

Life Sciences Reporting Summary

Nature Research wishes to improve the reproducibility of the work that we publish. This form is intended for publication with all accepted life science papers and provides structure for consistency and transparency in reporting. Every life science submission will use this form; some list items might not apply to an individual manuscript, but all fields must be completed for clarity.

For further information on the points included in this form, see [Reporting Life Sciences Research](#) [data availability policy](#) [Authors & Referees Editorial Policy Checklist](#)

Please do not complete any field with "not applicable" or n/a.

For final submission: please carefully check your responses for accuracy; you will not be able to make changes later.

► Experimental design

1. Sample size

Describe how sample size was determined.

Diffraction data was collected until crystallographic data statistics clearly show sufficient data sampling.

2. Data exclusions

Describe any data exclusions.

No data were excluded

3. Replication

Describe the measures taken to verify the reproducibility of the experimental findings.

Multiple crystal structures have been reproduced with similar data statistics for FAcD and other proteins in general.

4. Randomization

Describe how samples/organisms/participants were allocated into experimental groups.

Crystals were randomly deposited onto the crystal chip from the growth slurry.

5. Blinding

Describe whether the investigators were blinded to group allocation during data collection and/or analysis.

Macromolecular crystallography does not require blinding as structure determination from diffraction patterns does not result in bias.

Note: all in vivo studies must report how sample size was determined and whether blinding and randomization were used.

6.

For all figures and tables that use statistical methods, confirm that the following items are present in relevant figure legends (or in the Methods section if additional space is needed).

n/a Confirmed

- | | | |
|-------------------------------------|-------------------------------------|--|
| <input checked="" type="checkbox"/> | <input type="checkbox"/> | The <u>exact sample size</u> <i>n</i> |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | A description of how samples were collected, noting whether measurements were taken from distinct samples or whether the same sample was measured repeatedly |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> | A statement indicating how many times each experiment was replicated |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | The statistical test(s) used and whether they are one- or two-sided
Only common tests should be described solely by name; describe more complex techniques in the Methods section. |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> | A description of any assumptions or corrections, such as an adjustment for multiple comparisons |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> | Test values indicating whether an effect is present
Provide confidence intervals or give results of significance tests (e.g. <i>P</i> values) as exact values whenever appropriate and with effect sizes noted. |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | A clear description of statistics including <u>central tendency</u> <u>variation</u> |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> | Clearly defined error bars in <u>all</u> |

See the web collection on [statistics for biologists](#)

► Software

Policy information about [availability of computer code](#)

7. Software

Describe the software used to analyze the data in this study.

Data was analyzed using software published in the phenix software package (Ver. 1.13 - 2998) For PHASER and phenix.refine and POLDER maps. Structural refinement was conducted using coot (Ver. 0.8.8). END-RAPID software was used to calculate absolute value maps. nXDS (Ver. May 2018) for indexing, integration and scaling of diffraction data. PyMOL (Ver. 1.7) for molecular graphics.

For manuscripts utilizing custom algorithms or software that are central to the paper but not yet described in the published literature, software must be made available to editors and reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). Nature Methods [guidance for providing algorithms and software for publication](#)

► Materials and reagents

Policy information about [availability of materials](#)

8. Materials availability

Indicate whether there are restrictions on availability of unique materials or if these materials are only available for distribution by a third party.

All materials are available.

9. Antibodies

Describe the antibodies used and how they were validated for use in the system under study (i.e. assay and species).

No antibodies were used.

10. Eukaryotic cell lines

a. State the source of each eukaryotic cell line used.

No eukaryotic cell lines were used.

b. Describe the method of cell line authentication used.

No eukaryotic cell lines were used.

c. Report whether the cell lines were tested for mycoplasma contamination.

No eukaryotic cell lines were used.

d. [ICLAC](#)

No eukaryotic cell lines were used.

► Animals and human research participants

Policy information about [studies involving animals](#) [ARRIVE guidelines](#)

11. Description of research animals

Provide all relevant details on animals and/or animal-derived materials used in the study.

No animals were used.

Policy information about [studies involving human research participants](#)

12. Description of human research participants

Describe the covariate-relevant population characteristics of the human research participants.

Human research participants were not involved in this study.