

GeDiPNet Cluster 596 -- 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 03:23:13. · Rows: 15 · Generated: 2026-10-19 23:17:26

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
actin filament uncapping	GO:0051695	1	ACTN2	1	1	18687.00	5.351e-5	1.943e-3
phospholipase C-activating angiotensin-activated signaling pathway	GO:0086097	1	ACTN2	3	1	6229.00	1.605e-4	4.340e-3
microspike assembly	GO:0030035	1	ACTN2	4	1	4671.75	2.141e-4	5.314e-3
positive regulation of cation channel activity	GO:2001259	1	ACTN2	5	1	3737.40	2.676e-4	6.245e-3
positive regulation of endocytic recycling	GO:2001137	1	ACTN2	6	1	3114.50	3.211e-4	7.044e-3
negative regulation of potassium ion transport	GO:0043267	1	ACTN2	8	1	2335.88	4.281e-4	8.531e-3
positive regulation of potassium ion transport	GO:0043268	1	ACTN2	9	1	2076.33	4.816e-4	9.241e-3
negative regulation of protein localization to cell surface	GO:2000009	1	ACTN2	12	1	1557.25	6.422e-4	1.113e-2
postsynaptic actin cytoskeleton organization	GO:0098974	1	ACTN2	20	1	934.35	1.070e-3	1.514e-2
muscle cell development	GO:0055001	1	ACTN2	23	1	812.48	1.231e-3	1.640e-2
cardiac muscle cell development	GO:0055013	1	ACTN2	25	1	747.48	1.338e-3	1.709e-2
focal adhesion assembly	GO:0048041	1	ACTN2	28	1	667.39	1.498e-3	1.821e-2
anatomical structure formation involved in morphogenesis	GO:0048646	1	ACTN2	30	1	622.90	1.605e-3	1.885e-2
sarcomere organization	GO:0045214	1	ACTN2	43	1	434.58	2.301e-3	2.277e-2
regulation of membrane potential	GO:0042391	1	ACTN2	85	1	219.85	4.549e-3	3.200e-2