

GeDiPNet Cluster 119 -- 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: 2026-10-08 01:49:49

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
modulation of chemical synaptic transmission	GO:0050804	7	NLGN4X, IQSEC2, SYN1, SYP, GLRA2, GRIA3, NLGN3	121	106	10.20	5.749e-6	3.419e-4
presynaptic membrane assembly	GO:0097105	3	NLGN4X, IL1RAPL1, NLGN3	9	106	58.76	1.454e-5	7.104e-4
chromatin organization	GO:0006325	11	HCFC1, SMARCA1, OGT, TAF1, FAM50A, KDM5C, UBE2A, PHF8, PHIP, HDAC8, ATRX	449	106	4.32	4.875e-5	1.796e-3
synapse organization	GO:0050808	5	NLGN4X, PAK3, SYN1, RAB39B, NLGN3	72	106	12.24	5.525e-5	1.976e-3
brain development	GO:0007420	8	SMARCA1, AFF2, MECP2, UPF3B, PHF8, SOX3, AGTR2, SHROOM4	244	106	5.78	7.555e-5	2.511e-3
regulation of RNA splicing	GO:0043484	5	AFF2, FAM50A, HNRNPH1, HNRNPH2, PQBP1	78	106	11.30	8.115e-5	2.653e-3
positive regulation of transcription by RNA polymerase II	GO:0045944	18	HCFC1, SMARCA1, OGT, RPS6KA3, ARX, ZNF711, RBMX, MECP2, TAF1, ZFX, MED12, PHF8	1208	106	2.63	1.444e-4	4.063e-3
neuron differentiation	GO:0030182	7	NLGN4X, SMARCA1, IL1RAPL1, ACSL4, MECP2, OPHN1, SOX3	222	106	5.56	2.735e-4	6.406e-3
biogenic amine metabolic process	GO:0006576	2	MECP2, MAOA	5	106	70.52	3.152e-4	7.102e-3
social behavior	GO:0035176	4	NLGN4X, MECP2, PTCHD1, NLGN3	58	106	12.16	3.279e-4	7.285e-3
chromatin remodeling	GO:0006338	8	HCFC1, HUWE1, SMARCA1, TAF1, KDM5C, UBE2A, PHF8, ATRX	320	106	4.41	4.774e-4	9.487e-3
learning	GO:0007612	4	NLGN4X, FGF13, MECP2, NLGN3	64	106	11.02	4.784e-4	9.491e-3
positive regulation of synapse assembly	GO:0051965	4	IQSEC2, SLITRK2, IL1RAPL1, NLGN3	68	106	10.37	6.026e-4	1.108e-2
ubiquitin-dependent protein catabolic process	GO:0006511	7	HUWE1, KLHL15, TAF1, CUL4B, UBE2A, ZDHHC9, RLIM	257	106	4.80	6.572e-4	1.172e-2
neuron development	GO:0048666	4	THOC2, ARX, SYN1, DMD	77	106	9.16	9.631e-4	1.501e-2