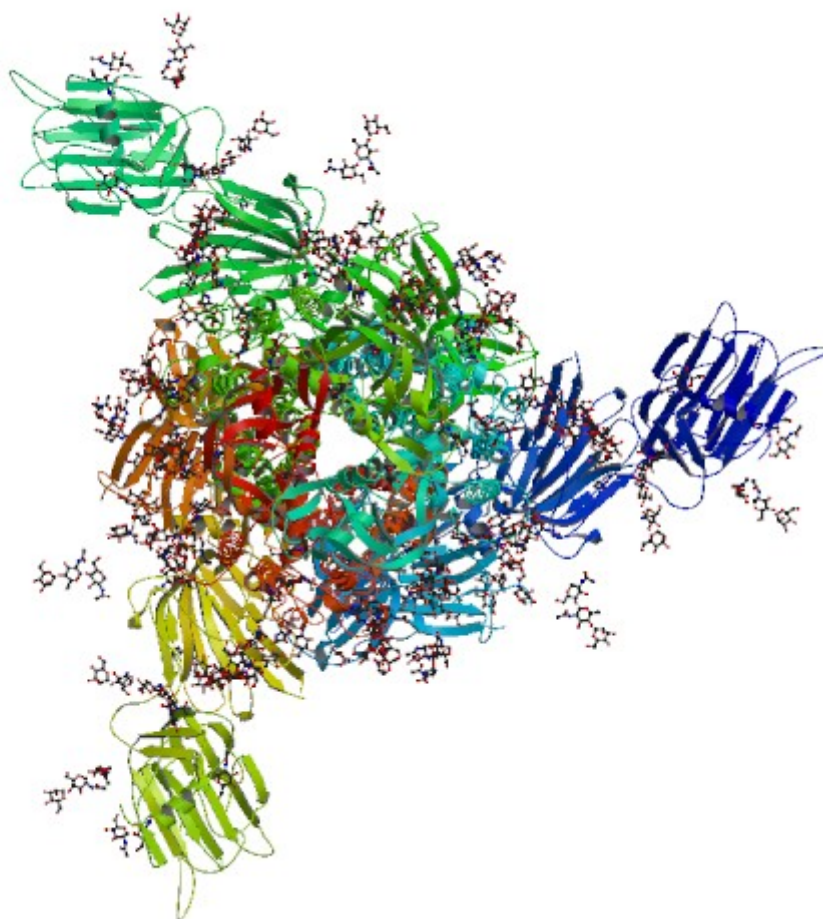


Navigation Tabs



Biological Assembly 1



 **3D View:** Structure | Ligand Interaction

Standalone Viewers (To be retired June 1st)

Protein Workshop | Ligand Explorer

Global Symmetry: Cyclic - C3 (3D View)

Global Stoichiometry: Homo 3-mer - A3

Find Similar Assemblies

Biological assembly 1 assigned by authors.

Biological Assembly Evidence: gel filtration

Display Files ▼

Download Files ▼

6JX7

Cryo-EM structure of spike protein of feline infectious peritonitis virus strain UU4

DOI: 10.2210/pdb6JX7/pdb **EMDataResource:** EMD-9891

Classification: VIRAL PROTEIN

Organism(s): Feline infectious peritonitis virus

Expression System: Homo sapiens

Deposited: 2019-04-22 **Released:** 2020-01-15

Deposition Author(s): Hsu, S.T.D., Yang, T.J., Ko, T.P., Draczkowski, P.

Funding Organization(s): Ministry of Science and Technology (Taiwan), Academia Sinica (Taiwan)

Experimental Data Snapshot

Method: ELECTRON MICROSCOPY

Resolution: 3.31 Å

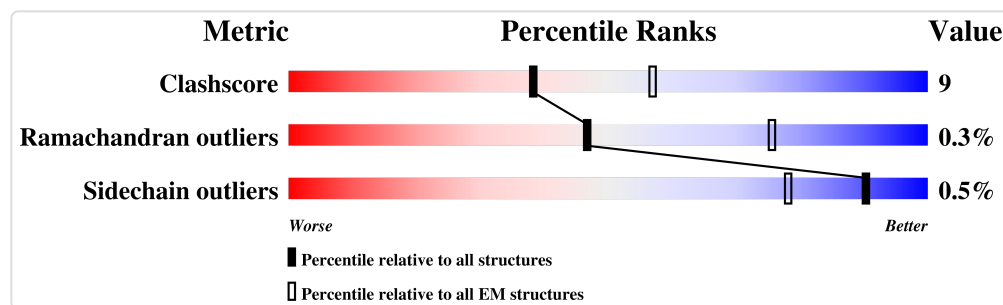
Aggregation State: PARTICLE

Reconstruction Method: SINGLE PARTICLE

wwPDB Validation

3D Report

Full Report



This is version 1.1 of the entry. See complete history.

Literature

Cryo-EM analysis of a feline coronavirus spike protein reveals a unique structure and camouflaging glycans.

Yang, T.J., Chang, Y.C., Ko, T.P., Draczkowski, P., Chien, Y.C., Chang, Y.C., Wu, K.P., Khoo, K.H., Chang, H.W., Hsu, S.D.

(2020) Proc Natl Acad Sci U S A **117**: 1438-1446

PubMed: [31900356](https://pubmed.ncbi.nlm.nih.gov/31900356/)

DOI: 10.1073/pnas.1908898117

Structures With Same Primary Citation

PubMed Abstract:

Macromolecules

Find similar proteins by: Sequence | Structure

Entity ID: 1				
Molecule	Chains	Sequence Length	Organism	Details
Feline Infectious Peritonitis Virus Spike Protein	A, B, C	1468	Feline infectious peritonitis virus	Mutation (s): 0
Protein Feature View is not available: No corresponding UniProt sequence found.				

Small Molecules

Ligands 4 Unique				
ID	Chains	Name / Formula / InChI Key	2D Diagram	3D Interactions
NAG	A, B, C	N-ACETYL-D-GLUCOSAMINE C ₈ H ₁₅ N O ₆ OVRNDRQMDRJTHS-FMDGEEDCSA-N		
BMA	A, B, C	BETA-D-MANNOSE C ₆ H ₁₂ O ₆ WQZGKKKJIJFFOK-RWOPYEJCSA-N		
MAN	A, B, C	ALPHA-D-MANNOSE C ₆ H ₁₂ O ₆ WQZGKKKJIJFFOK-PQMKYFCFSA-N		
FUC	A, B, C	ALPHA-L-FUCOSE C ₆ H ₁₂ O ₅ SHZGCJCMOBCMKK-SXUWKVJYSA-N		

Experimental Data & Validation

Experimental Data

Method: ELECTRON MICROSCOPY

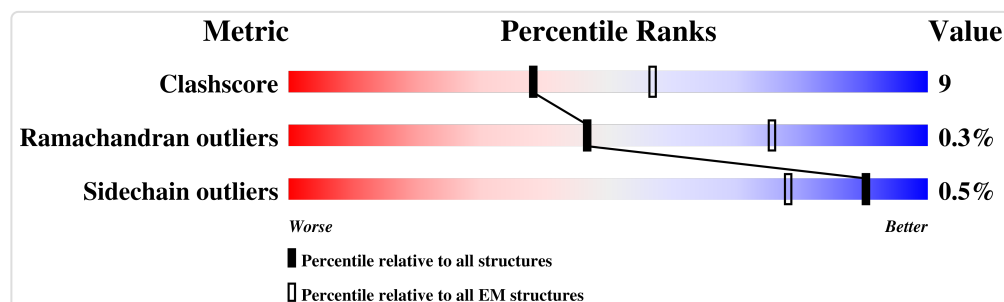
Resolution: 3.31 Å

Aggregation State: PARTICLE

Reconstruction Method: SINGLE PARTICLE

Structure Validation

[View Full Validation Report](#)



Entry History & Funding Information

Deposition Data

Deposited Date: 2019-04-22

Released Date: 2020-01-15

Deposition Author(s): Hsu, S.T.D., Yang, T.J., Ko, T.P., Draczkowski, P.

Funding Organization	Location	Grant Number
Ministry of Science and Technology (Taiwan)	Taiwan	106-2311-B-002-028-MY3
Ministry of Science and Technology (Taiwan)	Taiwan	107-2628-M-001-005-MY3
Academia Sinica (Taiwan)	Taiwan	AS-KPQ-105-TPP

Revision History

- **Version 1.0: 2020-01-15**
Type: Initial release
- **Version 1.1: 2020-02-05**
Changes: Database references

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