

GeDiPNet Cluster 47 -- 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: 2026-10-08 03:23:04. · Rows: 15 · Generated: 2026-10-07 22:40:59

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
nucleus organization	GO:0006997	3	LMNA, SYNE1, ZMPSTE24	34	17	96.99	3.677e-6	2.393e-4
nuclear membrane organization	GO:0071763	2	TMEM43, EMD	7	17	314.07	1.631e-5	7.760e-4
muscle organ development	GO:0007517	3	LMNA, EMD, FHL1	114	17	28.93	1.413e-4	4.000e-3
pharyngeal system development	GO:0060037	2	BMP5, HOXA2	21	17	104.69	1.619e-4	4.423e-3
nuclear migration	GO:0007097	2	LMNA, SYNE2	22	17	99.93	1.780e-4	4.755e-3
motor neuron axon guidance	GO:0008045	2	HOXA2, PLXNA3	24	17	91.60	2.125e-4	5.374e-3
nuclear envelope organization	GO:0006998	2	LMNA, ZMPSTE24	24	17	91.60	2.125e-4	5.374e-3
cellular response to gamma radiation	GO:0071480	2	ZMPSTE24, WRN	28	17	78.52	2.904e-4	6.684e-3
determination of adult lifespan	GO:0008340	2	ZMPSTE24, WRN	38	17	57.85	5.372e-4	1.021e-2
response to estrogen	GO:0043627	2	KMT2D, ESR1	49	17	44.87	8.933e-4	1.440e-2
beta-catenin-TCF complex assembly	GO:1904837	1	KMT2D	1	17	1099.24	9.097e-4	1.456e-2
negative regulation of cation transmembrane transport	GO:1904063	1	MMP9	1	17	1099.24	9.097e-4	1.456e-2
negative regulation of epithelial cell differentiation involved in kidney development	GO:2000697	1	MMP9	1	17	1099.24	9.097e-4	1.456e-2
negative regulation of cortisol secretion	GO:0051463	1	PTPN11	1	17	1099.24	9.097e-4	1.456e-2
negative regulation of growth hormone secretion	GO:0060125	1	PTPN11	1	17	1099.24	9.097e-4	1.456e-2