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CORRECTION

Correction to: An automated iterative approach for protein structure refinement using pseudocontact shifts

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In the original publication, the Figure 2 has been published incorrectly. The correct version is given below.

The original article has been corrected.

The original article can be found online at https://doi.org/10.1007/s10858-021-00376-8.

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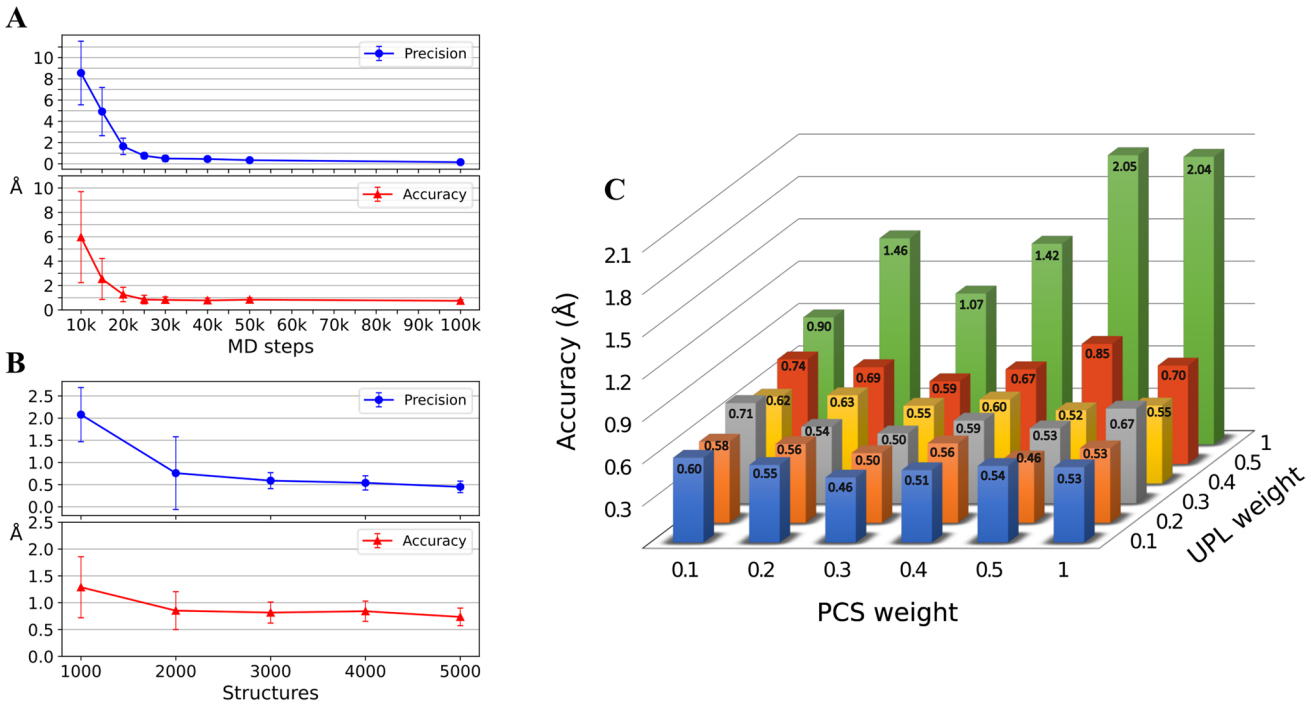

Fig. 2 Optimization of core parameters. a precision (top) and accuracy (bottom) versus the number of MD steps. Results are shown for calculating 2000 structures with **a** UPL:PCS weight of 1:0.1. **b** precision (top) and accuracy (bottom) versus the number of calculated structures computed with 25000 MD steps and a UPL:PCS weight of 1:0.1. **c** accuracy versus the UPL and PCS weights when computed with 2000 structures in 25000 MD steps