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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 our Editorial Policies and the Editorial Policy Checklist.

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St	at	101	11	$^{\sim}$

So	ftware and code
	Our web collection on <u>statistics for biologists</u> contains articles on many of the points above.
\boxtimes	Estimates of effect sizes (e.g. Cohen's d, Pearson's r), indicating how they were calculated
\boxtimes	For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
\boxtimes	For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
	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 Give <i>P</i> values as exact values whenever suitable.
	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)
\boxtimes	A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
\boxtimes	A description of all covariates tested
	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 statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
	$oxed{\boxtimes}$ The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement
n/a	Confirmed
FOI	an statistical analyses, commit that the following items are present in the figure legend, table legend, main text, or Methods section.

Policy information about <u>availability of computer code</u>

Data collection

MS acquisition: Xcalibur 4.1, Chromeleon Xpress 7.2 (Thermo Scientific); NMR acquisition: TopSpin 3.5./4.1 (Bruker); Microscopy: Visiview (Visitron)

Data analysis

MS: Xcalibur 4.1 (Thermo Scientific); NMR: MNova 14 (Mestrelab Research); Assays: Microsoft Excel 2019 (Microsoft), Prism 9.2 (GraphPad Software), Inkscape 0.92 (Open-source); DNA and protein sequences: Geneious 7.1.9 (Biomatters Limited.); Microscopy: Fiji 1.51 (Open-source)

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 Research guidelines for submitting code & software for further information.

Data

Policy information about availability of data

All manuscripts must include a <u>data availability statement</u>. 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 data supporting the findings of this study are available in this article and the Supplementary Information. The crystal structure of the affibody was fetched from the RCSB PDB (PDB 3MZW).

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MS/MS
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Only commercially available antibodies were used in ELISA for affibodies: Goat Anti-Affibody IgG (Affibody SE, catalog Nr.

Validation statments of the antibodies were supplied with the commercially available antibodies. Anti-goat IgG (Fc specific)-

20.1000.01.0005, Batch 1304-PB011), Anti-goat IgG (Fc specific)-Peroxidase antibody (Sigma Aldrich, catalog number

Peroxidase antibody was tested by ELISA, Western Blotting and Immunohistochemistry.

Antibodies

Validation

Antibodies used

SAB3700259-2MG, Lot RI34052)