

Resource Summary Report

Generated by [Kravitz](#) on Sep 17, 2026

Wasserman Lab Online Software Tools

RRID:SCR_002892

Type: Tool

Proper Citation

Wasserman Lab Online Software Tools (RRID:SCR_002892)

Resource Information

URL: <http://www.cisreg.ca/>

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Description: This portal leads to the numerous Wasserman Lab online software tools available for use. The following are list of active Software tools available: - ConSite: Transcription factor binding site detection using phylogenetic footprinting - dbMTN: Multiple Tissue Northern Blot Comparison Tool - Gene Set Builder: A tool for collation, curation and distribution of sets of genes - The Gene Characterization Index: a bioinformatics method for scoring the extent to which a protein-encoding gene is functionally described - JASPAR: Transcription Factor Binding Profile Database - MSCAN: Algorithm that detects clusters of transcription factor binding sites in genomic sequences - NHRscan: A computational predictor of nuclear hormone receptor binding sites - oPOSSUM: Web-based analysis of over-represented transcription factor binding sites - ORCA: Transcription factor binding site detection using phylogenetic footprinting (alternative to ConSite) - OrthoSeq: Alignment of DNA sequences - PAZAR: An open-access system for the collection and dissemination of regulatory sequence annotation - Phylofoot: Tools for phylogenetic footprinting - RAVEN: Regulatory analysis of Variation in ENhancers - SAGE2Splice: A tool that uses unmapped SAGE tags to predict novel splice junctions in the genome - TFBS: Perl modules for transcription factor binding site detection and analysis - TFCat: TFCat is a catalog of mouse and human TFs based on a reliable core collection of annotations obtained by expert review of the scientific literature. - TFe: An online encyclopedic collection of well-studied transcription factor proteins in the human, mouse, and rat genomes - Ulysses: Protein Interactions Conserved Across Evolution

Synonyms: Wasserman Software

Resource Type: software library, software resource, software toolkit

Keywords: lab, library, online, software, tool

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Wasserman Lab Online Software Tools

Resource ID: SCR_002892

Alternate IDs: nif-0000-25613

Record Creation Time: 20220129T080216+0000

Record Last Update: 20260912T195548+0000

Ratings and Alerts

No rating or validation information has been found for Wasserman Lab Online Software Tools.

No alerts have been found for Wasserman Lab Online Software Tools.

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 [Kravitz](#) .

Chan CC, et al. (2020) Type I interferon sensing unlocks dormant adipocyte inflammatory potential. Nature communications, 11(1), 2745.

Song YC, et al. (2019) HDAC1-mediated repression of the retinoic acid-responsive gene ripply3 promotes second heart field development. PLoS genetics, 15(5), e1008165.

Marquet S, et al. (2017) A Functional IL22 Polymorphism (rs2227473) Is Associated with Predisposition to Childhood Cerebral Malaria. Scientific reports, 7, 41636.

Chang TT, et al. (2014) Molecular mechanisms underlying the enhanced functions of three-dimensional hepatocyte aggregates. Biomaterials, 35(7), 2162.

Patnala R, et al. (2013) Candidate gene association studies: a comprehensive guide to useful in silico tools. BMC genetics, 14, 39.

Keasey MP, et al. (2013) Inhibition of a novel specific neuroglial integrin signaling pathway increases STAT3-mediated CNTF expression. Cell communication and signaling : CCS, 11, 35.

Kuo BY, et al. (2006) SAGE2Splice: unmapped SAGE tags reveal novel splice junctions. PLoS computational biology, 2(4), e34.

McKee AE, et al. (2006) Systems biology of gene regulation fulfills its promise. Genome biology, 7(5), 316.

Kemmer D, et al. (2004) Exploring the foundation of genomics: a northern blot reference set for the comparative analysis of transcript profiling technologies. *Comparative and functional genomics*, 5(8), 584.