

GeDiPNet Cluster 49 -- Enriched GO Terms (Biological Process)

GO term enrichment: Biological Process terms (gene2go, human/tax_id=9606 only), upper-tail hypergeometric test, fold enrichment = (overlap / cluster gene count) / (term gene count / universe size), Benjamini-Hochberg FDR-corrected. Top 15 terms per cluster by q-value. See scripts/build_cluster_go_enrichment.php on gedipnet.bicnirrh.res.in. Data as of: 2026-10-07 03:23:06. · Rows: 15 · Generated: 2026-10-07 14:59:26

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Ras protein signal transduction	GO:0007265	12	SOS1, SYNGAP1, HRAS, KRAS, NRAS, RIT1, SOS2, DHCR24, NF1, RRAS, MRAS, RRAS2	79	106	26.78	2.186e-14	1.339e-11
Schwann cell development	GO:0014044	7	SOS1, HRAS, MAP2K1, MAP2K2, RAF1, NF1, MAPK1	20	106	61.70	1.128e-11	4.117e-9
MAPK cascade	GO:0000165	11	LRRK2, BRAF, HRAS, KRAS, MAP2K1, MAP2K2, NRAS, RAF1, NF1, PPP1CB, MAPK1	147	106	13.19	7.178e-10	1.668e-7
face development	GO:0060324	6	ANKRD11, BRAF, MAP2K1, MAP2K2, RAF1, MAPK1	22	106	48.08	2.001e-9	4.134e-7
insulin-like growth factor receptor signaling pathway	GO:0048009	6	SOS1, MAP2K1, MAP2K2, RAF1, MAPK1, PIK3CA	33	106	32.05	2.824e-8	4.179e-6
regulation of intracellular signal transduction	GO:1902531	6	LRRK2, SYNGAP1, CBL, NF1, RASA1, RASA2	40	106	26.44	9.478e-8	1.151e-5
ERBB2-ERBB3 signaling pathway	GO:0038133	4	MAP2K1, MAP2K2, RAF1, MAPK1	9	106	78.35	1.206e-7	1.409e-5
Schwann cell migration	GO:0036135	3	NF1, RRAS, RRAS2	3	106	176.29	1.774e-7	1.956e-5
insulin receptor signaling pathway	GO:0008286	7	FOXC2, SOS1, HRAS, RAF1, SOS2, MAPK1, PIK3CA	80	106	15.43	3.498e-7	3.455e-5
thymus development	GO:0048538	6	BRAF, MAP2K1, MAP2K2, RAF1, ASXL1, MAPK1	50	106	21.16	3.748e-7	3.668e-5
thyroid gland development	GO:0030878	5	BRAF, MAP2K1, MAP2K2, RAF1, MAPK1	30	106	29.38	6.798e-7	6.056e-5
regulation of Golgi inheritance	GO:0090170	3	MAP2K1, MAP2K2, MAPK1	4	106	132.22	7.067e-7	6.271e-5
blood vessel morphogenesis	GO:0048514	5	SOS1, ANGPT2, FLT4, EPHA2, RASA1	34	106	25.93	1.304e-6	1.024e-4
regulation of long-term neuronal synaptic plasticity	GO:0048169	4	SYNGAP1, HRAS, KRAS, NF1	18	106	39.18	2.815e-6	1.892e-4
regulation of MAPK cascade	GO:0043408	5	PTPN11, SYNGAP1, SHOC2, SPRED1, NF1	41	106	21.50	3.402e-6	2.209e-4