



Full wwPDB EM Validation Report ⓘ

Oct 13, 2024 – 02:18 PM EDT

PDB ID : 7TF1
EMDB ID : EMD-25858
Title : Cryo-EM structure of SARS-CoV-2 Kappa (B.1.617.1) Q484I spike protein (focused refinement of RBD)
Authors : Zhu, X.; Saville, J.W.; Mannar, D.; Srivastava, S.S.; Berezuk, A.M.; Demers, J.P.; Zhou, S.; Tuttle, K.S.; Subramaniam, S.
Deposited on : 2022-01-06
Resolution : 3.57 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev113
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

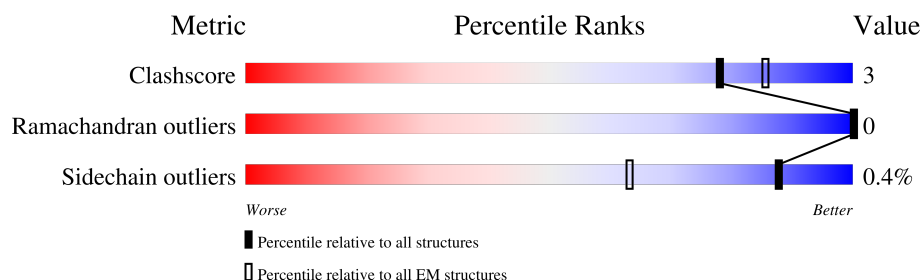
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.57 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1288	
1	B	1288	
1	C	1288	
1	D	1288	
1	E	1288	
1	F	1288	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 12786 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Spike glycoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	268	Total	C	N	O	S	0	0
			2103	1346	353	395	9		
1	B	268	Total	C	N	O	S	0	0
			2103	1346	353	395	9		
1	C	268	Total	C	N	O	S	0	0
			2103	1346	353	395	9		
1	D	268	Total	C	N	O	S	0	0
			2103	1346	353	395	9		
1	E	268	Total	C	N	O	S	0	0
			2103	1346	353	395	9		
1	F	268	Total	C	N	O	S	0	0
			2103	1346	353	395	9		

There are 570 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	154	LYS	GLU	variant	UNP P0DTC2
A	452	ARG	LEU	variant	UNP P0DTC2
A	484	ILE	GLU	variant	UNP P0DTC2
A	614	GLY	ASP	variant	UNP P0DTC2
A	681	ARG	PRO	variant	UNP P0DTC2
A	682	GLY	ARG	variant	UNP P0DTC2
A	683	SER	ARG	variant	UNP P0DTC2
A	685	SER	ARG	variant	UNP P0DTC2
A	817	PRO	PHE	variant	UNP P0DTC2
A	892	PRO	ALA	variant	UNP P0DTC2
A	899	PRO	ALA	variant	UNP P0DTC2
A	942	PRO	ALA	variant	UNP P0DTC2
A	986	PRO	LYS	variant	UNP P0DTC2
A	987	PRO	VAL	variant	UNP P0DTC2
A	1071	HIS	GLN	variant	UNP P0DTC2
A	1209	GLY	-	expression tag	UNP P0DTC2
A	1210	SER	-	expression tag	UNP P0DTC2
A	1211	GLY	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1212	TYR	-	expression tag	UNP P0DTC2
A	1213	ILE	-	expression tag	UNP P0DTC2
A	1214	PRO	-	expression tag	UNP P0DTC2
A	1215	GLU	-	expression tag	UNP P0DTC2
A	1216	ALA	-	expression tag	UNP P0DTC2
A	1217	PRO	-	expression tag	UNP P0DTC2
A	1218	ARG	-	expression tag	UNP P0DTC2
A	1219	ASP	-	expression tag	UNP P0DTC2
A	1220	GLY	-	expression tag	UNP P0DTC2
A	1221	GLN	-	expression tag	UNP P0DTC2
A	1222	ALA	-	expression tag	UNP P0DTC2
A	1223	TYR	-	expression tag	UNP P0DTC2
A	1224	VAL	-	expression tag	UNP P0DTC2
A	1225	ARG	-	expression tag	UNP P0DTC2
A	1226	LYS	-	expression tag	UNP P0DTC2
A	1227	ASP	-	expression tag	UNP P0DTC2
A	1228	GLY	-	expression tag	UNP P0DTC2
A	1229	GLU	-	expression tag	UNP P0DTC2
A	1230	TRP	-	expression tag	UNP P0DTC2
A	1231	VAL	-	expression tag	UNP P0DTC2
A	1232	LEU	-	expression tag	UNP P0DTC2
A	1233	LEU	-	expression tag	UNP P0DTC2
A	1234	SER	-	expression tag	UNP P0DTC2
A	1235	THR	-	expression tag	UNP P0DTC2
A	1236	PHE	-	expression tag	UNP P0DTC2
A	1237	LEU	-	expression tag	UNP P0DTC2
A	1238	GLY	-	expression tag	UNP P0DTC2
A	1239	ARG	-	expression tag	UNP P0DTC2
A	1240	SER	-	expression tag	UNP P0DTC2
A	1241	LEU	-	expression tag	UNP P0DTC2
A	1242	GLU	-	expression tag	UNP P0DTC2
A	1243	VAL	-	expression tag	UNP P0DTC2
A	1244	LEU	-	expression tag	UNP P0DTC2
A	1245	PHE	-	expression tag	UNP P0DTC2
A	1246	GLN	-	expression tag	UNP P0DTC2
A	1247	GLY	-	expression tag	UNP P0DTC2
A	1248	PRO	-	expression tag	UNP P0DTC2
A	1249	GLY	-	expression tag	UNP P0DTC2
A	1250	HIS	-	expression tag	UNP P0DTC2
A	1251	HIS	-	expression tag	UNP P0DTC2
A	1252	HIS	-	expression tag	UNP P0DTC2
A	1253	HIS	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1254	HIS	-	expression tag	UNP P0DTC2
A	1255	HIS	-	expression tag	UNP P0DTC2
A	1256	HIS	-	expression tag	UNP P0DTC2
A	1257	HIS	-	expression tag	UNP P0DTC2
A	1258	SER	-	expression tag	UNP P0DTC2
A	1259	ALA	-	expression tag	UNP P0DTC2
A	1260	TRP	-	expression tag	UNP P0DTC2
A	1261	SER	-	expression tag	UNP P0DTC2
A	1262	HIS	-	expression tag	UNP P0DTC2
A	1263	PRO	-	expression tag	UNP P0DTC2
A	1264	GLN	-	expression tag	UNP P0DTC2
A	1265	PHE	-	expression tag	UNP P0DTC2
A	1266	GLU	-	expression tag	UNP P0DTC2
A	1267	LYS	-	expression tag	UNP P0DTC2
A	1268	GLY	-	expression tag	UNP P0DTC2
A	1269	GLY	-	expression tag	UNP P0DTC2
A	1270	GLY	-	expression tag	UNP P0DTC2
A	1271	SER	-	expression tag	UNP P0DTC2
A	1272	GLY	-	expression tag	UNP P0DTC2
A	1273	GLY	-	expression tag	UNP P0DTC2
A	1274	GLY	-	expression tag	UNP P0DTC2
A	1275	GLY	-	expression tag	UNP P0DTC2
A	1276	SER	-	expression tag	UNP P0DTC2
A	1277	GLY	-	expression tag	UNP P0DTC2
A	1278	GLY	-	expression tag	UNP P0DTC2
A	1279	SER	-	expression tag	UNP P0DTC2
A	1280	ALA	-	expression tag	UNP P0DTC2
A	1281	TRP	-	expression tag	UNP P0DTC2
A	1282	SER	-	expression tag	UNP P0DTC2
A	1283	HIS	-	expression tag	UNP P0DTC2
A	1284	PRO	-	expression tag	UNP P0DTC2
A	1285	GLN	-	expression tag	UNP P0DTC2
A	1286	PHE	-	expression tag	UNP P0DTC2
A	1287	GLU	-	expression tag	UNP P0DTC2
A	1288	LYS	-	expression tag	UNP P0DTC2
B	154	LYS	GLU	variant	UNP P0DTC2
B	452	ARG	LEU	variant	UNP P0DTC2
B	484	ILE	GLU	variant	UNP P0DTC2
B	614	GLY	ASP	variant	UNP P0DTC2
B	681	ARG	PRO	variant	UNP P0DTC2
B	682	GLY	ARG	variant	UNP P0DTC2
B	683	SER	ARG	variant	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	685	SER	ARG	variant	UNP P0DTC2
B	817	PRO	PHE	variant	UNP P0DTC2
B	892	PRO	ALA	variant	UNP P0DTC2
B	899	PRO	ALA	variant	UNP P0DTC2
B	942	PRO	ALA	variant	UNP P0DTC2
B	986	PRO	LYS	variant	UNP P0DTC2
B	987	PRO	VAL	variant	UNP P0DTC2
B	1071	HIS	GLN	variant	UNP P0DTC2
B	1209	GLY	-	expression tag	UNP P0DTC2
B	1210	SER	-	expression tag	UNP P0DTC2
B	1211	GLY	-	expression tag	UNP P0DTC2
B	1212	TYR	-	expression tag	UNP P0DTC2
B	1213	ILE	-	expression tag	UNP P0DTC2
B	1214	PRO	-	expression tag	UNP P0DTC2
B	1215	GLU	-	expression tag	UNP P0DTC2
B	1216	ALA	-	expression tag	UNP P0DTC2
B	1217	PRO	-	expression tag	UNP P0DTC2
B	1218	ARG	-	expression tag	UNP P0DTC2
B	1219	ASP	-	expression tag	UNP P0DTC2
B	1220	GLY	-	expression tag	UNP P0DTC2
B	1221	GLN	-	expression tag	UNP P0DTC2
B	1222	ALA	-	expression tag	UNP P0DTC2
B	1223	TYR	-	expression tag	UNP P0DTC2
B	1224	VAL	-	expression tag	UNP P0DTC2
B	1225	ARG	-	expression tag	UNP P0DTC2
B	1226	LYS	-	expression tag	UNP P0DTC2
B	1227	ASP	-	expression tag	UNP P0DTC2
B	1228	GLY	-	expression tag	UNP P0DTC2
B	1229	GLU	-	expression tag	UNP P0DTC2
B	1230	TRP	-	expression tag	UNP P0DTC2
B	1231	VAL	-	expression tag	UNP P0DTC2
B	1232	LEU	-	expression tag	UNP P0DTC2
B	1233	LEU	-	expression tag	UNP P0DTC2
B	1234	SER	-	expression tag	UNP P0DTC2
B	1235	THR	-	expression tag	UNP P0DTC2
B	1236	PHE	-	expression tag	UNP P0DTC2
B	1237	LEU	-	expression tag	UNP P0DTC2
B	1238	GLY	-	expression tag	UNP P0DTC2
B	1239	ARG	-	expression tag	UNP P0DTC2
B	1240	SER	-	expression tag	UNP P0DTC2
B	1241	LEU	-	expression tag	UNP P0DTC2
B	1242	GLU	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1243	VAL	-	expression tag	UNP P0DTC2
B	1244	LEU	-	expression tag	UNP P0DTC2
B	1245	PHE	-	expression tag	UNP P0DTC2
B	1246	GLN	-	expression tag	UNP P0DTC2
B	1247	GLY	-	expression tag	UNP P0DTC2
B	1248	PRO	-	expression tag	UNP P0DTC2
B	1249	GLY	-	expression tag	UNP P0DTC2
B	1250	HIS	-	expression tag	UNP P0DTC2
B	1251	HIS	-	expression tag	UNP P0DTC2
B	1252	HIS	-	expression tag	UNP P0DTC2
B	1253	HIS	-	expression tag	UNP P0DTC2
B	1254	HIS	-	expression tag	UNP P0DTC2
B	1255	HIS	-	expression tag	UNP P0DTC2
B	1256	HIS	-	expression tag	UNP P0DTC2
B	1257	HIS	-	expression tag	UNP P0DTC2
B	1258	SER	-	expression tag	UNP P0DTC2
B	1259	ALA	-	expression tag	UNP P0DTC2
B	1260	TRP	-	expression tag	UNP P0DTC2
B	1261	SER	-	expression tag	UNP P0DTC2
B	1262	HIS	-	expression tag	UNP P0DTC2
B	1263	PRO	-	expression tag	UNP P0DTC2
B	1264	GLN	-	expression tag	UNP P0DTC2
B	1265	PHE	-	expression tag	UNP P0DTC2
B	1266	GLU	-	expression tag	UNP P0DTC2
B	1267	LYS	-	expression tag	UNP P0DTC2
B	1268	GLY	-	expression tag	UNP P0DTC2
B	1269	GLY	-	expression tag	UNP P0DTC2
B	1270	GLY	-	expression tag	UNP P0DTC2
B	1271	SER	-	expression tag	UNP P0DTC2
B	1272	GLY	-	expression tag	UNP P0DTC2
B	1273	GLY	-	expression tag	UNP P0DTC2
B	1274	GLY	-	expression tag	UNP P0DTC2
B	1275	GLY	-	expression tag	UNP P0DTC2
B	1276	SER	-	expression tag	UNP P0DTC2
B	1277	GLY	-	expression tag	UNP P0DTC2
B	1278	GLY	-	expression tag	UNP P0DTC2
B	1279	SER	-	expression tag	UNP P0DTC2
B	1280	ALA	-	expression tag	UNP P0DTC2
B	1281	TRP	-	expression tag	UNP P0DTC2
B	1282	SER	-	expression tag	UNP P0DTC2
B	1283	HIS	-	expression tag	UNP P0DTC2
B	1284	PRO	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1285	GLN	-	expression tag	UNP P0DTC2
B	1286	PHE	-	expression tag	UNP P0DTC2
B	1287	GLU	-	expression tag	UNP P0DTC2
B	1288	LYS	-	expression tag	UNP P0DTC2
C	154	LYS	GLU	variant	UNP P0DTC2
C	452	ARG	LEU	variant	UNP P0DTC2
C	484	ILE	GLU	variant	UNP P0DTC2
C	614	GLY	ASP	variant	UNP P0DTC2
C	681	ARG	PRO	variant	UNP P0DTC2
C	682	GLY	ARG	variant	UNP P0DTC2
C	683	SER	ARG	variant	UNP P0DTC2
C	685	SER	ARG	variant	UNP P0DTC2
C	817	PRO	PHE	variant	UNP P0DTC2
C	892	PRO	ALA	variant	UNP P0DTC2
C	899	PRO	ALA	variant	UNP P0DTC2
C	942	PRO	ALA	variant	UNP P0DTC2
C	986	PRO	LYS	variant	UNP P0DTC2
C	987	PRO	VAL	variant	UNP P0DTC2
C	1071	HIS	GLN	variant	UNP P0DTC2
C	1209	GLY	-	expression tag	UNP P0DTC2
C	1210	SER	-	expression tag	UNP P0DTC2
C	1211	GLY	-	expression tag	UNP P0DTC2
C	1212	TYR	-	expression tag	UNP P0DTC2
C	1213	ILE	-	expression tag	UNP P0DTC2
C	1214	PRO	-	expression tag	UNP P0DTC2
C	1215	GLU	-	expression tag	UNP P0DTC2
C	1216	ALA	-	expression tag	UNP P0DTC2
C	1217	PRO	-	expression tag	UNP P0DTC2
C	1218	ARG	-	expression tag	UNP P0DTC2
C	1219	ASP	-	expression tag	UNP P0DTC2
C	1220	GLY	-	expression tag	UNP P0DTC2
C	1221	GLN	-	expression tag	UNP P0DTC2
C	1222	ALA	-	expression tag	UNP P0DTC2
C	1223	TYR	-	expression tag	UNP P0DTC2
C	1224	VAL	-	expression tag	UNP P0DTC2
C	1225	ARG	-	expression tag	UNP P0DTC2
C	1226	LYS	-	expression tag	UNP P0DTC2
C	1227	ASP	-	expression tag	UNP P0DTC2
C	1228	GLY	-	expression tag	UNP P0DTC2
C	1229	GLU	-	expression tag	UNP P0DTC2
C	1230	TRP	-	expression tag	UNP P0DTC2
C	1231	VAL	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1232	LEU	-	expression tag	UNP P0DTC2
C	1233	LEU	-	expression tag	UNP P0DTC2
C	1234	SER	-	expression tag	UNP P0DTC2
C	1235	THR	-	expression tag	UNP P0DTC2
C	1236	PHE	-	expression tag	UNP P0DTC2
C	1237	LEU	-	expression tag	UNP P0DTC2
C	1238	GLY	-	expression tag	UNP P0DTC2
C	1239	ARG	-	expression tag	UNP P0DTC2
C	1240	SER	-	expression tag	UNP P0DTC2
C	1241	LEU	-	expression tag	UNP P0DTC2
C	1242	GLU	-	expression tag	UNP P0DTC2
C	1243	VAL	-	expression tag	UNP P0DTC2
C	1244	LEU	-	expression tag	UNP P0DTC2
C	1245	PHE	-	expression tag	UNP P0DTC2
C	1246	GLN	-	expression tag	UNP P0DTC2
C	1247	GLY	-	expression tag	UNP P0DTC2
C	1248	PRO	-	expression tag	UNP P0DTC2
C	1249	GLY	-	expression tag	UNP P0DTC2
C	1250	HIS	-	expression tag	UNP P0DTC2
C	1251	HIS	-	expression tag	UNP P0DTC2
C	1252	HIS	-	expression tag	UNP P0DTC2
C	1253	HIS	-	expression tag	UNP P0DTC2
C	1254	HIS	-	expression tag	UNP P0DTC2
C	1255	HIS	-	expression tag	UNP P0DTC2
C	1256	HIS	-	expression tag	UNP P0DTC2
C	1257	HIS	-	expression tag	UNP P0DTC2
C	1258	SER	-	expression tag	UNP P0DTC2
C	1259	ALA	-	expression tag	UNP P0DTC2
C	1260	TRP	-	expression tag	UNP P0DTC2
C	1261	SER	-	expression tag	UNP P0DTC2
C	1262	HIS	-	expression tag	UNP P0DTC2
C	1263	PRO	-	expression tag	UNP P0DTC2
C	1264	GLN	-	expression tag	UNP P0DTC2
C	1265	PHE	-	expression tag	UNP P0DTC2
C	1266	GLU	-	expression tag	UNP P0DTC2
C	1267	LYS	-	expression tag	UNP P0DTC2
C	1268	GLY	-	expression tag	UNP P0DTC2
C	1269	GLY	-	expression tag	UNP P0DTC2
C	1270	GLY	-	expression tag	UNP P0DTC2
C	1271	SER	-	expression tag	UNP P0DTC2
C	1272	GLY	-	expression tag	UNP P0DTC2
C	1273	GLY	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1274	GLY	-	expression tag	UNP P0DTC2
C	1275	GLY	-	expression tag	UNP P0DTC2
C	1276	SER	-	expression tag	UNP P0DTC2
C	1277	GLY	-	expression tag	UNP P0DTC2
C	1278	GLY	-	expression tag	UNP P0DTC2
C	1279	SER	-	expression tag	UNP P0DTC2
C	1280	ALA	-	expression tag	UNP P0DTC2
C	1281	TRP	-	expression tag	UNP P0DTC2
C	1282	SER	-	expression tag	UNP P0DTC2
C	1283	HIS	-	expression tag	UNP P0DTC2
C	1284	PRO	-	expression tag	UNP P0DTC2
C	1285	GLN	-	expression tag	UNP P0DTC2
C	1286	PHE	-	expression tag	UNP P0DTC2
C	1287	GLU	-	expression tag	UNP P0DTC2
C	1288	LYS	-	expression tag	UNP P0DTC2
D	154	LYS	GLU	variant	UNP P0DTC2
D	452	ARG	LEU	variant	UNP P0DTC2
D	484	ILE	GLU	variant	UNP P0DTC2
D	614	GLY	ASP	variant	UNP P0DTC2
D	681	ARG	PRO	variant	UNP P0DTC2
D	682	GLY	ARG	variant	UNP P0DTC2
D	683	SER	ARG	variant	UNP P0DTC2
D	685	SER	ARG	variant	UNP P0DTC2
D	817	PRO	PHE	variant	UNP P0DTC2
D	892	PRO	ALA	variant	UNP P0DTC2
D	899	PRO	ALA	variant	UNP P0DTC2
D	942	PRO	ALA	variant	UNP P0DTC2
D	986	PRO	LYS	variant	UNP P0DTC2
D	987	PRO	VAL	variant	UNP P0DTC2
D	1071	HIS	GLN	variant	UNP P0DTC2
D	1209	GLY	-	expression tag	UNP P0DTC2
D	1210	SER	-	expression tag	UNP P0DTC2
D	1211	GLY	-	expression tag	UNP P0DTC2
D	1212	TYR	-	expression tag	UNP P0DTC2
D	1213	ILE	-	expression tag	UNP P0DTC2
D	1214	PRO	-	expression tag	UNP P0DTC2
D	1215	GLU	-	expression tag	UNP P0DTC2
D	1216	ALA	-	expression tag	UNP P0DTC2
D	1217	PRO	-	expression tag	UNP P0DTC2
D	1218	ARG	-	expression tag	UNP P0DTC2
D	1219	ASP	-	expression tag	UNP P0DTC2
D	1220	GLY	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
D	1221	GLN	-	expression tag	UNP P0DTC2
D	1222	ALA	-	expression tag	UNP P0DTC2
D	1223	TYR	-	expression tag	UNP P0DTC2
D	1224	VAL	-	expression tag	UNP P0DTC2
D	1225	ARG	-	expression tag	UNP P0DTC2
D	1226	LYS	-	expression tag	UNP P0DTC2
D	1227	ASP	-	expression tag	UNP P0DTC2
D	1228	GLY	-	expression tag	UNP P0DTC2
D	1229	GLU	-	expression tag	UNP P0DTC2
D	1230	TRP	-	expression tag	UNP P0DTC2
D	1231	VAL	-	expression tag	UNP P0DTC2
D	1232	LEU	-	expression tag	UNP P0DTC2
D	1233	LEU	-	expression tag	UNP P0DTC2
D	1234	SER	-	expression tag	UNP P0DTC2
D	1235	THR	-	expression tag	UNP P0DTC2
D	1236	PHE	-	expression tag	UNP P0DTC2
D	1237	LEU	-	expression tag	UNP P0DTC2
D	1238	GLY	-	expression tag	UNP P0DTC2
D	1239	ARG	-	expression tag	UNP P0DTC2
D	1240	SER	-	expression tag	UNP P0DTC2
D	1241	LEU	-	expression tag	UNP P0DTC2
D	1242	GLU	-	expression tag	UNP P0DTC2
D	1243	VAL	-	expression tag	UNP P0DTC2
D	1244	LEU	-	expression tag	UNP P0DTC2
D	1245	PHE	-	expression tag	UNP P0DTC2
D	1246	GLN	-	expression tag	UNP P0DTC2
D	1247	GLY	-	expression tag	UNP P0DTC2
D	1248	PRO	-	expression tag	UNP P0DTC2
D	1249	GLY	-	expression tag	UNP P0DTC2
D	1250	HIS	-	expression tag	UNP P0DTC2
D	1251	HIS	-	expression tag	UNP P0DTC2
D	1252	HIS	-	expression tag	UNP P0DTC2
D	1253	HIS	-	expression tag	UNP P0DTC2
D	1254	HIS	-	expression tag	UNP P0DTC2
D	1255	HIS	-	expression tag	UNP P0DTC2
D	1256	HIS	-	expression tag	UNP P0DTC2
D	1257	HIS	-	expression tag	UNP P0DTC2
D	1258	SER	-	expression tag	UNP P0DTC2
D	1259	ALA	-	expression tag	UNP P0DTC2
D	1260	TRP	-	expression tag	UNP P0DTC2
D	1261	SER	-	expression tag	UNP P0DTC2
D	1262	HIS	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
D	1263	PRO	-	expression tag	UNP P0DTC2
D	1264	GLN	-	expression tag	UNP P0DTC2
D	1265	PHE	-	expression tag	UNP P0DTC2
D	1266	GLU	-	expression tag	UNP P0DTC2
D	1267	LYS	-	expression tag	UNP P0DTC2
D	1268	GLY	-	expression tag	UNP P0DTC2
D	1269	GLY	-	expression tag	UNP P0DTC2
D	1270	GLY	-	expression tag	UNP P0DTC2
D	1271	SER	-	expression tag	UNP P0DTC2
D	1272	GLY	-	expression tag	UNP P0DTC2
D	1273	GLY	-	expression tag	UNP P0DTC2
D	1274	GLY	-	expression tag	UNP P0DTC2
D	1275	GLY	-	expression tag	UNP P0DTC2
D	1276	SER	-	expression tag	UNP P0DTC2
D	1277	GLY	-	expression tag	UNP P0DTC2
D	1278	GLY	-	expression tag	UNP P0DTC2
D	1279	SER	-	expression tag	UNP P0DTC2
D	1280	ALA	-	expression tag	UNP P0DTC2
D	1281	TRP	-	expression tag	UNP P0DTC2
D	1282	SER	-	expression tag	UNP P0DTC2
D	1283	HIS	-	expression tag	UNP P0DTC2
D	1284	PRO	-	expression tag	UNP P0DTC2
D	1285	GLN	-	expression tag	UNP P0DTC2
D	1286	PHE	-	expression tag	UNP P0DTC2
D	1287	GLU	-	expression tag	UNP P0DTC2
D	1288	LYS	-	expression tag	UNP P0DTC2
E	154	LYS	GLU	variant	UNP P0DTC2
E	452	ARG	LEU	variant	UNP P0DTC2
E	484	ILE	GLU	variant	UNP P0DTC2
E	614	GLY	ASP	variant	UNP P0DTC2
E	681	ARG	PRO	variant	UNP P0DTC2
E	682	GLY	ARG	variant	UNP P0DTC2
E	683	SER	ARG	variant	UNP P0DTC2
E	685	SER	ARG	variant	UNP P0DTC2
E	817	PRO	PHE	variant	UNP P0DTC2
E	892	PRO	ALA	variant	UNP P0DTC2
E	899	PRO	ALA	variant	UNP P0DTC2
E	942	PRO	ALA	variant	UNP P0DTC2
E	986	PRO	LYS	variant	UNP P0DTC2
E	987	PRO	VAL	variant	UNP P0DTC2
E	1071	HIS	GLN	variant	UNP P0DTC2
E	1209	GLY	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
E	1210	SER	-	expression tag	UNP P0DTC2
E	1211	GLY	-	expression tag	UNP P0DTC2
E	1212	TYR	-	expression tag	UNP P0DTC2
E	1213	ILE	-	expression tag	UNP P0DTC2
E	1214	PRO	-	expression tag	UNP P0DTC2
E	1215	GLU	-	expression tag	UNP P0DTC2
E	1216	ALA	-	expression tag	UNP P0DTC2
E	1217	PRO	-	expression tag	UNP P0DTC2
E	1218	ARG	-	expression tag	UNP P0DTC2
E	1219	ASP	-	expression tag	UNP P0DTC2
E	1220	GLY	-	expression tag	UNP P0DTC2
E	1221	GLN	-	expression tag	UNP P0DTC2
E	1222	ALA	-	expression tag	UNP P0DTC2
E	1223	TYR	-	expression tag	UNP P0DTC2
E	1224	VAL	-	expression tag	UNP P0DTC2
E	1225	ARG	-	expression tag	UNP P0DTC2
E	1226	LYS	-	expression tag	UNP P0DTC2
E	1227	ASP	-	expression tag	UNP P0DTC2
E	1228	GLY	-	expression tag	UNP P0DTC2
E	1229	GLU	-	expression tag	UNP P0DTC2
E	1230	TRP	-	expression tag	UNP P0DTC2
E	1231	VAL	-	expression tag	UNP P0DTC2
E	1232	LEU	-	expression tag	UNP P0DTC2
E	1233	LEU	-	expression tag	UNP P0DTC2
E	1234	SER	-	expression tag	UNP P0DTC2
E	1235	THR	-	expression tag	UNP P0DTC2
E	1236	PHE	-	expression tag	UNP P0DTC2
E	1237	LEU	-	expression tag	UNP P0DTC2
E	1238	GLY	-	expression tag	UNP P0DTC2
E	1239	ARG	-	expression tag	UNP P0DTC2
E	1240	SER	-	expression tag	UNP P0DTC2
E	1241	LEU	-	expression tag	UNP P0DTC2
E	1242	GLU	-	expression tag	UNP P0DTC2
E	1243	VAL	-	expression tag	UNP P0DTC2
E	1244	LEU	-	expression tag	UNP P0DTC2
E	1245	PHE	-	expression tag	UNP P0DTC2
E	1246	GLN	-	expression tag	UNP P0DTC2
E	1247	GLY	-	expression tag	UNP P0DTC2
E	1248	PRO	-	expression tag	UNP P0DTC2
E	1249	GLY	-	expression tag	UNP P0DTC2
E	1250	HIS	-	expression tag	UNP P0DTC2
E	1251	HIS	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
E	1252	HIS	-	expression tag	UNP P0DTC2
E	1253	HIS	-	expression tag	UNP P0DTC2
E	1254	HIS	-	expression tag	UNP P0DTC2
E	1255	HIS	-	expression tag	UNP P0DTC2
E	1256	HIS	-	expression tag	UNP P0DTC2
E	1257	HIS	-	expression tag	UNP P0DTC2
E	1258	SER	-	expression tag	UNP P0DTC2
E	1259	ALA	-	expression tag	UNP P0DTC2
E	1260	TRP	-	expression tag	UNP P0DTC2
E	1261	SER	-	expression tag	UNP P0DTC2
E	1262	HIS	-	expression tag	UNP P0DTC2
E	1263	PRO	-	expression tag	UNP P0DTC2
E	1264	GLN	-	expression tag	UNP P0DTC2
E	1265	PHE	-	expression tag	UNP P0DTC2
E	1266	GLU	-	expression tag	UNP P0DTC2
E	1267	LYS	-	expression tag	UNP P0DTC2
E	1268	GLY	-	expression tag	UNP P0DTC2
E	1269	GLY	-	expression tag	UNP P0DTC2
E	1270	GLY	-	expression tag	UNP P0DTC2
E	1271	SER	-	expression tag	UNP P0DTC2
E	1272	GLY	-	expression tag	UNP P0DTC2
E	1273	GLY	-	expression tag	UNP P0DTC2
E	1274	GLY	-	expression tag	UNP P0DTC2
E	1275	GLY	-	expression tag	UNP P0DTC2
E	1276	SER	-	expression tag	UNP P0DTC2
E	1277	GLY	-	expression tag	UNP P0DTC2
E	1278	GLY	-	expression tag	UNP P0DTC2
E	1279	SER	-	expression tag	UNP P0DTC2
E	1280	ALA	-	expression tag	UNP P0DTC2
E	1281	TRP	-	expression tag	UNP P0DTC2
E	1282	SER	-	expression tag	UNP P0DTC2
E	1283	HIS	-	expression tag	UNP P0DTC2
E	1284	PRO	-	expression tag	UNP P0DTC2
E	1285	GLN	-	expression tag	UNP P0DTC2
E	1286	PHE	-	expression tag	UNP P0DTC2
E	1287	GLU	-	expression tag	UNP P0DTC2
E	1288	LYS	-	expression tag	UNP P0DTC2
F	154	LYS	GLU	variant	UNP P0DTC2
F	452	ARG	LEU	variant	UNP P0DTC2
F	484	ILE	GLU	variant	UNP P0DTC2
F	614	GLY	ASP	variant	UNP P0DTC2
F	681	ARG	PRO	variant	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
F	682	GLY	ARG	variant	UNP P0DTC2
F	683	SER	ARG	variant	UNP P0DTC2
F	685	SER	ARG	variant	UNP P0DTC2
F	817	PRO	PHE	variant	UNP P0DTC2
F	892	PRO	ALA	variant	UNP P0DTC2
F	899	PRO	ALA	variant	UNP P0DTC2
F	942	PRO	ALA	variant	UNP P0DTC2
F	986	PRO	LYS	variant	UNP P0DTC2
F	987	PRO	VAL	variant	UNP P0DTC2
F	1071	HIS	GLN	variant	UNP P0DTC2
F	1209	GLY	-	expression tag	UNP P0DTC2
F	1210	SER	-	expression tag	UNP P0DTC2
F	1211	GLY	-	expression tag	UNP P0DTC2
F	1212	TYR	-	expression tag	UNP P0DTC2
F	1213	ILE	-	expression tag	UNP P0DTC2
F	1214	PRO	-	expression tag	UNP P0DTC2
F	1215	GLU	-	expression tag	UNP P0DTC2
F	1216	ALA	-	expression tag	UNP P0DTC2
F	1217	PRO	-	expression tag	UNP P0DTC2
F	1218	ARG	-	expression tag	UNP P0DTC2
F	1219	ASP	-	expression tag	UNP P0DTC2
F	1220	GLY	-	expression tag	UNP P0DTC2
F	1221	GLN	-	expression tag	UNP P0DTC2
F	1222	ALA	-	expression tag	UNP P0DTC2
F	1223	TYR	-	expression tag	UNP P0DTC2
F	1224	VAL	-	expression tag	UNP P0DTC2
F	1225	ARG	-	expression tag	UNP P0DTC2
F	1226	LYS	-	expression tag	UNP P0DTC2
F	1227	ASP	-	expression tag	UNP P0DTC2
F	1228	GLY	-	expression tag	UNP P0DTC2
F	1229	GLU	-	expression tag	UNP P0DTC2
F	1230	TRP	-	expression tag	UNP P0DTC2
F	1231	VAL	-	expression tag	UNP P0DTC2
F	1232	LEU	-	expression tag	UNP P0DTC2
F	1233	LEU	-	expression tag	UNP P0DTC2
F	1234	SER	-	expression tag	UNP P0DTC2
F	1235	THR	-	expression tag	UNP P0DTC2
F	1236	PHE	-	expression tag	UNP P0DTC2
F	1237	LEU	-	expression tag	UNP P0DTC2
F	1238	GLY	-	expression tag	UNP P0DTC2
F	1239	ARG	-	expression tag	UNP P0DTC2
F	1240	SER	-	expression tag	UNP P0DTC2

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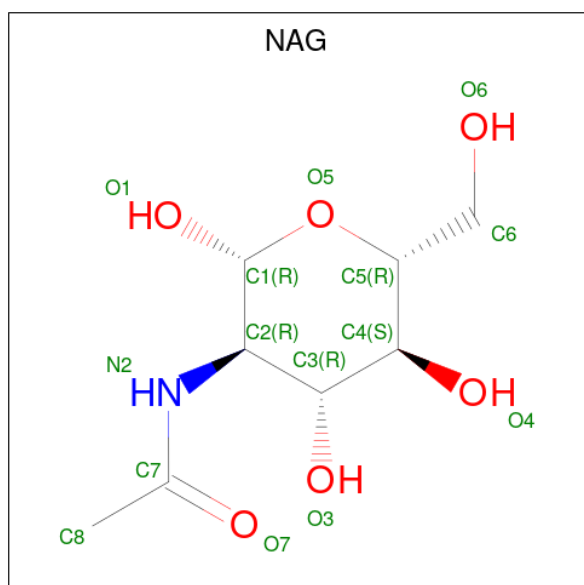
Chain	Residue	Modelled	Actual	Comment	Reference
F	1241	LEU	-	expression tag	UNP P0DTC2
F	1242	GLU	-	expression tag	UNP P0DTC2
F	1243	VAL	-	expression tag	UNP P0DTC2
F	1244	LEU	-	expression tag	UNP P0DTC2
F	1245	PHE	-	expression tag	UNP P0DTC2
F	1246	GLN	-	expression tag	UNP P0DTC2
F	1247	GLY	-	expression tag	UNP P0DTC2
F	1248	PRO	-	expression tag	UNP P0DTC2
F	1249	GLY	-	expression tag	UNP P0DTC2
F	1250	HIS	-	expression tag	UNP P0DTC2
F	1251	HIS	-	expression tag	UNP P0DTC2
F	1252	HIS	-	expression tag	UNP P0DTC2
F	1253	HIS	-	expression tag	UNP P0DTC2
F	1254	HIS	-	expression tag	UNP P0DTC2
F	1255	HIS	-	expression tag	UNP P0DTC2
F	1256	HIS	-	expression tag	UNP P0DTC2
F	1257	HIS	-	expression tag	UNP P0DTC2
F	1258	SER	-	expression tag	UNP P0DTC2
F	1259	ALA	-	expression tag	UNP P0DTC2
F	1260	TRP	-	expression tag	UNP P0DTC2
F	1261	SER	-	expression tag	UNP P0DTC2
F	1262	HIS	-	expression tag	UNP P0DTC2
F	1263	PRO	-	expression tag	UNP P0DTC2
F	1264	GLN	-	expression tag	UNP P0DTC2
F	1265	PHE	-	expression tag	UNP P0DTC2
F	1266	GLU	-	expression tag	UNP P0DTC2
F	1267	LYS	-	expression tag	UNP P0DTC2
F	1268	GLY	-	expression tag	UNP P0DTC2
F	1269	GLY	-	expression tag	UNP P0DTC2
F	1270	GLY	-	expression tag	UNP P0DTC2
F	1271	SER	-	expression tag	UNP P0DTC2
F	1272	GLY	-	expression tag	UNP P0DTC2
F	1273	GLY	-	expression tag	UNP P0DTC2
F	1274	GLY	-	expression tag	UNP P0DTC2
F	1275	GLY	-	expression tag	UNP P0DTC2
F	1276	SER	-	expression tag	UNP P0DTC2
F	1277	GLY	-	expression tag	UNP P0DTC2
F	1278	GLY	-	expression tag	UNP P0DTC2
F	1279	SER	-	expression tag	UNP P0DTC2
F	1280	ALA	-	expression tag	UNP P0DTC2
F	1281	TRP	-	expression tag	UNP P0DTC2
F	1282	SER	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
F	1283	HIS	-	expression tag	UNP P0DTC2
F	1284	PRO	-	expression tag	UNP P0DTC2
F	1285	GLN	-	expression tag	UNP P0DTC2
F	1286	PHE	-	expression tag	UNP P0DTC2
F	1287	GLU	-	expression tag	UNP P0DTC2
F	1288	LYS	-	expression tag	UNP P0DTC2

- Molecule 2 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				AltConf
2	A	1	Total	C	N	O	0
			14	8	1	5	
2	A	1	Total	C	N	O	0
			14	8	1	5	
2	B	1	Total	C	N	O	0
			14	8	1	5	
2	B	1	Total	C	N	O	0
			14	8	1	5	
2	C	1	Total	C	N	O	0
			14	8	1	5	
2	C	1	Total	C	N	O	0
			14	8	1	5	
2	D	1	Total	C	N	O	0
			14	8	1	5	
2	D	1	Total	C	N	O	0
			14	8	1	5	

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Mol	Chain	Residues	Atoms				AltConf
2	E	1	Total	C	N	O	0
			14	8	1	5	
2	E	1	Total	C	N	O	0
			14	8	1	5	
2	F	1	Total	C	N	O	0
			14	8	1	5	
2	F	1	Total	C	N	O	0
			14	8	1	5	

GLY	TLE	ASP	GLY	VAL	GLY	VAL	TLE
GLY	PRO	LYS	VAL	PHE	VAL	PHE	SER
GLY	GLY	TYR	TYR	ASP	GLY	GLY	SER
SER	ALA	PHE	ASP	VAL	SER	GLN	VAL
GLY	PRO	LYS	LYS	SER	ASN	LYS	LEU
GLY	ARG	ASN	ASN	ASN	GLY	ARG	ASN
SER	ASP	HIS	HIS	THR	THR	GLY	TLE
GLY	GLY	THR	THR	HIS	HIS	ASP	LEU
TRP	ALA	PRO	SER	TRP	PHE	GLY	ARG
SER	ALA	ASP	GLN	TRP	THR	ASP	SER
HIS	TYR	ASP	ASP	PHE	VAL	CYS	ARG
PRO	VAL	VAL	VAL	THR	THR	GLY	LEU
GLN	ARG	ASP	ASP	THR	LYS	ASP	ASP
PHE	LYS	LEU	LEU	GLN	GLY	GLY	PRO
GLU	ASP	GLY	ASP	ASN	HIS	TYR	PRO
LYS	GLY	ILE	ILE	PHE	PHE	LEU	GLA
	TRP	SER	GLY	GLU	GLU	MET	GLU
	VAL	GLY	ILE	GLU	SER	SER	VAL
	LEU	ILE	ILE	GLN	PHE	GLN	GLN
	LEU	ASN	ASN	ILE	PRO	TLE	TLE
	SER	ALA	ALA	ILE	GLN	ASP	ASP
	THR	SER	SER	ILE	SER	ARG	ARG
	PHE	VAL	VAL	THR	ALA	LEU	LEU
	LEU	VAL	VAL	THR	PRO	TLE	TLE
	GLY	ASN	ASN	ASP	HIS	GLY	GLY
	ARG	GLN	GLN	THR	VAL	VAL	ARG
	GLY	LEU	LEU	PHE	VAL	LEU	LEU
	GLU	GLU	GLU	VAL	PHE	GLN	GLN
	VAL	ILE	ILE	VAL	LEU	GLY	TLE
	LEU	ASP	ASP	SER	HIS	ASN	ARG
	PHE	ARG	ARG	ASN	PHE	ALA	ALA
	GLN	LEU	LEU	CYS	THR	GLU	GLU
	GLY	ASN	ASN	ASP	TYR	ARG	ARG
	PRO	GLU	GLU	VAL	VAL	PRO	ALA
	GLY	VAL	VAL	VAL	PRO	ILE	SER
	HIS	ALA	ALA	ILE	ALA	CYS	ASN
	HIS	LYS	LYS	GLY	THR	HIS	ALA
	HIS	ASN	ASN	ILE	VAL	ASP	LEU
	HIS	LEU	LEU	TYR	ALA	GLY	ALA
	ALA	ASP	ASP	ASP	ALA	LYS	ALA
	TRP	LEU	LEU	PRO	ALA	ALA	ALA
	SER	GLN	GLN	LEU	ILE	GLY	THR
	HIS	GLU	GLU	PRO	GLN	ALA	LYS
	PRO	LEU	LEU	GLY	THR	PHE	THR
	GLN	GLY	GLY	LEU	ASP	GLY	GLY
	PHE	TYR	TYR	LEU	SER	GLY	GLY
	GLU	GLU	GLU	ASP	GLU	GLY	SER
	GLY	TRP	TRP	LEU	GLU	ARG	CYS
	GLY	GLY	GLY	LEU	GLY	GLY	GLY

- Molecule 1: Spike glycoprotein



ASP	GLU	GLY	ASP	PRO	THR	VAL	ASP	L517	ASP	GLN	THR	CYS	LEU	GLY	ASN	ASN	VAL	THR	ASP	THR	ASN	GLY	LEU
GLU	MET	PRO	PRO	CYS	GLY	ALA	LEU	L518	LEU	LEU	ALA	THR	ALA	LYS	ASN	ASN	ALA	THR	PHE	THR	ASN	LYS	LEU
ILE	ALA	LYS	THR	ILE	SER	GLN	THR	H519	PRO	THR	SER	SER	HIS	ASN	ASN	ASN	THR	TRP	PHE	THR	ASN	GLY	LEU
GLN	GLN	PRO	ILE	LEU	ILE	ILE	THR	T523	THR	THR	PHE	THR	ARG	PHE	VAL	VAL	VAL	VAL	VAL	VAL	VAL	LYS	LEU
THR	THR	THR	THR	THR	THR	ALA	ARG	S555	ALA	ARG	VAL	VAL	TYR	ASN	TYR	TYR	TYR	TYR	TYR	TYR	ASN	TYR	LEU
LYS	ARG	GLN	THR	GLN	TYR	TYR	VAL	N556	GLU	GLY	GLY	GLY	THR	ARG	THR	THR	THR	THR	THR	THR	THR	THR	PRO
LEU	LEU	LEU	PRO	GLY	MET	MET	SER	G566	PRO	SER	ILE	ILE	PRO	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
LEU	LEU	LEU	LEU	THR	THR	THR	THR	I569	THR	THR	THR	THR	ASP	PHE	THR	THR	THR	THR	THR	THR	THR	THR	THR
ALA	ASP	GLY	GLY	GLY	LEU	LEU	GLY	A570	ASN	ASN	GLN	GLN	ASP	PHE	THR	THR	THR	THR	THR	THR	THR	THR	THR
THR	THR	THR	THR	THR	ALA	ALA	ASN	A575	PHE	PHE	ASN	ASN	SER	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE
GLY	LYS	GLY	LYS	ARG	VAL	VAL	THR	D578	GLN	GLN	ARG	ARG	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
TRP	VAL	VAL	VAL	ALA	ALA	ALA	ARG	T581	ALA	ALA	VAL	VAL	ALA	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
THR	THR	THR	THR	THR	THR	TYR	THR	D586	GLY	GLY	THR	P322	ALA	PHE	THR	THR	THR	THR	THR	THR	THR	THR	THR
GLY	GLY	GLY	GLY	ALA	ASN	ASN	CYS	P589	LEU	LEU	ILE	N353	ALA	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE
ALA	ASP	ALA	ALA	ILE	ASN	ASN	ILE	CYS	SER	SER	GLY	N360	VAL	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
PRO	PRO	GLY	GLY	VAL	ILE	ILE	GLY	SER	THR	THR	THR	H370	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
GLY	ILE	ILE	ILE	ILE	ILE	ILE	GLN	PHE	THR	THR	THR	S371	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
GLN	LYS	GLN	GLN	LYS	ASP	PRO	HIS	GLY	GLY	GLY	GLY	A372	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
ILE	ILE	ILE	ILE	THR	THR	ASN	VAL	VAL	VAL	VAL	VAL	S377	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
PRO	PHE	GLY	GLY	THR	THR	PHE	ASN	SER	SER	SER	SER	C379	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
PHE	PRO	MET	PRO	ASP	GLN	ILE	THR	ILE	THR	THR	THR	D389	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
GLN	LEU	GLN	LEU	CYS	VAL	VAL	SER	PRO	PRO	GLY	GLY	V401	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
MET	ALA	MET	GLY	GLY	THR	THR	CYS	THR	THR	THR	THR	G413	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
ALA	TYR	ILE	ILE	ILE	GLU	GLU	PRO	ASN	ASN	ASN	ASN	N439	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
THR	PHE	ALA	ALA	ALA	ILE	ILE	ILE	LYS	THR	THR	THR	N440	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
ASN	ASN	GLN	GLN	ARG	LYS	LYS	THR	THR	THR	THR	THR	K444	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
GLY	VAL	VAL	VAL	PHE	THR	THR	GLN	GLN	GLN	GLN	GLN	C432	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
ILE	ILE	ILE	ILE	ILE	SER	SER	VAL	VAL	VAL	VAL	VAL	N466	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
GLY	GLY	GLY	GLY	GLY	MET	MET	THR	THR	THR	THR	THR	Q493	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
VAL	VAL	VAL	VAL	VAL	THR	THR	GLN	GLY	GLY	GLY	GLY	F497	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	Y505	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	Y506	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	P507	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	Y508	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	R509	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR

[illegible]

- Molecule 1: Spike glycoprotein

[illegible]

TRP	SER	LEU	PRO	ALA	ALA	ASN	MET	CYS
	HIS	GLN	LEU	ILE	SER	THR	THR	LEU
	PRO	GLU	PRO	HIS	ASN	VAL	LEU	GLY
	GLN	GLY	GLU	ASP	LEU	LYS	TYR	ASP
	PHE	LYS	LEU	GLY	ALA	GLN	ARG	ALA
	GLU	TYR	ASP	LYS	ALA	LEU	PHE	ALA
	LYS	GLU	SER	ALA	THR	SER	ASN	ARG
	GLY	GLN	PHE	HIS	LYS	SER	GLY	LEU
	GLY	GLY	LYS	PHE	MET	ASN	ILE	ASP
	GLY	GLY	GLU	PRO	SER	PHE	GLY	ILE
GLY	SER	GLY	GLU	ARG	GLU	CYS	VAL	CYS
	GLY	TYR	LEU	GLU	THR	ALA	THR	ALA
	GLY	ASP	ASP	VAL	VAL	ILE	GLN	GLN
	GLY	PRO	TYR	PHE	GLN	SER	VAL	ASN
	GLY	GLU	PHE	VAL	GLN	VAL	LEU	ASN
	SER	LYS	LYS	SER	SER	LEU	TYR	GLY
	GLY	ARG	ASN	ASN	LYS	ASN	GLU	LEU
	ARG	ASP	HIS	GLY	ARG	ASP	ASN	THR
	GLY	GLY	THR	THR	VAL	ILE	GLN	VAL
	ALA	GLN	SER	HIS	ASP	LEU	LYS	LEU
TRP	GLN	VAL	PRO	PHE	PHE	ARG	ILE	PRO
	SER	TYR	ASP	PHE	CYS	ARG	ILE	PRO
	HIS	ALA	VAL	VAL	GLY	LEU	ALA	LEU
	PRO	VAL	VAL	VAL	THR	LEU	ALA	LEU
	SER	ARG	ASP	THR	LYS	ASP	ASN	LEU
	GLN	GLY	LEU	GLN	GLY	PRO	GLN	THR
	ASP	ASP	GLY	ARG	TYR	PRO	PHE	ASP
	GLY	GLY	ASP	ASN	HIS	GLU	ASN	GLU
	GLY	GLU	ILE	PHE	LEU	ALA	SER	MET
	THR	THR	SER	TYR	MET	GLU	ALA	ILE
GLY	VAL	VAL	GLY	GLU	SER	VAL	ILE	ALA
	LEU	LEU	ILE	PRO	PHE	GLN	GLY	GLN
	SER	SER	ALA	ILE	GLN	ASP	ILE	THR
	THR	THR	SER	ILE	SER	ARG	GLN	SER
	PHE	PHE	VAL	THR	ALA	LEU	ASP	ALA
	LEU	LEU	ASN	THR	PRO	ILE	SER	LEU
	GLY	GLY	ARG	ASP	HIS	THR	LEU	LEU
	ARG	SER	ILE	ASN	GLY	GLY	SER	ALA
	SER	SER	GLN	THR	VAL	ARG	SER	GLY
	LEU	LEU	LYS	PHE	VAL	LEU	THR	THR
GLU	GLU	GLU	ILE	VAL	PHE	GLN	THR	ILE
	VAL	VAL	ILE	VAL	LEU	SER	PRO	ILE
	VAL	VAL	ASP	GLY	LEU	SER	ALA	SER
	PHE	PHE	ARG	ASN	VAL	GLN	LEU	GLY
	GLN	GLN	LEU	CYS	THR	TYR	GLY	THR
	GLY	GLY	ASN	ASP	TYR	THR	LYS	THR
	PRO	PRO	VAL	VAL	VAL	VAL	LEU	PHE
	SER	SER	VAL	ILE	ALA	THR	GLN	GLY
	HIS	HIS	ALA	ILE	GLN	GLN	ASP	ALA
	HIS	HIS	ASN	VAL	HIS	GLY	VAL	PRO
GLY	HIS	HIS	ASN	ILE	LYS	ILE	ASN	ALA
	ASN	ASN	LEU	VAL	LYS	ILE	ASN	ALA
	GLU	GLU	ASN	THR	ARG	ARG	GLN	LEU
	THR	THR	THR	THR	PHE	ALA	GLN	GLN
	LEU	LEU	SER	VAL	THR	GLU	VAL	PRO
	LEU	LEU	THR	THR	THR	GLU	VAL	PRO
	THR	THR	THR	THR	THR	THR	THR	ALA
	THR	THR	THR	THR	THR	THR	THR	ALA
	THR	THR	THR	THR	THR	THR	THR	ALA
	THR	THR	THR	THR	THR	THR	THR	ALA

- Molecule 1: Spike glycoprotein

[illegible]

[illegible]

- Molecule 1: Spike glycoprotein

Chain F: 19% 79%

[illegible]

[illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	76565	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	1.104	Depositor
Minimum map value	-0.527	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.024	Depositor
Recommended contour level	0.24	Depositor
Map size (Å)	520.0, 520.0, 520.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.3, 1.3, 1.3	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NAG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.30	0/2157	0.55	1/2935 (0.0%)
1	B	0.29	0/2157	0.55	0/2935
1	C	0.31	0/2157	0.55	1/2935 (0.0%)
1	D	0.29	0/2157	0.54	0/2935
1	E	0.29	0/2157	0.54	0/2935
1	F	0.30	0/2157	0.58	1/2935 (0.0%)
All	All	0.30	0/12942	0.55	3/17610 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	391	CYS	CA-CB-SG	6.17	125.11	114.00
1	A	517	LEU	CA-CB-CG	6.04	129.19	115.30
1	C	505	TYR	C-N-CA	5.16	134.61	121.70

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2103	0	2024	10	0
1	B	2103	0	2024	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	2103	0	2024	11	0
1	D	2103	0	2024	13	0
1	E	2103	0	2024	8	0
1	F	2103	0	2024	17	0
2	A	28	0	26	0	0
2	B	28	0	26	0	0
2	C	28	0	26	0	0
2	D	28	0	26	0	0
2	E	28	0	26	0	0
2	F	28	0	26	0	0
All	All	12786	0	12300	67	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

All (67) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:383:SER:HB3	1:F:386:LYS:HB2	1.84	0.59
1:F:328:ARG:NH1	1:F:531:THR:O	2.36	0.59
1:E:411:ALA:HB3	1:E:414:GLN:HG3	1.84	0.58
1:C:439:ASN:ND2	1:F:437:ASN:OD1	2.37	0.58
1:F:327:VAL:HG11	1:F:528:LYS:HD2	1.86	0.57
1:C:353:TRP:O	1:C:466:ARG:NH1	2.38	0.56
1:D:442:ASP:O	1:D:448:ASN:ND2	2.38	0.56
1:F:577:ARG:HB2	1:F:584:ILE:HG13	1.87	0.55
1:F:403:ARG:NH1	1:F:405:ASP:OD2	2.40	0.54
1:A:358:ILE:HB	1:A:395:VAL:HB	1.89	0.54
1:C:401:VAL:HG22	1:C:509:ARG:HG2	1.89	0.54
1:B:418:ILE:HA	1:B:422:ASN:HB2	1.91	0.52
1:C:493:GLN:OE1	1:E:493:GLN:NE2	2.40	0.52
1:B:358:ILE:HB	1:B:395:VAL:HB	1.89	0.52
1:A:401:VAL:HG22	1:A:509:ARG:HG2	1.92	0.51
1:D:560:LEU:O	1:D:577:ARG:NH2	2.43	0.51
1:A:533:LEU:HD21	1:A:585:LEU:HD11	1.92	0.51
1:C:497:PHE:CG	1:C:507:PRO:HG3	2.46	0.51
1:D:366:SER:H	1:D:388:ASN:HD21	1.59	0.49
1:C:555:SER:HB3	1:C:586:ASP:HB2	1.94	0.49
1:F:577:ARG:HD2	1:F:582:LEU:HD22	1.95	0.48
1:E:329:PHE:HE2	1:E:528:LYS:HB3	1.79	0.48
1:B:396:TYR:HB2	1:B:514:SER:HB3	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:411:ALA:HB3	1:D:414:GLN:HG3	1.96	0.48
1:D:393:THR:HA	1:D:522:ALA:HA	1.95	0.48
1:F:577:ARG:HA	1:F:584:ILE:HA	1.95	0.47
1:A:357:ARG:HG2	1:A:396:TYR:HE1	1.79	0.47
1:D:358:ILE:HB	1:D:395:VAL:HB	1.97	0.46
1:D:578:ASP:OD2	1:D:581:THR:OG1	2.30	0.46
1:E:379:CYS:HA	1:E:432:CYS:HA	1.96	0.46
1:A:418:ILE:HA	1:A:422:ASN:HB2	1.96	0.46
1:A:379:CYS:HA	1:A:432:CYS:HA	1.98	0.46
1:C:360:ASN:H	1:C:523:THR:HB	1.81	0.46
1:C:566:GLY:N	1:C:575:ALA:O	2.48	0.46
1:D:360:ASN:H	1:D:523:THR:HB	1.81	0.46
1:C:444:LYS:HG3	1:F:372:ALA:HB1	1.99	0.45
1:B:453:TYR:HE2	1:B:455:LEU:HD13	1.81	0.45
1:D:457:ARG:NE	1:D:467:ASP:OD2	2.40	0.45
1:A:578:ASP:HB3	1:A:583:GLU:H	1.82	0.44
1:B:395:VAL:HG23	1:B:524:VAL:HG11	1.99	0.44
1:C:578:ASP:OD2	1:C:581:THR:OG1	2.31	0.44
1:E:497:PHE:CG	1:E:507:PRO:HG3	2.52	0.43
1:D:497:PHE:CG	1:D:507:PRO:HG3	2.53	0.43
1:B:497:PHE:CG	1:B:507:PRO:HG3	2.52	0.43
1:D:331:ASN:OD1	1:D:331:ASN:N	2.49	0.43
1:E:401:VAL:HG22	1:E:509:ARG:HG2	2.01	0.43
1:F:391:CYS:HB2	1:F:525:CYS:HA	2.00	0.43
1:B:379:CYS:HA	1:B:432:CYS:HA	1.99	0.43
1:E:418:ILE:HA	1:E:422:ASN:HB2	2.01	0.43
1:F:357:ARG:NH2	1:F:396:TYR:OH	2.50	0.42
1:A:403:ARG:HG3	1:A:406:GLU:HG3	2.00	0.42
1:B:533:LEU:HD21	1:B:585:LEU:HD11	2.00	0.42
1:E:403:ARG:NH2	1:E:405:ASP:OD2	2.52	0.42
1:F:376:THR:HG23	1:F:378:LYS:HG3	2.01	0.42
1:F:409:GLN:HA	1:F:414:GLN:HG2	2.01	0.42
1:F:457:ARG:NH1	1:F:459:SER:OG	2.52	0.42
1:A:328:ARG:HD2	1:A:533:LEU:HD13	2.01	0.42
1:B:401:VAL:HG22	1:B:509:ARG:HG2	2.01	0.42
1:F:418:ILE:HA	1:F:422:ASN:HB2	2.01	0.42
1:D:328:ARG:NH2	1:D:578:ASP:OD2	2.51	0.41
1:C:379:CYS:HA	1:C:432:CYS:HA	2.03	0.41
1:F:364:ASP:OD1	1:F:364:ASP:N	2.44	0.41
1:D:335:LEU:HD23	1:D:362:VAL:HG13	2.02	0.41
1:B:551:VAL:HB	1:B:588:THR:HB	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:393:THR:O	1:A:523:THR:OG1	2.38	0.40
1:B:365:TYR:HD2	1:B:387:LEU:HB3	1.85	0.40
1:F:410:ILE:HD12	1:F:410:ILE:HG23	1.86	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	266/1288 (21%)	257 (97%)	9 (3%)	0	100	100
1	B	266/1288 (21%)	262 (98%)	4 (2%)	0	100	100
1	C	266/1288 (21%)	257 (97%)	9 (3%)	0	100	100
1	D	266/1288 (21%)	261 (98%)	5 (2%)	0	100	100
1	E	266/1288 (21%)	258 (97%)	8 (3%)	0	100	100
1	F	266/1288 (21%)	261 (98%)	5 (2%)	0	100	100
All	All	1596/7728 (21%)	1556 (98%)	40 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	231/1115 (21%)	230 (100%)	1 (0%)	89	95
1	B	231/1115 (21%)	231 (100%)	0	100	100
1	C	231/1115 (21%)	231 (100%)	0	100	100
1	D	231/1115 (21%)	228 (99%)	3 (1%)	65	82
1	E	231/1115 (21%)	230 (100%)	1 (0%)	89	95
1	F	231/1115 (21%)	231 (100%)	0	100	100
All	All	1386/6690 (21%)	1381 (100%)	5 (0%)	88	95

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	558	LYS
1	D	573	THR
1	D	583	GLU
1	D	586	ASP
1	E	588	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

12 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and

the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	C	1302	1	14,14,15	0.46	0	17,19,21	0.65	1 (5%)
2	NAG	E	1302	1	14,14,15	0.36	0	17,19,21	0.57	0
2	NAG	D	1302	1	14,14,15	0.34	0	17,19,21	0.54	0
2	NAG	A	1301	1	14,14,15	0.30	0	17,19,21	0.42	0
2	NAG	D	1301	1	14,14,15	0.42	0	17,19,21	0.44	0
2	NAG	A	1302	1	14,14,15	0.37	0	17,19,21	0.67	1 (5%)
2	NAG	C	1301	1	14,14,15	0.40	0	17,19,21	0.44	0
2	NAG	B	1301	1	14,14,15	0.35	0	17,19,21	0.46	0
2	NAG	B	1302	1	14,14,15	0.45	0	17,19,21	0.61	1 (5%)
2	NAG	F	1301	1	14,14,15	0.97	2 (14%)	17,19,21	0.71	1 (5%)
2	NAG	E	1301	1	14,14,15	0.31	0	17,19,21	0.40	0
2	NAG	F	1302	1	14,14,15	0.40	0	17,19,21	0.59	1 (5%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	C	1302	1	-	2/6/23/26	0/1/1/1
2	NAG	E	1302	1	-	1/6/23/26	0/1/1/1
2	NAG	D	1302	1	-	2/6/23/26	0/1/1/1
2	NAG	A	1301	1	-	2/6/23/26	0/1/1/1
2	NAG	D	1301	1	-	0/6/23/26	0/1/1/1
2	NAG	A	1302	1	-	2/6/23/26	0/1/1/1
2	NAG	C	1301	1	-	0/6/23/26	0/1/1/1
2	NAG	B	1301	1	-	2/6/23/26	0/1/1/1
2	NAG	B	1302	1	-	2/6/23/26	0/1/1/1
2	NAG	F	1301	1	-	2/6/23/26	0/1/1/1
2	NAG	E	1301	1	-	2/6/23/26	0/1/1/1
2	NAG	F	1302	1	-	2/6/23/26	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	1301	NAG	O5-C1	2.72	1.48	1.43
2	F	1301	NAG	C1-C2	2.29	1.55	1.52

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	1301	NAG	C1-O5-C5	2.66	115.75	112.19
2	A	1302	NAG	C1-O5-C5	2.45	115.48	112.19
2	C	1302	NAG	C1-O5-C5	2.24	115.18	112.19
2	B	1302	NAG	C1-O5-C5	2.13	115.03	112.19
2	F	1302	NAG	C1-O5-C5	2.02	114.89	112.19

There are no chirality outliers.

All (19) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	1301	NAG	O5-C5-C6-O6
2	B	1302	NAG	O5-C5-C6-O6
2	C	1302	NAG	O5-C5-C6-O6
2	A	1302	NAG	O5-C5-C6-O6
2	E	1301	NAG	O5-C5-C6-O6
2	B	1301	NAG	C4-C5-C6-O6
2	A	1301	NAG	C4-C5-C6-O6
2	A	1301	NAG	O5-C5-C6-O6
2	F	1302	NAG	O5-C5-C6-O6
2	C	1302	NAG	C4-C5-C6-O6
2	B	1302	NAG	C4-C5-C6-O6
2	D	1302	NAG	C4-C5-C6-O6
2	E	1301	NAG	C4-C5-C6-O6
2	A	1302	NAG	C4-C5-C6-O6
2	E	1302	NAG	O5-C5-C6-O6
2	D	1302	NAG	O5-C5-C6-O6
2	F	1302	NAG	C4-C5-C6-O6
2	F	1301	NAG	C4-C5-C6-O6
2	F	1301	NAG	O5-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

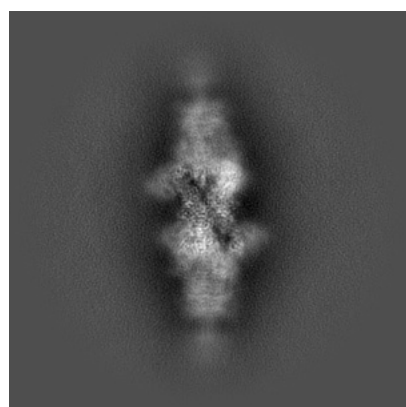
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-25858. These allow visual inspection of the internal detail of the map and identification of artifacts.

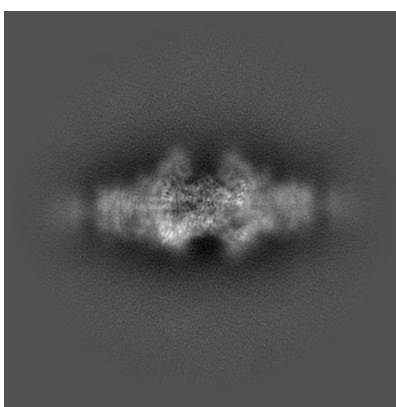
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

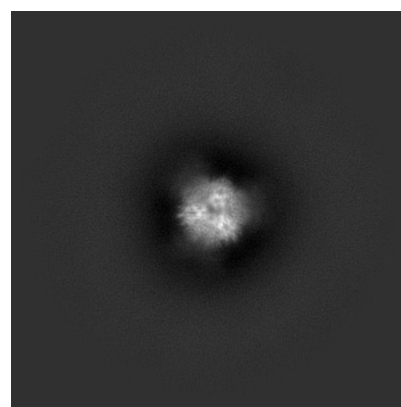
6.1.1 Primary map



X



Y

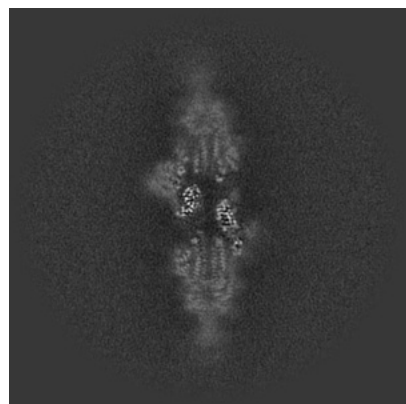


Z

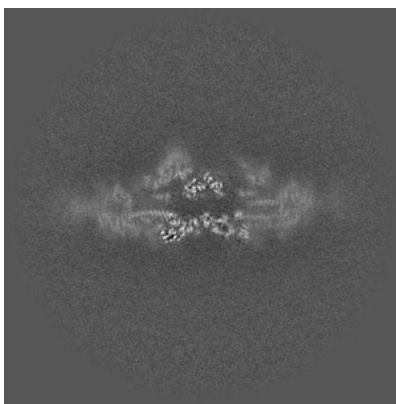
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

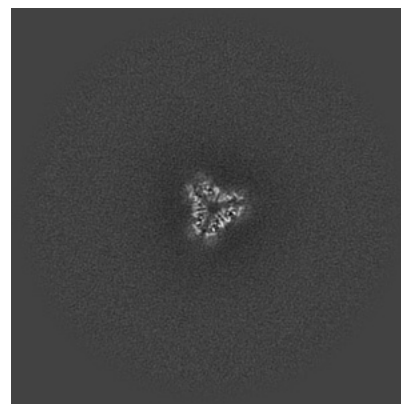
6.2.1 Primary map



X Index: 200



Y Index: 200

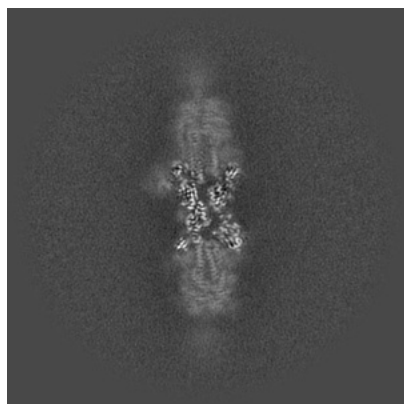


Z Index: 200

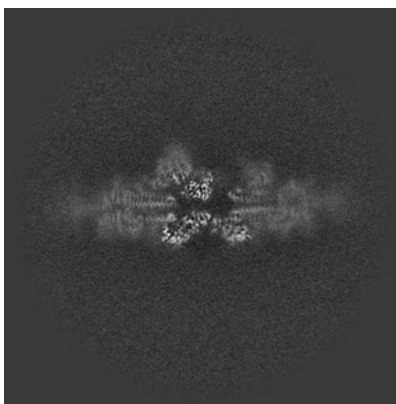
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

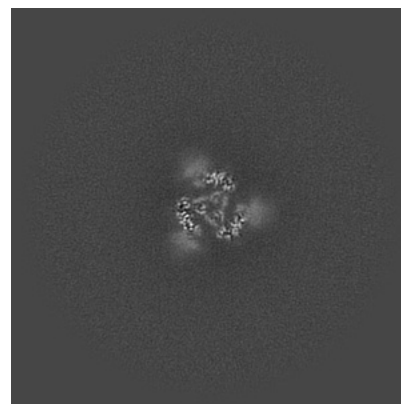
6.3.1 Primary map



X Index: 211



Y Index: 195

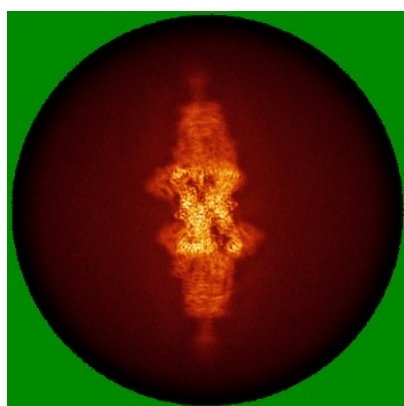


Z Index: 165

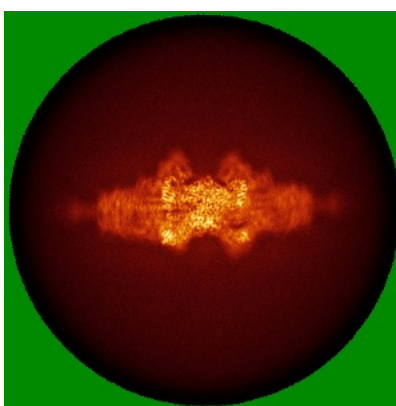
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

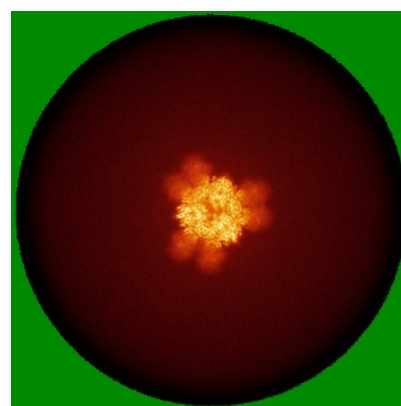
6.4.1 Primary map



X



Y

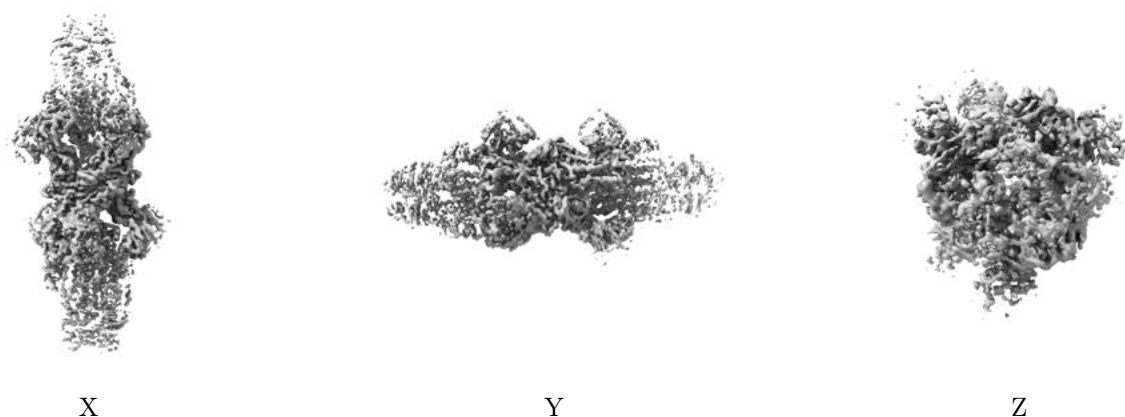


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.24. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

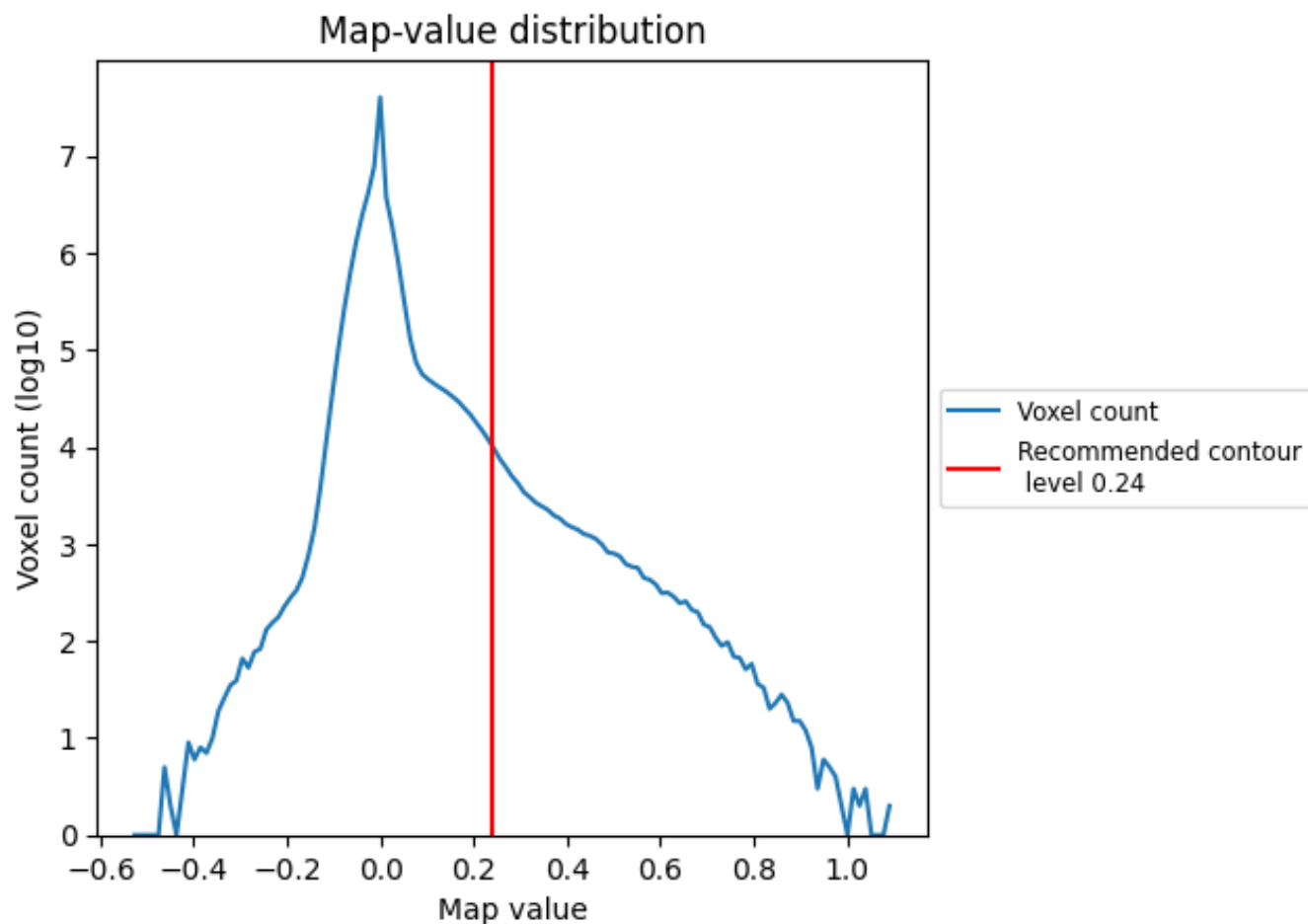
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

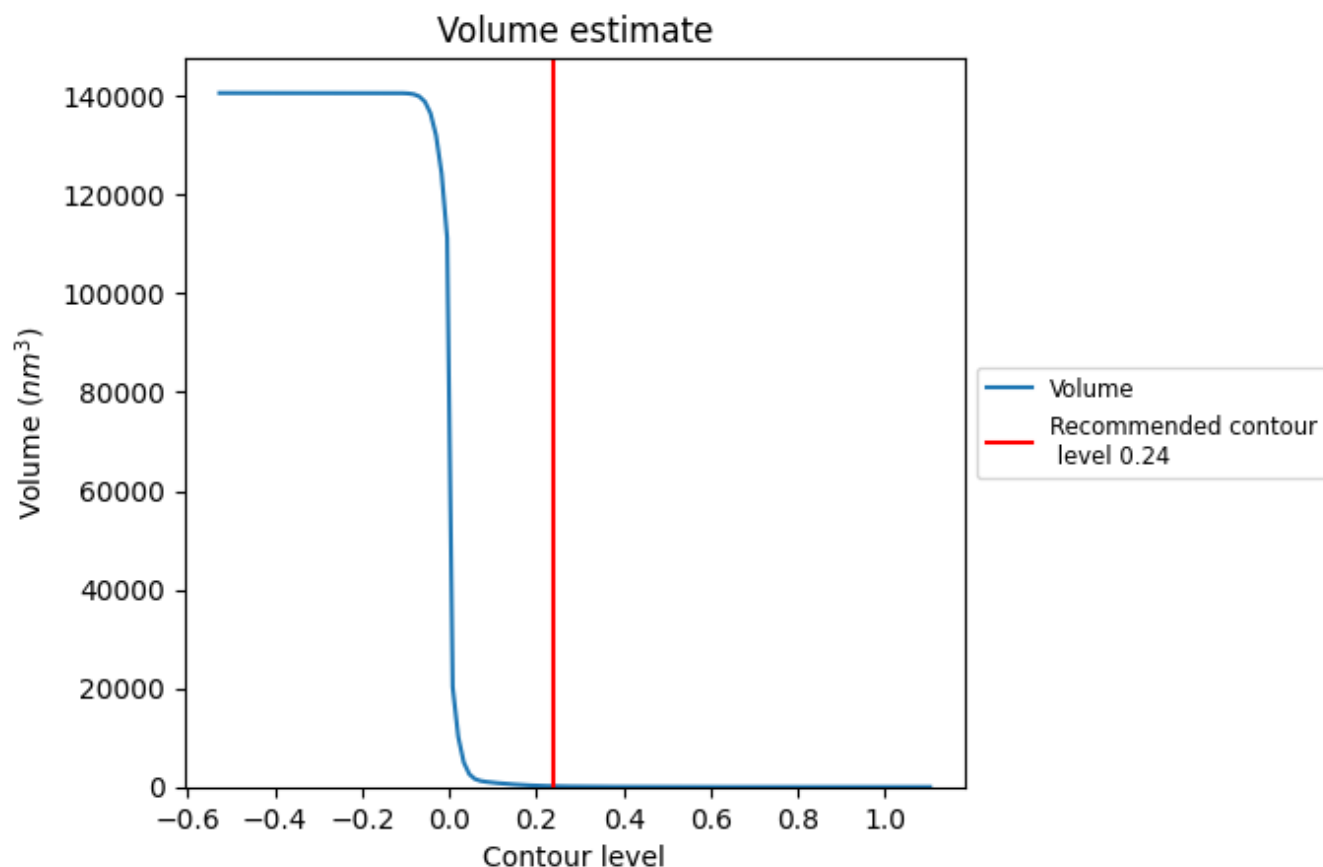
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

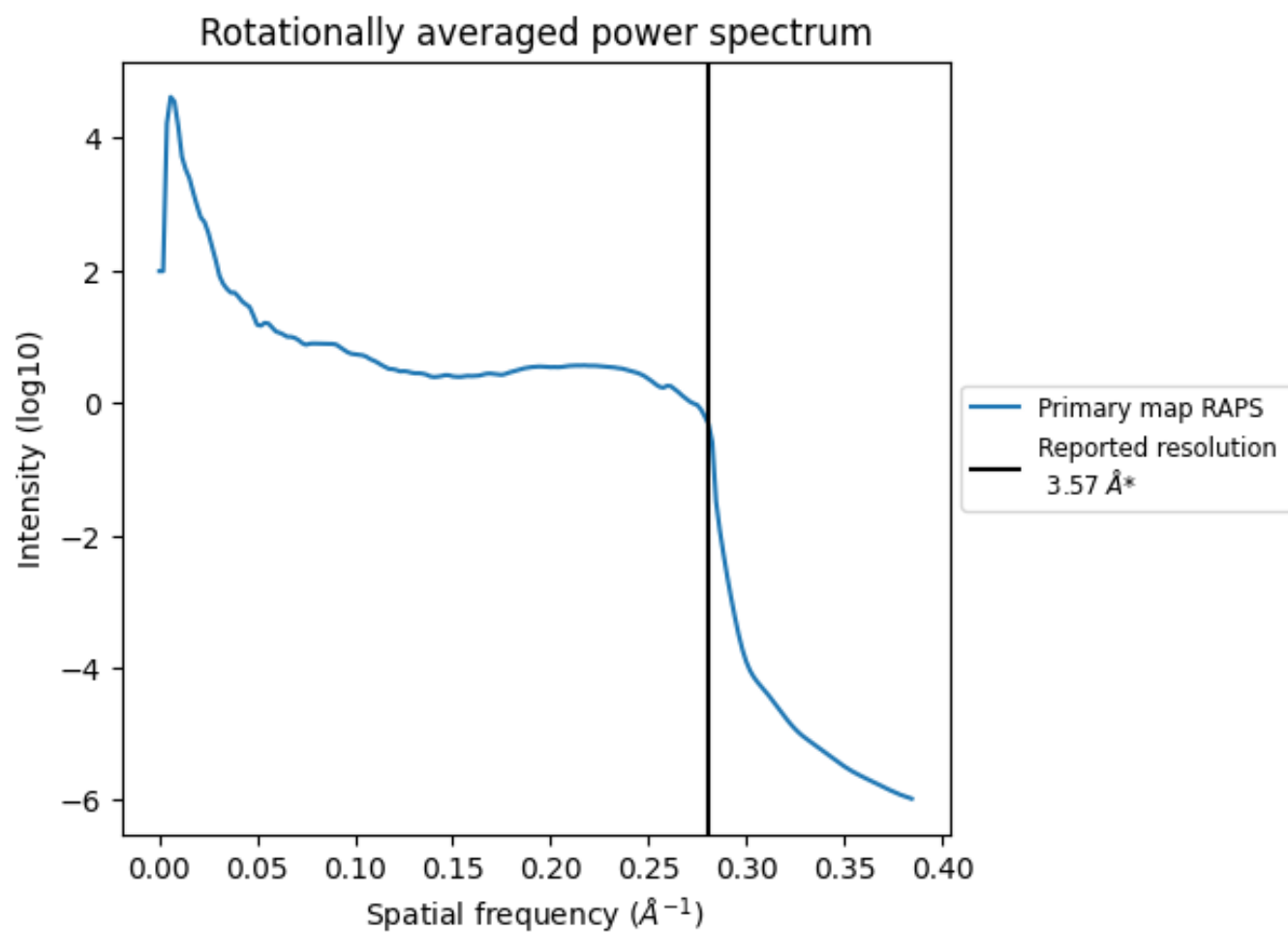
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 155 nm^3 ; this corresponds to an approximate mass of 140 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

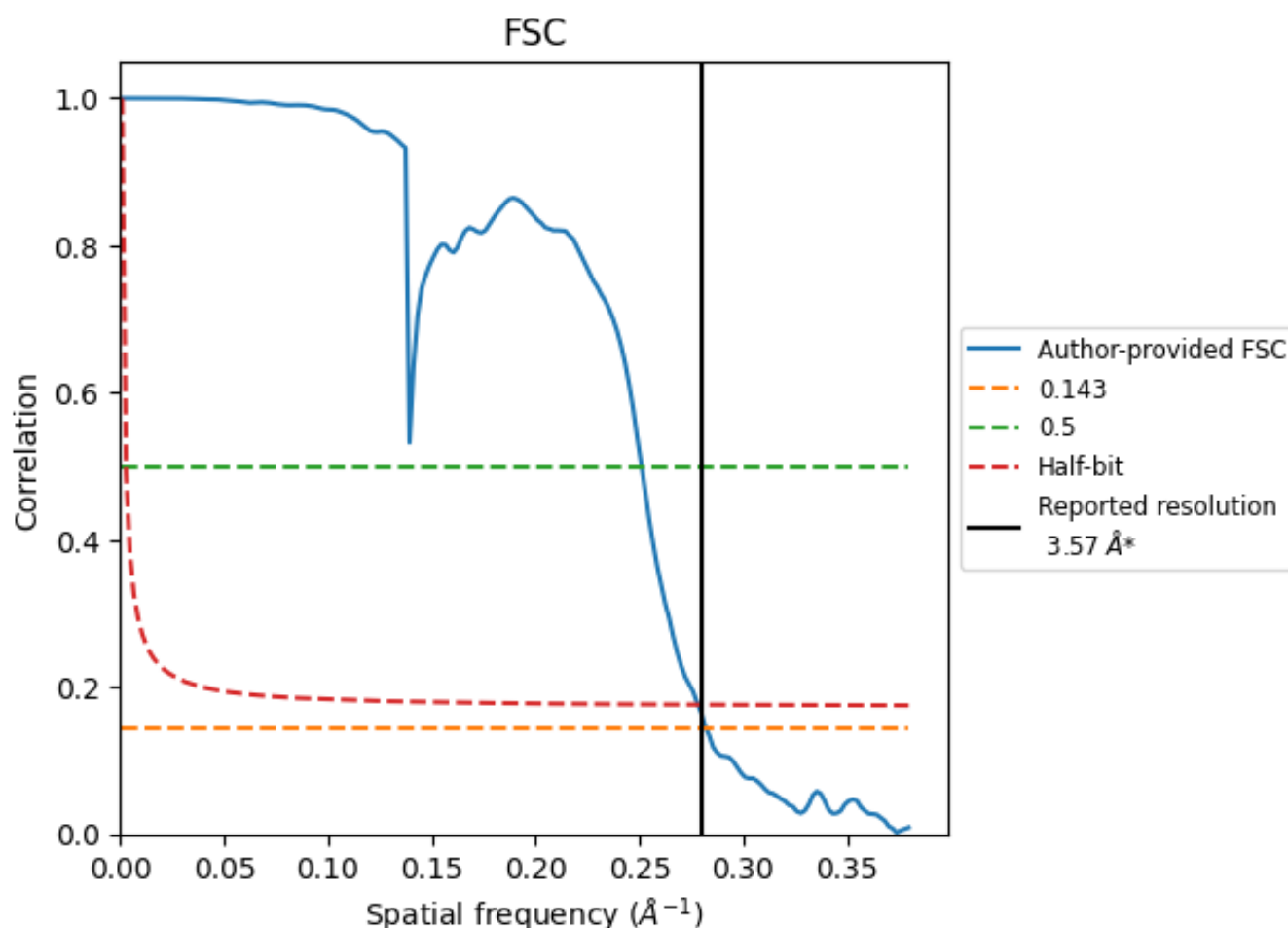


*Reported resolution corresponds to spatial frequency of 0.280 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.280 \AA^{-1}

8.2 Resolution estimates [i](#)

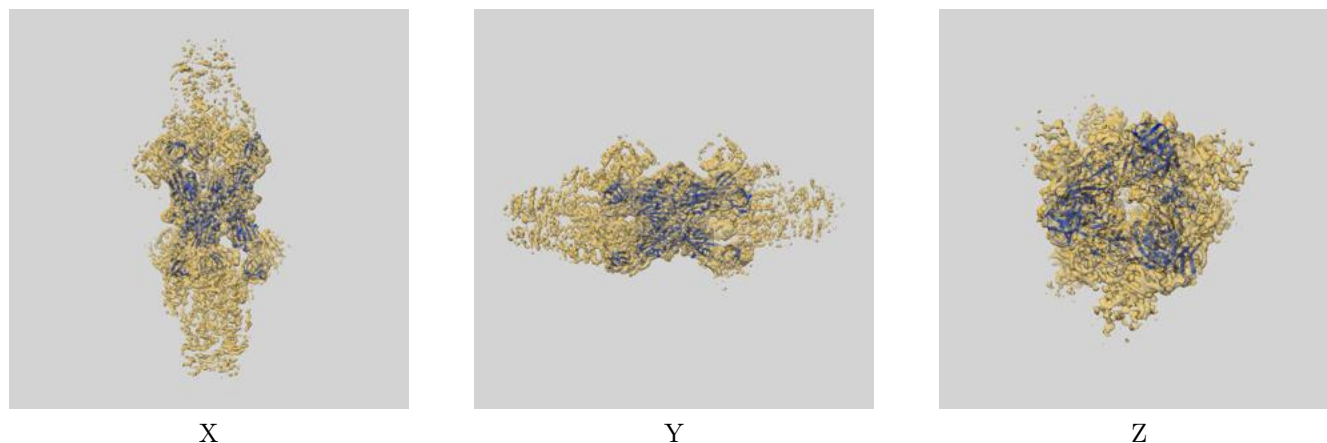
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.57	-	-
Author-provided FSC curve	3.54	3.98	3.59
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

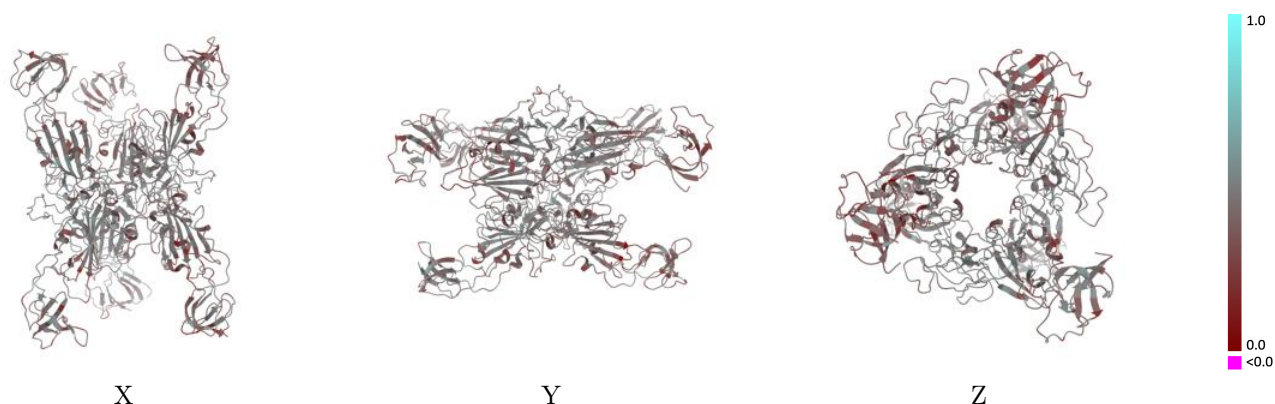
This section contains information regarding the fit between EMDB map EMD-25858 and PDB model 7TF1. Per-residue inclusion information can be found in section [3](#) on page [19](#).

9.1 Map-model overlay [i](#)



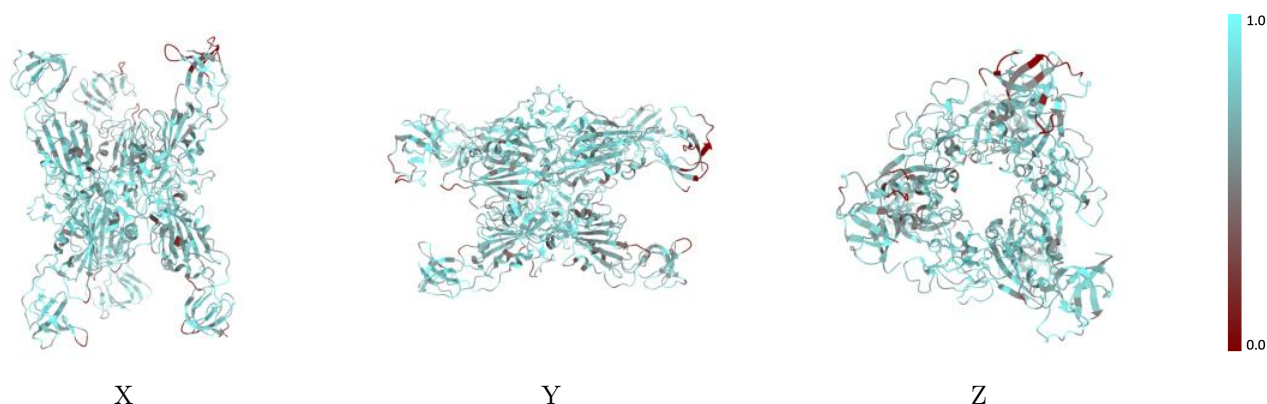
The images above show the 3D surface view of the map at the recommended contour level 0.24 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



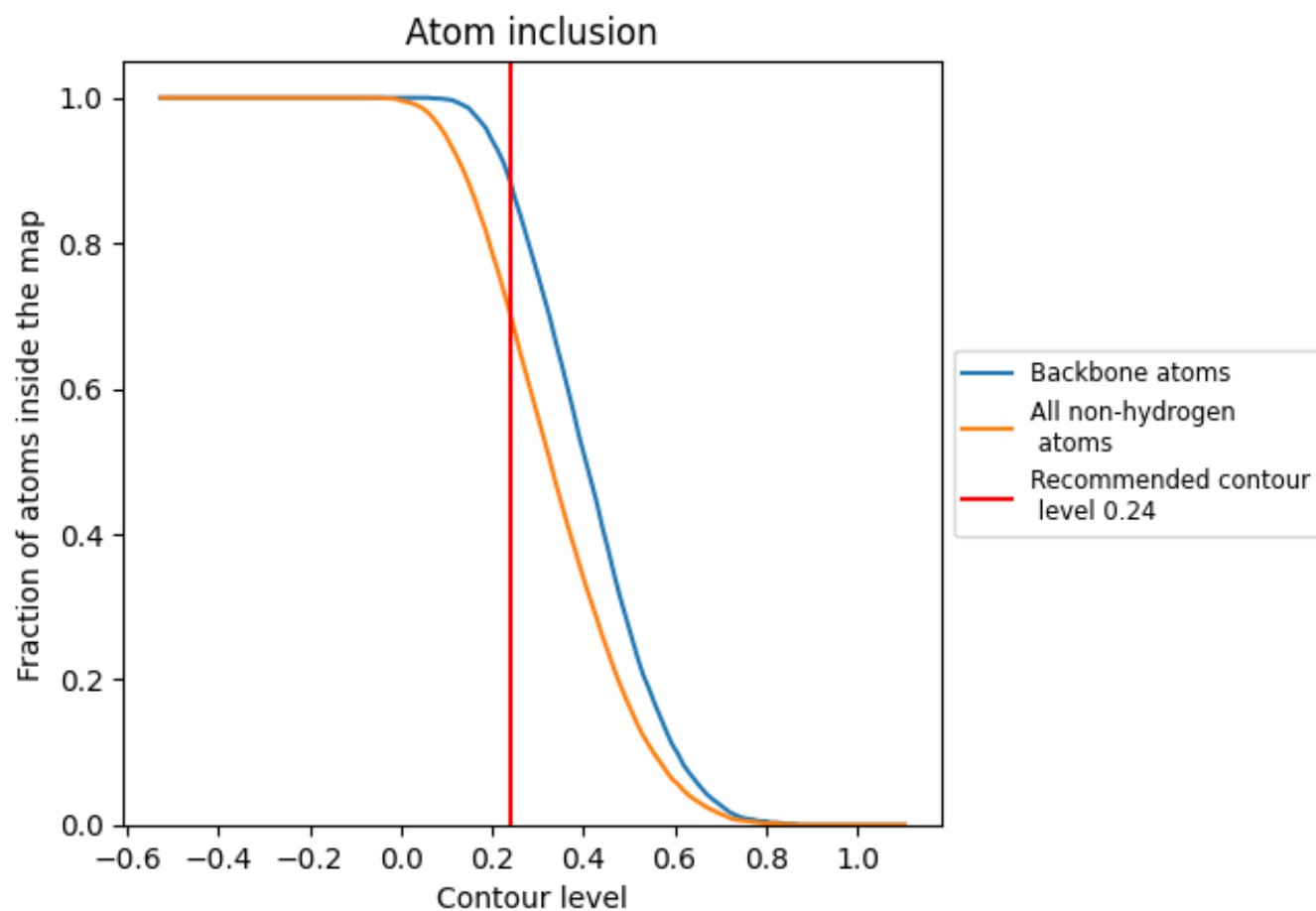
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.24).

9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 70% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.24) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div>0.7020</div>	<div><div></div>0.4170</div>
A	<div><div></div>0.7330</div>	<div><div></div>0.4320</div>
B	<div><div></div>0.6810</div>	<div><div></div>0.3970</div>
C	<div><div></div>0.7400</div>	<div><div></div>0.4370</div>
D	<div><div></div>0.6740</div>	<div><div></div>0.4130</div>
E	<div><div></div>0.7450</div>	<div><div></div>0.4430</div>
F	<div><div></div>0.6380</div>	<div><div></div>0.3780</div>

1.0

0.0

<0.0