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Retina enrichment

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Many of the genes associated with human [retinal diseases](#) are preferentially expressed in the retina, and this has motivated a search for retina-specific genes. In the Early Edition of the [Proceedings of the National Academy of Sciences](#), Katsanis *et al.* describe a [computational approach](#) to selecting genes that might be linked to retinopathies. They mined the human subset of the NCBI database of ESTs ([dbEST](#)) for transcripts expressed in human retinal cDNA libraries and performed an *in silico* subtraction to identify retina-enriched sequences. Over 900 nonredundant clusters were isolated, including many of the known retinopathy-associated genes and others that were confirmed experimentally. Katsanis *et al.* mapped the ESTs onto the human genome and identified several [candidate genes](#) for retinopathy disorders.

References

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