



Full wwPDB EM Validation Report ⓘ

Jun 3, 2024 – 05:17 PM EDT

PDB ID : 8T15
EMDB ID : EMD-40955
Title : Cryo-EM structure of dodecameric hub domain of CaMKII alpha
Authors : Chien, C.-T.; Chiu, W.; Khan, S.
Deposited on : 2023-06-01
Resolution : 2.70 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.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

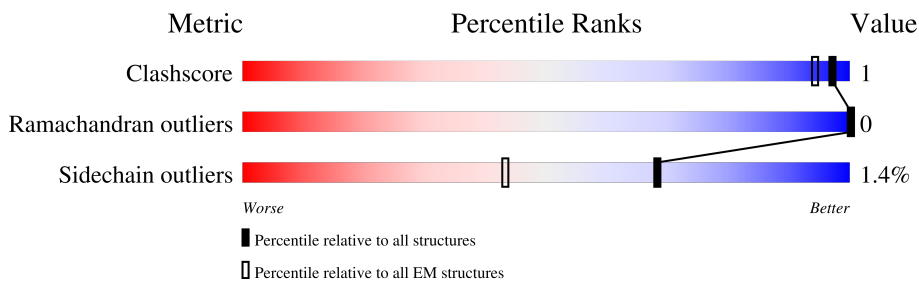
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.70 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	407	32% 67%
1	B	407	32% 67%
1	C	407	32% 67%
1	D	407	32% 67%
1	E	407	32% 67%
1	F	407	32% 67%
1	G	407	32% 67%
1	H	407	32% 67%

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Mol	Chain	Length	Quality of chain
1	I	407	
1	J	407	
1	K	407	
1	L	407	

2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 25656 atoms, of which 12612 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 Venus-tagged CaMKII Alpha Association Domain.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
1	A	134	2138	688	1051	195	199	5	0	0
1	B	134	2138	688	1051	195	199	5	0	0
1	C	134	2138	688	1051	195	199	5	0	0
1	D	134	2138	688	1051	195	199	5	0	0
1	E	134	2138	688	1051	195	199	5	0	0
1	F	134	2138	688	1051	195	199	5	0	0
1	G	134	2138	688	1051	195	199	5	0	0
1	H	134	2138	688	1051	195	199	5	0	0
1	I	134	2138	688	1051	195	199	5	0	0
1	J	134	2138	688	1051	195	199	5	0	0
1	K	134	2138	688	1051	195	199	5	0	0
1	L	134	2138	688	1051	195	199	5	0	0

There are 564 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	72	MET	-	initiating methionine	UNP P42212
A	73	GLY	-	expression tag	UNP P42212
A	74	SER	-	expression tag	UNP P42212
A	75	SER	-	expression tag	UNP P42212
A	76	HIS	-	expression tag	UNP P42212
A	77	HIS	-	expression tag	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
A	78	HIS	-	expression tag	UNP P42212
A	79	HIS	-	expression tag	UNP P42212
A	80	HIS	-	expression tag	UNP P42212
A	81	HIS	-	expression tag	UNP P42212
A	82	SER	-	expression tag	UNP P42212
A	83	SER	-	expression tag	UNP P42212
A	84	GLY	-	expression tag	UNP P42212
A	85	LEU	-	expression tag	UNP P42212
A	86	VAL	-	expression tag	UNP P42212
A	87	PRO	-	expression tag	UNP P42212
A	88	ARG	-	expression tag	UNP P42212
A	89	GLY	-	expression tag	UNP P42212
A	90	SER	-	expression tag	UNP P42212
A	91	HIS	-	expression tag	UNP P42212
A	92	VAL	-	expression tag	UNP P42212
A	137	LEU	PHE	conflict	UNP P42212
A	155	LEU	PHE	conflict	UNP P42212
A	156	GLY	SER	conflict	UNP P42212
A	159	LEU	VAL	conflict	UNP P42212
A	163	ALA	SER	conflict	UNP P42212
A	244	THR	MET	conflict	UNP P42212
A	254	ALA	VAL	conflict	UNP P42212
A	266	GLY	SER	conflict	UNP P42212
A	294	TYR	THR	conflict	UNP P42212
A	297	LYS	ALA	conflict	UNP P42212
A	322	LEU	HIS	conflict	UNP P42212
A	330	SER	-	linker	UNP P42212
A	331	GLY	-	linker	UNP P42212
A	332	LEU	-	linker	UNP P42212
A	333	ARG	-	linker	UNP P42212
A	334	SER	-	linker	UNP P42212
A	335	ARG	-	linker	UNP P42212
A	336	ALA	-	linker	UNP P42212
A	337	GLN	-	linker	UNP P42212
A	338	ALA	-	linker	UNP P42212
A	339	SER	-	linker	UNP P42212
A	340	ASN	-	linker	UNP P42212
A	341	SER	-	linker	UNP P42212
A	342	ALA	-	linker	UNP P42212
A	343	VAL	-	linker	UNP P42212
A	344	ASP	-	linker	UNP P42212
B	72	MET	-	initiating methionine	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
B	73	GLY	-	expression tag	UNP P42212
B	74	SER	-	expression tag	UNP P42212
B	75	SER	-	expression tag	UNP P42212
B	76	HIS	-	expression tag	UNP P42212
B	77	HIS	-	expression tag	UNP P42212
B	78	HIS	-	expression tag	UNP P42212
B	79	HIS	-	expression tag	UNP P42212
B	80	HIS	-	expression tag	UNP P42212
B	81	HIS	-	expression tag	UNP P42212
B	82	SER	-	expression tag	UNP P42212
B	83	SER	-	expression tag	UNP P42212
B	84	GLY	-	expression tag	UNP P42212
B	85	LEU	-	expression tag	UNP P42212
B	86	VAL	-	expression tag	UNP P42212
B	87	PRO	-	expression tag	UNP P42212
B	88	ARG	-	expression tag	UNP P42212
B	89	GLY	-	expression tag	UNP P42212
B	90	SER	-	expression tag	UNP P42212
B	91	HIS	-	expression tag	UNP P42212
B	92	VAL	-	expression tag	UNP P42212
B	137	LEU	PHE	conflict	UNP P42212
B	155	LEU	PHE	conflict	UNP P42212
B	156	GLY	SER	conflict	UNP P42212
B	159	LEU	VAL	conflict	UNP P42212
B	163	ALA	SER	conflict	UNP P42212
B	244	THR	MET	conflict	UNP P42212
B	254	ALA	VAL	conflict	UNP P42212
B	266	GLY	SER	conflict	UNP P42212
B	294	TYR	THR	conflict	UNP P42212
B	297	LYS	ALA	conflict	UNP P42212
B	322	LEU	HIS	conflict	UNP P42212
B	330	SER	-	linker	UNP P42212
B	331	GLY	-	linker	UNP P42212
B	332	LEU	-	linker	UNP P42212
B	333	ARG	-	linker	UNP P42212
B	334	SER	-	linker	UNP P42212
B	335	ARG	-	linker	UNP P42212
B	336	ALA	-	linker	UNP P42212
B	337	GLN	-	linker	UNP P42212
B	338	ALA	-	linker	UNP P42212
B	339	SER	-	linker	UNP P42212
B	340	ASN	-	linker	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
B	341	SER	-	linker	UNP P42212
B	342	ALA	-	linker	UNP P42212
B	343	VAL	-	linker	UNP P42212
B	344	ASP	-	linker	UNP P42212
C	72	MET	-	initiating methionine	UNP P42212
C	73	GLY	-	expression tag	UNP P42212
C	74	SER	-	expression tag	UNP P42212
C	75	SER	-	expression tag	UNP P42212
C	76	HIS	-	expression tag	UNP P42212
C	77	HIS	-	expression tag	UNP P42212
C	78	HIS	-	expression tag	UNP P42212
C	79	HIS	-	expression tag	UNP P42212
C	80	HIS	-	expression tag	UNP P42212
C	81	HIS	-	expression tag	UNP P42212
C	82	SER	-	expression tag	UNP P42212
C	83	SER	-	expression tag	UNP P42212
C	84	GLY	-	expression tag	UNP P42212
C	85	LEU	-	expression tag	UNP P42212
C	86	VAL	-	expression tag	UNP P42212
C	87	PRO	-	expression tag	UNP P42212
C	88	ARG	-	expression tag	UNP P42212
C	89	GLY	-	expression tag	UNP P42212
C	90	SER	-	expression tag	UNP P42212
C	91	HIS	-	expression tag	UNP P42212
C	92	VAL	-	expression tag	UNP P42212
C	137	LEU	PHE	conflict	UNP P42212
C	155	LEU	PHE	conflict	UNP P42212
C	156	GLY	SER	conflict	UNP P42212
C	159	LEU	VAL	conflict	UNP P42212
C	163	ALA	SER	conflict	UNP P42212
C	244	THR	MET	conflict	UNP P42212
C	254	ALA	VAL	conflict	UNP P42212
C	266	GLY	SER	conflict	UNP P42212
C	294	TYR	THR	conflict	UNP P42212
C	297	LYS	ALA	conflict	UNP P42212
C	322	LEU	HIS	conflict	UNP P42212
C	330	SER	-	linker	UNP P42212
C	331	GLY	-	linker	UNP P42212
C	332	LEU	-	linker	UNP P42212
C	333	ARG	-	linker	UNP P42212
C	334	SER	-	linker	UNP P42212
C	335	ARG	-	linker	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
C	336	ALA	-	linker	UNP P42212
C	337	GLN	-	linker	UNP P42212
C	338	ALA	-	linker	UNP P42212
C	339	SER	-	linker	UNP P42212
C	340	ASN	-	linker	UNP P42212
C	341	SER	-	linker	UNP P42212
C	342	ALA	-	linker	UNP P42212
C	343	VAL	-	linker	UNP P42212
C	344	ASP	-	linker	UNP P42212
D	72	MET	-	initiating methionine	UNP P42212
D	73	GLY	-	expression tag	UNP P42212
D	74	SER	-	expression tag	UNP P42212
D	75	SER	-	expression tag	UNP P42212
D	76	HIS	-	expression tag	UNP P42212
D	77	HIS	-	expression tag	UNP P42212
D	78	HIS	-	expression tag	UNP P42212
D	79	HIS	-	expression tag	UNP P42212
D	80	HIS	-	expression tag	UNP P42212
D	81	HIS	-	expression tag	UNP P42212
D	82	SER	-	expression tag	UNP P42212
D	83	SER	-	expression tag	UNP P42212
D	84	GLY	-	expression tag	UNP P42212
D	85	LEU	-	expression tag	UNP P42212
D	86	VAL	-	expression tag	UNP P42212
D	87	PRO	-	expression tag	UNP P42212
D	88	ARG	-	expression tag	UNP P42212
D	89	GLY	-	expression tag	UNP P42212
D	90	SER	-	expression tag	UNP P42212
D	91	HIS	-	expression tag	UNP P42212
D	92	VAL	-	expression tag	UNP P42212
D	137	LEU	PHE	conflict	UNP P42212
D	155	LEU	PHE	conflict	UNP P42212
D	156	GLY	SER	conflict	UNP P42212
D	159	LEU	VAL	conflict	UNP P42212
D	163	ALA	SER	conflict	UNP P42212
D	244	THR	MET	conflict	UNP P42212
D	254	ALA	VAL	conflict	UNP P42212
D	266	GLY	SER	conflict	UNP P42212
D	294	TYR	THR	conflict	UNP P42212
D	297	LYS	ALA	conflict	UNP P42212
D	322	LEU	HIS	conflict	UNP P42212
D	330	SER	-	linker	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
D	331	GLY	-	linker	UNP P42212
D	332	LEU	-	linker	UNP P42212
D	333	ARG	-	linker	UNP P42212
D	334	SER	-	linker	UNP P42212
D	335	ARG	-	linker	UNP P42212
D	336	ALA	-	linker	UNP P42212
D	337	GLN	-	linker	UNP P42212
D	338	ALA	-	linker	UNP P42212
D	339	SER	-	linker	UNP P42212
D	340	ASN	-	linker	UNP P42212
D	341	SER	-	linker	UNP P42212
D	342	ALA	-	linker	UNP P42212
D	343	VAL	-	linker	UNP P42212
D	344	ASP	-	linker	UNP P42212
E	72	MET	-	initiating methionine	UNP P42212
E	73	GLY	-	expression tag	UNP P42212
E	74	SER	-	expression tag	UNP P42212
E	75	SER	-	expression tag	UNP P42212
E	76	HIS	-	expression tag	UNP P42212
E	77	HIS	-	expression tag	UNP P42212
E	78	HIS	-	expression tag	UNP P42212
E	79	HIS	-	expression tag	UNP P42212
E	80	HIS	-	expression tag	UNP P42212
E	81	HIS	-	expression tag	UNP P42212
E	82	SER	-	expression tag	UNP P42212
E	83	SER	-	expression tag	UNP P42212
E	84	GLY	-	expression tag	UNP P42212
E	85	LEU	-	expression tag	UNP P42212
E	86	VAL	-	expression tag	UNP P42212
E	87	PRO	-	expression tag	UNP P42212
E	88	ARG	-	expression tag	UNP P42212
E	89	GLY	-	expression tag	UNP P42212
E	90	SER	-	expression tag	UNP P42212
E	91	HIS	-	expression tag	UNP P42212
E	92	VAL	-	expression tag	UNP P42212
E	137	LEU	PHE	conflict	UNP P42212
E	155	LEU	PHE	conflict	UNP P42212
E	156	GLY	SER	conflict	UNP P42212
E	159	LEU	VAL	conflict	UNP P42212
E	163	ALA	SER	conflict	UNP P42212
E	244	THR	MET	conflict	UNP P42212
E	254	ALA	VAL	conflict	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
E	266	GLY	SER	conflict	UNP P42212
E	294	TYR	THR	conflict	UNP P42212
E	297	LYS	ALA	conflict	UNP P42212
E	322	LEU	HIS	conflict	UNP P42212
E	330	SER	-	linker	UNP P42212
E	331	GLY	-	linker	UNP P42212
E	332	LEU	-	linker	UNP P42212
E	333	ARG	-	linker	UNP P42212
E	334	SER	-	linker	UNP P42212
E	335	ARG	-	linker	UNP P42212
E	336	ALA	-	linker	UNP P42212
E	337	GLN	-	linker	UNP P42212
E	338	ALA	-	linker	UNP P42212
E	339	SER	-	linker	UNP P42212
E	340	ASN	-	linker	UNP P42212
E	341	SER	-	linker	UNP P42212
E	342	ALA	-	linker	UNP P42212
E	343	VAL	-	linker	UNP P42212
E	344	ASP	-	linker	UNP P42212
F	72	MET	-	initiating methionine	UNP P42212
F	73	GLY	-	expression tag	UNP P42212
F	74	SER	-	expression tag	UNP P42212
F	75	SER	-	expression tag	UNP P42212
F	76	HIS	-	expression tag	UNP P42212
F	77	HIS	-	expression tag	UNP P42212
F	78	HIS	-	expression tag	UNP P42212
F	79	HIS	-	expression tag	UNP P42212
F	80	HIS	-	expression tag	UNP P42212
F	81	HIS	-	expression tag	UNP P42212
F	82	SER	-	expression tag	UNP P42212
F	83	SER	-	expression tag	UNP P42212
F	84	GLY	-	expression tag	UNP P42212
F	85	LEU	-	expression tag	UNP P42212
F	86	VAL	-	expression tag	UNP P42212
F	87	PRO	-	expression tag	UNP P42212
F	88	ARG	-	expression tag	UNP P42212
F	89	GLY	-	expression tag	UNP P42212
F	90	SER	-	expression tag	UNP P42212
F	91	HIS	-	expression tag	UNP P42212
F	92	VAL	-	expression tag	UNP P42212
F	137	LEU	PHE	conflict	UNP P42212
F	155	LEU	PHE	conflict	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
F	156	GLY	SER	conflict	UNP P42212
F	159	LEU	VAL	conflict	UNP P42212
F	163	ALA	SER	conflict	UNP P42212
F	244	THR	MET	conflict	UNP P42212
F	254	ALA	VAL	conflict	UNP P42212
F	266	GLY	SER	conflict	UNP P42212
F	294	TYR	THR	conflict	UNP P42212
F	297	LYS	ALA	conflict	UNP P42212
F	322	LEU	HIS	conflict	UNP P42212
F	330	SER	-	linker	UNP P42212
F	331	GLY	-	linker	UNP P42212
F	332	LEU	-	linker	UNP P42212
F	333	ARG	-	linker	UNP P42212
F	334	SER	-	linker	UNP P42212
F	335	ARG	-	linker	UNP P42212
F	336	ALA	-	linker	UNP P42212
F	337	GLN	-	linker	UNP P42212
F	338	ALA	-	linker	UNP P42212
F	339	SER	-	linker	UNP P42212
F	340	ASN	-	linker	UNP P42212
F	341	SER	-	linker	UNP P42212
F	342	ALA	-	linker	UNP P42212
F	343	VAL	-	linker	UNP P42212
F	344	ASP	-	linker	UNP P42212
G	72	MET	-	initiating methionine	UNP P42212
G	73	GLY	-	expression tag	UNP P42212
G	74	SER	-	expression tag	UNP P42212
G	75	SER	-	expression tag	UNP P42212
G	76	HIS	-	expression tag	UNP P42212
G	77	HIS	-	expression tag	UNP P42212
G	78	HIS	-	expression tag	UNP P42212
G	79	HIS	-	expression tag	UNP P42212
G	80	HIS	-	expression tag	UNP P42212
G	81	HIS	-	expression tag	UNP P42212
G	82	SER	-	expression tag	UNP P42212
G	83	SER	-	expression tag	UNP P42212
G	84	GLY	-	expression tag	UNP P42212
G	85	LEU	-	expression tag	UNP P42212
G	86	VAL	-	expression tag	UNP P42212
G	87	PRO	-	expression tag	UNP P42212
G	88	ARG	-	expression tag	UNP P42212
G	89	GLY	-	expression tag	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
G	90	SER	-	expression tag	UNP P42212
G	91	HIS	-	expression tag	UNP P42212
G	92	VAL	-	expression tag	UNP P42212
G	137	LEU	PHE	conflict	UNP P42212
G	155	LEU	PHE	conflict	UNP P42212
G	156	GLY	SER	conflict	UNP P42212
G	159	LEU	VAL	conflict	UNP P42212
G	163	ALA	SER	conflict	UNP P42212
G	244	THR	MET	conflict	UNP P42212
G	254	ALA	VAL	conflict	UNP P42212
G	266	GLY	SER	conflict	UNP P42212
G	294	TYR	THR	conflict	UNP P42212
G	297	LYS	ALA	conflict	UNP P42212
G	322	LEU	HIS	conflict	UNP P42212
G	330	SER	-	linker	UNP P42212
G	331	GLY	-	linker	UNP P42212
G	332	LEU	-	linker	UNP P42212
G	333	ARG	-	linker	UNP P42212
G	334	SER	-	linker	UNP P42212
G	335	ARG	-	linker	UNP P42212
G	336	ALA	-	linker	UNP P42212
G	337	GLN	-	linker	UNP P42212
G	338	ALA	-	linker	UNP P42212
G	339	SER	-	linker	UNP P42212
G	340	ASN	-	linker	UNP P42212
G	341	SER	-	linker	UNP P42212
G	342	ALA	-	linker	UNP P42212
G	343	VAL	-	linker	UNP P42212
G	344	ASP	-	linker	UNP P42212
H	72	MET	-	initiating methionine	UNP P42212
H	73	GLY	-	expression tag	UNP P42212
H	74	SER	-	expression tag	UNP P42212
H	75	SER	-	expression tag	UNP P42212
H	76	HIS	-	expression tag	UNP P42212
H	77	HIS	-	expression tag	UNP P42212
H	78	HIS	-	expression tag	UNP P42212
H	79	HIS	-	expression tag	UNP P42212
H	80	HIS	-	expression tag	UNP P42212
H	81	HIS	-	expression tag	UNP P42212
H	82	SER	-	expression tag	UNP P42212
H	83	SER	-	expression tag	UNP P42212
H	84	GLY	-	expression tag	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
H	85	LEU	-	expression tag	UNP P42212
H	86	VAL	-	expression tag	UNP P42212
H	87	PRO	-	expression tag	UNP P42212
H	88	ARG	-	expression tag	UNP P42212
H	89	GLY	-	expression tag	UNP P42212
H	90	SER	-	expression tag	UNP P42212
H	91	HIS	-	expression tag	UNP P42212
H	92	VAL	-	expression tag	UNP P42212
H	137	LEU	PHE	conflict	UNP P42212
H	155	LEU	PHE	conflict	UNP P42212
H	156	GLY	SER	conflict	UNP P42212
H	159	LEU	VAL	conflict	UNP P42212
H	163	ALA	SER	conflict	UNP P42212
H	244	THR	MET	conflict	UNP P42212
H	254	ALA	VAL	conflict	UNP P42212
H	266	GLY	SER	conflict	UNP P42212
H	294	TYR	THR	conflict	UNP P42212
H	297	LYS	ALA	conflict	UNP P42212
H	322	LEU	HIS	conflict	UNP P42212
H	330	SER	-	linker	UNP P42212
H	331	GLY	-	linker	UNP P42212
H	332	LEU	-	linker	UNP P42212
H	333	ARG	-	linker	UNP P42212
H	334	SER	-	linker	UNP P42212
H	335	ARG	-	linker	UNP P42212
H	336	ALA	-	linker	UNP P42212
H	337	GLN	-	linker	UNP P42212
H	338	ALA	-	linker	UNP P42212
H	339	SER	-	linker	UNP P42212
H	340	ASN	-	linker	UNP P42212
H	341	SER	-	linker	UNP P42212
H	342	ALA	-	linker	UNP P42212
H	343	VAL	-	linker	UNP P42212
H	344	ASP	-	linker	UNP P42212
I	72	MET	-	initiating methionine	UNP P42212
I	73	GLY	-	expression tag	UNP P42212
I	74	SER	-	expression tag	UNP P42212
I	75	SER	-	expression tag	UNP P42212
I	76	HIS	-	expression tag	UNP P42212
I	77	HIS	-	expression tag	UNP P42212
I	78	HIS	-	expression tag	UNP P42212
I	79	HIS	-	expression tag	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
I	80	HIS	-	expression tag	UNP P42212
I	81	HIS	-	expression tag	UNP P42212
I	82	SER	-	expression tag	UNP P42212
I	83	SER	-	expression tag	UNP P42212
I	84	GLY	-	expression tag	UNP P42212
I	85	LEU	-	expression tag	UNP P42212
I	86	VAL	-	expression tag	UNP P42212
I	87	PRO	-	expression tag	UNP P42212
I	88	ARG	-	expression tag	UNP P42212
I	89	GLY	-	expression tag	UNP P42212
I	90	SER	-	expression tag	UNP P42212
I	91	HIS	-	expression tag	UNP P42212
I	92	VAL	-	expression tag	UNP P42212
I	137	LEU	PHE	conflict	UNP P42212
I	155	LEU	PHE	conflict	UNP P42212
I	156	GLY	SER	conflict	UNP P42212
I	159	LEU	VAL	conflict	UNP P42212
I	163	ALA	SER	conflict	UNP P42212
I	244	THR	MET	conflict	UNP P42212
I	254	ALA	VAL	conflict	UNP P42212
I	266	GLY	SER	conflict	UNP P42212
I	294	TYR	THR	conflict	UNP P42212
I	297	LYS	ALA	conflict	UNP P42212
I	322	LEU	HIS	conflict	UNP P42212
I	330	SER	-	linker	UNP P42212
I	331	GLY	-	linker	UNP P42212
I	332	LEU	-	linker	UNP P42212
I	333	ARG	-	linker	UNP P42212
I	334	SER	-	linker	UNP P42212
I	335	ARG	-	linker	UNP P42212
I	336	ALA	-	linker	UNP P42212
I	337	GLN	-	linker	UNP P42212
I	338	ALA	-	linker	UNP P42212
I	339	SER	-	linker	UNP P42212
I	340	ASN	-	linker	UNP P42212
I	341	SER	-	linker	UNP P42212
I	342	ALA	-	linker	UNP P42212
I	343	VAL	-	linker	UNP P42212
I	344	ASP	-	linker	UNP P42212
J	72	MET	-	initiating methionine	UNP P42212
J	73	GLY	-	expression tag	UNP P42212
J	74	SER	-	expression tag	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
J	75	SER	-	expression tag	UNP P42212
J	76	HIS	-	expression tag	UNP P42212
J	77	HIS	-	expression tag	UNP P42212
J	78	HIS	-	expression tag	UNP P42212
J	79	HIS	-	expression tag	UNP P42212
J	80	HIS	-	expression tag	UNP P42212
J	81	HIS	-	expression tag	UNP P42212
J	82	SER	-	expression tag	UNP P42212
J	83	SER	-	expression tag	UNP P42212
J	84	GLY	-	expression tag	UNP P42212
J	85	LEU	-	expression tag	UNP P42212
J	86	VAL	-	expression tag	UNP P42212
J	87	PRO	-	expression tag	UNP P42212
J	88	ARG	-	expression tag	UNP P42212
J	89	GLY	-	expression tag	UNP P42212
J	90	SER	-	expression tag	UNP P42212
J	91	HIS	-	expression tag	UNP P42212
J	92	VAL	-	expression tag	UNP P42212
J	137	LEU	PHE	conflict	UNP P42212
J	155	LEU	PHE	conflict	UNP P42212
J	156	GLY	SER	conflict	UNP P42212
J	159	LEU	VAL	conflict	UNP P42212
J	163	ALA	SER	conflict	UNP P42212
J	244	THR	MET	conflict	UNP P42212
J	254	ALA	VAL	conflict	UNP P42212
J	266	GLY	SER	conflict	UNP P42212
J	294	TYR	THR	conflict	UNP P42212
J	297	LYS	ALA	conflict	UNP P42212
J	322	LEU	HIS	conflict	UNP P42212
J	330	SER	-	linker	UNP P42212
J	331	GLY	-	linker	UNP P42212
J	332	LEU	-	linker	UNP P42212
J	333	ARG	-	linker	UNP P42212
J	334	SER	-	linker	UNP P42212
J	335	ARG	-	linker	UNP P42212
J	336	ALA	-	linker	UNP P42212
J	337	GLN	-	linker	UNP P42212
J	338	ALA	-	linker	UNP P42212
J	339	SER	-	linker	UNP P42212
J	340	ASN	-	linker	UNP P42212
J	341	SER	-	linker	UNP P42212
J	342	ALA	-	linker	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
J	343	VAL	-	linker	UNP P42212
J	344	ASP	-	linker	UNP P42212
K	72	MET	-	initiating methionine	UNP P42212
K	73	GLY	-	expression tag	UNP P42212
K	74	SER	-	expression tag	UNP P42212
K	75	SER	-	expression tag	UNP P42212
K	76	HIS	-	expression tag	UNP P42212
K	77	HIS	-	expression tag	UNP P42212
K	78	HIS	-	expression tag	UNP P42212
K	79	HIS	-	expression tag	UNP P42212
K	80	HIS	-	expression tag	UNP P42212
K	81	HIS	-	expression tag	UNP P42212
K	82	SER	-	expression tag	UNP P42212
K	83	SER	-	expression tag	UNP P42212
K	84	GLY	-	expression tag	UNP P42212
K	85	LEU	-	expression tag	UNP P42212
K	86	VAL	-	expression tag	UNP P42212
K	87	PRO	-	expression tag	UNP P42212
K	88	ARG	-	expression tag	UNP P42212
K	89	GLY	-	expression tag	UNP P42212
K	90	SER	-	expression tag	UNP P42212
K	91	HIS	-	expression tag	UNP P42212
K	92	VAL	-	expression tag	UNP P42212
K	137	LEU	PHE	conflict	UNP P42212
K	155	LEU	PHE	conflict	UNP P42212
K	156	GLY	SER	conflict	UNP P42212
K	159	LEU	VAL	conflict	UNP P42212
K	163	ALA	SER	conflict	UNP P42212
K	244	THR	MET	conflict	UNP P42212
K	254	ALA	VAL	conflict	UNP P42212
K	266	GLY	SER	conflict	UNP P42212
K	294	TYR	THR	conflict	UNP P42212
K	297	LYS	ALA	conflict	UNP P42212
K	322	LEU	HIS	conflict	UNP P42212
K	330	SER	-	linker	UNP P42212
K	331	GLY	-	linker	UNP P42212
K	332	LEU	-	linker	UNP P42212
K	333	ARG	-	linker	UNP P42212
K	334	SER	-	linker	UNP P42212
K	335	ARG	-	linker	UNP P42212
K	336	ALA	-	linker	UNP P42212
K	337	GLN	-	linker	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
K	338	ALA	-	linker	UNP P42212
K	339	SER	-	linker	UNP P42212
K	340	ASN	-	linker	UNP P42212
K	341	SER	-	linker	UNP P42212
K	342	ALA	-	linker	UNP P42212
K	343	VAL	-	linker	UNP P42212
K	344	ASP	-	linker	UNP P42212
L	72	MET	-	initiating methionine	UNP P42212
L	73	GLY	-	expression tag	UNP P42212
L	74	SER	-	expression tag	UNP P42212
L	75	SER	-	expression tag	UNP P42212
L	76	HIS	-	expression tag	UNP P42212
L	77	HIS	-	expression tag	UNP P42212
L	78	HIS	-	expression tag	UNP P42212
L	79	HIS	-	expression tag	UNP P42212
L	80	HIS	-	expression tag	UNP P42212
L	81	HIS	-	expression tag	UNP P42212
L	82	SER	-	expression tag	UNP P42212
L	83	SER	-	expression tag	UNP P42212
L	84	GLY	-	expression tag	UNP P42212
L	85	LEU	-	expression tag	UNP P42212
L	86	VAL	-	expression tag	UNP P42212
L	87	PRO	-	expression tag	UNP P42212
L	88	ARG	-	expression tag	UNP P42212
L	89	GLY	-	expression tag	UNP P42212
L	90	SER	-	expression tag	UNP P42212
L	91	HIS	-	expression tag	UNP P42212
L	92	VAL	-	expression tag	UNP P42212
L	137	LEU	PHE	conflict	UNP P42212
L	155	LEU	PHE	conflict	UNP P42212
L	156	GLY	SER	conflict	UNP P42212
L	159	LEU	VAL	conflict	UNP P42212
L	163	ALA	SER	conflict	UNP P42212
L	244	THR	MET	conflict	UNP P42212
L	254	ALA	VAL	conflict	UNP P42212
L	266	GLY	SER	conflict	UNP P42212
L	294	TYR	THR	conflict	UNP P42212
L	297	LYS	ALA	conflict	UNP P42212
L	322	LEU	HIS	conflict	UNP P42212
L	330	SER	-	linker	UNP P42212
L	331	GLY	-	linker	UNP P42212
L	332	LEU	-	linker	UNP P42212

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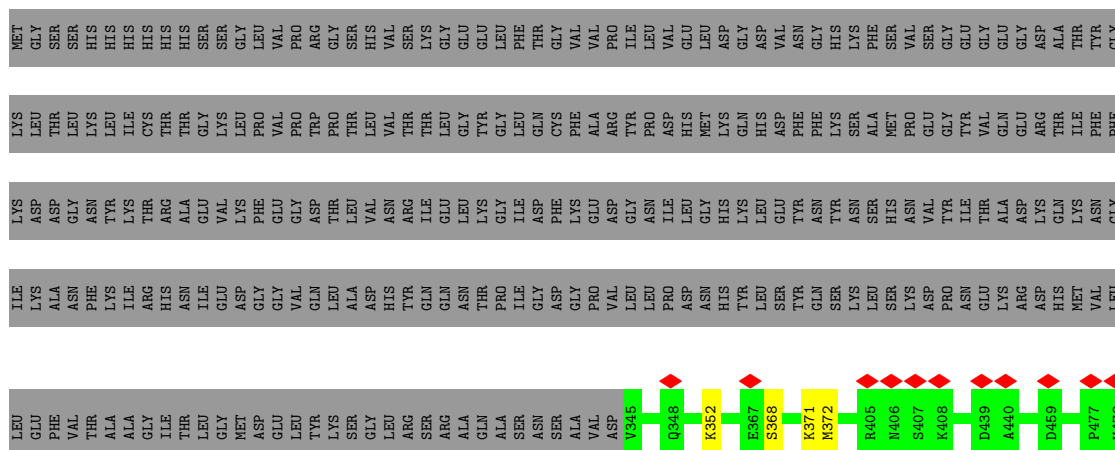
Chain	Residue	Modelled	Actual	Comment	Reference
L	333	ARG	-	linker	UNP P42212
L	334	SER	-	linker	UNP P42212
L	335	ARG	-	linker	UNP P42212
L	336	ALA	-	linker	UNP P42212
L	337	GLN	-	linker	UNP P42212
L	338	ALA	-	linker	UNP P42212
L	339	SER	-	linker	UNP P42212
L	340	ASN	-	linker	UNP P42212
L	341	SER	-	linker	UNP P42212
L	342	ALA	-	linker	UNP P42212
L	343	VAL	-	linker	UNP P42212
L	344	ASP	-	linker	UNP P42212

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.

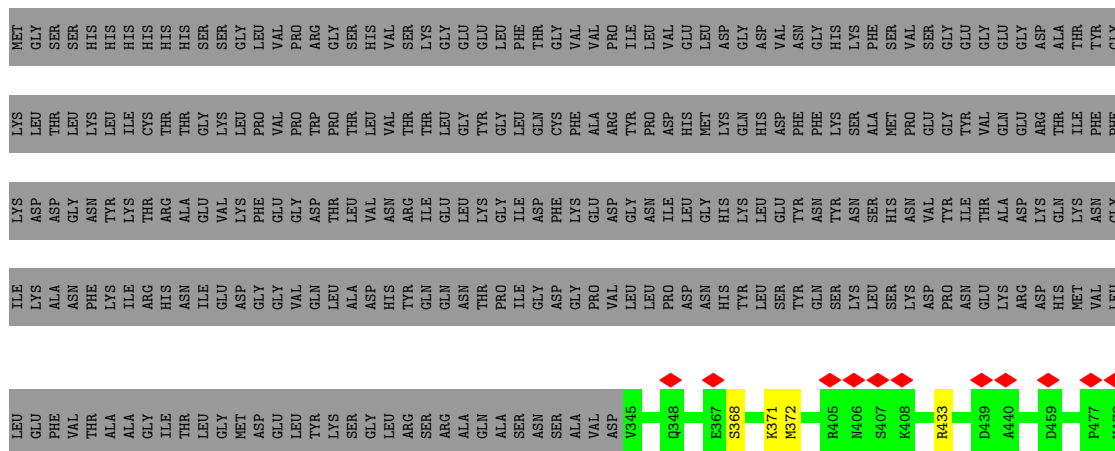
• Molecule 1: Venus-tagged CaMKII Alpha Association Domain

Chain A:

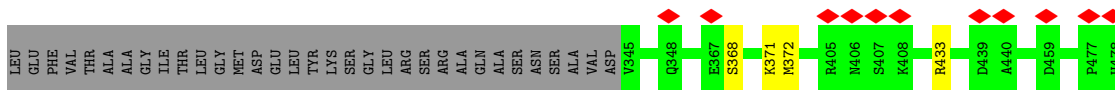


• Molecule 1: Venus-tagged CaMKII Alpha Association Domain

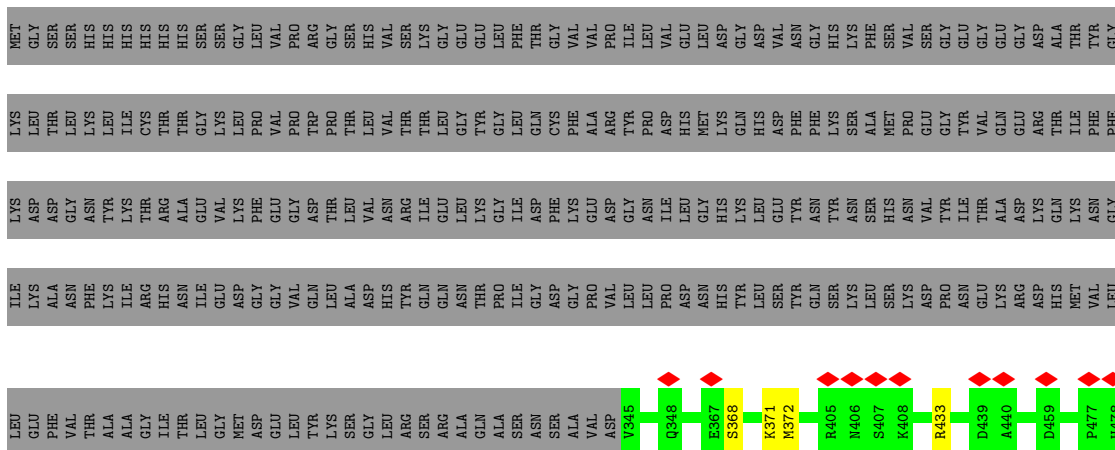
Chain B:



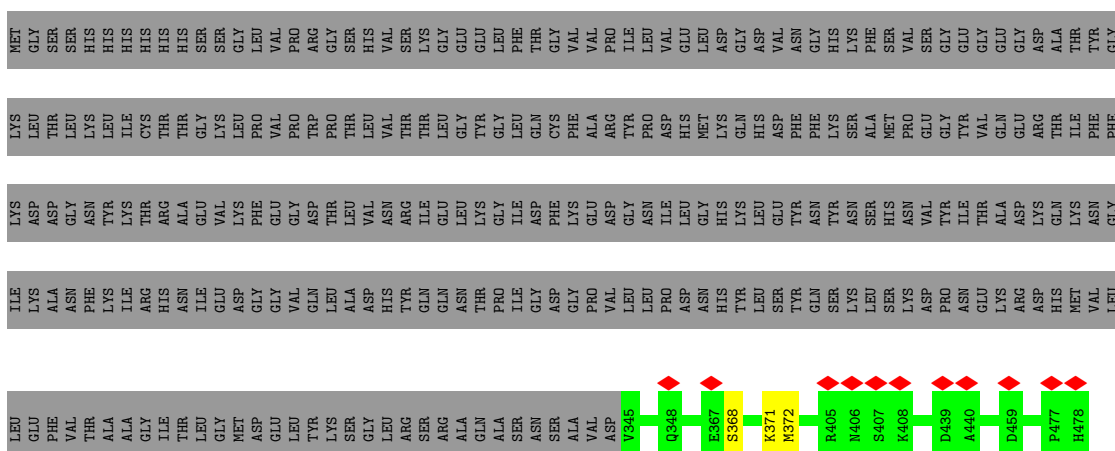
• Molecule 1: Venus-tagged CaMKII Alpha Association Domain



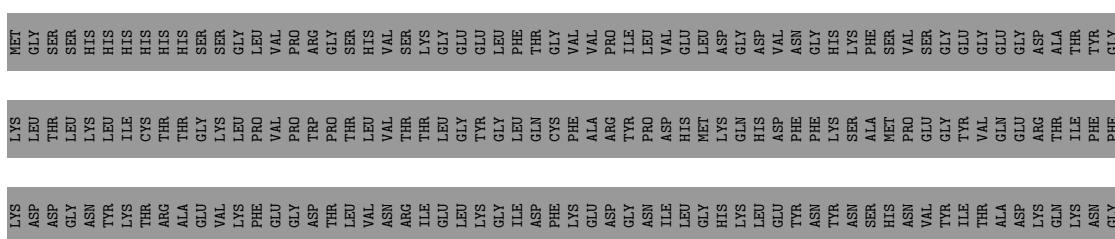
• Molecule 1: Venus-tagged CaMKII Alpha Association Domain

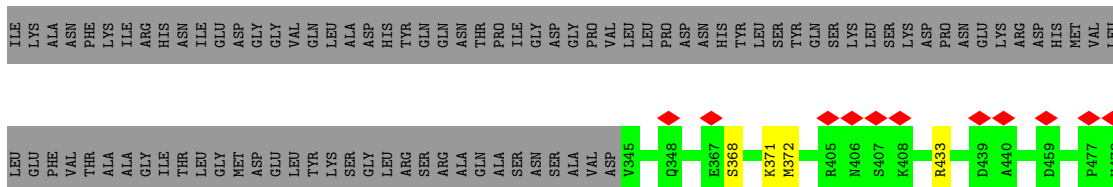


• Molecule 1: Venus-tagged CaMKII Alpha Association Domain

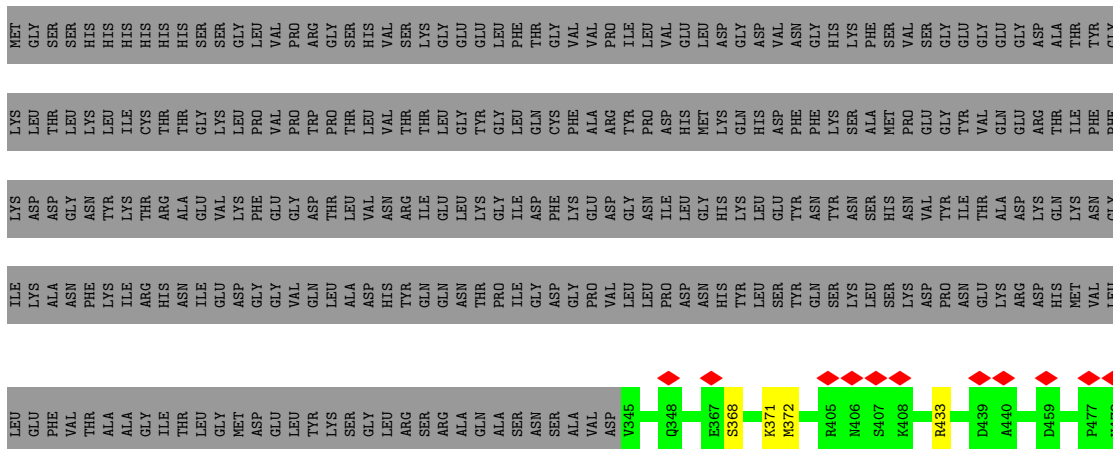


• Molecule 1: Venus-tagged CaMKII Alpha Association Domain





● Molecule 1: Venus-tagged CaMKII Alpha Association Domain



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	94506	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 ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	5.574	Depositor
Minimum map value	-3.057	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.097	Depositor
Recommended contour level	0.5	Depositor
Map size (Å)	284.544, 284.544, 284.544	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.741, 0.741, 0.741	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	0.24	0/1117	0.49	0/1513
1	B	0.24	0/1117	0.49	0/1513
1	C	0.24	0/1117	0.49	0/1513
1	D	0.24	0/1117	0.50	0/1513
1	E	0.24	0/1117	0.49	0/1513
1	F	0.24	0/1117	0.49	0/1513
1	G	0.24	0/1117	0.50	0/1513
1	H	0.24	0/1117	0.49	0/1513
1	I	0.24	0/1117	0.49	0/1513
1	J	0.24	0/1117	0.49	0/1513
1	K	0.24	0/1117	0.49	0/1513
1	L	0.24	0/1117	0.49	0/1513
All	All	0.24	0/13404	0.49	0/18156

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	1087	1051	1049	2	0
1	B	1087	1051	1049	1	0
1	C	1087	1051	1049	1	0
1	D	1087	1051	1049	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	1087	1051	1049	1	0
1	F	1087	1051	1049	1	0
1	G	1087	1051	1049	2	0
1	H	1087	1051	1049	1	0
1	I	1087	1051	1049	1	0
1	J	1087	1051	1049	1	0
1	K	1087	1051	1049	1	0
1	L	1087	1051	1049	1	0
All	All	13044	12612	12588	14	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 1.

All (14) 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:L:368:SER:O	1:L:372:MET:HG3	2.14	0.48
1:F:368:SER:O	1:F:372:MET:HG3	2.14	0.48
1:I:368:SER:O	1:I:372:MET:HG3	2.14	0.47
1:C:368:SER:O	1:C:372:MET:HG3	2.14	0.47
1:K:368:SER:O	1:K:372:MET:HG3	2.16	0.45
1:D:368:SER:O	1:D:372:MET:HG3	2.16	0.45
1:E:368:SER:O	1:E:372:MET:HG3	2.16	0.45
1:J:368:SER:O	1:J:372:MET:HG3	2.16	0.45
1:H:368:SER:O	1:H:372:MET:HG3	2.17	0.44
1:A:368:SER:O	1:A:372:MET:HG3	2.16	0.44
1:G:368:SER:O	1:G:372:MET:HG3	2.16	0.44
1:B:368:SER:O	1:B:372:MET:HG3	2.17	0.44
1:A:352:LYS:HB3	1:A:352:LYS:HE3	1.92	0.42
1:G:352:LYS:HB3	1:G:352:LYS:HE3	1.92	0.42

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	132/407 (32%)	130 (98%)	2 (2%)	0	100	100
1	B	132/407 (32%)	130 (98%)	2 (2%)	0	100	100
1	C	132/407 (32%)	130 (98%)	2 (2%)	0	100	100
1	D	132/407 (32%)	130 (98%)	2 (2%)	0	100	100
1	E	132/407 (32%)	130 (98%)	2 (2%)	0	100	100
1	F	132/407 (32%)	130 (98%)	2 (2%)	0	100	100
1	G	132/407 (32%)	130 (98%)	2 (2%)	0	100	100
1	H	132/407 (32%)	130 (98%)	2 (2%)	0	100	100
1	I	132/407 (32%)	130 (98%)	2 (2%)	0	100	100
1	J	132/407 (32%)	130 (98%)	2 (2%)	0	100	100
1	K	132/407 (32%)	130 (98%)	2 (2%)	0	100	100
1	L	132/407 (32%)	130 (98%)	2 (2%)	0	100	100
All	All	1584/4884 (32%)	1560 (98%)	24 (2%)	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	117/350 (33%)	116 (99%)	1 (1%)	78	92
1	B	117/350 (33%)	115 (98%)	2 (2%)	60	84
1	C	117/350 (33%)	115 (98%)	2 (2%)	60	84
1	D	117/350 (33%)	116 (99%)	1 (1%)	78	92
1	E	117/350 (33%)	115 (98%)	2 (2%)	60	84
1	F	117/350 (33%)	115 (98%)	2 (2%)	60	84
1	G	117/350 (33%)	116 (99%)	1 (1%)	78	92

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	H	117/350 (33%)	115 (98%)	2 (2%)	60	84
1	I	117/350 (33%)	115 (98%)	2 (2%)	60	84
1	J	117/350 (33%)	116 (99%)	1 (1%)	78	92
1	K	117/350 (33%)	115 (98%)	2 (2%)	60	84
1	L	117/350 (33%)	115 (98%)	2 (2%)	60	84
All	All	1404/4200 (33%)	1384 (99%)	20 (1%)	68	86

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	371	LYS
1	B	371	LYS
1	B	433	ARG
1	C	371	LYS
1	C	433	ARG
1	D	371	LYS
1	E	371	LYS
1	E	433	ARG
1	F	371	LYS
1	F	433	ARG
1	G	371	LYS
1	H	371	LYS
1	H	433	ARG
1	I	371	LYS
1	I	433	ARG
1	J	371	LYS
1	K	371	LYS
1	K	433	ARG
1	L	371	LYS
1	L	433	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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](#)

There are no chain breaks in this entry.

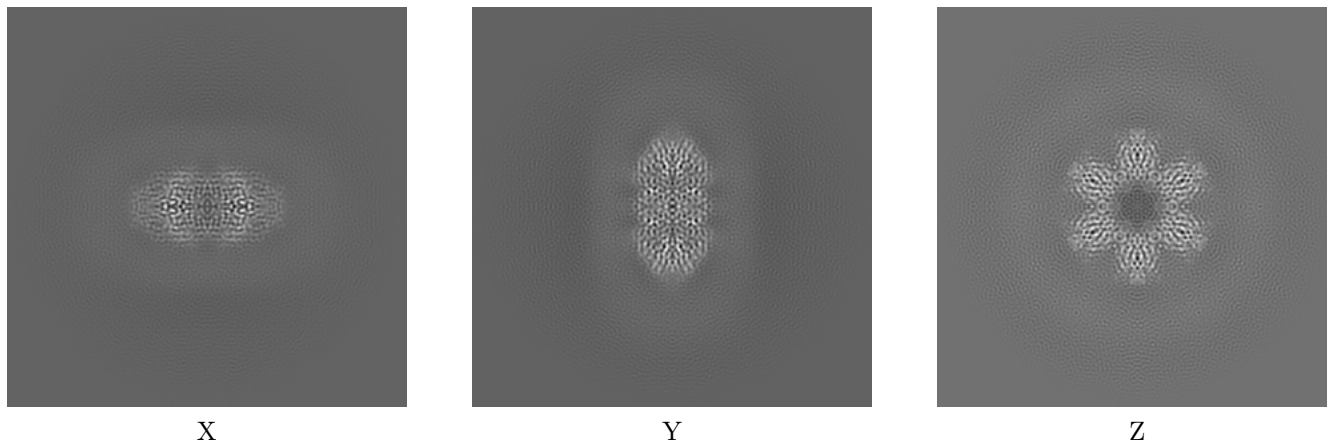
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-40955. These allow visual inspection of the internal detail of the map and identification of artifacts.

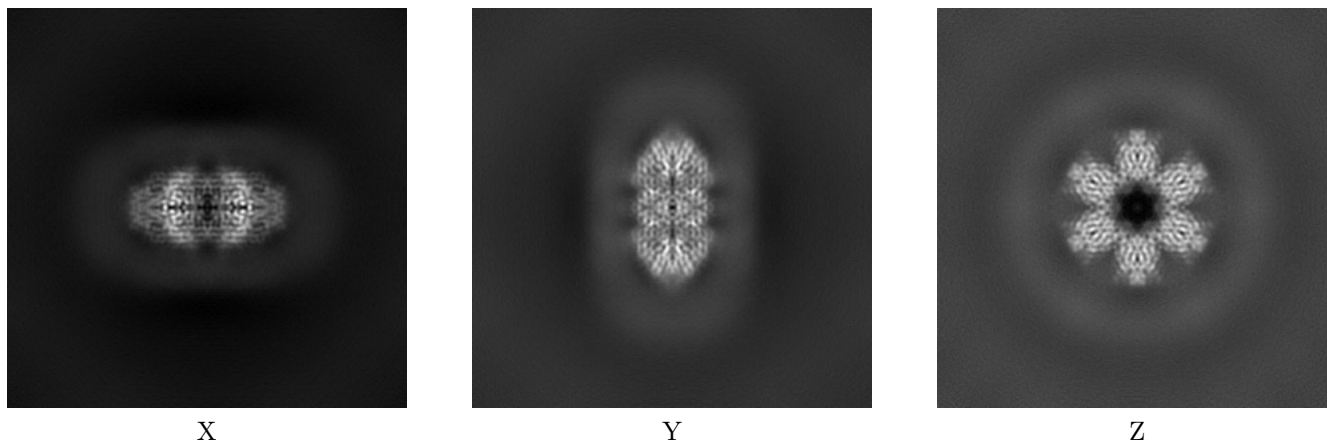
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



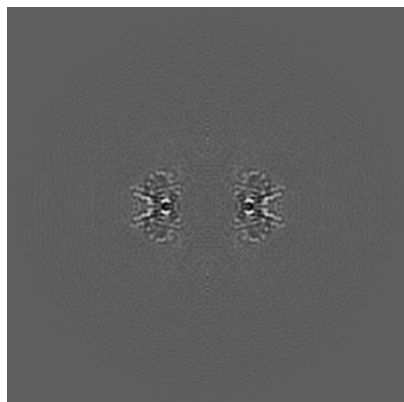
6.1.2 Raw map



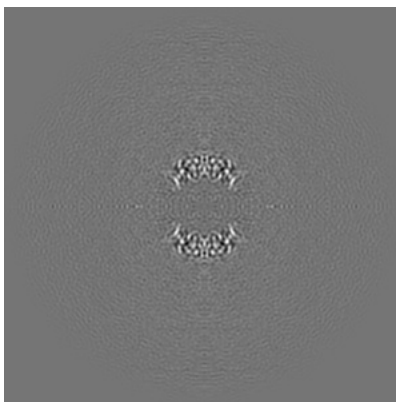
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

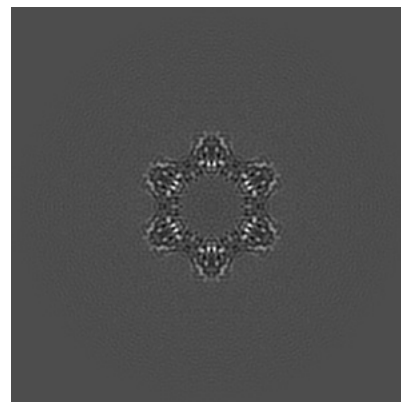
6.2.1 Primary map



X Index: 192

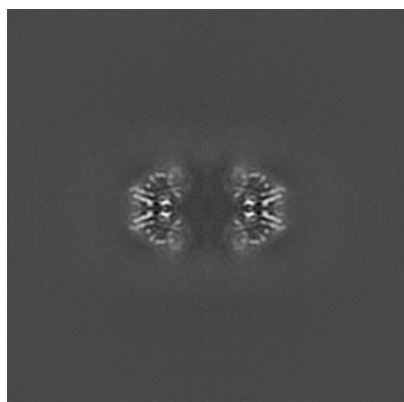


Y Index: 192

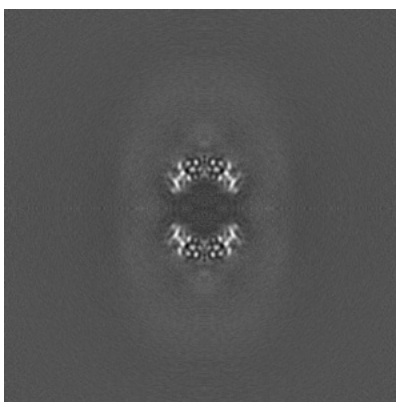


Z Index: 192

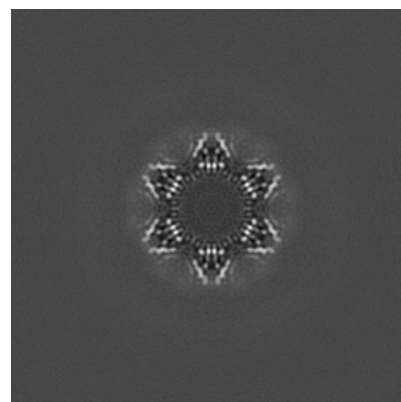
6.2.2 Raw map



X Index: 192



Y Index: 192

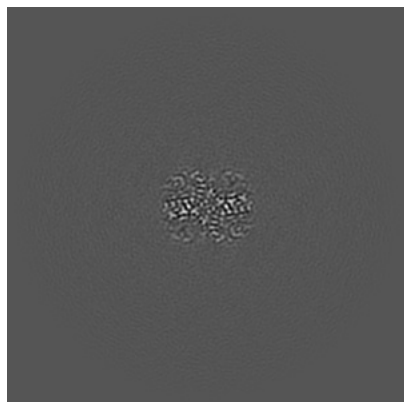


Z Index: 192

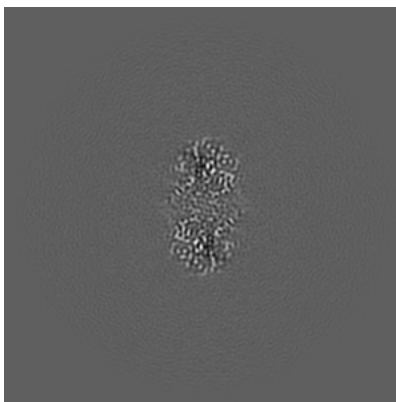
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

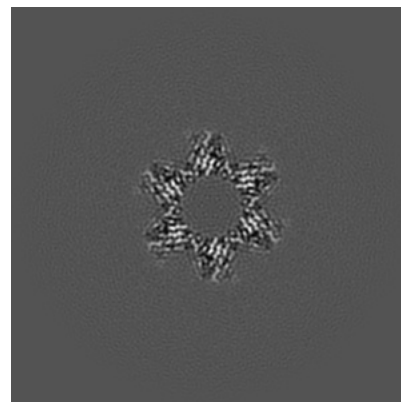
6.3.1 Primary map



X Index: 229

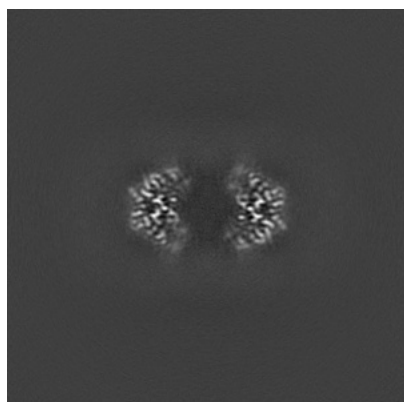


Y Index: 222

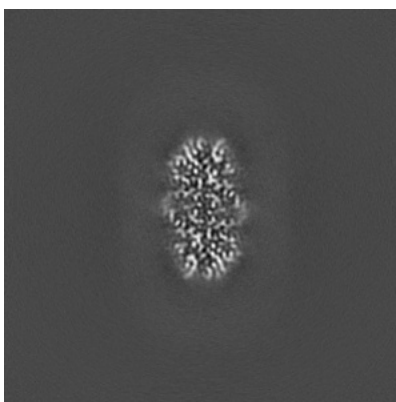


Z Index: 187

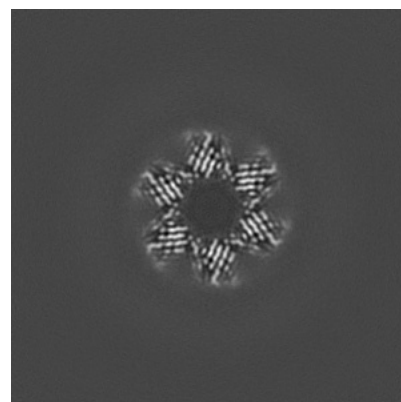
6.3.2 Raw map



X Index: 195



Y Index: 160

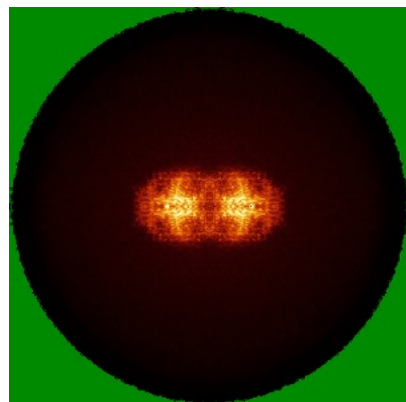


Z Index: 187

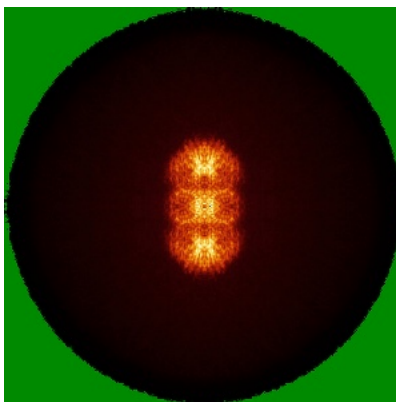
The images above show the largest variance slices of the map in three orthogonal directions.

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

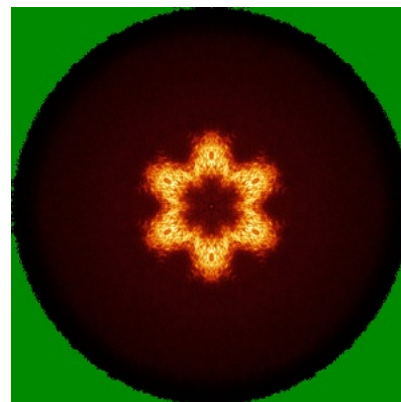
6.4.1 Primary map



X

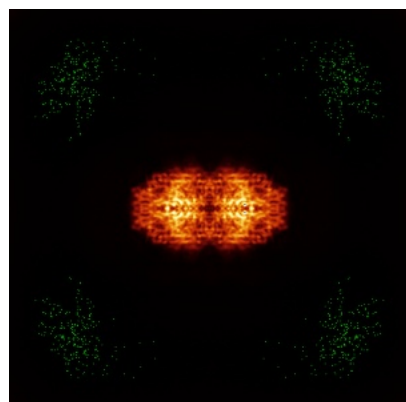


Y

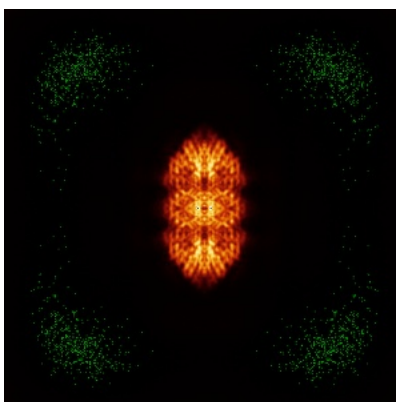


Z

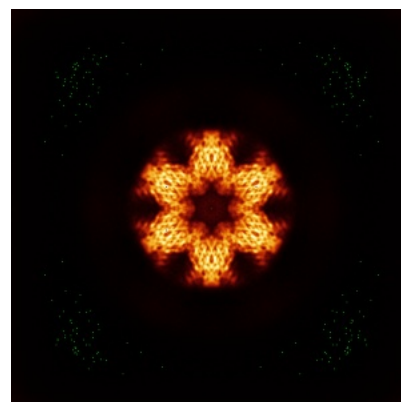
6.4.2 Raw map



X



Y

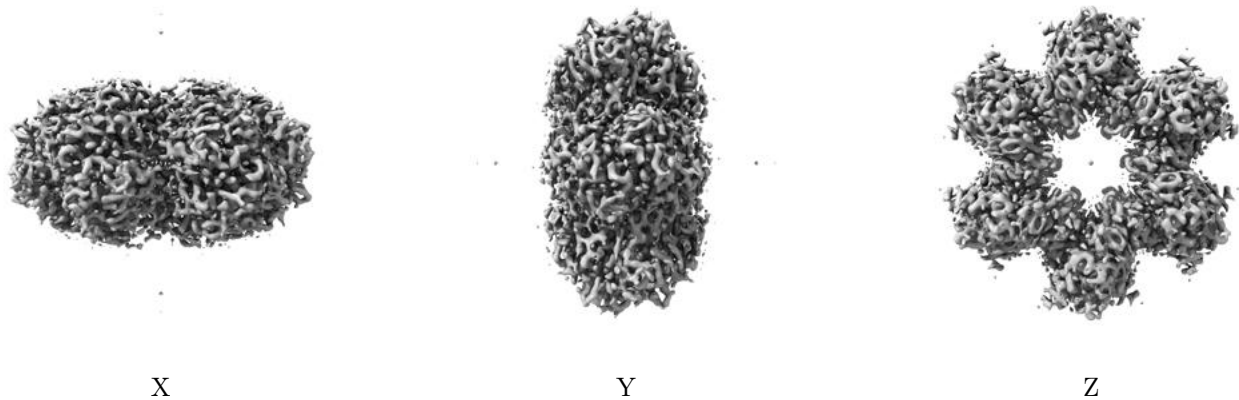


Z

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.

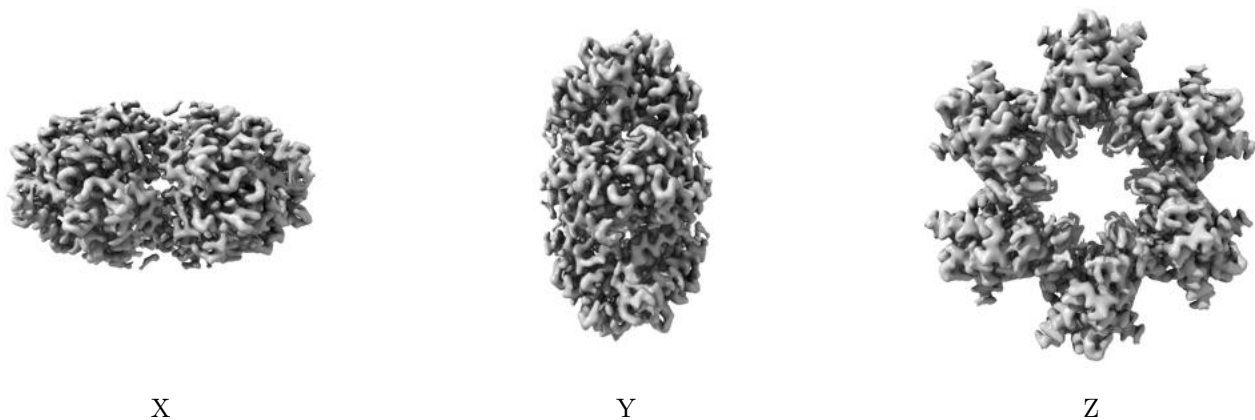
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.5. 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.

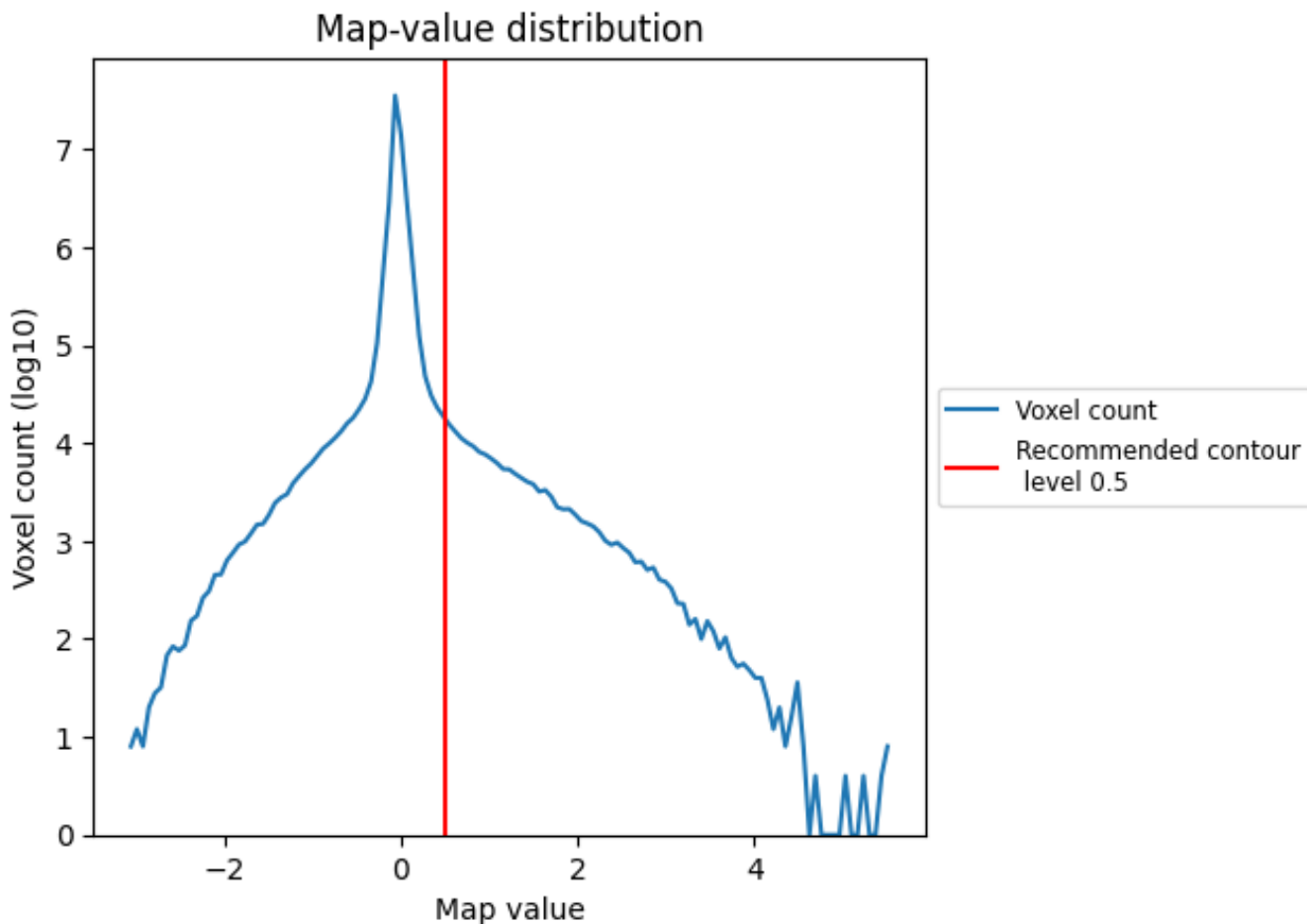
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

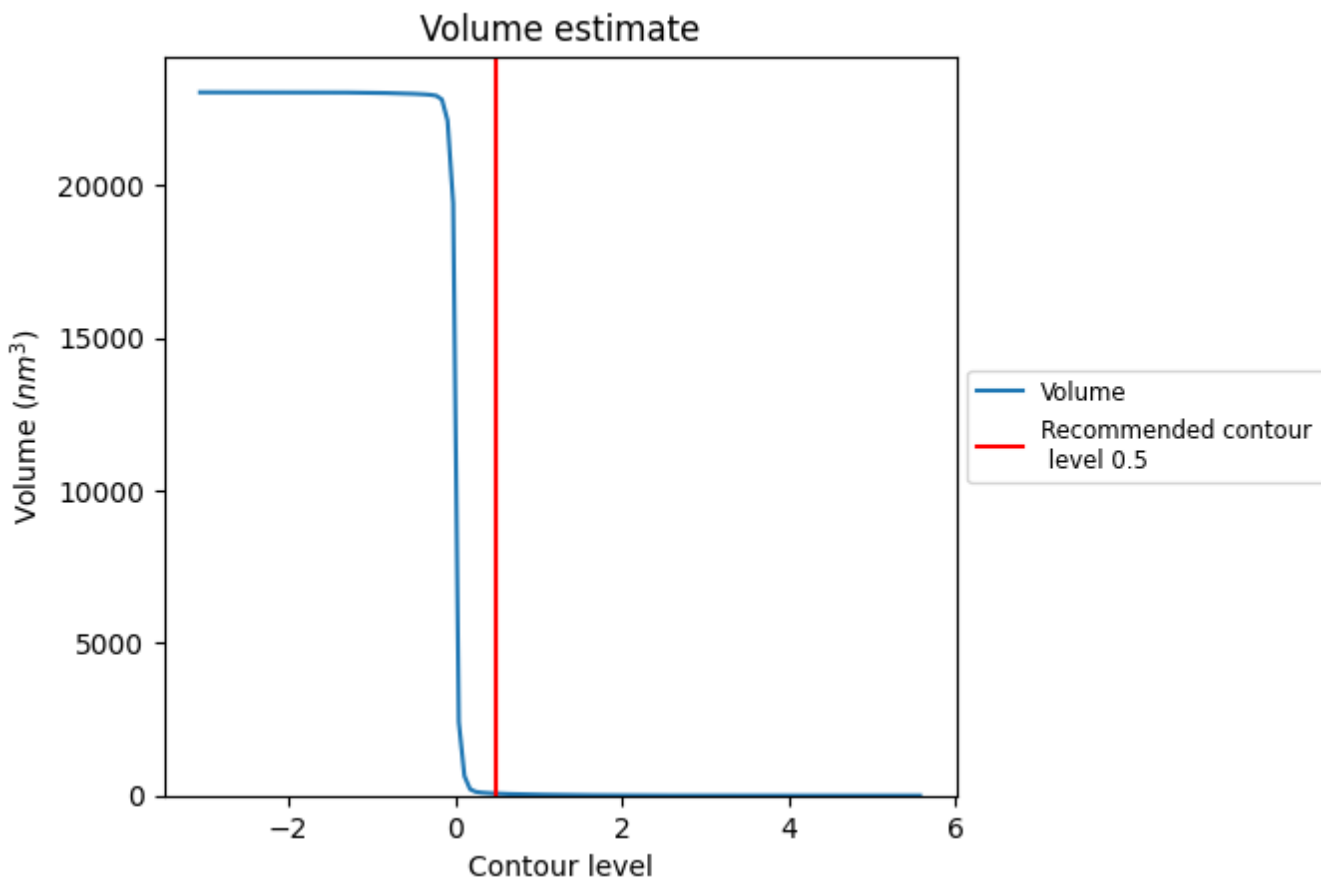
This section contains the results of statistical analysis of the map.

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.

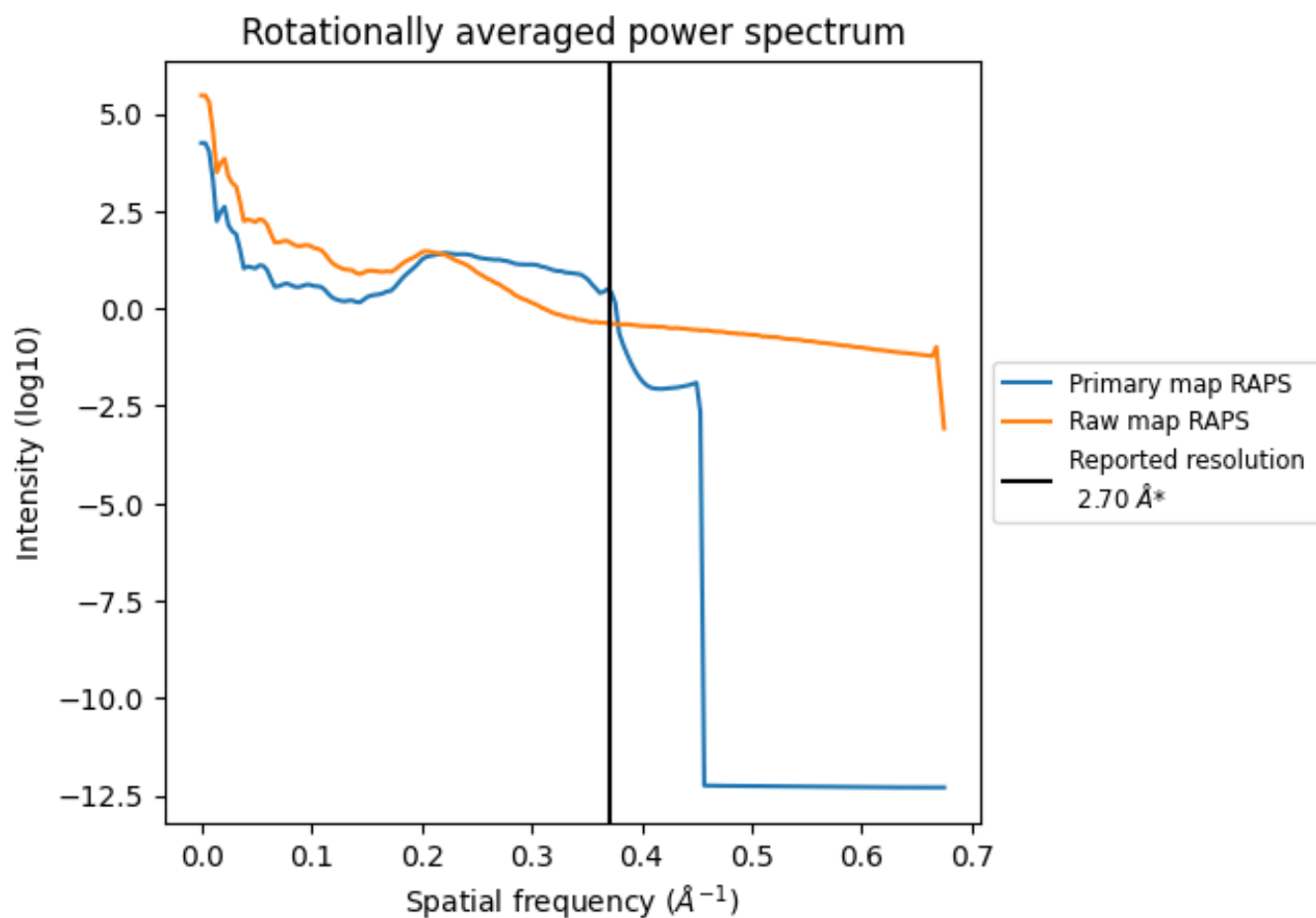
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 66 nm^3 ; this corresponds to an approximate mass of 59 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](#)

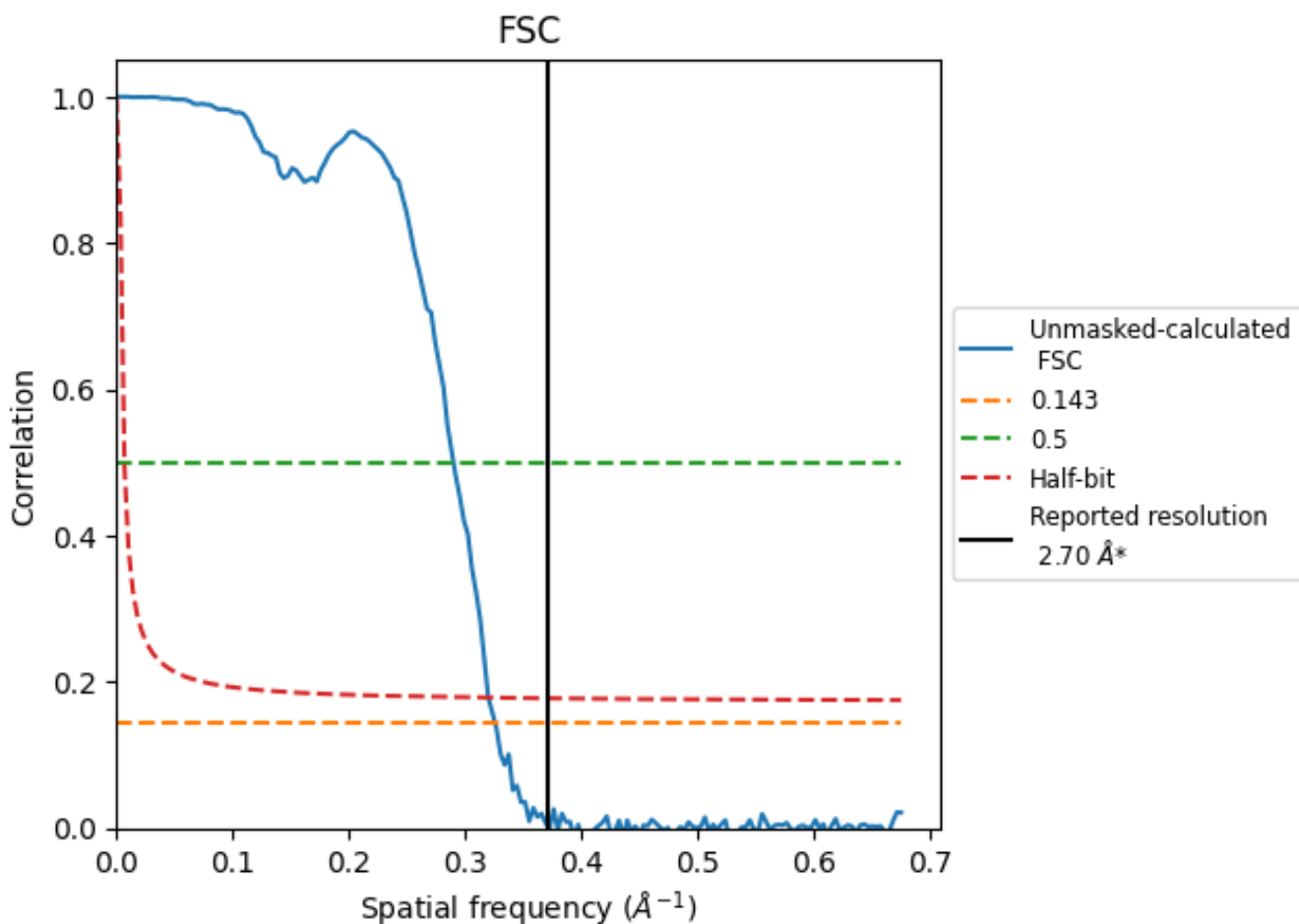


*Reported resolution corresponds to spatial frequency of 0.370 Å⁻¹

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 0.370 \AA^{-1}

8.2 Resolution estimates [i](#)

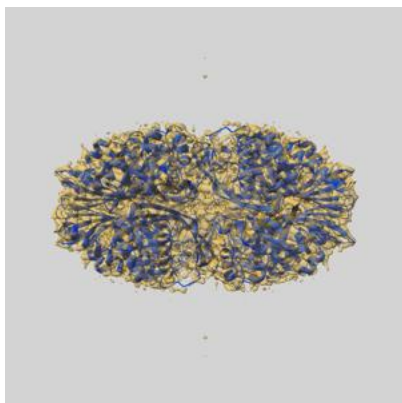
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.70	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.07	3.45	3.13

*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 3.07 differs from the reported value 2.7 by more than 10 %

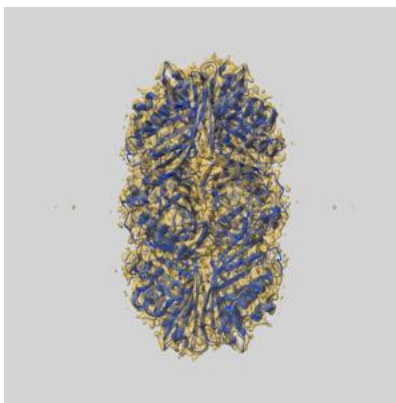
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-40955 and PDB model 8T15. Per-residue inclusion information can be found in section 3 on page 19.

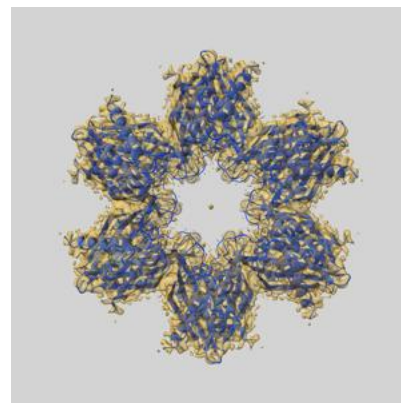
9.1 Map-model overlay [i](#)



X



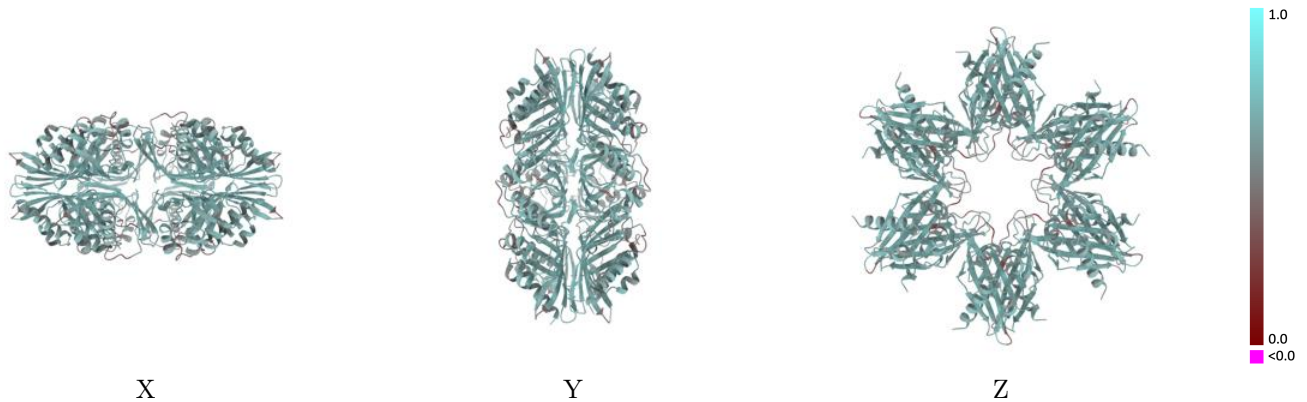
Y



Z

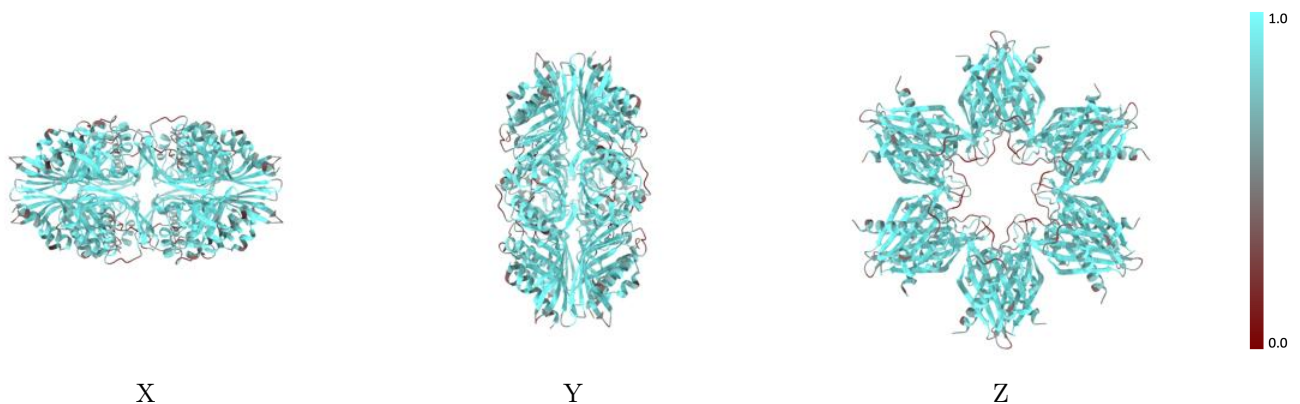
The images above show the 3D surface view of the map at the recommended contour level 0.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



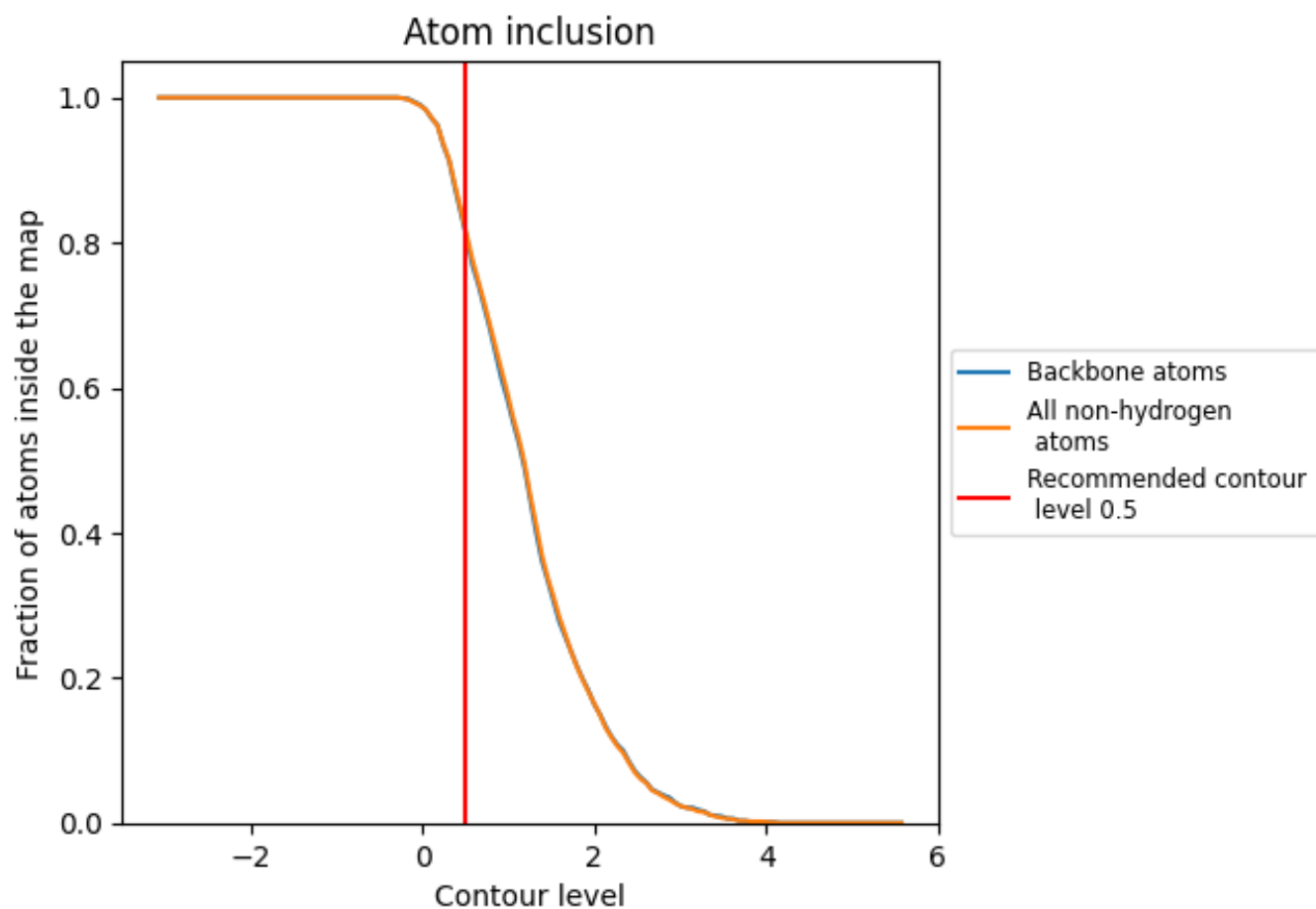
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.5).



























9.4 Atom inclusion [i](#)



At the recommended contour level, 82% of all backbone atoms, 82% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary [i](#)

The table lists the average atom inclusion at the recommended contour level (0.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8210	 0.6070
A	 0.8270	 0.6080
B	 0.8330	 0.6080
C	 0.8280	 0.6070
D	 0.8270	 0.6070
E	 0.8330	 0.6070
F	 0.8280	 0.6070
G	 0.8270	 0.6080
H	 0.8330	 0.6080
I	 0.8290	 0.6080
J	 0.8290	 0.6060
K	 0.8330	 0.6050
L	 0.8280	 0.6080

