

GeDiPNet Cluster 310 -- 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 00:26:30

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
detection of muscle stretch	GO:0035995	2	TTN, CAV3	7	15	355.94	1.260e-5	6.253e-4
visual perception	GO:0007601	4	BEST1, IMPG1, IMPG2, PRPH2	215	15	23.18	2.106e-5	9.358e-4
cardiac muscle hypertrophy	GO:0003300	2	TTN, CAV3	13	15	191.66	4.667e-5	1.706e-3
muscle filament sliding	GO:0030049	2	MYH7, TTN	15	15	166.11	6.277e-5	2.133e-3
detection of light stimulus involved in visual perception	GO:0050908	2	BEST1, PRPH2	24	15	103.82	1.643e-4	4.388e-3
striated muscle contraction	GO:0006941	2	MYH7, TTN	24	15	103.82	1.643e-4	4.388e-3
cardiac muscle cell development	GO:0055013	2	TTN, CAV3	25	15	99.66	1.785e-4	4.667e-3
regulation of calcium ion transport	GO:0051924	2	BEST1, CAV3	25	15	99.66	1.785e-4	4.667e-3
positive regulation of ubiquitin-dependent protein catabolic process	GO:2000060	2	VCP, CAV3	30	15	83.05	2.582e-4	6.050e-3
skeletal muscle contraction	GO:0003009	2	MYH7, TTN	32	15	77.86	2.942e-4	6.617e-3
ATP metabolic process	GO:0046034	2	VCP, MYH7	36	15	69.21	3.730e-4	7.800e-3
regulation of heart rate	GO:0002027	2	MYH7, CAV3	39	15	63.89	4.381e-4	8.716e-3
intracellular protein localization	GO:0008104	3	IMPG2, SQSTM1, CAV3	194	15	19.26	4.572e-4	8.993e-3
cardiac muscle contraction	GO:0060048	2	MYH7, TTN	43	15	57.94	5.328e-4	9.981e-3
sarcomere organization	GO:0045214	2	TTN, FLNC	43	15	57.94	5.328e-4	9.981e-3