

GeDiPNet Cluster 152 -- 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: 2026-10-08 03:23:04. · Rows: 15 · Generated: 2026-10-08 13:33:01

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
ureteric bud development	GO:0001657	6	FOXC2, BCL2, EYA1, FGFR2, SPRY1, WT1	41	168	16.28	1.673e-6	1.267e-4
branching involved in ureteric bud morphogenesis	GO:0001658	6	BCL2, EYA1, LAMA5, WNT4, WT1, PAX2	45	168	14.83	2.941e-6	2.004e-4
metanephros development	GO:0001656	5	FOXC2, BCL2, EYA1, SPRY1, WNT4	38	168	14.64	2.184e-5	9.755e-4
animal organ morphogenesis	GO:0009887	8	BCL2, EYA1, FGFR2, GREM1, LAMA5, NRP1, NTN4, SLIT3	130	168	6.85	2.314e-5	1.014e-3
camera-type eye development	GO:0043010	6	EFEMP1, FOXC2, FBN2, FOXP2, WT1, PAX2	74	168	9.02	5.396e-5	1.938e-3
gland morphogenesis	GO:0022612	3	BCL2, FGFR2, GDF7	9	168	37.08	5.762e-5	2.034e-3
mesenchymal to epithelial transition	GO:0060231	3	WNT4, WT1, PAX2	11	168	30.34	1.117e-4	3.351e-3
ventricular zone neuroblast division	GO:0021847	2	DCT, FGFR2	3	168	74.15	2.396e-4	5.840e-3
regulation of signal transduction	GO:0009966	6	CSF2, GPC6, GUCA1C, MGLL, SPRY1, WWOX	101	168	6.61	3.024e-4	6.905e-3
axon guidance	GO:0007411	8	EPHA4, TRIO, UNC5D, GDF7, KLF7, NRP1, NTN4, SLIT3	192	168	4.63	3.519e-4	7.672e-3
lung development	GO:0030324	6	ADA, AP3B1, CRISPLD2, FGFR2, FOXP2, LAMA5	108	168	6.18	4.336e-4	8.850e-3
eye morphogenesis	GO:0048592	2	COL5A1, STAU2	4	168	55.62	4.764e-4	9.477e-3
regulation of epidermal cell differentiation	GO:0045604	2	KLF7, MAFF	4	168	55.62	4.764e-4	9.477e-3
positive regulation of epithelial cell proliferation	GO:0050679	5	EYA1, FGFR2, FOXP2, TACR1, PAX2	73	168	7.62	5.075e-4	9.839e-3
positive regulation of bone mineralization	GO:0030501	4	ADRB2, FBN2, RXRA, WNT4	42	168	10.59	5.405e-4	1.027e-2