

Resource Summary Report

Generated by [kravitz2](#) on Sep 16, 2026

iMaps

RRID:SCR_016705

Type: Tool

Proper Citation

iMaps (RRID:SCR_016705)

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: 20260912T195843+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 11 mentions in open access literature.

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

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.