Resource Summary Report

Generated by NIF on May 7, 2025

EPDnew

RRID:SCR_002485
Type: Tool

Proper Citation

EPDnew (RRID:SCR_002485)

Resource Information

URL: https://epd.expasy.org/epd/

Proper Citation: EPDnew (RRID:SCR_002485)

Description: EPDnew databases are the result of merging Eukaryotic Promoter Database, EPD, promoters within house analysis of promoter specific high throughput data for selected organisms only. EPDnew is a set of species specific databases of experimentally validated promoters.

Abbreviations: HT-EPD, EPD

Synonyms: , Eukaryotic Promoter Database, Eukaryotic Promoter Database new

Resource Type: data or information resource, database

Defining Citation: PMID:27899657, PMID:23193273

Keywords: Promoter collection, eukaryotic promoter, promoter specific high throughput data, species specific data, experimentally validated promoter, promoter, data

Funding: Swiss Government ;
Swiss National Science Foundation

Availability: Free, Freely available

Resource Name: EPDnew

Resource ID: SCR_002485

Alternate IDs: nif-0000-02806

Alternate URLs: https://epd.expasy.org/

Record Creation Time: 20220129T080213+0000

Record Last Update: 20250507T060050+0000

Ratings and Alerts

No rating or validation information has been found for EPDnew.

No alerts have been found for EPDnew.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 26 mentions in open access literature.

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

Zhao Z, et al. (2024) Guide for phenotype-specific profiling of DNA G-quadruplex-regulated genes. STAR protocols, 5(1), 102820.

Daich Varela M, et al. (2023) Multidisciplinary team directed analysis of whole genome sequencing reveals pathogenic non-coding variants in molecularly undiagnosed inherited retinal dystrophies. Human molecular genetics, 32(4), 595.

Gr?bowski R, et al. (2023) The role of SOD2 and NOS2 genes in the molecular aspect of bladder cancer pathophysiology. Scientific reports, 13(1), 14491.

Mahat DB, et al. (2023) Single-cell nascent RNA sequencing using click-chemistry unveils coordinated transcription. bioRxiv : the preprint server for biology.

Lee YJ, et al. (2023) The EDN1/EDNRA/??arrestin axis promotes colorectal cancer progression by regulating STAT3 phosphorylation. International journal of oncology, 62(1).

Sahu B, et al. (2022) Sequence determinants of human gene regulatory elements. Nature genetics, 54(3), 283.

Nam H, et al. (2021) The TGF-?/HDAC7 axis suppresses TCA cycle metabolism in renal cancer. JCI insight, 6(22).

Elsakka EGE, et al. (2020) Androgen/androgen receptor affects gentamicin-induced nephrotoxicity through regulation of megalin expression. Life sciences, 251, 117628.

Peng F, et al. (2020) The transcription factor Sp1 modulates RNA polymerase III gene transcription by controlling BRF1 and GTF3C2 expression in human cells. The Journal of biological chemistry, 295(14), 4617.

Sakamoto A, et al. (2020) Polyamines regulate gene expression by stimulating translation of histone acetyltransferase mRNAs. The Journal of biological chemistry, 295(26), 8736.

Cserhati MF, et al. (2018) Motifome comparison between modern human, Neanderthal and Denisovan. BMC genomics, 19(1), 472.

Wang L, et al. (2018) Association study and mutation sequencing of genes on chromosome 15q11-q13 identified GABRG3 as a susceptibility gene for autism in Chinese Han population. Translational psychiatry, 8(1), 152.

Yen WH, et al. (2016) Sp1-mediated ectopic expression of T-cell lymphoma invasion and metastasis 2 in hepatocellular carcinoma. Cancer medicine, 5(3), 465.

Banik D, et al. (2015) MMP3-mediated tumor progression is controlled transcriptionally by a novel IRF8-MMP3 interaction. Oncotarget, 6(17), 15164.

Dreos R, et al. (2015) The Eukaryotic Promoter Database: expansion of EPDnew and new promoter analysis tools. Nucleic acids research, 43(Database issue), D92.

Kravatsky YV, et al. (2015) Genome-wide study of correlations between genomic features and their relationship with the regulation of gene expression. DNA research : an international journal for rapid publication of reports on genes and genomes, 22(1), 109.

Kalathur RK, et al. (2015) The unfolded protein response and its potential role in Huntington's disease elucidated by a systems biology approach. F1000Research, 4, 103.

Fan M, et al. (2014) Optimizations of siRNA design for the activation of gene transcription by targeting the TATA-box motif. PloS one, 9(9), e108253.

Stockinger H, et al. (2014) Fifteen years SIB Swiss Institute of Bioinformatics: life science databases, tools and support. Nucleic acids research, 42(Web Server issue), W436.

Chandrasekar V, et al. (2010) The brain-specific Neural Zinc Finger transcription factor 2b (NZF-2b/7ZFMyt1) causes suppression of cocaine-induced locomotor activity. Neurobiology of disease, 37(1), 86.