

Author Correction: A genetically encodable cell-type-specific protein synthesis inhibitorMaximilian Heumüller, Caspar Glock, Vidhya Rangaraju, Anne Biever and Erin M. Schuman Correction to: *Nature Methods* <https://doi.org/10.1038/s41592-019-0468-x>, published online 15 July 2019.

In the version of this Brief Communication originally published, the GenBank and Addgene accession numbers related to the constructs used in this paper were not provided in the ‘Data availability’ statement. The statement has now been amended in the online versions to read: “Source data for Figs. 1–3 are available online. The full vector sequences used in this study have been submitted to the NIH genetic sequence database (GenBank). The GenBank accession numbers are listed below: MN224153 (pCAMKIIa-TetOn3G), MN224154 (pCMV-FLEX-TetOn3G-3xHA-FLEX), MN224155 (pGFAP-TetOn3G), MN224156 (pTRE3G-Bi-a-Chain), MN224157 (pTRE3G-Bi-b-Chain), MN224158 (pTRE3G-Bi-gePSI-pCamk2a-AcGFP), MN224159 (pTRE3G-Bi-gePSI-pCMV-AcGFP), MN224160 (pTRE3G-Bi-gePSI-pGFAP-AcGFP), MN224161 (pTRE3G-Bi-ProRIP). The following plasmids have been deposited on Addgene (Addgene ID): pTRE3G-Bi-gePSI-pCMV-AcGFP (131008), pCAMKIIa-TetOn3G (133727), pGFAP-TetOn3G (133728), pCMV-FLEX-TetOn3G-3xHA-FLEX (133729), pTRE3G-Bi- α -chain (133730), pTRE3G-Bi- β -chain (133731), pTRE3G-Bi-gePSI-pCamk2a-AcGFP (133732), pTRE3G-Bi-gePSI-pGFAP-AcGFP (133733). Further data can be requested from the corresponding author upon request.”

Published online: 25 October 2019

<https://doi.org/10.1038/s41592-019-0662-x>

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Author Correction: Genome-wide high-throughput screening of T cell epitopes

Arunima Singh

Correction to: *Nature Methods* <https://doi.org/10.1038/s41592-019-0599-0>, published online 27 September 2019.

In the version of this Research Highlight originally published, in the sentence beginning “They also mapped...” it was mistakenly stated that “the TCR-peptide interface for three sets of Norwalk-like virus (NLV)-specific T cells” was mapped. Instead, the sentence should have read: “They also mapped the critical residues in the TCR-peptide interface for three CMV-specific TCRs, and were able to show that T-scan can detect subtle differences in TCR specificity for low-affinity interactions.” This has now been amended in the online versions of the Research Highlight.

Published online: 29 October 2019

<https://doi.org/10.1038/s41592-019-0660-z>

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Publisher Correction: Nuclear pores as versatile reference standards for quantitative superresolution microscopyJervis Verma, Thevathasan, Maurice Kahnwald, Konstanty Cieśliński, Philipp Hoess , Sudheer Kumar Peneti, Manuel Reitberger, Daniel Heid , Krishna Chaitanya Kasuba, Sarah Janice Hoerner , Yiming Li , Yu-Le Wu, Markus Mund, Ulf Matti , Pedro Matos Pereira, Ricardo Henriques , Bianca Nijmeijer, Moritz Kueblbeck, Vilma Jimenez Sabinina , Jan Ellenberg  and Jonas Ries Correction to: *Nature Methods* <https://doi.org/10.1038/s41592-019-0574-9>, published online 27 September 2019.

In the version of this Article originally published, at the end of the caption for Fig. 3f, the text ‘measured in GLOX/MEA’ was missing; this has now been corrected. Additionally, Supplementary Tables 3 and 4 were missing from the Supplementary Information, and their citations were missing from the main text. The Supplementary Information file has now been updated; and citations have been added in the main text to the sentence beginning “We thus extended our counting references...”, for Supplementary Table 3; and in the sentences beginning “Example images for all labels...” and “Typical acquisition parameters can be found...” for Supplementary Table 4.

Published online: 25 October 2019

<https://doi.org/10.1038/s41592-019-0659-5>

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