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WFDC2

WFDC1

CRISPLD2

BHMT2

BEX1

TCEAL2

PENK

PRIM

ZN   NDNF

RUNDC3B

ZNF655

PPP1R1A

SLC2A5

ATRNL1

TSHZ3

HMGCLL1

OAT

RGN

AMT

ASPA

Network Stats

number of nodes: 444	expected number of edges: 378
number of edges: 868	PPI enrichment p-value: < 1.0e-16
average node degree: 3.91	*your network has significantly more interactions*
avg. local clustering coefficient: 0.318	*than expected (what does that mean?)*

Functional enrichments in your network

explain columns

Biological Process (Gene Ontology)

GO-term	description	count in network	strength	false discovery rate
GO:0070458	Cellular detoxification of nitrogen compound	3 of 3	1.64	0.0160
GO:0018916	Nitrobenzene metabolic process	3 of 4	1.52	0.0231
GO:0060426	Lung vasculature development	3 of 6	1.34	0.0406
GO:0048251	Elastic fiber assembly	4 of 9	1.29	0.0128
GO:0031581	Hemidesmosome assembly	4 of 12	1.17	0.0231

(more ...)

Molecular Function (Gene Ontology)

GO-term	description	count in network	strength	false discovery rate
GO:0004364	Glutathione transferase activity	6 of 22	1.08	0.0078
GO:0004602	Glutathione peroxidase activity	5 of 20	1.04	0.0313
GO:0005201	Extracellular matrix structural constituent	14 of 119	0.71	0.00073
GO:0008201	Heparin binding	19 of 172	0.69	4.45e-05
GO:0019199	Transmembrane receptor protein kinase activity	9 of 81	0.69	0.0295

(more ...)

Cellular Component (Gene Ontology)

GO-term	description	count in network	strength	false discovery rate
GO:0090533	Cation-transporting atpase complex	5 of 19	1.06	0.0074
GO:0043034	Costamere	4 of 19	0.97	0.0486
GO:0014704	Intercalated disc	7 of 51	0.78	0.0128
GO:0030315	T-tubule	7 of 54	0.76	0.0169
GO:0042383	Sarcolemma	17 of 132	0.75	1.25e-05

(more ...)

Reference publications (PubMed)

publication	(year) title	count in network	strength	false discovery rate
PMID:32858538	(2021) Best Practice (Efficient) Immunohistologic Panel for ...	5 of 5	1.64	0.0495
PMID:23621580	(2013) Identification of new genes downregulated in prostat...	5 of 5	1.64	0.0495
PMID:23528302	(2013) Folate-receptor 1 (FOLR1) protein is elevated in the s...	5 of 5	1.64	0.0495
PMID:27597880	(2016) Functional networks inference from rule-based mach...	9 of 14	1.45	0.00049
PMID:30712971	(2019) Impact of Immune and Stromal Infiltration on Outco...	6 of 10	1.42	0.0401

(more ...)

Local network cluster (STRING)

cluster	description	count in network	strength	false discovery rate
CL:13066	Glutathione derivative metabolic process, and byssinosis	6 of 22	1.08	0.0261
CL:17920	Mixed, incl. annexin, and plasma membrane repair	7 of 26	1.07	0.0074
CL:25041	Mixed, incl. sparc/testican, calcium-binding domain, and olf...	8 of 52	0.83	0.0389
CL:16430	Collagen formation, and Matrix metalloproteinases	14 of 129	0.68	0.0057
CL:16429	Collagen formation, and Defective B3GALTL causes Peters-...	18 of 168	0.67	0.00085

KEGG Pathways

pathway	description	count in network	strength	false discovery rate
hsa00480	Glutathione metabolism	9 of 53	0.87	0.0014
hsa04350	TGF-beta signaling pathway	12 of 91	0.76	0.0010
hsa00982	Drug metabolism - cytochrome P450	8 of 64	0.74	0.0214
hsa05204	Chemical carcinogenesis	8 of 75	0.67	0.0319
hsa00980	Metabolism of xenobiotics by cytochrome P450	7 of 69	0.65	0.0407

(more ...)

Reactome Pathways

pathway	description	count in network	strength	false discovery rate
HSA-2129379	Molecules associated with elastic fibres	7 of 38	0.91	0.0300
HSA-1566948	Elastic fibre formation	8 of 45	0.89	0.0201
HSA-1474244	Extracellular matrix organization	25 of 301	0.56	0.00018
HSA-397014	Muscle contraction	16 of 193	0.56	0.0201

WikiPathways

pathway	description	count in network	strength	false discovery rate
WP98	Prostaglandin synthesis and regulation	8 of 45	0.89	0.0035
WP2840	Hair follicle development: cytodifferentiation - part 3 of 3	11 of 88	0.74	0.0028
WP2880	Glucocorticoid receptor pathway	8 of 70	0.7	0.0451
WP702	Metapathway biotransformation Phase I and II	16 of 180	0.59	0.0028
WP2882	Nuclear receptors meta-pathway	23 of 316	0.51	0.0016

(more ...)

Disease-gene associations (DISEASES)

disease	description	count in network	strength	false discovery rate
DOID:0050155	Sensory system disease	41 of 887	0.31	0.0499
DOID:7	Disease of anatomical entity	144 of 4452	0.15	0.0110

Permalink

Tissue expression (TISSUES)

	description	count in network	strength	false discovery rate
BTO:0003969	Hair follicle outer root sheath	3 of 3	1.64	0.0157
BTO:0002309	Myoepithelial cell	3 of 4	1.52	0.0218
BTO:0000554	Hair follicle	7 of 40	0.89	0.0078
BTO:0001702	Atrium	8 of 61	0.76	0.0228
BTO:0000903	Atrium	9 of 74	0.73	0.0093
				(more ...)

Subcellular localization (COMPARTMENTS)

compartment	description	count in network	strength	false discovery rate
GOCC:0090533	Cation-transporting atpase complex	5 of 15	1.17	0.0057
GOCC:0043034	Costamere	4 of 13	1.13	0.0275
GOCC:0045095	Keratin filament	4 of 16	1.04	0.0462
GOCC:0014704	Intercalated disc	5 of 29	0.88	0.0462
GOCC:0030018	Z disc	10 of 60	0.87	0.00049
				(more ...)

STRING is a Core Data Resource as designated by Global Biodata Coalition and ELIXIR.

Human Phenotype (Monarch)

phenotype	description	count in network	strength	false discovery rate
HP:0003555	Muscle fiber splitting	5 of 15	1.17	0.0227
HP:0030196	Fatigable weakness of respiratory muscles	8 of 49	0.86	0.0184
HP:0100266	Synostosis of carpals/tarsals	7 of 44	0.85	0.0337
HP:0001437	Abnormality of the musculature of the lower limbs	8 of 55	0.81	0.0243
HP:0003557	Increased variability in muscle fiber diameter	8 of 61	0.76	0.0368
				(more ...)

Annotated Keywords (UniProt)

keyword	description	count in network	strength	false discovery rate
KW-1060	Myofibrillar myopathy	3 of 7	1.28	0.0459
KW-0263	Epidermolysis bullosa	4 of 16	1.04	0.0369
KW-0084	Basement membrane	6 of 39	0.83	0.0203
KW-0403	Intermediate filament	11 of 75	0.81	0.00030
KW-0440	LIM domain	9 of 69	0.76	0.0038
				(more ...)

Protein Domains (Pfam)

domain	description	count in network	strength	false discovery rate
PF02798	Glutathione S-transferase, N-terminal domain	6 of 19	1.14	0.0165
PF00038	Intermediate filament protein	11 of 72	0.83	0.0075
PF00412	LIM domain	10 of 69	0.81	0.0165

Protein Domains and Features (InterPro)

domain	description	count in network	strength	false discovery rate
IPR026052	DNA-binding protein inhibitor	4 of 4	1.64	0.0211
IPR003081	Glutathione S-transferase, Mu class	4 of 5	1.55	0.0293
IPR040079	Glutathione Transferase family	7 of 27	1.06	0.0137
IPR004045	Glutathione S-transferase, N-terminal	6 of 24	1.04	0.0307
IPR026823	Complement Clr-like EGF domain	6 of 26	1.01	0.0334
				(more ...)

Protein Domains (SMART)

domain	description	count in network	strength	false discovery rate
SM01391	Intermediate filament protein	9 of 67	0.77	0.0214
SM00181	Epidermal growth factor-like domain.	16 of 201	0.55	0.0214

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	258 GO-terms significantly enriched; file-format: tab-delimited
Molecular Function (Gene Ontology)	download	19 GO-terms significantly enriched; file-format: tab-delimited
Cellular Component (Gene Ontology)	download	48 GO-terms significantly enriched; file-format: tab-delimited
Reference publications (PubMed)	download	108 publications significantly enriched; file-format: tab-delimited
Local network cluster (STRING)	download	5 clusters significantly enriched; file-format: tab-delimited
KEGG Pathways	download	13 pathways significantly enriched; file-format: tab-delimited
Reactome Pathways	download	4 pathways significantly enriched; file-format: tab-delimited
WikiPathways	download	6 pathways significantly enriched; file-format: tab-delimited
Disease-gene associations (DISEASES)	download	2 diseases significantly enriched; file-format: tab-delimited
Tissue expression (TISSUES)	download	33 tissues significantly enriched; file-format: tab-delimited
Subcellular localization (COMPARTMENTS)	download	42 compartments significantly enriched; file-format: tab-delimited
Human Phenotype (Monarch)	download	32 phenotypes significantly enriched; file-format: tab-delimited
Annotated Keywords (UniProt)	download	22 keywords significantly enriched; file-format: tab-delimited
Protein Domains (Pfam)	download	3 domains significantly enriched; file-format: tab-delimited
Protein Domains and Features (InterPro)	download	14 domains significantly enriched; file-format: tab-delimited
Protein Domains (SMART)	download	2 domains significantly enriched; file-format: tab-delimited
All enriched terms (without PubMed)	download	503 enriched terms in 15 categories; file-format: tab-delimited
Selected terms only	download	no enriched terms selected (click on any term above to select)

Table display settings

Table display settings

Row Visibility: Display only selected rows   UPDATE