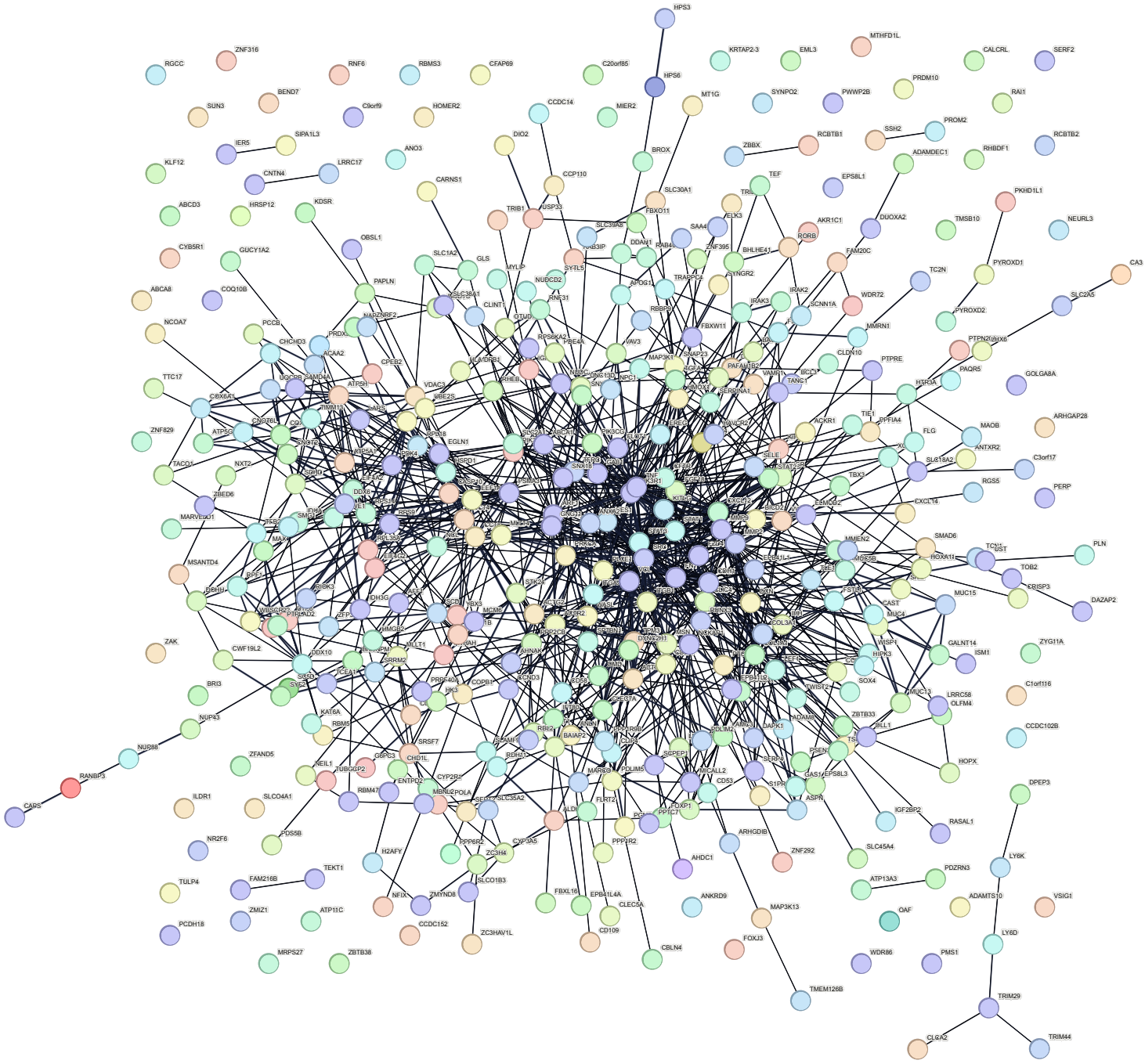
Version: 11.5 LOGIN REGISTER SURVEY



Network Stats

number of nodes: 426
number of edges: 1164
average node degree: 5.46
avg. local clustering coefficient: 0.393
expected number of edges: 945
PPI enrichment p-value: 3.45e-12

Functional enrichments in your network

Biological Process (Gene Ontology)

GO-term	description	count in network	strength	false discovery rate
GO:0036035	Osteoclast development	4 of 7	1.42	0.0057
GO:0001957	Intramembranous ossification	3 of 6	1.36	0.0401
GO:0030316	Osteoclast differentiation	8 of 42	0.94	0.0015
GO:0003413	Chondrocyte differentiation involved in endochondral bone ...	5 of 30	0.88	0.0437
GO:0060351	Cartilage development involved in endochondral bone morp...	7 of 43	0.87	0.0075

(more ...)

Molecular Function (Gene Ontology)

GO-term	description	count in network	strength	false discovery rate
GO:0002020	Protease binding	12 of 138	0.6	0.0330
GO:0005178	Integrin binding	12 of 147	0.57	0.0469
GO:0045296	Cadherin binding	25 of 334	0.54	0.00026
GO:0050839	Cell adhesion molecule binding	38 of 538	0.51	2.50e-06
GO:0003779	Actin binding	24 of 438	0.4	0.0244

(more ...)

Cellular Component (Gene Ontology)

GO-term	description	count in network	strength	false discovery rate
GO:0043034	Costamere	4 of 19	0.99	0.0292
GO:0031941	Filamentous actin	6 of 36	0.88	0.0069
GO:0044291	Cell-cell contact zone	10 of 72	0.8	0.00052
GO:0014704	Intercalated disc	7 of 51	0.8	0.0063
GO:0030864	Cortical actin cytoskeleton	9 of 68	0.78	0.0017

(more ...)

Reference publications (PubMed)

publication	(year) title	count in network	strength	false discovery rate
PMID:24228106	(2013) Cyclosporin A enhances the ability of trophoblasts to...	5 of 6	1.58	0.0446
PMID:21998672	(2011) Insights into the complex formed by matrix metallop...	5 of 6	1.58	0.0446
PMID:25218161	(2014) Astragaloside IV inhibits migration and invasion in h...	6 of 9	1.49	0.0400
PMID:19778905	(2007) A short guide to hereditary diffuse gastric cancer	6 of 9	1.49	0.0400

PMID:26097506	(2015) Testing multiple hypotheses through IMP weighted F...	6 of 10	1.44	0.0400

(more ...)

KEGG Pathways

pathway	*description*	*count in network*	*strength*	*false discovery rate*
hsa05100	Bacterial invasion of epithelial cells	10 of 70	0.82	0.0013
hsa04520	Adherens junction	8 of 67	0.74	0.0072
hsa04933	AGE-RAGE signaling pathway in diabetic complications	11 of 98	0.71	0.0024
hsa04670	Leukocyte transendothelial migration	11 of 109	0.67	0.0039
hsa05205	Proteoglycans in cancer	19 of 196	0.65	6.44e-05

(more ...)

Reactome Pathways

pathway	*description*	*count in network*	*strength*	*false discovery rate*
HSA-430116	GP1b-IX-V activation signalling	4 of 12	1.18	0.0298
HSA-180292	GAB1 signalosome	5 of 17	1.13	0.0165
HSA-3000170	Syndecan interactions	7 of 27	1.08	0.0027
HSA-9670439	Signaling by phosphorylated juxtamembrane, extracellular a...	5 of 20	1.06	0.0232
HSA-5083636	Defective GALNT12 causes colorectal cancer 1 (CRCS1)	4 of 16	1.06	0.0469

(more ...)

WikiPathways

pathway	*description*	*count in network*	*strength*	*false discovery rate*
WP4495	IL-10 anti-inflammatory signaling pathway	4 of 12	1.18	0.0341
WP3287	Overview of nanoparticle effects	4 of 19	0.99	0.0443
WP4564	Neural crest cell migration during development	7 of 39	0.92	0.0145
WP3972	PDGFR-beta pathway	5 of 29	0.9	0.0392
WP4565	Neural crest cell migration in cancer	7 of 42	0.88	0.0145

(more ...)

Tissue expression (TISSUES)

tissue	*description*	*count in network*	*strength*	*false discovery rate*
BTO:0000020	Abdomen	10 of 90	0.71	0.0019
BTO:0001703	Right atrium	6 of 54	0.71	0.0435
BTO:0001049	Pharynx	7 of 68	0.67	0.0287
BTO:0001356	Tendon	9 of 97	0.63	0.0122
BTO:0000140	Bone	12 of 138	0.6	0.0029

(more ...)

Subcellular localization (COMPARTMENTS)

compartment	*description*	*count in network*	*strength*	*false discovery rate*
GOCC:0043034	Costamere	4 of 13	1.15	0.0191
GOCC:0031941	Filamentous actin	4 of 19	0.99	0.0431
GOCC:0030864	Cortical actin cytoskeleton	8 of 46	0.9	0.0013
GOCC:0044291	Cell-cell contact zone	6 of 43	0.81	0.0240
GOCC:0030863	Cortical cytoskeleton	9 of 71	0.77	0.0034

(more ...)

Human Phenotype (Monarch)

phenotype	*description*	*count in network*	*strength*	*false discovery rate*
EFO:0009775	Threonine measurement	4 of 9	1.31	0.0141
HP:0001073	Cigarette-paper scars	4 of 10	1.26	0.0174
EFO:0008184	Interleukin 4 measurement	4 of 16	1.06	0.0428
HP:0006979	Sleep-wake cycle disturbance	5 of 28	0.91	0.0376
HP:0010051	Deviation of the hallux	6 of 40	0.84	0.0279

(more ...)

Annotated Keywords (UniProt)

keyword	*description*	*count in network*	*strength*	*false discovery rate*
KW-0272	Extracellular matrix	17 of 265	0.47	0.0121
KW-0130	Cell adhesion	24 of 474	0.37	0.0160
KW-0206	Cytoskeleton	53 of 1215	0.3	0.00042
KW-0007	Acetylation	117 of 3341	0.21	2.92e-05
KW-0832	Ubl conjugation	78 of 2383	0.18	0.0160

(more ...)

Statistical background

For the above enrichment analysis, the following statistical background is assumed: Whole Genome | ADD BACKGROUND | UPDATE

Save / Export

Biological Process (Gene Ontology)	download	*242 GO-terms significantly enriched; file-format: tab-delimited*
Molecular Function (Gene Ontology)	download	*11 GO-terms significantly enriched; file-format: tab-delimited*
Cellular Component (Gene Ontology)	download	*69 GO-terms significantly enriched; file-format: tab-delimited*
Reference publications (PubMed)	download	*199 publications significantly enriched; file-format: tab-delimited*
KEGG Pathways	download	*15 pathways significantly enriched; file-format: tab-delimited*
Reactome Pathways	download	*41 pathways significantly enriched; file-format: tab-delimited*
WikiPathways	download	*25 pathways significantly enriched; file-format: tab-delimited*
Tissue expression (TISSUES)	download	*71 tissues significantly enriched; file-format: tab-delimited*
Subcellular localization (COMPARTMENTS)	download	*63 compartments significantly enriched; file-format: tab-delimited*
Human Phenotype (Monarch)	download	*179 phenotypes significantly enriched; file-format: tab-delimited*
Annotated Keywords (UniProt)	download	*9 keywords significantly enriched; file-format: tab-delimited*
All enriched terms (without PubMed)	download	*725 enriched terms in 10 categories; file-format: tab-delimited*
Selected terms only	download	*no enriched terms selected (click on any term above to select)*

Table display settings

Row Visibility: Display only selected rows | UPDATE

There were no significant pathway annotations observed in the following categories:
Lowest reference subset (STRING): Brenda tissue enhanced, Compartments Experimental, Disease Binknowledge, and Reactome Pathways Domains (183448).

Server load: low (28%) [?]

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SIB - Swiss Institute of Bioinformatics

CPR - Novo Nordisk Foundation Center Protein Research

EMBL - European Molecular Biology Laboratory

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STRING is part of the ELIXIR infrastructure: it is one of ELIXIR's Core Data Resources.