

GeDiPNet Cluster 257 -- 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: 2026-10-10 03:23:27. · Rows: 15 · Generated: 2026-10-09 23:17:18

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
subthalamic nucleus development	GO:0021763	1	PITX2	1	5	3737.40	2.676e-4	6.409e-3
superior vena cava morphogenesis	GO:0060578	1	PITX2	1	5	3737.40	2.676e-4	6.409e-3
urate biosynthetic process	GO:0034418	1	PRPS1	2	5	1868.70	5.351e-4	1.032e-2
hypothalamus cell migration	GO:0021855	1	PITX2	2	5	1868.70	5.351e-4	1.032e-2
prolactin secreting cell differentiation	GO:0060127	1	PITX2	2	5	1868.70	5.351e-4	1.032e-2
left lung morphogenesis	GO:0060460	1	PITX2	2	5	1868.70	5.351e-4	1.032e-2
pulmonary vein morphogenesis	GO:0060577	1	PITX2	2	5	1868.70	5.351e-4	1.032e-2
cell proliferation involved in outflow tract morphogenesis	GO:0061325	1	PITX2	2	5	1868.70	5.351e-4	1.032e-2
hypoxanthine biosynthetic process	GO:0046101	1	PRPS1	2	5	1868.70	5.351e-4	1.032e-2
pulmonary myocardium development	GO:0003350	1	PITX2	3	5	1245.80	8.025e-4	1.353e-2
deltoid tuberosity development	GO:0035993	1	PITX2	3	5	1245.80	8.025e-4	1.353e-2
endodermal digestive tract morphogenesis	GO:0061031	1	PITX2	3	5	1245.80	8.025e-4	1.353e-2
ribonucleoside monophosphate biosynthetic process	GO:0009156	1	PRPS1	4	5	934.35	1.070e-3	1.625e-2
somatotropin secreting cell differentiation	GO:0060126	1	PITX2	4	5	934.35	1.070e-3	1.625e-2
atrioventricular valve development	GO:0003171	1	PITX2	5	5	747.48	1.337e-3	1.856e-2