

GeDiPNet Cluster 11 -- 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 06:49:55

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
spermatogenesis	GO:0007283	102	BRDT, DDX25, DMC1, ERCC1, KASH5, MCMDC2, MOV10L1, REC8, TDRD9, TDRKH, AKAP4, ARMC2	556	411	8.34	3.071e-65	1.790e-60
meiotic cell cycle	GO:0051321	45	BRDT, DMC1, HFM1, KASH5, MCMDC2, MEIOB, MSH5, REC8, SYCP3, TDRD9, TERB1, SLC26A8	137	411	14.93	1.235e-40	1.350e-36
cell differentiation	GO:0030154	88	BRDT, DDX25, SOX5, TDRD9, TDRKH, ARMC2, CATSPER1, CFAP69, SEPTIN12, SLC26A8, SPAG17, SPEF2	1051	411	3.81	2.643e-28	1.267e-24
piRNA processing	GO:0034587	17	HENMT1, MOV10L1, TDRD9, TDRKH, TDRD7, DDX4, FKBP6, GPAT2, MAEL, PIWIL1, PIWIL2, PLD6	21	411	36.81	2.623e-25	8.494e-22
flagellated sperm motility	GO:0030317	32	AKAP4, ARMC2, CATSPER1, CFAP251, CFAP43, CFAP44, CFAP65, CFAP69, DNAH1, DRC1, FSIP2, TTC21A	142	411	10.25	1.925e-23	5.140e-20
spermatid development	GO:0007286	28	DDX25, DMC1, REC8, SYCP3, TTC21A, ACTL7A, ADCY10, GALNTL5, PIWIL1, PLD6, SOX30, ZMYND15	120	411	10.61	4.269e-21	8.071e-18
male meiotic nuclear division	GO:0007140	15	BRDT, MEIOB, TDRD9, TDRKH, DDX4, MAEL, TDRD12, TEX11, ASZ1, SYCP2, TEX14, TEX15	31	411	22.00	2.307e-17	2.538e-14
fertilization	GO:0009566	18	MEIOB, REC8, TDRD9, TDRKH, ACTL9, AR, BAX, ACTL7A, CATSPER2, KLK14, MAEL, TDRD12	54	411	15.16	4.704e-17	4.826e-14
homologous chromosome pairing at meiosis	GO:0007129	15	DMC1, KASH5, MEIOB, REC8, TERB1, HORMAD1, MAEL, RNF212, TERB2, TEX15, MND1, MSH4	33	411	20.67	7.649e-17	7.515e-14
regulatory ncRNA-mediated gene silencing	GO:0031047	19	HENMT1, TDRD9, TDRKH, DROSHA, DDX4, FKBP6, MAEL, PIWIL1, PIWIL2, TDRD1, TDRD12, ASZ1	65	411	13.29	1.029e-16	9.834e-14
cilium movement	GO:0003341	17	CFAP251, CFAP43, CFAP70, TTC29, DNAAF4, CCDC40, DNAH11, DNAH3, DNAH5, DNAI1, ODAD2, CFAP61	48	411	16.10	1.080e-16	1.017e-13
oogenesis	GO:0048477	17	DMC1, ERCC1, KASH5, MCMDC2, KMT2D, NANOS2, HORMAD1, PIWIL2, NANOS1, STRA8, TAF4B, TERB2	53	411	14.58	7.435e-16	5.951e-13
cilium movement involved in cell motility	GO:0060294	13	DNAH1, DNAH17, DNAH10, DNAH11, DNAH3, DNAH5, DNAH6, DNAH7, DNAH8, DNAH2, TEK3, CFAP54	27	411	21.89	3.542e-15	2.539e-12
sperm axoneme assembly	GO:0007288	13	ARMC2, CFAP43, CFAP44, CFAP65, CFAP69, DNAH1, FSIP2, SPEF2, CCDC146, CEP131, CFAP58, TTC12	31	411	19.07	3.363e-14	2.000e-11
synaptonemal complex assembly	GO:0007130	12	MCMDC2, REC8, HORMAD1, SHOC1, TEX11, STAG3, SYCE1, SYCP2, TERB2, TEX15, MLH3, SPO11	25	411	21.82	4.389e-14	2.572e-11