

GeDiPNet Cluster 473 -- 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: 2026-10-19 23:19:00

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
determination of left/right symmetry	GO:0007368	3	CFAP53, ZIC3, NODAL	83	8	84.43	4.656e-6	2.999e-4
primitive streak formation	GO:0090009	2	ZIC3, NODAL	11	8	424.70	8.804e-6	4.925e-4
embryonic pattern specification	GO:0009880	2	ZIC3, NODAL	32	8	145.99	7.904e-5	2.599e-3
gastrulation	GO:0007369	2	ZIC3, NODAL	38	8	122.94	1.119e-4	3.352e-3
stem cell population maintenance	GO:0019827	2	ZIC3, NODAL	47	8	99.40	1.717e-4	4.550e-3
heart looping	GO:0001947	2	ZIC3, NODAL	64	8	73.00	3.190e-4	7.044e-3
central nervous system segmentation	GO:0035283	1	ZIC3	1	8	2335.88	4.281e-4	8.531e-3
positive regulation of connective tissue growth factor production	GO:0032723	1	ROCK2	1	8	2335.88	4.281e-4	8.531e-3
polarity specification of proximal/distal axis	GO:0010085	1	NODAL	1	8	2335.88	4.281e-4	8.531e-3
floor plate morphogenesis	GO:0033505	1	NODAL	1	8	2335.88	4.281e-4	8.531e-3
axial mesodermal cell fate specification	GO:0048327	1	NODAL	1	8	2335.88	4.281e-4	8.531e-3
epiblast cell-extraembryonic ectoderm cell signaling	GO:0060802	1	NODAL	1	8	2335.88	4.281e-4	8.531e-3
cell differentiation	GO:0030154	4	CFAP53, MYRF, ZIC3, NODAL	1051	8	8.89	5.802e-4	1.051e-2
trophectodermal cellular morphogenesis	GO:0001831	1	NODAL	2	8	1167.94	8.560e-4	1.331e-2
negative regulation of protein localization to lysosome	GO:0150033	1	ROCK2	2	8	1167.94	8.560e-4	1.331e-2