

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 |
| ☐ | ☒ The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement |
| ☒ | ☐ A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly |
| ☒ | ☐ 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> |
| ☒ | ☐ A description of all covariates tested |
| ☒ | ☐ A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons |
| ☐ | ☒ 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) |
| ☐ | ☒ 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> |
| ☒ | ☐ For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings |
| ☒ | ☐ For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes |
| ☐ | ☒ 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 The automated data collection program EPU (v 3.8) was used for cryoEM data collection.

Data analysis MotionCor2 (v 2.1.1); Gctf (v 1.18); RELION (v 4.0); CryoSparc (v 4.0); Coot (0.9.8.95); UCSF Chimera X (v 1.9); Phenix (v 1.20); MAFFT (v 7.490); Jalview (v 2.11.4.1); Clustal Omega (v 1.2.4); HMMER (v 3.4); MEME suite (v 5.5.7); FastTree (v 2.1.11); IQ-TREE 2 (v2.0.8); ggtree (v 3.14.0); ggtreeExtra (v 1.16.0); GTDB-tk (v 2.4.0);

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](#)

Our EM density maps and atomic models have been deposited in the EMDB and wwPDB, respectively, with accession codes EMD-56610 and PDB 28MF (Acinetobacter baylyi endogenous LolDF with lipoprotein); EMD-53525 and PDB 9R29 (AMP-PNP bound Acinetobacter baylyi LolDF); EMD-57113 and PDB 29EB (Acinetobacter baylyi LolA bound LolDF).

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	No statistical methods were used to predetermine sample size. 6,260 movies were collected for the Acinetobacter baylyi endogenous LoIDF with lipoprotein dataset; 2,852 movies were collected for the Acinetobacter baylyi LoIDF bound nucleotide dataset; and 5052 movies were collected for the LoIA bound LoIDF dataset. Number of movies collected was determined by the availability of the microscope time and particle density on the grids. Sample size was sufficient to obtain the reported resolution of map and model building.
Data exclusions	During cryo-EM data processing poor quality or damaged particles were removed from final reconstruction for achieving high resolution as to follow the standard processing procedure.
Replication	Each experiment was repeated at least three times independently. All attempts of replication were successful.
Randomization	This is not relevant to our study, because no grouping was needed.
Blinding	Blinding was not relevant to our study, because no grouping was needed.

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
☐	☒ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology and archaeology
☒	☐ Animals and other organisms
☒	☐ Human research participants
☒	☐ Clinical data
☒	☐ Dual use research of concern

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging

Antibodies

Antibodies used	Commercial antibodies: 1. Mouse monoclonal anti-Myc (MeRCK, Sigma-Aldrich, Catalog No: M4439; clone:9E10; 1:1000 dilution) 2. Mouse monoclonal anti-Flag (MeRCK, Sigma-Aldrich, Catalog No: F3165; clone:M2; 1:1000 dilution) 3. Mouse monoclonal anti-His (MeRCK, Sigma-Aldrich, Catalog No: SAB2702218; clone:GT359; 1:1000 dilution) 4. Mouse monoclonal anti-Strep (MeRCK, Sigma-Aldrich, Catalog No: SAB2702216; clone:GT661; 1:1000 dilution) 5. Rabbit anti-mouse IgG (MeRCK, Sigma-Aldrich, Catalog No: A9044; 1:5000 dilution)
Validation	All antibodies have been validated by the manufacturer for application of western blots.