

# BioHackathon Europe 2021 #1: CiTO annotations in BioHackrXiv



Published November 15, 2021

## Citation

Willighagen, E. (2021, November 15). BioHackathon Europe 2021 #1: CiTO annotations in BioHackrXiv. *Chem-bla-ics*. <https://doi.org/10.59350/5z9yt-vy941>

## Keywords

Cito, Biohackrxiv, Markdown, Pandoc, Biohackeu12

## Copyright

Copyright © None 2021. 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.

Serendipity. I did not plan this hack at the [BioHackathon Europe 2021](#) but it happened anyway. Based on earlier work in the [Journal of Cheminformatics](#), extending on the [work by Krewinkel et al.](#) I looked into the idea of using the Lua filter for [BioHackrXiv](#), a preprint server for BioHackathons. Actually, I started by looking at the Citation Styling Language file used by the BioHackrXiv tools. But that was just wrong.

Long story short: [it worked!](#) Thanks to the encouragements from [Pjotr](#) and [Tazro](#) and suggestions from [Lars](#) and some code on how to [dump a Lua data structure to stdout](#).

In the Markdown/BibTeX combination you would normally write `[@bibtexkey]` to add the reference to the article with the given key in the `.bib` file. To type the citation (to state the intention why you cite that source), for example because you use a method in it, you write `[@usesMethodIn:bibtexkey]`. This is different from [how it currently works for the Journal of Cheminformatics](#), where the intention cannot be given at citation level yet. You can even use more than one intention, e.g. `[@usesMethodIn:extends:bibtexkey]`.

If you want to try it, just create a compatible Markdown file with BibTeX file in a new GitHub repository, and post the repository URL on this [cool preview website](#).

Here's what the created PDF could look like:

## References

- Bolleman, J. T., Mungall, C. J., Strozzi, F., Baran, J., Dumontier, M., Bonnal, R. J., Buels, R., Hoehndorf, R., Fujisawa, T., Katayama, T., & Cock, P. J. (2016). FALDO: a semantic standard for describing the location of nucleotide and protein feature annotation. *J Biomed Semantics*, 7, 39. <https://doi.org/10.1186/s13326-016-0067-z> [cito:agreesWith]
- Byrd, W. E. (2009). *Relational programming in miniKanren: Techniques, applications, and implementations* [PhD thesis]. Indiana University.



- Chiba, H., Nishide, H., & Uchiyama, I. (2015). Construction of an ortholog database using the semantic web technology for integrative analysis of genomic data. *PLOS ONE*, 10(4), e0122802. <https://doi.org/10.1371/journal.pone.0122802>
- Friedman, D. P., Byrd, W. E., Kiselyov, O., & Hemann, J. (2018). *The Reasoned Schemer* (second edition). MIT Press. ISBN: 9780262535519 [cito:usesMethodIn] [cito:agreesWith]
- Queralt-Rosinach, N., Pinero, J., Bravo, À., Sanz, F., & Furlong, L. I. (2016). DisGeNET-RDF: harnessing the innovative power of the Semantic Web to explore the genetic basis of diseases. *Bioinformatics*, 32(14), 2236–2238. <https://doi.org/10.1093/bioinformatics/btw214>
- Wielemaker, J., Beek, W., Hildebrand, M., & Ossenbruggen, J. van. (2016). ClioPatria: A SWI-Prolog infrastructure for the Semantic Web. *Semantic Web*, 7(5), 529–541. <https://doi.org/10.3233/SW-150191>