

GeDiPNet Cluster 409 -- 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 15:45:18

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
positive regulation of NF-kappaB transcription factor activity	GO:0051092	2	RIPK4, CHUK	80	2	233.59	1.810e-5	8.295e-4
response to acetate	GO:0010034	1	CHUK	1	2	9343.50	1.070e-4	3.177e-3
response to cholecystokinin	GO:0061847	1	CHUK	2	2	4671.75	2.140e-4	5.282e-3
response to hydroperoxide	GO:0033194	1	CHUK	9	2	1038.17	9.630e-4	1.467e-2
striated muscle cell differentiation	GO:0051146	1	CHUK	20	2	467.18	2.139e-3	2.343e-2
pattern recognition receptor signaling pathway	GO:0002221	1	CHUK	21	2	444.93	2.246e-3	2.412e-2
response to amino acid	GO:0043200	1	CHUK	22	2	424.70	2.353e-3	2.480e-2
positive regulation of interferon-alpha production	GO:0032727	1	CHUK	26	2	359.37	2.781e-3	2.708e-2
skeletal muscle contraction	GO:0003009	1	CHUK	32	2	291.98	3.422e-3	3.030e-2
non-canonical NF-kappaB signal transduction	GO:0038061	1	CHUK	34	2	274.81	3.636e-3	3.139e-2
toll-like receptor 4 signaling pathway	GO:0034142	1	CHUK	42	2	222.46	4.490e-3	3.472e-2
negative regulation of NF-kappaB transcription factor activity	GO:0032088	1	CHUK	46	2	203.12	4.917e-3	3.634e-2
morphogenesis of an epithelium	GO:0002009	1	RIPK4	51	2	183.21	5.451e-3	3.835e-2
skin development	GO:0043588	1	RIPK4	55	2	169.88	5.878e-3	3.982e-2
tumor necrosis factor-mediated signaling pathway	GO:0033209	1	CHUK	60	2	155.73	6.411e-3	4.146e-2