



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 10:07 AM UTC

PDB ID : 8UXU / pdb_00008uxu
EMDB ID : EMD-42779
Title : Cryo-EM structure of a bacterial nitrilase filament with a covalent adduct derived from benzonitrile hydrolysis
Authors : Aguirre-Sampieri, S.; Casanal, A.; Emsley, P.; Garza-Ramos, G.
Deposited on : 2023-11-10
Resolution : 3.01 Å (reported)
Based on initial models : ., 2VHH

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 : 2022.3.0, CSD as543be (2022)
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

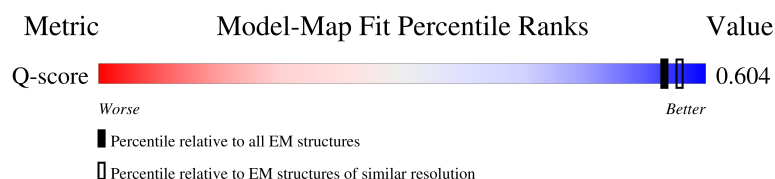
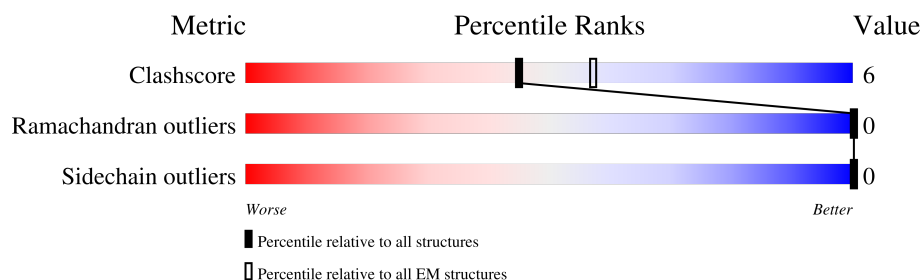
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.01 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	13882 (2.51 - 3.51)

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	327	 83% 14% .
1	B	327	 87% 9% .
1	C	327	 79% 18% .
1	D	327	 84% 13% .

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Mol	Chain	Length	Quality of chain
1	E	327	 83% 14% .
1	F	327	 82% 15% .
1	G	327	 84% 13% .
1	H	327	 85% 12% .
1	I	327	 87% 9% .
1	J	327	 84% 13% .
1	K	327	 81% 16% .
1	L	327	 82% 15% .
1	M	327	 83% 14% .
1	N	327	 80% 17% .

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 65716 atoms, of which 32157 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 Nitrilase.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	317	Total	C	H	N	O	S	0	0
			4683	1526	2290	426	429	12		
1	B	317	Total	C	H	N	O	S	0	0
			4681	1525	2290	418	436	12		
1	C	317	Total	C	H	N	O	S	0	0
			4613	1512	2249	414	426	12		
1	D	317	Total	C	H	N	O	S	0	0
			4696	1527	2303	424	430	12		
1	E	317	Total	C	H	N	O	S	0	0
			4561	1502	2212	410	425	12		
1	F	317	Total	C	H	N	O	S	0	0
			4726	1532	2322	427	433	12		
1	G	317	Total	C	H	N	O	S	0	0
			4685	1523	2301	424	425	12		
1	H	317	Total	C	H	N	O	S	0	0
			4756	1538	2339	428	439	12		
1	I	317	Total	C	H	N	O	S	0	0
			4635	1514	2267	415	427	12		
1	J	317	Total	C	H	N	O	S	0	0
			4702	1530	2300	424	436	12		
1	K	317	Total	C	H	N	O	S	0	0
			4653	1518	2275	417	431	12		
1	L	317	Total	C	H	N	O	S	0	0
			4709	1529	2308	421	439	12		
1	M	317	Total	C	H	N	O	S	0	0
			4709	1529	2313	422	433	12		
1	N	317	Total	C	H	N	O	S	0	0
			4725	1532	2318	424	439	12		

There are 14 discrepancies between the modelled and reference sequences:

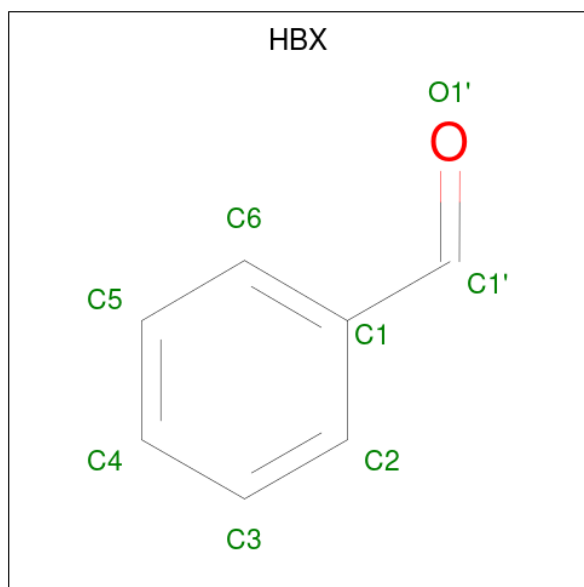
Chain	Residue	Modelled	Actual	Comment	Reference
A	32	ASN	ILE	conflict	UNP A4LA85
B	32	ASN	ILE	conflict	UNP A4LA85

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Chain	Residue	Modelled	Actual	Comment	Reference
C	32	ASN	ILE	conflict	UNP A4LA85
D	32	ASN	ILE	conflict	UNP A4LA85
E	32	ASN	ILE	conflict	UNP A4LA85
F	32	ASN	ILE	conflict	UNP A4LA85
G	32	ASN	ILE	conflict	UNP A4LA85
H	32	ASN	ILE	conflict	UNP A4LA85
I	32	ASN	ILE	conflict	UNP A4LA85
J	32	ASN	ILE	conflict	UNP A4LA85
K	32	ASN	ILE	conflict	UNP A4LA85
L	32	ASN	ILE	conflict	UNP A4LA85
M	32	ASN	ILE	conflict	UNP A4LA85
N	32	ASN	ILE	conflict	UNP A4LA85

- Molecule 2 is benzaldehyde (CCD ID: HBX) (formula: C₇H₆O).



Mol	Chain	Residues	Atoms				AltConf
2	A	1	Total	C	H	O	0
			13	7	5	1	
2	B	1	Total	C	H	O	0
			13	7	5	1	
2	C	1	Total	C	H	O	0
			13	7	5	1	
2	D	1	Total	C	H	O	0
			13	7	5	1	
2	E	1	Total	C	H	O	0
			13	7	5	1	

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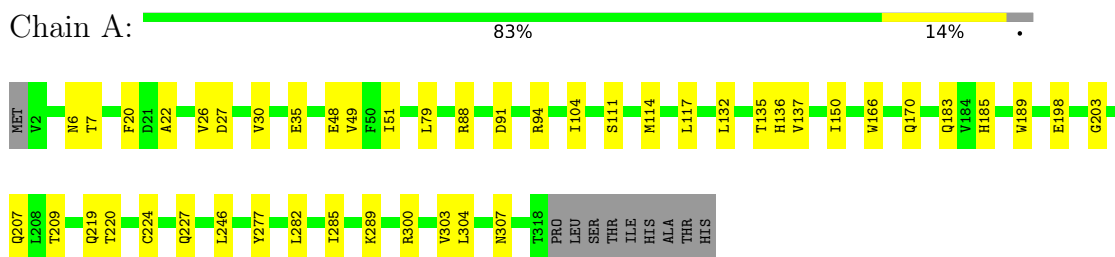
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Mol	Chain	Residues	Atoms				AltConf
2	F	1	Total 13	C 7	H 5	O 1	0
2	G	1	Total 13	C 7	H 5	O 1	0
2	H	1	Total 13	C 7	H 5	O 1	0
2	I	1	Total 13	C 7	H 5	O 1	0
2	J	1	Total 13	C 7	H 5	O 1	0
2	K	1	Total 13	C 7	H 5	O 1	0
2	L	1	Total 13	C 7	H 5	O 1	0
2	M	1	Total 13	C 7	H 5	O 1	0
2	N	1	Total 13	C 7	H 5	O 1	0

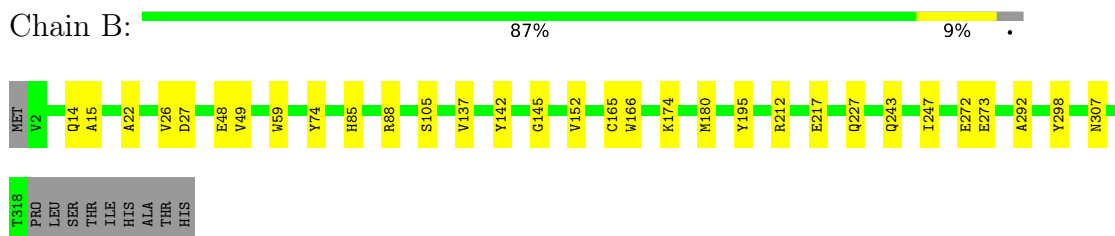
3 Residue-property plots [i](#)

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.

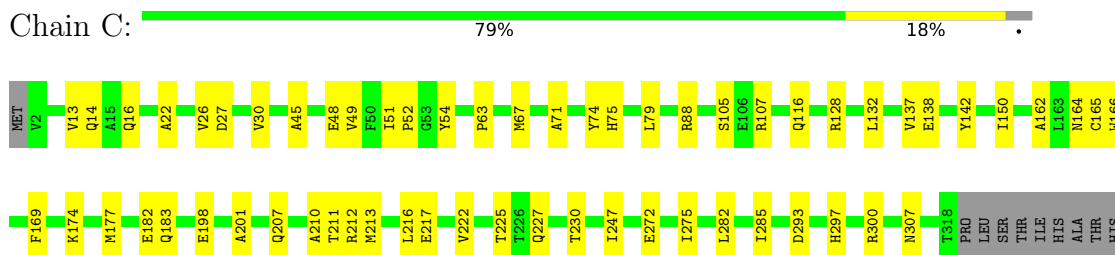
• Molecule 1: Nitrilase



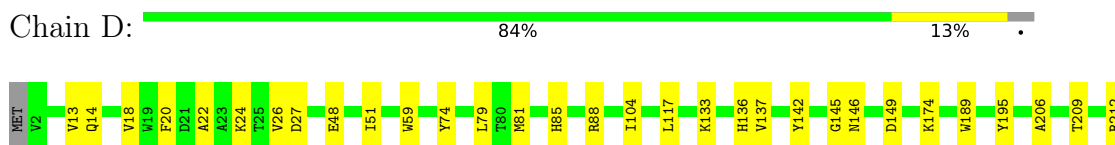
• Molecule 1: Nitrilase



• Molecule 1: Nitrilase



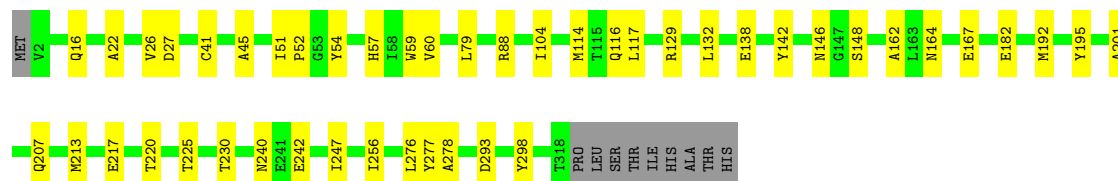
• Molecule 1: Nitrilase





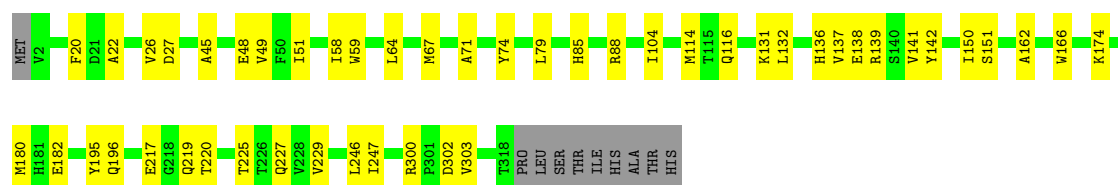
- Molecule 1: Nitrilase

Chain E: 83% 14% .



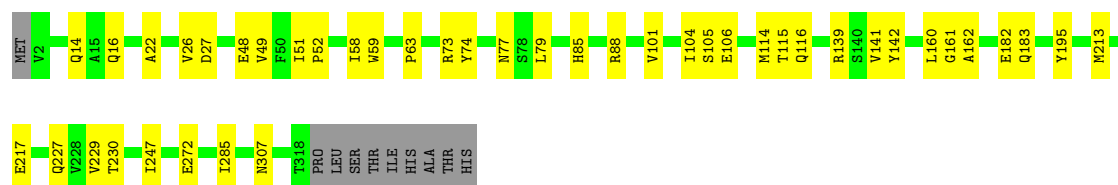
- Molecule 1: Nitrilase

Chain F: 82% 15% .



- Molecule 1: Nitrilase

Chain G: 84% 13% .



- Molecule 1: Nitrilase

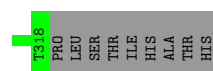
Chain H: 85% 12% .



- Molecule 1: Nitrilase

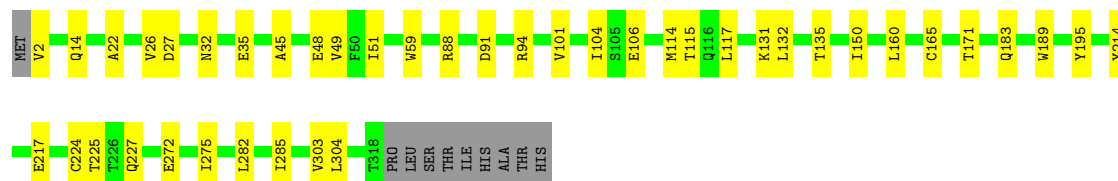
Chain I: 87% 9% .





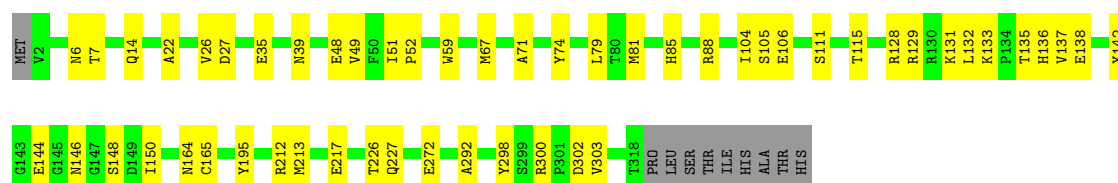
- Molecule 1: Nitrilase

Chain J: 84% 13% .



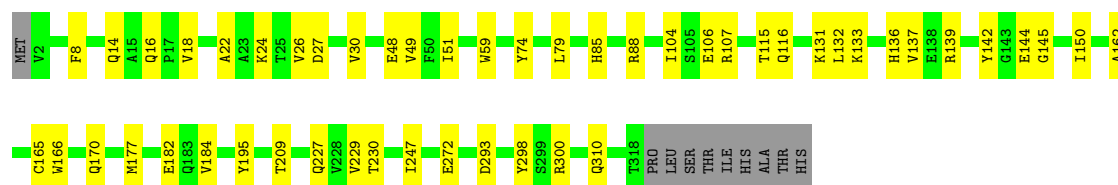
- Molecule 1: Nitrilase

Chain K: 81% 16% .



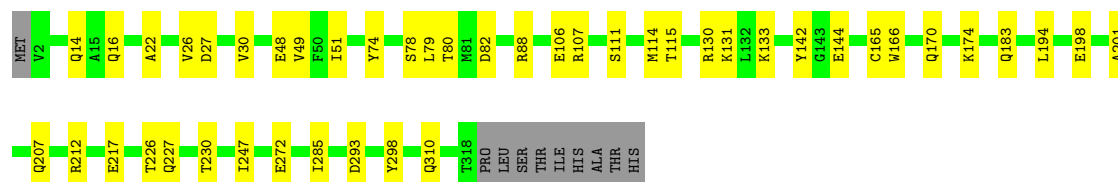
- Molecule 1: Nitrilase

Chain L: 82% 15% .



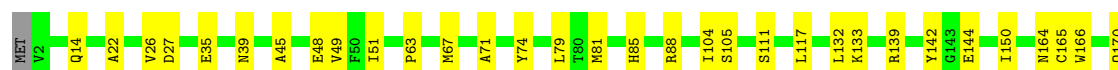
- Molecule 1: Nitrilase

Chain M: 83% 14% .



- Molecule 1: Nitrilase

Chain N: 80% 17% .



T173	K174	M177	E182	Q183	T209	M213	E217	T225	T226	Q227	T230	P231	C238	I247	R255	L268	E272	L276	L282	I285	A292	V295	Y298	T318	PRO	LEU	SER	THR	THR	ILE	HIS	ALA	THR	HIS
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

4 Experimental information

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=-72, -72°, rise=18.2573, 18.2573 Å, axial sym=D1, D1	Depositor
Number of segments used	56369	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 ($e^-/\text{Å}^2$)	1.0	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	75000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.186	Depositor
Minimum map value	-0.083	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.02	Depositor
Map size (Å)	374.4, 374.4, 374.4	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.04, 1.04, 1.04	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	0.20	0/2453	0.29	0/3349
1	B	0.20	0/2451	0.29	0/3347
1	C	0.22	0/2424	0.29	0/3314
1	D	0.21	0/2453	0.30	0/3349
1	E	0.18	0/2409	0.28	0/3296
1	F	0.19	0/2464	0.27	0/3362
1	G	0.22	0/2444	0.28	0/3337
1	H	0.21	0/2477	0.29	0/3378
1	I	0.20	0/2428	0.28	0/3319
1	J	0.20	0/2462	0.27	0/3360
1	K	0.22	0/2438	0.29	0/3331
1	L	0.22	0/2461	0.29	0/3360
1	M	0.22	0/2456	0.31	0/3352
1	N	0.23	0/2467	0.30	0/3367
All	All	0.21	0/34287	0.29	0/46821

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	A	2393	2290	2296	34	0
1	B	2391	2290	2287	23	0
1	C	2364	2249	2245	43	0
1	D	2393	2303	2301	29	0
1	E	2349	2212	2209	31	0
1	F	2404	2322	2319	36	0
1	G	2384	2301	2296	30	0
1	H	2417	2339	2336	26	0
1	I	2368	2267	2263	22	0
1	J	2402	2300	2307	27	0
1	K	2378	2275	2271	42	0
1	L	2401	2308	2303	42	0
1	M	2396	2313	2308	34	0
1	N	2407	2318	2314	41	0
2	A	8	5	5	0	0
2	B	8	5	5	0	0
2	C	8	5	5	0	0
2	D	8	5	5	0	0
2	E	8	5	5	0	0
2	F	8	5	5	0	0
2	G	8	5	5	0	0
2	H	8	5	5	0	0
2	I	8	5	5	0	0
2	J	8	5	5	0	0
2	K	8	5	5	0	0
2	L	8	5	5	0	0
2	M	8	5	5	0	0
2	N	8	5	5	0	0
All	All	33559	32157	32125	414	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 6.

The worst 5 of 414 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:D:27:ASP:OD1	1:D:88:ARG:NH2	1.99	0.96
1:B:27:ASP:OD1	1:B:88:ARG:NH2	2.06	0.87
1:I:16:GLN:OE1	1:I:230:THR:OG1	1.92	0.87
1:D:51:ILE:HG21	1:D:79:LEU:HD11	1.60	0.81
1:C:51:ILE:HG21	1:C:79:LEU:HD11	1.61	0.81

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	315/327 (96%)	308 (98%)	7 (2%)	0	100	100
1	B	315/327 (96%)	300 (95%)	15 (5%)	0	100	100
1	C	315/327 (96%)	303 (96%)	12 (4%)	0	100	100
1	D	315/327 (96%)	307 (98%)	8 (2%)	0	100	100
1	E	315/327 (96%)	309 (98%)	6 (2%)	0	100	100
1	F	315/327 (96%)	302 (96%)	13 (4%)	0	100	100
1	G	315/327 (96%)	307 (98%)	8 (2%)	0	100	100
1	H	315/327 (96%)	303 (96%)	12 (4%)	0	100	100
1	I	315/327 (96%)	304 (96%)	11 (4%)	0	100	100
1	J	315/327 (96%)	306 (97%)	9 (3%)	0	100	100
1	K	315/327 (96%)	305 (97%)	10 (3%)	0	100	100
1	L	315/327 (96%)	306 (97%)	9 (3%)	0	100	100
1	M	315/327 (96%)	306 (97%)	9 (3%)	0	100	100
1	N	315/327 (96%)	303 (96%)	12 (4%)	0	100	100
All	All	4410/4578 (96%)	4269 (97%)	141 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	237/270 (88%)	237 (100%)	0	100	100
1	B	239/270 (88%)	239 (100%)	0	100	100
1	C	231/270 (86%)	231 (100%)	0	100	100
1	D	238/270 (88%)	238 (100%)	0	100	100
1	E	227/270 (84%)	227 (100%)	0	100	100
1	F	241/270 (89%)	241 (100%)	0	100	100
1	G	236/270 (87%)	236 (100%)	0	100	100
1	H	245/270 (91%)	245 (100%)	0	100	100
1	I	234/270 (87%)	234 (100%)	0	100	100
1	J	241/270 (89%)	241 (100%)	0	100	100
1	K	236/270 (87%)	236 (100%)	0	100	100
1	L	242/270 (90%)	242 (100%)	0	100	100
1	M	240/270 (89%)	240 (100%)	0	100	100
1	N	243/270 (90%)	243 (100%)	0	100	100
All	All	3330/3780 (88%)	3330 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 33 such sidechains are listed below:

Mol	Chain	Res	Type
1	K	297	HIS
1	L	87	GLN
1	N	87	GLN
1	D	14	GLN
1	C	309	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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](#)

14 ligands 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	$\# Z > 2$
2	HBX	N	401	1	8,8,8	0.10	0	9,9,9	0.43	0
2	HBX	K	401	1	8,8,8	0.11	0	9,9,9	0.47	0
2	HBX	I	401	1	8,8,8	0.12	0	9,9,9	0.47	0
2	HBX	C	401	1	8,8,8	0.11	0	9,9,9	0.43	0
2	HBX	J	401	1	8,8,8	0.11	0	9,9,9	0.46	0
2	HBX	M	401	1	8,8,8	0.11	0	9,9,9	0.44	0
2	HBX	B	401	1	8,8,8	0.12	0	9,9,9	0.45	0
2	HBX	L	401	1	8,8,8	0.12	0	9,9,9	0.43	0
2	HBX	H	401	1	8,8,8	0.11	0	9,9,9	0.44	0
2	HBX	F	401	1	8,8,8	0.10	0	9,9,9	0.44	0
2	HBX	A	401	1	8,8,8	0.11	0	9,9,9	0.45	0
2	HBX	E	401	1	8,8,8	0.09	0	9,9,9	0.45	0
2	HBX	G	401	1	8,8,8	0.11	0	9,9,9	0.44	0
2	HBX	D	401	1	8,8,8	0.13	0	9,9,9	0.47	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
2	HBX	N	401	1	-	0/2/2/2	0/1/1/1
2	HBX	K	401	1	-	0/2/2/2	0/1/1/1
2	HBX	I	401	1	-	0/2/2/2	0/1/1/1
2	HBX	C	401	1	-	0/2/2/2	0/1/1/1
2	HBX	J	401	1	-	0/2/2/2	0/1/1/1
2	HBX	M	401	1	-	0/2/2/2	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	HBX	B	401	1	-	0/2/2/2	0/1/1/1
2	HBX	L	401	1	-	0/2/2/2	0/1/1/1
2	HBX	H	401	1	-	0/2/2/2	0/1/1/1
2	HBX	F	401	1	-	0/2/2/2	0/1/1/1
2	HBX	A	401	1	-	0/2/2/2	0/1/1/1
2	HBX	E	401	1	-	0/2/2/2	0/1/1/1
2	HBX	G	401	1	-	0/2/2/2	0/1/1/1
2	HBX	D	401	1	-	0/2/2/2	0/1/1/1

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.

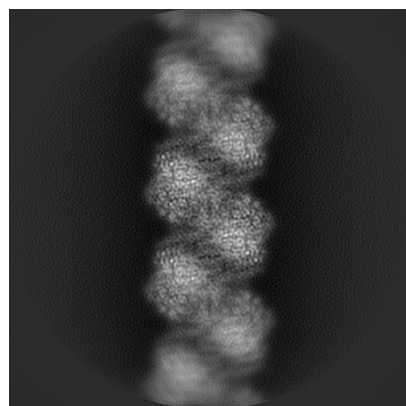
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-42779. These allow visual inspection of the internal detail of the map and identification of artifacts.

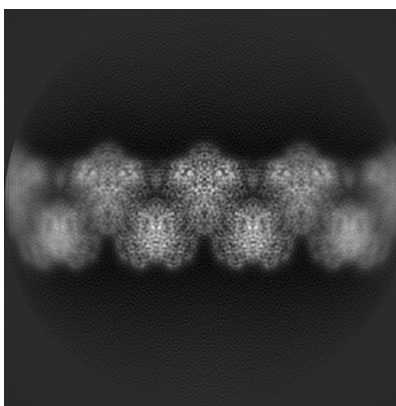
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

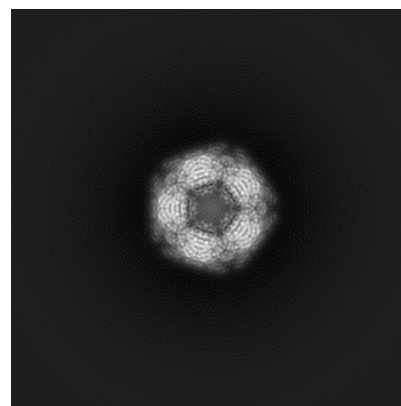
6.1.1 Primary map



X

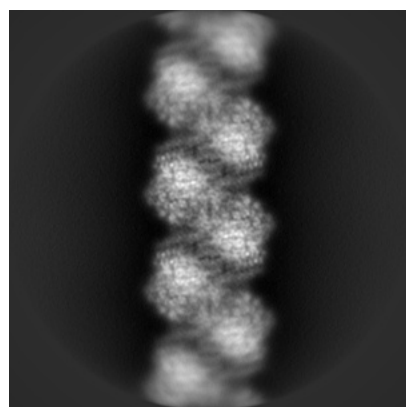


Y

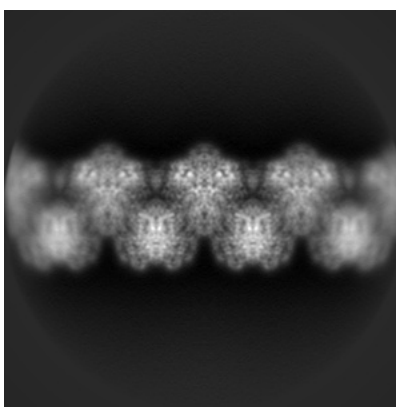


Z

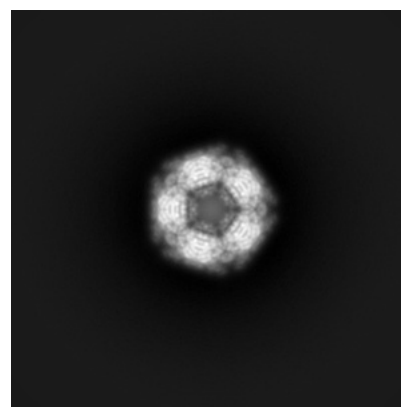
6.1.2 Raw map



X



Y

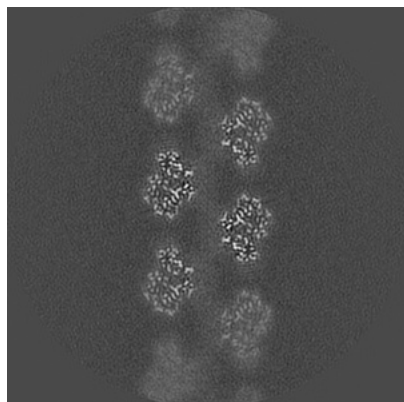


Z

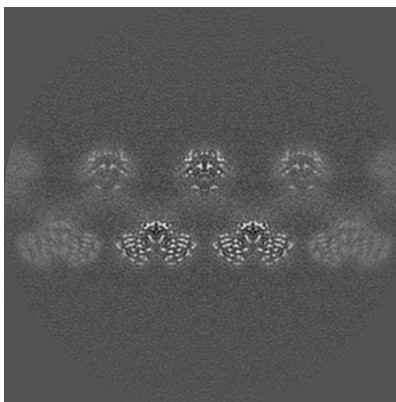
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

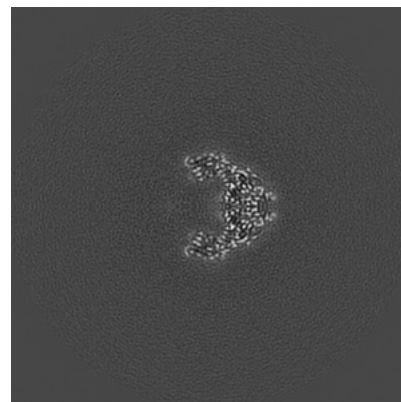
6.2.1 Primary map



X Index: 180

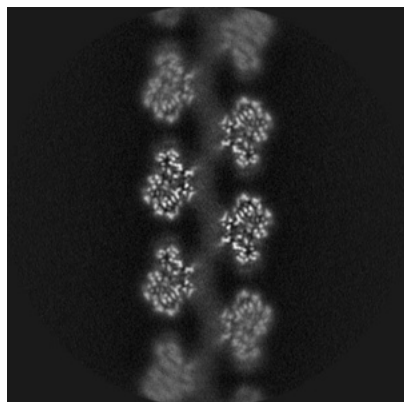


Y Index: 180

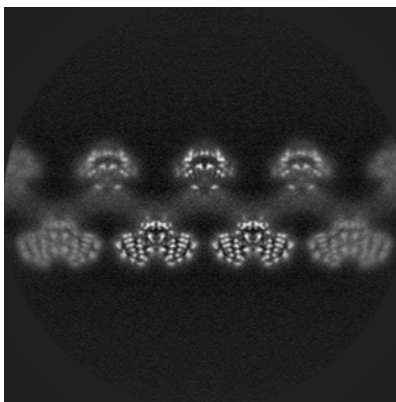


Z Index: 180

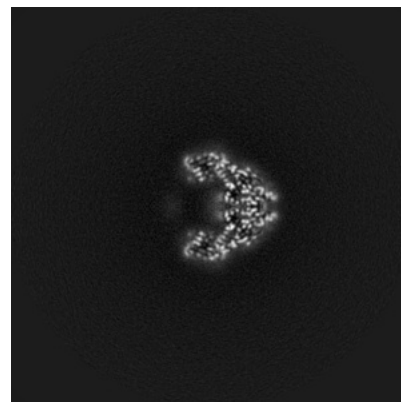
6.2.2 Raw map



X Index: 180



Y Index: 180

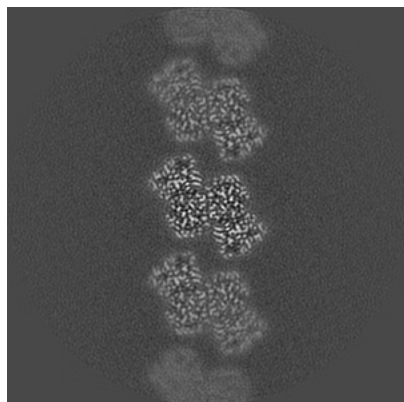


Z Index: 180

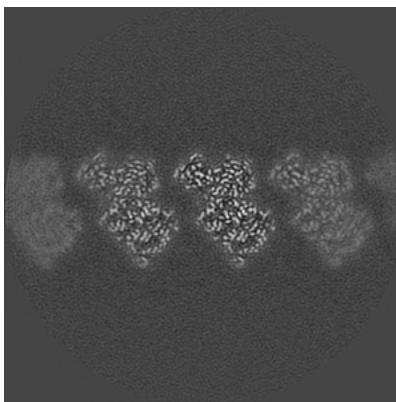
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

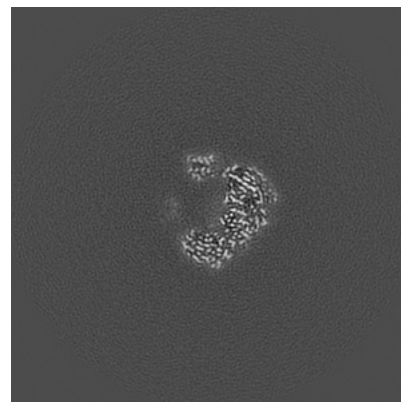
6.3.1 Primary map



X Index: 208

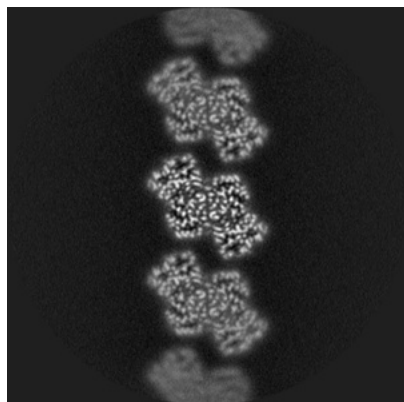


Y Index: 154

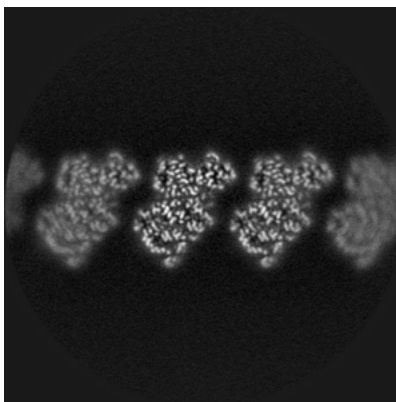


Z Index: 185

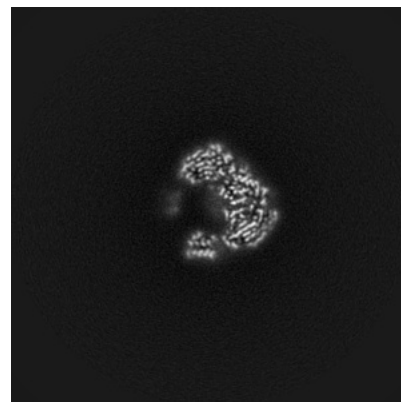
6.3.2 Raw map



X Index: 208



Y Index: 206

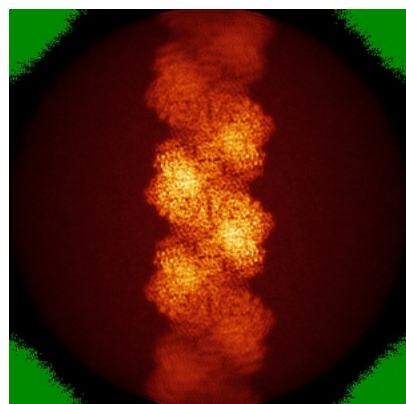


Z Index: 175

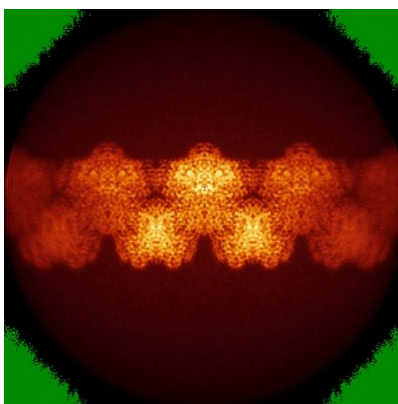
The images above show the largest variance slices of the map in three orthogonal directions.

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

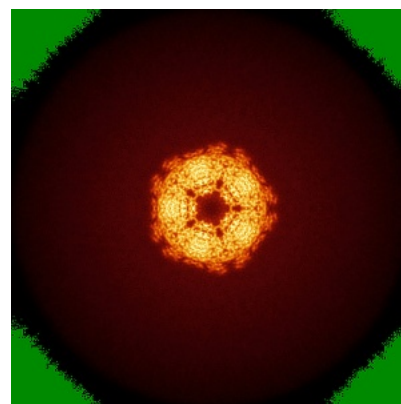
6.4.1 Primary map



X

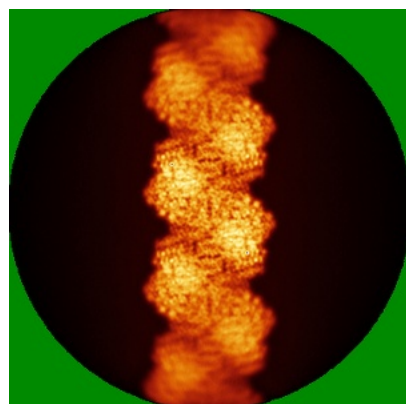


Y

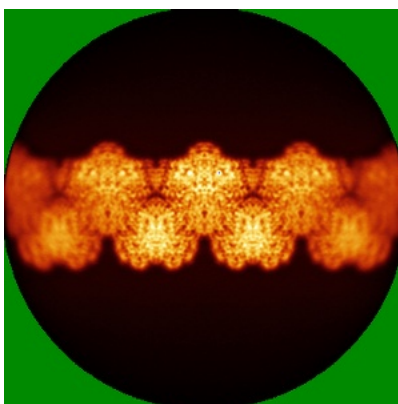


Z

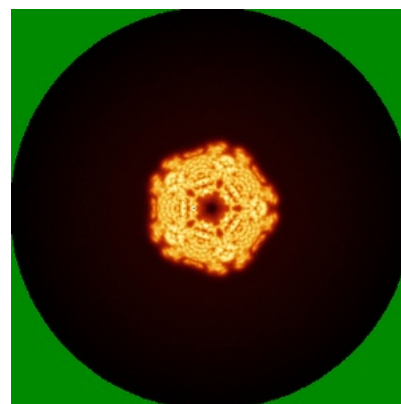
6.4.2 Raw map



X



Y

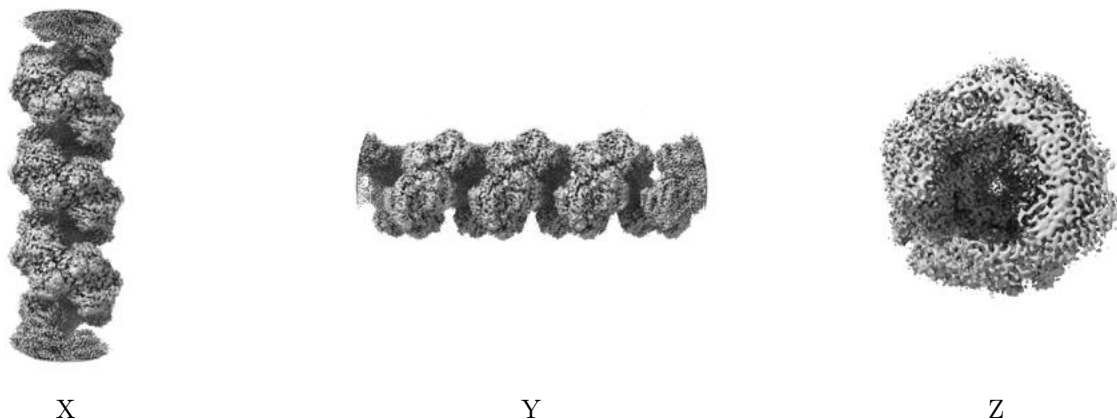


Z

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.

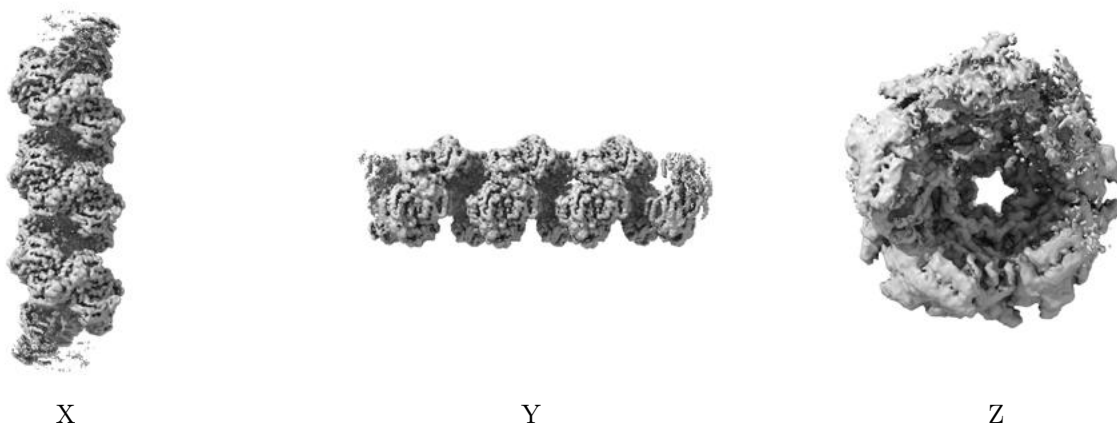
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.02. 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.

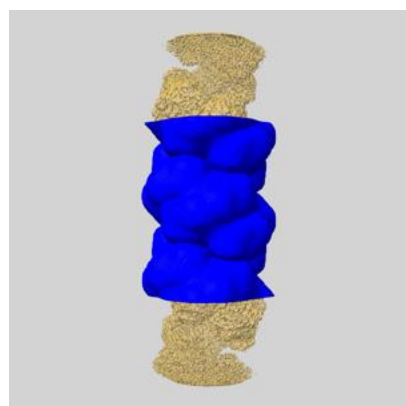
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

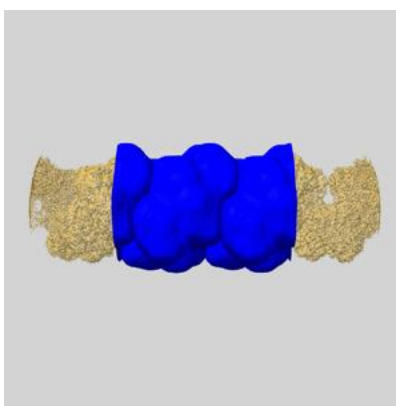
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

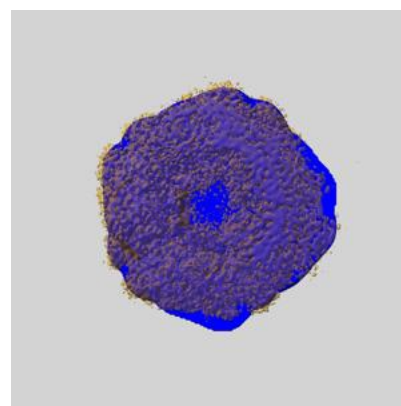
6.6.1 emd_42779_msk_1.map [i](#)



X



Y

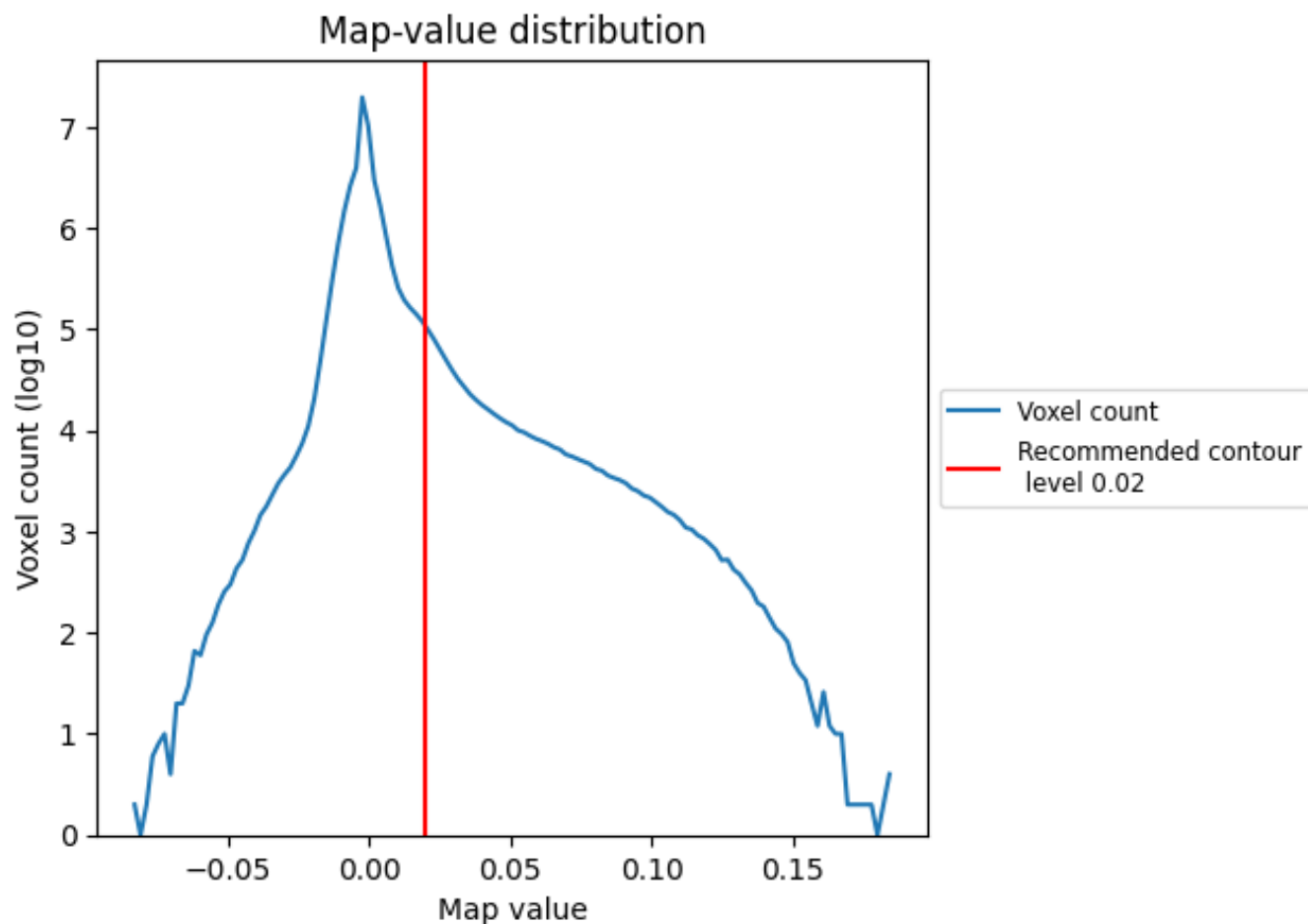


Z

7 Map analysis [i](#)

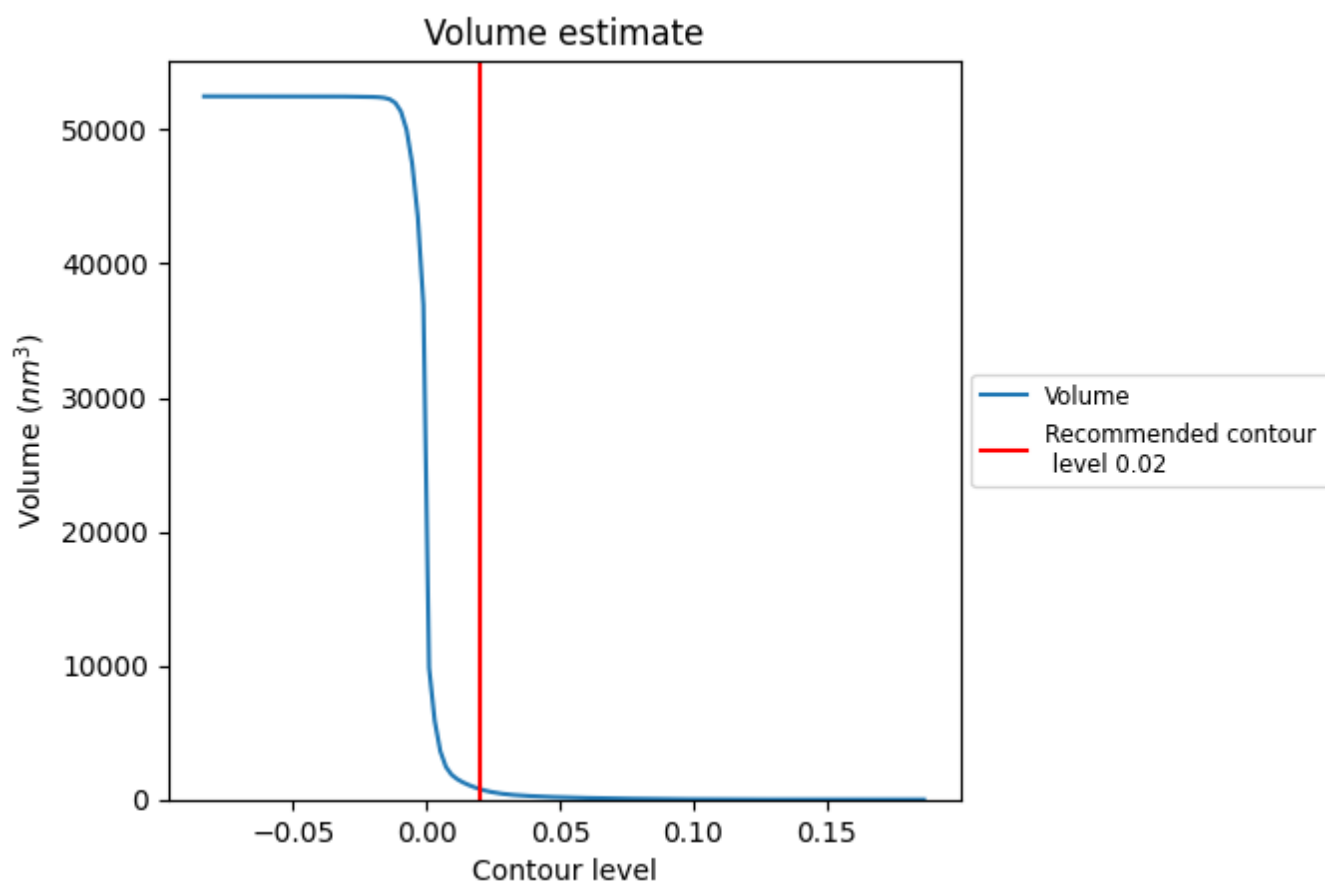
This section contains the results of statistical analysis of the map.

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.

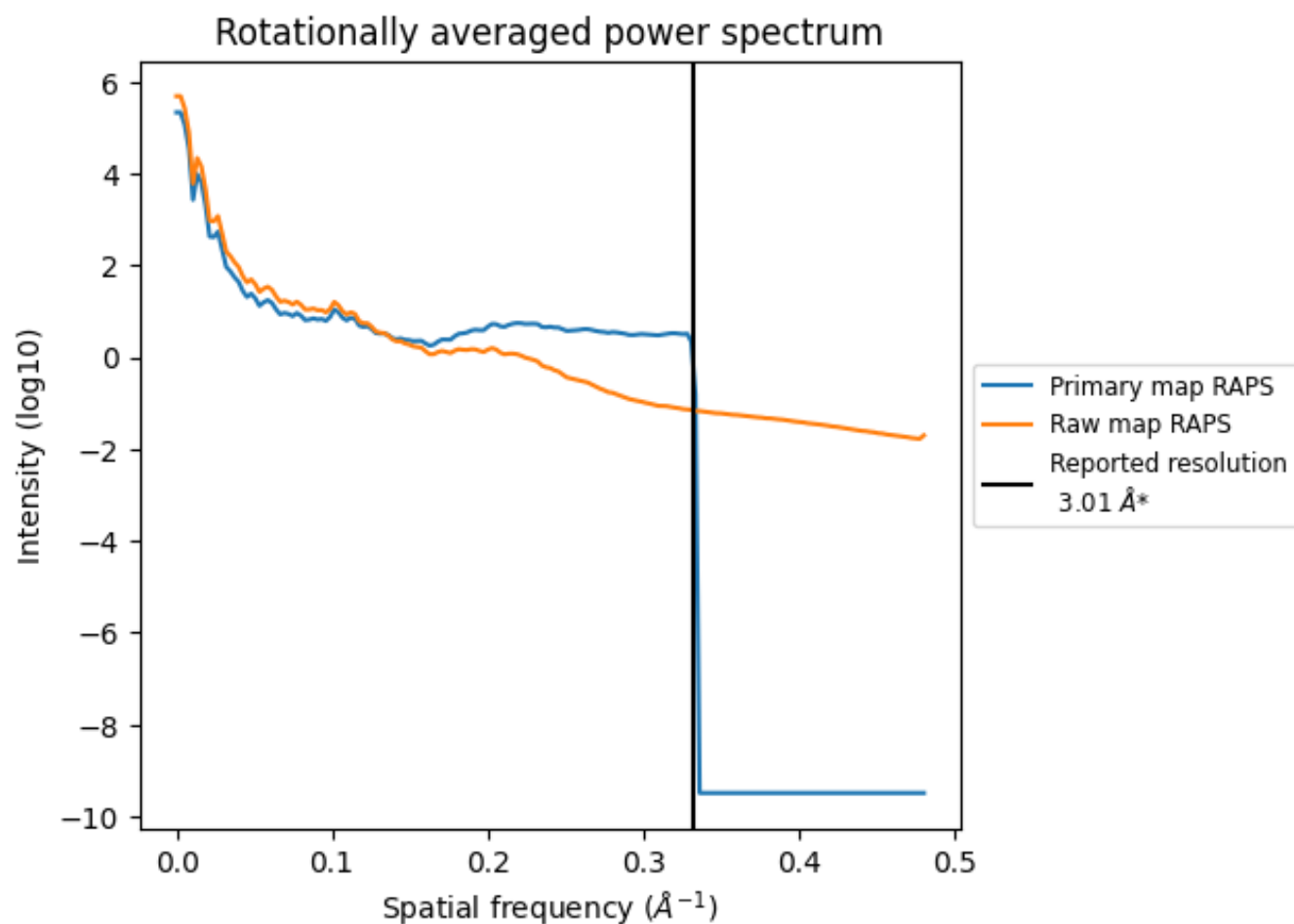
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 785 nm³; this corresponds to an approximate mass of 709 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 ⓘ

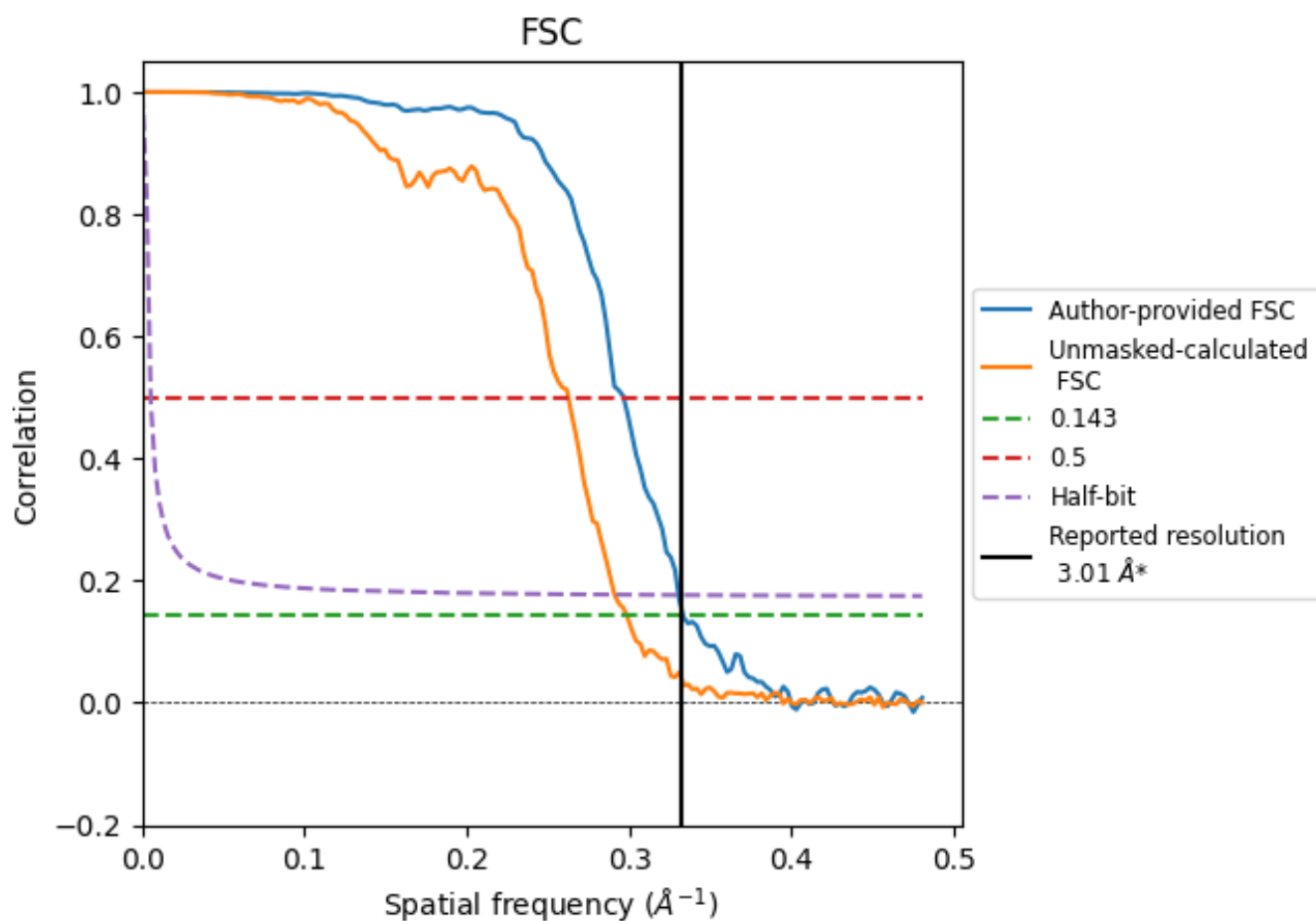


*Reported resolution corresponds to spatial frequency of 0.332 $\text{\AA}^{-1}$

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 $0.332 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

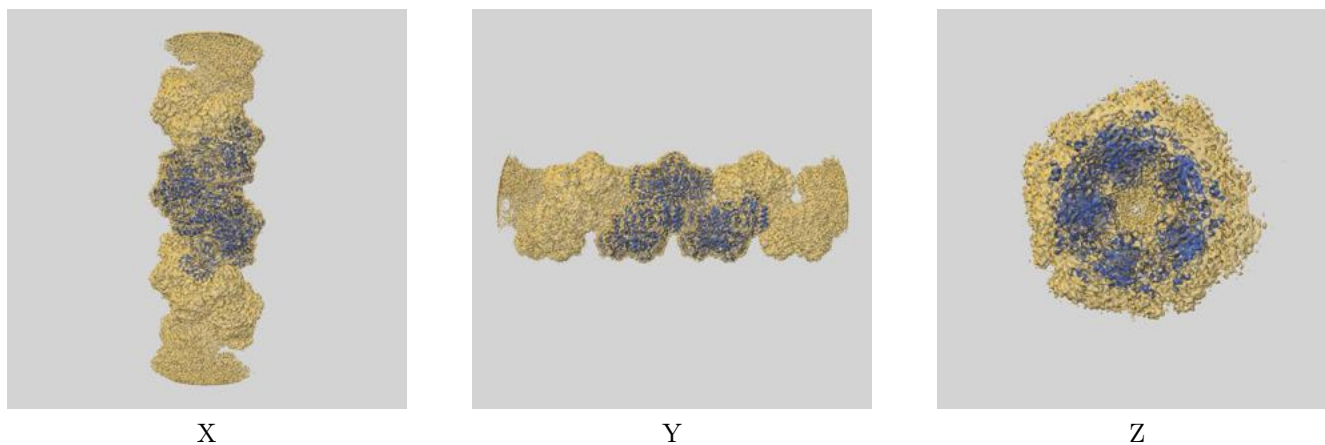
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.01	-	-
Author-provided FSC curve	3.00	3.37	3.02
Unmasked-calculated*	3.35	3.81	3.43

*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 3.35 differs from the reported value 3.01 by more than 10 %

9 Map-model fit [i](#)

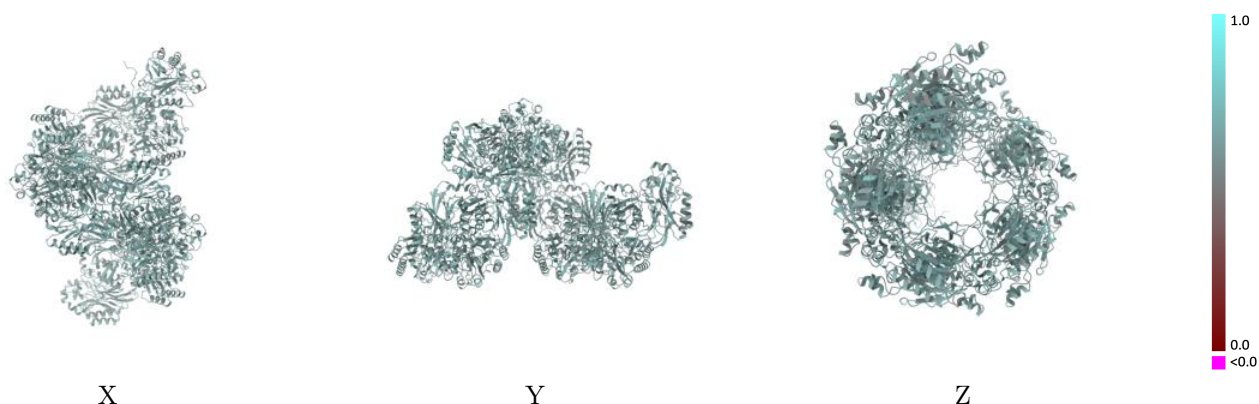
This section contains information regarding the fit between EMDB map EMD-42779 and PDB model 8UXU. Per-residue inclusion information can be found in [section 3](#) on [page 7](#).

9.1 Map-model overlay [i](#)



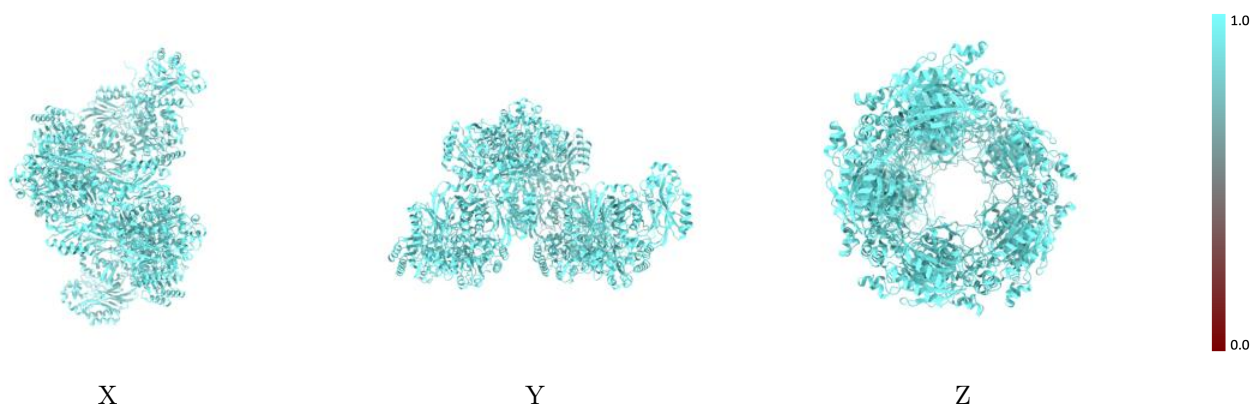
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



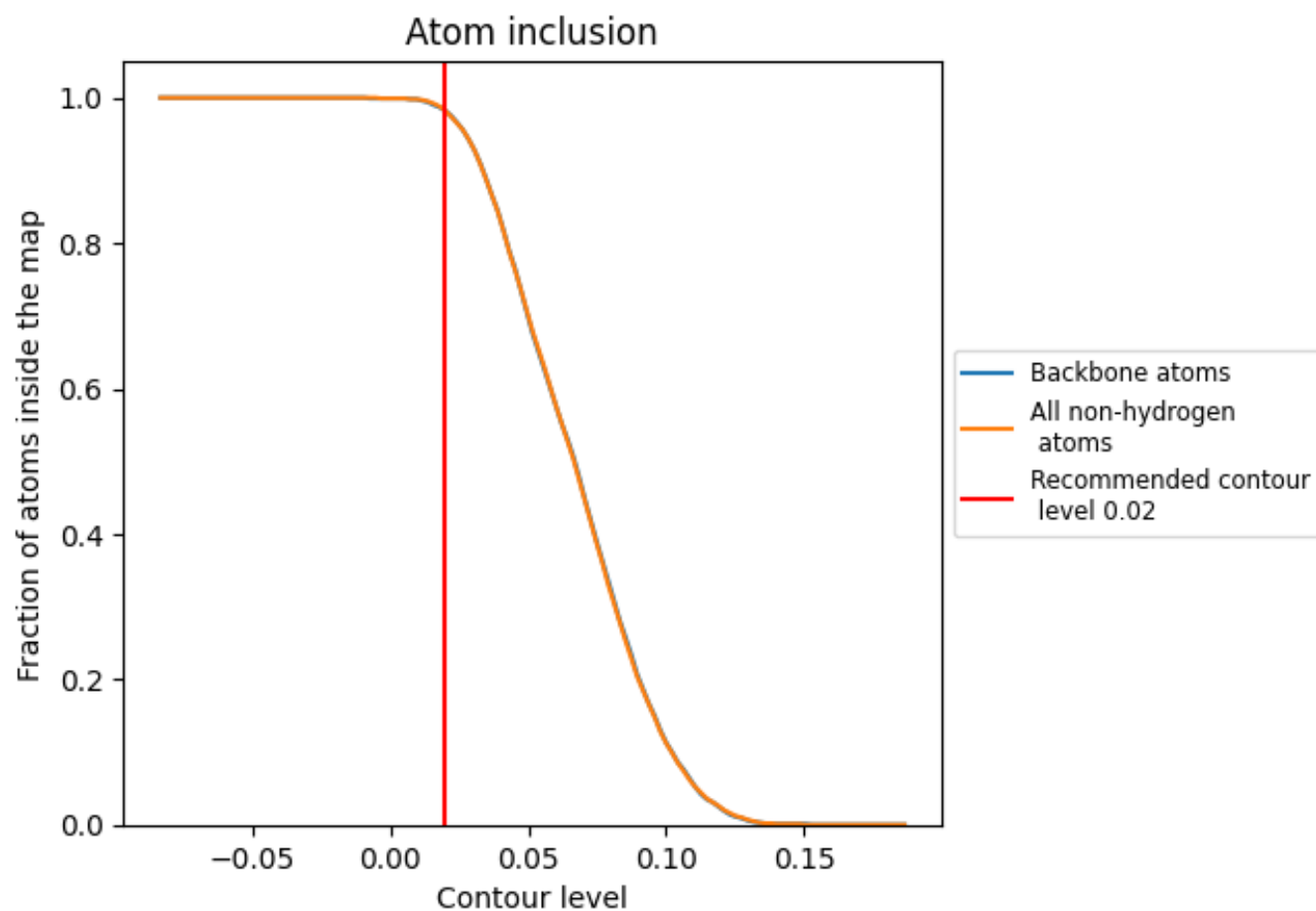
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.02).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 98% 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	0.9820	0.6040
A	0.9860	0.5970
B	0.9810	0.6010
C	0.9890	0.6060
D	0.9830	0.6070
E	0.9860	0.5920
F	0.9790	0.5960
G	0.9870	0.6090
H	0.9810	0.6060
I	0.9850	0.6010
J	0.9820	0.6000
K	0.9840	0.6110
L	0.9840	0.6070
M	0.9860	0.6080
N	0.9850	0.6090

1.0

0.0

<0.0