



MRMaid: Frequently Asked Questions

Q. *I have a problem, comment or feature request – is there someone I can tell?*

A. We are committed to developing and supporting MRMaid for some years to come, so please post your questions and comments to the MRMaid Google Group (<http://groups.google.com/group/mrmaid>) or email us directly via team@mrmaid.info.

Q. *How are the transitions calculated?*

A. Transitions are determined according to a number of different criteria derived from spectral data extracted from PRIDE. A poster outlining the general approach was presented at HUPO 2011, and a paper describing in detail the methods used is in preparation. In the meantime key aspects of the transition design process can be found in the original MRMaid paper: [Mead et al., Molecular & Cellular Proteomics, 2009, 8 \(4\), 696-705](#).

Q. *Is there a limit to the number of proteins I can look for in one search?*

A. We haven't set a limit but the transition table may become slow to respond if it grows beyond a few hundred rows, depending on the speed of your computer and the number of other people using MRMaid at the time. Use the various filters at the top of the transition table to keep things manageable – there will be a limit to the number of transitions you can monitor in the lab anyway.

Q. *Which browser should I use with MRMaid?*

A. MRMaid has been tested on recent versions of Chrome, Firefox, Safari and Internet Explorer, on various operating systems. The main thing you can do to improve your MRMaid experience is to maximise your browser window on a good size display because the transition tables are necessarily quite large.

Q. *Can I use MRMaid to design transitions for species other than those listed in the drop down box on the search page?*

A. No, but we will be increasing the number of species we support during the coming weeks. If you have a particular species that you would like to see included, let us know so we can move it up our list of priorities.

Q. *How reliable are MRMaid's transitions?*

A. Results of the original MRMaid were compared to published lists of validated transitions and found to be in good agreement – this was reported in our 2009 paper in MCP. We are currently carrying out similar tests on MRMaid 2.0 and it will remain in beta until the results of those tests are completed and in press. It is important to note that the results returned by MRMaid are only *suggested* transitions – we recommend that you validate them for your particular combination of instrument and sample prior to use.

Q. *Do you record or monitor which proteins I'm searching for, or do other creepy stuff?*

A. No. We don't monitor or store any information that links protein searches with IP addresses so we have no way of knowing who is studying which proteins. However, like most web sites we do record general statistical data about where our visitors come from and how they use the site to help us plan future development.

Q. *Can I use MRMAid to design transitions based on my own spectral dataset(s)?*

A. The web based version of MRMAid doesn't support the design of transitions based on a specific dataset. If you are interested in having your own instance of MRMAid installed in your organisation to derive transitions from your own in-house data, contact us (email team@mrm Maid.info) because we may be able to help.

Q. *Is MRMAid able to consider private PRIDE datasets when designing transitions?*

A. No, MRMAid is only able to access PRIDE's public datasets. If you would like your own private data to be considered by MRMAid, please let us know as this is something that could be explored.

Q. *How long does it take MRMAid to pick up new data from PRIDE?*

A. New builds of the transition database that powers MRMAid are created periodically. Normally this will be several days after a new PRIDE build is released – the date and version of the transition database build is shown at the bottom of the MRMAid search page and the MRMAid results page.

Q. *Can I use MRMAid to design transitions for anything other than proteins?*

A. No, not at present. If you would be interested in another version of MRMAid that supports other classes of molecules, please let us know (email team@mrm Maid.info).

Q. *Can I use MRMAid to design transitions for proteins that have been subjected to a specific post translational modification?*

A. No, not at present. If you would like MRMAid to support the design of PTM-specific transitions please let us know – the more support we can get for this feature, the sooner we can implement it.

Q. *What effect does changing the instrument type have in the transitions table?*

A. The instrument type setting is used to specify the type of instrument from which the transitions were inferred. So, selecting *ESI-ToF* will show transitions derived from spectral data which is unambiguously tagged in PRIDE as being from some kind of ESI-ToF.

Q. *Why does selecting the All instrument type give me more transitions than the three individual instrument types put together?*

A. PRIDE includes data from instruments other than the three listed in MRMAid, and includes some spectral data for which the instrument type is unclassified or ambiguous. Selecting the *All* instrument type makes MRMAid literally consider all PRIDE data, regardless of the instrument on which it was collected.