

GeDiPNet Cluster 346 -- 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 22:43:43

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
immunoglobulin V(D)J recombination	GO:0033152	2	LIG4, XRCC4	6	32	194.66	4.243e-5	1.622e-3
double-strand break repair via nonhomologous end joining	GO:0006303	3	LIG4, XRCC4, SETMAR	45	32	38.93	6.164e-5	2.145e-3
response to magnesium ion	GO:0032026	2	BMP6, KCNC2	12	32	97.33	1.855e-4	4.894e-3
cellular response to lithium ion	GO:0071285	2	LIG4, XRCC4	15	32	77.86	2.942e-4	6.751e-3
regulation of ARF protein signal transduction	GO:0032012	2	IQSEC1, PSD4	19	32	61.47	4.770e-4	9.482e-3
response to X-ray	GO:0010165	2	LIG4, XRCC4	19	32	61.47	4.770e-4	9.482e-3
positive regulation of chondrocyte differentiation	GO:0032332	2	BMP6, SOX5	20	32	58.40	5.295e-4	1.016e-2
heparan sulfate proteoglycan biosynthetic process	GO:0015012	2	HS6ST3, XYLT1	30	32	38.93	1.199e-3	1.725e-2
establishment of integrated proviral latency	GO:0075713	1	LIG4	1	32	583.97	1.712e-3	2.128e-2
meiotic cell cycle checkpoint signaling	GO:0033313	1	NSUN2	1	32	583.97	1.712e-3	2.128e-2
mitotic DNA integrity checkpoint signaling	GO:0044774	1	SETMAR	1	32	583.97	1.712e-3	2.128e-2
negative regulation of chromosome organization	GO:2001251	1	SETMAR	1	32	583.97	1.712e-3	2.128e-2
base-excision repair	GO:0006284	2	LIG4, XRCC4	37	32	31.57	1.823e-3	2.200e-2
positive regulation of bone mineralization	GO:0030501	2	BMP6, KL	42	32	27.81	2.344e-3	2.546e-2
mechanosensory behavior	GO:0007638	1	ETV1	2	32	291.98	3.422e-3	3.102e-2