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## Publisher Correction: Comparison of the Hi-C, GAM and SPRITE methods using polymer models of chromatin

Luca Fiorillo , Francesco Musella, Mattia Conte , Rieke Kempfer, Andrea M. Chiariello , Simona Bianco , Alexander Kukalev, Ibai Irastorza-Azcarate, Andrea Esposito , Alex Abraham , Antonella Prisco, Ana Pombo  and Mario Nicodemi 

Correction to: *Nature Methods* <https://doi.org/10.1038/s41592-021-01135-1>, published online 7 May 2021.

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Published online: 3 September 2021

<https://doi.org/10.1038/s41592-021-01251-y>

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## Publisher Correction: Towards resolving proteomes in single cells

Arunima Singh

Correction to: *Nature Methods* <https://doi.org/10.1038/s41592-021-01243-y>, published online 5 August 2021.

In the version of this Research Highlight initially published, the third paragraph, first sentence was unclear. The original sentence read, in part, “Nikolai Slavov and his research group at Northeastern University previously developed SCoPE-MS”; this sentence has been amended to read: “Nikolai Slavov of Northeastern University, along with Bogdan Budnik of Harvard University, and their colleagues, previously developed SCoPE-MS (Single-Cell Proteomics by Mass Spectrometry)—a single-cell proteomics method that originally made use of carrier cells with isobaric labeled proteins mixed with single cells of interest to reduce sample loss.”

The original Research Highlight has been corrected in the online version of the paper.

Published online: 16 September 2021

<https://doi.org/10.1038/s41592-021-01298-x>

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