



wwPDB EM Validation Summary Report ⓘ

Nov 22, 2022 – 07:15 PM JST

PDB ID : 7EVN
EMDB ID : EMD-31330
Title : The cryo-EM structure of the DDX42-SF3b complex
Authors : Zhang, X.; Zhan, X.; Shi, Y.
Deposited on : 2021-05-21
Resolution : 2.60 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.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.3

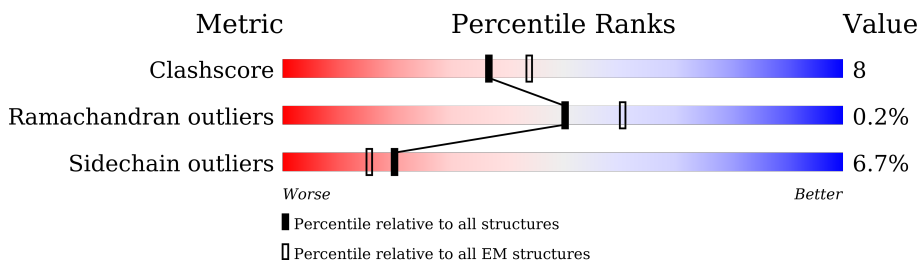
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.60 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	B	86	 81% 9% 9%
2	C	872	 70% 22% 7%
3	D	110	 5% 74% 10% 15%
4	A	1250	 5% 74% 18% 6%
5	E	958	 47% 47% 49%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 19668 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 Splicing factor 3B subunit 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	78	Total	C	N	O	S	0	0
			646	409	114	118	5		

- Molecule 2 is a protein called Splicing factor 3B subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	815	Total	C	N	O	S	0	0
			6487	4163	1121	1164	39		

There are 19 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	433	MET	-	initiating methionine	UNP O75533
C	434	ALA	-	expression tag	UNP O75533
C	435	SER	-	expression tag	UNP O75533
C	436	ASP	-	expression tag	UNP O75533
C	437	TYR	-	expression tag	UNP O75533
C	438	LYS	-	expression tag	UNP O75533
C	439	ASP	-	expression tag	UNP O75533
C	440	ASP	-	expression tag	UNP O75533
C	441	ASP	-	expression tag	UNP O75533
C	442	ASP	-	expression tag	UNP O75533
C	443	LYS	-	expression tag	UNP O75533
C	444	ALA	-	expression tag	UNP O75533
C	445	SER	-	expression tag	UNP O75533
C	446	ASP	-	expression tag	UNP O75533
C	447	GLU	-	expression tag	UNP O75533
C	448	VAL	-	expression tag	UNP O75533
C	449	ASP	-	expression tag	UNP O75533
C	450	ALA	-	expression tag	UNP O75533
C	451	GLY	-	expression tag	UNP O75533

- Molecule 3 is a protein called PHD finger-like domain-containing protein 5A.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	93	Total	C	N	O	S	0	0
			700	429	123	135	13		

- Molecule 4 is a protein called Splicing factor 3B subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	1177	Total	C	N	O	S	0	0
			9227	5858	1568	1756	45		

There are 33 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-32	TRP	-	expression tag	UNP Q15393
A	-31	SER	-	expression tag	UNP Q15393
A	-30	HIS	-	expression tag	UNP Q15393
A	-29	PRO	-	expression tag	UNP Q15393
A	-28	GLN	-	expression tag	UNP Q15393
A	-27	PHE	-	expression tag	UNP Q15393
A	-26	GLU	-	expression tag	UNP Q15393
A	-25	LYS	-	expression tag	UNP Q15393
A	-24	GLY	-	expression tag	UNP Q15393
A	-23	GLY	-	expression tag	UNP Q15393
A	-22	GLY	-	expression tag	UNP Q15393
A	-21	SER	-	expression tag	UNP Q15393
A	-20	GLY	-	expression tag	UNP Q15393
A	-19	GLY	-	expression tag	UNP Q15393
A	-18	GLY	-	expression tag	UNP Q15393
A	-17	SER	-	expression tag	UNP Q15393
A	-16	GLY	-	expression tag	UNP Q15393
A	-15	GLY	-	expression tag	UNP Q15393
A	-14	SER	-	expression tag	UNP Q15393
A	-13	ALA	-	expression tag	UNP Q15393
A	-12	TRP	-	expression tag	UNP Q15393
A	-11	SER	-	expression tag	UNP Q15393
A	-10	HIS	-	expression tag	UNP Q15393
A	-9	PRO	-	expression tag	UNP Q15393
A	-8	GLN	-	expression tag	UNP Q15393
A	-7	PHE	-	expression tag	UNP Q15393
A	-6	GLU	-	expression tag	UNP Q15393
A	-5	LYS	-	expression tag	UNP Q15393
A	-4	GLY	-	expression tag	UNP Q15393
A	-3	SER	-	expression tag	UNP Q15393
A	-2	ALA	-	expression tag	UNP Q15393

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	ALA	-	expression tag	UNP Q15393
A	0	ALA	-	expression tag	UNP Q15393

- Molecule 5 is a protein called ATP-dependent RNA helicase DDX42.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	486	Total	C	N	O	S	0	0
			2605	1555	505	542	3		

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	-19	MET	-	initiating methionine	UNP Q86XP3
E	-18	ALA	-	expression tag	UNP Q86XP3
E	-17	SER	-	expression tag	UNP Q86XP3
E	-16	ASP	-	expression tag	UNP Q86XP3
E	-15	TYR	-	expression tag	UNP Q86XP3
E	-14	LYS	-	expression tag	UNP Q86XP3
E	-13	ASP	-	expression tag	UNP Q86XP3
E	-12	ASP	-	expression tag	UNP Q86XP3
E	-11	ASP	-	expression tag	UNP Q86XP3
E	-10	ASP	-	expression tag	UNP Q86XP3
E	-9	LYS	-	expression tag	UNP Q86XP3
E	-8	ALA	-	expression tag	UNP Q86XP3
E	-7	SER	-	expression tag	UNP Q86XP3
E	-6	ASP	-	expression tag	UNP Q86XP3
E	-5	GLU	-	expression tag	UNP Q86XP3
E	-4	VAL	-	expression tag	UNP Q86XP3
E	-3	ASP	-	expression tag	UNP Q86XP3
E	-2	ALA	-	expression tag	UNP Q86XP3
E	-1	GLY	-	expression tag	UNP Q86XP3
E	0	THR	-	expression tag	UNP Q86XP3


- Molecule 6 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
6	D	3	Total	Zn	0
			3	3	

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.

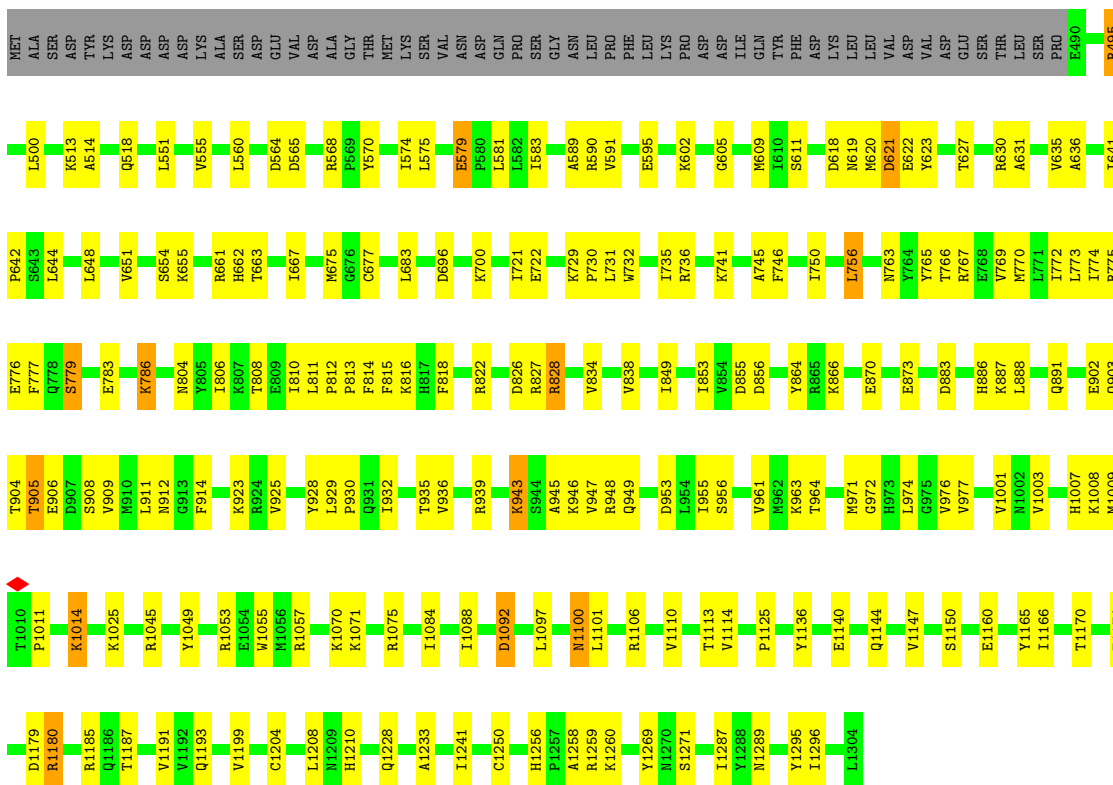
- Molecule 1: Splicing factor 3B subunit 5

Chain B: 



- Molecule 2: Splicing factor 3B subunit 1

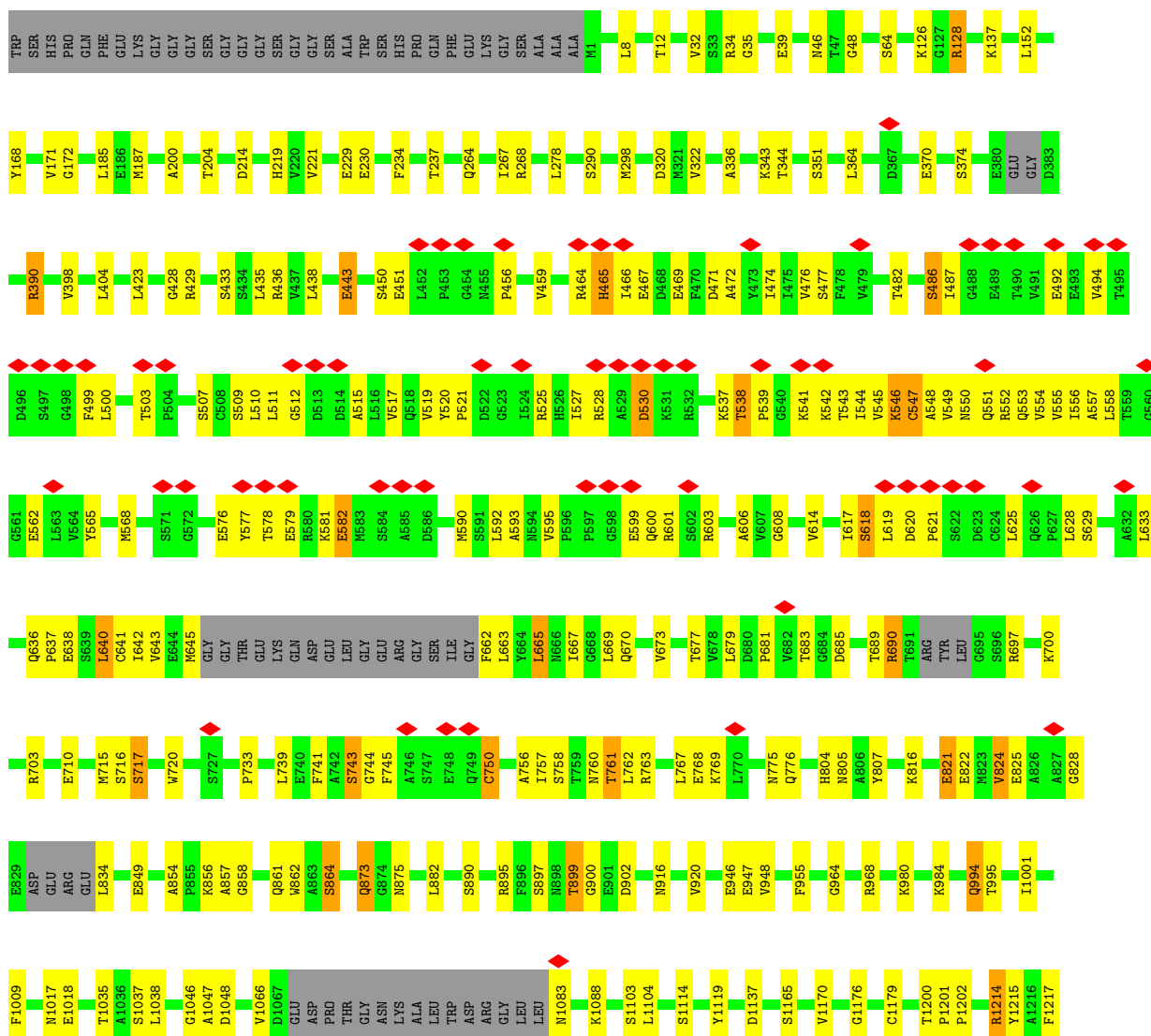
Chain C: 



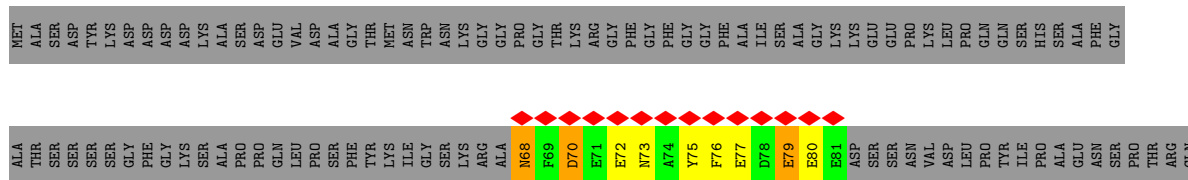
- Molecule 3: PHD finger-like domain-containing protein 5A

Chain D: 





- Molecule 5: ATP-dependent RNA helicase DDX42



PRO	GLY	THR	ASN	LEU	N538	L478	V358	K298	K238	GLU	GLN
LYS	ARG	TYR	GLN	GLY	K539	H479	A359	T299	L239	ASP	PHE
MET	HIS	PRO	LYS	TYR	N540	H480	V360	G300	N240	ASN	HIS
ASP	GLY	ALA	ALA	ARG	N541	G481	Y361	S301	L241	LEU	SER
VAL	GLY	ALA	SER	ARG	N542	P482	G363	G302	R242	TYR	PRO
ASP	ARG	ALA	SER	PRO	D543	S483	G364	K303	V243	ASP	VAL
GLY	GLY	GLY	ALA	GLY	F544	K484	G365	T304	S244	SER	ASP
SER	GLY	VAL	GLY	GLY	K545	V485	S366	A305	G245	GLY	ASP
ASN	ASN	ASN	ALA	SER	K546	N486	M366	A306	G246	ASN	SER
MET	SER	THR	GLY	GLY	K547	V487	W367	F307	A247	PRO	ASP
LYS	SER	ALA	TRP	MET	D548	L488	E368	I308	P248	ILE	ASP
VAL	ARG	SER	THR	ASP	I549	T489	Q369	W309	P249	ALA	D114
ASP	GLY	GLY	THR	ARG	P550	R490	A370	P310	R250	PRO	P115
SER	ASN	ASN	ALA	GLY	N551	D431	K371	M311	P251	THR	L116
THR	ASP	ASN	GLY	ASN	L552	R432	A372	L312	G252	LYS	E117
ASP	HIS	ARG	LEU	ASN	V553	Q433	L373	I313	S253	ILE	M120
THR	GLY	GLY	GLY	VAL	A554	T434	Q374	H314	S254	ASP	Q126
ALA	GLY	THR	VAL	SER	T555	L435	E375	I315	F255	PRO	D130
GLY	ASN	GLY	PRO	ASN	D556	L436	G376	M316	A256	PRO	H131
PHE	ARG	SER	THR	TYR	V557	F437	A377	D317	H257	ILE	K132
ALA	ASN	ASN	ALA	GLY	A558	S498	E378	Q318	F258	ASP	R133
VAL	HIS	TYR	ALA	TYR	A559	A439	I379	K319	G259	HIS	L134
PRO	GLY	LYS	GLN	LYS	H560	T440	V380	E320	F260	SER	E135
GLU	ALA	GLY	GLY	SER	G561	F441	V381	L321	D261	GLU	GLU
PRO	GLY	ARG	THR	THR	L562	R442	C382	E322	E262	ASP	LYS
LYS	GLY	TYR	ASN	GLY	D563	K443	T383	P223	Q263	LYS	ASP
ARG	HIS	THR	SER	ALA	I564	F504	P384	G324	L264	GLU	GLU
GLY	GLY	GLY	PRO	MET	P565	V505	G385	D325	M265	ARG	ARG
ASN	ASN	ARG	ASP	GLY	S566	T506	R386	G326	H266	LYS	LYS
ARG	ARG	GLY	PRO	ARG	I567	K507	L387	P327	Q267	ASN	VAL
TRP	GLY	SER	VAL	LEU	K568	L448	I388	A329	R269	VAL	K145
ASP	ALA	ARG	ALA	ALA	T569	A449	D389	H390	K270	GLU	G146
GLY	LYS	SER	ALA	LYS	N570	R450	H390	V330	S271	LYS	G147
ALA	ALA	HIS	LYS	ALA	I571	D451	V391	I331	E272	ASP	R148
ASN	GLY	GLY	GLY	ALA	N572	I452	K392	V332	E273	LYS	D149
GLY	ILE	GLU	ILE	PHE	V573	L453	K393	C333	Y273	ASN	D155
THR	PRO	THR	PRO	GLN	D574	I454	K394	P334	T274	GLY	E158
SER	GLY	GLY	GLY	SER	V575	D455	A395	T335	Q275	VAL	R162
ALA	ASN	ASN	PHE	GLN	A576	P456	T396	R336	P276	GLY	H167
LYS	GLY	ARG	GLY	TYR	R577	I457	N397	E337	T277	THR	PRO
GLU	HIS	HIS	ASN	LYS	D578	L458	L398	L338	P278	ALA	THR
ALA	ASP	ASP	GLY	SER	I579	V459	Q399	C339	I279	GLY	ALA
ARG	PRO	PRO	ILE	VAL	D580	Q460	R400	Q340	Q280	VAL	GLY
GLU	ARG	ARG	SER	ALA	T581	Q461	V401	I341	C281	VAL	VAL
SER	HIS	HIS	GLY	ALA	H582	G462	S402	I342	Q282	GLN	VAL
LYS	GLY	GLY	ALA	SER	T583	D463	Y403	H343	G283	GLU	GLU
MET	ASP	ASP	PRO	LEU	H584	I464	L404	A344	V284	GLU	GLU
GLU	VAL	GLY	VAL	SER	R585	G465	V405	E345	P285	GLU	GLU
					I586	E466	F406	C346	V286		
					G587	ALA	D407	K347	A287		
					R588	ASN	E408	R348	L288		
					T589	GLU	A409	F349	S289		
					G590	D470	D410	G350	G290		
					ALA	V471	R411	K351	R291		
					GLY	T472	M412	A352	D292		
						Q473	F413	Y353	M293		
					E594	I474	D414	N354	I294		
					K595	V475	M415	L355	G295		
					G596	E476	G416	R356	I296		
					V597	I477	F417	S357	A297		

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	234800	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)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.235	Depositor
Minimum map value	-0.133	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.02	Depositor
Map size (\AA)	260.88, 260.88, 260.88	wwPDB
Map dimensions	240, 240, 240	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.087, 1.087, 1.087	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	B	0.36	0/665	0.47	0/899
2	C	0.33	0/6609	0.48	1/8946 (0.0%)
3	D	0.36	0/709	0.49	0/952
4	A	0.34	0/9415	0.51	0/12775
5	E	0.40	0/2607	0.56	1/3593 (0.0%)
All	All	0.35	0/20005	0.51	2/27165 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	564	ASP	O-C-N	-5.13	114.49	122.70
5	E	271	SER	C-N-CA	5.03	134.27	121.70

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	646	0	608	6	0
2	C	6487	0	6700	148	0
3	D	700	0	682	6	0
4	A	9227	0	9154	140	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	E	2605	0	1378	63	0
6	D	3	0	0	0	0
All	All	19668	0	18522	317	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 8.

The worst 5 of 317 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)
2:C:786:LYS:NZ	5:E:72:GLU:HG3	1.52	1.22
2:C:741:LYS:HE3	5:E:79:GLU:HB2	1.19	1.15
4:A:221:VAL:CG1	5:E:146:GLY:HA3	1.82	1.10
2:C:741:LYS:CE	5:E:79:GLU:HB2	1.87	1.04
2:C:786:LYS:HZ1	5:E:72:GLU:HG3	0.87	1.01

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	B	76/86 (88%)	75 (99%)	1 (1%)	0	100	100
2	C	813/872 (93%)	784 (96%)	29 (4%)	0	100	100
3	D	91/110 (83%)	86 (94%)	5 (6%)	0	100	100
4	A	1165/1250 (93%)	1088 (93%)	76 (6%)	1 (0%)	51	75
5	E	474/958 (50%)	459 (97%)	12 (2%)	3 (1%)	25	47
All	All	2619/3276 (80%)	2492 (95%)	123 (5%)	4 (0%)	50	71

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	E	301	SER
5	E	595	LYS
5	E	275	GLN
4	A	234	PHE

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	B	69/77 (90%)	68 (99%)	1 (1%)	67	85
2	C	701/753 (93%)	664 (95%)	37 (5%)	22	45
3	D	80/95 (84%)	76 (95%)	4 (5%)	24	47
4	A	1020/1071 (95%)	945 (93%)	75 (7%)	13	28
5	E	51/787 (6%)	40 (78%)	11 (22%)	1	1
All	All	1921/2783 (69%)	1793 (93%)	128 (7%)	20	33

5 of 128 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	A	1214	ARG
5	E	79	GLU
4	A	171	VAL
4	A	152	LEU
5	E	126	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 39 such sidechains are listed below:

Mol	Chain	Res	Type
4	A	553	GLN
4	A	1017	ASN
4	A	776	GLN
4	A	870	ASN
4	A	1083	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

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.

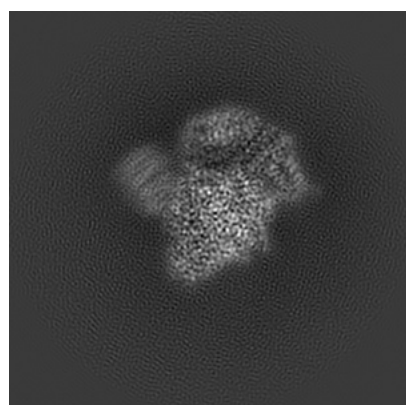
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-31330. These allow visual inspection of the internal detail of the map and identification of artifacts.

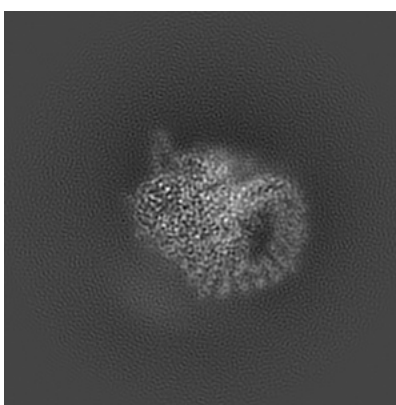
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

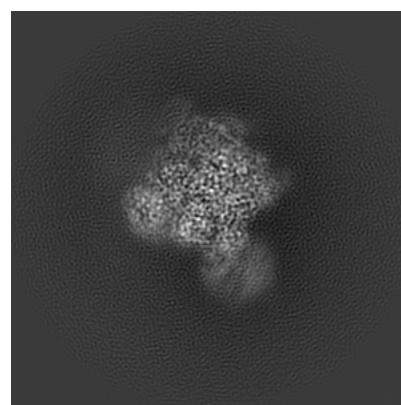
6.1.1 Primary map



X



Y

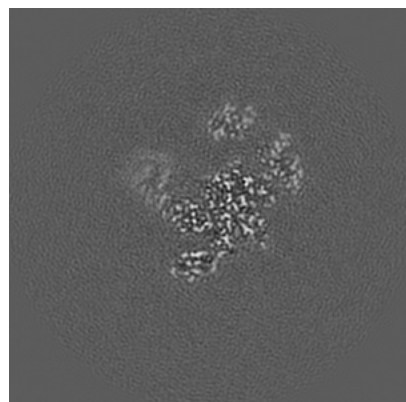


Z

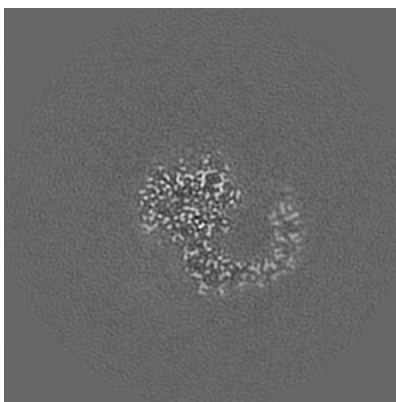
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

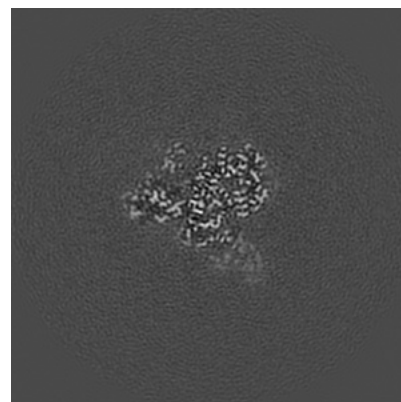
6.2.1 Primary map



X Index: 120



Y Index: 120

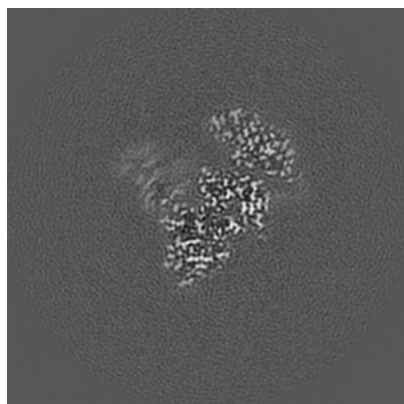


Z Index: 120

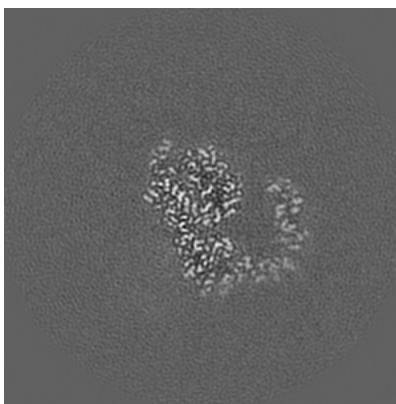
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

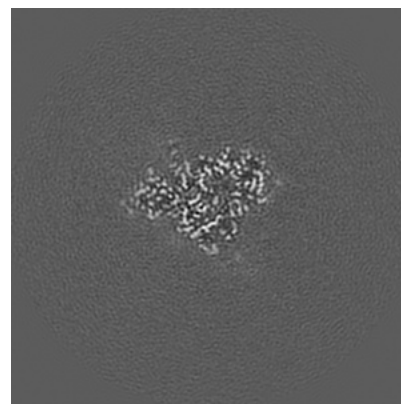
6.3.1 Primary map



X Index: 127



Y Index: 127



Z Index: 116

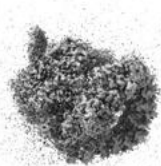
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.02. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

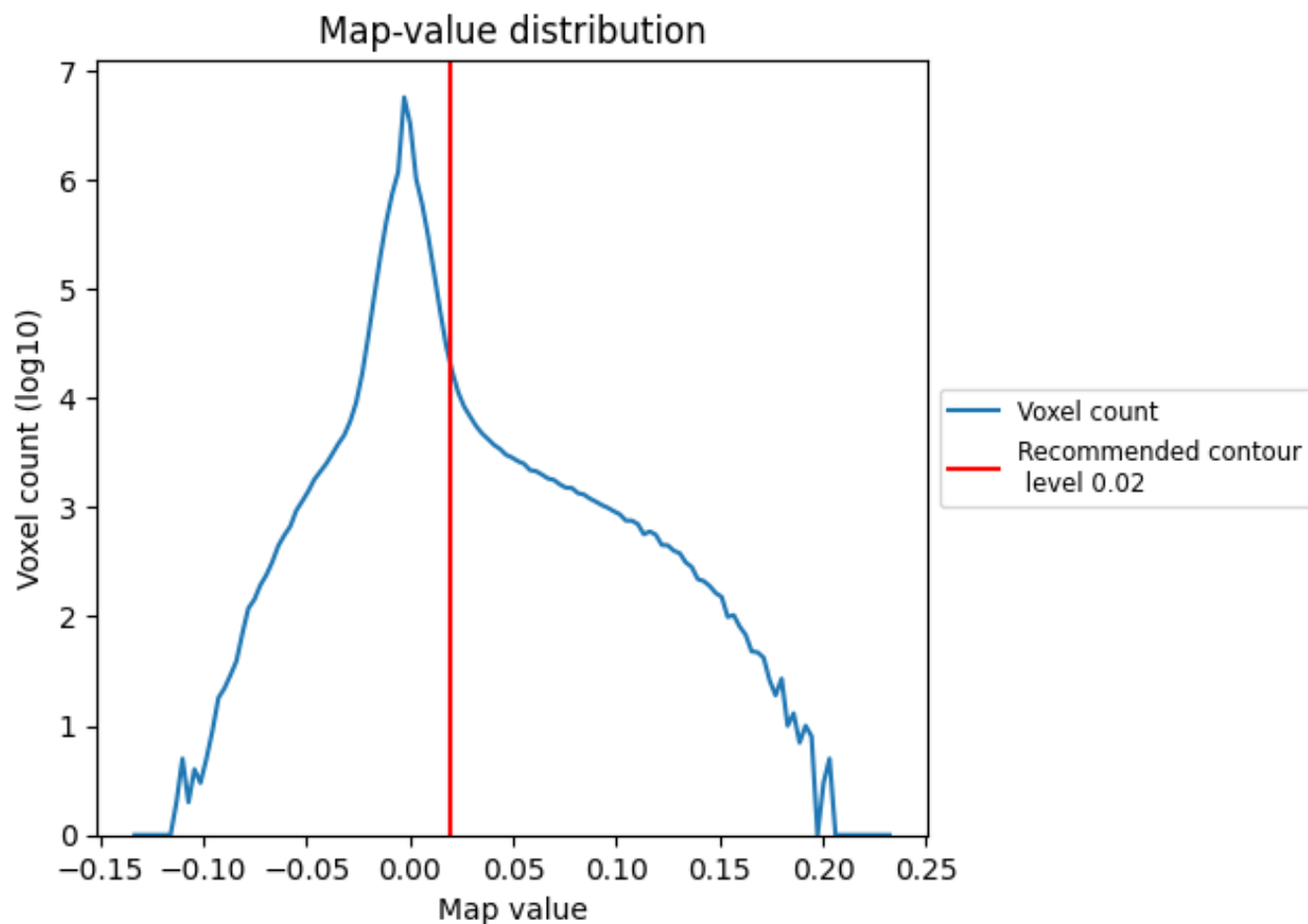
6.5 Mask visualisation

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

7 Map analysis [i](#)

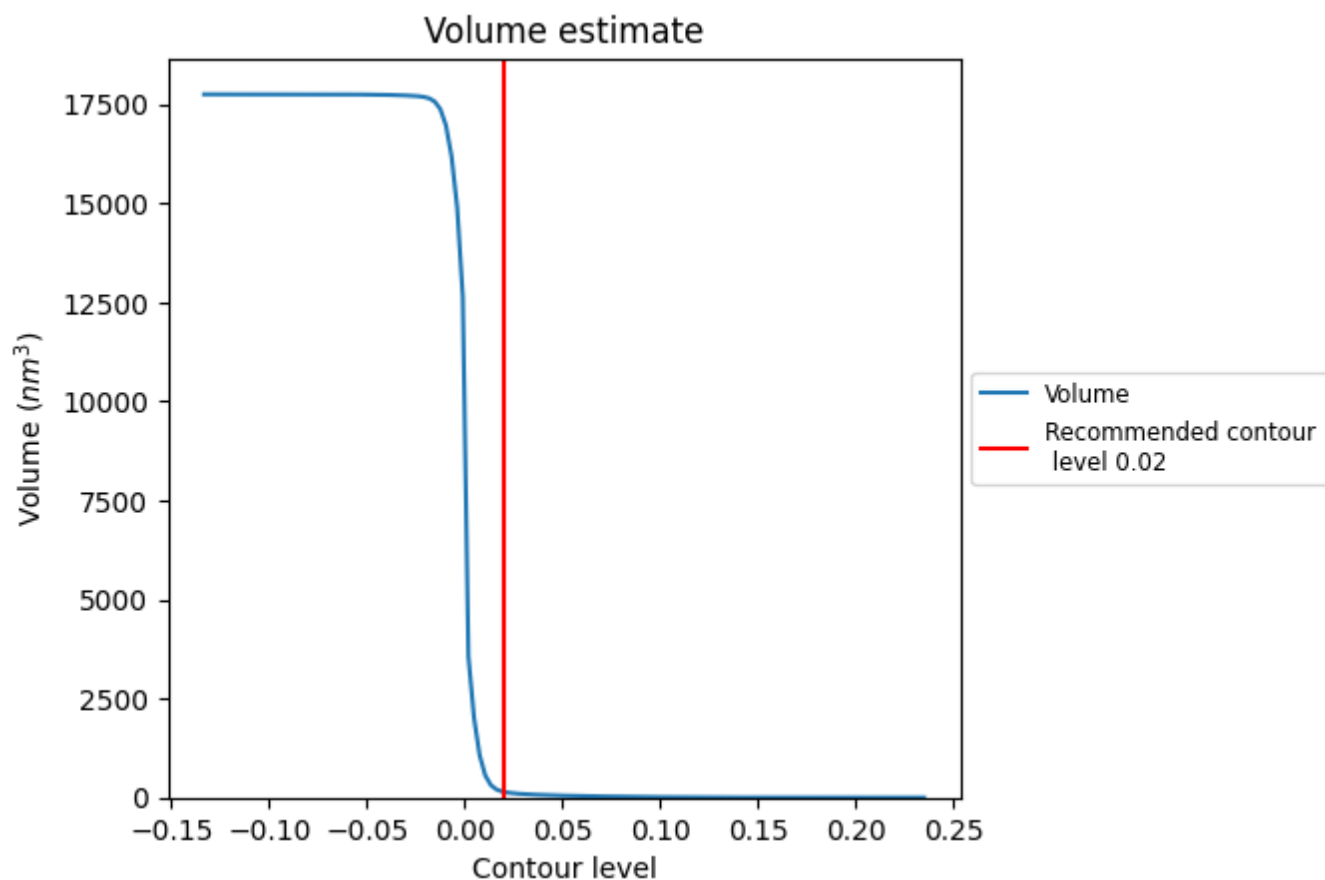
This section contains the results of statistical analysis of the map.

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.

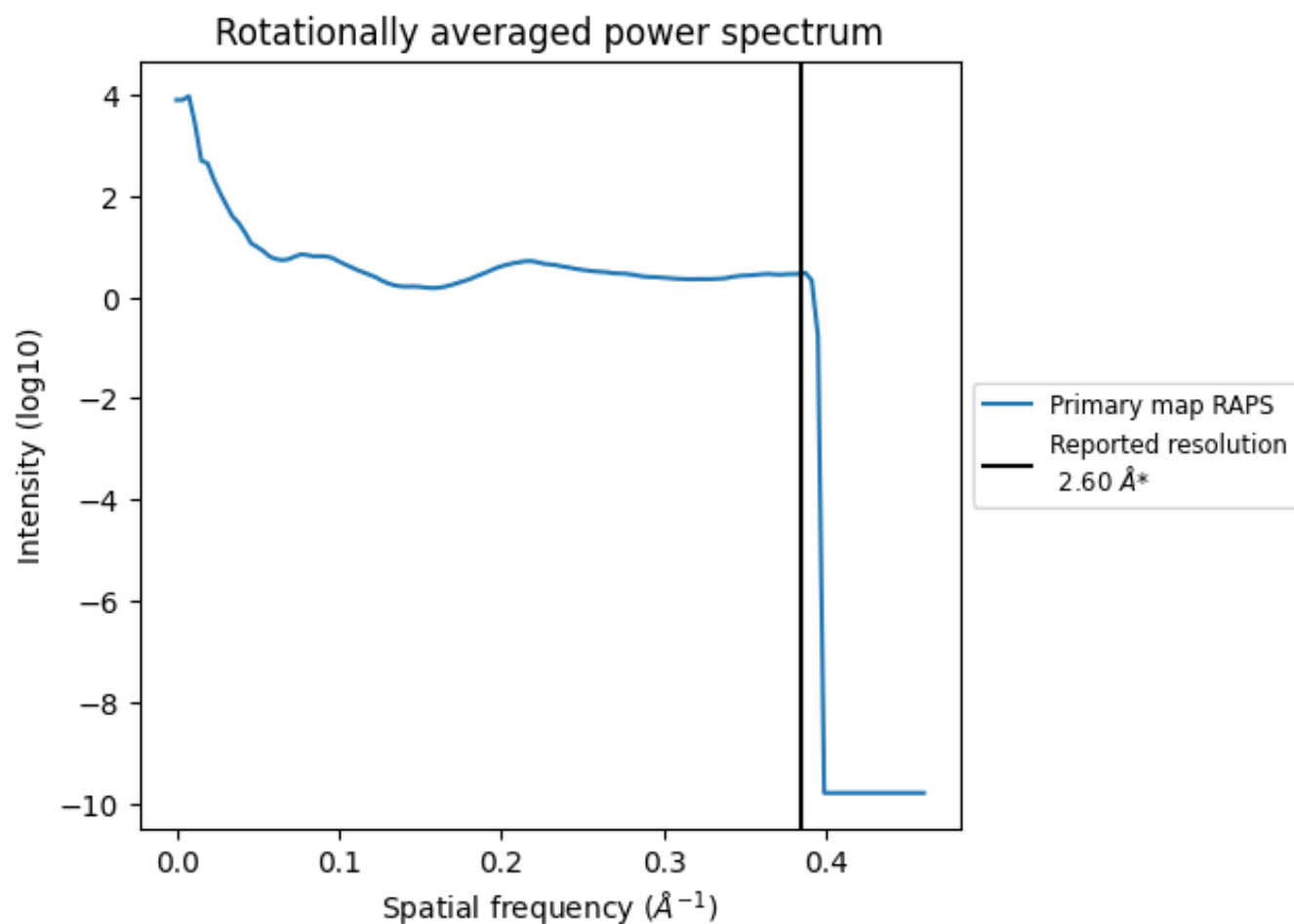
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 145 nm³; this corresponds to an approximate mass of 131 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 0.385 Å⁻¹

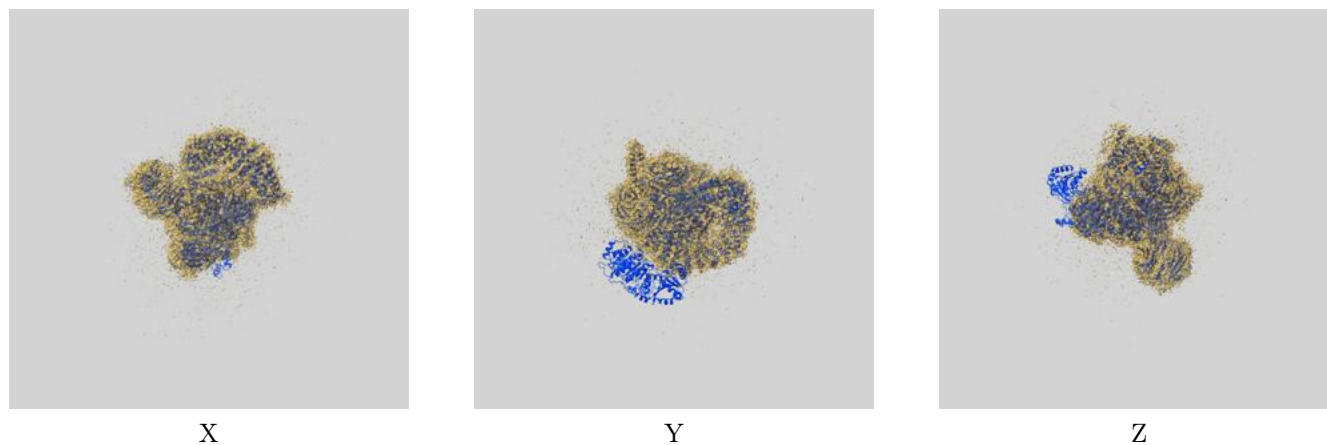
8 Fourier-Shell correlation

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-31330 and PDB model 7EVN. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlay [i](#)



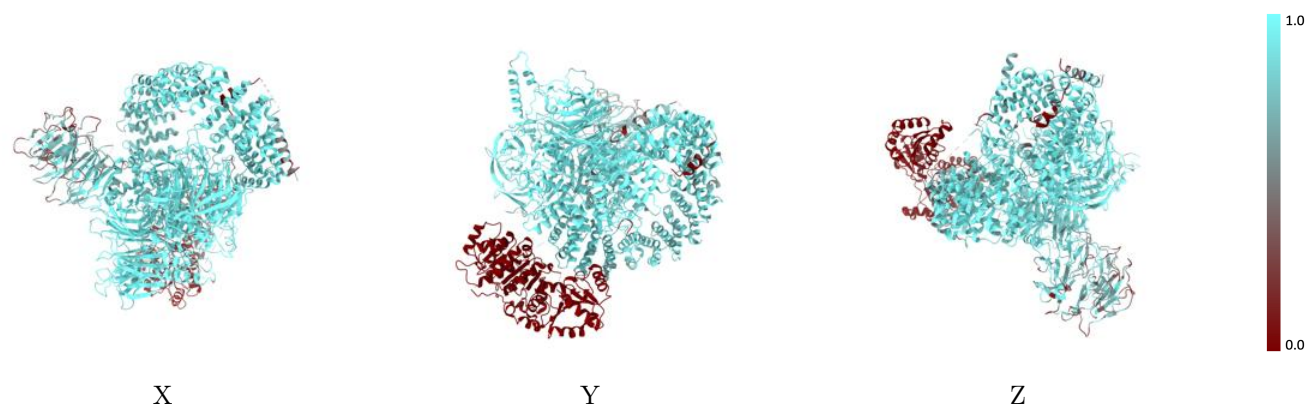
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



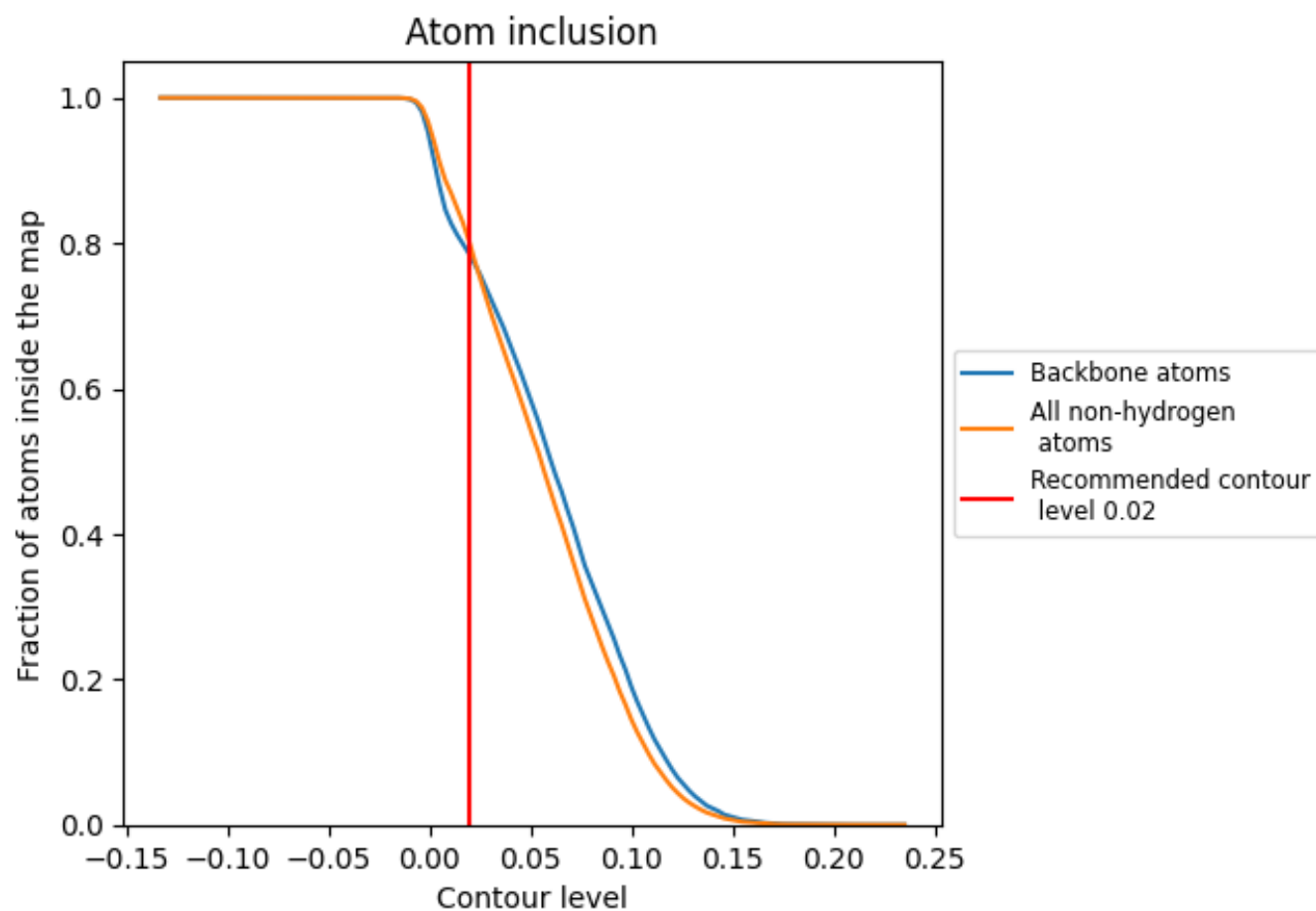
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.02).

9.4 Atom inclusion [i](#)



At the recommended contour level, 78% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.7993	<div></div> 0.5400
A	<div></div> 0.8871	<div></div> 0.6040
B	<div></div> 0.9842	<div></div> 0.6760
C	<div></div> 0.9296	<div></div> 0.6110
D	<div></div> 0.9242	<div></div> 0.6470
E	<div></div> 0.0952	<div></div> 0.0770

