

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 "lissencephaly spectrum disorder with complex brainstem malformation" (5 matching pairs). · Rows: 5 · Generated: 2026-10-10 15:07:55

Disease A	Disease B	Shared Genes	Corroborated Shared Genes	Shared Gene Names	Similarity Score	Overlap Coefficient	P-value	FDR Q-value	Shared Cluster
Lissencephaly	lissencephaly spectrum disorder with complex brainstem malformation	1	1	MACF1 (5)	0.01961	1.00000	3.247e-3	4.245e-3	
lissencephaly spectrum disorder with complex brainstem malformation	Sleep apnea	1	1	MACF1 (2)	0.02000	1.00000	3.182e-3	4.168e-3	
Diabetic eye disease	lissencephaly spectrum disorder with complex brainstem malformation	1	1	MACF1 (2)	0.02041	1.00000	3.117e-3	4.096e-3	73
Cerebellar hypoplasia/atrophy, epilepsy, and global developmental delay	lissencephaly spectrum disorder with complex brainstem malformation	1	1	MACF1 (2)	0.02703	1.00000	2.338e-3	3.243e-3	
Diabetic nephropathy type 2	lissencephaly spectrum disorder with complex brainstem malformation	1	1	MACF1 (2)	0.05263	1.00000	1.169e-3	1.895e-3	73