

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

SearchGUI

RRID:SCR_012054

Type: Tool

Proper Citation

SearchGUI (RRID:SCR_012054)

Resource Information

URL: <https://code.google.com/p/searchgui/>

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Description: Software providing a user-friendly, lightweight and open-source graphical user interface for configuring and running the freely available OMSSA and X!Tandem search engines simultaneously.

Resource Type: software resource

Defining Citation: [PMID:21337703](#)

Keywords: mac os x, unix/linux, windows

Availability: Apache License

Resource Name: SearchGUI

Resource ID: SCR_012054

Alternate IDs: OMICS_03352

Record Creation Time: 20220129T080308+0000

Record Last Update: 20260905T132719+0000

Ratings and Alerts

No rating or validation information has been found for SearchGUI.

No alerts have been found for SearchGUI.

Data and Source Information

Usage and Citation Metrics

We found 157 mentions in open access literature.

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

Choi KY, et al. (2026) Structural energetics of cold sensitivity. *Nature*, 653(8115), 962.

Troian EA, et al. (2026) Harnessing toxin-mediated ribosome stalling as a complementary tool to annotate bacterial ORFs. *Nucleic acids research*, 54(7).

Farag YM, et al. (2026) Automatic Selection of Search Parameter Values for Mass Spectrometry-Based Search Engines. *Journal of proteome research*, 25(2), 662.

Sadaow L, et al. (2025) Immunomics-guided biomarker discovery for human liver fluke infection and infection-associated cholangiocarcinoma. *Nature communications*, 16(1), 5965.

Kaiser A, et al. (2025) Transient ligand contacts of the intrinsically disordered N-terminus of neuropeptide Y2 receptor regulate arrestin-3 recruitment. *Nature communications*, 16(1), 8326.

Pipart J, et al. (2025) MultiStageSearch: An Iterative Workflow for Unbiased Taxonomic Analysis of Pathogens Using Proteogenomics. *Journal of proteome research*, 24(6), 2643.

Yan S, et al. (2025) Glycoproteomic and Single-Protein Glycomic Analyses Reveal Zwitterionic N-Glycans on Natural and Recombinant Proteins Derived From Insect Cells. *Molecular & cellular proteomics : MCP*, 24(6), 100981.

Canderan J, et al. (2025) Identification of microbial species and proteins associated with colorectal cancer by reanalyzing CPTAC proteomic datasets. *Scientific reports*, 15(1), 13926.

Choi KY, et al. (2025) The structural basis of cold sensitivity. *bioRxiv : the preprint server for biology*.

Vlasov PA, et al. (2025) Multiple human enhancer RNAs contain long translated open reading frames. *Genes & development*, 39(23-24), 1468.

Wang S, et al. (2025) An Approach to Integrate Metagenomics, Metatranscriptomics and Metaproteomics Data in Public Data Resources. *Proteomics*, 25(17-18), 33.

Meurs J, et al. (2025) High-Throughput Analysis of Protein Adsorption to a Large Library of Polymers Using Liquid Extraction Surface Analysis-Tandem Mass Spectrometry (LESA-MS/MS). *Analytical chemistry*, 97(24), 12776.

Hus KK, et al. (2024) Venom diversity in *Naja mossambica*: Insights from proteomic and immunochemical analyses reveal intraspecific differences. *PLoS neglected tropical diseases*, 18(4), e0012057.

Bertino F, et al. (2024) Dysregulation of FLVCR1a-dependent mitochondrial calcium handling in neural progenitors causes congenital hydrocephalus. *Cell reports. Medicine*, 5(7), 101647.

Delogu F, et al. (2024) Forecasting the dynamics of a complex microbial community using integrated meta-omics. *Nature ecology & evolution*, 8(1), 32.

Do K, et al. (2024) A novel clinical metaproteomics workflow enables bioinformatic analysis of host-microbe dynamics in disease. *mSphere*, 9(6), e0079323.

Ahmed TA, et al. (2024) The cross talk between type II diabetic microenvironment and the regenerative capacities of human adipose tissue-derived pericytes: a promising cell therapy. *Stem cell research & therapy*, 15(1), 36.

Kiseleva OI, et al. (2024) Multiomics Picture of Obesity in Young Adults. *Biology*, 13(4).

Nasr E, et al. (2024) microGalaxy: A gateway to tools, workflows, and training for reproducible and FAIR analysis of microbial data. *bioRxiv : the preprint server for biology*.

Kruk ME, et al. (2024) An integrated metaproteomics workflow for studying host-microbe dynamics in bronchoalveolar lavage samples applied to cystic fibrosis disease. *mSystems*, 9(7), e0092923.