

GeDiPNet Cluster 232 -- 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 00:26:53

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
establishment of skin barrier	GO:0061436	6	KRT1, ALOX12B, ALOXE3, ABCA12, UGCG, FLG	37	25	121.21	6.781e-12	2.592e-9
keratinocyte differentiation	GO:0030216	6	TGM1, ST14, ABCA12, CERS3, UGCG, FLG	69	25	65.00	3.400e-10	8.557e-8
ceramide biosynthetic process	GO:0046513	5	PNPLA1, ALOX12B, ALOXE3, CYP4F22, CERS3	41	25	91.16	2.031e-9	4.190e-7
peptide cross-linking	GO:0018149	4	TGM1, KRT1, FLG, KRT2	19	25	157.36	9.524e-9	1.638e-6
keratinization	GO:0031424	5	TGM1, KRT1, ABCA12, CASP14, KRT2	73	25	51.20	3.957e-8	5.563e-6
lipid metabolic process	GO:0006629	10	PNPLA1, ALOX12B, ALOXE3, CYP4F22, LIPN, CERS3, SULT2B1, UGCG, ABHD5, SLC27A4	840	25	8.90	5.642e-8	7.515e-6
cornification	GO:0070268	3	LIPN, CERS3, CASP14	8	25	280.31	1.179e-7	1.387e-5
epidermis development	GO:0008544	5	CERS3, CASP14, UGCG, COL7A1, KRT2	114	25	32.78	3.728e-7	3.653e-5
sphingolipid metabolic process	GO:0006665	4	ALOX12B, ALOXE3, CERS3, UGCG	59	25	50.68	1.079e-6	8.812e-5
protein lipidation	GO:0006497	2	ALOX12B, UGCG	4	25	373.74	1.029e-5	5.328e-4
lipid oxidation	GO:0034440	2	ALOX12B, ALOXE3	8	25	186.87	4.788e-5	1.738e-3
hepoxilin biosynthetic process	GO:0051122	2	ALOX12B, ALOXE3	8	25	186.87	4.788e-5	1.738e-3
lipid homeostasis	GO:0055088	3	PNPLA1, ABCA12, ABHD5	55	25	40.77	5.300e-5	1.883e-3
skin development	GO:0043588	3	ASPRV1, ERCC2, SLC27A4	55	25	40.77	5.300e-5	1.883e-3
lipoxygenase pathway	GO:0019372	2	ALOX12B, ALOXE3	11	25	135.91	9.381e-5	2.882e-3