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Reporting Summary

Nature Research 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 Research policies, see Authors & Referees and the Editorial Policy Checklist.

Statistical parameters

When statistical analyses are reported, confirm that the following items are present in the relevant location (e.g. 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
☐	☒	An indication of 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 statistics 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
☐	☒	Clearly defined error bars *State explicitly what error bars represent (e.g. SD, SE, CI)*

Our web collection on statistics for biologists may be useful.

Software and code

Policy information about availability of computer code

Data collection	Crystallography: HKL2000 for X-ray data collection. Leica SP8 laser scanning confocal: Leica Application Suite X and ImageJ version 2.0.0
Data analysis	Prism 7.00 was used to analyze and produce graphs. Protein structure statistics were produced, processed and analyzed by HKL2000, CCP4, Phenix 1.13, COOT 0.8.8, and PyMOL 1.8.6.0

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/reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research 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 list of figures that have associated raw data
- A description of any restrictions on data availability

The proteins coordinate and atomic structure factors have been deposited in the Protein Data Bank (PDB) under accession number 6BRP, 6BRT, 6BRO, 6BRQ. All other data are available from the corresponding author upon reasonable request.

Field-specific reporting

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

☒ Life sciences ☐ Behavioural & social sciences

For a reference copy of the document with all sections, see nature.com/authors/policies/ReportingSummary-flat.pdf

Life sciences

Study design

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

Sample size	Sample sizes were determined based on prior literature and best practices in the field; no statistical methods were used to pre determine sample size
Data exclusions	No data were excluded
Replication	Each experiment was reproduced at least three times on separate occasions. Experimental findings were reliably reproduced.
Randomization	Animal experiments were not performed in this study, so no randomization was needed.
Blinding	Animal experiments were not performed in this study, so Investigators were not blinded to the experiment

Materials & experimental systems

Policy information about availability of materials

n/a	Involved in the study
☒	☐ Unique materials
☐	☒ Antibodies
☐	☒ Eukaryotic cell lines
☒	☐ Research animals
☒	☐ Human research participants

Antibodies

Antibodies used	Antibodies were used for Western-Blotting: Anti-Glutathione-S-Transferase (GST) antibody- produced in rabbit (Sigma, G7781) Monoclonal Anti-polyHistidine, antibody produced in mouse (Sigma, H1029) Amersham ECL Mouse IgG, HRP-linked whole Ab (from sheep) Lot 9793520 Amersham ECL Rabbit IgG, HRP-linked whole Ab (from donkey) Lot 12219044
Validation	All Antibodies used in this study were certified and validated by manufacturers and vendors

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)	SF9 and High Five insect cells were used for recombinant protein expressions only
Authentication	Cells have been authenticated by the vendors. No further authentication was performed for commercially available cell lines.
Mycoplasma contamination	Cells were not tested for mycoplasma contamination.
Commonly misidentified lines (See ICLAC register)	no commonly misidentified cell lines were used

Method-specific reporting

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ Magnetic resonance imaging