***
- ✓ **Regulatory: 200,000+***
- ✓ **Conferences: 100,000+**
- ✓ **Companies: 260,000+**
- ✓ **Literature: 2,700,000+**
- ✓ **Broker research: 1,900,000+**
- ✓ **News: 560,000+**
- ✓ **Venture funding: 10,000+**

dupilumab

Snapshot: 高亮显示 检索关键词和同义词 < 上一个 下一个 >

Latest Press Releases: 研发概况

Latest Event Transcripts: 新内容: [关闭高亮显示]

Broker Research Reports: 概要

Development Profile

- Summary
- Patents & Generics
- Regulatory
- Postmarketing
- Premarketing
- Preclinical
- Additional Information

Literature Review

Development Status

Regulatory Designations

作用格局概览
APRIL receptor modulator
在研药物总数: 95 公司总数: 93

Status: Pre-registration Phase 3 Clinical Phase 2 Clinical Phase 1 Clinical Practical Discovery Suspended Discontinued Outlicensed

Companies: Juno Therapeutics Inc, Celgene Corp, Poseida Therapeutics Inc, Tenobio Inc, Allogene Therapeutics Inc, Amgen Inc, Autolus Therapeutics Ltd, bluebird bio Inc, Cartesian Therapeutics, Heidelberg Pharma Hold

Indications: Multiple myeloma, Cancer, Diffuse large B-cell lym, IgA nephropathy, Non-Hodgkin lympho, Acute lymphoblastic l, Advanced solid tumor, Amyloidosis, Autoimmune disease, Chronic lymphocytic l

Technologies: Biological therapeutic, Immuno-oncology, Intravenous formulat, Infusion, Protein fusion, Receptor chimeric, Chimeric antigen rece, Bispecific T cell engin, Parenteral formulatio, Antibody drug conjug

公司: Adagene Suzhou Limited

适应症: Advanced solid tumor

特殊审评: None

地理区域/国家或地区: US

变更跟踪

里程碑: Expected Trial Outcome Announcements

事件日期: 17-Sep-2018

5.5

Pha

In August 2021, results from phase Ib/II trial (ADG106-P2001/KEYNOTE-D12) of ADG-106 in combination with keytruda in patients with advanced or metastatic solid and hematological malignancies were expected in 2022 [2518135].

95

2024 Today

02-Mar-2026

21-Jun-2028

06-May-2029

1.9 years

2.3 years

0.9 years

Phase 2

Phase 3

Pre-Reg

57%

72%

95%

Time to Registration: 5.1 years

Probability of success: 37%

显示成功指标 >

Patents by Drug Relationship Type

Number of Patents

专利

药物安全信息平台 OFF-X



不良事件

美国食品和药品监督管理局将能够继续使用科睿唯安旗下药物安全信息平台 OFF-X™

近日，全球领先的专业信息服务提供商科睿唯安（纽约证券交易所股票代码：CLVT）宣布将与美国食品和药品监督管理局签署的《材料转移协议》(MTA) 延长三年，确保美国食品和药品监督管理局能够继续使用科睿唯安旗下药物安全信息平台 OFF-X™。该平台提供综合的临床前毒理、临床和上市后不良事件数据、可视化工具和分析。

临床研究的成功可能会受到意外安全问题的影响。在药物研发过程中，尽早识别潜在安全责任至关重要。通过融合临床前和临床的药物安全数据转化，可以减少患者负担并提高研发成功率。

随着双方合作关系进入第六个年头，美国食品和药品监督管理局将继续使用 OFF-X，以识别与分子靶点，新药及上市药物相关的潜在不良事件，并为监管审查过程提供支持。该协议通过评估加强人用药品及相关分子靶点安全性评价的方法，继续支持美国食品和药品监督管理局履行保护公众健康的使命。

科睿唯安合作伙伴关系副总裁 Gavin Coney 表示：“科睿唯安利用深度数据、深厚的洞察力和专业知识，帮助生命科学合作伙伴预测并克服向患者提供创新治疗的障碍。美国食品和药品监督管理局与科睿唯安之间的这项协议将赋能研究人员和药物安全专业人员在药物研发和上市后所有阶段预测和监测潜在安全责任的准备。”



Master view

Showing 1,784 adverse events for 25 System Organ Classes

Filter Columns View AE/SOC

Adverse event • System Organ Class	OFF-X Target/Class Score	Classifier tags	Number of alerts	Alert type	Alert phase
Death • General disorders and administration site conditions	Very high	On-Target Causality Severity	227	40 10 7 217 40	9 8
Decreased appetite • Metabolism and nutrition disorders	Very high	On-Target Causality Severity Pharmacogenomics	449	66 12 9 437 66	0 0
Dermatitis acneiform • Skin and subcutaneous tissue disorders	Very high	On-Target Causality Severity Pharmacogenomics	347	50 16 7 331 50	1 2
Diarrhoea • Gastrointestinal disorders	Very high	On-Target Causality Severity Pharmacogenomics	1114	81 44 14 1070 81	18 8
Hypomagnesaemia • Metabolism and nutrition disorders	Very high	On-Target Causality Severity	138	26 10 4 128 25	1 1
Interstitial lung disease • Respiratory, thoracic and mediastinal disorders	Very high	On-Target Causality Severity Pharmacogenomics	323	28 20 8 303 28	2 2
Mucosal inflammation • General disorders and administration site conditions	Very high	On-Target Causality Severity Pharmacogenomics	189	25 19 9 170 25	0 0

Filter Columns View AE/SOC

Adverse event • System Organ Class	OFF-X Target/Class Score	Biological Role & Preclinical Pharmacological Evidence				Clinical Pharmacological Evidence						
		Target Expression	Human Genetic variants	KO/ND animal data	In vitro Data / Patient samples	Preclinical	Phase I	Phase II	Phase III	Clinical Regulatory	Postmarketing	Phase not specified
Weight decreased • Investigations	Medium				Species 4	30 17	25 22	54 23	24 11	28 14	9 6	9 4
Mutagenic effect • Congenital, familial and genetic disorders	Not associated				Species 3	7 6					1 1	
Diarrhoea • Gastrointestinal disorders	Very high	DN	1		Species 1	1 2	202 74	312 47	137 23	66 15	258 21	199 28
Infertility male • Reproductive system and breast disorders	Very low	DN			Species 3	12 7				1 1	1 1	
Foetal disorder • Pregnancy, puerperium and perinatal conditions	Medium				Species 2	10 8	1 1		1 1	12 10		

Metacore, Metadrug



Table of Contents

- General
 - Gene Details
 - Thomson Reuters Integrity
 - External Databases
 - Vendors
- Groups/Variants
- Pathways and Processes
 - Pathway Maps
 - Process Networks
 - GO Processes
 - GO Molecular Functions
- Diseases
 - Associated Diseases
 - Drug Target for
 - Disease Ontologies
- Reactions
 - Metabolic Reactions
 - Posttranslational Modification
 - Interactions

Pathways and Processes

Pathway Maps

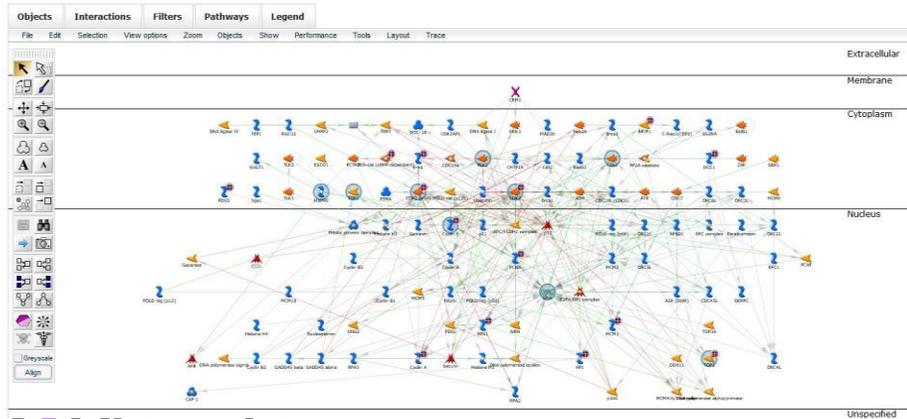
#	Name
1	Activation of Ca2+-dependent neuronal cell death in Huntington's disease
2	Angiotensin II Signaling in Cardiac Hypertrophy
3	Antioxidant effects of statins in COPD
4	Apoptosis and survival Anti-apoptotic action of nuclear ESR1 and ESR2
5	Apoptosis and survival Inhibition of ROS-induced apoptosis by 17beta-estradiol
6	Cigarette smoke-induced oxidative stress and apoptosis in airway epithelial cells
7	Development Lipoxin inhibitory action on PDGF, EGF and LTD4 signaling
8	GLP-1 in beta cell apoptosis in type 2 diabetes
9	Immune response MIF - the neuroendocrine-macrophage connector
10	Impaired Lipoxin A4 signaling in CF
11	Influence of low doses of Arsenite on Glucose stimulated Insulin secretion in pancreatic cells
12	LRRK2 in neuronal apoptosis in Parkinson's disease
13	NALP3 inflammasome activation in age-related macular degeneration (AMD)
14	Neuroprotective action of lithium
15	NRF2 regulation of oxidative stress response
16	Oxidative stress Role of ASK1 under oxidative stress
17	Oxidative stress Role of Sirtuin1 and PGC1-alpha in activation of antioxidant defense system
18	Oxidative stress ROS-induced cellular signaling
19	Role of inflammasome in macrophages, adipocytes and pancreatic beta cells in type 2 diabetes
20	The innate immune response to contact allergens

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 - GO Molecular Functions
- Diseases
 - Associated Diseases
 - Drug Target for
 - Disease Ontologies
- Reactions
 - Metabolic Reactions
 - Posttranslational Modification
 - Interactions

Interactions

#	From	To	Direction	Effect	Mechanism	Link info
3	Thioredoxin	APEX	Outgoing	Activation	Binding	
4	Thioredoxin	ESR1 (nuclear)	Outgoing	Activation	Binding	
5	Thioredoxin	FKHR	Outgoing	Activation	Binding	
6	Thioredoxin	HIF1A	Outgoing	Activation	Binding	
7	Thioredoxin	Lipocalin_1	Outgoing	Activation	Binding	
8	Thioredoxin	MEK4(MAP2K4)	Outgoing	Activation	Binding	
9	Thioredoxin	NF-kB1 (p50)	Outgoing	Activation	Binding	
10	Thioredoxin	NSF	Outgoing	Activation	Binding	
11	Thioredoxin	Oct-3/4	Outgoing	Activation	Binding	
12	Thioredoxin	SHP-1	Outgoing	Activation	Binding	
13	Thioredoxin	DNAJB5	Outgoing	Activation	Covalent modification	
14	Thioredoxin	HDAC4	Outgoing	Activation	Covalent modification	
15	Thioredoxin	Hdi-2	Outgoing	Activation	Covalent modification	
16	Thioredoxin	NF-kB_p65/p65	Outgoing	Activation	Covalent modification	
17	Thioredoxin	PTP-1B	Outgoing	Activation	Covalent modification	Unspecified
18	Thioredoxin	CYP11A1	Outgoing	Activation	Unspecified	
19	Thioredoxin	CYP11B1	Outgoing	Activation	Unspecified	
20	Thioredoxin	IFN-gamma	Outgoing	Activation	Influence on expression	



- Accelerate disease research, biomarker, and drug target identification
加快疾病研究、生物标志物和药物靶标鉴定进程
- MetaCore has prepared the code and algorithms, and the data can be uploaded for omics data analysis
MetaCore已做好代码和算法，上传数据即可进行组学数据分析
- Build the signaling network you want
构建您想要的信号传导网络

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 (原GeneGo产品) 概览

加快疾病研究、生物标志物和药物靶标鉴定进程

METACORE
数据挖掘与分子通路分析



METACORE 可用于:

- 药物发现 (drug discovery) 中组学 (OMICS) 数据的通路分析
- 在数据库中进行知识挖掘, 产生假设
- 靶标和生物标记物的评估与验证
- 全面疾病通路的建立和发病机制的研究
- 病患分层、综合性比对和功能性指纹图谱

适合以下专业人员:

- 生物学家研究人员
- 发现生物学家
- 生物信息学家
- 生物标记小组和临床前研究人员
- 治疗领域方向高层人员
- 首席调研员 (临床医生等 PI)
- 转化医学研究人员

- ◆ **数据精准:** 完全通过人工阅读全文文献和实验数据后进行整合的高准确率的数据库, 包含分子互作用, 通路, 基因与疾病关联, 化学代谢物与毒理信息。
- ◆ **功能强大:** 涵盖药物研究各个方面, 包括药物靶标的发现及验证; 药物代谢的通路分析及药物作用靶标及活性和毒性的预测; 药物临床实验数据的功能分析等。
- ◆ **使用方便:** 从实验数据的上传、统计分析一直到靶标的验证、新的靶标的选择和生物标记物的发现都可以实时显示, 图形界面和可视化工具非常友好。

近年来利用MetaCore发表的高影响力文章部分列表

1. (2023) Subcellular location defines GPCR signal transduction. *Science Advances* IF=13.6
2. (2023) Exploring the possible mechanism(s) underlying the nephroprotective effect of Zhenwu Decoction in diabetic kidney disease: An integrated analysis. *PHYTOMEDICINE* IF=7.9
3. (2022) A lymphocyte–microglia–astrocyte axis in chronic active multiple sclerosis. *Nature*, IF=64.2
4. (2021) Deletion of *Abi3* gene locus exacerbates neuropathological features of Alzheimer’s disease in a mouse model of A β amyloidosis. *Science Advances* IF=13.6
5. (2021) Differences in transcriptome response to air pollution exposure between adult residents with and without chronic obstructive pulmonary disease in Beijing: A panel study. *JOURNAL OF HAZARDOUS MATERIALS* IF=13.6
6. (2019) Metastatic-niche labelling reveals parenchymal cells with stem features. *Nature*, IF=64.2
7. (2016) Dual Targeting of P53 and C-Myc Selectively Eliminates Leukaemic Stem Cells. *Nature* IF= 64.2
8. (2016) A Core Viral Protein Binds Host Nucleosomes to Sequester Immune Danger Signals. *Nature* IF= 64.2
9. (2013) Molecular Profiling of Human Mammary Gland Links Breast Cancer Risk to a p27(+) Cell Population with Progenitor Characteristics. *Cell Stem Cell*. IF=23.9
10. (2011) The JAK2/STAT3 signaling pathway is required for growth of CD44⁺CD24⁻ stem cell-like breast cancer cells in human tumors. *J Clin Invest.*; IF=12.812
11. (2008). Core signaling pathways in human pancreatic cancers revealed by global genomic analyses. *Science*. IF=56.9
12. (2008). An integrated genomic analysis of human glioblastoma multiforme. *Science* . IF=56.9
13. (2008). Regulation of *in situ* to invasive breast carcinoma transition. *Cancer Cell*. IF=50.3
14. (2007). The genomic landscapes of human breast and colorectal cancers. *Science* IF=56.9

Metacore是组学分析的有效分析工具

Article | Published: 08 September 2021

A lymphocyte–microglia–astrocyte axis in chronic active multiple sclerosis

Martina Absinta , Dragan Maric, Marjan Gharagozloo, Thomas Garton, Matthew D. Smith, Jing Jin, Kathryn C. Fitzgerald, Anya Song, Poching Liu, Jing-Ping Lin, Tianxia Wu, Kory R. Johnson, Dorian B. McGavern, Dorothy P. Schafer, Peter A. Calabresi & Daniel S. Reich 

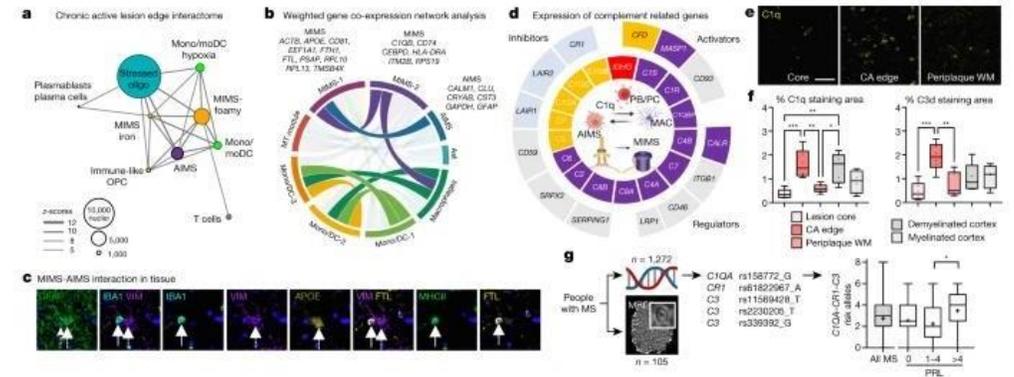
Nature 597, 709–714 (2021) | [Cite this article](#)

42k Accesses | 270 Citations | 213 Altmetric | [Metrics](#)

Abstract

Multiple sclerosis (MS) lesions that do not resolve in the months after they form harbour ongoing demyelination and axon degeneration, and are identifiable in vivo by their paramagnetic rims on MRI scans^{1,2,3}. Here, to define mechanisms underlying this disabling, progressive neurodegenerative state^{4,5,6} and foster development of new therapeutic agents, we used MRI-informed single-nucleus RNA sequencing to profile the edge of demyelinated white matter lesions at various stages of inflammation. We uncovered notable glial and immune cell diversity, especially at the chronically inflamed lesion edge. We define ‘microglia inflamed in MS’ (MIMS) and ‘astrocytes inflamed in MS’, glial phenotypes that demonstrate

Fig. 3: MIMS–AIMS interactions anchor the glial interactome, and C1q and C3 activity is increased in chronic active white matter lesions.



a, Glial interactome map of the chronic active lesion edge (first 20 significant connections, $P < 0.05$). Each node indicates a cell-type cluster; node size is proportional to number of nuclei and connector thickness is proportional to z-scores of the **MetaCore** interactome output. **b**, Correlations among gene modules in immune and astrocyte clusters using WGCNA, retaining only genes that are differentially expressed in chronic active edge versus control white matter; module size < 50 genes. Ribbon colour scale: eigengene adjacency matrix values (highest quartile, dark colour; corresponding heat map and scale bar are shown in Extended Data Fig. 8c). MIMS and AIMS gene modules are highly correlated. DC, dendritic cells. MT, mitochondria. **c**, Spatial interaction between MIMS (dashed white arrow) and AIMS (white arrow) in tissue at the chronic active edge. **d**, z-scores (>1.5 relative to all

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- [National Center for Biotechnology Information \(NCBI\)](#)
- [National Institutes of Health \(NIH\)](#)
- [The Harvard Clinical and Translational Science Center](#)

Bioinformatics Databases and Tools

[Metacore](#) -- genomic analytical tool and pathway analyzer. [See here for access and registration info.](#)

[TAIR](#) -- The Arabidopsis Information Resources maintains a database of genetic and molecular biology data for Arabidopsis thaliana.

[NCBI](#) (National Center for Biotechnology Information) -- collection public databases for research in computational biology, genome data, and biomedical information.

[Ensembl](#) -- software system which produces and maintains automatic annotation on selected eukaryotic genomes.

[BLAST](#) -- analysis tool that finds regions of similarity between biological sequences.

What is MetaCore?

MetaCore is an integrated software suite for functional analysis of experimental data. MetaCore is based on a curated database of human protein-protein, protein-DNA interactions, transcription factors, signaling and metabolic pathways, disease and toxicity, and the effects of bioactive molecules.

Use MetaCore for functional analysis of:

- gene expression
- metabolomics
- proteomics
- siRNA
- SNPs
- HCS

Questions?

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AND/OR by type of content: Books Calculator Clinical Practice Guidelines

MetaCore	Curates high quality biological systems content in context, giving you essential data and analytical tools to accelerate scientific research. Register OR Login to MetaCore
MetaDrug	Incorporates extensive manually curated information on biological effects of small molecule compounds. Request an account OR Login

ADDITIONAL RESOURCES

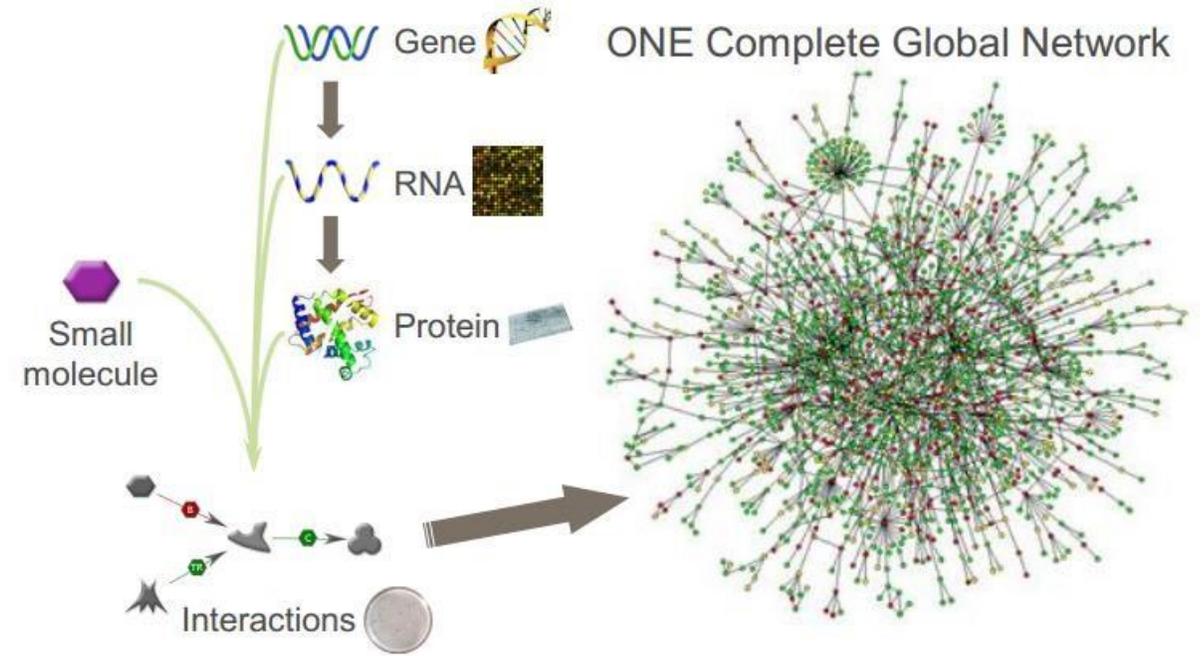
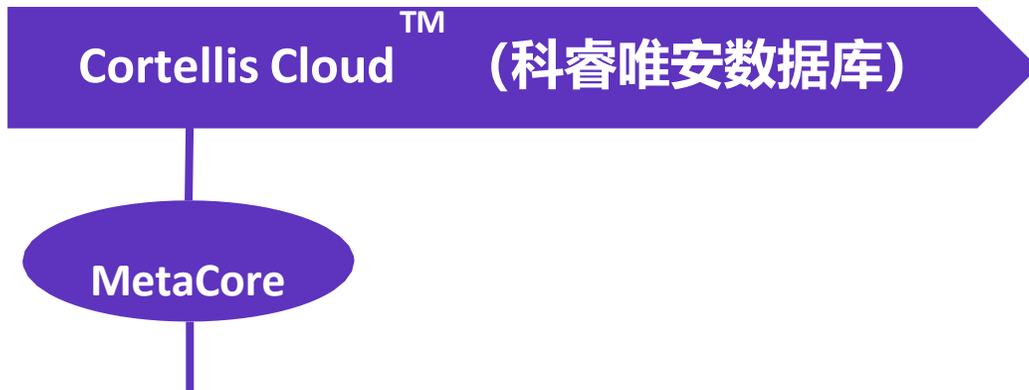
Report an Access Problem: askyalemedicallibrary@yale.edu

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- New to the Collection
- Mobile Apps
- eJournals & eBooks

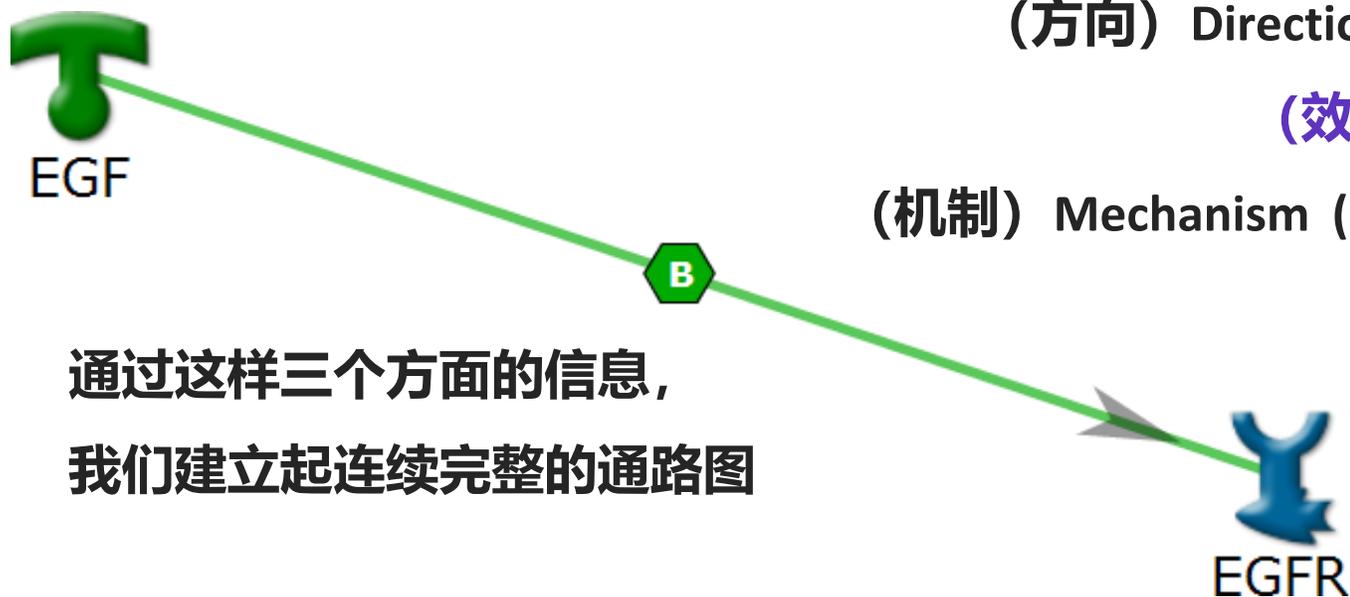
什么是MetaCore?

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

NETWORKS	MAPS
Up-regulated (+) Object has user data with positive value	
Down-regulated (-) Object has user data with negative value	
Mixed-signal (+/-) Object has user data with both positive and negative values	
Gene variants Object has user data with gene variants	
Mixed data Object has user data with both expression values and gene variants	

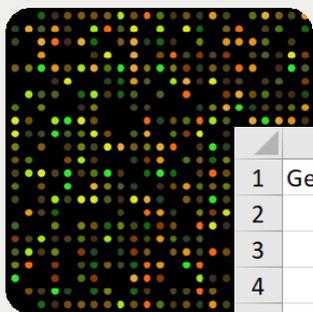
Network Objects

ENZYMES	GENERIC CLASSES
Generic enzyme	Receptor ligand
KINASE	Transcription factor
Generic kinase	Protein
Protein kinase	Compound
Lipid kinase	Predicted metabolite or user's structure
PHOSPHATASE	Inorganic ion
Generic phosphatase	Reaction
Protein phosphatase	DNA
Lipid phosphatase	RNA
PHOSPHOLIPASE	Generic binding protein
Generic phospholipase	Cell membrane glycoprotein
PROTEASE	G PROTEIN ADAPTOR/REGULATORS
Generic protease	G beta/gamma
Metalloprotease	Regulators (GDI, GAP, GET, etc.)
CHANNELS/TRANSPORTERS	RECEPTORS
Generic channel	Generic Receptor
Ligand-gated ion channel	GPCR
Voltage-gated ion channel	Receptors with kinase activity
Transporter	
	GROUPS OF OBJECTS
	A complex or a group Proteins physically connected into a complex or related as a family
	Logical association Proteins linked by logical relations or physical interactions
	Custom association Group of collapsed objects chosen by user

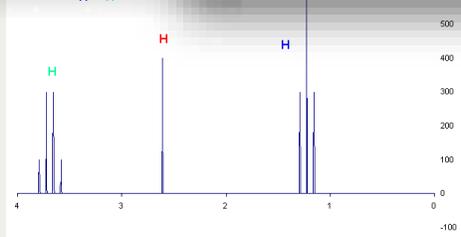
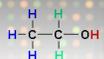


搜索/浏览

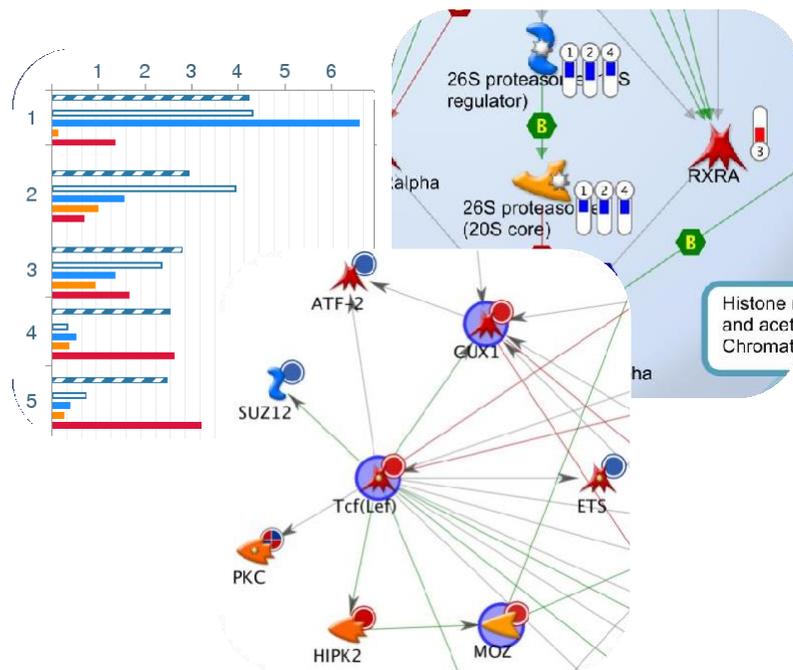
组学分析



	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

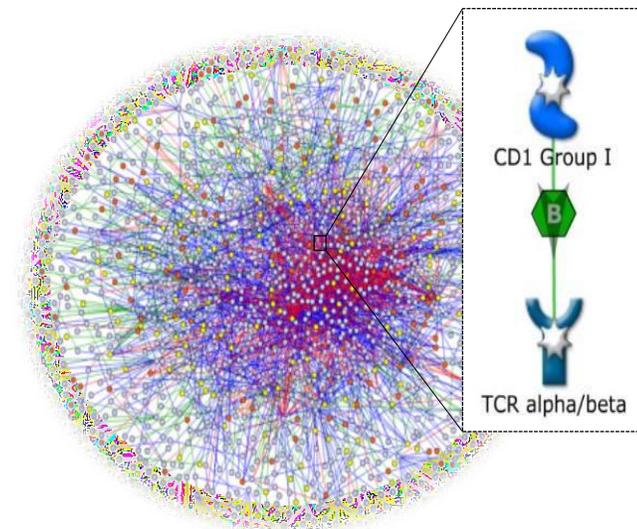


- 在经过验证的生物途径的背景下了解实验数据
- 生成并确认新靶标和生物标志物的假设

MetaBase



3700 种期刊, 由科学家手动策划



MetaCore / MetaBase的数据 载量

Content Overview

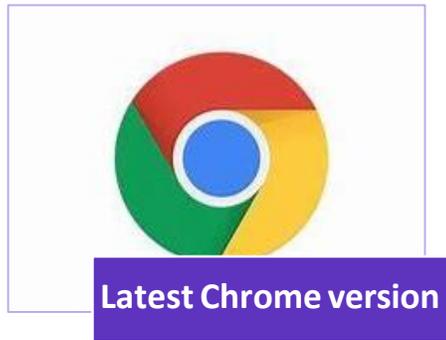
- 每季度更新
- 科学家手动上传

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

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

File Edit View Tools Help

Activate/Deactivate

Home > My 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		
Active Data		

Home > Active Data

Name	Type	Date
------	------	------

[...] 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。

Activate
Please, drag one or more experiments from the upper frame and drop
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 Analysis Most Popular Questions Upload Workflows & Reports One-click Analysis Build Network Custom Content Predict Compound Activity (MetaDrug) Search & Browse Content

1 Genomic Va 2 3 4 5 6 7 8 9

- Genomic Variant Analysis
- Cohort Analysis
- Somatic Mutation Detection
- Trio Analysis
- Genomic 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。

Hide Description

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 interactions analysis.

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

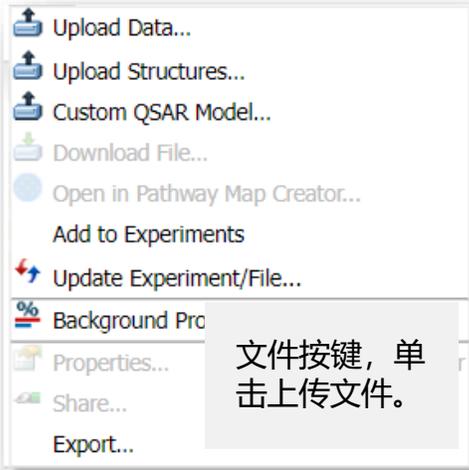
Cohort Analysis: This tool allows you to create a cohort of variants from a list of gene names or a group of variants.

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

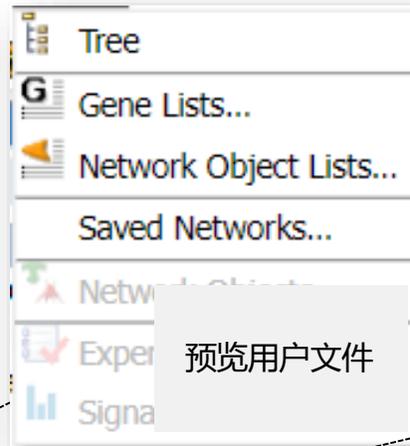
Trio Analysis: Analyse family trios for inherited variants, filter for autosomal recessive and sex linked variants in active dataset.

Compound Variant Filter: Filter variants based on compound variant analysis.

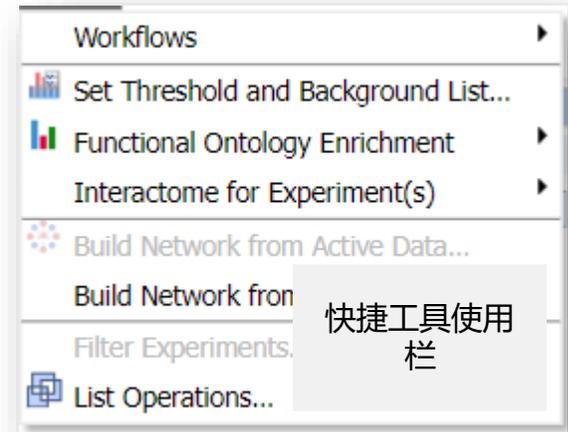
此区域为注释区，功能为对方所选择的模块功能进行备注。



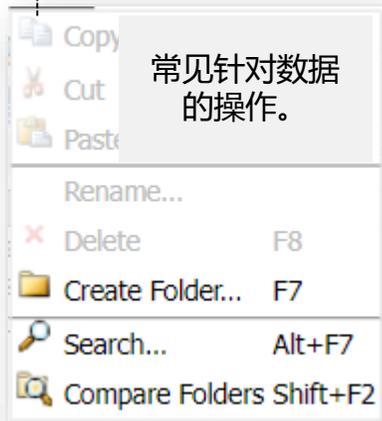
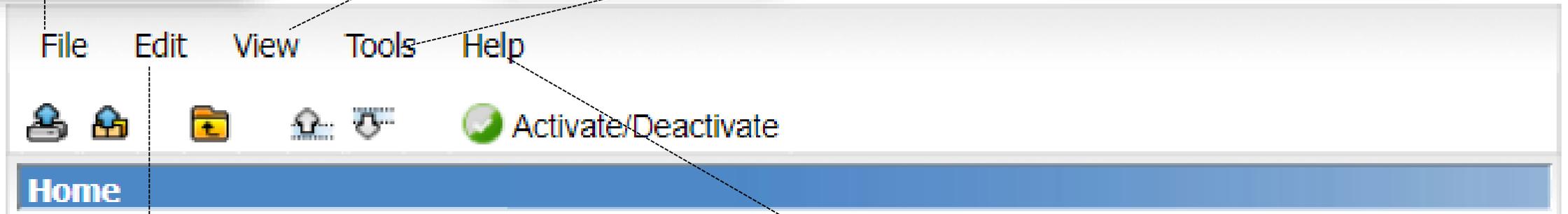
文件按键，单击上传文件。



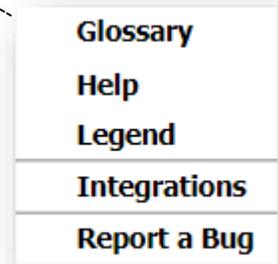
预览用户文件



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

上传基因组变异数据，协助进行分析

Metacore使用常见问题

上传数据按钮

Metacore workflow按钮，上传数据后一键获得结果。

一键分析功能

协助用户使用自己的数据建立网路途径

协助用户使用自己的数据建立网路途径

预测化合物毒性按钮

搜索基因或疾病按钮



Genomic Analysis



Most Popular Questions



Upload



Workflows & Reports



One-click Analysis



Build Network



Custom Content



Predict Compound Activity (MetaDrug)



Search & Browse Content

- [Upload Genomic Variants](#)
- [Cohort Analysis](#)
- [Somatic Mutation Detection](#)
- [Trio Analysis](#)
- [Genomic Variant Filter](#)

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

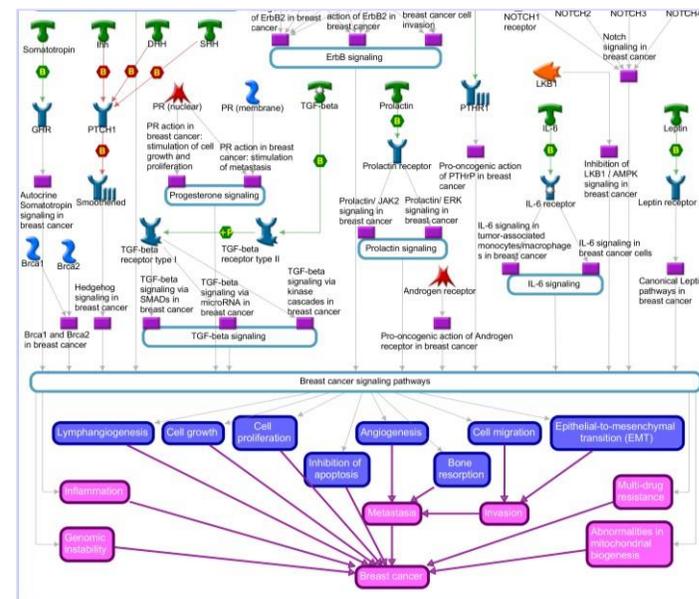
第四部分：内容回顾与总结

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**
- 3 M+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



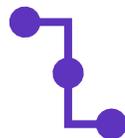
MetaCore 基础功能与应用价值-概述



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

PD-1 Search

EZ Search

Name: PD-1

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: Network Objects that interact

PD-1 Network object | Build Network

Table of Contents

- General
 - Gene Details
 - Protein Details
 - Thomson Reuters Integrity
 - External Databases
 - Vendors
- Groups/Variants
- Pathways and Processes
- Diseases
- Interactions

	Human	Mouse
Gene Details		
PDCD1		
Symbols		PDCD1, CD279, hPD-1, H
Full Name		programmed cell death 1
Synonyms		protein PD-1, systemic lupus erythematosus, programmed cell death pr
Description		This gene encodes a cell surface protein that belongs to the immunoglobulin superfamily. This protein is expressed in a variety of tissues and has a role in their differentiation. It is also expressed in 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: *Pdcd1* (*Mus musculus*)
Clarivate Analytics Integrity: *Pdcd1* (*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** **Pdcd1_predicted** programmed cell death 1 (predicted) (*Rattus norvegicus*)
Synonyms: programmed cell death 1 (predicted), programmed cell death protein 1-like
Genes: *Pdcd1* (*Rattus norvegicus*)
Clarivate Analytics Integrity: *Pdcd1* (*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

Table of Contents

- General
 - [Protein Details](#)
 - [Clarivate Analytics Integrity](#)
 - [External Databases](#)
 - [Vendors](#)
- Groups/Variants
- Pathways and Processes
 - [Pathway Maps](#)
 - [Process Networks](#)
 - [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/PKtheta 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

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

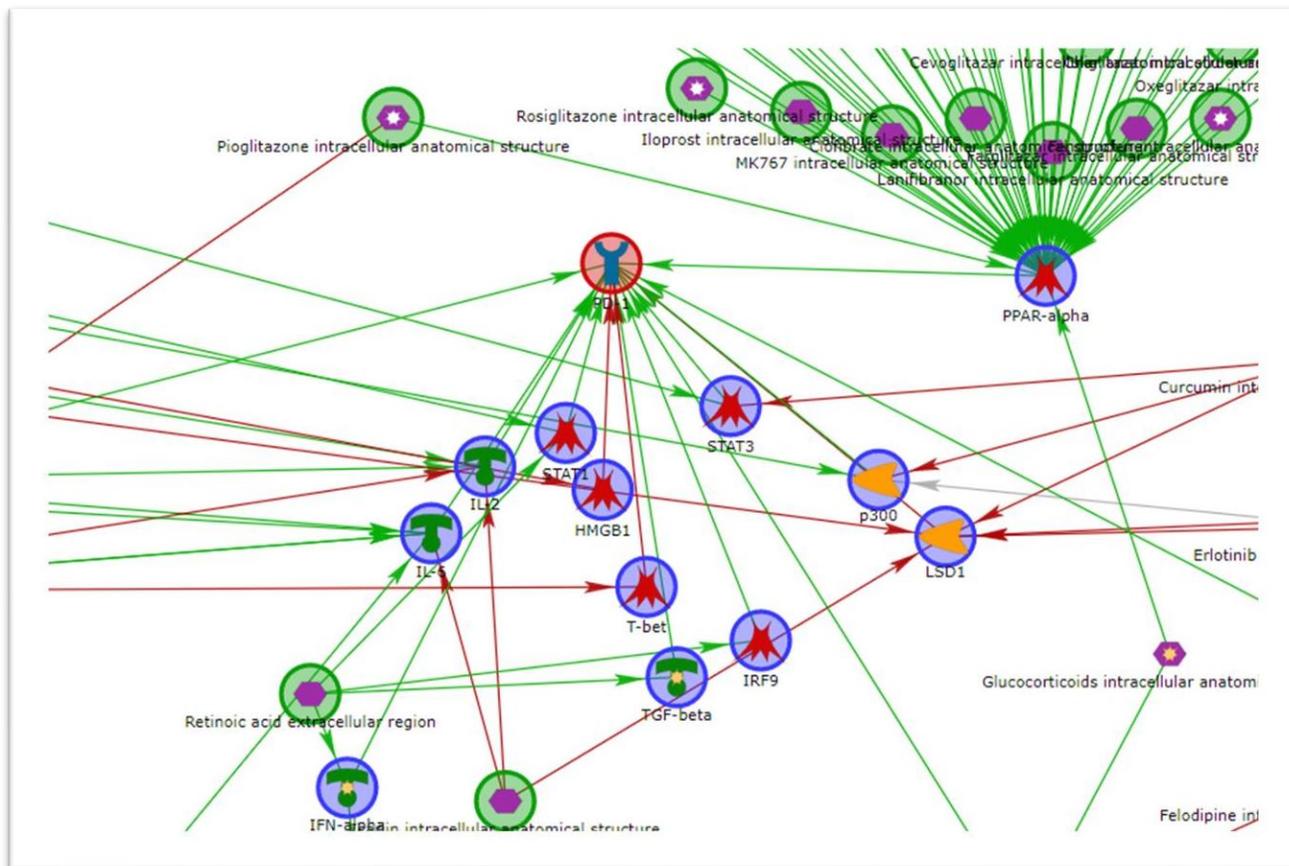
Indirect Activators

▼ Activators of 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

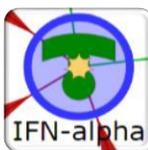
Indirect Activators



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.

- 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

GO Localizations | Network Objects

Export | Export to image | Reorder enrichment

1 cytoplasmic part

2 membrane-bounded organelle

3 vesicle

4 intracellular organelle

5 cell periphery

6 plasma membrane

7 organelle

Network Objects

Export | Build Network | highlight text... 0/0

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

#	Name	Score
1	A630077B13Rik	2.817
2	ABCC5	5.070
3	ACSL1	30.025
4	Adenosine A2a receptor	3.043
5	plasma membrane	5.195
6		2.056
7		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

plasma membrane

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

EZ Search

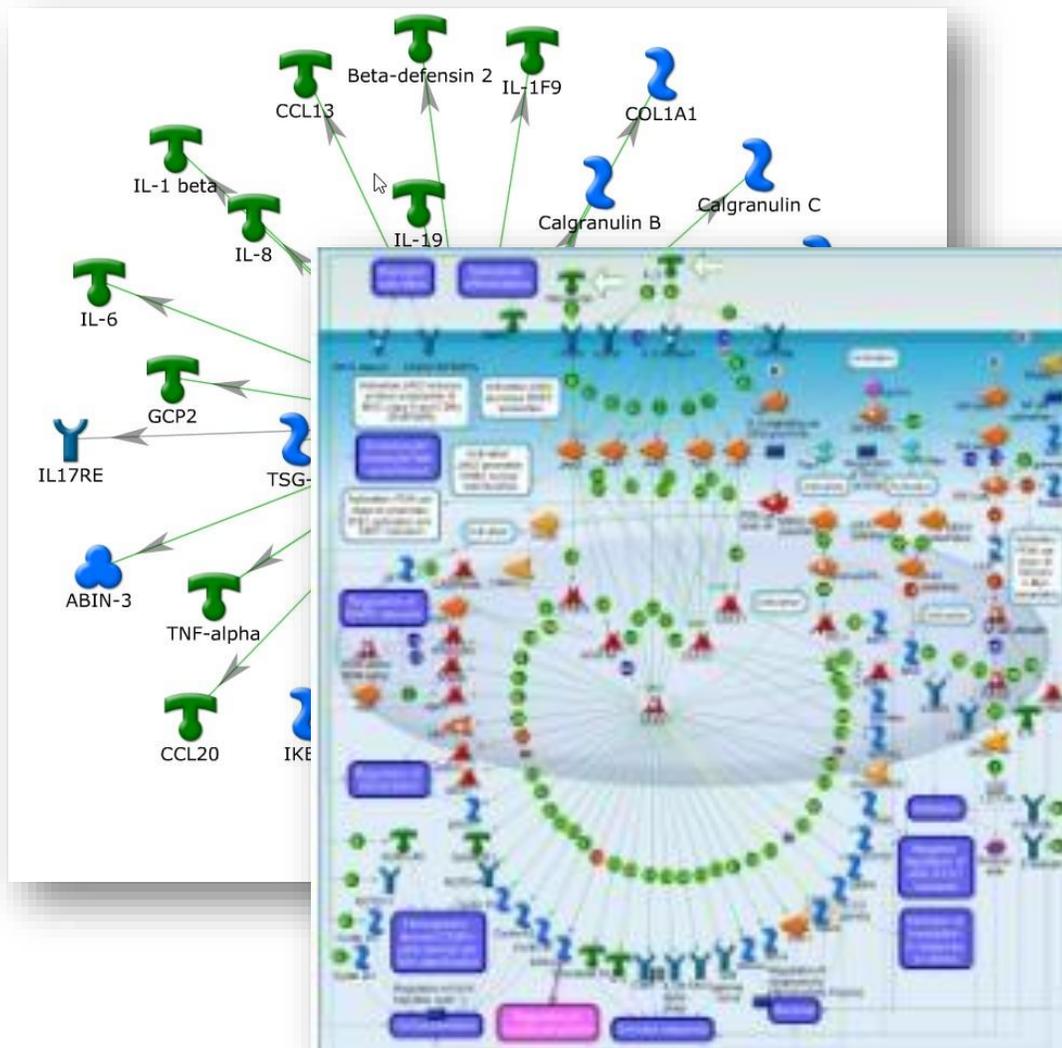
Name

Objects Found

- Genes (3)
- Gene Aberrations (152)
- Proteins (13)
- RNA (18)
- Network Objects (1)
- Interactions (938)
- GO Processes (5)
- Genes, associated with GO Processes (47)

Table of Contents

- General
 - Gene Details
 - Protein Details
 - Clarivate Analytics Integrity
 - External Databases
 - Vendors
- Groups/Variants
- Pathways and Processes
 - Pathway Maps
 - Process Networks
 - GO Processes
 - GO Molecular Functions
- Diseases
 - Interactions



- 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'. The 'Network Objects' tab is selected. Below the tabs, there are three buttons: 'Export', 'Export to image', and 'Reorder enrichment profile'. A list of maps is displayed, with the following entries:

#	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' popup window is open, showing a link between 'IL-3' and 'IL-3 receptor'. The link is represented by a green arrow pointing from 'IL-3' to 'IL-3 receptor', with a green circle containing the letter 'B' in the middle. Below the link, there are two buttons: 'Hide All Details' and 'Show All Details', and an 'Export to EndNote' button.

- 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 passway List

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

#	Genes Code	Species	Location
1	CCL2	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: highlight text..

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

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:

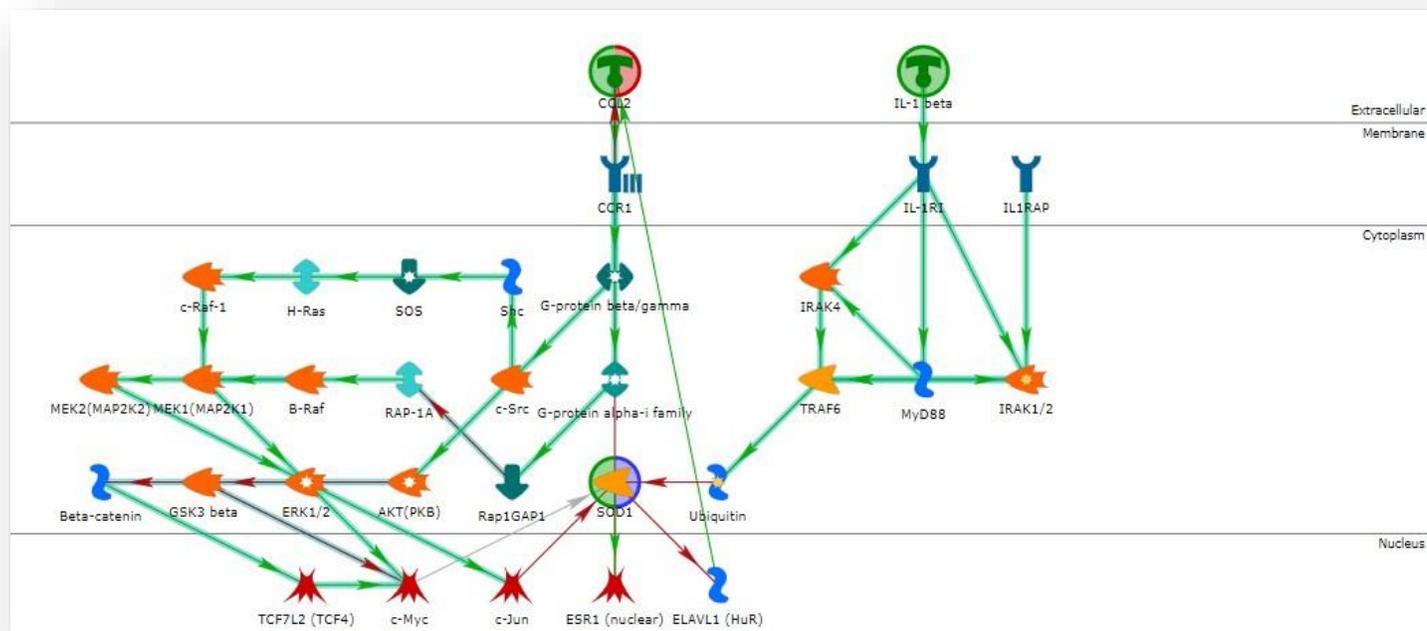
- Activation
- Inhibition
- Unspecified

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 shows a software interface for network analysis. A menu titled 'About network' is open, listing 'Network description', 'Network statistics', and 'Legend'. Below the menu, a table titled 'Toxic Pathologies' is displayed, listing various pathologies with their corresponding percentages, p-values, and the number of genes from active data.

#	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

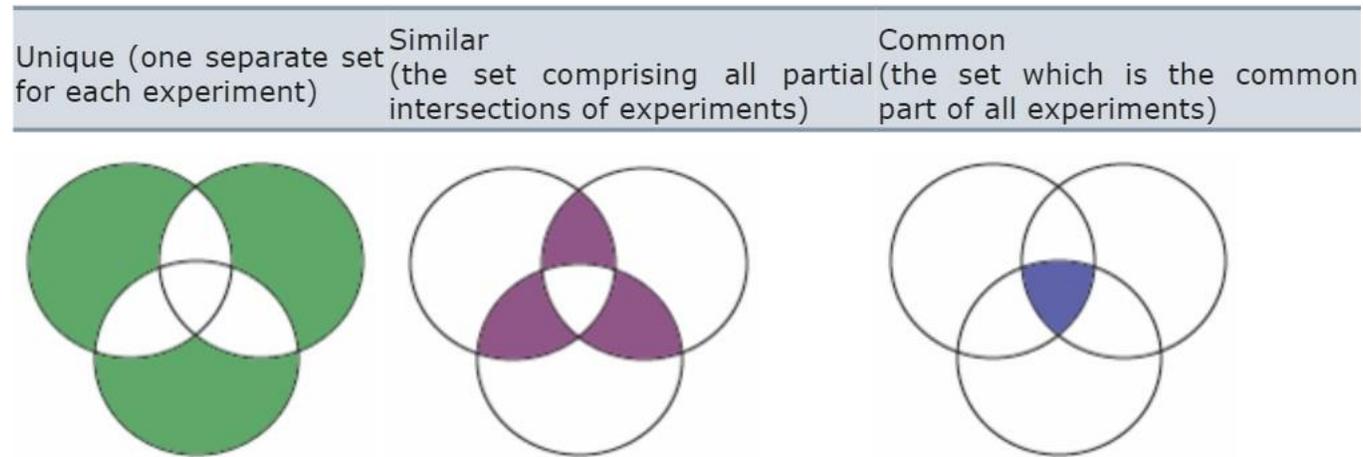
实用场景

- 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

vs

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

Workflows & Reports

Data Analysis Workflows
A set of simple step-by-step wizards for analysis of your data.

- Enrichment Analysis
- Analyze Single Experiment
- Compare Experiments**
- Compare Compounds
- Toxicity Analysis
- Biomarker Assessment
- Interactome Analysis

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

Comparison Results

Pathway Maps

GO Processes

Process Networks

Diseases (by Biomarkers)

Network Statistics

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:

P-value:

Signals: up, down, both

▼ Comparison Results

#	Unique	Similar	Common	Recalculate
1	2452	42	5052	<input type="button" value="Selected"/>

[back to top](#)

▼ Pathway Maps

Export | Export to image | Filter by Map Categories ⚠ Filtered | Sorting method: Similarity by maps

#	Maps	-log(pValue)	pValue	err(-log(pValue))	FDR	Ratio
1	Cigarette smoke-induced proliferation, metaplasia and survival of airway epithelial cells	1.000e+0	1.000e+0	0.850	1.000e+0	0/50
		1.922e-3	9.448e-3		9.448e-3	14/50
		2.419e-1	4.482e-1		4.482e-1	5/50
		3.472e-2	5.768e-2		5.768e-2	1/50
2	NF-κB-, AP-1- and MAPKs-mediated proinflammatory cytokine production by eosinophils in asthma	1.000e+0	1.000e+0	1.000	1.000e+0	0/43
		6.967e-2	1.282e-1		1.282e-1	9/43
		6.518e-2	2.047e-1		2.047e-1	6/43
		1.000e+0	1.000e+0		1.000e+0	0/43
3	Role of type 2 innate lymphoid cells in asthma	1.000e+0	1.000e+0	1.000	1.000e+0	0/38
		3.475e-2	7.530e-2		7.530e-2	9/38
		3.900e-2	1.496e-1		1.496e-1	6/38
		1.000e+0	1.000e+0		1.000e+0	0/38
4	Role of integrins in eosinophil degranulation in asthma	1.000e+0	1.000e+0	1.000	1.000e+0	0/58

Compare Experiments Workflow-结果

Export ✕ close

Name:

To: [Select columns to export](#)

Genes/Network object of

Homo sa
 Mus mus
 Rattus ni

Through:

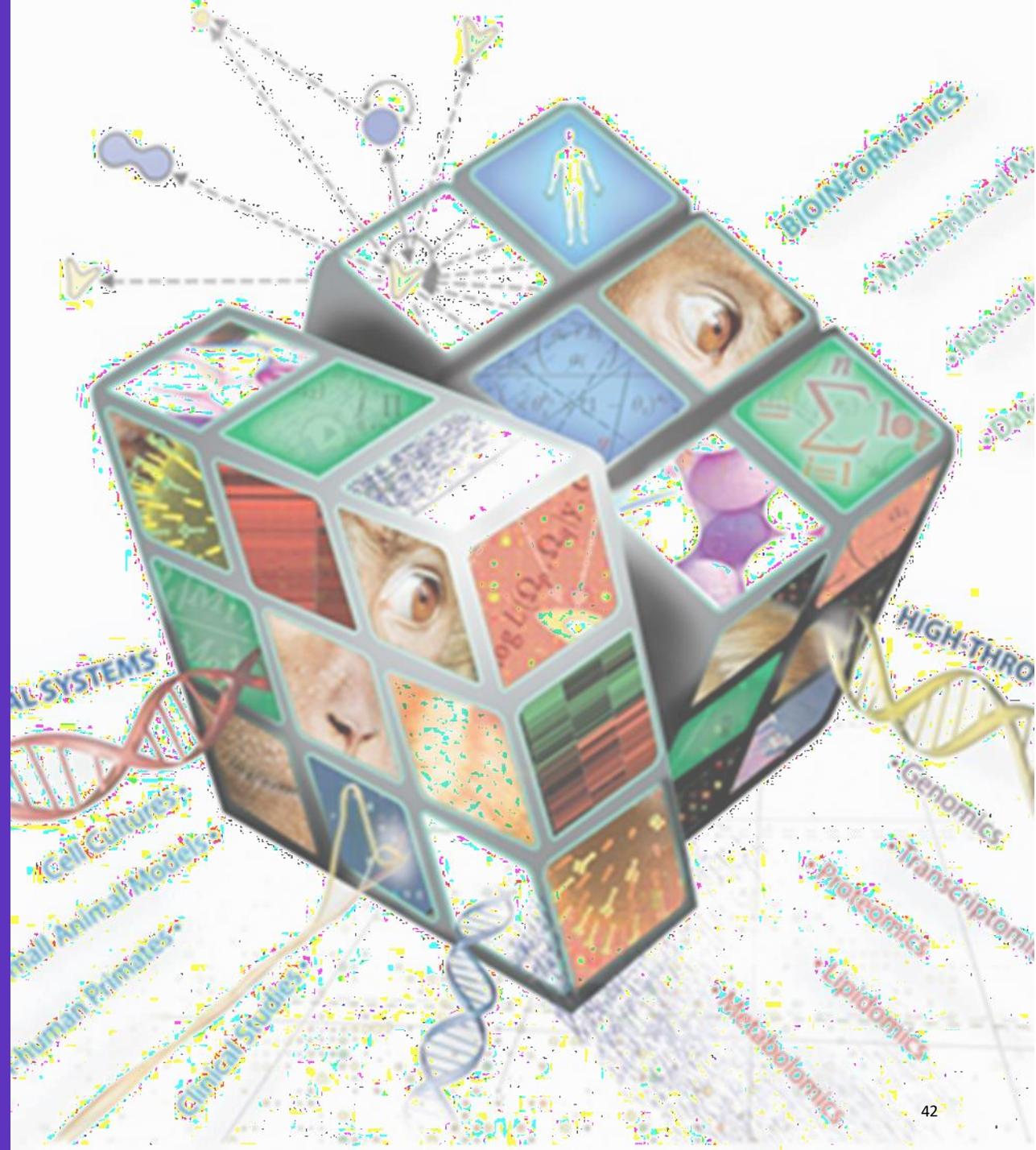
[Show additional options](#)

Exporting...

MetaCore Data							CDDI Data					PNC_392.4_genelist		PNC_453.2_genelist	
#	Input ID	Network Object Na	Gene Symbol	Unit (protein or chem)	Object Type	Description	Therapeutic Drugs	CDDI Biomark	CDDI Biomarker Rol	CDDI Biomarker Typ	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 18; SMAD family member 2	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 ERCC 1	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; autophagy-101; ADP observation	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	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

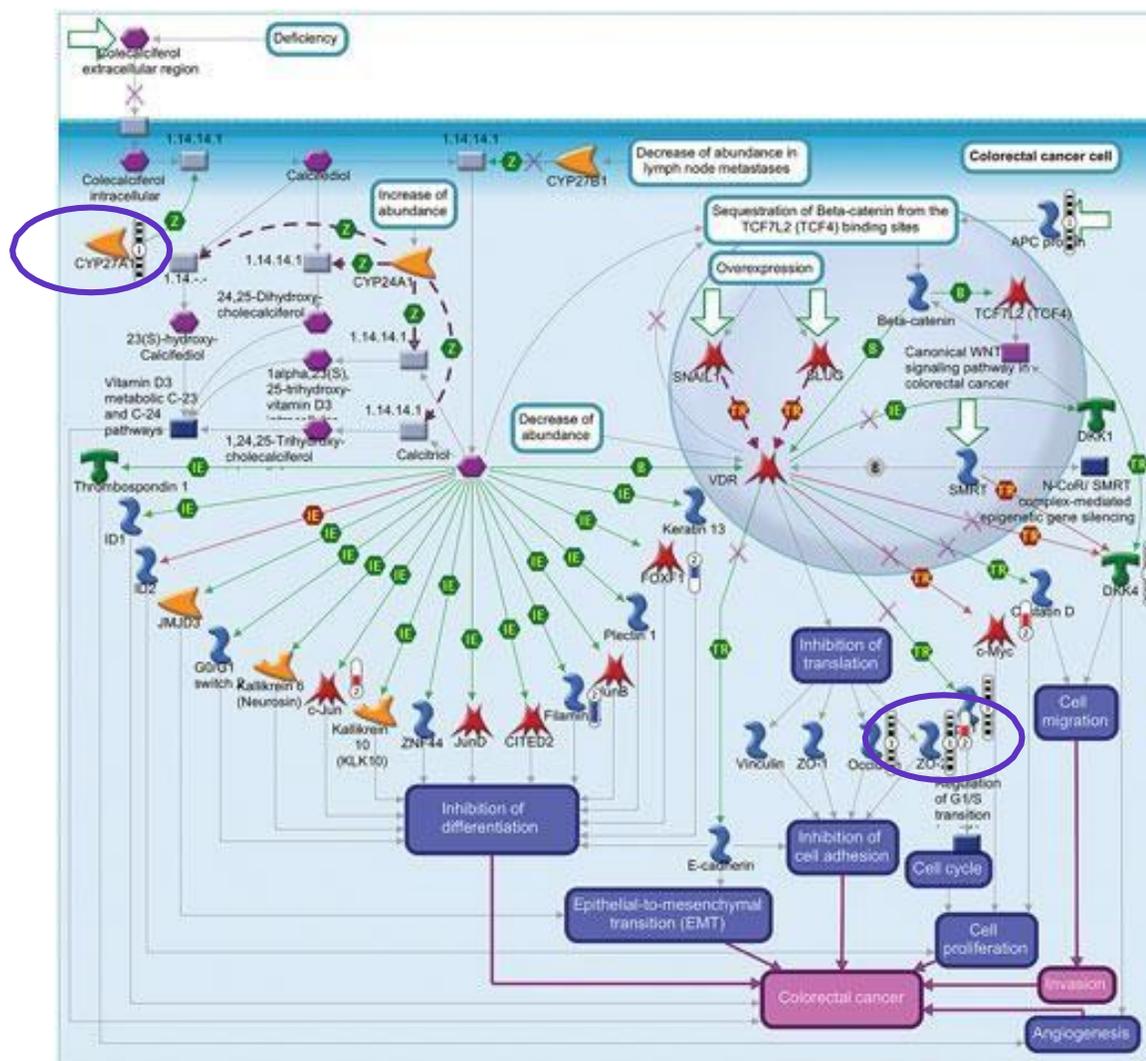
Name	Type	Date
T2D Genetic Variants	VX	07/22/2013 11:45:19
pre diabetic metabolites	MX	11/07/2012 09:55:03
Diabetes vs. Normal Gene Expression	GX	11/20/2012 15:24:43

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。

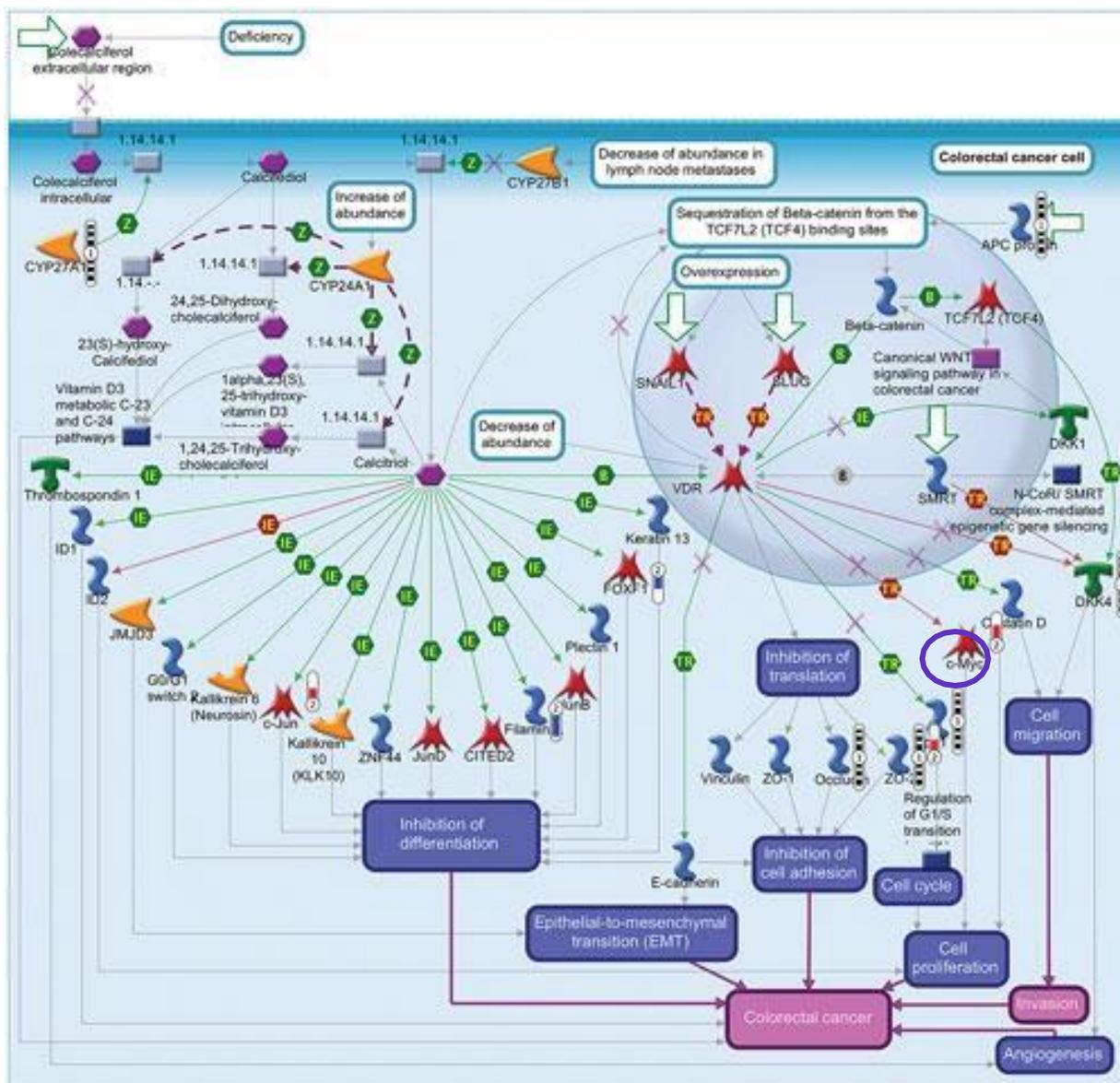
案例说明：围绕CRC的机制提出了多个假设，使用MetaCore中可用的知识和数据驱动方法的组合。

结果解读



1. CYP27A1 (过滤后的三个变体) 催化胆钙化醇 (colexcalciferol) 转化为骨化二醇 (calcifediol), 后者通过另一种酶转化为骨化三醇。CRC 中骨化三醇信号下调; 因此, 这些 CYP27A1 突变可能代表功能缺失突变, 这些突变降低了胆钙化醇的催化作用和整体降低的 VDR 信号传导。
2. CRC基因组数据显示ZO2 (TJP2基因) 在C>T SNP 71865988位置的变异, 转录组学数据显示 TJP2基因上调1.8倍 (p值= .021)。可以假设这种变异导致TJP2的产生增加, 并改变生物过程, 例如通过细胞粘附机制的CRC进展。

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:

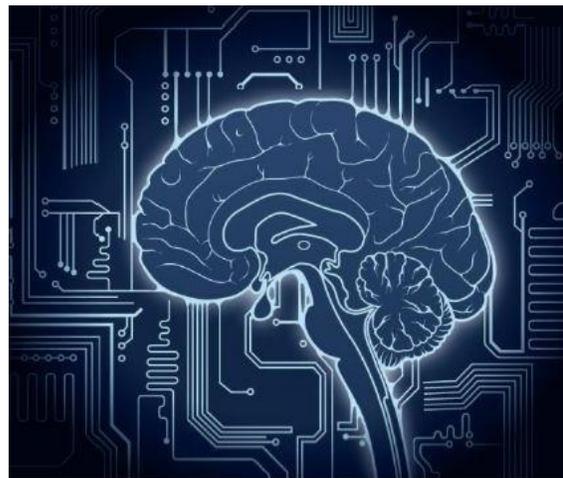
- 灵活方便（对于VCF文件等）

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



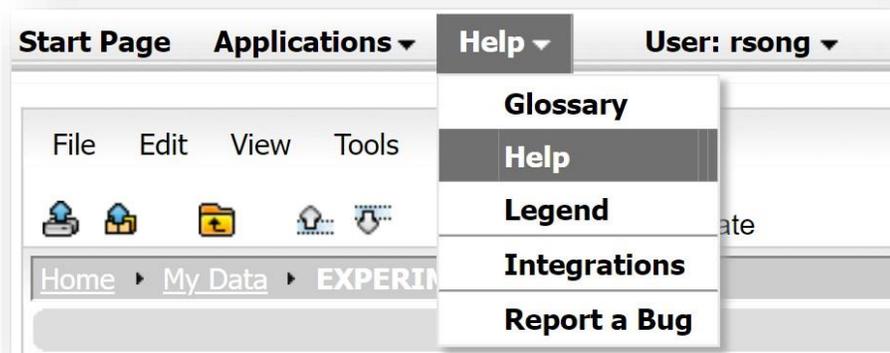
操作简便

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

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：**组织俱乐部活动，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](tel:4008424896)；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/>