



Author Correction: Glycopeptide database search and de novo sequencing with PEAKS GlycanFinder enable highly sensitive glycoproteomics

Correction to: *Nature Communications*
<https://doi.org/10.1038/s41467-023-39699-5>,
published online 08 July 2023

<https://doi.org/10.1038/s41467-024-45153-x>

Published online: 24 January 2024



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The original version of this article contained an error in the Code Availability Statement, which incorrectly omitted from the end the following: ‘Our glycan de novo sequencing tool GlycoNovo uses the Python glypy library [50]’. This has been corrected in both the PDF and HTML versions of the article.

The original version of this article omitted a reference to previous work in ‘Klein, J. & Zaia, J. glypy - An open source glycoinformatics library. *J. Proteome Res.* **18**, 3532–3537 (2019)’. This has been added as reference [50] in the Code Availability Statement: ‘Our glycan de novo sequencing tool GlycoNovo uses the Python glypy library [50]’. This has been corrected in the PDF and HTML versions of the article.

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