



wwPDB EM Validation Summary Report ⓘ

Apr 22, 2024 – 09:28 pm BST

PDB ID : 7AQO
EMDB ID : EMD-11871
Title : yeast THO-Sub2 complex dimer
Authors : Schuller, S.K.; Schuller, J.M.; Prabu, R.J.; Baumgartner, M.; Bonneau, F.;
basquin, J.; Conti, E.
Deposited on : 2020-10-22
Resolution : 4.50 Å(reported)
Based on initial model : 7APX

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:

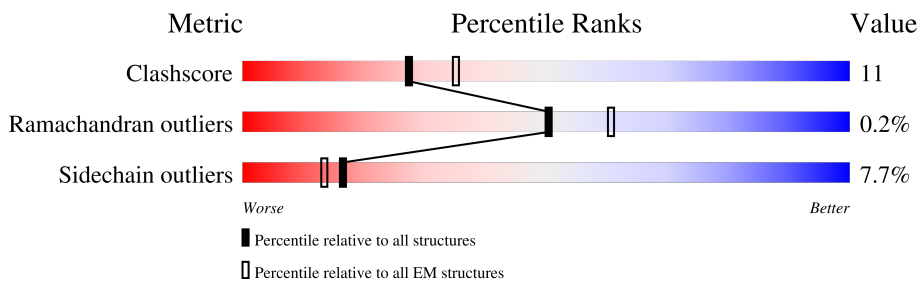
EMDB validation analysis : 0.0.1.dev92
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36.2

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 4.50 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.





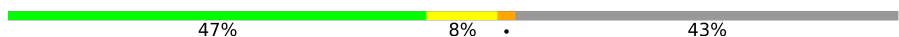
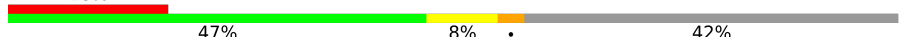
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	1601	
1	G	1601	
2	B	720	
2	H	720	
3	E	380	
3	K	380	
4	F	400	
4	L	400	

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Mol	Chain	Length	Quality of chain
5	C	261	 62% 19% 5% 13% 20%
5	J	261	 64% 19% 5% 12% 20%
6	D	392	 47% 8% 43% 18%
6	I	392	 47% 8% 42% 18%

2 Entry composition i

There are 6 unique types of molecules in this entry. The entry contains 40261 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 THO complex subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	G	1079	Total	C	N	O	S	0	0
			7785	5074	1304	1379	28		
1	A	1079	Total	C	N	O	S	0	0
			7785	5074	1304	1379	28		

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	-3	GLY	-	expression tag	UNP A0A6A5Q535
G	-2	ALA	-	expression tag	UNP A0A6A5Q535
G	-1	ALA	-	expression tag	UNP A0A6A5Q535
G	0	SER	-	expression tag	UNP A0A6A5Q535
A	-3	GLY	-	expression tag	UNP A0A6A5Q535
A	-2	ALA	-	expression tag	UNP A0A6A5Q535
A	-1	ALA	-	expression tag	UNP A0A6A5Q535
A	0	SER	-	expression tag	UNP A0A6A5Q535

- Molecule 2 is a protein called THO complex subunit HPR1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	H	563	Total	C	N	O	S	0	0
			4143	2713	693	721	16		
2	B	563	Total	C	N	O	S	0	0
			4143	2713	693	721	16		

- Molecule 3 is a protein called TEX1 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	K	348	Total	C	N	O	S	0	0
			2357	1530	402	414	11		
3	E	348	Total	C	N	O	S	0	0
			2357	1530	402	414	11		

- Molecule 4 is a protein called EM14S01-3B_G0007820.mRNA.1.CDS.1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	L	361	Total	C	N	O	S	0	0
			2818	1783	491	535	9		
4	F	361	Total	C	N	O	S	0	0
			2818	1783	491	535	9		

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	47	GLY	-	expression tag	UNP A0A6A5Q316
L	48	ALA	-	expression tag	UNP A0A6A5Q316
L	49	ALA	-	expression tag	UNP A0A6A5Q316
L	50	SER	-	expression tag	UNP A0A6A5Q316
F	47	GLY	-	expression tag	UNP A0A6A5Q316
F	48	ALA	-	expression tag	UNP A0A6A5Q316
F	49	ALA	-	expression tag	UNP A0A6A5Q316
F	50	SER	-	expression tag	UNP A0A6A5Q316

- Molecule 5 is a protein called BJ4_G0025130.mRNA.1.CDS.1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	J	230	Total	C	N	O	S	1	0
			1588	997	278	310	3		
5	C	227	Total	C	N	O	S	1	0
			1573	988	275	307	3		

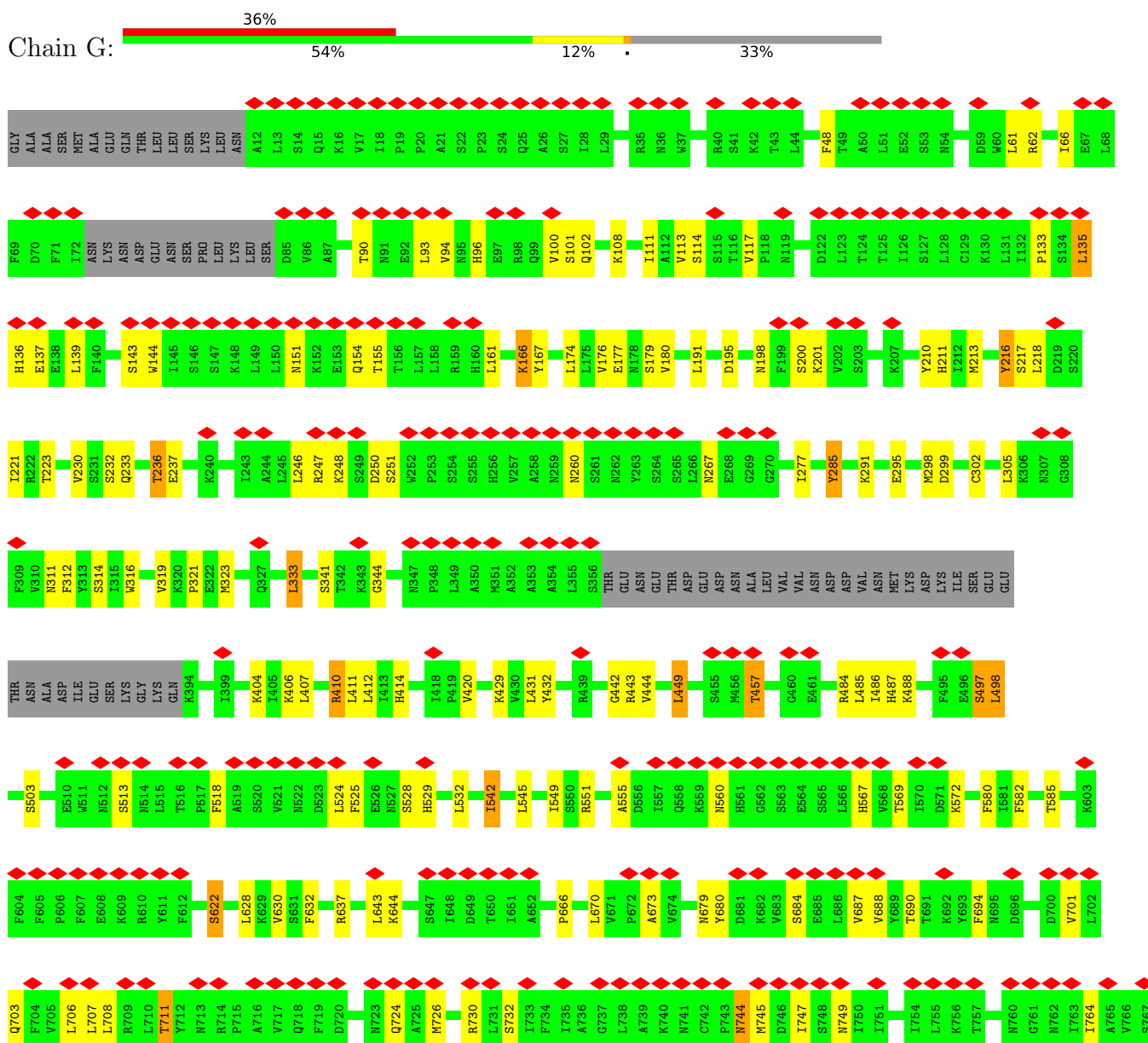
- Molecule 6 is a protein called THO complex subunit MFT1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	I	227	Total	C	N	O	S	0	0
			1452	902	267	282	1		
6	D	225	Total	C	N	O	S	0	0
			1442	896	265	280	1		

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: THO complex subunit 2

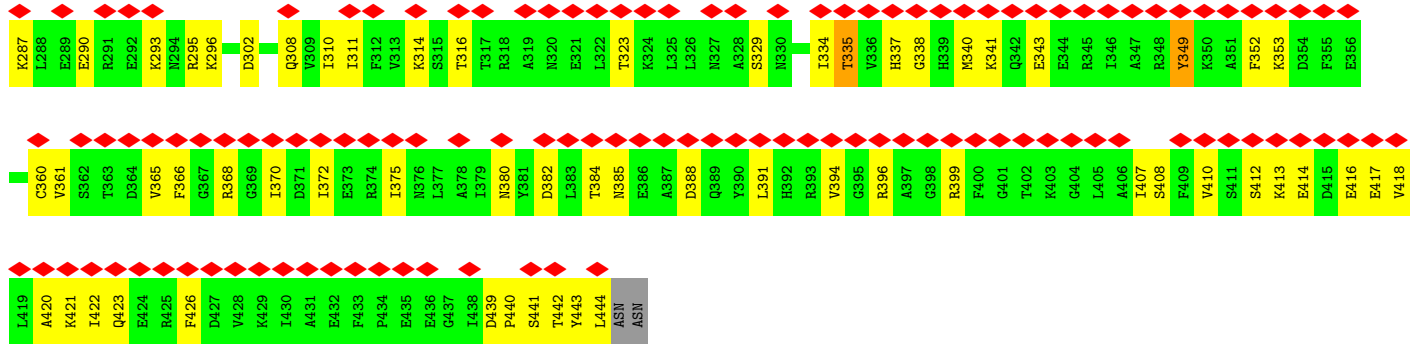


S134	L135	H136	E137	E138	L139	S143	W144	M151	Q154	T155	L158	L161	K166	Y167	E168	L169	L174	L175	V176	E177	N178	S179	V180	L191	D195	N198	K201	L206	Y210	H211	I212	M213	Y216	S217	L218	D219	S220	I221	R222	T223	V230	S231	S232	Q233						
T236	E237	L246	R247	K248	S249	D250	S251	M260	M267	I277	L285	K291	E295	M298	D299	C302	L305	N311	F312	Y313	S314	W316	F322	M323	L333	S341	G344	S356	THR	GLU	ASN	GLU	THR	ASP	GLU	ASN	ASN	ALA												
LEU	VAL	VAL	ASN	ASP	VAL	ASN	MET	LYS	ASP	ILE	SER	GLU	THR	ASN	ALA	ASP	ILE	GLU	SER	LYS	GLY	LYS	GLN	K394	L401	K404	I405	K406	L407	R410	L411	L412	I413	H414	V420	K425	K429	V430	L431	Y432	G442	R443	V444	L449	T457	R484				
L485	I486	H487	K488	S487	L488	S513	F518	L524	F525	S528	H529	L532	S533	I534	I542	L545	I549	S550	R551	A555	M560	H567	V568	T569	I570	D571	K572	F580	I581	F582	T585	S622	L630	S631	F632	R637	L643	K644	P666											
L670	A673	N679	Y680	S684	V687	Y688	Y689	T690	F694	W701	L702	Q703	L707	L708	I711	Q724	A725	M726	R730	L731	S732	M744	W745	D746	I747	S748	N749	K756	I764	I768	I773	L782	L791	M792	L793	M794	S797	Q801	R811											
S818	S819	R820	S823	I831	I834	N842	L843	N846	H851	Y852	K853	L854	L855	F869	I870	F871	L872	I873	C876	N883	T900	P901	W902	T903	I906	F907	R908	L915	F932	S941	F945	T946	T947	F948	R950	L951	S952	L953	H957	F958										
S971	GLY	ASN	THR	HIS	MET	ASN	THR	D992	L993	L994	W1018	ASN	LYS	ASN	ASP	CYS	GLY	E1024	K1028	L1031	Q1032	M1033	C1034	V1035	F1041	F1051	L1078	L1079	F1080	C1081	L1092	F1093	F1094	D1096	V1097	L1098	L1101	W1121	L1121	S952	M1143	M1148	V1151							
F1155	PRO	VAL	VAL	LYS	ALA	HIS	ILE	LEU	ASN	ARG	VAL	TYR	THR	ASN	ILE	LEU	LYS	LEU	ILE	LYS	PRO	SER	SER	ALA	ALA	GLY	HIS	LEU	ALA	LYS	ASP	ALA	LEU	LEU	GLU	LEU	VAL	ALA	SER	GLU	PHE	THR	THR	GLY	GLU	ALA				
GLU	GLN	LYS	ARG	ILE	ARG	GLU	MET	THR	ASN	TYR	LEU	THR	ASN	GLN	CYS	GLM	VAL	VAL	LEU	ARG	LYS	PRO	SER	GLM	GLN	LYS	SER	GLM	ASN	PRO	PRO	LYS	LEU	VAL	VAL	ALA	SER	GLY	GLY	ALA	GLU	GLY	GLY	ASP	LYS	ASP				
ARG	TYR	THR	TYR	SER	ARG	ASN	GLU	PRO	VAL	SER	THR	GLN	TRP	SER	TYR	ARG	THR	VAL	THR	LYS	VAL	THR	ILE	GLN	ARG	HIS	ASN	GLN	ALA	TYR	HIS	LYS	GLN	GLN	LYS	ALA	VAL	VAL	ASP	ASP	ASP	ASP	ASP	ASP	LEU	LEU				
SER	LYS	ASN	GLN	MET	ILE	PHE	ASN	THR	THR	LEU	PRO	THR	ARG	TYR	ASN	GLY	GLY	GLY	ASN	PRO	GLN	ASP	PRO	ASP	ASN	ASP	ALA	ALA	ASP	ALA	ILE	LYS	ASN	ASN	ILE	VAL	VAL	GLU	GLU	GLU	TYR	THR	THR	THR	THR	THR	TYR			
SER	GLY	ALA	ALA	PRO	TYR	THR	THR	TYR	THR	TYR	THR	GLY	ALA	GLY	GLY	GLY	GLY	GLY	ASP	TYR	ASN	ASP	PRO	PRO	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA		
SER	LYS	SER	LYS	THR	ASN	ASP	ASP	ARG	ARG	THR	PRO	ARG	ARG	TYR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	
ALA	ASN	PRO	GLN	ALA	SER	SER	LEU	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO
ASN	ARG	LYS	SER	THR	GLN	ALA	LEU	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO

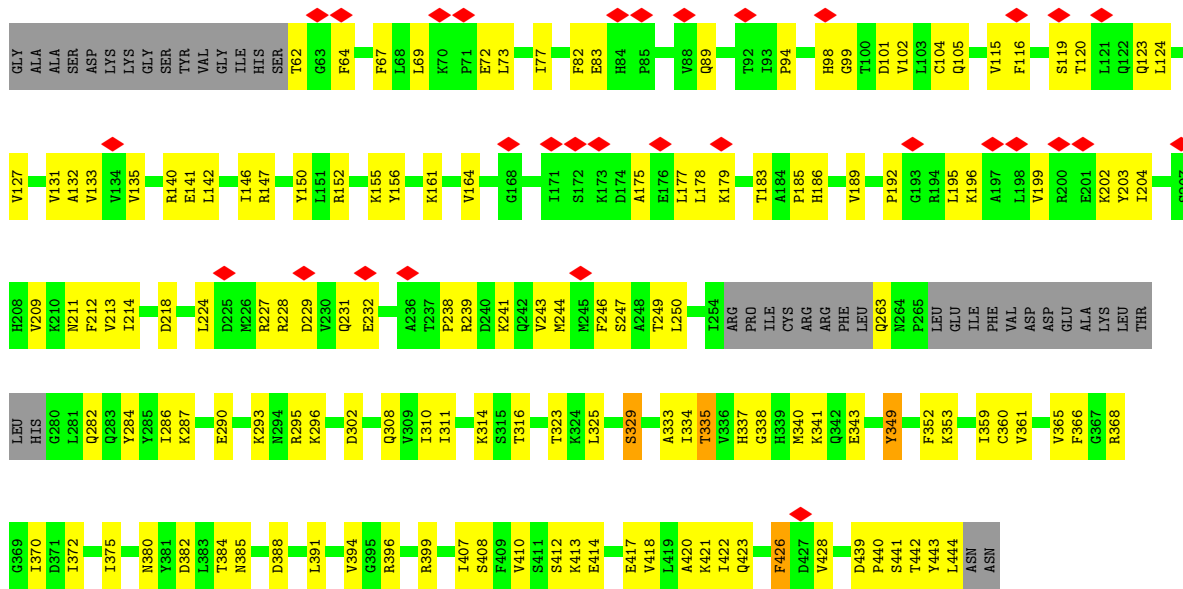
● Molecule 2: THO complex subunit HPR1



MET	S2	M3	T4	E5	E6	L7	I8	Q9	N10	S11	I12	G13	F14	L15	Q16	K17	T18	F19	K20	A21	L22	P23	V24	S25	F26	D27	S28	I29	H31	E32	P33	L34	P35	S36	S37	M38	L39	H40	A41	S42	V43	L44	N45	F46	E47	W48	E49	P50	L51	E52	K53	N54	I55	S56	A57	I58	H59	D60
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• Molecule 4: EM14S01-3B_G0007820.mRNA.1.CDS.1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	113076	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 ($e^-/\text{\AA}^2$)	55.0	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.789	Depositor
Minimum map value	-0.636	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.060	Depositor
Recommended contour level	0.25	Depositor
Map size (Å)	414.0, 414.0, 414.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.38, 1.38, 1.38	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	0.39	0/7953	0.48	0/10871
1	G	0.39	0/7953	0.48	0/10871
2	B	0.36	0/4246	0.46	0/5811
2	H	0.36	0/4246	0.46	0/5811
3	E	0.31	0/2411	0.47	0/3318
3	K	0.32	0/2411	0.47	0/3318
4	F	0.25	0/2862	0.46	0/3865
4	L	0.26	0/2862	0.46	0/3865
5	C	0.75	0/1595	0.84	0/2184
5	J	0.74	0/1609	0.83	0/2202
6	D	0.71	0/1454	0.79	1/1989 (0.1%)
6	I	0.68	0/1464	0.79	1/2003 (0.0%)
All	All	0.43	0/41066	0.54	2/56108 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
6	I	0	1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	I	81	THR	CB-CA-C	-6.00	95.40	111.60
6	D	81	THR	CB-CA-C	-5.98	95.47	111.60

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	I	206	ASN	Mainchain

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	7785	0	7050	140	0
1	G	7785	0	7050	132	0
2	B	4143	0	3661	76	0
2	H	4143	0	3661	76	0
3	E	2357	0	1985	28	0
3	K	2357	0	1985	30	0
4	F	2818	0	2793	102	0
4	L	2818	0	2793	99	0
5	C	1573	0	1319	77	0
5	J	1588	0	1324	77	0
6	D	1442	0	1153	46	0
6	I	1452	0	1157	48	0
All	All	40261	0	35931	824	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 11.

The worst 5 of 824 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)
5:C:67:ARG:O	5:C:71:ASP:OD1	1.58	1.21
5:J:67:ARG:O	5:J:71:ASP:OD1	1.58	1.20
3:K:50:SER:CB	3:E:46:ILE:HD12	1.71	1.20
5:C:117:TYR:CZ	6:D:120:ARG:HD3	1.84	1.12
5:J:117:TYR:CZ	6:I:120:ARG:HD3	1.84	1.11

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	1069/1601 (67%)	1002 (94%)	66 (6%)	1 (0%)	51	85
1	G	1069/1601 (67%)	1002 (94%)	66 (6%)	1 (0%)	51	85
2	B	555/720 (77%)	503 (91%)	51 (9%)	1 (0%)	47	81
2	H	555/720 (77%)	503 (91%)	51 (9%)	1 (0%)	47	81
3	E	344/380 (90%)	320 (93%)	24 (7%)	0	100	100
3	K	344/380 (90%)	320 (93%)	24 (7%)	0	100	100
4	F	355/400 (89%)	346 (98%)	9 (2%)	0	100	100
4	L	355/400 (89%)	346 (98%)	9 (2%)	0	100	100
5	C	224/261 (86%)	211 (94%)	9 (4%)	4 (2%)	8	42
5	J	225/261 (86%)	213 (95%)	9 (4%)	3 (1%)	12	48
6	D	221/392 (56%)	208 (94%)	12 (5%)	1 (0%)	29	68
6	I	223/392 (57%)	210 (94%)	12 (5%)	1 (0%)	34	72
All	All	5539/7508 (74%)	5184 (94%)	342 (6%)	13 (0%)	50	81

5 of 13 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	G	993	ILE
1	A	993	ILE
5	C	194	TYR
2	H	442	GLU
2	B	442	GLU

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	702/1468 (48%)	640 (91%)	62 (9%)	10	33
1	G	702/1468 (48%)	640 (91%)	62 (9%)	10	33
2	B	367/670 (55%)	343 (94%)	24 (6%)	17	44
2	H	367/670 (55%)	343 (94%)	24 (6%)	17	44
3	E	186/344 (54%)	172 (92%)	14 (8%)	13	40
3	K	186/344 (54%)	171 (92%)	15 (8%)	11	37
4	F	299/351 (85%)	293 (98%)	6 (2%)	55	73
4	L	299/351 (85%)	293 (98%)	6 (2%)	55	73
5	C	129/242 (53%)	112 (87%)	17 (13%)	4	20
5	J	129/242 (53%)	112 (87%)	17 (13%)	4	20
6	D	102/363 (28%)	88 (86%)	14 (14%)	3	19
6	I	102/363 (28%)	88 (86%)	14 (14%)	3	19
All	All	3570/6876 (52%)	3295 (92%)	275 (8%)	16	39

5 of 275 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	I	22	THR
6	I	109	ASP
5	C	176	ASN
3	K	309	ILE
3	K	248	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 79 such sidechains are listed below:

Mol	Chain	Res	Type
4	F	186	HIS
5	C	109	HIS
4	F	385	ASN
5	J	180	GLN
6	D	25	ASN

5.3.3 RNA

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
5	J	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	J	235:LYS	C	236:ILE	N	3.04

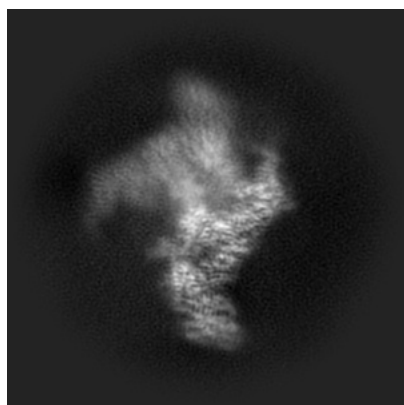
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11871. These allow visual inspection of the internal detail of the map and identification of artifacts.

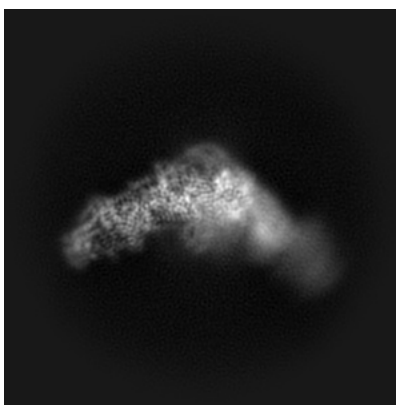
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

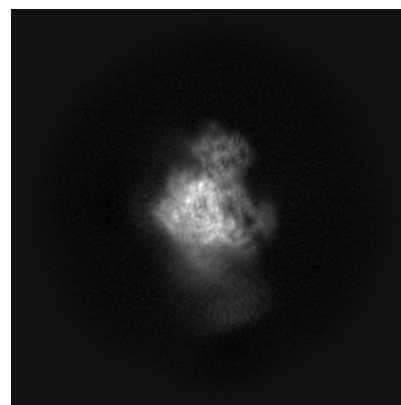
6.1.1 Primary map



X



Y

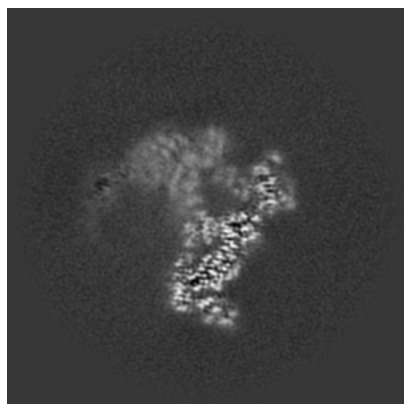


Z

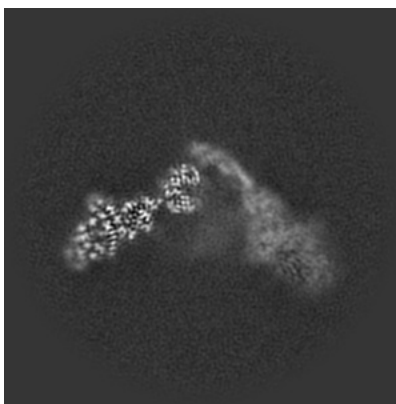
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

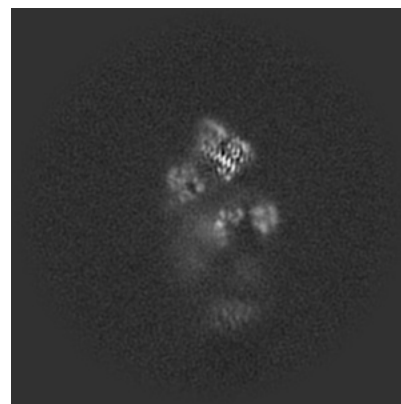
6.2.1 Primary map



X Index: 150



Y Index: 150

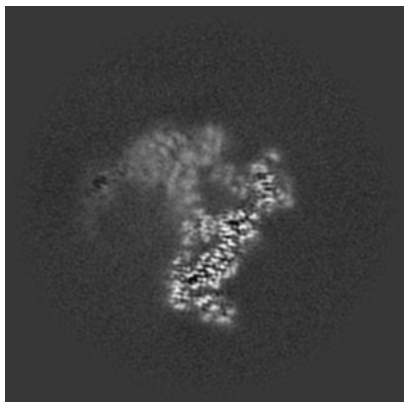


Z Index: 150

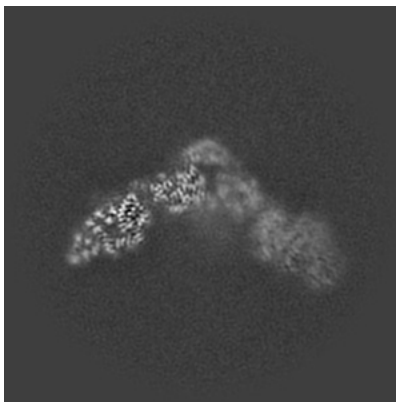
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

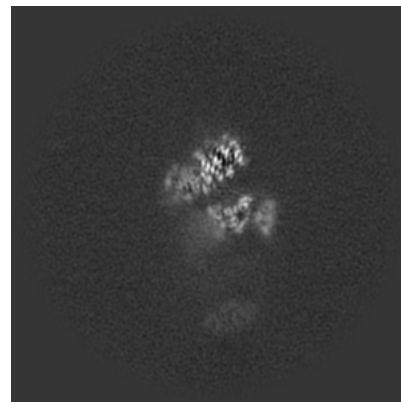
6.3.1 Primary map



X Index: 150



Y Index: 141



Z Index: 144

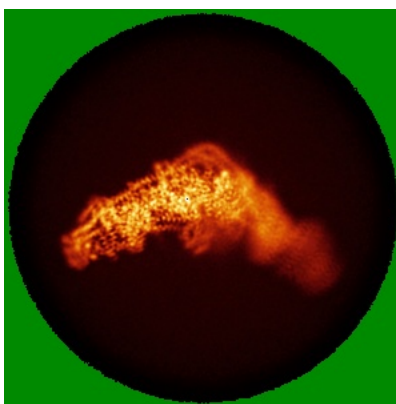
The images above show the largest variance slices of the map in three orthogonal directions.

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

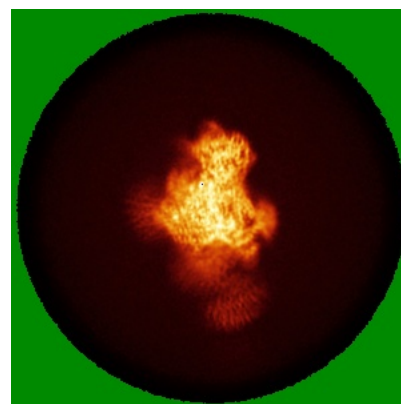
6.4.1 Primary map



X



Y

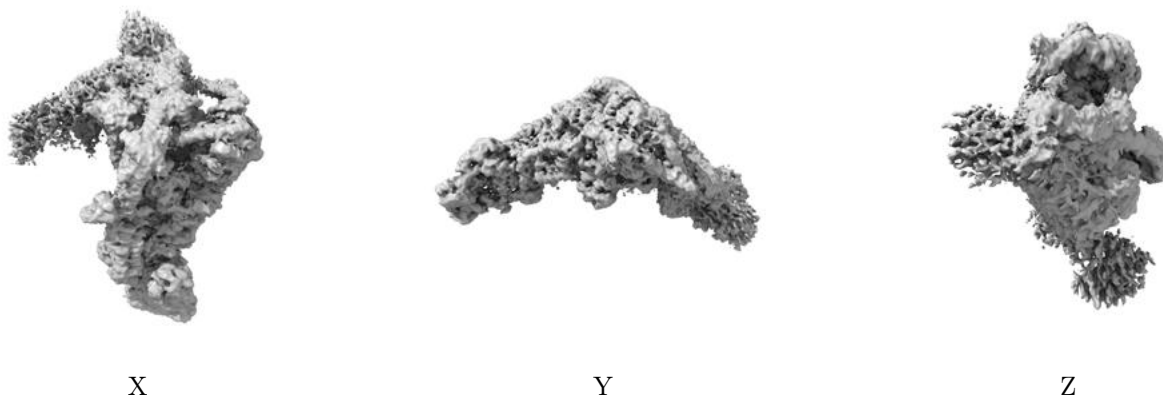


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.25. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

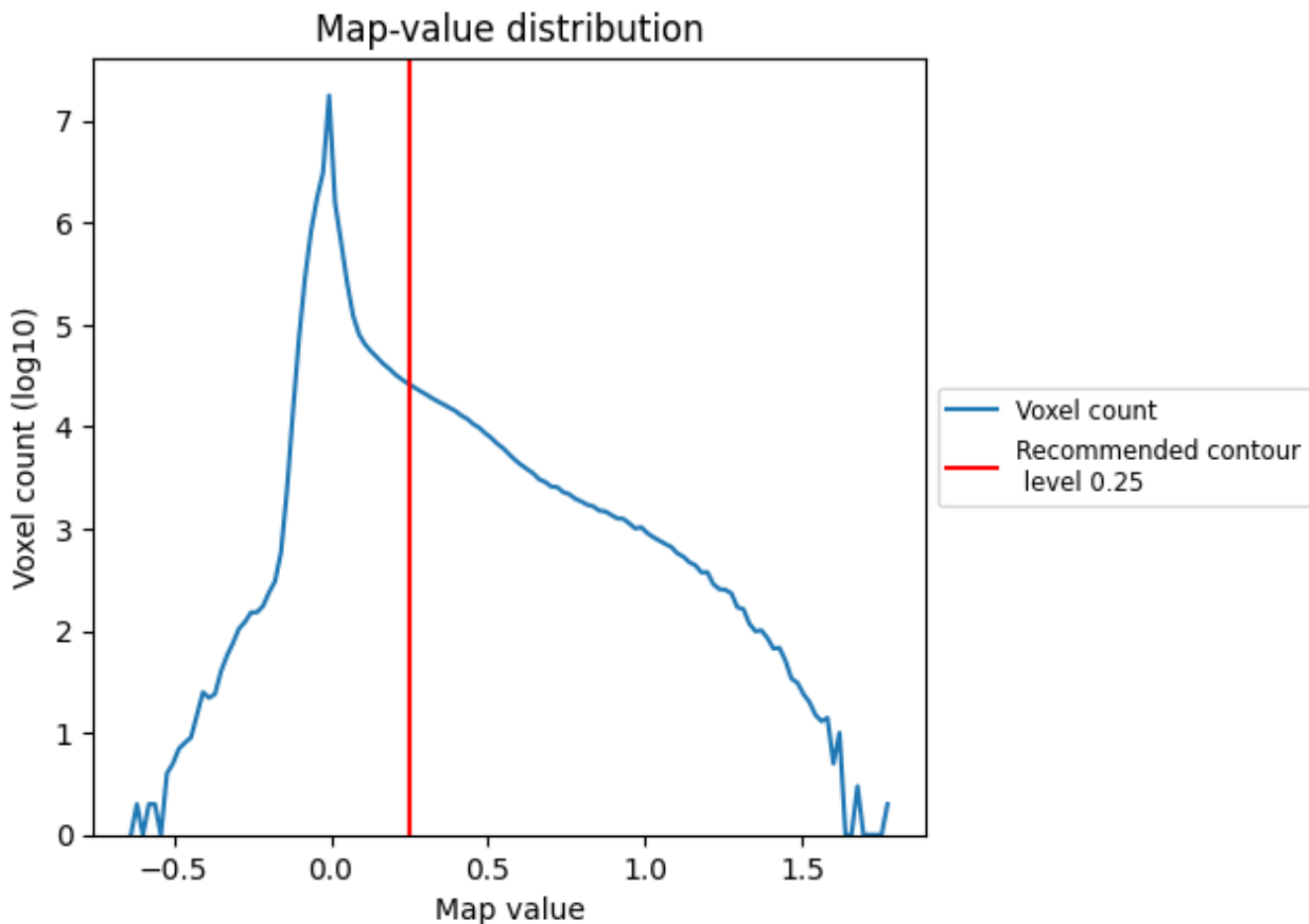
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

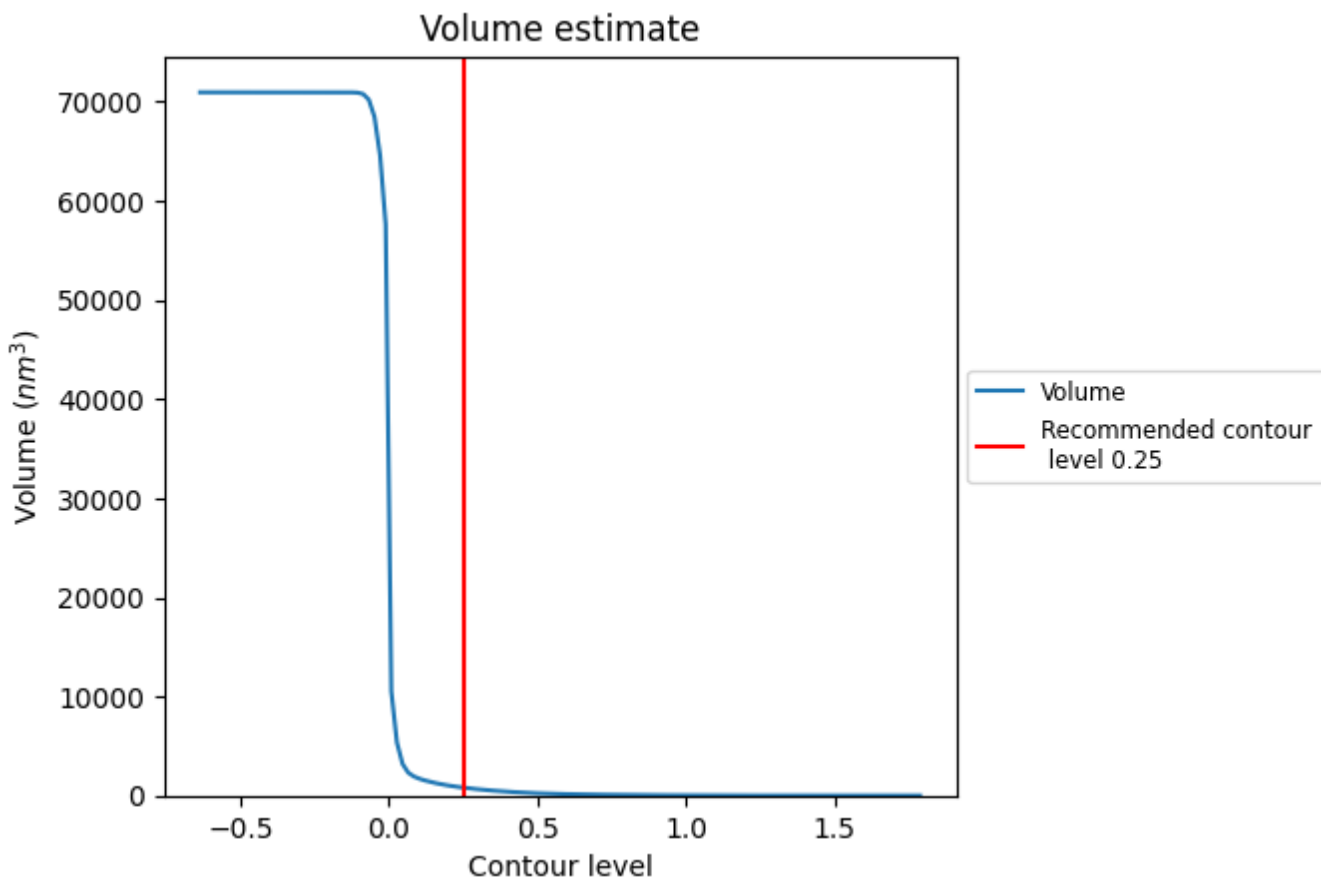
This section contains the results of statistical analysis of the map.

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.

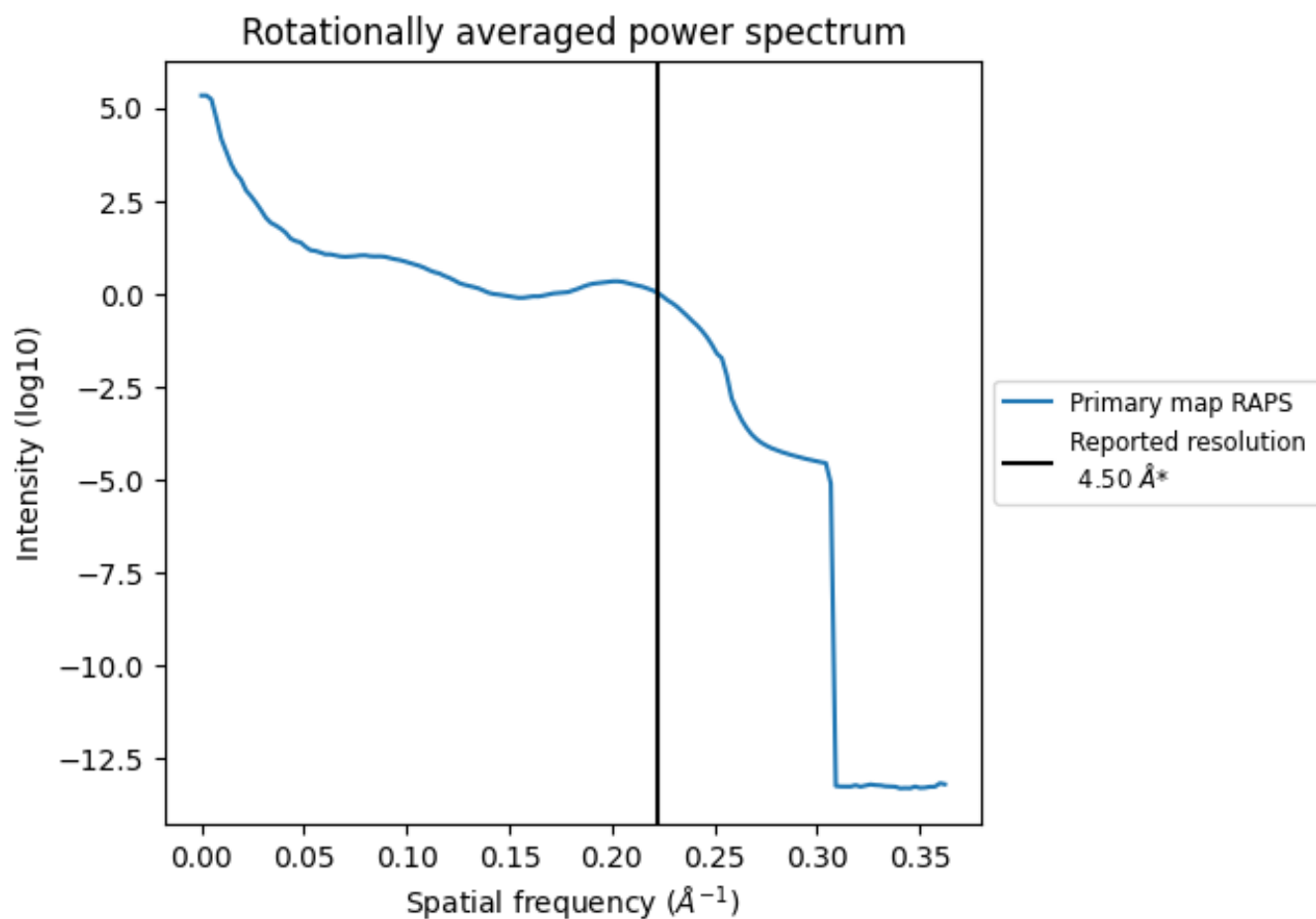
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 804 nm³; this corresponds to an approximate mass of 726 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum [i](#)



*Reported resolution corresponds to spatial frequency of 0.222\AA^{-1}

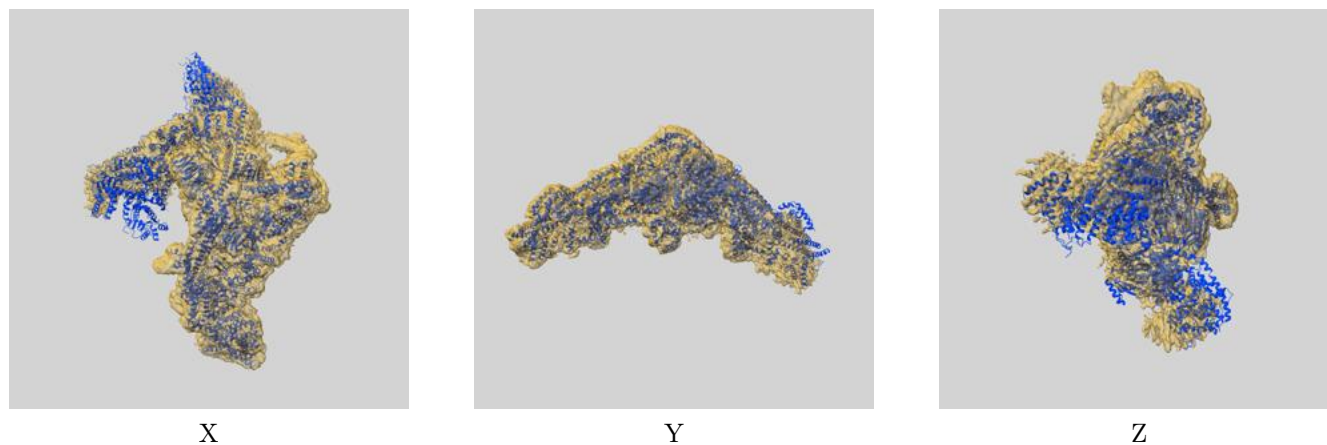
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

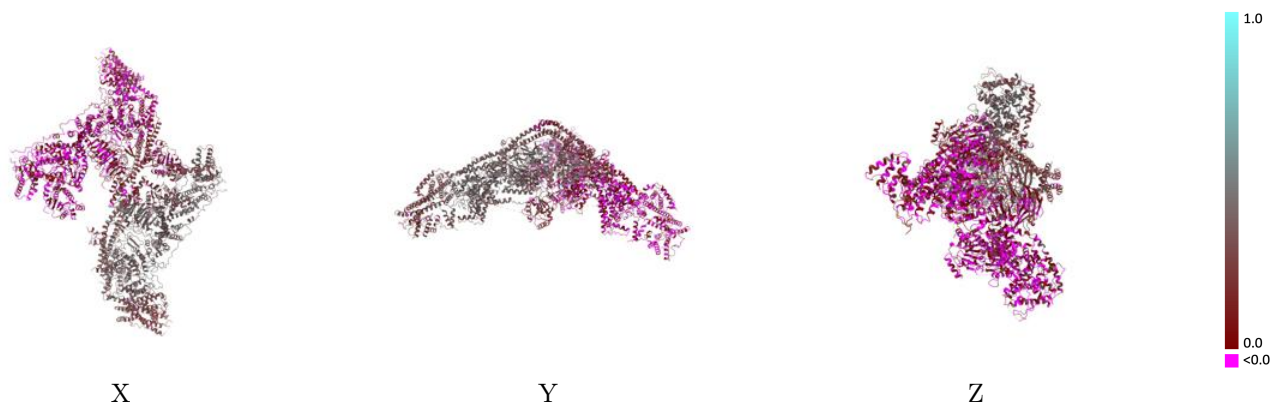
This section contains information regarding the fit between EMDB map EMD-11871 and PDB model 7AQO. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlay [i](#)



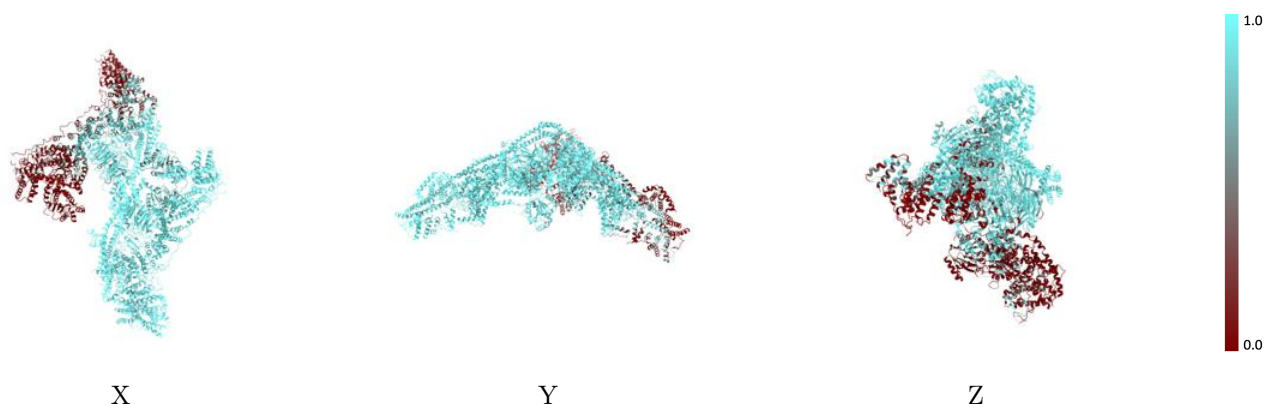
The images above show the 3D surface view of the map at the recommended contour level 0.25 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



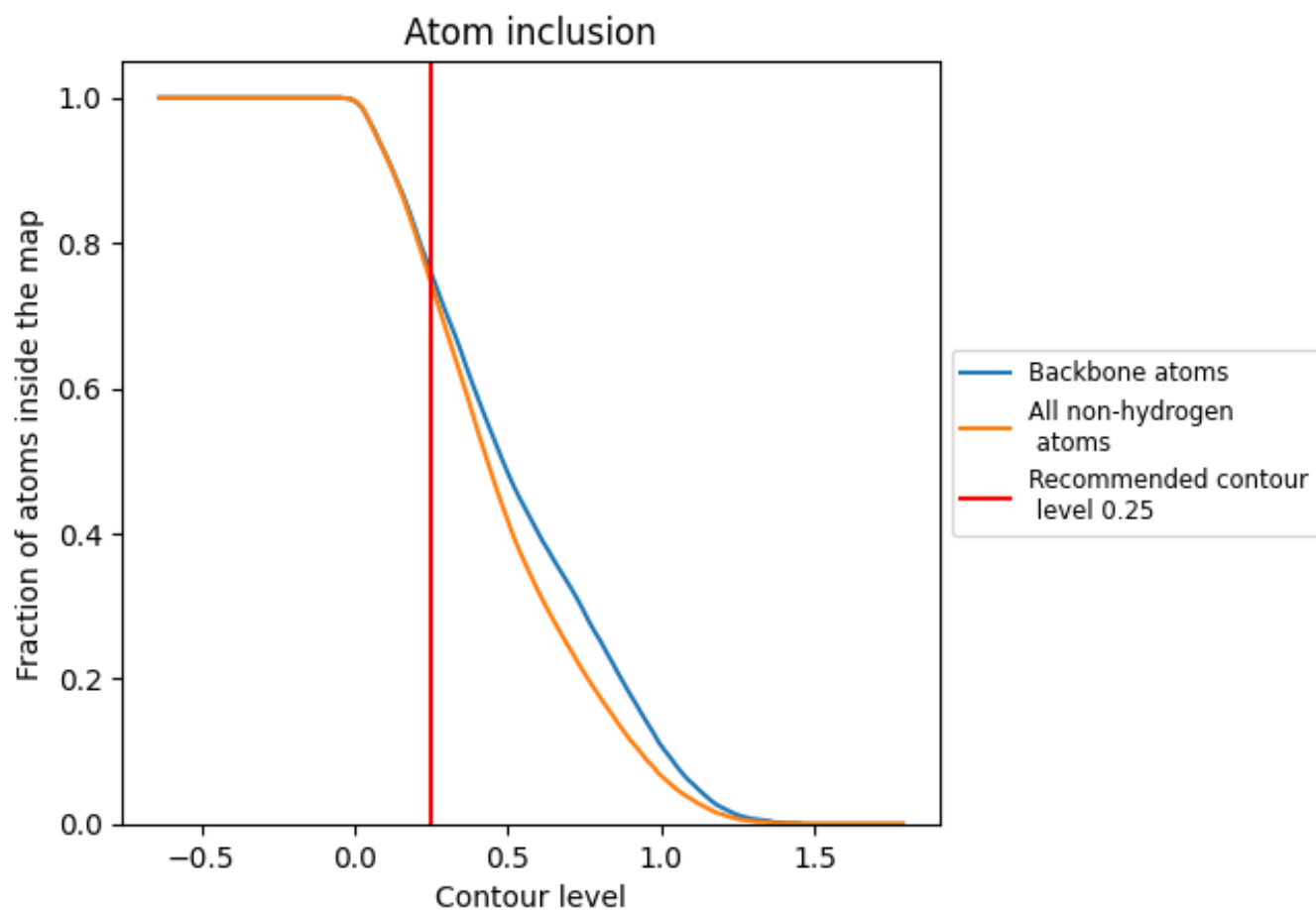
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.25).



























9.4 Atom inclusion [i](#)



At the recommended contour level, 76% of all backbone atoms, 74% 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 (0.25) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7450	 0.1890
A	 0.9870	 0.3920
B	 0.9820	 0.3790
C	 0.9700	 0.3400
D	 0.9740	 0.3130
E	 0.9930	 0.4000
F	 0.8170	 0.1320
G	 0.4690	 0.0170
H	 0.5790	 0.0200
I	 0.6440	 0.0790
J	 0.7470	 0.0910
K	 0.9340	 0.0960
L	 0.1040	 0.0020

