

GeDiPNet Cluster 495 -- 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: 2026-10-19 23:18:23

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
endocardial cushion cell development	GO:0061444	1	JAG1	1	5	3737.40	2.676e-4	6.245e-3
response to cortisone	GO:0051413	1	GLB1	1	5	3737.40	2.676e-4	6.245e-3
keratan sulfate proteoglycan catabolic process	GO:0042340	1	GLB1	2	5	1868.70	5.351e-4	9.880e-3
response to Thyroglobulin triiodothyronine	GO:1904016	1	GLB1	2	5	1868.70	5.351e-4	9.880e-3
distal tubule development	GO:0072017	1	JAG1	3	5	1245.80	8.025e-4	1.283e-2
loop of Henle development	GO:0072070	1	JAG1	3	5	1245.80	8.025e-4	1.283e-2
ciliary body morphogenesis	GO:0061073	1	JAG1	4	5	934.35	1.070e-3	1.514e-2
cardiac neural crest cell development involved in outflow tract morphogenesis	GO:0061309	1	JAG1	4	5	934.35	1.070e-3	1.514e-2
galactose catabolic process	GO:0019388	1	GLB1	5	5	747.48	1.337e-3	1.709e-2
inhibition of neuroepithelial cell differentiation	GO:0002085	1	JAG1	5	5	747.48	1.337e-3	1.709e-2
positive regulation of myeloid cell differentiation	GO:0045639	1	JAG1	5	5	747.48	1.337e-3	1.709e-2
positive regulation of cardiac epithelial to mesenchymal transition	GO:0062043	1	JAG1	5	5	747.48	1.337e-3	1.709e-2
pulmonary artery morphogenesis	GO:0061156	1	JAG1	6	5	622.90	1.605e-3	1.885e-2
negative regulation of endothelial cell differentiation	GO:0045602	1	JAG1	7	5	533.91	1.872e-3	2.050e-2
ganglioside catabolic process	GO:0006689	1	GLB1	8	5	467.18	2.139e-3	2.189e-2