

# MetWare: metabolomics database project started on SourceForge

id

Published November 22, 2007

## Citation

Willighagen, E. (2007, November 22). MetWare: metabolomics database project started on SourceForge. *Chem-bla-ics*. <https://doi.org/10.59350/j6f3x-a2q13>

## Keywords

Metabolomics, Metware

## Copyright

Copyright © None 2007. Distributed under the terms of the [Creative Commons Attribution 4.0 International License](#), which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

## **chem-bla-ics**

The Applied Bioinformatics at [PRI](#) group where I now work in [Wageningen](#) and the group of [Steffen Neumann](#) in Halle have started the [MetWare](#) project on [Sourceforge](#) to develop opensource databases for metabolomics data.

The databases design will be based on and ideally compatible with proposed standards like ArMet (DOI:[10.1038/nbt1041](https://doi.org/10.1038/nbt1041)) and those recently written up by the [Metabolomics Standards Initiative](#) (see the issue around DOI:[10.1007/s11306-007-0070-6](https://doi.org/10.1007/s11306-007-0070-6)).

One important design goal is that the project will use [BioMart](#), which will allow easy integration of the database content in data analysis programs like [Taverna](#) and [R](#) using the [biomaRt](#) package (see DOI:[10.1093/bioinformatics/bti525](https://doi.org/10.1093/bioinformatics/bti525)).

Though the software will be opensource, it is yet unsure how much data will be open.