

GeDiPNet Cluster 515 -- 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 03:23:13. · Rows: 15 · Generated: 2026-10-20 00:01:13

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
ventricular trabecula myocardium morphogenesis	GO:0003222	3	DLL4, NOTCH1, RBPJ	15	8	467.18	2.338e-8	3.698e-6
blood vessel lumenization	GO:0072554	2	DLL4, RBPJ	2	8	2335.88	1.604e-7	1.890e-5
endocardium morphogenesis	GO:0003160	2	NOTCH1, RBPJ	2	8	2335.88	1.604e-7	1.890e-5
auditory receptor cell fate commitment	GO:0009912	2	NOTCH1, RBPJ	3	8	1557.25	4.810e-7	4.720e-5
regulation of cell adhesion involved in heart morphogenesis	GO:0061344	2	NOTCH1, RBPJ	3	8	1557.25	4.810e-7	4.720e-5
endocardium development	GO:0003157	2	NOTCH1, RBPJ	5	8	934.35	1.603e-6	1.267e-4
epidermal cell fate specification	GO:0009957	2	NOTCH1, RBPJ	5	8	934.35	1.603e-6	1.267e-4
cardiac atrium morphogenesis	GO:0003209	2	DLL4, NOTCH1	6	8	778.63	2.404e-6	1.760e-4
pericardium morphogenesis	GO:0003344	2	DLL4, NOTCH1	7	8	667.39	3.364e-6	2.299e-4
positive regulation of transcription of Notch receptor target	GO:0007221	2	NOTCH1, RBPJ	7	8	667.39	3.364e-6	2.299e-4
dorsal aorta morphogenesis	GO:0035912	2	DLL4, RBPJ	8	8	583.97	4.485e-6	2.903e-4
cardiac ventricle morphogenesis	GO:0003208	2	DLL4, NOTCH1	10	8	467.18	7.204e-6	4.218e-4
cardiac left ventricle morphogenesis	GO:0003214	2	NOTCH1, RBPJ	11	8	424.70	8.804e-6	4.925e-4
cardiac muscle cell myoblast differentiation	GO:0060379	2	NOTCH1, RBPJ	11	8	424.70	8.804e-6	4.925e-4
epithelial to mesenchymal transition involved in endocardial cushion formation	GO:0003198	2	NOTCH1, RBPJ	13	8	359.37	1.248e-5	6.462e-4