



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 01:27 PM UTC

PDB ID : 7EVN / pdb_00007evn
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:

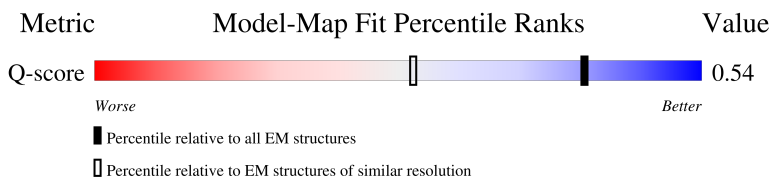
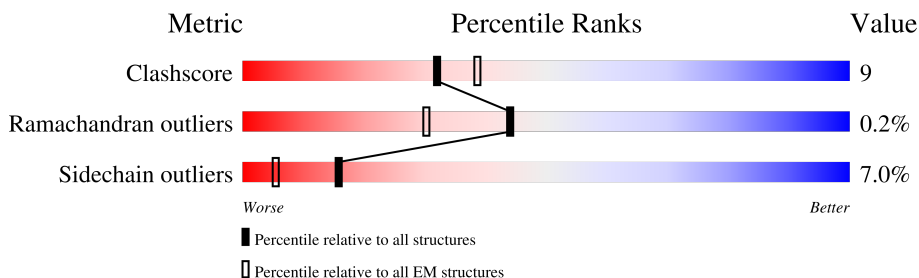
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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.



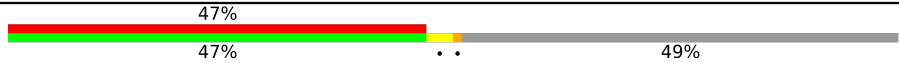
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	8728 (2.10 - 3.10)

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	80% (green), 8% (yellow), 9% (grey)
2	C	872	69% (green), 23% (yellow), 7% (grey)
3	D	110	5% (red), 75% (green), 9% (yellow), 15% (grey)
4	A	1250	5% (red), 73% (green), 19% (yellow), 6% (grey)

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
5	E	958	 <p>A horizontal bar chart representing the quality of chain. The bar is divided into three segments: a green segment on the left labeled '47%', a red segment in the middle labeled '47%', and a grey segment on the right labeled '49%'. There are two small black dots on the bar between the red and grey segments.</p>

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
			Total	C	N	O	S		
1	B	78	646	409	114	118	5	0	0

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

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

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
			Total	C	N	O	S		
3	D	93	700	429	123	135	13	0	0

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

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

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

Continued on next page...

Continued from previous page...

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
			Total	C	N	O	S		
5	E	486	2605	1555	505	542	3	0	0

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 (CCD ID: 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 [i](#)

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.

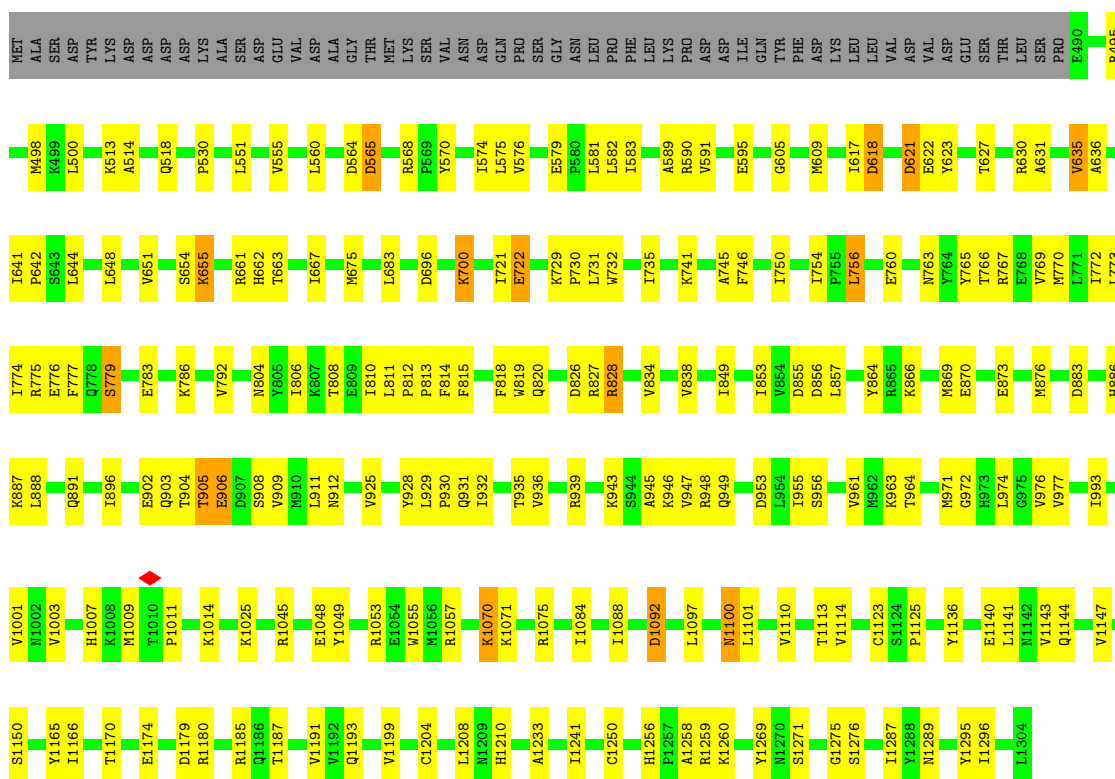
- Molecule 1: Splicing factor 3B subunit 5

Chain B: 




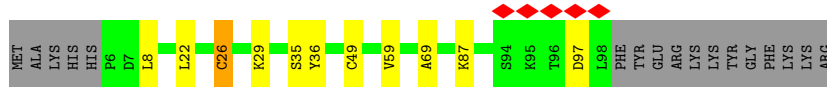
- Molecule 2: Splicing factor 3B subunit 1

Chain C: 

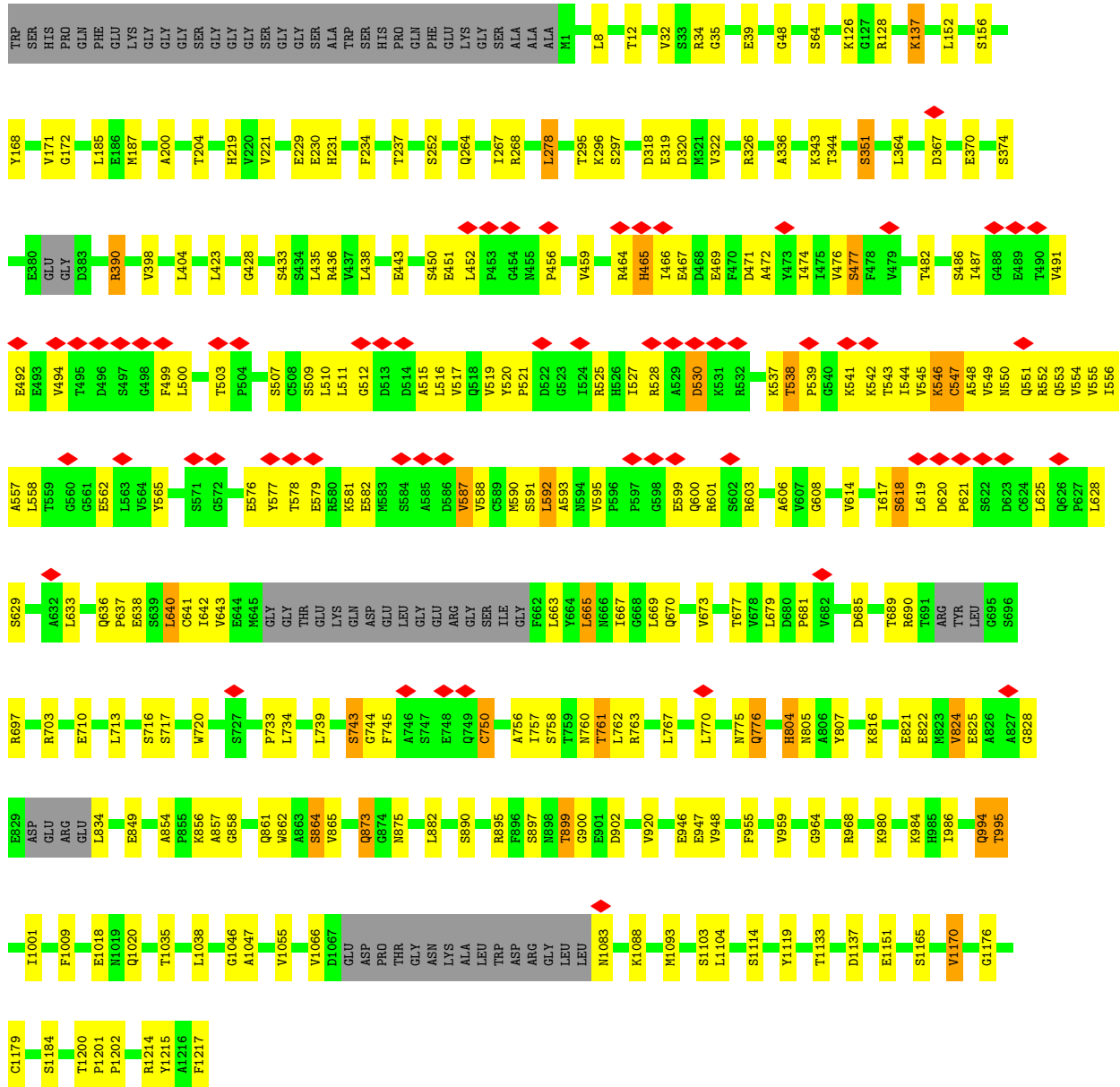
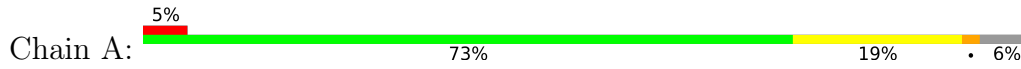


- Molecule 3: PHD finger-like domain-containing protein 5A

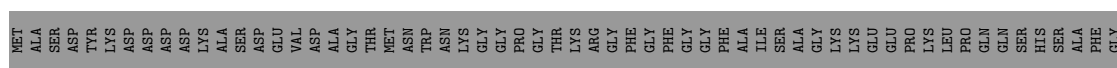
Chain D: 



• Molecule 4: Splicing factor 3B subunit 3



• Molecule 5: ATP-dependent RNA helicase DDX42



PRO	LYS	ARG	GLY	THR	THR	ASN	LEU	A598	N538	L478	E418	V388	K298	K238	GLU	ASP	ALA	N68	F69	D70	E71	E72	N73	A74	Y75	F76	E77	D78	E79	E80	E81	ASP	SER	ASN	VAL	ASP	LEU	PRO	TYR	ILE	PRO	ALA	GLU	ASN	PRO	THR	ARG	GLN
LYS	GLY	THR	GLY	TYR	TYR	GLN	GLY	Y599	K639	H479	Y419	A359	T299	L239	ASP	ASN	THR	F69	D70	E71	E72	N73	A74	Y75	F76	E77	D78	E79	E80	E81	ASP	SER	ASN	VAL	ASP	LEU	PRO	TYR	ILE	PRO	ALA	GLU	ASN	PRO	THR	ARG	GLN	
MET	GLU	HIS	ASP	GLY	PRO	ALA	ARG	T600	V540	S480	Q420	V360	G300	M240	LEU	ASN	THR	F69	D70	E71	E72	N73	A74	Y75	F76	E77	D78	E79	E80	E81	ASP	SER	ASN	VAL	ASP	LEU	PRO	TYR	ILE	PRO	ALA	GLU	ASN	PRO	THR	ARG	GLN	
PRO	LYS	VAL	VAL	TYR	ALA	ALA	ARG	L601	I641	G481	V421	Y361	S301	L241	PRO	ASN	THR	F69	D70	E71	E72	N73	A74	Y75	F76	E77	D78	E79	E80	E81	ASP	SER	ASN	VAL	ASP	LEU	PRO	TYR	ILE	PRO	ALA	GLU	ASN	PRO	THR	ARG	GLN	
ASP	VAL	ASP	GLY	ALA	PRO	ALA	ARG	L602	S542	P482	S422	G362	K302	V242	ASP	ASN	THR	F69	D70	E71	E72	N73	A74	Y75	F76	E77	D78	E79	E80	E81	ASP	SER	ASN	VAL	ASP	LEU	PRO	TYR	ILE	PRO	ALA	GLU	ASN	PRO	THR	ARG	GLN	
ASP	VAL	ASP	GLY	ALA	PRO	ALA	ARG	T603	D643	S483	S423	G363	K303	V243	ASP	ASN	THR	F69	D70	E71	E72	N73	A74	Y75	F76	E77	D78	E79	E80	E81	ASP	SER	ASN	VAL	ASP	LEU	PRO	TYR	ILE	PRO	ALA	GLU	ASN	PRO	THR	ARG	GLN	
ASP	VAL	ASP	GLY	ALA	PRO	ALA	ARG	P604	F444	K484	I424	G364	T304	S244	ASP	ASN	THR	F69	D70	E71	E72	N73	A74	Y75	F76	E77	D78	E79	E80	E81	ASP	SER	ASN	VAL	ASP	LEU	PRO	TYR	ILE	PRO	ALA	GLU	ASN	PRO	THR	ARG	GLN	
ASP	VAL	ASP	GLY	ALA	PRO	ALA	ARG	K605	K645	W485	A425	S365	A305	G245	ASP	ASN	THR	F69	D70	E71	E72	N73	A74	Y75	F76	E77	D78	E79	E80	E81	ASP	SER	ASN	VAL	ASP	LEU	PRO	TYR	ILE	PRO	ALA	GLU	ASN	PRO	THR	ARG	GLN	
ASP	VAL	ASP	GLY	ALA	PRO	ALA	ARG	D606	K546	W486	S426	S366	A306	G246	ASP	ASN	THR	F69	D70	E71	E72	N73	A74	Y75	F76	E77	D78	E79	E80	E81	ASP	SER	ASN	VAL	ASP	LEU	PRO	TYR	ILE	PRO	ALA	GLU	ASN	PRO	THR	ARG	GLN	
ASP	VAL	ASP	GLY	ALA	PRO	ALA	ARG	S607	K647	W487	H427	W367	F307	A247	ASP	ASN	THR	F69	D70	E71	E72	N73	A74	Y75	F76	E77	D78	E79	E80	E81	ASP	SER	ASN	VAL	ASP	LEU	PRO	TYR	ILE	PRO	ALA	GLU	ASN	PRO	THR	ARG	GLN	
ASP	VAL	ASP	GLY	ALA	PRO	ALA	ARG	N608	D548	L488	V428	E388	I308	P248	ASP	ASN	THR	F69	D70	E71	E72	N73	A74	Y75	F76	E77	D78	E79	E80	E81	ASP	SER	ASN	VAL	ASP	LEU	PRO	TYR	ILE	PRO	ALA	GLU	ASN	PRO	THR	ARG	GLN	
ASP	VAL	ASP	GLY	ALA	PRO	ALA	ARG	F609	I649	T489	R429	Q369	W309	P249	ASP	ASN	THR	F69	D70	E71	E72	N73	A74	Y75	F76	E77	D78	E79	E80	E81	ASP	SER	ASN	VAL	ASP	LEU	PRO	TYR	ILE	PRO	ALA	GLU	ASN	PRO	THR	ARG	GLN	
ASP	VAL	ASP	GLY	ALA	PRO	ALA	ARG	A610	P550	A370	R490	K310	M310	R250	ASP	ASN	THR	F69	D70	E71	E72	N73	A74	Y75	F76	E77	D78	E79	E80	E81	ASP	SER	ASN	VAL	ASP	LEU	PRO	TYR	ILE	PRO	ALA	GLU	ASN	PRO	THR	ARG	GLN	
ASP	VAL	ASP	GLY	ALA	PRO	ALA	ARG	G611	V651	R491	D431	M311	K311	R251	ASP	ASN	THR	F69	D70	E71	E72	N73	A74	Y75	F76	E77	D78	E79	E80	E81	ASP	SER	ASN	VAL	ASP	LEU	PRO	TYR	ILE	PRO	ALA	GLU	ASN	PRO	THR	ARG	GLN	
ASP	VAL	ASP	GLY	ALA	PRO	ALA	ARG	D612	L552	L492	R452	L312	M312	R252	ASP	ASN	THR	F69	D70	E71	E72	N73	A74	Y75	F76	E77	D78	E79	E80	E81	ASP	SER	ASN	VAL	ASP	LEU	PRO	TYR	ILE	PRO	ALA	GLU	ASN	PRO	THR	ARG	GLN	
ASP	VAL	ASP	GLY	ALA	PRO	ALA	ARG	L613	V653	V493	Q433	L373	I313	G253	ASP	ASN	THR	F69	D70	E71	E72	N73	A74	Y75	F76	E77	D78	E79	E80	E81	ASP	SER	ASN	VAL	ASP	LEU	PRO	TYR	ILE	PRO	ALA	GLU	ASN	PRO	THR	ARG	GLN	
ASP	VAL	ASP	GLY	ALA	PRO	ALA	ARG	V614	A554	E494	T434	Q374	H314	S254	ASP	ASN	THR	F69	D70	E71	E72	N73	A74	Y75	F76	E77	D78	E79	E80	E81	ASP	SER	ASN	VAL	ASP	LEU	PRO	TYR	ILE	PRO	ALA	GLU	ASN	PRO	THR	ARG	GLN	
ASP	VAL	ASP	GLY	ALA	PRO	ALA	ARG	R615	T655	F495	L435	E375	I315	F255	ASP	ASN	THR	F69	D70	E71	E72	N73	A74	Y75	F76	E77	D78	E79	E80	E81	ASP	SER	ASN	VAL	ASP	LEU	PRO	TYR	ILE	PRO	ALA	GLU	ASN	PRO	THR	ARG	GLN	
ASP	VAL	ASP	GLY	ALA	PRO	ALA	ARG	N616	D556	T496	L436	G376	M316	A256	ASP	ASN	THR	F69	D70	E71	E72	N73	A74	Y75	F76	E77	D78	E79	E80	E81	ASP	SER	ASN	VAL	ASP	LEU	PRO	TYR	ILE	PRO	ALA	GLU	ASN	PRO	THR	ARG	GLN	
ASP	VAL	ASP	GLY	ALA	PRO	ALA	ARG	L617	V657	S497	F437	A377	D317	H257	ASP	ASN	THR	F69	D70	E71	E72	N73	A74	Y75	F76	E77	D78	E79	E80	E81	ASP	SER	ASN	VAL	ASP	LEU	PRO	TYR	ILE	PRO	ALA	GLU	ASN	PRO	THR	ARG	GLN	
ASP	VAL	ASP	GLY	ALA	PRO	ALA	ARG	E618	A558	S498	S438	E378	M318	A258	ASP	ASN	THR	F69	D70	E71	E72	N73	A74	Y75	F76	E77	D78	E79	E80	E81	ASP	SER	ASN	VAL	ASP	LEU	PRO	TYR	ILE	PRO	ALA	GLU	ASN	PRO	THR	ARG	GLN	
ASP	VAL	ASP	GLY	ALA	PRO	ALA	ARG	G619	A559	G499	A439	I379	Q319	G259	ASP	ASN	THR	F69	D70	E71	E72	N73	A74	Y75	F76	E77	D78	E79	E80	E81	ASP	SER	ASN	VAL	ASP	LEU	PRO	TYR	ILE	PRO	ALA	GLU	ASN	PRO	THR	ARG	GLN	
ASP	VAL	ASP	GLY	ALA	PRO	ALA	ARG	A620	R560	S500	T440	V380	E320	F260	ASP	ASN	THR	F69	D70	E71	E72	N73	A74	Y75	F76	E77	D78	E79	E80	E81	ASP	SER	ASN	VAL	ASP	LEU	PRO	TYR	ILE	PRO	ALA	GLU	ASN	PRO	THR	ARG	GLN	
ASP	VAL	ASP	GLY	ALA	PRO	ALA	ARG	N621	G561	V501	F441	V381	L321	D261	ASP	ASN	THR	F69	D70	E71	E72	N73	A74	Y75	F76	E77	D78	E79	E80	E81	ASP	SER	ASN	VAL	ASP	LEU	PRO	TYR	ILE	PRO	ALA	GLU	ASN	PRO	THR	ARG	GLN	
ASP	VAL	ASP	GLY	ALA	PRO	ALA	ARG	Q622	L562	L502	R442	C382	E322	E262	ASP	ASN	THR	F69	D70	E71	E72	N73	A74	Y75	F76	E77	D78	E79	E80	E81	ASP	SER	ASN	VAL	ASP	LEU	PRO	TYR	ILE	PRO	ALA	GLU	ASN	PRO	THR	ARG	GLN	
ASP	VAL	ASP	GLY	ALA	PRO	ALA	ARG	H623	D563	L503	K443	T383	P323	Q263	ASP	ASN	THR	F69	D70	E71	E72	N73	A74	Y75	F76	E77	D78	E79	E80	E81	ASP	SER	ASN	VAL	ASP	LEU	PRO	TYR	ILE	PRO	ALA	GLU	ASN	PRO	THR	ARG	GLN	
ASP	VAL	ASP	GLY	ALA	PRO	ALA	ARG	V624	I564	F504	K444	P384	G324	L264	ASP	ASN	THR	F69	D70	E71	E72	N73	A74	Y75	F76	E77	D78	E79	E80	E81	ASP	SER	ASN	VAL	ASP	LEU	PRO	TYR	ILE	PRO	ALA	GLU	ASN	PRO	THR	ARG	GLN	
ASP	VAL	ASP	GLY	ALA	PRO	ALA	ARG	S625	P565	V505	I445	G385	D325	M265	ASP	ASN	THR	F69	D70	E71	E72	N73	A74	Y75	F76	E77	D78	E79	E80	E81	ASP	SER	ASN	VAL	ASP	LEU	PRO	TYR	ILE	PRO	ALA	GLU	ASN	PRO	THR	ARG	GLN	
ASP	VAL	ASP	GLY	ALA	PRO	ALA	ARG	K626	S566	T506	E446	R386	G326	H266	ASP	ASN	THR	F69	D70	E71	E72	N73	A74	Y75	F76	E77	D78	E79	E80	E81	ASP	SER	ASN	VAL	ASP	LEU	PRO	TYR	ILE	PRO	ALA	GLU	ASN	PRO	THR	ARG	GLN	
ASP	VAL	ASP	GLY	ALA	PRO	ALA	ARG	E627	I567	K507	L447	L387	P327	Q267	ASP	ASN	THR	F69	D70	E71	E72	N73	A74	Y75	F76	E77	D78	E79	E80	E81	ASP	SER	ASN	VAL	ASP	LEU	PRO	TYR	ILE	PRO	ALA	GLU	ASN	PRO	THR	ARG	GLN	
ASP	VAL	ASP	GLY	ALA	PRO	ALA	ARG	L628	K568	K508	L448	I388	I328	I268	ASP	ASN	THR	F69	D70	E71	E72	N73	A74	Y75	F76	E77	D78	E79	E80	E81	ASP	SER	ASN	VAL	ASP	LEU	PRO	TYR	ILE	PRO	ALA	GLU	ASN	PRO	THR	ARG	GLN	
ASP	VAL	ASP	GLY	ALA	PRO	ALA	ARG	L629	T569	A509	A449	D389	I329	I269	ASP	ASN	THR	F69	D70	E71	E72	N73	A74	Y75	F76	E77	D78	E79	E80	E81	ASP	SER	ASN	VAL	ASP	LEU	PRO	TYR	ILE	PRO	ALA	GLU	ASN	PRO	THR	ARG	GLN	
ASP	VAL	ASP	GLY	ALA	PRO	ALA	ARG	D630	V570	N510	R450	H390	V330	K270	ASP	ASN	THR	F69	D70	E71	E72	N73	A74	Y75	F76	E77	D78	E79	E80	E81	ASP	SER	ASN	VAL	ASP	LEU	PRO	TYR	ILE	PRO	ALA	GLU	ASN	PRO	THR	ARG	GLN	
ASP	VAL	ASP	GLY	ALA	PRO	ALA	ARG	L631	I571	A511	D451	V391	I331	S271	ASP	ASN	THR	F69	D70	E71	E72	N73	A74	Y75	F76	E77	D78	E79	E80	E81	ASP	SER	ASN	VAL	ASP	LEU	PRO	TYR	ILE	PRO	ALA	GLU	ASN	PRO	THR	ARG	GLN	
ASP	VAL	ASP	GLY	ALA	PRO	ALA	ARG	A632	N572	E512	I462	K392	V332	E272	ASP	ASN	THR	F69	D70	E71	E72	N73	A74	Y75	F76	E77	D78	E79	E80	E81	ASP	SER	ASN	VAL	ASP	LEU	PRO	TYR	ILE	PRO	ALA	GLU	ASN	PRO	THR	ARG	GLN	
ASP	VAL	ASP	GLY	ALA	PRO	ALA	ARG	M633	Y573	E513	L453	K393	C333	Y273	ASP	ASN	THR	F69	D70	E71	E72	N73	A74	Y75	F76	E77	D78	E79	E80	E81	ASP	SER	ASN	VAL	ASP	LEU	PRO	TYR	ILE	PRO	ALA	GLU	ASN	PRO	THR	ARG	GLN	
ASP	VAL	ASP	GLY	ALA	PRO	ALA	ARG	Q634	D574	L514	I464	K394	P334	T274	ASP	ASN	THR	F69	D70	E71	E72	N73	A74	Y75	F76	E77	D78	E79	E80	E81	ASP	SER	ASN	VAL	ASP	LEU	PRO	TYR	ILE	PRO	ALA	GLU	ASN	PRO	THR	ARG	GLN	
ASP	VAL	ASP	GLY	ALA	PRO	ALA	ARG	N635	A575	A515	D455	A395	T335	Q275	ASP	ASN	THR																															

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	0.27	0/665	0.50	0/899
2	C	0.25	0/6609	0.48	2/8946 (0.0%)
3	D	0.29	0/709	0.47	0/952
4	A	0.27	1/9415 (0.0%)	0.46	1/12775 (0.0%)
5	E	0.62	0/2607	0.98	5/3593 (0.1%)
All	All	0.34	1/20005 (0.0%)	0.56	8/27165 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	804	HIS	C-O	6.55	1.32	1.23

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	E	275	GLN	CA-C-N	-8.04	111.73	119.85
5	E	275	GLN	C-N-CA	-8.04	111.73	119.85
5	E	271	SER	CA-C-N	6.98	134.27	121.70
5	E	271	SER	C-N-CA	6.98	134.27	121.70
2	C	565	ASP	N-CA-C	-5.91	104.74	113.61

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	157	0
3	D	700	0	682	6	0
4	A	9227	0	9154	142	0
5	E	2605	0	1378	67	0
6	D	3	0	0	0	0
All	All	19668	0	18522	330	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 9.

The worst 5 of 330 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
5:E:120:MET:HA	5:E:120:MET:HE2	1.24	1.18
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

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%)	48	70

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	E	474/958 (50%)	459 (97%)	12 (2%)	3 (1%)	21	42
All	All	2619/3276 (80%)	2492 (95%)	123 (5%)	4 (0%)	44	66

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 [i](#)

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%)	65 (94%)	4 (6%)	18	39
2	C	701/753 (93%)	666 (95%)	35 (5%)	22	46
3	D	80/95 (84%)	77 (96%)	3 (4%)	29	56
4	A	1020/1071 (95%)	940 (92%)	80 (8%)	11	26
5	E	51/787 (6%)	39 (76%)	12 (24%)	1	1
All	All	1921/2783 (69%)	1787 (93%)	134 (7%)	16	31

5 of 134 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	A	1103	SER
4	A	1170	VAL
5	E	148	ARG
4	A	229	GLU
4	A	171	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 48 such sidechains are listed below:

Mol	Chain	Res	Type
4	A	307	GLN
4	A	796	ASN
4	A	417	ASN
4	A	553	GLN
4	A	805	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](#)

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.

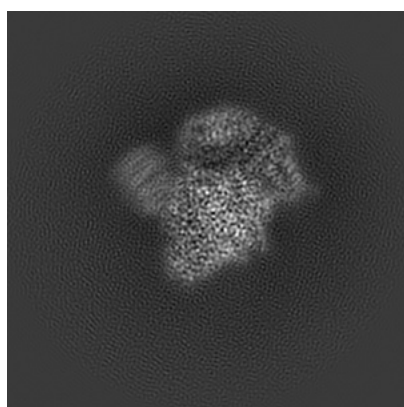
6 Map visualisation [i](#)

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.

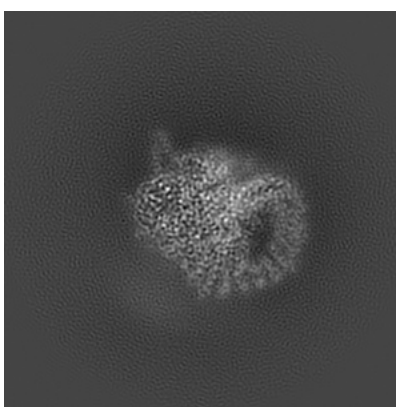
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

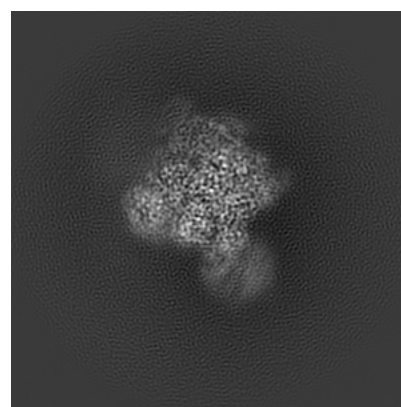
6.1.1 Primary map



X



Y

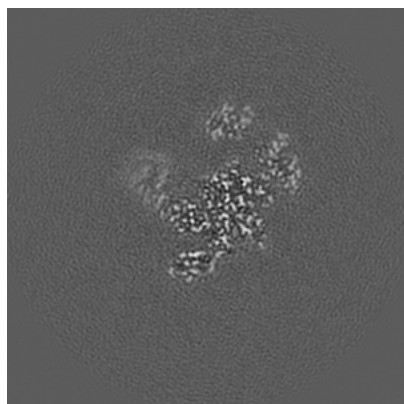


Z

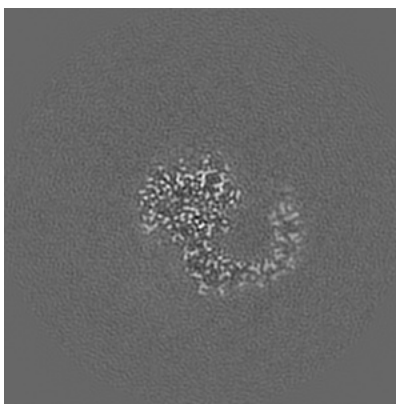
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

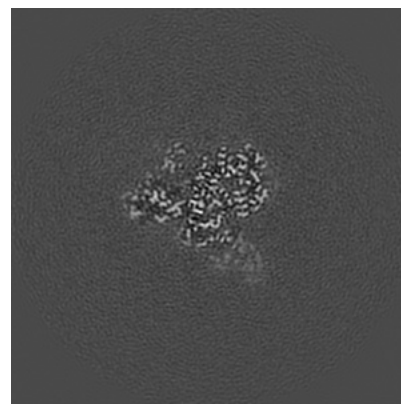
6.2.1 Primary map



X Index: 120



Y Index: 120

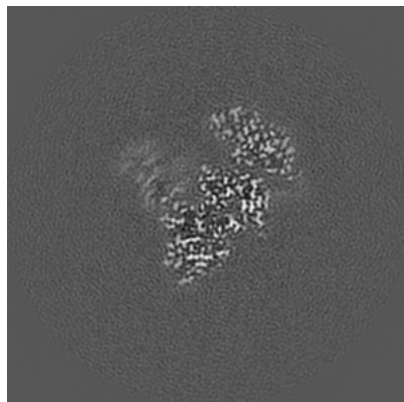


Z Index: 120

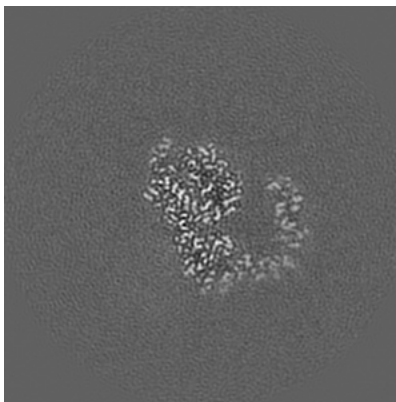
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

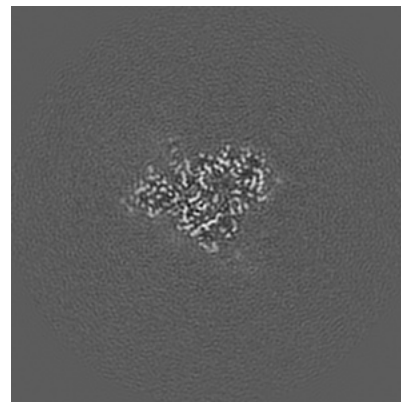
6.3.1 Primary map



X Index: 127



Y Index: 127

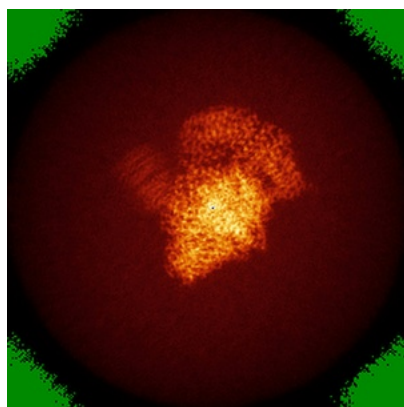


Z Index: 116

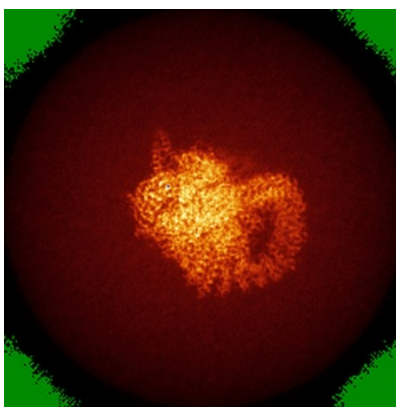
The images above show the largest variance slices of the map in three orthogonal directions.

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

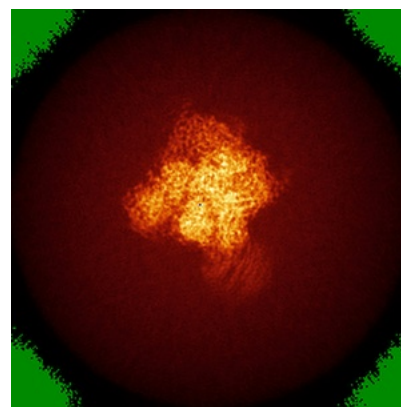
6.4.1 Primary map



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

This section was not generated.

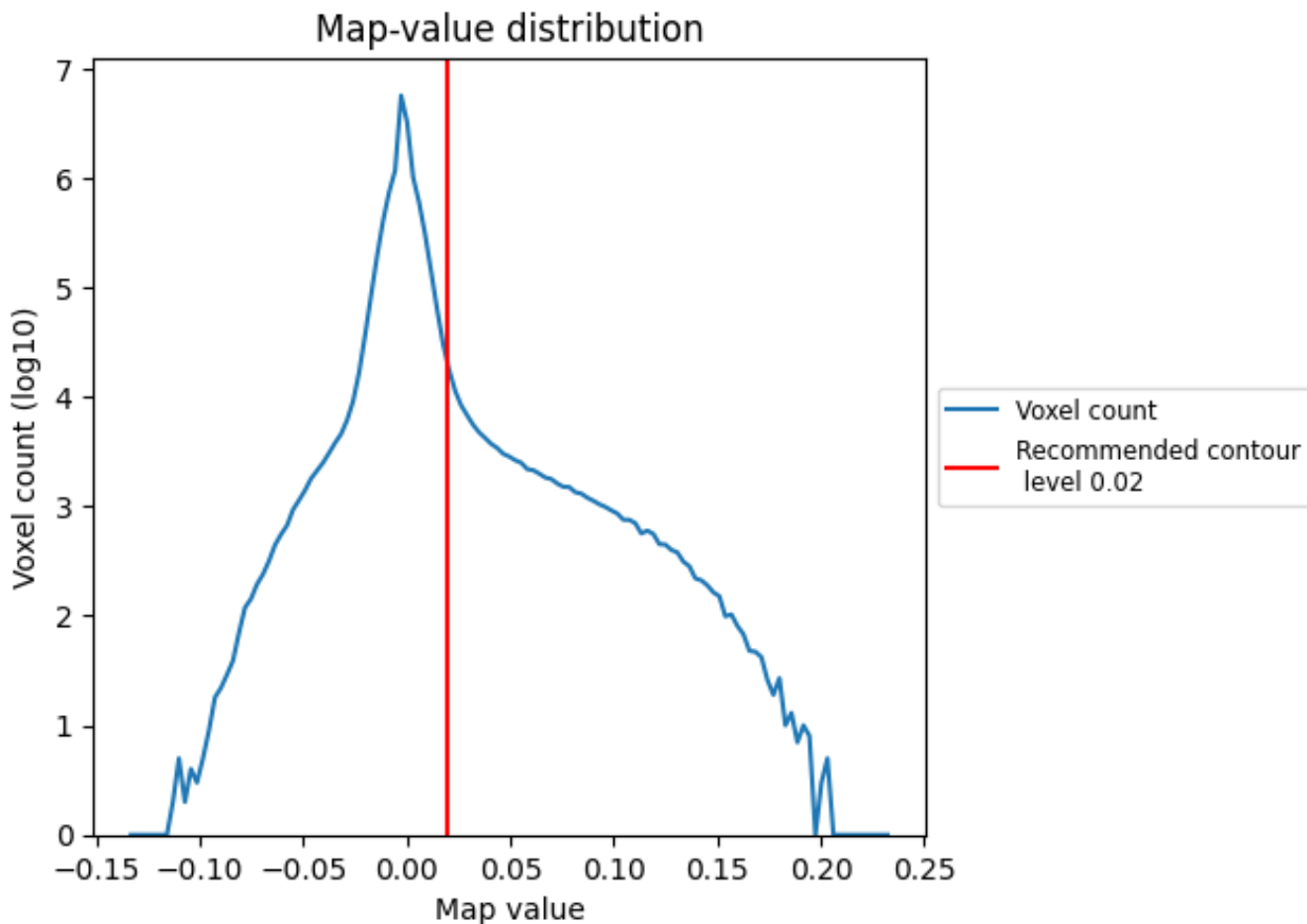
6.6 Mask visualisation

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

7 Map analysis [i](#)

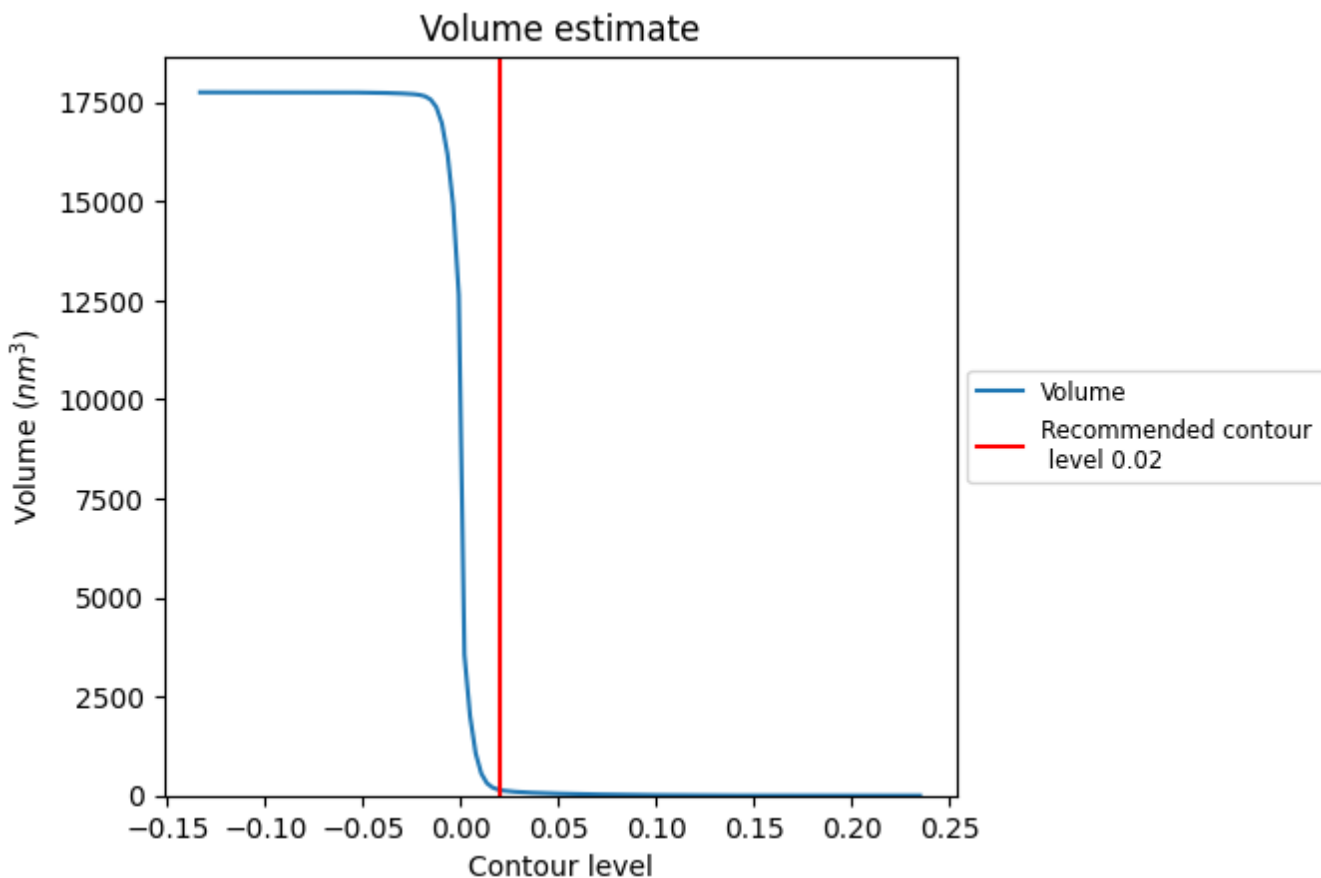
This section contains the results of statistical analysis of the map.

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.

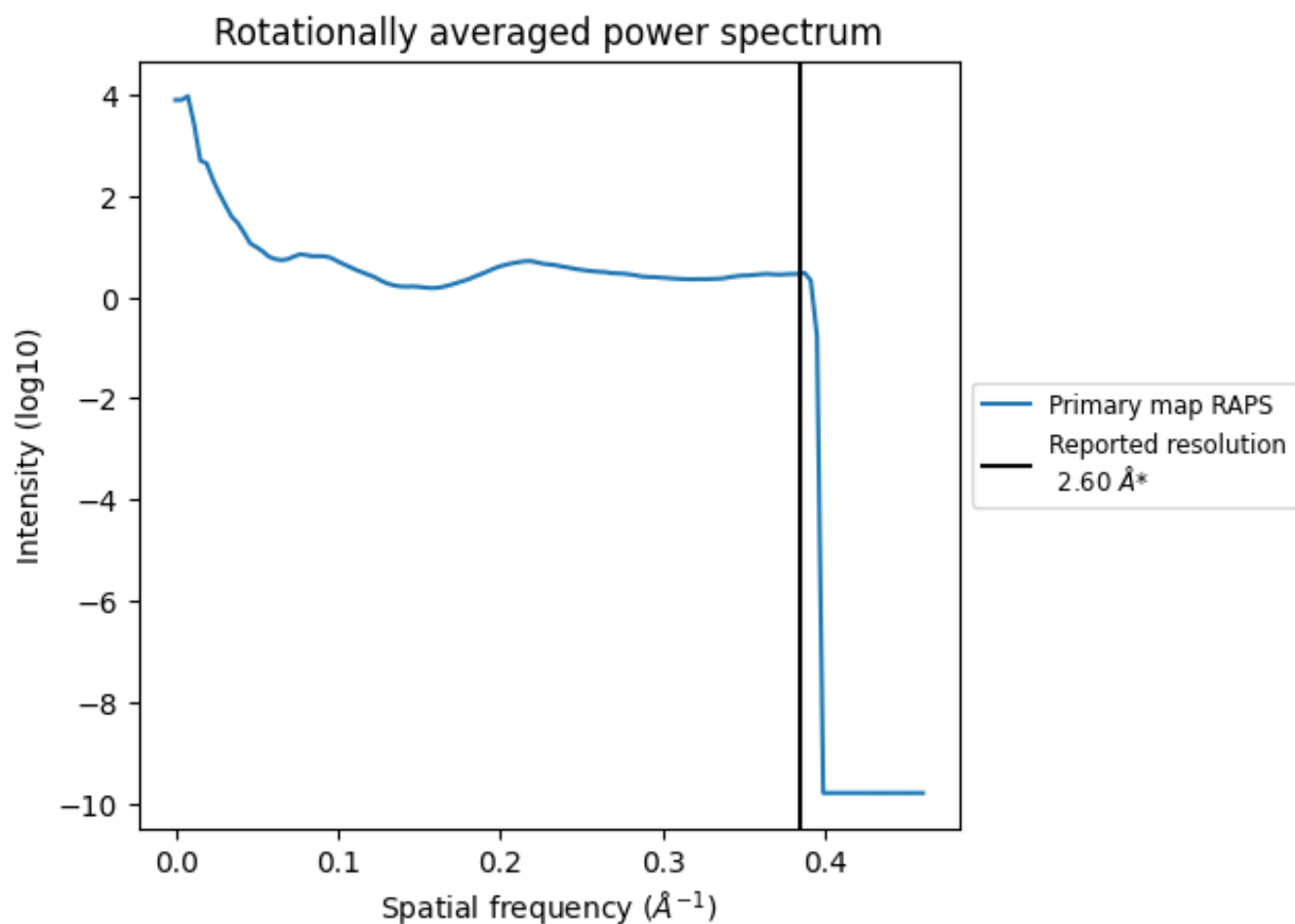
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 145 nm^3 ; 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 i



*Reported resolution corresponds to spatial frequency of 0.385 \AA^{-1}

8 Fourier-Shell correlation

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

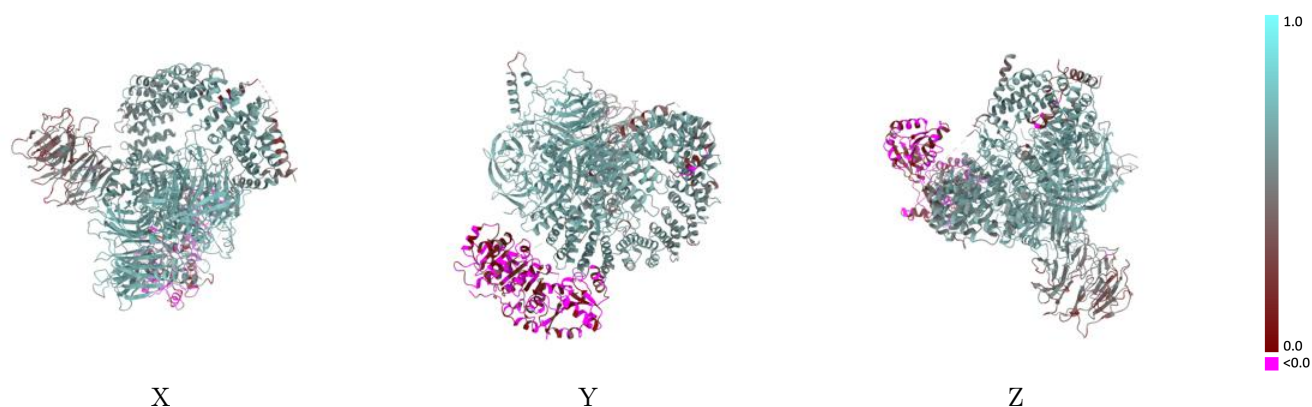
9 Map-model fit [i](#)

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 7.

9.1 Map-model overlay [i](#)

This section was not generated.

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

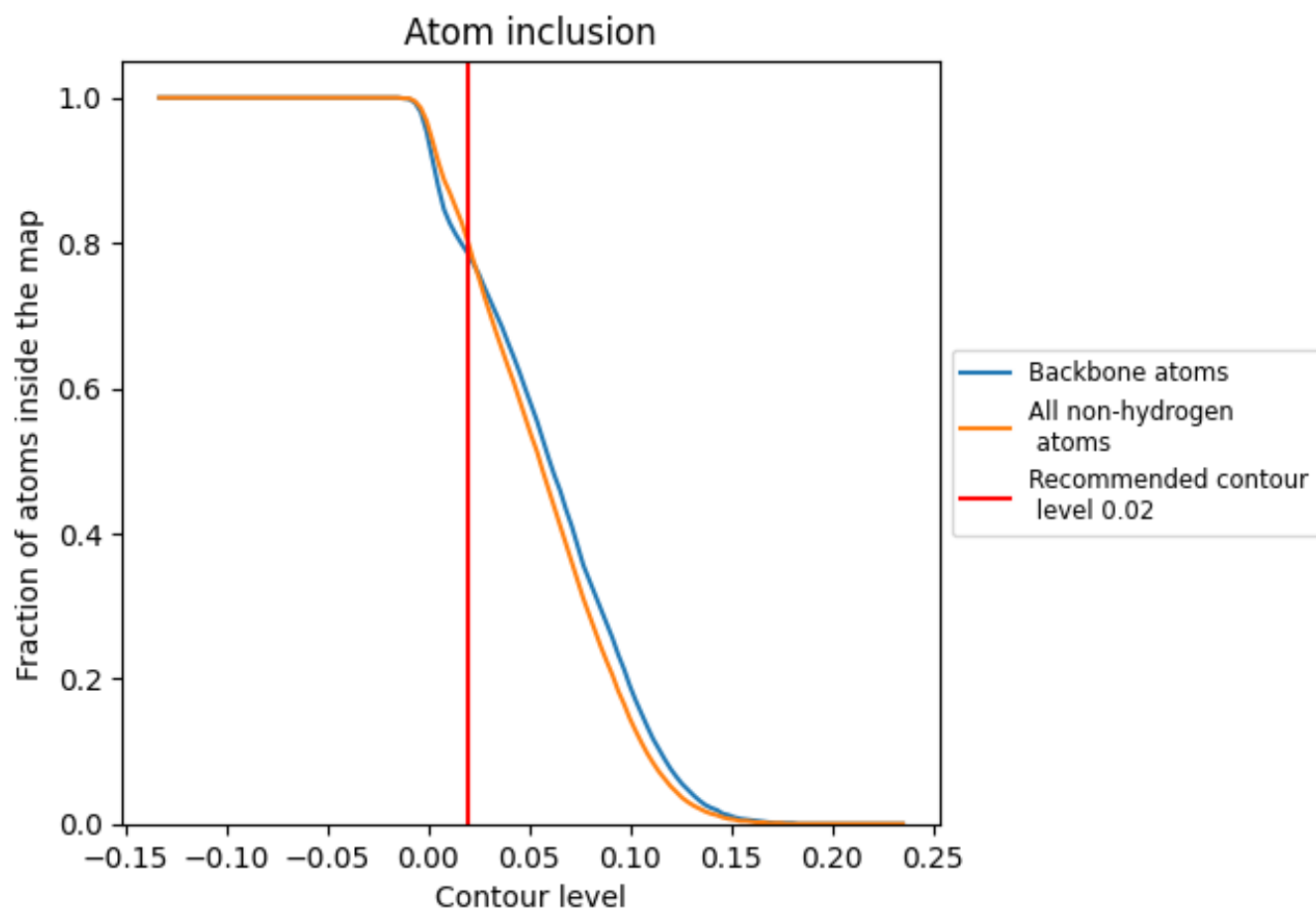


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 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	 0.7990	 0.5400
A	 0.8870	 0.6040
B	 0.9840	 0.6760
C	 0.9300	 0.6110
D	 0.9240	 0.6470
E	 0.0950	 0.0770

