

GeDiPNet Cluster 210 -- 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 20:36:14

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
digestion	GO:0007586	4	PRSS1, PRSS2, CCK, SST	26	60	47.92	1.361e-6	1.059e-4
intestinal cholesterol absorption	GO:0030299	3	ABCG5, ABCG8, CEL	11	60	84.94	5.098e-6	3.055e-4
negative regulation of intestinal phytosterol absorption	GO:0010949	2	ABCG5, ABCG8	2	60	311.45	1.014e-5	5.270e-4
negative regulation of intestinal cholesterol absorption	GO:0045796	2	ABCG5, ABCG8	2	60	311.45	1.014e-5	5.270e-4
adenylate cyclase-activating G protein-coupled receptor signaling pathway	GO:0007189	6	CASR, ADRB2, CNR1, CNR2, HTR4, PTHLH	161	60	11.61	1.270e-5	6.288e-4
G protein-coupled receptor signaling pathway, coupled to cyclic nucleotide second messenger	GO:0007187	4	CCL2, CNR1, CNR2, HTR4	54	60	23.07	2.693e-5	1.127e-3
cannabinoid signaling pathway	GO:0038171	2	CNR1, CNR2	3	60	207.63	3.035e-5	1.230e-3
negative regulation of synaptic transmission, GABAergic	GO:0032229	2	CNR2, STXBP1	4	60	155.73	6.058e-5	2.071e-3
adenylate cyclase-activating G protein-coupled cAMP receptor signaling pathway	GO:0140582	2	CASR, PTHLH	5	60	124.58	1.008e-4	3.039e-3
chemosensory behavior	GO:0007635	2	CASR, TRPV1	6	60	103.82	1.508e-4	4.112e-3
bile acid secretion	GO:0032782	2	CASR, ABCB4	6	60	103.82	1.508e-4	4.112e-3
acute-phase response	GO:0006953	3	INS, SERPINA1, IL1RN	37	60	25.25	2.262e-4	5.498e-3
triglyceride homeostasis	GO:0070328	3	ABCG5, ABCG8, LPL	38	60	24.59	2.451e-4	5.834e-3
positive regulation of T cell activation	GO:0050870	3	CCL2, HLA-DQA1, HLA-DRB1	45	60	20.76	4.057e-4	8.295e-3
epidermis development	GO:0008544	4	HLA-DRB1, PPP3CA, PTCH1, PTHLH	114	60	10.93	4.923e-4	9.455e-3