

GeDiPNet Cluster 468 -- 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: 2026-10-19 23:18:33

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
negative regulation of hair cycle	GO:0042636	1	TRPV3	1	5	3737.40	2.676e-4	6.245e-3
spermatocyte division	GO:0048137	1	SPATA22	2	5	1868.70	5.351e-4	9.880e-3
bone maturation	GO:0070977	1	MBTPS2	3	5	1245.80	8.025e-4	1.283e-2
meiotic DNA repair synthesis	GO:0000711	1	SPATA22	3	5	1245.80	8.025e-4	1.283e-2
regulation of response to endoplasmic reticulum stress	GO:1905897	1	MBTPS2	4	5	934.35	1.070e-3	1.514e-2
keratinocyte migration	GO:0051546	1	KRT16	6	5	622.90	1.605e-3	1.885e-2
reproductive system development	GO:0061458	1	SPATA22	7	5	533.91	1.872e-3	2.050e-2
ATF6-mediated unfolded protein response	GO:0036500	1	MBTPS2	8	5	467.18	2.139e-3	2.189e-2
mammary gland duct morphogenesis	GO:0060603	1	PERP	8	5	467.18	2.139e-3	2.189e-2
desmosome organization	GO:0002934	1	PERP	8	5	467.18	2.139e-3	2.189e-2
positive regulation of T cell apoptotic process	GO:0070234	1	PERP	9	5	415.27	2.406e-3	2.324e-2
osmosensory signaling pathway	GO:0007231	1	TRPV3	9	5	415.27	2.406e-3	2.324e-2
regulation of cholesterol biosynthetic process	GO:0045540	1	MBTPS2	12	5	311.45	3.207e-3	2.689e-2
amelogenesis	GO:0097186	1	PERP	12	5	311.45	3.207e-3	2.689e-2
membrane protein intracellular domain proteolysis	GO:0031293	1	MBTPS2	14	5	266.96	3.741e-3	2.900e-2