

GeDiPNet Cluster 564 -- 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 00:01:21

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
DNA repair	GO:0006281	3	PNKP, APTX, SETX	420	6	22.25	2.144e-4	5.321e-3
positive regulation of termination of DNA-templated transcription	GO:0060566	1	SETX	1	6	3114.50	3.211e-4	7.044e-3
involuntary skeletal muscle contraction	GO:0003011	1	ATP8A2	1	6	3114.50	3.211e-4	7.044e-3
DNA damage response	GO:0006974	3	PNKP, APTX, SETX	577	6	16.19	5.463e-4	1.004e-2
positive regulation of neuron projection development	GO:0010976	2	SETX, ATP8A2	121	6	51.48	6.132e-4	1.092e-2
positive regulation of termination of RNA polymerase II transcription, poly(A)-coupled	GO:2000806	1	SETX	3	6	1038.17	9.630e-4	1.423e-2
positive regulation of phospholipid translocation	GO:0061092	1	ATP8A2	4	6	778.63	1.284e-3	1.669e-2
retinal blood vessel morphogenesis	GO:0061304	1	LAMA1	6	6	519.08	1.925e-3	2.069e-2
regulation of basement membrane organization	GO:0110011	1	LAMA1	6	6	519.08	1.925e-3	2.069e-2
termination of RNA polymerase II transcription	GO:0006369	1	SETX	7	6	444.93	2.246e-3	2.244e-2
aminophospholipid translocation	GO:0140331	1	ATP8A2	7	6	444.93	2.246e-3	2.244e-2
positive regulation of DNA-templated transcription initiation	GO:2000144	1	SETX	8	6	389.31	2.566e-3	2.402e-2
neurofilament cytoskeleton organization	GO:0060052	1	ATP8A2	10	6	311.45	3.207e-3	2.689e-2
morphogenesis of an epithelial sheet	GO:0002011	1	LAMA1	10	6	311.45	3.207e-3	2.689e-2
branching involved in salivary gland morphogenesis	GO:0060445	1	LAMA1	12	6	259.54	3.847e-3	2.937e-2