

Component GO terms

#term ID	term description	observed gene count	background gene count
GO:0031252	cell leading edge	8	371
GO:0030027	lamellipodium	6	185
GO:0030175	filopodium	5	96
GO:0005856	cytoskeleton	12	2068
GO:0043232	intracellular non-membrane-bounded organelle	14	4005
GO:0120025	plasma membrane bounded cell projection	10	1900
GO:0005925	focal adhesion	4	134
GO:0001726	ruffle	4	164
GO:0097433	dense body	2	6
GO:0031209	SCAR complex	2	8
GO:0005884	actin filament	3	67
GO:0005829	cytosol	14	4958
GO:0015629	actin cytoskeleton	5	432
GO:0031941	filamentous actin	2	16
GO:0031258	lamellipodium membrane	2	22
GO:0045335	phagocytic vesicle	3	122
GO:0060076	excitatory synapse	2	29
GO:0031256	leading edge membrane	3	150
GO:0099568	cytoplasmic region	4	402
GO:0031410	cytoplasmic vesicle	8	2226
GO:0045202	synapse	5	849
GO:0005938	cell cortex	3	230
GO:0120038	plasma membrane bounded cell projection part	6	1316
GO:0030054	cell junction	5	1006
GO:0031253	cell projection membrane	3	317
GO:0098590	plasma membrane region	5	1061
GO:0099513	polymeric cytoskeletal fiber	4	645
GO:0044456	synapse part	4	705
GO:0098793	presynapse	3	354
GO:0044306	neuron projection terminus	2	115
GO:0043197	dendritic spine	2	143
GO:0030141	secretory granule	4	828
GO:0071944	cell periphery	11	5254
GO:0098794	postsynapse	3	435

Function GO terms

#term ID	term description	observed gene count	background gene count
GO:0008092	cytoskeletal protein binding	11	882
GO:0005522	profilin binding	4	10
GO:0003779	actin binding	8	413
GO:0017048	Rho GTPase binding	5	162
GO:0070064	proline-rich region binding	2	20
GO:0017124	SH3 domain binding	3	125
GO:0019904	protein domain specific binding	5	706

GO:0030554	adenyl nucleotide binding	7	1524
GO:0019899	enzyme binding	8	2197
GO:0048365	Rac GTPase binding	2	60
GO:0005524	ATP binding	6	1462
GO:0005200	structural constituent of cytoskeleton	2	106
GO:0005515	protein binding	13	6605

Process GO terms

#term ID	term description	observed gene count	background gene count
GO:0030036	actin cytoskeleton organization	10	418
GO:0030838	positive regulation of actin filament polymerization	6	81
GO:0031334	positive regulation of protein complex assembly	7	241
GO:0038096	Fc-gamma receptor signaling pathway involved in phagocytosis	5	73
GO:0007015	actin filament organization	6	200
GO:0097435	supramolecular fiber organization	7	383
GO:0051493	regulation of cytoskeleton organization	7	477
GO:1900027	regulation of ruffle assembly	3	27
GO:0032989	cellular component morphogenesis	7	720
GO:0008154	actin polymerization or depolymerization	3	43
GO:0008360	regulation of cell shape	4	143
GO:0016043	cellular component organization	15	5163
GO:0120032	regulation of plasma membrane bounded cell projection assembly	4	163
GO:0007409	axonogenesis	5	346
GO:0002252	immune effector process	7	927
GO:2000601	positive regulation of Arp2/3 complex-mediated actin nucleation	2	7
GO:0048010	vascular endothelial growth factor receptor signaling pathway	3	67
GO:0048468	cell development	8	1493
GO:1900029	positive regulation of ruffle assembly	2	13
GO:0120034	positive regulation of plasma membrane bounded cell projection assembly	3	93
GO:0007169	transmembrane receptor protein tyrosine kinase signaling pathway	5	499
GO:0006897	endocytosis	5	510
GO:0016601	Rac protein signal transduction	2	20
GO:0051128	regulation of cellular component organization	9	2306
GO:0022607	cellular component assembly	9	2343
GO:0120035	regulation of plasma membrane bounded cell projection organization	5	600
GO:0034329	cell junction assembly	3	135
GO:0031346	positive regulation of cell projection organization	4	343
GO:0009653	anatomical structure morphogenesis	8	1992
GO:0050808	synapse organization	3	189
GO:0016192	vesicle-mediated transport	7	1699

GO:0007411	axon guidance	3	220
GO:0042221	response to chemical	11	4153
GO:0071417	cellular response to organonitrogen compound	4	485
GO:0099173	postsynapse organization	2	54
GO:0030239	myofibril assembly	2	59
GO:0010243	response to organonitrogen compound	5	876
GO:0032233	positive regulation of actin filament bundle assembly	2	60
GO:0002376	immune system process	8	2370
GO:1900006	positive regulation of dendrite development	2	65
GO:0006928	movement of cell or subcellular component	6	1355
GO:0022603	regulation of anatomical structure morphogenesis	5	961
GO:0051289	protein homotetramerization	2	78
GO:0051492	regulation of stress fiber assembly	2	78
GO:0048013	ephrin receptor signaling pathway	2	79
GO:0001843	neural tube closure	2	86
GO:0051260	protein homooligomerization	3	312
GO:0007166	cell surface receptor signaling pathway	7	2198
GO:0007399	nervous system development	7	2206
GO:0010033	response to organic substance	8	2815
GO:0030154	cell differentiation	9	3457
GO:0040011	locomotion	5	1144
GO:0071310	cellular response to organic substance	7	2219
GO:0061024	membrane organization	4	729

false discovery rate matching proteins in your network (IDs)

5.93E-07 ENSP00000245932,ENSP00000290378,ENS
3.80E-06 ENSP00000245932,ENSP00000290378,ENS
4.17E-06 ENSP00000245932,ENSP00000290378,ENS
1.16E-05 ENSP00000225655,ENSP00000245932,ENS
0.0002 ENSP00000225655,ENSP00000245932,ENS
0.00024 ENSP00000245932,ENSP00000290378,ENS
0.00028 ENSP00000245932,ENSP00000355809,ENS
0.00043 ENSP00000316338,ENSP00000354251,ENS
0.00043 ENSP00000349960,ENSP00000458162
0.00065 ENSP00000354251,ENSP00000481038
0.00069 ENSP00000290378,ENSP00000354251,ENS
0.00095 ENSP00000225655,ENSP00000245932,ENS
0.00095 ENSP00000245932,ENSP00000290378,ENS
0.0016 ENSP00000354251,ENSP00000458162
0.0027 ENSP00000245932,ENSP00000354251
0.0027 ENSP00000329219,ENSP00000376652,ENS
0.0041 ENSP00000316338,ENSP00000481038
0.0045 ENSP00000245932,ENSP00000354251,ENS
0.0063 ENSP00000225655,ENSP00000316338,ENS
0.0108 ENSP00000316338,ENSP00000321348,ENS
0.0121 ENSP00000316338,ENSP00000349960,ENS
0.0125 ENSP00000225655,ENSP00000329219,ENS
0.0131 ENSP00000245932,ENSP00000316338,ENS
0.021 ENSP00000245932,ENSP00000355809,ENS
0.0252 ENSP00000245932,ENSP00000354251,ENS
0.0252 ENSP00000245932,ENSP00000316338,ENS
0.0252 ENSP00000290378,ENSP00000316338,ENS
0.0318 ENSP00000316338,ENSP00000349960,ENS
0.0318 ENSP00000316338,ENSP00000349960,ENS
0.0335 ENSP00000316338,ENSP00000481038
0.0494 ENSP00000316338,ENSP00000481038
0.0495 ENSP00000316338,ENSP00000351777,ENS
0.0495 ENSP00000225655,ENSP00000245932,ENS
0.0495 ENSP00000316338,ENSP00000417901,ENS

false discovery rate matching proteins in your network (IDs)

4.13E-08 ENSP00000225655,ENSP00000245932,ENS
5.19E-08 ENSP00000245932,ENSP00000329219,ENS
2.42E-07 ENSP00000225655,ENSP00000245932,ENS
2.07E-05 ENSP00000225655,ENSP00000321348,ENS
0.0038 ENSP00000225655,ENSP00000316338
0.0044 ENSP00000245932,ENSP00000355809,ENS
0.0082 ENSP00000245932,ENSP00000316338,ENS

0.0082 ENSP00000225655,ENSP00000290378,ENS
0.012 ENSP00000225655,ENSP00000321348,ENS
0.0164 ENSP00000329219,ENSP00000481038
0.0255 ENSP00000290378,ENSP00000349960,ENS
0.0333 ENSP00000349960,ENSP00000458162
0.0411 ENSP00000225655,ENSP00000245932,ENS

false discovery rate matching proteins in your network (IDs)

5.22E-09 ENSP00000225655,ENSP00000245932,ENS

9.07E-08 ENSP00000225655,ENSP00000245932,ENS

7.87E-07 ENSP00000225655,ENSP00000245932,ENS

1.94E-06 ENSP00000316338,ENSP00000349960,ENS

3.07E-06 ENSP00000245932,ENSP00000290378,ENS

4.90E-06 ENSP00000245932,ENSP00000290378,ENS

1.73E-05 ENSP00000225655,ENSP00000245932,ENS

0.00012 ENSP00000225655,ENSP00000376652,ENS

0.00018 ENSP00000245932,ENSP00000290378,ENS

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0.00066 ENSP00000316338,ENSP00000349960,ENS

0.0007 ENSP00000354251,ENSP00000481038

0.00093 ENSP00000316338,ENSP00000354251,ENS

0.0015 ENSP00000245932,ENSP00000290378,ENS

0.0017 ENSP00000225655,ENSP00000481038

0.002 ENSP00000225655,ENSP00000354251,ENS

0.0021 ENSP00000316338,ENSP00000349960,ENS

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0.0032 ENSP00000354251,ENSP00000481038

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0.005 ENSP00000225655,ENSP00000316338,ENS

0.0075 ENSP00000225655,ENSP00000245932,ENS

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0.0444 ENSP00000245932,ENSP00000329219,ENS
0.0449 ENSP00000316338,ENSP00000349960,ENS
0.0467 ENSP00000316338,ENSP00000349960,ENS

matching proteins in your network (labels)

ACTC1,BAIAP2,CYFIP1,DIAPH1,ENAH,EVL,NCKAP1,VASP
ACTC1,CYFIP1,ENAH,EVL,NCKAP1,VASP
ACTC1,BAIAP2,CYFIP1,ENAH,VASP
ACTB,ACTBL2,ACTC1,ACTG1,BAIAP2,DIAPH1,ENAH,EVL,GPHN,NCKAP1,PFN1,VASP
ACTB,ACTBL2,ACTC1,ACTG1,BAIAP2,DIAPH1,DIAPH2,ENAH,EVL,GPHN,NCKAP1,PFN1,VASP,VCP
ACTC1,BAIAP2,CYFIP1,DIAPH1,ENAH,EVL,FMNL1,GPHN,NCKAP1,VASP
ACTG1,ENAH,EVL,VASP
BAIAP2,CYFIP1,DIAPH1,NCKAP1
ACTB,ACTG1
CYFIP1,NCKAP1
ACTC1,ACTG1,NCKAP1
ACTB,ACTC1,ACTG1,BAIAP2,CYFIP1,DIAPH1,DIAPH2,ENAH,EVL,FMNL1,NCKAP1,PFN1,VASP,VCP
ACTB,ACTC1,ACTG1,NCKAP1,VASP
ACTG1,NCKAP1
NCKAP1,VASP
ACTG1,EVL,FMNL1
BAIAP2,CYFIP1
DIAPH1,NCKAP1,VASP
BAIAP2,FMNL1,PFN1,POTEF
ACTG1,BAIAP2,CYFIP1,DIAPH1,DIAPH2,EVL,FMNL1,VCP
ACTB,BAIAP2,CYFIP1,ENAH,GPHN
FMNL1,PFN1,POTEF
BAIAP2,CYFIP1,DIAPH1,GPHN,NCKAP1,VASP
ACTG1,ENAH,EVL,GPHN,VASP
DIAPH1,NCKAP1,VASP
BAIAP2,DIAPH1,GPHN,NCKAP1,VASP
ACTC1,ACTG1,BAIAP2,NCKAP1
ACTB,BAIAP2,CYFIP1,GPHN
ACTB,BAIAP2,CYFIP1
BAIAP2,CYFIP1
BAIAP2,CYFIP1
BAIAP2,CYFIP1,DIAPH1,VCP
ACTB,ACTG1,BAIAP2,DIAPH1,ENAH,FMNL1,GPHN,NCKAP1,PFN1,POTEF,VASP
BAIAP2,CYFIP1,GPHN

matching proteins in your network (labels)

ACTB,ACTC1,BAIAP2,CYFIP1,DIAPH1,DIAPH2,ENAH,EVL,FMNL1,PFN1,VASP
ACTG1,EVL,FMNL1,VASP
CYFIP1,DIAPH1,DIAPH2,ENAH,EVL,FMNL1,PFN1,VASP
CYFIP1,DIAPH1,DIAPH2,FMNL1,PFN1
BAIAP2,PFN1
ENAH,EVL,VASP
BAIAP2,ENAH,EVL,VASP,VCP

ACTB,ACTBL2,ACTC1,ACTG1,GPHN,PFN1,VCP
ACTB,ACTG1,CYFIP1,DIAPH1,DIAPH2,FMNL1,PFN1,VCP
CYFIP1,FMNL1
ACTB,ACTBL2,ACTC1,ACTG1,GPHN,VCP
ACTB,ACTG1
ACTB,ACTC1,ACTG1,BAIAP2,CYFIP1,DIAPH1,DIAPH2,ENAH,EVL,FMNL1,PFN1,VASP,VCP

matching proteins in your network (labels)

ACTB,ACTC1,ACTG1,BAIAP2,DIAPH1,DIAPH2,EVL,FMNL1,PFN1,VASP

BAIAP2,CYFIP1,EVL,NCKAP1,PFN1,VASP
BAIAP2,CYFIP1,EVL,NCKAP1,PFN1,VASP,VCP

ACTB,ACTG1,BAIAP2,CYFIP1,NCKAP1
ACTC1,BAIAP2,DIAPH1,DIAPH2,EVL,VASP
ACTC1,ACTG1,BAIAP2,DIAPH1,DIAPH2,EVL,VASP
BAIAP2,CYFIP1,DIAPH1,EVL,NCKAP1,PFN1,VASP
CYFIP1,EVL,PFN1
ACTC1,ACTG1,BAIAP2,CYFIP1,ENAH,EVL,VASP
DIAPH1,EVL,VASP
BAIAP2,CYFIP1,DIAPH1,FMNL1
ACTB,ACTC1,ACTG1,BAIAP2,CYFIP1,DIAPH1,DIAPH2,ENAH,EVL,FMNL1,GPHN,NCKAP1,PFN1,VASP,VCP

CYFIP1,EVL,NCKAP1,PFN1
BAIAP2,CYFIP1,ENAH,EVL,VASP
ACTB,ACTG1,BAIAP2,CYFIP1,DIAPH1,NCKAP1,VCP

CYFIP1,NCKAP1

BAIAP2,CYFIP1,NCKAP1
ACTC1,ACTG1,BAIAP2,CYFIP1,DIAPH2,ENAH,EVL,VASP
CYFIP1,PFN1

CYFIP1,NCKAP1,PFN1

ACTB,ACTG1,BAIAP2,CYFIP1,NCKAP1
ACTB,ACTG1,BAIAP2,CYFIP1,NCKAP1
CYFIP1,NCKAP1
BAIAP2,CYFIP1,DIAPH1,EVL,FMNL1,NCKAP1,PFN1,VASP,VCP
ACTB,ACTC1,ACTG1,BAIAP2,CYFIP1,DIAPH1,EVL,VASP,VCP

BAIAP2,CYFIP1,EVL,NCKAP1,PFN1
ACTB,ACTG1,VASP

BAIAP2,CYFIP1,NCKAP1,PFN1
ACTC1,ACTG1,BAIAP2,CYFIP1,ENAH,EVL,PFN1,VASP
ACTB,CYFIP1,GPHN
ACTB,ACTG1,BAIAP2,CYFIP1,DIAPH1,NCKAP1,VCP

ENAH,EVL,VASP
ACTB,ACTC1,ACTG1,BAIAP2,CYFIP1,DIAPH1,ENAH,EVL,GPHN,VASP,VCP
ACTB,BAIAP2,CYFIP1,DIAPH1
ACTB,GPHN
ACTC1,ACTG1
ACTB,BAIAP2,CYFIP1,DIAPH1,VCP

EVL,PFN1
ACTB,ACTG1,BAIAP2,CYFIP1,DIAPH1,EVL,NCKAP1,VCP
BAIAP2,CYFIP1
ACTB,ACTC1,ENAH,EVL,FMNL1,VASP

BAIAP2,CYFIP1,DIAPH1,FMNL1,PFN1
EVL,VASP
EVL,PFN1
ACTB,ACTG1
PFN1,VASP
EVL,VASP,VCP
ACTB,ACTG1,BAIAP2,CYFIP1,EVL,NCKAP1,PFN1
BAIAP2,CYFIP1,ENAH,EVL,NCKAP1,PFN1,VASP
ACTB,ACTC1,ACTG1,BAIAP2,CYFIP1,DIAPH1,EVL,VCP
ACTC1,ACTG1,BAIAP2,CYFIP1,DIAPH2,ENAH,EVL,KIAA1522,VASP
ACTB,ENAH,EVL,FMNL1,VASP
ACTB,ACTG1,BAIAP2,CYFIP1,DIAPH1,EVL,VCP
ACTB,ACTG1,BAIAP2,GPHN