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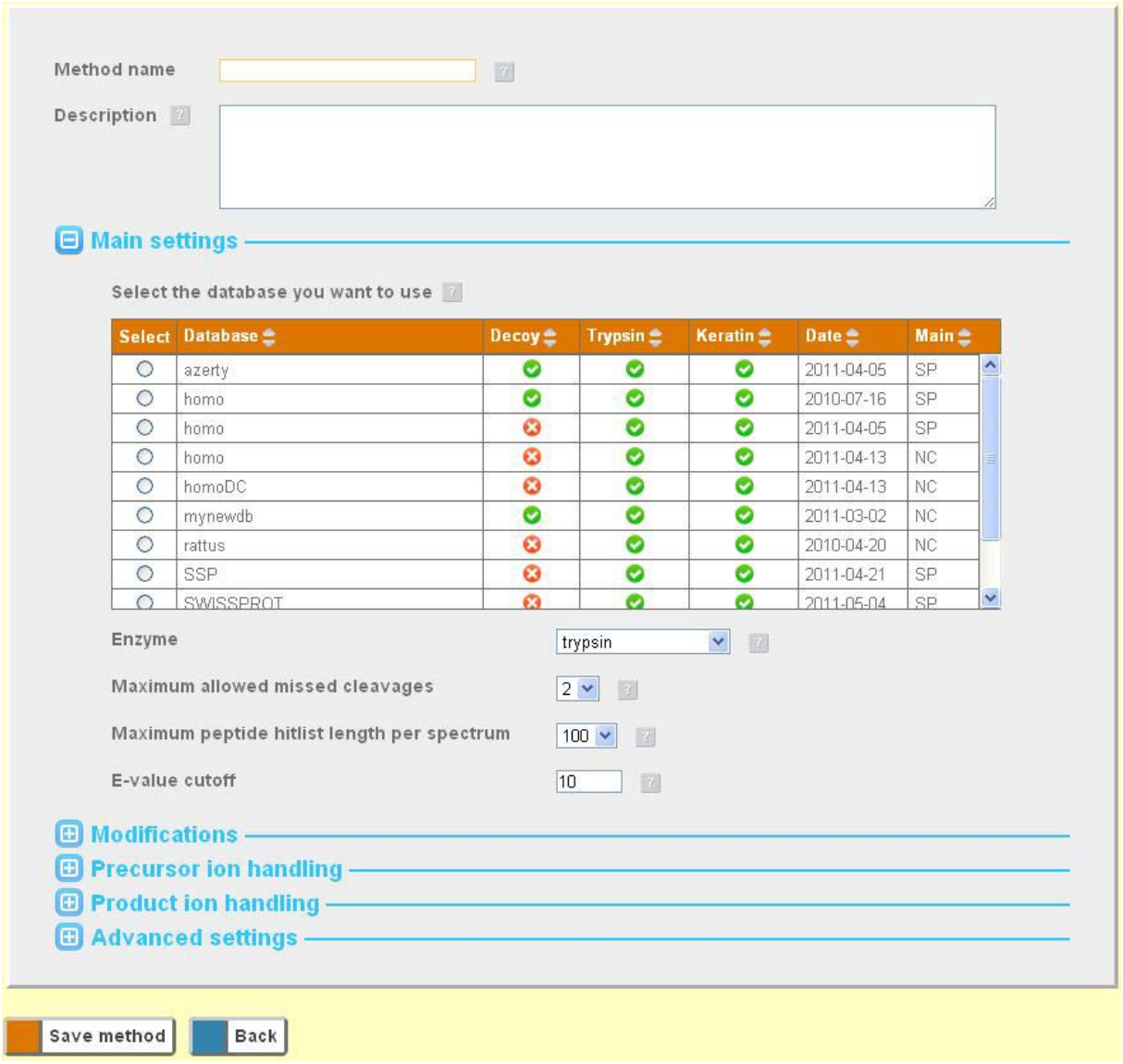
MSDA tutorial: How to refine OMSSA search parameters

MSDA and OMSSA enable all search parameters to be user-adjusted. A set of settings is stored into a method named by the user. You can generate your own protein databases and post-translational modifications, save and store your methods to reuse them for further searches. Every user has a predefined default method.

Create your own method

You need to enter a method name and set your parameters at adapted values for your searches. The grey boxes with an interrogation mark contain a definition of the parameter. A method is divided into five parts: the main settings, modifications, precursor & product ion handling, and advanced settings.



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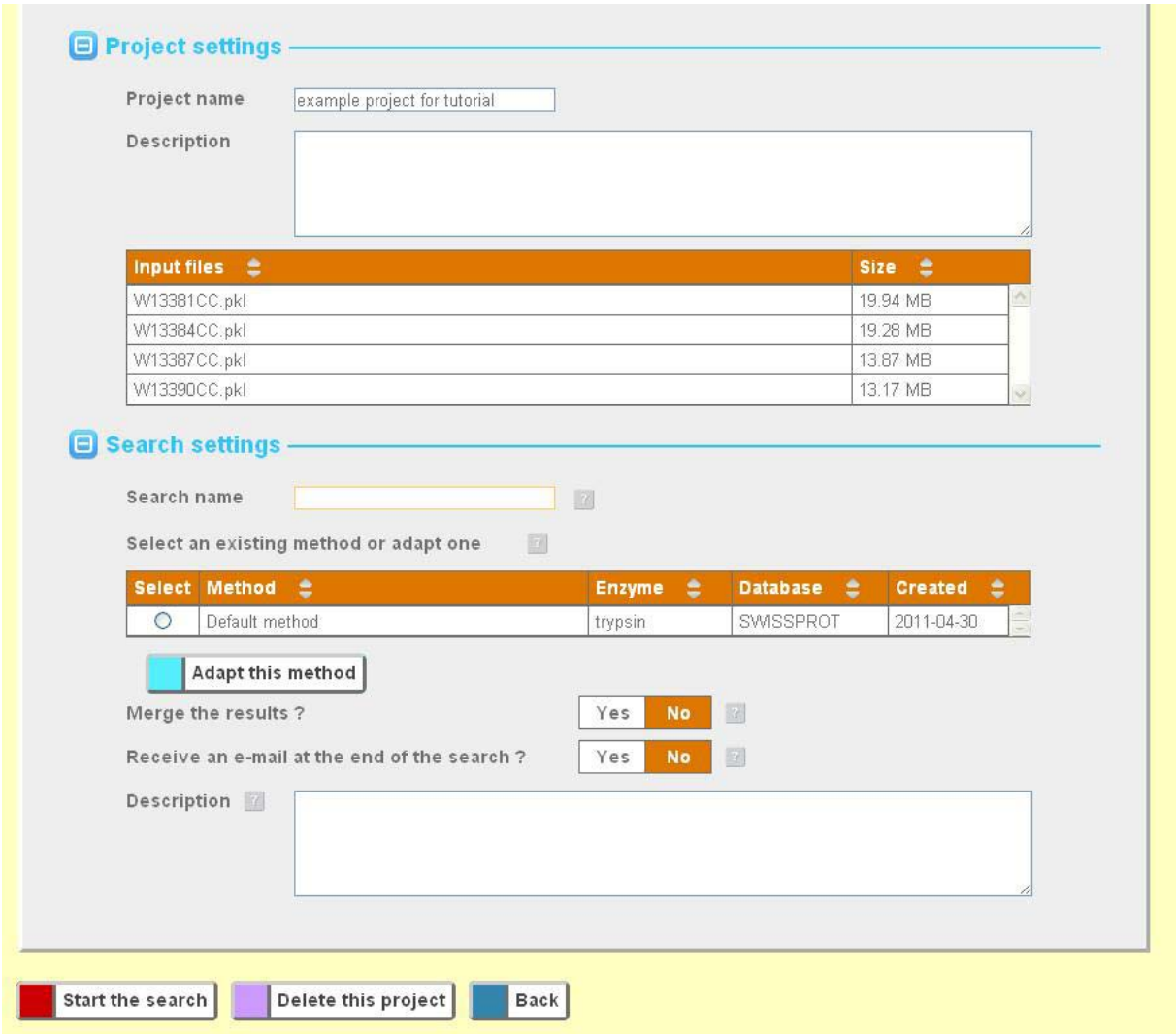
Adapt a method to your search

If you want to run a search with parameters close to an existing method, select this method and click "Adapt the method". This will open the method and allows you to change any parameter in it. **The adapted method will only be used in your search**.



Use your own databases or generate a new one

The database toolbox is a set of tools designed to generate any databases you want. You can **generate** a database including selected taxonomies, add sequences and/or accession numbers. You can **upload** your own FASTA files into MSDA. You can also **merge** your databases. The toolbox can generate decoy entries, add trypsin and/or keratins to your database. The toolbox will also remove any redundant entries in the file (redundancy based on identical accession numbers).

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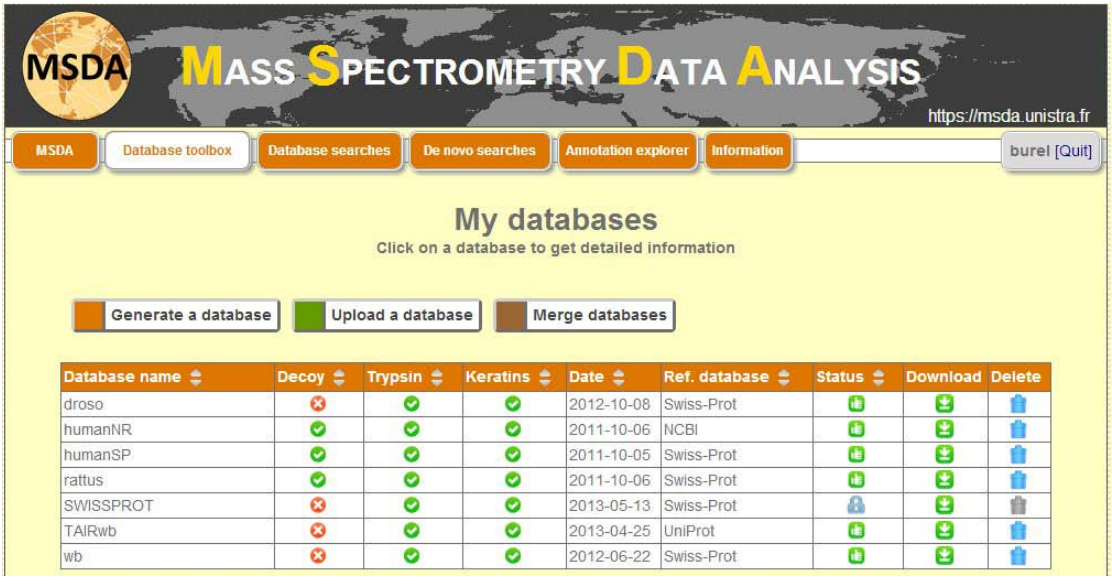

Create your own post-translational modifications

The default protein modifications listed on MSDA are extracted from Unimod (http://www.unimod.org), but you can define and insert your own modifications if necessary.