



Login | Register

Transcription Pathways Ontologies Diseases/Drugs Cell Types Misc Legacy Crowd

Description AML_UP (857 genes)



ChEA 2016

Bar Graph

Table

Grid

Network

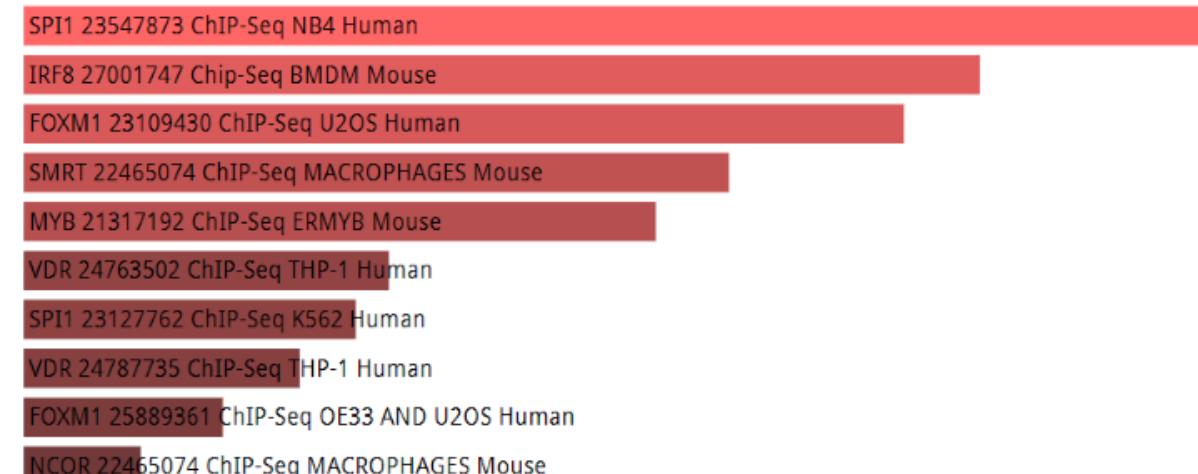
Clustergram

Appyter



Click the bars to sort. Now sorted by p-value ranking.

SVG PNG JPG



ENCODE and ChEA Consensus TFs from ChIP-X

ARCHS4 TFs Coexp

TF Perturbations Followed by Expression





Login | Register

Transcription Pathways Ontologies Diseases/Drugs Cell Types Misc Legacy Crowd

Description AML_UP (857 genes)



ChEA 2016

Bar Graph

Table

Grid

Network

Clustergram

Appyter



Hover each row to see the overlapping genes.

10 entries per page

Search:

Index	Name	P-value	Adjusted p-value	Odds Ratio	Combined score
1	FOXM1 23109430 ChIP-Seq U2OS Human	1.102e-16	2.358e-14	4.99	183.39
2	SPI1 23547873 ChIP-Seq NB4 Human	1.377e-19	8.839e-17	2.12	91.86
3	IRF8 27001747 Chip-Seq BMDM Mouse	2.038e-17	6.542e-15	2.27	87.14
4	MYB 21317192 ChIP-Seq ERMYB Mouse	2.784e-14	3.575e-12	2.65	82.72
5	SMRT 22465074 ChIP-Seq MACROPHAGES Mouse	5.462e-15	8.766e-13	2.14	70.31
6	VDR 24787735 ChIP-Seq THP-1 Human	7.877e-11	6.321e-9	2.46	57.18
7	VDR 24763502 ChIP-Seq THP-1 Human	1.074e-11	1.149e-9	2.20	55.44
8	SPI1 23127762 ChIP-Seq K562 Human	2.243e-11	2.057e-9	2.13	52.15
9	FOXM1 25889361 ChIP-Seq OE33 AND U2OS Human	4.351e-10	3.104e-8	2.28	49.08
10	TRP63 18441228 ChIP-ChIP KERATINOCYTES Mouse	0.00001167	0.0004409	3.48	39.50

Showing 1 to 10 of 642 entries | Export entries to table

Previous Next

Terms marked with an * have an overlap of less than 5

ENCODE and ChEA Consensus TFs from ChIP-X

ARCHS4 TFs Coexp

Activate Windows

Go to Settings to activate Windows.



Type here to search



05:17 ب.م
ENGLISH
11/IV



Transcription Pathways On

Description AML_UP (857 genes)

ChEA 2016

Bar Graph

Hover each row to see the overlap

10 entries per page

Index	Name	Odds Ratio	Combined score
1	FOXM1 23109430 ChIP-seq NB4 Human	4.99	183.39
2	SPI1 23547873 ChIP-Seq NB4 Human	8.839e-17	2.12
3	IRF8 27001747 Chip-Seq BMDM Mouse	2.038e-17	91.86
4	MYB 21317192 ChIP-Seq ERMYB Mouse	2.784e-14	2.27
5	SMRT 22465074 ChIP-Seq MACROPHAGES Mouse	5.462e-15	87.14
6	VDR 24787735 ChIP-Seq THP-1 Human	8.777e-11	2.65
7	VDR 24763502 ChIP-Seq THP-1 Human	2.243e-11	82.72
8	SPI1 23127762 ChIP-Seq K562 Human	2.405e-10	70.31
9	FOXM1 25889361 ChIP-Seq OE33 AND U2OS Human	4.351e-10	55.44
10	TRP63 18441228 ChIP-ChIP KERATINOCYTES Mouse	0.00001167	52.15

Showing 1 to 10 of 642 entries | Export entries to table

Terms marked with an * have an overlap of less than 5

Legacy Crowd

Copypter

ENCODE and ChEA Consensus TFs from ChIP-X

ARCHS4 TFs Coexp

Activate Windows
Go to Settings to activate Windows.

Type here to search



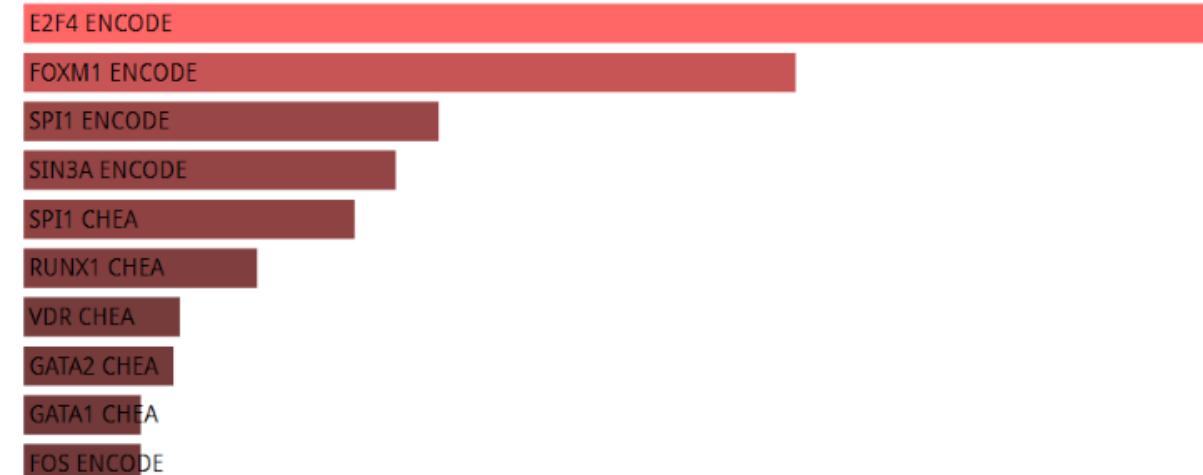
ChEA 2016

ENCODE and ChEA Consensus TFs from ChIP-X

Bar Graph Table Clustergram Appyter

Click the bars to sort. Now sorted by p-value ranking.

SVG PNG JPG



ARCHS4 TFs Coexp

TF Perturbations Followed by Expression

TRRUST Transcription Factors 2019

Activate Windows
Go to Settings to activate Windows.

ChEA 2016

ENCODE and ChEA Consensus TFs from ChIP-X

[Bar Graph](#) [Table](#) [Clustergram](#) [Appyter](#)

Hover each row to see t

10 entries per

GABPB2, CCNF, HJURP, BUB1B, SMC6, MKI67, CDC20, BSG, HMGN2, GTF51, GEN1, ZGRF1, ESCO2, NEIL3, MELK, CCNE2, TMEM258, CCNE1, FANCD2, KIF20A, KIF20B, PRR11, ASF1B, CDC42, ANAPC15, CDC43, CDC44, TROAP, ARHGAP19, CDC48, IQGAP3, NCAPH, KIAA1524, ORC1, RACGAP1, PLK4, XRCC4, PLX1, LARP7, NDC80, TPX2, DIAPH3, KIF4A, CDK1, TOP2A, C2CD3, KIF14, MCM10, KIF11, BRCA1, FOXM1, BRCA2, KIF15, CKS1B, NUF2, PBK, MYBL2, ZNF367, CEP55, DLGAP5, RAB8A, KIF23, MASTL, CIT, CCNA2, ASPM, TFPD1, ESPL1, DEPDCL, MTFR2, ALDOA, PCNA, ATL3, TTK, AURKB, AURKA, RECQL4, POLD3, EMC3, E2F2, E2F7, E2F8, POLO, CENPW, CDKN2C, SPAG5, MYO9B, TICRR, CENPF, RAD51, KIAA0101, PRC1, RPWD3, TRMT6, NCAPD2, SPC24, SPC25

Search:

Index	Name	Adjusted p-value	Odds Ratio	Combined score
1	FOXM1 ENCODE	1.007e-14	9.62	347.93
2	E2F4 ENCODE	1.399e-24	1.455e-22	211.91
3	SPI1 ENCODE	2.570e-9	8.909e-8	38.12
4	SIN3A ENCODE	1.836e-8	4.773e-7	35.86
5	SPI1 CHEA	1.229e-7	0.000002557	31.41
6	VDR CHEA	0.0003763	0.005591	30.09
7	RUNX1 CHEA	0.00001066	0.0001848	19.49
8	ESR1 CHEA	0.002584	0.02443	14.51
9	GATA2 CHEA	0.0005058	0.006576	12.82
10	IRF8 CHEA	0.005769	0.04615	12.78

Showing 1 to 10 of 104 entries | [Export entries to table](#)

Terms marked with an * have an overlap of less than 5

[Previous](#) [Next](#)

ARCHS4 TFs Coexp

TF Perturbations Followed by Expression

TRRUST Transcription Factors 2019

Activate Windows
Go to Settings to activate Windows.

Type here to search

^ ENG 05:18 ب.م
If..//IV

ChEA 2016

ENCODE and ChEA Consensus TFs from ChIP-X

ARCHS4 TFs Coexp

Bar Graph

Table

Clustergram

Appyter



Click the bars to sort. Now sorted by p-value ranking.

SVG PNG JPG

JDP2 human tf ARCHS4 coexpression

ZNF438 human tf ARCHS4 coexpression

TFEC human tf ARCHS4 coexpression

HLX human tf ARCHS4 coexpression

MTF1 human tf ARCHS4 coexpression

PLEK human tf ARCHS4 coexpression

SEMA4A human tf ARCHS4 coexpression

CEBPB human tf ARCHS4 coexpression

ZNF385A human tf ARCHS4 coexpression

MAFB human tf ARCHS4 coexpression

TF Perturbations Followed by Expression

TRRUST Transcription Factors 2019

IncHIIIR IncRNA Co-Expression

Activate Windows
Go to Settings to activate Windows.

Type here to search



ChEA 2016

ENCODE and ChEA Consensus TFs from ChIP-X

ARCHS4 TFs Coexp

Hover each row to see the overlapping genes.

10 entries per page

Index	Name	Par-Graph	Table	Clustergram	Annotate	?	
1	JDP2 human tf ARCHS4 coexpression	SP1, NCF1, NCF2, NCF4, JIF30, CXCL16, ADGRA2, CLEC5A, C3AR1, TOM1, SIRPA, IL13RA1, PRKCD, C10ORF54, CYBB, CYBA, MPEM1, OSCAR, TYROBP, KCNQ1, CD300C, FTI, CSF1R, RAB5C, NCF1C, GPR84, CFP, RASGRP4, PIK3R5, ADGRG3, TRPM2, ADAP2, CLEC7A, CD300LB, HMOX1, CD14, SLC15A3, NADK, CCR1, CD163, PILRA, IGF2R, FOSL2, MAFB, BCL6, MAN2B1, SIGLEC9, ITGAM, ELL, FKBP15, MS4A7, ITGB2, SIRPB2, ARRB2, SQORDL, TREMT, FGFR3A, STAB1, EFHD2, ITGAX, CTSH, QSOX1, CTSD, ZNF385A, CT58, SLC36A1, FCER1G, NFAM1, PLAUR, GAB2, GMIP, TNFRSF1B, IL17RA, FGR, HCK, MMP19, TLR8, TLR4, PLCB2, TLR2, LILRA6, C1Q1A, GRN, LRP1, CEBPD, UNC93B1, DENND3, OA0H, NOD2, GNAI2, TYMP, ALOX5, SH3BP2, LRRK25, SEMA4A, LILRB1, MYO9B, LILRB4, SNX18, CD4, ZYX, CD68, FCGR2B, MYO1F	2.167e-66	3.686e-63	13.42	2029.14	combined score
2	ZNF438 human tf ARCHS4 coexpression		1.392e-57	1.184e-54	11.77	1540.86	
3	TFEC human tf ARCHS4 coexpression		1.880e-55	4.570e-53	11.38	1434.14	
4	HLX human tf ARCHS4 coexpression		1.880e-55	4.570e-53	11.38	1434.14	
5	MTF1 human tf ARCHS4 coexpression		1.880e-55	4.570e-53	11.38	1434.14	
6	PLEK human tf ARCHS4 coexpression		1.880e-55	4.570e-53	11.38	1434.14	
7	SEMA4A human tf ARCHS4 coexpression		1.880e-55	4.570e-53	11.38	1434.14	
8	CEBPB human tf ARCHS4 coexpression		2.375e-53	5.049e-51	11.00	1333.05	
9	ZNF385A human tf ARCHS4 coexpression		2.802e-51	4.766e-49	10.63	1237.38	
10	MAFB human tf ARCHS4 coexpression		2.802e-51	4.766e-49	10.63	1237.38	

Showing 1 to 10 of 1,701 entries | Export entries to table

Terms marked with an * have an overlap of less than 5

Previous Next

Activate Windows

Go to Settings to activate Windows.



Type here to search

^ ENG 05:18 ب.م
I.../I/I/V

maayanlab.cloud/Enrichr/enrich#

ENCODE and ChEA Consensus TFs from ChIP-X

ARCHS4 TFs Coexp

TF Perturbations Followed by Expression

Bar Graph Table Clustergram Appyter

Click the bars to sort. Now sorted by p-value ranking.

SVG PNG JPG

Experiment	Condition	Gene	Direction	p-value ranking
ZNF750 KD HUMAN GSE38039 CREEDSID	GENE 2704	ZNF750	DOWN	1
ZNF750 KD HUMAN GSE38039 CREEDSID	GENE 204	ZNF750	UP	2
AIRE KO MOUSE GSE30129 CREEDSID	GENE 1676	AIRE	UP	3
MBD2 KO MOUSE GSE48653 CREEDSID	GENE 1051	MBD2	UP	4
MAF OE MACROPHAGE HUMAN GSE98368 RNASEQ		MAF	UP	5
MAF SIRNA MACROPHAGE HUMAN GSE98368 RNASEQ		MAF	DOWN	6
KCNIP3 KO MOUSE GSE16874 CREEDSID	GENE 1030	KCNIP3	UP	7
FOXO1 KO MOUSE GSE40655 CREEDSID	GENE 508	FOXO1	UP	8
RORC KO MOUSE GSE27241 CREEDSID	GENE 1686	RORC	DOWN	9
PIN1 DEPLETION HUMAN GSE26262 CREEDSID	GENE 477	PIN1	DOWN	10

TRRUST Transcription Factors 2019

IncHUB IncRNA Co-Expression

Activate Windows
Go to Settings to activate Windows.

maayanlab.cloud/Enrichr/enrich#

Bar Graph Table Clustergram Appyter i

Hover each row to see the overlapping genes.

10 entries per page

Index	Name				
1	ZNF750 KD HUMAN GSE38039 CREEDSID GENE 2704 DOWN	7.289e-49	9.490e-46	9.60	1064.05
2	ZNF750 KD HUMAN GSE38039 CREEDSID GENE 204 UP	9.723e-49	9.490e-46	9.56	1056.71
3	AIRE KO MOUSE GSE30129 CREEDSID GENE 1676 UP	7.694e-44	5.006e-41	9.80	973.02
4	MBD2 KO MOUSE GSE48653 CREEDSID GENE 1051 UP	3.723e-39	1.817e-36	7.16	633.86
5	KCNIP3 KO MOUSE GSE16874 CREEDSID GENE 1030 UP	4.564e-32	1.273e-29	7.28	525.50
6	FLI1 KD HUMAN GSE27524 CREEDSID GENE 1597 DOWN	3.429e-29	5.578e-27	8.01	525.24
7	FOXO1 KO MOUSE GSE40655 CREEDSID GENE 508 UP	7.160e-32	1.747e-29	7.08	508.08
8	FLI1 KD HUMAN GSE27524 CREEDSID GENE 1596 DOWN	2.959e-29	5.250e-27	7.50	492.69
9	FLI1 KD HUMAN GSE27524 CREEDSID GENE 1599 DOWN	5.526e-29	8.297e-27	7.56	492.15
10	PIN1 DEPLETION HUMAN GSE26262 CREEDSID GENE 477 DOWN	5.019e-30	9.797e-28	6.64	448.03

Showing 1 to 10 of 1,952 entries | [Export entries to table](#)

Previous Next

Terms marked with an * have an overlap of less than 5

TRRUST Transcription Factors 2019

IncHUB IncRNA Co-Expression

Activate Windows
Go to Settings to activate Windows.

Enrichr Submissions TF Gene Cooccurrence



Type here to search



05:19 ب.م.
ENGLISH
فارسی/انگلیش

Enrichr Submissions TF-Gene Cooccurrence

TRANSFAC and JASPAR PWMs

Bar Graph Table Grid Network Clustergram Appyter

Click the bars to sort. Now sorted by p-value ranking.

SVG PNG JPG



Epigenomics Roadmap HM ChIP-seq

TargetScan microRNA 2017

miRTarBase 2017

ENCODE TF ChIP-seq 2015

Activate Windows
Go to Settings to activate Windows.



Type here to search



05:19 ب.م
ENGLISH
11/11/IV

Enrichr Submissions TF-Gene Cooccurrence

TRANSFAC and JASPAR PWMs

Bar Graph Table Grid Network Clustergram Appyter ⚙ ⓘ

Hover each row to see the overlapping genes.

10 entries per page

Search:

Index	Name	P-value	Adjusted p-value	Odds Ratio	Combined score
1	NFYB (human)	0.001494	0.2315	5.62	36.54
2	ELF3 (human)	0.0005431	0.1683	1.49	11.20
3	NR4A2 (human)	0.05240	1.000	2.18	6.43
4	E2F4 (human)	0.02393	1.000	1.71	6.37
5	IRF8 (human)	0.02024	1.000	1.29	5.04
6	ATF2 (human)	0.02301	1.000	1.29	4.85
7	ZNF281 (human)	0.02746	1.000	1.34	4.82
8	HNF4A (human)	0.02678	1.000	1.24	4.48
9	THR8 (human)	0.03179	1.000	1.23	4.25
10	PURA (human)	0.05229	1.000	1.41	4.17

Showing 1 to 10 of 310 entries | [Export entries to table](#)

Terms marked with an * have an overlap of less than 5

Previous Next

Epigenomics Roadmap HM ChIP-seq

TargetScan microRNA 2017

miRTarBase 2017

Activate Windows
Go to Settings to activate Windows.



Type here to search



5:19 ۱۰/۱۱/۲۰۲۳ ENG

maayanlab.cloud/Enrichr/enrich#

ARCHS4 TFs Coexp

TF Perturbations Followed by Expression

TRRUST Transcription Factors 2019

Bar Graph Table Clustergram Appyter

Click the bars to sort. Now sorted by p-value ranking.

SVG PNG JPG

Transcription Factor	Species
SPI1	human
SPI1	mouse
E2F4	mouse
TP53	human
JUN	mouse
E2F1	human
ETS1	mouse
NFKB1	human
USF2	human
ATM	human

IncHUB lncRNA Co-Expression

Enrichr Submissions TF-Gene Cooccurrence

Activate Windows
Go to Settings to activate Windows.

Type here to search

05:19 ب.م
ENGLISH
11/11/V

ARCHS4 TFs Coexp

TF Perturbations Followed by Expression

TRRUST Transcription Factors 2019

Bar Graph Table Clustergram Appyter ⓘ

Hover each row to see the overlapping genes.

10 entries per page

Search:

Index	Name	P-value	Adjusted p-value	Odds Ratio	Combined score
1	E2F4 mouse	CD163, ITGAM, NCF2, ITGB2, PRG2, CYBB, RNASE2, CSF2RA, HCK, BCL6, CCL5, ITGAX, CTSG, BPI, PRTN3, MNDA, FCGR1A, CD68, TLR4, ELANE	4.451e-1451	33.74	462.80
2	SPI1 human		5.864e-13	2.316e-10	306.07
3	SPI1 mouse		5.197e-10	1.026e-7	12.21
4	NUPR1 mouse		0.001423	0.01653	22.41
5	ZBTB7A mouse		0.001423	0.01653	146.92
6	E2F3 human		0.0001378	0.003202	14.04
7	RBL2 mouse		0.0005714	0.009028	14.96
8	SNAI1 human		0.0005714	0.009028	111.69
9	TFDP1 human		0.0005714	0.009028	111.69
10	ATM human		0.00002508	0.0009122	10.50

Showing 1 to 10 of 395 entries | [Export entries to table](#)

Previous Next

Terms marked with an * have an overlap of less than 5

IncHUB IncRNA Co-Expression

Enrichr Submissions TF-Gene Cooccurrence

Activate Windows

Go to Settings to activate Windows.

TF Perturbations Followed by Expression

TRRUST Transcription Factors 2019

IncHUB lncRNA Co-Expression

Bar Graph

Table

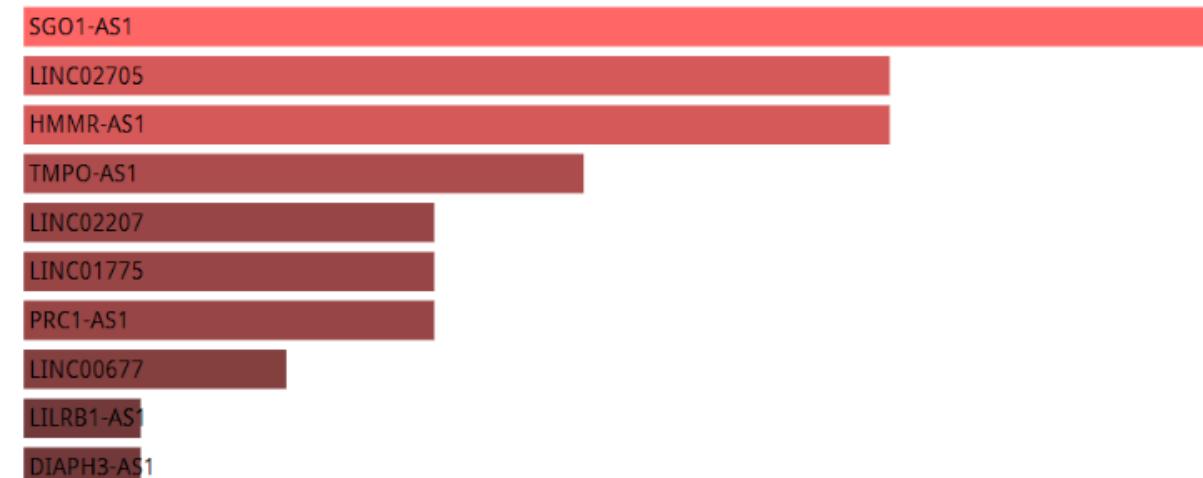
Clustergram

Appyter



Click the bars to sort. Now sorted by p-value ranking.

SVG PNG JPG



Enrichr Submissions TF-Gene Cooccurrence

TRANSFAC and JASPAR PWMs

Epigenomics Roadmap HM ChIP-seq

Activate Windows

Go to Settings to activate Windows.

TRRUST Transcription Factors 2019

IncHUB IncRNA Co-Expression

Bar Graph

Table

Clustergram

Appyter



Hover each row to see the overlapping genes.

10 entries per page

Search:

CCNF, HJURP, KIF14, BUB1B, MCM10, KIF11, BRCA1, MKI67, KIF15, NUF2, KPNA2, GTSE1, DLGAP5, CEP55, KIF23, KNL1, ESCO2, SGO1, CCNA2, ASPM, MELK, ESPL1, FANCQ2, DEPDCL, KIF20A, MTRR2, KIF20B, FAM72D, FAM72B, FAM72A, TROAP, TTK, HMMR, NCAPH, AURKA, CCNB2, RACGAP1, E2F8, PLK4, POLQ, PLK1, TICRR, TPX2, CENPE, CENPF, RAD51, PRC1, KIF4A, CDK1, SPC25

Index	Name	P-value	Adjusted p-value		
1	SGO1-AS1	1.299e-41	4.086e-38	23.66	2227.38
2	LINC02705	6.721e-39	7.046e-36	21.78	1914.63
3	HMMR-AS1	6.721e-39	7.046e-36	21.78	1914.63
4	TMPO-AS1	2.953e-36	2.321e-33	20.05	1640.34
5	LINC02207	5.819e-35	2.614e-32	19.23	1516.15
6	LINC01775	5.819e-35	2.614e-32	19.23	1516.15
7	PRC1-AS1	5.819e-35	2.614e-32	19.23	1516.15
8	LINC00677	1.101e-33	4.327e-31	18.45	1399.89
9	LILRB1-AS1	1.997e-32	5.710e-30	17.69	1291.08
10	DIAPH3-AS1	1.997e-32	5.710e-30	17.69	1291.08

Showing 1 to 10 of 3,145 entries | [Export entries to table](#)

Terms marked with an * have an overlap of less than 5

Previous Next

Enrichr Submissions TF-Gene Cooccurrence

Activate Windows
Go to Settings to activate Windows.



Type here to search



05:20 ب.م
ENGLISH
1/1/V

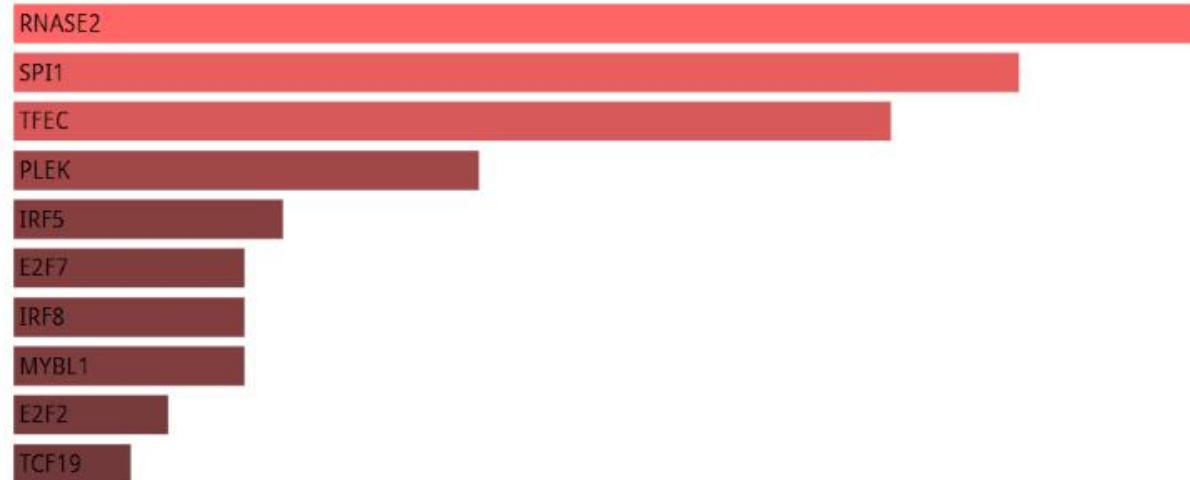
TRRUST Transcription Factors 2019

IncHUB lncRNA Co-Expression

Enrichr Submissions TF-Gene Cooccurrence

[Bar Graph](#) [Table](#) [Clustergram](#) [Appyter](#) [⚙](#) [ℹ](#)

Click the bars to sort. Now sorted by p-value ranking.

[SVG](#) [PNG](#) [JPG](#)

TRANSFAC and JASPAR PWMs

Epigenomics Roadmap HM ChIP-seq

TargetScan microRNA 2017

Activate Windows
Go to Settings to activate Windows.

maayanlab.cloud/Enrichr/enrich#

TRRUST Transcription Factors 2019

IncHUB IncRNA Co-Expression

Enrichr Submissions TF-Gene Cooccurrence

Bar Graph Table Clustergram

Hover each row to see the overlapping genes.

10 entries per page

Index	Name	P-value	Adjusted p-value	Cluster	Group
1	RNASE2	1.955e-80	3.364e-77	10.22	2370.80
2	SPI1	1.207e-75	1.038e-72	15.24	2628.88
3	TFEC	4.012e-72	2.302e-69	14.54	2389.70
4	PLEK	7.835e-61	3.371e-58	12.37	1712.06
5	IRF5	1.880e-55	6.473e-53	11.38	1434.14
6	E2F7	2.131e-54	4.584e-52	11.19	1382.90
7	IRF8	2.131e-54	4.584e-52	11.19	1382.90
8	MYBL1	2.131e-54	4.584e-52	11.19	1382.90
9	E2F2	2.602e-52	4.975e-50	10.81	1284.55
10	TCF19	2.802e-51	4.384e-49	10.63	1237.38

Showing 1 to 10 of 1,721 entries | [Export entries to table](#)

Terms marked with an * have an overlap of less than 5

Activate Windows
Go to Settings to activate Windows.

TRANSFAC and JASPAR PWMs

Bar Graph Table Grid Network Clustergram Appyter ⚙ ⓘ

Click the bars to sort. Now sorted by p-value ranking.

SVG PNG JPG

TF	Ortholog	p-value ranking
ELF3	(human)	1
NFYB	(human)	2
IRF8	(human)	3
ATF2	(human)	4
E2F4	(human)	5
HNF4A	(human)	6
ZNF281	(human)	7
THRB	(human)	8
NR5A2	(human)	9
TFAP2D	(human)	10

Epigenomics Roadmap HM ChIP-seq

TargetScan microRNA 2017

miRTarBase 2017

ENCODE TF ChIP-seq 2015

TF-LOF Expression from GEO

Activate Windows
Go to Settings to activate Windows.



Type here to search



05:20 ۱۰.۰۱.۲۰۲۳ ENG

TRANSFAC and JASPAR PWMs

[Bar Graph](#) **Table** [Grid](#) [Network](#) [Clustergram](#) [Appyter](#)

Hover each row to see the overlapping genes.

10 entries per page

Search:

Index	Name	P-value	Adjusted p-value	Odds Ratio	Combined score
1	NFYB (human)	0.001494	0.2315	5.62	36.54
2	ELF3 (human)	0.0005431	0.1683	1.49	11.20
3	NR4A2 (human)	0.05240	1.000	2.18	6.43
4	E2F4 (human)	0.02393	1.000	1.71	6.37
5	IRF8 (human)	0.02024	1.000	1.29	5.04
6	ATF2 (human)	0.02301	1.000	1.29	4.85
7	ZNF281 (human)	0.02746	1.000	1.34	4.82
8	HNF4A (human)	0.02678	1.000	1.24	4.48
9	THR8 (human)	0.03179	1.000	1.23	4.25
10	PURA (human)	0.05229	1.000	1.41	4.17

Showing 1 to 10 of 310 entries | [Export entries to table](#)

Terms marked with an * have an overlap of less than 5

[Previous](#) [Next](#)[Epigenomics Roadmap HM ChIP-seq](#)[TargetScan microRNA 2017](#)[miRTarBase 2017](#)[ENCODE TF ChIP-seq 2015](#)[TF-L OF Expression from GFO](#)

Activate Windows

Go to Settings to activate Windows.



Type here to search

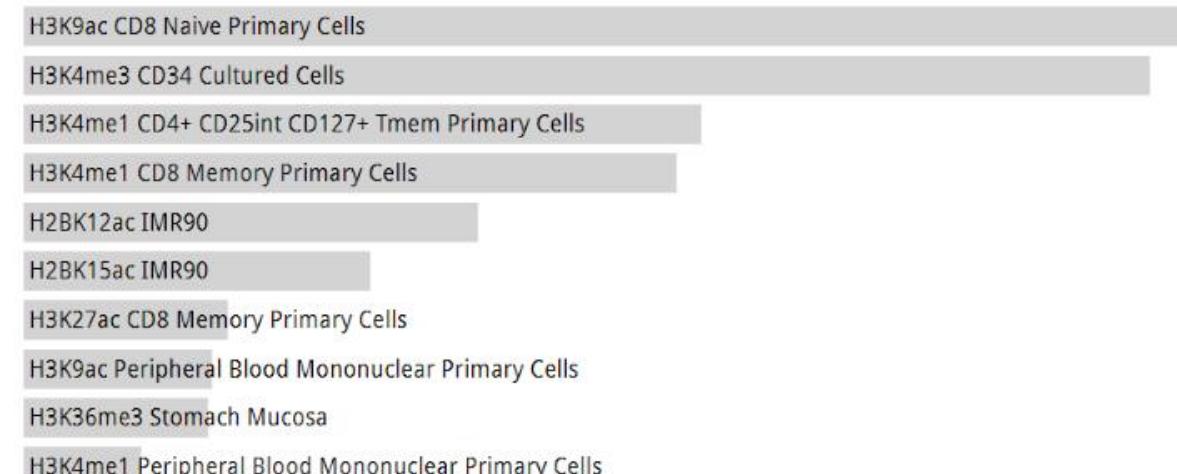


TRANSFAC and JASPAR PWMs

Epigenomics Roadmap HM ChIP-seq

[Bar Graph](#) [Table](#) [Grid](#) [Network](#) [Clustergram](#) [Appyter](#) [⚙️](#) [ℹ️](#)

Click the bars to sort. Now sorted by p-value ranking.

[SVG](#) [PNG](#) [JPG](#)

TargetScan microRNA 2017

miRTarBase 2017

ENCODE TF ChIP-seq 2015

TF-LOF Expression from GEO

Activate Windows
Go to Settings to activate Windows.



Type here to search

^ ENG 05:20 ب.م
I.../I/V

TRANSFAC and JASPAR PWMs

Epigenomics Roadmap HM ChIP-seq

Bar Graph Table Grid Network Clustergram Appyter ⚙ ⓘ

Hover each row to see the overlapping genes.

10 entries per page

Search:

Index	Name	P-value	Adjusted p-value	Odds Ratio	Combined score
1	H3K9ac CD8 Naive Primary Cells	0.2150	1.000	1.07	1.65
2	H3K4me3 CD34 Cultured Cells	0.2253	1.000	1.06	1.57
3	H3K4me1 CD4+ CD25int CD127+ Tmem Primary Cells	0.3325	1.000	1.05	1.15
4	H3K4me1 CD8 Memory Primary Cells	0.3397	1.000	1.04	1.12
5	H2BK12ac IMR90	0.4035	1.000	1.03	0.93
6	H2BK15ac IMR90	0.4428	1.000	1.02	0.83
7	H3K27ac CD8 Memory Primary Cells	0.5014	1.000	1.00	0.69
8	H3K36me3 Stomach Mucosa	0.5100	1.000	1.03	0.69
9	H3K9ac Peripheral Blood Mononuclear Primary Cells	0.5081	1.000	1.00	0.68
10	H3K4me1 Peripheral Blood Mononuclear Primary Cells	0.5406	1.000	0.99	0.61

Showing 1 to 10 of 369 entries | [Export entries to table](#)

Previous Next

Terms marked with an * have an overlap of less than 5

TargetScan microRNA 2017

miRTarBase 2017

ENCODE TF ChIP-seq 2015

Activate Windows
Go to Settings to activate Windows.

Type here to search



IncHUB lncRNA Co-Expression

Enrichr Submissions TF-Gene Cooccurrence

TRANSFAC and JASPAR PWMs

Epigenomics Roadmap HM ChIP-seq

TargetScan microRNA 2017

Bar Graph

Table

Clustergram

Appyter



Click the bars to sort. Now sorted by p-value ranking.

mmu-miR-5130

p-value: 0.00002989
q-value: 0.01299
odds ratio: 1.68
combined score: 17.55

mmu-let-7c

mmu-let-7b

mmu-let-7a

mmu-let-7g

mmu-miR-98

mmu-miR-1961

mmu-let-7f

mmu-let-7d

mmu-let-7i

Activate Windows

Go to Settings to activate Windows.

miRTarBase 2017

TRANSFAC and JASPAR PWMs

Epigenomics Roadmap HM ChIP-seq

TargetScan microRNA 2017

Bar Graph

Table

Clustergram

Appyter



Hover each row to see the overlapping genes.

10 entries per page

Search:

Index	Name	P-value	Adjusted p-value	Odds Ratio	Combined score
1	mmu-miR-5130	0.00002989	0.01299	1.68	17.55
2	hsa-miR-487b	0.0009441	0.03224	2.18	15.19
3	mmu-let-7c	0.0002093	0.01299	1.47	12.42
4	mmu-let-7b	0.0002093	0.01299	1.47	12.42
5	mmu-let-7a	0.0002093	0.01299	1.47	12.42
6	mmu-let-7g	0.0002093	0.01299	1.47	12.42
7	mmu-miR-98	0.0002093	0.01299	1.47	12.42
8	mmu-miR-1961	0.0002093	0.01299	1.47	12.42
9	mmu-let-7f	0.0002093	0.01299	1.47	12.42
10	mmu-let-7d	0.0002093	0.01299	1.47	12.42

Showing 1 to 10 of 683 entries | [Export entries to table](#)
Terms marked with an * have an overlap of less than 5[Previous](#) [Next](#)

CD86, RB1, CLPB, ITSN1, CCNF, IRS2, PRDM1, BACH1, C3AR1, KPNA6, GEN1, NUP210, ENTPD7, FNDC3B, UBE2E2, PRKCA, ATP11A, PLPP6, CACNB4, CCNY, ZNF318, PPIF, TRIB1, ANAPC15, EPB41, TOR1AIP2, ADRB2, NID1, DTX4, ZNF25, GNS, ARPP19, DPP3, RDH10, SLAMF6, PAG1, IGF2R, SSH1, TADA2B, MARCH1, NCEH1, DIAPH3, REEP5, CPD, AAK1, SNAI1, NABP1, CALM1, CPEB4, DENND1C, CPM, DAGLA, SNAP23, CHD7, KIF14, CD3G, PTPRJ, KIF11, HK2, ASGR2, ENC1, EFHD2, CTSC, CTSB, SLC36A1, NCOAT1, WARS, NFAM1, TET2, AEN, GAB2, HBA1, RHOF, TNFRSF1B, IL17RA, PARP8, TGFBR3, FGR, NCOR1, ESPL1, MTF1, CNKS3, ZNF516, ATP6V1B2, SMCR8, TLR7, TLR5, GAS7, OX3CR1, CEBPD, DOT1L, ASAP1, DENND3, NOD2, SNX30, CBL, THBS1, AGPAT3, POLD3, GGA3, FGD6, SH3BP2, PLAGL2, E2F2, MEF2D, E2F7, TMEM30A, SLC31A1, CCDC59, TTL4, GNPD1, SLC31A1, ABI3, FAS, SMAP2, MYO1F

miRTarBase 2017

ENCODE TF ChIP-seq 2015

Activate Windows
Go to Settings to activate Windows.

TargetScan microRNA 2017

miRTarBase 2017

Bar Graph

Table

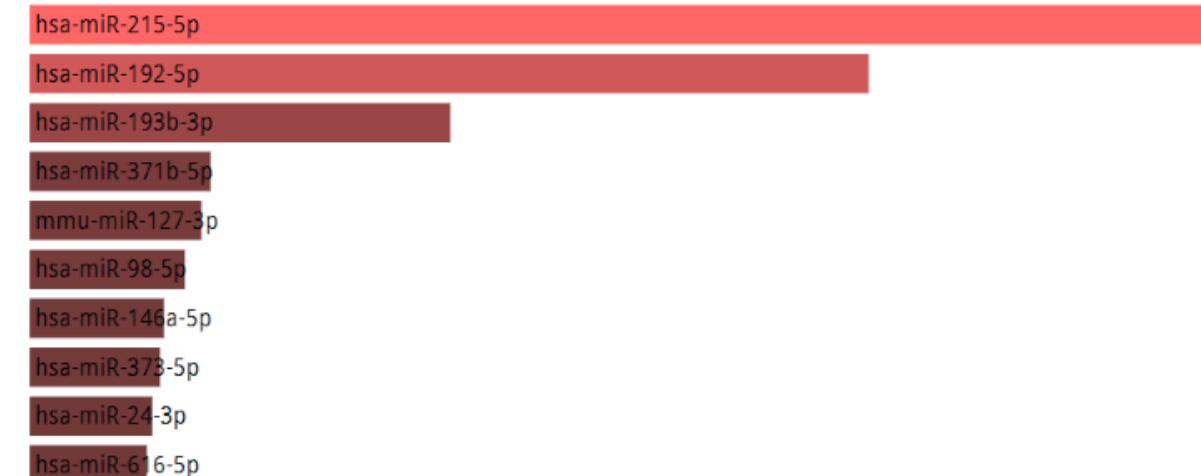
Clustergram

Appyter



Click the bars to sort. Now sorted by p-value ranking.

SVG PNG JPG



ENCODE TF ChIP-seq 2015

TF-LOF Expression from GEO

ENCODE Histone Modifications 2015

Transcription Factor PPIs

Activate Windows
Go to Settings to activate Windows.

TargetScan microRNA 2017

miRTarBase 2017

Bar Graph

Table

Clustergram

Appyter



Hover each row to see the overlapping genes.

10 entries per page

Search:

Index	Name		Adjusted p-value	Odds Ratio	Combined score
1	mmu-miR-1	RB1, CRYBG3, CHD7, HJURP, KIF14, BUB1B, MCM10, PLOD1, ILTRAP, BRCA1, MKI67, BRCAl, TNFSF13B, KIF15, EPS8, CDC20, UBASH3B, NUF2, ENC1, SLC16A6, UPP1, CEP55, DLGAP5, GEN1, GAS2L3, FNDC3B, ENTPD7, KIF23, KN1, GAB2, CIT, KAT2B, ASPM, NEIL3, CCNY, NRG4, CCNE1, DEPDCl, KCTD12, KIF20A, KIF20B, HBEGF, ANAPC15, CDCA4, TROAP, ARHGAP19, TMTC2, TTK, IOGAP1, HMMR, NOD2, NID1, SAMHD1, NCAPH, BCCL11, ORC1, RACGAP1, ZMAT3, PLAGL2, ECT2, E2F8, PLK4, TMEM30A, CDKN2A, PPP1CA, TICRR, CENPE, PTPRE, ANLN, CENPF, RAD51, NCEH1, SLC03A1, WT1, ARTN, RFWD3	0.01734	22.46	233.89
2	hsa-miR-5		0.1014	12.82	90.37
3	hsa-miR-215-5p	3.564e-12	1.028e-8	2.65	69.75
4	hsa-miR-553	0.007504	0.2186	9.60	46.98
5	mmu-miR-1224-5p	0.007504	0.2186	9.60	46.98
6	hsa-miR-192-5p	7.834e-10	0.000001130	2.21	46.36
7	mmu-miR-7116-3p	0.02452	0.3133	11.19	41.50
8	mmu-miR-6951-3p	0.02452	0.3133	11.19	41.50
9	hsa-miR-3713	0.002522	0.1738	6.24	37.30
10	hsa-miR-5188	0.03337	0.3248	8.95	30.44

Showing 1 to 10 of 2,884 entries | [Export entries to table](#)

Terms marked with an * have an overlap of less than 5

Previous Next

ENCODE TF ChIP-seq 2015

TF-LOF Expression from GEO

ENCODE Histone Modifications 2015

Transcription Factor PPIs

Activate Windows

Go to Settings to activate Windows.



Type here to search



05:21 ۱۰.۰۷.۲۰۲۳
ENGLISH
100% / 100%

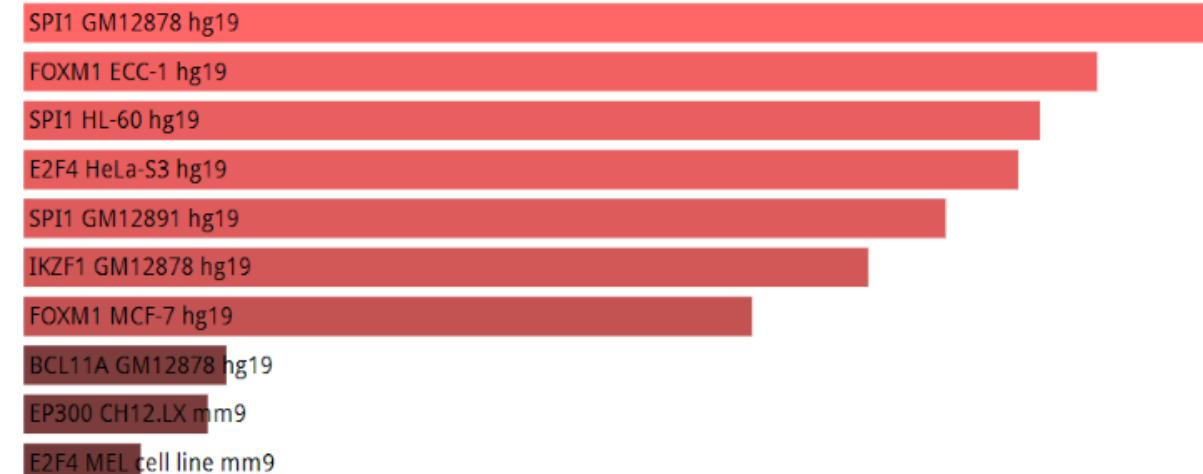
ENRICHR BASE 2017

ENCODE TF ChIP-seq 2015

Bar Graph Table Grid Network Clustergram Appyter

Click the bars to sort. Now sorted by p-value ranking.

SVG PNG JPG



TF-LOF Expression from GEO

ENCODE Histone Modifications 2015

Transcription Factor PPIs

Genome Browser PWMs

Activate Windows
Go to Settings to activate Windows.



Type here to search



^ ENG 05:21 ب.م
11/11/IV

maayanlab.cloud/Enrichr/enrich#

ENCODE TF ChIP-seq 2015

Bar Graph Table Grid Network Clustergram

Hover each row to see the overlapping genes.

10 entries per page

Index	Name	P-value	Adjusted p-value		
1	FOXM1 MCF-7 hg19	2.707e-11	3.156		
2	FOXM1 ECC-1 hg19	1.146e-14	4.677e-13		
3	SPI1 GM12878 hg19	1.044e-15	8.520e-13	2.16	74.51
4	SPI1 HL-60 hg19	4.183e-14	1.138e-11	2.39	73.62
5	E2F4 HeLa-S3 hg19	6.787e-14	1.384e-11	2.42	73.36
6	SPI1 GM12891 hg19	3.481e-13	5.681e-11	2.43	69.81
7	IKZF1 GM12878 hg19	1.991e-12	2.708e-10	2.00	53.90
8	BCL11A GM12878 hg19	0.000003721	0.0003795	1.78	22.24
9	E2F4 MEL cell line mm9	0.00002559	0.002088	2.05	21.67
10	EP300 CH12.LX mm9	0.000005663	0.0005135	1.59	19.19

Showing 1 to 10 of 816 entries | [Export entries to table](#)

Terms marked with an * have an overlap of less than 5

CD86, RB1, GLTP, CD84, IL1RN, NCF1, NCF2, NCF4, EIF4A3, SMC6, IKZF3, CXCL16, ICAM1, RG52, RASSF2, PNP, SLC16A6, MS4A14, BANF1, AP153, AZ2, TMSB10, GEN1, CD93, SP110, BROX, PRKCD, RNASE6, CYBB, CYBA, IPCEF1, TUBA4A, MPEG1, HIST2H3A, TYROBP, NAAA, ZNF318, BOLA2, ATP6V0D1, HIST2H3C, FTL, ASF1B, RAB5C, SP140, NCF1B, IQGAP1, CD1D, ADRB2, CFP, CORO1A, GNS, ARPP19, SAMSN1, NCAPH, BOLA2B, PIK3R5, BCL2L11, CLEC7A, ZMAT3, RDH10, STAP1, CD14, SLC15A3, NADK, ARSB, S100A11, LY86, NETO2, DIAPH2, NCEH1, REEPS, RPL27A, TADA3, MAN2B1, IL7R, APOBEC3B, DENND1C, SMG1, ITGAM, FKBP15, CITED2, LRRK1, SNAP23, PLEK, MS4A7, SIRPB2, AP2A1, ARRBB2, FOXM1, OSBP11, LYST, SIRPB1, TNFSF13B, CKS1B, LFNG, HSD3BP4, KYNU, FFHD2, ITGB7, QSOX1, RAC1, CD33, CEP55, RAB8A, CTSB, HAVCR2, EIF5A, DUSP5, MYOF, GMIP, PARP8, MS4A6A, MTF1, SMCR8, TLR7, LCPT1, FAM72D, ST6GALNAC4, PLCB2, TLR4, FAM72B, FAM72A, VAC14, CSTA, SELPLG, UNC93B1, WBP2, RAB1B, FGLL2, FAM129A, NEDD9, ASAP1, CBL, LILRA2, GNAI2, PSM83, MFN2, E2F4, POLR2J, LRRK25, PTPN18, TMEM30A, SLC31A1, CCDC59, NAGA, LILRB1, TPD52L2, SCIMP, LILRB4, USF1, TMEM154, TTL4, RAD51, GLB1, AB3, IL2RB, TRMT6, ALOX5AP, MNDA, TRIM38, FCGR2B, CD68, FCGR2C, PTPN2

Previous Next

TF-LOF Expression from GEO

ENCODE Histone Modifications 2015

Transcription Factor PPIs

Genome Browser PWMs

Activate Windows
Go to Settings to activate Windows.

maayanlab.cloud/Enrichr/enrich#

ENCODE TF ChIP-seq 2015

TF-LOF Expression from GEO

Bar Graph Table Grid Network Clustergram Appyter

Click the bars to sort. Now sorted by p-value ranking.

SVG PNG JPG

- foxa1 21151129 mcfdash7 lof human gpl10558 gse25315 up
- myc 20940306 e13dot5 erythroblast purified from liver gof mouse gpl6885 gse18558 up
- foxa2 20483781 p15 lung lof mouse gpl1261 gse19204 up
- gata1 15860665 megakaryocytes lof mouse gpl1261 gds1245 up
- ccnd1 18413728 imr neuroblastoma lof human gpl570 gse8866 down
- pou5f1 16518401 mesc lof mouse gpl1261 gds1824 up
- ets 00000000 2008 ovarian cancer cells gof human gpl6244 gse21129 up
- hsf1 19179333 rko colon carcinoma lof human gpl6244 gse12762 down
- gfi1b 22201127 amulv gof mouse gpl6246 gds4302 up
- prdm1 21670299 e18dot5 small intestine lof mouse gpl6887 gse29658 down

ENCODE Histone Modifications 2015

Transcription Factor PPIs

Genome Browser PWMs

Activate Windows
Go to Settings to activate Windows.



Type here to search



maayanlab.cloud/Enrichr/enrich#

OVEREXPRESSION IN TUMOR CELLS

Bar Graph Table Grid Network Clustergram Appyter ⚙ ⓘ

Hover each row to see the overlapping genes

10 entries per page

Index	Name			Combined score		
1	myc 20940306 e13dot5 erythroid from liver gof mouse gpl6887	RB1, CCNF, HJURP, FAM107B, CDC20, CLEC5A, TOM1, FAM53B, KPNA2, HMGN2, GTF1, MELK, CCNE1, FANCO2, PSME3, KIF20A, KIF20B, S100A9, PRR11, FTL, ASF1B, CDC42, CDC43, CDC44, TROAP, COX17, CDC48, HMMR, GNS, CCNB2, NCSTN, BCL2L11, RACGAP1, ZMAT3, LPXN, ST3GAL5, HMOX1, S100A11, CTSA, PLX4, FHDC1, NDC80, ANLN, TPX2, DIAPH3, KIF4A, CDK1, PLXNB2, CALM1, COPS8, TOP2A, CPM, B4GALT1, CITED2, SH3KBP1, SUV39H1, CITED4, FAF2, ARHGAP1, KIF14, MCIM10, KIF11, BRCA1, FOXM1, HSPB11, CTKS18, SCPEP1, CA2, ENC1, PBK, EFHD2, FLVCR2, CTSH, UPP1, CD36, DLGAP5, CTSC, CEP55, TUBB, MYOF, KIF23, MASTL, TUBG1, SERPINB8, CCNA2, KAT2B, ASPM, TFPD1, ESPL1, FAM72D, SGK1, FBPI, FAM72B, SLFN5, RBM47, GRN, PCNA, FAM129A, NEDD9, ASAP1, DENND3, TTK, THBS1, AURKB, PAPSS2, AURKA, RECQL4, NFLI3, ALOX5, E2F2, PDSS1, E2F7, POLQ, CENPW, SULF2, CENPE, GNPD1, KIAA0101, PRC1, RWD3, NCAPP2, SPC25	2.241e-16	5.804e-14	2.50	109.08
2	foxa1 21151129 mcfdash7 lolo gpl10558 gse25315 up					90.16
3	foxa2 20483781 p15 lung lof mouse gpl1261 gse19204 up		1.164e-11	1.005e-9	2.88	72.61
4	ccnd1 18413728 imr neuroblastoma lof human gpl570 gse8866 down		4.899e-9	2.537e-7	2.31	44.21
5	prdm1 21670299 e18dot5 small intestine lof mouse gpl6887 gse29658 down		0.00001081	0.0002800	3.36	38.47
6	gata1 15860665 megakaryocytes lof mouse gpl1261 gds1245 up		1.435e-9	9.291e-8	1.58	32.10
7	pou5f1 16518401 mesc lof mouse gpl1261 gds1824 up		9.997e-7	0.00004315	2.23	30.76
8	hsf1 19179333 rko colon carcinoma lof human gpl6244 gse12762 down		0.000006471	0.0002095	2.12	25.34
9	gfi1b 22201127 amulv gof mouse gpl6246 gds4302 up		0.000007574	0.0002180	1.92	22.69
10	irf8 00000000 splenic cd11bplusgrdash1 hdash2b gen background lof mouse gpl6887 gse39228 down		0.00002610	0.0006145	1.80	19.01

Showing 1 to 10 of 259 entries | [Export entries to table](#)

Terms marked with an * have an overlap of less than 5

Previous Next

ENCODE Histone Modifications 2015

Transcription Factor PPIs

Activate Windows
Go to Settings to activate Windows.



Type here to search



05:22 ۱۰/۱۱/۲۰۲۳ ENG

maayanlab.cloud/Enrichr/enrich#

ENCODE BASE 2017

ENCODE TF ChIP-seq 2015

TF-LOF Expression from GEO

ENCODE Histone Modifications 2015

Bar Graph Table Grid Network Clustergram Appyter ⚙ ⓘ

Click the bars to sort. Now sorted by p-value ranking.

H3K4me1 T-cell acute lymphoblastic leukemia hg19

H3K4me2 T-cell acute lymphoblastic leukemia hg19

H3K4me2 B cell hg19

H3K36me3 CD14-positive monocyte hg19

H3K4me3 myotube hg19

H3K79me3 C2C12 mm9

H3K4me1 olfactory bulb mm9

H3K79me2 C2C12 mm9

H3K9ac T-cell acute lymphoblastic leukemia hg19

H3K79me2 myocyte mm9

Transcription Factor PPIs

Genome Browser PWMs

Activate Windows
Go to Settings to activate Windows.

Type here to search

O File Mail Word App Store U Microsoft Edge Google Chrome G Mail

05:22 ۱۰/۱۱/۲۰۲۳ ENG

ENCODE TF ChIP-seq 2015

TF-LOF Expression from GEO

ENCODE Histone Modifications 2015

Bar Graph Table Grid Network Clustergram Appyter ⚙ ⓘ

Hover each row to see the overlapping genes.

10 entries per page

Search:

Index	Name	P-value	Adjusted p-value	Odds Ratio	Combined score
1	H3K4me1 T-cell acute lymphoblastic leukemia hg19	0.03530	1.000	1.23	4.10
2	H3K4me2 T-cell acute lymphoblastic leukemia hg19	0.1530	1.000	1.13	2.12
3	H3K4me2 B cell hg19	0.1813	1.000	1.11	1.90
4	H3K36me3 CD14-positive monocyte hg19	0.2128	1.000	1.10	1.70
5	H3K4me3 myotube hg19	0.2474	1.000	1.09	1.52
6	H3K79me3 C2C12 mm9	0.2849	1.000	1.07	1.35
7	H3K4me1 olfactory bulb mm9	0.2849	1.000	1.07	1.35
8	H3K79me2 C2C12 mm9	0.3251	1.000	1.06	1.19
9	H3K9ac T-cell acute lymphoblastic leukemia hg19	0.3251	1.000	1.06	1.19
10	H3K79me2 myocyte mm9	0.3251	1.000	1.06	1.19

Showing 1 to 10 of 411 entries | [Export entries to table](#)

Previous Next

Terms marked with an * have an overlap of less than 5

Transcription Factor PPIs

Genome Browser PWMs

Activate Windows
Go to Settings to activate Windows.

INTERACTOME 2017

ENCODE TF ChIP-seq 2015

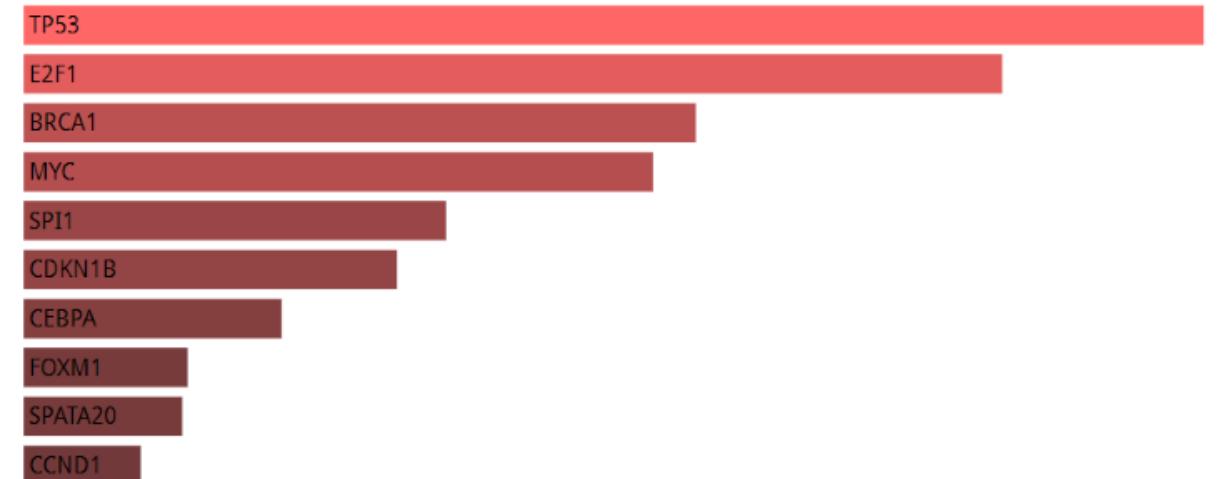
TF-LOF Expression from GEO

ENCODE Histone Modifications 2015

Transcription Factor PPIs

[Bar Graph](#) [Table](#) [Grid](#) [Network](#) [Clustergram](#) [Appyter](#) [⚙](#) [ℹ](#)

Click the bars to sort. Now sorted by p-value ranking.

[SVG](#) [PNG](#) [JPG](#)

Genome Browser PWMs

Activate Windows
Go to Settings to activate Windows.

Type here to search

^ ENG 05:22 ب.م
۱۰/۱۱/۱۴

ENCODE TF ChIP-seq 2015

TF-LOF Expression from GEO

ENCODE Histone Modifications 2015

Transcription Factor PPIs

[Bar Graph](#) [Table](#) [Grid](#) [Network](#) [Clustergram](#) [Appyter](#) [⚙️](#) [ⓘ](#)

Hover each row to see the overlapping genes.

10

entries per page

Search:

Index	Name	P-value	Adjusted p-value	Odds Ratio	Combined score
1	SPATA20	0.001834	0.04524	38286.00	241249.11
2	E2F1	0.00002719	0.003018	3.53	37.15
3	FOXM1	0.001786	0.04524	5.39	34.12
4	USF2	0.003710	0.05752	5.61	31.40
5	SPI1	0.0004734	0.02102	4.02	30.81
6	PRDM1	0.007753	0.08385	5.99	30.06
7	CCNT2	0.01625	0.1164	RB1, TOP2A, SMG1, ELL, GFI1, UBE2D3, BRCA1, BRCA2, BACH1, PNP, PBK, KPNA2, ZNF385A, PRKCD, PRKCA, CCNA2, KAT2B, ASPM, NCOR1, TFDP1, PSME3, PPIF, PADI4, CSNK1G1, PCNA, COX17, TTK, PHB, THBS1, TAF5L, AURKB, AURKA, ZMAT3, ECT2, HEXIM1, CDKN2C, CDKN2A, VDR, SMURF1, PLK1, PPP1CA, RAD51, KIAA0101, WT1, RWD3, TADA3, SNAI1, CDK1, FAS, MND1, COP58	
8	CDKN1B	0.0006081	0.02250	2.04	23.51
9	TP53	0.000009657	0.002144	2.93	19.98
10	CEBPA	0.001102	0.03494		

Showing 1 to 10 of 222 entries | [Export entries to table](#)

Terms marked with an * have an overlap of less than 5

[Previous](#) [Next](#)

Genome Browser PWMs

Activate Windows
Go to Settings to activate Windows.

Type here to search



^ ENG 05:22 ۱۰/۱۱/۲۰۲۳

maayanlab.cloud/Enrichr/enrich#

ENCODE TF ChIP-seq 2015

TF-LOF Expression from GEO

ENCODE Histone Modifications 2015

Transcription Factor PPIs

Genome Browser PWMs

Bar Graph Table Grid Network Clustergram Appyter ⚙ ⓘ

Click the bars to sort. Now sorted by p-value ranking.

V\$ELF1 Q6
V\$PEA3 Q6
V\$IRF1 Q6
RYTTCCTG V\$ETS2 B
V\$E2F1 Q4
V\$ICSBP Q6
RYCACNNRRNRNCAG UNKNOWN
V\$SRF O1
V\$IRF Q6
V\$MAF Q6

Activate Windows
Go to Settings to activate Windows.

Type here to search

O E W M U C G

05:22 ۱۰/۱۱/۲۰۲۳

ENGLISH

maayanlab.cloud/Enrichr/enrich#

ENCODE TF ChIP-seq 2015

TF-LOF Expression from GEO

ENCODE Histone Modifications 2015

Transcription Factor PPIs

Genome Browser PWMs

Bar Graph Table Grid Network Clustergram Appyter ⚙ ⓘ

Hover each row to see the overlapping genes.

10 entries per page Search:

Index	Name	P-value	Adjusted p-value	Odds Ratio	Combined score
1	V\$ELF1 Q6	0.0002007	0.1186	2.41	20.53
2	V\$PEA3 Q6	0.001046	0.3091	2.16	14.84
3	V\$IRF1 Q6	0.01007	1.000	1.85	8.51
4	RYCACNNRRNCAG UNKNOWN	0.04671	1.000	2.24	6.87
5	V\$SRF O1	0.06641	1.000	2.44	6.61
6	V\$E2F1 Q4	0.02408	1.000	1.73	6.46
7	V\$ICSBP Q6	0.02580	1.000	1.72	6.29
8	GGCKCATGS UNKNOWN	0.07079	1.000	2.17	5.75
9	RYTTCCTG V\$ETS2 B	0.01879	1.000	1.35	5.35
10	CCAWWNAAGG V\$SRF Q4	0.08323	1.000	1.94	4.82

Showing 1 to 10 of 591 entries | [Export entries to table](#)

Terms marked with an * have an overlap of less than 5

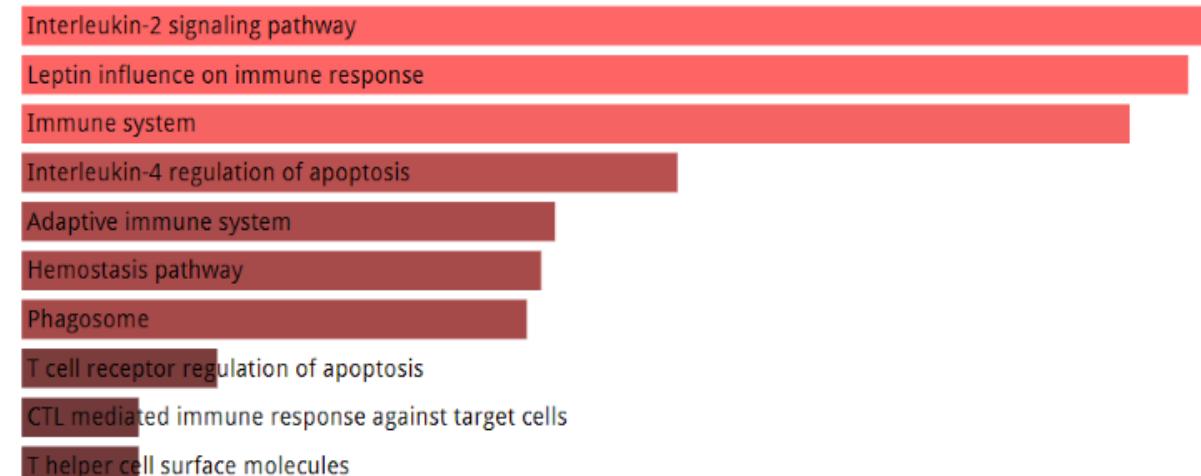
Previous Next

Activate Windows
Go to Settings to activate Windows.



Type here to search



[Login](#) | [Register](#)[Transcription](#) **Pathways** [Ontologies](#) [Diseases/Drugs](#) [Cell Types](#) [Misc](#) [Legacy](#) [Crowd](#)**Description** AML_UP (857 genes)**BioPlanet 2019****Bar Graph**[Table](#)[Clustergram](#)[Appyter](#)Click the bars to sort. Now sorted by **p-value ranking**.[SVG](#) [PNG](#) [JPG](#)**WikiPathway 2021 Human****KEGG 2021 Human****ARCHS4 Kinases Coexp**

Activate Windows

Go to Settings to activate Windows.



Login | Register

Transcription Pathways Ontologies Diseases/Drugs Cell Types Misc Legacy Crowd

Description AML_UP (857 genes)



BioPlanet 2019

Bar Graph

Table

Clustergram

Appyter



Hover each row to see the overlapping genes.

10 entries per page

Search:

Index	Name	P-value	Adjusted p-value	Odds Ratio	Combined score	
1	Cross-presentation of particulate exogenous antigens (phagosomes)	1.582e-7	0.000009118	67.48	1056.64	
2	CTL mediated immune response against target cells	1.170e-8	0.000001281	36.07	658.73	
3	T helper cell surface molecules	1.170e-8	0.000001281	36.07	658.73	
4	Oxygen/carbon dioxide exchange in erythrocytes	0.000007178	0.0002456	C3CR1, IL1RN, ITGAM, NCF2, NCF4, PRF1, IL1RAP, CD3E, CD3D, CXCL16, ACAT1, C2, CCL5, ITGAX, BANF1, CD36, TIMP1, CCR2, CCR1, FCER1G, LYZ, VEGFA, CD4, STAR, ALOX5AP, IRF8, TLR8, MNDA, IL7R, FCGR2B		
5	Leptin influence on immune response	1.762e-16	9.648e-14	8.64	313.56	
6	HIV-induced T cell apoptosis	0.00001558	0.0004489	28.08	310.83	
7	Interleukin-17 signaling pathway	0.000001232	0.00005620	19.70	268.03	
8	G0 and early G1 pathway	3.602e-8	0.000003034	15.06	258.04	
9	Malaria	1.865e-8	0.000001857	8.58	152.62	
10	FOXM1 transcription factor network	8.890e-8	0.000005726	9.36	151.97	

Showing 1 to 10 of 1,095 entries | [Export entries to table](#)

Terms marked with an * have an overlap of less than 5

Previous Next

WikiPathway 2021 Human

Activate Windows

Go to Settings to activate Windows.

KEGG 2021 Human



Type here to search



5:28 ب.م
ENGLISH
05:28 ب.م
10/11/14



Login | Register

Transcription Pathways Ontologies Diseases/Drugs Cell Types Misc Legacy Crowd

Description AML_UP (857 genes)



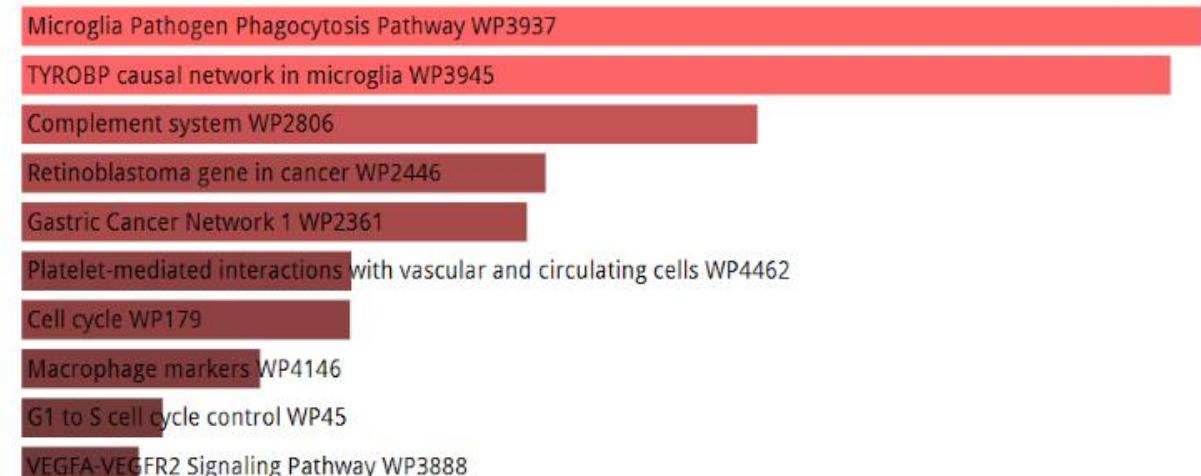
BioPlanet 2019

WikiPathway 2021 Human

Bar Graph Table Clustergram Appyter

Click the bars to sort. Now sorted by p-value ranking.

SVG PNG JPG



KEGG 2021 Human

Activate Windows
Go to Settings to activate Windows.

ARCHS4 Kinases Coexp



Type here to search



^ ENG 05:29 ب.م
I.../I/V

BioPlanet 2019

WikiPathway 2021 Human

Bar Graph

Table

Clustergram

Appyter



Hover each row to see the overlapping genes.

10 entries per page

Search:

Index	Name	P-value	Adjusted p-value	Odds	Combined
1	Microglia Pathogen Phagocytosis Pathway WP3937	2.692e-12	1.047e-9	15.16	403.76
2	Macrophage markers WP4146	0.00001558	0.0009016	28.08	310.83
3	TYROBP causal network in microglia WP3945	4.523e-12	1.047e-9	10.31	269.35
4	Platelet-mediated interactions with vascular and circulating cells WP4462	0.000003452	0.0002327	15.76	198.16
5	Gastric Cancer Network 1 WP2361	1.888e-7	0.00001748	11.88	183.99
6	Complement system WP2806	4.194e-9	6.472e-7	5.92	114.13
7	Nanomaterial-induced inflammasome activation WP3890	0.002410	0.03100	16.81	101.32
8	Retinoblastoma gene in cancer WP2446	1.392e-7	0.00001611	5.51	87.06
9	Pathogenesis of SARS-CoV-2 Mediated by nsp9-nsp10 Complex WP4884	0.0001897	0.006757	8.99	77.05
10	ApoE and miR-146 in inflammation and atherosclerosis WP3926	0.003734	0.04217	13.45	75.17

Showing 1 to 10 of 463 entries | [Export entries to table](#)

Terms marked with an * have an overlap of less than 5

Previous Next

KEGG 2021 Human

ARCHS4 Kinases Coexp

Activate Windows
Go to Settings to activate Windows.

maayanlab.cloud/Enrichr/enrich#

BIOLOGICAL PATHWAYS

WikiPathway 2021 Human

KEGG 2021 Human

Bar Graph Table Clustergram Appyter ⚙️ ⓘ

Click the bars to sort. Now sorted by p-value ranking.

Phagosome
Osteoclast differentiation
Malaria
Neutrophil extracellular trap formation
Hematopoietic cell lineage
Lysosome
Cell cycle
Tuberculosis
Fc gamma R-mediated phagocytosis
Leishmaniasis

SVG PNG JPG

ARCHS4 Kinases Coexp

Elsevier Pathway Collection

MSigDB Hallmark 2020

Activate Windows
Go to Settings to activate Windows.

maayanlab.cloud/Enrichr/enrich#

WikiPathway 2021 Human

KEGG 2021 Human

Bar Graph Table Clustergram Appyter ⚙ ⓘ

Hover each row to see the overlapping genes.

10 entries per page Search:

Index	Name	P-value	Adjusted p-value	Odds	Combined
1	Malaria	1.476e-9	1.392e-7	RAB5C, ITGAM, NCF1, NCF2, NCF4, ITGB2, MPO, CORO1A, THBS1, ACTB, FCAR, FCGR3A, CLEC7A, MRC1, CD14, CD36, RAC1, FCGR1A, TUBB, CYBB, CYBA, IGH, TUBA4A, FCGR2A, ATP6V1B2, ATP6V0D1, FCGR2B, TLR4, FCGR2C, TLR2	
2	Phagosome	1.893e-12	5.358e-10	5.66	152.66
3	Osteoclast differentiation	7.889e-10	1.116e-7	5.33	111.63
4	Hematopoietic cell lineage	3.506e-8	0.000001985	5.40	92.74
5	Neutrophil extracellular trap formation	2.363e-9	1.672e-7	4.16	82.54
6	African trypanosomiasis	0.00001968	0.0003978	7.25	78.51
7	Leishmaniasis	0.000004302	0.0001217	5.03	62.15
8	Lysosome	5.256e-7	0.00002479	4.21	60.89
9	Fc gamma R-mediated phagocytosis	0.000003442	0.0001082	4.48	56.32
10	Cell cycle	0.000001365	0.00005520	4.11	55.51

Showing 1 to 10 of 283 entries | [Export entries to table](#)

Previous Next

Terms marked with an * have an overlap of less than 5

ARCHS4 Kinases Coexp

Elsevier Pathway Collection

MSigDB Hallmark 2020

Activate Windows
Go to Settings to activate Windows.

BioPlanet 2019

WikiPathway 2021 Human

KEGG 2021 Human

ARCHS4 Kinases Coexp

Bar Graph

Table

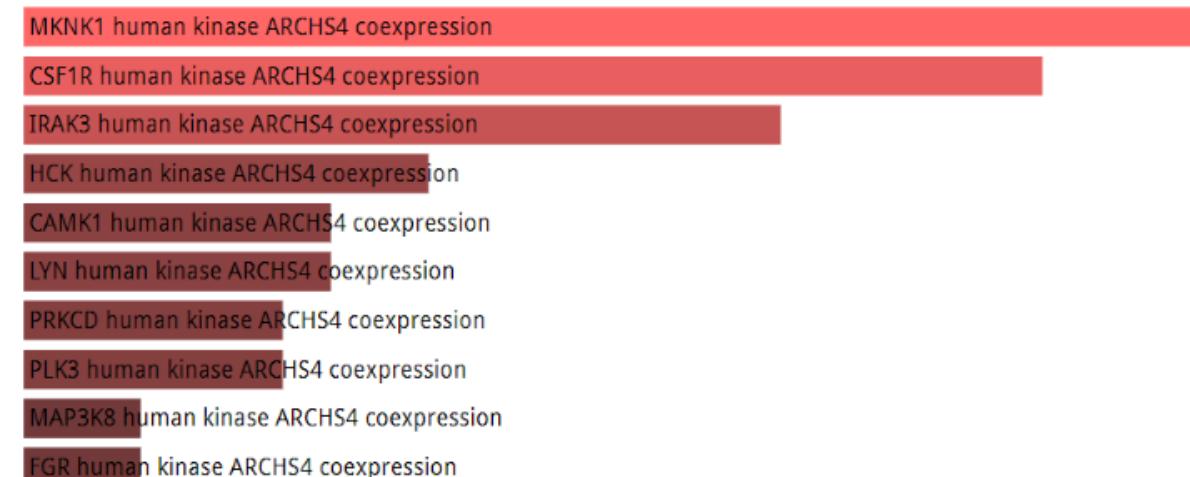
Clustergram

Appyter



Click the bars to sort. Now sorted by p-value ranking.

SVG PNG JPG



Elsevier Pathway Collection

MSigDB Hallmark 2020

Activate Windows

Go to Settings to activate Windows.

KEGG 2021 Human

ARCHS4 Kinases Coexp

Bar Graph

Hover each row to see the overlapping genes.

10 entries per page

Index Name

1	MKNK1 human kinase ARCHS4 coexpression	2.167e-66	1.070e-63	13.42	2029.14
2	CSF1R human kinase ARCHS4 coexpression	4.919e-63	1.215e-60	12.78	1833.96
3	IRAK3 human kinase ARCHS4 coexpression	1.392e-57	2.293e-55	11.77	1540.86
4	HCK human kinase ARCHS4 coexpression	2.966e-50	3.664e-48	10.45	1191.50
5	CAMK1 human kinase ARCHS4 coexpression	3.157e-48	2.599e-46	10.09	1103.52
6	LYN human kinase ARCHS4 coexpression	3.157e-48	2.599e-46	10.09	1103.52
7	PRKCD human kinase ARCHS4 coexpression	3.173e-47	1.959e-45	9.91	1061.38
8	PLK3 human kinase ARCHS4 coexpression	3.173e-47	1.959e-45	9.91	1061.38
9	MAP3K8 human kinase ARCHS4 coexpression	2.898e-44	1.193e-42	9.40	941.99
10	FGR human kinase ARCHS4 coexpression	2.898e-44	1.193e-42	9.40	941.99

Showing 1 to 10 of 494 entries | [Export entries to table](#)
Terms marked with an * have an overlap of less than 5[Previous](#) [Next](#)

Elsevier Pathway Collection

Activate Windows
Go to Settings to activate Windows.

Type here to search

05:30 ب.م.
ENGLISH
100% / 100%

maayanlab.cloud/Enrichr/enrich#

KEGG 2021 Human

ARCHS4 Kinases Coexp

Elsevier Pathway Collection Bar Graph Table Clustergram Appyter ⚙️ ⓘ

Click the bars to sort. Now sorted by p-value ranking.

SVG PNG JPG

- Neutrophil Degranulation via FPR1/IL8
- Neutrophil Degranulation via FPR1 Signaling
- Proteins Involved in Glomerulonephritis
- Neutrophil Activation via Adherence on Endothelial Cells
- Low-Density Lipoproteins and Chemokines in Atherosclerosis
- Monoblast → Promonocyte Surface Expression Markers
- Neutrophil Activation via FCGR3B
- Kinetochore Assembly
- Proteins Involved in Rheumatoid Arthritis
- Proteins Involved in Gout

MSigDB Hallmark 2020

BioCarta 2016

Reactome 2016

Activate Windows
Go to Settings to activate Windows.

KEGG 2021 Human

ARCHS4 Kinases Coexp

Elsevier Pathway Collection

Bar Graph

Table

Clustergram

Appyter



Hover each row to see the overlapping genes.

10 entries per page

Search:

Index	Name	P-value	Adjusted p-value	Odds Ratio	Combined score
1	Metaphase/Anaphase Phase Transition	1.582e-7	0.000009966	67.48	1056.64
2	Monoblast -> Promonocyte Surface Expression Markers	2.028e-11	4.269e-9	35.54	875.16
3	Low-Density Lipoproteins and Chemokines in Atherosclerosis	1.545e-11	3.904e-8	1056.64	875.16
4	Neutrophil Degranulation via FPR1/IL8	7.090e-16	8.954e-13	12.85	448.20
5	Neutrophil Degranulation via FPR1 Signaling	4.139e-15	2.614e-12	12.58	416.72
6	Neutrophil Activation via Adherence on Endothelial Cells	1.141e-12	3.602e-10	11.40	313.47
7	Proteins Involved in Gout	6.034e-10	7.621e-8	14.03	297.74
8	Sister Chromatid Cohesion	3.283e-7	0.00001658	18.03	269.16
9	Myeloid Progenitor Cell -> GEMM - CFU Surface Expression Markers	3.283e-7	0.00001658	18.03	269.16
10	Chromosome Condensation	0.000001232	0.00005556	19.70	268.03

Showing 1 to 10 of 1,263 entries | [Export entries to table](#)

Terms marked with an * have an overlap of less than 5

Previous Next

MSigDB Hallmark 2020

BioCarta 2016

Activate Windows

Go to Settings to activate Windows.

ARCHS4 Kinases Coexp

Elsevier Pathway Collection

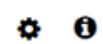
MSigDB Hallmark 2020

Bar Graph

Table

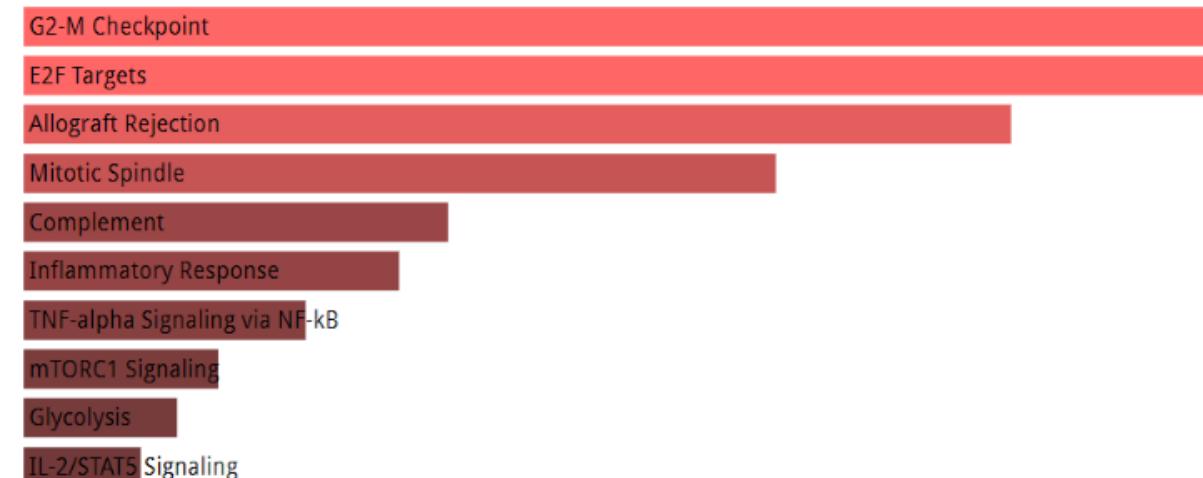
Clustergram

Appyter



Click the bars to sort. Now sorted by p-value ranking.

SVG PNG JPG



BioCarta 2016

Reactome 2016

HumanCyc 2016

Activate Windows

Go to Settings to activate Windows.

ARCHS4 Kinases Coexp

Elsevier Pathway Collection

MSigDB Hallmark 2020

Bar Graph

Table

Clustergram

Appyter



Hover each row to see the overlapping genes.

10 entries per page

Search:

TOP2A, SUV39H1, TROAP, CCNF, TTK, KIF11, HMMR, MKI67, BRCA2, AURKB, KIF15, CKS1B, AURKA, CDC20, CCNB2, MT2A, RACGAP1, PBK, E2F2, MYBL2, KMT5A, E2F4, KPNA2, HMGN2, PLK4, POLQ, CDKN2C, PLK1, KIF23, KNL1, NDC80, CCNA2, TPX2, SLC7A5, CENPE, CENPF, TFPD1, ESPL1, PRC1, KIF4A, CDK1, KIF20B

score

Index	Name	P-value	Adjusted p-value		
1	G2-M Checkpoint	6.305e-18	1.576e-16	6.19	245.24
2	E2F Targets	6.305e-18	1.576e-16	6.19	245.24
3	Allograft Rejection	1.355e-15	2.259e-14	5.62	192.44
4	Mitotic Spindle	9.499e-13	1.187e-11	4.93	136.40
5	Complement	8.869e-9	8.869e-8	3.89	72.05
6	Inflammatory Response	3.468e-8	2.890e-7	3.73	63.99
7	Angiogenesis	0.0001143	0.0004395	6.43	58.39
8	TNF-alpha Signaling via NF-kB	4.685e-7	0.000003346	3.41	49.71
9	mTORC1 Signaling	0.000005321	0.00003325	3.10	37.71
10	IL-6/JAK/STAT3 Signaling	0.00008145	0.0003394	3.97	37.37

Showing 1 to 10 of 50 entries | [Export entries to table](#)

Previous Next

Terms marked with an * have an overlap of less than 5

BioCarta 2016

Reactome 2016

HumanCyc 2016

Activate Windows

Go to Settings to activate Windows.



Type here to search



05:30 ب.م
ENGLISH
11/11/V

Elsevier Pathway Collection

MSigDB Hallmark 2020

BioCarta 2016

Bar Graph

Table

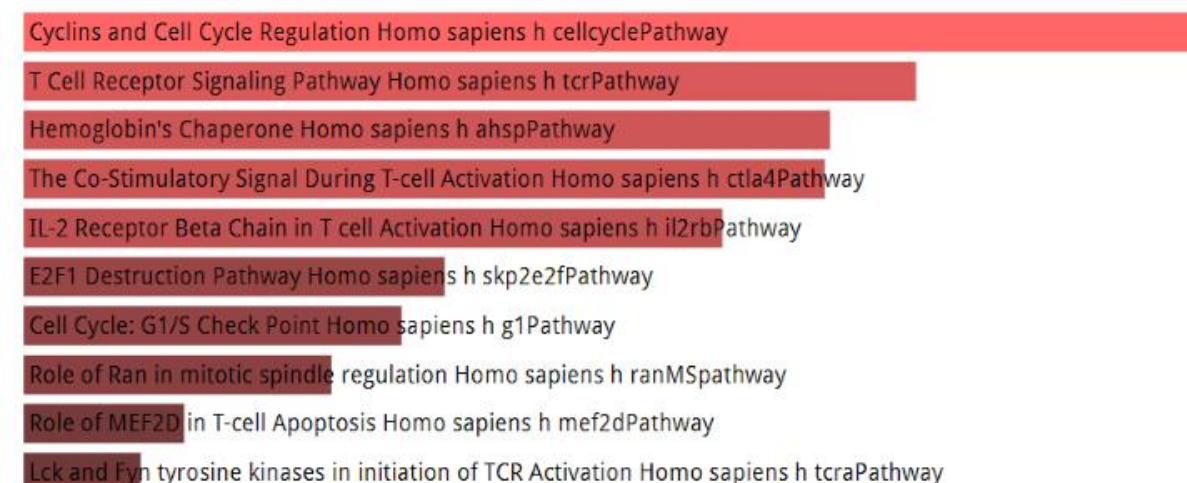
Clustergram

Appyter



Click the bars to sort. Now sorted by p-value ranking.

SVG PNG JPG



Reactome 2016

HumanCyc 2016

NCT-Nature 2016

Activate Windows
Go to Settings to activate Windows.



Type here to search



maayanlab.cloud/Enrichr/enrich#

Index	Name	P-value	Adjusted p-value	Odds Ratio	Combined score
1	Hemoglobin's Chaperone Homo sapiens h ahspPathway	0.0001378	0.005553	14.04	124.78
2	E2F1 Destruction Pathway Homo sapiens h skp2e2fPathway	0.0005714	0.01505	14.96	111.69
3	Cyclins and Cell Cycle Regulation Homo sapiens h cellcyclePathway	0.00003472	0.005403	RB1, CCNA1, CDKN2C, TFDP1, CDKN2A, CCNE1, CDK1	
4	Role of Ran in mitotic spindle regulation Homo sapiens h ranMSpathway	0.0008676	0.01713	12.82	90.37
5	The Co-Stimulatory Signal During T-cell Activation Homo sapiens h cta4Pathway	0.0001406	0.005553	9.63	85.45
6	CBL mediated ligand-induced downregulation of EGF receptors Homo sapiens h cblPathway	0.003734	0.04917	13.45	75.17
7	Lck and Fyn tyrosine kinases in initiation of TCR Activation Homo sapiens h tcratPathway	0.001755	0.02521	9.97	63.26
8	Regulation of p27 Phosphorylation during Cell Cycle Progression Homo sapiens h p27Pathway	0.001755	0.02521	9.97	63.26
9	Cyclin E Destruction Pathway Homo sapiens h fbw7Pathway	0.005424	0.06592	11.20	58.45
10	Cell Cycle: G1/S Check Point Homo sapiens h g1Pathway	0.0006702	0.01513	6.74	49.27

Showing 1 to 10 of 158 entries | [Export entries to table](#)

Terms marked with an * have an overlap of less than 5

Previous Next

Reactome 2016

HumanCyc 2016

NCI-Nature 2016

Activate Windows
Go to Settings to activate Windows.

maayanlab.cloud/Enrichr/enrich#

MSigDB Hallmark 2020

BioCarta 2016

Reactome 2016

Bar Graph Table Clustergram Appyter

Click the bars to sort. Now sorted by p-value ranking.

SVG PNG JPG

- Immune System Homo sapiens R-HSA-168256
- Adaptive Immune System Homo sapiens R-HSA-1280218
- Hemostasis Homo sapiens R-HSA-109582
- Cell Cycle, Mitotic Homo sapiens R-HSA-69278
- Cell Cycle Homo sapiens R-HSA-1640170
- Immunoregulatory interactions between a Lymphoid and a non-Lymphoid cell Homo sapiens R-HSA-198933
- Innate Immune System Homo sapiens R-HSA-168249
- Signaling by Rho GTPases Homo sapiens R-HSA-194315
- G0 and Early G1 Homo sapiens R-HSA-1538133
- Platelet activation, signaling and aggregation Homo sapiens R-HSA-76002

HumanCyc 2016

NCI-Nature 2016

Panther 2016

Activate Windows
Go to Settings to activate Windows.

maayanlab.cloud/Enrichr/enrich#

Entries per page: 10 | Search:

Index	Name	P-value	Adjusted p-value	Odds Ratio	Combined score	
1	Cross-presentation of particulate exogenous antigens (phagosomes) Homo sapiens R-HSA-1236973	1.582e-7	0.00001555	67.48	1056.64	
2	Erythrocytes take up oxygen and release carbon dioxide Homo sapiens R-HSA-1247673	0.000007178	0.0003880	37.44	443.47	
3	G0 and Early G1 Homo sapiens R-HSA-1538133	3.602e-8	0.000004327	15.06	258.04	
4	TP53 Regulates Transcription of Genes Involved in G1 Cell Cycle Arrest Homo sapiens R-HSA-6804116	0.000008057	0.0003959	19.27	226.07	
5	RHO GTPases Activate NADPH Oxidases Homo sapiens R-HSA-5668599	0.000008057	0.0003959	19.27	226.07	
6	Erythrocytes take up carbon dioxide and release oxygen Homo sapiens R-HSA-1237044	0.00008791	0.002568	CD86, IL1RN, NCF1, NCF2, IGHV3-23, UBE2D3, NCF4, EIF4A3, JNPL1, IRS2, IL1RAP, IFE30, ACTB, ICAM1, CDC20, MT2A, IGHG1, IGHG2, GRAP2, CLECSA, C3AR1, AP153, KPNA2, CD96, NUP210, PRKCD, CD180, UBE2E2, CYBB, CYBA, PRKCA, OSCAR, TYROBP, CD8A, PSM3, CD300E, PRTN3, KIF20A, CD300C, ATP6V0D1, VCL, CFD, CSF1R, CSAR2, IQGAP1, CD1D, PHB, PLD1, DTX4, CSF2RA, RASGRP4, C2, RASGRP3, KLRK1, RACGAP1, CLEC7A, CD300LB, SLAMF6, CD14, MAP2K7, PAG1, CTSA, VCAM1, SMURF1, SH2D1A, LY86, ARTN, KIF4B, KIF4A, TAB3, CALM1, IL7R, IGHM, ITK, SIGLEC9, ITGAM, FLT3, SH3KBP1, ITGB2, CD3G, PTPRJ, AP2A1, ARR82, KIF11, CD3E, CD3D, TREM1, SIRPB1, TNFSF13B, KIF15, FCGR3A, MRC1, CASP1, CTLA4, CTSH, ITGB7, CD36, RAC1, CTSE, CTSD, CD33, CTSC, CT5B, CCR2, HAVCR2, DUSP5, FCER1G, KIF23, GAB2, TNFRSF1B, IL17RA, VAV2, FGR, HKC, NR4A, ATP6V1B2, IGHD, IRF8, TLR8, BPI, TLR7, TLR5, TLR4, HBEGF, TLR2, LILRA6, C1QA, UNC93B1, NOD2, CBL, SAMHD1, LILRA2, FYB, IGKC, PSMB3, FCGR1A, FCGR1B, WASF2, POLR2K, IL32, TRAT1, MYO9B, LILRB1, LILRB4, CENPE, CD4, FCGR2A, IL2RB, TRIM38, FCGR2B, PTPN2		
7	O2/CO2 exchange in erythrocytes Homo sapiens R-HSA-1480926	0.00008791	0.002568			
8	Phosphorylation of Emi1 Homo sapiens R-HSA-176417	0.001423	0.02262			
9	Immunoregulatory interactions between a Lymphoid and a non-Lymphoid cell Homo sapiens R-HSA-198933	4.525e-12	8.152e-10			
10	Immune System Homo sapiens R-HSA-168256	2.321e-22	2.509e-19	2.72	135.45	

Showing 1 to 10 of 1,081 entries | [Export entries to table](#)
Terms marked with an * have an overlap of less than 5

Previous Next

[HumanCyc 2016](#)[NCI-Nature 2016](#)

Activate Windows
Go to Settings to activate Windows.



Type here to search



5:31 ب.م.
ENGLISH
05:31 ب.م.
10/10/2023

HumanCyc 2016

Bar Graph Table Clustergram Appyter ⚙ ⓘ

Click the bars to sort. Now sorted by p-value ranking.

SVG PNG JPG

superpathway of conversion of glucose to acetyl CoA and entry into the TCA cycle Homo sapiens PWY66-407

TCA cycle Homo sapiens PWY66-398

glycolysis Homo sapiens PWY66-400

gluconeogenesis Homo sapiens PWY66-399

GDP-mannose biosynthesis Homo sapiens PWY-5659

UDP-N-acetyl-D-galactosamine biosynthesis II Homo sapiens PWY-5514

3-phosphoinositide biosynthesis Homo sapiens PWY-6352

chondroitin sulfate biosynthesis Homo sapiens PWY-6569

superpathway of inositol phosphate compounds Homo sapiens PWY-6371

protein citrullination Homo sapiens PWY-4921

NCI-Nature 2016

Panther 2016

BioPlex 2017

huMAP

Activate Windows
Go to Settings to activate Windows.



Type here to search



^ ENG 05:31 ب.م
۱۰/۱۱/۲۰۲۳

HumanCyc 2016

Bar Graph

Table

Clustergram

Appyter



Hover each row to see the overlapping genes.

10 ▾ entries per page

Search:

Index	Name	P-value	Adjusted p-value	Odds Ratio	Combined score
1	GDP-mannose biosynthesis Homo sapiens PWY-5659	0.02452	0.2648	11.19	41.50
2	TCA cycle Homo sapiens PWY66-398	0.005095	0.1376	6.90	36.43
3	superpathway of conversion of glucose to acetyl CoA and entry into the TCA cycle Homo sapiens PWY66-407	0.0006750	0.03645	4.74	34.59
4	UDP-N-acetyl-D-galactosamine biosynthesis II Homo sapiens PWY-5514	0.05405	0.4864	6.39	18.66
5	glycolysis Homo sapiens PWY66-400	0.01795	0.2423	4.48	18.03
6	gluconeogenesis Homo sapiens PWY66-399	0.01795	0.2423	4.48	18.03
7	protein citrullination Homo sapiens PWY-4921	0.1967	0.5321	5.59	9.09
8	tetrapyrrole biosynthesis Homo sapiens PWY-5189	0.1967	0.5321	5.59	9.09
9	ketogenesis Homo sapiens PWY66-367	0.1967	0.5321	5.59	9.09
10	histidine degradation Homo sapiens PWY-5030	0.1967	0.5321	5.59	9.09

Showing 1 to 10 of 54 entries | [Export entries to table](#)

Terms marked with an * have an overlap of less than 5

Previous Next

NCI-Nature 2016

Panther 2016

BioPlex 2017

Activate Windows

Go to Settings to activate Windows.



Type here to search



^ ENG 05:31 ب.م
۱۰/۱۱/۱۷

HumanCyc 2016

NCI-Nature 2016

Bar Graph

Table

Clustergram

Appyter



Click the bars to sort. Now sorted by p-value ranking.

SVG PNG JPG

PLK1 signaling events Homo sapiens e5e87977-6194-11e5-8ac5-06603eb7f303

IL8- and CXCR1-mediated signaling events Homo sapiens f6a58ef3-6193-11e5-8ac5-06603eb7f303

TCR signaling in naive CD4+ T cells Homo sapiens 0c2862fa-6196-11e5-8ac5-06603eb7f303

FOXM1 transcription factor network Homo sapiens c51cda49-6192-11e5-8ac5-06603eb7f303

E2F transcription factor network Homo sapiens bb4d0fd3-6191-11e5-8ac5-06603eb7f303

RAC1 signaling pathway Homo sapiens faffa4fc-6194-11e5-8ac5-06603eb7f303

Thromboxane A2 receptor signaling Homo sapiens 27d5800d-6196-11e5-8ac5-06603eb7f303

IL8- and CXCR2-mediated signaling events Homo sapiens fe78e284-6193-11e5-8ac5-06603eb7f303

Beta2 integrin cell surface interactions Homo sapiens 95b6b434-618d-11e5-8ac5-06603eb7f303

CXCR4-mediated signaling events Homo sapiens 46a5529b-6191-11e5-8ac5-06603eb7f303

Panther 2016

BioPlex 2017

huMAP

PPI Hub Proteins

Activate Windows

Go to Settings to activate Windows.



Type here to search



5:31 ب.م
ENGLISH
11/11/IV

maayanlab.cloud/Enrichr/enrich#

Index	Name	P-value	Adjusted p-value	Odds Ratio	Combined score
1	IL8- and CXCR1-mediated signaling events Homo sapiens f6a58ef3-6193-11e5-8ac5-06603eb7f303	1.286e-7	0.00001158	12.54	199.03
2	PLK1 signaling events Homo sapiens e5e87977-6194-11e5-8ac5-06603eb7f303	4.104e-8	0.000007387	8.92	151.71
3	Class IB PI3K non-lipid kinase events Homo sapiens 263703f8-6191-11e5-8ac5-06603eb7f303	0.001423	0.01024	22.41	146.92
4	FOXM1 transcription factor network Homo sapiens c51cda49-6192-11e5-8ac5-06603eb7f303	6.194e-7	0.00002788	8.57	122.50
5	IL8- and CXCR2-mediated signaling events Homo sapiens fe78e284-6193-11e5-8ac5-06603eb7f303	0.000009313	0.0002095	8.12	94.02
6	TCR signaling in naive CD4+ T cells Homo sapiens 0c2862fa-6196-11e5-8ac5-06603eb7f303	4.111e-7	0.00002467	6.34	93.25
7	Beta2 integrin cell surface interactions Homo sapiens 95b6b434-618d-11e5-8ac5-06603eb7f303	0.00002115	0.0004056	8.58	92.35
8	RAC1 signaling pathway Homo sapiens faffa4fc-6194-11e5-8ac5-06603eb7f303	0.000002310	0.00006931	6.46	83.82
9	Thromboxane A2 receptor signaling Homo sapiens 27d5800d-6196-11e5-8ac5-06603eb7f303	0.000003476	0.00008938	6.16	77.48
10	E2F transcription factor network Homo sapiens bb4d0fd3-6191-11e5-8ac5-06603eb7f303	0.000001867	0.00006721	5.46	72.09

Showing 1 to 10 of 180 entries | [Export entries to table](#)
Terms marked with an * have an overlap of less than 5

Previous Next

Panther 2016**BioPlex 2017**

Activate Windows
Go to Settings to activate Windows.



Type here to search



5:32 ب.م
ENGLISH
5/11/19

maayanlab.cloud/Enrichr/enrich

BioPlanet 2019

- Interleukin-2 signaling pathway
- Leptin influence on immune response
- Immune system
- Interleukin-4 regulation of apoptosis
- Adaptive immune system

WikiPathway 2021 Human

- Microglia Pathogen Phagocytosis Pathway V
- TYROBP causal network in microglia WP394
- Complement system WP2806
- Retinoblastoma gene in cancer WP2446
- Gastric Cancer Network 1 WP2361

KEGG 2021 Human

- Phagosome
- Osteoclast differentiation
- Malaria
- Neutrophil extracellular trap formation
- Hematopoietic cell lineage

ARCHS4 Kinases Coexp

- MKNK1 human kinase ARCHS4 coexpression
- CSF1R human kinase ARCHS4 coexpression
- IRAK3 human kinase ARCHS4 coexpression
- HCK human kinase ARCHS4 coexpression
- CAMK1 human kinase ARCHS4 coexpression

Elsevier Pathway Collection

- Neutrophil Degranulation via FPR1/IL8
- Neutrophil Degranulation via FPR1 Signaling
- Proteins Involved in Glomerulonephritis
- Neutrophil Activation via Adherence on End
- Low-Density Lipoproteins and Chemokines I

MSigDB Hallmark 2020

- G2-M Checkpoint
- E2F Targets
- Allograft Rejection
- Mitotic Spindle
- Complement

BioCarta 2016

- Cyclins and Cell Cycle Regulation Homo sapiens
- T Cell Receptor Signaling Pathway Homo sapiens
- Hemoglobin's Chaperone Homo sapiens
- The Co-Stimulatory Signal During T-cell Activation Homo sapiens
- IL-2 Receptor Beta Chain in T cell Activation Homo sapiens

Reactome 2016

- Immune System Homo sapiens R-HSA-1682
- Adaptive Immune System Homo sapiens R-HSA-109582
- Hemostasis Homo sapiens R-HSA-109582
- Cell Cycle: Mitotic Homo sapiens R-HSA-692
- Cell Cycle Homo sapiens R-HSA-1640170

HumanCyc 2016

- superpathway of conversion of glucose to a
- TCA cycle Homo sapiens PWY66-398
- glycolysis Homo sapiens PWY66-400
- gluconeogenesis Homo sapiens PWY66-399
- GDP-mannose biosynthesis Homo sapiens P

NCI-Nature 2016

- PLK1 signaling events Homo sapiens e5e879
- IL8- and CXCR1-mediated signaling events Homo sapiens
- TCR signaling in naïve CD4+ T cells Homo sapiens
- FOXM1 transcription factor network Homo sapiens

Panther 2016

- Glycolysis Homo sapiens P00024
- Alpha adrenergic receptor signaling pathway Homo sapiens
- Toll receptor signaling pathway Homo sapiens
- Dopamine receptor mediated signaling pathway Homo sapiens

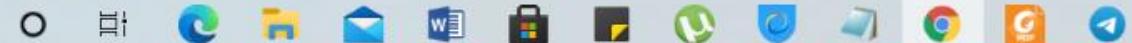
BioPlex 2017

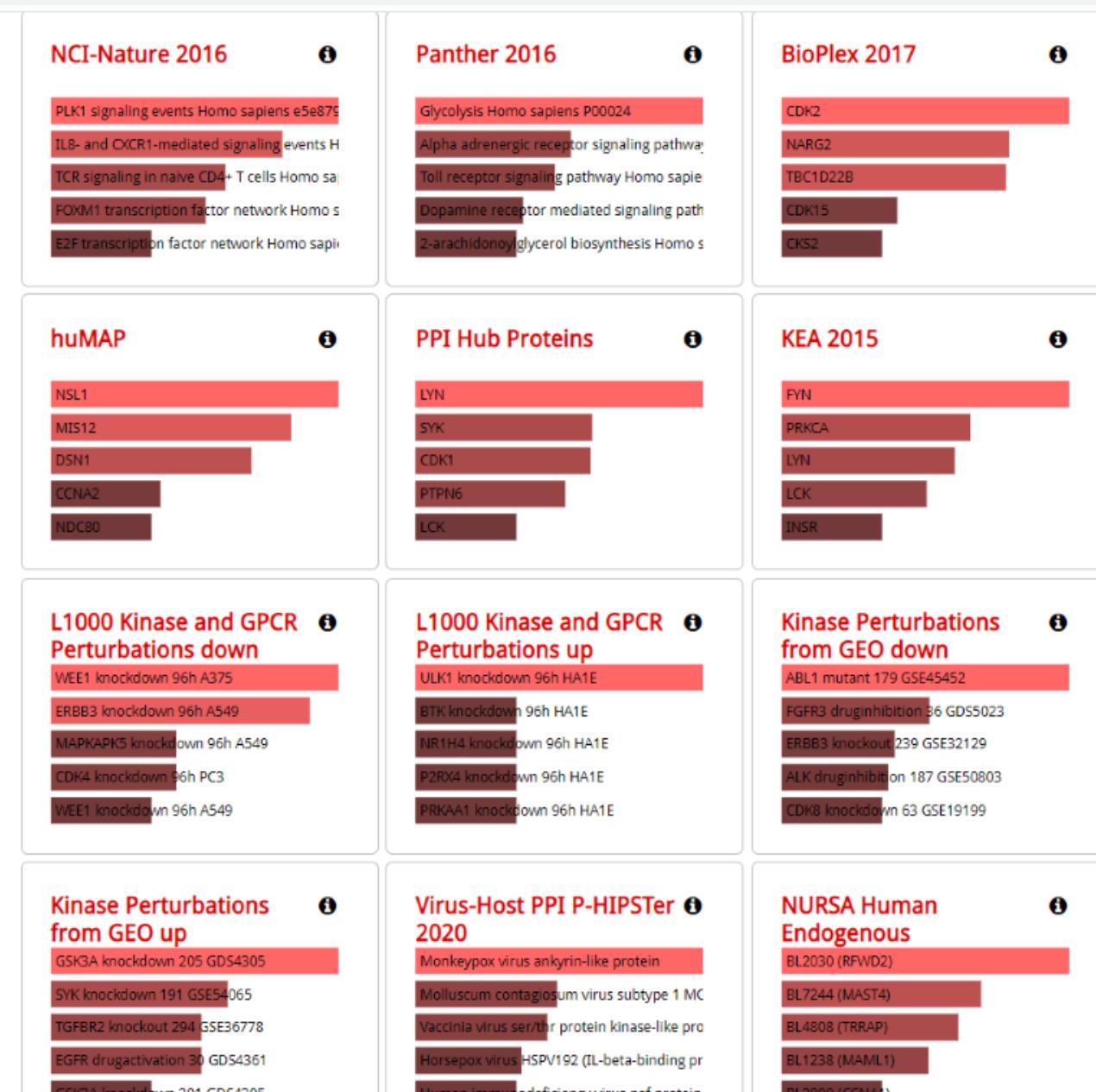
- CDK2
- NARG2
- TBC1D22B
- CDK15

Activate Windows
Go to Settings to activate Windows.



Type here to search





Activate Windows
Go to Settings to activate Windows.



Type here to search



maayanlab.cloud/Enrichr/enrich

L1000 Kinase and GPCR Perturbations down

- WEE1 knockdown 96h A375
- EPBB3 knockdown 96h A549
- MAPKAPK5 knockdown 96h A549
- CDK4 knockdown 96h PC3
- WEE1 knockdown 96h A549

L1000 Kinase and GPCR Perturbations up

- ULK1 knockdown 96h HA1E
- BTK knockdown 96h HA1E
- NR1H4 knockdown 96h HA1E
- P2RX4 knockdown 96h HA1E
- PRKAA1 knockdown 96h HA1E

Kinase Perturbations from GEO down

- ABL1 mutant 179 GSE45452
- FGFR3 drug inhibition 56 GD55023
- ERBB3 knockout 239 GSE32129
- ALK drug inhibition 187 GSE50803
- CDK8 knockdown 63 GSE19199

Kinase Perturbations from GEO up

- GSK3A knockdown 205 GDS4305
- SYK knockdown 191 GSE54065
- TGFBR2 knockout 294 GSE36778
- EGFR drugactivation 30 GDS4361
- GSK3A knockdown 201 GDS4305

Virus-Host PPI P-HIPSTer 2020

- Monkeypox virus ankyrin-like protein
- Molluscum contagiosum virus subtype 1 MC
- Vaccinia virus ser/thr protein kinase-like pro
- Horsepox virus HSPV192 (IL-beta-binding pr)
- Human immunodeficiency virus nef protein

NURSA Human Endogenous

- BL2030 (RFWD2)
- BL7244 (MAST4)
- BL4808 (TRRAP)
- BL1238 (MAML1)
- BL2800 (CCNA1)

CORUM

- NDC80 kinetochore complex (human)
- Cd3d-Cd3g-Cd3e-Cd247 complex (mouse)
- BRCC complex (human)
- Cell cycle kinase complex CDC2 (human)
- PCNA-PAF complex (human)

SILAC Phosphoproteomics

- up metaphase anaphase telophase 60min n
- down metaphase anaphase telophase 15min
- down 7min cross-link ZAP-70 null vs reconst
- down 5min cross-link ZAP-70 null vs reconst
- up metaphase anaphase telophase 15min n

HMS LINCS KinomeScan

- Tozasertib
- Barasertib
- XMD-12
- WZ4002
- ZM-447439

Phosphatase Substrates from DEPOD

- PPP1CA
- PTPN5
- PTPN11
- ACP1
- PPP6C

SubCell BarCode

- H322 Unclassified Unclassified 30609389
- H251 Cytosol Unclassified 30609389
- H322 Cytosol Unclassified 30609389
- HCCB27 Cytosol C2 30609389
- MCF7 Unclassified Unclassified 30609389

Activate Windows
Go to Settings to activate Windows.

Type here to search

05:41 ٦.٢ ENG ١٠٠/١١/١٩

Hover each row to see the overlapping genes.

10 entries per page

Search:

Index	Name	P-value	Adjusted p-value	Odds Ratio	Combined score
1	Cross-presentation of particulate exogenous antigens (phagosomes) Homo sapiens R-HSA-1236973	1.582e-7	0.00001555	67.48	1056.64
2	Erythrocytes take up oxygen and release carbon dioxide Homo sapiens R-HSA-1247673	0.000007178	0.0003880	37.44	443.47
3	G0 and Early G1 Homo sapiens R-HSA-1538133	3.602e-8	0.000004327	15.06	258.04
4	TP53 Regulates Transcription of Genes Involved in G1 Cell Cycle Arrest Homo sapiens R-HSA-6804116	0.000008057	0.0003959	19.27	226.07
5	RHO GTPases Activate NADPH Oxidases Homo sapiens R-HSA-5668599	0.000008057	0.0003959	19.27	226.07
6	Erythrocytes take up carbon dioxide and release oxygen Homo sapiens R-HSA-1237044	0.00000724	0.000560	16.04	149.83
7	O2/CO2 exchange in erythrocytes Homo sapiens R-HSA-1480926	0.00000724	0.000560	16.04	149.83
8	Phosphorylation of Emery-Dreifuss muscular dystrophy protein 1 Homo sapiens R-HSA-176417	0.00000724	0.000560	22.41	146.92
9	Immunoregulatory interactions in Lymphoid and a non-Lymphoid tissue Homo sapiens R-HSA-198933	0.00000724	0.000560	5.43	141.88
10	Immune System Homo sapiens R-HSA-168256	2.521e-22	2.509e-19	2.72	135.45

Showing 1 to 10 of 1,081 entries | [Export entries to table](#)

Terms marked with an * have an overlap of less than 5

[Previous](#) [Next](#)

HumanCyc 2016

Activate Windows

Go to Settings to activate Windows.

NCI-Nature 2016



Type here to search



[Login](#) | [Register](#)[Transcription](#) [Pathways](#) **Ontologies** [Diseases/Drugs](#) [Cell Types](#) [Misc](#) [Legacy](#) [Crowd](#)**Description** No description available (857 genes)**GO Biological Process 2021**

neutrophil activation involved in immune re
neutrophil degranulation (GO:0043312)
neutrophil mediated immunity (GO:0002446)
cytokine-mediated signaling pathway (GO:0002447)
regulation of immune response (GO:005077)

GO Molecular Function 2021

kinase binding (GO:0019900)
cyclin-dependent protein serine/threonine kinase activity (GO:0002448)
protein kinase binding (GO:0019901)
superoxide-generating NAD(P)H oxidase activity (GO:0002449)
microtubule motor activity (GO:0003777)

GO Cellular Component 2021

secretory granule membrane (GO:0030667)
azurophil granule (GO:0042582)
specific granule (GO:0042581)
secretory granule lumen (GO:0034774)
specific granule membrane (GO:0035579)

MGI Mammalian Phenotype Level 4 2021

abnormal neutrophil physiology MP:000246
abnormal macrophage physiology MP:000247
increased susceptibility to bacterial infection MP:000248
increased inflammatory response MP:00018
decreased CD4-positive, alpha beta T cell number MP:00019

Human Phenotype Ontology

Splenomegaly (HP:0001744)
Recurrent abscess formation (HP:0002722)
Hepatomegaly (HP:0002240)
Meningitis (HP:0001287)
Recurrent bacterial skin infections (HP:0005100)

Jensen TISSUES

Blood
Monocyte
Immune system
Bone marrow
Dendritic cell

Jensen COMPARTMENTS

Interleukin-12 complex
B cell receptor complex
IgG immunoglobulin complex
Interleukin-23 complex
NF-kappaB complex

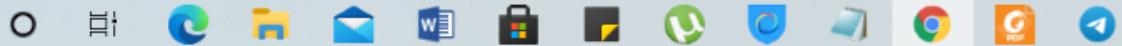
Jensen DISEASES

Arthritis
Vasculitis
Lung disease
Chronic granulomatous disease
Uveitis

Activate Windows
Go to Settings to activate Windows.



Type here to search

5:44 ب.م
ENGLISH
05:44 ب.م
IF..//IV



Input data

Expand a gene, a term, or a variant into a gene set:

e.g. STAT3, breast cancer, or rs28897756



Try an example

Include the top 100 most relevant genes



Paste a set of valid Entrez gene symbols on each row in the text-box below. [Try a gene set example.](#)

```
NBPF1  
TBC1D3B  
PMS2P1  
CT47A7  
NBPF14  
TBC1D3F  
CT47B1  
CT47A11  
IGHV3-75
```

2578 gene(s) entered

Down AML

Contribute your set so it can be searched by others

Submit

Please acknowledge Enrichr in your publications by citing the following references:

Chen EY, Tan CM, Kou Y, Duan Q, Wang Z, Meirelles GV, Clark NR, Ma'ayan A.

Enrichr: interactive and collaborative HTML5 gene list enrichment analysis tool. *BMC Bioinformatics*. 2013; 128(14).

Kuleshov MV, Jones MR, Rouillard AD, Fernandez NF, Duan Q, Wang Z, Koplev S, Jenkins SL, Jagodnik KM, Lachmann A, McDermott MG, Monteiro CD, Gundersen GW, Ma'ayan A.

Enrichr: a comprehensive gene set enrichment analysis web server 2016 update. *Nucleic Acids Research*. 2016; gkw377.

Xie Z, Bailey A, Kuleshov MV, Clarke DJB., Evangelista JE, Jenkins SL, Lachmann A, Wojciechowicz ML, Kropiwnicki E, Jagodnik KM, Jeon M, & Ma'ayan A.

Gene set knowledge discovery with Enrichr. *Current Protocols*, 1, e90. 2021. doi: 10.1002/cp21.90

modEnrichr

A suite of gene set enrichment analysis tools

FlyEnrichr

A suite of gene set enrichment analysis tools

YeastEnrichr

A suite of gene set enrichment analysis tools

WormEnrichr

A suite of gene set enrichment analysis tools

FishEnrichr

A suite of gene set enrichment analysis tools



Input data

Expand a gene, a term, or a variant into a gene set:

e.g. STAT3, breast cancer, or rs28897756



Try an example

Include the top 100 most relevant genes



Paste a set of valid Entrez gene symbols on each row in the text-box below. [Try a gene set example.](#)

```
NBPF1  
TBC1D3B  
PMS2P1  
CT47A7  
NBPF14  
TBC1D3F  
CT47B1  
CT47A11  
IGHV3-75
```

2577 gene(s) entered

Down_AML

Contribute your set so it can be searched by others

Submit

Please acknowledge Enrichr in your publications by citing the following references:

Chen EY, Tan CM, Kou Y, Duan Q, Wang Z, Meirelles GV, Clark NR, Ma'ayan A.

Enrichr: interactive and collaborative HTML5 gene list enrichment analysis tool. *BMC Bioinformatics*. 2013; 128(14).

Kuleshov MV, Jones MR, Rouillard AD, Fernandez NF, Duan Q, Wang Z, Koplev S, Jenkins SL, Jagodnik KM, Lachmann A, McDermott MG, Monteiro CD, Gundersen GW, Ma'ayan A.

Enrichr: a comprehensive gene set enrichment analysis web server 2016 update. *Nucleic Acids Research*. 2016; gkw377.

Xie Z, Bailey A, Kuleshov MV, Clarke DJB., Evangelista JE, Jenkins SL, Lachmann A, Wojciechowicz ML, Kropiwnicki E, Jagodnik KM, Jeon M, & Ma'ayan A.

Gene set knowledge discovery with Enrichr. *Current Protocols*, 1, e90. 2021. doi: 10.1002/cp21.90



A suite of gene set enrichment analysis tools



FlyEnrichr



YeastEnrichr



WormEnrichr



FishEnrichr



Login | Register

[Transcription](#) [Pathways](#) [Ontologies](#) [Diseases/Drugs](#) [Cell Types](#) [Misc](#) [Legacy](#) [Crowd](#)

Description Down_AML (2577 genes)

**ChEA 2016**

FOXM1 23109430 ChIP-Seq U205 Human
SPI1 23127762 ChIP-Seq K562 Human
NR1H3 23393188 ChIP-Seq ATHEROSCLEROTIC
SPI1 23547873 ChIP-Seq NB4 Human
VDR 24763502 ChIP-Seq THP-1 Human

ENCODE and ChEA Consensus TFs from

FOXM1 ENCODE
E2F4 ENCODE
SPI1 CHEA
GATA2 CHEA
RUNX1 CHEA

ARCHS4 TFs Coexp

JDP2 human tf ARCHS4 coexpression
CEBPB human tf ARCHS4 coexpression
PLEK human tf ARCHS4 coexpression
SEMA4A human tf ARCHS4 coexpression
ZNF385A human tf ARCHS4 coexpression

TF Perturbations Followed by Expression

MAF SIRNA MACROPHAGE HUMAN GSE9836
AIRE KO MOUSE GSE30129 CREEDSID GENE
ZNF750 KD HUMAN GSE38039 CREEDSID GE
ZNF750 KD HUMAN GSE38039 CREEDSID GE
MAF OE MACROPHAGE HUMAN GSE98368 R

TRRUST Transcription Factors 2019

SPI1 human
GATA1 human
RUNX1 human
SPI1 mouse
E2F4 mouse

IncHUB lncRNA Co-Expression

LINC02705
SGO1-AS1
TMPO-AS1
LINC02207
CSRP3-AS1

Enrichr Submissions TF-Gene Cooccurrence

SPI1
RNASE2
TFEC
MYBL1
IKZF1

TRANSFAC and JASPAR PWMs

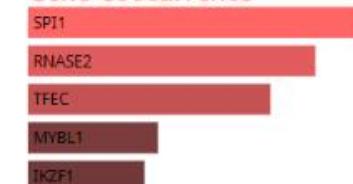
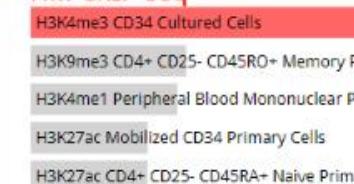
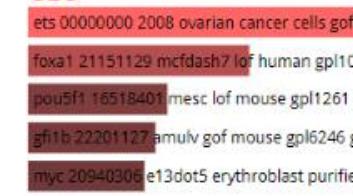
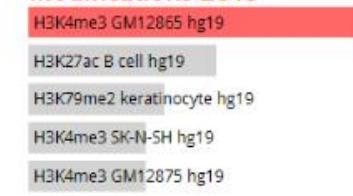
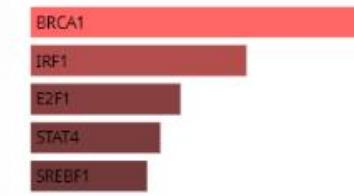
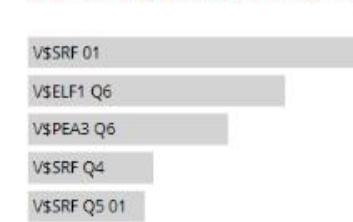
NFYB (human)
TEAD2 (human)
SOX10 (human)
TLX1::NFIC (human)
EWSR1::FLI1 (human)

Epigenomics Roadmap HM ChIP-seq

H3K4me3 CD34 Cultured Cells
H3K9me3 CD4+ CD25- CD45RO- Memory Pr
H3K4me1 Peripheral Blood Mononuclear Pr
H3K27ac Mobilized CD34 Primary Cells
H3K27ac CD4+ CD25- CD45RA+ Naive Prima

<>C

maayanlab.cloud/Enrichr/enrich

**ENRICHMENT SUBMISSIONS TO ENRICHR**
Gene Cooccurrence**TRANSFAC and JASPAR**
PWMs**epigenomics Roadmap**
HM ChIP-seq**TargetScan microRNA 2017****miRTarBase 2017****ENCODE TF ChIP-seq 2015****TF-LOF Expression from GEO****ENCODE Histone Modifications 2015****Transcription Factor PPIs****Genome Browser PWMs**



Login | Register

Transcription Pathways Ontologies Diseases/Drugs Cell Types Misc Legacy Crowd

Description Down_AML (2577 genes)



BioPlanet 2019

Interleukin-2 signaling pathway
Phagosome
Leptin influence on immune response
Lysosome
MHC class II antigen presentation

WikiPathway 2021 Human

TYROBP causal network in microglia WP394
Microglia Pathogen Phagocytosis Pathway W
VEGFA-VEGFR2 Signaling Pathway WP3888
Complement system WP2806
Cell cycle WP179

KEGG 2021 Human

Phagosome
Lysosome
Progesterone-mediated oocyte maturation
Osteoclast differentiation
Fc gamma R-mediated phagocytosis

ARCHS4 Kinases Coexp

CSF1R human kinase ARCHS4 coexpression
MKNK1 human kinase ARCHS4 coexpression
TRAK3 human kinase ARCHS4 coexpression
PRKCD human kinase ARCHS4 coexpression
CAMK1 human kinase ARCHS4 coexpression

Elsevier Pathway Collection

Neutrophil Degranulation via FPR1 Signaling
Neutrophil Degranulation via FPR1/IL8
Neutrophil Activation via Adherence on End
Neutrophil Activation via FCGR3B
Monoblast -> Promonocyte Surface Expressi

MSigDB Hallmark 2020

G2-M Checkpoint
Mitotic Spindle
Allograft Rejection
E2F Targets
mTORC1 Signaling

BioCarta 2016

Cell Cycle: G1/S Check Point Homo sapiens
Thrombin signaling and protease-activated
IL-7 Signal Transduction Homo sapiens h IL7
IL-2 Receptor Beta Chain in T cell Activation
Hemoglobin's Chaperone Homo sapiens h a

Reactome 2016

Immune System Homo sapiens R-HSA-1682
Adaptive Immune System Homo sapiens R-I
Hemostasis Homo sapiens R-HSA-109582
MHC class II antigen presentation Homo sap
Signaling by Rho GTPases Homo sapiens R-I

HumanCyc 2016

superpathway of conversion of glucose to a
glycolysis Homo sapiens PWY66-400
gluconeogenesis Homo sapiens PWY66-399
TCA cycle Homo sapiens PWY66-398
GDP-mannose biosynthesis Homo sapiens P

BioCarta 2016

Cell Cycle: G1/S Check Point Homo sapiens
 Thrombin signaling and protease-activated
 IL-7 Signal Transduction Homo sapiens h il7
 IL-2 Receptor Beta Chain in T cell Activation
 Hemoglobin's Chaperone Homo sapiens h a

Reactome 2016

Immune System Homo sapiens R-HSA-1682
 Adaptive Immune System Homo sapiens R-HSA-1682
 Hemostasis Homo sapiens R-HSA-109582
 MHC class II antigen presentation Homo sapiens
 Signaling by Rho GTPases Homo sapiens R-HSA-1682

HumanCyc 2016

superpathway of conversion of glucose to acetyl-CoA Homo sapiens P0Y66-400
 glycolysis Homo sapiens P0Y66-400
 gluconeogenesis Homo sapiens P0Y66-399
 TCA cycle Homo sapiens P0Y66-398
 GDP-mannose biosynthesis Homo sapiens P0Y66-398

NCI-Nature 2016

RAC1 signaling pathway Homo sapiens P00024
 PLK1 signaling events Homo sapiens e5e879
 Thromboxane A2 receptor signaling Homo sapiens P00024
 CXCR4-mediated signaling events Homo sapiens P00024
 E2F transcription factor network Homo sapiens P00024

Panther 2016

Glycolysis Homo sapiens P00024
 Cytoskeletal regulation by Rho GTPase Homo sapiens P00024
 Interleukin signaling pathway Homo sapiens P00024
 Endothelin signaling pathway Homo sapiens P00024
 p53 pathway Homo sapiens P00059

BioPlex 2017

GMNN
 SAMD1
 KCTD17
 CDK2
 FLYWCH2

huMAP

PLEKHG3
 ARPC4
 RAI14
 SSH2
 MPPED1

PPI Hub Proteins

CDK1
 CBL
 RAC1
 PIK3R1
 LYN

KEA 2015

HCK
 LCK
 IGF1R
 INSR
 FYN

L1000 Kinase and GPCR Perturbations down

WEE1 knockdown 96h A375
 CSNK1A1 knockdown 96h A375
 ERBB3 knockdown 96h A549
 CDK4 knockdown 96h PC3
 MST1R knockdown 96h A549

L1000 Kinase and GPCR Perturbations up

NR1H4 knockdown 96h HA1E
 ULK1 knockdown 96h HA1E
 DAPK1 knockdown 96h HA1E
 KCNK2 knockdown 96h HA1E
 PAK3 knockdown 96h HA1E

Kinase Perturbations from GEO down

ABL1 mutant 179 GSE45452
 FGFR3 druginhibition 36 GDS5023
 CDK9 knockdown 71 GSE21751
 ROCK1 knockdown 156 GSE34769
 BRAF druginhibition 175 GSE42872

Activate Windows
 Go to Settings to activate Windows.

< > C

maayanlab.cloud/Enrichr/enrich



L1000 Kinase and GPCR Perturbations down

- WEE1 knockdown 96h A375
- CSNK1A1 knockdown 96h A375
- ERBB3 knockdown 96h A549
- CDK4 knockdown 96h PC3
- MST1R knockdown 96h A549

L1000 Kinase and GPCR Perturbations up

- NR1H4 knockdown 96h HA1E
- ULK1 knockdown 96h HA1E
- DAPK1 knockdown 96h HA1E
- KCNK2 knockdown 96h HA1E
- PAK3 knockdown 96h HA1E

Kinase Perturbations from GEO down

- ABL1 mutant 179 GSE45452
- FGFR3 druginhibition 36 GD55023
- CDK9 knockdown 71 GSE21751
- ROCK1 knockdown 156 GSE34769
- BRAF druginhibition 175 GSE42872

Kinase Perturbations from GEO up

- SYK knockdown 191 GSE54065
- LRRK2 activemutant 159 GSE36321
- LRRK2 mutant 33 GDS4401
- EGFR drugactivation 30 GDS4361
- PIK3CA knockdown 182 GSE46869

Virus-Host PPI P-HIPSTer 2020

- Horsepox virus HSPV189 (Serine/threonine)
- Cowpox virus CPXV206 protein (gene: CPXV2
- Mariola virus semaphorin-like protein (gene:
- Measles virus strain Edmonston-Zagreb nuc
- Measles virus strain MVi/Pennsylvania.USA.

NURSA Human Endogenous

- a-PTEN (WG) (PTEN)
- BL2393 (CDT1)
- BL1744 (CITED1)
- BL1096 (DYRK2)
- BL461 (RBM14)

CORUM

- NDC80 kinetochore complex (human)
- Cofilin-actin-CAP1 complex (human)
- Itgax-Itgb2-Icam4 complex (mouse)
- ELMO1-DOCK1-RAC1 complex (human)
- CIN85-SH3GL3-CBL complex (human)

SILAC Phosphoproteomics

- up metaphase anaphase telophase 15min n
- down 20min EGF vs ctrl HeLa (Human) (1708)
- up metaphase anaphase telophase 60min n
- down 5min cross-link ZAP-70 null vs reconstr
- up 10min PPase inhibitors vs ctrl Hepa-1-6 (I

HMS LINCS KinomeScan

- W24003
- XMD8-92
- WZ4002
- Tozasertib
- NVP-TAE684

Phosphatase Substrates from DEPOD

- PPP1CA
- PTPN11
- PTPN12
- SSH1
- PTPN13

SubCell BarCode

- U251 Cytosol Unclassified 30609389
- HCCB27 Cytosol C2 30609389
- MCF7 Cytosol Unclassified 30609389
- H322 Cytosol Unclassified 30609389

Type here to search





Transcription Pathways Ontologies Diseases/Drugs Cell Types Misc Legacy Crowd

Description Down_AML (2577 genes)



GO Biological Process 2021

neutrophil activation involved in immune re
neutrophil degranulation (GO:0043312)
neutrophil mediated immunity (GO:0002446)
mitotic cytokinesis (GO:0000281)
cytoskeleton-dependent cytokinesis (GO:006

GO Molecular Function 2021

GTPase regulator activity (GO:0030695)
GTPase activator activity (GO:0005096)
kinase binding (GO:0019900)
protein kinase binding (GO:0019901)
microtubule motor activity (GO:0003777)

GO Cellular Component 2021

azurophil granule (GO:0042582)
polymeric cytoskeletal fiber (GO:0099513)
secretory granule membrane (GO:0030667)
vacuolar lumen (GO:0005775)
azurophil granule lumen (GO:0035578)

MGI Mammalian Phenotype Level 4 2021

decreased CD4-positive, alpha beta T cell nu
increased B cell number MP:0005014
abnormal neutrophil physiology MP:000246
abnormal dendritic cell antigen presentation
increased monocyte cell number MP:000022

Human Phenotype Ontology

Splenomegaly (HP:0001744)
Chronic obstructive pulmonary disease (HP:
Obstructive lung disease (HP:0006536)
Abnormality of cells of the lymphoid lineage
Meningitis (HP:0001287)

Jensen TISSUES

Blood
Immune system
Monocyte
Uterus
Thymus

Jensen COMPARTMENTS

B cell receptor complex
Astral microtubule
Midbody
Centralspinidin complex
Vacuole

Jensen DISEASES

Chronic granulomatous disease
Vasculitis
Cancer
Hemorrhagic disease
Arthritis

Activate Windows
Go to Settings to activate Windows.



Type here to search

06:02 ب.م
ENGLISH
107