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	Leginon was employed to collect data from the Talos 200C electron microscope (EM), while the 200 kV Glacios cryo-transmission electron microscope (cryo-TEM) and EPU were used for cryo-EM data collection. The processing of cryo-EM data was carried out using publicly available software detailed in the paper.
Data analysis	GraphPad Prism 10 was used for scientific graphing and statistical analysis. EM images were processed and analyzed using Appion software. Molecular replacement and refinement of crystal structures were accomplished with software including CryoSPARC Live, Relion 3.0 or 4.0b1, and Phenix. GetContacts was utilized to assess and visualize molecular interactions derived from protein structures and their dynamics. Processing of Cryo-EM data employed publicly available software detailed in the paper.

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

nsEM and cryoEM maps and models are deposited in the Electron Microscopy DataBank under accession IDs EMD-48510-48512, 48679-48690, 48692-48696, and in the Protein DataBank under accession IDs 9MQ1, 9MQ2, and 9MQ3.

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	*Use the terms sex (biological attribute) and gender (shaped by social and cultural circumstances) carefully in order to avoid confusing both terms. Indicate if findings apply to only one sex or gender; describe whether sex and gender were considered in study design; whether sex and/or gender was determined based on self-reporting or assigned and methods used.* *Provide in the source data disaggregated sex and gender data, where this information has been collected, and if consent has been obtained for sharing of individual-level data; provide overall numbers in this Reporting Summary. Please state if this information has not been collected.* *Report sex- and gender-based analyses where performed, justify reasons for lack of sex- and gender-based analysis.*
Reporting on race, ethnicity, or other socially relevant groupings	*Please specify the socially constructed or socially relevant categorization variable(s) used in your manuscript and explain why they were used. Please note that such variables should not be used as proxies for other socially constructed/relevant variables (for example, race or ethnicity should not be used as a proxy for socioeconomic status).* *Provide clear definitions of the relevant terms used, how they were provided (by the participants/respondents, the researchers, or third parties), and the method(s) used to classify people into the different categories (e.g. self-report, census or administrative data, social media data, etc.)* *Please provide details about how you controlled for confounding variables in your analyses.*
Population characteristics	*Describe the covariate-relevant population characteristics of the human research participants (e.g. age, genotypic information, past and current diagnosis and treatment categories). If you filled out the behavioural & social sciences study design questions and have nothing to add here, write "See above."*
Recruitment	*Describe how participants were recruited. Outline any potential self-selection bias or other biases that may be present and how these are likely to impact results.*
Ethics oversight	*Identify the organization(s) that approved the study protocol.*

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	The experimental size of the animals was determined based on previous studies conducted on mice. For both prophylactic and therapeutic studies, the mice were divided into either four or three groups, each containing five mice (n=5) for each administered antibody. Viral titers in the lungs were measured in two groups of three mice (n=3) for each antibody administered.
Data exclusions	No data was excluded.
Replication	All experiments had multiple biological and/or technical replicates and are indicated in the Figure legends.
Randomization	Samples were not randomized since only a limited number of mAbs were characterized, and it was important to evaluate the effect of each antibody individually. In animal studies, mice were randomly allocated from large batches obtained from the vendor to different experimental groups with an age-matched distribution.
Blinding	Investigators were not blinded during the data collection. In this study, blinding was not essential to reduce bias since the research focused on

Blinding	objective outcomes, specifically the mortality rate in animals following the administration of antibodies and challenge studies involving infection with the virus in mice.

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
☒	☐ Plants

Methods

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

Antibodies

Antibodies used	Here is a list of monoclonal antibodies from previous studies and synthesized in-house: - anti-hemagglutinin (HA) antibody, CR9114. https://doi.org:10.1126/science.1222908. - anti-neuraminidase (NA) antibody, 1G01. https://doi.org:10.1038/s41467-022-35586-7. - anti-severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) spike antibody. https://doi.org:10.1016/j.celrep.2024.114922. Additionally, here is a list of monoclonal antibodies specific to this study, and synthesized in-house: - H5N1_1A1 - H5N1_12C11 - H5N1_12G9 - H5N1_13B9 - H5N1_13E8 - H5N1_1H2 - H5N1_17E3 - H5N1_20D10 - H5N1_6G1 - H5N1_7G4 - H5N1_7G11 - H5N1_12G8 - H5N1_17C12 - H5N1_7H10 - H5N1_14B8 - H5N1_12G1
Validation	Monoclonal antibodies generated in-house were validated using ELISAs and neutralization assays. The concentrations of the monoclonal antibodies were standardized according to the assay, and the starting concentration is detailed in the methods section.

Eukaryotic cell lines

Policy information about cell lines and Sex and Gender in Research

Cell line source(s)	Madin-Darby canine kidney (MDCK) cells (ATCC) Expi293F cells (ThermoFisher)
Authentication	Cells grew and propagated as expected. None of the cell lines used were authenticated.
Mycoplasma contamination	Cell lines were not tested for mycoplasma contamination.
Commonly misidentified lines (See ICLAC register)	No commonly misindentified cell lines were used in this study

Animals and other research organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research, and Sex and Gender in Research

Laboratory animals	Eight to twelve-week-old female H2L2 Harbour Mice® and six to eight-week-old female BALB/c mice were housed in groups of three to five. The mice were kept under ABSL-2 conditions with 12-hour light/dark cycles, along with controlled temperature and humidity.
Wild animals	No wild animals were used in this study.
Reporting on sex	A total of 5 female H2L2 Harbour Mice® and 248 female BALB/c mice were used. Female mice were used to allow co-housing in groups without animal fighting, which could adversely impact immune responses.
Field-collected samples	No field collected samples were used in this study.
Ethics oversight	Icahn School of Medicine at Mount Sinai Institutional Animal Care and Use Committee (IACUC).

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

Plants

Seed stocks	*Report on the source of all seed stocks or other plant material used. If applicable, state the seed stock centre and catalogue number. If plant specimens were collected from the field, describe the collection location, date and sampling procedures.*
Novel plant genotypes	*Describe the methods by which all novel plant genotypes were produced. This includes those generated by transgenic approaches, gene editing, chemical/radiation-based mutagenesis and hybridization. For transgenic lines, describe the transformation method, the number of independent lines analyzed and the generation upon which experiments were performed. For gene-edited lines, describe the editor used, the endogenous sequence targeted for editing, the targeting guide RNA sequence (if applicable) and how the editor was applied.*
Authentication	*Describe any authentication procedures for each seed stock used or novel genotype generated. Describe any experiments used to assess the effect of a mutation and, where applicable, how potential secondary effects (e.g. second site T-DNA insertions, mosiacism, off-target gene editing) were examined.*