

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 "anterior segment dysgenesis 8" (5 matching pairs). · Rows: 5 · Generated: 2026-10-11 09:12:59

Disease A	Disease B	Shared Genes	Corroborated Shared Genes	Shared Gene Names	Similarity Score	Overlap Coefficient	P-value	FDR Q-value	Shared Cluster
anterior segment dysgenesis 8	Cataract	1	1	CPAMD8 (2)	0.00495	1.00000	1.305e-2	1.458e-2	
anterior segment dysgenesis 8	Retinal detachment	1	1	CPAMD8 (2)	0.02128	1.00000	2.987e-3	3.949e-3	
anterior segment dysgenesis 8	Selective iga deficiency disease	1	1	CPAMD8 (2)	0.03125	1.00000	2.013e-3	2.901e-3	
Anterior segment dysgenesis	anterior segment dysgenesis 8	1	1	CPAMD8 (5)	0.04167	1.00000	1.494e-3	2.313e-3	
anterior segment dysgenesis 8	Anterior segment mesenchymal dysgenesis	1	1	CPAMD8 (3)	0.06667	1.00000	9.092e-4	1.576e-3	