

Resource Summary Report

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BiQAnalyzer HT

RRID:SCR_008045

Type: Tool

Proper Citation

BiQAnalyzer HT (RRID:SCR_008045)

Resource Information

URL: <http://biq-analyzer-ht.bioinf.mpi-inf.mpg.de/>

Proper Citation: BiQAnalyzer HT (RRID:SCR_008045)

Description: Software that currently allows to process an amount of bisulfite sequencing reads obtained in one or several bisulfite sequencing experiments.

Abbreviations: BiQAnalyzer HT

Resource Type: software resource

Resource Name: BiQAnalyzer HT

Resource ID: SCR_008045

Alternate IDs: OMICS_00631

Record Creation Time: 20220129T080245+0000

Record Last Update: 20260725T190647+0000

Ratings and Alerts

No rating or validation information has been found for BiQAnalyzer HT.

No alerts have been found for BiQAnalyzer HT.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 12 mentions in open access literature.

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

Almomani SN, et al. (2021) Identification and validation of DNA methylation changes in pre-eclampsia. *Placenta*, 110, 16.

Gianmoena K, et al. (2021) Epigenomic and transcriptional profiling identifies impaired glyoxylate detoxification in NAFLD as a risk factor for hyperoxaluria. *Cell reports*, 36(8), 109526.

Gasparoni G, et al. (2018) DNA methylation analysis on purified neurons and glia dissects age and Alzheimer's disease-specific changes in the human cortex. *Epigenetics & chromatin*, 11(1), 41.

Giehr P, et al. (2018) Two are better than one: HPoxBS - hairpin oxidative bisulfite sequencing. *Nucleic acids research*, 46(15), e88.

Pangeson T, et al. (2017) Association of Tissue-Specific DNA Methylation Alterations with α -Thalassemia Southeast Asian Deletion. *Genetics & epigenetics*, 9, 1179237X17736107.

Pietrzak M, et al. (2016) Non-random distribution of methyl-CpG sites and non-CpG methylation in the human rDNA promoter identified by next generation bisulfite sequencing. *Gene*, 585(1), 35.

Su Y, et al. (2016) Genome-wide DNA methylation profile of developing deciduous tooth germ in miniature pigs. *BMC genomics*, 17, 134.

Bharti P, et al. (2015) AtROS1 overexpression provides evidence for epigenetic regulation of genes encoding enzymes of flavonoid biosynthesis and antioxidant pathways during salt stress in transgenic tobacco. *Journal of experimental botany*, 66(19), 5959.

Höbaus J, et al. (2013) Increased copy-number and not DNA hypomethylation causes overexpression of the candidate proto-oncogene CYP24A1 in colorectal cancer. *International journal of cancer*, 133(6), 1380.

Steenpass L, et al. (2013) Human PPP1R26P1 functions as cis-repressive element in mouse Rb1. *PloS one*, 8(9), e74159.

Höbaus J, et al. (2013) Epigenetic regulation of the 1,25-dihydroxyvitamin D3 24-hydroxylase (CYP24A1) in colon cancer cells. *The Journal of steroid biochemistry and molecular biology*, 136, 296.

Lutsik P, et al. (2011) BiQ Analyzer HT: locus-specific analysis of DNA methylation by high-throughput bisulfite sequencing. *Nucleic acids research*, 39(Web Server issue), W551.