

GeDiPNet Cluster 466 -- 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 00:01:23

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
rhombomere 6 development	GO:0021572	1	MAFB	1	3	6229.00	1.605e-4	4.340e-3
microtubule cytoskeleton organization	GO:0000226	2	TOGARAM1, TUBB4A	149	3	83.61	1.885e-4	4.882e-3
rhombomere 5 development	GO:0021571	1	MAFB	2	3	3114.50	3.211e-4	7.044e-3
abducens nerve formation	GO:0021599	1	MAFB	2	3	3114.50	3.211e-4	7.044e-3
brain segmentation	GO:0035284	1	MAFB	3	3	2076.33	4.816e-4	9.241e-3
cornified envelope assembly	GO:1903575	1	MAFB	6	3	1038.17	9.630e-4	1.423e-2
regulation of myeloid cell differentiation	GO:0045637	1	MAFB	8	3	778.63	1.284e-3	1.669e-2
segment specification	GO:0007379	1	MAFB	8	3	778.63	1.284e-3	1.669e-2
negative regulation of erythrocyte differentiation	GO:0045647	1	MAFB	10	3	622.90	1.605e-3	1.885e-2
negative regulation of microtubule polymerization	GO:0031115	1	TUBB4A	13	3	479.15	2.086e-3	2.170e-2
integrated stress response signaling	GO:0140467	1	MAFB	25	3	249.16	4.008e-3	3.008e-2
sensory organ development	GO:0007423	1	MAFB	27	3	230.70	4.329e-3	3.113e-2
positive regulation of microtubule polymerization	GO:0031116	1	TOGARAM1	27	3	230.70	4.329e-3	3.113e-2
negative regulation of osteoclast differentiation	GO:0045671	1	MAFB	30	3	207.63	4.809e-3	3.273e-2
respiratory gaseous exchange by respiratory system	GO:0007585	1	MAFB	31	3	200.94	4.969e-3	3.329e-2