

Resource Summary Report

Generated by [SPARC SAWG](#) on Jul 29, 2026

[iMaps](#)

RRID:SCR_016705

Type: Tool

Proper Citation

iMaps (RRID:SCR_016705)

Resource Information

URL: <https://imaps.genialis.com/iclip>

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Description: Web server for analysis of high-resolution sequencing data. It can be used with all variants of CLIP, as well as with methods that interrogate RNA or DNA methylation, RNA processing, RNA structure or protein-DNA interactions.

Resource Type: service resource, data or information resource, data analysis service, production service resource, analysis service resource, portal

Keywords: Genialis, analysis, high-resolution, sequencing, data, RNA, DNA, protein, interaction

Availability: Free, Registration required

Resource Name: iMaps

Resource ID: SCR_016705

Record Creation Time: 20220129T080331+0000

Record Last Update: 20260729T044425+0000

Ratings and Alerts

No rating or validation information has been found for iMaps.

No alerts have been found for iMaps.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 9 mentions in open access literature.

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

Klein P, et al. (2024) m6a methylation orchestrates IMP1 regulation of microtubules during human neuronal differentiation. Nature communications, 15(1), 4819.

Horste EL, et al. (2023) Subcytoplasmic location of translation controls protein output. Molecular cell, 83(24), 4509.

Nicastro G, et al. (2023) Direct m6A recognition by IMP1 underlays an alternative model of target selection for non-canonical methyl-readers. Nucleic acids research, 51(16), 8774.

Avolio R, et al. (2022) Coordinated post-transcriptional control of oncogene-induced senescence by UNR/CSDE1. Cell reports, 38(2), 110211.

D'Angeli V, et al. (2022) Polypyrimidine tract binding protein 1 regulates the activation of mouse CD8 T cells. European journal of immunology, 52(7), 1058.

Gong C, et al. (2021) Sequential inverse dysregulation of the RNA helicases DDX3X and DDX3Y facilitates MYC-driven lymphomagenesis. Molecular cell, 81(19), 4059.

Dermitt M, et al. (2020) Subcellular mRNA Localization Regulates Ribosome Biogenesis in Migrating Cells. Developmental cell, 55(3), 298.

Briese M, et al. (2019) A systems view of spliceosomal assembly and branchpoints with iCLIP. Nature structural & molecular biology, 26(10), 930.

Blazquez L, et al. (2018) Exon Junction Complex Shapes the Transcriptome by Repressing Recursive Splicing. Molecular cell, 72(3), 496.