

GeDiPNet Cluster 586 -- 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
olfactory nerve development	GO:0021553	2	SALL1, CHD7	3	5	2491.60	1.718e-7	1.992e-5
olfactory bulb development	GO:0021772	2	SALL1, CHD7	27	5	276.84	2.005e-5	9.249e-4
limb development	GO:0060173	2	SALL1, CHD7	56	5	133.48	8.770e-5	2.807e-3
inductive cell-cell signaling	GO:0031129	1	SALL1	1	5	3737.40	2.676e-4	6.245e-3
right ventricular compact myocardium morphogenesis	GO:0003226	1	CHD7	1	5	3737.40	2.676e-4	6.245e-3
cellular response to selenite ion	GO:0072715	1	EIF4A3	1	5	3737.40	2.676e-4	6.245e-3
negative regulation of selenocysteine incorporation	GO:1904570	1	EIF4A3	1	5	3737.40	2.676e-4	6.245e-3
rhombomere 3 morphogenesis	GO:0021658	1	HOXA2	1	5	3737.40	2.676e-4	6.245e-3
olfactory bulb mitral cell layer development	GO:0061034	1	SALL1	2	5	1868.70	5.351e-4	9.880e-3
ureteric bud invasion	GO:0072092	1	SALL1	2	5	1868.70	5.351e-4	9.880e-3
rhombomere 2 development	GO:0021568	1	HOXA2	2	5	1868.70	5.351e-4	9.880e-3
negative regulation of protein localization to nucleolus	GO:1904750	1	POLR1A	2	5	1868.70	5.351e-4	9.880e-3
rRNA processing	GO:0006364	2	EIF4A3, CHD7	162	5	46.14	7.342e-4	1.226e-2
rhombomere 3 development	GO:0021569	1	HOXA2	3	5	1245.80	8.025e-4	1.283e-2
brain segmentation	GO:0035284	1	HOXA2	3	5	1245.80	8.025e-4	1.283e-2