


 Cite this: *RSC Adv.*, 2022, 12, 35778

## Correction: Rapid prediction of possible inhibitors for SARS-CoV-2 main protease using docking and FPL simulations

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DOI: 10.1039/d2ra90114e

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 Correction for 'Rapid prediction of possible inhibitors for SARS-CoV-2 main protease using docking and FPL simulations' by Minh Quan Pham *et al.*, *RSC Adv.*, 2020, 10, 31991–31996, <https://doi.org/10.1039/D0RA06212J>.

In the original article at the time of publication, ref. 44 had only been uploaded to ChemRxiv (DOI: <https://doi.org/10.26434/chemrxiv.12771068.v1>) and had not been published in a finalised format, so the full reference information was not included. The research described in ref. 44 has been published, and the full details of this reference are included below:

44 S. T. Ngo, H. M. Nguyen, L. T. Thuy Huong, P. M. Quan, V. K. Truong, N. T. Tung and V. V. Vu, Assessing potential inhibitors of SARS-CoV-2 main protease from available drugs using free energy perturbation simulations, *RSC Adv.*, 2020, 10, 40284–40290.

The Royal Society of Chemistry apologises for these errors and any consequent inconvenience to authors and readers.

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