Resource Summary Report

Generated by dkNET on Apr 18, 2025

Open Reading Frame Finder

RRID:SCR_016643
Type: Tool

Proper Citation

Open Reading Frame Finder (RRID:SCR_016643)

Resource Information

URL: https://www.ncbi.nlm.nih.gov/orffinder

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Description: Software tool to search for open reading frames (ORFs) in the DNA sequence. The program returns the range of each ORF, along with its protein translation. Used to search newly sequenced DNA for potential protein encoding segments, verify predicted protein. Limited to the subrange of the query sequence up to 50 kb long.

Abbreviations: ORF finder

Synonyms: Open Reading Frame finder, Open Reading Frame Finder

Resource Type: data processing software, software application, service resource, data analysis software, sequence analysis software, software resource, production service resource, analysis service resource

Keywords: search, open, reading, frame, DNA, sequence, ORF, protein, translation, data, encoding, segment, verify

Funding:

Availability: Free, Available for download, Freely available

Resource Name: Open Reading Frame Finder

Resource ID: SCR_016643

Record Creation Time: 20220129T080331+0000

Record Last Update: 20250418T055453+0000

Ratings and Alerts

No rating or validation information has been found for Open Reading Frame Finder.

No alerts have been found for Open Reading Frame Finder.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1281 mentions in open access literature.

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

Xu Z, et al. (2025) An orphan viral genome with unclear evolutionary status sheds light on a distinct lineage of flavi-like viruses infecting plants. Virus evolution, 11(1), veaf001.

Basmenj ER, et al. (2025) Computational epitope-based vaccine design with bioinformatics approach; a review. Heliyon, 11(1), e41714.

Debat H, et al. (2025) RNA Virus Discovery Sheds Light on the Virome of a Major Vineyard Pest, the European Grapevine Moth (Lobesia botrana). Viruses, 17(1).

Li Z, et al. (2025) Characterisation of a Betasatellite Associated With Tomato Yellow Leaf Curl Guangdong Virus and Discovery of an Unusual Modulation of Virus Infection Associated With C4 Protein. Molecular plant pathology, 26(1), e70051.

Shao D, et al. (2025) The Functional Identification of the CYP2E1 Gene in the Kidney of Lepus yarkandensis. International journal of molecular sciences, 26(2).

Zhang L, et al. (2025) p18 encoded by FgGMTV1 is responsible for asymptomatic infection in Fusarium graminearum. mBio, 16(1), e0306624.

Patil MP, et al. (2025) Complete Mitochondrial Genome of Niphon spinosus (Perciformes: Niphonidae): Genome Characterization and Phylogenetic Analysis. Biomolecules, 15(1).

Zhang Y, et al. (2025) Morphological Characteristics, Mitochondrial Genome, and Evolutionary Insights Into a New Sea Squirt From the Beibu Gulf. Ecology and evolution, 15(1), e70639.

Astaraki S, et al. (2025) High-throughput sequencing revealed the symptomatic common bean (Phaseolus vulgaris L.) virome in Iran. Scientific reports, 15(1), 1621.

Wang P, et al. (2025) The StbHLH47 transcription factor negatively regulates drought tolerance in potato (Solanum tuberosum L.). BMC plant biology, 25(1), 14.

Guo D, et al. (2025) LncRNA81246 regulates resistance against tea leaf spot by interrupting the miR164d-mediated degradation of NAC1. The Plant journal : for cell and molecular biology, 121(1), e17173.

Lan P, et al. (2025) Molecular and biological characterization of infectious full-length cDNA clones of two viruses in Paris yunnanensis, including a novel potyvirus. Scientific reports, 15(1), 473.

Prigigallo MI, et al. (2025) Resistance-breaking strains of tomato spotted wilt virus hamper photosynthesis and protein synthesis pathways in a virus accumulation-dependent manner in Sw5-carrying tomatoes. Scientific reports, 15(1), 3630.

Yang J, et al. (2025) MARTRE family proteins negatively regulate CCR4-NOT activity to protect poly(A) tail length and promote translation of maternal mRNA. Nature communications, 16(1), 248.

Zhu Z, et al. (2025) Integrative multi-omics analysis reveals the translational landscape of the plant-parasitic nematode Meloidogyne incognita. Communications biology, 8(1), 140.

Policarpo R, et al. (2025) The MIR-NAT MAPT-AS1 does not regulate Tau expression in human neurons. PloS one, 20(1), e0314973.

Bates L, et al. (2024) A Novel Method to Profile Transcripts Encoding SH2 Domains in the Patiria miniata Mature Egg Transcriptome. Cells, 13(22).

Gupta P, et al. (2024) A parasite odyssey: An RNA virus concealed in Toxoplasma gondii. Virus evolution, 10(1), veae040.

Camilleri-Robles C, et al. (2024) Long non-coding RNAs involved in Drosophila development and regeneration. NAR genomics and bioinformatics, 6(3), lqae091.

Russell JN, et al. (2024) Whole-genome sequencing of Western Canadian Borrelia spp. collected from diverse tick and animal hosts reveals short-lived local genotypes interspersed with longer-lived continental genotypes. Microbial genomics, 10(8).