

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: 2026-10-20 03:00:20. Filters applied: disease name contains "Anterior segment dysgenesis 8" (5 matching pairs). · Rows: 5 · Generated: 2026-10-20 00:05:31

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 (3)	0.00472	1.00000	1.362e-2	1.498e-2	
Anterior segment dysgenesis 8	Retinal detachment	1	1	CPAMD8 (3)	0.02128	1.00000	2.970e-3	3.788e-3	
Anterior segment dysgenesis 8	Selective iga deficiency disease	1	1	CPAMD8 (3)	0.03125	1.00000	2.002e-3	2.719e-3	
Anterior segment dysgenesis	Anterior segment dysgenesis 8	1	1	CPAMD8 (6)	0.04000	1.00000	1.550e-3	2.192e-3	75
Anterior segment dysgenesis 8	Anterior segment mesenchymal dysgenesis	1	1	CPAMD8 (4)	0.06667	1.00000	9.039e-4	1.411e-3	75