

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: 2026-10-12 03:00:13. Filters applied: disease name contains "Congenital anosmia" (4 matching pairs). · Rows: 4 · Generated: 2026-10-12 15:35:26

Disease A	Disease B	Shared Genes	Corroborated Shared Genes	Shared Gene Names	Similarity Score	Overlap Coefficient	P-value	FDR Q-value	Shared Cluster
Anosmia	Congenital anosmia	2	2	CNGA2 (2), TENM1 (2)	0.66667	1.00000	8.436e-9	6.818e-8	
Congenital anosmia	Moyamoya angiopathy	1	0	TENM1 (1)	0.02632	0.50000	4.671e-3	5.787e-3	
Cerebral palsy	Congenital anosmia	1	1	TENM1 (2)	0.02083	0.50000	5.966e-3	7.186e-3	
Congenital anosmia	Hearing loss	1	0	TENM1 (1)	0.00257	0.50000	4.964e-2	5.144e-2	