

Reporting Summary

Nature Portfolio wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Portfolio policies, see our [Editorial Policies](#) and the [Editorial Policy Checklist](#).

Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

n/a Confirmed

- | | | |
|-------------------------------------|-------------------------------------|--|
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> | The statistical test(s) used AND whether they are one- or two-sided
<i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i> |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> | A description of all covariates tested |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> | A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals) |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> | For null hypothesis testing, the test statistic (e.g. F , t , r) with confidence intervals, effect sizes, degrees of freedom and P value noted
<i>Give P values as exact values whenever suitable.</i> |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> | For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> | For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> | Estimates of effect sizes (e.g. Cohen's d , Pearson's r), indicating how they were calculated |

Our web collection on [statistics for biologists](#) contains articles on many of the points above.

Software and code

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

Data collection

Data analysis

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio [guidelines for submitting code & software](#) for further information.

Data

Policy information about [availability of data](#)

All manuscripts must include a [data availability statement](#). This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our [policy](#)

The cryo-EM maps have been deposited in the Electron Microscopy Data bank (EMDB) under the accession numbers EMD-15370 [<https://www.ebi.ac.uk/pdbe/entry/emdb/EMD-15370>] (L1A), EMD-15371 [<https://www.ebi.ac.uk/pdbe/entry/emdb/EMD-15371>] (L1B), EMD-15372 [<https://www.ebi.ac.uk/pdbe/entry/emdb/EMD-15372>] (L1C), EMD-15148 [<https://www.ebi.ac.uk/pdbe/entry/emdb/EMD-15148>] (L2A), EMD-15369 [<https://www.ebi.ac.uk/pdbe/entry/emdb/EMD-15369>] (L2B), and EMD-15388 [<https://www.ebi.ac.uk/pdbe/entry/emdb/EMD-15388>] (L3A). The corresponding atomic models have been deposited in the Protein Data Bank (PDB) under the accession numbers: 8ADU [<https://doi.org/10.2210/pdb8ADU/pdb>] (L1A), 8ADV [<https://doi.org/10.2210/pdb8ADV/pdb>] (L1B), 8ADW [<https://doi.org/10.2210/pdb8ADW/pdb>] (L1C), 8A4L [<https://doi.org/10.2210/pdb8A4L/pdb>] (L2A), 8ADS [<https://doi.org/10.2210/pdb8ADS/pdb>] (L2B), and 8AEX [<https://doi.org/10.2210/pdb8AEX/pdb>] (L3A). The data generated in this study are provided in the Source Data file. The data that support the findings of this study

are available from the corresponding author upon reasonable request.

Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

- Life sciences Behavioural & social sciences Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see [nature.com/documents/nr-reporting-summary-flat.pdf](https://www.nature.com/documents/nr-reporting-summary-flat.pdf)

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	We collected three datasets, one for each aggregation protocol. For the three datasets we collected 4,589, 4,324, and 4,542 micrographs, respectively. Number of datasets collected and the number of micrographs collected was limited by microscope measurement time and data processing time.
Data exclusions	Standard image classification procedures (Scheres, J. <i>Struc. Biol.</i> 180: 519-530, (2012)) were employed to select particle images with the goal to reach highest resolution reconstructions. Details of the number of selected images are given in Supplementary Table S1.
Replication	All determined fibril structures were replicated at least once from the three collected datasets. For the MD simulations, we performed eight replica simulations for each simulated polymorph.
Randomization	Randomization was not performed. We considered only three aggregation conditions. Randomization would therefore not remove any bias.
Blinding	Blinding was not performed, because the risk of bias in the results was considered negligible.

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

n/a	Involved in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> Antibodies
<input checked="" type="checkbox"/>	<input type="checkbox"/> Eukaryotic cell lines
<input checked="" type="checkbox"/>	<input type="checkbox"/> Palaeontology and archaeology
<input checked="" type="checkbox"/>	<input type="checkbox"/> Animals and other organisms
<input checked="" type="checkbox"/>	<input type="checkbox"/> Human research participants
<input checked="" type="checkbox"/>	<input type="checkbox"/> Clinical data
<input checked="" type="checkbox"/>	<input type="checkbox"/> Dual use research of concern

Methods

n/a	Involved in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> ChIP-seq
<input checked="" type="checkbox"/>	<input type="checkbox"/> Flow cytometry
<input checked="" type="checkbox"/>	<input type="checkbox"/> MRI-based neuroimaging