

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 (<i>n</i>) 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. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> 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 <i>d</i> , Pearson's <i>r</i>), 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	Xcalibur 4.6 and Tune 4.0 (Thermo Scientific)
Data analysis	Proteome Discoverer v2.1 (Thermo Scientific), XlinkX version v2.0 stand-alone (Liu et al. Nature Communications 2017), AlphaFold multimer v2.3, AlphaFold3, python v3.10, Cytoscape v3.7.2, Xinet (https://crosslinkviewer.org/), MaxQuant v1.6.2.6a and v2.0.3.0, R v4.4, pymol v2.4

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 mass spectrometry proteomics data have been deposited to the ProteomeXchange Consortium via the PRIDE partner repository with the dataset identifier PXD047422 (<https://proteomecentral.proteomexchange.org/cgi/GetDataset?ID=PX047422>). AlphaFold models are available via figshare under: <https://doi.org/10.6084/m9.figshare.24639279.v2> (AF2.3) or <https://doi.org/10.6084/m9.figshare.29064041.v1> (AF3). A summary on the performed experiments and raw files is available in Supplementary Data 7. Source data are provided with this paper.

Research involving human participants, their data, or biological material

Policy information about studies with [human participants or human data](#). See also policy information about [sex, gender \(identity/presentation\), and sexual orientation](#) and [race, ethnicity and racism](#).

Reporting on sex and gender	no human participants/data
Reporting on race, ethnicity, or other socially relevant groupings	no human participants/data
Population characteristics	no human participants/data
Recruitment	no human participants/data
Ethics oversight	no human participants/data

Note that full information on the approval of the study protocol must also be provided in the manuscript.

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	Sample size of all experiments were chosen based on preliminary experiments and common practice in the field; without any statistical sample size calculations
Data exclusions	No data were excluded from our analysis
Replication	XL-MS experiments were performed in two biological replicates. SILAC experiments were performed in two biological replicates (label-swap). For all other experiments, three biological replicates were analyzed.
Randomization	This is a molecular biology study. There were no experimental groups for which randomization would be relevant.
Blinding	This is a molecular biology study. There were no experimental groups for which blinding would be relevant.

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
☒	☐ Clinical data
☒	☐ Dual use research of concern
☒	☐ Plants

Methods

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

Antibodies

Antibodies used

anti-DDB1 (rabbit polyclonal, Bethyl Laboratories, A300-462A, lot #3, working concentration: 0.5 µg/mL)
 anti-HA (rat clone 3F10, Roche, ROAHAHA, lot 60789700, working concentration: 0.2 µg/mL)
 anti-UL48 (mouse clone 1-21, Santa Cruz Biotechnology, sc-7545, lot #H1021, working concentration: 0.5 µg/mL)
 anti-ICP4 (mouse clone H943, Santa Cruz Biotechnology, sc-69809, lot #L1317, working concentration: 0.5 µg/mL)

Validation

All antibodies were validated by the manufacturers and validation data are available on the vendors website by searching for the catalog numbers.

Eukaryotic cell lines

Policy information about [cell lines and Sex and Gender in Research](#)

Cell line source(s)

Human embryonic lung fibroblasts (HELFS) were obtained from the institute of virology, Charité, Berlin, Germany

Authentication

Cell line was not further authenticated.

Mycoplasma contamination

HELFS were tested negative for Mycoplasma contamination.

Commonly misidentified lines
(See [ICLAC](#) register)

No commonly misidentified cell lines were used.

Plants

Seed stocks

No plants were used in this study.

Novel plant genotypes

No plants were used in this study.

Authentication

No plants were used in this study.