



Network Stats

number of nodes: 16	expected number of edges: 5
number of edges: 30	PPI enrichment p-value: 3.1e-14
average node degree: 3.75	<i>your network has significantly more interactions than expected (what does that mean?)</i>
avg. local clustering coefficient: 0.594	

Functional enrichments in your network

[explain columns](#)

Biological Process (Gene Ontology)				
<i>GO-term</i>	<i>description</i>	<i>count in network</i>	<i>strength</i>	<i>false discovery rate</i>
GO:0042297	Vocal learning	3 of 6	2.79	0.00019
GO:0086029	Purkinje myocyte to ventricular cardiac muscle cell signaling	2 of 5	2.69	0.0044
GO:0050957	Equilibrioception	2 of 7	2.55	0.0064
GO:0033275	Actin-myosin filament sliding	3 of 13	2.45	0.00035
GO:0097105	Presynaptic membrane assembly	2 of 10	2.39	0.0102
(more ...)				

Molecular Function (Gene Ontology)				
<i>GO-term</i>	<i>description</i>	<i>count in network</i>	<i>strength</i>	<i>false discovery rate</i>
GO:0000146	Microfilament motor activity	3 of 37	2.0	0.0105
GO:0005509	Calcium ion binding	8 of 717	1.14	0.00016

Cellular Component (Gene Ontology)				
<i>GO-term</i>	<i>description</i>	<i>count in network</i>	<i>strength</i>	<i>false discovery rate</i>
GO:0033018	Sarcoplasmic reticulum lumen	2 of 10	2.39	0.0092
GO:0014701	Junctional sarcoplasmic reticulum membrane	2 of 10	2.39	0.0092
GO:0005859	Muscle myosin complex	2 of 15	2.22	0.0122
GO:0060077	Inhibitory synapse	2 of 21	2.07	0.0186
GO:0044295	Axonal growth cone	2 of 25	1.99	0.0231
(more ...)				

Reference publications (PubMed)				
<i>publication</i>	<i>(year) title</i>	<i>count in network</i>	<i>strength</i>	<i>false discovery rate</i>
PMID:34162222	(2021) Functional Calsequestrin-1 Is Expressed in the Heart ...	3 of 3	3.09	0.0018
PMID:22396703	(2012) Catecholaminergic polymorphic ventricular tachycar...	3 of 3	3.09	0.0018
PMID:20713040	(2010) Potential adverse interaction of human cardiac calse...	3 of 3	3.09	0.0018
PMID:20161689	(2010) The Genetic Basis of Thought Disorder and Languag...	3 of 3	3.09	0.0018
PMID:38253398	(2024) ent-Verticilide B1 Inhibits Type 2 Ryanodine Receptor...	2 of 2	3.09	0.0333
(more ...)				

Local network cluster (STRING)				
<i>cluster</i>	<i>description</i>	<i>count in network</i>	<i>strength</i>	<i>false discovery rate</i>
CL:24822	Autosomal recessive nonsyndromic deafness 23	2 of 5	2.69	0.0066
CL:22631	Muscle myosin complex	2 of 6	2.61	0.0072
CL:22730	Junctional sarcoplasmic reticulum membrane, and Terminal...	3 of 14	2.42	0.00023
CL:22988	Vocalization behavior	2 of 10	2.39	0.0133
CL:22576	Striated muscle contraction pathway, and Myosin II complex	3 of 44	1.92	0.0040
(more ...)				

KEGG Pathways				
<i>pathway</i>	<i>description</i>	<i>count in network</i>	<i>strength</i>	<i>false discovery rate</i>
hsa04260	Cardiac muscle contraction	3 of 87	1.63	0.0083
hsa04514	Cell adhesion molecules	3 of 138	1.43	0.0210
hsa04020	Calcium signaling pathway	4 of 191	1.41	0.0052
hsa04261	Adrenergic signaling in cardiomyocytes	3 of 146	1.4	0.0210

Reactome Pathways				
<i>pathway</i>	<i>description</i>	<i>count in network</i>	<i>strength</i>	<i>false discovery rate</i>
HSA-5578775	Ion homeostasis	3 of 54	1.84	0.0143
HSA-9662360	Sensory processing of sound by inner hair cells of the cochl...	3 of 68	1.73	0.0184
HSA-2672351	Stimuli-sensing channels	3 of 106	1.54	0.0399
HSA-397014	Muscle contraction	5 of 203	1.48	0.0011

WikiPathways				
<i>pathway</i>	<i>description</i>	<i>count in network</i>	<i>strength</i>	<i>false discovery rate</i>
WP4875	Disruption of postsynaptic signaling by CNV	3 of 33	2.05	0.0024

Disease-gene associations (DISEASES)				
<i>disease</i>	<i>description</i>	<i>count in network</i>	<i>strength</i>	<i>false discovery rate</i>
DOID:0111275	Speech-language disorder-1	2 of 3	2.91	0.0142
DOID:0110831	Usher syndrome type 1D	2 of 3	2.91	0.0142
DOID:0090130	Cortical dysplasia-focal epilepsy syndrome	2 of 3	2.91	0.0142
DOID:0110481	Autosomal recessive nonsyndromic deafness 23	2 of 4	2.79	0.0142
DOID:0110467	Autosomal recessive nonsyndromic deafness 12	2 of 4	2.79	0.0142
(more ...)				

Tissue expression (TISSUES)				
<i>tissue</i>	<i>description</i>	<i>count in network</i>	<i>strength</i>	<i>false discovery rate</i>
BTO:0005824	Vestibular hair cell	2 of 5	2.69	0.0026
BTO:0005823	Hair-cell stereocilium	2 of 5	2.69	0.0026
BTO:0003667	Inner hair cell	2 of 5	2.69	0.0026
BTO:0005822	Cochlear hair cell	2 of 6	2.61	0.0026
BTO:0003666	Outer hair cell	2 of 6	2.61	0.0026
(more ...)				

Subcellular localization (COMPARTMENTS)				
<i>compartment</i>	<i>description</i>	<i>count in network</i>	<i>strength</i>	<i>false discovery rate</i>
GOCC:0033018	Sarcoplasmic reticulum lumen	2 of 7	2.55	0.0046
GOCC:0014701	Junctional sarcoplasmic reticulum membrane	2 of 9	2.44	0.0065
GOCC:0060077	Inhibitory synapse	2 of 15	2.22	0.0137
GOCC:0005859	Muscle myosin complex	2 of 15	2.22	0.0137
GOCC:0098982	GABA-ergic synapse	2 of 21	2.07	0.0222
(more ...)				

Human Phenotype (Monarch)				
<i>phenotype</i>	<i>description</i>	<i>count in network</i>	<i>strength</i>	<i>false discovery rate</i>
EFO:0007864	Sulfate measurement	2 of 4	2.79	0.0188
EFO:0009885	Frailty measurement	2 of 8	2.49	0.0483
HP:0002321	Vertigo	3 of 74	1.7	0.0483
HP:0001751	Vestibular dysfunction	4 of 101	1.69	0.0040
EFO:0008579	Risk-taking behaviour	5 of 223	1.44	0.0032
(more ...)				

Annotated Keywords (UniProt)				
<i>keyword</i>	<i>description</i>	<i>count in network</i>	<i>strength</i>	<i>false discovery rate</i>
KW-0836	Usher syndrome	2 of 12	2.31	0.0063
KW-0514	Muscle protein	5 of 64	1.98	1.29e-06
KW-1269	Autism	2 of 26	1.98	0.0172
KW-1009	Hearing	3 of 43	1.93	0.0015
KW-0703	Sarcoplasmic reticulum	3 of 48	1.89	0.0015
(more ...)				

Protein Domains and Features (InterPro)				
<i>domain</i>	<i>description</i>	<i>count in network</i>	<i>strength</i>	<i>false discovery rate</i>
IPR041860	Calsequestrin, C-terminal TRX-fold domain	2 of 2	3.09	0.0266
IPR041859	Calsequestrin, N-terminal TRX-fold domain	2 of 2	3.09	0.0266
IPR041858	Calsequestrin, middle TRX-fold domain	2 of 2	3.09	0.0266
IPR018233	Calsequestrin, conserved site	2 of 2	3.09	0.0266
IPR001393	Calsequestrin	2 of 2	3.09	0.0266

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	70 GO-terms significantly enriched; file-format: tab-delimited
Molecular Function (Gene Ontology)	download	2 GO-terms significantly enriched; file-format: tab-delimited
Cellular Component (Gene Ontology)	download	24 GO-terms significantly enriched; file-format: tab-delimited
Reference publications (PubMed)	download	851 publications significantly enriched; file-format: tab-delimited
Local network cluster (STRING)	download	6 clusters significantly enriched; file-format: tab-delimited
KEGG Pathways	download	4 pathways significantly enriched; file-format: tab-delimited
Reactome Pathways	download	4 pathways significantly enriched; file-format: tab-delimited
WikiPathways	download	one single pathway is enriched; file-format: tab-delimited
Disease-gene associations (DISEASES)	download	16 diseases significantly enriched; file-format: tab-delimited

Tissue expression (TISSUES)	download	18 tissues significantly enriched; file-format: tab-delimited
Subcellular localization (COMPARTMENTS)	download	17 compartments significantly enriched; file-format: tab-delimited
Human Phenotype (Monarch)	download	8 phenotypes significantly enriched; file-format: tab-delimited
Annotated Keywords (UniProt)	download	12 keywords significantly enriched; file-format: tab-delimited
Protein Domains and Features (InterPro)	download	5 domains significantly enriched; file-format: tab-delimited
All enriched terms (without PubMed)	download	187 enriched terms in 13 categories; file-format: tab-delimited
Selected terms only	download	no enriched terms selected (click on any term above to select)

Table display settings

Maximum FDR shown:

FDR <= 0.05

UPDATE

Minimum strength shown:

strength >= 0.01

Minimum count in network:

2

Row Visibility:

Display only selected rows

There were **no** significant pathway enrichments observed in the following categories:
Protein Domains (Pfam), Protein Domains (SMART).

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	References	Use scenarios	APIs	Datasources
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STRING is a Core Data Resource as designated by Global Biodata Coalition and ELIXIR.