

GeDiPNet Cluster 517 -- 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 00:01:43

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
protein import into mitochondrial intermembrane space	GO:0045041	1	AIFM1	3	4	1557.25	6.421e-4	1.113e-2
mitochondrial disulfide relay system	GO:0160203	1	AIFM1	3	4	1557.25	6.421e-4	1.113e-2
L-valine catabolic process	GO:0006574	1	HIBCH	5	4	934.35	1.070e-3	1.514e-2
mitochondrial respiratory chain complex assembly	GO:0033108	1	AIFM1	6	4	778.63	1.284e-3	1.669e-2
articular cartilage development	GO:0061975	1	BGN	6	4	778.63	1.284e-3	1.669e-2
cellular response to aldosterone	GO:1904045	1	AIFM1	7	4	667.39	1.498e-3	1.821e-2
positive regulation of necroptotic process	GO:0060545	1	AIFM1	8	4	583.97	1.711e-3	1.958e-2
response to L-glutamate	GO:1902065	1	AIFM1	12	4	389.31	2.566e-3	2.402e-2
positive regulation of programmed cell death	GO:0043068	1	AIFM1	17	4	274.81	3.634e-3	2.863e-2
Rab protein signal transduction	GO:0032482	1	RAB33A	17	4	274.81	3.634e-3	2.863e-2
cellular response to nitric oxide	GO:0071732	1	AIFM1	17	4	274.81	3.634e-3	2.863e-2
branched-chain amino acid catabolic process	GO:0009083	1	HIBCH	18	4	259.54	3.848e-3	2.937e-2
intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress	GO:0070059	1	AIFM1	36	4	129.77	7.684e-3	4.089e-2
cellular response to estradiol stimulus	GO:0071392	1	AIFM1	36	4	129.77	7.684e-3	4.089e-2
blood vessel remodeling	GO:0001974	1	BGN	42	4	111.23	8.961e-3	4.406e-2