

GeDiPNet Cluster 262 -- 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: 2026-10-08 03:23:04. · Rows: 15 · Generated: 2026-10-08 19:06:18

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
intracellular iron ion homeostasis	GO:0006879	4	CP, FTL, ATP13A2, FTH1	71	18	58.49	5.623e-7	5.220e-5
coenzyme A biosynthetic process	GO:0015937	2	PANK2, COASY	10	18	207.63	3.925e-5	1.528e-3
glutamate secretion	GO:0014047	2	GJA1, BEST1	11	18	188.76	4.795e-5	1.772e-3
iron ion transport	GO:0006826	2	FTL, FTH1	31	18	66.98	4.008e-4	8.390e-3
microtubule-based transport	GO:0099111	1	GJA1	1	18	1038.17	9.632e-4	1.501e-2
spermine transmembrane transport	GO:1903710	1	ATP13A2	1	18	1038.17	9.632e-4	1.501e-2
regulation of sebum secreting cell proliferation	GO:1904002	1	FA2H	1	18	1038.17	9.632e-4	1.501e-2
regulation of acinar cell proliferation	GO:1904697	1	FA2H	1	18	1038.17	9.632e-4	1.501e-2
autophagy	GO:0006914	3	WDR45, ATP13A2, C19orf12	221	18	14.09	1.168e-3	1.702e-2
gamma-aminobutyric acid secretion, neurotransmission	GO:0061534	1	BEST1	2	18	519.08	1.926e-3	2.259e-2
negative regulation of gonadotropin secretion	GO:0032277	1	GJA1	2	18	519.08	1.926e-3	2.259e-2
positive regulation of morphogenesis of an epithelium	GO:1905332	1	GJA1	2	18	519.08	1.926e-3	2.259e-2
sebaceous gland cell differentiation	GO:0001949	1	FA2H	2	18	519.08	1.926e-3	2.259e-2
extracellular exosome biogenesis	GO:0097734	1	ATP13A2	2	18	519.08	1.926e-3	2.259e-2
glucosylceramide biosynthetic process	GO:0006679	1	FA2H	2	18	519.08	1.926e-3	2.259e-2