

Life Sciences Reporting Summary

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Please do not complete any field with "not applicable" or n/a. Refer to the help text for what text to use if an item is not relevant to your study. [For final submission](#): please carefully check your responses for accuracy; you will not be able to make changes later.

► Experimental design

1. Sample size

Describe how sample size was determined.

Sample size was chosen such that 10% more data points gave no significant change in the estimated value. Standard Deviation values and histograms of the data are given in order to enable direct classification of data quality.

2. Data exclusions

Describe any data exclusions.

No data were excluded from the analysis.

3. Replication

Describe the measures taken to verify the reproducibility of the experimental findings.

Reproducibility of the data was ensured by repeating the experiments at least with three independent protein preparations with comparable results.

4. Randomization

Describe how samples/organisms/participants were allocated into experimental groups.

All proteins used in this study are defined 100% by their DNA sequence and are therefore not relevant for randomization processes.

5. Blinding

Describe whether the investigators were blinded to group allocation during data collection and/or analysis.

The identity of all constructs used in this study is absolute and therefore not relevant for blinding purposes.

Note: all in vivo studies must report how sample size was determined and whether blinding and randomization were used.

6. Statistical parameters

For all figures and tables that use statistical methods, confirm that the following items are present in relevant figure legends (or in the Methods section if additional space is needed).

- | n/a | Confirmed |
|-------------------------------------|---|
| ☐ | ☒ The <u>exact sample size</u> (<i>n</i>) for each experimental group/condition, given as a discrete number and unit of measurement (animals, litters, cultures, etc.) |
| ☐ | ☒ A description of how samples were collected, noting whether measurements were taken from distinct samples or whether the same sample was measured repeatedly |
| ☐ | ☒ A statement indicating how many times each experiment was replicated |
| ☐ | ☒ 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 any assumptions or corrections, such as an adjustment for multiple comparisons |
| ☐ | ☒ Test values indicating whether an effect is present
<i>Provide confidence intervals or give results of significance tests (e.g. <i>P</i> values) as exact values whenever appropriate and with effect sizes noted.</i> |
| ☐ | ☒ A clear description of statistics including <u>central tendency</u> (e.g. median, mean) and <u>variation</u> (e.g. standard deviation, interquartile range) |
| ☐ | ☒ Clearly defined error bars in <u>all</u> relevant figure captions (with explicit mention of central tendency and variation) |

See the web collection on [statistics for biologists](#) for further resources and guidance.

► Software

Policy information about [availability of computer code](#)

7. Software

Describe the software used to analyze the data in this study.

Commercially available ASTRA 6 software (Wyatt technology) and NanoTemper analysis software (NanoTemper Technologies GmbH) along with custom written codes using the MATLAB software (MathWorks) were used in this study.

For manuscripts utilizing custom algorithms or software that are central to the paper but not yet described in the published literature, software must be made available to editors and reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). *Nature Methods* [guidance for providing algorithms and software for publication](#) provides further information on this topic.

► Materials and reagents

Policy information about [availability of materials](#)

8. Materials availability

Indicate whether there are restrictions on availability of unique materials or if these materials are only available for distribution by a third party.

No unique materials were used in this study.

9. Antibodies

Describe the antibodies used and how they were validated for use in the system under study (i.e. assay and species).

No antibodies were used in this study.

10. Eukaryotic cell lines

a. State the source of each eukaryotic cell line used.

Commercial Sf9 cells (*Spodoptera frugiperda*) from ThermoFisher (Cat-No: 12659017) were used exclusively for recombinant protein expression.

b. Describe the method of cell line authentication used.

Certificate of analysis is provided by the manufacturer (Cell Growth and recovery; bacterial and fungal contamination; Mycoplasma qPCR Assay)

c. Report whether the cell lines were tested for mycoplasma contamination.

Because Sf9 cells are used exclusively for recombinant protein expression and due to the lack of any indication, cells were not tested for mycoplasma contamination in this study.

d. If any of the cell lines used are listed in the database of commonly misidentified cell lines maintained by [ICLAC](#), provide a scientific rationale for their use.

No commonly misidentified cell lines were used in this study.

► Animals and human research participants

Policy information about [studies involving animals](#); when reporting animal research, follow the [ARRIVE guidelines](#)

11. Description of research animals

Provide all relevant details on animals and/or animal-derived materials used in the study.

No animals were used in this study.

Policy information about [studies involving human research participants](#)

12. Description of human research participants

Describe the covariate-relevant population characteristics of the human research participants.

The study did not involve human research participants.