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 "Chondrodysplasia with multiple dislocations and amelogenesis imperfecta" (5 matching pairs). · Rows: 5 · Generated: 2026-10-20 04:21:38

Disease A	Disease B	Shared Genes	Corroborated Shared Genes	Shared Gene Names	Similarity Score	Overlap Coefficient	P-value	FDR Q-value	Shared Cluster
Chondrodysplasia with multiple dislocations and amelogenesis imperfecta	Short stature, amelogenesis imperfecta, and skeletal dysplasia with scoliosis	1	1	SLC10A7 (2)	0.50000	1.00000	6.457e-5	1.985e-4	
Chondrodysplasia with multiple dislocations and amelogenesis imperfecta	Headache	1	1	SLC10A7 (2)	0.09091	1.00000	6.457e-4	1.087e-3	
Chondrodysplasia with multiple dislocations and amelogenesis imperfecta	Short stature	1	0	SLC10A7 (1)	0.04545	1.00000	1.356e-3	1.965e-3	
Chondrodysplasia with multiple dislocations and amelogenesis imperfecta	Skeletal dysplasia	1	0	SLC10A7 (1)	0.02326	1.00000	2.712e-3	3.483e-3	
Bone fragility with contractures, arterial rupture, and deafness	Chondrodysplasia with multiple dislocations and amelogenesis imperfecta	1	1	SLC10A7 (2)	0.02000	1.00000	3.164e-3	4.003e-3	