

MetWare: metabolomics database project started on SourceForge

Egon Willighagen 

Published November 22, 2007

Citation

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

Keywords

Metabolomics, Metware

Copyright

Copyright © Egon Willighagen 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](#)) and those recently written up by the [Metabolomics Standards Initiative](#) (see the issue around DOI:[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](#)).

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