nature portfolio

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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
☐	☒ The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement
☐	☒ A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
☒	☐ The statistical test(s) used AND whether they are one- or two-sided *Only common tests should be described solely by name; describe more complex techniques in the Methods section.*
☒	☐ A description of all covariates tested
☒	☐ A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
☒	☐ 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)
☒	☐ For null hypothesis testing, the test statistic (e.g. *F*, *t*, *r*) with confidence intervals, effect sizes, degrees of freedom and *P* value noted *Give P values as exact values whenever suitable.*
☒	☐ For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
☒	☐ For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
☒	☐ 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	The ensemble fluorescence was collected by a real-time PCR cycler (Rotor-Gene Q, QIAGEN, Germany), and the data was collected by the cycler's software. Single-molecule fluorescence was collected by a Nikon inverted microscope (ECLIPSE, Ti–U) with TIRF excitation. The data was collected by Solis software.
Data analysis	The single-molecule fluorescence was analyzed by Matlab code, and the ensemble fluorescence was analyzed by Graphpad software.

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

The data supporting the results in this study are available within the main text and supplementary information. The raw data are available from the author's

reasonable request, subject to approval from the Academic Board of the Beijing University of Chemical Technology. Non-clinical data generated in this study, including source data and the data used to make the figures, are available as Supplementary information.

Human research participants

Policy information about studies involving human research participants and Sex and Gender in Research.

Reporting on sex and gender	Age and sex were not controlled, for detailed information about the samples is provided in Table S1 in the Supplementary Information.
Population characteristics	All samples were from a single institution, China-Japan Friendship Hospital , China. Age and sex were not controlled, for detailed information about the samples is provided in Table 2 in the Supplementary Information.
Recruitment	Clinicians recruited subjects who presented with COVID-19-related symptoms or who were suspected of SARS-CoV-2 infection.
Ethics oversight	The study was approved by the Ethics Review Board of Joint Biomedical Engineering Center of China-Japan Friendship Hospital and Beijing University of Chemical Technology, Beijing, China.

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

Life sciences study design

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

Sample size	We used 12 clinical samples (6 COVID-19 positive and 6 COVID-19 negative). Our clinical study was conducted to test the feasibility of the developed assay, and we collected samples that became available on a rolling basis.
Data exclusions	No data were excluded from the analyses
Replication	Single-molecule fluorescence and ensemble fluorescence were validated by 2 or 3 repeats per experiment.
Randomization	Randomization was not relevant to the study, because the main purpose of the study was to report a new property of enzyme and its potential applications.
Blinding	The investigator was not blinded to group allocation during the experiment. Blinding was not relevant because the main purpose of the study was to report a new property of enzyme and its potential applications.

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
☒	☐ Antibodies
☐	☒ Eukaryotic cell lines
☒	☐ Palaeontology and archaeology
☒	☐ Animals and other organisms
☒	☐ Clinical data
☒	☐ Dual use research of concern

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging

Eukaryotic cell lines

Policy information about cell lines and Sex and Gender in Research

Cell line source(s)	A549 cell line (CCL-185) from ATCC. A549 cells were isolated from the lung tissue of a White, 58-year-old male with lung cancer. This cell line can be used in cancer, immuno-oncology, and toxicology research.
Authentication	All the cell lines used were directly procured from reputed commercial sources and authenticated by the source.
Mycoplasma contamination	No Mycoplasma contamination for all used cell lines
Commonly misidentified lines (See ICLAC register)	No commonly misidentified line used.