

Resource Summary Report

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MAxEntScan

RRID:SCR_016707

Type: Tool

Proper Citation

MAxEntScan (RRID:SCR_016707)

Resource Information

URL: http://genes.mit.edu/burgelab/maxent/Xmaxentscan_scoreseq.html

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Description: Software tool as a framework for modeling the sequences of short sequence motifs based on the maximum entropy principle (MEP). Used for sequence motifs such as those involved in RNA splicing.

Abbreviations: MAxEntScan

Synonyms: Maximum Entropy Scan, MAxEntScan, MAMaximumEntropyScan

Resource Type: simulation software, software resource, service resource, software application

Defining Citation: [PMID:15285897](#)

Keywords: modeling, sequence, short, motif, maximum, entropy, principle, MEP, RNA, splicing

Funding: NSF Grant 0218506;
NIH ;
Lee Kuan Yew Scholarship for the government of Singapore

Availability: Free, Available for download, Freely available

Resource Name: MAxEntScan

Resource ID: SCR_016707

Record Creation Time: 20220129T080332+0000

Record Last Update: 20260803T040728+0000

Ratings and Alerts

No rating or validation information has been found for MAXEntScan.

No alerts have been found for MAXEntScan.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 65 mentions in open access literature.

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

García-Ruiz S, et al. (2025) Splicing accuracy varies across human introns, tissues, age and disease. *Nature communications*, 16(1), 1068.

Michel L, et al. (2025) Unraveling variability in young children's brain responses to varied sensory stimulations. *iScience*, 28(11), 113773.

Spangsberg Petersen US, et al. (2024) Regulating PCCA gene expression by modulation of pseudoexon splicing patterns to rescue enzyme activity in propionic acidemia. *Molecular therapy. Nucleic acids*, 35(1), 102101.

Riaz H, et al. (2024) The spectrum of novel ABCB11 gene variations in children with progressive familial intrahepatic cholestasis type 2 in Pakistani cohorts. *Scientific reports*, 14(1), 18876.

Zhang C, et al. (2024) A Novel Splice Site Mutation in the FBN2 Gene in a Chinese Family with Congenital Contractural Arachnodactyly. *Biochemical genetics*, 62(4), 2495.

Koczkowska M, et al. (2023) Analysis of 200 unrelated individuals with a constitutional NF1 deep intronic pathogenic variant reveals that variants flanking the alternatively spliced NF1 exon 31 [23a] cause a classical neurofibromatosis type 1 phenotype while altering predominantly NF1 isoform type II. *Human genetics*, 142(7), 849.

García-Ruiz S, et al. (2023) Splicing accuracy varies across human introns, tissues and age. *bioRxiv : the preprint server for biology*.

Okada E, et al. (2023) All reported non-canonical splice site variants in GLA cause aberrant splicing. *Clinical and experimental nephrology*, 27(9), 737.

Yi T, et al. (2023) Genetic aetiology distribution of 398 fetuses with congenital heart disease in the prenatal setting. *ESC heart failure*, 10(2), 917.

Lu F, et al. (2022) Estimating the frequency of causal genetic variants in fetuses with congenital heart defects: a Chinese cohort study. *Orphanet journal of rare diseases*, 17(1), 2.

Barbosa P, et al. (2022) Computational prediction of human deep intronic variation. *GigaScience*, 12.

Yu B, et al. (2021) Mutation of c.244G>T in NR5A1 gene causing 46, XY DSD by affecting RNA splicing. *Orphanet journal of rare diseases*, 16(1), 370.

Pio MG, et al. (2021) A novel mutation in intron 11 donor splice site, responsible of a rare genotype in thyroglobulin gene by altering the pre-mRNA splicing process. *Cell expression and bioinformatic analysis. Molecular and cellular endocrinology*, 522, 111124.

Wang X, et al. (2021) mRNA analysis identifies deep intronic variants causing Alport syndrome and overcomes the problem of negative results of exome sequencing. *Scientific reports*, 11(1), 18097.

Pio MG, et al. (2021) Curating the gnomAD database: Report of novel variants in the thyroglobulin gene using in silico bioinformatics algorithms. *Molecular and cellular endocrinology*, 534, 111359.

Wang S, et al. (2021) Detection of TSC1/TSC2 mosaic variants in patients with cardiac rhabdomyoma and tuberous sclerosis complex by hybrid-capture next-generation sequencing. *Molecular genetics & genomic medicine*, 9(10), e1802.

Guo L, et al. (2021) Deficiency of TMEM53 causes a previously unknown sclerosing bone disorder by dysregulation of BMP-SMAD signaling. *Nature communications*, 12(1), 2046.

Austena LMI, et al. (2021) A first exon termination checkpoint preferentially suppresses extragenic transcription. *Nature structural & molecular biology*, 28(4), 337.

Lu X, et al. (2021) Novel Intronic Mutations Introduce Pseudoexons in DMD That Cause Muscular Dystrophy in Patients. *Frontiers in genetics*, 12, 657040.

Akhavanfard S, et al. (2021) Germline EGFR variants are over-represented in adolescents and young adults (AYA) with adrenocortical carcinoma. *Human molecular genetics*, 29(22), 3679.