



wwPDB EM Validation Summary Report ⓘ

Mar 10, 2026 – 12:29 AM UTC

PDB ID : 7FJN / pdb_00007fjn
EMDB ID : EMD-31624
Title : Cryo-EM structure of South African (B.1.351) SARS-CoV-2 spike glycoprotein
in complex with two T6 Fab
Authors : Wang, X.; Zhang, L.; Zhang, S.; Liang, Q.
Deposited on : 2021-08-04
Resolution : 3.25 Å(reported)

This is a wwPDB EM Validation Summary 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:

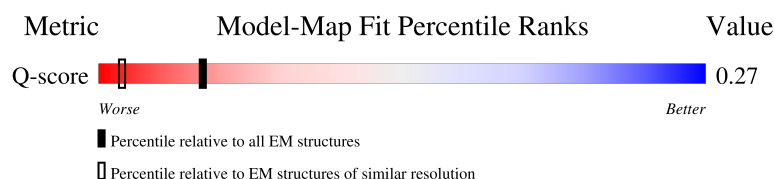
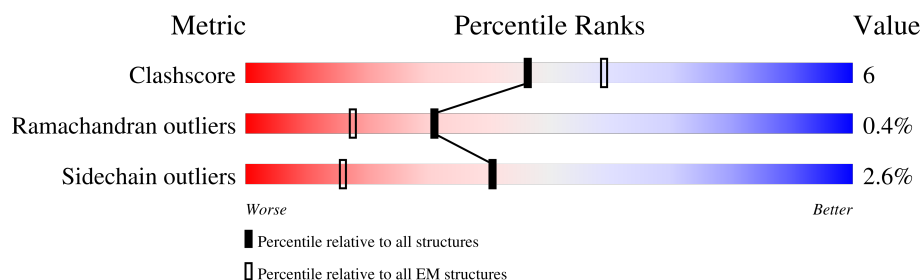
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

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 3.25 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14599 (2.75 - 3.75)

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	1280	 6% 73% 5% 22%
1	B	1280	 1% 73% 5% 22%
1	C	1280	 5% 73% 5% 22%
2	H	117	 61% 57% 32% 9%

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Mol	Chain	Length	Quality of chain
2	I	117	86% 60%29%9%
3	J	113	84% 65%29%5%
3	L	113	52% 65%28%5%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 26824 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,Envelope glycoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	993	Total	C	N	O	S	0	0
			7687	4917	1277	1458	35		
1	B	993	Total	C	N	O	S	0	0
			7691	4921	1277	1458	35		
1	C	992	Total	C	N	O	S	0	0
			7678	4916	1279	1448	35		

There are 237 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	18	PHE	LEU	variant	UNP P0DTC2
A	80	ALA	ASP	variant	UNP P0DTC2
A	215	GLY	ASP	variant	UNP P0DTC2
A	?	-	LEU	deletion	UNP P0DTC2
A	?	-	LEU	deletion	UNP P0DTC2
A	?	-	ALA	deletion	UNP P0DTC2
A	305	THR	SER	engineered mutation	UNP P0DTC2
A	417	ASN	LYS	variant	UNP P0DTC2
A	484	LYS	GLU	variant	UNP P0DTC2
A	501	TYR	ASN	variant	UNP P0DTC2
A	614	GLY	ASP	variant	UNP P0DTC2
A	682	GLY	ARG	engineered mutation	UNP P0DTC2
A	683	SER	ARG	engineered mutation	UNP P0DTC2
A	685	SER	ARG	engineered mutation	UNP P0DTC2
A	701	VAL	ALA	variant	UNP P0DTC2
A	986	PRO	LYS	engineered mutation	UNP P0DTC2
A	987	PRO	VAL	engineered mutation	UNP P0DTC2
A	1209	GLY	-	linker	UNP P0DTC2
A	1210	SER	-	linker	UNP P0DTC2
A	1239	ARG	-	expression tag	UNP M1E1E4
A	1240	SER	-	expression tag	UNP M1E1E4
A	1241	LEU	-	expression tag	UNP M1E1E4
A	1242	GLU	-	expression tag	UNP M1E1E4
A	1243	VAL	-	expression tag	UNP M1E1E4

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1244	LEU	-	expression tag	UNP M1E1E4
A	1245	PHE	-	expression tag	UNP M1E1E4
A	1246	GLN	-	expression tag	UNP M1E1E4
A	1247	GLY	-	expression tag	UNP M1E1E4
A	1248	PRO	-	expression tag	UNP M1E1E4
A	1249	GLY	-	expression tag	UNP M1E1E4
A	1250	HIS	-	expression tag	UNP M1E1E4
A	1251	HIS	-	expression tag	UNP M1E1E4
A	1252	HIS	-	expression tag	UNP M1E1E4
A	1253	HIS	-	expression tag	UNP M1E1E4
A	1254	HIS	-	expression tag	UNP M1E1E4
A	1255	HIS	-	expression tag	UNP M1E1E4
A	1256	HIS	-	expression tag	UNP M1E1E4
A	1257	HIS	-	expression tag	UNP M1E1E4
A	1258	SER	-	expression tag	UNP M1E1E4
A	1259	ALA	-	expression tag	UNP M1E1E4
A	1260	TRP	-	expression tag	UNP M1E1E4
A	1261	SER	-	expression tag	UNP M1E1E4
A	1262	HIS	-	expression tag	UNP M1E1E4
A	1263	PRO	-	expression tag	UNP M1E1E4
A	1264	GLN	-	expression tag	UNP M1E1E4
A	1265	PHE	-	expression tag	UNP M1E1E4
A	1266	GLU	-	expression tag	UNP M1E1E4
A	1267	LYS	-	expression tag	UNP M1E1E4
A	1268	GLY	-	expression tag	UNP M1E1E4
A	1269	GLY	-	expression tag	UNP M1E1E4
A	1270	GLY	-	expression tag	UNP M1E1E4
A	1271	SER	-	expression tag	UNP M1E1E4
A	1272	GLY	-	expression tag	UNP M1E1E4
A	1273	GLY	-	expression tag	UNP M1E1E4
A	1274	GLY	-	expression tag	UNP M1E1E4
A	1275	GLY	-	expression tag	UNP M1E1E4
A	1276	SER	-	expression tag	UNP M1E1E4
A	1277	GLY	-	expression tag	UNP M1E1E4
A	1278	GLY	-	expression tag	UNP M1E1E4
A	1279	SER	-	expression tag	UNP M1E1E4
A	1280	ALA	-	expression tag	UNP M1E1E4
A	1281	TRP	-	expression tag	UNP M1E1E4
A	1282	SER	-	expression tag	UNP M1E1E4
A	1283	HIS	-	expression tag	UNP M1E1E4
A	1284	PRO	-	expression tag	UNP M1E1E4
A	1285	GLN	-	expression tag	UNP M1E1E4

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1286	PHE	-	expression tag	UNP M1E1E4
A	1287	GLU	-	expression tag	UNP M1E1E4
A	1288	LYS	-	expression tag	UNP M1E1E4
A	1289	GLY	-	expression tag	UNP M1E1E4
A	1290	SER	-	expression tag	UNP M1E1E4
A	1291	ASP	-	expression tag	UNP M1E1E4
A	1292	TYR	-	expression tag	UNP M1E1E4
A	1293	LYS	-	expression tag	UNP M1E1E4
A	1294	ASP	-	expression tag	UNP M1E1E4
A	1295	ASP	-	expression tag	UNP M1E1E4
A	1296	ASP	-	expression tag	UNP M1E1E4
A	1297	ASP	-	expression tag	UNP M1E1E4
A	1298	LYS	-	expression tag	UNP M1E1E4
B	18	PHE	LEU	variant	UNP P0DTC2
B	80	ALA	ASP	variant	UNP P0DTC2
B	215	GLY	ASP	variant	UNP P0DTC2
B	?	-	LEU	deletion	UNP P0DTC2
B	?	-	LEU	deletion	UNP P0DTC2
B	?	-	ALA	deletion	UNP P0DTC2
B	305	THR	SER	engineered mutation	UNP P0DTC2
B	417	ASN	LYS	variant	UNP P0DTC2
B	484	LYS	GLU	variant	UNP P0DTC2
B	501	TYR	ASN	variant	UNP P0DTC2
B	614	GLY	ASP	variant	UNP P0DTC2
B	682	GLY	ARG	engineered mutation	UNP P0DTC2
B	683	SER	ARG	engineered mutation	UNP P0DTC2
B	685	SER	ARG	engineered mutation	UNP P0DTC2
B	701	VAL	ALA	variant	UNP P0DTC2
B	986	PRO	LYS	engineered mutation	UNP P0DTC2
B	987	PRO	VAL	engineered mutation	UNP P0DTC2
B	1209	GLY	-	linker	UNP P0DTC2
B	1210	SER	-	linker	UNP P0DTC2
B	1239	ARG	-	expression tag	UNP M1E1E4
B	1240	SER	-	expression tag	UNP M1E1E4
B	1241	LEU	-	expression tag	UNP M1E1E4
B	1242	GLU	-	expression tag	UNP M1E1E4
B	1243	VAL	-	expression tag	UNP M1E1E4
B	1244	LEU	-	expression tag	UNP M1E1E4
B	1245	PHE	-	expression tag	UNP M1E1E4
B	1246	GLN	-	expression tag	UNP M1E1E4
B	1247	GLY	-	expression tag	UNP M1E1E4
B	1248	PRO	-	expression tag	UNP M1E1E4

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1249	GLY	-	expression tag	UNP M1E1E4
B	1250	HIS	-	expression tag	UNP M1E1E4
B	1251	HIS	-	expression tag	UNP M1E1E4
B	1252	HIS	-	expression tag	UNP M1E1E4
B	1253	HIS	-	expression tag	UNP M1E1E4
B	1254	HIS	-	expression tag	UNP M1E1E4
B	1255	HIS	-	expression tag	UNP M1E1E4
B	1256	HIS	-	expression tag	UNP M1E1E4
B	1257	HIS	-	expression tag	UNP M1E1E4
B	1258	SER	-	expression tag	UNP M1E1E4
B	1259	ALA	-	expression tag	UNP M1E1E4
B	1260	TRP	-	expression tag	UNP M1E1E4
B	1261	SER	-	expression tag	UNP M1E1E4
B	1262	HIS	-	expression tag	UNP M1E1E4
B	1263	PRO	-	expression tag	UNP M1E1E4
B	1264	GLN	-	expression tag	UNP M1E1E4
B	1265	PHE	-	expression tag	UNP M1E1E4
B	1266	GLU	-	expression tag	UNP M1E1E4
B	1267	LYS	-	expression tag	UNP M1E1E4
B	1268	GLY	-	expression tag	UNP M1E1E4
B	1269	GLY	-	expression tag	UNP M1E1E4
B	1270	GLY	-	expression tag	UNP M1E1E4
B	1271	SER	-	expression tag	UNP M1E1E4
B	1272	GLY	-	expression tag	UNP M1E1E4
B	1273	GLY	-	expression tag	UNP M1E1E4
B	1274	GLY	-	expression tag	UNP M1E1E4
B	1275	GLY	-	expression tag	UNP M1E1E4
B	1276	SER	-	expression tag	UNP M1E1E4
B	1277	GLY	-	expression tag	UNP M1E1E4
B	1278	GLY	-	expression tag	UNP M1E1E4
B	1279	SER	-	expression tag	UNP M1E1E4
B	1280	ALA	-	expression tag	UNP M1E1E4
B	1281	TRP	-	expression tag	UNP M1E1E4
B	1282	SER	-	expression tag	UNP M1E1E4
B	1283	HIS	-	expression tag	UNP M1E1E4
B	1284	PRO	-	expression tag	UNP M1E1E4
B	1285	GLN	-	expression tag	UNP M1E1E4
B	1286	PHE	-	expression tag	UNP M1E1E4
B	1287	GLU	-	expression tag	UNP M1E1E4
B	1288	LYS	-	expression tag	UNP M1E1E4
B	1289	GLY	-	expression tag	UNP M1E1E4
B	1290	SER	-	expression tag	UNP M1E1E4

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1291	ASP	-	expression tag	UNP M1E1E4
B	1292	TYR	-	expression tag	UNP M1E1E4
B	1293	LYS	-	expression tag	UNP M1E1E4
B	1294	ASP	-	expression tag	UNP M1E1E4
B	1295	ASP	-	expression tag	UNP M1E1E4
B	1296	ASP	-	expression tag	UNP M1E1E4
B	1297	ASP	-	expression tag	UNP M1E1E4
B	1298	LYS	-	expression tag	UNP M1E1E4
C	18	PHE	LEU	variant	UNP P0DTC2
C	80	ALA	ASP	variant	UNP P0DTC2
C	215	GLY	ASP	variant	UNP P0DTC2
C	?	-	LEU	deletion	UNP P0DTC2
C	?	-	LEU	deletion	UNP P0DTC2
C	?	-	ALA	deletion	UNP P0DTC2
C	305	THR	SER	engineered mutation	UNP P0DTC2
C	417	ASN	LYS	variant	UNP P0DTC2
C	484	LYS	GLU	variant	UNP P0DTC2
C	501	TYR	ASN	variant	UNP P0DTC2
C	614	GLY	ASP	variant	UNP P0DTC2
C	682	GLY	ARG	engineered mutation	UNP P0DTC2
C	683	SER	ARG	engineered mutation	UNP P0DTC2
C	685	SER	ARG	engineered mutation	UNP P0DTC2
C	701	VAL	ALA	variant	UNP P0DTC2
C	986	PRO	LYS	engineered mutation	UNP P0DTC2
C	987	PRO	VAL	engineered mutation	UNP P0DTC2
C	1209	GLY	-	linker	UNP P0DTC2
C	1210	SER	-	linker	UNP P0DTC2
C	1239	ARG	-	expression tag	UNP M1E1E4
C	1240	SER	-	expression tag	UNP M1E1E4
C	1241	LEU	-	expression tag	UNP M1E1E4
C	1242	GLU	-	expression tag	UNP M1E1E4
C	1243	VAL	-	expression tag	UNP M1E1E4
C	1244	LEU	-	expression tag	UNP M1E1E4
C	1245	PHE	-	expression tag	UNP M1E1E4
C	1246	GLN	-	expression tag	UNP M1E1E4
C	1247	GLY	-	expression tag	UNP M1E1E4
C	1248	PRO	-	expression tag	UNP M1E1E4
C	1249	GLY	-	expression tag	UNP M1E1E4
C	1250	HIS	-	expression tag	UNP M1E1E4
C	1251	HIS	-	expression tag	UNP M1E1E4
C	1252	HIS	-	expression tag	UNP M1E1E4
C	1253	HIS	-	expression tag	UNP M1E1E4

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1254	HIS	-	expression tag	UNP M1E1E4
C	1255	HIS	-	expression tag	UNP M1E1E4
C	1256	HIS	-	expression tag	UNP M1E1E4
C	1257	HIS	-	expression tag	UNP M1E1E4
C	1258	SER	-	expression tag	UNP M1E1E4
C	1259	ALA	-	expression tag	UNP M1E1E4
C	1260	TRP	-	expression tag	UNP M1E1E4
C	1261	SER	-	expression tag	UNP M1E1E4
C	1262	HIS	-	expression tag	UNP M1E1E4
C	1263	PRO	-	expression tag	UNP M1E1E4
C	1264	GLN	-	expression tag	UNP M1E1E4
C	1265	PHE	-	expression tag	UNP M1E1E4
C	1266	GLU	-	expression tag	UNP M1E1E4
C	1267	LYS	-	expression tag	UNP M1E1E4
C	1268	GLY	-	expression tag	UNP M1E1E4
C	1269	GLY	-	expression tag	UNP M1E1E4
C	1270	GLY	-	expression tag	UNP M1E1E4
C	1271	SER	-	expression tag	UNP M1E1E4
C	1272	GLY	-	expression tag	UNP M1E1E4
C	1273	GLY	-	expression tag	UNP M1E1E4
C	1274	GLY	-	expression tag	UNP M1E1E4
C	1275	GLY	-	expression tag	UNP M1E1E4
C	1276	SER	-	expression tag	UNP M1E1E4
C	1277	GLY	-	expression tag	UNP M1E1E4
C	1278	GLY	-	expression tag	UNP M1E1E4
C	1279	SER	-	expression tag	UNP M1E1E4
C	1280	ALA	-	expression tag	UNP M1E1E4
C	1281	TRP	-	expression tag	UNP M1E1E4
C	1282	SER	-	expression tag	UNP M1E1E4
C	1283	HIS	-	expression tag	UNP M1E1E4
C	1284	PRO	-	expression tag	UNP M1E1E4
C	1285	GLN	-	expression tag	UNP M1E1E4
C	1286	PHE	-	expression tag	UNP M1E1E4
C	1287	GLU	-	expression tag	UNP M1E1E4
C	1288	LYS	-	expression tag	UNP M1E1E4
C	1289	GLY	-	expression tag	UNP M1E1E4
C	1290	SER	-	expression tag	UNP M1E1E4
C	1291	ASP	-	expression tag	UNP M1E1E4
C	1292	TYR	-	expression tag	UNP M1E1E4
C	1293	LYS	-	expression tag	UNP M1E1E4
C	1294	ASP	-	expression tag	UNP M1E1E4
C	1295	ASP	-	expression tag	UNP M1E1E4

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1296	ASP	-	expression tag	UNP M1E1E4
C	1297	ASP	-	expression tag	UNP M1E1E4
C	1298	LYS	-	expression tag	UNP M1E1E4

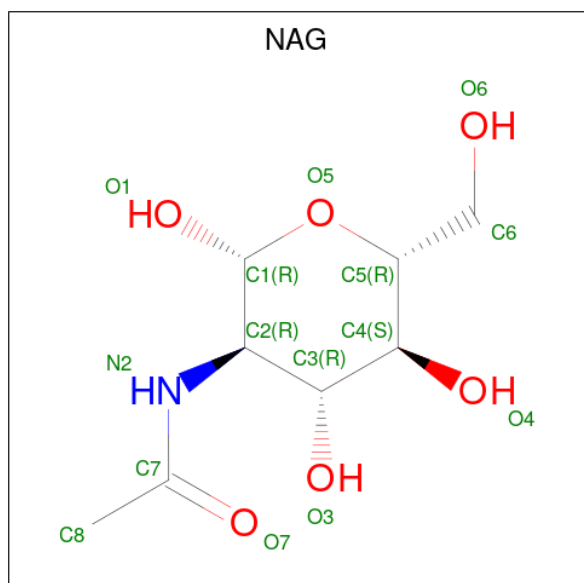
- Molecule 2 is a protein called T6 heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	H	107	Total	C	N	O	S	0	0
			823	517	132	170	4		
2	I	107	Total	C	N	O	S	0	0
			823	517	132	170	4		

- Molecule 3 is a protein called T6 light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	J	113	Total	C	N	O	S	0	0
			886	564	146	174	2		
3	L	113	Total	C	N	O	S	0	0
			886	564	146	174	2		

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				AltConf
4	A	1	Total	C	N	O	0
			14	8	1	5	

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

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Mol	Chain	Residues	Atoms				AltConf
4	C	1	Total	C	N	O	0
			14	8	1	5	
4	C	1	Total	C	N	O	0
			14	8	1	5	
4	C	1	Total	C	N	O	0
			14	8	1	5	

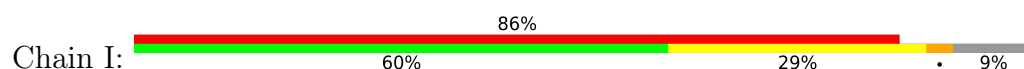
LYS	LEU	GLY	ILE	ASP	LEU	ARG	LEU	ASN	GLY	VAL	GLY	ALA	LYS	ASN	LEU	ASN	GLY	SER	HIS	LEU	ILE	SER	ALA	ASP	LEU	GLN	HIS	LEU	PRO	GLY	GLY	GLY	LYS	TYR	GLY	GLN	GLY	GLY	SER	GLY	TYR	ILE	GLY	PRO	ALA	SER	GLY	PRO	ARG	ASP	GLY	ALA	GLY	TRP	SER	ALA	TYR	VAL	ARG	VAL	ASP	LYS	GLY	GLY	LEU	ASP	THR	ASP	LEU	GLY	ARG	SER
LEU	VAL	LEU	PHE	GLN	GLY	PRO	GLY	THR	GLY	L11	V12	N13	P14	G15	A16	S17	L18	K19	M20	S21	C22	Y32	I33	I34	H35	W36	V37	K38	Q39	T40	F41	G42	Q43	G44	L45	E46	W47	T48	G49	A50	I51	F52	P53	E54	N55	D56	D57	T58	S59	Y60	S61	Q62	F63	K65	G66	K67	A68															

• Molecule 2: T6 heavy chain



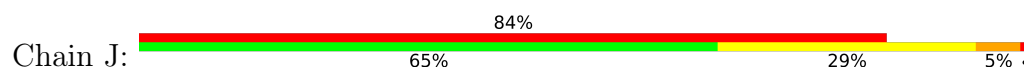
T69	L70	T71	T72	D73	T74	S75	S76	S77	T78	A79	Y80	H81	G82	L83	S84	S85	L86	T87	S88	E89	D90	S91	A92	W93	Y94	Y95	C96	A97	R98	M102	V103	L104	D105	Y106	W107	G108	Q109	G110	T111	S112	V113	T114	V115	S116	S117																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																				

• Molecule 2: T6 heavy chain



GLN																															VAL			GLN			LEU			GLN			GLN			PRO			GLY			THR			GLU			L11			V12			M13			P14			G15			A16			S17			L18			K19			M20			S21			C22			K23			T24			S25			G26			Y27			R28			F29			T30			S31			Y32			I33			I34			H35			K36			V37			K38			Q39			T40			F41			G42			Q43			G44			L45			I48			G49			A50			W51			F52			P53			N54			E54			M55			D56			D57			T58			S59			Y60			S61		
Q62																															K63			F64			K65			G66			K67			A68			T69			L70			T71			T72			D73			T74			S75			S76			S77			T78			A79			Y80			H81			Q82			L83			S84			S85			L86			T87			S88			E89			D90			S91			A92			V93			Y94			Y95			C96			A97			R98			D99			G100			E101			N102			V103			M104			D105			Y106			W107			G108			Q109			G110			T111			S112			V113			T114			V115			S116			S117														

• Molecule 3: T6 light chain



Q1	I2	V3	L4	T5	Q6	S7	P8	S9	S10	L11	A12	V13	S14	V15	G16	E17	K18	V19	T20	L21	S22	C23	K24	S25	S26	Q27	S28	L29	L30	Y31	S32	N33	N34	Q35	K36	N37	Y38	Q39	Q43	Q44	K45	S46	K47	R48	S49	P50	K51	L52	L53	H54	H55	W56	T57	S58	T59	R60	E61	S62	G63
V64	P65	D66	R67	T68	F69	G70	S71	G72	S73	G74	T75	D76	F77	T78	L79	T80	I81	S82	S83	V84	K85	A86	E87	D88	L89	A90	V91	Y92	Y93	C94	Q95	Y96	Y97	Y98	T99	Y100	F101	F104	G105	G106	G107	T108	K109	L110	E111	I112	K113												

• Molecule 3: T6 light chain



Q1	I2	V3	L4	T5	Q6	S7	P8	S9	S10	L11	A12	V13	S14	V15	G16	E17	K18	V19	T20	L21	S22	C23	K24	S25	S26	Q27	S28	L29	L30	Y31	S32	N33	N34	Q35	Y38	Q43	Q44	K45	S46	K47	R48	L53	L54	H55	W56	T57	V64	S73	G74	T75	D76	F77	S83
A86	L89	A90	V91	Y92	Y93	C94	Q95	Q96	Y97	Y98	T99	Y100	P101	W102	T103	F104	G105	G106	G107	T108	K109	L110	E111	I112	K113																												

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	286245	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.058	Depositor
Minimum map value	-0.018	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.007	Depositor
Map size ($\text{\AA}$)	351.328, 351.328, 351.328	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.0979, 1.0979, 1.0979	Depositor

5 Model quality

5.1 Standard geometry

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	0.67	0/7858	1.08	4/10696 (0.0%)
1	B	0.68	0/7864	1.10	11/10706 (0.1%)
1	C	0.67	0/7853	1.08	4/10696 (0.0%)
2	H	1.02	0/842	1.17	0/1144
2	I	1.02	0/842	1.17	0/1144
3	J	1.05	1/907 (0.1%)	1.15	1/1231 (0.1%)
3	L	1.05	1/907 (0.1%)	1.15	1/1231 (0.1%)
All	All	0.73	2/27073 (0.0%)	1.10	21/36848 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
1	B	0	1
3	J	0	1
3	L	0	1
All	All	0	5

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	L	106	GLY	CA-C	7.30	1.63	1.52
3	J	106	GLY	CA-C	7.29	1.62	1.52

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	527	PRO	N-CA-C	7.17	121.81	111.13
1	C	986	PRO	N-CA-C	6.53	118.66	110.70
3	L	106	GLY	N-CA-C	-6.09	104.09	112.25
3	J	106	GLY	N-CA-C	-6.09	104.09	112.25
1	B	986	PRO	N-CA-C	6.05	118.08	110.70

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	332	ILE	Peptide
1	A	34	ARG	Sidechain
1	B	577	ARG	Sidechain
3	J	106	GLY	Mainchain
3	L	106	GLY	Mainchain

5.2 Too-close contacts ⓘ

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	7687	0	7472	84	0
1	B	7691	0	7484	89	0
1	C	7678	0	7478	51	0
2	H	823	0	779	43	0
2	I	823	0	779	33	0
3	J	886	0	872	57	0
3	L	886	0	872	58	0
4	A	112	0	104	0	0
4	B	112	0	104	0	0
4	C	126	0	117	0	0
All	All	26824	0	26061	321	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 6.

The worst 5 of 321 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:A:521:PRO:CG	1:B:230:PRO:HB2	1.18	1.62
1:C:498:GLN:CB	1:C:501:TYR:CE2	1.75	1.60
1:B:456:PHE:CZ	2:H:54:GLU:HG2	1.32	1.59
1:A:521:PRO:HG2	1:B:230:PRO:CB	1.14	1.58
1:A:498:GLN:HB2	1:A:501:TYR:CE2	1.42	1.52

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	975/1280 (76%)	893 (92%)	78 (8%)	4 (0%)	30	59
1	B	975/1280 (76%)	891 (91%)	80 (8%)	4 (0%)	30	59
1	C	976/1280 (76%)	899 (92%)	74 (8%)	3 (0%)	36	66
2	H	105/117 (90%)	97 (92%)	8 (8%)	0	100	100
2	I	105/117 (90%)	97 (92%)	8 (8%)	0	100	100
3	J	111/113 (98%)	108 (97%)	2 (2%)	1 (1%)	14	42
3	L	111/113 (98%)	108 (97%)	2 (2%)	1 (1%)	14	42
All	All	3358/4300 (78%)	3093 (92%)	252 (8%)	13 (0%)	31	59

5 of 13 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	986	PRO
1	A	197	ILE
1	C	112	SER
1	B	137	ASN
1	B	334	ASN

5.3.2 Protein sidechains ⓘ

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	849/1103 (77%)	839 (99%)	10 (1%)	63	74
1	B	851/1103 (77%)	847 (100%)	4 (0%)	81	82
1	C	848/1103 (77%)	842 (99%)	6 (1%)	76	79
2	H	92/101 (91%)	76 (83%)	16 (17%)	2	8
2	I	92/101 (91%)	75 (82%)	17 (18%)	1	7
3	J	100/100 (100%)	88 (88%)	12 (12%)	5	20
3	L	100/100 (100%)	88 (88%)	12 (12%)	5	20
All	All	2932/3711 (79%)	2855 (97%)	77 (3%)	41	62

5 of 77 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	J	55	HIS
3	L	64	VAL
3	J	64	VAL
3	L	15	VAL
3	L	111	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 58 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	804	GLN
2	I	82	GLN
1	C	188	ASN
2	H	102	ASN
1	C	1002	GLN

5.3.3 RNA ⓘ

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](#)

25 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	$\# Z > 2$
4	NAG	A	1302	1	14,14,15	0.29	0	17,19,21	0.73	0
4	NAG	C	1302	1	14,14,15	0.31	0	17,19,21	0.72	0
4	NAG	B	1307	1	14,14,15	0.29	0	17,19,21	0.69	0
4	NAG	C	1301	1	14,14,15	0.28	0	17,19,21	0.57	0
4	NAG	B	1304	1	14,14,15	0.27	0	17,19,21	0.55	0
4	NAG	A	1301	1	14,14,15	0.28	0	17,19,21	1.05	1 (5%)
4	NAG	B	1306	1	14,14,15	0.26	0	17,19,21	0.98	1 (5%)
4	NAG	B	1303	1	14,14,15	0.29	0	17,19,21	0.65	0
4	NAG	B	1305	1	14,14,15	0.25	0	17,19,21	0.98	1 (5%)
4	NAG	C	1309	1	14,14,15	0.29	0	17,19,21	0.62	0
4	NAG	B	1308	1	14,14,15	0.30	0	17,19,21	0.53	0
4	NAG	C	1306	1	14,14,15	0.26	0	17,19,21	1.01	1 (5%)
4	NAG	C	1303	1	14,14,15	0.28	0	17,19,21	1.15	2 (11%)
4	NAG	C	1304	1	14,14,15	0.25	0	17,19,21	0.58	0
4	NAG	B	1302	1	14,14,15	0.25	0	17,19,21	0.97	1 (5%)
4	NAG	A	1304	1	14,14,15	0.28	0	17,19,21	0.53	0
4	NAG	C	1307	1	14,14,15	0.28	0	17,19,21	0.48	0
4	NAG	A	1305	1	14,14,15	0.28	0	17,19,21	0.67	0
4	NAG	A	1303	1	14,14,15	0.27	0	17,19,21	0.59	0
4	NAG	A	1306	1	14,14,15	0.28	0	17,19,21	0.65	0
4	NAG	B	1301	1	14,14,15	0.27	0	17,19,21	0.63	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NAG	A	1308	1	14,14,15	0.30	0	17,19,21	0.68	1 (5%)
4	NAG	A	1307	1	14,14,15	0.29	0	17,19,21	0.66	0
4	NAG	C	1305	1	14,14,15	0.28	0	17,19,21	0.57	0
4	NAG	C	1308	1	14,14,15	0.30	0	17,19,21	1.17	2 (11%)

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
4	NAG	A	1302	1	-	2/6/23/26	0/1/1/1
4	NAG	C	1302	1	-	0/6/23/26	0/1/1/1
4	NAG	B	1307	1	-	2/6/23/26	0/1/1/1
4	NAG	C	1301	1	-	3/6/23/26	0/1/1/1
4	NAG	B	1304	1	-	1/6/23/26	0/1/1/1
4	NAG	A	1301	1	-	4/6/23/26	0/1/1/1
4	NAG	B	1306	1	-	3/6/23/26	0/1/1/1
4	NAG	B	1303	1	-	1/6/23/26	0/1/1/1
4	NAG	B	1305	1	-	4/6/23/26	0/1/1/1
4	NAG	C	1309	1	-	0/6/23/26	0/1/1/1
4	NAG	B	1308	1	-	0/6/23/26	0/1/1/1
4	NAG	C	1306	1	-	4/6/23/26	0/1/1/1
4	NAG	C	1303	1	-	4/6/23/26	0/1/1/1
4	NAG	C	1304	1	-	2/6/23/26	0/1/1/1
4	NAG	B	1302	1	-	4/6/23/26	0/1/1/1
4	NAG	A	1304	1	-	1/6/23/26	0/1/1/1
4	NAG	C	1307	1	-	3/6/23/26	0/1/1/1
4	NAG	A	1305	1	-	1/6/23/26	0/1/1/1
4	NAG	A	1303	1	-	1/6/23/26	0/1/1/1
4	NAG	A	1306	1	-	0/6/23/26	0/1/1/1
4	NAG	B	1301	1	-	2/6/23/26	0/1/1/1
4	NAG	A	1308	1	-	1/6/23/26	0/1/1/1
4	NAG	A	1307	1	-	2/6/23/26	0/1/1/1
4	NAG	C	1305	1	-	1/6/23/26	0/1/1/1
4	NAG	C	1308	1	-	4/6/23/26	0/1/1/1

There are no bond length outliers.

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1301	NAG	C2-N2-C7	3.18	127.17	122.90
4	C	1303	NAG	C2-N2-C7	2.78	126.62	122.90
4	C	1308	NAG	C2-N2-C7	2.74	126.57	122.90
4	C	1308	NAG	C1-O5-C5	2.69	115.80	112.19
4	B	1302	NAG	C2-N2-C7	2.45	126.18	122.90

There are no chirality outliers.

5 of 50 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1301	NAG	C1-C2-N2-C7
4	A	1301	NAG	C8-C7-N2-C2
4	A	1301	NAG	O7-C7-N2-C2
4	A	1302	NAG	C8-C7-N2-C2
4	A	1302	NAG	O7-C7-N2-C2

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

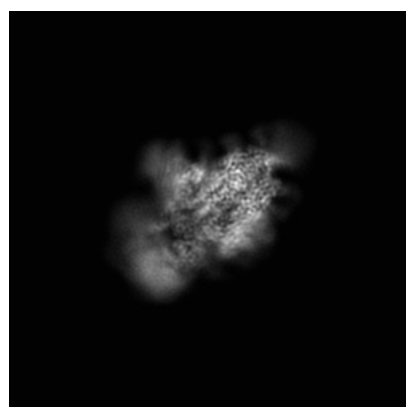
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-31624. These allow visual inspection of the internal detail of the map and identification of artifacts.

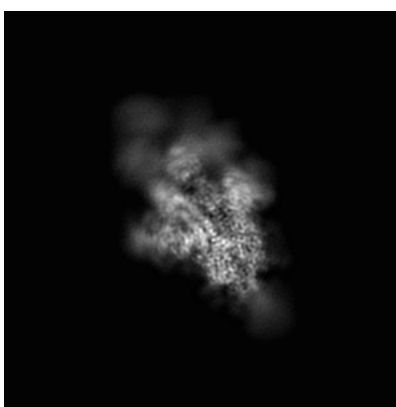
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

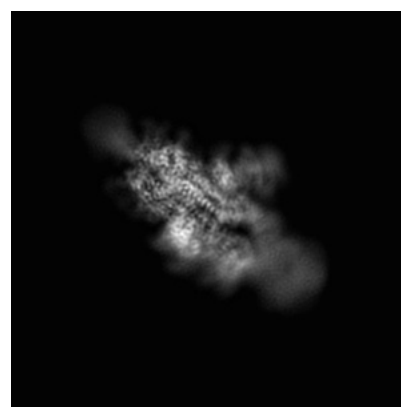
6.1.1 Primary map



X



Y

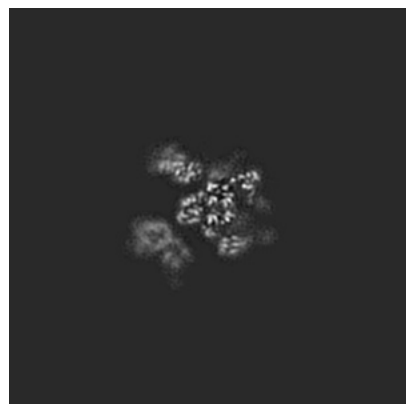


Z

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

6.2 Central slices [i](#)

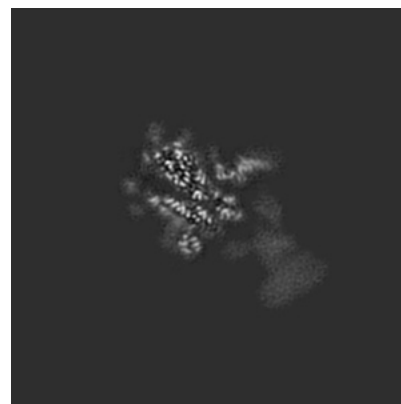
6.2.1 Primary map



X Index: 160



Y Index: 160

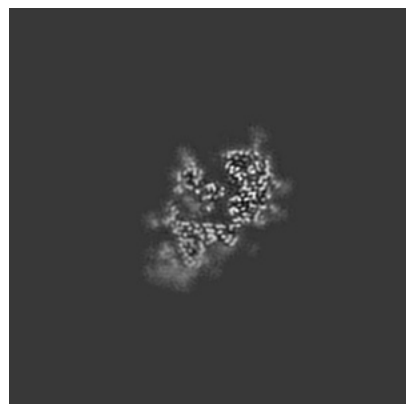


Z Index: 160

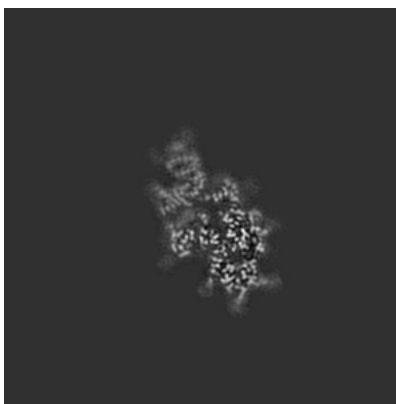
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

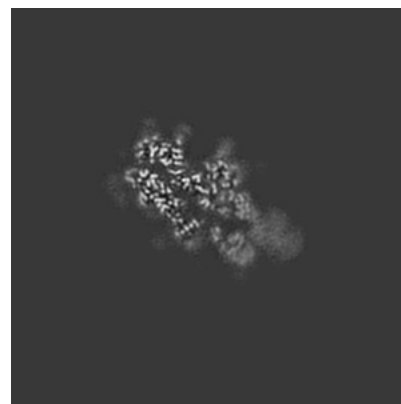
6.3.1 Primary map



X Index: 135



Y Index: 182

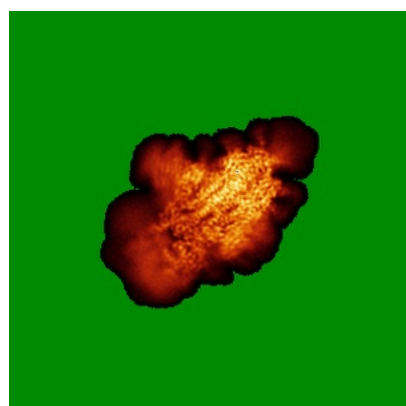


Z Index: 180

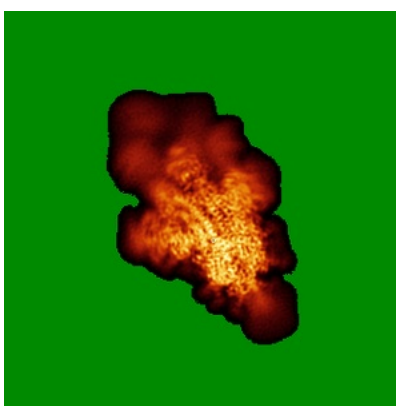
The images above show the largest variance slices of the map in three orthogonal directions.

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

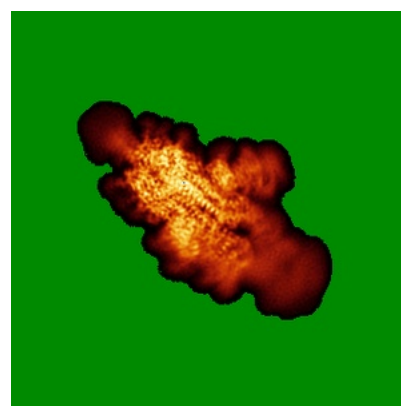
6.4.1 Primary map



X



Y

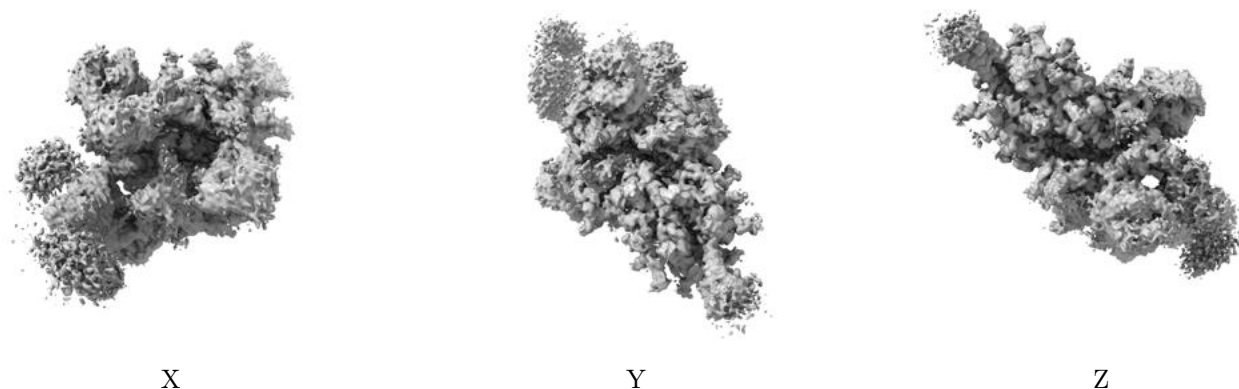


Z

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 0.007. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

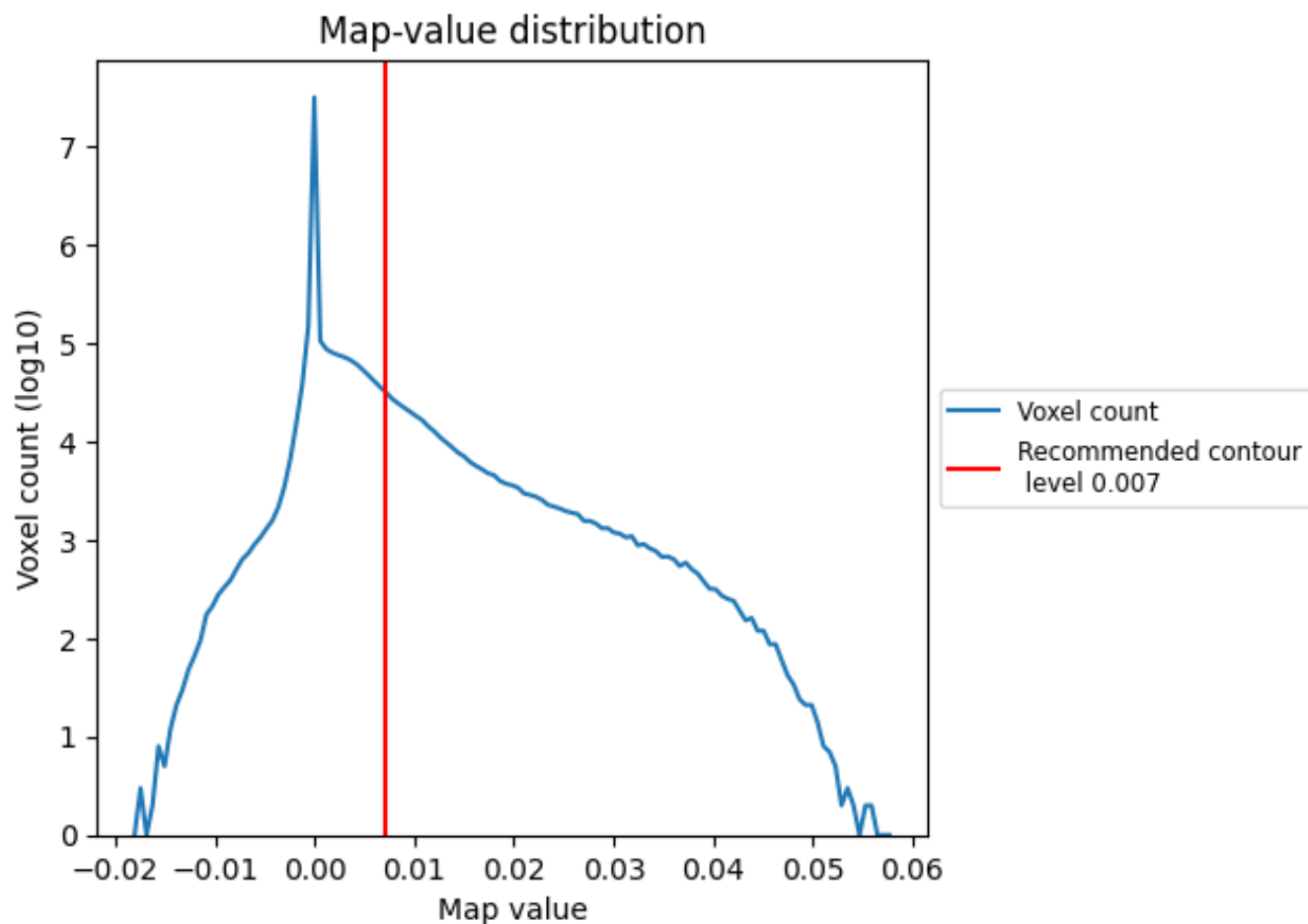
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

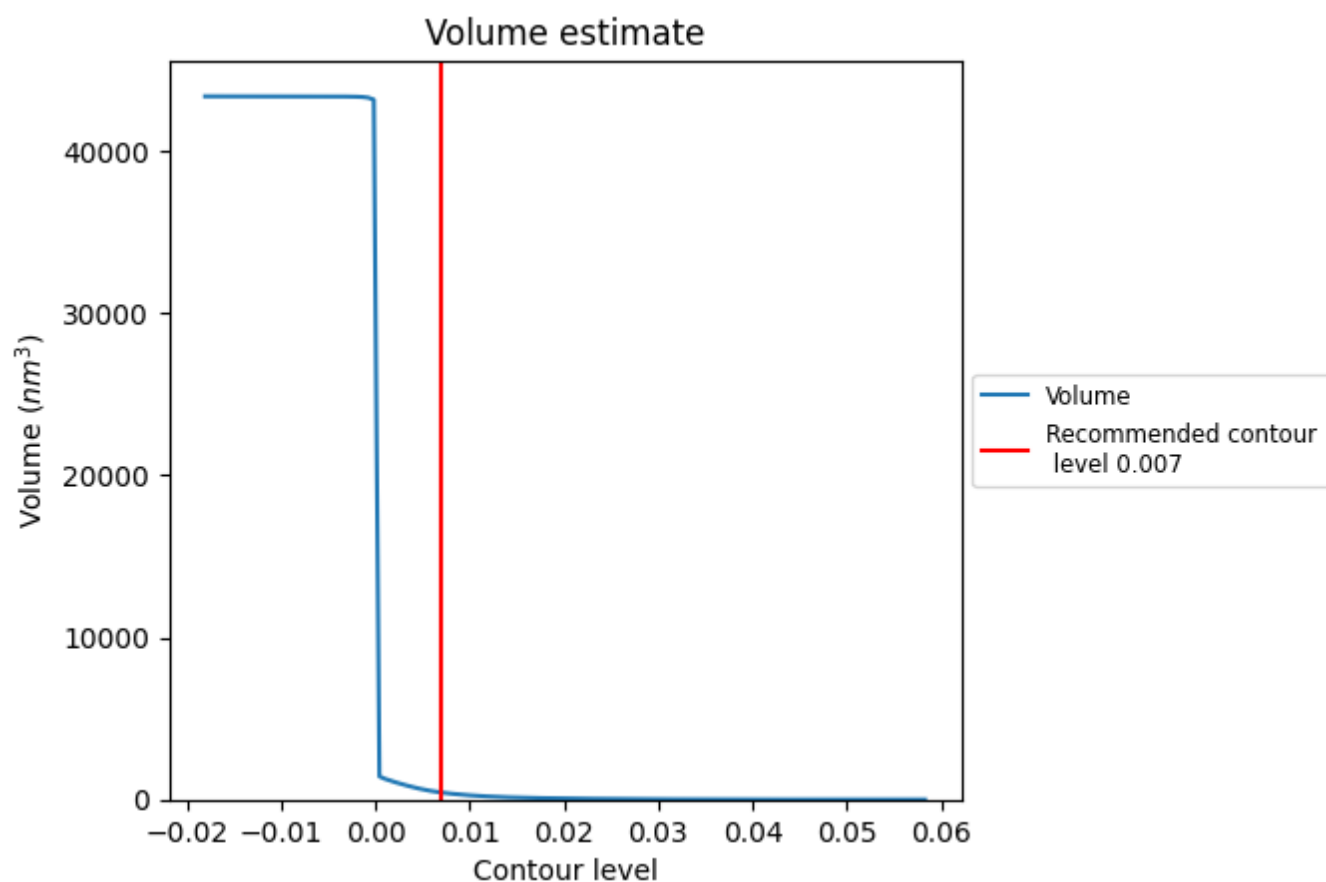
This section contains the results of statistical analysis of the map.

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.

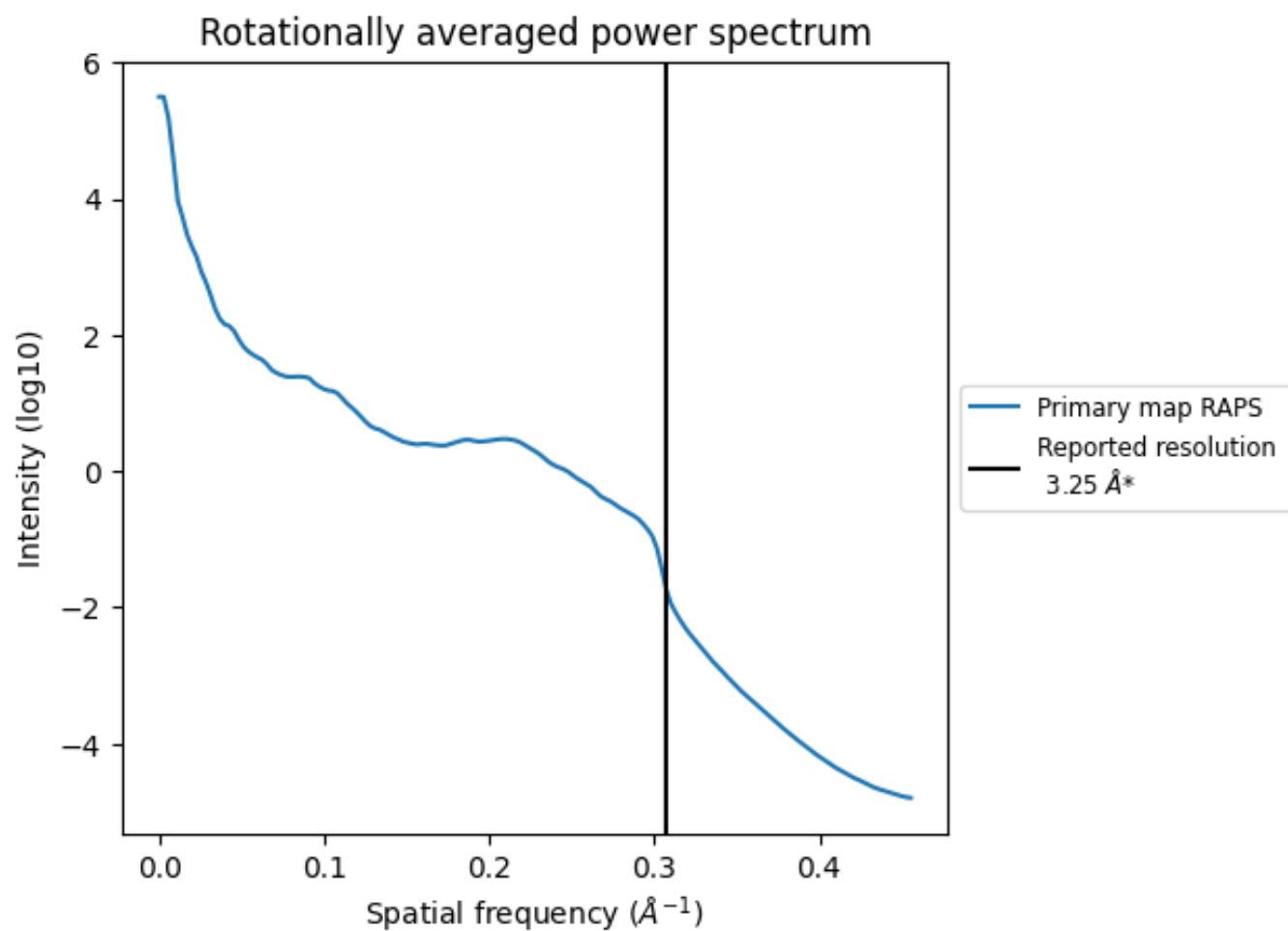
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 433 nm³; this corresponds to an approximate mass of 391 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 0.308 Å⁻¹

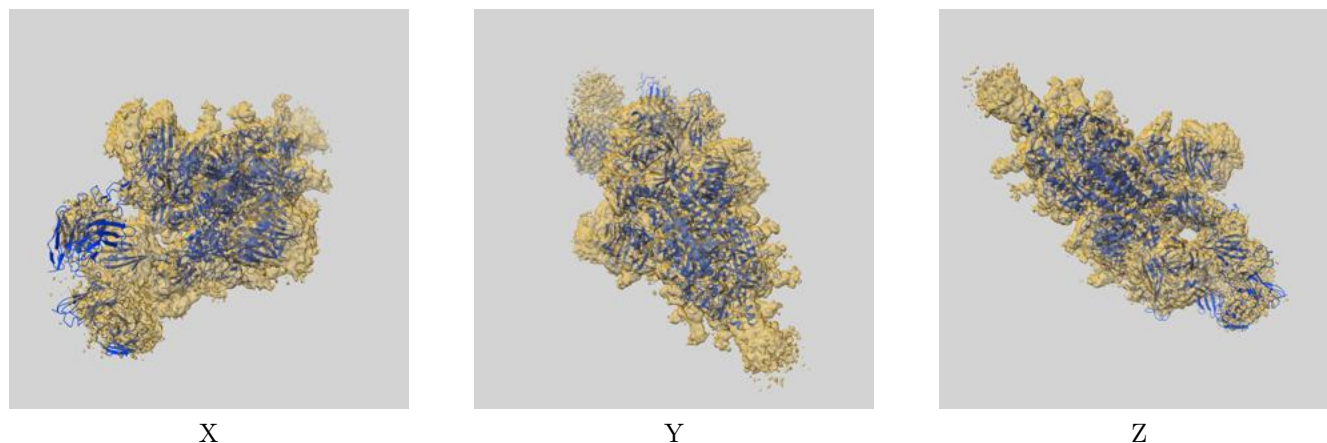
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

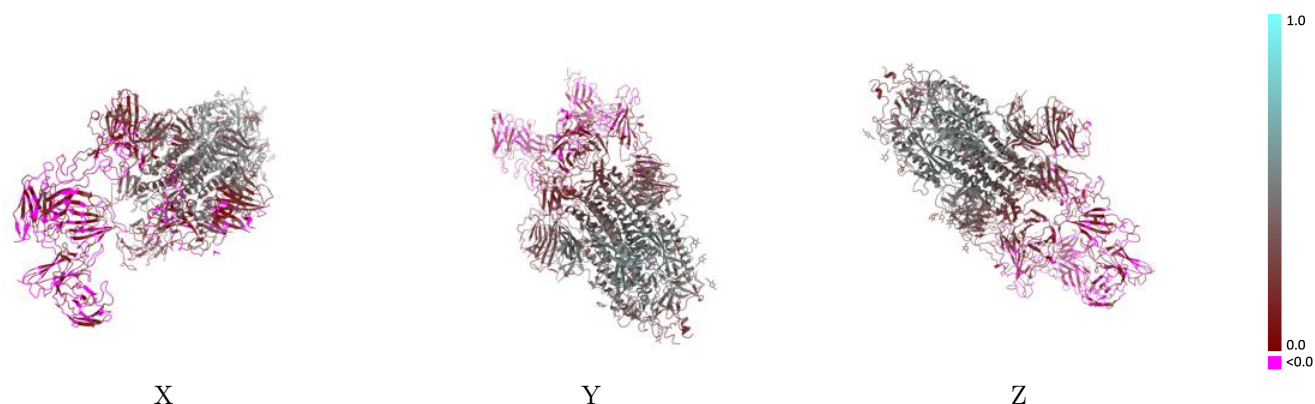
This section contains information regarding the fit between EMDB map EMD-31624 and PDB model 7FJN. Per-residue inclusion information can be found in section [3](#) on page [13](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.007 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](#)



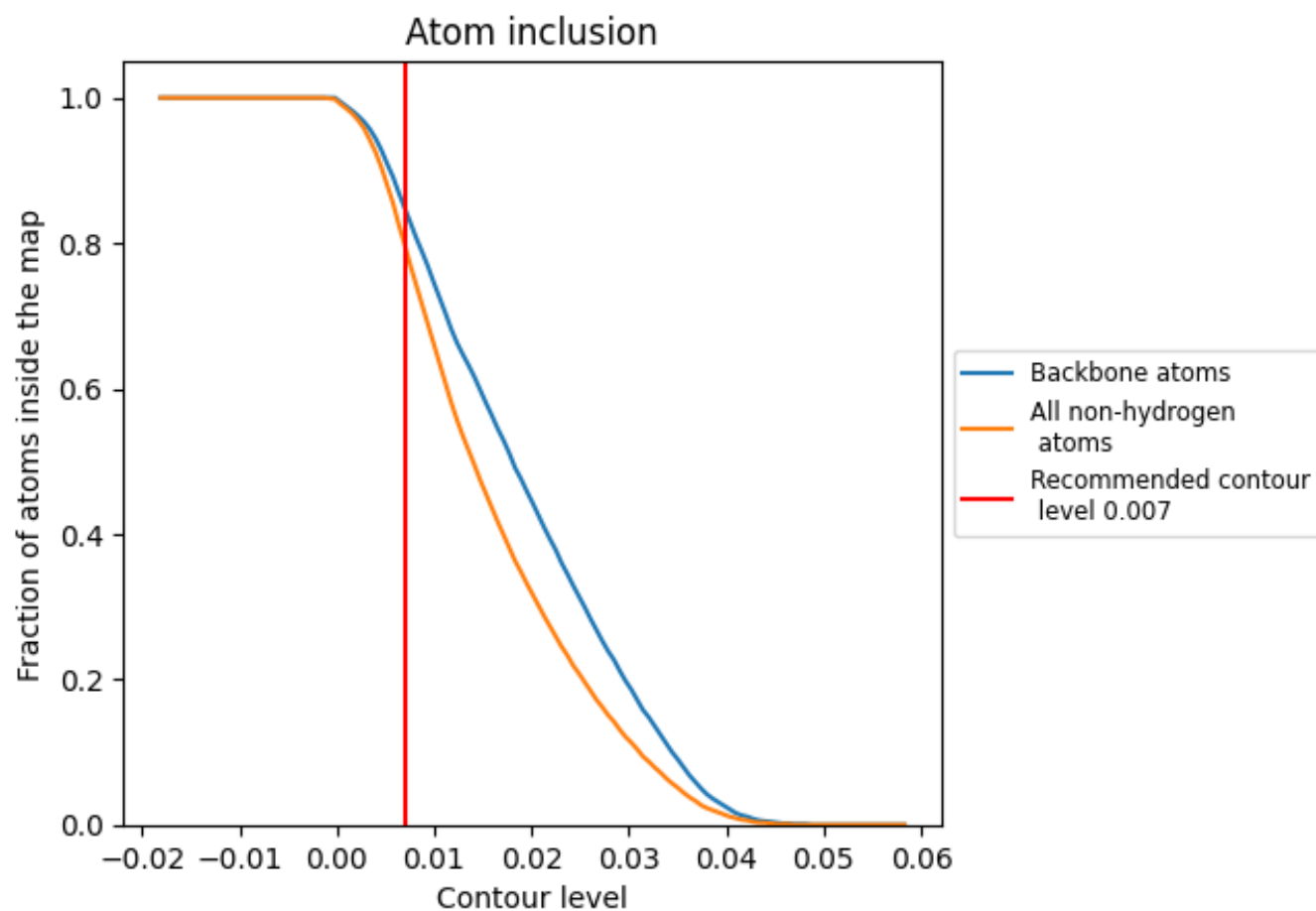
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.007).

9.4 Atom inclusion [i](#)



At the recommended contour level, 85% of all backbone atoms, 80% 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 (0.007) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7970	0.2700
A	0.8620	0.2910
B	0.8880	0.3010
C	0.8720	0.3260
H	0.3470	0.0260
I	0.0950	0.0320
J	0.1480	0.0060
L	0.4780	0.0100

1.0

0.0

<0.0