

GeDiPNet Cluster 248 -- 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: 2026-10-09 03:23:08. · Rows: 15 · Generated: 2026-10-09 03:30:15

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
positive regulation of lysosomal protein catabolic process	GO:1905167	2	LRP1, LDLR	5	25	298.99	1.714e-5	7.999e-4
defense response to Gram-positive bacterium	GO:0050830	4	CALCA, TAC1, TNF, REG3G	135	25	22.15	2.929e-5	1.207e-3
positive regulation of action potential	GO:0045760	2	TAC1, TNF	7	25	213.57	3.594e-5	1.408e-3
negative regulation of macromolecule metabolic process	GO:0010605	2	LRP1, LDLR	7	25	213.57	3.594e-5	1.408e-3
amyloid-beta clearance by cellular catabolic process	GO:0150094	2	LRP1, LDLR	8	25	186.87	4.788e-5	1.749e-3
negative regulation of heart rate	GO:0010459	2	TAC1, TNF	12	25	124.58	1.125e-4	3.311e-3
antifungal humoral response	GO:0019732	2	CALCA, TAC1	13	25	115.00	1.328e-4	3.754e-3
response to yeast	GO:0001878	2	CALCA, TAC1	16	25	93.44	2.038e-4	5.118e-3
amyloid-beta clearance	GO:0097242	2	LRP1, LDLR	17	25	87.94	2.308e-4	5.569e-3
negative regulation of systemic arterial blood pressure	GO:0003085	2	TAC1, TNF	18	25	83.05	2.595e-4	6.076e-3
regulation of protein metabolic process	GO:0051246	2	LRP1, LDLR	24	25	62.29	4.658e-4	9.199e-3
lysosomal transport	GO:0007041	2	LRP1, VPS53	26	25	57.50	5.476e-4	1.023e-2
antimicrobial humoral immune response mediated by antimicrobial peptide	GO:0061844	3	CALCA, TAC1, REG3G	124	25	18.08	5.895e-4	1.080e-2
artery morphogenesis	GO:0048844	2	LDLR, NOTCH3	27	25	55.37	5.909e-4	1.082e-2
negative regulation of blood pressure	GO:0045776	2	CALCA, ABAT	28	25	53.39	6.358e-4	1.140e-2