

Resource Summary Report

Generated by [ASWG](#) on Aug 2, 2026

SearchGUI

RRID:SCR_012054

Type: Tool

Proper Citation

SearchGUI (RRID:SCR_012054)

Resource Information

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

Proper Citation: SearchGUI (RRID:SCR_012054)

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: 20260801T190430+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 154 mentions in open access literature.

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

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

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.

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

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.

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

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

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.

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).

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

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

5(7), 101647.

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.

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

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*.

Ducker C, et al. (2024) A diterpene synthase from the sandfly *Lutzomyia longipalpis* produces the pheromone sobralene. *Proceedings of the National Academy of Sciences of the United States of America*, 121(12), e2322453121.

Chen R, et al. (2024) HDX-MS finds that partial unfolding with sequential domain activation controls condensation of a cellular stress marker. *Proceedings of the National Academy of Sciences of the United States of America*, 121(13), e2321606121.

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.

Walcher S, et al. (2024) Deciphering fucosylated protein-linked O-glycans in oral *Tannerella serpentina*: Insights from NMR spectroscopy and glycoproteomics. *Glycobiology*, 34(12).