Resource Summary Report

Generated by dkNET on Apr 18, 2025

JASPAR

RRID:SCR_003030
Type: Tool

Proper Citation

JASPAR (RRID:SCR_003030)

Resource Information

URL: http://jaspar.genereg.net

Proper Citation: JASPAR (RRID:SCR_003030)

Description: Open source database of curated, non-redundant set of profiles derived from published collections of experimentally defined transcription factor binding sites for multicellular eukaryotes. Consists of open data access, non-redundancy and quality. JASPAR CORE is smaller set that is non-redundant and curated. Collection of transcription factor DNA-binding preferences, modeled as matrices. These can be converted into Position Weight Matrices (PWMs or PSSMs), used for scanning genomic sequences. Web interface for browsing, searching and subset selection, online sequence analysis utility and suite of programming tools for genome-wide and comparative genomic analysis of regulatory regions. New functions include clustering of matrix models by similarity, generation of random matrices by sampling from selected sets of existing models and a language-independent Web Service applications programming interface for matrix retrieval.

Abbreviations: JASPAR

Synonyms: JASPAR, JASPAR CORE, JASPAR CORE database, JASPAR database

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

Defining Citation: PMID:18006571, PMID:16381983, PMID:14681366

Keywords: structural class, transcription factor binding site, profile, regulatory region, genome, genomic, matrix, transcription factor, binding site, dna, FASEB list

Funding: Novo Nordisk Foundation ;
European Union ;

EMBRACEa Sixth Framework Network of Excellence ;
Sars Centre ;
Carlsberg Foundation

Availability: Free, Freely available

Resource Name: JASPAR

Resource ID: SCR_003030

Alternate IDs: OMICS_00538, nif-0000-03061

Old URLs: http://129.177.120.189/cgi-bin/jaspar2010/jaspar_db.pl, http://jaspar.cgb.ki.se

Record Creation Time: 20220129T080216+0000

Record Last Update: 20250418T055010+0000

Ratings and Alerts

No rating or validation information has been found for JASPAR.

No alerts have been found for JASPAR.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 4045 mentions in open access literature.

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

Su S, et al. (2025) Analysis of the CHS Gene Family Reveals Its Functional Responses to Hormones, Salinity, and Drought Stress in Moso Bamboo (Phyllostachys edulis). Plants (Basel, Switzerland), 14(2).

Du X, et al. (2025) Synthetic Retinoid Sulfarotene Selectively Inhibits Tumor-Repopulating Cells of Intrahepatic Cholangiocarcinoma via Disrupting Cytoskeleton by P-Selectin/PSGL1 N-Glycosylation Blockage. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(3), e2407519.

Chen X, et al. (2025) Enhancing immunotherapy efficacy in colorectal cancer: targeting the FGR-AKT-SP1-DKK1 axis with DCC-2036 (Rebastinib). Cell death & disease, 16(1), 8.

Tong L, et al. (2025) YBX1 alleviates ferroptosis in osteoporosis via the ATF4/FSP1 axis in

an m5C manner. Journal of orthopaedic surgery and research, 19(1), 685.

Qian S, et al. (2025) Downregulation of FcRn promotes ferroptosis in herpes simplex virus-1-induced lung injury. Cellular and molecular life sciences : CMLS, 82(1), 36.

Wang H, et al. (2025) Targeting EGFR-binding protein SLC7A11 enhancing antitumor immunity of T cells via inducing MHC-I antigen presentation in nasopharyngeal carcinoma. Cell death & disease, 16(1), 21.

Zhou C, et al. (2025) The transcription factor GABPA is a master regulator of naive pluripotency. Nature cell biology, 27(1), 48.

She P, et al. (2025) The transcriptional repressor HEY2 regulates mitochondrial oxidative respiration to maintain cardiac homeostasis. Nature communications, 16(1), 232.

An W, et al. (2025) Exploration of the shared diagnostic genes and molecular mechanism between obesity and atherosclerosis via bioinformatic analysis. Scientific reports, 15(1), 2301.

Pampari A, et al. (2025) ChromBPNet: bias factorized, base-resolution deep learning models of chromatin accessibility reveal cis-regulatory sequence syntax, transcription factor footprints and regulatory variants. bioRxiv : the preprint server for biology.

Lin Z, et al. (2025) NOX4 exacerbates Parkinson's disease pathology by promoting neuronal ferroptosis and neuroinflammation. Neural regeneration research, 20(7), 2038.

Katayama M, et al. (2025) Exercise-induced methylation of the Serhl2 promoter and implication for lipid metabolism in rat skeletal muscle. Molecular metabolism, 92, 102081.

Zhong Y, et al. (2025) ZmCCD8 regulates sugar and amino acid accumulation in maize kernels via strigolactone signalling. Plant biotechnology journal, 23(2), 492.

Luo Y, et al. (2025) Characterization and functional analysis of conserved non-coding sequences among poaceae: insights into gene regulation and phenotypic variation in maize. BMC genomics, 26(1), 46.

Liu TW, et al. (2025) The steroid hormone 20-hydroxyecdysone inhibits RAPTOR expression by repressing Hox gene transcription to induce autophagy. The Journal of biological chemistry, 301(1), 108093.

Fanourgakis G, et al. (2025) DNA methylation modulates nucleosome retention in sperm and H3K4 methylation deposition in early mouse embryos. Nature communications, 16(1), 465.

Li XY, et al. (2025) Tryptophan metabolism-related gene CYP1B1 serves as a shared biomarker for both Parkinson's disease and insomnia. Scientific reports, 15(1), 1362.

Ikawa T, et al. (2025) Impact of Hyaluronic Acid on the Cutaneous T-Cell Lymphoma Microenvironment: A Novel Anti-Tumor Mechanism of Bexarotene. Cancers, 17(2).

Aggarwal N, et al. (2025) Insights into expression and localization of HPV16 LCR-associated transcription factors and association with LCR activity in HNSCC. Molecular therapy. Oncology, 33(1), 200926.

Grant ZL, et al. (2025) Dose-dependent sensitivity of human 3D chromatin to a heart disease-linked transcription factor. bioRxiv : the preprint server for biology.