

GeDiPNet Cluster 408 -- 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 00:56:49

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
ERBB2-ERBB3 signaling pathway	GO:0038133	2	ERBB3, ERBB2	9	20	207.63	3.900e-5	1.499e-3
epidermal growth factor receptor signaling pathway	GO:0007173	3	PTPN11, ERBB3, ERBB2	64	20	43.80	4.190e-5	1.583e-3
atrioventricular canal development	GO:0036302	2	GATA4, PTPN11	11	20	169.88	5.951e-5	2.057e-3
wound healing	GO:0042060	3	GATA4, ERBB3, ERBB2	76	20	36.88	7.012e-5	2.326e-3
positive regulation of hormone secretion	GO:0046887	2	EDN3, PTPN11	12	20	155.73	7.136e-5	2.357e-3
endocardial cushion development	GO:0003197	2	GATA4, ERBB3	13	20	143.75	8.429e-5	2.672e-3
myofibril assembly	GO:0030239	2	LMOD1, MYL9	15	20	124.58	1.133e-4	3.329e-3
heart development	GO:0007507	4	GATA4, PTPN11, ERBB3, ERBB2	273	20	13.69	1.795e-4	4.680e-3
Schwann cell development	GO:0014044	2	ERBB3, ERBB2	20	20	93.44	2.044e-4	5.130e-3
smooth muscle contraction	GO:0006939	2	MYH11, MYLK	24	20	77.86	2.961e-4	6.695e-3
peripheral nervous system development	GO:0007422	2	ERBB3, ERBB2	26	20	71.87	3.483e-4	7.493e-3
positive regulation of intracellular signal transduction	GO:1902533	2	PTPN11, ERBB2	43	20	43.46	9.572e-4	1.485e-2
phthalate metabolic process	GO:0018963	1	SRD5A2	1	20	934.35	1.070e-3	1.580e-2
tonic smooth muscle contraction	GO:0014820	1	MYLK	1	20	934.35	1.070e-3	1.580e-2
negative regulation of cortisol secretion	GO:0051463	1	PTPN11	1	20	934.35	1.070e-3	1.580e-2