

GeDiPNet Cluster 421 -- 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 02:40:36

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
'de novo' NAD+ biosynthetic process from L-tryptophan	GO:0034354	3	KYNU, HAAO, NADSYN1	9	5	1245.80	7.721e-10	1.779e-7
NAD+ biosynthetic process	GO:0009435	3	KYNU, HAAO, NADSYN1	13	5	862.48	2.628e-9	5.253e-7
anthranilate metabolic process	GO:0043420	2	KYNU, HAAO	3	5	2491.60	1.718e-7	1.907e-5
quinolinate biosynthetic process	GO:0019805	2	KYNU, HAAO	4	5	1868.70	3.436e-7	3.405e-5
L-tryptophan catabolic process	GO:0006569	2	KYNU, HAAO	9	5	830.53	2.060e-6	1.473e-4
pyridine nucleotide biosynthetic process	GO:0019363	2	KYNU, HAAO	11	5	679.53	3.147e-6	2.073e-4
purine-containing compound metabolic process	GO:0072521	1	KYNU	1	5	3737.40	2.676e-4	6.199e-3
response to vitamin B6	GO:0034516	1	KYNU	2	5	1868.70	5.351e-4	9.981e-3
nucleotide-sugar metabolic process	GO:0009225	1	TGDS	2	5	1868.70	5.351e-4	9.981e-3
quinolinate metabolic process	GO:0046874	1	HAAO	2	5	1868.70	5.351e-4	9.981e-3
L-kynurenine catabolic process	GO:0097053	1	KYNU	4	5	934.35	1.070e-3	1.569e-2
dicarboxylic acid metabolic process	GO:0043648	1	HAAO	5	5	747.48	1.337e-3	1.795e-2
L-tryptophan catabolic process to kynurenine	GO:0019441	1	KYNU	5	5	747.48	1.337e-3	1.795e-2
nucleoside phosphate metabolic process	GO:0006753	1	KYNU	6	5	622.90	1.605e-3	1.983e-2
NAD+ biosynthetic process via the salvage pathway	GO:0034355	1	NADSYN1	17	5	219.85	4.541e-3	3.499e-2