

GeDiPNet Cluster 120 -- 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 02:57:40

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
behavioral response to ethanol	GO:0048149	3	DRD4, DBH, OPRM1	10	35	160.17	7.158e-7	6.342e-5
G protein-coupled receptor signaling pathway, coupled to cyclic nucleotide second messenger	GO:0007187	4	DRD4, HTR1B, OPRD1, OPRM1	54	35	39.55	3.051e-6	2.023e-4
cellular response to alkaloid	GO:0071312	2	ABCB1, HTR1B	6	35	177.97	5.088e-5	1.824e-3
fear response	GO:0042596	2	DRD4, DBH	8	35	133.48	9.475e-5	2.904e-3
G protein-coupled opioid receptor signaling pathway	GO:0038003	2	OPRD1, OPRM1	9	35	118.65	1.217e-4	3.509e-3
mitotic spindle midzone assembly	GO:0051256	2	KIF23, RACGAP1	11	35	97.08	1.855e-4	4.794e-3
dopamine catabolic process	GO:0042420	2	MAOA, DBH	11	35	97.08	1.855e-4	4.794e-3
cerebellar Purkinje cell layer development	GO:0021680	2	HSPA5, FAIM2	12	35	88.99	2.223e-4	5.431e-3
erythrocyte differentiation	GO:0030218	3	CDIN1, RACGAP1, KLF1	65	35	24.64	2.428e-4	5.790e-3
maternal behavior	GO:0042711	2	DBH, BRINP1	14	35	76.27	3.058e-4	6.808e-3
adenylate cyclase-inhibiting G protein-coupled receptor signaling pathway	GO:0007193	3	HTR1B, OPRD1, OPRM1	73	35	21.94	3.422e-4	7.348e-3
vasoconstriction	GO:0042310	2	HTR1B, DBH	18	35	59.32	5.117e-4	9.703e-3
hematopoietic stem cell proliferation	GO:0071425	2	ETV6, MECOM	25	35	42.71	9.951e-4	1.502e-2
acyl-CoA metabolic process	GO:0006637	2	GCDH, ACSM2A	28	35	38.14	1.249e-3	1.732e-2
interleukin-1-mediated signaling pathway	GO:0070498	2	IRAK4, IL1R1	28	35	38.14	1.249e-3	1.732e-2