

# Resource Summary Report

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## Bycom

RRID:SCR\_000659

Type: Tool

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### Proper Citation

Bycom (RRID:SCR\_000659)

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### Resource Information

**URL:** <http://sourceforge.net/projects/bycom/>

**Proper Citation:** Bycom (RRID:SCR\_000659)

**Description:** A software which can perform methylcytosine calling from BS-seq (WGBS and RRBS), and permits either unmapped reads (FASTQ) or mapped reads (SAM/BAM) to be used as the input data. Certain SNPs (C>A/G) can also be selected in the output.

**Resource Type:** software resource

**Defining Citation:** [PMID:25255082](#)

**Keywords:** methylcytosine, bs-seq, fastq, sam, bam, snps, snp, wgbs, rrbs, sorftw

**Availability:** Free, Available for download, Freely available

**Resource Name:** Bycom

**Resource ID:** SCR\_000659

**Alternate IDs:** OMICS\_00594

**Record Creation Time:** 20220129T080202+0000

**Record Last Update:** 20260815T182730+0000

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### Ratings and Alerts

No rating or validation information has been found for Bycom.

No alerts have been found for Bycom.

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### Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We have not found any literature mentions for this resource.