

GeDiPNet Cluster 460 -- 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 03:23:14. · Rows: 15 · Generated: 2026-10-20 00:01:14

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
ganglioside catabolic process	GO:0006689	3	HEXA, GM2A, HEXB	8	4	1751.91	2.060e-10	5.841e-8
lipid storage	GO:0019915	3	HEXA, GM2A, HEXB	32	4	437.98	1.822e-8	2.969e-6
neuromuscular process controlling balance	GO:0050885	3	HEXA, GM2A, HEXB	53	4	264.44	8.600e-8	1.114e-5
dermatan sulfate proteoglycan catabolic process	GO:0030209	2	HEXA, HEXB	4	4	2335.88	2.062e-7	2.318e-5
oligosaccharide catabolic process	GO:0009313	2	GM2A, HEXB	12	4	778.63	2.267e-6	1.680e-4
glycosaminoglycan metabolic process	GO:0030203	2	HEXA, HEXB	12	4	778.63	2.267e-6	1.680e-4
hyaluronan catabolic process	GO:0030214	2	HEXA, HEXB	16	4	583.97	4.120e-6	2.713e-4
sexual reproduction	GO:0019953	2	HEXA, HEXB	17	4	549.62	4.669e-6	3.006e-4
carbohydrate derivative metabolic process	GO:1901135	2	HEXA, HEXB	18	4	519.08	5.252e-6	3.288e-4
N-glycan processing	GO:0006491	2	HEXA, HEXB	19	4	491.76	5.869e-6	3.597e-4
lysosome organization	GO:0007040	2	HEXA, HEXB	65	4	143.75	7.116e-5	2.399e-3
myelination	GO:0042552	2	HEXA, HEXB	73	4	127.99	8.986e-5	2.859e-3
locomotory behavior	GO:0007626	2	HEXA, HEXB	99	4	94.38	1.656e-4	4.434e-3
positive regulation of termination of DNA-templated transcription	GO:0060566	1	SETX	1	4	4671.75	2.141e-4	5.314e-3
male courtship behavior	GO:0008049	1	HEXB	1	4	4671.75	2.141e-4	5.314e-3