

Resource Summary Report

Generated by PRECISE-TBI on Sep 8, 2026

Dinucleotide Property Database

RRID:SCR_007128

Type: Tool

Proper Citation

Dinucleotide Property Database (RRID:SCR_007128)

Resource Information

URL: <http://diprodb.fli-leibniz.de>

Proper Citation: Dinucleotide Property Database (RRID:SCR_007128)

Description: The Dinucleotide Property Database is designed to collect and analyse thermodynamic, structural and other dinucleotide properties. The table presenting all the dinucleotide properties can be pruned and rearranged by different criteria. The database contains different export and analysis functions.

Synonyms: DiProDB

Resource Type: data or information resource, database

Keywords: dinucleotide

Related Condition: Aging

Resource Name: Dinucleotide Property Database

Resource ID: SCR_007128

Alternate IDs: nif-0000-02753

Record Creation Time: 20220129T080240+0000

Record Last Update: 20260905T133138+0000

Ratings and Alerts

No rating or validation information has been found for Dinucleotide Property Database.

No alerts have been found for Dinucleotide Property Database.

Data and Source Information

Usage and Citation Metrics

We found 9 mentions in open access literature.

Listed below are recent publications. The full list is available at [PRECISE-TBI](#) .

Savina EA, et al. (2023) Core Promoter Regions of Antisense and Long Intergenic Non-Coding RNAs. International journal of molecular sciences, 24(9).

Melikhova AV, et al. (2022) Evolutionary Invariant of the Structure of DNA Double Helix in RNAP II Core Promoters. International journal of molecular sciences, 23(18).

Yella VR, et al. (2020) Delving into Eukaryotic Origins of Replication Using DNA Structural Features. ACS omega, 5(23), 13601.

Meher PK, et al. (2020) miRNALoc: predicting miRNA subcellular localizations based on principal component scores of physico-chemical properties and pseudo compositions of di-nucleotides. Scientific reports, 10(1), 14557.

Batmanov K, et al. (2017) Predicting Variation of DNA Shape Preferences in Protein-DNA Interaction in Cancer Cells with a New Biophysical Model. Genes, 8(9).

Singh VK, et al. (2016) Context based computational analysis and characterization of ARS consensus sequences (ACS) of Saccharomyces cerevisiae genome. Genomics data, 9, 130.

Il'icheva IA, et al. (2016) Structural features of DNA that determine RNA polymerase II core promoter. BMC genomics, 17(1), 973.

Tsai ZT, et al. (2015) Contribution of Sequence Motif, Chromatin State, and DNA Structure Features to Predictive Models of Transcription Factor Binding in Yeast. PLoS computational biology, 11(8), e1004418.

Pan J, et al. (2011) A hierarchical combination of factors shapes the genome-wide topography of yeast meiotic recombination initiation. Cell, 144(5), 719.