

GeDiPNet Cluster 562 -- 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 00:01:14

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
immature T cell proliferation in thymus	GO:0033080	2	ERBB2, WNT4	5	28	266.96	2.159e-5	9.799e-4
positive regulation of DNA metabolic process	GO:0051054	2	AGER, ATAD5	6	28	222.46	3.236e-5	1.328e-3
ERBB2-ERBB3 signaling pathway	GO:0038133	2	ERBB2, RAF1	9	28	148.31	7.744e-5	2.558e-3
cellular response to transforming growth factor beta stimulus	GO:0071560	3	CAV1, FOS, WNT4	67	28	29.88	1.353e-4	3.837e-3
wound healing	GO:0042060	3	PPP3CA, ERBB2, RAF1	76	28	26.34	1.968e-4	5.024e-3
type II interferon-mediated signaling pathway	GO:0060333	2	RAF1, TP53	15	28	88.99	2.246e-4	5.507e-3
apoptotic signaling pathway	GO:0097190	3	CAV1, TP53, WNT4	84	28	23.84	2.647e-4	6.212e-3
cellular response to starvation	GO:0009267	3	CAV1, EHMT2, WNT4	90	28	22.25	3.244e-4	7.084e-3
oocyte development	GO:0048599	2	EHMT2, WNT4	19	28	70.25	3.644e-4	7.703e-3
Schwann cell development	GO:0014044	2	ERBB2, RAF1	20	28	66.74	4.045e-4	8.237e-3
response to muscle stretch	GO:0035994	2	FOS, RAF1	20	28	66.74	4.045e-4	8.237e-3
negative regulation of telomere maintenance via telomerase	GO:0032211	2	STN1, TP53	22	28	60.67	4.909e-4	9.368e-3
protein import into nucleus	GO:0006606	3	PPP3CA, KPNB1, TP53	110	28	18.20	5.840e-4	1.056e-2
cell population proliferation	GO:0008283	4	ATAD5, CAV1, ERBB2, TP53	263	28	10.15	6.017e-4	1.078e-2
positive regulation of activated T cell proliferation	GO:0042104	2	PPP3CA, AGER	28	28	47.67	7.989e-4	1.283e-2