

GeDiPNet Cluster 324 -- 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 12:42:11

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
dosage compensation by inactivation of X chromosome	GO:0009048	2	SMCHD1, LRIF1	10	6	622.90	3.862e-6	2.440e-4
lymphocyte mediated immunity	GO:0002449	1	LYST	1	6	3114.50	3.211e-4	7.027e-3
mast cell secretory granule organization	GO:0033364	1	LYST	2	6	1557.25	6.421e-4	1.127e-2
endosome to lysosome transport via multivesicular body sorting pathway	GO:0032510	1	LYST	6	6	519.08	1.925e-3	2.203e-2
nose development	GO:0043584	1	SMCHD1	8	6	389.31	2.566e-3	2.584e-2
negative regulation of G0 to G1 transition	GO:0070317	1	DUX4	9	6	346.06	2.887e-3	2.764e-2
leukocyte chemotaxis	GO:0030595	1	LYST	16	6	194.66	5.127e-3	3.713e-2
positive regulation of double-strand break repair via nonhomologous end joining	GO:2001034	1	SMCHD1	17	6	183.21	5.447e-3	3.835e-2
defense response to other organism	GO:0098542	1	LYST	19	6	163.92	6.086e-3	4.052e-2
melanosome organization	GO:0032438	1	LYST	25	6	124.58	8.001e-3	4.595e-2
defense response to protozoan	GO:0042832	1	LYST	30	6	103.82	9.595e-3	5.006e-2
negative regulation of double-strand break repair via homologous recombination	GO:2000042	1	SMCHD1	30	6	103.82	9.595e-3	5.006e-2
pigmentation	GO:0043473	1	LYST	39	6	79.86	1.246e-2	5.716e-2
natural killer cell mediated cytotoxicity	GO:0042267	1	LYST	41	6	75.96	1.309e-2	5.853e-2
positive regulation of DNA repair	GO:0045739	1	SMCHD1	46	6	67.71	1.468e-2	6.161e-2