## **Resource Summary Report**

Generated by dkNET on May 5, 2025

# **GobyWeb**

RRID:SCR\_005443

Type: Tool

### **Proper Citation**

GobyWeb (RRID:SCR\_005443)

#### Resource Information

URL: http://campagnelab.org/software/gobyweb/

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**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

**Funding:** 

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:** 20250420T014251+0000

### **Ratings and Alerts**

No rating or validation information has been found for GobyWeb.

No alerts have been found for GobyWeb.

#### Data and Source Information

Source: SciCrunch Registry

## **Usage and Citation Metrics**

We found 3 mentions in open access literature.

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

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.

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

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.