

## 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](#).

### Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

- |                                     |  |
|-------------------------------------|--|
| n/a                                 | Confirmed  |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> The exact sample size ( $n$ ) for each experimental group/condition, given as a discrete number and unit of measurement  |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly  |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> The statistical test(s) used AND whether they are one- or two-sided<br><i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i>   |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> A description of all covariates tested  |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons   |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> 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) |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> For null hypothesis testing, the test statistic (e.g. $F$ , $t$ , $r$ ) with confidence intervals, effect sizes, degrees of freedom and $P$ value noted<br><i>Give <math>P</math> values as exact values whenever suitable.</i>                                       |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings  |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes  |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Estimates of effect sizes (e.g. Cohen's $d$ , Pearson's $r$ ), indicating how they were calculated  |

*Our web collection on [statistics for biologists](#) contains articles on many of the points above.*

### Software and code

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

**Data collection** Fluorescence data was collected using Pro-Data SX (Applied Photophysics) for stopped-flow experiments, and FluorEssence (Horiba) for anisotropy experiments. Liquid scintillation data was collected using QuantaSmart (Perkin Elmer). Cryo-EM data collection was performed using software EM-TOOLS (TVIPS GmbH), SW EPU 2.1 (ThermoFisher) and CETCORPLUS 4.6.9 (CEOS). All software is commercially available.

**Data analysis** Analytical fit of fluorescence traces and reaction time courses was performed in GraphPad Prism v8. All software is commercially available. All software used for Cryo-EM data analysis has been described in Methods and is publicly available free-of-charge: MCOR2, GAUTOMATCH, RELION 2.1, RELION 3.0, PHENIX 1.16, UCSF ChimeraX 0.91.

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 [data availability statement](#). 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

Cryo-EM maps/associated coordinates of atomic models have been deposited in the Electron Microscopy Data Bank/Protein Data Bank with the following accession codes: EMD-10905/PDB 6YSR [<https://doi.org/10.2210/pdb6YSR/pdb>] (P+9 stalled complex), EMD-10906/PDB 6YSS [<https://doi.org/10.2210/pdb6YSS/pdb>] (P+9 post-hydrolysis), EMD-10907/PDB 6YST [<https://doi.org/10.2210/pdb6YST/pdb>] (P+9 tRNA hybrid state), EMD-10908/PDB 6YSU [<https://doi.org/10.2210/pdb6YSU/pdb>] (P+0 post-hydrolysis). Cryo-EM micrographs and particle images have been deposited in the EMPIAR database with accession code EMPIAR-10443. The authors

declare that all other data supporting the findings of this study are available within the paper and its supplementary information files. Raw kinetic data can be supplied by authors upon reasonable request.

## Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

Life sciences       Behavioural & social sciences       Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see [nature.com/documents/nr-reporting-summary-flat.pdf](https://www.nature.com/documents/nr-reporting-summary-flat.pdf)

## Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size      The number of datapoints for each technical replicate in the stopped-flow is 2000, which is a default setting of the stopped flow machine. The number of points is sufficient to ensure the precision of the fit is below 1%.

Data exclusions      No data were omitted.

Replication      All biochemical experiments have been repeated as independent experiments, as indicated in the figure legends.

Randomization      Does not apply to our study, because we do not separate data into treatment groups.

Blinding      Does not apply to our study, because we avoid bias by using all data for analysis

## Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

### Materials & experimental systems

n/a	Involved in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> Antibodies
<input checked="" type="checkbox"/>	<input type="checkbox"/> Eukaryotic cell lines
<input checked="" type="checkbox"/>	<input type="checkbox"/> Palaeontology and archaeology
<input checked="" type="checkbox"/>	<input type="checkbox"/> Animals and other organisms
<input checked="" type="checkbox"/>	<input type="checkbox"/> Human research participants
<input checked="" type="checkbox"/>	<input type="checkbox"/> Clinical data
<input checked="" type="checkbox"/>	<input type="checkbox"/> Dual use research of concern

### Methods

n/a	Involved in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> ChIP-seq
<input checked="" type="checkbox"/>	<input type="checkbox"/> Flow cytometry
<input checked="" type="checkbox"/>	<input type="checkbox"/> MRI-based neuroimaging