

GeDiPNet Shared-Gene Disease Pairs

Similarity: Jaccard index on shared curated genes (disease_gdp). Significance: upper-tail hypergeometric test ($P(X \geq k)$), Benjamini-Hochberg FDR-corrected across all tested pairs. Corroborated Shared Genes: count of shared genes backed by ≥ 2 distinct disease_gdp.main_source values combined across both diseases (e.g. GWAS-backed for one, ClinVar-backed for the other still counts); Shared Gene Names lists each gene's own source count in parentheses. Overlap Coefficient: shared genes / MIN(each disease's own total gene count) -- complements the Jaccard-based Similarity Score by showing how much of the SMALLER disease's entire known gene-set is covered by this pair, which Jaccard (dividing by the union) can understate. Shared Cluster: cluster id if both diseases fall in the same label-propagation cluster (scripts/build_disease_clusters.php), blank otherwise. See scripts/build_related.php on gedipnet.bicnirrh.res.in. Data as of: 2026-10-10 03:00:13. Filters applied: disease name contains "STT3A-congenital disorder of glycosylation" (5 matching pairs). · Rows: 5 · Generated: 2026-10-10 13:39:38

Disease A	Disease B	Shared Genes	Corroborated Shared Genes	Shared Gene Names	Similarity Score	Overlap Coefficient	P-value	FDR Q-value	Shared Cluster
Autism	STT3A-congenital disorder of glycosylation	1	1	STT3A (2)	0.00068	1.00000	9.501e-2	9.603e-2	
Bipolar disorder	STT3A-congenital disorder of glycosylation	1	1	STT3A (2)	0.00082	1.00000	7.923e-2	8.034e-2	
Attention deficit hyperactivity disorder	STT3A-congenital disorder of glycosylation	1	1	STT3A (2)	0.00090	1.00000	7.176e-2	7.308e-2	
Congenital disorder of glycosylation	STT3A-congenital disorder of glycosylation	1	1	STT3A (5)	0.01000	1.00000	6.429e-3	7.682e-3	
congenital disorder of glycosylation, type 1w, autosomal dominant	STT3A-congenital disorder of glycosylation	1	0	STT3A (1)	0.50000	1.00000	6.494e-5	2.331e-4	