Resource Summary Report

Generated by NIF on Apr 27, 2025

Ancora

RRID:SCR_001623
Type: Tool

Proper Citation

Ancora (RRID:SCR_001623)

Resource Information

URL: http://ancora.genereg.net/

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Description: Web resource that provides data and tools for exploring genomic organization of highly conserved noncoding elements (HCNEs) for multiple genomes. It includes a genome browser that shows HCNE locations and features novel HCNE density plots as a powerful tool to discover developmental regulatory genes and distinguish their regulatory elements and domains. They identify HCNEs as non-exonic regions of high similarity between genome sequences from distantly related organisms, such as human and fish, and provide tools for studying the distribution of HCNEs along chromosomes. Major peaks of HCNE density along chromosomes most often coincide with developmental regulatory genes. Their aim with this site is to aid discovery of developmental regulatory genes, their regulatory domains and their fundamental regulatory elements.

Abbreviations: Ancora

Synonyms: Atlas of Noncoding Conserved Regions in Animals

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

Defining Citation: PMID:18279518

Keywords: genome, highly conserved noncoding element, noncoding element, regulatory gene, regulatory domain, regulatory element, developmental regulatory gene, evolution, enhancer

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Availability: Acknowledgement requested

Resource Name: Ancora

Resource ID: SCR_001623

Alternate IDs: nlx_153891

Record Creation Time: 20220129T080208+0000

Record Last Update: 20250426T055451+0000

Ratings and Alerts

No rating or validation information has been found for Ancora.

No alerts have been found for Ancora.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 19 mentions in open access literature.

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

Iliopoulou E, et al. (2024) Extensive Loss and Gain of Conserved Noncoding Elements During Early Teleost Evolution. Genome biology and evolution, 16(4).

Chua EHZ, et al. (2022) The importance of considering regulatory domains in genome-wide analyses - the nearest gene is often wrong! Biology open, 11(4).

Inoue J, et al. (2021) dbCNS: A New Database for Conserved Noncoding Sequences. Molecular biology and evolution, 38(4), 1665.

Joshi M, et al. (2021) Impact of Genetic Variation in Gene Regulatory Sequences: A Population Genomics Perspective. Frontiers in genetics, 12, 660899.

Pérez-Palma E, et al. (2020) Copy number variants in lipid metabolism genes are associated with gallstones disease in men. European journal of human genetics : EJHG, 28(2), 264.

Fishman V, et al. (2019) 3D organization of chicken genome demonstrates evolutionary conservation of topologically associated domains and highlights unique architecture of

erythrocytes' chromatin. Nucleic acids research, 47(2), 648.

Harmston N, et al. (2017) Topologically associating domains are ancient features that coincide with Metazoan clusters of extreme noncoding conservation. Nature communications, 8(1), 441.

Kim S, et al. (2016) Understanding Editing Behaviors in Multilingual Wikipedia. PloS one, 11(5), e0155305.

Liu T, et al. (2015) Gene Coexpression and Evolutionary Conservation Analysis of the Human Preimplantation Embryos. BioMed research international, 2015, 316735.

Li CF, et al. (2015) Identification of Critical Region Responsible for Split Hand/Foot Malformation Type 3 (SHFM3) Phenotype through Systematic Review of Literature and Mapping of Breakpoints Using Microarray Data. Microarrays (Basel, Switzerland), 5(1).

Makunin IV, et al. (2014) Underreplicated regions in Drosophila melanogaster are enriched with fast-evolving genes and highly conserved noncoding sequences. Genome biology and evolution, 6(8), 2050.

Lybæk H, et al. (2014) RevSex duplication-induced and sex-related differences in the SOX9 regulatory region chromatin landscape in human fibroblasts. Epigenetics, 9(3), 416.

Sharma Y, et al. (2014) Computational characterization of modes of transcriptional regulation of nuclear receptor genes. PloS one, 9(2), e88880.

Díaz-Castillo C, et al. (2012) Evaluation of the role of functional constraints on the integrity of an ultraconserved region in the genus Drosophila. PLoS genetics, 8(2), e1002475.

Winkelmann J, et al. (2011) Genome-wide association study identifies novel restless legs syndrome susceptibility loci on 2p14 and 16q12.1. PLoS genetics, 7(7), e1002171.

Harewood L, et al. (2010) Bilateral renal agenesis/hypoplasia/dysplasia (BRAHD): postmortem analysis of 45 cases with breakpoint mapping of two de novo translocations. PloS one, 5(8), e12375.

Navratilova P, et al. (2009) Systematic human/zebrafish comparative identification of cis-regulatory activity around vertebrate developmental transcription factor genes. Developmental biology, 327(2), 526.

Previti C, et al. (2009) Profile analysis and prediction of tissue-specific CpG island methylation classes. BMC bioinformatics, 10, 116.

Engström PG, et al. (2008) Ancora: a web resource for exploring highly conserved noncoding elements and their association with developmental regulatory genes. Genome biology, 9(2), R34.