

GeDiPNet Cluster 445 -- 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: 2026-10-20 03:23:14. · Rows: 15 · Generated: 2026-10-20 00:00:46

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
negative regulation of Ras protein signal transduction	GO:0046580	2	RABGEF1, MFN2	25	31	48.22	7.802e-4	1.266e-2
dendritic transport	GO:0098935	1	RABGEF1	1	31	602.81	1.659e-3	1.929e-2
pyrimidine nucleoside transport	GO:0015864	1	SLC28A3	1	31	602.81	1.659e-3	1.929e-2
Spemann organizer formation at the anterior end of the primitive streak	GO:0060064	1	WNT3	1	31	602.81	1.659e-3	1.929e-2
hypoxanthine catabolic process	GO:0009114	1	XDH	1	31	602.81	1.659e-3	1.929e-2
xanthine catabolic process	GO:0009115	1	XDH	1	31	602.81	1.659e-3	1.929e-2
visceral mesoderm-endoderm interaction involved in midgut development	GO:0007495	1	FOXL1	1	31	602.81	1.659e-3	1.929e-2
inosine catabolic process	GO:0006148	1	XDH	2	31	301.40	3.315e-3	2.752e-2
deoxyinosine catabolic process	GO:0006149	1	XDH	2	31	301.40	3.315e-3	2.752e-2
negative regulation of mast cell cytokine production	GO:0032764	1	RABGEF1	2	31	301.40	3.315e-3	2.752e-2
negative regulation of Kit signaling pathway	GO:1900235	1	RABGEF1	2	31	301.40	3.315e-3	2.752e-2
positive regulation of collateral sprouting in absence of injury	GO:0048697	1	WNT3	2	31	301.40	3.315e-3	2.752e-2
guanine catabolic process	GO:0006147	1	XDH	2	31	301.40	3.315e-3	2.752e-2
deoxyguanosine catabolic process	GO:0006161	1	XDH	2	31	301.40	3.315e-3	2.752e-2
regulation of neurotransmitter receptor transport, endosome to postsynaptic membrane	GO:0099152	1	ARHGAP44	2	31	301.40	3.315e-3	2.752e-2