

GeDiPNet Cluster 276 -- 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 12:07:59

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
apoptotic mitochondrial changes	GO:0008637	2	SLC25A4, SOD2	20	7	266.96	2.278e-5	9.930e-4
acetylcholine-mediated vasodilation involved in regulation of systemic arterial blood pressure	GO:0003069	1	SOD2	1	7	2669.57	3.746e-4	7.813e-3
erythrocyte differentiation	GO:0048773	1	SOD2	1	7	2669.57	3.746e-4	7.813e-3
response to magnetism	GO:0071000	1	SOD2	1	7	2669.57	3.746e-4	7.813e-3
negative regulation of membrane hyperpolarization	GO:1902631	1	SOD2	2	7	1334.79	7.491e-4	1.251e-2
detection of oxygen	GO:0003032	1	SOD2	3	7	889.86	1.123e-3	1.623e-2
positive regulation of vascular associated smooth muscle cell differentiation involved in phenotypic switching	GO:1905932	1	SOD2	3	7	889.86	1.123e-3	1.623e-2
fructose catabolic process to hydroxyacetone phosphate and glyceraldehyde-3-phosphate	GO:0061624	1	TKFC	3	7	889.86	1.123e-3	1.623e-2
response to L-ascorbic acid	GO:0033591	1	SOD2	4	7	667.39	1.498e-3	1.912e-2
negative regulation of MDA-5 signaling pathway	GO:0039534	1	TKFC	4	7	667.39	1.498e-3	1.912e-2
response to silicon dioxide	GO:0034021	1	SOD2	4	7	667.39	1.498e-3	1.912e-2
response to isolation stress	GO:0035900	1	SOD2	4	7	667.39	1.498e-3	1.912e-2
positive regulation of hydrogen peroxide biosynthetic process	GO:0010729	1	SOD2	4	7	667.39	1.498e-3	1.912e-2
response to manganese ion	GO:0010042	1	SOD2	5	7	533.91	1.872e-3	2.187e-2
response to superoxide	GO:0000303	1	SOD2	5	7	533.91	1.872e-3	2.187e-2