

GeDiPNet Cluster 478 -- 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 00:01:17

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
vitamin B6 metabolic process	GO:0042816	1	PLPBP	1	6	3114.50	3.211e-4	7.044e-3
glycine betaine biosynthetic process from choline	GO:0019285	1	ALDH7A1	2	6	1557.25	6.421e-4	1.113e-2
regulation of platelet-derived growth factor receptor-alpha signaling pathway	GO:2000583	1	CBL	3	6	1038.17	9.630e-4	1.423e-2
choline catabolic process	GO:0042426	1	ALDH7A1	4	6	778.63	1.284e-3	1.669e-2
regulation of Rap protein signal transduction	GO:0032487	1	CBL	4	6	778.63	1.284e-3	1.669e-2
positive regulation of chemokine (C-C motif) ligand 5 production	GO:0071651	1	ADCYAP1	7	6	444.93	2.246e-3	2.244e-2
ubiquitin-dependent endocytosis	GO:0070086	1	CBL	7	6	444.93	2.246e-3	2.244e-2
positive regulation of growth hormone secretion	GO:0060124	1	ADCYAP1	9	6	346.06	2.887e-3	2.555e-2
aldehyde metabolic process	GO:0006081	1	ALDH7A1	13	6	239.58	4.167e-3	3.062e-2
regulation of signaling	GO:0023051	1	CBL	15	6	207.63	4.807e-3	3.273e-2
activation of adenylate cyclase activity	GO:0007190	1	ADCYAP1	15	6	207.63	4.807e-3	3.273e-2
positive regulation of cAMP/PKA signal transduction	GO:0141163	1	ADCYAP1	16	6	194.66	5.127e-3	3.369e-2
cell surface receptor signaling pathway	GO:0007166	2	ADGRE3, CBL	373	6	16.70	5.652e-3	3.533e-2
negative regulation of epidermal growth factor receptor signaling pathway	GO:0042059	1	CBL	21	6	148.31	6.725e-3	3.838e-2
positive regulation of receptor-mediated endocytosis	GO:0048260	1	CBL	21	6	148.31	6.725e-3	3.838e-2