Cryo-electron microscopy structure of a coronavirus spike glycoprotein trimer

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The tremendous pandemic potential of coronaviruses was demonstrated twice in the past few decades by two global outbreaks of deadly pneumonia. Entry of coronaviruses into cells is mediated by the transmembrane spike glycoprotein S, which forms a trimer carrying receptor-binding and membrane fusion functions1. S also contains the principal antigenic determinants and is the target of neutralizing antibodies. Here we present the structure of a mouse coronavirus S trimer ectodomain determined at 4.0 Å resolution by single particle cryo-electron microscopy. It reveals the metastable pre-fusion architecture of S and highlights key interactions stabilizing it. The structure shares a common core with paramyxovirus F proteins2,3, implicating mechanistic similarities and an evolutionary connection between these viral fusion proteins. The accessibility of the highly conserved fusion peptide at the periphery of the trimer indicates potential vaccineology strategies to elicit broadly neutralizing antibodies against coronavirus S domains. Finally, comparison with crystal structures of human coronavirus S domains allows rationalization of the molecular basis for species specificity based on the use of spatially contiguous but distinct domains.

Coronaviruses are enveloped viruses responsible for 30% of mild respiratory infections and atypical pneumonia in humans worldwide4. The emergence of the severe acute respiratory syndrome coronavirus (SARS-CoV) in 2002 and of the Middle East respiratory syndrome coronavirus (MERS-CoV) in 2012 demonstrated that these zoonotic viruses can transmit to humans from various animal species, and suggested that additional emergence events are likely to occur. The fatality rate of SARS-CoV and MERS-CoV infections are about 10–37%1,4 and transmission to and is zipped against the central helix via hydrophobic contacts by the presence of long α-helices (Figs 2b–d and 3a). A central helix (α30) stretches 75 Å along the three-fold molecular axis towards the viral membrane (Fig. 3a). It is located immediately downstream of the HR1 motif, which folds as four consecutive α-helices (α26−α29; Fig. 3a and Extended Data Fig. 6a, b), in sharp contrast to the 120-Å-long HR1 helix observed in the post-fusion S structures5. The 55-Å-long upstream helix (α30), so named because it is located immediately upstream of the S′ cleavage site, runs parallel to and is zipped against the central helix via hydrophobic contacts.

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largely following a heptad-repeat pattern. A core antiparallel \( \beta \)-sheet (\( \beta_{46} - \beta_{50} \)) is present at the viral membrane proximal end and is assembled from an N-terminal \( \beta \)-strand (\( \beta_{46} \)), preceding the upstream helix, and a C-terminal \( \beta \)-hairpin (\( \beta_{50} - \beta_{50} \)), located downstream of the central helix.

MHV S2 features a topology similar to the paramyxovirus F proteins (such as respiratory syncytial virus (RSV) F) root mean squared deviation (R.M.S.D.) 4 Å over 125 residues), with a comparable 3D organization of the core \( \beta \)-sheet, the upstream helix and the central helix (Fig. 3a, b). Importantly, these motifs were shown to remain invariant in the pre- and post-fusion F structures\(^2,3\). The conservation of these motifs among coronavirus S and paramyxovirus F proteins suggests that these fusion proteins have evolved from a distant common ancestor. Although the density is too weak to trace the polypeptide chain downstream from \( \beta_{50} \), secondary structure predictions suggest that the domain directly preceding HR2 could adopt a similar fold in coronavirus S and paramyxovirus F proteins.

In the S trimer, the three central helices are packed via their central portions whereas the two ends splay away from the three-fold axis (Extended Data Fig. 7a–c). Additional contacts between the upstream and central helices participate to inter-protomer interactions. Furthermore, the S1 subunits interlock to form a crown around the S2 trimer stabilizing it in the pre-fusion conformation (Fig. 3c, d and Supplementary Table 3). This is illustrated by the large surface area buried at the interface between each S1 subunit and the S2 subunits of the three protomers (1,970 Å\(^2\)). Many of these contacts involve the HR1 helices and the fusion peptide region. These polypeptide segments undergo major refolding during the fusogenic conformational changes (Extended Data Fig. 6a–c), which supports the notion that the S1 subunits maintain the S2 fusion machinery in its metastable state. Substitutions of the conserved alanine 994 by valine in helix \( \alpha_{28} \) or of the conserved leucine 1062 by phenylalanine in the central helix were shown to attenuate fusogenicity\(^21,22\). Our structure suggests that the former substitution would strengthen hydrophobic packing against the core \( \beta \)-sheet (Extended Data Fig. 7b), and that the later substitution could reinforce molecular stapling of the central helices (Extended Data Fig. 7a, c). The expected modification of the energy landscape between pre-fusion and post-fusion conformations would explain the reduction in fusion activity of these mutants\(^21,22\).

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**Figure 1** | 3D reconstruction of the MHV S trimer determined by single-particle cryoEM. a–c, 3D map filtered at 4.0 Å resolution coloured by protomer. Two different views of the S trimer (from the side (a) and from the top, looking towards the viral membrane (b)), and a side view of one S protomer (c) are shown. d–f, Ribbon diagrams showing the MHV S atomic model oriented as in a–c.

**Figure 2** | Architecture of the MHV S protomer. a, Schematic diagram of the S glycoprotein organization. Black and grey dashed lines denote regions unresolved in the reconstruction and regions that were not part of the construct, respectively. BH, \( \beta \)-hairpin (\( \beta_{46} - \beta_{50} \)); CH, central helix; CT, cytoplasmic tail; FP, fusion peptide; HR1/HR2, heptad-repeats; TM, transmembrane domain; UH, upstream helix. b–d, Ribbon diagrams depicting three views of the S protomer coloured as in a. Asterisk denotes the MHV S receptor-binding region. Disulfide bonds are shown as green sticks except for residues 453–535, for which they are not shown.
The predicted fusion peptide includes the C-terminal half of helix \( \alpha_{21} \) and extends up to the N-terminal half of \( \alpha_{22} \) (refs 6 and 23) (Fig. 2c). \( \alpha_{21} \) is an amphipathic helix located at the periphery of the S trimer, burying hydrophobic side chains towards the S2 centre and exposing charged residues to solvent (Fig. 2c and Extended Data Fig. 7b, c). In the case of porcine epidemic diarrhoea coronavirus, trypsin processing at the S2' site can only occur after host cell attachment24. This indicates that receptor binding could allosterically increase the accessibility of the S2' site, which is located within helix \( \alpha_{21} \). The acidic pH of the endo-lysosomes could also contribute to exposing the S2' cleavage site for coronaviruses requiring cleavage in this compartment. The fact that helix \( \alpha_{21} \) appears dynamic and is found immediately downstream from a disordered loop suggests that it could undergo considerable ‘breathing’ motions. Regardless of the mechanism promoting cleavage, the MHV S structure reported here explains the requirement for processing at the S2' site, as it frees the fusion peptide from the S2 N-terminal region, which is a prerequisite for its insertion ~200 Å away in the target membrane. The peripheral position of the fusion peptide is similar to what has been observed in the parainfluenza virus 5 F3 and HIV gp41 (ref. 25) prefusion structures (Extended Data Fig. 8a–c). The notable accessibility of the fusion peptide and its sequence conservation among coronaviruses6,23 suggest that it would be an ideal target for epitope-focused vaccinology initiatives aimed at raising broadly neutralizing antibodies against S glycoproteins (Fig. 4a–c and Extended Data Fig. 9). Major

![Figure 3](image-url) Pre-fusion structure of the coronavirus fusion machinery. a, b, Topology and ribbon diagrams showing the structural similarity between coronavirus MHV S2 (starting at residue 755) (a) and paramyxovirus RSV F (PDB 5C6B) (b). For clarity, only part of RSV F is shown, with conserved secondary structural elements coloured identically as for MHV S2. *#* denotes motifs participating to the post-fusion HR1 coiled–coil. c, d, Two different views of the MHV S trimer (from the side (c) and top, looking towards the host cell membrane (d)) highlighting how S1 (ribbon diagram and semi-transparent surface) wraps around the S2 fusion machinery (ribbon diagram) to stabilize it.

![Figure 4](image-url) Potential strategy for neutralizing coronavirus infections. a, Surface representation of the MHV S trimer coloured according to sequence conservation using the alignment presented in Extended Data Fig. 9. The fusion peptide sequence is highly conserved among coronavirus S proteins. b, Surface representation of the MHV S trimer highlighting the peripheral position of the fusion peptide (blue and cyan). c, Ribbon diagrams of the MHV S trimer showing the overlapping positions of the fusion peptide (residues 870–887, blue and cyan) and of a major antigenic determinant identified for MHV and SARS-CoV (residues 875–905, magenta spheres).
antigenic determinants (inducing neutralizing antibodies) of MHV and SARS-CoV S proteins overlap with the fusion peptide region and support the suitability of this approach. Antibodies binding to this site will not only hinder insertion of the fusion peptide into the target membrane, but will also putatively prevent fusogenic conformational changes. This epitope-focused strategy has proven successful to obtain neutralizing antibodies against RSV F.

The spatial proximity of domains A and B in the S trimer allows rationalization of their alternative use among coronaviruses to interact with host receptors. MHV uses the viral membrane distal loops decorating domain A to interact with CEACAM1 (ref. 13), whereas MERS-CoV and SARS-CoV rely on the β-motif protruding from domain B to bind to DPP4 (ref. 11) or ACE2 (refs 12 and 14), respectively (Extended Data Fig. 5a–d). The poor sequence conservation of the β domain among coronavirus S proteins, its considerable length variation among MHV strains (Extended Data Fig. 9) and our density-guided homology model of this motif indicate structural and functional differences. These structural variations constitute the molecular basis underlying coronavirus species specificity and cell tropism using a single S architectural scaffold.

Sequence comparisons indicate that the MHV spike S1 and S2 subunits respectively share ~25% and ~40% sequence similarity with many other coronavirus S proteins (Extended Data Fig. 9). Therefore, the structure reported here is representative of the architecture of other coronavirus S such as those of MERS-CoV and SARS-CoV. This hypothesis is further supported by the structural similarity of (1) the MHV13 and bovine coronavirus17 A domains; (2) the MHV, MERS-CoV11, SARS-CoV12 and HKU4 (ref. 29) B domains (Extended Data Fig. 10); (3) the post-fusion cores of MHV, SARS-CoV8,12 and MERS-CoV; and (4) the isolation of infectious coronavirus species featuring a deletion of the A domain and using domain B as the receptor-binding domain30. Our results now provide a framework to understand coronavirus entry and suggest ways for preventing or treating future coronavirus outbreaks.

Online Content
Methods, along with any additional Extended Data display items and Source Data, are available in the online version of the paper; references unique to these sections appear only in the online paper.

Received 17 November 2015; accepted 13 January 2016.
Published online 8 February 2016.

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Supplementary Information
is available in the online version of the paper.

Acknowledgements
Research reported in this publication was supported by the National Institute of General Medical Sciences (NIGMS) of the National Institutes of Health (NIH) under Award Number T32GM008268 (A.C.W.). Part of this research was facilitated by the National Resource for Automated Molecular Microscopy (award number GM103310), and the Hyak supercomputer system at the University of Washington. We thank W. Bartelink, B. Tummers and B. van der Kooij for assistance in cloning, protein expression and characterization. We are also grateful to B. Baron for assistance with the Thermophoresis experiments.

Author Contributions
M.A.T., B.-J.B., P.J.M.R., F.A.R. and D.V. designed the experiments. B.-J.B. and P.J.M.R. designed and cloned the protein constructs. B.-J.B. and M.A.T. carried out protein expression, purification and biophysical characterization. D.V. performed cryoEM sample preparation and data collection. A.C.W. and D.V. processed the cryoEM data. A.C.W., B.F. and D.V. built the atomic model. A.C.W., M.A.T., B.F., B.J.B., F.D., F.A.R. and D.V. analysed the cryoEM data. A.C.W., F.A.R. and D.V. prepared the manuscript, with input from all authors.

Author Information
The cryoEM map and the atomic model have been deposited in the Electron Microscopy Data Bank (EMD) and the Protein Data Bank (PDB) under accession codes EMD-6526 and 3JCL, respectively. Reprints and permissions information is available at www.nature.com/reprints. The authors declare no competing financial interests. Readers are welcome to comment on the online version of the paper. Correspondence and requests for materials should be addressed to D.V. (dveesler@uw.edu) or F.A.R. (felix.rey@pasteur.fr).

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No statistical methods were used to predetermine sample size.

Plasmids. A human codon-optimized gene encoding the MHV spike gene (UniProt: P11224) was synthesized with an Arg17Ser amino acid mutation to abolish the furin cleavage site at the S₁–S₂ junction (S₂ cleavage site). From this gene, the fragment encoding the MHV ectodomain (residues 15–1231) was PCR-amplified and ligated to a gene fragment encoding a GCN4 trimmerization motif (IRKRKKQGKEDKIEEIKSKQKKNKIARKQRK)17–19, a thrombin cleavage site (LYIVV)20, an 8-residue long Strep-Tag (WSHPQFEK) and a stop codon. This construct results in fusing the GCN4 trimmerization motif in register with the HR2 helix at the C-terminal end of the MHV S-encoding sequence. This gene was cloned into the pMT/BiP/His expression vector (Invitrogen) in frame with the Drosophila BiP secretion signal downstream the metallothionein promoter. The D1 domain of mouse CEACAM1a (residues 35–142; gb NP_001034274.1) was amplified by PCR and cloned into a mammalian expression plasmid21, in frame with a CD5 signal sequence at the N-terminus, and with a sequence encoding a thrombin cleavage site, a glycine linker and the Fc domain of human IgG1 at the C-terminus, creating the pCD5-MHV-R-T-Fc vector.

Production of recombinant CEACAM1a ectodomain by transient transfection. 293-F cells were grown in suspension using FreeStyle 293 Expression Medium (Life technologies) at 37 °C in a humidified 5% CO₂ incubator on a Cellrorn shaker platform (Infors HT) rotating at 130 r.p.m. (for 11 culture flasks). Twenty-four hours before transfection, cell density was adjusted at 1.5 × 10⁶ cells ml⁻¹ and culture grown overnight in the same conditions as mentioned above to reach 3 × 10⁶ cells ml⁻¹ before transfection. Cell density was adjusted at 1.5 × 10⁶ cells ml⁻¹ and a 1:1 mixture was incubated at 1,250 r.p.m. for 5 min, and resuspended in fresh FreeStyle 293 Expression Medium (Life technologies) without antibiotics at a density of 2.5 × 10⁶ cells ml⁻¹. To produce recombinant CEACAM1a ectodomain, 400 μg of pCD5-MHV-R-T-Fc vector (purified using EndoFree plasmid kit from Qiagen) were added to 200 ml of suspension cells. The cultures were swirled for 5 min on shaker in the culture incubator before adding 9 μg ml⁻¹ of Linear polyethyleneimine (PEI) solution (25 kDa, Polysciences). Twenty-four hours after transfection, cells were diluted 1:1 with FreeStyle 293 Expression Medium and the transfected cells were cultivated for 6 days. Clarified cell supernatants were concentrated tenfold using Vivaflow tangential filtration cassettes (Sartorius, 10-kDa cut-off) before affinity purification using a Protein A column (GE Life Sciences) followed by gel filtration chromatography using a Superdex 200 10/300 GL column (GE Life Sciences) equilibrated in 20 mM Tris-HCl, pH 7.5, 100 mM NaCl. The purified protein was quantified using absorption at 280 nm and concentrated to approximately 10 μg ml⁻¹.

Production of recombinant MHV S ectodomain in Drosophila S2 cells. To generate a stable Drosophila S2 cell line expressing recombinant MHV spike ectodomain, we used Effectene (Qiagen) and 2 μg of the plasmid encoding the MHV S protein ectodomain. A second plasmid, encoding blasticidin S deaminase was cloned into the pMT/BiP/V5/His expression vector (Invitrogen) in frame with a blasticidin S expression cassette (purified using EndoFree plasmid kit from Qiagen) were added to 200 ml of suspension cells. The cultures were swirled for 5 min on shaker in the culture incubator before adding 9 μg ml⁻¹ of Linear polyethyleneimine (PEI) solution (25 kDa, Polysciences). Twenty-four hours after transfection, cells were diluted 1:1 with FreeStyle 293 Expression Medium and the transfected cells were cultivated for 6 days. Clarified cell supernatants were concentrated tenfold using Vivaflow tangential filtration cassettes (Sartorius, 10-kDa cut-off) before affinity purification using a Protein A column (GE Life Sciences) followed by gel filtration chromatography using a Superdex 200 10/300 GL column (GE Life Sciences) equilibrated in 20 mM Tris-HCl, pH 7.5, 100 mM NaCl. The Fc tag was removed by trypsin cleavage in a reaction mixture containing 7 μg of recombinant CEACAM1a ectodomain and 5 μg of trypsin in 100 mM Tris-HCl, pH 8.0 and 20 mM CaCl₂. The mixture was incubated at 25 °C overnight and re-loaded in a Protein A column to remove uncleaved protein and the Fc tag. The cleaved protein was further purified by gel filtration using a Superdex 75 column 10/300 GL (GE Life Sciences) equilibrated in 20 mM Tris-HCl, pH 7.5, 100 mM NaCl. The purified protein was quantified using absorption at 280 nm and concentrated to approximately 10 μg ml⁻¹.

CryoEM sample preparation and data collection. Three microlitres of MHV spike at 1.85 mg ml⁻¹ was applied to a 1.2/1.3 C-flat grid (Protosnips), which had been glow-discharged for 30 s at 20 mA. Thereafter, grids were plunge-frozen in liquid ethane using a Gatan CP3 and a blotting time of 3.5 s. Data were acquired using an FEI Titan Krios transmission electron microscope operated at 300 kV and equipped with a Gatan K2 Summit direct detector. Cona-free alignment was performed using the Leginon software25. Automated data collection was carried out using Leginon25 to control both the FEI Titan Krios (used in microscope mode at a nominal magnification of 22,500 ×) and the Gatan K2 Summit operated in counted mode (pixel size: 1.315 Å) at a dose rate of ~9 counts per physical pixel per s, which corresponds to ~12 electrons per physical pixels per s (when accounting for coincidence loss)20. Each video had a total accumulated exposure of 53e− Å⁻² fractionated in 38 frames of 200 ms (yielding movies of 7.6 s). A data set of ~1,600 micrographs was acquired in a single session using a defocus range of between 2.0 and 5.0 μm.

CryoEM data processing. Whole-frame alignment was carried out using the software developed previously26, which is integrated into the Appion pipeline26, to account for stage drift and beam-induced motion. The parameters of the microscope contrast transfer function were estimated for each micrograph using ctf3d (ref. 37). Micrographs were manually masked using Appion to exclude the visible carbon supporting film for further processing. Particles were automatically picked in a reference-free manner using DogPicker38. Extraction of particle images was performed using Relion 1.4 with a box size of 320 pixels and applying a windowing operation in Fourier space to yield a final box size of 288 pixels (corresponding to a pixel size of 1.46 Å). From the 1.2 million particles initially picked, a subset of 50,000 particles were randomly selected to generate class averages using RELION4. An initial 3D model was generated using OPTIMOD49 within the Appion pipeline. The entire data set was subjected to 2D alignment and clustering using RELION and particles belonging to the best-defined class averages were retained (~500,000 particles). These ~500,000 particles were then subjected to RELION 3D classification with four classes (using c1 symmetry) starting with our initial model low-pass filtered to 40 Å resolution. We subsequently used the ~230,000 best particles (selected from the 3D classification) and the map corresponding to the best 3D class (low-pass filtered at 40 Å resolution) to run Relion 3D auto-refine (c₃ symmetry), which led to a reconstruction at 4.4 Å resolution. We used the particle polishing procedure in RELION 1.4 to correct for individual particle movement and radiation damage50,51. A second round of 3D classification with 6 classes (c₃ symmetry) was performed using the polished particles resulting in the selection of 82,000 particles. A new 3D auto-refine run (c₃ symmetry) using the selected 82,000 particles and the map corresponding to the best 3D class (low-pass filtered at 40 Å resolution) yielded a map at 4.0 Å resolution following post-processing in RELION. The final map was sharpened with an empirically determined B factor of ~220 Å using Relion post processing. Reported resolutions are based on the gold-standard Fourier shell correlation (FSC) = 0.143 criterion41, and Fourier shell correlation curves were corrected for the effects of soft masking by high-resolution noise substitution44. The soft mask used for FSC calculation had a 10 pixel cosine edge fall-off. The overall shape and dimensions of our reconstruction agree with previous data although the HR2 stem connecting to the membrane is not resolved50.

Model building and analysis. Fitting of atomic models into cryoEM maps was performed using UCSF Chimera54 and Coot55,56. We initially docked the MHV domain A structure (PDB 3R4D) and used a crystal structure of a bovine coronavirus domain A (PDB 4H14) to model the three-stranded α-sheet and the β-sheet and the α-helix present on the viral membrane proximal side of the gactin-like domain. Next, the MERS-CoV domain B crystal structure (PDB 4KQZ) was also fit into the density, and rebuilt and refined using RosettaCM57. Although we could accurately align the sequences corresponding to the core β-sheet of the MHV and MERS-CoV B domains, the ~100 residues forming the β-sheet motif extension (residues 453–555, MERS-CoV/SARS-CoV receptor-binding moiety) could not be aligned with confidence. We used RosettaM to build models of each of the NBS possible disulfide patterns into the density for domain B. For each disulfide arrangement, 50 models were generated, and there was a very clear energy signal for a single such arrangement (Extended Data Fig. 3c). Then, 1,000 models with this disulfide arrangement were sampled, and the lowest energy model (using the Rosetta force field...
augmented with a fit-to-density score term) was selected. Owing to the poor quality of the reconstruction at the apex of the S trimer, the confidence of the model is lowest for the segment corresponding to residues 453–535, as homology modelling was used to fill in details missing in the map.

A backbone model was then manually built for the rest of the S polypeptide using Coot. Sequence register was assigned by visual inspection where side chain density was clearly visible. This initial hand-built model was used as an initial model for Rosetta de novo. The Rosetta-derived model largely agreed with the hand-built model. Rosetta de novo successfully identified fragments allowing to anchor the sequence register for domains C and D as well as for helices α21–α25. Given these anchoring positions, RosettaCM augmented with a novel density-guided model-growing protocol was able to rebuild domains C and D in full. The final model was refined by applying strict non-crystallographic symmetry constraints using Rosetta. Model refinement was performed using a training map corresponding to one of the two maps generated by the gold-standard refinement procedure in Relion. The second map (testing map) was used only for calculation of the FSC compared to the atomic model and preventing overfitting. The quality of the final model was analysed with Molprobity andDALI servers. The sequence alignment was generated using MultAlin and coloured with ESPript. All figures were generated with UCSF Chimera.

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Extended Data Figure 1 | Biophysical characterization of the MHV S ectodomain. a, The MHV S molecular mass was determined to be 463.2 ± 0.3 kDa (mean ± s.e.m.) (corresponding to a trimer) using size-exclusion chromatography coupled in-line with multi-angle light scattering and refractometry. The blue line represents the normalized refractive index (right ordinate axis) and the red line shows the estimated molecular mass (expressed in Da, left ordinate axis). b, MHV S binds with high-affinity to the soluble mouse CEACAM1a receptor. Thermophoresis signal plotted against the MHV S concentration. The dissociation constant ($K_d$) was determined to be 48.5 ± 3.8 nM. Values correspond to the average of two independent experiments. The concentration of CEACAM1a used was 500 nM.
Extended Data Figure 2 | CryoEM analysis of the MHV S trimer. 

a, b, Representative electron micrograph (defocus: 4.6 μm) (a) and class averages (b) of the MHV S trimer embedded in vitreous ice. Scale bars: 573 Å (micrograph) and 44 Å (class averages). c, Gold-standard (blue) and model/map (red) Fourier shell correlation (FSC) curves. The resolution was determined to 4.0 Å. The 0.143 and 0.5 cut-off values are indicated by horizontal grey bars.
Extended Data Figure 3 | CryoEM density for selected regions of the MHV S reconstruction, local resolution analysis and density-guided homology modelling of residues 453–535. The atomic model is shown with the corresponding region of the map. a, b, Upstream helix. c–e, Helix belonging to domain A (residues 284–296). f–h, Core β-sheet. i, j, CryoEM density corresponding to the MHV S trimer (i) and a single protomer (j), coloured according to local resolution determined with the software Resmap. We interpret Resmap results as a qualitative (rather than quantitative) estimate of map quality. k, Rebuilding of the MHV S domain B using RosettaCM. Plot showing the energy mean and s.d. of the models corresponding to the 30 lowest energy disulfide arrangements (out of 945) for domain B.
Extended Data Figure 4 | Refinement and model statistics.

| Data collection                  | Value               |
|----------------------------------|---------------------|
| Number of particles             | 82,000              |
| Pixel size (Å)                  | 1.315 (rescaled to 1.46) |
| Defocus range (µm)              | 2.5                 |
| Voltage (kV)                     | 300                 |
| Electron dose (e/Å²)             | 53                  |

| Refinement                      | Value   |
|----------------------------------|---------|
| Resolution                       | 4.0     |
| Map sharpening B factor (Å²)     | -220    |

| Model validation                | Value   |
|----------------------------------|---------|
| Molprobity score (percentile)    | 1.55 (94%) |
| All-atom clashscore (percentile)| 3.68 (97%) |
| Poor rotamers (%)                | 0       |
| Ramachandran favored (%)         | 94.26   |
| Ramachandran allowed (%)         | 99.44   |
| Ramachandran outliers (%)        | 0.56    |
| r.m.s.d bonds (Å)                | 0.018   |
| r.m.s.d angles (°)               | 1.8     |
Extended Data Figure 5 | Structural organization of the $S_1$ subunit.

a, Ribbon diagram showing a single $S_1$ protomer. b, Close-up view of the MHV $S$ domain B. The structural motif used as a receptor-interacting moiety by MERS-CoV and SARS-CoV is indicated. The density was too weak to allow tracing of this segment (residues 453–535), which has been traced by density-guided homology modelling using Rosetta. c, d, Ribbon diagrams of the $S_1$ trimer viewed from the side (c) and from the top (looking towards the viral membrane) (d).
Extended Data Figure 6 | Mechanisms of membrane fusion promoted by coronavirus S glycoproteins. **a**, Ribbon diagram of the MHV S2 pre-fusion structure. Disulfide bonds are shown as green sticks. **b**, Topology diagram of the MHV S2 pre-fusion structure. PP, di-proline that will act as a helix breaker. The presence of these di-proline motifs indicates that the post-fusion HR1 coiled–coil could not extend up to the fusion peptide as a single helix. This hypothesis is further supported by the observation of a conserved disulfide bond formed between residues Cys894 and Cys905 (labelled 14 in **a** and **b**), which will prevent refolding of helices α22 and α23 as a single extended helix. **c**, Ribbon diagram of the SARS-CoV post-fusion HR1 helix obtained by X-ray crystallography (PDB 1WYY). The residue numbers corresponding to the MHV A59 sequence are indicated. **d**, Topology diagram showing the expected coronavirus S post-fusion conformation derived from our MHV S structure and the SARS-CoV post-fusion core crystal structure shown in **c**. **e**, Ribbon diagram of a model of the MHV S2 post-fusion conformation. Residues belonging to α21, α22, α23, β48, α24 and α25 are not represented owing to a lack of structural information.
Extended Data Figure 7 | Structural organization of the S₂ fusion machinery. a, Ribbon diagram of the trimer of central helices. b, c, Ribbon diagrams of the S₂ trimer (starting at residue 755) viewed from the side (b) and from the bottom (looking towards the host cell membrane) (c). Residues Ala994 and Leu1062, which are discussed in the text, are shown in stick format.
Extended Data Figure 8 | Class I viral fusion proteins with exposed fusion peptide. a, MHV S (residues 870–887). b, Parainfluenza virus 5 F (PIV5 F, residues 103–128, PDB 2B9B). c, HIV-1 gp41 (residues 518–528, PDB 4TVP). The trimeric fusion proteins are shown as grey ribbon diagrams with the fusion peptides rendered in magenta.
Extended Data Figure 9 | Sequence conservation among coronavirus S glycoproteins. a, Sequence alignment of coronavirus S proteins. Bovine-CoV, bovine respiratory coronavirus AH187 (gi 253756585); HKU1, human coronavirus HKU1 (gi 545299280); HKU4, tylonycteris bat coronavirus HKU4 (gi 126030114); HKU5, pipistrellus bat coronavirus HKU5 (gi 126030124); MERS-CoV, Middle East respiratory syndrome coronavirus (gi 836600681); MHV-A59, mouse hepatitis virus A59 (gi 1352862); MHV-JHM, mouse hepatitis virus JHM (gi 60115395); MHV-2, mouse hepatitis virus 2 (gi 5565844); OC43, human coronavirus OC43 (gi 744516696); SARS-CoV, severe acute respiratory syndrome coronavirus ZJ01 (gi 39980889); Waterbuck-CoV, waterbuck coronavirus US/OH-WD358-TC/1994 (gi 215478096). Asparagine residues featuring N-linked glycan chains visible in the MHV S reconstruction are indicated with a star. The S2 and S2′ cleavage sites are indicated with scissors at positions corresponding to the MHV S sequence. Cysteine residues involved in the formation of disulfide bonds are numbered according to Supplementary Table 2. The secondary structure elements observed in our MHV S reconstruction are indicated above the sequence. The black dotted lines above the sequence indicate regions poorly defined in the density. Although the viral membrane distal loops of the A domains are weakly defined in the density, the availability of a crystal structure of this domain from the same virus (PDB 3R4D) helped with the modelling.
Extended Data Figure 10 | Structural similarity of B domains among coronavirus S glycoproteins. a, MHV (pink). b, MERS-CoV (orange, PDB 4KQZ). c, SARS-CoV (red, PDB 2AJF). d, HKU4 (blue, PDB 4QZV).