Resource Summary Report

Generated by RRID on Aug 31, 2026

MAxEntScan

RRID:SCR_016707
Type: Tool

Proper Citation

MAxEntScan (RRID:SCR_016707)

Resource Information

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

Proper Citation: MAxEntScan (RRID:SCR_016707)

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, MAximumEntropyScan

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

Defining Citation: PMID:15285897

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

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

Availability: Free, Available for download, Freely available

Resource Name: MAxEntScan

Resource ID: SCR_016707

Record Creation Time: 20220129T080332+0000

Record Last Update: 20260829T182521+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 70 mentions in open access literature.

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

Shi T, et al. (2026) Functional reassessment of extended splice region variants in MYO7A with hearing loss and Usher syndrome. The Journal of pathology, 269(2), 222.

Zhang J, et al. (2025) Novel pathogenic splicing mutation in COL11A1 in a patient with Stickler syndrome verified by minigene splicing assay. Frontiers in genetics, 16, 1642604.

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.

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

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.

Fang Y, et al. (2023) Genetic analysis and prenatal diagnosis of short-rib thoracic dysplasia 3 with or without polydactyly caused by compound heterozygous variants of DYNC2H1 gene in four Chinese families. Frontiers in genetics, 14, 1075187.

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

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

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

Yi T, et al. (2022) Genetic and Clinical Features of Heterotaxy in a Prenatal Cohort. Frontiers in genetics, 13, 818241.

Li L, et al. (2022) Description of the Molecular and Phenotypic Spectrum of Lesch-Nyhan Disease in Eight Chinese Patients. Frontiers in genetics, 13, 868942.

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

Pio MG, et al. (2021) Curating the gnomAD database: Report of novel variants in the thyrogobulin 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.

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 splincing 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.