

GeDiPNet Cluster 529 -- 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: 2026-10-19 23:18:51

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
cellular response to interleukin-3	GO:0036016	2	SH2B3, JAK2	7	4	1334.79	7.214e-7	6.577e-5
thrombopoietin-mediated signaling pathway	GO:0038163	2	SH2B3, JAK2	7	4	1334.79	7.214e-7	6.577e-5
erythropoietin-mediated signaling pathway	GO:0038162	2	EPOR, JAK2	9	4	1038.17	1.237e-6	1.022e-4
cellular response to virus	GO:0098586	2	JAK2, CALR	89	4	104.98	1.337e-4	3.802e-3
nuclear receptor-mediated mineralocorticoid signaling pathway	GO:0031959	1	JAK2	1	4	4671.75	2.141e-4	5.314e-3
symbiont-induced defense-related programmed cell death	GO:0034050	1	JAK2	1	4	4671.75	2.141e-4	5.314e-3
interleukin-35-mediated signaling pathway	GO:0070757	1	JAK2	1	4	4671.75	2.141e-4	5.314e-3
negative regulation of Kit signaling pathway	GO:1900235	1	SH2B3	2	4	2335.88	4.281e-4	8.531e-3
response to interleukin-12	GO:0070671	1	JAK2	2	4	2335.88	4.281e-4	8.531e-3
positive regulation of growth factor dependent skeletal muscle satellite cell proliferation	GO:1902728	1	JAK2	2	4	2335.88	4.281e-4	8.531e-3
regulation of postsynapse to nucleus signaling pathway	GO:1905539	1	JAK2	2	4	2335.88	4.281e-4	8.531e-3
monocyte homeostasis	GO:0035702	1	SH2B3	3	4	1557.25	6.421e-4	1.113e-2
response to biphenyl	GO:1904614	1	CALR	3	4	1557.25	6.421e-4	1.113e-2
regulation of alpha-beta T cell activation	GO:0046634	1	JAK2	3	4	1557.25	6.421e-4	1.113e-2
positive regulation of growth hormone receptor signaling pathway	GO:0060399	1	JAK2	3	4	1557.25	6.421e-4	1.113e-2