

GeDiPNet Cluster 187 -- 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 12:43:41

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
response to oxidative stress	GO:0006979	6	KRT1, CAT, KEAP1, MPO, NFE2L2, TP53	146	12	64.00	1.824e-10	4.926e-8
intermediate filament organization	GO:0045109	4	KRT1, KRT10, KRT16, KRT9	70	12	88.99	8.735e-8	1.076e-5
morphogenesis of an epithelium	GO:0002009	3	KRT10, KRT16, KRT9	51	12	91.60	4.141e-6	2.579e-4
response to xenobiotic stimulus	GO:0009410	4	AHR, CAT, NFE2L2, TP53	248	12	25.12	1.378e-5	6.709e-4
protein heterotetramerization	GO:0051290	2	KRT1, KRT10	16	12	194.66	4.514e-5	1.669e-3
peptide cross-linking	GO:0018149	2	KRT1, KRT10	19	12	163.92	6.425e-5	2.171e-3
hydrogen peroxide catabolic process	GO:0042744	2	CAT, MPO	21	12	148.31	7.885e-5	2.534e-3
positive regulation of reactive oxygen species metabolic process	GO:2000379	2	NFE2L2, TP53	34	12	91.60	2.097e-4	5.211e-3
establishment of skin barrier	GO:0061436	2	KRT1, KRT16	37	12	84.18	2.486e-4	5.900e-3
reactive oxygen species metabolic process	GO:0072593	2	NFE2L2, TP53	45	12	69.21	3.685e-4	7.727e-3
cellular response to glucose starvation	GO:0042149	2	NFE2L2, TP53	50	12	62.29	4.552e-4	8.970e-3
response to UV	GO:0009411	2	CAT, TP53	54	12	57.68	5.310e-4	9.979e-3
response to amitrole	GO:0072722	1	CAT	1	12	1557.25	6.422e-4	1.127e-2
negative regulation of helicase activity	GO:0051097	1	TP53	1	12	1557.25	6.422e-4	1.127e-2
regulation of intrinsic apoptotic signaling pathway by p53 class mediator	GO:1902253	1	TP53	1	12	1557.25	6.422e-4	1.127e-2