

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: 2026-10-11 03:00:14. Filters applied: disease name contains "enhanced s-cone syndrome" (5 matching pairs). · Rows: 5 · Generated: 2026-10-10 21:38:21

Disease A	Disease B	Shared Genes	Corroborated Shared Genes	Shared Gene Names	Similarity Score	Overlap Coefficient	P-value	FDR Q-value	Shared Cluster
enhanced s-cone syndrome	Optic atrophy	1	1	NR2E3 (2)	0.00549	1.00000	1.175e-2	1.316e-2	
Cone-rod dystrophy	enhanced s-cone syndrome	1	1	NR2E3 (2)	0.01333	1.00000	4.806e-3	5.921e-3	
enhanced s-cone syndrome	Leber congenital amaurosis	1	1	NR2E3 (2)	0.01370	1.00000	4.676e-3	5.787e-3	
enhanced s-cone syndrome	inherited retinal dystrophy	1	0	NR2E3 (1)	0.06250	1.00000	9.742e-4	1.665e-3	
enhanced s-cone syndrome	Goldmann-favre syndrome	1	1	NR2E3 (4)	0.50000	1.00000	6.494e-5	2.331e-4	