

Reporting Summary

Nature Portfolio 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 Portfolio 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 (<i>n</i>) 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 checked="" type="checkbox"/> | <input type="checkbox"/> 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> |
| <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. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted
<i>Give P 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 <i>d</i> , Pearson's <i>r</i>), 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	<div>Octet BLI Discovery (12.2)</div>
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Data analysis

Typhoon (AMERSHAM TYPHOON version 5)
 Kaleidagraph (version 5.0)
 ImageQuant (version 5.2)
 Snakemake (v6.3.0)
 Cutadapt (v3.4)
 Bowtie (v1.3.0)
 Samtools (v1.16.1)
 Bedtools (v2.30.0)
 Octet BLI Analysis (12.2)
 Microsoft Excel (Version 16.89.1)
 Modeller (10.4)
 Snapgene 6.0.7 (ClustalOmega algorithm)
 AlphaFold (Version 3)
 Gene Designer from DNA 2.0 (now ATUM)
 R version 3.6.0 for generating 3' read counts
 R version 4.2.1 for creating plots

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](#)

Source data are provided with this paper.

Research involving human participants, their data, or biological material

Policy information about studies with [human participants or human data](#). See also policy information about [sex, gender \(identity/presentation\), and sexual orientation](#) and [race, ethnicity and racism](#).

Reporting on sex and gender

Not applicable

Reporting on race, ethnicity, or other socially relevant groupings

Not applicable

Population characteristics

Not applicable

Recruitment

Not applicable

Ethics oversight

Not applicable

Note that full information on the approval of the study protocol must also be provided in the manuscript.

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

Sample sizes are provided within figure legends. No statistical method was used to determine sample sizes. Quantified PIVOT assays were performed in triplicate, except in Figure 4d, in which case the main observation was validated by 4 independent anti-sense RNAs, each in duplicate. Biolayer interferometry experiments were performed in triplicate, and each dataset was independently globally fit to the same 1:1 binding model. Exonuclease footprinting assays were performed in duplicate but the effect size is substantial and supported by the kinetic nature of the assay. In vivo NET-seq was performed in singlet because it was sufficient for identifying candidate pause sites, and because we did not need to quantitatively evaluate pause strength from this in vivo dataset; relevant candidate pause sites found in vivo were validated in vitro.

Data exclusions	No data were excluded in this manuscript
Replication	Replicate information is provided in the figure legends. All experiments comparing conditions (e.g., minus versus plus factors) were performed side-by-side and in identical environments to maximize reproducibility and robustness. Where experiments are performed in less than triplicate, conclusions are supported by alternative conditions or orthogonal approaches.
Randomization	Randomization is not relevant to this study because it did not involve human or animal subjects. All data can be evaluated objectively.
Blinding	Blinding is not relevant to this study because it did not involve human or animal subjects, and because results can be evaluated objectively.

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 type="checkbox"/>	<input checked="" 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"/> Clinical data
<input checked="" type="checkbox"/>	<input type="checkbox"/> Dual use research of concern
<input checked="" type="checkbox"/>	<input type="checkbox"/> Plants

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

Antibodies

Antibodies used	PSE monoclonal antibody Alkaline phosphatase conjugated goat-anti mouse IgG (Pierce)
Validation	The hybridoma producing the PSE mAb was produced in the 1990s, a time when it was thought that <i>B. fragilis</i> produces only two capsular polysaccharides, PSA and PSB. With the subsequent demonstration that this organism produces eight capsular polysaccharides, we were able to determine that this mAb reacts to PSE. As these data are unpublished, we provide a western immunoblot showing that this mAb reacts with all seven other polysaccharide mutants, but not with the PSE mutant (Supplementary Figure 5).

Plants

Seed stocks	Not applicable
Novel plant genotypes	Not applicable
Authentication	Not applicable