

GeDiPNet Cluster 620 -- 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: 2026-10-20 03:23:14. · Rows: 15 · Generated: 2026-10-20 00:00:48

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
neuronal dense core vesicle exocytosis	GO:0099011	1	UNC13A	2	2	4671.75	2.140e-4	5.314e-3
dense core granule priming	GO:0061789	1	UNC13A	3	2	3114.50	3.211e-4	7.044e-3
regulation of miRNA metabolic process	GO:2000628	1	DROSHA	3	2	3114.50	3.211e-4	7.044e-3
regulation of regulatory T cell differentiation	GO:0045589	1	DROSHA	8	2	1167.94	8.560e-4	1.331e-2
miRNA metabolic process	GO:0010586	1	DROSHA	12	2	778.63	1.284e-3	1.669e-2
synaptic vesicle docking	GO:0016081	1	UNC13A	13	2	718.73	1.391e-3	1.753e-2
primary miRNA processing	GO:0031053	1	DROSHA	13	2	718.73	1.391e-3	1.753e-2
pre-miRNA processing	GO:0031054	1	DROSHA	14	2	667.39	1.498e-3	1.821e-2
miRNA processing	GO:0035196	1	DROSHA	17	2	549.62	1.819e-3	2.024e-2
synaptic vesicle priming	GO:0016082	1	UNC13A	19	2	491.76	2.033e-3	2.137e-2
positive regulation of dendrite extension	GO:1903861	1	UNC13A	23	2	406.24	2.460e-3	2.361e-2
neurotransmitter secretion	GO:0007269	1	UNC13A	29	2	322.19	3.101e-3	2.654e-2
regulation of synaptic transmission, glutamatergic	GO:0051966	1	UNC13A	33	2	283.14	3.529e-3	2.816e-2
synaptic transmission, glutamatergic	GO:0035249	1	UNC13A	45	2	207.63	4.811e-3	3.273e-2
regulatory ncRNA-mediated gene silencing	GO:0031047	1	DROSHA	65	2	143.75	6.945e-3	3.907e-2