

GeDiPNet Cluster 428 -- 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 07:18:39

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
tetrahydrofolate biosynthetic process	GO:0046654	2	SLC46A1, DHFR	7	15	355.94	1.260e-5	6.253e-4
folic acid metabolic process	GO:0046655	2	SLC46A1, DHFR	15	15	166.11	6.277e-5	2.133e-3
hematopoietic stem cell proliferation	GO:0071425	2	MECOM, RUNX1	25	15	99.66	1.785e-4	4.667e-3
response to axon injury	GO:0048678	2	SARM1, EPO	37	15	67.34	3.941e-4	8.112e-3
interstrand cross-link repair	GO:0036297	2	ERCC6L2, FANCC	39	15	63.89	4.381e-4	8.716e-3
negative regulation of erythrocyte apoptotic process	GO:1902251	1	EPO	1	15	1245.80	8.027e-4	1.302e-2
negative regulation of MyD88-independent toll-like receptor signaling pathway	GO:0034128	1	SARM1	1	15	1245.80	8.027e-4	1.302e-2
molybdopterin cofactor metabolic process	GO:0043545	1	MOCOS	1	15	1245.80	8.027e-4	1.302e-2
erythrocyte differentiation	GO:0030218	2	EPO, IKZF1	65	15	38.33	1.215e-3	1.704e-2
response to methotrexate	GO:0031427	1	DHFR	2	15	622.90	1.605e-3	1.983e-2
methotrexate transport	GO:0051958	1	SLC46A1	2	15	622.90	1.605e-3	1.983e-2
intestinal folate absorption	GO:0098829	1	SLC46A1	2	15	622.90	1.605e-3	1.983e-2
NAD+ catabolic process	GO:0019677	1	SARM1	3	15	415.27	2.406e-3	2.497e-2
regulation of plasminogen activation	GO:0010755	1	RUNX1	3	15	415.27	2.406e-3	2.497e-2
regulation of connective tissue replacement	GO:1905203	1	RUNX1	3	15	415.27	2.406e-3	2.497e-2