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.

Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

- 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

Aggregation/solubility algorithms used in the study were accessed using web servers with URLs listed in the Methods section. SAP input script was performed using CHARMM (version 43b1)

Data analysis

Provide a description of all commercial, open source and custom code used to analyse the data in this study, specifying the version used OR state that no software was used.

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. 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 raw data is available in the University of Leeds data repository https://doi.org/10.5518/739

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.

X Life sciences

X Behavioural & social sciences

X Ecological, evolutionary & environmental sciences
Life sciences study design

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

| Sample size          | Not applicable. Measures to assess reproducibility are described below |
|----------------------|-------------------------------------------------------------------------|
| Data exclusions      | No data excluded                                                        |
| Replication          | All measurements were repeated (usually in triplicate). Where n>2 this is stated and the use of technical or biological repeats stated. |
| Randomization        | No randomisation                                                         |
| Blinding             | No blinding                                                             |

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            |
|                                 | x   | Eukaryotic cell lines |
|                                 | x   | Palaeontology         |
|                                 | x   | Animals and other organisms |
|                                 | x   | Human research participants |
|                                 | x   | Clinical data         |

| Methods                        | n/a | Involved in the study |
|--------------------------------|-----|-----------------------|
|                                |     | ChiP-seq              |
|                                |     | Flow cytometry        |
|                                | x   | MRI-based neuroimaging |

Antibodies

Antibodies used

Antibodies for AC-SINS:

AffiniPure goat anti-human IgG Fox Fragment specific, Jackson ImmunoResearch, 109-005-098

ChromePure Goat IgG, whole molecule, Jackson ImmunoResearch, 005-000-003

All other antibodies described in this study are not used as experimental tools/methods but are subjects of the study.

Validation

Describe the validation of each primary antibody for the species and application, noting any validation statements on the manufacturer’s website, relevant citations, antibody profiles in online databases, or data provided in the manuscript.