

# Resource Summary Report

Generated by [dkNET](#) on Sep 21, 2026

## [iMaps](#)

RRID:SCR\_016705

Type: Tool

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### Proper Citation

iMaps (RRID:SCR\_016705)

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### Resource Information

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

**Proper Citation:** iMaps (RRID:SCR\_016705)

**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:** analysis service resource, data analysis service, data or information resource, portal, production service resource, service resource

**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:** 20260919T195327+0000

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### Ratings and Alerts

No rating or validation information has been found for iMaps.

No alerts have been found for iMaps.

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### Data and Source Information

**Source:** [SciCrunch Registry](#)

## Usage and Citation Metrics

We found 11 mentions in open access literature.

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

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

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.

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

Petkau G, et al. (2022) The timing of differentiation and potency of CD8 effector function is set by RNA binding proteins. *Nature communications*, 13(1), 2274.

Matheson LS, et al. (2022) Multiomics analysis couples mRNA turnover and translational control of glutamine metabolism to the differentiation of the activated CD4+ T cell. *Scientific reports*, 12(1), 19657.

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.