Resource Summary Report

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PReMod

RRID:SCR_003403
Type: Tool

Proper Citation

PReMod (RRID:SCR_003403)

Resource Information

URL: http://genomequebec.mcgill.ca/PReMod

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Description: Database that describes more than 100,000 computational predicted transcriptional regulatory modules within the human genome. These modules represent the regulatory potential for 229 transcription factors families and are the first genome-wide / transcription factor-wide collection of predicted regulatory modules for the human genome. The algorithm used involves two steps: (i) Identification and scoring of putative transcription factor binding sites using 481 TRANSFAC 7.2 position weight matrices (PWMs) for vertebrate transcription factors. To this end, each non-coding position of the human genome was evaluated for its similarity to each PWM using a log-likelihood ratio score with a local GC-parameterized third-order Markov background model. Corresponding orthologous positions in mouse and rat genomes were evaluated similarly and a weighted average of the human, mouse, and rat log-likelihood scores at aligned positions (based on a Multiz (Blanchette et al. 2004) genome-wide alignment of these three species) was used to define the matrix score for each genomic position and each PWM. (ii) Detection of clustered putative binding sites. To assign a module score to a given region, the five transcription factors with the highest total scoring hits are identified, and a p-value is assigned to the total score observed of the top 1, 2, 3, 4, or 5 factors. The p-value computation takes into consideration the number of factors involved (1 to 5), their total binding site scores, and the length and GC content of the region under evaluation. Users can retrieve all information for a given region, a given PWM, a given gene and so on. Several options are given for textual output or visualization of the data.

Abbreviations: PReMod

Synonyms: Predicted Regulatory Modules

Resource Type: database, data or information resource

Defining Citation: PMID:17148480

Keywords: cis-regulatory module, genome, transcription factor binding site, chromosome, module, predict, gene

Funding:

Resource Name: PReMod

Resource ID: SCR_003403

Alternate IDs: nif-0000-03334, OMICS_01873

Record Creation Time: 20220129T080218+0000

Record Last Update: 20250420T015459+0000

Ratings and Alerts

No rating or validation information has been found for PReMod.

No alerts have been found for PReMod.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 11 mentions in open access literature.

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

Villalba GC, et al. (2021) Fantastic databases and where to find them: Web applications for researchers in a rush. Genetics and molecular biology, 44(2), e20200203.

Huang CL, et al. (2021) Add-On Selective Estrogen Receptor Modulators for Methadone Maintenance Treatment. Frontiers in endocrinology, 12, 638884.

Rezaeian A, et al. (2021) Methylation Status of MTHFR Promoter and Oligozoospermia Risk: An Epigenetic Study and in Silico Analysis. Cell journal, 22(4), 482.

Mohammadpanah M, et al. (2020) Relationship of hypomethylation CpG islands in interleukin-6 gene promoter with IL-6 mRNA levels in patients with coronary atherosclerosis.

Journal of cardiovascular and thoracic research, 12(3), 214.

Yang D, et al. (2018) A two-level model for the role of complex and young genes in the formation of organism complexity and new insights into the relationship between evolution and development. EvoDevo, 9, 22.

Chiang YC, et al. (2017) Reduced dosing and liability in methadone maintenance treatment by targeting oestrogen signal for morphine addiction. Journal of cellular and molecular medicine, 21(12), 3552.

Lin VC, et al. (2017) Vitamin D receptor-binding site variants affect prostate cancer progression. Oncotarget, 8(43), 74119.

Kleftogiannis D, et al. (2016) Progress and challenges in bioinformatics approaches for enhancer identification. Briefings in bioinformatics, 17(6), 967.

Chan LW, et al. (2015) Novel structural co-expression analysis linking the NPM1-associated ribosomal biogenesis network to chronic myelogenous leukemia. Scientific reports, 5, 10973.

Hajjari M, et al. (2014) Characterizing the Retinoblastoma 1 locus: putative elements for Rb1 regulation by in silico analysis. Frontiers in genetics, 5, 2.

McKee AE, et al. (2006) Systems biology of gene regulation fulfills its promise. Genome biology, 7(5), 316.