



2018 IPA 系統生物學分析軟體暨資料庫 基礎操作課程



National Yang Ming University

Sample to Insight





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By NGS Data analysis workflow









A. Expression Application – Ingenuity Pathway Analysis

- 1. What's New in IPA 2017 Winter Release
- 2. Getting Start with IPA

大綱

IPA介紹與啟動IPA

B. Searching and Accessing the Knowledge Base

- 1. Introduction for Search Tools
- 2. My List

利用IPA進行搜尋

C. Building and Editing a Pathway for Publication

- 1. My Pathway
- 2. Path Designer

使用IPA進行分子模型建構並繪製訊息傳遞路徑

D. Q & A





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IPA是 All-in-one, web-based 的分析軟體與資料庫,幫助研究人員分析手上分子生物學實驗後的資料,可以快速提供研究人員更多的證據與文獻去解釋複雜的實驗背景與實驗成因並建構可以延伸的假設。





IPA 支援的物種(orthologous):

IPA

Arabidopsis thaliana Bos taurus (bovine) Caenorhabditis elegans Gallus gallus (chicken) Pan troglodytes (chimpanzee) Danio rerio (zebrafish) Canis lupus familiaris (canine) Drosophila melanogaster Macaca mulatta (Rhesus Monkey) Saccharomyces cerevisiae Schizosaccharomyces pombe

IPA 支援的實驗平台與技術:

- 基因表現實驗:
 - qPCR analysis
 - Microarray
 - RNA-Seq (NGS)
 - microRNA
 - mRNA
- 蛋白質體實驗
 PhosphoProteomics^{New}
- 代謝體實驗

IPA 的應用:

- 生物標記開發研究
- 藥物活性機轉研究
- 藥物毒性機制研究
- 疾病發生機制研究



Understand Complex 'Omics Data

IPA helps you understand complex 'omics data at multiple levels by integrating data from a variety of experimental platforms and providing insight into the molecular and chemical interactions, cellular phenotypes, and disease processes of your system.





>14,000 publications that used IPA -- and growing!

Se	arch results	Results by year
Iter	ms: 1 to 20 of 1707 << First < Prev Page 1 of 86 Next> Last>	
1.	Causal analysis approaches in Ingenuity Pathway Analysis.	<
1.	Krämer A, Green J, Pollard J Jr, Tugendreich S. Bioinformatics. 2014 Feb 15:30(4):523-30. doi: 10.1093/bioinformatics/btt703. Epub 2013 Dec 13.	Dow
	PMID: 24336805 Free PMC Article	
	Similar articles	Related searches
	Genome-wide analysis of genetic variations assisted by Ingenuity Pathway Analysis to	ingenuity pathway analysis gene
2.	comprehensively investigate potential genetic targets associated with the progression of	ingenuity pathway analysis mirna
	hepatocellular carcinoma.	ingenuity pathway analysis network
	Yu F, Shen XY, Fan L, Yu ZC.	
	Eur Rev Med Pharmacol Sci. 2014;18(15):2102-8. PMID: 25070813 Free Article	ingenuity pathway analysis proteomi
	Similar articles	
		PMC Images search for ingenuity
	Potential predictive plasma biomarkers for cervical cancer by 2D-DIGE proteomics and Ingenuity	pathway analysis
3.	Pathway Analysis.	
	Guo X, Hao Y, Kamilijiang M, Hasimu A, Yuan J, Wu G, Reyimu H, Kadeer N, Abudula A.	n lass at land a t
	Tumour Biol. 2015 Mar;36(3):1711-20. doi: 10.1007/s13277-014-2772-5. Epub 2014 Nov 27. PMID: 25427637	The second secon
	Similar articles	
	Gene set enrichment analysis and ingenuity pathway analysis of metastatic clear cell renal cell	
4.	carcinoma cell line.	
	Khan MI, Dębski KJ, Dabrowski M, Czarnecka AM, Szczylik C.	
	Am J Physiol Renal Physiol. 2016 Aug 1;311(2):F424-36. doi: 10.1152/ajprenal.00138.2016. Epub 2016 Jun 8.	()))보 ()))보 🖉 👘
	PMID: 27279483	

QIAGEN

>10,000 publications that used IPA -- and growing!





Integrate and compare genomics, transcriptomics, proteomics and metabolomics data to see the big picture on your focus research

RESEARCH ARTICLE

A Multi-Omics Approach Identifies Key Hubs Associated with Cell Type-Specific Responses of Airway Epithelial Cells to Staphylococcal Alpha-Toxin



Multi

Experiment

Phosphorylation

Protein



用IPA來發掘實驗資料中各類型關係









Gather this type of information for nearly every gene. Inferences can be made from the resulting networks.



□ Synonyms, Protein Family, Domains

- GO, Entrez Gene, Pfam

□ Tissue and Biofluid Expression & Location

- GNF, Plasma Proteome

□ Molecular Interactions

- BIND, DIP, MIPS, IntAct, Biogrid^{New}, MINT, Cognia, etc.

miRNA/mRNA target databases

TarBase, TargetScan, miRecords

Gene to Disease Associations

OMIM, GWAS databases

□ Metabolomics

HumanCyc^{New}

Clinical Trial information

- ClinicalTrials.gov

Sample to Insight







From full text, contextual detail, experimentally demonstrated

Original sentence from publication	Ingenuity Expert Findings
nNOS overexpression mice showed reduced myocardial contractility.	Transgenic nNOS in myocardium from mouse heart decreases the contractility of myocardium in left ventricle from mouse heart.
Francisella organisms efficiently induce IL-1beta processing and release.	Francisella tularensis subsp. novicida U112 increases (in a time- dependent manner) release of human IL1B protein from human monocytes.

- Contextual details: Manual curation process captures relevant details
- Experimentally demonstrated: Findings are from full text articles – includes tables and figures
- Structured: Supports computation and answering in-depth biological questions in the relevant context
- High quality: QC'd to ensure accuracy

Timely information: Weekly updates so up to date information is captured





Unique Tools for Biological Analysis and Interpretation





Unique Tools for Biological Analysis and Interpretation

AGEN	IsoProfiler; Universe = Human isoforms from RefSeq with Exp Fold Change and Exp Intensity/RPKM/FPKM/Counts	ቶ ር
	FGL1 fibrinogen like 1	CREATE DATASET CUSTOMIZE TABLE 🔊 Symbol A18G - AARD (p1 of 756) 🗸 🖾 More Info
IsoProfiler	1200 My Pathways	■ FCL1-204] tion × Gene × Expression Patterns × M × Tr × Ra × Iso × Iso ×
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	P an P cale Z A Y A A A A A A A A A A A A A A A A A	
	Summary Canonical Pathways Upstream Analysis Diseases & Functions Regulator Effects	
	Canonical Pathways Upstream Analysis Diseases & Functions Regulator Energy	
Multi-omics	Chart Heatmap	regulator Effects (Elsts (Molecules (Comparison Settings)
Overlay		
,	Settings/Legend	Pathway Molecules
	FILTER More Info	Cardiomyocyte Differentiation via BMP Receptors
Phosphorylation	Expression Analysis - Mock vs. WNV-TE Ensembl Jan2015 FC >1 p<0.05 RPKM>10 in o	
	Summary \ Canonical Pathways \ Upstream Analysis \ Diseases & Functions \ Regulator Effects \	
Analysis	VIEW AS HEATMAP VIEW COMPARISON CUSTOMIZE TABLE	z-score overall 71.83891386274442 - 57.4973960 (p1 of 23) 🔻 📧 🚺 More
	Analysis Name TX Project	$\mathbf{X} \times \mathbf{CP}$ $\mathbf{Y} \times \mathbf{CP}$
	GSE48210_GPL6246_test4-type 1 diabetes mellitus[spleen]ant - 2017-08-1 MouseDisease	spleen CellType:CellDescription:SamplingTime[hours] 85.63 76.16 63.48 62.08 71.84
Comparison	GSE53166_GPL6244_test2-NA[peripheral blood]NS1-deleted PR8 - 2017-08HumanDisease GSE18686_GPL6947_test2-NA[peripheral blood]IFN gamma;lipop - 2017-08 HumanDisease	periphera Treatment => N\$1-deleted PR8 virus vs none 77.46 83.67 69.11 54.96 71.30 periphera Treatment => IFN gamma;lipopolysaccharide 68.31 81.85 64.65 66.93 70.43
	GSE45251_GPL4133_test1-normal control[pulmonary airway]TNF - 2017-08-HumanDisease	pulmonar Treatment => TNF alpha vs none 73.03 84.26 58.59 60.38 69.07
Analysis	GSE18686_GPL6947_test1-NA[peripheral blood]IFN gamma - 2017-08-10 (HumanDisease	periphera Treatment => IFN gamma vs lipopolysacchari 57.74 82.46 72.28 60.38 68.21
	GSE61141_GPL11154_test1-asthma[tracheal epithelium]Infecti - 2017-08-1[HumanDisease	tracheal e DiseaseState:Infection => asthma -> HRV16 68.31 82.46 66.91 54.01 67.92
	GSE31022_GPL6887_test3-influenza A[lung]NA - 2017-08-11 05:12 PM MouseDisease GSE61141_GPL11154_test2-normal control[tracheal epithelium - 2017-08-1 HumanDisease	lung SamplingTime[dpi] => 3 vs baseline 77.46 74.83 57.30 61.24 67.71 tracheal e DiseaseState:Infection => normal control -> 68.31 84.26 65.79 52.04 67.60
Analysis Match*	GSE49709_GPL10558_test1-normal control[peripheral blood]li = 2017-08-1[HumanDisease	periphera Treatment:PreTreatment => fluticasone (Flove 73.03 84.26 58.59 53.03 67.23
OmicSoft Lands	GSE52405_GPL11002_test14-influenza A[lung]SubjectInfection - 2017-08-1 MouseDisease	lung SubjectInfection:SamplingTime[dpi]:AnimalStra 68.31 78.10 62.29 58.63 66.84
OfficSoft Lanus	GSE42606_GPL10558_test2-normal control[peripheral blood]C 2017-08- HumanDisease	periphera Treatment:TreatTime[hours] => 24 -> C. alb 68.31 83.07 59.85 55.90 66.78
	GSE44595_GPL7202_test9-influenza A[lung]NA - 2017-08-11 06:34 PM MouseDisease GSE42638_GPL6887_test3-influenza A[lung]NA - 2017-08-11 06:16 PM MouseDisease	lung SamplingTime[dpi]:SubjectInfection => 5 -> i 68.31 79.37 62.29 54.96 66.24 lung SubjectTreatment:SamplingTime => 2 days 68.31 78.74 59.85 56.83 65.93
	GSE72008_GPL10787_test1-influenza A[lung]SubjectInfection 2017-08-14MouseDisease	lung Subjectinection:SamplingTime[dpi] => $1 -> i 63.25$ 79.37 68.02 53.03 65.92
	GSE68945_GPL11202_test6-influenza A[lung]SubjectInfection 2017-08-14MouseDisease	lung SubjectInfection:SamplingTime[dpi] => 2 -> i 63.25 78.10 70.18 52.04 65.89
	GSE49709_GPL10558_test2-normal control[peripheral blood]li - 2017-08-1 HumanDisease	periphera Treatment:PreTreatment => none -> lipopoly 63.25 78.74 66.91 54.01 65.73
	GSE31022_GPL6887_test5-influenza A[lung]NA - 2017-08-11 05:12 PM MouseDisease GSE53166_GPL6244_test1-NA[peripheral blood]lipopolysacchar - 2017-08- HumanDisease	lung SamplingTime[dpi] => 5 vs baseline 68.31 73.48 62.29 58.63 65.68 periphera Treatment => lipopolysaccharide (LPS) vs none 73.03 81.24 51.83 55.90 65.50
	GSE64798_GPL8833_test2-influenza A[lung]NA - 2017-08-14 08:05 PM MouseDisease	Iung SamplingTime[dpi]:AnimalStrain => 12951/Sv 63.25 76.16 64.65 57.74 65.45
	GSE49706_GPL10558_test3-normal control[peripheral blood]IF - 2017-08-1 HumanDisease	periphera Treatment => IFN gamma vs none 68.31 72.11 72.28 48.95 65.41
	GSE53454_GPL16311_test15-normal control[pancreatic islets] - 2017-08-17HumanDisease	pancreati Treatment:TreatTime[hours] => 72 -> IL-1 b 57.74 79.37 68.02 55.90 65.26
	GSE13168_GPL96_test14-normal control[airway smooth muscle] - 2017-08- HumanDisease	airway sm Transfection:Treatment => PKI-GFP -> IL-1 77.46 81.24 51.83 50.00 65.13
	GSE48757_GPL570_test1-normal control[foreskin]IFN alpha;IF = 2017-08-12 HumanDisease GSE68945_GPL11202_test9-influenza A[lung]SubjectInfection_ = 2017-08-14 MouseDisease	foreskin Treatment => IFN alpha;IFN gamma;IL-1 beta 63.25 80.62 65.79 50.00 64.91 lung SubjectInfection:SamplingTime[dpi] => 4 -> i 57.74 76.16 66.91 58.63 64.86
	GSE52405_GPL11202_test29-viral infectious disease[lung]Sub = 2017-08-14MouseDisease	lung Subjectinection:SamplingTime[dpi]=>4=>1 57.74 70.10 00.91 58.03 04.80
	CCC7021 CDI 1261 testi immunologie deficience emdeemologie 2017 00 Mouro Disease	Transmont Transmitime (bound) > 4 > influen (52.35 70.37 61.09 54.06 64.67

*Q4 2017



Entry Points in IPA





Sample to Insight





Basic Module

- Canonical Pathway
- Molecule Activity Predictor (MAP)
- Mechanistic Network
- Upstream regulator Analysis
- Downstream Effects Analysis
- Regulator Effects
- Network Analysis
- Comparison Analysis
- MicroRNA Target Filter
- Isoform View
- Disease View
- Tox Lists and Tox Functions
- Gene and Chem View
- Interactive Disease and Functions Nodes
- Biomarker filter
- Path Designer

https://www.qiagenbioinformatics.com/products/features/

Advanced Analytics (AA)

- Causal Network Analysis
- BioProfiler
- Relationship Export
- IsoProfiler
- PhosphoProteomics Analysis
- Analysis Match (Pay extra)





Content Updates Time Line

Summer Release (June 2017)

- IsoProfiler with new GTEx human tissue expression data.
- Easily navigate to each of your open windows in IPA
- ~120,000 new findings (bringing total to greater than 6 million findings)
- New Canonical Pathway: Osteoarthritis Pathway

Winter Release (2017 December)

- Enhancements to Analysis Match updated additional analyses from OmicSoft
- Focus on the most important z-scores in the heat map by setting a threshold
- Entering metadata for a dataset help you quickly find and search those datasets
- New criteria to select, highlight or trimming nodes on networks and pathways
- New findings, including 120,000 (bringing total to over 6.3 million findings)
- New Canonical Pathways Opioid Signaling Pathway

Spring Release (March 2018)

- Predict Activity of Metabolic Pathways
- New Datasets for Analysis Match
- 130,000 new findings (bringing total to over 6.4 million findings)
- New Canonical Pathways
 - -Adrenomedullin signaling pathway, Iron homeostasis signaling pathway



- Predict Activity of Metabolic Pathways
- New Datasets for Analysis Match
- Content Updates
- New Canonical Pathways
 - Adrenomedullin signaling pathway
 - Iron homeostasis signaling pathway

~130,000 new findings (bringing total to over 6.4 million findings), including:

~40,000 new Expert findings

- ~62,000 new mutation-to-disease findings from ClinVar
- ~14,000 new cancer mutation disease association findings from COSMIC
- ~1,800 drug-to-disease findings from ClinicalTrials.gov
- ~1,700 new disease-to-target findings from ClinicalTrials.gov
- ~2,000 new functional annotations from Gene Ontology
- ${\sim}11{,}500$ new protein-protein interactions from the BioGRID database
- ~1,000 new protein-protein interactions from the IntAct database
- ~600 new mouse knockout-to-phenotype findings from MGD (JAX Labs)





- Predict Activity of Metabolic Pathways
- New Datasets for Analysis Match
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- New Canonical Pathways
 - Adrenomedullin signaling pathway
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Land	Repository	Q4 2017 (December)	Q1 2018 (March)	Increase
	HumanDisease	3239	3762	523
DiseaseLand	MouseDisease	2516	2798	282
DiseaseLand	Hematology	108	108	0
	RatDisease (New)	0	124	124
	OncoGEO	1028	1169	141
OncoLand	TCGA	24	24	0
Uncoland	MetastaticCancer	53	53	0
	Pediatrics (New)	0	127	127

There are 1,100+ new datasets for Analysis Match in this release, bringing the total available in IPA to >8,000. This includes two new repositories, RatDisease (under DiseaseLand) and Pediatrics (under OncoLand). Table 1 compares the repositories and their respective sizes in this release versus the prior one.



- Predict Activity of Metabolic Pathways
- New Datasets for Analysis Match
- Content Updates
- New Canonical Pathways
 - Adrenomedullin signaling pathway
 - Iron homeostasis signaling pathway









Curation, Processing, & QA











- DiseaseLand
 - HumanDisease (2,929)
 - MouseDisease (2,257)
- OncoLand
 - OncoGEO (986)
 - TCGA (25)
 - Hematology (68)

Total datasets for release: 6000+





Human DiseaseLand

- 350 diseases
- 185 tissues of origin
- 48 expression platforms (primarily array), >450 RNA-seq studies

Mouse DiseaseLand

- 194 diseases
- 145 tissues of origin
- 39 expression platforms (primarily array), >500 RNA-seq studies

OncoGEO

- 98 cancers
- 49 tissues of origin
- 27 expression platforms (primarily array), >160 RNA-seq studies

TCGA

• 23 cancers (23 tissues)

Hematology

- 7 tissues of origin
- 16 diseases



Visualizing an individual gene across comparisons





Highest-quality interpretation of genomics and sequencing data





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Searching Basics

Searching

- Gene/chemical search and results
- Function/Disease search and results
- Pathway tox list search and results
- Advanced search: Limiting results to a molecule type, family or subcellular location





• Finding:

- A single piece of evidence from a literature source or database in the **Ingenuity Knowledge Base**
- Includes context of the fact such as experiment type, species, tissue/cell location, etc.

Canonical Pathway (Signaling and Metabolic)

- Are generated prior to data input, based on the literature
- Do NOT change upon data input
- Do have directionality





Set of Genes and Chemicals Set of Genes and Chemicals associated with Disease/Function associated with Disease/Function (with relationship information) (without relationship information) Chemical Gene

Sample to Insight




Live Demo

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BioProfiler

BioProfiler allows you to make novel discoveries by providing you the ability to filter the fine-grained relationships between molecules (genes, RNAs, proteins, and chemicals) and diseases or functions.

BioProfiler										
ADD TO MY PA	THWAY ADD T	O MY LIST DISPL	AY AS NETWORK	CREATE DATA	SET 📃 手	LIMIT TO DATAS	ET Genentech BMC	<u>T</u>		
Molecule Add/Remove column(s)							Disease or Function Evidence			
🛆 Sym 🝸	Mole 🝸 🗵	ID 🗵	Expr 🝸 🗶	Expr 🝸 🗶	Expr 🍸 🕱	Mole 🝸 🗵	Effect on D 🝸 🗵	Disease or Function 🔳	Muta 🝸 🗵	
►ABCB9	transporter	214209_s_at	† 1.072	3.59E-04	1.30E-03	increased ac	affects,increases	Adenosquamous all 6	heterozygou.	
ABHD17A	enzyme	221267_s_at	↓ -0.602	3.44E-04	1.26E-03	unknown ch	affects	Acute myeloid leu all 4	heterozygou.	
►ABI2	other	225112_at	† 0.091	3.92E-01	6.19E-01	decreased a	affects,decreases,i	Abnormal morp all 25	heterozygou.	
►ACAT2	enzyme	209608_s_at	↓ -0.787	1.12E-02	2.92E-02	decreased a	affects,decreases,i	Absorption of ch all 23	homozygou	
►ACTN4	transcription	200601_at	† 1.464	8.88E-16	2.48E-14	decreased a	affects,decreases,i	Abnormal morp all 81	dominant,he.	
ADAM28	peptidase	205997_at	† 1.646	9.07E-01	1.00E00	decreased a	affects,decreases,i	Adhesion of end all 19	frameshift,h	
► ADAMDEC1	peptidase	206134_at	† 1.399	1.00E00	1.00E00	increased ac	affects	Adenosquamous all 8	heterozygou.	
ADAP2	other	222876_s_at	† 1.021	9.60E-01	1.00E00	increased ac	affects	Advanced stage all 4	heterozygou.	
►ADGRE5	G-protein co	202910_s_at	† 1.182	1.80E-06	1.05E-05	decreased a	affects,decreases,i	Accumulation of all 36	homozygou	
► ADGRL1	G-protein co	203488_at	† 1.334	1.11E-13	2.18E-12	decreased a	affects,decreases,i	Abnormal functi all 10	homozygou	
ADNP2	other	203321_s_at	↓ -0.466	3.03E-03	8.99E-03	increased ac	affects,decreases,i	Cell death all 7	heterozygou.	
►AGPAT4	enzyme	228667_at	↓ -1.675	2.74E-06	1.52E-05	decreased a	affects	Abnormal quantit all 8	heterozygou.	
► AK3	kinase	224655_at	↓ -1.323	2.52E-05	1.14E-04	decreased a	affects,decreases	Cell viability of m all 6	frameshift,wi.	
AKAP11	other	203156_at	↓ -1.330	2.72E-09	2.65E-08	decreased a	affects,decreases,i	Abnormal morp all 24	heterozygou.	
► AKAP8	other	203847_s_at	† 0.630	5.05E-09	4.71E-08	decreased a	affects,increases	Cleft palate synd all 11	heterozygou.	
► AKAP8L	other	218064_s_at	† 1.058	6.40E-12	9.58E-11	decreased a	affects,decreases,i	Activation of DN all 17	heterozygou.	
►ALG5	enzyme	218203_at	+-0.653	3.14E-08	2.47E-07	increased ac	affects	Adenosquamous all 8	heterozygou.	
ALS2	other	226291_at	1 0.375	1.01E-03	3.34E-03	decreased a	affects,decreases,i	Abnormal morp all 64	frameshift,h	
► ANAPC5	other	200098_s_at	† 0.471	1.72E-04	6.74E-04	decreased a	affects	Liver carcinoma all 6	missense,sile.	
►ANKRD33B	other	231963_at	† 2.676	2.66E-15	6.59E-14	unknown ch	affects	Cutaneous melan all 3	frameshift,h	
►ANP32E	other	221505_at	† 0.544	2.78E-04	1.04E-03	unknown ch	affects	Endometrioid en all 3	missense,no	
AP2B1	transporter	200612_s_at	↓ -1.040	1.15E-04	4.66E-04	decreased a	affects,decreases,i	Activation of RNA all 7	nonsense,un	
►AP3D1	transporter	206592_s_at	↓ -0.410	1.04E-04	4.25E-04	decreased a	affects,decreases,i	Acidification of all 23	frameshift,h	
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When will I use BioProfiler?

- Targets of toxicity: Which genes when [decreased] in activity [increase][liver cholestasis]? What types of [genetic] evidence support this?
- Target discovery:- What [heterozygous knockouts] in [mouse] can [decrease] [asthma]?
- Which drugs or which targets have been in late stage clinical trials or approved to decrease [diabetes]?
- Biomarker research: Which genes are potential [diagnosis OR prognosis] biomarkers of [breast cancer] and are [upregulated] in breast cancer?

ADD TO MY PATHWAY AE	DD TO MY LIST DISPLAY AS N			opterin - val ((p1 of 1) ▼ <
Molecule	Add column(s)	E Durease or Function Evi	idence		Add column(s) 🖽
△ Symbol	Molecule Type	Add Column(s) to section	Effect on Dise 🝸 🕱	Causal or Corr	Add Column(s) to section
(6R)-tetrahydrobiopt		Symbol	decreases	causal	Molecule Activity
ABAT	enzyme		affects	correlation	
acamprosate	chemical drug	Molecule Type	decreases	causal	Effect on Disease or Function
ACHE	enzyme	Disease Count	affects	correlation	Disease or Function
ADRA1A	G-protein coupled	r 🗆 Synonym(s)	affects	correlation	Mutation evidence
ADRA1B	G-protein coupled		affects	correlation	Biomarker Application Evidence
ADRA1D	G-protein coupled	r	affects	correlation	
ADRA2A	G-protein coupled	Tissue/Cell Line	affects	correlation	Species Evidence
ADRA2B	G-protein coupled	Location	affects	correlation	Drug target evidence
ADRA2C	G-protein coupled		affects	correlation	Expression evidence
ALDH5A1	enzyme	Apply Cancel	affects	correlation	Causal or Correlated
aripiprazole	chemical drug	increased activity	decreases	causal	
				causal	Tissue/Cell Line
				causal	Findings
				causal	Apply Cancel
				correlation	Apply Cancel
				causal	11





- 1. What disease is BCR (the kinase) associated with? Please list one of them.
- 2. How many categorized literature findings are in Ingenuity knowledge base on BCR (the kinase)?
- 3. Search for genes associated with the function antigen presentation in IPA. How many genes are associated with the function activation of antigen presenting cells?
- 4. Find the common genes between Diabetes mellitus and Alzheimer disease





1. What **disease** is **BCR (the kinase)** associated with? Please list one of them.

Chronic myeloid leukemia, adenocarcinoma, epithelial cancer, hyperactive behavior, leukemogenesis, hemangioblastoma, capillary hemangioma, squamous-cell carcinoma, melanoma, melanoma cancer, gliosis, edema, squamous cell cancer, weight loss, bipolar disorder, acute lymphocytic leukemia, sepsis, T-cell leukemia, ectopia, B-cell leukemia, Philadelphia-positive acute lymphoblastic leukemia, acute myeloid leukemia, carcinoma, hypertrophy, productive infection by HIV-1, tumorigenesis, Parkinson's disease, serous ovarian carcinoma, serous ovarian adenocarcinoma

2. How many categorized literature findings are in Ingenuity knowledge base on BCR (the kinase)?

1,569

3. Search for genes associated with the function antigen presentation in IPA. How many genes are associated with the function **activation of antigen presenting cells**?

671

4. Find the common genes between Diabetes mellitus and Alzheimer disease



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D. Q&A











ぞ 創源生技 GGA

Introduction to Pathway Building Key Terminology Adding Molecules to a New Pathway General pathway navigating Using the Build Tools Understanding the legend Using the Overlay tools Saving work for future analyses

How to build pathway





Networks:

- Generated de novo based upon input data
- Do NOT have directionality

Canonical Pathways (Signaling and Metabolic):

- Are pre-built and generated prior to data input, based on the literature
- Do have directionality (proceed "from A to Z")

My Pathways and Path Designer Pathways:

Custom built pathways manually created based on user input

Relationship Type:

- An interaction between two molecules in IPA (seen as a line)
- Direct (physical contact) and Indirect (do NOT require physical contact)

Node

Single molecule in Network such as Gene, Chemicals, Disease, and Pathway



 Using one molecule of interest as a starting point, the Grow feature allows you to find (and add) other molecules of interest to a pathway. You can also grow to functions and diseases.



Grow





- Calculates the "Shortest Path" between 2 molecules or 2 sets of molecules
- If 2 molecules/sets don't have specific connections in IPA, Path Explorer will find how many and which molecules can be added to this pathway to create the shortest path
 - Shortest Path (n)
 - Shortest Path + 1 (n+1)





 Connect allows you to see specific molecular interactions between nodes or groups of nodes.



Connect



 Overlay tools allows you to compare and contrast different kinds of information within networks



Overlay



Path Designer



 Use Path Designer to transform your networks and pathways in IPA into publication quality pathway graphics rich with color, customized text and fonts, biological icons, organelles, and custom backdrops.







- 1. Search for the following genes in IPA and add them to a pathway: A2M, APOE, APP, HFE2, LRP1, PSEN1, PSEN2, SLC40A1, TRF2
- 2. What are the connections between these molecules that occur in nervous system tissues and CNS cell lines?
- 3. Are these molecules involved in any Canonical Pathways?
- 4. Add at least one organelle or other cellular structure to your pathway and move the molecules on your pathway to the appropriate location.



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Q&A







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Sample to Insight

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