Resource Summary Report

Generated by NIF on May 19, 2025

ECRbase

RRID:SCR_001052
Type: Tool

Proper Citation

ECRbase (RRID:SCR_001052)

Resource Information

URL: http://ecrbase.dcode.org/

Proper Citation: ECRbase (RRID:SCR_001052)

Description: ECRbase is the Database of Evolutionary Conserved Regions (ECRs), Promoters, and Transcription Factor Binding Sites in Vertebrate Genomes created using ECR Browser alignments. Currently there are over 26 million ECRs available in the ECRbase that correspond to regions extracted from pairwise comparisons of all the available species.

Synonyms: ECRbase

Resource Type: database, data or information resource

Defining Citation: PMID:17090579

Keywords: ecr, evolutionary conserved region

Funding:

Resource Name: ECRbase

Resource ID: SCR_001052

Alternate IDs: nif-0000-02785

Record Creation Time: 20220129T080205+0000

Record Last Update: 20250517T055453+0000

Ratings and Alerts

No rating or validation information has been found for ECRbase.

No alerts have been found for ECRbase.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 7 mentions in open access literature.

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

Li L, et al. (2022) SoxD genes are required for adult neural stem cell activation. Cell reports, 38(5), 110313.

Zhang Q, et al. (2020) Axenfeld-Rieger syndrome-associated mutants of the transcription factor FOXC1 abnormally regulate NKX2-5 in model zebrafish embryos. The Journal of biological chemistry, 295(33), 11902.

Shumay E, et al. (2017) New Repeat Polymorphism in the AKT1 Gene Predicts Striatal Dopamine D2/D3 Receptor Availability and Stimulant-Induced Dopamine Release in the Healthy Human Brain. The Journal of neuroscience : the official journal of the Society for Neuroscience, 37(19), 4982.

Guan D, et al. (2014) PTHGRN: unraveling post-translational hierarchical gene regulatory networks using PPI, ChIP-seq and gene expression data. Nucleic acids research, 42(Web Server issue), W130.

Sandhu KS, et al. (2012) Large-scale functional organization of long-range chromatin interaction networks. Cell reports, 2(5), 1207.

Roessler E, et al. (2012) Unique alterations of an ultraconserved non-coding element in the 3'UTR of ZIC2 in holoprosencephaly. PloS one, 7(7), e39026.

Re A, et al. (2009) Genome-wide survey of microRNA-transcription factor feed-forward regulatory circuits in human. Molecular bioSystems, 5(8), 854.