

GeDiPNet Cluster 85 -- 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: 2026-10-08 03:23:04. · Rows: 15 · Generated: 2026-10-08 12:08:59

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
cardiac muscle contraction	GO:0060048	6	MYBPC3, MYH7, TTN, CASQ2, KCNQ1, RYR2	43	29	89.91	4.713e-11	1.448e-8
striated muscle contraction	GO:0006941	4	MYH7, TTN, CASQ2, RYR2	24	29	107.40	4.863e-8	6.659e-6
positive regulation of heart rate	GO:0010460	4	EDN1, NPPA, KCNQ1, RYR2	25	29	103.10	5.784e-8	7.641e-6
regulation of heart rate	GO:0002027	4	MYH7, CASQ2, KCNQ1, RYR2	39	29	66.09	3.705e-7	3.670e-5
cellular response to caffeine	GO:0071313	3	SELENON, CASQ2, RYR2	11	29	175.74	5.498e-7	5.120e-5
Purkinje myocyte to ventricular cardiac muscle cell signaling	GO:0086029	2	CASQ2, RYR2	2	29	644.38	2.325e-6	1.658e-4
response to muscle stretch	GO:0035994	3	EDN1, NPPA, RYR2	20	29	96.66	3.763e-6	2.439e-4
glomerular endothelium development	GO:0072011	2	EDN1, PECAM1	5	29	257.75	2.319e-5	1.015e-3
regulation of atrial cardiac muscle cell membrane repolarization	GO:0060372	2	NPPA, KCNQ1	6	29	214.79	3.475e-5	1.390e-3
sarcomere organization	GO:0045214	3	FLNC, MYBPC3, TTN	43	29	44.96	3.977e-5	1.543e-3
positive regulation of cardiac muscle contraction	GO:0060452	2	NPPA, KCNQ1	9	29	143.20	8.315e-5	2.697e-3
gastric acid secretion	GO:0001696	2	HRH2, KCNQ1	9	29	143.20	8.315e-5	2.697e-3
mitochondrial DNA replication	GO:0006264	2	POLG, RRM2B	11	29	117.16	1.268e-4	3.681e-3
cellular response to epinephrine stimulus	GO:0071872	2	KCNQ1, RYR2	12	29	107.40	1.520e-4	4.219e-3
cardiac muscle hypertrophy	GO:0003300	2	TTN, RYR2	13	29	99.14	1.795e-4	4.778e-3