

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: 2026-10-13 03:00:13. Filters applied: disease name contains "Rin2 syndrome" (5 matching pairs). · Rows: 5 · Generated: 2026-10-13 08:12:58

Disease A	Disease B	Shared Genes	Corroborated Shared Genes	Shared Gene Names	Similarity Score	Overlap Coefficient	P-value	FDR Q-value	Shared Cluster
Cerebral atherosclerosis	Rin2 syndrome	1	1	RIN2 (5)	0.07692	1.00000	7.793e-4	1.405e-3	
Glioblastoma	Rin2 syndrome	1	1	RIN2 (5)	0.00164	1.00000	3.942e-2	4.128e-2	
Central nervous system cancer	Rin2 syndrome	1	1	RIN2 (5)	0.00152	1.00000	4.260e-2	4.439e-2	
Glioma	Rin2 syndrome	1	1	RIN2 (5)	0.00132	1.00000	4.923e-2	5.102e-2	
Colorectal cancer	Rin2 syndrome	1	1	RIN2 (5)	0.00102	1.00000	6.338e-2	6.481e-2	