

GeDiPNet Cluster 62 -- 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: 2026-10-09 03:23:08. · Rows: 15 · Generated: 2026-10-09 09:23:07

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
gap junction-mediated intercellular transport	GO:1990349	2	GJB2, GJB6	6	16	389.31	1.029e-5	5.373e-4
cell communication by electrical coupling	GO:0010644	2	GJB2, GJB6	7	16	333.70	1.440e-5	6.992e-4
gap junction assembly	GO:0016264	2	GJB2, GJB6	8	16	291.98	1.919e-5	8.765e-4
cell communication	GO:0007154	3	GJB2, GJB6, GJB3	80	16	43.80	4.064e-5	1.546e-3
peptide cross-linking	GO:0018149	2	LORICRIN, KRT2	19	16	122.94	1.165e-4	3.401e-3
hematopoietic stem cell homeostasis	GO:0061484	2	ARMCX5-GPRASP2, GPRASP2	30	16	77.86	2.948e-4	6.673e-3
sensory perception of sound	GO:0007605	3	GJB2, GJB6, POU3F4	162	16	21.63	3.296e-4	7.218e-3
omega-hydroxyceramide biosynthetic process	GO:0106342	1	PNPLA1	1	16	1167.94	8.562e-4	1.377e-2
mitochondrial ncRNA surveillance	GO:0035945	1	SUPV3L1	1	16	1167.94	8.562e-4	1.377e-2
mitochondrial mRNA surveillance	GO:0035946	1	SUPV3L1	1	16	1167.94	8.562e-4	1.377e-2
mitochondrial RNA surveillance	GO:2000827	1	SUPV3L1	1	16	1167.94	8.562e-4	1.377e-2
cell-cell signaling	GO:0007267	3	GJB2, GJB6, GJB3	234	16	14.97	9.623e-4	1.485e-2
urate biosynthetic process	GO:0034418	1	PRPS1	2	16	583.97	1.712e-3	2.101e-2
hypoxanthine biosynthetic process	GO:0046101	1	PRPS1	2	16	583.97	1.712e-3	2.101e-2
keratinocyte activation	GO:0032980	1	KRT2	2	16	583.97	1.712e-3	2.101e-2