

MASH Native App

MASH Native, developed by the Ying Ge research group, is a comprehensive, universal, and user-friendly, free software environment for top-down native and denatured proteomics. MASH Native builds on previous work with MASH Suite, MASH Suite Pro, and MASH Explorer.

MASH Native allows data import from various vendor data formats. This software accommodates several deconvolution and database search pipelines for spectral deconvolution and protein identifications. The program also allows quantification of various proteoforms in different biological/experimental conditions. MASH Native allows visualization of the complex top-down and tandem mass spectra for the validation of deconvolution and protein identification results. It is developed by an interdisciplinary team consisting of experts in top-down mass spectrometry-based proteomics, computational data science, and bioinformatics/biostatistics.

More information can be found on the [MASH Website](#).

MASH Native Citation

Please cite the following publications if the software is used:

- Wu, Z.; Roberts, D.S.; Melby, J.A.; Wenger, K.; Wetzel, M.; Gu, Y.; Ramanathan, S.G.; Bayne, E.F.; Liu, X.; Sun, R.; Ong, I.M.; McIlwain, S.J.; **Ge, Y.** MASH Explorer: A Universal Software Environment for Top-Down Proteomics., *J. Proteome Res.*, 2020, Online ahead of print.
- Cai, W.; Guner, H.; Gregorich, Z.R.; Chen, A.J.; Ayaz - Guner, S.; Peng, Y.; Valeja, S.G.; Liu, X.; Ge, Y. MASH Suite Pro: A Comprehensive Software Tool for Top - down Proteomics, *Mol. Cell. Proteomics*. Epub ahead of print.mcp.O115.054387.

Also, please cite the supporting software you use within MASH Native (see “Supporting Software References” below).

Development Information

This application is written in C# using Microsoft Visual Studio Professional 2019.

Funding

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License

Copyright © 2019-2022 Ying Ge Research Group, University of Wisconsin - Madison, School of Medicine and Public Health. UW-Madison Human Proteomics Program.

Installation Requirements

Please see our [Installation Guide](#) for a detailed description of how to install the required supporting software. The same information can be found in the **User Installation Guide** (MASH Native -> Help -> Documentation -> User Installation Guide.pdf) included with your MASH Native download.

Getting Started

The [Getting Started Webpage](#) and the **Getting Started file** (MASH Native -> Help -> Documentation -> GettingStarted.pdf) document included with the MASH Native download contains sample data files and a tutorial of how to use Discovery Mode and Targeted Mode.

User Manual

Please see the **User Manual** (MASH Native -> Help -> Documentation -> UserManual.pdf) included with the MASH Native download, for a detailed description of how to use MASH Native's functions. You can also access the [User Manual](#) online

Supported Mass Spectra Data Files

- Thermo *.raw files
- Bruker *.d, *.Baf and *.ascii files

- *.mzXML files
- *.mzML files
- *.mgf files
- Waters *.raw files

Supported Algorithms

Informed Proteomics:

- [ProMex and MSPathFinderT Website](#)
- [Manual and Other Information](#)

MS-Align+:

- [Ms-Deconv Information](#)
- [MS-Align+ Information](#)

pTop:

- [pParseTD Manual and Other Information](#)
- [pTop Manual and Other Information](#)

THRASH:

- [THRASH Paper](#)

TopPIC:

- [Manual and Other Information](#)

OpenMS:

- [FLASHDeconv information](#)

UniDec:

- [UniDec information](#)
- [UniDec software license](#)

Versions

The current MASH Native software is version 1.0. A description of software updates and release notes can be found in the **Release Notes** (MASH Native -> Help -> Documentation -> ReleaseNotes.pdf). You can also access the [Release Notes](#) online.

User Support

Please email mash-support@g-groups.wisc.edu for technical assistance. The MASH development team responds to these emails.

Email Lists

MASH Announcements: mash-announce@g-groups.wisc.edu (Note that you cannot send email to this list – it is only for the MASH team to send announcements to MASH users.)

- Provides emails with news about MASH software updates
- To join, go to <https://groups.google.com/a/g-groups.wisc.edu/g/mash-announce> and click the “Ask to join group” button.
- To leave the group once you’ve joined, go to <https://groups.google.com/a/g-groups.wisc.edu/g/mash-announce/membership> and click the “Leave group” button.

MASH App Forum: mashforum@googlegroups.com.

- Provides a forum for MASH users to post questions, etc. Questions can be answered by other MASH users or by the MASH team.
- To join, go to <https://groups.google.com/g/mashforum> and click the “Ask to join group” button.
- To leave the group once you’ve joined, go to <https://groups.google.com/g/mashforum> and click the “Leave group” button.

MASH Team

Active Team Members

- Dr. Ying Ge, Principal Investigator
- Dr. Irene Ong, Co-Investigator
- Dr. Sean McIlwain, Co-Investigator
- Dr. Xiaowen Liu, Collaborator
- Dr. Ruixiang Sun, Collaborator
- Kent Wenger, Software Developer
- Jake Melby, Graduate Student
- David Roberts, Graduate Student
- Eli Larson, Graduate Student

Previous Team Members

- Dr. Wenxuan Cai
- Yiwen Gu Sudharshanan
- Govindaraj Ramanathan
- Molly Wetzel, Software Developer
- Yiran Yan, Undergraduate Assistant
- Zhijie (Abe) Wu, Graduate Student
- Kyndalanne Pike, Graduate Student
- Anna Janicek, Undergraduate Assistant
- Harini Josyer, Undergraduate Assistant

Supporting Software References

Please cite the appropriate publications from the following list according to the supporting software that you use within MASH Native.

CompassXtract: This software uses CompassXtract software. Copyright © 2011 by Bruker Daltonik GmbH. All rights reserved.

DeconEngine: N. Jaitly, A. Mayampurath, K. Littlefield, J. N. Adkins, G. A. Anderson, and R. D. Smith. Decon2LS: An open-source software package for automated processing and visualization of high resolution mass spectrometry data. *BMC Bioinformatics*, 2009, 10: 87. [Link](#)

Informed Proteomics: J. Park, P. D. Piehowski, C. Wilkins, M. Zhou, J. Mendoza, G. M. Fujimoto, B. C. Gibbons, J. B. Shaw, Y. Shen, A. K. Shukla, R. J. Moore, T. Liu, V. A. Petyuk, N. Tolic, L. Pasa-Tolic, R. D. Smith, S. H. Payne, and S. Kim. Informed-Proteomics: Open Source Software Package for Top-down Proteomics. *Nature Methods*, 2017, 14: 9. 909-914. [Link](#)

MS-Align+: X. Liu, Y. Sirotkin, Y. Shen, G. Anderson, Y. S. Tsai, Y. S. Ting, D. R. Goodlett, R. D. Smith, V. Bafna, and P. A. Pevzner. Protein Identification Using Top-Down Spectra. *Molecular & Cellular Proteomics*, 2012, 11: 6. [Link](#)

Ms-Deconv: X. Liu, Y. Inbar, P. C. Dorrestein, C. Wynne, N. Edwards, P. Souda, J. P. Whitelegge, V. Bafna, and P. A. Pevzner. Deconvolution and Database Search of Complex Tandem Mass Spectra of Intact Proteins. *Molecular & Cellular Proteomics*, 2010, 9, 12: 2772-2782. [Link](#)

MSFileReaderT: MSFileReader file reading tool. Copyright © 2009 - 2014 by Thermo Fisher Scientific, Inc. All rights reserved.

pParseTD: Z.-F. Yuan, C. Liu, H.-P. Wang, R.-X. Sun, Y. Fu, J.-F. Zhang, L.-H. Wang, H. Chi, Y. Li, L.-Y. Xiu, W.-P. Wang, S.-M. He. pParse: a method for accurate determination of monoisotopic peaks in high-resolution mass spectra. *Proteomics*, 2012, 12: 2, 226–235. [Link](#)

ProteoWizard: M.C. Chambers, B. MacLean, R. Burke, D. Amode, D.L. Ruderman, S. Neumann, L. Gatto, B. Fischer, B. Pratt, J. Egertson, K. Hoff, D. Kessner, N. Tasman, N. Shulman, B. Frewen, T.A. Baker, M.-Y. Brusniak, C. Paulse, D. Creasy, L. Flashner, K. Kani, C. Moulding, S. L. Seymour, L. M. Nuwaysir, B. Lefebvre, F. Kuhlmann, J. Roark, P. Rainer, S. Detlev, T. Hemenway, A. Huhmer, J. Langridge, B. Connolly, T. Chadick, K. Holly, J. Eckels, E. W. Deutsch, R. L. Moritz, J. E. Katz, D. B. Agus, M. MacCoss, D. L. Tabb, & P. Mallick. A cross-platform toolkit for mass spectrometry and proteomics. *Nature Biotechnology*, 2012, 30, 918-920. [Link](#)

pTop: R.-X. Sun, L. Luo, L. Wu, R.-M. Wang, W.-F. Zeng, H. Chi, C. Liu, and S.-M. He. pTop 1.0: a High-accuracy and High-efficiency Search Engine for Intact Protein Identification. *Analytical Chemistry*, 2016, 88, 3082-3090. [Link](#)

THRASH: D. M. Horn, R. A. Zubarev, and F. W. McLafferty. Automated reduction and interpretation of high resolution electrospray mass spectra of large molecules, *Journal of the American Society for Mass Spectrometry*, 2000, 11: 4, 320-332. [Link](#)

TopPIC Suite: Q. Kou, L. Xun, and X. Liu. TopPIC: a software tool for top-down mass spectrometry-based proteoform identification and characterization. *Bioinformatics*, 2016, 32, 3495-3497. [Link](#)

FLASHDeconv: K. Jeong, J. Kim, M. Gaikwad, S. N. Hidayah, L. Heikaus, H. Schlüter, and O. Kohlbacher, “FLASHDeconv: Ultrafast, high-quality feature deconvolution for top-down proteomics,” *Cell Systems*, vol. 10, iss. 2, p. 213–218, 2020. [Link](#)

UniDec: M. T. Marty , A. J. Baldwin , E. G. Marklund , G. K. A. Hochberg , J. L. P. Benesch , and C. V. Robinson. "Bayesian Deconvolution of Mass and Ion Mobility Spectra: From Binary Interactions to Polydisperse Ensembles" *Analytical Chemistry*, 2015, DOI: 10.1021/acs.analchem.5b00140. [Link](#)

Additional Resources

- [UniProt Database Website](#)
- [UW Human Proteomics Program](#)
- [Ying Ge Research Group](#)

- [Consortium for Top-down Proteomics](#)