

Resource Summary Report

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Online Nucleosomes Position Prediction by Genomic Sequence

RRID:SCR_004210

Type: Tool

Proper Citation

Online Nucleosomes Position Prediction by Genomic Sequence (RRID:SCR_004210)

Resource Information

URL: http://genie.weizmann.ac.il/software/nucleo_prediction.html

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Description: This tool allows you to submit a genomic sequence and to receive a prediction of the nucleosomes positions on it, based on the nucleosome-DNA interaction model that we developed in these papers: * Segal et al., A Genomic Code for Nucleosome Positioning, Nature 2006 * Field et al., Distinct Modes of Regulation by Chromatin Encoded through Nucleosome Positioning Signals, PLoS Comp Biol. 2008 * Kaplan et al., The DNA-Encoded Nucleosome Organization of a Eukaryotic Genome, Nature 2008 We recommend using the latest version of the model (Version 3), which is applicable to all species. Paste in a sequence to analyze or upload file. You can provide multiple sequences in fasta format (separate sequences by lines starting with ">" followed by the sequence name). The length of each sequence must be between 147bp and 40kb bp. Note: Due to boundary effects, we highly recommend that you add at least 5000 bp of flanking sequence around your sequence of interest. You can generate the nucleosomes positioning predictions on your own machine using our executable and wrapping Perl scripts.

Synonyms: Nucleosomes Position Prediction

Resource Type: production service resource, data analysis service, software resource, service resource, analysis service resource

Defining Citation: [PMID:16862119](#)

Resource Name: Online Nucleosomes Position Prediction by Genomic Sequence

Resource ID: SCR_004210

Alternate IDs: nlx_23258

Record Creation Time: 20220129T080223+0000

Record Last Update: 20260815T182248+0000

Ratings and Alerts

No rating or validation information has been found for Online Nucleosomes Position Prediction by Genomic Sequence.

No alerts have been found for Online Nucleosomes Position Prediction by Genomic Sequence.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 14 mentions in open access literature.

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

Kharerin H, et al. (2021) Thermodynamic modeling of genome-wide nucleosome depleted regions in yeast. PLoS computational biology, 17(1), e1008560.

Xiong J, et al. (2016) Dissecting relative contributions of cis- and trans-determinants to nucleosome distribution by comparing Tetrahymena macronuclear and micronuclear chromatin. Nucleic acids research, 44(21), 10091.

Hettiarachchi N, et al. (2016) GC Content Heterogeneity Transition of Conserved Noncoding Sequences Occurred at the Emergence of Vertebrates. Genome biology and evolution, 8(11), 3377.

Parmar JJ, et al. (2016) Theoretical estimates of exposure timescales of protein binding sites on DNA regulated by nucleosome kinetics. Nucleic acids research, 44(4), 1630.

Kharerin H, et al. (2016) Role of transcription factor-mediated nucleosome disassembly in PHO5 gene expression. Scientific reports, 6, 20319.

Liu J, et al. (2015) DNA sequence templates adjacent nucleosome and ORC sites at gene amplification origins in Drosophila. Nucleic acids research, 43(18), 8746.

Cui F, et al. (2014) Prediction of nucleosome rotational positioning in yeast and human genomes based on sequence-dependent DNA anisotropy. BMC bioinformatics, 15(1), 313.

Hettiarachchi N, et al. (2014) Lineage-specific conserved noncoding sequences of plant genomes: their possible role in nucleosome positioning. Genome biology and evolution,

6(9), 2527.

Gubelmann C, et al. (2013) A yeast one-hybrid and microfluidics-based pipeline to map mammalian gene regulatory networks. *Molecular systems biology*, 9, 682.

Stanlie A, et al. (2012) The DSIF subunits Spt4 and Spt5 have distinct roles at various phases of immunoglobulin class switch recombination. *PLoS genetics*, 8(4), e1002675.

Pedone F, et al. (2012) Preferential nucleosome occupancy at high values of DNA helical rise. *DNA research : an international journal for rapid publication of reports on genes and genomes*, 19(1), 81.

Palermo RD, et al. (2011) RNA polymerase II stalling promotes nucleosome occlusion and pTEFb recruitment to drive immortalization by Epstein-Barr virus. *PLoS pathogens*, 7(10), e1002334.

Mahapatra S, et al. (2011) Yeast H2A.Z, FACT complex and RSC regulate transcription of tRNA gene through differential dynamics of flanking nucleosomes. *Nucleic acids research*, 39(10), 4023.

Caserta M, et al. (2009) A translational signature for nucleosome positioning in vivo. *Nucleic acids research*, 37(16), 5309.