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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
☐	☒ 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	Biacore X100 was used for binding kinetic studies and Varioskan LUX Microplate Spectrophotometer was used for pseudovirus neutralization assay and ELISA
Data analysis	The programs IMGT/V-QUEST (http://www.imgt.org/IMGT_vquest/vquest), MIXCR (https://mixcr.r eadthedocs.io/en/master/) and VDJtools (https://vdjtools-doc.readthedocs.io/en/master/overlap.html) tools were applied to analyze gene germline, complementarity determining region (CDR) 3 length. The CDR3 length was calculated from amino acids sequences. Graphs were presented by GraphPad Prism version 8, , R version 0.1; Pymol was used to visualize molecular structures and freely available from https://www.pymol.org/2//.

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

The accession number for cryo-EM reported in this study is PDB 7E3K and 7E3L.Other data generated or analyzed during this study are included in this published article (and its supplementary information files). Any other raw data pertaining to this study are available from the corresponding 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

Life sciences study design

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

Sample size	Not applicable to this study, because no sample size calculation was performed to design the study
Data exclusions	No data were excluded.
Replication	All experiments successfully repeated at least twice except for the authentic virus neutralization assay performed in BSL-3 once.
Randomization	Not applicable for this study as no treatment strategies are compared.
Blinding	No blinding was conducted since there was no specific grouping.

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
☒	☐ Human research participants
☒	☐ Clinical data
☒	☐ Dual use research of concern

Methods

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

Antibodies

Antibodies used	ALP-conjugated Goat F(ab')2 Anti-Human (IgG (Fab')2) secondary antibody (Abcam, ab98532, 1:2000) HRP-conjugated Goat-anti-human Fc antibody (Abcam, ab99759, 1:10000)
Validation	Primary antibodies reported in this study were described previously in Han et al. (doi.org/10.1101/2020.08.19.253369). Target validation was done with multiple binding assays and structural studies using cryo-EM in this article. A previously described anti-SARS S-protein human antibody CR3022 (PMID: 32245784) was used as a control antibody. ALP-conjugated Goat F(ab')2 Anti-Human (IgG (Fab')2) secondary antibody (https://www.abcam.cn/goat-fab2-human-igg-fab2-alkaline-phosphatase-ab98532.html) HRP-conjugated Goat-anti-human Fc antibody (https://www.abcam.cn/mouse-monoclonal-jdc-10-human-igg-fc-hrp-ab99759.html)

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)	X293T (TAKARA 632180) HEK293T/ACE2 (derived from 293T); new cell line generated in this study Expi293 cells (ThermoFisher, A14528)
Authentication	Not authenticated after purchase.
Mycoplasma contamination	We confirm that all cell lines were negative for mycoplasma contamination

Commonly misidentified lines (See ICLAC register)	No commonly misidentified cell lines were used.