

Resource Summary Report

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ESTScan

RRID:SCR_005742

Type: Tool

Proper Citation

ESTScan (RRID:SCR_005742)

Resource Information

URL: <http://estscan.sourceforge.net/>

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Description: ESTScan is a program that can detect coding regions in DNA sequences, even if they are of low quality. ESTScan will also detect and correct sequencing errors that lead to frameshifts. ESTScan is not a gene prediction program, nor is it an open reading frame detector. In fact, its strength lies in the fact that it does not require an open reading frame to detect a coding region. As a result, the program may miss a few translated amino acids at either the N or the C terminus, but will detect coding regions with high selectivity and sensitivity. ESTScan takes advantages of the bias in hexanucleotide usage found in coding regions relative to non-coding regions. This bias is formalized as an inhomogeneous 3-periodic fifth-order Hidden Markov Model (HMM). Additionally, the HMM of ESTScan has been extended to allow insertions and deletions when these improve the coding region statistics.

Abbreviations: ESTScan

Synonyms: ESTScan project

Resource Type: software application, software resource, data analysis software, data processing software

Defining Citation: [PMID:10786296](#)

Keywords: dna, dna sequence, coding region, perl module, c, btlb perl module

Resource Name: ESTScan

Resource ID: SCR_005742

Alternate IDs: OMICS_08423, nlx_149202

Alternate URLs: <https://sources.debian.org/src/estscan/>

Record Creation Time: 20220129T080232+0000

Record Last Update: 20260729T044120+0000

Ratings and Alerts

No rating or validation information has been found for ESTScan.

No alerts have been found for ESTScan.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 289 mentions in open access literature.

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

Mo C, et al. (2025) The role of ACS genes in sex differentiation of *Siraitia grosvenorii* revealed by comparative transcriptomic analysis. *BMC plant biology*, 25(1), 1579.

Ma H, et al. (2025) Functional annotation and analysis of the hard tick *Dermacentor nuttalli* midgut genes. *Parasitology research*, 124(5), 52.

Brun G, et al. (2025) Seed metabolites headstart haustoriogenesis and potentiate aggressiveness of parasitic weeds. *Science advances*, 11(50), eaea1449.

Das SP, et al. (2025) Transcriptome profile of early matured *Macrobrachium rosenbergii* (Giant Freshwater Prawn) from Taiwan. *Scientific data*, 12(1), 932.

Deng J, et al. (2024) Transcriptomic analysis of spleen-derived macrophages in response to lipopolysaccharide shows dependency on the MyD88-independent pathway in Chinese giant salamanders (*Andrias davidianus*). *BMC genomics*, 25(1), 1005.

Ochieng WA, et al. (2023) Transcriptome Analysis of Macrophytes' *Myriophyllum spicatum* Response to Ammonium Nitrogen Stress Using the Whole Plant Individual. *Plants (Basel, Switzerland)*, 12(22).

Ji Z, et al. (2023) Functional characterization of triterpene synthases in *Cibotium barometz*. *Synthetic and systems biotechnology*, 8(3), 437.

Shah S, et al. (2023) Diallyl Trisulfide Causes Male Infertility with Oligoasthenoteratospermia in *Sitotroga cerealella* through the Ubiquitin-Proteasome Pathway. *Cells*, 12(20).

Xiao F, et al. (2023) Full-length transcriptome characterization and comparative analysis of *Gleditsia sinensis*. *BMC genomics*, 24(1), 757.

Wu LJ, et al. (2023) Proteome Analysis of Male Accessory Gland Secretions in the Diamondback Moth, *Plutella xylostella* (Lepidoptera: Plutellidae). *Insects*, 14(2).

Yang W, et al. (2023) Integrated transcriptome and proteome revealed that the declined expression of cell cycle-related genes associated with follicular atresia in geese. *BMC genomics*, 24(1), 24.

Liu XY, et al. (2023) Biosynthetic pathway of prescription bergenin from *Bergenia purpurascens* and *Ardisia japonica*. *Frontiers in plant science*, 14, 1259347.

Jiang H, et al. (2022) Single-Molecule Real-Time Sequencing of Full-Length Transcriptome and Identification of Genes Related to Male Development in *Cannabis sativa*. *Plants (Basel, Switzerland)*, 11(24).

Song N, et al. (2022) Transcriptome analysis of the bivalve *Placuna placenta* mantle reveals potential biomineralization-related genes. *Scientific reports*, 12(1), 4743.

Sun C, et al. (2022) Transcriptome Analysis Revealed Genes Related to γ -Irradiation Induced Emergence Failure in Third-Instar Larvae of *Bactrocera dorsalis*. *Insects*, 13(11).

Funayama S, et al. (2022) A novel peptide identified from visceral ganglia induces oocyte maturation, spermatozoa active motility, and spawning in the pen shell *Atrinapectinata*. *Biochemical and biophysical research communications*, 598, 9.

Li D, et al. (2022) De novo assembly and analysis of *Polygonatum cyrtonema* Hua and identification of genes involved in polysaccharide and saponin biosynthesis. *BMC genomics*, 23(1), 195.

Joffré E, et al. (2022) Analysis of Growth Phases of Enterotoxigenic *Escherichia coli* Reveals a Distinct Transition Phase before Entry into Early Stationary Phase with Shifts in Tryptophan, Fucose, and Putrescine Metabolism and Degradation of Neurotransmitter Precursors. *Microbiology spectrum*, 10(4), e0175521.

Nachtigall PG, et al. (2021) CodAn: predictive models for precise identification of coding regions in eukaryotic transcripts. *Briefings in bioinformatics*, 22(3).

Xin M, et al. (2021) Dynamic Analyses of Transcriptome and Metabolic Profiling: Revealing Molecular Insight of Aroma Synthesis of Mango (*Mangifera indica* L. Var. Tainong). *Frontiers in plant science*, 12, 666805.