Resource Summary Report

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NEIBank

RRID:SCR_007294
Type: Tool

Proper Citation

NEIBank (RRID:SCR_007294)

Resource Information

URL: http://neibank.nei.nih.gov

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Description: An integrated resource for genomics and bioinformatics in vision research including expressed sequence tag (EST) data and sequence-verified cDNA clones for multiple eye tissues of several species, web-based access to human eye-specific SAGE data through EyeSAGE, and comprehensive, annotated databases of known human eye disease genes and candidate disease gene loci. All expression- and disease-related data are integrated in EyeBrowse, an eye-centric genome browser. NEIBank provides a comprehensive overview of current knowledge of the transcriptional repertoires of eye tissues and their relation to pathology. The data can be interrogated in several ways. Specific gene names can be entered into the search window. Alternatively, regions of the genome can be displayed. For example, entering two STS markers separated by a semicolon (e.g. RH18061;RH80175) allows the display of the entire chromosomal region associated with the mapping of a specific disease locus. ESTs for each tissue can then be displayed to help in the selection of candidate genes. In addition, sequences can be entered into a BLAST search and rapidly aligned on the genome, again showing eye derived ESTs for the same region. To see the same region at the full UCSC site, cut and paste the location from the position window of the genome browser. EyeBrowse includes a custom track display SAGE data for human eye tissues derived from the EyeSAGE project. The track shows the normalized sum of SAGE tag counts from all published eye-related SAGE datasets centered on the position of each identifiable Unigene cluster. This indicates relative activity of each gene locus in eye. Clicking on the vertical count bar for a particular location will bring up a display listing gene details and linking to specific SAGE counts for each eye SAGE library and comparisons with normalized sums for neural and non-neural tissues. To view or alter settings for the EyeSAGE track on EyeBrowse, click on the vertical gray bar at the left of the display. Other custom tracks display known eye disease genes and mapped intervals for candidate loci for retinal disease, cataract, myopia and cornea disease. These link back to

further information at NEIBank.

Abbreviations: NEIBank

Synonyms: NEI Bank

Resource Type: database, service resource, production service resource, data analysis service, analysis service resource, data or information resource

Defining Citation: PMID:18648525

Keywords: ear, taste, genetics, cdna, chicken, ciliary body, cornea, fovea, dog, guinea pig, human, iris, lacrimal gland, lens, mouse, ocular surface system, optic nerve, rabbit, rat, retina, rpe, choroid, sequence data, trabecular meshwork, whole eye, zebrafish, library, vision, eye, gene, library, disease, loci, ocular genomics, cdna library, expressed sequence tag, blast, cataract, cornea, glaucoma, myopia, retinal disease, genomics, eye tracking device

Related Condition: Eye disease, Cataract, Glaucoma, Myopia, Retinal disease

Funding: NIH Blueprint for Neuroscience Research ;
NEI R01 EY13315;
NEI R01 EY11286;
NEI P30EY0054722

Resource Name: NEIBank

Resource ID: SCR_007294

Alternate IDs: nif-0000-00097

Record Creation Time: 20220129T080241+0000

Record Last Update: 20250418T055146+0000

Ratings and Alerts

No rating or validation information has been found for NEIBank.

No alerts have been found for NEIBank.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 15 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Gross C, et al. (2023) The Ins and Outs of Clusterin: Its Role in Cancer, Eye Diseases and Wound Healing. International journal of molecular sciences, 24(17).

Shinde V, et al. (2021) Pathogenic alleles in microtubule, secretory granule and extracellular matrix-related genes in familial keratoconus. Human molecular genetics, 30(8), 658.

Rosa-Fernandes L, et al. (2020) Cellular Imprinting Proteomics Assay: A Novel Method for Detection of Neural and Ocular Disorders Applied to Congenital Zika Virus Syndrome. Journal of proteome research, 19(11), 4496.

Shiels A, et al. (2020) TRPM3_miR-204: a complex locus for eye development and disease. Human genomics, 14(1), 7.

Paraoan L, et al. (2020) Secretory proteostasis of the retinal pigmented epithelium: Impairment links to age-related macular degeneration. Progress in retinal and eye research, 79, 100859.

Zhang J, et al. (2019) Novel Mutations Associated With Various Types of Corneal Dystrophies in a Han Chinese Population. Frontiers in genetics, 10, 881.

Kim MS, et al. (2019) Genetic Mutation Profiles in Korean Patients with Inherited Retinal Diseases. Journal of Korean medical science, 34(21), e161.

Ansar M, et al. (2018) Bi-allelic Loss-of-Function Variants in DNMBP Cause Infantile Cataracts. American journal of human genetics, 103(4), 568.

Liu Y, et al. (2017) Major review: Molecular genetics of primary open-angle glaucoma. Experimental eye research, 160, 62.

Wistow G, et al. (2012) The human crystallin gene families. Human genomics, 6(1), 26.

Larsson M, et al. (2011) GWAS findings for human iris patterns: associations with variants in genes that influence normal neuronal pattern development. American journal of human genetics, 89(2), 334.

Hildebrand MS, et al. (2007) Gene expression profiling analysis of the inner ear. Hearing research, 225(1-2), 1.

Wyatt K, et al. (2006) Lengsin is a survivor of an ancient family of class I glutamine synthetases re-engineered by evolution for a role in the vertebrate lens. Structure (London, England : 1993), 14(12), 1823.

Wiggs JL, et al. (2004) A genomewide scan identifies novel early-onset primary open-angle glaucoma loci on 9q22 and 20p12. American journal of human genetics, 74(6), 1314.

Pompeia C, et al. (2004) Gene expression profile of the mouse organ of Corti at the onset of hearing. Genomics, 83(6), 1000.