Corrections & amendments

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

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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 Glyco-Novo 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.