

Life Sciences Reporting Summary

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For further information on the points included in this form, see [Reporting Life Sciences Research](#). For further information on Nature Research policies, including our [data availability policy](#), see [Authors & Referees](#) and the [Editorial Policy Checklist](#).

► Experimental design

1. Sample size

Describe how sample size was determined.

As typical in biochemical and biophysical experiments; 3 repetitions were made

2. Data exclusions

Describe any data exclusions.

n.a.

3. Replication

Describe whether the experimental findings were reliably reproduced.

Measurements were performed at least in triplicates. Errors are in the usual range

4. Randomization

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

SpFRET measurements were performed and evaluated by Don C. Lamb and co-workers; Stopped Flow measurements were performed and evaluated by Jochen Reinstein and co-workers, biochemical analyses were performed by Johannes Buchner and co-workers. Computational studies were performed by Iris Antes and co-workers.

5. Blinding

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

The different groups involved worked independently on their analyses. Results were discussed later.

Note: all studies involving animals and/or human research participants must disclose 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 the Methods section if additional space is needed).

n/a Confirmed

- ☐ ☒ The exact sample size (n) 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 (note: only common tests should be described solely by name; more complex techniques should be described in the Methods section)
- ☒ ☐ A description of any assumptions or corrections, such as an adjustment for multiple comparisons
- ☒ ☐ The test results (e.g. p values) given as exact values whenever possible and with confidence intervals noted
- ☒ ☐ A summary of the descriptive statistics, including central tendency (e.g. median, mean) and variation (e.g. standard deviation, interquartile range)
- ☐ ☒ Clearly defined error bars

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.

For spFRET measurements, the custom software package PAM written in MATLAB was used. Visualization of single-molecule FRET efficiency histograms was performed using OriginLab8.

For computational studies the BiPPred, PSIPRED, and PROMALS3D webserver, and the MODELLER, Biopython 1.69, AmberTools16, IRECS, and DynaCell softwares were used. Visualisation of the H/DX data was performed by VMD, using home written scripts.

For all studies, we encourage code deposition in a community repository (e.g. GitHub). Authors must make computer code available to editors and reviewers upon request. The *Nature Methods* [guidance for providing algorithms and software for publication](#) may be useful for any submission.

► 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 for-profit company.

MABA-ADP

9. Antibodies

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

n.a.

10. Eukaryotic cell lines

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

n.a.

b. Describe the method of cell line authentication used.

n.a.

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

n.a.

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

n.a.

► 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 details on animals and/or animal-derived materials used in the study.

n.a.

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.

n.a.