

Resource Summary Report

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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: database, data or information resource

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, Available for download, 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

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 27 mentions in open access literature.

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

Yildiz Y, et al. (2025) Gelsolin Facilitates Estrogen Receptor Beta Nuclear Translocation and Transcriptional Repression of Genes Associated with Alzheimer Disease. *Receptors (Basel, Switzerland)*, 4(2).

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.

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

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*.

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.

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

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

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.