

GeDiPNet Cluster 464 -- 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 00:01:13

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
positive regulation of myoblast differentiation	GO:0045663	2	SOX4, SMARCA2	47	10	79.52	2.751e-4	6.370e-3
positive regulation of DNA-templated transcription	GO:0045893	4	PPARGC1A, SOX4, SMARCA2, KLF7	778	10	9.61	5.120e-4	9.649e-3
viral RNA genome packaging	GO:0019074	1	DDX6	2	10	934.35	1.070e-3	1.514e-2
pro-B cell differentiation	GO:0002328	1	SOX4	4	10	467.18	2.139e-3	2.189e-2
ascending aorta morphogenesis	GO:0035910	1	SOX4	4	10	467.18	2.139e-3	2.189e-2
regulation of epidermal cell differentiation	GO:0045604	1	KLF7	4	10	467.18	2.139e-3	2.189e-2
protein localization to paranode region of axon	GO:0002175	1	UGT8	4	10	467.18	2.139e-3	2.189e-2
glucose homeostasis	GO:0042593	2	SOX4, KLF7	134	10	27.89	2.212e-3	2.242e-2
positive regulation of transcription by RNA polymerase II	GO:0045944	4	PPARGC1A, SOX4, SMARCA2, KLF7	1208	10	6.19	2.662e-3	2.457e-2
atrial septum primum morphogenesis	GO:0003289	1	SOX4	5	10	373.74	2.673e-3	2.457e-2
glial cell development	GO:0021782	1	SOX4	5	10	373.74	2.673e-3	2.457e-2
galactosylceramide biosynthetic process	GO:0006682	1	UGT8	6	10	311.45	3.207e-3	2.689e-2
paranodal junction assembly	GO:0030913	1	UGT8	6	10	311.45	3.207e-3	2.689e-2
positive regulation of fatty acid oxidation	GO:0046321	1	PPARGC1A	6	10	311.45	3.207e-3	2.689e-2
regulation of DNA damage response, signal transduction by p53 class mediator	GO:0043516	1	SOX4	7	10	266.96	3.741e-3	2.900e-2