Resource Summary Report

Generated by NIF on Apr 22, 2025

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

Defining Citation: PMID:21346861

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

Funding:

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: 20250422T055801+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 NIF.

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.

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

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. Bioinformation, 5(2), 49.