

GeDiPNet Cluster 224 -- 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 00:30:58

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
positive regulation of long-term synaptic potentiation	GO:1900273	2	INS, SHANK3	24	9	173.03	5.660e-5	1.972e-3
cognition	GO:0050890	2	INS, SHANK3	64	9	64.89	4.093e-4	8.347e-3
epinephrine secretion	GO:0048242	1	VIP	1	9	2076.33	4.816e-4	9.305e-3
regulation of protein localization	GO:0032880	2	INS, VIP	89	9	46.66	7.901e-4	1.297e-2
negative regulation of glycogen catabolic process	GO:0045818	1	INS	2	9	1038.17	9.630e-4	1.467e-2
guanylate kinase-associated protein clustering	GO:0097117	1	SHANK3	2	9	1038.17	9.630e-4	1.467e-2
positive regulation of synapse structural plasticity	GO:0051835	1	SHANK3	3	9	692.11	1.444e-3	1.871e-2
positive regulation of nitric-oxide synthase activity	GO:0051000	1	INS	3	9	692.11	1.444e-3	1.871e-2
prolactin secretion	GO:0070459	1	VIP	3	9	692.11	1.444e-3	1.871e-2
olefinic compound metabolic process	GO:0120254	1	CYP17A1	4	9	519.08	1.925e-3	2.203e-2
positive regulation of nitric oxide mediated signal transduction	GO:0010750	1	INS	4	9	519.08	1.925e-3	2.203e-2
striatal medium spiny neuron differentiation	GO:0021773	1	SHANK3	4	9	519.08	1.925e-3	2.203e-2
AMPA glutamate receptor clustering	GO:0097113	1	SHANK3	5	9	415.27	2.406e-3	2.497e-2
NMDA glutamate receptor clustering	GO:0097114	1	SHANK3	5	9	415.27	2.406e-3	2.497e-2
positive regulation of dendritic spine maintenance	GO:1902952	1	INS	5	9	415.27	2.406e-3	2.497e-2