

GeDiPNet Cluster 378 -- 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 09:45:58

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
cellular detoxification of cadmium ion	GO:0098849	2	ABCB6, SLC39A8	3	17	732.82	2.336e-6	1.630e-4
somatic diversification of immune receptors via somatic mutation	GO:0002566	1	ADAR	1	17	1099.24	9.097e-4	1.420e-2
negative regulation of post-transcriptional gene silencing by regulatory ncRNA	GO:1900369	1	ADAR	1	17	1099.24	9.097e-4	1.420e-2
regulation of protein K63-linked ubiquitination	GO:1900044	1	SASH1	1	17	1099.24	9.097e-4	1.420e-2
regulation of protein autoubiquitination	GO:1902498	1	SASH1	1	17	1099.24	9.097e-4	1.420e-2
mercury ion transport	GO:0015694	1	SLC39A8	1	17	1099.24	9.097e-4	1.420e-2
leukocyte adhesion to arterial endothelial cell	GO:0061757	1	SLC39A8	1	17	1099.24	9.097e-4	1.420e-2
plasma membrane selenite transport	GO:0097080	1	SLC39A8	1	17	1099.24	9.097e-4	1.420e-2
mitochondrial manganese ion transmembrane transport	GO:1990540	1	SLC39A8	1	17	1099.24	9.097e-4	1.420e-2
tetrapyrrole metabolic process	GO:0033013	1	ABCB6	1	17	1099.24	9.097e-4	1.420e-2
iron ion import across plasma membrane	GO:0098711	1	SLC39A8	2	17	549.62	1.819e-3	2.147e-2
heme transmembrane transport	GO:0035351	1	ABCB6	2	17	549.62	1.819e-3	2.147e-2
positive regulation of synapse structural plasticity	GO:0051835	1	FRMPD4	3	17	366.41	2.727e-3	2.685e-2
base conversion or substitution editing	GO:0016553	1	ADAR	4	17	274.81	3.634e-3	3.139e-2
establishment of body hair planar orientation	GO:0048105	1	ASTN2	4	17	274.81	3.634e-3	3.139e-2