

Resource Summary Report

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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, sequence analysis software, service resource, data analysis software, software resource, software application, production service resource, analysis service resource

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

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: 20260731T043011+0000

Ratings and Alerts

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

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1428 mentions in open access literature.

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

Pasha AVK, et al. (2026) Immunoinformatics-Based Multi-Epitope Vaccine Targeting Helicobacter Pylori. Cancer reports (Hoboken, N.J.), 9(1), e70441.

Shu X, et al. (2026) LncRNA HAND2OT encoding micropeptide regulates the estradiol secretion, proliferation and apoptosis of ovarian follicular theca cells in chickens. Poultry science, 105(1), 106206.

Wu W, et al. (2025) Transposable Element Landscape in the Monotypic Species Barthea barthei (Hance) Krass (Melastomataceae) and Its Role in Ecological Adaptation. Biomolecules, 15(3).

Nancarrow N, et al. (2025) Hidden diversity of yellow dwarf viruses in Australian cereals. Archives of virology, 171(1), 3.

Nath R, et al. (2025) Lineage-Specific Class-A GPCR Dynamics Reflect Diverse Chemosensory Adaptations in Lophotrochozoa. Molecular biology and evolution, 42(3).

Ma Y, et al. (2025) Short-term antiretroviral therapy may not correct the dysregulations of plasma virome and cytokines induced by HIV-1 infection. Virulence, 16(1), 2467168.

Duarte AC, et al. (2025) A new bacteriophage infecting Staphylococcus epidermidis with potential for removing biofilms by combination with chimeric lysin CHAPSH3b and vancomycin. mSphere, 10(3), e0101424.

Moreno-Justicia R, et al. (2025) Human skeletal muscle fiber heterogeneity beyond myosin heavy chains. Nature communications, 16(1), 1764.

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

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.

Ma J, et al. (2025) Detection and characterization of bovine hepatitis virus in cattle and sheep from Hulunbuir, northeastern China. Frontiers in cellular and infection microbiology, 15, 1540849.

Fehér E, et al. (2025) Occurrence of Recombinant Canine Coronavirus, Picodistrovirus, and Circovirus in Red Foxes (*Vulpes vulpes*) Implies Frequent Virus Transmission Events Among Carnivores. *Transboundary and emerging diseases*, 2025, 6681119.

Minařík M, et al. (2025) Atoh1 is required for the formation of lateral line electroreceptors and hair cells, whereas FoxG1 represses an electrosensory fate. *eLife*, 14.

Lu L, et al. (2025) Two novel phages infecting *Erythrobacter* isolated from the epipelagic ocean. *Frontiers in microbiology*, 16, 1592355.

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

Gu XH, et al. (2025) Integrated evidence reveals a new subspecies of the genus *Seuratascaris* (Nematoda: Ascaridomorpha), with characterization of the complete mitochondrial genome. *Parasite (Paris, France)*, 32, 14.

Dias D, et al. (2025) Coding-complete genome sequence of a divergent member of the genus *Gordisvirus* detected in *Sabethes* (*Peytonulus*) *undosus* Coquillett mosquitoes (Diptera: Culicidae) from Brazil. *Microbiology resource announcements*, 14(6), e0127524.

Funaguma S, et al. (2025) Retrotrans-genomics identifies aberrant THE1B endogenous retrovirus fusion transcripts in the pathogenesis of sarcoidosis. *Nature communications*, 16(1), 1318.

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

Qu M, et al. (2025) Molecular Characterization of a Transcriptional Regulator GntR for Gluconate Metabolism in Industrial 2-Ketogluconate Producer *Pseudomonas plecoglossicida* JUIM01. *Microorganisms*, 13(6).