

GeDiPNet Cluster 183 -- 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 18:01:43

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
positive regulation of male gonad development	GO:2000020	4	DMRT1, NR5A1, SOX9, SRY	8	12	778.63	6.812e-12	2.601e-9
male gonad development	GO:0008584	6	DMRT1, NR5A1, SOX9, LHCGR, INHA, INHBB	117	12	79.86	4.743e-11	1.469e-8
male sex determination	GO:0030238	4	DMRT1, NR5A1, SOX9, SRY	12	12	519.08	4.811e-11	1.488e-8
female gonad development	GO:0008585	4	NR5A1, NR2F2, LHCGR, INHBB	27	12	230.70	1.697e-9	3.587e-7
Sertoli cell differentiation	GO:0060008	3	DMRT1, NR5A1, SOX9	9	12	519.08	1.696e-8	2.710e-6
negative regulation of follicle-stimulating hormone secretion	GO:0046882	2	INHA, INHBB	3	12	1038.17	1.134e-6	9.164e-5
response to gonadotropin	GO:0034698	2	LHCGR, INHBB	4	12	778.63	2.267e-6	1.591e-4
ovarian follicle development	GO:0001541	3	LHCGR, INHA, INHBB	47	12	99.40	3.229e-6	2.119e-4
positive regulation of follicle-stimulating hormone secretion	GO:0046881	2	INHA, INHBB	6	12	519.08	5.662e-6	3.312e-4
sex determination	GO:0007530	2	NR5A1, SOX3	8	12	389.31	1.056e-5	5.431e-4
cell differentiation	GO:0030154	6	DMRT1, SOX9, SRY, NR2F2, INHA, INHBB	1051	12	8.89	2.150e-5	9.527e-4
Sertoli cell development	GO:0060009	2	DMRT1, SOX9	13	12	239.58	2.937e-5	1.202e-3
positive regulation of transcription by RNA polymerase II	GO:0045944	6	DMRT1, NR5A1, SOX3, SOX9, SRY, NR2F2	1208	12	7.73	4.747e-5	1.728e-3
oocyte development	GO:0048599	2	DMRT1, INHBB	19	12	163.92	6.425e-5	2.171e-3
seminiferous tubule development	GO:0072520	2	LHCGR, INHBB	21	12	148.31	7.885e-5	2.534e-3