

Resource Summary Report

Generated by [dkNET](#) on Sep 5, 2026

xFITOM

RRID:SCR_014445

Type: Tool

Proper Citation

xFITOM (RRID:SCR_014445)

Resource Information

URL: <http://erilllab.umbc.edu/research/software/xfitom/>

Proper Citation: xFITOM (RRID:SCR_014445)

Description: A fully customizable program that uses a graphical user interface to locate transcription factor-binding sites in genomic sequences. xFITOM scans DNA or RNA sequences for putative binding sites as defined by a collection of aligned known sites, a consensus sequence in IUPAC degenerate-base format, or a combination of the two.

Resource Type: data analysis software, data processing software, sequence analysis software, software application, software resource, standalone software

Defining Citation: [PMID:21346861](#)

Keywords: transcription factor, binding site, information theory, customizable program, sequence analysis software

Availability: Available for download, Acknowledgement requested

Resource Name: xFITOM

Resource ID: SCR_014445

Alternate URLs: <http://www.mybiosoftware.com/fitom-1-0-detection-binding-sites-dna-rna-sequences.html>

Old URLs: compbio.umbc.edu/Software/xFITOM/ <http://research.umbc.edu/~erill/>

License: GPL

License URLs: Free for use and redistribution

Record Creation Time: 20220129T080320+0000

Record Last Update: 20260903T235802+0000

Ratings and Alerts

No rating or validation information has been found for xFITOM.

No alerts have been found for xFITOM.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 7 mentions in open access literature.

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

Caruso SM, et al. (2019) A Novel Genus of Actinobacterial Tectiviridae. *Viruses*, 11(12).

Qi W, et al. (2019) New insights on *Pseudoalteromonas haloplanktis* TAC125 genome organization and benchmarks of genome assembly applications using next and third generation sequencing technologies. *Scientific reports*, 9(1), 16444.

Erill I, et al. (2016) The Verrucomicrobia LexA-Binding Motif: Insights into the Evolutionary Dynamics of the SOS Response. *Frontiers in molecular biosciences*, 3, 33.

Walter BM, et al. (2014) The LexA regulated genes of the *Clostridium difficile*. *BMC microbiology*, 14, 88.

Sanchez-Alberola N, et al. (2012) Analysis of the SOS response of *Vibrio* and other bacteria with multiple chromosomes. *BMC genomics*, 13, 58.

Cambray G, et al. (2011) Prevalence of SOS-mediated control of integron integrase expression as an adaptive trait of chromosomal and mobile integrons. *Mobile DNA*, 2(1), 6.

Bhargava N, et al. (2010) xFITOM: a generic GUI tool to search for transcription factor binding sites. *Bioinformatics*, 5(2), 49.