

Resource Summary Report

Generated by [kravitz2](#) on Sep 5, 2026

IRESite

RRID:SCR_007754

Type: Tool

Proper Citation

IRESite (RRID:SCR_007754)

Resource Information

URL: <http://www.iresite.org>

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Description: The IRESite database presents information about the experimentally studied IRES (Internal Ribosome Entry Site) segments. Based on some experimental evidence there are at least 62 viruses and at least 90 eukaryotic cellular mRNAs reported to contain IRES. The experimental data about viral and cellular IRESs are contained in more than 189 and 318 publications, respectively. IRESite database covers at the moment 25 viral and 51 cellular IRES segments. Over 300 records contain the actual experimental results covering some of these IRESs in a greater detail. IRES regions are known to attract eukaryotic ribosomal translation initiation complex and thus promote translation initiation independently of the presence of the commonly utilized 5'-terminal 7mG cap structure. It is not yet clear whether the activity could be attributed to a common sequence or to a common secondary structure present in them. Such IRES regions were found in a broad range of +RNA viruses and in some eukaryotic cellular mRNAs. Certain IRESs have been predicted based on the fact that closely related viruses should share its features and indeed, their sequences are in some regions conserved enough to allow identification of a new IRES. In contrast, cellular IRESs do not have almost anything in common in terms of their sequence or secondary structure. Therefore, cellular IRESs cannot be predicted. Either way, IRESite is focused only on IRESs which have been at least to some extent experimentally proven. To allow the cross-correlation of the experimental results the IRESite database was specifically designed to store not only the primary experimental results (sequence, structure, measured values) but also the most important methodological characteristics of the experiments.

Synonyms: IRESite

Resource Type: data or information resource, database

Resource Name: IRESite

Resource ID: SCR_007754

Alternate IDs: nif-0000-03047

Record Creation Time: 20220129T080243+0000

Record Last Update: 20260903T234920+0000

Ratings and Alerts

No rating or validation information has been found for IRESite.

No alerts have been found for IRESite.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 24 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#).

Zhang T, et al. (2025) Small open reading frame-encoded microproteins in cancer: identification, biological functions and clinical significance. *Molecular cancer*, 24(1), 105.

Li S, et al. (2025) Functional characterization of a novel protein-coding circular RNA, circRNA_1193, from the mAAP gene in silkworm and its role in antiviral defense against BmCPV. *mBio*, 16(5), e0012525.

Zhou H, et al. (2025) A foundation language model to decipher diverse regulation of RNAs. *Genome biology*, 26(1), 301.

Ran N, et al. (2023) Long Non-Coding RNA IncWOX11a Suppresses Adventitious Root Formation of Poplar by Regulating the Expression of PeWOX11a. *International journal of molecular sciences*, 24(6).

Li M, et al. (2023) CircRNA Profiling of Skeletal Muscle in Two Pig Breeds Reveals CircIGF1R Regulates Myoblast Differentiation via miR-16. *International journal of molecular sciences*, 24(4).

Han Z, et al. (2023) A special satellite-like RNA of a novel hypovirus from *Pestalotiopsis fici* broadens the definition of fungal satellite. *PLoS pathogens*, 19(6), e1010889.

Zhang Y, et al. (2022) Micropeptide vsp21 translated by Reovirus circular RNA 000048 attenuates viral replication. *International journal of biological macromolecules*, 209(Pt A), 1179.

Hayer J, et al. (2021) Four novel picornaviruses detected in Magellanic Penguins (*Spheniscus magellanicus*) in Chile. *Virology*, 560, 116.

- Lu Y, et al. (2021) Translation role of circRNAs in cancers. *Journal of clinical laboratory analysis*, 35(7), e23866.
- Liu S, et al. (2021) Virus-derived sequences from the transcriptomes of two snail vectors of schistosomiasis, *Biomphalaria pfeifferi* and *Bulinus globosus* from Kenya. *PeerJ*, 9, e12290.
- Xiao Q, et al. (2021) Comprehensive Analysis of Peripheral Exosomal circRNAs in Large Artery Atherosclerotic Stroke. *Frontiers in cell and developmental biology*, 9, 685741.
- Wang X, et al. (2020) Circular RNAs in Human Cancer. *Frontiers in oncology*, 10, 577118.
- Watson SF, et al. (2020) ILF3 contributes to the establishment of the antiviral type I interferon program. *Nucleic acids research*, 48(1), 116.
- Wang H, et al. (2020) Internal Ribosome Entry Sites Mediate Cap-Independent Translation of Bmi1 in Nasopharyngeal Carcinoma. *Frontiers in oncology*, 10, 1678.
- Wu H, et al. (2020) LNC473 Regulating APAF1 IRES-Dependent Translation via Competitive Sponging miR574 and miR15b: Implications in Colorectal Cancer. *Molecular therapy*. *Nucleic acids*, 21, 764.
- Wu P, et al. (2020) Emerging role of tumor-related functional peptides encoded by lncRNA and circRNA. *Molecular cancer*, 19(1), 22.
- Yang Y, et al. (2019) IRES-mediated cap-independent translation, a path leading to hidden proteome. *Journal of molecular cell biology*, 11(10), 911.
- Corona AK, et al. (2018) Enteroviruses Remodel Autophagic Trafficking through Regulation of Host SNARE Proteins to Promote Virus Replication and Cell Exit. *Cell reports*, 22(12), 3304.
- Kolekar P, et al. (2016) IRESPred: Web Server for Prediction of Cellular and Viral Internal Ribosome Entry Site (IRES). *Scientific reports*, 6, 27436.
- Hong JJ, et al. (2013) Viral IRES prediction system - a web server for prediction of the IRES secondary structure in silico. *PLoS one*, 8(11), e79288.