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The data presented in this manuscript did not require sample size calculations.

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All information regarding number of repeats as well as detection of outliers can be found in Results, sections "AF2 generates multiple conformations of all eight target proteins" and "Predicted conformational fluctuations correlate with implied conformational dynamics" as well as in the caption of Figure 2.

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No p-values are used in this research. All reported R-squared values presented here correspond to the Pearson correlation coefficient and can be found in Results.

(For large datasets, or papers with a very large number of statistical tests, you may upload a single table file with tests, Ns, etc., with reference to sections in the manuscript.)

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The data plotted in Figures 1-3, the scripts used to analyze data shown in Figures 2 and 3, and the code used to plot the Figures are publicly available and can be found at github.com/delalamo/af2\_conformations. This link is provided in Methods.