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Reporting Summary

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For al	statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.
n/a (Confirmed
	extstyle ext
	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. <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.
	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 <u>statistics for biologists</u> contains articles on many of the points above.
Soft	ware and code

Policy information about availability of computer code

Data collection

TopSpin 3.6.1 and 4.1.4, MO.Control software version 2.3 (Nano Temper Technologies)

Data analysis

CcpNMR Analysis 2.4.2, ARIA 2.3.1, nmrPipe 9.8, TITAN 1.6, TALOS+, Clustal Omega (EBI tools webservice), MO.Affinity software version 2.3 (Nano Temper Technologies)

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

Protein sequences with the following accession codes were downloaded from the UniProt and NCBI database (Q5JRA6, Q0VC16, Q8BI84, F1R5N2, Q9VMA7, A0A5B7CJZ6, A0A5N5SML6, Q96PC5, A0A3Q1LM15, Q91ZV0, A5PLB3, Q9NRC9, Q16674, P12931, P62993, P00519, P06241, L0C412103, P08572, P29400, P53420, Q01955, Q14031). The NMR assignments for TANGO1(30-139) from Drosophila melanogaster and human MOTH domain of TANGO1(21-131) are deposited in the

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Population characteristics not applicable Ethics oversight not applicable Ethics oversight not applicable Determine not applicable Ethics oversight not applicable Determine not applicable	licy information abo	ut studies involving human research participants and Sex and Gender in Research.
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Materials & experimental systems		Methods	
n/a	Involved in the study	n/a	Involved in the study
\boxtimes	Antibodies	\boxtimes	ChIP-seq
\times	Eukaryotic cell lines	\boxtimes	Flow cytometry
\times	Palaeontology and archaeology	\boxtimes	MRI-based neuroimaging
\times	Animals and other organisms		
\times	Clinical data		
\boxtimes	Dual use research of concern		