# Resource Summary Report

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# BiQ Analyzer: A Software Tool for DNA Methylation Analysis

RRID:SCR_008423
Type: Tool

## Proper Citation

BiQ Analyzer: A Software Tool for DNA Methylation Analysis (RRID:SCR_008423)

## Resource Information

**URL:** http://biq-analyzer.bioinf.mpi-sb.mpg.de

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**Description:** BiQ Analyzer is a software tool for easy visualization and quality control of DNA methylation data from bisulfite sequencing. Highlights: - End-to-end support of the analysis process: from raw sequence files to a comprehensive documentation and visualization. - Automatically generate publication-quality lollipop diagrams (show example.) - Integrated 1-click multiple sequence alignment. - Automated CpG highlighting- never spend your time highlighting CpGs by hand anymore. - Open electropherogram files to check for sequencing problems (requires an electropherogram viewer such as Chromas LITE.) - Generate MethDB-compatible DNA methylation files for database submission. - Factor 5 speedup of sequence analysis while at the same time achieving better data quality. Intended users: - Anyone who works with DNA methylation data from bisulfite sequencing. - Occasional users as well as experts (the former will benefit from the help that the program gives in order to achieve a good quality management whereas the latter will save hours and days of tedious work.) Sponsors: This resource is supported by the Max Planck Institute. Keywords: Software, Visualization, DNA, Methylation, Data, Bisulfite, Sequencing, Electropherogram, Analysis,

**Synonyms:** BiQ

**Resource Type:** software application, data processing software, data visualization software, data analysis software, software resource

**Funding:**

**Resource Name:** BiQ Analyzer: A Software Tool for DNA Methylation Analysis

**Resource ID:** SCR_008423

**Alternate IDs:** nif-0000-30169

**Record Creation Time:** 20220129T080247+0000

**Record Last Update:** 20250423T060442+0000

## Ratings and Alerts

No rating or validation information has been found for BiQ Analyzer: A Software Tool for DNA Methylation Analysis.

No alerts have been found for BiQ Analyzer: A Software Tool for DNA Methylation Analysis.

## Data and Source Information

**Source:** SciCrunch Registry

## Usage and Citation Metrics

We found 18 mentions in open access literature.

**Listed below are recent publications.** The full list is available at dkNET.

Jiang Q, et al. (2020) G9a Plays Distinct Roles in Maintaining DNA Methylation, Retrotransposon Silencing, and Chromatin Looping. Cell reports, 33(4), 108315.

Carofino BL, et al. (2019) Head and neck squamous cancer progression is marked by CLIC4 attenuation in tumor epithelium and reciprocal stromal upregulation of miR-142-3p, a novel post-transcriptional regulator of CLIC4. Oncotarget, 10(68), 7251.

Yi Y, et al. (2018) Ultraviolet A irradiation induces senescence in human dermal fibroblasts by down-regulating DNMT1 via ZEB1. Aging, 10(2), 212.

Lin B, et al. (2018) c?Jun suppresses the expression of WNT inhibitory factor 1 through transcriptional regulation and interaction with DNA methyltransferase 1 in gallbladder cancer. Molecular medicine reports, 17(6), 8180.

Jiang CL, et al. (2017) Air pollution and DNA methylation alterations in lung cancer: A systematic and comparative study. Oncotarget, 8(1), 1369.

Myrick DA, et al. (2017) KDM1A/LSD1 regulates the differentiation and maintenance of spermatogonia in mice. PloS one, 12(5), e0177473.

Li N, et al. (2017) Hypermethylation of brain natriuretic peptide gene is associated with the risk of rheumatic heart disease. Bioscience reports, 37(1).

Nordström L, et al. (2015) DNA methylation and histone modifications regulate SOX11 expression in lymphoid and solid cancer cells. BMC cancer, 15, 273.

Hillemacher T, et al. (2015) Alterations in DNA-methylation of the dopamine-receptor 2 gene are associated with abstinence and health care utilization in individuals with a lifetime history of pathologic gambling. Progress in neuro-psychopharmacology & biological psychiatry, 63, 30.

Xu G, et al. (2014) Small nucleolar RNA 113-1 suppresses tumorigenesis in hepatocellular carcinoma. Molecular cancer, 13, 216.

Wang XQ, et al. (2013) Epigenetic regulation of pluripotent genes mediates stem cell features in human hepatocellular carcinoma and cancer cell lines. PloS one, 8(9), e72435.

Bettscheider M, et al. (2012) Optimized analysis of DNA methylation and gene expression from small, anatomically-defined areas of the brain. Journal of visualized experiments : JoVE(65), e3938.

Braunschweig MH, et al. (2011) Relationship of porcine IGF2 imprinting status to DNA methylation at the H19 DMD and the IGF2 DMRs 1 and 2. BMC genetics, 12, 47.

Nijland MJ, et al. (2010) Epigenetic modification of fetal baboon hepatic phosphoenolpyruvate carboxykinase following exposure to moderately reduced nutrient availability. The Journal of physiology, 588(Pt 8), 1349.

Zhai Y, et al. (2010) Loss of estrogen receptor 1 enhances cervical cancer invasion. The American journal of pathology, 177(2), 884.

Schalkwyk LC, et al. (2010) Allelic skewing of DNA methylation is widespread across the genome. American journal of human genetics, 86(2), 196.

Jahnke S, et al. (2009) Epigenetic resetting of a gene imprinted in plant embryos. Current biology : CB, 19(19), 1677.

Röhrs S, et al. (2009) Hypomethylation and expression of BEX2, IGSF4 and TIMP3 indicative of MLL translocations in acute myeloid leukemia. Molecular cancer, 8, 86.