



Full wwPDB EM Validation Report ⓘ

Aug 23, 2026 – 04:20 PM JST

PDB ID : 22DZ / pdb_000022dz
EMDB ID : EMD-68190
Title : Local structure of MERS-CoV RBD protein bound with receptor DPP4 in the conformation 2 (2 up RBD and 2 DPP4 bound)
Authors : Wang, Y.J.; Sun, L.
Deposited on : 2026-01-07
Resolution : 3.01 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.dev133
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) : 2.50

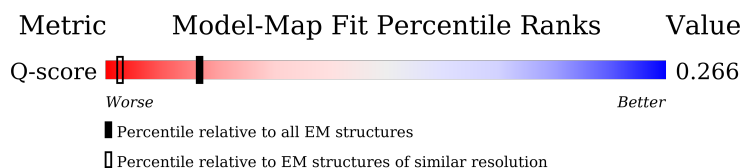
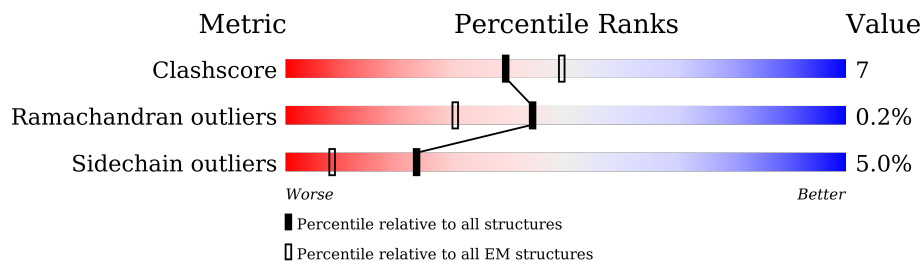
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.01 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	13882 (2.51 - 3.51)

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	C	1340	 9% 46% 11% 34%
1	F	1340	 21% 6% 73%
1	H	1340	 7% 92%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 9730 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	H	111	Total	C	N	O	S	0	0
			857	532	149	169	7		
1	F	366	Total	C	N	O	S	0	0
			2828	1786	462	559	21		
1	C	773	Total	C	N	O	S	0	0
			6045	3836	1004	1168	37		

There are 147 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	1292	GLY	-	expression tag	UNP K9N5Q8
H	1293	SER	-	expression tag	UNP K9N5Q8
H	1294	GLY	-	expression tag	UNP K9N5Q8
H	1295	TYR	-	expression tag	UNP K9N5Q8
H	1296	ILE	-	expression tag	UNP K9N5Q8
H	1297	PRO	-	expression tag	UNP K9N5Q8
H	1298	GLU	-	expression tag	UNP K9N5Q8
H	1299	ALA	-	expression tag	UNP K9N5Q8
H	1300	PRO	-	expression tag	UNP K9N5Q8
H	1301	ARG	-	expression tag	UNP K9N5Q8
H	1302	ASP	-	expression tag	UNP K9N5Q8
H	1303	GLY	-	expression tag	UNP K9N5Q8
H	1304	GLN	-	expression tag	UNP K9N5Q8
H	1305	ALA	-	expression tag	UNP K9N5Q8
H	1306	TYR	-	expression tag	UNP K9N5Q8
H	1307	VAL	-	expression tag	UNP K9N5Q8
H	1308	ARG	-	expression tag	UNP K9N5Q8
H	1309	LYS	-	expression tag	UNP K9N5Q8
H	1310	ASP	-	expression tag	UNP K9N5Q8
H	1311	GLY	-	expression tag	UNP K9N5Q8
H	1312	GLU	-	expression tag	UNP K9N5Q8
H	1313	TRP	-	expression tag	UNP K9N5Q8
H	1314	VAL	-	expression tag	UNP K9N5Q8
H	1315	LEU	-	expression tag	UNP K9N5Q8

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Chain	Residue	Modelled	Actual	Comment	Reference
H	1316	LEU	-	expression tag	UNP K9N5Q8
H	1317	SER	-	expression tag	UNP K9N5Q8
H	1318	THR	-	expression tag	UNP K9N5Q8
H	1319	PHE	-	expression tag	UNP K9N5Q8
H	1320	LEU	-	expression tag	UNP K9N5Q8
H	1321	GLY	-	expression tag	UNP K9N5Q8
H	1322	ARG	-	expression tag	UNP K9N5Q8
H	1323	SER	-	expression tag	UNP K9N5Q8
H	1324	LEU	-	expression tag	UNP K9N5Q8
H	1325	GLU	-	expression tag	UNP K9N5Q8
H	1326	VAL	-	expression tag	UNP K9N5Q8
H	1327	LEU	-	expression tag	UNP K9N5Q8
H	1328	PHE	-	expression tag	UNP K9N5Q8
H	1329	GLN	-	expression tag	UNP K9N5Q8
H	1330	GLY	-	expression tag	UNP K9N5Q8
H	1331	PRO	-	expression tag	UNP K9N5Q8
H	1332	GLY	-	expression tag	UNP K9N5Q8
H	1333	HIS	-	expression tag	UNP K9N5Q8
H	1334	HIS	-	expression tag	UNP K9N5Q8
H	1335	HIS	-	expression tag	UNP K9N5Q8
H	1336	HIS	-	expression tag	UNP K9N5Q8
H	1337	HIS	-	expression tag	UNP K9N5Q8
H	1338	HIS	-	expression tag	UNP K9N5Q8
H	1339	HIS	-	expression tag	UNP K9N5Q8
H	1340	HIS	-	expression tag	UNP K9N5Q8
F	1292	GLY	-	expression tag	UNP K9N5Q8
F	1293	SER	-	expression tag	UNP K9N5Q8
F	1294	GLY	-	expression tag	UNP K9N5Q8
F	1295	TYR	-	expression tag	UNP K9N5Q8
F	1296	ILE	-	expression tag	UNP K9N5Q8
F	1297	PRO	-	expression tag	UNP K9N5Q8
F	1298	GLU	-	expression tag	UNP K9N5Q8
F	1299	ALA	-	expression tag	UNP K9N5Q8
F	1300	PRO	-	expression tag	UNP K9N5Q8
F	1301	ARG	-	expression tag	UNP K9N5Q8
F	1302	ASP	-	expression tag	UNP K9N5Q8
F	1303	GLY	-	expression tag	UNP K9N5Q8
F	1304	GLN	-	expression tag	UNP K9N5Q8
F	1305	ALA	-	expression tag	UNP K9N5Q8
F	1306	TYR	-	expression tag	UNP K9N5Q8
F	1307	VAL	-	expression tag	UNP K9N5Q8
F	1308	ARG	-	expression tag	UNP K9N5Q8

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Chain	Residue	Modelled	Actual	Comment	Reference
F	1309	LYS	-	expression tag	UNP K9N5Q8
F	1310	ASP	-	expression tag	UNP K9N5Q8
F	1311	GLY	-	expression tag	UNP K9N5Q8
F	1312	GLU	-	expression tag	UNP K9N5Q8
F	1313	TRP	-	expression tag	UNP K9N5Q8
F	1314	VAL	-	expression tag	UNP K9N5Q8
F	1315	LEU	-	expression tag	UNP K9N5Q8
F	1316	LEU	-	expression tag	UNP K9N5Q8
F	1317	SER	-	expression tag	UNP K9N5Q8
F	1318	THR	-	expression tag	UNP K9N5Q8
F	1319	PHE	-	expression tag	UNP K9N5Q8
F	1320	LEU	-	expression tag	UNP K9N5Q8
F	1321	GLY	-	expression tag	UNP K9N5Q8
F	1322	ARG	-	expression tag	UNP K9N5Q8
F	1323	SER	-	expression tag	UNP K9N5Q8
F	1324	LEU	-	expression tag	UNP K9N5Q8
F	1325	GLU	-	expression tag	UNP K9N5Q8
F	1326	VAL	-	expression tag	UNP K9N5Q8
F	1327	LEU	-	expression tag	UNP K9N5Q8
F	1328	PHE	-	expression tag	UNP K9N5Q8
F	1329	GLN	-	expression tag	UNP K9N5Q8
F	1330	GLY	-	expression tag	UNP K9N5Q8
F	1331	PRO	-	expression tag	UNP K9N5Q8
F	1332	GLY	-	expression tag	UNP K9N5Q8
F	1333	HIS	-	expression tag	UNP K9N5Q8
F	1334	HIS	-	expression tag	UNP K9N5Q8
F	1335	HIS	-	expression tag	UNP K9N5Q8
F	1336	HIS	-	expression tag	UNP K9N5Q8
F	1337	HIS	-	expression tag	UNP K9N5Q8
F	1338	HIS	-	expression tag	UNP K9N5Q8
F	1339	HIS	-	expression tag	UNP K9N5Q8
F	1340	HIS	-	expression tag	UNP K9N5Q8
C	1292	GLY	-	expression tag	UNP K9N5Q8
C	1293	SER	-	expression tag	UNP K9N5Q8
C	1294	GLY	-	expression tag	UNP K9N5Q8
C	1295	TYR	-	expression tag	UNP K9N5Q8
C	1296	ILE	-	expression tag	UNP K9N5Q8
C	1297	PRO	-	expression tag	UNP K9N5Q8
C	1298	GLU	-	expression tag	UNP K9N5Q8
C	1299	ALA	-	expression tag	UNP K9N5Q8
C	1300	PRO	-	expression tag	UNP K9N5Q8
C	1301	ARG	-	expression tag	UNP K9N5Q8

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1302	ASP	-	expression tag	UNP K9N5Q8
C	1303	GLY	-	expression tag	UNP K9N5Q8
C	1304	GLN	-	expression tag	UNP K9N5Q8
C	1305	ALA	-	expression tag	UNP K9N5Q8
C	1306	TYR	-	expression tag	UNP K9N5Q8
C	1307	VAL	-	expression tag	UNP K9N5Q8
C	1308	ARG	-	expression tag	UNP K9N5Q8
C	1309	LYS	-	expression tag	UNP K9N5Q8
C	1310	ASP	-	expression tag	UNP K9N5Q8
C	1311	GLY	-	expression tag	UNP K9N5Q8
C	1312	GLU	-	expression tag	UNP K9N5Q8
C	1313	TRP	-	expression tag	UNP K9N5Q8
C	1314	VAL	-	expression tag	UNP K9N5Q8
C	1315	LEU	-	expression tag	UNP K9N5Q8
C	1316	LEU	-	expression tag	UNP K9N5Q8
C	1317	SER	-	expression tag	UNP K9N5Q8
C	1318	THR	-	expression tag	UNP K9N5Q8
C	1319	PHE	-	expression tag	UNP K9N5Q8
C	1320	LEU	-	expression tag	UNP K9N5Q8
C	1321	GLY	-	expression tag	UNP K9N5Q8
C	1322	ARG	-	expression tag	UNP K9N5Q8
C	1323	SER	-	expression tag	UNP K9N5Q8
C	1324	LEU	-	expression tag	UNP K9N5Q8
C	1325	GLU	-	expression tag	UNP K9N5Q8
C	1326	VAL	-	expression tag	UNP K9N5Q8
C	1327	LEU	-	expression tag	UNP K9N5Q8
C	1328	PHE	-	expression tag	UNP K9N5Q8
C	1329	GLN	-	expression tag	UNP K9N5Q8
C	1330	GLY	-	expression tag	UNP K9N5Q8
C	1331	PRO	-	expression tag	UNP K9N5Q8
C	1332	GLY	-	expression tag	UNP K9N5Q8
C	1333	HIS	-	expression tag	UNP K9N5Q8
C	1334	HIS	-	expression tag	UNP K9N5Q8
C	1335	HIS	-	expression tag	UNP K9N5Q8
C	1336	HIS	-	expression tag	UNP K9N5Q8
C	1337	HIS	-	expression tag	UNP K9N5Q8
C	1338	HIS	-	expression tag	UNP K9N5Q8
C	1339	HIS	-	expression tag	UNP K9N5Q8
C	1340	HIS	-	expression tag	UNP K9N5Q8



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	188119	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	2.569	Depositor
Minimum map value	-1.129	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.030	Depositor
Recommended contour level	0.2	Depositor
Map size (Å)	372.8, 372.8, 372.8	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.932, 0.932, 0.932	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	C	0.14	0/6185	0.38	0/8399
1	F	0.14	0/2889	0.42	0/3925
1	H	0.11	0/864	0.38	0/1161
All	All	0.14	0/9938	0.39	0/13485

There are no bond length outliers.

There are no bond angle outliers.

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	C	6045	0	5798	81	0
1	F	2828	0	2711	49	0
1	H	857	0	836	10	0
All	All	9730	0	9345	137	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 7.

All (137) 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:694:ARG:H	1:F:694:ARG:HH11	1.34	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:543:LYS:HB3	1:C:554:LEU:HB3	1.81	0.62
1:C:568:GLN:O	1:C:568:GLN:NE2	2.31	0.62
1:C:92:ALA:HA	1:C:98:GLN:HB2	1.80	0.61
1:H:826:GLN:O	1:H:826:GLN:NE2	2.33	0.61
1:C:425:CYS:HA	1:C:478:CYS:HA	1.80	0.61
1:C:155:ASN:HA	1:C:161:MET:HA	1.83	0.61
1:C:472:SER:HA	1:C:520:ALA:HB1	1.82	0.61
1:C:1075:LEU:O	1:C:1079:ASN:ND2	2.33	0.61
1:F:464:ILE:HA	1:F:468:ASN:HB2	1.83	0.61
1:C:685:THR:HG21	1:C:694:ARG:HB3	1.84	0.60
1:F:368:ALA:O	1:F:614:ARG:NH2	2.35	0.59
1:F:494:PRO:HD3	1:F:567:LEU:HD22	1.84	0.59
1:C:531:PRO:HG3	1:C:543:LYS:HB2	1.85	0.59
1:F:401:ARG:NH1	1:C:260:ALA:O	2.35	0.59
1:C:368:ALA:O	1:C:614:ARG:NH2	2.34	0.59
1:C:240:MET:SD	1:C:240:MET:N	2.76	0.58
1:F:603:CYS:SG	1:F:614:ARG:NH2	2.76	0.58
1:C:493:LYS:HD3	1:C:567:LEU:HD22	1.85	0.58
1:C:246:THR:O	1:C:269:ARG:NH2	2.36	0.58
1:C:471:GLN:HB3	1:C:477:THR:HG21	1.86	0.57
1:C:471:GLN:NE2	1:C:478:CYS:O	2.34	0.57
1:F:645:ASP:OD2	1:F:647:ASN:ND2	2.37	0.57
1:C:691:ARG:HG3	1:C:694:ARG:HH21	1.69	0.57
1:F:380:GLY:H	1:F:587:LYS:HZ1	1.54	0.56
1:C:24:ASP:HA	1:C:229:LYS:HD3	1.86	0.56
1:F:511:ARG:NH1	1:C:432:ALA:O	2.39	0.56
1:F:674:PHE:HB3	1:F:677:VAL:HB	1.88	0.55
1:F:462:GLY:O	1:F:468:ASN:ND2	2.39	0.55
1:C:810:VAL:O	1:C:1074:ARG:NH1	2.40	0.55
1:F:394:PRO:HG2	1:F:400:LYS:HB2	1.89	0.55
1:C:167:HIS:H	1:C:186:ILE:HG12	1.71	0.55
1:F:677:VAL:O	1:F:713:CYS:N	2.39	0.55
1:C:808:GLN:O	1:C:812:ASN:ND2	2.40	0.55
1:C:910:ASP:HA	1:C:913:MET:HE2	1.90	0.53
1:H:810:VAL:O	1:H:1074:ARG:NH1	2.41	0.53
1:C:375:VAL:HA	1:C:607:SER:HB2	1.90	0.53
1:C:460:SER:O	1:C:466:GLN:NE2	2.35	0.52
1:C:509:ASP:O	1:C:511:ARG:NE	2.38	0.52
1:F:633:ASP:OD1	1:F:637:ASN:N	2.41	0.52
1:F:433:ILE:O	1:F:438:TYR:OH	2.26	0.52
1:H:824:TYR:OH	1:H:1068:ASP:OD1	2.26	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:826:GLN:HB2	1:C:829:SER:HB2	1.93	0.51
1:F:425:CYS:HA	1:F:478:CYS:HA	1.93	0.50
1:F:406:ASN:HD22	1:F:582:ASN:HB2	1.75	0.50
1:C:94:GLY:HA2	1:C:304:GLN:HB3	1.92	0.50
1:C:691:ARG:HA	1:C:694:ARG:HE	1.76	0.50
1:C:43:THR:HA	1:C:84:MET:HE1	1.94	0.50
1:F:657:VAL:HG13	1:F:677:VAL:HG21	1.94	0.49
1:C:172:LEU:HD11	1:C:206:THR:HG21	1.93	0.49
1:C:46:ARG:HH12	1:C:123:ALA:HB2	1.78	0.49
1:F:426:SER:OG	1:F:427:GLN:NE2	2.46	0.49
1:F:452:MET:HB3	1:F:455:ASP:HB3	1.93	0.49
1:F:449:PRO:HG3	1:F:561:VAL:HG21	1.94	0.49
1:C:1052:GLY:O	1:C:1056:GLN:NE2	2.46	0.49
1:C:694:ARG:H	1:C:694:ARG:HD3	1.78	0.48
1:F:442:ILE:HB	1:F:574:THR:HG23	1.95	0.48
1:C:448:TYR:HE2	1:C:456:LEU:HD22	1.78	0.48
1:F:432:ALA:O	1:F:436:ASN:ND2	2.31	0.48
1:F:381:VAL:HG22	1:F:407:CYS:HA	1.96	0.48
1:C:464:ILE:HD13	1:C:468:ASN:HD22	1.80	0.47
1:F:409:TYR:OH	1:F:433:ILE:O	2.29	0.47
1:C:448:TYR:OH	1:C:452:MET:O	2.26	0.47
1:C:462:GLY:O	1:C:465:SER:OG	2.32	0.47
1:C:167:HIS:HB3	1:C:184:TYR:CZ	2.50	0.47
1:F:388:LEU:HD11	1:F:571:PHE:HE1	1.79	0.47
1:C:418:PHE:HD2	1:C:484:VAL:HG21	1.79	0.47
1:F:435:SER:HA	1:F:586:PRO:HG3	1.95	0.47
1:C:592:ASN:HA	1:C:595:LYS:HE3	1.96	0.47
1:H:1053:ASP:OD1	1:C:612:SER:OG	2.32	0.47
1:C:154:GLY:HA3	1:C:165:PHE:HE2	1.80	0.46
1:C:48:ILE:HD13	1:C:119:ARG:HH21	1.78	0.46
1:F:402:LEU:HB2	1:F:443:LEU:HB3	1.98	0.46
1:C:496:LYS:NZ	1:C:560:THR:OG1	2.48	0.46
1:C:37:GLN:HG3	1:C:39:PHE:H	1.81	0.46
1:C:933:LYS:NZ	1:C:934:VAL:O	2.45	0.46
1:H:1075:LEU:HD23	1:H:1078:LEU:HD12	1.98	0.45
1:C:100:LEU:HD11	1:C:207:TYR:HB3	1.98	0.45
1:C:472:SER:HB3	1:C:521:ASN:HB2	1.99	0.45
1:C:603:CYS:SG	1:C:614:ARG:NH2	2.81	0.45
1:F:660:SER:HB2	1:F:673:LEU:HB3	1.98	0.45
1:C:400:LYS:H	1:C:445:TYR:HB3	1.81	0.45
1:F:543:LYS:HD2	1:F:545:LEU:HD23	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:216:ASP:OD1	1:C:217:GLY:N	2.49	0.45
1:C:645:ASP:OD2	1:C:647:ASN:ND2	2.50	0.45
1:C:652:ARG:HG3	1:C:653:ALA:H	1.81	0.45
1:F:444:ASP:O	1:F:572:GLY:N	2.37	0.45
1:C:173:PRO:HA	1:C:180:LEU:HA	1.99	0.45
1:H:814:PHE:HE2	1:H:1055:ILE:HD13	1.82	0.45
1:F:367:GLU:O	1:F:688:GLN:NE2	2.40	0.45
1:F:365:SER:HA	1:F:659:VAL:HG23	1.99	0.44
1:F:631:VAL:HB	1:F:640:GLY:HA3	1.99	0.44
1:C:252:GLU:OE2	1:C:269:ARG:NH1	2.50	0.44
1:F:529:ILE:H	1:F:529:ILE:HG13	1.51	0.44
1:C:404:PHE:HB2	1:C:441:LEU:HD23	1.99	0.44
1:C:493:LYS:HD3	1:C:567:LEU:H	1.83	0.44
1:F:672:THR:HB	1:F:715:LEU:HB2	2.00	0.43
1:C:625:VAL:HG12	1:C:628:GLN:H	1.83	0.43
1:F:393:PRO:HG3	1:F:567:LEU:HD21	2.00	0.43
1:F:662:ILE:HB	1:F:671:ALA:HB3	2.00	0.43
1:C:34:ASP:HB2	1:C:99:LYS:HD3	1.99	0.43
1:C:57:ILE:HG12	1:C:278:MET:HE3	1.99	0.43
1:H:926:ALA:HA	1:H:929:VAL:HG22	2.00	0.43
1:C:64:TYR:HB3	1:C:67:ILE:HD11	2.01	0.43
1:C:464:ILE:HA	1:C:468:ASN:HB2	2.00	0.43
1:C:627:GLN:HE21	1:C:627:GLN:HB3	1.71	0.43
1:H:1059:ASP:OD1	1:H:1059:ASP:N	2.43	0.42
1:C:804:VAL:HA	1:C:932:TYR:HA	2.01	0.42
1:C:424:THR:HG23	1:C:479:LEU:HB2	2.01	0.42
1:C:433:ILE:HD13	1:C:433:ILE:H	1.84	0.42
1:C:643:SER:HB2	1:C:649:TYR:HE2	1.85	0.42
1:F:410:ASN:ND2	1:F:412:THR:OG1	2.50	0.42
1:F:411:LEU:HD23	1:F:434:ALA:HB2	2.01	0.42
1:C:531:PRO:HG2	1:C:556:ALA:HB3	2.01	0.42
1:H:927:GLN:HG2	1:H:932:TYR:CE2	2.54	0.42
1:F:481:LEU:HD23	1:F:570:GLY:HA3	2.01	0.42
1:C:504:SER:HA	1:C:516:GLN:H	1.84	0.42
1:C:652:ARG:HD2	1:C:652:ARG:HA	1.92	0.42
1:F:694:ARG:H	1:F:694:ARG:HD2	1.85	0.42
1:H:804:VAL:HG22	1:H:932:TYR:HB2	2.02	0.42
1:F:632:TYR:HA	1:F:638:LEU:HA	2.02	0.42
1:C:189:PRO:HB3	1:C:196:PRO:HB2	2.02	0.41
1:C:475:ASN:OD1	1:C:576:GLN:HB2	2.21	0.41
1:C:599:GLN:HG2	1:C:602:ASN:HB3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:382:GLU:C	1:F:407:CYS:HB2	2.46	0.41
1:F:496:LYS:HE2	1:F:496:LYS:HB3	1.91	0.41
1:C:599:GLN:OE1	1:C:602:ASN:ND2	2.51	0.41
1:C:33:VAL:HG12	1:C:100:LEU:HB2	2.03	0.41
1:F:393:PRO:HA	1:F:394:PRO:HD3	1.94	0.41
1:C:67:ILE:HD12	1:C:69:ILE:HD11	2.03	0.41
1:C:589:GLU:OE1	1:C:595:LYS:NZ	2.43	0.40
1:F:529:ILE:HG12	1:F:543:LYS:HB2	2.04	0.40
1:F:696:MET:HG3	1:F:715:LEU:HD23	2.04	0.40
1:F:529:ILE:HD12	1:F:530:VAL:H	1.86	0.40
1:C:88:SER:OG	1:C:89:ALA:N	2.55	0.40
1:C:259:THR:OG1	1:C:260:ALA:N	2.53	0.40
1:C:1066:GLN:OE1	1:C:1069:ARG:NH2	2.55	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	C	761/1340 (57%)	704 (92%)	54 (7%)	3 (0%)	30	63
1	F	356/1340 (27%)	320 (90%)	36 (10%)	0	100	100
1	H	105/1340 (8%)	102 (97%)	3 (3%)	0	100	100
All	All	1222/4020 (30%)	1126 (92%)	93 (8%)	3 (0%)	44	75

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	534	VAL
1	C	529	ILE
1	C	530	VAL

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	C	671/1159 (58%)	637 (95%)	34 (5%)	21	54
1	F	326/1159 (28%)	311 (95%)	15 (5%)	24	57
1	H	92/1159 (8%)	87 (95%)	5 (5%)	20	52
All	All	1089/3477 (31%)	1035 (95%)	54 (5%)	23	54

All (54) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	814	PHE
1	H	815	GLN
1	H	826	GLN
1	H	1056	GLN
1	H	1057	ARG
1	F	381	VAL
1	F	400	LYS
1	F	427	GLN
1	F	438	TYR
1	F	456	LEU
1	F	496	LYS
1	F	506	PHE
1	F	513	GLU
1	F	529	ILE
1	F	568	GLN
1	F	574	THR
1	F	579	THR
1	F	596	ILE
1	F	694	ARG
1	F	697	LEU
1	C	101	PHE
1	C	132	ILE
1	C	172	LEU
1	C	176	CYS
1	C	178	THR
1	C	179	LEU

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Mol	Chain	Res	Type
1	C	240	MET
1	C	303	ILE
1	C	377	GLN
1	C	383	CYS
1	C	389	LEU
1	C	433	ILE
1	C	456	LEU
1	C	475	ASN
1	C	488	LEU
1	C	495	LEU
1	C	506	PHE
1	C	523	TYR
1	C	527	VAL
1	C	528	SER
1	C	529	ILE
1	C	533	THR
1	C	534	VAL
1	C	537	ASP
1	C	540	TYR
1	C	543	LYS
1	C	563	MET
1	C	564	THR
1	C	568	GLN
1	C	569	MET
1	C	574	THR
1	C	588	LEU
1	C	620	CYS
1	C	815	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (37) such sidechains are listed below:

Mol	Chain	Res	Type
1	H	808	GLN
1	H	815	GLN
1	H	826	GLN
1	H	915	GLN
1	H	1031	GLN
1	H	1072	ASN
1	F	398	ASN
1	F	406	ASN
1	F	410	ASN
1	F	427	GLN

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Mol	Chain	Res	Type
1	F	487	ASN
1	F	544	GLN
1	F	568	GLN
1	F	599	GLN
1	F	670	HIS
1	C	37	GLN
1	C	60	GLN
1	C	98	GLN
1	C	218	ASN
1	C	220	ASN
1	C	236	ASN
1	C	264	HIS
1	C	277	ASN
1	C	280	GLN
1	C	522	GLN
1	C	566	GLN
1	C	568	GLN
1	C	592	ASN
1	C	627	GLN
1	C	628	GLN
1	C	647	ASN
1	C	808	GLN
1	C	812	ASN
1	C	815	GLN
1	C	915	GLN
1	C	1031	GLN
1	C	1085	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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.

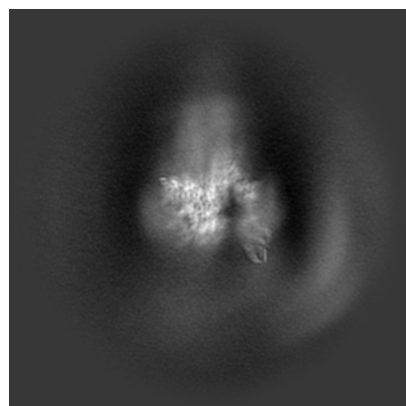
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-68190. These allow visual inspection of the internal detail of the map and identification of artifacts.

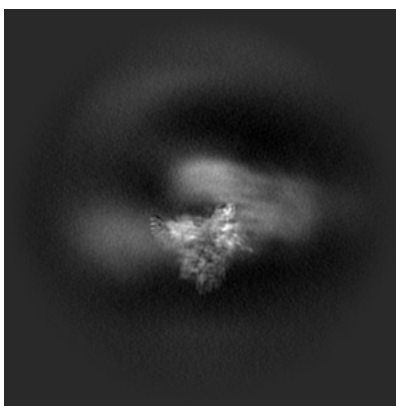
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

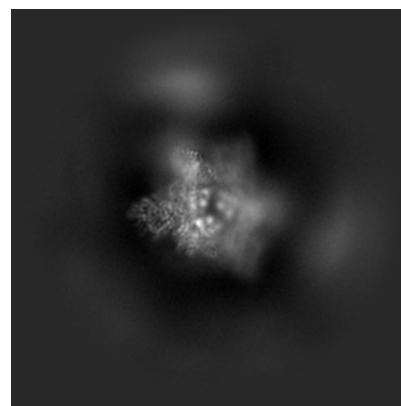
6.1.1 Primary map



X

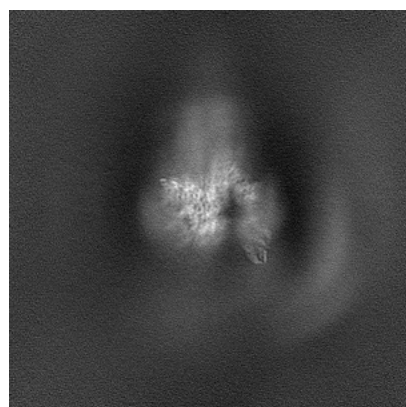


Y

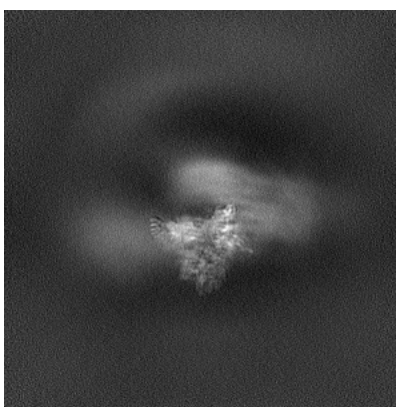


Z

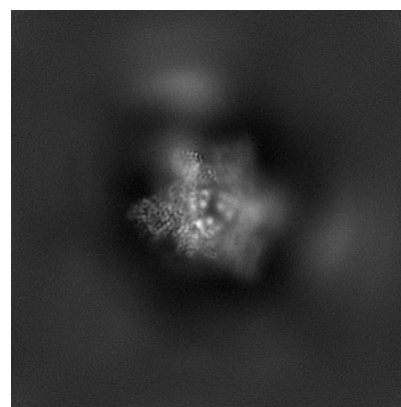
6.1.2 Raw map



X



Y

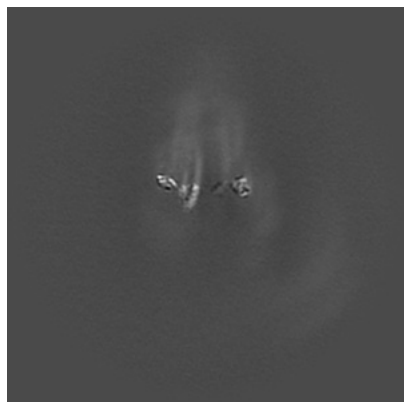


Z

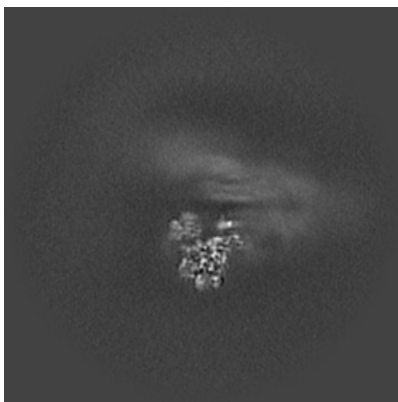
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

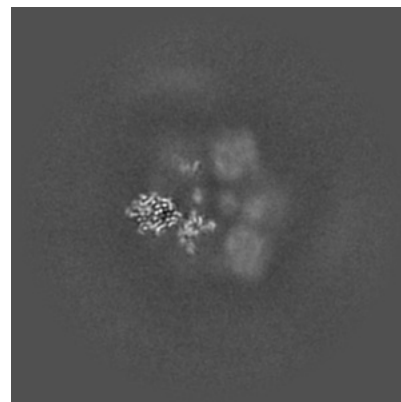
6.2.1 Primary map



X Index: 200

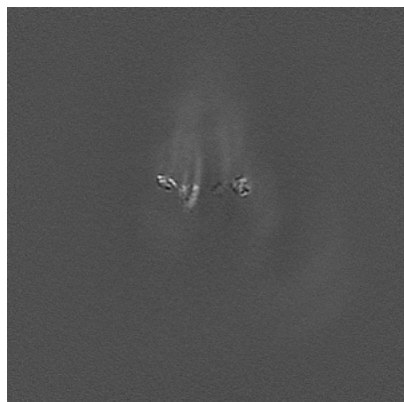


Y Index: 200

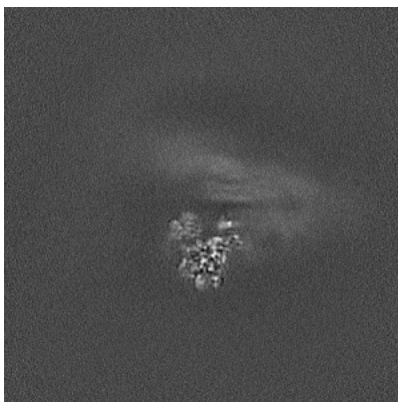


Z Index: 200

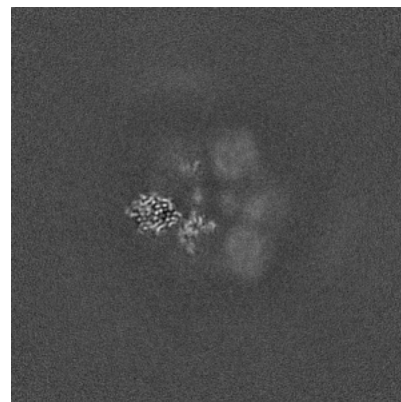
6.2.2 Raw map



X Index: 200



Y Index: 200

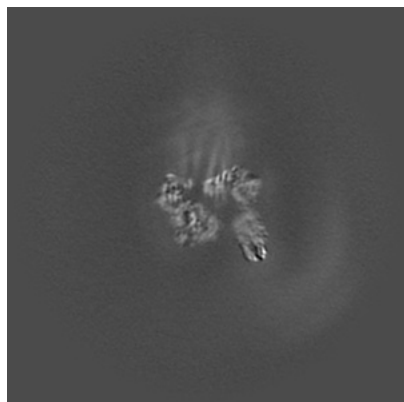


Z Index: 200

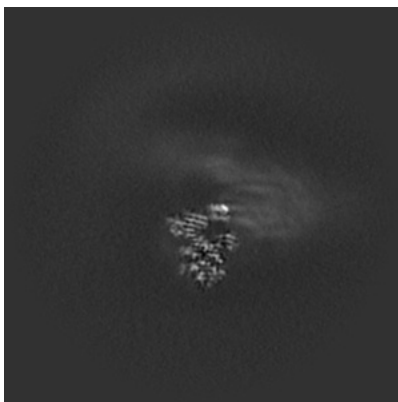
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

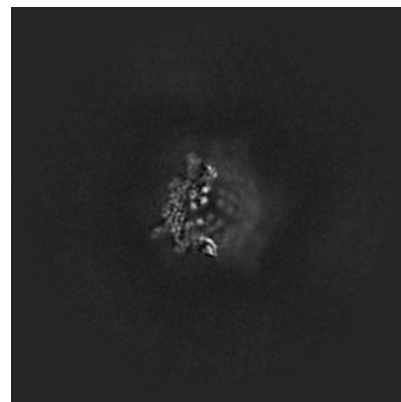
6.3.1 Primary map



X Index: 181

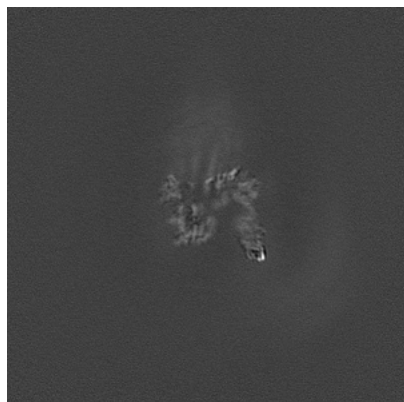


Y Index: 188

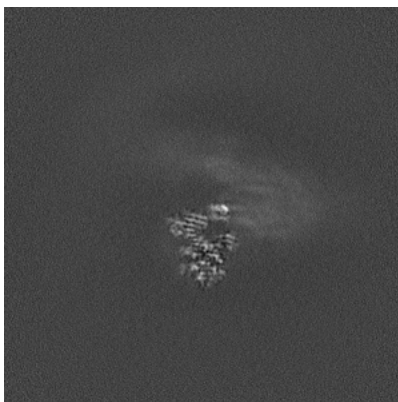


Z Index: 225

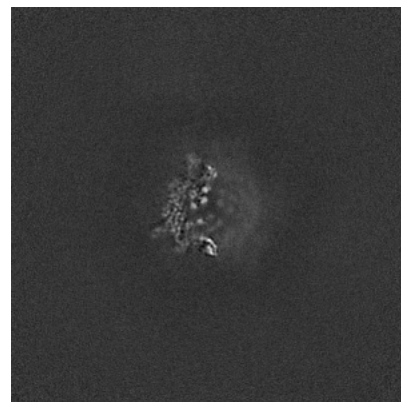
6.3.2 Raw map



X Index: 184



Y Index: 188

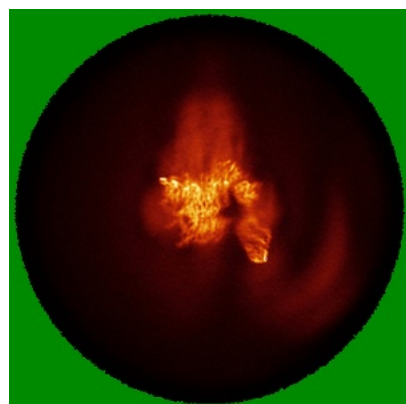


Z Index: 225

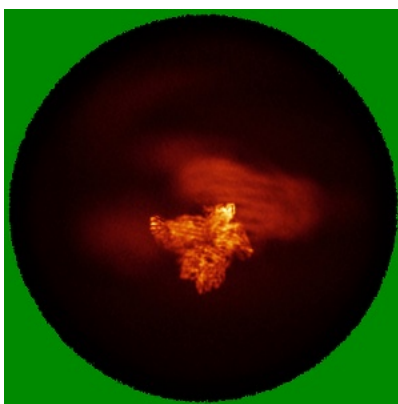
The images above show the largest variance slices of the map in three orthogonal directions.

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

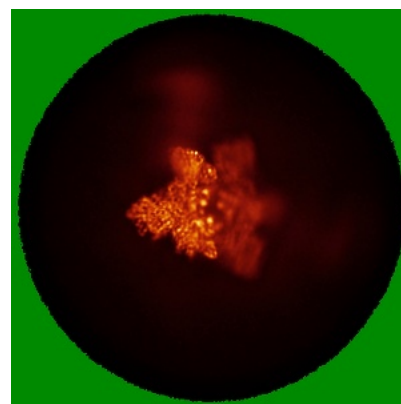
6.4.1 Primary map



X

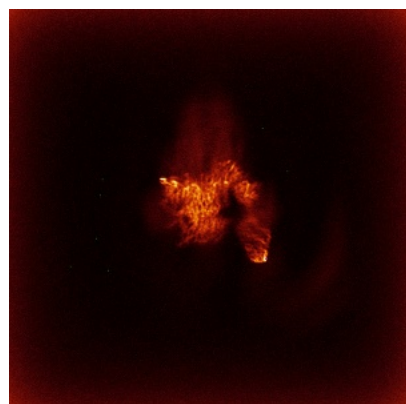


Y

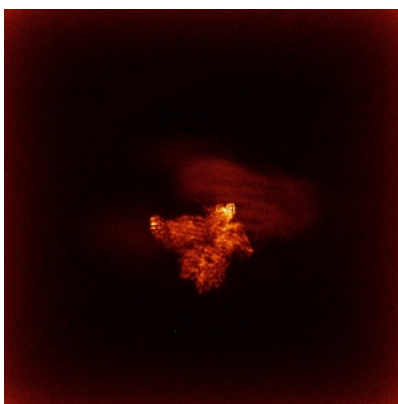


Z

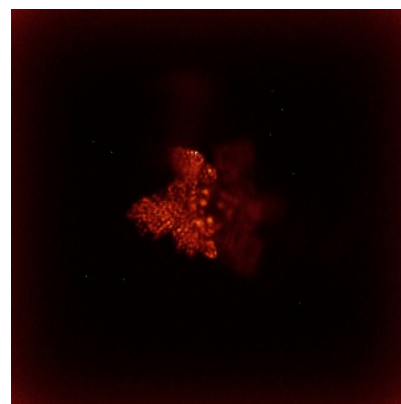
6.4.2 Raw map



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.

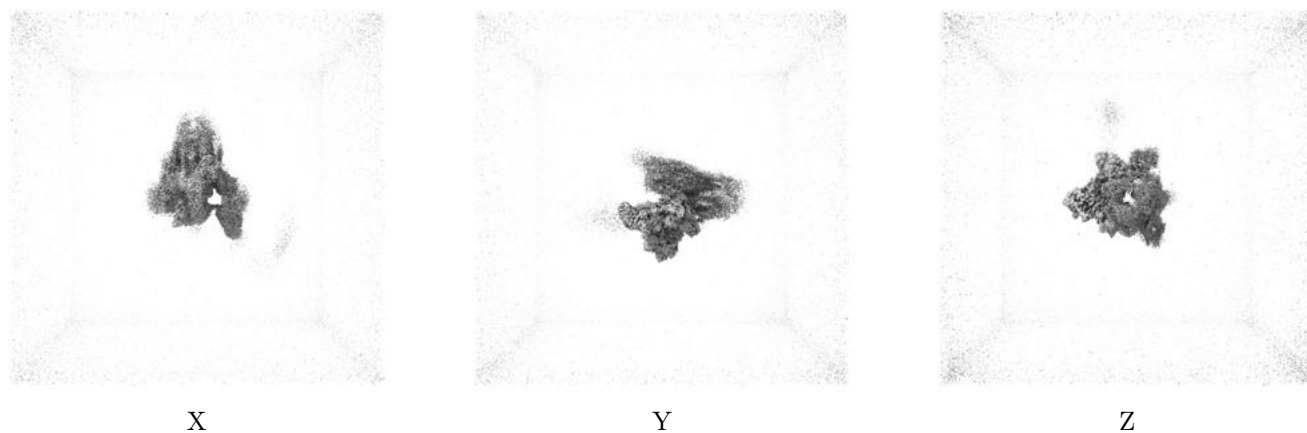
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.2. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

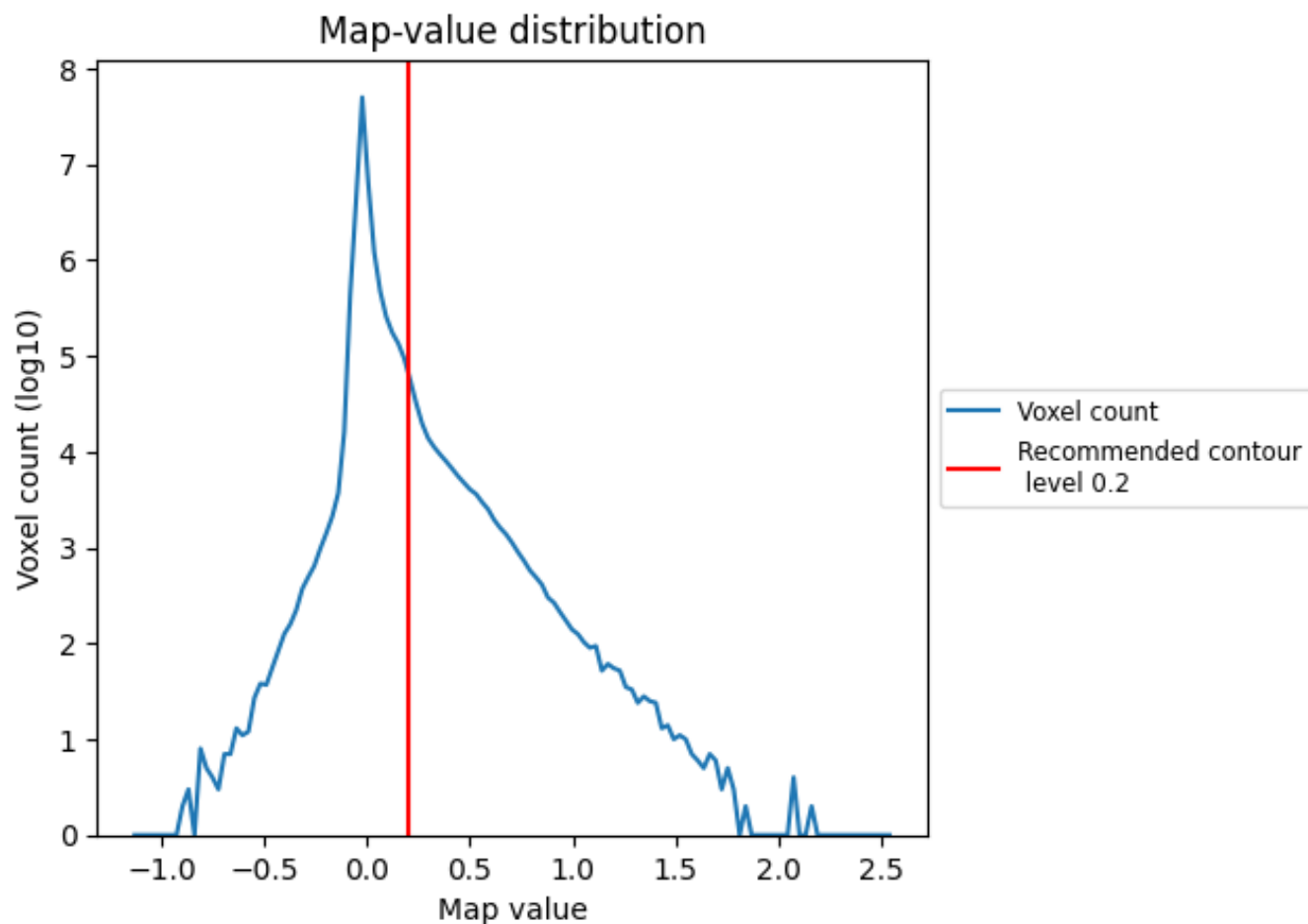
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

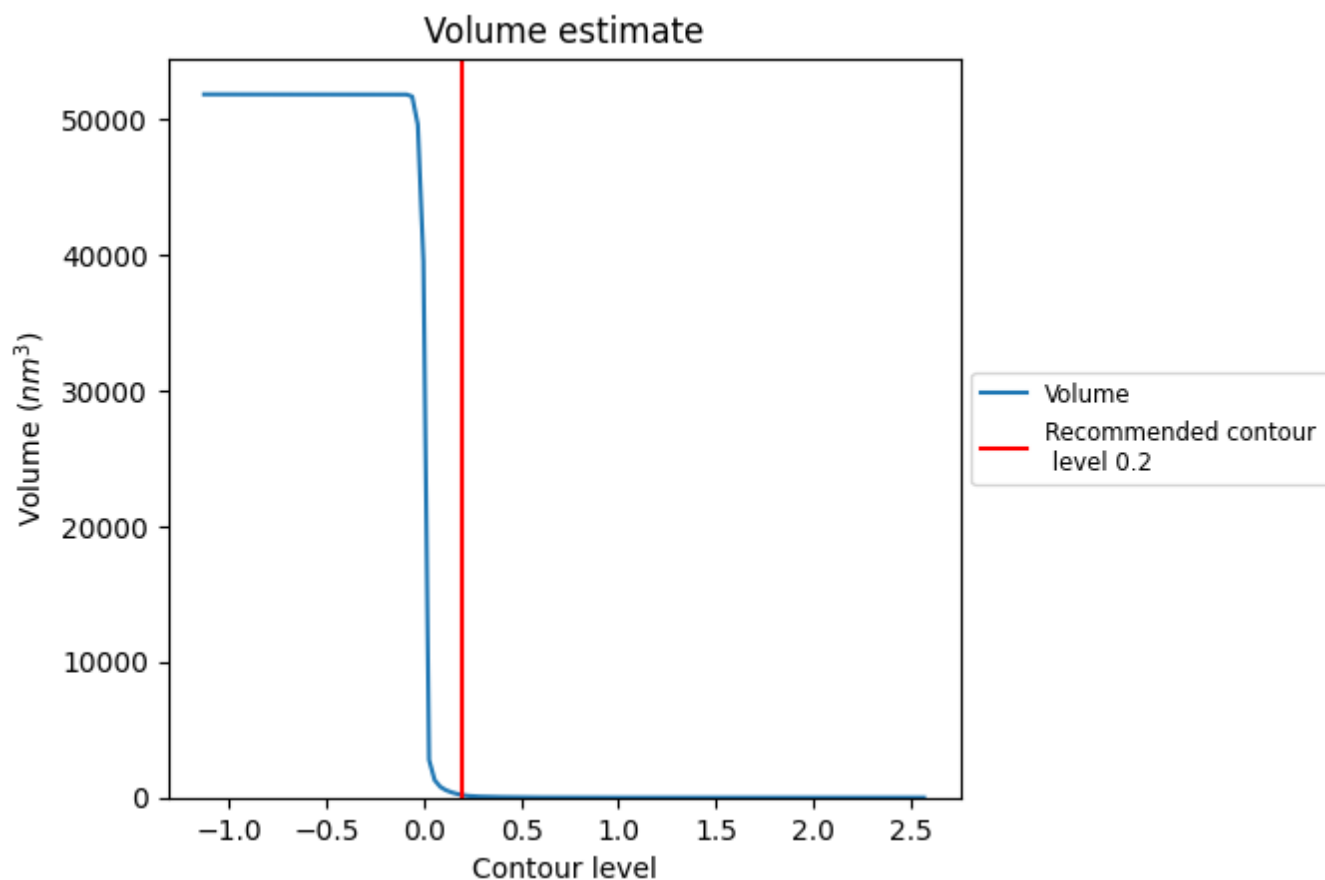
This section contains the results of statistical analysis of the map.

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.

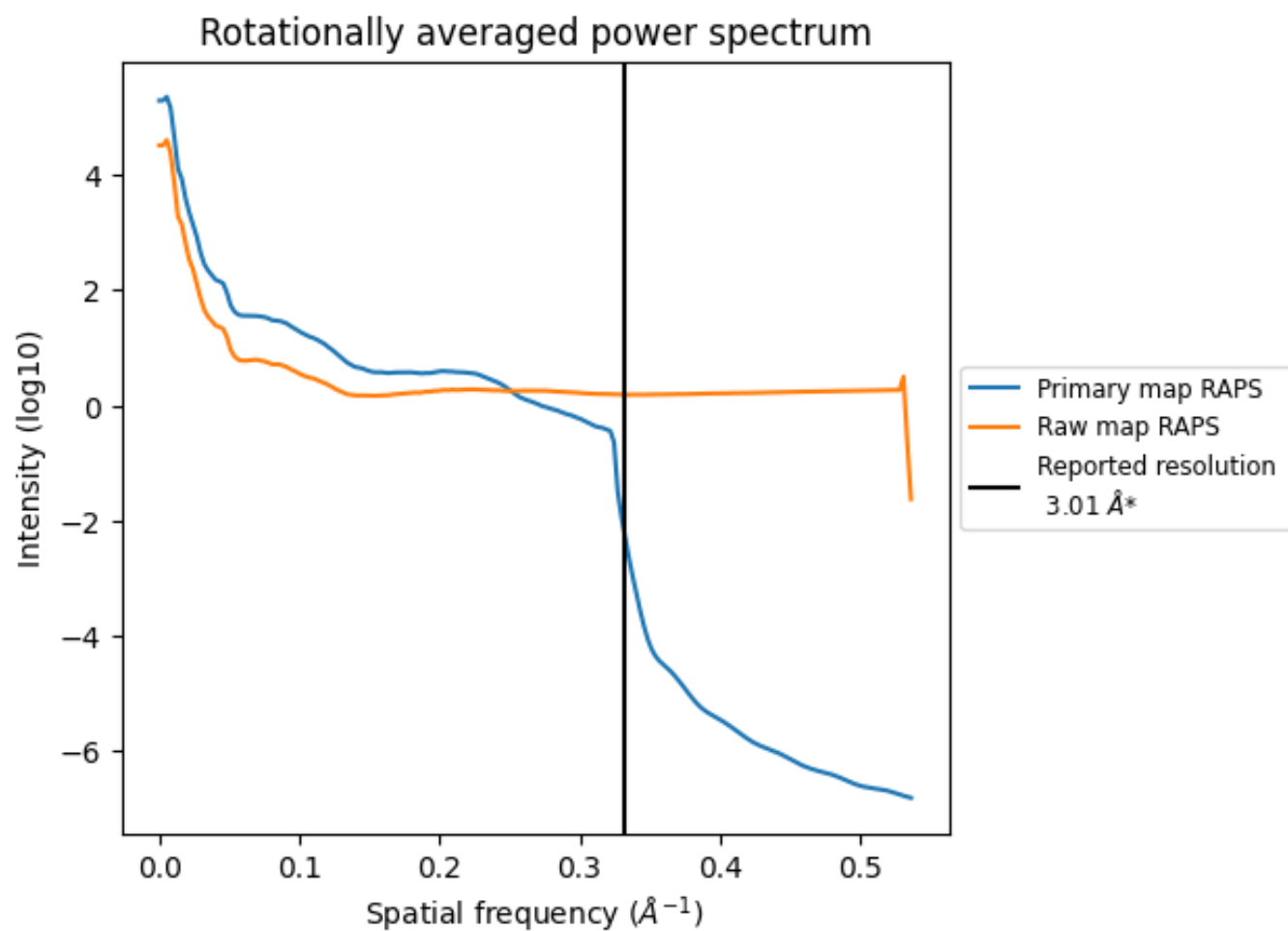
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 179 nm^3 ; this corresponds to an approximate mass of 161 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 ⓘ

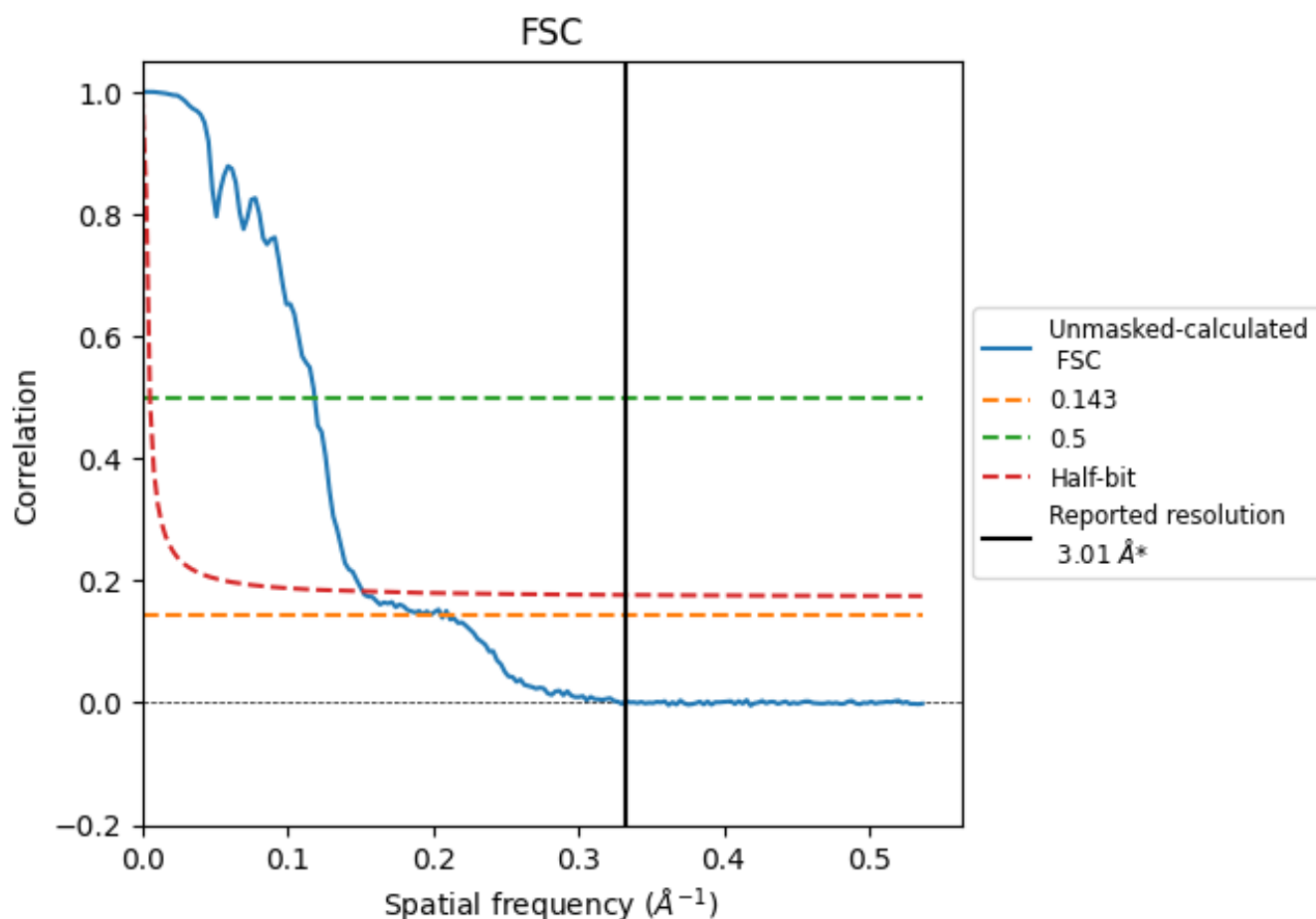


*Reported resolution corresponds to spatial frequency of 0.332 $\text{\AA}^{-1}$

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 0.332 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

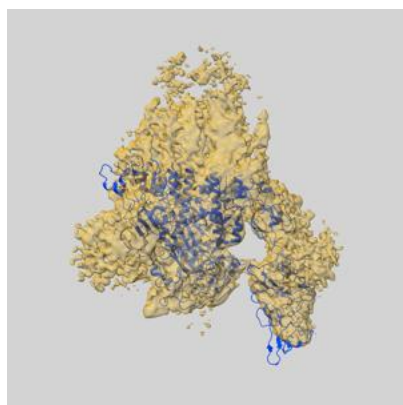
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.01	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.86	8.43	6.59

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.86 differs from the reported value 3.01 by more than 10 %

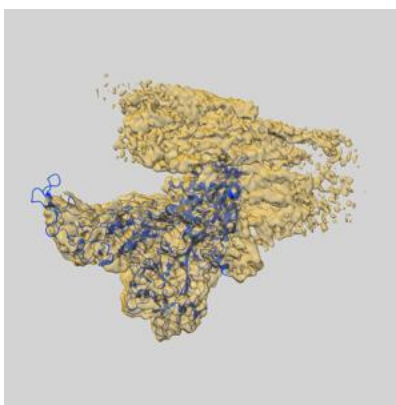
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-68190 and PDB model 22DZ. Per-residue inclusion information can be found in section [3](#) on page [7](#).

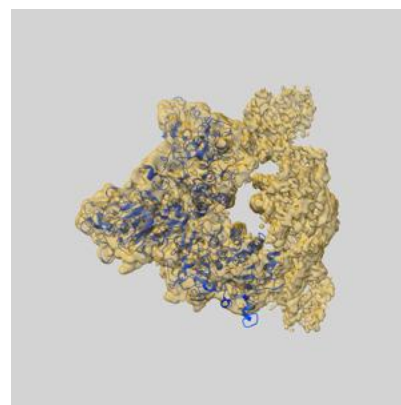
9.1 Map-model overlay [i](#)



X



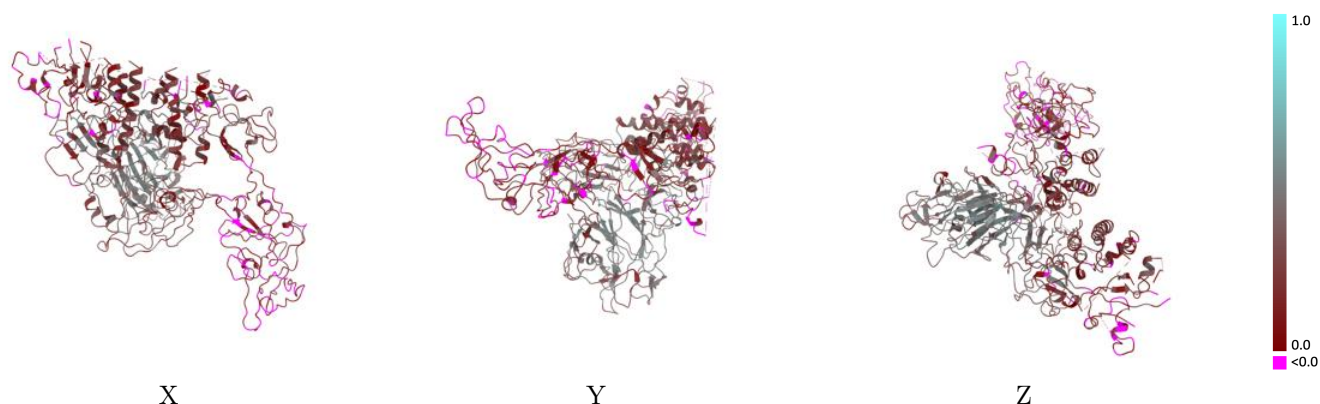
Y



Z

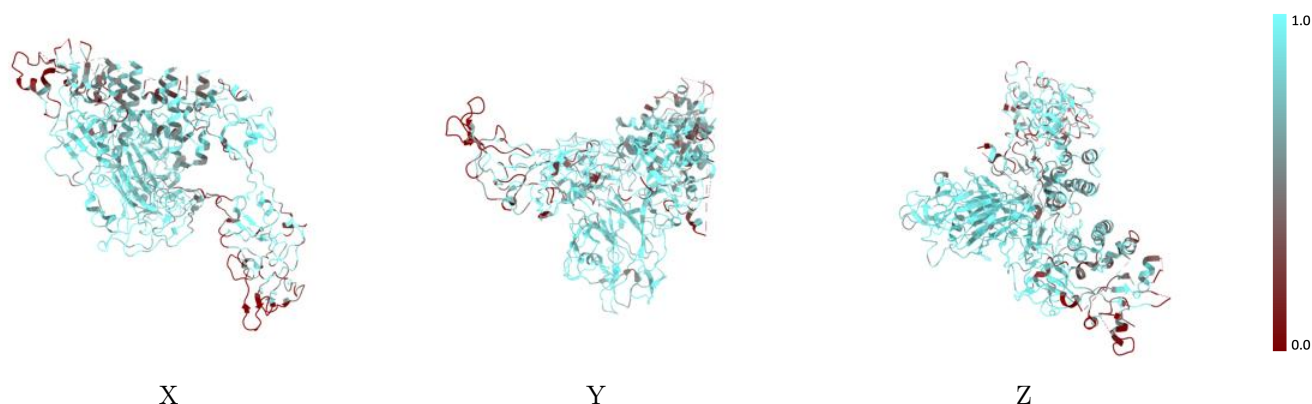
The images above show the 3D surface view of the map at the recommended contour level 0.2 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



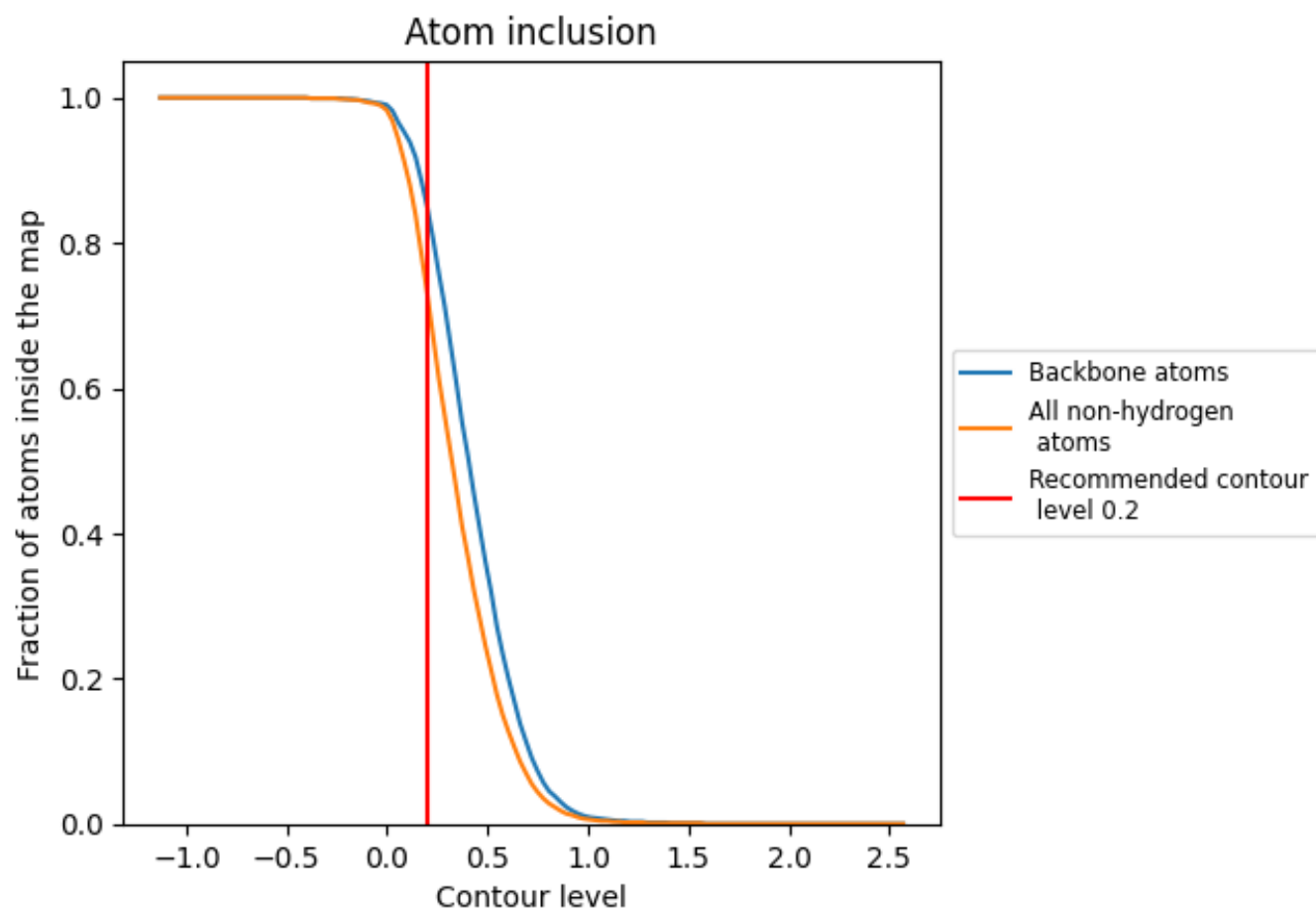
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.2).

9.4 Atom inclusion ⓘ



At the recommended contour level, 85% of all backbone atoms, 73% 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 (0.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7300	0.2660
C	0.7380	0.2670
F	0.7250	0.2770
H	0.6900	0.2190

