GeDiPNet Shared-Gene Disease Pairs

Similarity: Jaccard index on shared curated genes (disease_gdp). Significance: upper-tail hypergeometric test (P(X>=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: 2026-10-20 03:00:20. Filters applied: disease name contains "Merrf syndrome" (4 matching pairs). · Rows: 4 · Generated: 2026-10-20 04:13:21

Disease A	Disease B	Shared Genes	Corroborated Shared Genes	Shared Gene Names	Similarity Score	Overlap Coefficient	P-value	FDR Q-value	Shared Cluster
Merrf syndrome	Optic atrophy	1	0	TRNK (1)	0.00524	0.50000	2.426e-2	2.580e-2	
Merrf syndrome	Mitochondrial myopathy	1	0	TRNP (1)	0.05263	0.50000	2.194e-3	2.917e-3	
Merrf syndrome	Sensorineural hearing impairment	1	0	TRNK (1)	0.16667	0.50000	5.165e-4	9.125e-4	
Merrf syndrome	Multiple symmetric lipomatosis	1	0	TRNK (1)	0.33333	1.00000	1.291e-4	3.269e-4	