

# Resource Summary Report

Generated by [PRECISE-TBI](#) on Aug 1, 2026

## GobyWeb

RRID:SCR\_005443

Type: Tool

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### Proper Citation

GobyWeb (RRID:SCR\_005443)

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### Resource Information

**URL:** <http://campagnelab.org/software/gobyweb/>

**Proper Citation:** GobyWeb (RRID:SCR\_005443)

**Description:** Web application that facilitates the management and analysis of high-throughput sequencing (HTS) data. In the back-end, it uses the Goby framework, BWA, STAR, Last, GSNAP, Samtools, VCF-tools, along with a cluster of servers to provide rapid alignment and efficient analyses. GobyWeb makes it possible to analyze hundreds of samples in consistent ways without having to use command line tools. GobyWeb provides tools that streamline frequent data analyses for RNA-Seq, Methyl-Seq, RRBS, or DNA-Seq datasets and to enable teams of investigators to share reads and results of analyses. GobyWeb can be extended for new analyses by developing plugins.

**Abbreviations:** GobyWeb

**Resource Type:** software resource

**Defining Citation:** [PMID:23936070](#)

**Keywords:** high-throughput sequencing, gene expression, dna methylation, sequencing, bio.tools

**Availability:** Acknowledgement requested, GNU Lesser General Public License, v3

**Resource Name:** GobyWeb

**Resource ID:** SCR\_005443

**Alternate IDs:** OMICS\_00601, biotools:gobyweb

**Alternate URLs:** <https://bio.tools/gobyweb>

**Record Creation Time:** 20220129T080230+0000

**Record Last Update:** 20260801T190259+0000

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## Ratings and Alerts

No rating or validation information has been found for GobyWeb.

No alerts have been found for GobyWeb.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 3 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [PRECISE-TBI](#) .

Mesnard L, et al. (2016) Exome Sequencing and Prediction of Long-Term Kidney Allograft Function. PLoS computational biology, 12(9), e1005088.

Ruiz S, et al. (2016) A mouse model of hereditary hemorrhagic telangiectasia generated by transmammary-delivered immunoblocking of BMP9 and BMP10. Scientific reports, 5, 37366.

Marcinkiewicz KM, et al. (2014) Altered histone mark deposition and DNA methylation at homeobox genes in human oral squamous cell carcinoma. Journal of cellular physiology, 229(10), 1405.