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CGTGTCCGCGCGAAGATAAGGCTTGTGATGGCACTGCGGAAAGGTTAAAGCGGAG
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GACCCGAGGCAAGGATGAGGATCCGAATCGAGCTCCGCGCAAGCTGCGCGCAGCTG
AGCACCAACCAACCACTGAGATCCGCTGTAACAAGCGGAAAGGAGCTGAGTTGG
CTGTCCCGCTGAGCAATAACTGATAACCTTGGGGCTTAAACCGGCTTGGAGGG
TTTTTGTGAAAGGAGAACTATCCGGAT

Primer set 1 F 5'-GCCAGGATAGGGGATTTGATGCTCATGTTGGAGAGGGC-3'
R 5'-CGGCTATGCTGGCCGAGGAACCTGGCGAAGAT-3'
Primer set 2 F 5'-TGGAGGAGGCGGGTGTGAGAGACTGATGCTGCTGGG-3'

	<p>R 5'-ACCGCCTCCCTCCAAACAGATGAGCATCAATCCGCCTATGCCTGG-3' Primer set 3 F 5'-GCCAGAAATAGAAGGATTTGATGCTCATCTGTTGAGAAGG-3' R 5'-CCTTCTATTTCTGGCCAGGAACCTGGCGAA-3' Primer set 4 F 5'-TGGAGGAGCGGAGTCTGAGAACTACTGAGTGCCTTGGG-3' R 5'-ACTCGCCTCCCTCCAAACAGATGAGCATCAATCCCTCTATTCTGG-3' Primer set 5 F 5'-AAAGGAAAAGAGGTGATGCTCATCTGTTGGAGAAGG-3' R 5'-ACCTCCTTTTCTTTTGGCCAGGAAGTGGCG-3' Primer set 6 F 5'-CATCGTGTGAAAGGCGAAGTGTGAGAACTACTGAGT-3' R 5'-CTTCTACCACCATGAGCATCACCTCTTTCTTTTGGCCAA-3' Primer set 7 F 5'-TGACCGGGCGGTCGCGAGTCTCGGCGCAAAA-3' R 5'-GACCGGGCGGTCACCATGCTATAGCCCTCAAG-3' Primer set 8 F 5'-TGGAGGAGCGGAGTCTGAAAGAACTACTGAGTGCCTTGGG-3' R 5'-ACTCGCCTCCCTCCAAACAGATGAGCATCAATCCCTTTATTCTGG-3'</p>	
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Cell materials	Indicate where provided: section/figure legend	N/A
Cell lines: Provide species information, strain. Provide accession number in repository OR supplier name, catalog number, clone number, OR RRID.	Mentioned in the material and method section	
Primary cultures: Provide species, strain, sex of origin, genetic modification status.		N/A

Experimental animals	Indicate where provided: section/figure legend	N/A
Laboratory animals or Model organisms: Provide species, strain, sex, age, genetic modification status. Provide accession number in repository OR supplier name, catalog number, clone number, OR RRID.		N/A
Animal observed in or captured from the field: Provide species, sex, and age where possible.		N/A

Plants and microbes	Indicate where provided: section/figure legend	N/A
Plants: provide species and strain, ecotype and cultivar where relevant, unique accession number if available, and source (including location for collected wild specimens).		N/A
Microbes: provide species and strain, unique accession number if available, and source.		N/A

Human research participants	Indicate where provided: section/figure legend) or state if these demographics were not collected	N/A
If collected and within the bounds of privacy constraints report on age, sex, gender and ethnicity for all study participants.		N/A

Design:

Study protocol	Indicate where provided: section/figure legend	N/A
If the study protocol has been pre-registered, provide DOI. For clinical trials, provide the trial registration number OR cite DOI.		N/A

Laboratory protocol	Indicate where provided: section/figure legend	N/A
Provide DOI OR other citation details if detailed step-by-step protocols are available.	Details provided in the material and method section, or references given to protocols	

Experimental study design (statistics details) *		
For in vivo studies: State whether and how the following have been done	Indicate where provided: section/figure legend. If it could have been done, but was not, write "not done"	N/A
Sample size determination		N/A
Randomisation		N/A
Blinding		N/A
Inclusion/exclusion criteria		N/A

Sample definition and in-laboratory replication	Indicate where provided: section/figure legend	N/A
State number of times the experiment was replicated in the laboratory.	Each NMR experiment was performed once. All biological data was repeated at least three times (see figure legends)	
Define whether data describe technical or biological replicates.	Biological replicates	N/A

Ethics	Indicate where provided: section/submission form	N/A

Studies involving human participants: State details of authority granting ethics approval (IRB or equivalent committee(s), provide reference number for approval.		N/A
Studies involving experimental animals: State details of authority granting ethics approval (IRB or equivalent committee(s), provide reference number for approval.		N/A
Studies involving specimen and field samples: State if relevant permits obtained, provide details of authority approving study; if none were required, explain why.		N/A

Dual Use Research of Concern (DURC)	Indicate where provided: section/submission form	N/A
If study is subject to dual use research of concern regulations, state the authority granting approval and reference number for the regulatory approval.		N/A

Analysis:

Attrition	Indicate where provided: section/figure legend	N/A
Describe whether exclusion criteria were pre-established. Report if sample or data points were omitted from analysis. If yes, report if this was due to attrition or intentional exclusion and provide justification.	NMR data points were excluded when peaks were overlapping or unambiguously assigned	

Statistics	Indicate where provided: section/figure legend	N/A
Describe statistical tests used and justify choice of tests.	One-way ANOVA with Dunnet post-test – as we compare multiple groups to one control.	N/A

Data availability	Indicate where provided: section/submission form	N/A
For newly created and reused datasets, the manuscript includes a data availability statement that provides details for access (or notes restrictions on access).	There is a Data availability section just before the references.	
When newly created datasets are publicly available, provide accession number in repository OR DOI and licensing details where available.	Newly created NMR data is available in BioMagResBank under the accession number 51695 (accessible upon publication)	

	Newly created simulation data and models are available at Github at https://github.com/Niels-Bohr-Institute-XNS-StructBiophys/PRLRmodel and https://doi.org/10.5281/zenodo.7011481	
If reused data is publicly available provide accession number in repository OR DOI, OR URL, OR citation.	PDB ID codes 2N7I, 5L04, 4PO6, 4Z32, are available via https://rcsb.org/ . Chemical shift data code 25806 available at bmr.io	

Code availability	Indicate where provided: section/figure legend	N/A
For any computer code/software/mathematical algorithms essential for replicating the main findings of the study, whether newly generated or re-used, the manuscript includes a data availability statement that provides details for access or notes restrictions.	There is a Data availability section at just before the references	
Where newly generated code is publicly available, provide accession number in repository, OR DOI OR URL and licensing details where available. State any restrictions on code availability or accessibility.	Code and data are available at https://github.com/Niels-Bohr-Institute-XNS-StructBiophys/PRLRmodel .	
If reused code is publicly available provide accession number in repository OR DOI OR URL, OR citation.	We use NumPy (https://numpy.org/), SciPy (https://scipy.org/), Scikit-Learn (https://scikit-learn.org/stable/), Gromacs (https://www.gromacs.org/), and Martini2 (2.2) http://cgmartini.nl/index.php/224-m22 and Martini 3 (3.0.b.3.2) http://cgmartini.nl/index.php/martini3beta	

Reporting:

The MDAR framework recommends adoption of discipline-specific guidelines, established and endorsed through community initiatives.

Adherence to community standards	Indicate where provided: section/figure legend	N/A
State if relevant guidelines (e.g., ICMJE, MIBBI, ARRIVE, STRANGE) have been followed, and whether a checklist (e.g., CONSORT, PRISMA, ARRIVE) is provided with the manuscript.		N/A

* We provide the following guidance regarding transparent reporting and statistics; we also refer authors to [Ten common statistical mistakes to watch out for when writing or reviewing a manuscript](#).

Sample-size estimation

- You should state whether an appropriate sample size was computed when the study was being designed
- You should state the statistical method of sample size computation and any required assumptions
- If no explicit power analysis was used, you should describe how you decided what sample (replicate) size (number) to use

Replicates

- You should report how often each experiment was performed
- You should include a definition of biological versus technical replication
- The data obtained should be provided and sufficient information should be provided to indicate the number of independent biological and/or technical replicates
- If you encountered any outliers, you should describe how these were handled
- Criteria for exclusion/inclusion of data should be clearly stated
- High-throughput sequence data should be uploaded before submission, with a private link for reviewers provided (these are available from both GEO and ArrayExpress)

Statistical reporting

- Statistical analysis methods should be described and justified
- Raw data should be presented in figures whenever informative to do so (typically when N per group is less than 10)
- For each experiment, you should identify the statistical tests used, exact values of N, definitions of center, methods of multiple test correction, and dispersion and precision measures (e.g., mean, median, SD, SEM, confidence intervals; and, for the major substantive results, a measure of effect size (e.g., Pearson's r, Cohen's d)
- Report exact p-values wherever possible alongside the summary statistics and 95% confidence intervals. These should be reported for all key questions and not only when the p-value is less than 0.05.

Group allocation

- Indicate how samples were allocated into experimental groups (in the case of clinical studies, please specify allocation to treatment method); if randomization was used, please also state if restricted randomization was applied
- Indicate if masking was used during group allocation, data collection and/or data analysis