



Full wwPDB EM Validation Report ⓘ

Mar 27, 2026 – 08:41 AM UTC

PDB ID : 6PZK / pdb_00006pzk
EMDB ID : EMD-20536
Title : Cryo-EM Structure of the Respiratory Syncytial Virus Polymerase (L) Protein
Bound by the Tetrameric Phosphoprotein (P)
Authors : Gilman, M.S.A.; McLellan, J.S.
Deposited on : 2019-08-01
Resolution : 3.20 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.dev132
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

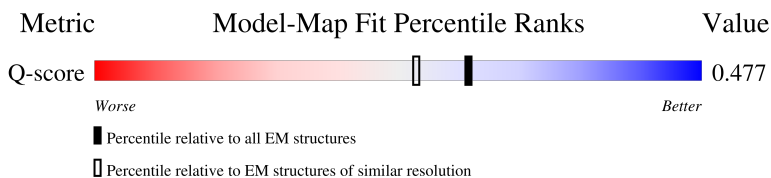
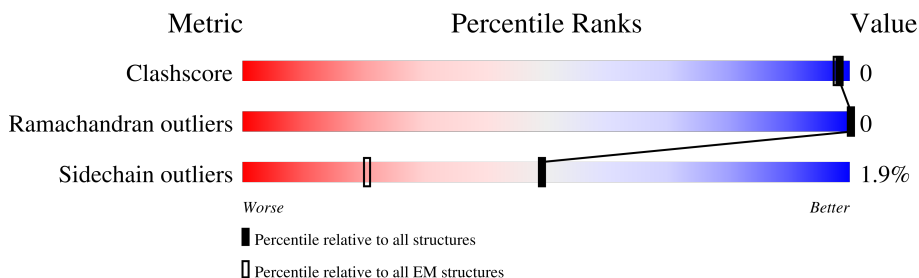
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 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	15020 (2.70 - 3.70)

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	2201	
2	B	256	
2	C	256	
2	D	256	

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Mol	Chain	Length	Quality of chain
2	E	256	 A horizontal bar chart showing the quality of chain E. The bar is divided into three segments: a red segment at the beginning labeled '11%', a green segment labeled '20%', and a grey segment at the end labeled '79%'. The total length of the bar represents 100%.

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 13153 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 RNA-directed RNA polymerase L.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1361	Total	C	N	O	S	0	0
			11106	7155	1863	2031	57		

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-35	MET	-	initiating methionine	UNP P28887
A	-34	GLY	-	expression tag	UNP P28887
A	-33	SER	-	expression tag	UNP P28887
A	-32	TRP	-	expression tag	UNP P28887
A	-31	SER	-	expression tag	UNP P28887
A	-30	HIS	-	expression tag	UNP P28887
A	-29	PRO	-	expression tag	UNP P28887
A	-28	GLN	-	expression tag	UNP P28887
A	-27	PHE	-	expression tag	UNP P28887
A	-26	GLU	-	expression tag	UNP P28887
A	-25	LYS	-	expression tag	UNP P28887
A	-24	GLY	-	expression tag	UNP P28887
A	-23	SER	-	expression tag	UNP P28887
A	-22	GLY	-	expression tag	UNP P28887
A	-21	SER	-	expression tag	UNP P28887
A	-20	GLY	-	expression tag	UNP P28887
A	-19	SER	-	expression tag	UNP P28887
A	-18	SER	-	expression tag	UNP P28887
A	-17	TRP	-	expression tag	UNP P28887
A	-16	SER	-	expression tag	UNP P28887
A	-15	HIS	-	expression tag	UNP P28887
A	-14	PRO	-	expression tag	UNP P28887
A	-13	GLN	-	expression tag	UNP P28887
A	-12	PHE	-	expression tag	UNP P28887
A	-11	GLU	-	expression tag	UNP P28887
A	-10	LYS	-	expression tag	UNP P28887
A	-9	GLY	-	expression tag	UNP P28887
A	-8	SER	-	expression tag	UNP P28887

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	GLY	-	expression tag	UNP P28887
A	-6	SER	-	expression tag	UNP P28887
A	-5	LEU	-	expression tag	UNP P28887
A	-4	VAL	-	expression tag	UNP P28887
A	-3	PRO	-	expression tag	UNP P28887
A	-2	ARG	-	expression tag	UNP P28887
A	-1	GLY	-	expression tag	UNP P28887
A	0	SER	-	expression tag	UNP P28887

- Molecule 2 is a protein called Phosphoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	98	Total	C	N	O	S	0	0
			762	462	137	157	6		
2	C	57	Total	C	N	O	S	0	0
			437	269	80	85	3		
2	D	55	Total	C	N	O	S	0	0
			424	260	78	83	3		
2	E	53	Total	C	N	O	S	0	0
			424	261	79	80	4		

There are 60 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	242	LYS	-	expression tag	UNP P03421
B	243	GLY	-	expression tag	UNP P03421
B	244	GLU	-	expression tag	UNP P03421
B	245	ASN	-	expression tag	UNP P03421
B	246	LYS	-	expression tag	UNP P03421
B	247	TYR	-	expression tag	UNP P03421
B	248	PHE	-	expression tag	UNP P03421
B	249	GLN	-	expression tag	UNP P03421
B	250	GLY	-	expression tag	UNP P03421
B	251	HIS	-	expression tag	UNP P03421
B	252	HIS	-	expression tag	UNP P03421
B	253	HIS	-	expression tag	UNP P03421
B	254	HIS	-	expression tag	UNP P03421
B	255	HIS	-	expression tag	UNP P03421
B	256	HIS	-	expression tag	UNP P03421
C	242	LYS	-	expression tag	UNP P03421
C	243	GLY	-	expression tag	UNP P03421
C	244	GLU	-	expression tag	UNP P03421

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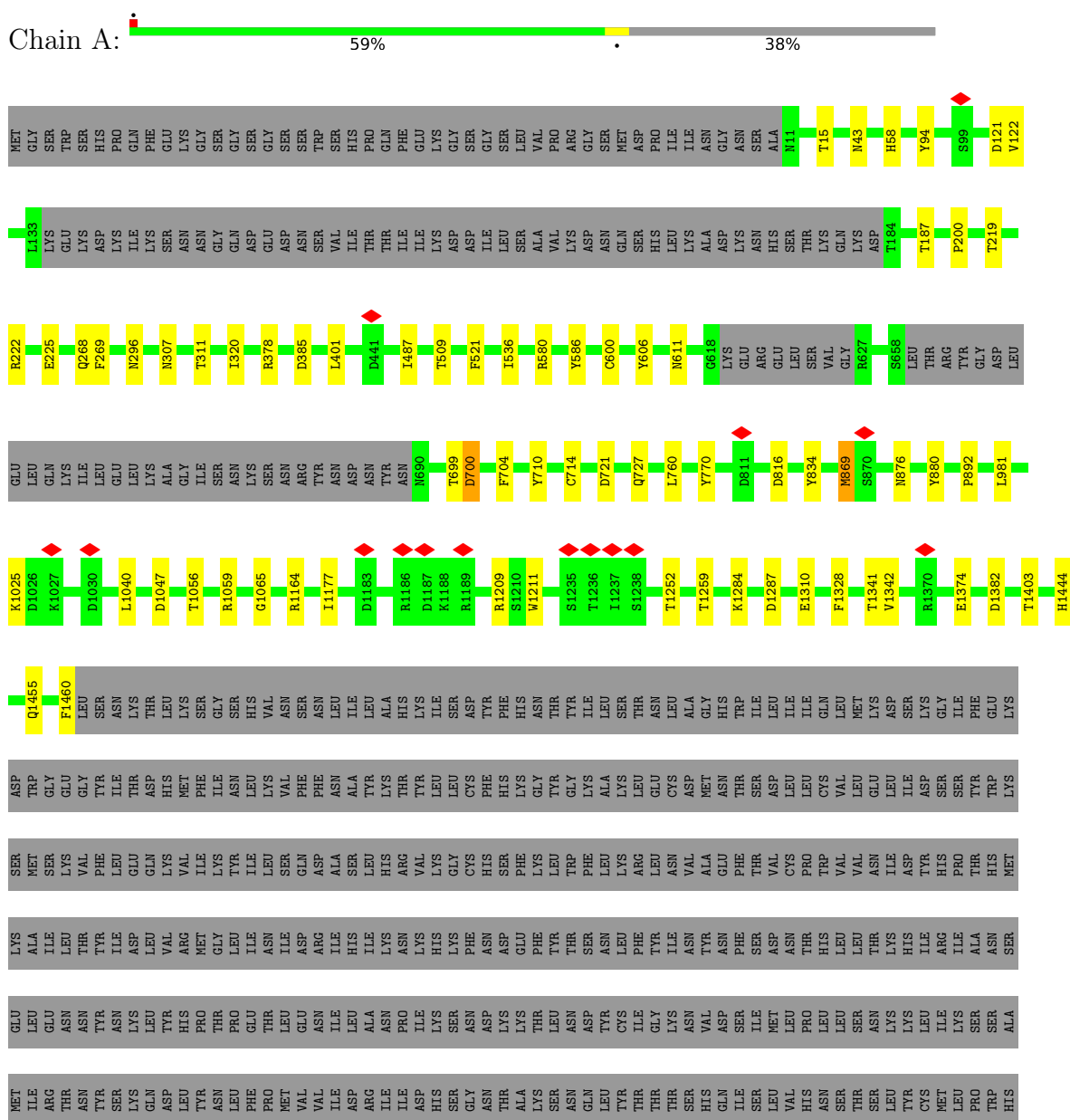
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Chain	Residue	Modelled	Actual	Comment	Reference
C	245	ASN	-	expression tag	UNP P03421
C	246	LYS	-	expression tag	UNP P03421
C	247	TYR	-	expression tag	UNP P03421
C	248	PHE	-	expression tag	UNP P03421
C	249	GLN	-	expression tag	UNP P03421
C	250	GLY	-	expression tag	UNP P03421
C	251	HIS	-	expression tag	UNP P03421
C	252	HIS	-	expression tag	UNP P03421
C	253	HIS	-	expression tag	UNP P03421
C	254	HIS	-	expression tag	UNP P03421
C	255	HIS	-	expression tag	UNP P03421
C	256	HIS	-	expression tag	UNP P03421
D	242	LYS	-	expression tag	UNP P03421
D	243	GLY	-	expression tag	UNP P03421
D	244	GLU	-	expression tag	UNP P03421
D	245	ASN	-	expression tag	UNP P03421
D	246	LYS	-	expression tag	UNP P03421
D	247	TYR	-	expression tag	UNP P03421
D	248	PHE	-	expression tag	UNP P03421
D	249	GLN	-	expression tag	UNP P03421
D	250	GLY	-	expression tag	UNP P03421
D	251	HIS	-	expression tag	UNP P03421
D	252	HIS	-	expression tag	UNP P03421
D	253	HIS	-	expression tag	UNP P03421
D	254	HIS	-	expression tag	UNP P03421
D	255	HIS	-	expression tag	UNP P03421
D	256	HIS	-	expression tag	UNP P03421
E	242	LYS	-	expression tag	UNP P03421
E	243	GLY	-	expression tag	UNP P03421
E	244	GLU	-	expression tag	UNP P03421
E	245	ASN	-	expression tag	UNP P03421
E	246	LYS	-	expression tag	UNP P03421
E	247	TYR	-	expression tag	UNP P03421
E	248	PHE	-	expression tag	UNP P03421
E	249	GLN	-	expression tag	UNP P03421
E	250	GLY	-	expression tag	UNP P03421
E	251	HIS	-	expression tag	UNP P03421
E	252	HIS	-	expression tag	UNP P03421
E	253	HIS	-	expression tag	UNP P03421
E	254	HIS	-	expression tag	UNP P03421
E	255	HIS	-	expression tag	UNP P03421
E	256	HIS	-	expression tag	UNP P03421

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: RNA-directed RNA polymerase L



[illegible]

- Molecule 2: Phosphoprotein

[illegible]

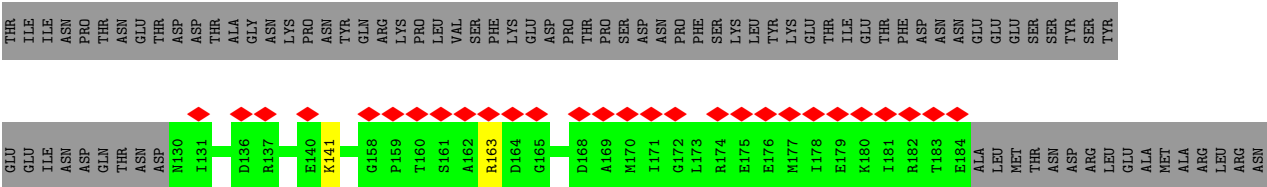
- Molecule 2: Phosphoprotein

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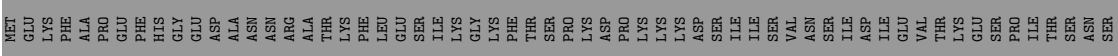
- Molecule 2: Phosphoprotein



MET	GLU	LYS	LYS	PHE	ALA	PRO	GLU	PHE	HIS	GLY	GLU	ASP	ALA	ASN	ASN	ARG	ALA	THR	LYS	PHE	LEU	GLU	SER	ILE	LYS	GLY	LYS	PHE	THR	SER	PRO	ASP	LYS	LYS	LYS	ASP	ASP	ILE	ILE	SER	VAL	ASN	SER	ILE	ASP	ILE	GLU	GLU	THR	LYS	GLU	SER	PRO	ILE	THR	SER	ASN
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● Molecule 2: Phosphoprotein



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	196720	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	48	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	3.980	Depositor
Minimum map value	-2.351	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.088	Depositor
Recommended contour level	0.35	Depositor
Map size (Å)	275.2, 275.2, 275.2	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.075, 1.075, 1.075	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	A	0.73	0/11340	1.36	34/15352 (0.2%)
2	B	0.77	0/764	1.42	3/1024 (0.3%)
2	C	0.80	0/438	1.44	1/587 (0.2%)
2	D	0.82	0/425	1.35	1/569 (0.2%)
2	E	0.79	0/423	1.40	1/563 (0.2%)
All	All	0.74	0/13390	1.37	40/18095 (0.2%)

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	7

There are no bond length outliers.

All (40) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1444	HIS	CA-CB-CG	9.00	122.80	113.80
1	A	869	MET	N-CA-C	7.77	121.49	110.23
1	A	378	ARG	NE-CZ-NH2	7.41	125.87	119.20
1	A	521	PHE	CA-C-N	6.93	133.47	122.59
1	A	521	PHE	C-N-CA	6.93	133.47	122.59
1	A	1444	HIS	CB-CA-C	-6.78	99.49	110.74
1	A	700	ASP	CA-CB-CG	6.70	119.30	112.60
1	A	721	ASP	CA-CB-CG	6.48	119.08	112.60
1	A	1328	PHE	CA-CB-CG	6.37	120.17	113.80
1	A	1287	ASP	CA-CB-CG	6.35	118.95	112.60
1	A	816	ASP	CA-CB-CG	6.07	118.67	112.60
1	A	1047	ASP	CA-CB-CG	5.93	118.53	112.60
1	A	200	PRO	N-CA-CB	5.93	106.30	103.22

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	981	LEU	CB-CA-C	5.92	117.98	109.11
2	B	212	ASP	CA-CB-CG	5.83	118.44	112.60
1	A	1382	ASP	CA-C-N	5.76	128.56	122.11
1	A	1382	ASP	C-N-CA	5.76	128.56	122.11
2	D	163	ARG	NE-CZ-NH2	5.68	124.31	119.20
1	A	880	TYR	CB-CA-C	5.67	115.55	110.44
1	A	58	HIS	CB-CG-CD2	-5.57	123.96	131.20
1	A	1460	PHE	CA-CB-CG	5.55	119.35	113.80
1	A	1444	HIS	CB-CG-CD2	-5.54	124.00	131.20
1	A	296	ASN	CA-CB-CG	5.53	118.13	112.60
1	A	385	ASP	CA-CB-CG	5.47	118.07	112.60
2	C	150	HIS	CB-CG-CD2	-5.45	124.12	131.20
1	A	1341	THR	CA-C-N	5.41	128.17	122.11
1	A	1341	THR	C-N-CA	5.41	128.17	122.11
1	A	580	ARG	N-CA-C	5.29	119.03	112.47
1	A	1374	GLU	CB-CA-C	5.09	119.17	110.56
2	B	167	ARG	NE-CZ-NH2	5.09	123.78	119.20
2	B	224	ASN	CA-CB-CG	5.09	117.69	112.60
1	A	222	ARG	NE-CZ-NH2	5.08	123.78	119.20
2	E	191	ARG	NE-CZ-NH2	5.07	123.77	119.20
1	A	1455	GLN	OE1-CD-NE2	-5.07	117.53	122.60
1	A	704	PHE	CA-CB-CG	5.06	118.86	113.80
1	A	892	PRO	N-CA-C	5.04	120.39	113.84
1	A	1444	HIS	CA-C-N	5.04	127.29	120.38
1	A	1444	HIS	C-N-CA	5.04	127.29	120.38
1	A	1209	ARG	NE-CZ-NH2	5.04	123.73	119.20
1	A	611	ASN	CA-CB-CG	5.02	117.62	112.60

There are no chirality outliers.

All (7) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1059	ARG	Sidechain
1	A	1164	ARG	Sidechain
1	A	269	PHE	Sidechain
1	A	586	TYR	Sidechain
1	A	606	TYR	Sidechain
1	A	770	TYR	Sidechain
1	A	834	TYR	Sidechain

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	11106	0	11295	6	0
2	B	762	0	780	1	0
2	C	437	0	459	1	0
2	D	424	0	443	1	0
2	E	424	0	450	0	0
All	All	13153	0	13427	8	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 0.

All (8) 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:1056:THR:HG21	1:A:1211:TRP:CH2	2.34	0.62
1:A:710:TYR:CE2	1:A:714:CYS:SG	3.04	0.49
1:A:121:ASP:OD1	1:A:187:THR:HG22	2.14	0.48
1:A:1056:THR:HG21	1:A:1211:TRP:CZ3	2.53	0.43
1:A:487:ILE:O	2:D:141:LYS:HE2	2.20	0.42
1:A:1065:GLY:HA3	1:A:1211:TRP:CH2	2.54	0.42
2:B:152:LEU:HB3	2:B:171:ILE:HD11	2.01	0.41
2:C:173:LEU:H	2:C:173:LEU:HD12	1.86	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	A	1353/2201 (62%)	1297 (96%)	56 (4%)	0	100	100
2	B	96/256 (38%)	93 (97%)	3 (3%)	0	100	100
2	C	55/256 (22%)	53 (96%)	2 (4%)	0	100	100
2	D	53/256 (21%)	53 (100%)	0	0	100	100
2	E	49/256 (19%)	49 (100%)	0	0	100	100
All	All	1606/3225 (50%)	1545 (96%)	61 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	1265/2041 (62%)	1236 (98%)	29 (2%)	44	70
2	B	85/233 (36%)	85 (100%)	0	100	100
2	C	47/233 (20%)	47 (100%)	0	100	100
2	D	46/233 (20%)	46 (100%)	0	100	100
2	E	46/233 (20%)	46 (100%)	0	100	100
All	All	1489/2973 (50%)	1460 (98%)	29 (2%)	49	73

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	15	THR
1	A	43	ASN
1	A	94	TYR
1	A	122	VAL
1	A	219	THR
1	A	225	GLU
1	A	268	GLN
1	A	307	ASN
1	A	311	THR
1	A	320	ILE

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Mol	Chain	Res	Type
1	A	401	LEU
1	A	509	THR
1	A	536	ILE
1	A	600	CYS
1	A	699	THR
1	A	700	ASP
1	A	727	GLN
1	A	760	LEU
1	A	869	MET
1	A	876	ASN
1	A	1025	LYS
1	A	1040	LEU
1	A	1177	ILE
1	A	1252	THR
1	A	1259	THR
1	A	1284	LYS
1	A	1310	GLU
1	A	1342	VAL
1	A	1403	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	43	ASN
1	A	52	GLN
1	A	216	ASN
1	A	307	ASN
1	A	417	ASN
1	A	590	ASN
1	A	650	ASN
1	A	739	HIS
1	A	827	GLN
1	A	895	ASN
1	A	930	ASN
1	A	936	GLN
1	A	943	ASN
1	A	1021	ASN
1	A	1098	GLN
1	A	1149	ASN
1	A	1285	GLN
1	A	1420	HIS
2	B	224	ASN

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Mol	Chain	Res	Type
2	E	189	ASN

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](#)

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.

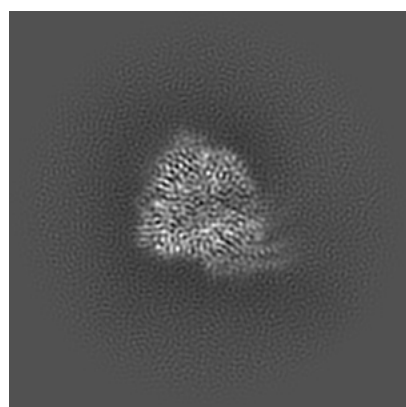
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-20536. These allow visual inspection of the internal detail of the map and identification of artifacts.

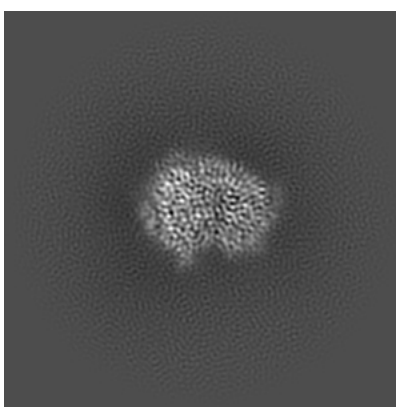
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

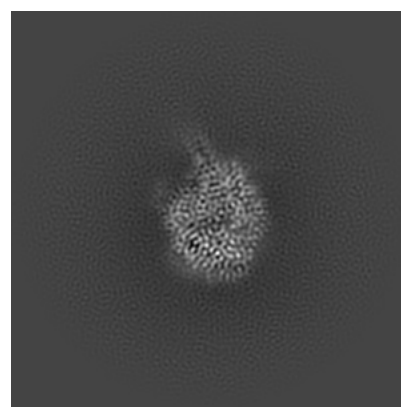
6.1.1 Primary map



X



Y

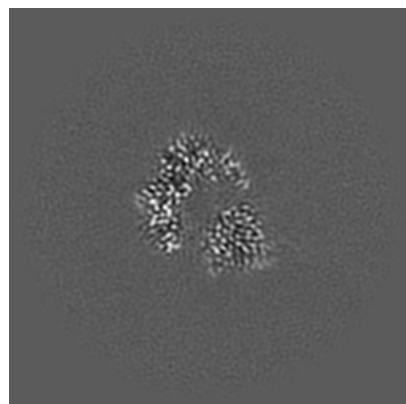


Z

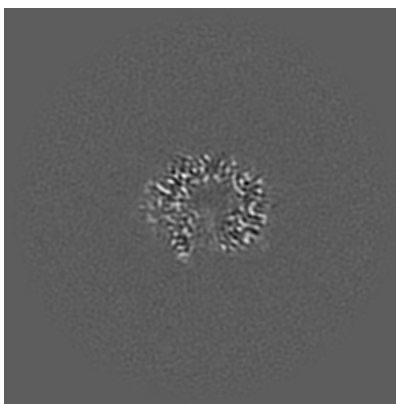
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

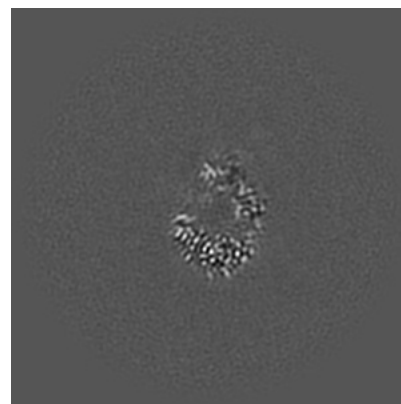
6.2.1 Primary map



X Index: 128



Y Index: 128

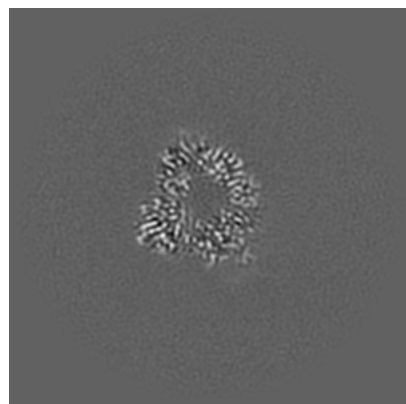


Z Index: 128

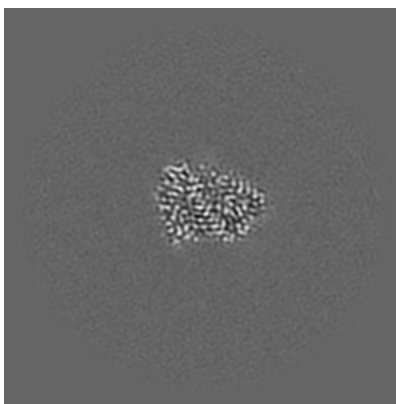
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

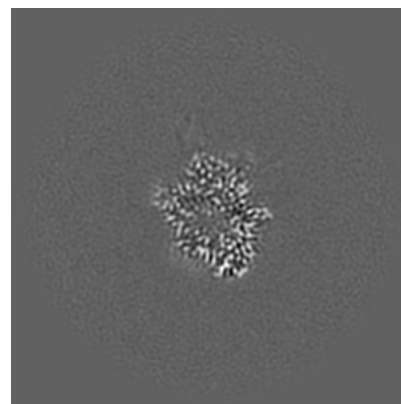
6.3.1 Primary map



X Index: 138



Y Index: 102

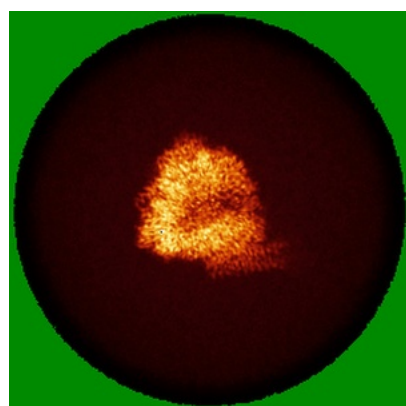


Z Index: 113

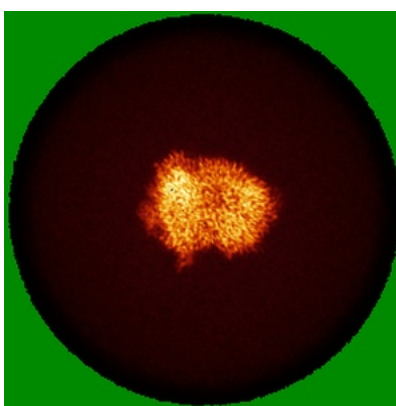
The images above show the largest variance slices of the map in three orthogonal directions.

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

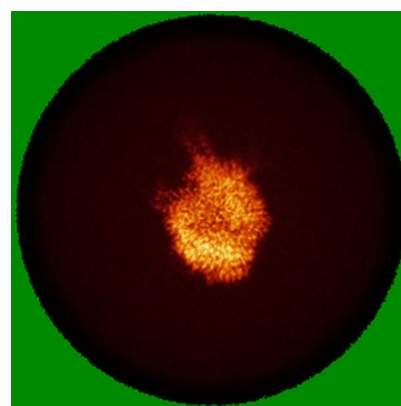
6.4.1 Primary map



X



Y

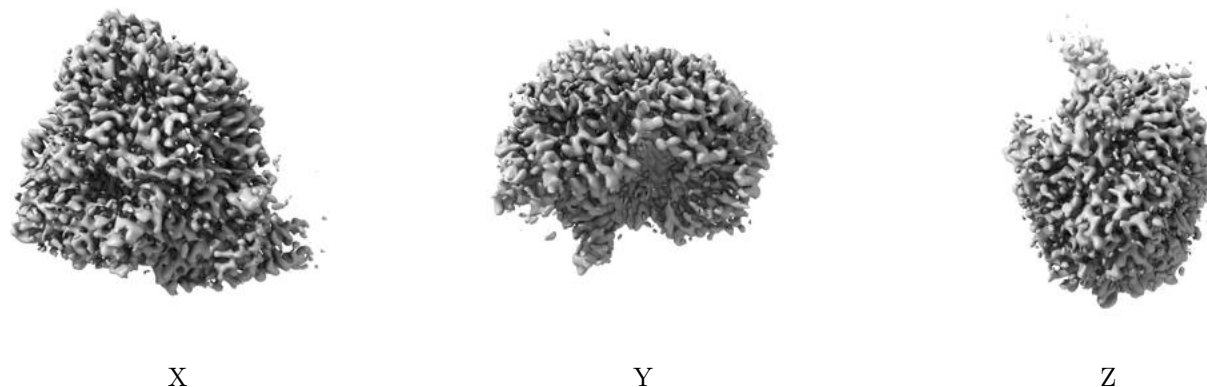


Z

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

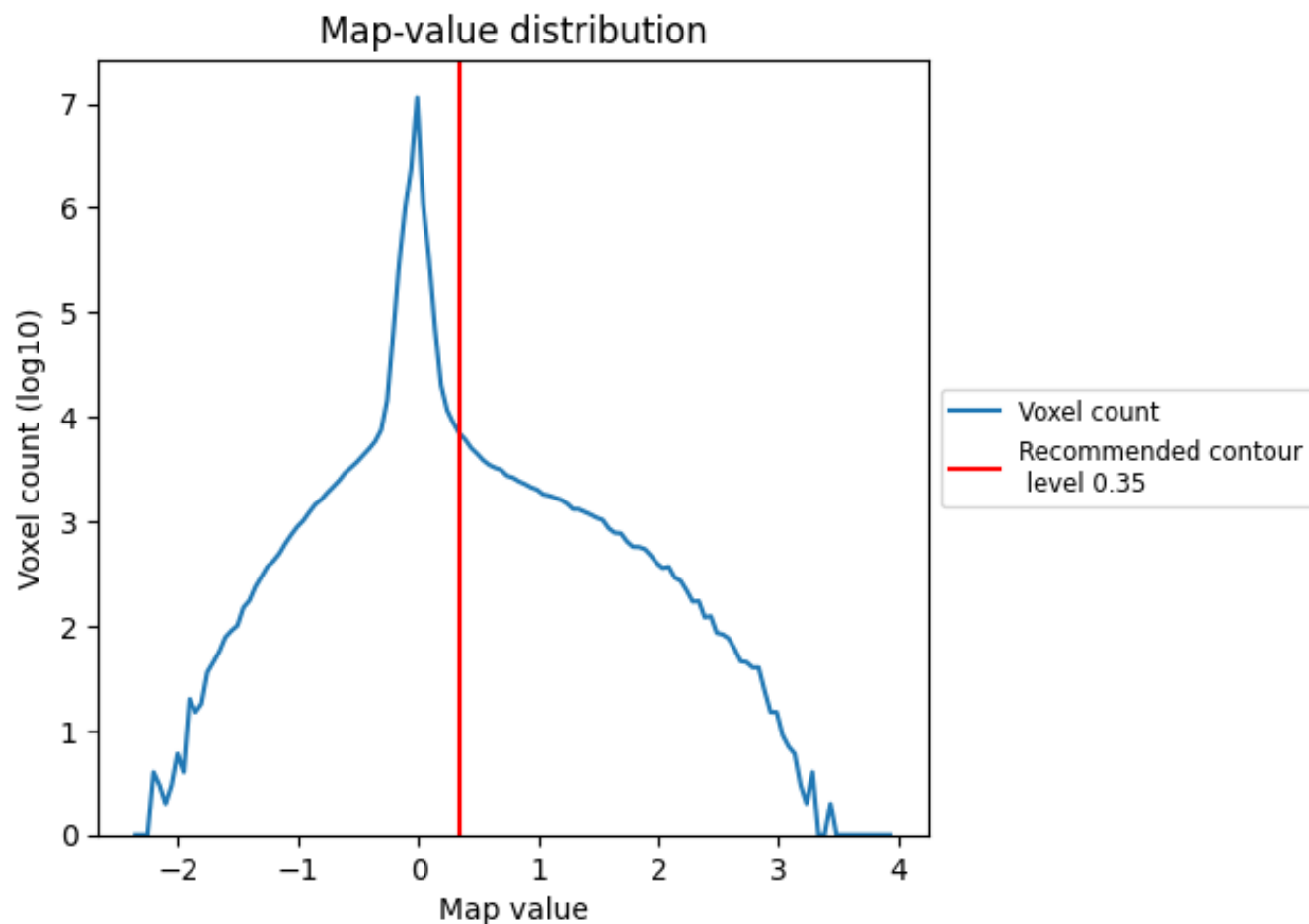
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

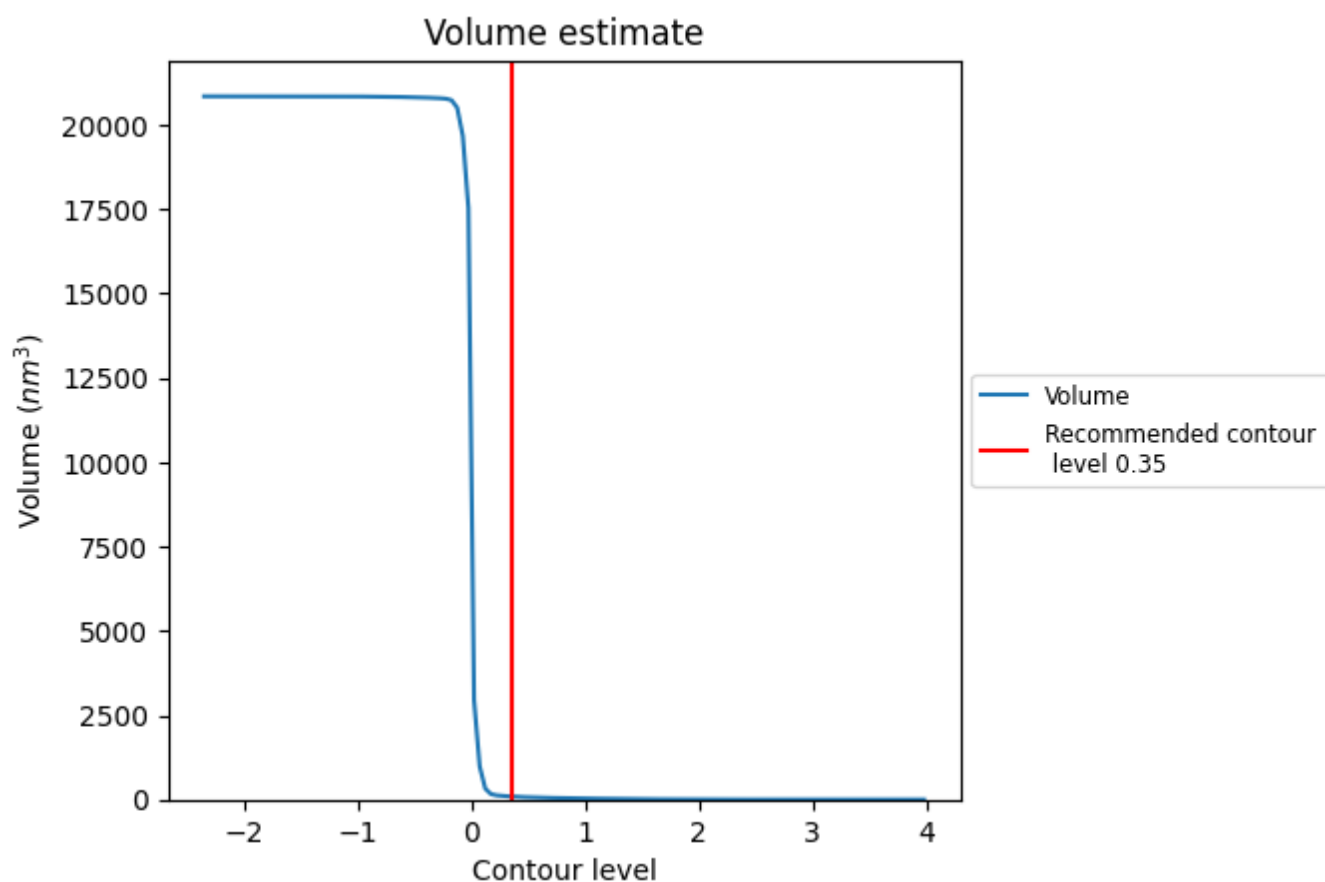
This section contains the results of statistical analysis of the map.

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.

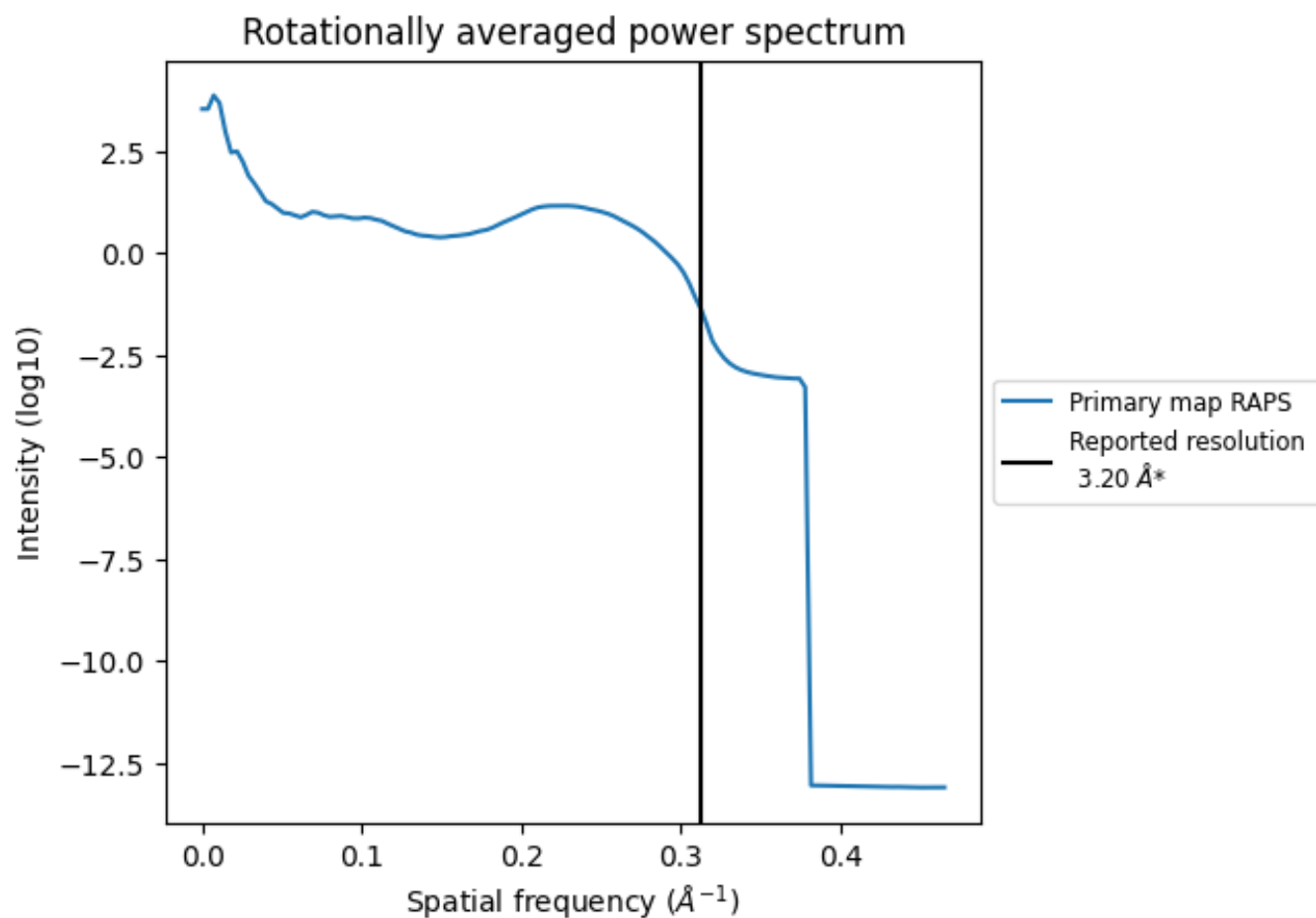
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 91 nm³; this corresponds to an approximate mass of 82 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 ⓘ

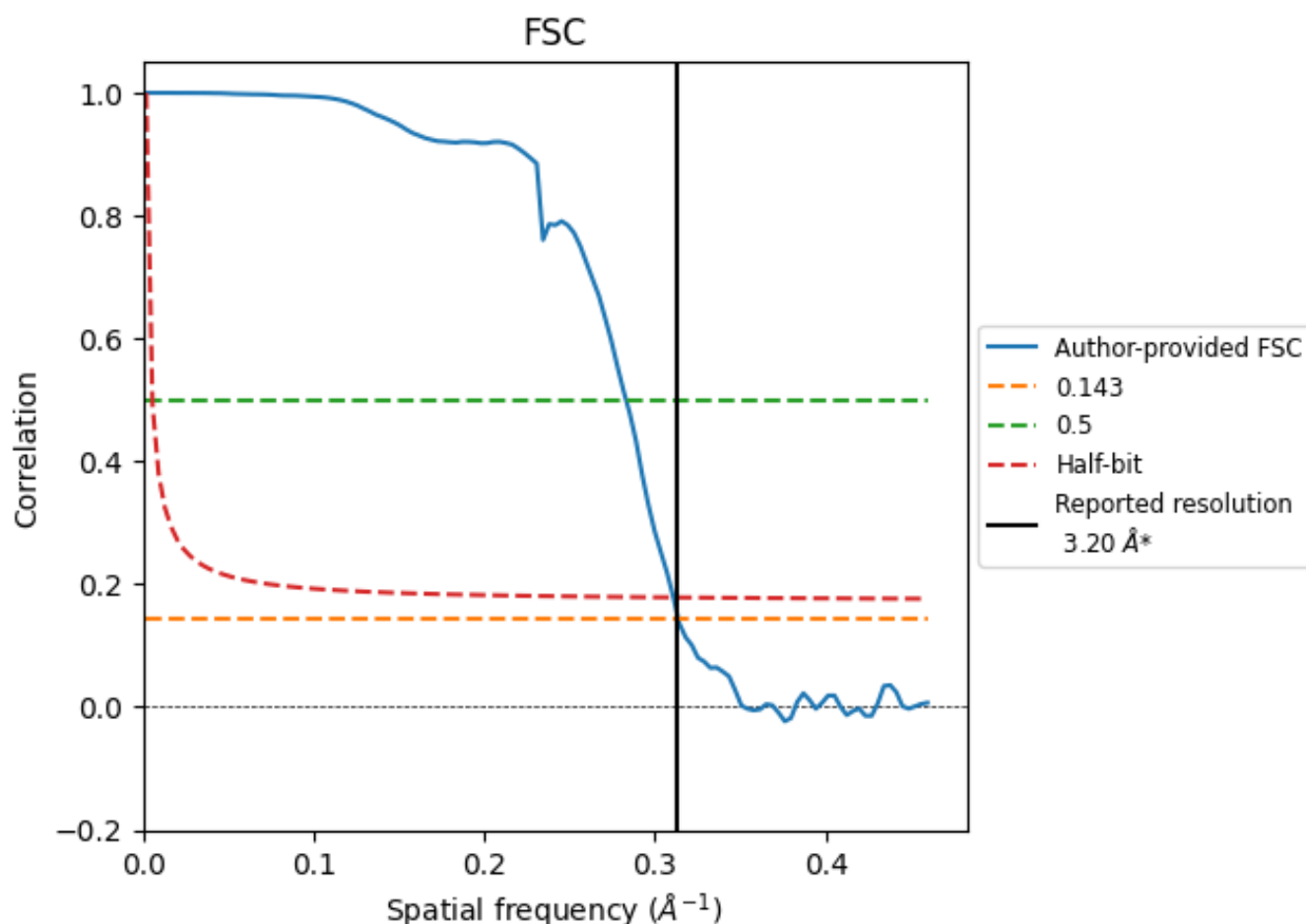


*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

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 0.312 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

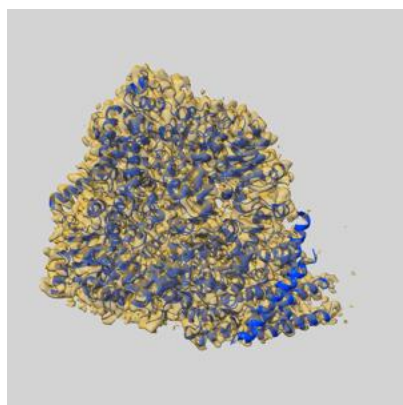
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	3.19	3.53	3.22
Unmasked-calculated*	-	-	-

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

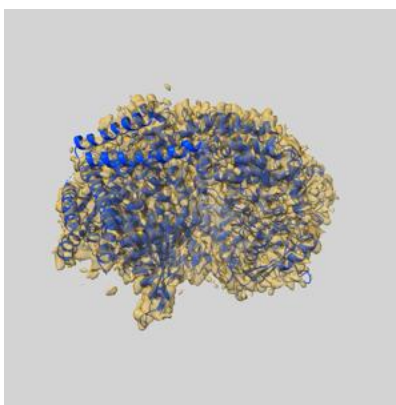
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-20536 and PDB model 6PZK. Per-residue inclusion information can be found in section 3 on page 7.

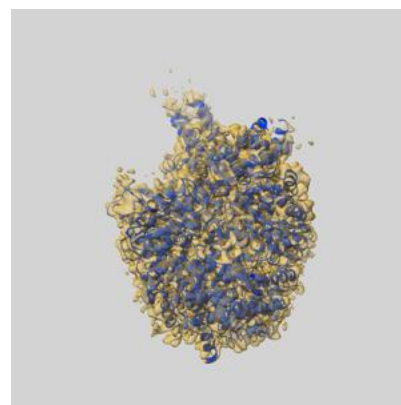
9.1 Map-model overlay [i](#)



X



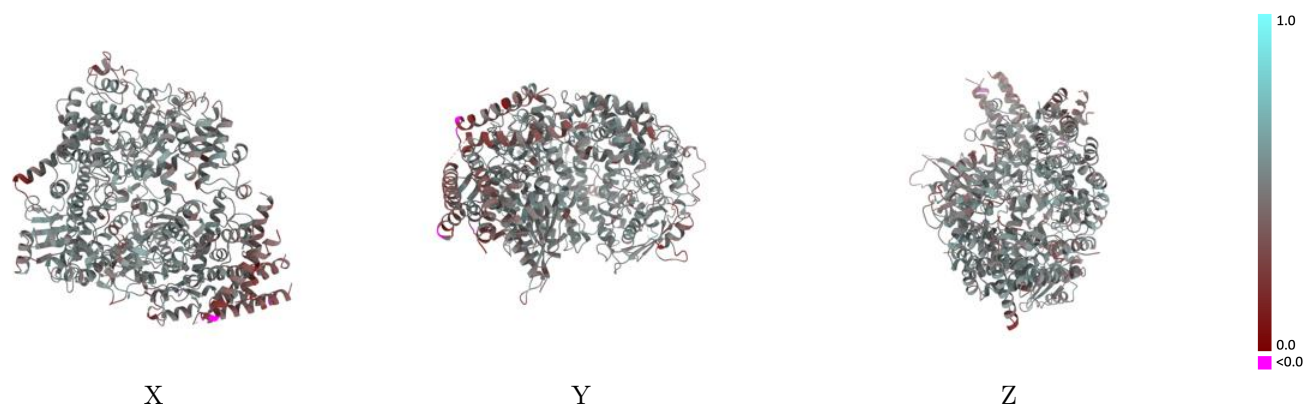
Y



Z

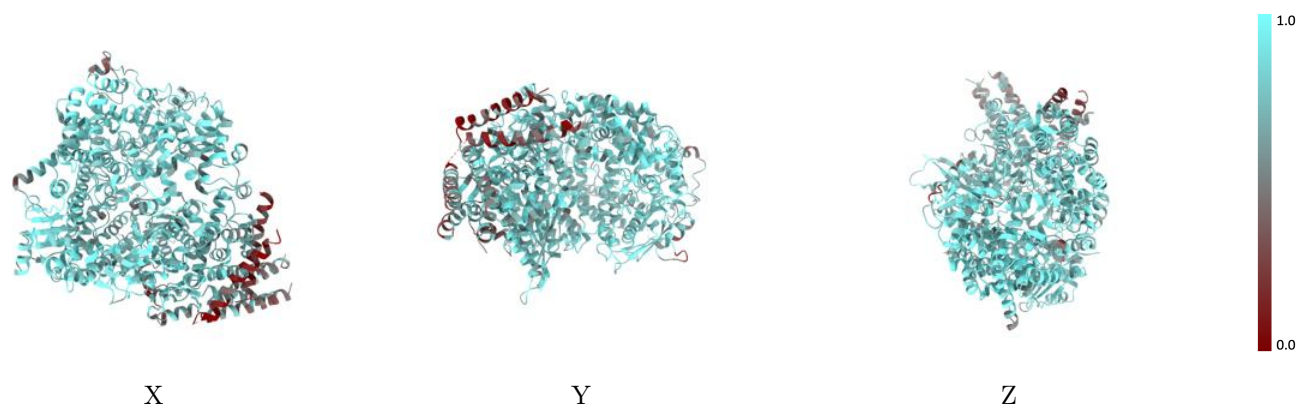
The images above show the 3D surface view of the map at the recommended contour level 0.35 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



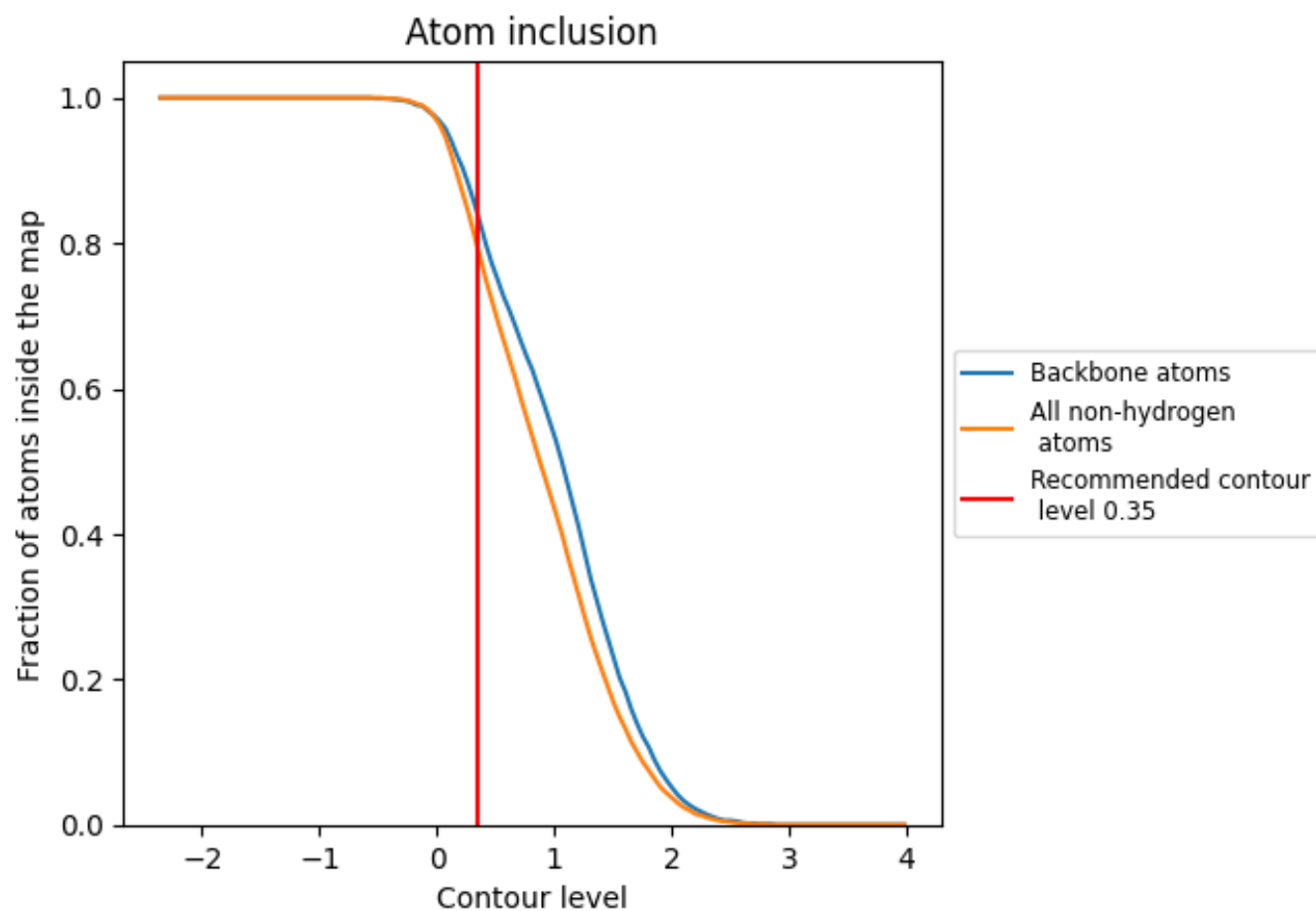
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.35).

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 79% 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 (0.35) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7920	0.4770
A	0.8340	0.4930
B	0.6460	0.4140
C	0.7130	0.4350
D	0.4150	0.3490
E	0.4020	0.3470

