

GeDiPNet Cluster 554 -- 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 00:00:31

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 gene expression	GO:0010628	16	CXCL8, MMP12, NR1I2, PPARG, RELA, VDR, AGO3, ALDH1A2, APOB, BCL3, GDF7, CLDN19	504	95	6.24	4.801e-9	9.252e-7
cellular oxidant detoxification	GO:0098869	6	GPX3, GPX7, PTGS2, MGST1, NNT, APOE	66	95	17.88	1.046e-6	8.905e-5
liver development	GO:0001889	6	HGF, RELA, ALDH1A2, RPGRIP1L, HNF1B, SOD2	87	95	13.57	5.334e-6	3.331e-4
response to oxidative stress	GO:0006979	7	GPX3, GPX7, PTGS2, MSRA, APOE, SOD2, TP53	146	95	9.43	9.575e-6	5.253e-4
negative regulation of apoptotic process	GO:0043066	12	HGF, MCL1, PTGS2, RELA, SLC9A1, BCL3, DUSP1, NNT, ASIC2, HNF1B, SOD2, TP53	524	95	4.50	1.375e-5	6.966e-4
negative regulation of membrane hyperpolarization	GO:1902631	2	CRTC1, SOD2	2	95	196.71	2.557e-5	1.109e-3
response to acidic pH	GO:0010447	3	SLC9A1, SST, ASIC2	12	95	49.18	2.709e-5	1.158e-3
positive regulation of mitochondrial membrane permeability	GO:0035794	2	SLC9A1, TP53	3	95	131.14	7.647e-5	2.535e-3
apoptotic process involved in mammary gland involution	GO:0060057	2	VDR, CDKN2A	3	95	131.14	7.647e-5	2.535e-3
cyclooxygenase pathway	GO:0019371	2	CTHRC1, PTGS2	3	95	131.14	7.647e-5	2.535e-3
histamine transport	GO:0051608	2	SLC22A2, SLC22A3	3	95	131.14	7.647e-5	2.535e-3
negative regulation of cell population proliferation	GO:0008285	10	CDH13, CXCL8, SST, VDR, ALDH1A2, DUSP1, CLDN19, SOD2, TP53, CDKN2A	444	95	4.43	8.639e-5	2.775e-3
positive regulation of apoptotic process involved in mammary gland involution	GO:0060058	2	VDR, CDKN2A	4	95	98.35	1.524e-4	4.192e-3
spermidine transmembrane transport	GO:1903711	2	SLC22A2, SLC22A3	4	95	98.35	1.524e-4	4.192e-3
histamine uptake	GO:0051615	2	SLC22A2, SLC22A3	4	95	98.35	1.524e-4	4.192e-3