

GeDiPNet Cluster 112 -- 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 11:05:27

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
urea cycle	GO:0000050	4	ARG1, ASL, NAGS, SLC25A15	12	28	222.46	1.979e-9	4.094e-7
amino acid biosynthetic process	GO:0008652	4	ASL, CTH, PHGDH, PSPH	27	28	98.87	6.909e-8	8.902e-6
one-carbon metabolic process	GO:0006730	3	AHCY, MAT1A, GNMT	21	28	95.34	3.935e-6	2.478e-4
short-chain fatty acid catabolic process	GO:0019626	2	PCCA, PCCB	3	28	444.93	6.489e-6	3.691e-4
L-arginine biosynthetic process	GO:0006526	2	ASL, NAGS	4	28	333.70	1.297e-5	6.400e-4
branched-chain amino acid metabolic process	GO:0009081	2	PCCA, PCCB	5	28	266.96	2.159e-5	9.543e-4
cysteine metabolic process	GO:0006534	2	CTH, GCLC	6	28	222.46	3.236e-5	1.294e-3
L-serine biosynthetic process	GO:0006564	2	PHGDH, PSPH	6	28	222.46	3.236e-5	1.294e-3
L-leucine catabolic process	GO:0006552	2	HMGCL, IVD	7	28	190.68	4.526e-5	1.671e-3
arginine metabolic process	GO:0006525	2	ARG1, ASL	8	28	166.85	6.028e-5	2.062e-3
L-serine metabolic process	GO:0006563	2	PHGDH, PSPH	10	28	133.48	9.671e-5	2.947e-3
protein homotetramerization	GO:0051289	3	CTH, MAT1A, GNMT	66	28	30.34	1.294e-4	3.675e-3
L-arginine transmembrane transport	GO:1903826	2	SLC25A15, SLC7A7	15	28	88.99	2.246e-4	5.471e-3
glutamate metabolic process	GO:0006536	2	GCLC, NAGS	15	28	88.99	2.246e-4	5.471e-3
branched-chain amino acid catabolic process	GO:0009083	2	ALDH6A1, IVD	18	28	74.15	3.264e-4	7.107e-3