nature portfolio

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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 *Only common tests should be described solely by name; describe more complex techniques in the Methods section.*
☒	☐	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 *Give P values as exact values whenever suitable.*
☒	☐	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	Molecular dynamics simulation data were generated using GROMACS 5.1.4. and OpenMM. Procedures are described in the manuscript. Both softwares are open and free software.
Data analysis	Data analysis of molecular dynamics simulations were carried out using the PYEMMA and MDTRAJ Python Libraries, both are open and free software. Data-analysis pipelines will be made available along with the manuscript. Mathematica 11.3 was used. XDS: Version January 26, 2018; Phaser 2.8.2; Refmac 5.8.0258; Coot 0.9.6

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

All experimental and simulation data will be made available upon final publication of the manuscript. Crystal-structure of Ubq-G53(D)T has deposited in the protein data-bank: 7OOJ. Source data have been deposited in Edmond: https://doi.org/10.17617/3.8o and https://edmond.mpdl.mpg.de/dataset.xhtml?persistentId=doi:10.17617/3.AVKYZC

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

Life sciences study design

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

Sample size	In the NMR experiments, each increment was signal averaged over 32 scans (titration) or 16 scans (relaxation dispersion). Each relaxation dispersion profile was determined by measuring the R2,eff at 14 different controlled experiments. Number of scans were predetermined from the signal to noise of respective HSQC experiments.
Data exclusions	no data were excluded
Replication	The full kex vs concentration curves were determined by measurements over 7 controlled samples where concentrations of one constituent were changed. The whole set of experiments were repeated in another spectrometer at a different field-strength. All replications were successful.
Randomization	The order of the experiments were randomized in order to avoid any systematic error.
Blinding	no blinding. It would not be possible to do for the NMR experiments since one needs to know the salient parameters: radio frequency power and duration of irradiation for the analysis.

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