



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 07:50 AM UTC

PDB ID : 6UXV / pdb_00006uxv
EMDB ID : EMD-20933
Title : SWI/SNF Body Module
Authors : He, Y.; Han, Y.
Deposited on : 2019-11-08
Resolution : 4.70 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:

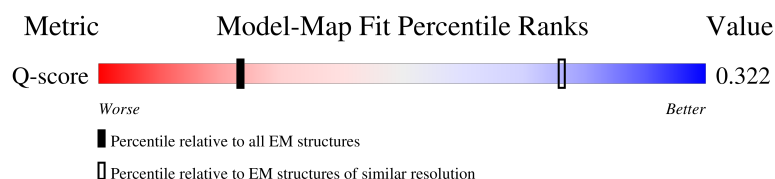
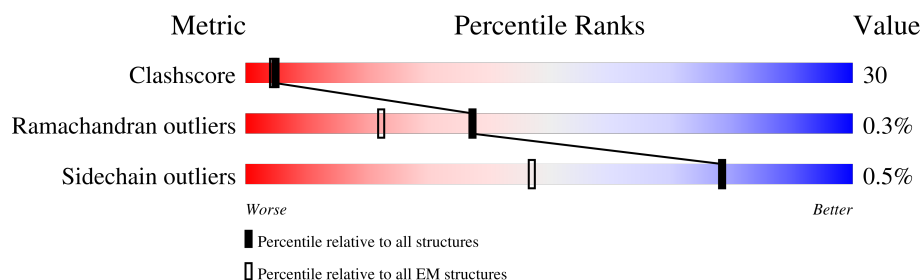
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 4.70 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.



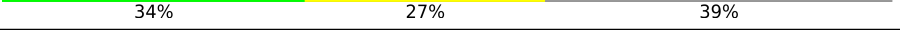
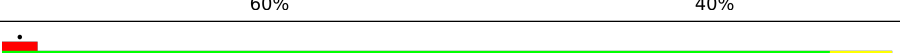
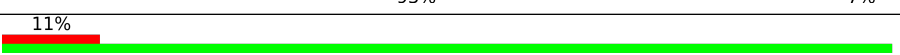
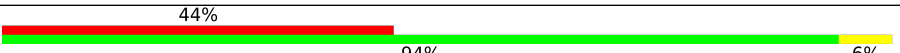
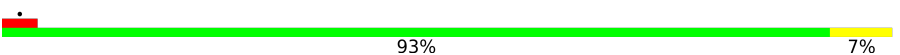
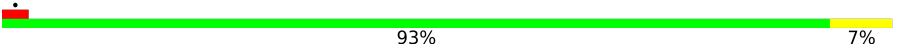
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	1989 (4.20 - 5.20)

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	1703	92%
2	B	1314	5% 15% 22% 63%
3	C	905	5% 10% 17% 73%
4	D	825	8% 11% 81%

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Mol	Chain	Length	Quality of chain
4	E	825	
4	F	825	
4	G	825	
5	H	566	
6	I	179	
7	J	67	
8	K	28	
9	L	18	
9	O	18	
10	M	83	
11	N	30	

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 16649 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 Transcription regulatory protein SNF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	140	Total	C	N	O	S	0	0
			1133	715	196	220	2		

- Molecule 2 is a protein called SWI/SNF chromatin-remodeling complex subunit SWI1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	482	Total	C	N	O	S	0	0
			3890	2519	637	723	11		

- Molecule 3 is a protein called SWI/SNF chromatin-remodeling complex subunit SNF5.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	245	Total	C	N	O	S	0	0
			2005	1256	346	395	8		

- Molecule 4 is a protein called SWI/SNF complex subunit SWI3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	159	Total	C	N	O	S	0	0
			1322	853	225	239	5		
4	E	139	Total	C	N	O	S	0	0
			1152	746	198	205	3		
4	F	221	Total	C	N	O	S	0	0
			1583	987	287	304	5		
4	G	197	Total	C	N	O	S	0	0
			1435	904	258	268	5		

- Molecule 5 is a protein called Transcription regulatory protein SNF12.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	H	257	Total	C	N	O	S	0	0
			2085	1323	355	400	7		

- Molecule 6 is a protein called Transcription regulatory protein SNF6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	I	109	Total	C	N	O	S	0	0
			818	504	155	156	3		

- Molecule 7 is a protein called Unknown protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	J	67	Total	C	N	O	0	0
			336	201	67	68		

- Molecule 8 is a protein called Unknown protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	K	28	Total	C	N	O	0	0
			141	84	28	29		

- Molecule 9 is a protein called Unknown protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	L	18	Total	C	N	O	0	0
			91	54	18	19		
9	O	18	Total	C	N	O	0	0
			91	54	18	19		

- Molecule 10 is a protein called SWI/SNF global transcription activator complex subunit SWP82.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	M	83	Total	C	N	O	0	0
			416	249	83	84		

- Molecule 11 is a protein called Unknown protein.

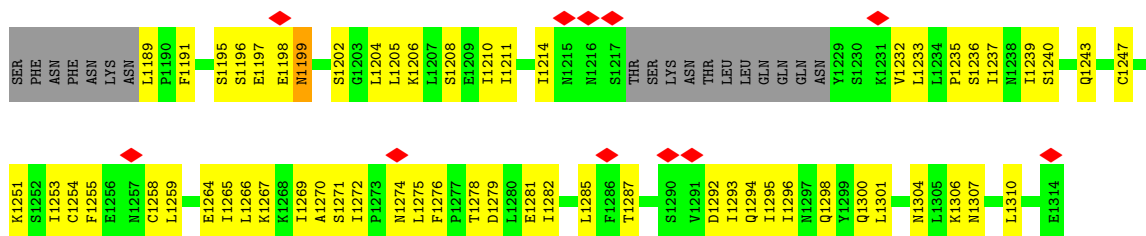
Mol	Chain	Residues	Atoms				AltConf	Trace
11	N	30	Total	C	N	O	0	0
			151	90	30	31		

[illegible]

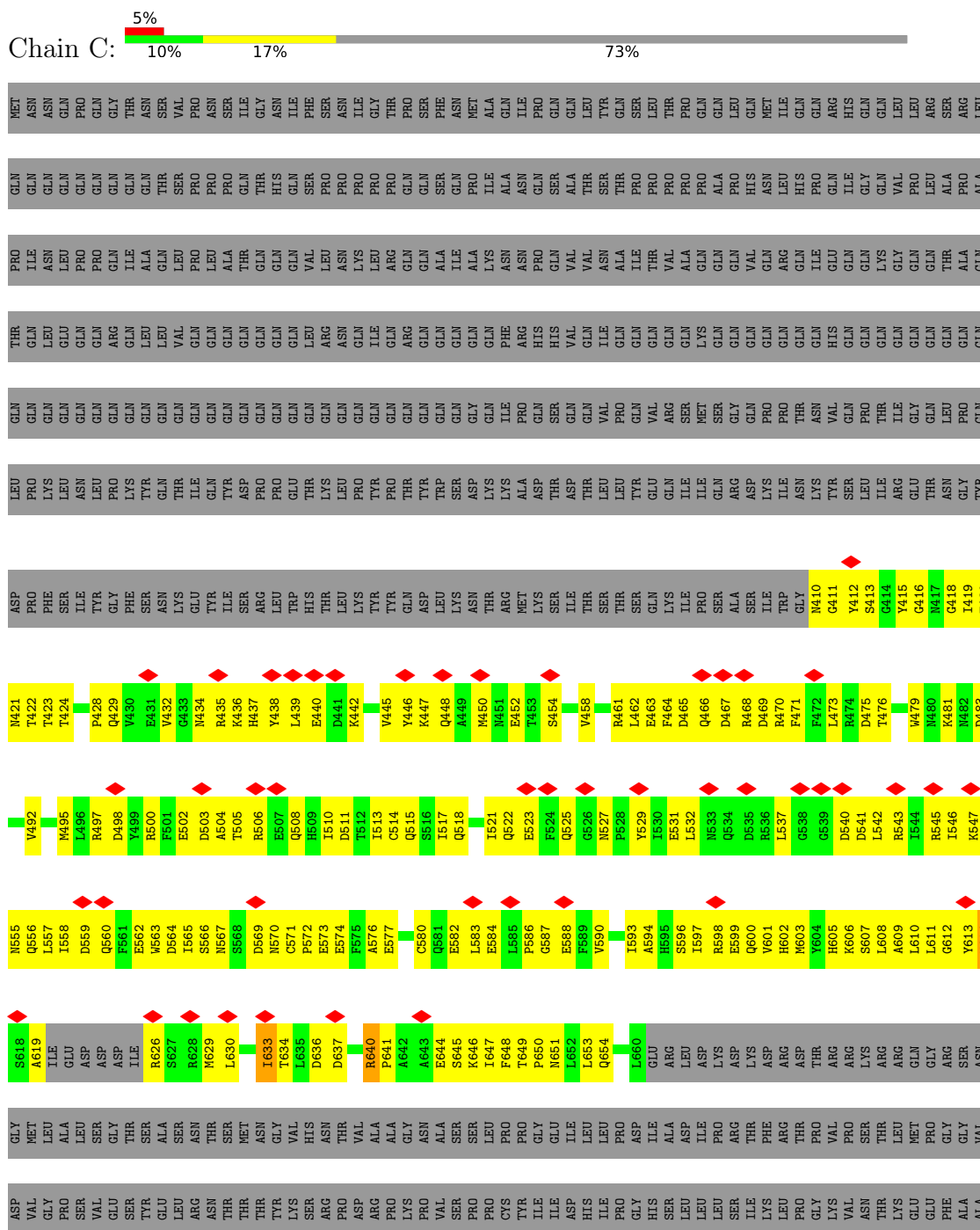
- Molecule 2: SWI/SNF chromatin-remodeling complex subunit SWI1

[illegible]



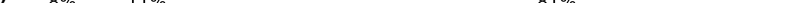


• Molecule 3: SWI/SNF chromatin-remodeling complex subunit SNF5



ALA	ALA	SER	LYS	SER	VAL	PRO	THR	PRO	SER	LEU	ILE	ALA	PRO	PRO	VAL	ALA	PRO	HIS	ASP	SER	GLU	ALA	THR	LEU	LEU	THR	ASN	SER	ASN	ASN	GLY	SER	SER	ASN	ASN	ASN	THR	GLN	ASN	THR
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- Molecule 4: SWI/SNF complex subunit SWI3

Chain D:  8% 11% 81%

PRO	ASN	THR	ARG	ASP	GLU	ALA	GLU	SER	GLU	ALA	ALA	THR	VAL	THR	ALA	LYS	GLN	GLN	PRO	THR	GLN	ASN	LYS	LEU	ASP	SER	GLN	GLU	THR	PRO	SER	THR	GLU	GLU	ARG	ALA	ALA	GLN	ASN	VAL	PHE	GLY	GLN	ASP	ASN	GLU	ASP	SER	ASP	ASN	LEU	PHE	GLY	GLU	THR	GLU	SER	SER
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VAL	SER	ASN	GLU	ALA	ASN	THR	PRO	THR	ASN	PRO	VAL	ASP	ASN	GLU	ASN	ASN	LYS	PRO	ALA	ILE	LYS	GLU	ASP	SER	THR	ILE	GLN	ASP	SER	ASN	GLY	ASP	VAL	LYS	ASN	MET	ILE	LYS	GLN	LYS	GLU	GLU	PRO	GLU	ASN	ASN	THR	VAL	ILE	GLU	GLY
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VAL	LYS	GLU	SER	GLN	PRO	ASP	GLU	ASN	THR	LYS	GLU	MET	ASP	GLU	VAL	GLU	GLU	ASP	ASP	GLN	PRO	PRO	MET	ILE	SER	SER	PRO	ASP	ASN	SER	ILE	PHE	GLY	ASP	THR	LYS	SER	GLU	LYS	GLN	LEU	GLY	ASN	THR	SER	VAL	ALA	ASN	THR	PRO	GLU	ILE	PRO
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ASP	ALA	HIS	LYS	ALA	GLU	GLN	GLU	ASP	ILE	ILE	GLU	LYS	THR	GLU	VAL	ASP	SER	SER	GLY	GLU	GLU	ARG	ASN	GLN	GLU	ARG	GLU	ILE	ILE	MET	ASP	ASN	LYS	SER	HIS	ASP	ASP	GLY	GLU	THR	THR	ILE	THR	ARG	VAL	GLU	PRO	GLU	THR	PHE	GLU	GLU	ILE	PRO
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[illegible]

A367	A368	A369	A370	A371	A372	A373	A374	A375	A376	A377	A378	A379	A380	A381	A382	A383	A384	A385	A386	A387	A388	A389	A390	A391	A392	A393	A394	A395	A396	A397	A398	A399	A400	A401	A402	A403	A404	A405	A406	A407	A408	A409	A410	A411	A412	A413	A414	A415	A416	A417	A418	A419	A420	A421	A422	A423	A424	A425	A426	A427	A428	A429	A430	A431	A432	A433	A434	A435	A436	A437	A438	A439	A440	A441	A442	A443	A444	A445	A446	A447	A448	A449	A450	A451	A452	A453	A454	A455	A456	A457	A458	A459	A460	A461	A462	A463	A464	A465	A466	A467	A468	A469	A470	A471	A472	A473	A474	A475	A476	A477	A478	A479	A480	A481	A482	A483	A484	A485	A486	A487	A488	A489	A490	A491	A492	A493	A494	A495	A496	A497	A498	A499	A500
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Residue	Position	Frequency (%)	Conservation Score
K441	1	0.8	0.9
K442	2	0.7	0.8
M443	3	0.6	0.7
M444	4	0.5	0.6
N445	5	0.4	0.5
T446	6	0.3	0.4
S447	7	0.2	0.3
D448	8	0.1	0.2
S449	9	0.0	0.1
E450	10	0.9	0.9
S451	11	0.8	0.8
T452	12	0.7	0.7
L453	13	0.6	0.6
Y454	14	0.5	0.5
K455	15	0.4	0.4
Y456	16	0.3	0.3
L457	17	0.2	0.2
K458	18	0.1	0.1
E459	19	0.9	0.9
S460	20	0.8	0.8
K461	21	0.7	0.7
R462	22	0.6	0.6
LYS	23	0.5	0.5
TYR	24	0.4	0.4
ASP	25	0.3	0.3
GLU	26	0.2	0.2
ILE	27	0.1	0.1
THR	28	0.0	0.0
HIS	29	0.9	0.9
PRO	30	0.8	0.8
PRO	31	0.7	0.7
SER	32	0.6	0.6
THR	33	0.5	0.5
THR	34	0.4	0.4
ASP	35	0.3	0.3
ASP	36	0.2	0.2
GLU	37	0.1	0.1
GLN	38	0.9	0.9
GLY	39	0.8	0.8
ASP	40	0.7	0.7
LYS	41	0.6	0.6
ASN	42	0.5	0.5
ASP	43	0.4	0.4
ASN	44	0.3	0.3
GLY	45	0.2	0.2
GLY	46	0.1	0.1
LYS	47	0.9	0.9
MET	48	0.8	0.8
ASN	49	0.7	0.7
ASN	50	0.6	0.6
GLU	51	0.5	0.5
VAL	52	0.4	0.4
SER	53	0.3	0.3
THR	54	0.2	0.2
SER	55	0.1	0.1
THR	56	0.9	0.9
MET	57	0.8	0.8
THR	58	0.7	0.7

GLY	ASP	ALA	ASN	LEU	LEU	GLU	GLU	GLY	THR	SER	ARG	PRO	LEU	LYS	LYS	VAL	LYS	ILE	LEU	GLU	GLN	ILE	ASP	GLU	ASN	TRP	SER	LYS	GLY	ASP	LEU	LYS	GLN	GLU	PHE	GLY	ALA	ASP	TRP	TYR	LYS	VAL	ALA	LYS	ASN	VAL	GLY	ASN	LYS	SER	LYS	PRO	GLU
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[illegible]

PRO	LYS	THR	VAL	GLN	SER	MET	THR	GLN	ARG	ALA	ILE	ALA	GLN	SER	ALA	GLU	GLY	SER	ILE	LYS	SER	GLN	LYS	GLU	GLU	ILE	ILE	ASP	ASN	GLN	LYS	GLN	PRO	PRO	ILE	ILE	GLU	GLY	SER	GLU	ILE	ILE	ALA	ALA	SER	SER	HIS	ILE	PHE	TYR	ARG	SER	HIS	ILE	ILE	GLY	GLY	THR	ALA	GLN	GLN	GLU	GLU	ARG	GLN	MET
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ASN	PHE	LEU	THR	ASN	GLU	LEU	I LE	ARG	LEU	GLN	MET	MET	GLU	LYS	LEU	ASN	HIS	LEU	LYS	LYS	LEU	GLU	LYS	PHE	MET	MET	GLU	LEU	GLU	ARG	LYS	THR	LEU	GLU	ARG	GLN	GLN	GLN	ARG	LEU	ASN	LEU	LEU	LEU	I LE	ILE	GLN	GLN	ASN	SER	SER	LYS	ILE	VAL	ASN	ASN
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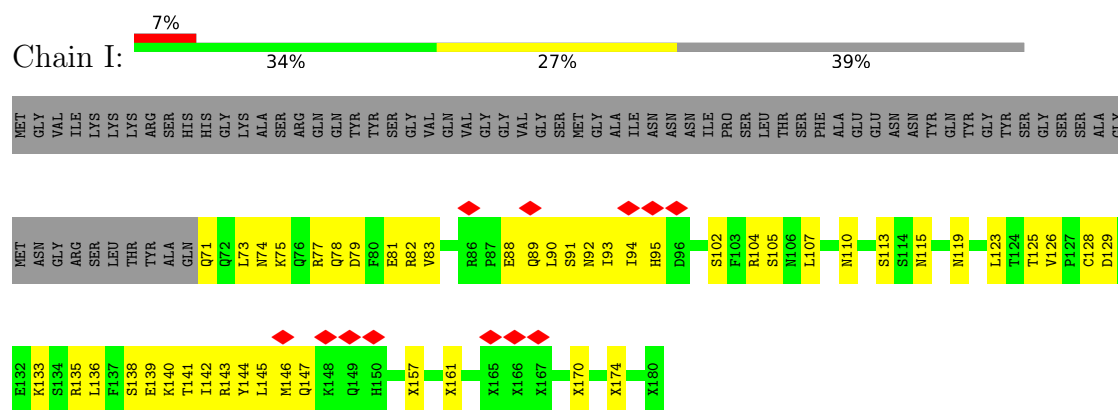
LEU SER
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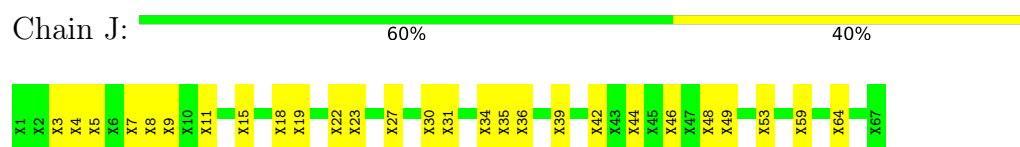
- Molecule 4: SWI/SNF complex subunit SWI3

Chain E: 8% 9% 83%

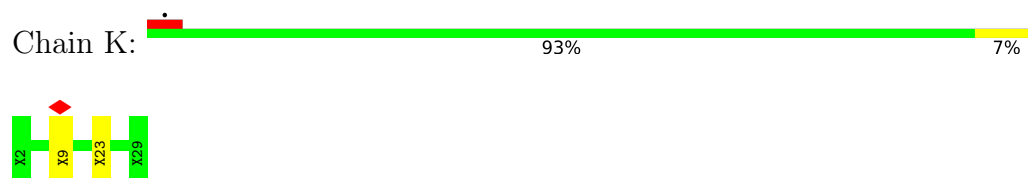




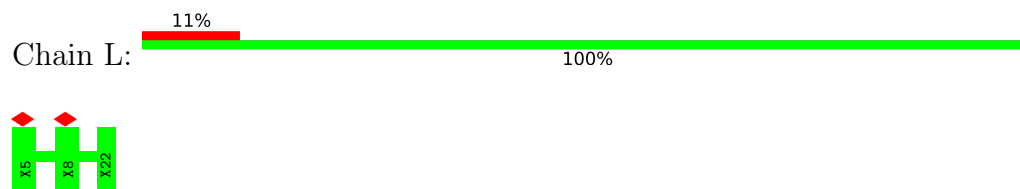
- Molecule 7: Unknown protein



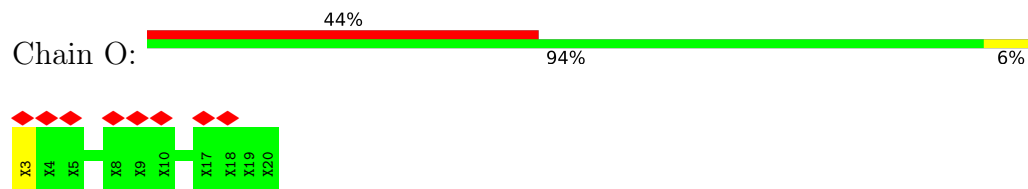
- Molecule 8: Unknown protein



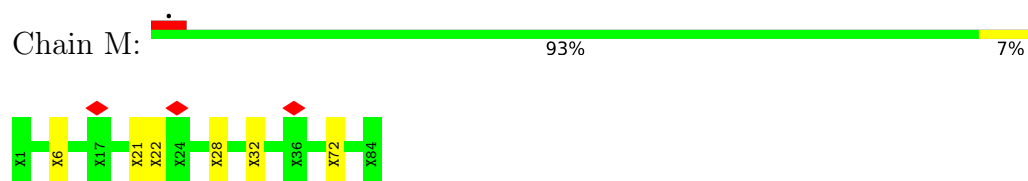
- Molecule 9: Unknown protein



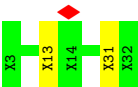
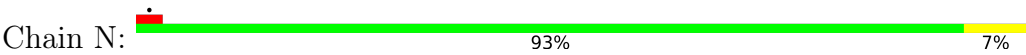
- Molecule 9: Unknown protein



- Molecule 10: SWI/SNF global transcription activator complex subunit SWP82



- Molecule 11: Unknown protein



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	61518	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY; CTF amplitude correction was performed following 3D auto refinement in relion.	Depositor
Microscope	JEOL 3200FS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	76.5	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	0.093	Depositor
Minimum map value	-0.040	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.035	Depositor
Map size ($\text{\AA}$)	430.08002, 430.08002, 430.08002	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.12, 1.12, 1.12	Depositor

5 Model quality

5.1 Standard geometry

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	0.31	0/1154	0.46	0/1572
2	B	0.35	0/3958	0.53	0/5364
3	C	0.31	0/2040	0.64	2/2756 (0.1%)
4	D	0.26	0/1359	0.45	0/1838
4	E	0.34	0/1189	0.53	0/1616
4	F	0.29	0/1596	0.58	5/2154 (0.2%)
4	G	0.32	0/1446	0.58	3/1949 (0.2%)
5	H	0.33	1/2119 (0.0%)	0.47	0/2856
6	I	0.29	0/682	0.45	0/913
All	All	0.32	1/15543 (0.0%)	0.53	10/21018 (0.0%)

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
2	B	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	H	544	ASN	CA-C	-5.00	1.44	1.52

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	640	ARG	CA-C-N	10.75	133.28	119.84
3	C	640	ARG	C-N-CA	10.75	133.28	119.84
4	F	649	PRO	N-CA-CB	8.31	110.58	103.35
4	F	606	PRO	N-CA-CB	7.99	111.64	103.25
4	F	599	PRO	N-CA-CB	7.17	110.36	103.19

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	776	ASP	Peptide
2	B	932	ASP	Peptide

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	1133	0	1122	88	0
2	B	3890	0	4008	263	0
3	C	2005	0	1939	171	0
4	D	1322	0	1325	100	0
4	E	1152	0	1137	87	0
4	F	1583	0	1397	78	0
4	G	1435	0	1294	63	0
5	H	2085	0	2104	149	0
6	I	818	0	708	68	0
7	J	336	0	70	18	0
8	K	141	0	33	3	0
9	L	91	0	21	0	0
9	O	91	0	21	2	0
10	M	416	0	92	4	0
11	N	151	0	41	3	0
All	All	16649	0	15312	945	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 30.

The worst 5 of 945 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)
4:D:412:TYR:CD1	5:H:560:ILE:HG23	1.62	1.34
4:D:412:TYR:CD1	5:H:560:ILE:CG2	2.12	1.32
4:D:412:TYR:CG	5:H:560:ILE:HG21	1.93	1.02
1:A:570:LYS:HE2	6:I:90:LEU:H	1.25	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:412:TYR:HD1	5:H:560:ILE:HG23	1.16	0.95

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	138/1703 (8%)	118 (86%)	20 (14%)	0	100	100
2	B	468/1314 (36%)	364 (78%)	104 (22%)	0	100	100
3	C	241/905 (27%)	176 (73%)	63 (26%)	2 (1%)	16	53
4	D	157/825 (19%)	131 (83%)	26 (17%)	0	100	100
4	E	137/825 (17%)	113 (82%)	24 (18%)	0	100	100
4	F	215/825 (26%)	186 (86%)	27 (13%)	2 (1%)	14	49
4	G	189/825 (23%)	164 (87%)	24 (13%)	1 (0%)	24	63
5	H	249/566 (44%)	217 (87%)	32 (13%)	0	100	100
6	I	78/179 (44%)	67 (86%)	11 (14%)	0	100	100
All	All	1872/7967 (24%)	1536 (82%)	331 (18%)	5 (0%)	37	72

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	F	606	PRO
3	C	614	ASN
4	G	572	ASP
4	F	648	LYS
3	C	612	GLY

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	129/1520 (8%)	129 (100%)	0	100	100
2	B	460/1218 (38%)	459 (100%)	1 (0%)	87	86
3	C	222/823 (27%)	220 (99%)	2 (1%)	70	77
4	D	150/751 (20%)	150 (100%)	0	100	100
4	E	129/751 (17%)	129 (100%)	0	100	100
4	F	138/751 (18%)	138 (100%)	0	100	100
4	G	127/751 (17%)	126 (99%)	1 (1%)	73	78
5	H	239/517 (46%)	235 (98%)	4 (2%)	53	68
6	I	79/133 (59%)	79 (100%)	0	100	100
All	All	1673/7215 (23%)	1665 (100%)	8 (0%)	78	82

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	H	562	SER
5	H	561	LEU
5	H	494	LEU
4	G	571	GLU
5	H	538	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 66 such sidechains are listed below:

Mol	Chain	Res	Type
5	H	102	GLN
5	H	118	ASN
6	I	76	GLN
2	B	1260	ASN
2	B	1243	GLN

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
6	I	1
10	M	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	I	150:HIS	C	152:UNK	N	20.17
1	M	22:UNK	C	24:UNK	N	7.86

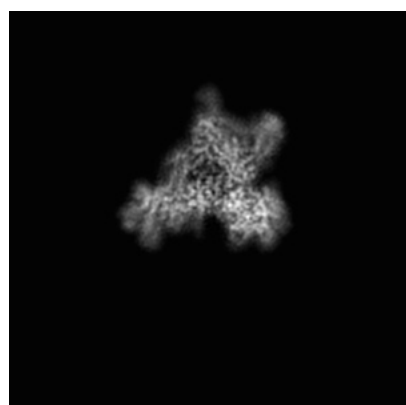
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-20933. These allow visual inspection of the internal detail of the map and identification of artifacts.

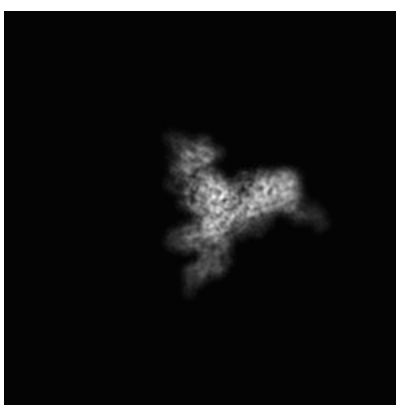
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

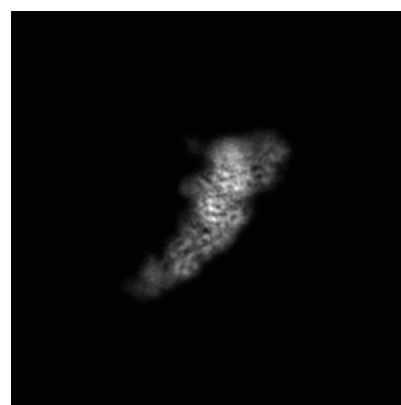
6.1.1 Primary map



X



Y

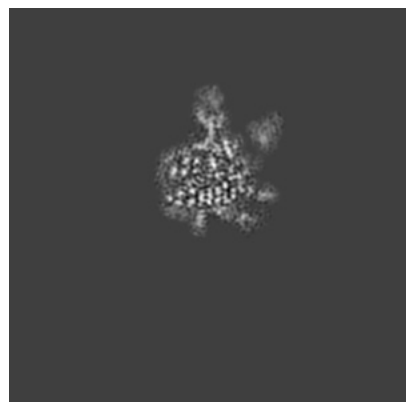


Z

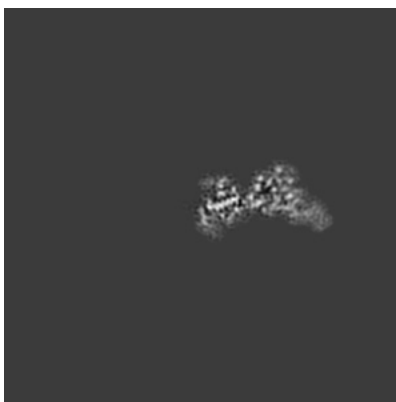
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

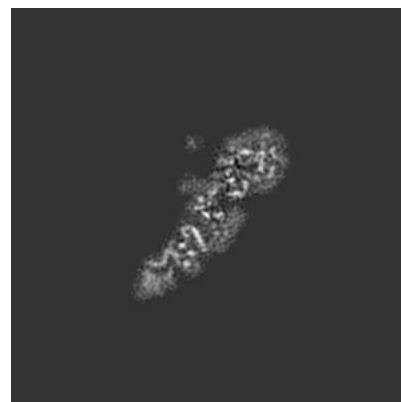
6.2.1 Primary map



X Index: 192



Y Index: 192

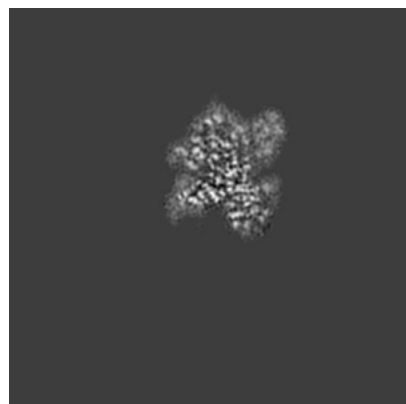


Z Index: 192

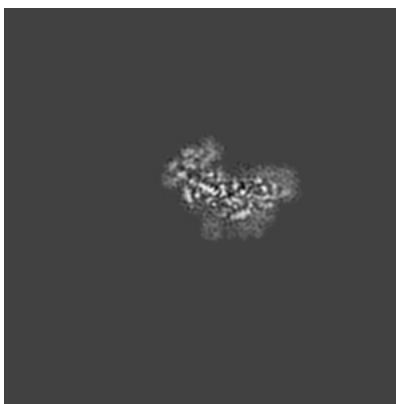
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 204



Y Index: 218

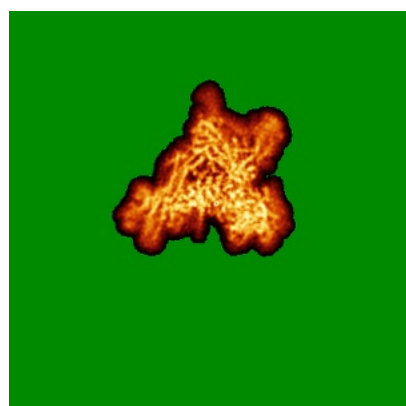


Z Index: 197

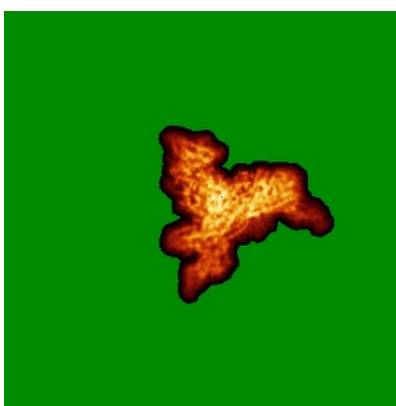
The images above show the largest variance slices of the map in three orthogonal directions.

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

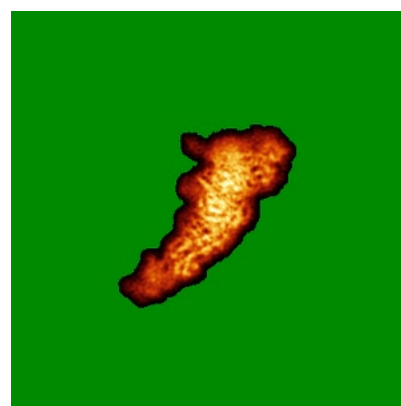
6.4.1 Primary map



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

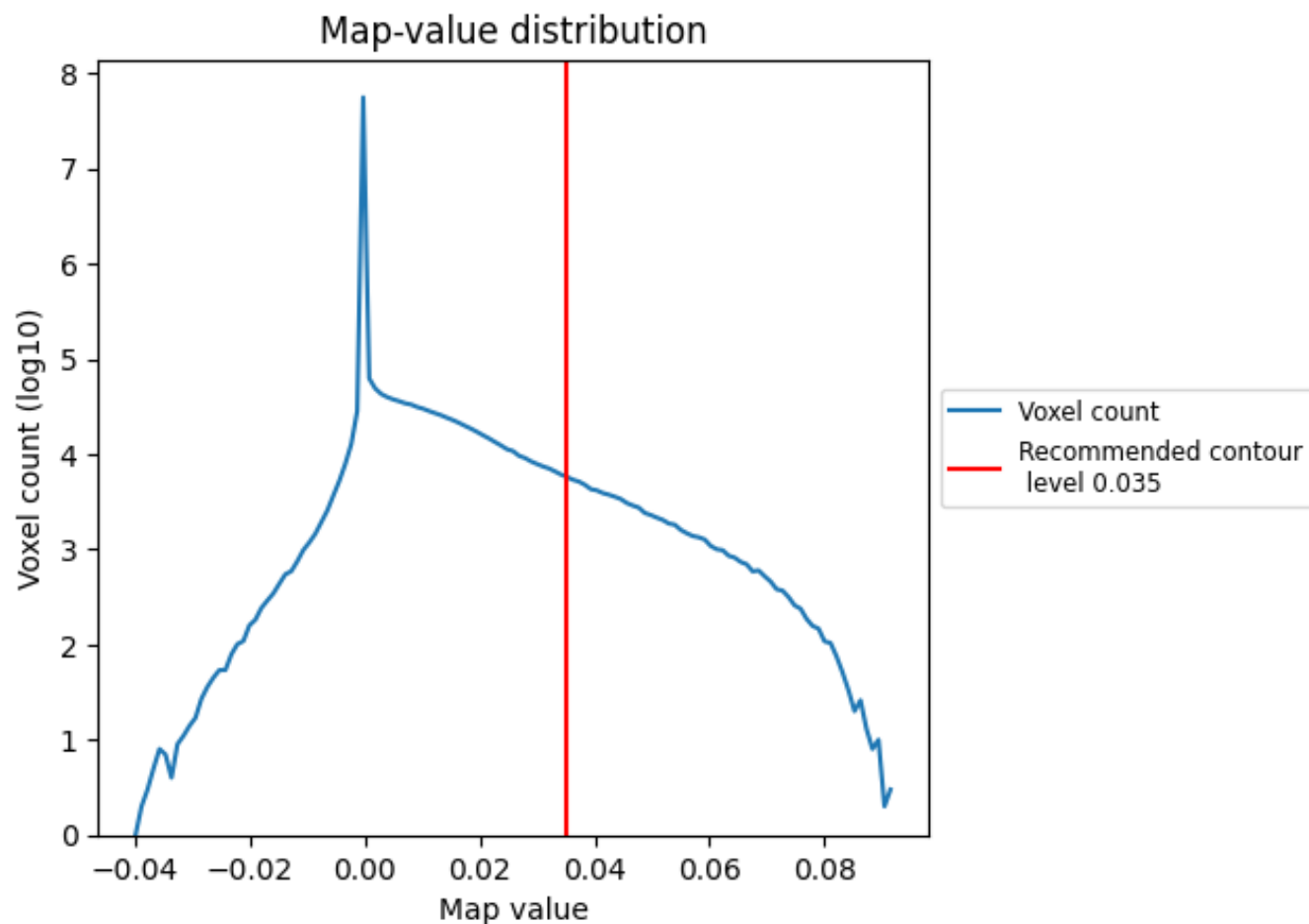
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

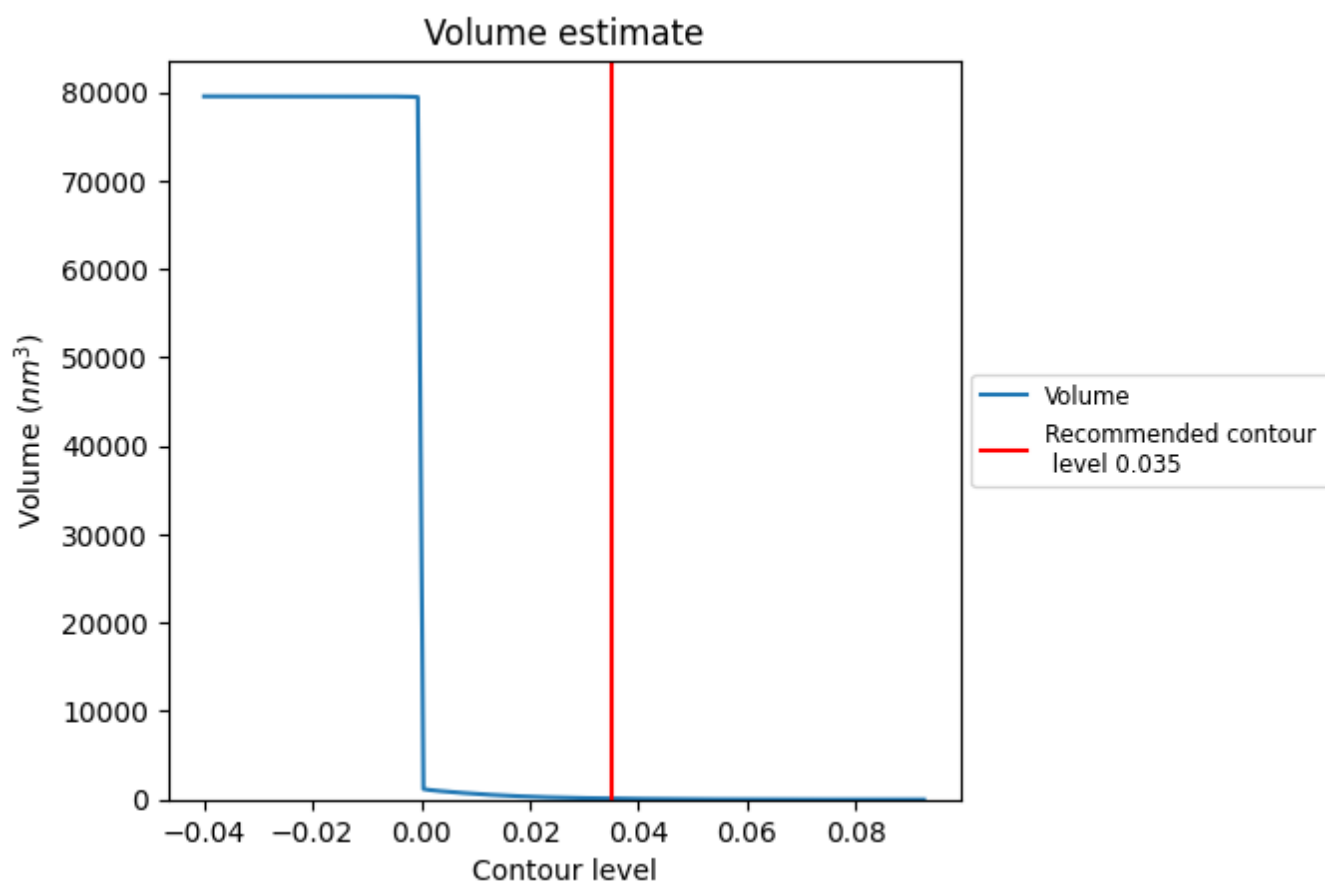
This section contains the results of statistical analysis of the map.

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.

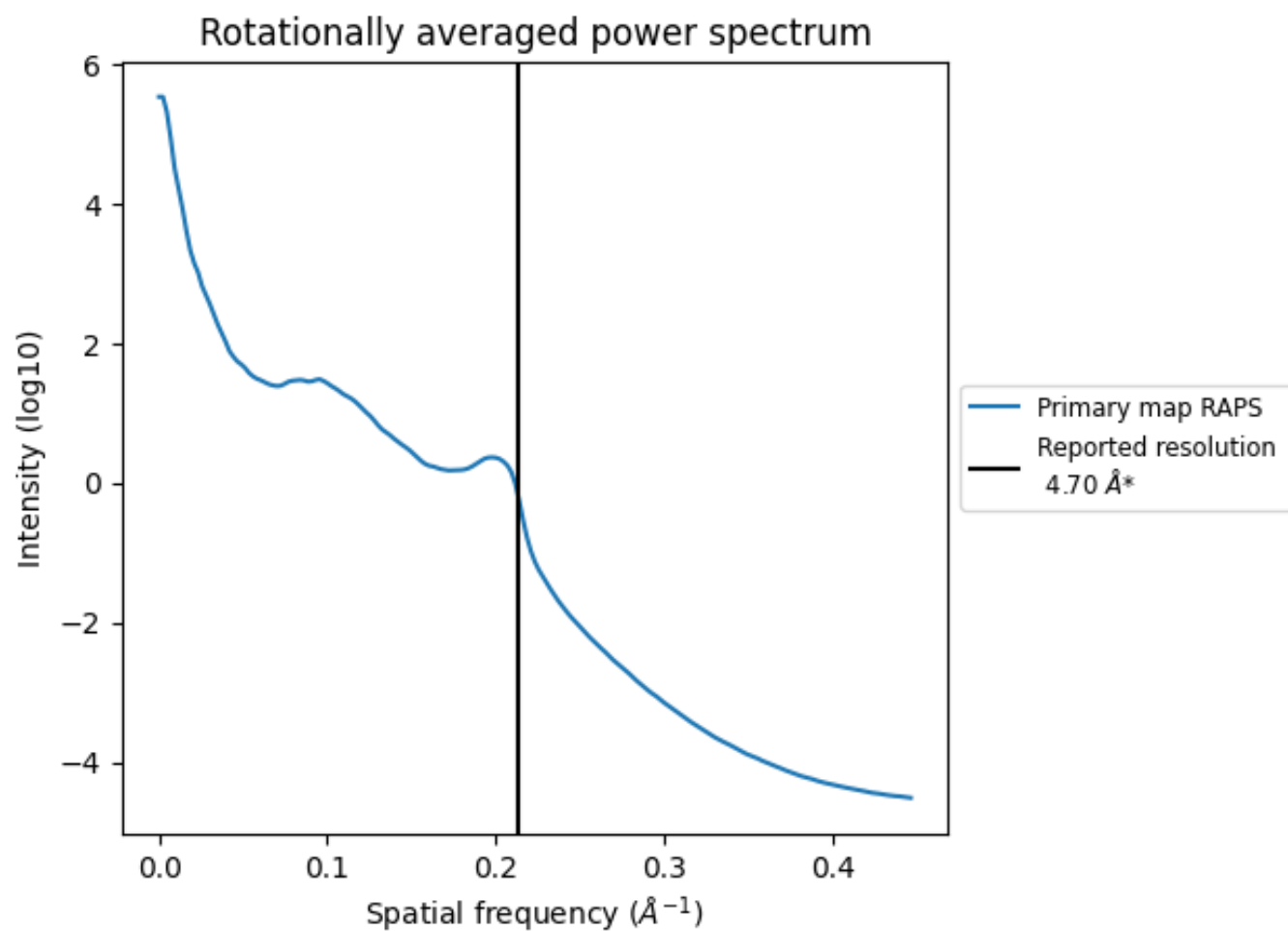
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 118 nm³; this corresponds to an approximate mass of 107 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 ⓘ

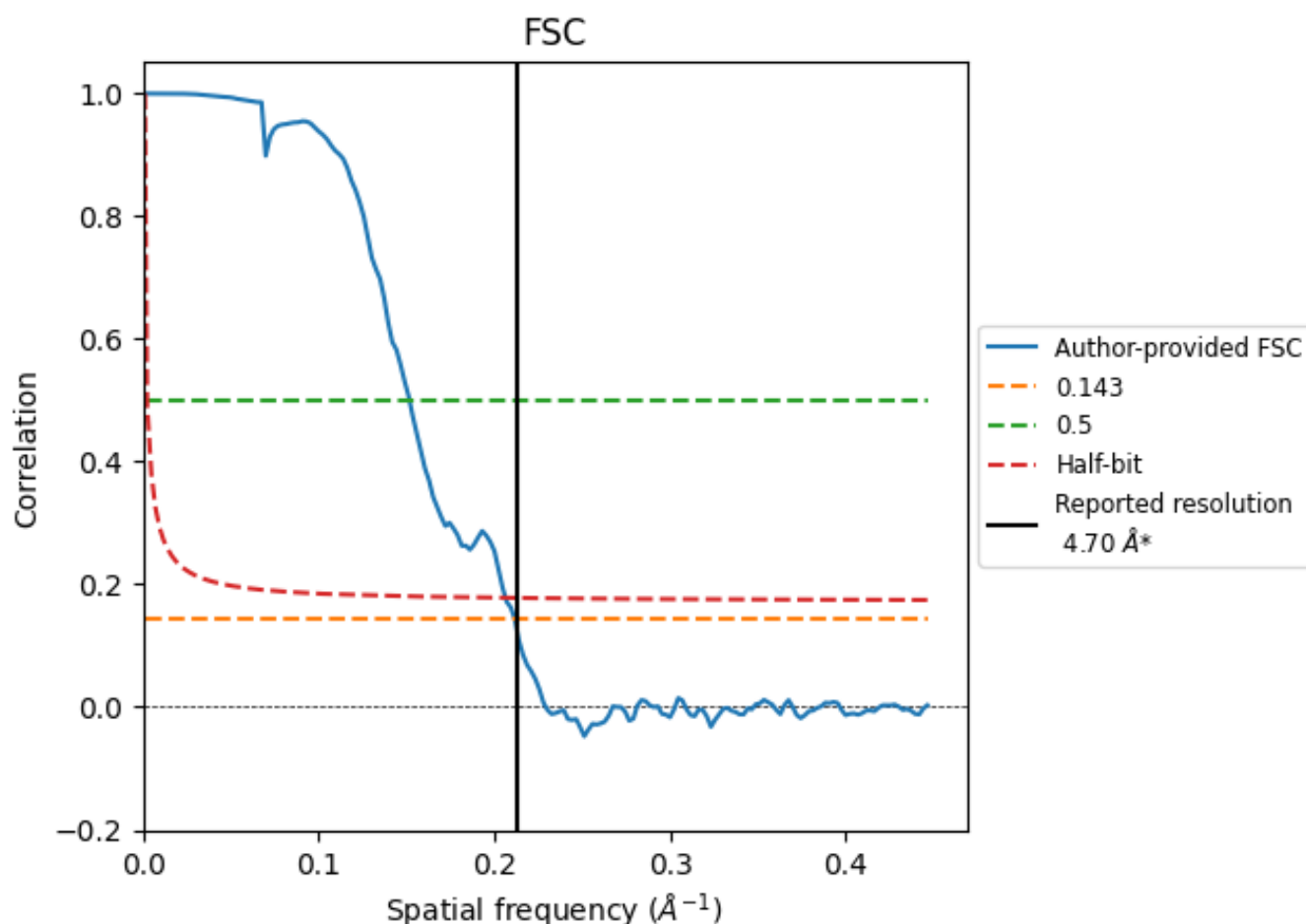


*Reported resolution corresponds to spatial frequency of 0.213 Å⁻¹

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 0.213 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.70	-	-
Author-provided FSC curve	4.73	6.60	4.85
Unmasked-calculated*	-	-	-

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

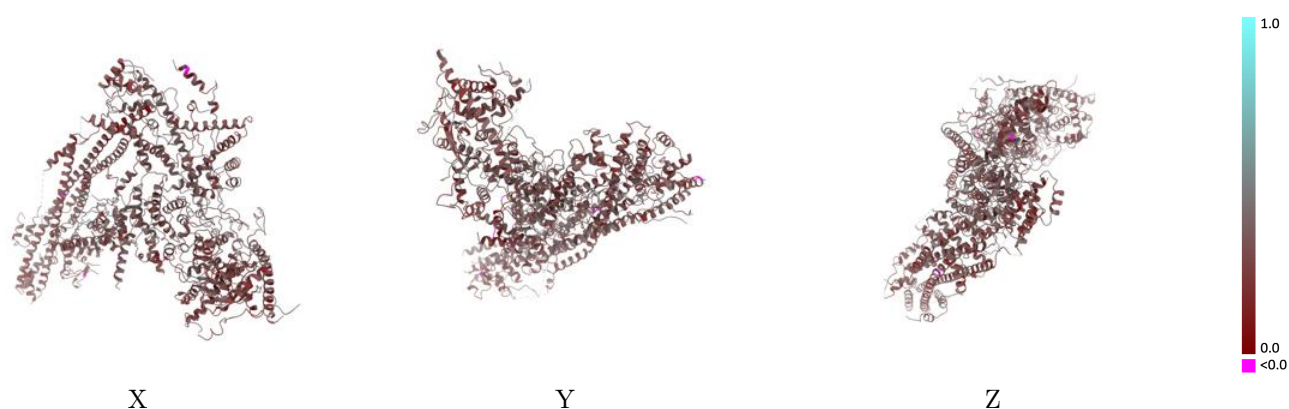
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-20933 and PDB model 6UXV. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlay [i](#)

This section was not generated.

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

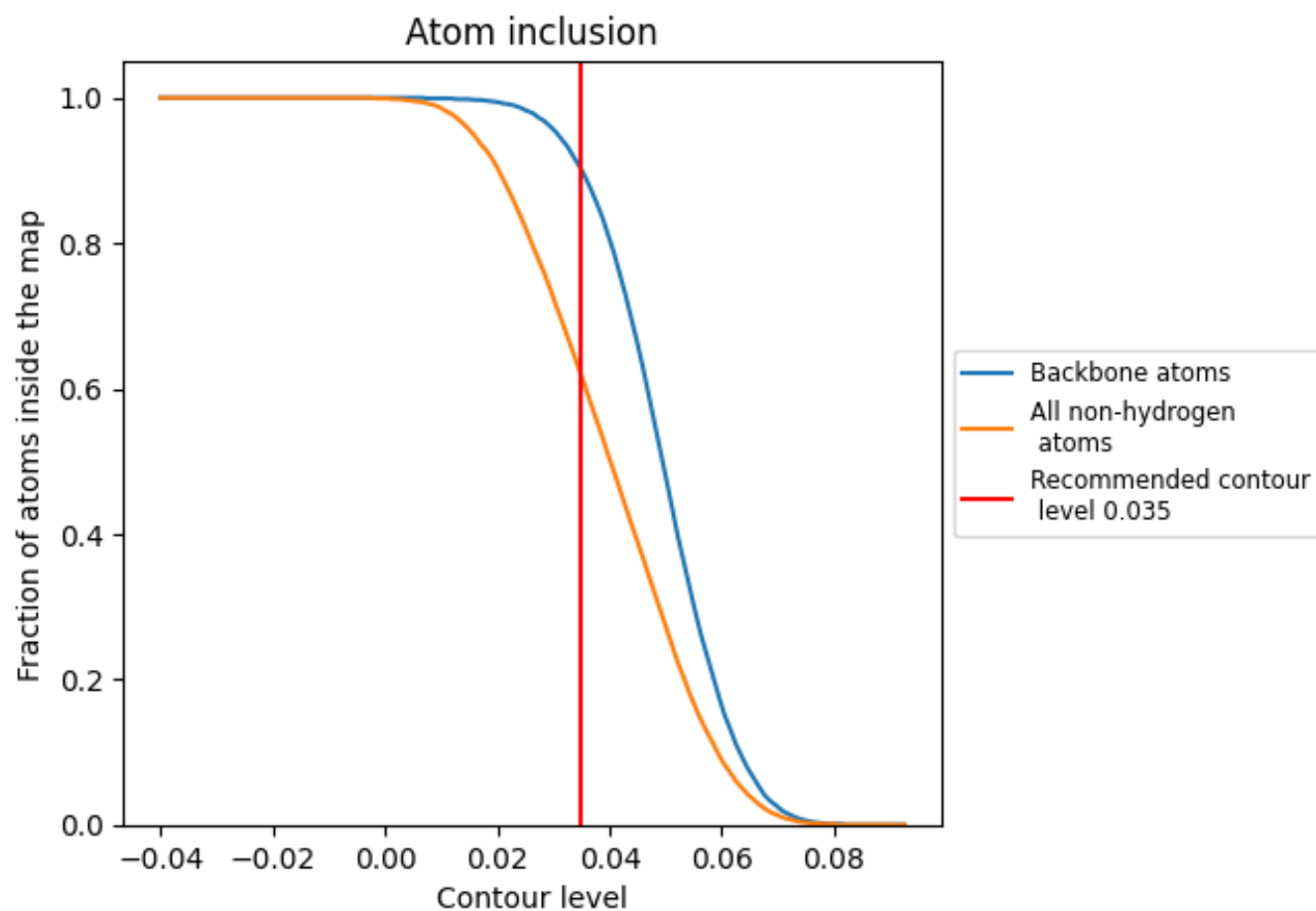


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 62% 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 (0.035) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6170	0.3220
A	0.6270	0.3330
B	0.5990	0.3360
C	0.5540	0.3140
D	0.5780	0.3070
E	0.6410	0.3420
F	0.6220	0.2950
G	0.6530	0.3150
H	0.5500	0.2930
I	0.6320	0.3310
J	0.9170	0.3710
K	0.8650	0.4030
L	0.7580	0.2930
M	0.8650	0.3650
N	0.8740	0.4630
O	0.4400	0.1680

1.0

0.0

<0.0