



## Full wwPDB EM Validation Report ⓘ

Apr 5, 2026 – 09:32 PM UTC

PDB ID : 9KQ0 / pdb\_00009kq0  
EMDB ID : EMD-62493  
Title : Structure of TolQRA complex at pH 8.0 from E.coli  
Authors : Dong, C.; Zhang, Z.  
Deposited on : 2024-11-24  
Resolution : 3.60 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

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<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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev132  
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

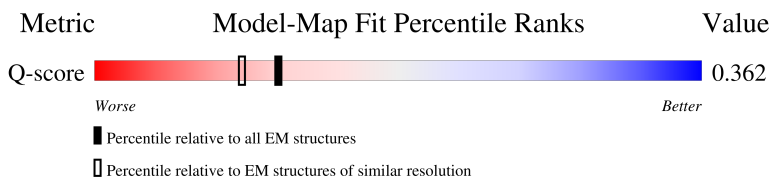
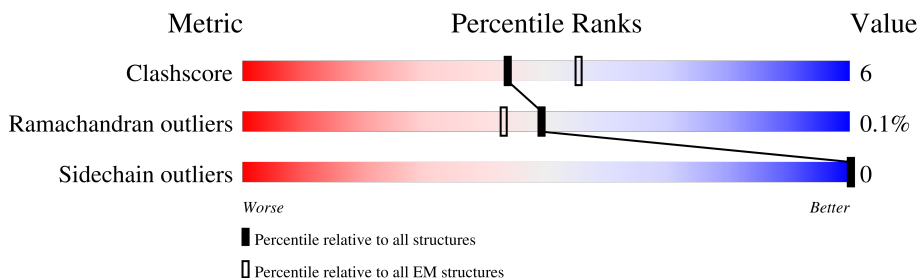
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.60 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.







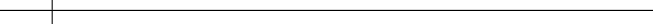



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	12797 ( 3.10 - 4.10 )

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  $\geq 3$ , 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	232	
1	B	232	
1	C	232	
1	D	232	

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Mol	Chain	Length	Quality of chain
1	E	232	 76%19%5%
2	F	142	 11%6%84%
2	G	142	 15%1%82%
3	H	557	 5%95%
3	I	557	 5%95%
3	J	557	 1%96%
3	K	557	 1%97%
3	L	557	 1%1%95%

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 10048 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 Tol-Pal system protein TolQ.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	228	Total	C	N	O	S	0	0
			1784	1148	307	321	8		
1	B	221	Total	C	N	O	S	0	0
			1738	1122	299	309	8		
1	C	224	Total	C	N	O	S	0	0
			1758	1134	302	314	8		
1	D	219	Total	C	N	O	S	0	0
			1705	1106	290	302	7		
1	E	221	Total	C	N	O	S	0	0
			1737	1123	299	307	8		

There are 15 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	MET	-	initiating methionine	UNP P0ABU9
A	0	GLY	-	expression tag	UNP P0ABU9
A	1	VAL	-	expression tag	UNP P0ABU9
B	-1	MET	-	initiating methionine	UNP P0ABU9
B	0	GLY	-	expression tag	UNP P0ABU9
B	1	VAL	-	expression tag	UNP P0ABU9
C	-1	MET	-	initiating methionine	UNP P0ABU9
C	0	GLY	-	expression tag	UNP P0ABU9
C	1	VAL	-	expression tag	UNP P0ABU9
D	-1	MET	-	initiating methionine	UNP P0ABU9
D	0	GLY	-	expression tag	UNP P0ABU9
D	1	VAL	-	expression tag	UNP P0ABU9
E	-1	MET	-	initiating methionine	UNP P0ABU9
E	0	GLY	-	expression tag	UNP P0ABU9
E	1	VAL	-	expression tag	UNP P0ABU9

- Molecule 2 is a protein called Tol-Pal system protein TolR.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	F	23	Total	C	N	O	S	0	0
			179	123	25	30	1		
2	G	25	Total	C	N	O	S	0	0
			191	131	27	32	1		

- Molecule 3 is a protein called Ubiquitin-like protein SMT3,Tol-Pal system protein TolA.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	H	28	Total	C	N	O	0	0
			214	145	34	35		
3	I	30	Total	C	N	O	0	0
			237	158	40	39		
3	J	24	Total	C	N	O	0	0
			164	110	28	26		
3	K	18	Total	C	N	O	0	0
			129	85	23	21		
3	L	28	Total	C	N	O	0	0
			212	142	35	35		

There are 200 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	-134	MET	-	initiating methionine	UNP Q12306
H	-133	GLY	-	expression tag	UNP Q12306
H	-132	HIS	-	expression tag	UNP Q12306
H	-131	HIS	-	expression tag	UNP Q12306
H	-130	HIS	-	expression tag	UNP Q12306
H	-129	HIS	-	expression tag	UNP Q12306
H	-128	HIS	-	expression tag	UNP Q12306
H	-127	HIS	-	expression tag	UNP Q12306
H	-126	HIS	-	expression tag	UNP Q12306
H	-125	HIS	-	expression tag	UNP Q12306
H	-124	GLY	-	expression tag	UNP Q12306
H	-123	SER	-	expression tag	UNP Q12306
H	-122	LEU	-	expression tag	UNP Q12306
H	-121	GLN	-	expression tag	UNP Q12306
H	-23	ALA	-	linker	UNP Q12306
H	-22	ALA	-	linker	UNP Q12306
H	-21	ASP	-	linker	UNP Q12306
H	-20	TYR	-	linker	UNP Q12306
H	-19	GLY	-	linker	UNP Q12306
H	-18	GLY	-	linker	UNP Q12306
H	-17	ASP	-	linker	UNP Q12306

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Chain	Residue	Modelled	Actual	Comment	Reference
H	-16	ILE	-	linker	UNP Q12306
H	-15	PRO	-	linker	UNP Q12306
H	-14	THR	-	linker	UNP Q12306
H	-13	THR	-	linker	UNP Q12306
H	-12	GLU	-	linker	UNP Q12306
H	-11	ASN	-	linker	UNP Q12306
H	-10	LEU	-	linker	UNP Q12306
H	-9	TYR	-	linker	UNP Q12306
H	-8	PHE	-	linker	UNP Q12306
H	-7	GLN	-	linker	UNP Q12306
H	-6	GLY	-	linker	UNP Q12306
H	-5	ALA	-	linker	UNP Q12306
H	-4	ALA	-	linker	UNP Q12306
H	-3	ALA	-	linker	UNP Q12306
H	-2	ASP	-	linker	UNP Q12306
H	-1	ILE	-	linker	UNP Q12306
H	0	GLY	-	linker	UNP Q12306
H	1	SER	-	linker	UNP Q12306
H	2	VAL	-	linker	UNP Q12306
I	-134	MET	-	initiating methionine	UNP Q12306
I	-133	GLY	-	expression tag	UNP Q12306
I	-132	HIS	-	expression tag	UNP Q12306
I	-131	HIS	-	expression tag	UNP Q12306
I	-130	HIS	-	expression tag	UNP Q12306
I	-129	HIS	-	expression tag	UNP Q12306
I	-128	HIS	-	expression tag	UNP Q12306
I	-127	HIS	-	expression tag	UNP Q12306
I	-126	HIS	-	expression tag	UNP Q12306
I	-125	HIS	-	expression tag	UNP Q12306
I	-124	GLY	-	expression tag	UNP Q12306
I	-123	SER	-	expression tag	UNP Q12306
I	-122	LEU	-	expression tag	UNP Q12306
I	-121	GLN	-	expression tag	UNP Q12306
I	-23	ALA	-	linker	UNP Q12306
I	-22	ALA	-	linker	UNP Q12306
I	-21	ASP	-	linker	UNP Q12306
I	-20	TYR	-	linker	UNP Q12306
I	-19	GLY	-	linker	UNP Q12306
I	-18	GLY	-	linker	UNP Q12306
I	-17	ASP	-	linker	UNP Q12306
I	-16	ILE	-	linker	UNP Q12306
I	-15	PRO	-	linker	UNP Q12306

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Chain	Residue	Modelled	Actual	Comment	Reference
I	-14	THR	-	linker	UNP Q12306
I	-13	THR	-	linker	UNP Q12306
I	-12	GLU	-	linker	UNP Q12306
I	-11	ASN	-	linker	UNP Q12306
I	-10	LEU	-	linker	UNP Q12306
I	-9	TYR	-	linker	UNP Q12306
I	-8	PHE	-	linker	UNP Q12306
I	-7	GLN	-	linker	UNP Q12306
I	-6	GLY	-	linker	UNP Q12306
I	-5	ALA	-	linker	UNP Q12306
I	-4	ALA	-	linker	UNP Q12306
I	-3	ALA	-	linker	UNP Q12306
I	-2	ASP	-	linker	UNP Q12306
I	-1	ILE	-	linker	UNP Q12306
I	0	GLY	-	linker	UNP Q12306
I	1	SER	-	linker	UNP Q12306
I	2	VAL	-	linker	UNP Q12306
J	-134	MET	-	initiating methionine	UNP Q12306
J	-133	GLY	-	expression tag	UNP Q12306
J	-132	HIS	-	expression tag	UNP Q12306
J	-131	HIS	-	expression tag	UNP Q12306
J	-130	HIS	-	expression tag	UNP Q12306
J	-129	HIS	-	expression tag	UNP Q12306
J	-128	HIS	-	expression tag	UNP Q12306
J	-127	HIS	-	expression tag	UNP Q12306
J	-126	HIS	-	expression tag	UNP Q12306
J	-125	HIS	-	expression tag	UNP Q12306
J	-124	GLY	-	expression tag	UNP Q12306
J	-123	SER	-	expression tag	UNP Q12306
J	-122	LEU	-	expression tag	UNP Q12306
J	-121	GLN	-	expression tag	UNP Q12306
J	-23	ALA	-	linker	UNP Q12306
J	-22	ALA	-	linker	UNP Q12306
J	-21	ASP	-	linker	UNP Q12306
J	-20	TYR	-	linker	UNP Q12306
J	-19	GLY	-	linker	UNP Q12306
J	-18	GLY	-	linker	UNP Q12306
J	-17	ASP	-	linker	UNP Q12306
J	-16	ILE	-	linker	UNP Q12306
J	-15	PRO	-	linker	UNP Q12306
J	-14	THR	-	linker	UNP Q12306
J	-13	THR	-	linker	UNP Q12306

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Chain	Residue	Modelled	Actual	Comment	Reference
J	-12	GLU	-	linker	UNP Q12306
J	-11	ASN	-	linker	UNP Q12306
J	-10	LEU	-	linker	UNP Q12306
J	-9	TYR	-	linker	UNP Q12306
J	-8	PHE	-	linker	UNP Q12306
J	-7	GLN	-	linker	UNP Q12306
J	-6	GLY	-	linker	UNP Q12306
J	-5	ALA	-	linker	UNP Q12306
J	-4	ALA	-	linker	UNP Q12306
J	-3	ALA	-	linker	UNP Q12306
J	-2	ASP	-	linker	UNP Q12306
J	-1	ILE	-	linker	UNP Q12306
J	0	GLY	-	linker	UNP Q12306
J	1	SER	-	linker	UNP Q12306
J	2	VAL	-	linker	UNP Q12306
K	-134	MET	-	initiating methionine	UNP Q12306
K	-133	GLY	-	expression tag	UNP Q12306
K	-132	HIS	-	expression tag	UNP Q12306
K	-131	HIS	-	expression tag	UNP Q12306
K	-130	HIS	-	expression tag	UNP Q12306
K	-129	HIS	-	expression tag	UNP Q12306
K	-128	HIS	-	expression tag	UNP Q12306
K	-127	HIS	-	expression tag	UNP Q12306
K	-126	HIS	-	expression tag	UNP Q12306
K	-125	HIS	-	expression tag	UNP Q12306
K	-124	GLY	-	expression tag	UNP Q12306
K	-123	SER	-	expression tag	UNP Q12306
K	-122	LEU	-	expression tag	UNP Q12306
K	-121	GLN	-	expression tag	UNP Q12306
K	-23	ALA	-	linker	UNP Q12306
K	-22	ALA	-	linker	UNP Q12306
K	-21	ASP	-	linker	UNP Q12306
K	-20	TYR	-	linker	UNP Q12306
K	-19	GLY	-	linker	UNP Q12306
K	-18	GLY	-	linker	UNP Q12306
K	-17	ASP	-	linker	UNP Q12306
K	-16	ILE	-	linker	UNP Q12306
K	-15	PRO	-	linker	UNP Q12306
K	-14	THR	-	linker	UNP Q12306
K	-13	THR	-	linker	UNP Q12306
K	-12	GLU	-	linker	UNP Q12306
K	-11	ASN	-	linker	UNP Q12306

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Chain	Residue	Modelled	Actual	Comment	Reference
K	-10	LEU	-	linker	UNP Q12306
K	-9	TYR	-	linker	UNP Q12306
K	-8	PHE	-	linker	UNP Q12306
K	-7	GLN	-	linker	UNP Q12306
K	-6	GLY	-	linker	UNP Q12306
K	-5	ALA	-	linker	UNP Q12306
K	-4	ALA	-	linker	UNP Q12306
K	-3	ALA	-	linker	UNP Q12306
K	-2	ASP	-	linker	UNP Q12306
K	-1	ILE	-	linker	UNP Q12306
K	0	GLY	-	linker	UNP Q12306
K	1	SER	-	linker	UNP Q12306
K	2	VAL	-	linker	UNP Q12306
L	-134	MET	-	initiating methionine	UNP Q12306
L	-133	GLY	-	expression tag	UNP Q12306
L	-132	HIS	-	expression tag	UNP Q12306
L	-131	HIS	-	expression tag	UNP Q12306
L	-130	HIS	-	expression tag	UNP Q12306
L	-129	HIS	-	expression tag	UNP Q12306
L	-128	HIS	-	expression tag	UNP Q12306
L	-127	HIS	-	expression tag	UNP Q12306
L	-126	HIS	-	expression tag	UNP Q12306
L	-125	HIS	-	expression tag	UNP Q12306
L	-124	GLY	-	expression tag	UNP Q12306
L	-123	SER	-	expression tag	UNP Q12306
L	-122	LEU	-	expression tag	UNP Q12306
L	-121	GLN	-	expression tag	UNP Q12306
L	-23	ALA	-	linker	UNP Q12306
L	-22	ALA	-	linker	UNP Q12306
L	-21	ASP	-	linker	UNP Q12306
L	-20	TYR	-	linker	UNP Q12306
L	-19	GLY	-	linker	UNP Q12306
L	-18	GLY	-	linker	UNP Q12306
L	-17	ASP	-	linker	UNP Q12306
L	-16	ILE	-	linker	UNP Q12306
L	-15	PRO	-	linker	UNP Q12306
L	-14	THR	-	linker	UNP Q12306
L	-13	THR	-	linker	UNP Q12306
L	-12	GLU	-	linker	UNP Q12306
L	-11	ASN	-	linker	UNP Q12306
L	-10	LEU	-	linker	UNP Q12306
L	-9	TYR	-	linker	UNP Q12306

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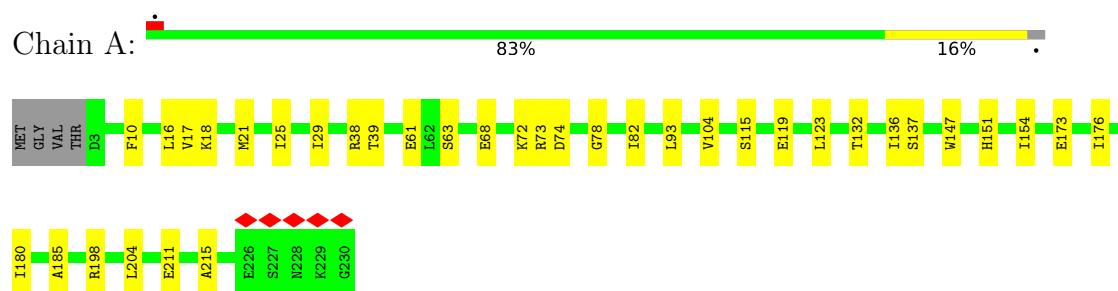
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Chain	Residue	Modelled	Actual	Comment	Reference
L	-8	PHE	-	linker	UNP Q12306
L	-7	GLN	-	linker	UNP Q12306
L	-6	GLY	-	linker	UNP Q12306
L	-5	ALA	-	linker	UNP Q12306
L	-4	ALA	-	linker	UNP Q12306
L	-3	ALA	-	linker	UNP Q12306
L	-2	ASP	-	linker	UNP Q12306
L	-1	ILE	-	linker	UNP Q12306
L	0	GLY	-	linker	UNP Q12306
L	1	SER	-	linker	UNP Q12306
L	2	VAL	-	linker	UNP Q12306

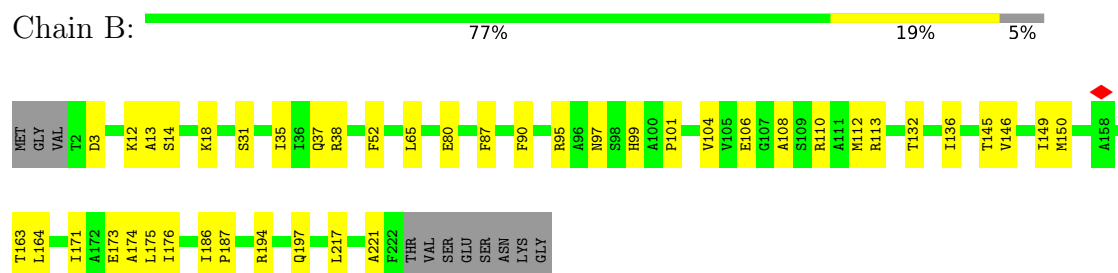
### 3 Residue-property plots [i](#)

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.

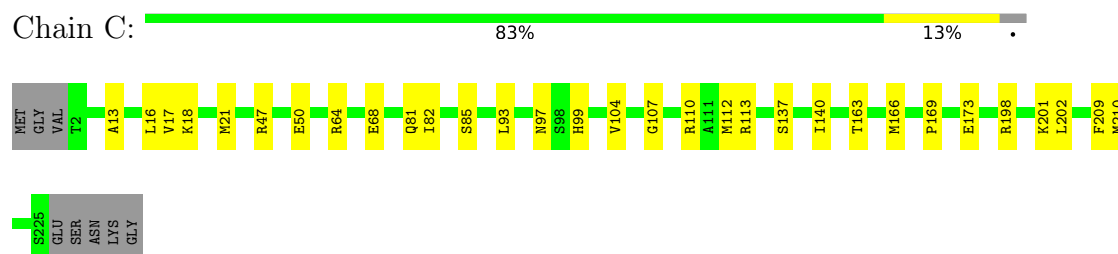
#### • Molecule 1: Tol-Pal system protein TolQ



#### • Molecule 1: Tol-Pal system protein TolQ

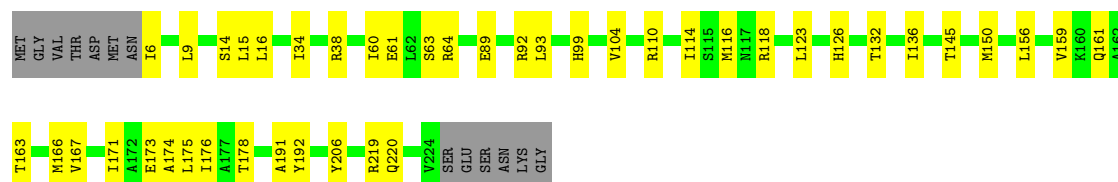


#### • Molecule 1: Tol-Pal system protein TolQ



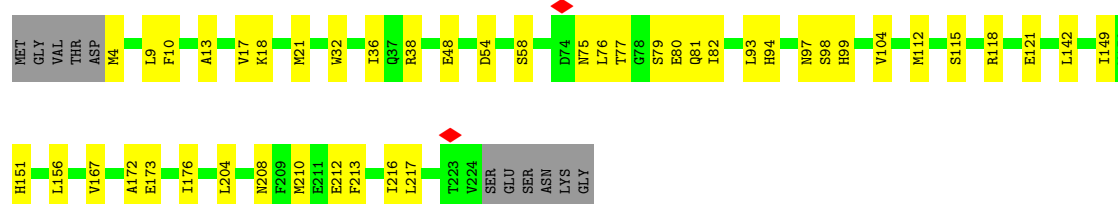
#### • Molecule 1: Tol-Pal system protein TolQ





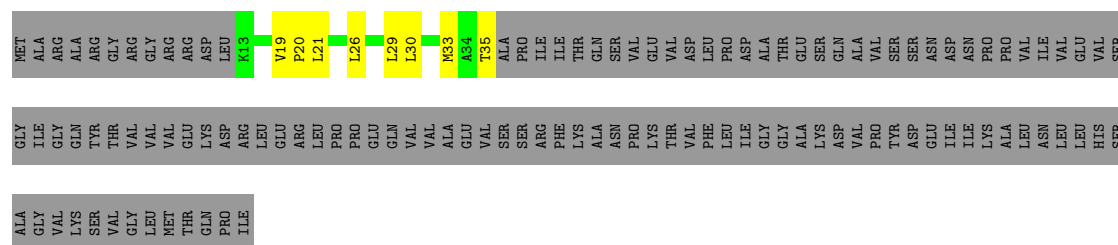
• Molecule 1: Tol-Pal system protein TolQ

Chain E: 76% 19% 5%



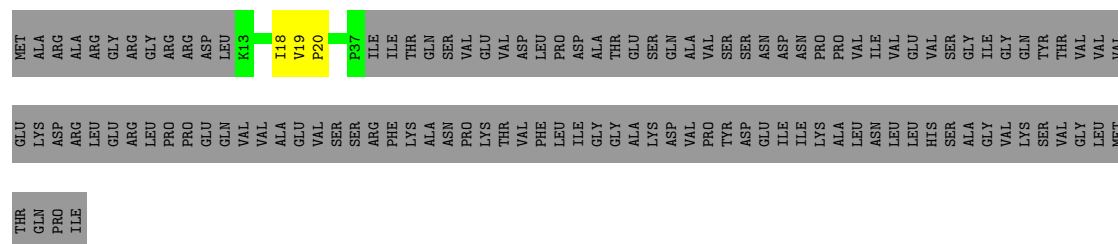
• Molecule 2: Tol-Pal system protein TolR

Chain F: 11% 6% 84%



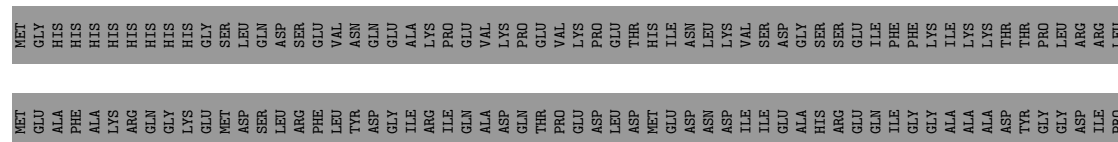
• Molecule 2: Tol-Pal system protein TolR

Chain G: 15% 82%



• Molecule 3: Ubiquitin-like protein SMT3, Tol-Pal system protein TolA

Chain H: 5% 95%



ALA	THR	ALA	GLY	ALA	ALA	LYS	GLN	THR
PRO	GLY	GLU	LYS	GLU	ALA	LYS	GLN	GLU
ASP	GLY	ALA	ALA	ALA	LEU	LYS	GLN	SER
MET	ALA	ALA	ALA	LYS	LEU	ALA	ALA	ASN
LEU	LYS	ALA	ALA	LYS	LYS	GLU	ARG	LEU
LEU	GLY	GLU	GLU	LYS	LYS	GLU	ARG	TYR
ASP	ASN	LYS	LYS	ALA	ALA	ALA	SER	GLN
ILE	ASN	ALA	ALA	GLU	ALA	ALA	ASP	GLY
LYS	ALA	ALA	ALA	ALA	ALA	LYS	GLU	ALA
PRO	SER	ASP	ASP	GLU	ALA	LYS	ARG	ALA
ALA	ASN	ALA	ALA	ALA	ALA	LYS	GLN	ALA
LEU	THR	GLY	GLY	ALA	ALA	LYS	GLN	VAL
ALA	ASN	ALA	ALA	ALA	GLU	LYS	GLN	SER
PRO	GLY	ALA	ALA	ALA	ALA	LYS	GLN	LYS
ASP	THR	LYS	LYS	ARG	ALA	ALA	GLN	ALA
GLY	ASN	ALA	ALA	LYS	LYS	ALA	ALA	THR
LEU	ASN	ALA	ALA	LYS	LYS	GLU	GLU	GLU
ALA	ALA	ALA	ALA	ALA	ALA	ALA	LEU	GLS
LEU	GLY	ASP	LYS	THR	ALA	ASP	ARG	F3S
ALA	SER	LYS	LYS	GLU	ALA	LYS	GLU	ASP
ALA	GLY	ALA	ALA	ALA	ALA	ALA	LYS	GLU
PRO	ALA	ALA	ALA	GLU	GLU	ALA	GLN	ASN
LYS	GLY	GLU	GLU	GLU	GLU	LYS	ALA	ILE
LEU	ILE	ALA	ALA	LYS	LYS	GLU	ALA	GLU
ALA	ASN	ALA	LYS	ALA	ALA	ALA	GLU	ALA
LYS	ASN	LYS	ALA	LYS	LYS	ASP	GLU	SER
ILE	TYR	ALA	ALA	ALA	LYS	ALA	GLN	ALA
PRO	ALA	ALA	ALA	ALA	ALA	LYS	GLU	ALA
LYS	GLY	ALA	ALA	GLU	GLU	LYS	ARG	ALA
PRO	GLN	GLU	GLU	GLU	ALA	ALA	LEU	GLY
PRO	PRO	ILE	LYS	GLU	GLU	ALA	GLN	GLY
SER	GLN	LYS	ALA	LYS	LYS	ASP	LEU	GLY
ALA	ALA	ALA	ALA	ALA	ALA	ALA	GLU	GLY
VAL	ILE	ALA	ALA	ALA	ALA	LYS	LYS	SER
TYR	GLU	LYS	LYS	ALA	ALA	LYS	GLU	SER
GLU	SER	ALA	ALA	GLU	GLU	LYS	ARG	ILE
VAL	VAL	LYS	ALA	LYS	LYS	ALA	LEU	ASP
LYS	LYS	TYR	GLU	ALA	ALA	GLU	ALA	ALA
ASN	ASP	GLN	ALA	ALA	ALA	GLU	ALA	VAL
ALA	ALA	ASP	ALA	ALA	ASP	GLU	GLN	MET
PRO	SER	ASP	ASP	LYS	LYS	ALA	GLU	VAL
ASP	SER	ILE	ILE	LYS	ALA	LYS	LYS	ASP
LEU	ASP	PHE	PHE	ALA	ALA	ALA	GLN	GLY
PHE	PHE	ALA	GLY	GLY	ALA	ALA	ALA	ALA
LYS	LYS	GLY	LYS	LYS	GLU	GLU	ALA	VAL
PRO	PRO	THR	LYS	LEU	GLU	GLU	GLU	VAL
				SER	SER	LYS	GLU	GLN
	CYS	THR	LYS	GLY	ALA	GLN	ALA	GLN
	LEU	LEU	LYS	GLY	ALA	LYS	ALA	TYR
	ARG	THR	LYS	ALA	ALA	LYS	LYS	LYS
	ILE	ILE	ALA	ASN	ASP	ALA	GLN	ARG
	LYS	LYS	ALA	ALA	LYS	GLU	ALA	MET
	LEU	PRO	LYS	LYS	LYS	ALA	GLN	GLN
	LEU	LEU	LYS	PRO	ALA	ALA	LEU	SER

- Molecule 3: Ubiquitin-like protein SMT3, Tol-Pal system protein TolA

Chain I:  5% 95%

[illegible]

- Molecule 3: Ubiquitin-like protein SMT3, Tol-Pal system protein TolA

Chain J:  96%

MET GLY HIS HIS HIS HIS HIS HIS HIS HIS GLY SER LEU GLN ASP SER ASP GLU VAL ASN GLN GLU GLU LYS PRO PRO GLU VAL LYS PRO LYS GLU VAL VAL LYS PRO GLU GLU THR HIS HIS ILE ASN ASP GLY SER SER SER LEU LYS LYS THR THR PRO PRO LEU ARG ARG LEU

[illegible]

- Molecule 3: Ubiquitin-like protein SMT3, Tol-Pal system protein TolA

Chain K:  97%

[illegible]

- Chain L:  95%

Chain L:  95%

[illegible]

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	160613	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.573	Depositor
Minimum map value	-0.434	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.016	Depositor
Recommended contour level	0.05	Depositor
Map size (Å)	251.99998, 251.99998, 251.99998	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.84, 0.84, 0.84	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	0.11	0/1818	0.26	0/2455
1	B	0.13	0/1772	0.28	0/2395
1	C	0.12	0/1792	0.30	0/2423
1	D	0.13	0/1738	0.32	0/2352
1	E	0.11	0/1771	0.26	0/2394
2	F	0.15	0/180	0.31	0/245
2	G	0.16	0/193	0.36	0/264
3	H	0.04	0/218	0.13	0/297
3	I	0.06	0/241	0.16	0/326
3	J	0.05	0/164	0.17	0/224
3	K	0.05	0/129	0.15	0/175
3	L	0.05	0/215	0.13	0/292
All	All	0.12	0/10231	0.28	0/13842

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	1784	0	1806	22	0
1	B	1738	0	1765	29	0
1	C	1758	0	1786	21	0
1	D	1705	0	1730	27	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	1737	0	1770	32	0
2	F	179	0	207	10	0
2	G	191	0	219	2	0
3	H	214	0	221	0	0
3	I	237	0	249	1	0
3	J	164	0	177	0	0
3	K	129	0	138	1	0
3	L	212	0	225	3	0
All	All	10048	0	10293	132	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.

All (132) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:149:ILE:HD13	2:F:26:LEU:HD13	1.57	0.87
1:B:145:THR:HG23	1:B:174:ALA:HB1	1.69	0.74
1:A:215:ALA:HB2	1:D:110:ARG:HH21	1.54	0.73
1:C:17:VAL:HG12	1:C:21:MET:HE2	1.73	0.70
1:C:93:LEU:HD23	1:C:104:VAL:HA	1.73	0.70
1:D:156:LEU:HB2	1:D:167:VAL:HG11	1.74	0.69
1:B:37:GLN:HE22	1:B:38:ARG:HH21	1.39	0.69
1:E:142:LEU:HD23	2:F:20:PRO:HB2	1.75	0.67
1:C:17:VAL:HG11	1:C:173:GLU:HB2	1.76	0.67
2:F:26:LEU:HA	2:F:29:LEU:HD12	1.77	0.67
1:B:31:SER:O	1:B:35:ILE:HG12	1.95	0.66
1:E:17:VAL:HG12	1:E:21:MET:HE1	1.79	0.66
1:E:93:LEU:HB3	1:E:104:VAL:HG22	1.78	0.66
1:D:38:ARG:NH1	1:D:123:LEU:O	2.29	0.65
1:D:219:ARG:HH21	1:D:220:GLN:HB3	1.60	0.65
1:A:17:VAL:HG12	1:A:21:MET:HE2	1.79	0.64
1:A:93:LEU:HD23	1:A:104:VAL:HA	1.78	0.64
1:E:112:MET:HE2	1:E:210:MET:HG3	1.80	0.63
1:D:93:LEU:HD23	1:D:104:VAL:HG13	1.81	0.63
1:D:145:THR:HG1	1:D:178:THR:HG1	1.44	0.62
1:B:106:GLU:OE1	1:B:110:ARG:NH2	2.33	0.62
1:A:68:GLU:OE1	1:A:72:LYS:NZ	2.30	0.62
1:A:211:GLU:OE1	1:D:110:ARG:NH1	2.32	0.62
1:A:39:THR:HG23	1:A:198:ARG:HH12	1.65	0.61
1:D:145:THR:HG23	1:D:174:ALA:HB1	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:164:LEU:HD11	2:F:35:THR:HG22	1.83	0.60
1:A:78:GLY:N	1:A:119:GLU:OE2	2.34	0.60
1:C:13:ALA:O	1:C:18:LYS:NZ	2.35	0.60
1:E:204:LEU:O	1:E:208:ASN:ND2	2.35	0.60
1:E:156:LEU:HB2	1:E:167:VAL:HG11	1.84	0.60
1:E:81:GLN:OE1	1:E:115:SER:OG	2.23	0.57
1:B:194:ARG:O	1:B:197:GLN:HG2	2.05	0.57
1:E:76:LEU:HD22	1:E:80:GLU:HB3	1.87	0.57
1:A:211:GLU:O	1:D:110:ARG:NH2	2.38	0.57
1:B:52:PHE:HE1	1:B:65:LEU:HD21	1.71	0.56
1:C:81:GLN:OE1	1:C:85:SER:OG	2.24	0.56
1:C:113:ARG:NH2	1:E:212:GLU:OE2	2.39	0.56
1:C:137:SER:HA	1:C:140:ILE:HD12	1.90	0.54
1:C:82:ILE:HB	1:C:209:PHE:HE2	1.74	0.53
1:B:108:ALA:HB1	1:B:112:MET:HE3	1.91	0.52
1:A:38:ARG:NH1	1:A:123:LEU:O	2.43	0.52
1:B:146:VAL:HA	1:B:149:ILE:HG12	1.92	0.52
1:A:137:SER:HB2	1:A:185:ALA:HB2	1.92	0.51
1:E:97:ASN:OD1	1:E:99:HIS:NE2	2.43	0.51
1:E:173:GLU:HA	1:E:176:ILE:HD12	1.91	0.51
1:B:101:PRO:HB3	1:B:221:ALA:HB1	1.93	0.51
1:E:142:LEU:HD21	2:F:21:LEU:HB2	1.93	0.51
1:C:112:MET:HE2	1:C:210:MET:HG3	1.93	0.50
1:E:54:ASP:O	1:E:58:SER:OG	2.29	0.50
1:D:60:ILE:HD12	1:D:64:ARG:HH12	1.76	0.50
2:G:19:VAL:HB	2:G:20:PRO:HD3	1.94	0.49
2:F:30:LEU:HA	2:F:33:MET:HG2	1.93	0.49
1:A:82:ILE:HG22	1:A:115:SER:HB3	1.93	0.49
1:A:29:ILE:HA	3:K:23:HIS:CE1	2.48	0.49
1:D:6:ILE:HG23	1:D:9:LEU:HD23	1.94	0.48
1:B:175:LEU:HD13	1:E:149:ILE:HG23	1.95	0.48
1:C:64:ARG:NH2	1:C:68:GLU:OE2	2.46	0.48
1:E:118:ARG:O	1:E:121:GLU:HG3	2.14	0.48
1:E:9:LEU:HD23	1:E:176:ILE:HD11	1.96	0.47
1:A:25:ILE:HG13	1:A:180:ILE:HD11	1.96	0.47
1:A:173:GLU:O	1:A:176:ILE:HG22	2.15	0.47
1:E:94:HIS:O	1:E:98:SER:HB3	2.15	0.47
1:E:48:GLU:OE2	1:E:77:THR:OG1	2.32	0.47
1:D:14:SER:OG	1:D:15:LEU:N	2.47	0.46
1:A:151:HIS:HA	1:A:154:ILE:HG12	1.98	0.46
1:E:172:ALA:O	1:E:176:ILE:HG13	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:95:ARG:HD3	1:B:95:ARG:HA	1.69	0.46
2:F:19:VAL:O	2:F:20:PRO:C	2.59	0.46
1:A:61:GLU:HG3	1:A:63:SER:H	1.81	0.45
1:B:173:GLU:O	1:B:176:ILE:HG22	2.17	0.45
1:E:38:ARG:HA	1:E:38:ARG:HD3	1.77	0.45
1:C:17:VAL:HG21	1:C:173:GLU:HG3	1.99	0.45
1:D:114:ILE:HG22	1:D:118:ARG:NE	2.31	0.45
2:F:19:VAL:HG22	2:G:18:ILE:HD11	1.99	0.44
1:B:110:ARG:HA	1:B:113:ARG:HG2	1.99	0.44
1:A:16:LEU:HD23	1:A:147:TRP:CD1	2.53	0.44
1:A:132:THR:O	1:A:136:ILE:HG12	2.16	0.44
1:E:4:MET:N	3:L:34:SER:HB2	2.32	0.44
2:F:26:LEU:O	2:F:29:LEU:HB2	2.17	0.44
1:A:10:PHE:O	1:A:18:LYS:NZ	2.44	0.44
1:B:12:LYS:HA	1:B:12:LYS:HD2	1.72	0.44
1:B:14:SER:O	1:B:18:LYS:HG3	2.18	0.44
1:C:16:LEU:HB2	3:L:30:LEU:HD11	1.99	0.44
1:C:18:LYS:HA	1:C:21:MET:HE3	2.00	0.43
1:D:173:GLU:O	1:D:176:ILE:HG22	2.17	0.43
1:A:73:ARG:HH11	1:A:74:ASP:HB2	1.82	0.43
1:D:34:ILE:HD13	1:D:126:HIS:HB3	2.01	0.43
1:E:216:ILE:HG23	1:E:217:LEU:HD12	2.00	0.43
1:C:198:ARG:O	1:C:201:LYS:HG2	2.19	0.43
1:D:61:GLU:HG3	1:D:63:SER:H	1.83	0.43
1:D:89:GLU:HG2	1:D:92:ARG:HH21	1.84	0.43
1:D:92:ARG:NH2	1:D:93:LEU:HB2	2.34	0.43
1:E:13:ALA:O	1:E:18:LYS:NZ	2.51	0.43
1:B:132:THR:O	1:B:136:ILE:HG12	2.19	0.43
1:D:171:ILE:O	1:D:175:LEU:HG	2.19	0.42
1:A:72:LYS:O	1:A:74:ASP:N	2.50	0.42
1:C:47:ARG:O	1:C:50:GLU:HG3	2.19	0.42
1:D:15:LEU:HG	1:D:16:LEU:HD22	2.01	0.42
1:C:107:GLY:HA2	1:C:110:ARG:HG2	2.01	0.42
1:C:163:THR:H	1:C:166:MET:HE2	1.85	0.42
1:D:132:THR:O	1:D:136:ILE:HG12	2.20	0.42
1:D:163:THR:HG21	1:D:166:MET:HE3	2.01	0.42
1:D:159:VAL:HG12	1:D:161:GLN:H	1.85	0.42
1:A:204:LEU:HD23	1:A:204:LEU:HA	1.86	0.42
1:B:97:ASN:HB2	1:B:99:HIS:CD2	2.55	0.42
1:C:202:LEU:HD23	1:C:202:LEU:HA	1.85	0.42
1:B:104:VAL:HG12	1:B:217:LEU:HD21	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:149:ILE:HG13	1:B:150:MET:N	2.34	0.42
1:C:97:ASN:HB2	1:C:99:HIS:CD2	2.54	0.42
1:E:79:SER:HA	1:E:82:ILE:HD12	2.02	0.41
1:E:32:TRP:O	1:E:36:ILE:HG12	2.20	0.41
1:E:75:ASN:OD1	1:E:75:ASN:N	2.53	0.41
1:D:171:ILE:HD12	1:D:171:ILE:H	1.85	0.41
1:B:52:PHE:CG	1:B:80:GLU:HG3	2.56	0.41
1:C:169:PRO:O	1:C:173:GLU:OE1	2.38	0.41
1:B:171:ILE:O	1:B:175:LEU:HG	2.21	0.41
1:B:149:ILE:HB	2:F:30:LEU:HD11	2.03	0.41
1:B:186:ILE:HB	1:B:187:PRO:HD3	2.02	0.41
1:D:191:ALA:O	1:D:192:TYR:C	2.63	0.41
1:E:17:VAL:HG12	1:E:21:MET:CE	2.49	0.41
1:E:18:LYS:HA	1:E:21:MET:HE2	2.03	0.41
1:C:113:ARG:NH2	1:E:208:ASN:HB3	2.36	0.41
1:B:13:ALA:O	1:B:18:LYS:NZ	2.37	0.40
1:B:87:PHE:HA	1:B:90:PHE:HB3	2.03	0.40
1:D:150:MET:HE3	1:D:150:MET:HB3	2.00	0.40
1:E:112:MET:HE1	1:E:213:PHE:HB3	2.03	0.40
1:E:10:PHE:O	1:E:18:LYS:HE3	2.22	0.40
1:B:163:THR:OG1	1:B:164:LEU:N	2.54	0.40
1:D:116:MET:SD	1:D:206:TYR:HB3	2.61	0.40
3:I:10:ASP:O	3:I:14:ARG:HG3	2.21	0.40
1:B:3:ASP:HB3	1:E:151:HIS:CE1	2.57	0.40
3:L:11:LYS:HA	3:L:11:LYS:HD3	1.96	0.40

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	226/232 (97%)	222 (98%)	4 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	219/232 (94%)	211 (96%)	8 (4%)	0	100	100
1	C	222/232 (96%)	212 (96%)	10 (4%)	0	100	100
1	D	217/232 (94%)	207 (95%)	9 (4%)	1 (0%)	24	57
1	E	219/232 (94%)	217 (99%)	2 (1%)	0	100	100
2	F	21/142 (15%)	20 (95%)	1 (5%)	0	100	100
2	G	23/142 (16%)	23 (100%)	0	0	100	100
3	H	26/557 (5%)	26 (100%)	0	0	100	100
3	I	28/557 (5%)	28 (100%)	0	0	100	100
3	J	22/557 (4%)	22 (100%)	0	0	100	100
3	K	16/557 (3%)	16 (100%)	0	0	100	100
3	L	26/557 (5%)	26 (100%)	0	0	100	100
All	All	1265/4229 (30%)	1230 (97%)	34 (3%)	1 (0%)	49	79

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	99	HIS

### 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	184/188 (98%)	184 (100%)	0	100	100
1	B	179/188 (95%)	179 (100%)	0	100	100
1	C	182/188 (97%)	182 (100%)	0	100	100
1	D	173/188 (92%)	173 (100%)	0	100	100
1	E	179/188 (95%)	179 (100%)	0	100	100
2	F	22/123 (18%)	22 (100%)	0	100	100
2	G	23/123 (19%)	23 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	H	22/384 (6%)	22 (100%)	0	100	100
3	I	25/384 (6%)	25 (100%)	0	100	100
3	J	15/384 (4%)	15 (100%)	0	100	100
3	K	13/384 (3%)	13 (100%)	0	100	100
3	L	22/384 (6%)	22 (100%)	0	100	100
All	All	1039/3106 (34%)	1039 (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. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	5	ASN
1	A	193	ASN
1	B	200	ASN
1	C	43	ASN
1	C	75	ASN
1	C	151	HIS
1	C	220	GLN
1	D	75	ASN
1	D	97	ASN
1	D	126	HIS
1	D	151	HIS
1	D	200	ASN
1	D	208	ASN
1	D	220	GLN
1	E	117	ASN
1	E	193	ASN
1	E	220	GLN

### 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](#)

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.



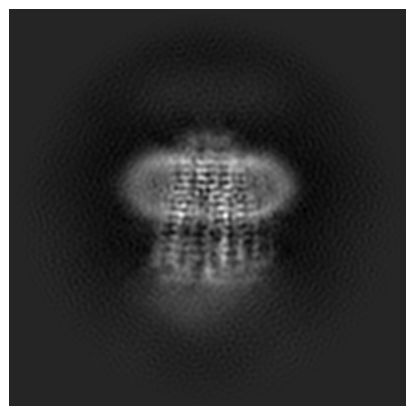
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-62493. These allow visual inspection of the internal detail of the map and identification of artifacts.

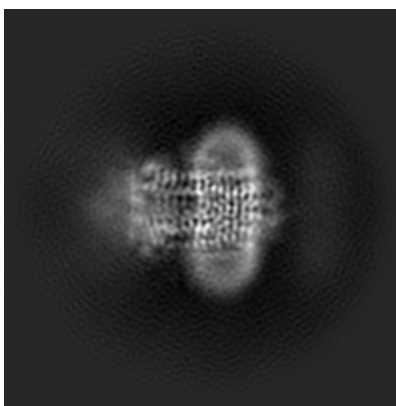
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

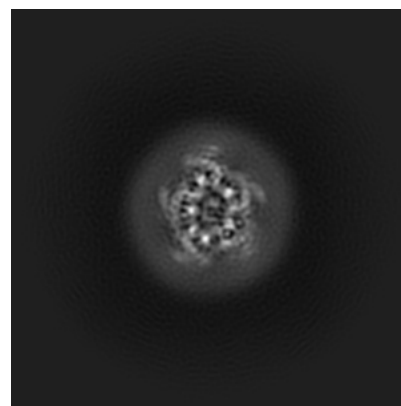
#### 6.1.1 Primary map



X

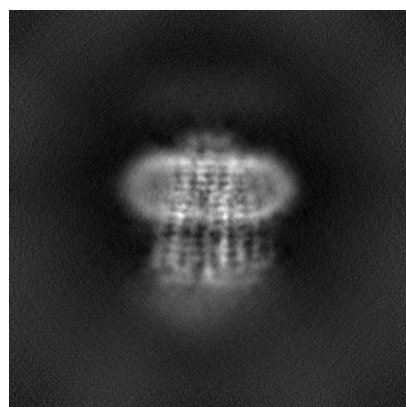


Y

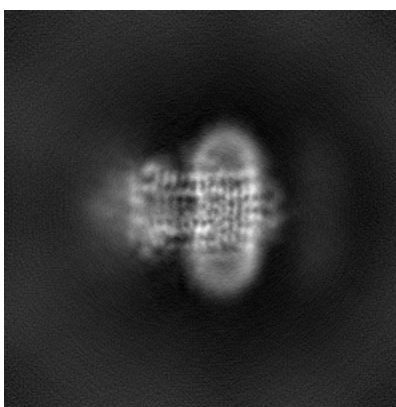


Z

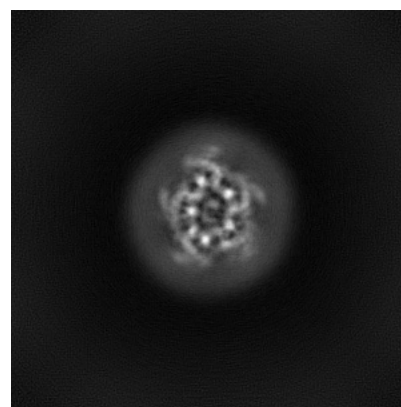
#### 6.1.2 Raw map



X



Y

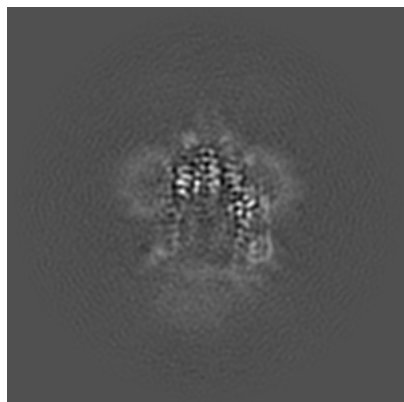


Z

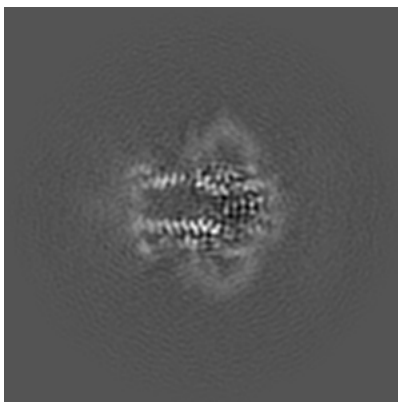
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

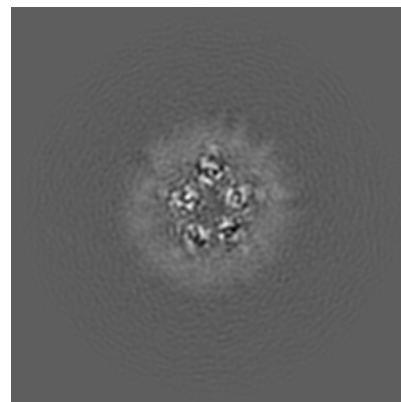
### 6.2.1 Primary map



X Index: 150

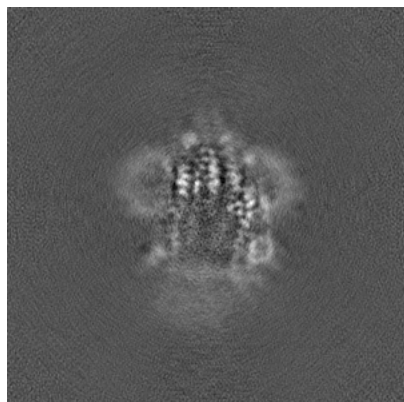


Y Index: 150

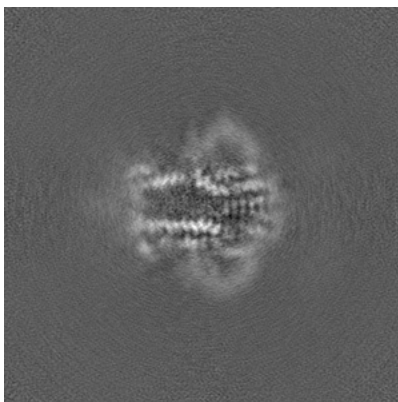


Z Index: 150

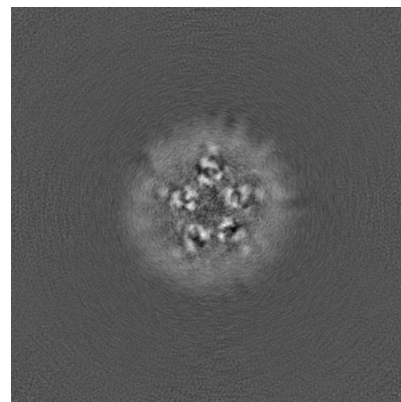
### 6.2.2 Raw map



X Index: 150



Y Index: 150

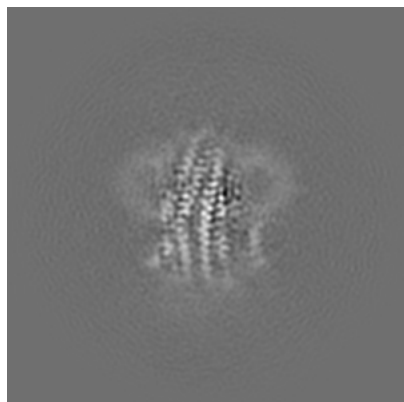


Z Index: 150

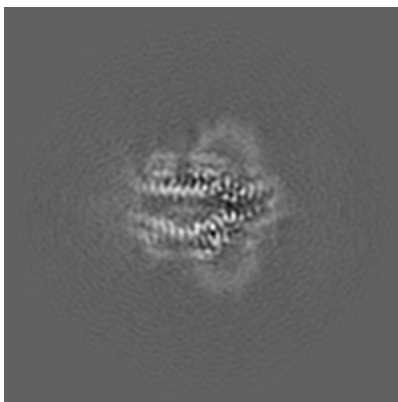
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

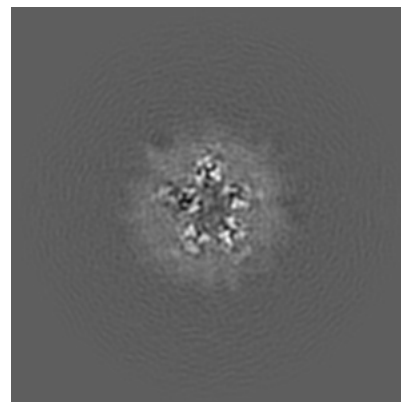
### 6.3.1 Primary map



X Index: 135

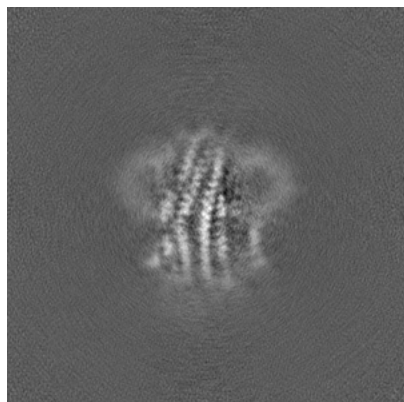


Y Index: 161

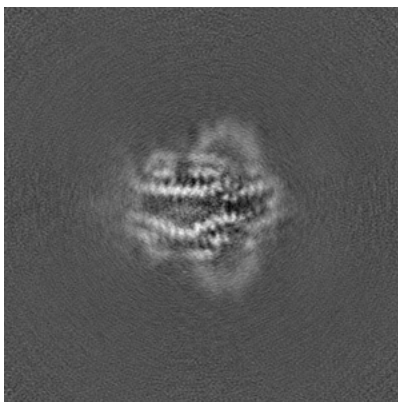


Z Index: 146

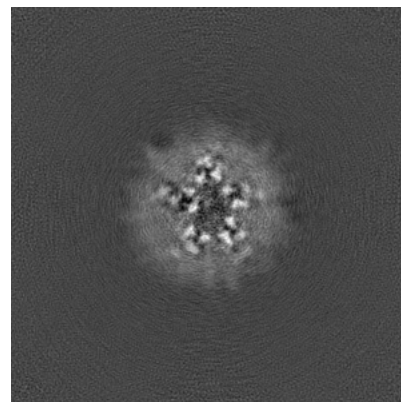
### 6.3.2 Raw map



X Index: 135



Y Index: 161

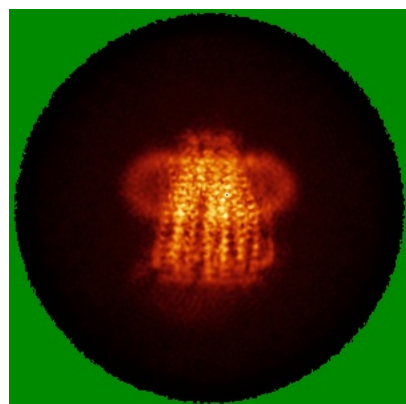


Z Index: 146

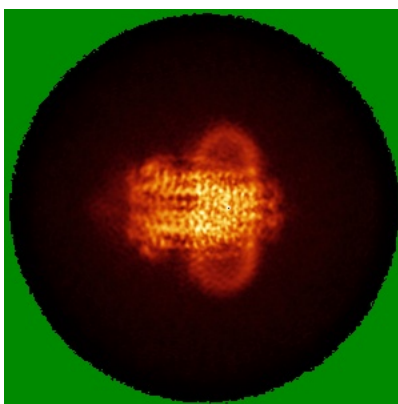
The images above show the largest variance slices of the map in three orthogonal directions.

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

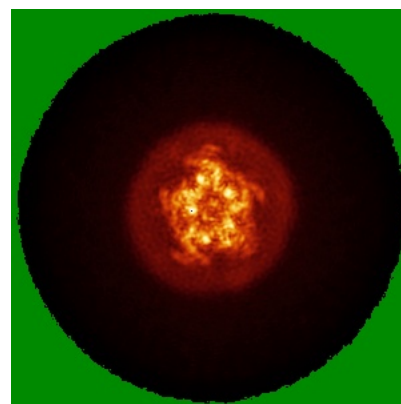
### 6.4.1 Primary map



X

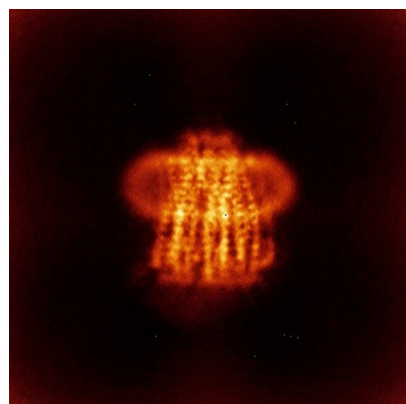


Y

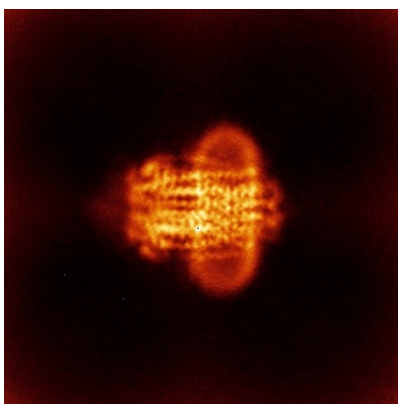


Z

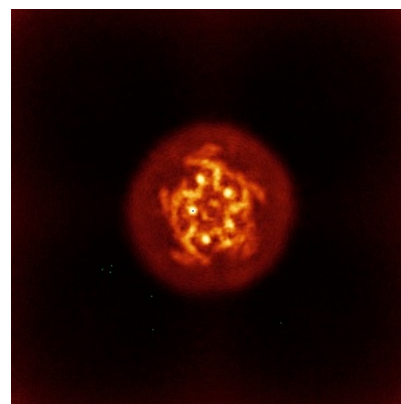
### 6.4.2 Raw map



X



Y

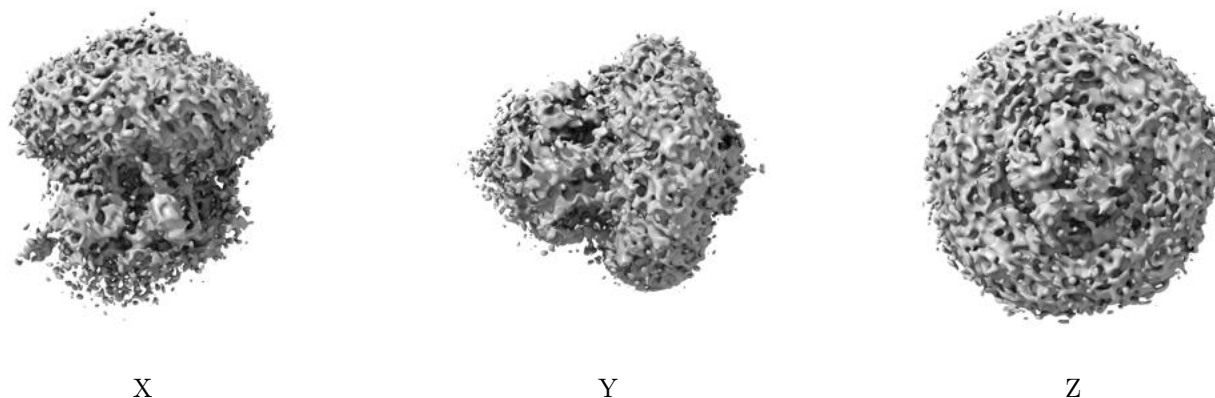


Z

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.

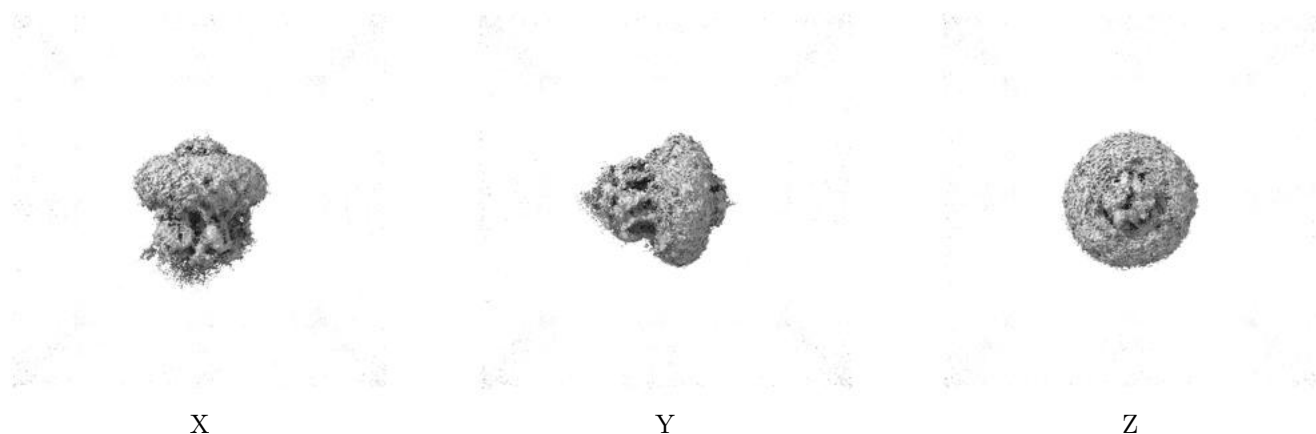
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.05. 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.



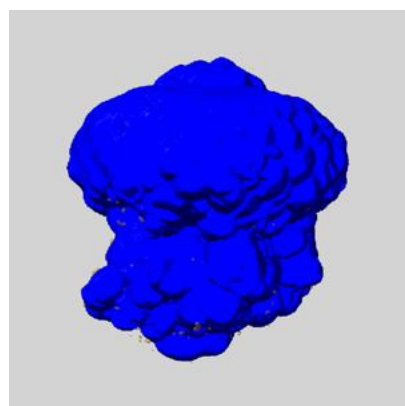
## 6.6 Mask visualisation [i](#)

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

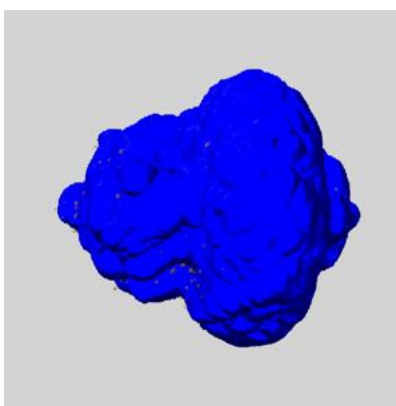
A mask typically either:

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

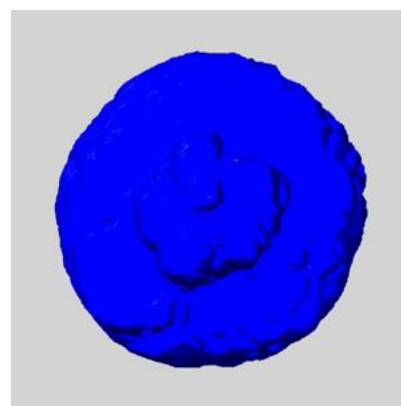
### 6.6.1 emd\_62493\_msk\_1.map [i](#)



X



Y

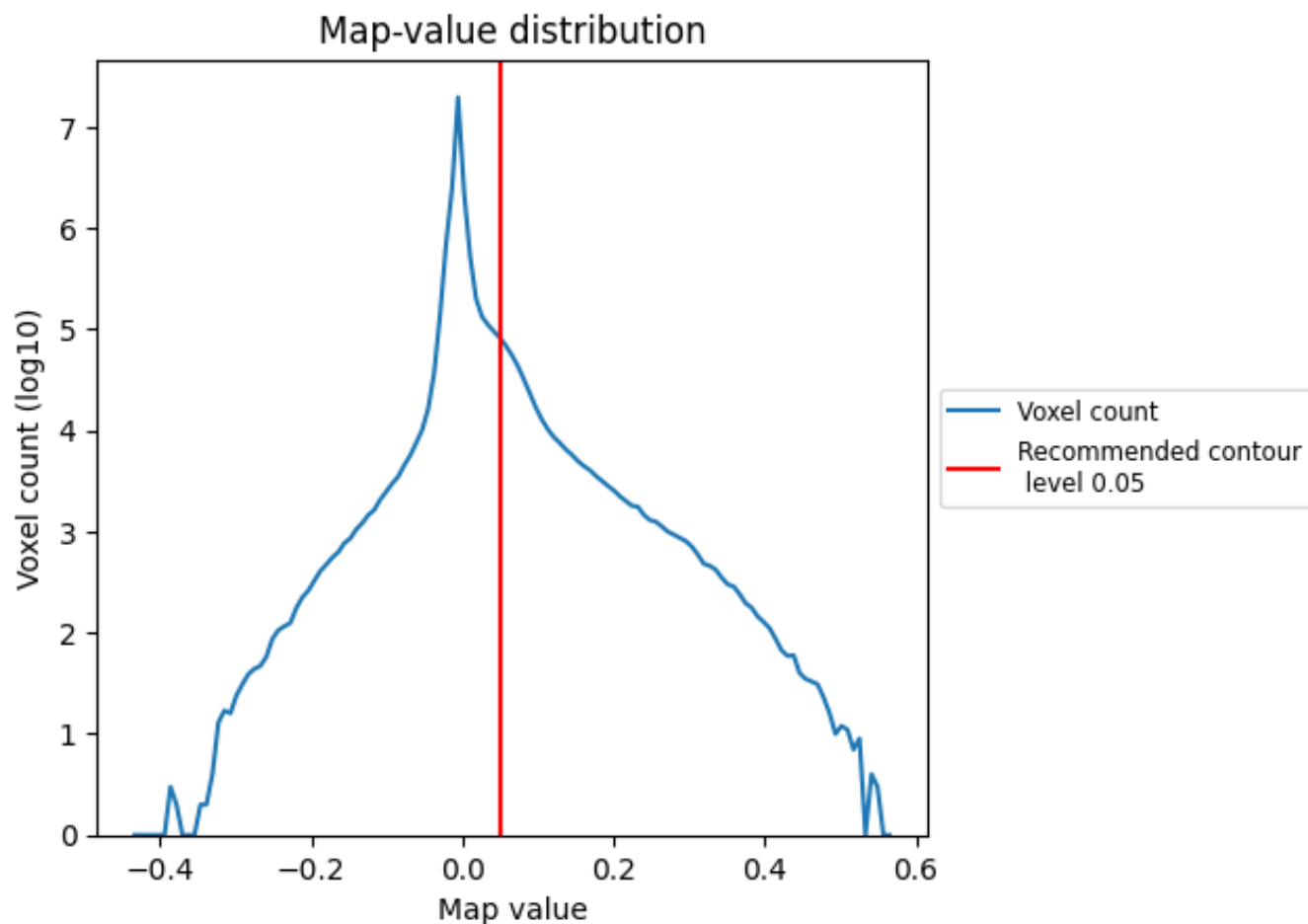


Z

## 7 Map analysis [i](#)

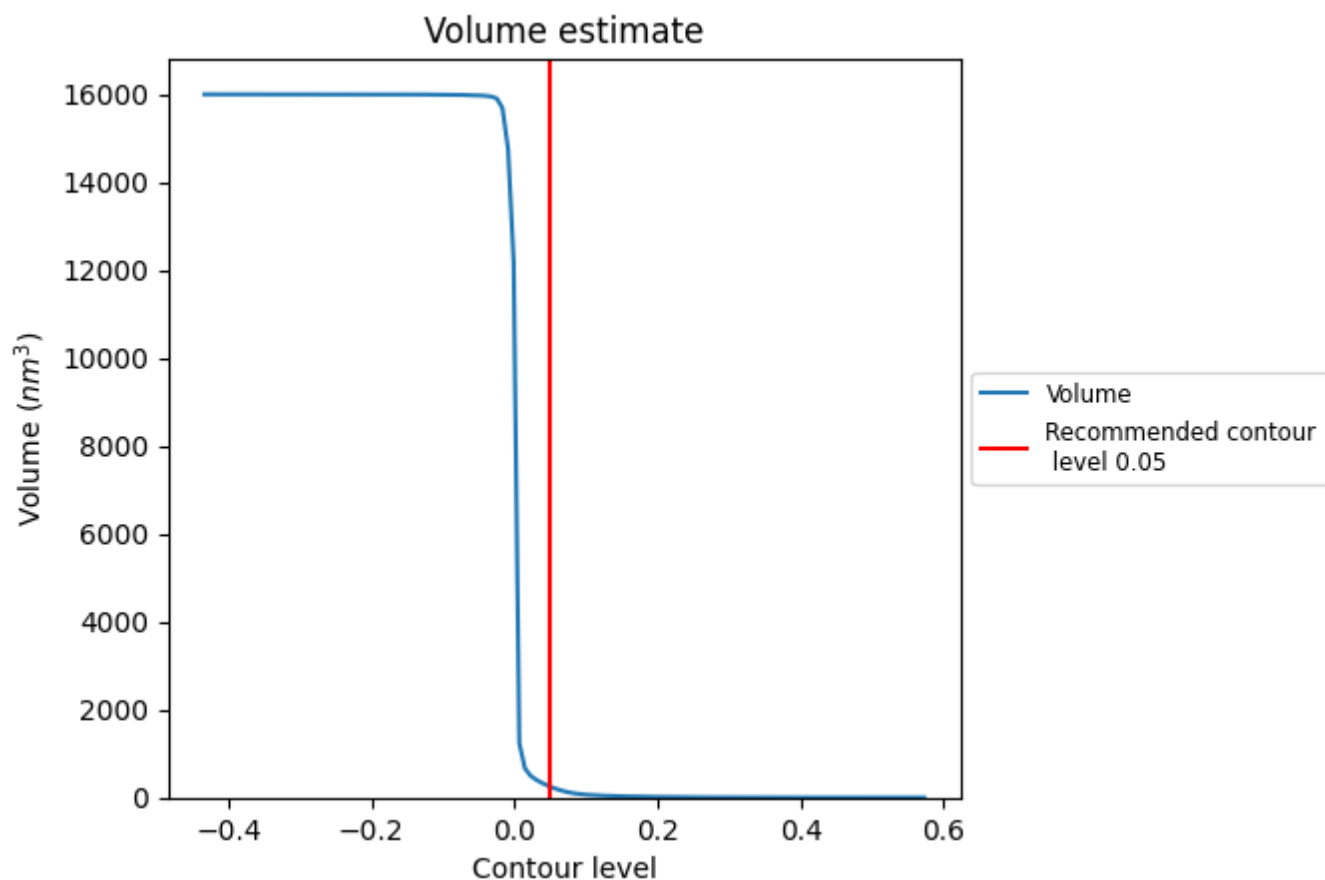
This section contains the results of statistical analysis of the map.

### 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](#)

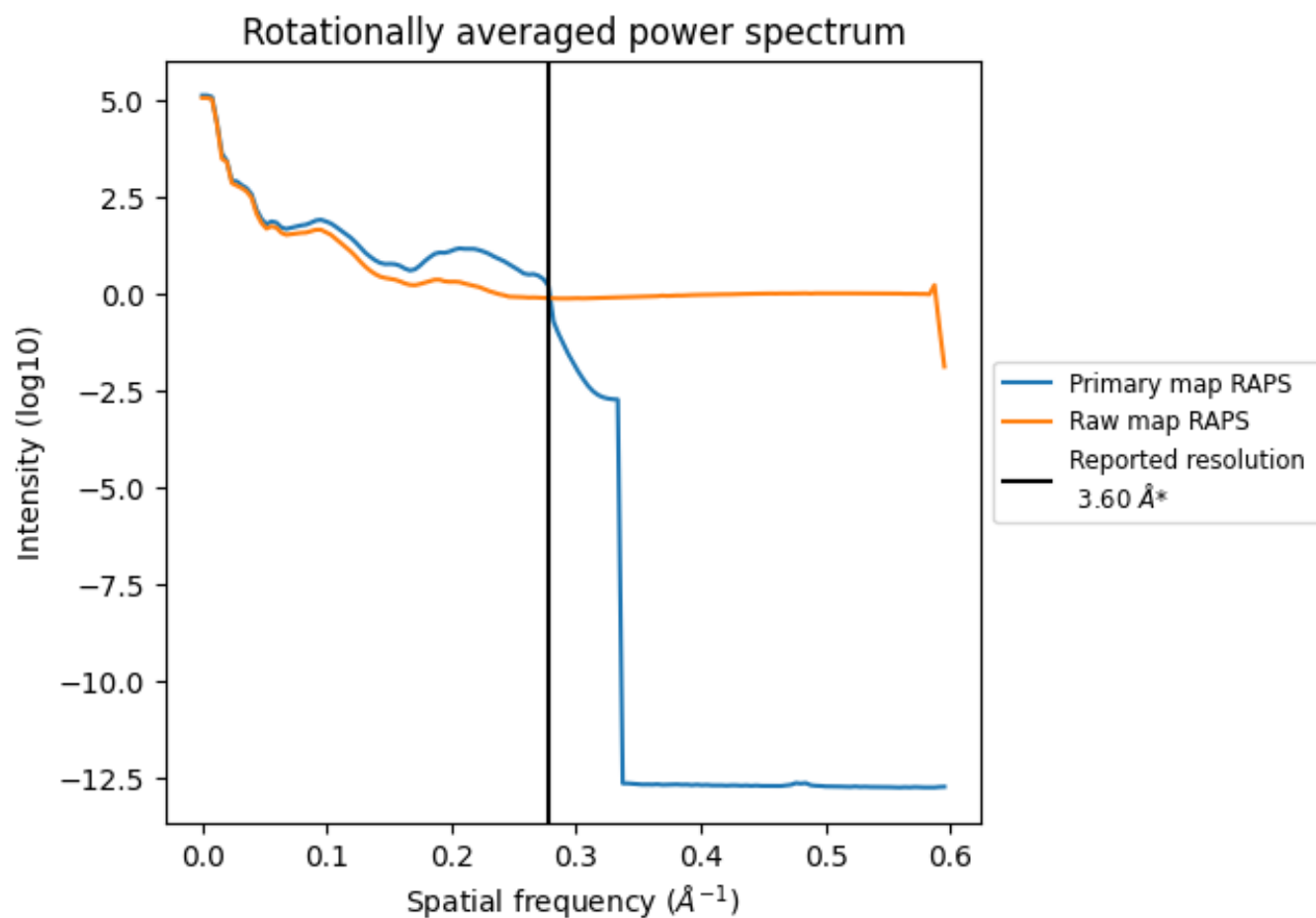


The volume at the recommended contour level is 248 nm<sup>3</sup>; this corresponds to an approximate mass of 224 kDa.

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 ⓘ

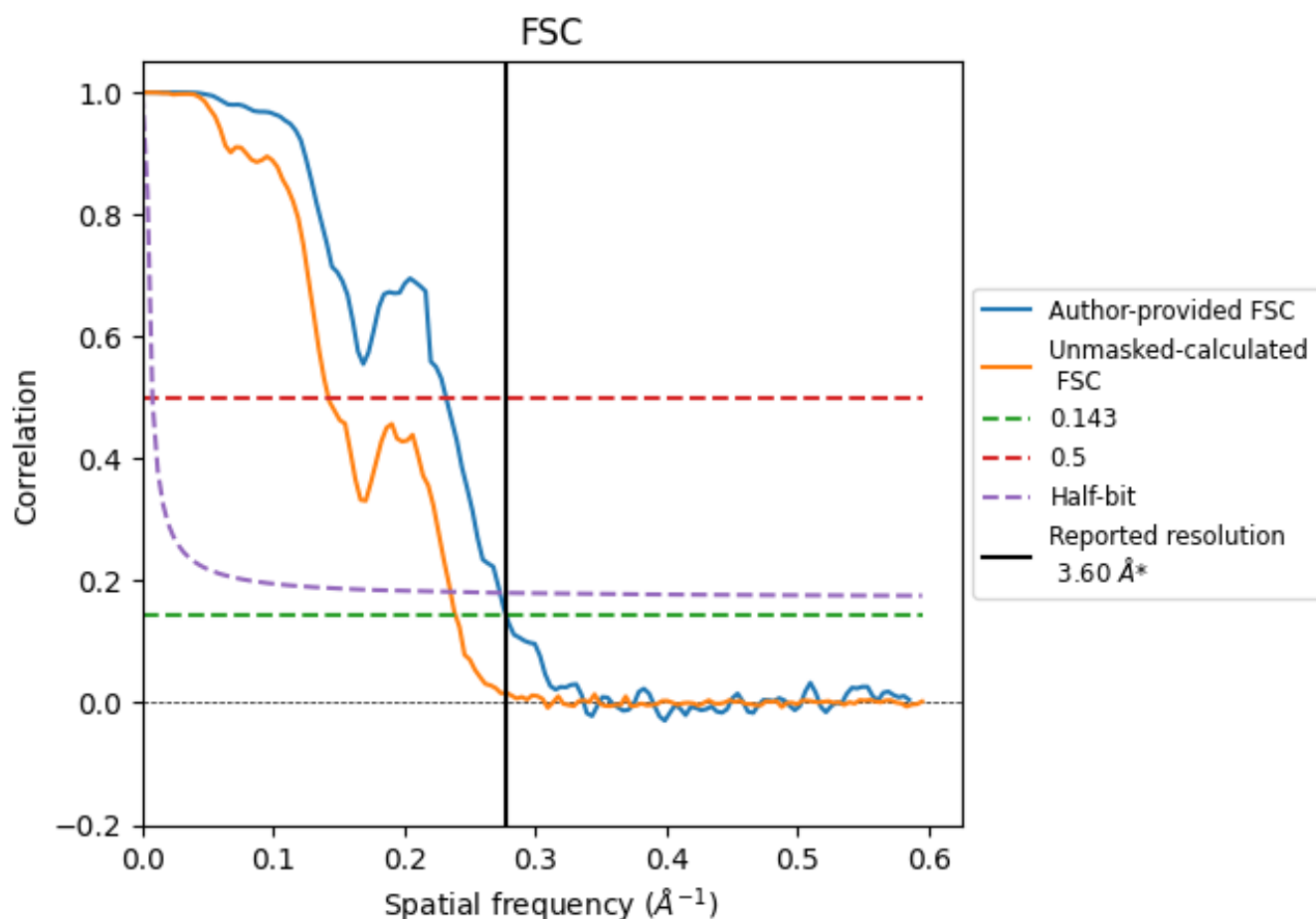


\*Reported resolution corresponds to spatial frequency of 0.278 Å<sup>-1</sup>

## 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 0.278 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

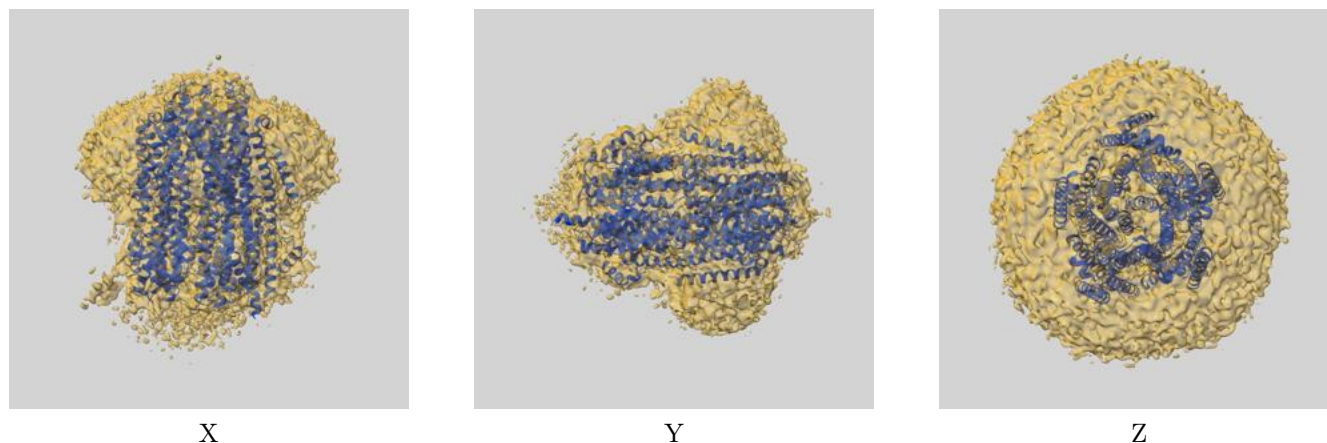
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.60	-	-
Author-provided FSC curve	3.60	4.31	3.66
Unmasked-calculated*	4.18	7.04	4.25

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.18 differs from the reported value 3.6 by more than 10 %

## 9 Map-model fit [i](#)

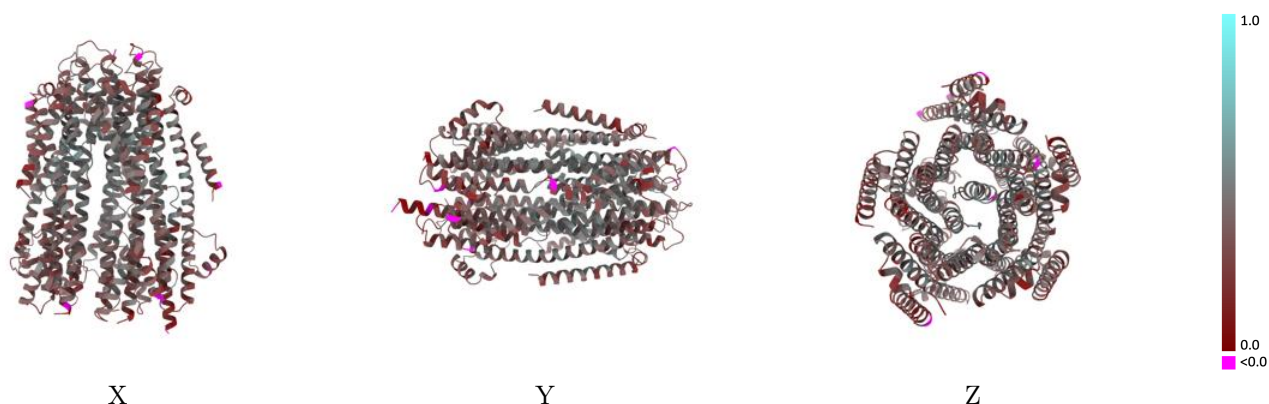
This section contains information regarding the fit between EMDB map EMD-62493 and PDB model 9KQ0. Per-residue inclusion information can be found in section 3 on page 11.

### 9.1 Map-model overlay [i](#)



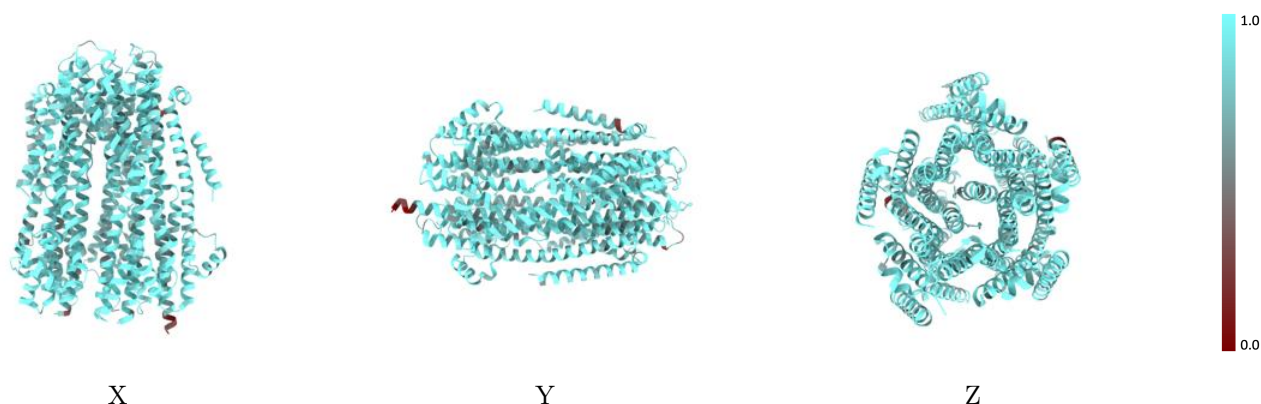
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



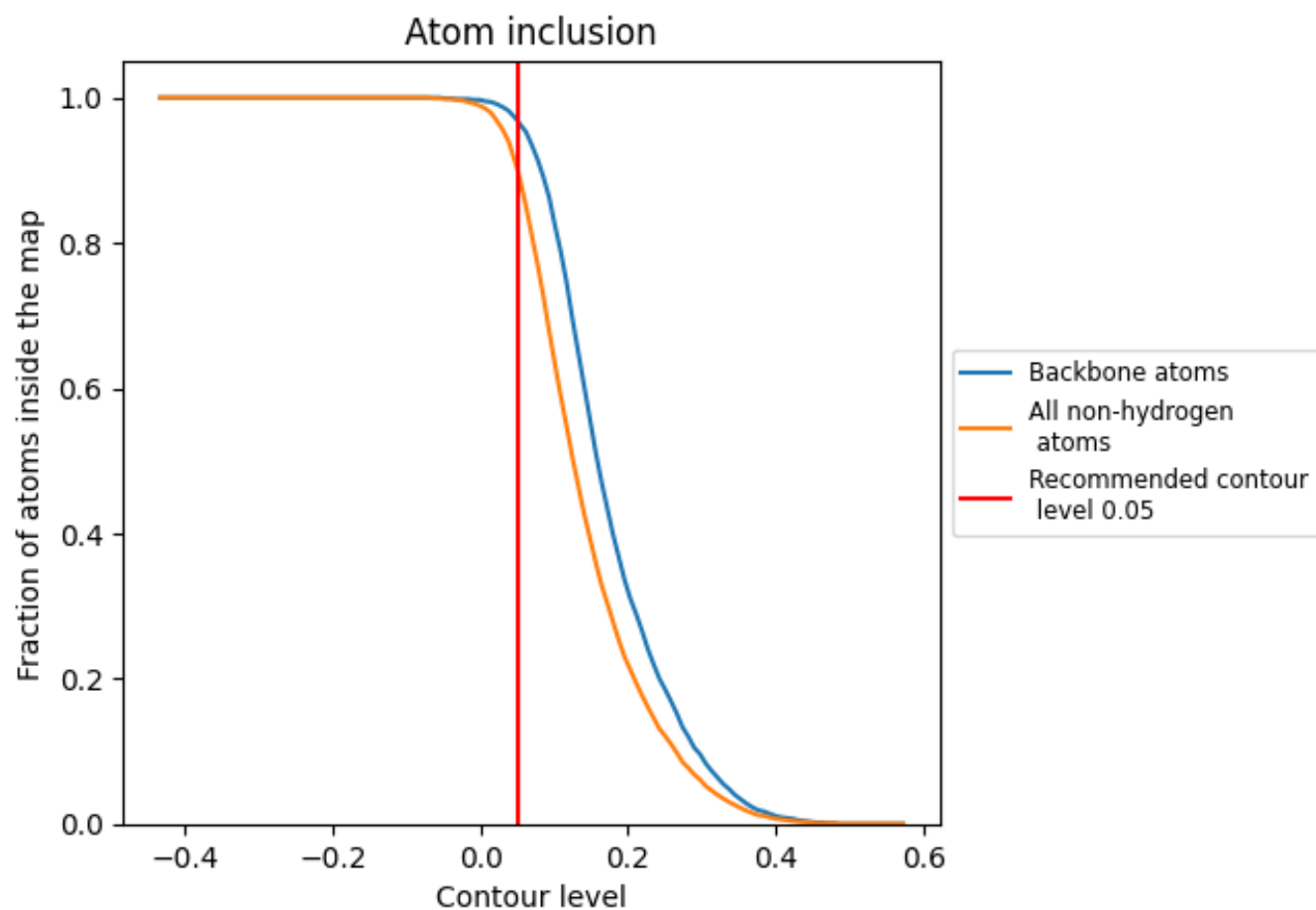
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.05).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 90% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div>0.9020</div>	<div><div></div>0.3620</div>
A	<div><div></div>0.8950</div>	<div><div></div>0.3440</div>
B	<div><div></div>0.9010</div>	<div><div></div>0.3540</div>
C	<div><div></div>0.9230</div>	<div><div></div>0.3820</div>
D	<div><div></div>0.9070</div>	<div><div></div>0.3690</div>
E	<div><div></div>0.9180</div>	<div><div></div>0.3850</div>
F	<div><div></div>0.8380</div>	<div><div></div>0.4370</div>
G	<div><div></div>0.8530</div>	<div><div></div>0.4300</div>
H	<div><div></div>0.8310</div>	<div><div></div>0.2410</div>
I	<div><div></div>0.8890</div>	<div><div></div>0.3150</div>
J	<div><div></div>0.8350</div>	<div><div></div>0.3010</div>
K	<div><div></div>0.8680</div>	<div><div></div>0.3040</div>
L	<div><div></div>0.8860</div>	<div><div></div>0.3290</div>

1.0

0.0

<0.0