



wwPDB EM Validation Summary Report ⓘ

Apr 28, 2026 – 04:30 pm BST

PDB ID : 9HN5 / pdb_00009hn5
EMDB ID : EMD-52307
Title : Cryo-EM structure of human separase bound to phosphorylated SCC1 (100-320 aa)
Authors : Yu, J.; Schmidt, S.; Botto, M.; Boland, A.
Deposited on : 2024-12-10
Resolution : 2.96 Å(reported)
Based on initial model : 7NJ1

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
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

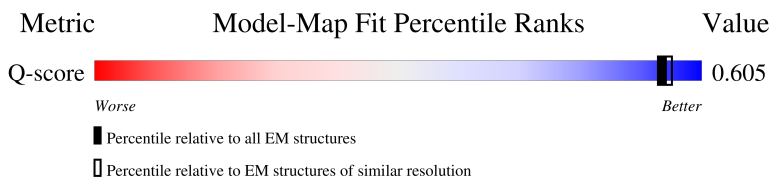
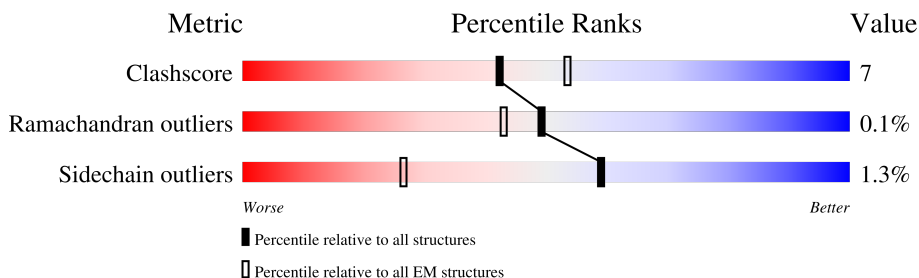
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.96 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	13155 (2.46 - 3.46)

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	227	
2	A	2172	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 11314 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 Double-strand-break repair protein rad21 homolog.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	B	38	Total	C	N	O	P	S	0	0
			283	166	45	67	2	3		

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	136	ILE	ASN	conflict	UNP O60216
B	245	GLU	-	insertion	UNP O60216
B	246	ILE	-	insertion	UNP O60216
B	247	MET	-	insertion	UNP O60216
B	248	ARG	-	insertion	UNP O60216
B	249	GLU	-	insertion	UNP O60216
B	250	GLY	-	insertion	UNP O60216

- Molecule 2 is a protein called Separin.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	1480	Total	C	N	O	S	0	0
			11030	7006	1927	2043	54		

There are 113 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-54	MET	-	initiating methionine	UNP Q14674
A	-53	ASP	-	expression tag	UNP Q14674
A	-52	TYR	-	expression tag	UNP Q14674
A	-51	LYS	-	expression tag	UNP Q14674
A	-50	ASP	-	expression tag	UNP Q14674
A	-49	HIS	-	expression tag	UNP Q14674
A	-48	ASP	-	expression tag	UNP Q14674
A	-47	GLY	-	expression tag	UNP Q14674
A	-46	ASP	-	expression tag	UNP Q14674
A	-45	TYR	-	expression tag	UNP Q14674

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-44	LYS	-	expression tag	UNP Q14674
A	-43	ASP	-	expression tag	UNP Q14674
A	-42	HIS	-	expression tag	UNP Q14674
A	-41	ASP	-	expression tag	UNP Q14674
A	-40	ILE	-	expression tag	UNP Q14674
A	-39	ASP	-	expression tag	UNP Q14674
A	-38	TYR	-	expression tag	UNP Q14674
A	-37	LYS	-	expression tag	UNP Q14674
A	-36	ASP	-	expression tag	UNP Q14674
A	-35	ASP	-	expression tag	UNP Q14674
A	-34	ASP	-	expression tag	UNP Q14674
A	-33	ASP	-	expression tag	UNP Q14674
A	-32	LYS	-	expression tag	UNP Q14674
A	-31	SER	-	expression tag	UNP Q14674
A	-30	GLY	-	expression tag	UNP Q14674
A	-29	PRO	-	expression tag	UNP Q14674
A	-28	GLY	-	expression tag	UNP Q14674
A	-27	GLY	-	expression tag	UNP Q14674
A	-26	SER	-	expression tag	UNP Q14674
A	-25	GLY	-	expression tag	UNP Q14674
A	-24	GLY	-	expression tag	UNP Q14674
A	-23	SER	-	expression tag	UNP Q14674
A	-22	GLY	-	expression tag	UNP Q14674
A	-21	GLY	-	expression tag	UNP Q14674
A	-20	GLY	-	expression tag	UNP Q14674
A	-19	SER	-	expression tag	UNP Q14674
A	-18	GLY	-	expression tag	UNP Q14674
A	-17	GLY	-	expression tag	UNP Q14674
A	-16	GLY	-	expression tag	UNP Q14674
A	-15	SER	-	expression tag	UNP Q14674
A	-14	GLY	-	expression tag	UNP Q14674
A	-13	GLU	-	expression tag	UNP Q14674
A	-12	ASN	-	expression tag	UNP Q14674
A	-11	LEU	-	expression tag	UNP Q14674
A	-10	TYR	-	expression tag	UNP Q14674
A	-9	PHE	-	expression tag	UNP Q14674
A	-8	GLN	-	expression tag	UNP Q14674
A	-7	GLY	-	expression tag	UNP Q14674
A	-6	GLY	-	expression tag	UNP Q14674
A	-5	GLY	-	expression tag	UNP Q14674
A	-4	SER	-	expression tag	UNP Q14674
A	-3	GLY	-	expression tag	UNP Q14674

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP Q14674
A	-1	SER	-	expression tag	UNP Q14674
A	0	GLY	-	expression tag	UNP Q14674
A	25	ASP	ALA	conflict	UNP Q14674
A	116	VAL	ALA	conflict	UNP Q14674
A	1372	SER	ARG	conflict	UNP Q14674
A	1525	GLY	-	linker	UNP Q14674
A	1526	LEU	-	linker	UNP Q14674
A	1527	GLU	-	linker	UNP Q14674
A	1528	VAL	-	linker	UNP Q14674
A	1529	LEU	-	linker	UNP Q14674
A	1530	PHE	-	linker	UNP Q14674
A	1531	GLN	-	linker	UNP Q14674
A	1532	GLY	-	linker	UNP Q14674
A	1533	PRO	-	linker	UNP Q14674
A	1534	GLY	-	linker	UNP Q14674
A	1535	SER	-	linker	UNP Q14674
A	1536	GLY	-	linker	UNP Q14674
A	1561	GLN	ARG	conflict	UNP Q14674
A	2029	SER	CYS	engineered mutation	UNP Q14674
A	2037	HIS	ARG	conflict	UNP Q14674
A	2121	SER	-	expression tag	UNP Q14674
A	2122	SER	-	expression tag	UNP Q14674
A	2123	LEU	-	expression tag	UNP Q14674
A	2124	ALA	-	expression tag	UNP Q14674
A	2125	GLU	-	expression tag	UNP Q14674
A	2126	GLU	-	expression tag	UNP Q14674
A	2127	ASN	-	expression tag	UNP Q14674
A	2128	LEU	-	expression tag	UNP Q14674
A	2129	TYR	-	expression tag	UNP Q14674
A	2130	PHE	-	expression tag	UNP Q14674
A	2131	GLN	-	expression tag	UNP Q14674
A	2132	SER	-	expression tag	UNP Q14674
A	2133	TRP	-	expression tag	UNP Q14674
A	2134	SER	-	expression tag	UNP Q14674
A	2135	HIS	-	expression tag	UNP Q14674
A	2136	PRO	-	expression tag	UNP Q14674
A	2137	GLN	-	expression tag	UNP Q14674
A	2138	PHE	-	expression tag	UNP Q14674
A	2139	GLU	-	expression tag	UNP Q14674
A	2140	LYS	-	expression tag	UNP Q14674
A	2141	GLY	-	expression tag	UNP Q14674

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Chain	Residue	Modelled	Actual	Comment	Reference
A	2142	GLY	-	expression tag	UNP Q14674
A	2143	GLY	-	expression tag	UNP Q14674
A	2144	SER	-	expression tag	UNP Q14674
A	2145	GLY	-	expression tag	UNP Q14674
A	2146	GLY	-	expression tag	UNP Q14674
A	2147	GLY	-	expression tag	UNP Q14674
A	2148	SER	-	expression tag	UNP Q14674
A	2149	GLY	-	expression tag	UNP Q14674
A	2150	GLY	-	expression tag	UNP Q14674
A	2151	GLY	-	expression tag	UNP Q14674
A	2152	SER	-	expression tag	UNP Q14674
A	2153	TRP	-	expression tag	UNP Q14674
A	2154	SER	-	expression tag	UNP Q14674
A	2155	HIS	-	expression tag	UNP Q14674
A	2156	PRO	-	expression tag	UNP Q14674
A	2157	GLN	-	expression tag	UNP Q14674
A	2158	PHE	-	expression tag	UNP Q14674
A	2159	GLU	-	expression tag	UNP Q14674
A	2160	LYS	-	expression tag	UNP Q14674

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
3	A	1	Total 1	Zn 1	0

LYS	V2046	E1867	SER	SER	LYS	THR	PRO	ARG	D1182	GLN	ALA	V802	Q644	L503	T405
	L2047	L1873	LEU	SER	LYS	ASP	GLY	SER	L1183	LEU	VAL	L806	T645	H604	T409
	M2061	V1877	GLN	LYS	VAL	GLY	GLY	GLY	V1186	PRO	T968	S816	L650	R505	Y409
	L2056	Q1881	PRO	LEU	PRO	ALA	ALA	ARG	C1191	GLY	Y978	T820	R664	R507	Q413
	D2068	V1885	ARG	PRO	ARG	PRO	ARG	LYS	L1206	LEU	Q979	Q821	L882	L509	I417
	I2069	F1676	VAL	VAL	VAL	GLN	VAL	ALA	L1223	PHE	X960	L822	Y685	Q510	A421
	L2089	H1699	ALA	ALA	ALA	ALA	GLN	GLY	L1235	ARG	Y983	L823	I686	L514	L423
	I2106	L1699	GLY	GLY	GLY	VAL	VAL	ALA	N1236	PRO	E986	A832	Q704	L426	T424
	A2112	L1711	ASN	ASN	ASN	GLN	GLN	LEU	S1242	LEU	Y987	L836	ALA	L427	Q425
	P2116	A1712	PRO	PRO	PRO	THR	THR	SER	V1246	GLY	L994	A839	PRO	L428	T426
	V2117	A1714	LEU	LEU	LEU	ASN	ASN	LEU	V1250	VAL	H997	L843	ASN	L429	V427
	R2120	Q1717	GLY	GLY	GLY	THR	THR	THR	G1250	ALA	K1008	L856	LEU	M526	V434
	SER	T1724	PRO	PRO	PRO	ASN	ASN	GLN	V1254	VAL	E1013	C860	GLY	V527	M437
	LEU	L1730	ARG	ARG	ARG	GLY	GLY	GLY	L1261	ALA	E1028	L861	PHE	I528	V441
	ALA	T1743	LYS	LYS	LYS	ASP	ASP	LEU	W1264	PRO	V1032	L863	VAL	M530	L441
	GLU	L1748	VAL	VAL	VAL	ASP	ASP	GLY	I1271	PRO	L1033	R864	ASP	L534	E448
	ASN	H1749	ALA	ALA	ALA	GLY	GLY	ARG	G1278	ILE	K1034	S894	LEU	T450	L449
	LEU	L1750	SER	SER	SER	PRO	PRO	PRO	GLY	SER	E1038	K895	ASN	D451	H452
	TYR	A1935	ALA	ALA	ALA	VAL	VAL	CYS	GLY	THR	E1063	A896	ASP	M453	M455
	PHE	F1949	THR	THR	THR	SER	SER	THR	SER	ASN	PHE	W897	LEU	G154	G156
	SER	F1757	GLY	GLY	GLY	ALA	ALA	ASN	GLY	GLN	GLY	Y898	GLN	M455	T456
	TRP	Q1764	PRO	PRO	PRO	GLY	GLY	PRO	CYS	LEU	GLY	L899	GLY	Y459	T460
	HIS	H1955	ARG	ARG	ARG	GLY	GLY	LYS	TYR	THR	THR	Q903	ASP	T463	L463
	PRO	N1956	ALA	ALA	ALA	ALA	ALA	ALA	GLY	LYS	LYS	P915	ARG	F467	F467
	GLN	N1957	GLY	GLY	GLY	GLY	GLY	GLY	L1284	VAL	VAL	N918	SER	H470	K471
	PHE	R1976	LEU	LEU	LEU	LEU	LEU	LEU	L1287	GLN	GLN	W832	PRO	K471	L472
	GLU	E1981	ALA	ALA	ALA	ALA	ALA	ALA	S1290	LYS	HIS	L914	ASP	E474	A474
	LYS	V1982	GLY	GLY	GLY	GLY	GLY	GLY	W1294	THR	LEU	P915	ASP	E475	E475
	GLY	A1991	GLY	GLY	GLY	GLY	GLY	GLY	P1297	PRO	PRO	W832	LYS	E812	S480
	SER	H1995	GLY	GLY	GLY	GLY	GLY	GLY	LEU	PRO	VAL	E936	VAL	E812	C484
	GLY	H2003	GLY	GLY	GLY	GLY	GLY	GLY	ILE	GLN	GLN	I937	VAL	I607	Q485
	GLY	A2014	SER	SER	SER	SER	SER	SER	LYS	GLN	GLN	A938	GLN	C608	H486
	GLY	V2015	LEU	LEU	LEU	LEU	LEU	LEU	C1146	LYS	HIS	L952	ALA	P815	L487
	GLY	L2016	LEU	LEU	LEU	LEU	LEU	LEU	L1150	VAL	LEU	L939	GLN	P815	G488
	SER	R2017	ILE	ILE	ILE	ILE	ILE	ILE	C1151	GLY	GLY	L946	GLY	G821	L489
	TRP	L2018	ALA	ALA	ALA	ALA	ALA	ALA	L1156	LYS	LYS	R947	LYS	V630	P499
	SER	Q1817	GLY	GLY	GLY	GLY	GLY	GLY	V1159	GLN	GLN	L952	GLN	A633	P500
	HIS	R1821	ARG	ARG	ARG	ARG	ARG	ARG	R1162	VAL	VAL	M954	GLN	Q634	L836
	PRO	L2024	GLN	GLN	GLN	GLN	GLN	GLN	W1163	THR	THR	T961	VAL	V635	C837
	GLN	L2025	LEU	LEU	LEU	LEU	LEU	LEU	V1164	GLN	GLN	Q962	PRO	L836	C837
	PHE	L2026	GLY	GLY	GLY	GLY	GLY	GLY	L1165	GLY	CYS	T961	CYS	L836	C837
	GLU	S2031	LEU	LEU	LEU	LEU	LEU	LEU	V1166	LYS	PRO	Q962	PRO	T642	F641
											PRO	ALA	PRO	K501	K502

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	195231	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	130000	Depositor
Image detector	TFS FALCON 4i (4k x 4k)	Depositor
Maximum map value	21.826	Depositor
Minimum map value	-0.266	Depositor
Average map value	-0.019	Depositor
Map value standard deviation	0.354	Depositor
Recommended contour level	2.5	Depositor
Map size (Å)	360.96002, 360.96002, 360.96002	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.9024001, 0.9024001, 0.9024001	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SEP, 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	0.84	0/259	1.08	0/343
2	A	0.40	0/11241	0.57	0/15311
All	All	0.42	0/11500	0.59	0/15654

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

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	283	0	243	9	0
2	A	11030	0	10738	143	0
3	A	1	0	0	0	0
All	All	11314	0	10981	149	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 7.

The worst 5 of 149 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:B:188:THR:HG23	1:B:190:ASN:H	1.37	0.89
1:B:167:ASP:HA	2:A:1773:LYS:HD2	1.57	0.86
2:A:1750:LEU:HD11	2:A:1798:VAL:HG13	1.62	0.79
2:A:427:VAL:HG21	2:A:475:GLU:HB3	1.64	0.79
2:A:894:SER:HB3	2:A:897:TRP:HD1	1.47	0.78

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	30/227 (13%)	26 (87%)	3 (10%)	1 (3%)	3	7
2	A	1466/2172 (68%)	1437 (98%)	29 (2%)	0	100	100
All	All	1496/2399 (62%)	1463 (98%)	32 (2%)	1 (0%)	49	72

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	184	VAL

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	27/200 (14%)	26 (96%)	1 (4%)	30	55

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	A	1113/1814 (61%)	1099 (99%)	14 (1%)	61	78
All	All	1140/2014 (57%)	1125 (99%)	15 (1%)	59	78

5 of 15 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	1290	SER
2	A	2046	VAL
2	A	1881	GLN
2	A	2117	VAL
2	A	1982	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 27 such sidechains are listed below:

Mol	Chain	Res	Type
2	A	918	ASN
2	A	1053	GLN
2	A	1957	ASN
2	A	1022	GLN
2	A	1203	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

2 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
1	SEP	B	185	1	8,9,10	0.64	0	8,12,14	0.61	0
1	SEP	B	175	1	8,9,10	0.65	0	8,12,14	0.62	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	SEP	B	185	1	-	0/5/8/10	-
1	SEP	B	175	1	-	0/5/8/10	-

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.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	185	SEP	1	0
1	B	175	SEP	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 1 ligands modelled in this entry, 1 is 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 ⓘ

There are no chain breaks in this entry.

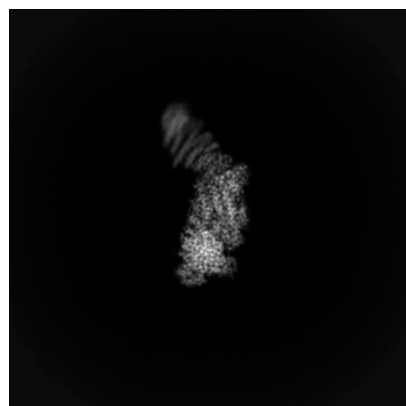
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-52307. These allow visual inspection of the internal detail of the map and identification of artifacts.

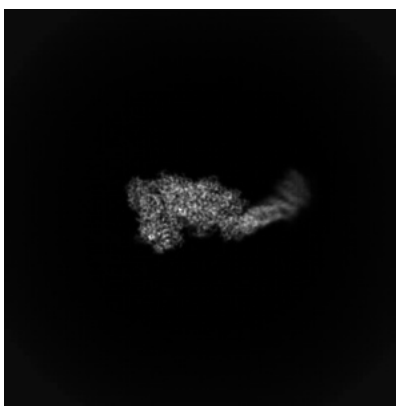
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

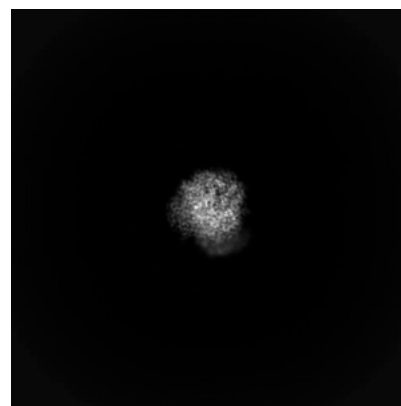
6.1.1 Primary map



X

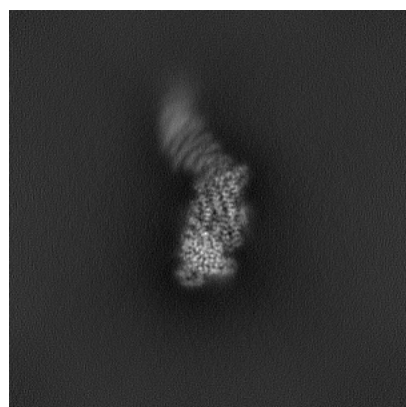


Y

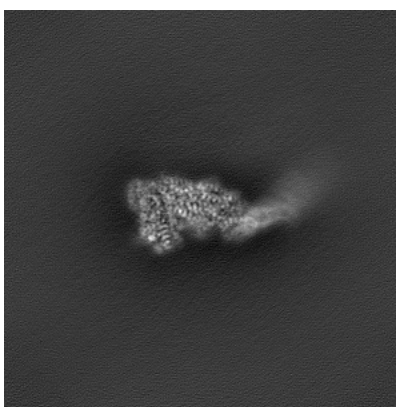


Z

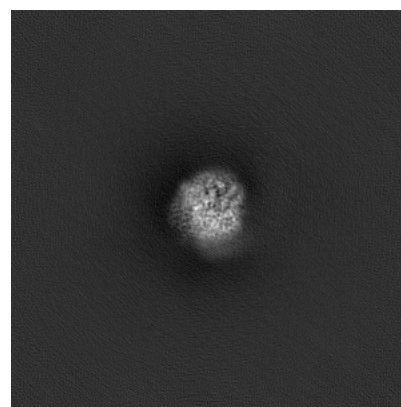
6.1.2 Raw map



X



Y

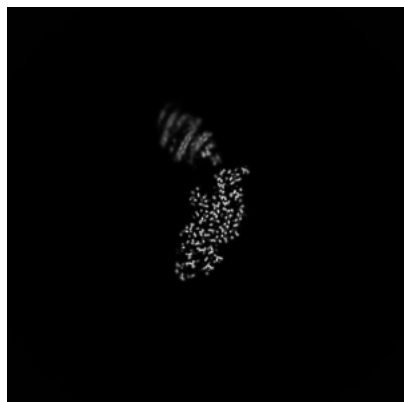


Z

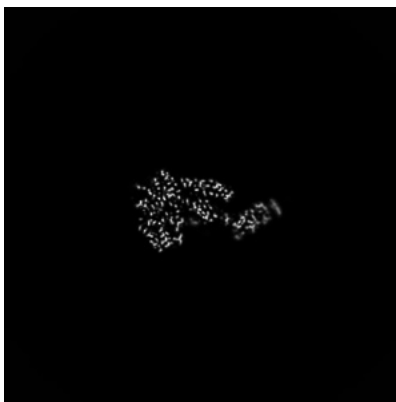
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

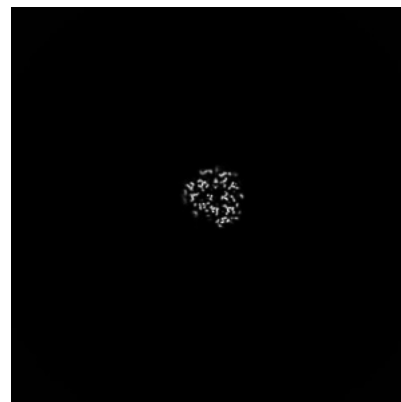
6.2.1 Primary map



X Index: 200

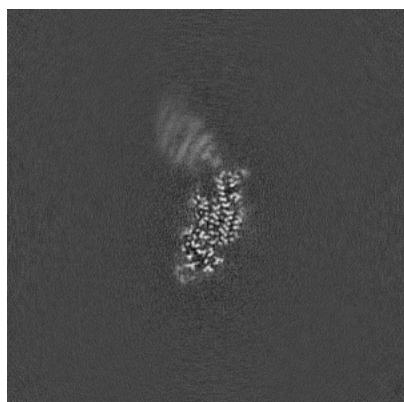


Y Index: 200

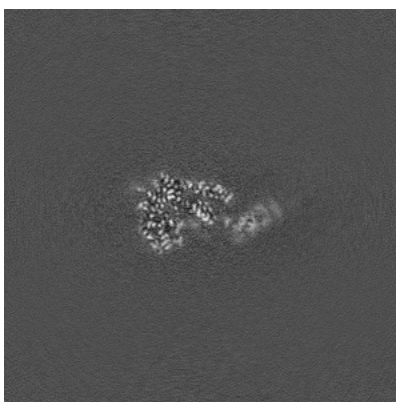


Z Index: 200

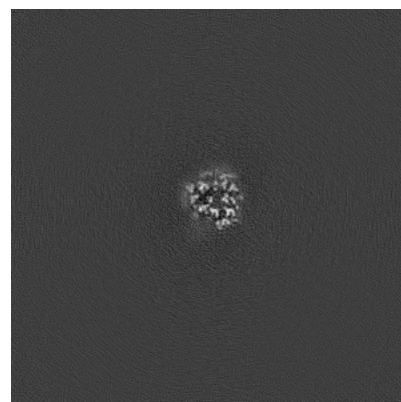
6.2.2 Raw map



X Index: 200



Y Index: 200

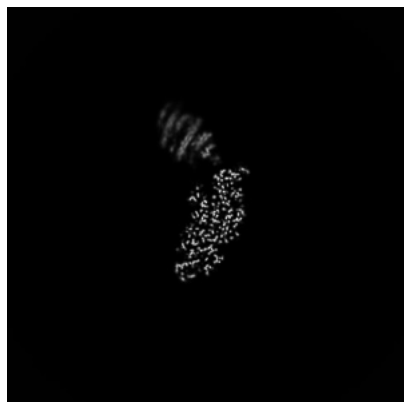


Z Index: 200

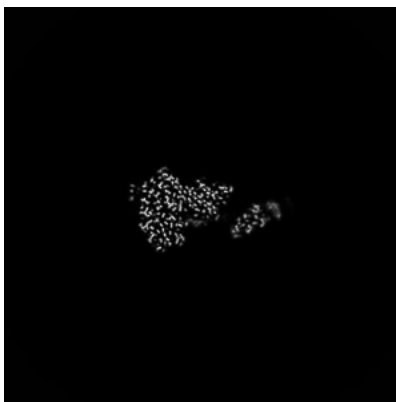
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

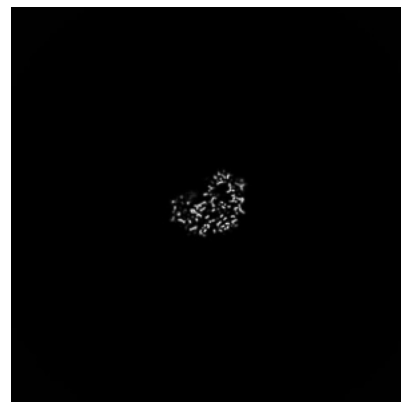
6.3.1 Primary map



X Index: 201

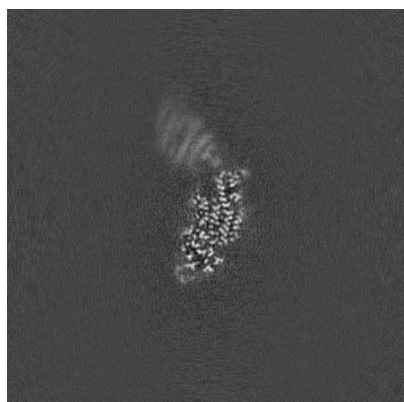


Y Index: 196

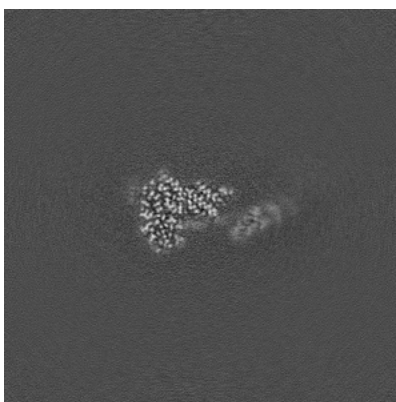


Z Index: 167

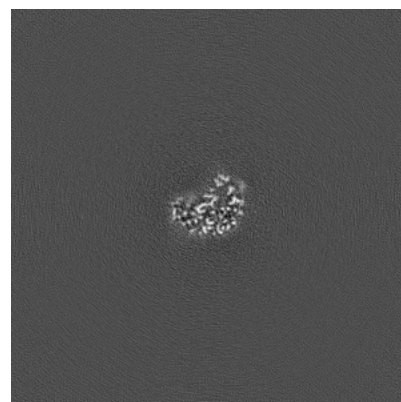
6.3.2 Raw map



X Index: 200



Y Index: 196

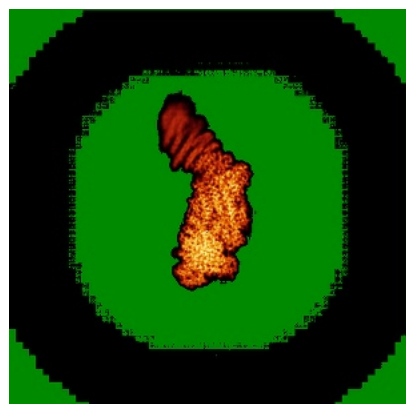


Z Index: 166

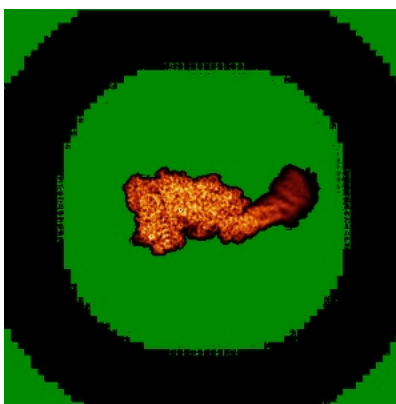
The images above show the largest variance slices of the map in three orthogonal directions.

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

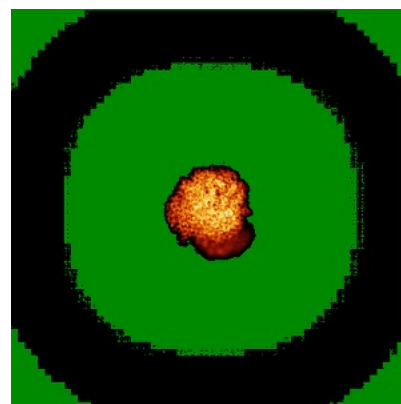
6.4.1 Primary map



X

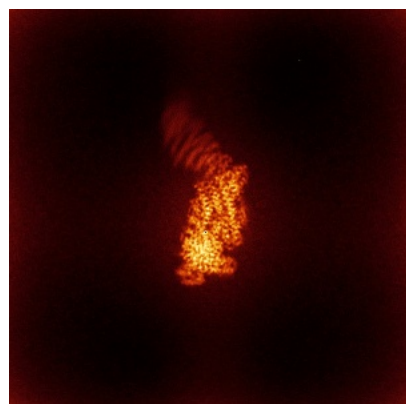


Y

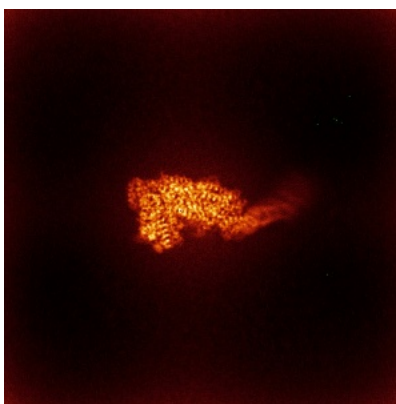


Z

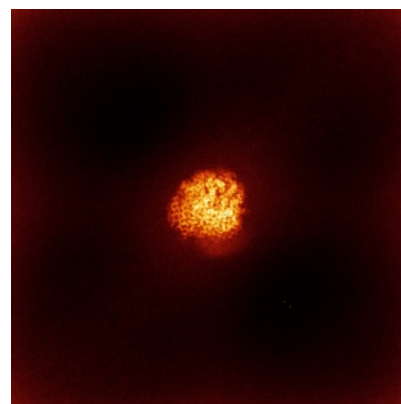
6.4.2 Raw map



X



Y

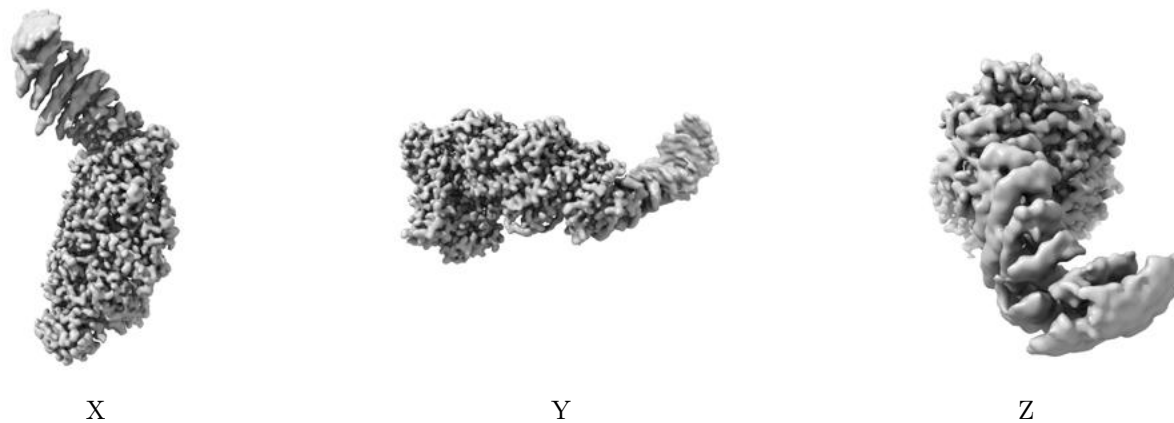


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

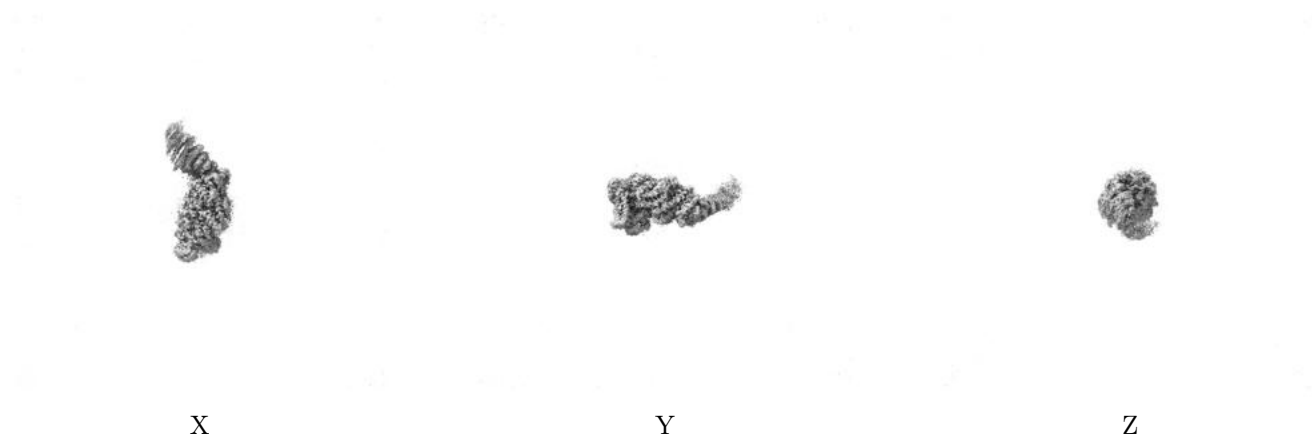
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 2.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 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.

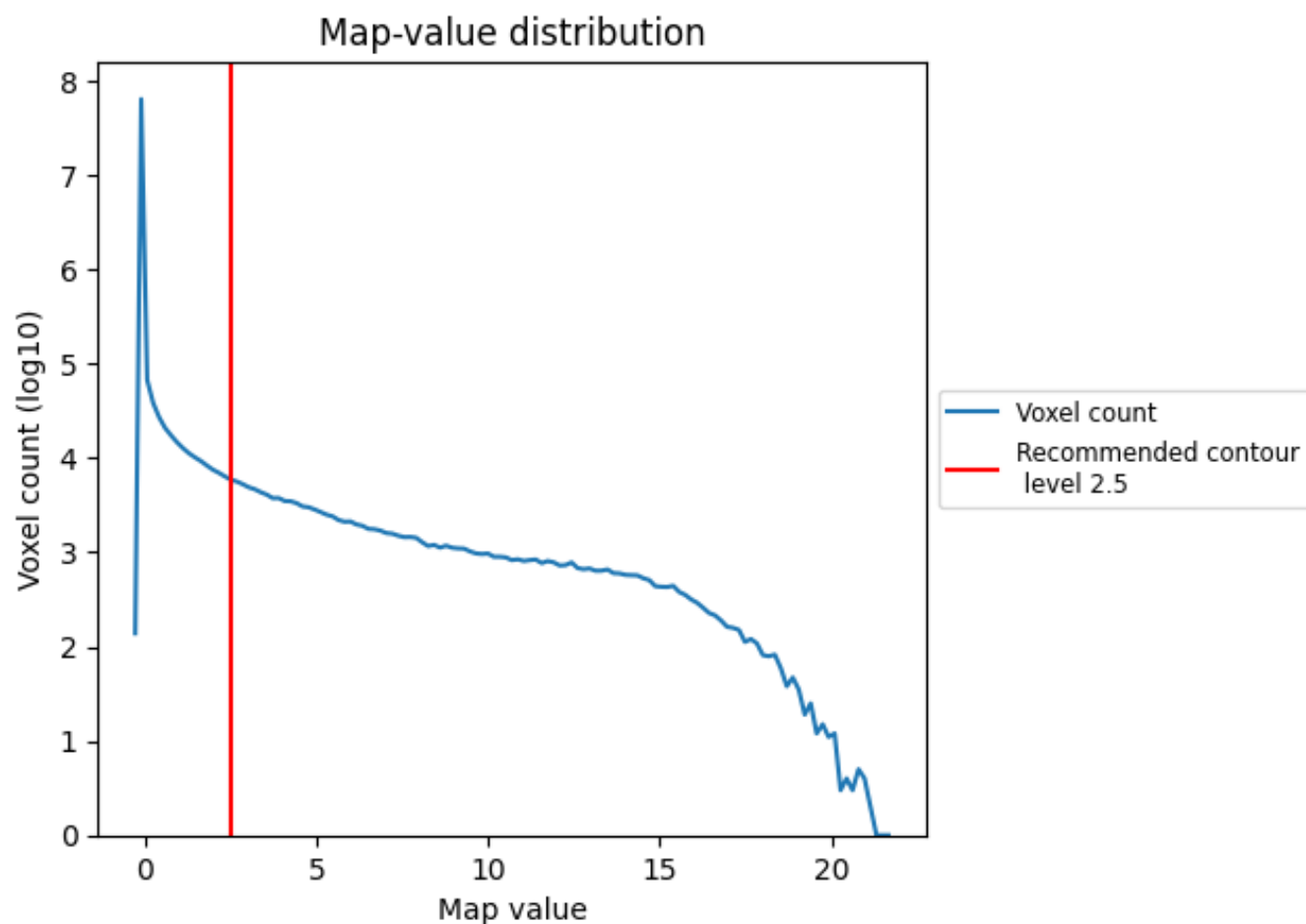
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

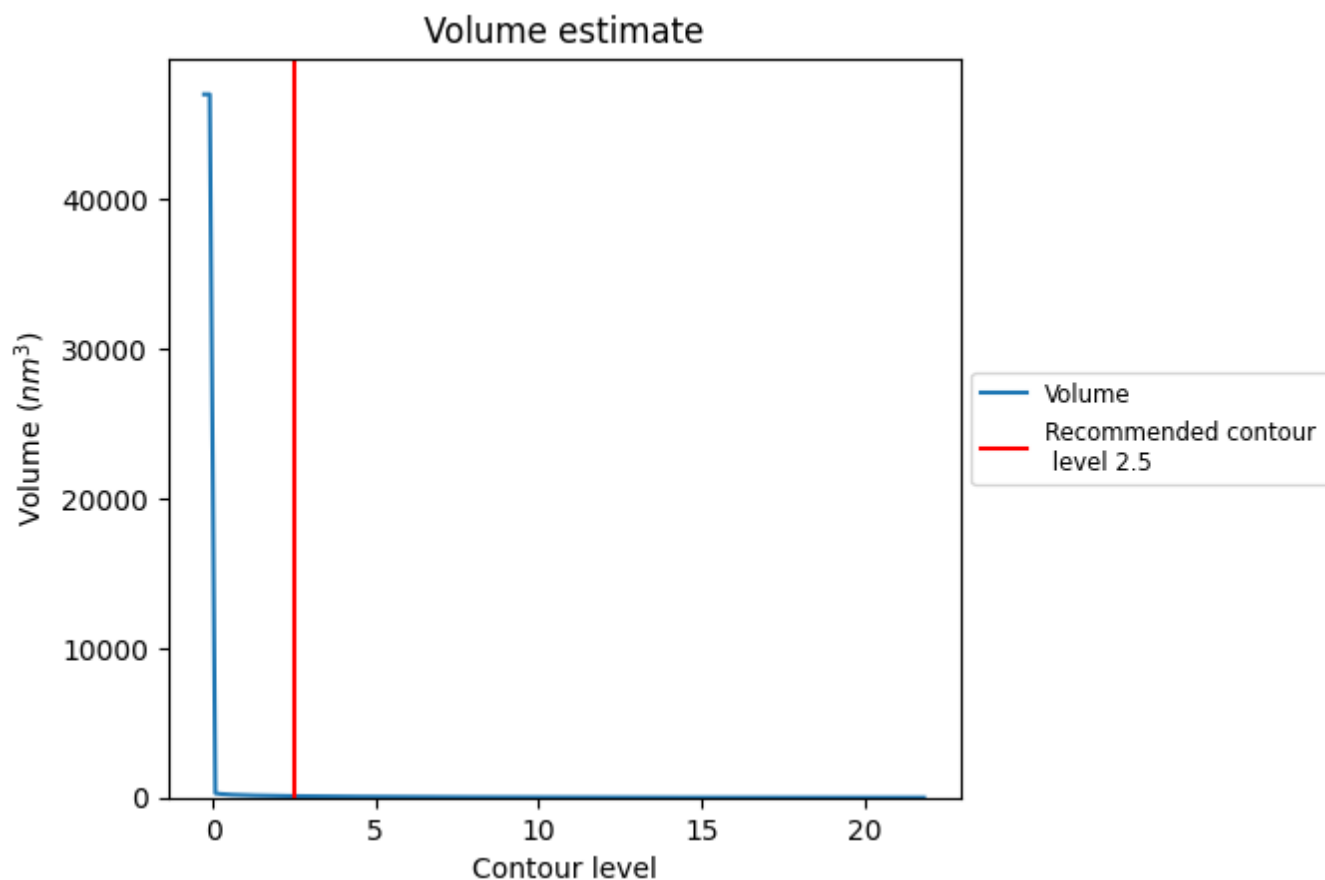
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

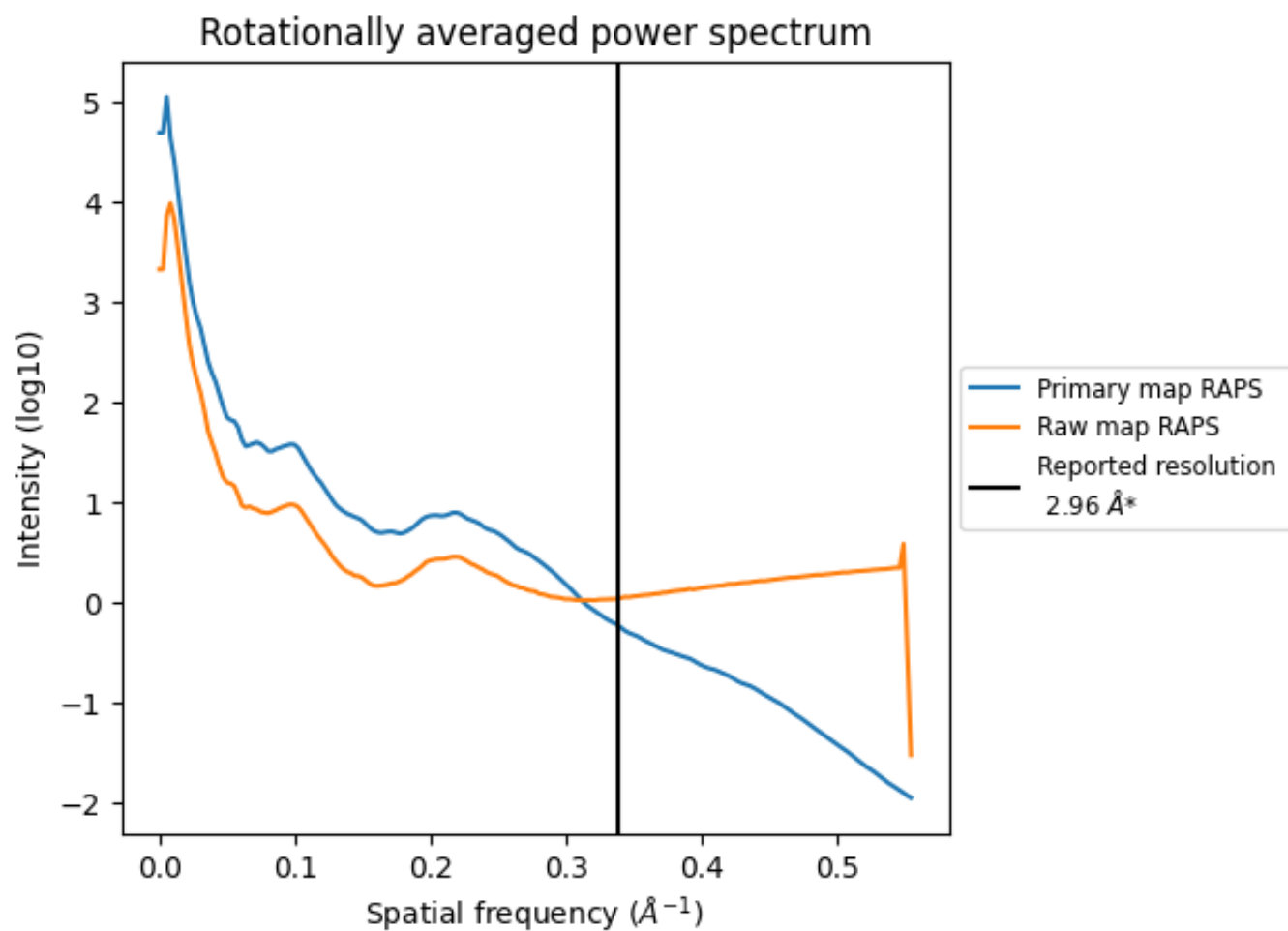
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 97 nm^3 ; this corresponds to an approximate mass of 87 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 ⓘ

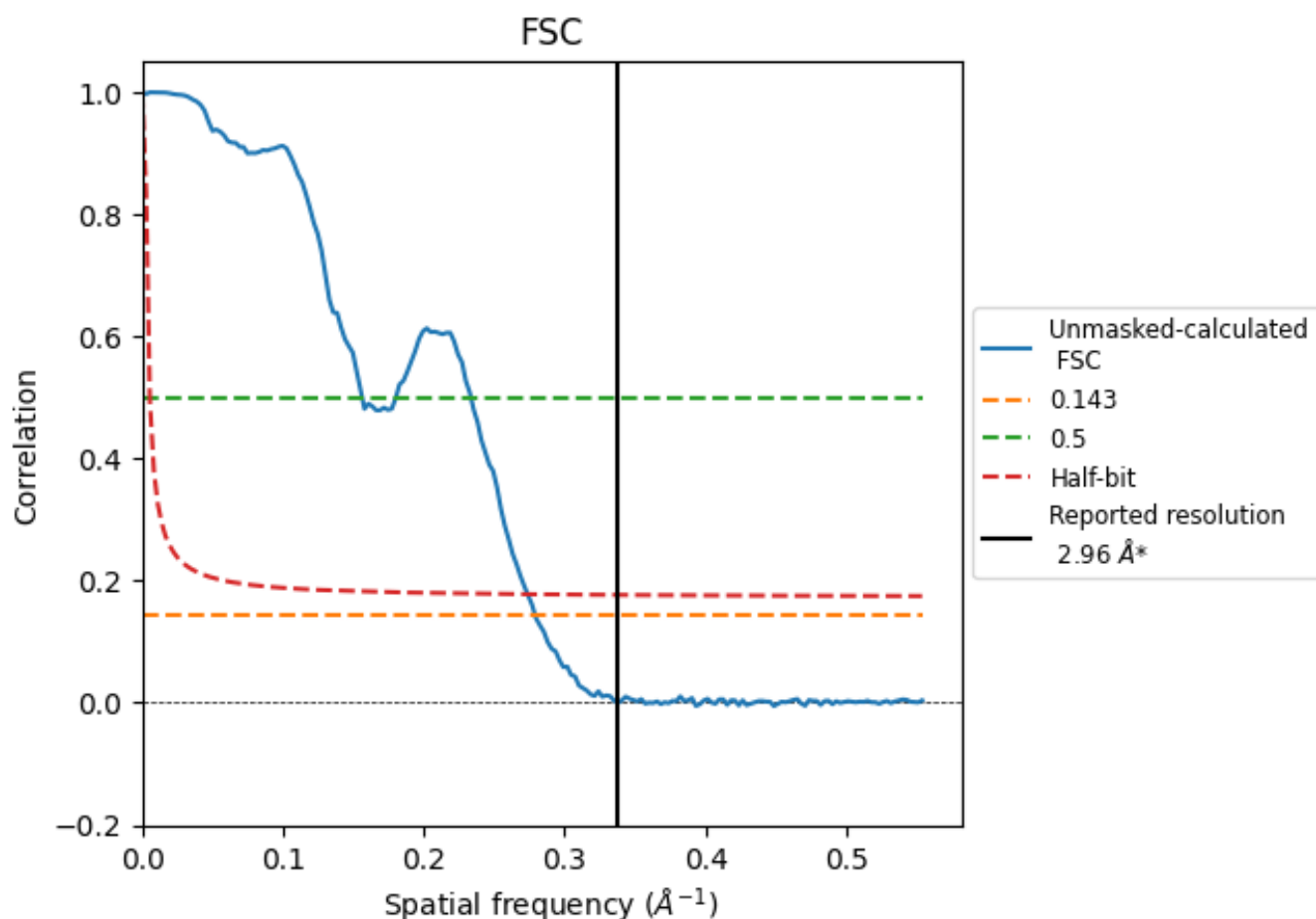


*Reported resolution corresponds to spatial frequency of 0.338 Å⁻¹

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 0.338 Å⁻¹

8.2 Resolution estimates [i](#)

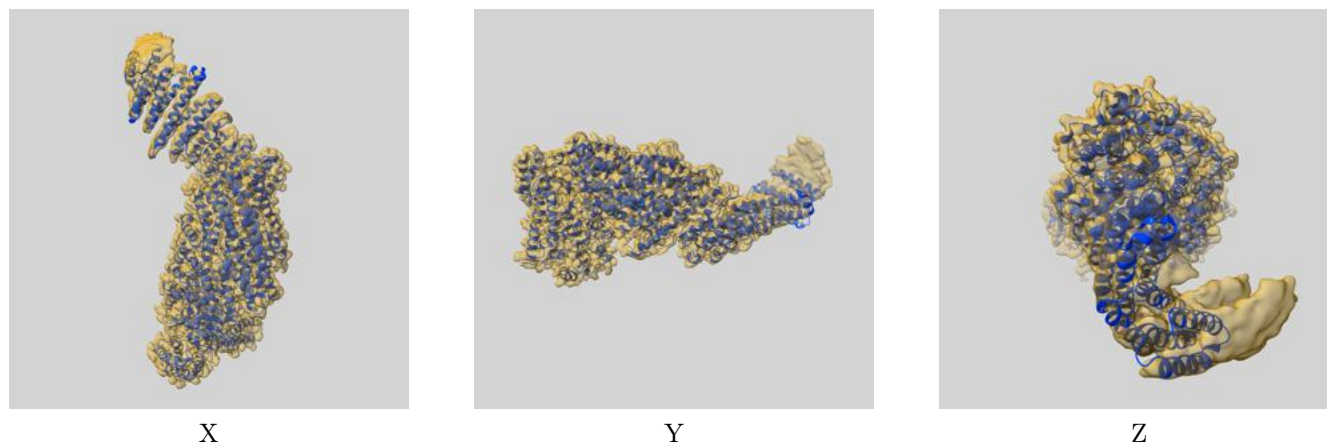
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.96	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.58	6.40	3.65

*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 3.58 differs from the reported value 2.96 by more than 10 %

9 Map-model fit [i](#)

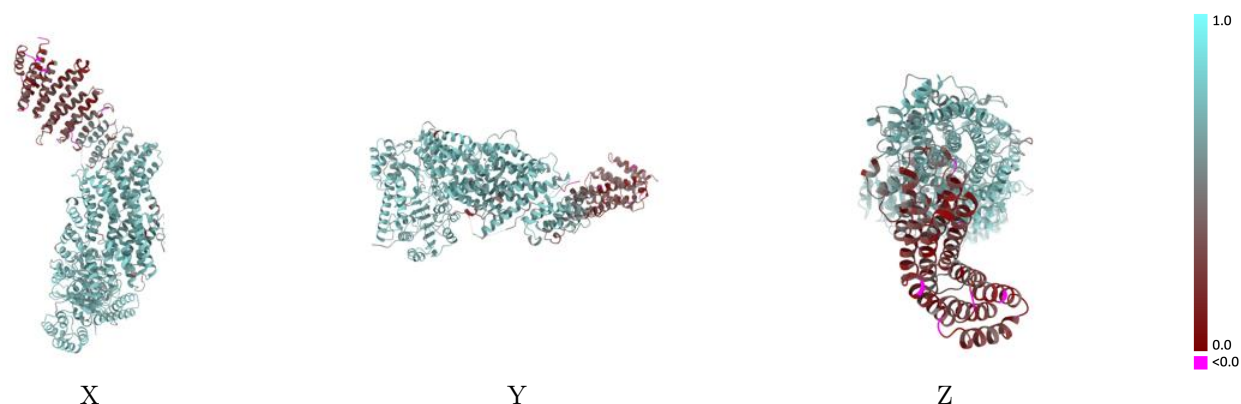
This section contains information regarding the fit between EMDB map EMD-52307 and PDB model 9HN5. Per-residue inclusion information can be found in section [3](#) on page [7](#).

9.1 Map-model overlay [i](#)



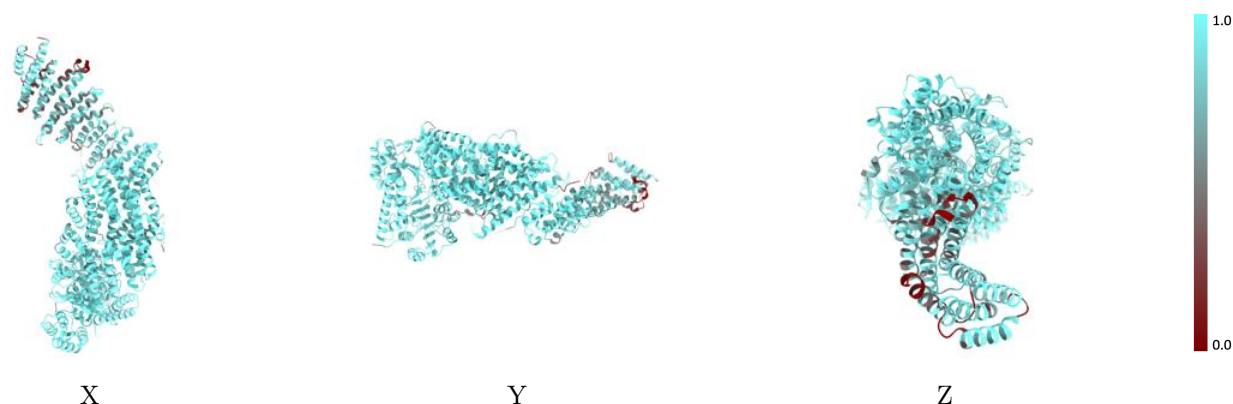
The images above show the 3D surface view of the map at the recommended contour level 2.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



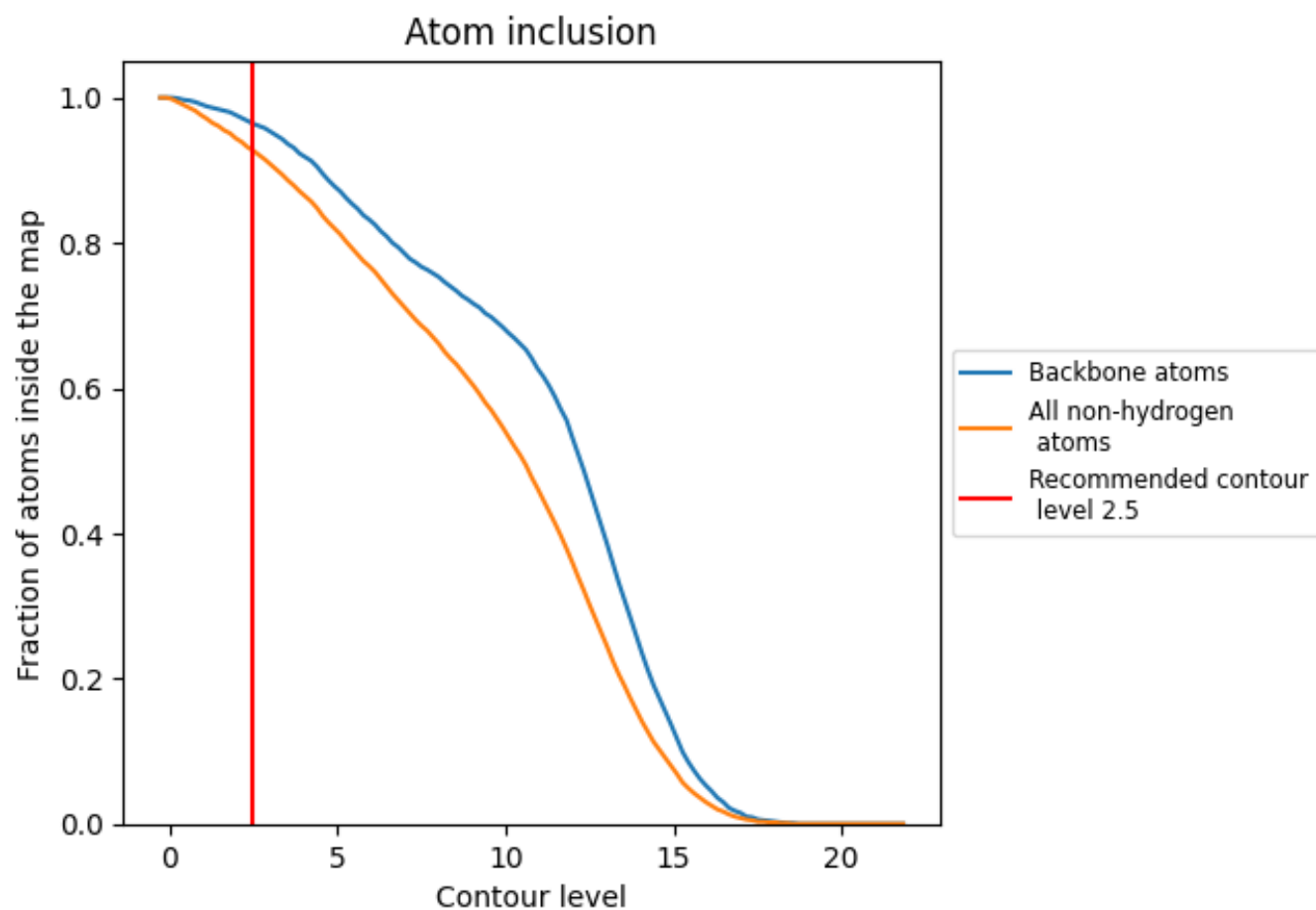
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2.5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 93% 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 (2.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9270	0.6050
A	0.9340	0.6110
B	0.6440	0.3810

