

Resource Summary Report

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[COHCAP](#)

RRID:SCR_006499

Type: Tool

Proper Citation

COHCAP (RRID:SCR_006499)

Resource Information

URL: <http://sourceforge.net/projects/cohcap/>

Proper Citation: COHCAP (RRID:SCR_006499)

Description: An algorithm to analyze single-nucleotide resolution methylation data (Illumina 450k methylation array, targeted BS-Seq, etc.). It provides QC metrics, differential methylation for CpG Sites, differential methylation for CpG Islands, integration with gene expression data, and visualization of methylation values.

Abbreviations: COHCAP

Synonyms: City of Hope CpG Island Analysis Pipeline, COHCAP - City of Hope CpG Island Analysis Pipeline

Resource Type: software resource

Defining Citation: [PMID:23598999](#)

Keywords: java, perl, s/r, java swing, bio.tools

Availability: Acknowledgement requested, Attribution Assurance License

Resource Name: COHCAP

Resource ID: SCR_006499

Alternate IDs: biotools:cohcap, OMICS_00595

Alternate URLs: <https://bio.tools/cohcap>

Record Creation Time: 20220129T080236+0000

Record Last Update: 20260801T190309+0000

Ratings and Alerts

No rating or validation information has been found for COHCAP.

No alerts have been found for COHCAP.

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 [RRID](#).

Sun JX, et al. (2024) Upregulation of GPR133 expression impaired the phagocytosis of macrophages in recurrent spontaneous miscarriage. *Epigenetics*, 19(1), 2337087.

Elhai M, et al. (2023) The long non-coding RNA HOTAIR contributes to joint-specific gene expression in rheumatoid arthritis. *Nature communications*, 14(1), 8172.

Zhang W, et al. (2022) Epigenetic study of early breast cancer (EBC) based on DNA methylation and gene integration analysis. *Scientific reports*, 12(1), 1989.

Wang G, et al. (2022) Uncovering potential genes in colorectal cancer based on integrated and DNA methylation analysis in the gene expression omnibus database. *BMC cancer*, 22(1), 138.

Xu Y, et al. (2021) Epigenetic Study of Esophageal Carcinoma Based on Methylation, Gene Integration and Weighted Correlation Network Analysis. *OncoTargets and therapy*, 14, 3133.

Tini G, et al. (2020) DNA methylation during human adipogenesis and the impact of fructose. *Genes & nutrition*, 15(1), 21.

Ren J, et al. (2020) Identification of Methylated Gene Biomarkers in Patients with Alzheimer's Disease Based on Machine Learning. *BioMed research international*, 2020, 8348147.

Sun XJ, et al. (2018) An integrated analysis of genome-wide DNA methylation and gene expression data in hepatocellular carcinoma. *FEBS open bio*, 8(7), 1093.

Huang J, et al. (2018) Use of methylation profiling to identify significant differentially methylated genes in bone marrow mesenchymal stromal cells from acute myeloid leukemia. *International journal of molecular medicine*, 41(2), 679.

Gerhard GS, et al. (2018) Differentially methylated loci in NAFLD cirrhosis are associated with key signaling pathways. *Clinical epigenetics*, 10(1), 93.

Wang Y, et al. (2018) Identification of methylated genes and miRNA signatures in nasopharyngeal carcinoma by bioinformatics analysis. *Molecular medicine reports*, 17(4),

Men C, et al. (2017) Identification of DNA methylation associated gene signatures in endometrial cancer via integrated analysis of DNA methylation and gene expression systematically. *Journal of gynecologic oncology*, 28(6), e83.

Frank-Bertoncelj M, et al. (2017) Epigenetically-driven anatomical diversity of synovial fibroblasts guides joint-specific fibroblast functions. *Nature communications*, 8, 14852.

Yang Y, et al. (2017) Identification of regulatory role of DNA methylation in colon cancer gene expression via systematic bioinformatics analysis. *Medicine*, 96(47), e8487.

Geoghegan F, et al. (2017) Bioenergetics of acquired cisplatin resistant H1299 non-small cell lung cancer and P31 mesothelioma cells. *Oncotarget*, 8(55), 94711.

Hui L, et al. (2017) Identification of potentially critical differentially methylated genes in nasopharyngeal carcinoma: A comprehensive analysis of methylation profiling and gene expression profiling. *Oncology letters*, 14(6), 7171.

Hua Y, et al. (2017) Abnormal expression of mRNA, microRNA alteration and aberrant DNA methylation patterns in rectal adenocarcinoma. *PloS one*, 12(3), e0174461.

Gevaert O, et al. (2015) Pancancer analysis of DNA methylation-driven genes using MethylMix. *Genome biology*, 16(1), 17.