

GeDiPNet Cluster 595 -- 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 00:01:13

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
glomerular capillary formation	GO:0072104	1	NOTCH3	3	3	2076.33	4.816e-4	9.241e-3
chorionic trophoblast cell differentiation	GO:0060718	1	HTRA1	6	3	1038.17	9.630e-4	1.423e-2
neuroblast differentiation	GO:0014016	1	NOTCH3	7	3	889.86	1.123e-3	1.550e-2
retina homeostasis	GO:0001895	1	ARMS2	15	3	415.27	2.406e-3	2.324e-2
artery morphogenesis	GO:0048844	1	NOTCH3	27	3	230.70	4.329e-3	3.113e-2
regulation of developmental process	GO:0050793	1	NOTCH3	32	3	194.66	5.129e-3	3.369e-2
neuron fate commitment	GO:0048663	1	NOTCH3	33	3	188.76	5.289e-3	3.427e-2
programmed cell death	GO:0012501	1	HTRA1	42	3	148.31	6.728e-3	3.838e-2
placenta development	GO:0001890	1	HTRA1	48	3	129.77	7.687e-3	4.089e-2
positive regulation of smooth muscle cell proliferation	GO:0048661	1	NOTCH3	52	3	119.79	8.325e-3	4.252e-2
positive regulation of miRNA transcription	GO:1902895	1	NOTCH3	56	3	111.23	8.964e-3	4.407e-2
negative regulation of neuron differentiation	GO:0045665	1	NOTCH3	63	3	98.87	1.008e-2	4.670e-2
negative regulation of cell differentiation	GO:0045596	1	NOTCH3	75	3	83.05	1.199e-2	5.062e-2
negative regulation of BMP signaling pathway	GO:0030514	1	HTRA1	75	3	83.05	1.199e-2	5.062e-2
forebrain development	GO:0030900	1	NOTCH3	76	3	81.96	1.215e-2	5.104e-2