



Full wwPDB EM Validation Report ⓘ

Nov 23, 2022 – 01:30 PM EST

PDB ID : 7UN3
EMDB ID : EMD-26612
Title : Complex of UBE2O with NAP1L1 and ubiquitylated uL2
Authors : Yip, M.C.J.; Sedor, S.F.; Shao, S.
Deposited on : 2022-04-08
Resolution : 3.50 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.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) : 2.31.2

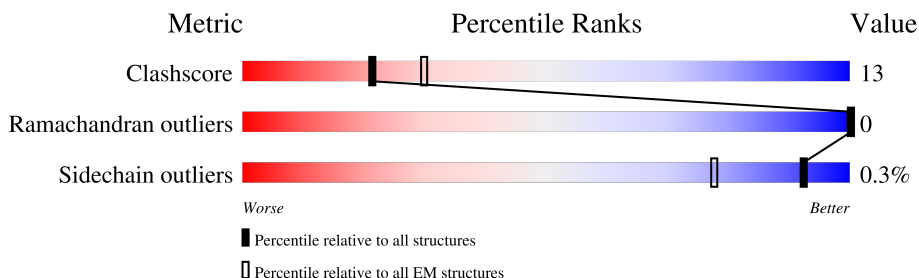
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.50 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	A	1744	<div> <div>9%</div> <div>27%</div> <div>11%</div> <div>63%</div> </div>
1	D	1744	<div> <div>96%</div> </div>
2	B	416	<div> <div>13%</div> <div>39%</div> <div>14%</div> <div>46%</div> </div>
2	C	416	<div> <div>15%</div> <div>39%</div> <div>13%</div> <div>47%</div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 9423 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 Ubiquitin,60S ribosomal protein L8,(E3-independent) E2 ubiquitin-conjugating enzyme fusion.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	D	73	Total	C	N	O	S	0	0
			582	368	99	114	1		
1	A	649	Total	C	N	O	S	0	0
			5196	3329	894	947	26		

There are 244 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	-46	MET	-	initiating methionine	UNP P62987
D	-45	ALA	-	expression tag	UNP P62987
D	-44	SER	-	expression tag	UNP P62987
D	-43	TRP	-	expression tag	UNP P62987
D	-42	SER	-	expression tag	UNP P62987
D	-41	HIS	-	expression tag	UNP P62987
D	-40	PRO	-	expression tag	UNP P62987
D	-39	GLN	-	expression tag	UNP P62987
D	-38	PHE	-	expression tag	UNP P62987
D	-37	GLU	-	expression tag	UNP P62987
D	-36	LYS	-	expression tag	UNP P62987
D	-35	GLY	-	expression tag	UNP P62987
D	-34	ALA	-	expression tag	UNP P62987
D	-33	TRP	-	expression tag	UNP P62987
D	-32	SER	-	expression tag	UNP P62987
D	-31	HIS	-	expression tag	UNP P62987
D	-30	PRO	-	expression tag	UNP P62987
D	-29	GLN	-	expression tag	UNP P62987
D	-28	PHE	-	expression tag	UNP P62987
D	-27	GLU	-	expression tag	UNP P62987
D	-26	LYS	-	expression tag	UNP P62987
D	-25	GLY	-	expression tag	UNP P62987
D	-24	SER	-	expression tag	UNP P62987
D	-23	TRP	-	expression tag	UNP P62987
D	-22	SER	-	expression tag	UNP P62987

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-21	HIS	-	expression tag	UNP P62987
D	-20	PRO	-	expression tag	UNP P62987
D	-19	GLN	-	expression tag	UNP P62987
D	-18	PHE	-	expression tag	UNP P62987
D	-17	GLU	-	expression tag	UNP P62987
D	-16	LYS	-	expression tag	UNP P62987
D	-15	GLY	-	expression tag	UNP P62987
D	-14	PRO	-	expression tag	UNP P62987
D	-13	ALA	-	expression tag	UNP P62987
D	-12	GLY	-	expression tag	UNP P62987
D	-11	SER	-	expression tag	UNP P62987
D	-10	GLU	-	expression tag	UNP P62987
D	-9	ASN	-	expression tag	UNP P62987
D	-8	LEU	-	expression tag	UNP P62987
D	-7	TYR	-	expression tag	UNP P62987
D	-6	PHE	-	expression tag	UNP P62987
D	-5	GLN	-	expression tag	UNP P62987
D	-4	GLY	-	expression tag	UNP P62987
D	-3	SER	-	expression tag	UNP P62987
D	-2	GLY	-	expression tag	UNP P62987
D	-1	ILE	-	expression tag	UNP P62987
D	0	ARG	-	expression tag	UNP P62987
D	76	VAL	GLY	engineered mutation	UNP P62987
D	77	GLY	-	linker	UNP P62987
D	78	SER	-	linker	UNP P62987
D	176	VAL	ILE	conflict	UNP P62917
D	336	GLY	-	linker	UNP P62917
D	337	GLY	-	linker	UNP P62917
D	338	SER	-	linker	UNP P62917
D	339	GLY	-	linker	UNP P62917
D	340	LEU	-	linker	UNP P62917
D	341	GLU	-	linker	UNP P62917
D	342	VAL	-	linker	UNP P62917
D	343	LEU	-	linker	UNP P62917
D	344	PHE	-	linker	UNP P62917
D	345	GLN	-	linker	UNP P62917
D	346	GLY	-	linker	UNP P62917
D	347	PRO	-	linker	UNP P62917
D	348	GLY	-	linker	UNP P62917
D	349	GLY	-	linker	UNP P62917
D	350	SER	-	linker	UNP P62917
D	351	GLY	-	linker	UNP P62917

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Chain	Residue	Modelled	Actual	Comment	Reference
D	352	GLY	-	linker	UNP P62917
D	353	GLY	-	linker	UNP P62917
D	354	SER	-	linker	UNP P62917
D	355	GLY	-	linker	UNP P62917
D	356	LEU	-	linker	UNP P62917
D	357	GLU	-	linker	UNP P62917
D	358	VAL	-	linker	UNP P62917
D	359	LEU	-	linker	UNP P62917
D	360	PHE	-	linker	UNP P62917
D	361	GLN	-	linker	UNP P62917
D	362	GLY	-	linker	UNP P62917
D	363	PRO	-	linker	UNP P62917
D	364	GLY	-	linker	UNP P62917
D	365	GLY	-	linker	UNP P62917
D	366	SER	-	linker	UNP P62917
D	367	GLY	-	linker	UNP P62917
D	368	TYR	-	linker	UNP P62917
D	369	PRO	-	linker	UNP P62917
D	370	TYR	-	linker	UNP P62917
D	371	ASP	-	linker	UNP P62917
D	372	VAL	-	linker	UNP P62917
D	373	PRO	-	linker	UNP P62917
D	374	ASP	-	linker	UNP P62917
D	375	TYR	-	linker	UNP P62917
D	376	ALA	-	linker	UNP P62917
D	377	GLY	-	linker	UNP P62917
D	378	TYR	-	linker	UNP P62917
D	379	PRO	-	linker	UNP P62917
D	380	TYR	-	linker	UNP P62917
D	381	ASP	-	linker	UNP P62917
D	382	VAL	-	linker	UNP P62917
D	383	PRO	-	linker	UNP P62917
D	384	ASP	-	linker	UNP P62917
D	385	TYR	-	linker	UNP P62917
D	386	ALA	-	linker	UNP P62917
D	387	GLY	-	linker	UNP P62917
D	388	SER	-	linker	UNP P62917
D	389	TYR	-	linker	UNP P62917
D	390	PRO	-	linker	UNP P62917
D	391	TYR	-	linker	UNP P62917
D	392	ASP	-	linker	UNP P62917
D	393	VAL	-	linker	UNP P62917

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Chain	Residue	Modelled	Actual	Comment	Reference
D	394	PRO	-	linker	UNP P62917
D	395	ASP	-	linker	UNP P62917
D	396	TYR	-	linker	UNP P62917
D	397	ALA	-	linker	UNP P62917
D	398	GLY	-	linker	UNP P62917
D	399	SER	-	linker	UNP P62917
D	400	ALA	-	linker	UNP P62917
D	401	ILE	-	linker	UNP P62917
D	402	ARG	-	linker	UNP P62917
D	403	ASP	-	linker	UNP P62917
D	404	ARG	-	linker	UNP P62917
D	405	THR	-	linker	UNP P62917
D	1445	LYS	CYS	engineered mutation	UNP Q9C0C9
A	-451	MET	-	initiating methionine	UNP P62987
A	-450	ALA	-	expression tag	UNP P62987
A	-449	SER	-	expression tag	UNP P62987
A	-448	TRP	-	expression tag	UNP P62987
A	-447	SER	-	expression tag	UNP P62987
A	-446	HIS	-	expression tag	UNP P62987
A	-445	PRO	-	expression tag	UNP P62987
A	-444	GLN	-	expression tag	UNP P62987
A	-443	PHE	-	expression tag	UNP P62987
A	-442	GLU	-	expression tag	UNP P62987
A	-441	LYS	-	expression tag	UNP P62987
A	-440	GLY	-	expression tag	UNP P62987
A	-439	ALA	-	expression tag	UNP P62987
A	-438	TRP	-	expression tag	UNP P62987
A	-437	SER	-	expression tag	UNP P62987
A	-436	HIS	-	expression tag	UNP P62987
A	-435	PRO	-	expression tag	UNP P62987
A	-434	GLN	-	expression tag	UNP P62987
A	-433	PHE	-	expression tag	UNP P62987
A	-432	GLU	-	expression tag	UNP P62987
A	-431	LYS	-	expression tag	UNP P62987
A	-430	GLY	-	expression tag	UNP P62987
A	-429	SER	-	expression tag	UNP P62987
A	-428	TRP	-	expression tag	UNP P62987
A	-427	SER	-	expression tag	UNP P62987
A	-426	HIS	-	expression tag	UNP P62987
A	-425	PRO	-	expression tag	UNP P62987
A	-424	GLN	-	expression tag	UNP P62987
A	-423	PHE	-	expression tag	UNP P62987

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-422	GLU	-	expression tag	UNP P62987
A	-421	LYS	-	expression tag	UNP P62987
A	-420	GLY	-	expression tag	UNP P62987
A	-419	PRO	-	expression tag	UNP P62987
A	-418	ALA	-	expression tag	UNP P62987
A	-417	GLY	-	expression tag	UNP P62987
A	-416	SER	-	expression tag	UNP P62987
A	-415	GLU	-	expression tag	UNP P62987
A	-414	ASN	-	expression tag	UNP P62987
A	-413	LEU	-	expression tag	UNP P62987
A	-412	TYR	-	expression tag	UNP P62987
A	-411	PHE	-	expression tag	UNP P62987
A	-410	GLN	-	expression tag	UNP P62987
A	-409	GLY	-	expression tag	UNP P62987
A	-408	SER	-	expression tag	UNP P62987
A	-407	GLY	-	expression tag	UNP P62987
A	-406	ILE	-	expression tag	UNP P62987
A	-405	ARG	-	expression tag	UNP P62987
A	-329	VAL	GLY	engineered mutation	UNP P62987
A	-328	GLY	-	linker	UNP P62987
A	-327	SER	-	linker	UNP P62987
A	-229	VAL	ILE	conflict	UNP P62917
A	-69	GLY	-	linker	UNP P62917
A	-68	GLY	-	linker	UNP P62917
A	-67	SER	-	linker	UNP P62917
A	-66	GLY	-	linker	UNP P62917
A	-65	LEU	-	linker	UNP P62917
A	-64	GLU	-	linker	UNP P62917
A	-63	VAL	-	linker	UNP P62917
A	-62	LEU	-	linker	UNP P62917
A	-61	PHE	-	linker	UNP P62917
A	-60	GLN	-	linker	UNP P62917
A	-59	GLY	-	linker	UNP P62917
A	-58	PRO	-	linker	UNP P62917
A	-57	GLY	-	linker	UNP P62917
A	-56	GLY	-	linker	UNP P62917
A	-55	SER	-	linker	UNP P62917
A	-54	GLY	-	linker	UNP P62917
A	-53	GLY	-	linker	UNP P62917
A	-52	GLY	-	linker	UNP P62917
A	-51	SER	-	linker	UNP P62917
A	-50	GLY	-	linker	UNP P62917

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-49	LEU	-	linker	UNP P62917
A	-48	GLU	-	linker	UNP P62917
A	-47	VAL	-	linker	UNP P62917
A	-46	LEU	-	linker	UNP P62917
A	-45	PHE	-	linker	UNP P62917
A	-44	GLN	-	linker	UNP P62917
A	-43	GLY	-	linker	UNP P62917
A	-42	PRO	-	linker	UNP P62917
A	-41	GLY	-	linker	UNP P62917
A	-40	GLY	-	linker	UNP P62917
A	-39	SER	-	linker	UNP P62917
A	-38	GLY	-	linker	UNP P62917
A	-37	TYR	-	linker	UNP P62917
A	-36	PRO	-	linker	UNP P62917
A	-35	TYR	-	linker	UNP P62917
A	-34	ASP	-	linker	UNP P62917
A	-33	VAL	-	linker	UNP P62917
A	-32	PRO	-	linker	UNP P62917
A	-31	ASP	-	linker	UNP P62917
A	-30	TYR	-	linker	UNP P62917
A	-29	ALA	-	linker	UNP P62917
A	-28	GLY	-	linker	UNP P62917
A	-27	TYR	-	linker	UNP P62917
A	-26	PRO	-	linker	UNP P62917
A	-25	TYR	-	linker	UNP P62917
A	-24	ASP	-	linker	UNP P62917
A	-23	VAL	-	linker	UNP P62917
A	-22	PRO	-	linker	UNP P62917
A	-21	ASP	-	linker	UNP P62917
A	-20	TYR	-	linker	UNP P62917
A	-19	ALA	-	linker	UNP P62917
A	-18	GLY	-	linker	UNP P62917
A	-17	SER	-	linker	UNP P62917
A	-16	TYR	-	linker	UNP P62917
A	-15	PRO	-	linker	UNP P62917
A	-14	TYR	-	linker	UNP P62917
A	-13	ASP	-	linker	UNP P62917
A	-12	VAL	-	linker	UNP P62917
A	-11	PRO	-	linker	UNP P62917
A	-10	ASP	-	linker	UNP P62917
A	-9	TYR	-	linker	UNP P62917
A	-8	ALA	-	linker	UNP P62917

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	GLY	-	linker	UNP P62917
A	-6	SER	-	linker	UNP P62917
A	-5	ALA	-	linker	UNP P62917
A	-4	ILE	-	linker	UNP P62917
A	-3	ARG	-	linker	UNP P62917
A	-2	ASP	-	linker	UNP P62917
A	-1	ARG	-	linker	UNP P62917
A	0	THR	-	linker	UNP P62917
A	1040	LYS	CYS	engineered mutation	UNP Q9C0C9

- Molecule 2 is a protein called Nucleosome assembly protein 1-like 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	223	Total	C	N	O	S	0	0
			1838	1190	308	333	7		
2	C	219	Total	C	N	O	S	0	0
			1807	1169	304	327	7		

There are 52 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-24	MET	-	initiating methionine	UNP P55209
B	-23	ASP	-	expression tag	UNP P55209
B	-22	TYR	-	expression tag	UNP P55209
B	-21	LYS	-	expression tag	UNP P55209
B	-20	ASP	-	expression tag	UNP P55209
B	-19	HIS	-	expression tag	UNP P55209
B	-18	ASP	-	expression tag	UNP P55209
B	-17	GLY	-	expression tag	UNP P55209
B	-16	ASP	-	expression tag	UNP P55209
B	-15	TYR	-	expression tag	UNP P55209
B	-14	LYS	-	expression tag	UNP P55209
B	-13	ASP	-	expression tag	UNP P55209
B	-12	HIS	-	expression tag	UNP P55209
B	-11	ASP	-	expression tag	UNP P55209
B	-10	ILE	-	expression tag	UNP P55209
B	-9	ASP	-	expression tag	UNP P55209
B	-8	TYR	-	expression tag	UNP P55209
B	-7	LYS	-	expression tag	UNP P55209
B	-6	ASP	-	expression tag	UNP P55209
B	-5	ASP	-	expression tag	UNP P55209
B	-4	ASP	-	expression tag	UNP P55209

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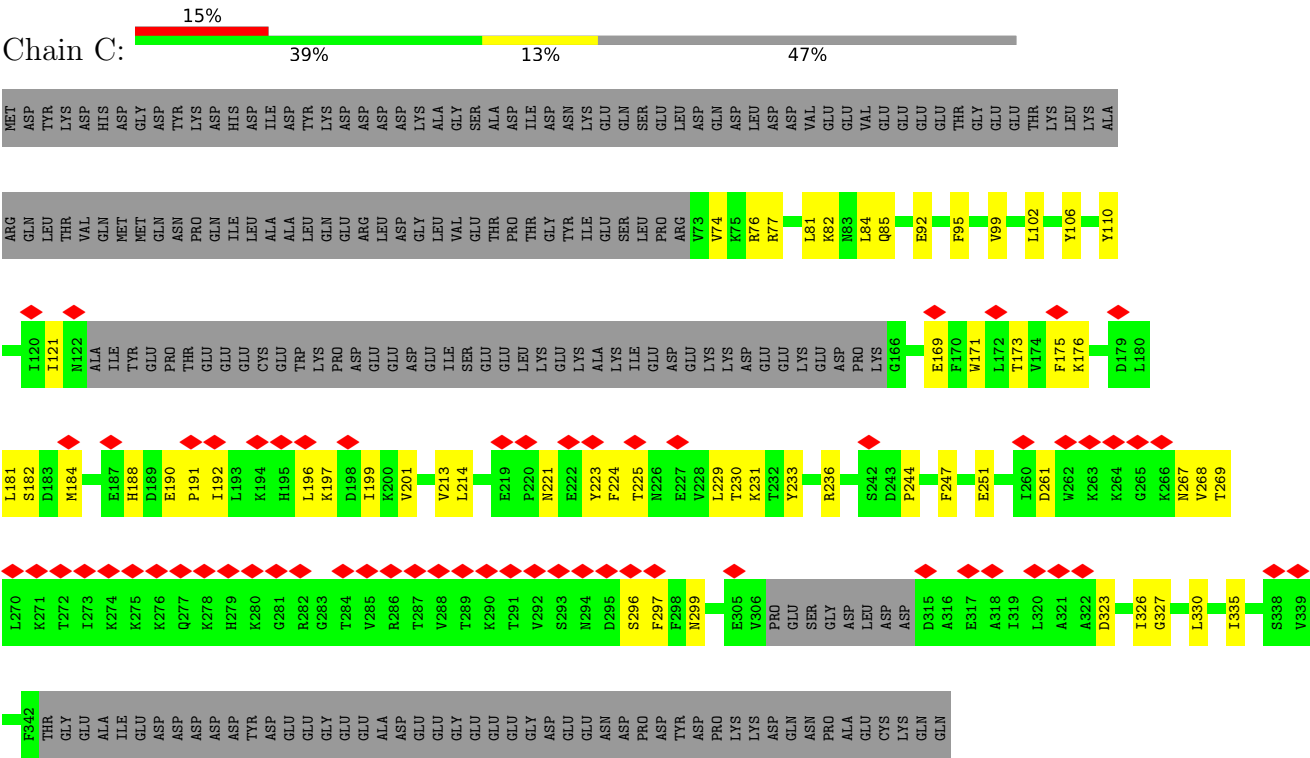
Chain	Residue	Modelled	Actual	Comment	Reference
B	-3	ASP	-	expression tag	UNP P55209
B	-2	LYS	-	expression tag	UNP P55209
B	-1	ALA	-	expression tag	UNP P55209
B	0	GLY	-	expression tag	UNP P55209
B	1	SER	-	expression tag	UNP P55209
C	-24	MET	-	initiating methionine	UNP P55209
C	-23	ASP	-	expression tag	UNP P55209
C	-22	TYR	-	expression tag	UNP P55209
C	-21	LYS	-	expression tag	UNP P55209
C	-20	ASP	-	expression tag	UNP P55209
C	-19	HIS	-	expression tag	UNP P55209
C	-18	ASP	-	expression tag	UNP P55209
C	-17	GLY	-	expression tag	UNP P55209
C	-16	ASP	-	expression tag	UNP P55209
C	-15	TYR	-	expression tag	UNP P55209
C	-14	LYS	-	expression tag	UNP P55209
C	-13	ASP	-	expression tag	UNP P55209
C	-12	HIS	-	expression tag	UNP P55209
C	-11	ASP	-	expression tag	UNP P55209
C	-10	ILE	-	expression tag	UNP P55209
C	-9	ASP	-	expression tag	UNP P55209
C	-8	TYR	-	expression tag	UNP P55209
C	-7	LYS	-	expression tag	UNP P55209
C	-6	ASP	-	expression tag	UNP P55209
C	-5	ASP	-	expression tag	UNP P55209
C	-4	ASP	-	expression tag	UNP P55209
C	-3	ASP	-	expression tag	UNP P55209
C	-2	LYS	-	expression tag	UNP P55209
C	-1	ALA	-	expression tag	UNP P55209
C	0	GLY	-	expression tag	UNP P55209
C	1	SER	-	expression tag	UNP P55209

MET	ALA	SER	TRP	SER	HIS	PRO	GLN	PHE	GLU	LYS	GLY	ALA	TRP	SER	HIS	PRO	GLN	PHE	GLU	LYS	GLY	SER	TRP	SER	HIS	PRO	GLN	PHE	GLU	LYS	GLY	SER	TRP
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● Molecule 2: Nucleosome assembly protein 1-like 1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	201743	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 ($e^-/\text{\AA}^2$)	59.6	Depositor
Minimum defocus (nm)	1400	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.954	Depositor
Minimum map value	-2.153	Depositor
Average map value	-0.002	Depositor
Map value standard deviation	0.043	Depositor
Recommended contour level	0.3	Depositor
Map size (Å)	280.5, 280.5, 280.5	wwPDB
Map dimensions	340, 340, 340	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.825, 0.825, 0.825	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	0.27	0/5314	0.52	0/7200
1	D	0.25	0/588	0.49	0/792
2	B	0.26	0/1882	0.49	0/2533
2	C	0.26	0/1850	0.49	0/2491
All	All	0.26	0/9634	0.50	0/13016

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5196	0	5187	156	0
1	D	582	0	610	12	0
2	B	1838	0	1836	47	0
2	C	1807	0	1799	46	0
All	All	9423	0	9432	247	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 13.

All (247) 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:154:ARG:NH1	1:A:161:SER:O	1.97	0.96
2:B:181:LEU:HD11	2:B:330:LEU:HD11	1.54	0.87
2:C:296:SER:N	2:C:299:ASN:OD1	2.09	0.85
1:A:144:ASP:OD1	1:A:553:THR:OG1	1.94	0.84
1:D:54:ARG:NH1	1:D:58:ASP:OD2	2.12	0.83
2:C:236:ARG:NH2	2:C:251:GLU:OE1	2.14	0.80
2:C:196:LEU:HD21	2:C:199:ILE:HD11	1.62	0.79
1:A:79:VAL:HG12	1:A:124:VAL:HG22	1.64	0.79
1:A:1023:SER:OG	1:A:1035:ASP:O	2.00	0.79
1:A:1068:ILE:HG12	1:A:1072:ILE:HD12	1.65	0.78
1:A:603:VAL:HG23	1:A:634:ILE:HD12	1.64	0.78
2:C:201:VAL:HG13	2:C:335:ILE:HD13	1.67	0.77
1:A:215:ASP:OD1	1:A:216:LEU:N	2.18	0.76
1:A:656:THR:N	1:A:681:VAL:O	2.17	0.76
2:B:339:VAL:HG22	2:C:81:LEU:HD22	1.66	0.76
2:B:83:ASN:OD1	2:B:87:LYS:NZ	2.16	0.76
1:A:226:ASN:ND2	2:B:344:GLY:O	2.19	0.75
2:B:175:PHE:HD1	2:B:181:LEU:HD13	1.50	0.75
1:A:623:LYS:HB2	1:A:634:ILE:HD11	1.70	0.74
1:A:162:GLN:OE1	1:A:561:ASP:N	2.22	0.73
1:A:171:ILE:CD1	1:A:553:THR:HG22	2.18	0.73
1:A:144:ASP:OD2	1:A:553:THR:HG23	1.89	0.72
2:B:166:GLY:O	2:C:77:ARG:NH2	2.22	0.72
2:C:197:LYS:O	2:C:197:LYS:NZ	2.18	0.72
1:A:145:ARG:NH2	1:A:156:MET:SD	2.63	0.71
2:B:339:VAL:HG21	2:C:85:GLN:HB2	1.73	0.70
2:B:198:ASP:OD1	2:B:199:ILE:N	2.24	0.70
2:B:117:ARG:HD3	2:C:81:LEU:HD21	1.72	0.70
1:D:68:HIS:NE2	1:A:663:GLY:O	2.25	0.70
2:B:340:LEU:HB3	2:B:346:ALA:HB2	1.76	0.68
1:A:203:TYR:O	1:A:339:LEU:N	2.25	0.68
1:D:52:ASP:OD1	1:D:53:GLY:N	2.26	0.68
1:A:224:LEU:HD23	1:A:292:PHE:CD1	2.29	0.68
1:A:1259:PHE:O	1:A:1261:LEU:HD12	1.95	0.67
1:A:936:PRO:O	1:A:942:LYS:NZ	2.25	0.67
1:A:167:ILE:HD11	1:A:558:MET:HB2	1.77	0.66
1:A:583:GLU:OE2	1:A:615:ARG:NH1	2.28	0.66
2:B:267:ASN:OD1	2:B:268:VAL:N	2.28	0.66
2:B:175:PHE:CD1	2:B:181:LEU:HD13	2.30	0.66
1:D:60:ASN:O	1:D:62:GLN:NE2	2.30	0.65
1:A:236:ASP:OD1	1:A:239:LYS:NZ	2.21	0.65
2:C:74:VAL:HG22	2:C:77:ARG:NH2	2.11	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:649:PRO:O	1:A:652:ARG:NH1	2.30	0.64
1:A:136:LYS:HA	1:A:136:LYS:HE3	1.80	0.64
1:D:21:ASP:OD1	1:D:22:THR:N	2.31	0.63
2:B:103:GLU:OE1	2:B:331:ARG:NH2	2.32	0.63
2:C:201:VAL:HG12	2:C:214:LEU:HD23	1.81	0.63
1:A:171:ILE:HD12	1:A:553:THR:HG22	1.81	0.63
1:A:585:CYS:N	1:A:588:ASP:OD2	2.33	0.62
1:A:330:GLN:HA	1:A:333:LEU:HD13	1.81	0.62
2:B:235:MET:HG2	2:B:252:ILE:HD13	1.81	0.61
2:C:221:ASN:OD1	2:C:224:PHE:N	2.32	0.61
1:A:1139:VAL:HG11	1:A:1277:ARG:NE	2.15	0.60
1:A:1129:GLN:O	1:A:1133:THR:HG22	2.01	0.60
1:A:1019:PHE:CZ	1:A:1064:VAL:HG11	2.36	0.60
2:B:339:VAL:HG22	2:C:81:LEU:CD2	2.32	0.60
1:A:220:ILE:HD11	1:A:260:PHE:CD2	2.37	0.60
1:A:1149:HIS:HB2	1:A:1261:LEU:HD13	1.83	0.59
1:A:999:ASP:HB2	1:A:1138:LEU:HD21	1.84	0.59
1:A:1030:ASN:OD1	1:A:1031:PRO:HD2	2.02	0.59
1:A:210:LEU:HD13	1:A:660:ILE:HD11	1.84	0.59
2:C:326:ILE:O	2:C:330:LEU:HD23	2.02	0.59
2:B:234:ARG:NH2	2:B:256:THR:OG1	2.36	0.59
1:A:66:VAL:CG1	1:A:140:LEU:HD21	2.33	0.58
1:A:1133:THR:HG23	1:A:1133:THR:O	2.03	0.58
2:B:202:LYS:NZ	2:B:215:GLU:OE2	2.36	0.58
1:A:222:LEU:HD11	1:A:232:MET:HE2	1.86	0.58
1:A:285:VAL:HG13	2:B:345:GLU:HG2	1.86	0.58
1:A:590:VAL:O	1:A:605:GLY:N	2.34	0.58
1:A:709:ASN:OD1	1:A:710:ILE:N	2.37	0.57
1:A:1024:GLN:HG3	1:A:1114:GLN:OE1	2.04	0.57
1:A:656:THR:O	1:A:656:THR:HG23	2.04	0.57
2:B:340:LEU:HD21	2:C:244:PRO:HB2	1.85	0.57
2:C:121:ILE:HB	2:C:197:LYS:HZ3	1.69	0.57
1:A:65:LEU:HD12	1:A:551:THR:OG1	2.04	0.57
1:A:580:ASP:OD2	1:A:615:ARG:NH1	2.37	0.57
2:C:196:LEU:HD21	2:C:199:ILE:CD1	2.33	0.57
1:A:983:ASP:OD2	1:A:1007:GLN:NE2	2.38	0.57
1:A:1030:ASN:ND2	1:A:1072:ILE:HG23	2.20	0.57
1:A:270:ALA:O	1:A:286:LEU:HD12	2.05	0.56
1:A:689:LYS:HG2	1:A:703:LEU:HD23	1.86	0.56
1:A:140:LEU:HD23	1:A:141:LYS:N	2.20	0.56
1:A:936:PRO:HG2	1:A:942:LYS:HZ2	1.69	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:972:GLY:O	1:A:990:LYS:NZ	2.36	0.56
1:A:232:MET:HB3	1:A:276:VAL:HG12	1.87	0.56
1:A:1028:ARG:NH1	1:A:1031:PRO:O	2.39	0.56
1:D:31:GLN:O	1:D:35:GLY:N	2.37	0.55
1:A:301:VAL:O	1:A:330:GLN:NE2	2.38	0.55
2:B:88:CYS:HG	2:C:110:TYR:HE2	1.52	0.55
2:C:221:ASN:ND2	2:C:224:PHE:O	2.39	0.55
1:A:302:VAL:HG12	1:A:303:GLU:HG2	1.87	0.55
1:A:222:LEU:HD11	1:A:232:MET:CE	2.36	0.55
1:A:705:GLN:OE1	1:A:706:HIS:ND1	2.35	0.55
1:A:192:LEU:HD13	1:A:353:CYS:SG	2.47	0.54
1:A:693:VAL:HG23	1:A:693:VAL:O	2.07	0.54
2:B:113:LEU:HB3	2:C:84:LEU:HD21	1.89	0.54
1:A:327:VAL:HG23	1:A:327:VAL:O	2.07	0.54
1:A:66:VAL:HG12	1:A:140:LEU:HD21	1.89	0.54
1:A:552:MET:CE	1:A:569:ARG:HE	2.20	0.54
2:B:340:LEU:O	2:B:346:ALA:N	2.41	0.54
2:C:229:LEU:HD12	2:C:230:THR:H	1.74	0.53
1:A:82:ILE:HG22	1:A:83:HIS:N	2.23	0.53
1:A:687:SER:OG	1:A:688:SER:N	2.41	0.53
2:B:236:ARG:NE	2:B:238:GLU:OE2	2.41	0.53
2:C:176:LYS:O	2:C:182:SER:OG	2.25	0.53
1:A:975:VAL:HG12	1:A:987:ALA:HB2	1.90	0.53
1:A:1011:ILE:HG22	1:A:1011:ILE:O	2.08	0.53
1:A:1061:LEU:O	1:A:1065:LEU:HD23	2.08	0.53
1:A:1074:VAL:HG22	1:A:1075:ASN:H	1.74	0.53
2:B:255:CYS:SG	2:B:256:THR:N	2.82	0.52
2:C:171:TRP:CE3	2:C:199:ILE:HD12	2.44	0.52
2:B:98:GLU:O	2:B:102:LEU:HD23	2.09	0.52
1:A:1139:VAL:HG11	1:A:1277:ARG:HE	1.74	0.51
1:A:66:VAL:HB	1:A:140:LEU:HD21	1.93	0.51
1:A:210:LEU:HD12	1:A:678:VAL:CG1	2.41	0.51
2:B:267:ASN:OD1	2:B:269:THR:N	2.43	0.51
1:A:60:LEU:HD11	1:A:140:LEU:HD22	1.91	0.51
1:A:210:LEU:HD11	1:A:658:ILE:HG21	1.93	0.51
1:A:1079:TYR:CD2	1:A:1088:ARG:NH1	2.78	0.51
1:A:235:GLU:N	1:A:235:GLU:OE1	2.43	0.50
1:A:691:GLU:OE2	1:A:691:GLU:HA	2.11	0.50
1:D:72:ARG:C	1:D:73:LEU:HD12	2.32	0.50
1:A:991:GLY:HA2	1:A:1073:LEU:HD23	1.93	0.50
1:A:66:VAL:HB	1:A:140:LEU:HD11	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:225:THR:OG1	2:C:261:ASP:OD2	2.29	0.50
2:C:267:ASN:OD1	2:C:268:VAL:N	2.44	0.50
1:A:576:VAL:HG23	1:A:576:VAL:O	2.11	0.50
1:A:196:TRP:CD1	1:A:299:VAL:HG11	2.47	0.50
1:A:82:ILE:HG22	1:A:83:HIS:H	1.77	0.49
2:B:210:MET:SD	2:B:237:SER:OG	2.65	0.49
2:C:106:TYR:O	2:C:110:TYR:HD1	1.94	0.49
1:A:658:ILE:HD12	1:A:658:ILE:H	1.77	0.49
1:A:196:TRP:NE1	1:A:299:VAL:HG11	2.27	0.49
2:B:107:ALA:O	2:B:111:GLN:OE1	2.31	0.49
1:A:989:ILE:HD13	1:A:1068:ILE:HG21	1.93	0.49
1:A:273:PHE:HZ	1:A:294:VAL:HG11	1.77	0.48
2:C:95:PHE:O	2:C:99:VAL:HG23	2.13	0.48
1:A:1124:GLU:O	1:A:1128:ARG:NH1	2.46	0.48
2:B:343:THR:HG22	2:B:343:THR:O	2.11	0.48
1:A:66:VAL:CB	1:A:140:LEU:HD11	2.42	0.48
1:A:955:PHE:HA	1:A:958:VAL:HG22	1.94	0.48
2:B:238:GLU:N	2:B:238:GLU:OE1	2.46	0.48
2:C:231:LYS:NZ	2:C:233:TYR:CZ	2.81	0.48
1:A:129:GLU:O	1:A:129:GLU:HG2	2.14	0.48
1:A:222:LEU:HD21	1:A:232:MET:HE1	1.96	0.48
1:A:693:VAL:HG12	1:A:699:LYS:HG2	1.95	0.48
2:B:178:VAL:HG11	2:B:329:PHE:HE1	1.79	0.47
1:A:150:ARG:HG3	1:A:656:THR:HG22	1.97	0.47
1:A:166:VAL:HG12	1:A:557:VAL:HG22	1.96	0.47
1:D:46:ALA:HB1	1:A:624:LEU:HD22	1.97	0.47
2:C:169:GLU:O	2:C:173:THR:HG23	2.14	0.47
1:A:154:ARG:HB2	1:A:574:PHE:CE1	2.49	0.47
1:A:1136:TRP:NE1	1:A:1280:LEU:HD23	2.29	0.47
2:B:231:LYS:HD2	2:B:233:TYR:HE1	1.80	0.47
1:A:629:ASP:O	1:A:703:LEU:HD12	2.15	0.47
2:B:106:TYR:CD1	2:B:109:LEU:HD12	2.49	0.47
1:A:64:ASP:OD1	1:A:146:SER:N	2.43	0.46
2:B:333:ARG:NE	2:B:341:TYR:OH	2.39	0.46
1:A:147:VAL:HG13	1:A:166:VAL:HG11	1.96	0.46
2:C:201:VAL:HG12	2:C:214:LEU:CD2	2.45	0.46
1:A:58:ARG:NH2	1:A:82:ILE:HG21	2.29	0.46
1:D:46:ALA:HB3	1:D:48:LYS:NZ	2.30	0.46
1:A:1126:GLU:O	1:A:1129:GLN:HG3	2.16	0.46
1:A:210:LEU:HD12	1:A:678:VAL:HG13	1.97	0.46
1:A:149:PRO:HA	1:A:166:VAL:HG23	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1024:GLN:OE1	1:A:1024:GLN:N	2.48	0.46
2:B:233:TYR:HD2	2:B:252:ILE:HD12	1.80	0.46
2:C:267:ASN:OD1	2:C:269:THR:N	2.48	0.46
1:A:623:LYS:CB	1:A:634:ILE:HD11	2.42	0.45
2:C:213:VAL:CG1	2:C:230:THR:HG23	2.46	0.45
1:A:149:PRO:HB3	1:A:655:THR:HG21	1.99	0.45
2:B:232:THR:HG22	2:B:233:TYR:N	2.31	0.45
2:B:332:GLU:HG3	2:B:333:ARG:HG2	1.99	0.45
1:A:1072:ILE:HG22	1:A:1073:LEU:HD12	1.97	0.45
1:A:1261:LEU:HD23	1:A:1265:PHE:HE2	1.81	0.45
1:A:974:MET:HG2	1:A:988:LEU:HD11	1.99	0.45
2:C:188:HIS:O	2:C:191:PRO:HD2	2.17	0.44
1:A:691:GLU:OE2	1:A:701:ILE:HG22	2.17	0.44
1:A:580:ASP:OD1	1:A:582:ASN:N	2.40	0.44
1:A:662:ILE:HG22	1:A:663:GLY:N	2.32	0.44
2:C:233:TYR:OH	2:C:323:ASP:O	2.30	0.44
1:A:66:VAL:CB	1:A:140:LEU:HD21	2.47	0.44
1:A:581:ASN:OD1	1:A:581:ASN:O	2.36	0.44
1:A:147:VAL:CG1	1:A:166:VAL:HG11	2.48	0.44
2:C:106:TYR:O	2:C:110:TYR:CD1	2.71	0.44
1:A:975:VAL:HG12	1:A:987:ALA:CB	2.47	0.44
1:A:1031:PRO:CB	1:A:1081:GLU:HB2	2.48	0.44
1:A:79:VAL:CG1	1:A:124:VAL:HG22	2.41	0.43
1:A:655:THR:HG22	1:A:656:THR:N	2.33	0.43
2:B:196:LEU:HD21	2:B:199:ILE:HD11	2.00	0.43
1:A:149:PRO:O	1:A:150:ARG:HB2	2.17	0.43
1:A:620:LYS:HB3	1:A:622:PHE:CE2	2.52	0.43
1:D:41:GLN:HB2	1:D:69:LEU:HD11	2.00	0.43
1:A:173:CYS:HB2	1:A:548:VAL:HG13	2.01	0.43
1:A:655:THR:HG23	1:A:682:ALA:O	2.17	0.43
1:A:1146:LEU:HD23	1:A:1270:ARG:CZ	2.48	0.43
1:A:994:ARG:O	1:A:1075:ASN:ND2	2.51	0.43
1:A:997:TYR:O	1:A:1000:GLY:N	2.51	0.43
1:A:1127:ILE:CG2	1:A:1128:ARG:NH2	2.82	0.43
1:A:222:LEU:HD23	1:A:294:VAL:HG21	2.00	0.43
1:A:600:ASP:O	1:A:603:VAL:HG12	2.19	0.43
1:A:940:SER:HB3	1:A:984:LEU:HD22	2.01	0.43
1:A:1261:LEU:HD12	1:A:1261:LEU:H	1.84	0.43
1:A:983:ASP:OD1	1:A:983:ASP:N	2.52	0.42
1:A:615:ARG:O	1:A:615:ARG:HG3	2.19	0.42
1:A:997:TYR:HD1	1:A:1002:TYR:HH	1.65	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:75:LYS:HA	2:B:78:VAL:HG22	2.01	0.42
1:A:1031:PRO:HD3	1:A:1100:TYR:CZ	2.54	0.42
1:A:222:LEU:HD23	1:A:294:VAL:CB	2.50	0.42
2:C:192:ILE:HG12	2:C:223:TYR:CD2	2.54	0.42
2:C:233:TYR:CE2	2:C:327:GLY:HA3	2.54	0.42
1:A:181:ASN:OD1	1:A:181:ASN:O	2.38	0.42
1:D:37:PRO:O	1:D:41:GLN:OE1	2.37	0.42
2:B:339:VAL:HG11	2:C:82:LYS:HA	2.01	0.42
1:A:997:TYR:OH	1:A:1029:LEU:O	2.15	0.42
1:A:63:HIS:N	1:A:79:VAL:O	2.41	0.42
1:A:689:LYS:CG	1:A:703:LEU:HD23	2.48	0.42
1:A:1031:PRO:HB2	1:A:1081:GLU:HB2	2.00	0.42
1:A:595:VAL:HG11	1:A:1275:GLN:OE1	2.20	0.41
2:C:181:LEU:HA	2:C:184:MET:HE2	2.02	0.41
2:C:184:MET:HB3	2:C:297:PHE:HA	2.02	0.41
1:A:1031:PRO:HG2	1:A:1080:ASN:HB2	2.03	0.41
2:B:111:GLN:N	2:B:112:PRO:HD2	2.36	0.41
2:C:81:LEU:O	2:C:81:LEU:HD23	2.20	0.41
1:A:264:GLN:O	1:A:295:VAL:HA	2.21	0.41
1:A:1136:TRP:CD1	1:A:1280:LEU:HD23	2.56	0.41
2:C:92:GLU:OE1	2:C:247:PHE:O	2.38	0.41
1:A:603:VAL:CG2	1:A:634:ILE:HD12	2.44	0.41
2:C:201:VAL:HG13	2:C:335:ILE:CD1	2.41	0.41
2:B:102:LEU:HG	2:C:102:LEU:HD11	2.03	0.41
2:B:174:VAL:HG11	2:B:334:ILE:HG23	2.02	0.41
1:D:70:VAL:HG12	1:D:71:LEU:N	2.36	0.41
1:A:643:TYR:OH	1:A:1102:GLU:OE1	2.13	0.40
1:A:1074:VAL:HG22	1:A:1075:ASN:N	2.34	0.40
1:A:1261:LEU:HD23	1:A:1265:PHE:CE2	2.56	0.40
2:B:171:TRP:HZ3	2:B:334:ILE:HG22	1.86	0.40
2:C:175:PHE:CD1	2:C:181:LEU:CD2	3.04	0.40
1:A:129:GLU:OE1	1:A:129:GLU:N	2.55	0.40
2:B:104:ARG:O	2:B:107:ALA:HB3	2.21	0.40
1:A:172:ASP:O	1:A:552:MET:HB2	2.22	0.40
1:A:1009:PRO:HD3	1:A:1017:PRO:HA	2.03	0.40
1:A:1079:TYR:HB3	1:A:1088:ARG:HH12	1.86	0.40
2:B:258:CYS:O	2:B:260:ILE:HD12	2.21	0.40
2:B:288:VAL:HG22	2:B:289:THR:N	2.36	0.40
1:A:700:THR:HG22	1:A:701:ILE:N	2.37	0.40
1:A:1085:ASP:O	1:A:1088:ARG:HD3	2.22	0.40
2:C:190:GLU:HG2	2:C:191:PRO:HD3	2.03	0.40

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	A	629/1744 (36%)	587 (93%)	42 (7%)	0	100	100
1	D	71/1744 (4%)	71 (100%)	0	0	100	100
2	B	217/416 (52%)	209 (96%)	8 (4%)	0	100	100
2	C	213/416 (51%)	203 (95%)	10 (5%)	0	100	100
All	All	1130/4320 (26%)	1070 (95%)	60 (5%)	0	100	100

There are no Ramachandran outliers to report.

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	A	585/1461 (40%)	583 (100%)	2 (0%)	92	97
1	D	67/1461 (5%)	67 (100%)	0	100	100
2	B	204/377 (54%)	204 (100%)	0	100	100
2	C	200/377 (53%)	199 (100%)	1 (0%)	88	94
All	All	1056/3676 (29%)	1053 (100%)	3 (0%)	92	97

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	959	ARG
1	A	976	LYS
2	C	76	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	75	HIS
2	B	188	HIS

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](#)

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.

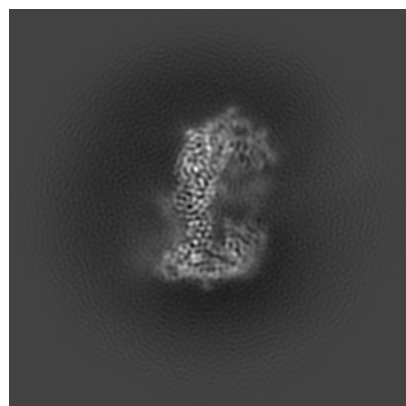
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-26612. These allow visual inspection of the internal detail of the map and identification of artifacts.

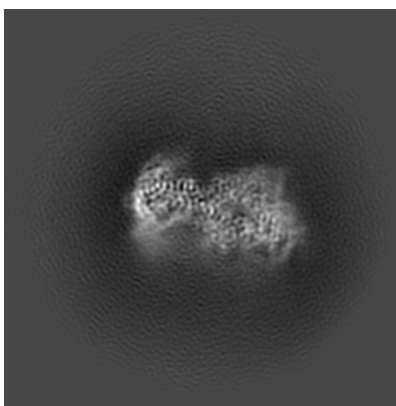
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

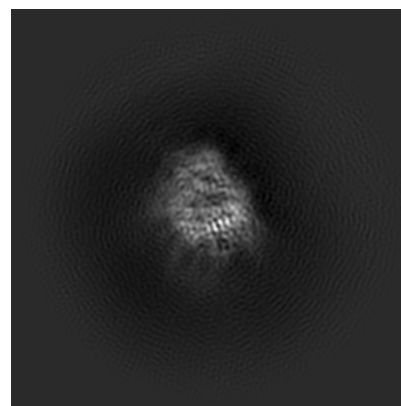
6.1.1 Primary map



X

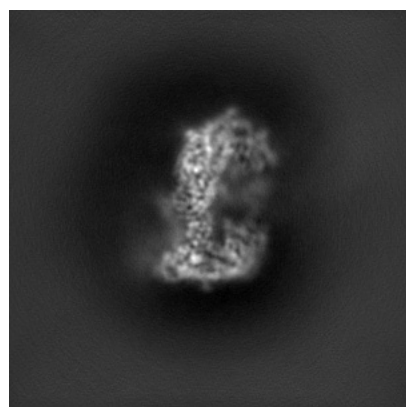


Y

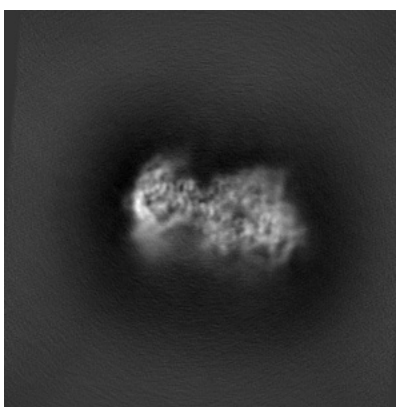


Z

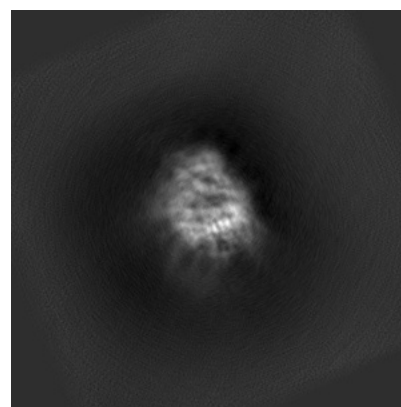
6.1.2 Raw map



X



Y

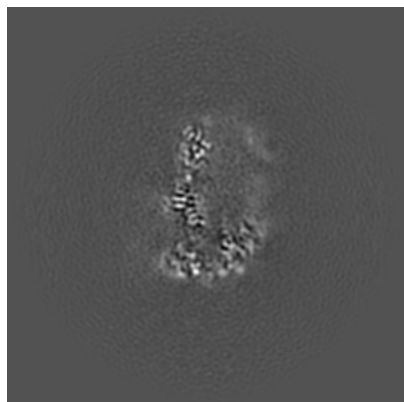


Z

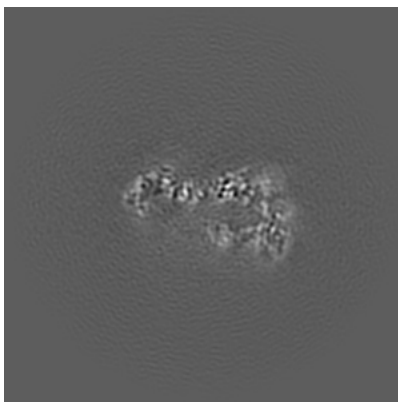
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

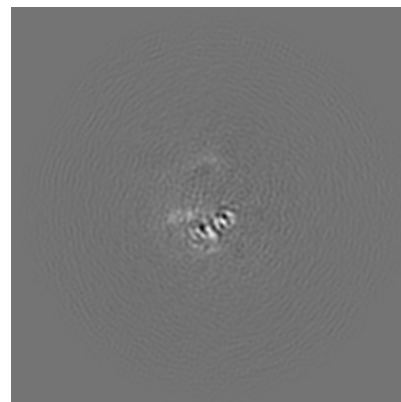
6.2.1 Primary map



X Index: 170

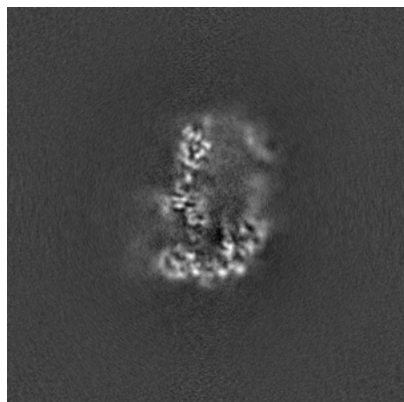


Y Index: 170

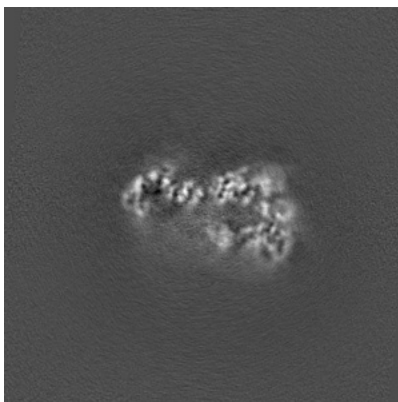


Z Index: 170

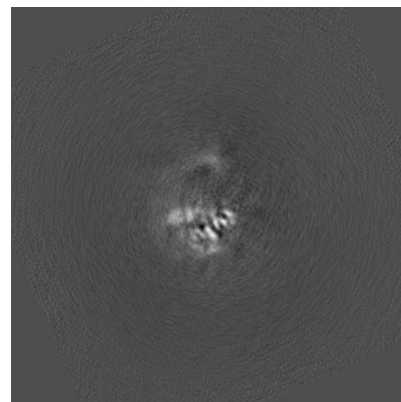
6.2.2 Raw map



X Index: 170



Y Index: 170

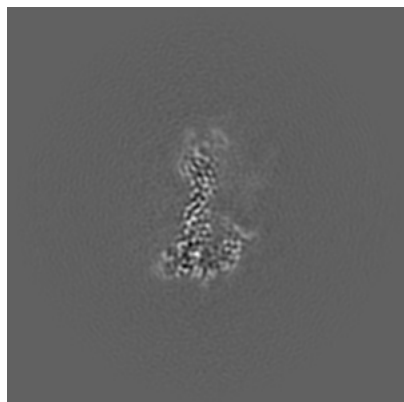


Z Index: 170

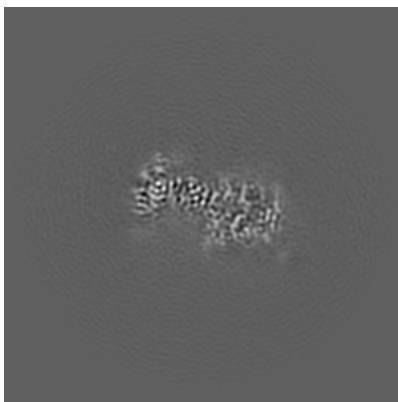
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

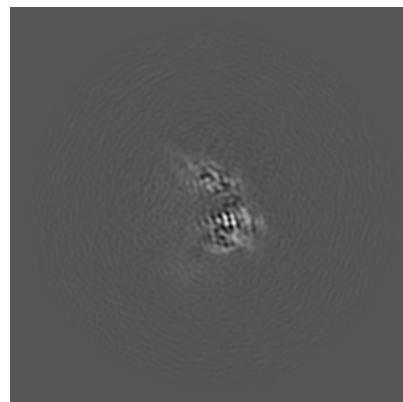
6.3.1 Primary map



X Index: 182

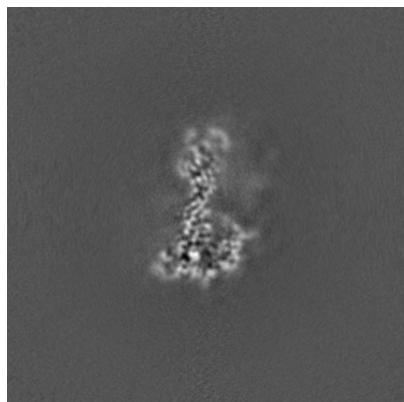


Y Index: 157

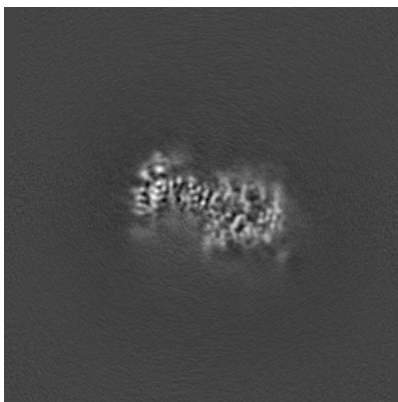


Z Index: 130

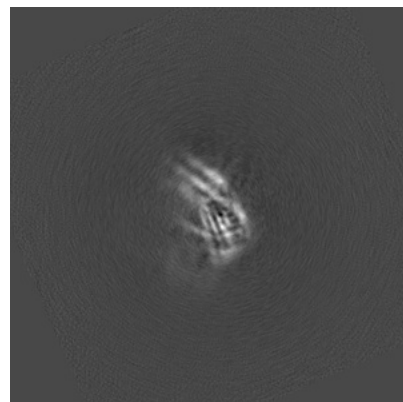
6.3.2 Raw map



X Index: 183



Y Index: 157

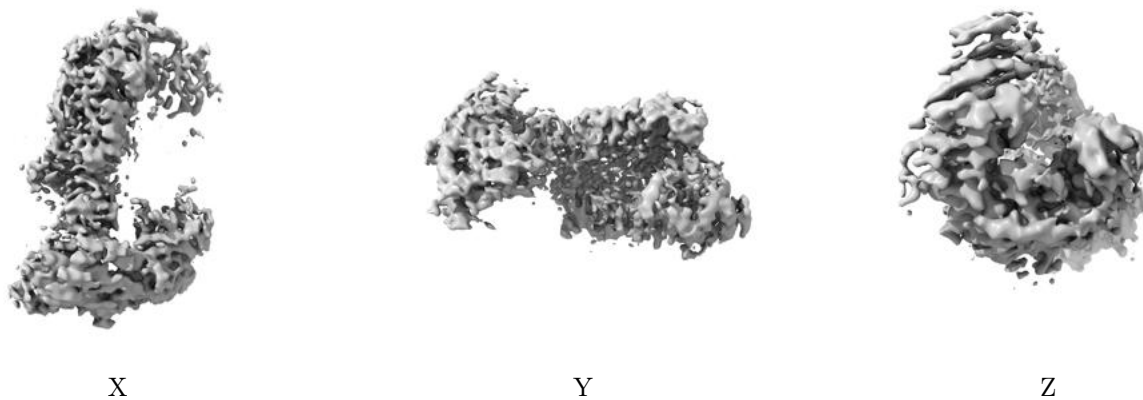


Z Index: 116

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

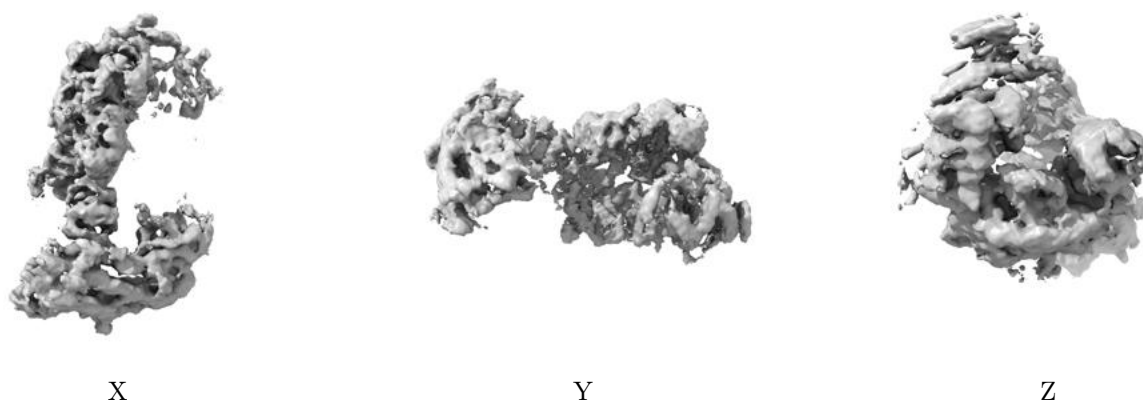
6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.3. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 Raw map



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

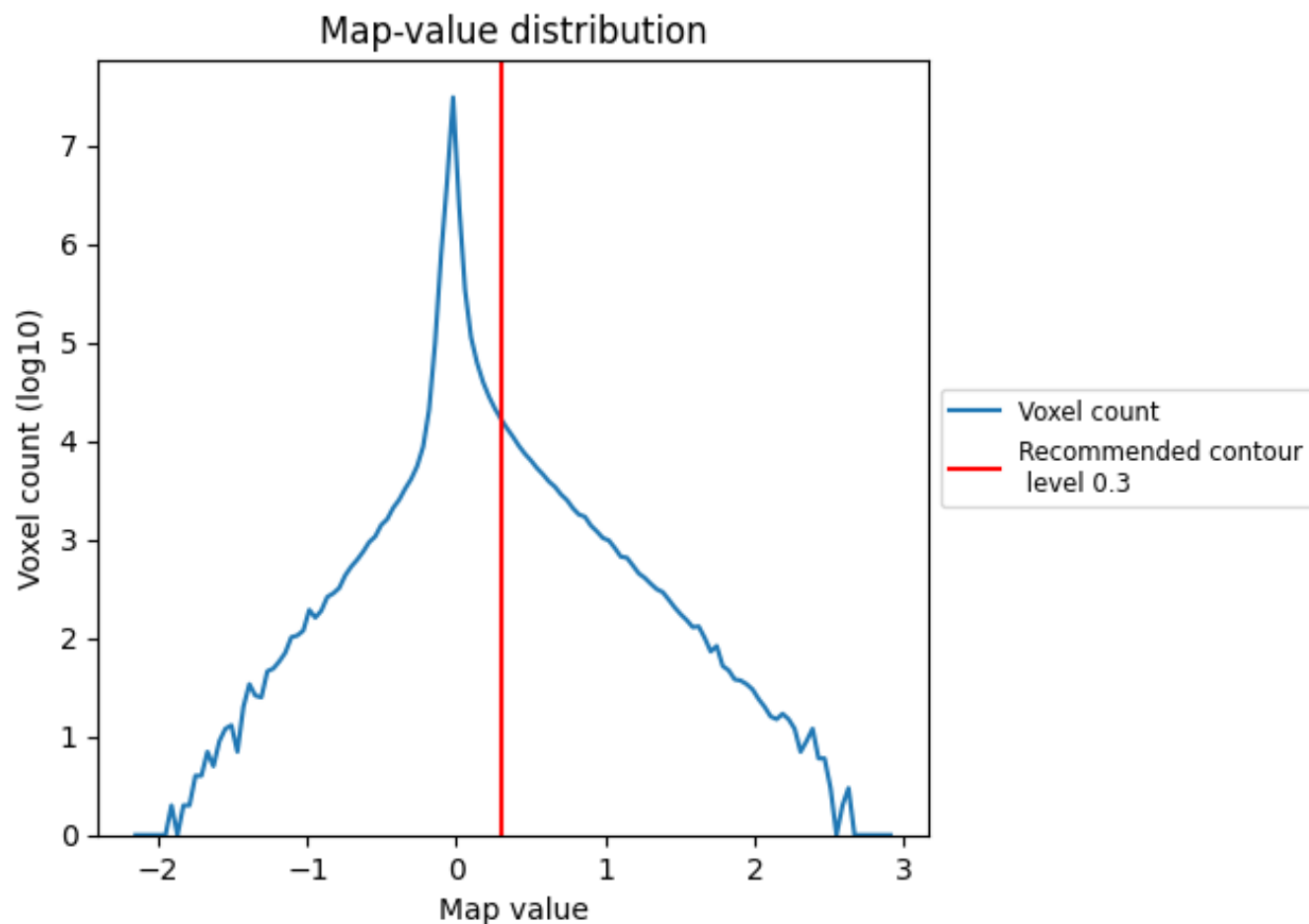
6.5 Mask visualisation [i](#)

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

7 Map analysis [i](#)

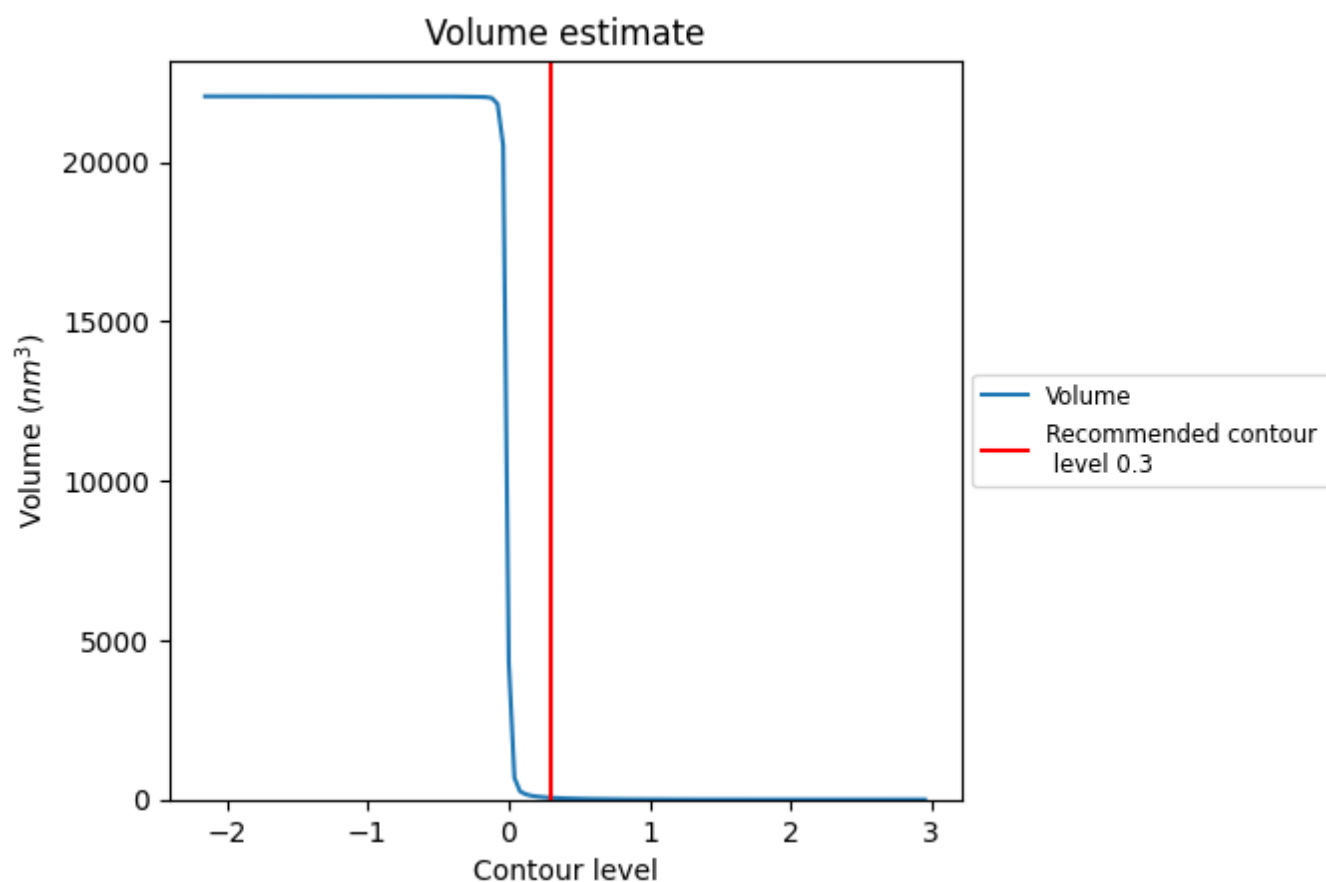
This section contains the results of statistical analysis of the map.

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.

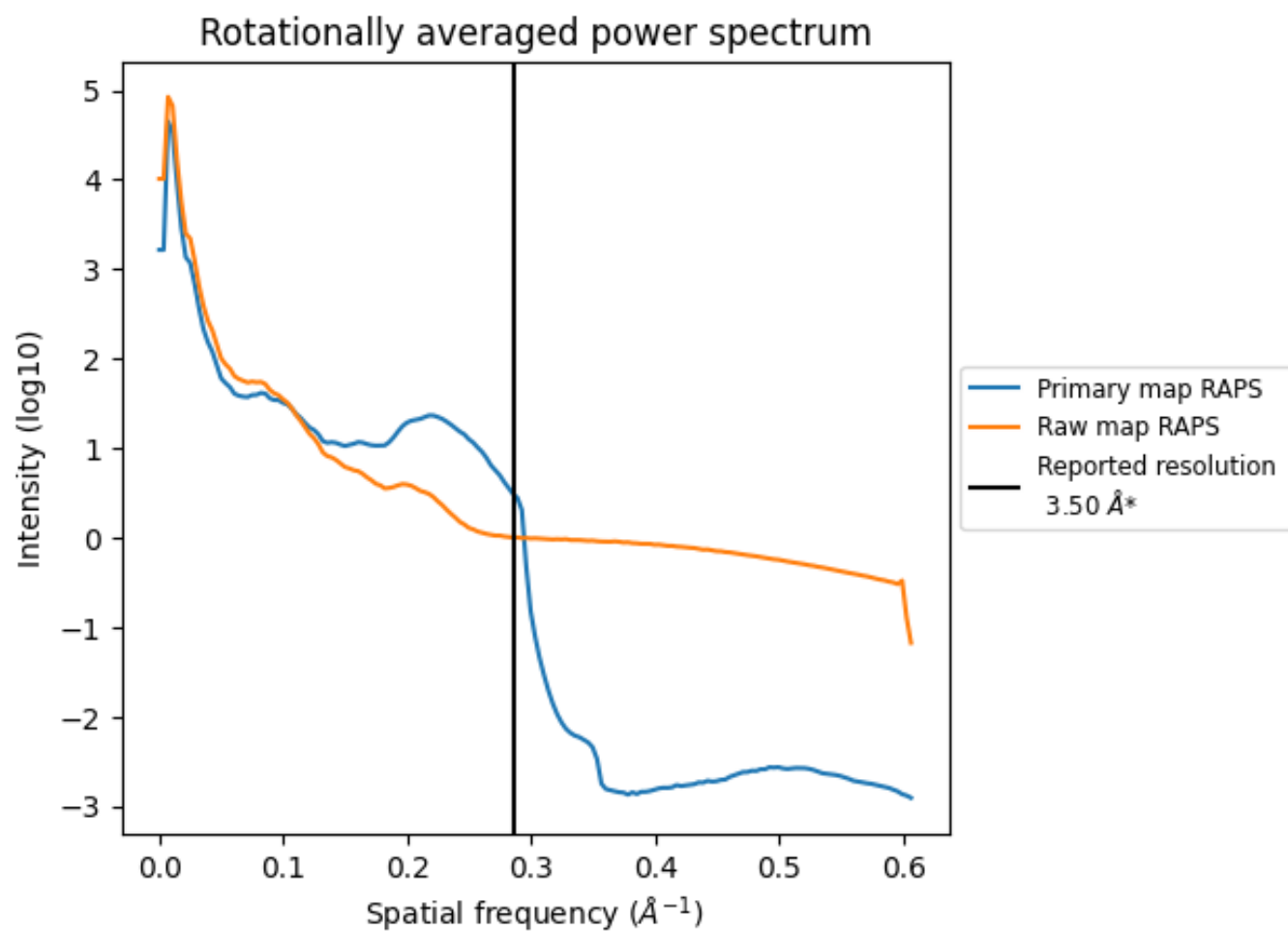
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 58 nm³; this corresponds to an approximate mass of 52 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 ⓘ

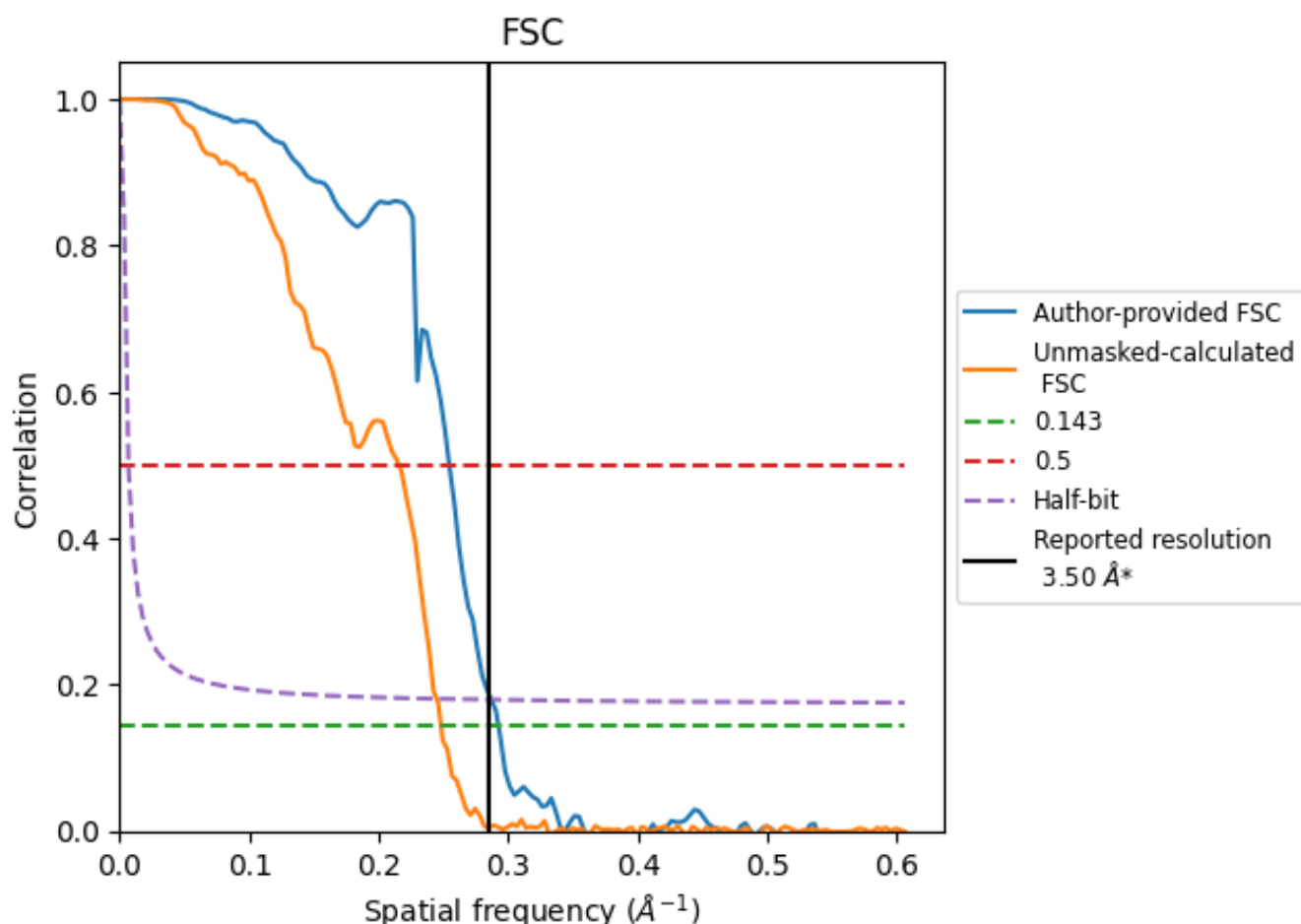


*Reported resolution corresponds to spatial frequency of 0.286 Å⁻¹

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 0.286 Å⁻¹

8.2 Resolution estimates [i](#)

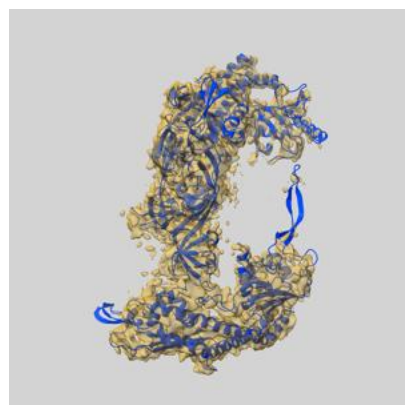
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	3.42	3.93	3.48
Unmasked-calculated*	4.03	4.64	4.08

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.03 differs from the reported value 3.5 by more than 10 %

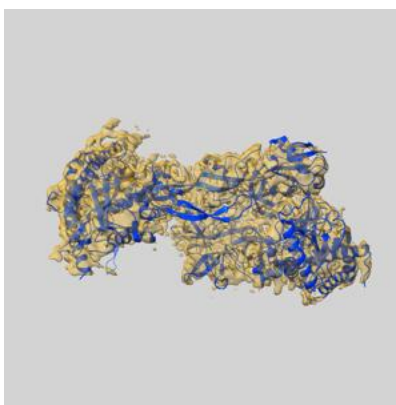
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-26612 and PDB model 7UN3. Per-residue inclusion information can be found in section [3](#) on page [11](#).

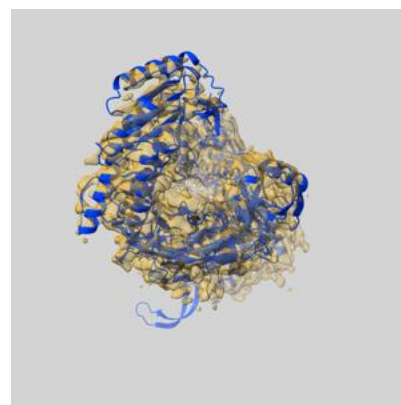
9.1 Map-model overlay [i](#)



X



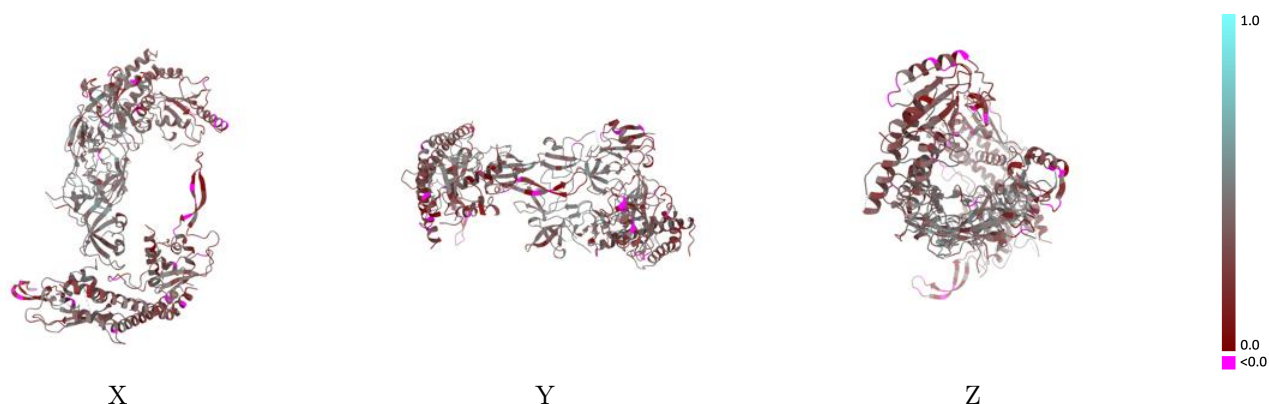
Y



Z

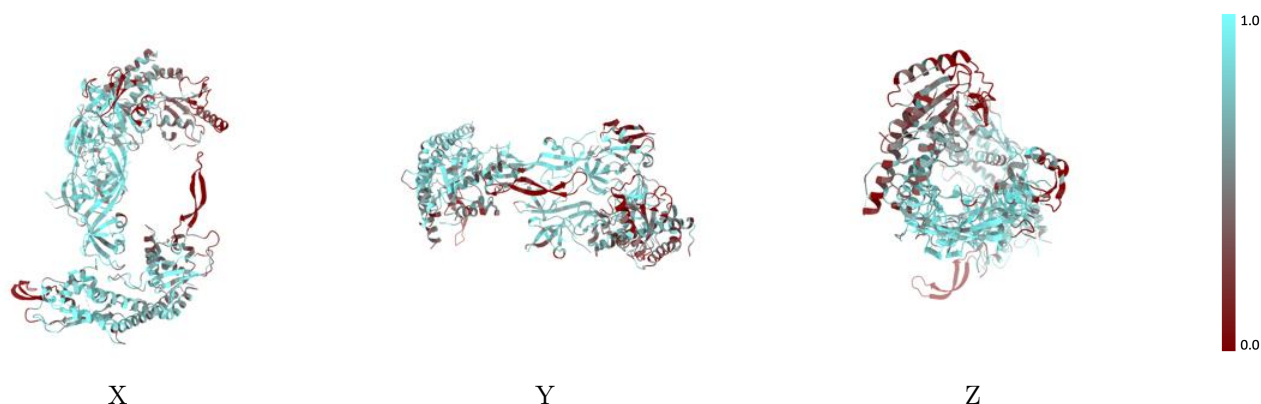
The images above show the 3D surface view of the map at the recommended contour level 0.3 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



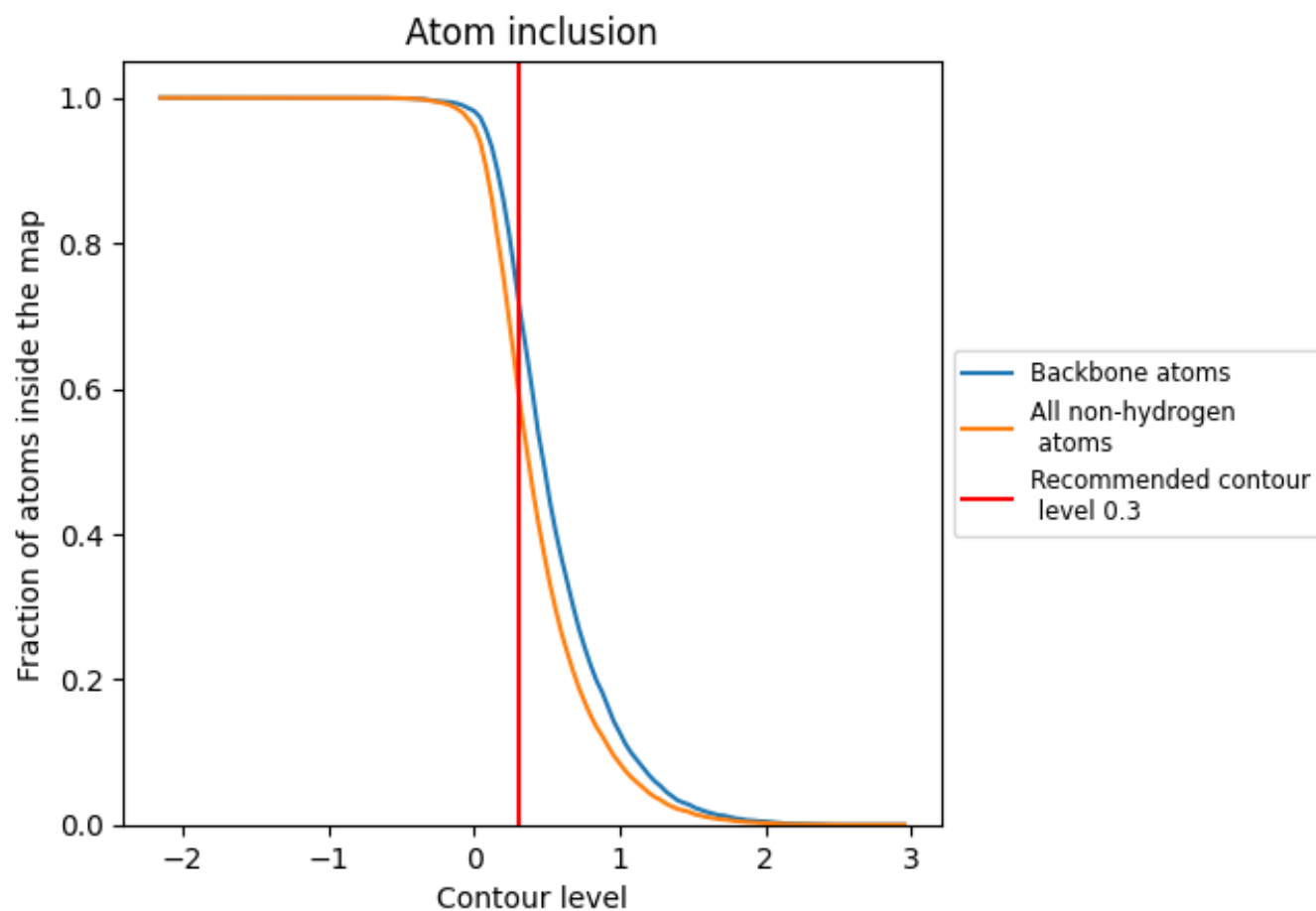
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.3).

9.4 Atom inclusion [i](#)



At the recommended contour level, 73% of all backbone atoms, 60% 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 (0.3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.5997	<div></div> 0.3340
A	<div></div> 0.6248	<div></div> 0.3620
B	<div></div> 0.6117	<div></div> 0.3130
C	<div></div> 0.5554	<div></div> 0.2920
D	<div></div> 0.4765	<div></div> 0.2920

