

Resource Summary Report

Generated by ASWG on Aug 9, 2026

University of Freiburg Bioinformatics Group: Servers and Web-Applications

RRID:SCR_008256

Type: Tool

Proper Citation

University of Freiburg Bioinformatics Group: Servers and Web-Applications
(RRID:SCR_008256)

Resource Information

URL: <http://www.bioinf.uni-freiburg.de/Software>

Proper Citation: University of Freiburg Bioinformatics Group: Servers and Web-Applications (RRID:SCR_008256)

Description: This resource takes you to the Server and Web-Applications of the University of Freiburg Bioinformatics Group. Sponsors: This resource is supported by University of Freiburg. Keywords: Server, Web application, Bioinformatics, Software,

Synonyms: Freiburg Bioinformatics Group

Resource Type: data or information resource, portal, topical portal

Resource Name: University of Freiburg Bioinformatics Group: Servers and Web-Applications

Resource ID: SCR_008256

Alternate IDs: nif-0000-30196

Record Creation Time: 20220129T080246+0000

Record Last Update: 20260808T185906+0000

Ratings and Alerts

No rating or validation information has been found for University of Freiburg Bioinformatics Group: Servers and Web-Applications.

No alerts have been found for University of Freiburg Bioinformatics Group: Servers and Web-Applications.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 9 mentions in open access literature.

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

Hao J, et al. (2023) Lnc-SNHG5 Promoted Hepatocellular Carcinoma Progression Through the RPS3-NF κ B Pathway. International journal of general medicine, 16, 5651.

Kleinkauf R, et al. (2015) antaRNA--Multi-objective inverse folding of pseudoknot RNA using ant-colony optimization. BMC bioinformatics, 16, 389.

Wright PR, et al. (2014) CopraRNA and IntaRNA: predicting small RNA targets, networks and interaction domains. Nucleic acids research, 42(Web Server issue), W119.

Mann M, et al. (2014) Atom mapping with constraint programming. Algorithms for molecular biology : AMB, 9(1), 23.

Mann M, et al. (2014) Memory-efficient RNA energy landscape exploration. Bioinformatics (Oxford, England), 30(18), 2584.

Silva IJ, et al. (2013) An RpoS-dependent sRNA regulates the expression of a chaperone involved in protein folding. RNA (New York, N.Y.), 19(9), 1253.

Li W, et al. (2012) Predicting sRNAs and their targets in bacteria. Genomics, proteomics & bioinformatics, 10(5), 276.

Marín RM, et al. (2012) Optimal use of conservation and accessibility filters in microRNA target prediction. PloS one, 7(2), e32208.

Richter AS, et al. (2012) Accessibility and conservation: general features of bacterial small RNA-mRNA interactions? RNA biology, 9(7), 954.