

GeDiPNet Cluster 155 -- 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 15:46:30

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
homocysteine metabolic process	GO:0050667	4	MTHFR, MTRR, MTR, CBS	10	25	298.99	5.202e-10	1.253e-7
methionine biosynthetic process	GO:0009086	4	MTHFR, MTRR, MTR, MTHFD1	11	25	271.81	8.167e-10	1.868e-7
methionine metabolic process	GO:0006555	3	MTHFR, GNMT, MTHFD1	6	25	373.74	4.219e-8	5.863e-6
cobalamin metabolic process	GO:0009235	3	MTRR, MMADHC, MTR	9	25	249.16	1.767e-7	1.951e-5
non-motile cilium assembly	GO:1905515	4	CSNK1D, CC2D2A, RPGRIP1L, VANGL2	57	25	52.45	9.380e-7	7.889e-5
folic acid metabolic process	GO:0046655	3	MTRR, SLC46A1, MTHFD1	15	25	149.50	9.522e-7	7.982e-5
neural tube closure	GO:0001843	4	CC2D2A, MTHFR, VANGL2, MTHFD1	85	25	35.18	4.688e-6	2.854e-4
amino acid biosynthetic process	GO:0008652	3	MTRR, MTR, CBS	27	25	83.05	6.057e-6	3.497e-4
S-adenosylmethionine metabolic process	GO:0046500	2	MTHFR, GNMT	4	25	373.74	1.029e-5	5.328e-4
homocysteine catabolic process	GO:0043418	2	MTRR, CBS	4	25	373.74	1.029e-5	5.328e-4
serine family amino acid metabolic process	GO:0009069	2	CBS, MTHFD1	4	25	373.74	1.029e-5	5.328e-4
transsulfuration	GO:0019346	2	CBS, MTHFD1	5	25	298.99	1.714e-5	7.947e-4
positive regulation of extrinsic apoptotic signaling pathway	GO:2001238	3	AGT, PYCARD, TNF	38	25	59.01	1.730e-5	8.003e-4
positive regulation of inflammatory response	GO:0050729	4	AGT, CASP1, PYCARD, TNF	122	25	24.51	1.967e-5	8.861e-4
response to folic acid	GO:0051593	2	MTHFR, CBS	8	25	186.87	4.788e-5	1.738e-3