

Resource Summary Report

Generated by [kravitz2](#) on Sep 18, 2026

TMAP

RRID:SCR_000687

Type: Tool

Proper Citation

TMAP (RRID:SCR_000687)

Resource Information

URL: <https://github.com/iontorrent/TMAP>

Proper Citation: TMAP (RRID:SCR_000687)

Description: Alignment software for short and long nucleotide sequences produced by next-generation sequencing technologies.

Abbreviations: TMAP

Synonyms: TMAP - torrent mapping alignment program, Torrent Mapping Alignment Program

Resource Type: software resource

Keywords: next-generation sequencing

Availability: Free, Available for download, Freely available

Resource Name: TMAP

Resource ID: SCR_000687

Alternate IDs: OMICS_00694

Record Creation Time: 20220129T080203+0000

Record Last Update: 20260912T195513+0000

Ratings and Alerts

No rating or validation information has been found for TMAP.

No alerts have been found for TMAP.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 23 mentions in open access literature.

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

Hu K, et al. (2025) Development and Application of MiMouse, a Comprehensive Genomic Profiling Panel for Credentialing Mouse Tumor Models. Cancer research communications, 5(10), 1910.

Bustamante BLM, et al. (2024) Breast cancer screening needs assessment in 19 Northern California counties: geography, poverty, and racial/ethnic identity composition. Cancer causes & control : CCC.

Papoutsoglou P, et al. (2019) The TGFB2-AS1 lncRNA Regulates TGF- β Signaling by Modulating Corepressor Activity. Cell reports, 28(12), 3182.

Saeb ATM, et al. (2018) Current Bioinformatics resources in combating infectious diseases. Bioinformation, 14(1), 31.

Zhang S, et al. (2018) Alternative polyadenylation drives genome-to-phenome information detours in the AMPK α 1 and AMPK α 2 knockout mice. Scientific reports, 8(1), 6462.

Rasmussen TB, et al. (2018) Full-length genome sequences of porcine epidemic diarrhoea virus strain CV777; Use of NGS to analyse genomic and sub-genomic RNAs. PloS one, 13(3), e0193682.

Gómez-Manjón I, et al. (2018) Noninvasive Prenatal Testing: Comparison of Two Mappers and Influence in the Diagnostic Yield. BioMed research international, 2018, 9498140.

Kijak GH, et al. (2017) Rare HIV-1 transmitted/founder lineages identified by deep viral sequencing contribute to rapid shifts in dominant quasiespecies during acute and early infection. PLoS pathogens, 13(7), e1006510.

Giner-Lamia J, et al. (2017) Identification of the direct regulon of NtcA during early acclimation to nitrogen starvation in the cyanobacterium Synechocystis sp. PCC 6803. Nucleic acids research, 45(20), 11800.

Saeb AT, et al. (2017) The Use of Next-Generation Sequencing in the Identification of a Fastidious Pathogen: A Lesson From a Clinical Setup. Evolutionary bioinformatics online, 12, 1176934316686072.

Dacic S, et al. (2016) ALK FISH patterns and the detection of ALK fusions by next generation sequencing in lung adenocarcinoma. Oncotarget, 7(50), 82943.

Németh D, et al. (2016) Clinical Use of Next-Generation Sequencing in the Diagnosis of Wilson's Disease. Gastroenterology research and practice, 2016, 4548039.

Baranzoni GM, et al. (2016) Complete Genome Sequences of Escherichia coli O157:H7 Strains SRCC 1675 and 28RC, Which Vary in Acid Resistance. Genome announcements, 4(4).

Iwata S, et al. (2016) Engineering new balancer chromosomes in C. elegans via CRISPR/Cas9. Scientific reports, 6, 33840.

Li Y, et al. (2016) Comparative Transcriptome Analysis Reveals Effects of Exogenous Hematin on Anthocyanin Biosynthesis during Strawberry Fruit Ripening. International journal of genomics, 2016, 6762731.

Yuan Y, et al. (2016) An optimized protocol for generation and analysis of Ion Proton sequencing reads for RNA-Seq. BMC genomics, 17, 403.

Gorokhova S, et al. (2015) Comparing targeted exome and whole exome approaches for genetic diagnosis of neuromuscular disorders. Applied & translational genomics, 7, 26.

Flagel LE, et al. (2015) Genetic markers for western corn rootworm resistance to Bt toxin. G3 (Bethesda, Md.), 5(3), 399.

Olson ND, et al. (2015) International interlaboratory study comparing single organism 16S rRNA gene sequencing data: Beyond consensus sequence comparisons. Biomolecular detection and quantification, 3, 17.

Juntawong P, et al. (2014) Elucidation of the molecular responses to waterlogging in Jatropha roots by transcriptome profiling. Frontiers in plant science, 5, 658.