

Resource Summary Report

Generated by [Kravitz](#) on Sep 17, 2026

BMap

RRID:SCR_016044

Type: Tool

Proper Citation

BMap (RRID:SCR_016044)

Resource Information

URL: <http://itolab.med.kyushu-u.ac.jp/BMap/index.html>

Proper Citation: BMap (RRID:SCR_016044)

Description: Software that maps whole-genome and targeted bisulfite sequence reads to reference genomes. It is especially useful for reads obtained using post-bisulfite adaptor tagging (PBAT)., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Resource Type: alignment software, data analysis software, data processing software, image analysis software, sequence analysis software, software application, software resource, source code

Defining Citation: [PMID:22649061](#)

Keywords: mapper, whole-genome, bisulfite, sequencing, post-bisulfite, adaptor, tagging, pbat, reads, mapping

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: BMap

Resource ID: SCR_016044

License: GNU GPL v3

Record Creation Time: 20220129T080328+0000

Record Last Update: 20260912T195834+0000

Ratings and Alerts

No rating or validation information has been found for BMap.

No alerts have been found for BMap.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 29 mentions in open access literature.

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

Bucciarelli V, et al. (2025) Influence of statistical approaches on Probabilistic Sweet Spots computation in Deep Brain Stimulation for severe Essential Tremor. *NeuroImage. Clinical*, 47, 103820.

Ku AT, et al. (2025) Radiogenomic Profiling of Prostate Tumors prior to External Beam Radiotherapy Converges on a Transcriptomic Signature of TGF- β Activity Driving Tumor Recurrence. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 31(24), 5211.

Chen X, et al. (2025) DNA methylation protects cancer cells against senescence. *Nature communications*, 16(1), 5901.

Yamaguchi K, et al. (2024) Non-canonical functions of UHRF1 maintain DNA methylation homeostasis in cancer cells. *Nature communications*, 15(1), 2960.

Cousins T, et al. (2024) Accurate inference of population history in the presence of background selection. *bioRxiv : the preprint server for biology*.

Ito T, et al. (2024) DNMT1 can induce primary germ layer differentiation through de novo DNA methylation. *Genes to cells : devoted to molecular & cellular mechanisms*, 29(7), 549.

Yakhou L, et al. (2023) A genetic screen identifies BEND3 as a regulator of bivalent gene expression and global DNA methylation. *Nucleic acids research*, 51(19), 10292.

Horisawa K, et al. (2023) Transcription factor-mediated direct cellular reprogramming yields cell-type specific DNA methylation signature. *Scientific reports*, 13(1), 22317.

Suzuki T, et al. (2023) Crucial role of iron in epigenetic rewriting during adipocyte differentiation mediated by JMJD1A and TET2 activity. *Nucleic acids research*, 51(12), 6120.

Zou Z, et al. (2022) ChIP-Atlas 2021 update: a data-mining suite for exploring epigenomic landscapes by fully integrating ChIP-seq, ATAC-seq and Bisulfite-seq data. *Nucleic acids research*, 50(W1), W175.

Furuta Y, et al. (2022) A GCDGC-specific DNA (cytosine-5) methyltransferase that methylates the GCWGC sequence on both strands and the GCSGC sequence on one strand. *PloS one*, 17(3), e0265225.

Sugimachi K, et al. (2022) Persistent epigenetic alterations in transcription factors after a sustained virological response in hepatocellular carcinoma. *JGH open : an open access journal of gastroenterology and hepatology*, 6(12), 854.

Kuribayashi W, et al. (2021) Limited rejuvenation of aged hematopoietic stem cells in young bone marrow niche. *The Journal of experimental medicine*, 218(3).

Yoshioka K, et al. (2021) Hoxa10 mediates positional memory to govern stem cell function in adult skeletal muscle. *Science advances*, 7(24).

Gully BS, et al. (2021) The cryo-EM structure of the endocytic receptor DEC-205. *The Journal of biological chemistry*, 296, 100127.

Kameda T, et al. (2021) Neuronal activation modulates enhancer activity of genes for excitatory synaptogenesis through de novo DNA methylation. *The Journal of reproduction and development*, 67(6), 369.

Yoshida K, et al. (2020) ATF7-Dependent Epigenetic Changes Are Required for the Intergenerational Effect of a Paternal Low-Protein Diet. *Molecular cell*, 78(3), 445.

Araki H, et al. (2019) Base-Resolution Methylome of Retinal Pigment Epithelial Cells Used in the First Trial of Human Induced Pluripotent Stem Cell-Based Autologous Transplantation. *Stem cell reports*, 13(4), 761.

Matsuda T, et al. (2019) Pioneer Factor NeuroD1 Rearranges Transcriptional and Epigenetic Profiles to Execute Microglia-Neuron Conversion. *Neuron*, 101(3), 472.

Miura F, et al. (2019) Highly efficient single-stranded DNA ligation technique improves low-input whole-genome bisulfite sequencing by post-bisulfite adaptor tagging. *Nucleic acids research*, 47(15), e85.