

GeDiPNet Cluster 197 -- 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 05:22:06

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
hindlimb morphogenesis	GO:0035137	2	TFAP2B, PITX1	9	33	125.84	1.080e-4	3.198e-3
negative regulation of smooth muscle cell differentiation	GO:0051151	2	FOXO4, MECP2	10	33	113.25	1.349e-4	3.783e-3
neuromuscular process controlling posture	GO:0050884	2	SCN1A, MECP2	15	33	75.50	3.130e-4	6.929e-3
cartilage development	GO:0051216	3	SATB2, COL2A1, PITX1	89	33	19.09	5.138e-4	9.728e-3
coronary vasculature development	GO:0060976	2	DYNC2H1, ABCC9	27	33	41.95	1.033e-3	1.538e-2
vascular process in circulatory system	GO:0003018	1	ABCC9	1	33	566.27	1.766e-3	2.107e-2
response to hydrogen sulfide	GO:1904880	1	ABCC9	1	33	566.27	1.766e-3	2.107e-2
trans-synaptic signaling by BDNF	GO:0099191	1	MECP2	1	33	566.27	1.766e-3	2.107e-2
kidney development	GO:0001822	3	DYNC2H1, TFAP2B, CEP290	146	33	11.64	2.147e-3	2.348e-2
skeletal system development	GO:0001501	3	RPS6KA3, COL2A1, PITX1	151	33	11.25	2.362e-3	2.486e-2
negative regulation of blood vessel endothelial cell migration	GO:0043537	2	CSNK2B, MECP2	43	33	26.34	2.610e-3	2.617e-2
skeletal system morphogenesis	GO:0048705	2	ANKRD11, COL2A1	45	33	25.17	2.855e-3	2.759e-2
potassium ion import across plasma membrane	GO:1990573	2	SLC12A6, ABCC9	46	33	24.62	2.982e-3	2.816e-2
regulation of system process	GO:0044057	1	DMD	2	33	283.14	3.529e-3	3.080e-2
regulation of muscle system process	GO:0090257	1	DMD	2	33	283.14	3.529e-3	3.080e-2