***eLife’s* transparent reporting form**

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**Sample-size estimation**

* You should state whether an appropriate sample size was computed when the study was being designed
* You should state the statistical method of sample size computation and any required assumptions
* If no explicit power analysis was used, you should describe how you decided what sample (replicate) size (number) to use

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn’t apply to your submission:

Does not apply to the reported structure determination of a molecular complex.

**Replicates**

* You should report how often each experiment was performed
* You should include a definition of biological versus technical replication
* The data obtained should be provided and sufficient information should be provided to indicate the number of independent biological and/or technical replicates
* If you encountered any outliers, you should describe how these were handled
* Criteria for exclusion/inclusion of data should be clearly stated
* High-throughput sequence data should be uploaded before submission, with a private link for reviewers provided (these are available from both GEO and ArrayExpress)

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn’t apply to your submission:

Structures were determined once each by several technologically independent , using two different (biological) expression constructs. The overall strategy is rationalized in the Experimental Design subsection of the Methods section, with details throughout the manuscript. The inbuilt redundancy goes far beyond the usual in the field, with rigor in the consistency of results from independent experimental approaches, two approaches to cryo-EM, cryo-ET and mass spectrometry.

**Statistical reporting**

* Statistical analysis methods should be described and justified
* Raw data should be presented in figures whenever informative to do so (typically when N per group is less than 10)
* For each experiment, you should identify the statistical tests used, exact values of N, definitions of center, methods of multiple test correction, and dispersion and precision measures (e.g., mean, median, SD, SEM, confidence intervals; and, for the major substantive results, a measure of effect size (e.g., Pearson's r, Cohen's d)
* Report exact p-values wherever possible alongside the summary statistics and 95% confidence intervals. These should be reported for all key questions and not only when the p-value is less than 0.05.

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The reported structure determinations are not dependent upon such statistical analyses.

(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.)

**Group allocation**

* Indicate how samples were allocated into experimental groups (in the case of clinical studies, please specify allocation to treatment method); if randomization was used, please also state if restricted randomization was applied
* Indicate if masking was used during group allocation, data collection and/or data analysis

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn’t apply to your submission:

In the methods section, in the Cryo tomography subsection, is the description of the picking of particles from the EM images and classification, prior to the generation of signal-averaged tomographic maps. In the Single particle cryo-EM subsection (SPA), are corresponding descriptions for SPA (paragraphs 1, 2)

**Additional data files (“source data”)**

* We encourage you to upload relevant additional data files, such as numerical data that are represented as a graph in a figure, or as a summary table
* Where provided, these should be in the most useful format, and they can be uploaded as “Source data” files linked to a main figure or table
* Include model definition files including the full list of parameters used
* Include code used for data analysis (e.g., R, MatLab)
* Avoid stating that data files are “available upon request”

Please indicate the figures or tables for which source data files have been provided:

For figures 2, 6, 8 & 9 and tables 1 & 2, the underlying electron microscopic maps and atomic structures will be available from the electron microscopy and protein data banks (<https://www.ebi.ac.uk/pdbe/emdb/> & <https://www.rcsb.org/>), with accession codes EMD-0553, PDB ID 6NZ0 respectively. For figure 3 and 2C/D, the four tomographic classes of the MBP-PKD1-5/AAV2 complex are deposited in the electron microscopy data bank (<https://www.ebi.ac.uk/pdbe/emdb/>) with identifiers: EMD-0621, EMD-0622, EMD-0623 and EMD-0624.