



Full wwPDB EM Validation Report ⓘ

Mar 20, 2026 – 06:21 AM UTC

PDB ID : 6Y5B / pdb_00006y5b
EMDB ID : EMD-10693
Title : 5-HT3A receptor in Salipro (apo, asymmetric)
Authors : Zhang, Y.; Dijkman, P.M.; Zou, R.; Zandl-Lang, M.; Sanchez, R.M.; Eckhardt-Strelau, L.; Koefeler, H.; Vogel, H.; Yuan, S.; Kudryashev, M.
Deposited on : 2020-02-25
Resolution : 3.10 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.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

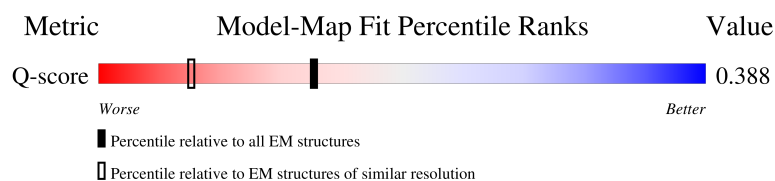
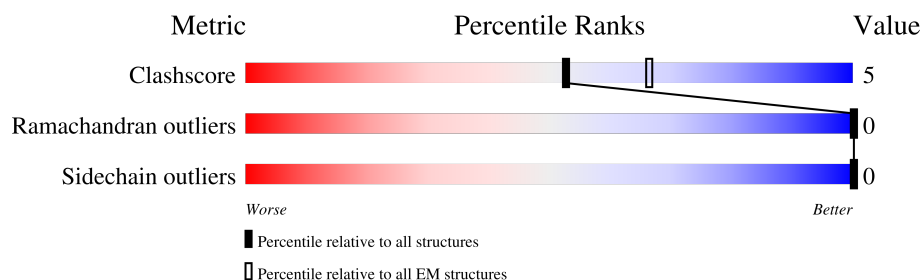
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.10 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	14724 (2.60 - 3.60)

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	538	
1	B	538	
1	C	538	
1	D	538	

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Mol	Chain	Length	Quality of chain
1	E	538	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 31429 atoms, of which 15794 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 5-hydroxytryptamine receptor 3A.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	378	Total	C	H	N	O	S	0	0
			6299	2067	3166	509	548	9		
1	B	375	Total	C	H	N	O	S	0	0
			6243	2046	3138	505	545	9		
1	C	378	Total	C	H	N	O	S	0	0
			6293	2066	3162	508	548	9		
1	D	377	Total	C	H	N	O	S	0	0
			6281	2061	3156	508	547	9		
1	E	379	Total	C	H	N	O	S	0	0
			6313	2071	3172	511	550	9		

There are 415 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-75	MET	-	initiating methionine	UNP P23979
A	-74	TRP	-	expression tag	UNP P23979
A	-73	SER	-	expression tag	UNP P23979
A	-72	HIS	-	expression tag	UNP P23979
A	-71	PRO	-	expression tag	UNP P23979
A	-70	GLN	-	expression tag	UNP P23979
A	-69	PHE	-	expression tag	UNP P23979
A	-68	GLU	-	expression tag	UNP P23979
A	-67	LYS	-	expression tag	UNP P23979
A	-66	GLY	-	expression tag	UNP P23979
A	-65	GLY	-	expression tag	UNP P23979
A	-64	GLY	-	expression tag	UNP P23979
A	-63	SER	-	expression tag	UNP P23979
A	-62	GLY	-	expression tag	UNP P23979
A	-61	GLY	-	expression tag	UNP P23979
A	-60	GLY	-	expression tag	UNP P23979
A	-59	SER	-	expression tag	UNP P23979
A	-58	GLY	-	expression tag	UNP P23979
A	-57	GLY	-	expression tag	UNP P23979
A	-56	GLY	-	expression tag	UNP P23979

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-55	SER	-	expression tag	UNP P23979
A	-54	TRP	-	expression tag	UNP P23979
A	-53	SER	-	expression tag	UNP P23979
A	-52	HIS	-	expression tag	UNP P23979
A	-51	PRO	-	expression tag	UNP P23979
A	-50	GLN	-	expression tag	UNP P23979
A	-49	PHE	-	expression tag	UNP P23979
A	-48	GLU	-	expression tag	UNP P23979
A	-47	LYS	-	expression tag	UNP P23979
A	-46	GLY	-	expression tag	UNP P23979
A	-45	GLY	-	expression tag	UNP P23979
A	-44	GLY	-	expression tag	UNP P23979
A	-43	SER	-	expression tag	UNP P23979
A	-42	GLY	-	expression tag	UNP P23979
A	-41	GLY	-	expression tag	UNP P23979
A	-40	GLY	-	expression tag	UNP P23979
A	-39	SER	-	expression tag	UNP P23979
A	-38	GLY	-	expression tag	UNP P23979
A	-37	GLY	-	expression tag	UNP P23979
A	-36	GLY	-	expression tag	UNP P23979
A	-35	SER	-	expression tag	UNP P23979
A	-34	TRP	-	expression tag	UNP P23979
A	-33	SER	-	expression tag	UNP P23979
A	-32	HIS	-	expression tag	UNP P23979
A	-31	PRO	-	expression tag	UNP P23979
A	-30	GLN	-	expression tag	UNP P23979
A	-29	PHE	-	expression tag	UNP P23979
A	-28	GLU	-	expression tag	UNP P23979
A	-27	LYS	-	expression tag	UNP P23979
A	-26	GLY	-	expression tag	UNP P23979
A	-25	GLY	-	expression tag	UNP P23979
A	-24	GLY	-	expression tag	UNP P23979
A	-23	SER	-	expression tag	UNP P23979
A	-22	GLY	-	expression tag	UNP P23979
A	-21	GLY	-	expression tag	UNP P23979
A	-20	GLY	-	expression tag	UNP P23979
A	-19	SER	-	expression tag	UNP P23979
A	-18	GLY	-	expression tag	UNP P23979
A	-17	GLY	-	expression tag	UNP P23979
A	-16	GLY	-	expression tag	UNP P23979
A	-15	SER	-	expression tag	UNP P23979
A	-14	TRP	-	expression tag	UNP P23979

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-13	SER	-	expression tag	UNP P23979
A	-12	HIS	-	expression tag	UNP P23979
A	-11	PRO	-	expression tag	UNP P23979
A	-10	GLN	-	expression tag	UNP P23979
A	-9	PHE	-	expression tag	UNP P23979
A	-8	GLU	-	expression tag	UNP P23979
A	-7	LYS	-	expression tag	UNP P23979
A	-6	GLU	-	expression tag	UNP P23979
A	-5	ASN	-	expression tag	UNP P23979
A	-4	LEU	-	expression tag	UNP P23979
A	-3	TYR	-	expression tag	UNP P23979
A	-2	PHE	-	expression tag	UNP P23979
A	-1	GLN	-	expression tag	UNP P23979
A	0	GLY	-	expression tag	UNP P23979
A	1	ALA	-	expression tag	UNP P23979
A	2	THR	-	expression tag	UNP P23979
A	3	GLN	-	expression tag	UNP P23979
A	4	ALA	-	expression tag	UNP P23979
A	5	ARG	-	expression tag	UNP P23979
A	277	ALA	-	insertion	UNP P23979
A	461	SER	TYR	conflict	UNP P23979
B	-75	MET	-	initiating methionine	UNP P23979
B	-74	TRP	-	expression tag	UNP P23979
B	-73	SER	-	expression tag	UNP P23979
B	-72	HIS	-	expression tag	UNP P23979
B	-71	PRO	-	expression tag	UNP P23979
B	-70	GLN	-	expression tag	UNP P23979
B	-69	PHE	-	expression tag	UNP P23979
B	-68	GLU	-	expression tag	UNP P23979
B	-67	LYS	-	expression tag	UNP P23979
B	-66	GLY	-	expression tag	UNP P23979
B	-65	GLY	-	expression tag	UNP P23979
B	-64	GLY	-	expression tag	UNP P23979
B	-63	SER	-	expression tag	UNP P23979
B	-62	GLY	-	expression tag	UNP P23979
B	-61	GLY	-	expression tag	UNP P23979
B	-60	GLY	-	expression tag	UNP P23979
B	-59	SER	-	expression tag	UNP P23979
B	-58	GLY	-	expression tag	UNP P23979
B	-57	GLY	-	expression tag	UNP P23979
B	-56	GLY	-	expression tag	UNP P23979
B	-55	SER	-	expression tag	UNP P23979

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-54	TRP	-	expression tag	UNP P23979
B	-53	SER	-	expression tag	UNP P23979
B	-52	HIS	-	expression tag	UNP P23979
B	-51	PRO	-	expression tag	UNP P23979
B	-50	GLN	-	expression tag	UNP P23979
B	-49	PHE	-	expression tag	UNP P23979
B	-48	GLU	-	expression tag	UNP P23979
B	-47	LYS	-	expression tag	UNP P23979
B	-46	GLY	-	expression tag	UNP P23979
B	-45	GLY	-	expression tag	UNP P23979
B	-44	GLY	-	expression tag	UNP P23979
B	-43	SER	-	expression tag	UNP P23979
B	-42	GLY	-	expression tag	UNP P23979
B	-41	GLY	-	expression tag	UNP P23979
B	-40	GLY	-	expression tag	UNP P23979
B	-39	SER	-	expression tag	UNP P23979
B	-38	GLY	-	expression tag	UNP P23979
B	-37	GLY	-	expression tag	UNP P23979
B	-36	GLY	-	expression tag	UNP P23979
B	-35	SER	-	expression tag	UNP P23979
B	-34	TRP	-	expression tag	UNP P23979
B	-33	SER	-	expression tag	UNP P23979
B	-32	HIS	-	expression tag	UNP P23979
B	-31	PRO	-	expression tag	UNP P23979
B	-30	GLN	-	expression tag	UNP P23979
B	-29	PHE	-	expression tag	UNP P23979
B	-28	GLU	-	expression tag	UNP P23979
B	-27	LYS	-	expression tag	UNP P23979
B	-26	GLY	-	expression tag	UNP P23979
B	-25	GLY	-	expression tag	UNP P23979
B	-24	GLY	-	expression tag	UNP P23979
B	-23	SER	-	expression tag	UNP P23979
B	-22	GLY	-	expression tag	UNP P23979
B	-21	GLY	-	expression tag	UNP P23979
B	-20	GLY	-	expression tag	UNP P23979
B	-19	SER	-	expression tag	UNP P23979
B	-18	GLY	-	expression tag	UNP P23979
B	-17	GLY	-	expression tag	UNP P23979
B	-16	GLY	-	expression tag	UNP P23979
B	-15	SER	-	expression tag	UNP P23979
B	-14	TRP	-	expression tag	UNP P23979
B	-13	SER	-	expression tag	UNP P23979

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-12	HIS	-	expression tag	UNP P23979
B	-11	PRO	-	expression tag	UNP P23979
B	-10	GLN	-	expression tag	UNP P23979
B	-9	PHE	-	expression tag	UNP P23979
B	-8	GLU	-	expression tag	UNP P23979
B	-7	LYS	-	expression tag	UNP P23979
B	-6	GLU	-	expression tag	UNP P23979
B	-5	ASN	-	expression tag	UNP P23979
B	-4	LEU	-	expression tag	UNP P23979
B	-3	TYR	-	expression tag	UNP P23979
B	-2	PHE	-	expression tag	UNP P23979
B	-1	GLN	-	expression tag	UNP P23979
B	0	GLY	-	expression tag	UNP P23979
B	1	ALA	-	expression tag	UNP P23979
B	2	THR	-	expression tag	UNP P23979
B	3	GLN	-	expression tag	UNP P23979
B	4	ALA	-	expression tag	UNP P23979
B	5	ARG	-	expression tag	UNP P23979
B	277	ALA	-	insertion	UNP P23979
B	461	SER	TYR	conflict	UNP P23979
C	-75	MET	-	initiating methionine	UNP P23979
C	-74	TRP	-	expression tag	UNP P23979
C	-73	SER	-	expression tag	UNP P23979
C	-72	HIS	-	expression tag	UNP P23979
C	-71	PRO	-	expression tag	UNP P23979
C	-70	GLN	-	expression tag	UNP P23979
C	-69	PHE	-	expression tag	UNP P23979
C	-68	GLU	-	expression tag	UNP P23979
C	-67	LYS	-	expression tag	UNP P23979
C	-66	GLY	-	expression tag	UNP P23979
C	-65	GLY	-	expression tag	UNP P23979
C	-64	GLY	-	expression tag	UNP P23979
C	-63	SER	-	expression tag	UNP P23979
C	-62	GLY	-	expression tag	UNP P23979
C	-61	GLY	-	expression tag	UNP P23979
C	-60	GLY	-	expression tag	UNP P23979
C	-59	SER	-	expression tag	UNP P23979
C	-58	GLY	-	expression tag	UNP P23979
C	-57	GLY	-	expression tag	UNP P23979
C	-56	GLY	-	expression tag	UNP P23979
C	-55	SER	-	expression tag	UNP P23979
C	-54	TRP	-	expression tag	UNP P23979

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-53	SER	-	expression tag	UNP P23979
C	-52	HIS	-	expression tag	UNP P23979
C	-51	PRO	-	expression tag	UNP P23979
C	-50	GLN	-	expression tag	UNP P23979
C	-49	PHE	-	expression tag	UNP P23979
C	-48	GLU	-	expression tag	UNP P23979
C	-47	LYS	-	expression tag	UNP P23979
C	-46	GLY	-	expression tag	UNP P23979
C	-45	GLY	-	expression tag	UNP P23979
C	-44	GLY	-	expression tag	UNP P23979
C	-43	SER	-	expression tag	UNP P23979
C	-42	GLY	-	expression tag	UNP P23979
C	-41	GLY	-	expression tag	UNP P23979
C	-40	GLY	-	expression tag	UNP P23979
C	-39	SER	-	expression tag	UNP P23979
C	-38	GLY	-	expression tag	UNP P23979
C	-37	GLY	-	expression tag	UNP P23979
C	-36	GLY	-	expression tag	UNP P23979
C	-35	SER	-	expression tag	UNP P23979
C	-34	TRP	-	expression tag	UNP P23979
C	-33	SER	-	expression tag	UNP P23979
C	-32	HIS	-	expression tag	UNP P23979
C	-31	PRO	-	expression tag	UNP P23979
C	-30	GLN	-	expression tag	UNP P23979
C	-29	PHE	-	expression tag	UNP P23979
C	-28	GLU	-	expression tag	UNP P23979
C	-27	LYS	-	expression tag	UNP P23979
C	-26	GLY	-	expression tag	UNP P23979
C	-25	GLY	-	expression tag	UNP P23979
C	-24	GLY	-	expression tag	UNP P23979
C	-23	SER	-	expression tag	UNP P23979
C	-22	GLY	-	expression tag	UNP P23979
C	-21	GLY	-	expression tag	UNP P23979
C	-20	GLY	-	expression tag	UNP P23979
C	-19	SER	-	expression tag	UNP P23979
C	-18	GLY	-	expression tag	UNP P23979
C	-17	GLY	-	expression tag	UNP P23979
C	-16	GLY	-	expression tag	UNP P23979
C	-15	SER	-	expression tag	UNP P23979
C	-14	TRP	-	expression tag	UNP P23979
C	-13	SER	-	expression tag	UNP P23979
C	-12	HIS	-	expression tag	UNP P23979

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-11	PRO	-	expression tag	UNP P23979
C	-10	GLN	-	expression tag	UNP P23979
C	-9	PHE	-	expression tag	UNP P23979
C	-8	GLU	-	expression tag	UNP P23979
C	-7	LYS	-	expression tag	UNP P23979
C	-6	GLU	-	expression tag	UNP P23979
C	-5	ASN	-	expression tag	UNP P23979
C	-4	LEU	-	expression tag	UNP P23979
C	-3	TYR	-	expression tag	UNP P23979
C	-2	PHE	-	expression tag	UNP P23979
C	-1	GLN	-	expression tag	UNP P23979
C	0	GLY	-	expression tag	UNP P23979
C	1	ALA	-	expression tag	UNP P23979
C	2	THR	-	expression tag	UNP P23979
C	3	GLN	-	expression tag	UNP P23979
C	4	ALA	-	expression tag	UNP P23979
C	5	ARG	-	expression tag	UNP P23979
C	277	ALA	-	insertion	UNP P23979
C	461	SER	TYR	conflict	UNP P23979
D	-75	MET	-	initiating methionine	UNP P23979
D	-74	TRP	-	expression tag	UNP P23979
D	-73	SER	-	expression tag	UNP P23979
D	-72	HIS	-	expression tag	UNP P23979
D	-71	PRO	-	expression tag	UNP P23979
D	-70	GLN	-	expression tag	UNP P23979
D	-69	PHE	-	expression tag	UNP P23979
D	-68	GLU	-	expression tag	UNP P23979
D	-67	LYS	-	expression tag	UNP P23979
D	-66	GLY	-	expression tag	UNP P23979
D	-65	GLY	-	expression tag	UNP P23979
D	-64	GLY	-	expression tag	UNP P23979
D	-63	SER	-	expression tag	UNP P23979
D	-62	GLY	-	expression tag	UNP P23979
D	-61	GLY	-	expression tag	UNP P23979
D	-60	GLY	-	expression tag	UNP P23979
D	-59	SER	-	expression tag	UNP P23979
D	-58	GLY	-	expression tag	UNP P23979
D	-57	GLY	-	expression tag	UNP P23979
D	-56	GLY	-	expression tag	UNP P23979
D	-55	SER	-	expression tag	UNP P23979
D	-54	TRP	-	expression tag	UNP P23979
D	-53	SER	-	expression tag	UNP P23979

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-52	HIS	-	expression tag	UNP P23979
D	-51	PRO	-	expression tag	UNP P23979
D	-50	GLN	-	expression tag	UNP P23979
D	-49	PHE	-	expression tag	UNP P23979
D	-48	GLU	-	expression tag	UNP P23979
D	-47	LYS	-	expression tag	UNP P23979
D	-46	GLY	-	expression tag	UNP P23979
D	-45	GLY	-	expression tag	UNP P23979
D	-44	GLY	-	expression tag	UNP P23979
D	-43	SER	-	expression tag	UNP P23979
D	-42	GLY	-	expression tag	UNP P23979
D	-41	GLY	-	expression tag	UNP P23979
D	-40	GLY	-	expression tag	UNP P23979
D	-39	SER	-	expression tag	UNP P23979
D	-38	GLY	-	expression tag	UNP P23979
D	-37	GLY	-	expression tag	UNP P23979
D	-36	GLY	-	expression tag	UNP P23979
D	-35	SER	-	expression tag	UNP P23979
D	-34	TRP	-	expression tag	UNP P23979
D	-33	SER	-	expression tag	UNP P23979
D	-32	HIS	-	expression tag	UNP P23979
D	-31	PRO	-	expression tag	UNP P23979
D	-30	GLN	-	expression tag	UNP P23979
D	-29	PHE	-	expression tag	UNP P23979
D	-28	GLU	-	expression tag	UNP P23979
D	-27	LYS	-	expression tag	UNP P23979
D	-26	GLY	-	expression tag	UNP P23979
D	-25	GLY	-	expression tag	UNP P23979
D	-24	GLY	-	expression tag	UNP P23979
D	-23	SER	-	expression tag	UNP P23979
D	-22	GLY	-	expression tag	UNP P23979
D	-21	GLY	-	expression tag	UNP P23979
D	-20	GLY	-	expression tag	UNP P23979
D	-19	SER	-	expression tag	UNP P23979
D	-18	GLY	-	expression tag	UNP P23979
D	-17	GLY	-	expression tag	UNP P23979
D	-16	GLY	-	expression tag	UNP P23979
D	-15	SER	-	expression tag	UNP P23979
D	-14	TRP	-	expression tag	UNP P23979
D	-13	SER	-	expression tag	UNP P23979
D	-12	HIS	-	expression tag	UNP P23979
D	-11	PRO	-	expression tag	UNP P23979

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-10	GLN	-	expression tag	UNP P23979
D	-9	PHE	-	expression tag	UNP P23979
D	-8	GLU	-	expression tag	UNP P23979
D	-7	LYS	-	expression tag	UNP P23979
D	-6	GLU	-	expression tag	UNP P23979
D	-5	ASN	-	expression tag	UNP P23979
D	-4	LEU	-	expression tag	UNP P23979
D	-3	TYR	-	expression tag	UNP P23979
D	-2	PHE	-	expression tag	UNP P23979
D	-1	GLN	-	expression tag	UNP P23979
D	0	GLY	-	expression tag	UNP P23979
D	1	ALA	-	expression tag	UNP P23979
D	2	THR	-	expression tag	UNP P23979
D	3	GLN	-	expression tag	UNP P23979
D	4	ALA	-	expression tag	UNP P23979
D	5	ARG	-	expression tag	UNP P23979
D	277	ALA	-	insertion	UNP P23979
D	461	SER	TYR	conflict	UNP P23979
E	-75	MET	-	initiating methionine	UNP P23979
E	-74	TRP	-	expression tag	UNP P23979
E	-73	SER	-	expression tag	UNP P23979
E	-72	HIS	-	expression tag	UNP P23979
E	-71	PRO	-	expression tag	UNP P23979
E	-70	GLN	-	expression tag	UNP P23979
E	-69	PHE	-	expression tag	UNP P23979
E	-68	GLU	-	expression tag	UNP P23979
E	-67	LYS	-	expression tag	UNP P23979
E	-66	GLY	-	expression tag	UNP P23979
E	-65	GLY	-	expression tag	UNP P23979
E	-64	GLY	-	expression tag	UNP P23979
E	-63	SER	-	expression tag	UNP P23979
E	-62	GLY	-	expression tag	UNP P23979
E	-61	GLY	-	expression tag	UNP P23979
E	-60	GLY	-	expression tag	UNP P23979
E	-59	SER	-	expression tag	UNP P23979
E	-58	GLY	-	expression tag	UNP P23979
E	-57	GLY	-	expression tag	UNP P23979
E	-56	GLY	-	expression tag	UNP P23979
E	-55	SER	-	expression tag	UNP P23979
E	-54	TRP	-	expression tag	UNP P23979
E	-53	SER	-	expression tag	UNP P23979
E	-52	HIS	-	expression tag	UNP P23979

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-51	PRO	-	expression tag	UNP P23979
E	-50	GLN	-	expression tag	UNP P23979
E	-49	PHE	-	expression tag	UNP P23979
E	-48	GLU	-	expression tag	UNP P23979
E	-47	LYS	-	expression tag	UNP P23979
E	-46	GLY	-	expression tag	UNP P23979
E	-45	GLY	-	expression tag	UNP P23979
E	-44	GLY	-	expression tag	UNP P23979
E	-43	SER	-	expression tag	UNP P23979
E	-42	GLY	-	expression tag	UNP P23979
E	-41	GLY	-	expression tag	UNP P23979
E	-40	GLY	-	expression tag	UNP P23979
E	-39	SER	-	expression tag	UNP P23979
E	-38	GLY	-	expression tag	UNP P23979
E	-37	GLY	-	expression tag	UNP P23979
E	-36	GLY	-	expression tag	UNP P23979
E	-35	SER	-	expression tag	UNP P23979
E	-34	TRP	-	expression tag	UNP P23979
E	-33	SER	-	expression tag	UNP P23979
E	-32	HIS	-	expression tag	UNP P23979
E	-31	PRO	-	expression tag	UNP P23979
E	-30	GLN	-	expression tag	UNP P23979
E	-29	PHE	-	expression tag	UNP P23979
E	-28	GLU	-	expression tag	UNP P23979
E	-27	LYS	-	expression tag	UNP P23979
E	-26	GLY	-	expression tag	UNP P23979
E	-25	GLY	-	expression tag	UNP P23979
E	-24	GLY	-	expression tag	UNP P23979
E	-23	SER	-	expression tag	UNP P23979
E	-22	GLY	-	expression tag	UNP P23979
E	-21	GLY	-	expression tag	UNP P23979
E	-20	GLY	-	expression tag	UNP P23979
E	-19	SER	-	expression tag	UNP P23979
E	-18	GLY	-	expression tag	UNP P23979
E	-17	GLY	-	expression tag	UNP P23979
E	-16	GLY	-	expression tag	UNP P23979
E	-15	SER	-	expression tag	UNP P23979
E	-14	TRP	-	expression tag	UNP P23979
E	-13	SER	-	expression tag	UNP P23979
E	-12	HIS	-	expression tag	UNP P23979
E	-11	PRO	-	expression tag	UNP P23979
E	-10	GLN	-	expression tag	UNP P23979

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-9	PHE	-	expression tag	UNP P23979
E	-8	GLU	-	expression tag	UNP P23979
E	-7	LYS	-	expression tag	UNP P23979
E	-6	GLU	-	expression tag	UNP P23979
E	-5	ASN	-	expression tag	UNP P23979
E	-4	LEU	-	expression tag	UNP P23979
E	-3	TYR	-	expression tag	UNP P23979
E	-2	PHE	-	expression tag	UNP P23979
E	-1	GLN	-	expression tag	UNP P23979
E	0	GLY	-	expression tag	UNP P23979
E	1	ALA	-	expression tag	UNP P23979
E	2	THR	-	expression tag	UNP P23979
E	3	GLN	-	expression tag	UNP P23979
E	4	ALA	-	expression tag	UNP P23979
E	5	ARG	-	expression tag	UNP P23979
E	277	ALA	-	insertion	UNP P23979
E	461	SER	TYR	conflict	UNP P23979

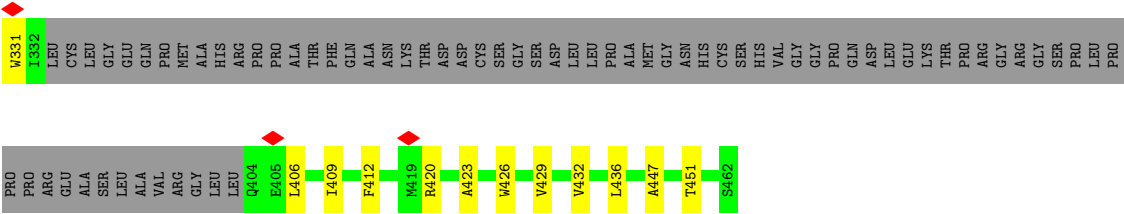
[illegible]

Chain D: 64% 6% 30%

Position	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30
Met																														
Ser																														
Thr																														
His																														
Pro																														
Gln																														
Phe																														
Leu																														
Val																														
Ala																														
Arg																														
Asp																														
Asn																														
Lys																														
Glu																														
Trp																														
Ile																														
Met																														
Val																														
Leu																														
Ala																														
Arg																														
Asp																														
Asn																														
Lys																														
Glu																														
Trp																														
Ile																														
Met																														

Chain E:

Met	TRP	SER	HIS	PRO	GLN	PHE	GLU	LYS	GLY	GLY	SER	GLY	GLY	GLY	SER	TRP	SER	HIS	PRO	GLN	PHE	GLU	LYS	GLY	GLY	GLY	GLY	GLY	GLY															
SER	TRP	SER	HIS	PRO	GLN	PHE	GLU	LYS	GLU	ASN	LEU	TVR	PHE	GLN	GLY	ALA	THR	GLN	ALA	ARG	ASP	THR	T8	R14	L15	L49	D52	D56	T59	Y64	Y67	P77	E78	D79	N82	L86	K108	Q124	L129	Q130	L137	D138	I139	Y146



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	152877	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 ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.416	Depositor
Minimum map value	-0.117	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.017	Depositor
Recommended contour level	0.1	Depositor
Map size (Å)	266.24, 266.24, 266.24	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.83199996, 0.83199996, 0.83199996	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	0.34	0/3220	0.58	4/4397 (0.1%)
1	B	0.42	2/3190 (0.1%)	0.63	2/4356 (0.0%)
1	C	0.30	0/3218	0.53	0/4397
1	D	0.30	0/3212	0.51	0/4386
1	E	0.38	1/3228 (0.0%)	0.61	5/4409 (0.1%)
All	All	0.35	3/16068 (0.0%)	0.57	11/21945 (0.1%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	24	LYS	C-N	7.24	1.43	1.33
1	B	420	ARG	C-O	-5.95	1.17	1.24
1	E	268	ILE	C-O	-5.42	1.17	1.24

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	436	LEU	CA-C-N	5.37	127.74	120.44
1	A	436	LEU	C-N-CA	5.37	127.74	120.44
1	E	268	ILE	N-CA-CB	5.36	117.83	110.54
1	E	268	ILE	CA-C-O	-5.33	115.41	120.95
1	E	282	LEU	CA-C-N	5.32	127.35	120.70
1	E	282	LEU	C-N-CA	5.32	127.35	120.70
1	B	420	ARG	CA-C-O	-5.29	114.94	120.55
1	B	24	LYS	O-C-N	5.23	129.33	123.27
1	A	10	PRO	CA-C-N	5.15	127.45	120.44
1	A	10	PRO	C-N-CA	5.15	127.45	120.44
1	E	269	VAL	N-CA-C	-5.13	105.50	110.42

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3133	3166	3167	50	0
1	B	3105	3138	3138	35	0
1	C	3131	3162	3162	26	0
1	D	3125	3156	3156	20	0
1	E	3141	3172	3172	46	0
All	All	15635	15794	15795	167	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 5.

All (167) 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:E:265:PHE:O	1:E:269:VAL:HG23	1.79	0.82
1:E:15:LEU:HD23	1:E:86:LEU:HD22	1.64	0.78
1:A:10:PRO:O	1:A:14:ARG:HG2	1.84	0.77
1:D:262:TYR:HH	1:D:441:TYR:HH	1.26	0.77
1:A:255:LYS:NZ	1:A:294:LEU:O	2.21	0.73
1:B:451:THR:O	1:B:455:LEU:HD13	1.88	0.72
1:B:302:ILE:HA	1:B:305:VAL:HG12	1.72	0.71
1:E:108:LYS:N	1:E:130:GLN:OE1	2.25	0.69
1:A:80:PHE:O	1:A:83:VAL:HG23	1.96	0.66
1:B:53:GLU:O	1:B:56:GLN:NE2	2.29	0.65
1:D:196:PHE:O	1:D:197:LYS:HG3	1.96	0.65
1:A:188:GLU:HG3	1:A:189:LEU:H	1.62	0.65
1:A:451:THR:O	1:A:455:LEU:HD13	1.97	0.64
1:A:188:GLU:HG3	1:A:189:LEU:N	2.11	0.64
1:E:64:TYR:HB2	1:E:129:LEU:HD12	1.78	0.63
1:B:29:PRO:HG3	1:B:70:ASP:OD1	1.99	0.63
1:C:262:TYR:OH	1:C:441:TYR:OH	2.17	0.62
1:E:265:PHE:CD2	1:E:269:VAL:CG2	2.83	0.62
1:A:15:LEU:HD23	1:A:86:LEU:HD22	1.83	0.61
1:C:268:ILE:O	1:C:272:THR:N	2.34	0.61
1:A:413:LEU:HD22	1:E:409:ILE:HG13	1.84	0.59
1:A:105:ASP:CG	1:A:106:VAL:H	2.11	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:420:ARG:HG3	1:E:423:ALA:HB3	1.84	0.59
1:B:423:ALA:O	1:B:427:LEU:HG	2.03	0.58
1:C:159:THR:HG23	1:D:116:TYR:OH	2.02	0.58
1:A:155:SER:OG	1:A:158:HIS:O	2.21	0.58
1:A:237:VAL:HG12	1:A:258:LEU:HD21	1.85	0.58
1:E:321:LEU:HD21	1:E:429:VAL:HG11	1.86	0.58
1:C:227:LEU:CD2	1:C:273:LEU:HD11	2.34	0.58
1:B:416:ARG:O	1:B:420:ARG:N	2.37	0.57
1:A:90:THR:N	1:A:113:PRO:O	2.37	0.57
1:C:264:VAL:HA	1:C:267:ILE:HD12	1.85	0.57
1:A:413:LEU:HD11	1:E:412:PHE:CE2	2.39	0.57
1:C:53:GLU:OE1	1:C:274:PRO:HG3	2.04	0.56
1:E:67:TYR:CD1	1:E:124:GLN:HG2	2.40	0.56
1:E:146:VAL:O	1:E:146:VAL:HG23	2.04	0.56
1:E:282:LEU:C	1:E:282:LEU:HD12	2.31	0.56
1:C:45:MET:HG3	1:C:189:LEU:HD11	1.87	0.56
1:A:139:ILE:O	1:A:139:ILE:HG22	2.05	0.55
1:A:297:SER:HB2	1:A:437:LEU:HD13	1.88	0.55
1:C:322:ARG:HA	1:C:325:VAL:HG22	1.88	0.55
1:A:246:PRO:CG	1:A:427:LEU:HD11	2.37	0.55
1:E:328:ARG:O	1:E:331:TRP:N	2.40	0.54
1:D:196:PHE:O	1:D:197:LYS:CG	2.55	0.54
1:B:217:ARG:NH1	1:B:459:TRP:O	2.39	0.54
1:A:434:ASP:O	1:A:434:ASP:OD1	2.25	0.54
1:E:420:ARG:CG	1:E:423:ALA:HB3	2.37	0.53
1:A:412:PHE:HB2	1:B:413:LEU:HD22	1.90	0.53
1:B:42:ASP:OD2	1:B:65:ARG:NH2	2.42	0.53
1:C:108:LYS:N	1:C:130:GLN:OE1	2.41	0.53
1:E:247:ASP:OD1	1:E:248:SER:N	2.42	0.53
1:C:93:ILE:HD11	1:C:115:VAL:HG21	1.91	0.53
1:A:428:ARG:O	1:A:432:VAL:HG23	2.08	0.52
1:D:233:PHE:O	1:D:237:VAL:HG23	2.09	0.52
1:A:53:GLU:O	1:A:56:GLN:NE2	2.42	0.52
1:E:139:ILE:CD1	1:E:276:THR:HB	2.39	0.52
1:C:300:GLU:HG3	1:C:433:LEU:HD11	1.91	0.52
1:A:105:ASP:CG	1:A:106:VAL:N	2.66	0.52
1:E:188:GLU:HB2	1:E:219:ARG:CZ	2.40	0.52
1:B:42:ASP:OD2	1:B:169:ARG:NE	2.43	0.52
1:E:139:ILE:HD11	1:E:276:THR:HB	1.90	0.52
1:A:102:GLU:OE1	1:B:46:TYR:OH	2.28	0.51
1:A:434:ASP:OD1	1:A:437:LEU:HD23	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:262:TYR:OH	1:D:441:TYR:OH	2.01	0.51
1:B:139:ILE:HG22	1:B:139:ILE:O	2.11	0.51
1:E:139:ILE:HD11	1:E:279:GLY:O	2.11	0.51
1:B:29:PRO:CG	1:B:70:ASP:OD1	2.59	0.50
1:A:42:ASP:OD2	1:A:169:ARG:NE	2.44	0.50
1:E:189:LEU:HD12	1:E:215:ILE:O	2.11	0.50
1:A:329:ILE:HA	1:A:332:ILE:HD12	1.93	0.50
1:B:239:ILE:HG23	1:B:438:PHE:HE1	1.77	0.50
1:E:447:ALA:O	1:E:451:THR:HG23	2.12	0.50
1:B:410:ARG:HG3	1:B:413:LEU:HD23	1.93	0.49
1:E:301:THR:O	1:E:305:VAL:HG23	2.13	0.49
1:A:297:SER:OG	1:A:437:LEU:CD2	2.61	0.49
1:B:235:MET:O	1:B:239:ILE:HG13	2.12	0.49
1:E:56:GLN:HA	1:E:137:LEU:HD12	1.95	0.49
1:D:77:PRO:O	1:D:82:ASN:N	2.45	0.49
1:E:49:LEU:HB2	1:E:59:THR:HG23	1.95	0.49
1:A:255:LYS:HZ1	1:A:297:SER:HB3	1.78	0.48
1:B:234:LEU:HD22	1:B:262:TYR:CE1	2.48	0.48
1:C:232:ILE:O	1:C:236:VAL:HG23	2.13	0.48
1:C:420:ARG:HA	1:C:423:ALA:HB3	1.95	0.48
1:D:265:PHE:O	1:D:269:VAL:HG23	2.14	0.48
1:C:319:ASP:OD1	1:C:320:TRP:N	2.47	0.48
1:C:301:THR:O	1:C:305:VAL:HG23	2.14	0.48
1:A:246:PRO:HG2	1:A:427:LEU:HD11	1.96	0.47
1:E:265:PHE:CE2	1:E:269:VAL:HG22	2.49	0.47
1:A:297:SER:OG	1:A:437:LEU:HD22	2.15	0.47
1:E:64:TYR:HB2	1:E:129:LEU:CD1	2.43	0.47
1:A:297:SER:HB2	1:A:437:LEU:CD1	2.44	0.47
1:E:282:LEU:HD12	1:E:283:ILE:N	2.30	0.47
1:A:139:ILE:O	1:A:139:ILE:CG2	2.63	0.47
1:B:199:PHE:O	1:B:207:TYR:N	2.40	0.47
1:A:413:LEU:HD12	1:A:416:ARG:HD2	1.97	0.47
1:A:94:TRP:CD1	1:B:114:TYR:HH	2.33	0.46
1:A:65:ARG:HG2	1:A:126:TYR:HD1	1.79	0.46
1:D:268:ILE:O	1:D:272:THR:N	2.42	0.46
1:B:265:PHE:O	1:B:269:VAL:HG22	2.16	0.46
1:D:300:GLU:OE1	1:D:437:LEU:HD11	2.15	0.46
1:E:429:VAL:HA	1:E:432:VAL:HG22	1.97	0.46
1:B:102:GLU:OE1	1:C:46:TYR:OH	2.34	0.45
1:B:53:GLU:HA	1:B:137:LEU:HD12	1.99	0.45
1:C:321:LEU:HD12	1:C:426:TRP:CZ3	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:52:ASP:O	1:E:56:GLN:N	2.49	0.45
1:A:217:ARG:HD2	1:A:459:TRP:CE2	2.51	0.45
1:B:155:SER:OG	1:B:158:HIS:O	2.35	0.45
1:E:14:ARG:NH2	1:E:79:ASP:O	2.49	0.45
1:A:188:GLU:CG	1:A:189:LEU:H	2.28	0.45
1:B:406:LEU:HA	1:B:409:ILE:HG22	1.98	0.45
1:A:158:HIS:CB	1:A:163:ILE:HD12	2.45	0.45
1:A:188:GLU:CG	1:A:189:LEU:N	2.79	0.45
1:D:236:VAL:O	1:D:240:VAL:HG23	2.17	0.45
1:C:67:TYR:CD1	1:C:124:GLN:HG2	2.52	0.45
1:C:302:ILE:HB	1:D:244:LEU:HD21	1.98	0.44
1:D:53:GLU:OE2	1:D:218:ARG:NH2	2.50	0.44
1:A:446:LEU:HG	1:A:450:ILE:CD1	2.46	0.44
1:B:254:PHE:O	1:B:257:THR:OG1	2.33	0.44
1:E:64:TYR:CB	1:E:129:LEU:CD1	2.96	0.44
1:E:148:ASN:OD1	1:E:148:ASN:C	2.60	0.44
1:E:406:LEU:HA	1:E:409:ILE:HG22	2.00	0.44
1:A:409:ILE:HD12	1:B:409:ILE:HG21	1.98	0.44
1:B:153:PHE:N	1:B:210:MET:O	2.49	0.44
1:E:190:LEU:HD12	1:E:215:ILE:HG22	2.00	0.44
1:E:321:LEU:HD11	1:E:429:VAL:HG21	1.98	0.44
1:A:237:VAL:HG12	1:A:258:LEU:CD2	2.47	0.43
1:A:229:LEU:HB2	1:A:230:PRO:HD3	2.00	0.43
1:A:237:VAL:HG12	1:A:258:LEU:CG	2.48	0.43
1:D:448:TYR:O	1:D:452:LEU:HG	2.18	0.43
1:E:232:ILE:O	1:E:236:VAL:HG23	2.17	0.43
1:B:239:ILE:HG23	1:B:438:PHE:CE1	2.54	0.43
1:D:196:PHE:C	1:D:197:LYS:HG3	2.44	0.43
1:C:282:LEU:HD13	1:C:286:TYR:HE1	1.83	0.43
1:E:307:LEU:HD22	1:E:426:TRP:CD2	2.54	0.43
1:A:430:GLY:O	1:A:433:LEU:HB3	2.18	0.42
1:D:137:LEU:HD22	1:D:147:GLN:HG2	2.01	0.42
1:E:154:THR:OG1	1:E:208:ALA:O	2.23	0.42
1:B:131:LEU:C	1:B:131:LEU:HD12	2.44	0.42
1:D:307:LEU:O	1:D:426:TRP:NE1	2.53	0.42
1:E:432:VAL:O	1:E:436:LEU:HD23	2.19	0.42
1:B:237:VAL:HA	1:B:240:VAL:HG22	2.02	0.42
1:B:428:ARG:O	1:B:432:VAL:HG13	2.19	0.42
1:C:227:LEU:HD11	1:C:269:VAL:HG12	2.01	0.42
1:C:283:ILE:HG23	1:C:448:TYR:OH	2.20	0.42
1:B:269:VAL:O	1:B:273:LEU:N	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:166:THR:HG22	1:D:167:LEU:H	1.85	0.42
1:A:265:PHE:O	1:A:269:VAL:HG23	2.20	0.41
1:C:227:LEU:HD22	1:C:273:LEU:HD21	2.02	0.41
1:E:77:PRO:O	1:E:82:ASN:N	2.52	0.41
1:B:141:ASN:O	1:B:145:ASP:N	2.53	0.41
1:A:105:ASP:OD1	1:B:108:LYS:HB2	2.20	0.41
1:E:321:LEU:CD2	1:E:429:VAL:HG11	2.50	0.41
1:A:131:LEU:HD12	1:A:131:LEU:O	2.20	0.41
1:E:268:ILE:HG13	1:E:272:THR:HG23	2.01	0.41
1:A:131:LEU:HD12	1:A:131:LEU:C	2.46	0.41
1:C:428:ARG:O	1:C:432:VAL:HG22	2.20	0.41
1:B:302:ILE:HA	1:B:305:VAL:CG1	2.45	0.41
1:D:52:ASP:O	1:D:56:GLN:N	2.52	0.41
1:A:144:PHE:CD2	1:A:455:LEU:HB3	2.55	0.41
1:C:158:HIS:CB	1:C:163:ILE:HD12	2.50	0.41
1:C:282:LEU:HD13	1:C:286:TYR:CE1	2.55	0.41
1:D:297:SER:HA	1:D:437:LEU:HD13	2.03	0.41
1:E:322:ARG:HA	1:E:325:VAL:HG22	2.03	0.41
1:A:423:ALA:O	1:A:424:ARG:NH1	2.50	0.41
1:E:189:LEU:HD12	1:E:190:LEU:H	1.85	0.40
1:E:67:TYR:CE1	1:E:124:GLN:HG2	2.56	0.40
1:E:265:PHE:CE2	1:E:269:VAL:CG2	3.05	0.40

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	372/538 (69%)	368 (99%)	4 (1%)	0	100	100
1	B	369/538 (69%)	364 (99%)	5 (1%)	0	100	100
1	C	372/538 (69%)	366 (98%)	6 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	371/538 (69%)	360 (97%)	11 (3%)	0	100	100
1	E	373/538 (69%)	363 (97%)	10 (3%)	0	100	100
All	All	1857/2690 (69%)	1821 (98%)	36 (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	354/470 (75%)	354 (100%)	0	100	100
1	B	352/470 (75%)	352 (100%)	0	100	100
1	C	354/470 (75%)	354 (100%)	0	100	100
1	D	353/470 (75%)	353 (100%)	0	100	100
1	E	355/470 (76%)	355 (100%)	0	100	100
All	All	1768/2350 (75%)	1768 (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 (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	74	GLN
1	C	55	ASN
1	C	118	HIS
1	C	323	HIS
1	D	148	ASN

5.3.3 RNA [i](#)

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 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.

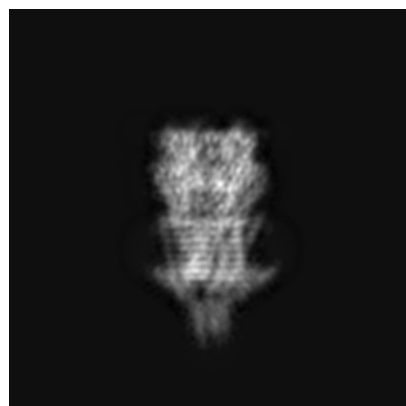
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10693. These allow visual inspection of the internal detail of the map and identification of artifacts.

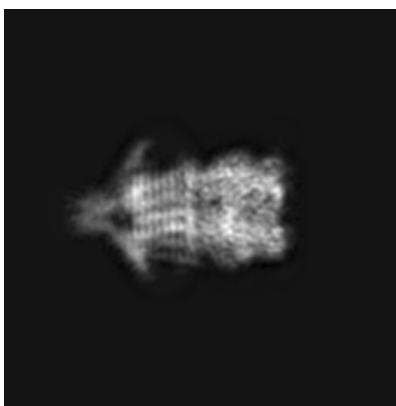
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

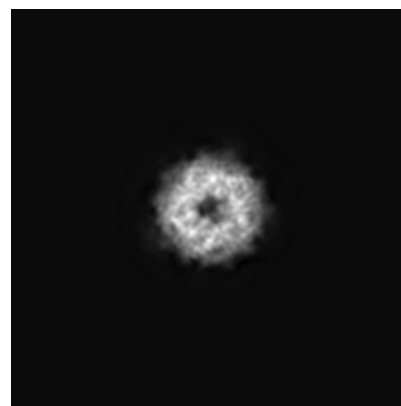
6.1.1 Primary map



X

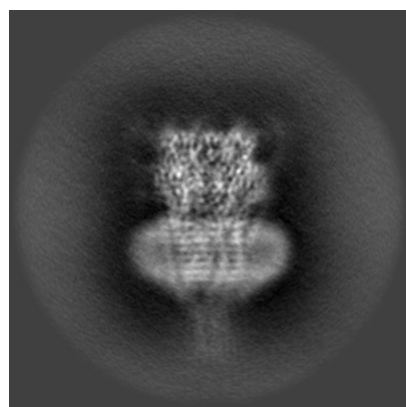


Y

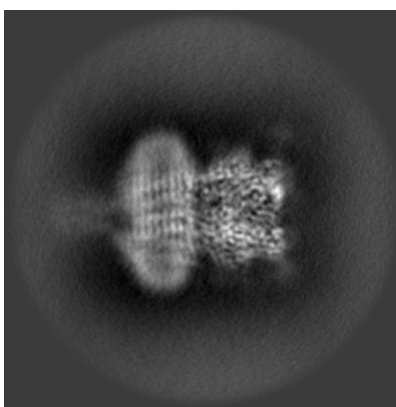


Z

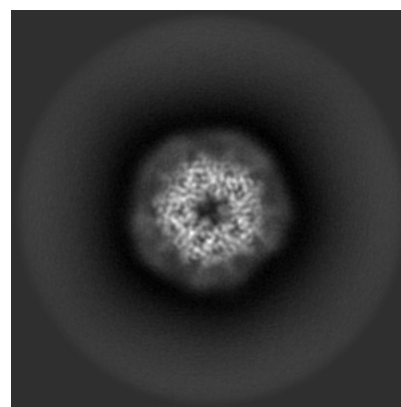
6.1.2 Raw map



X



Y

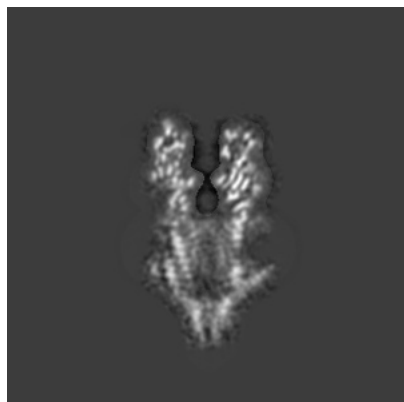


Z

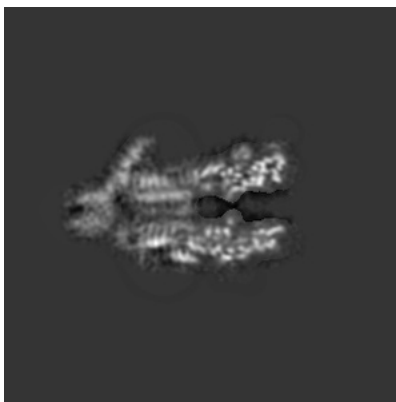
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

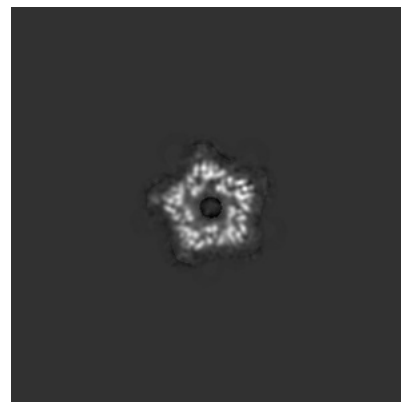
6.2.1 Primary map



X Index: 160

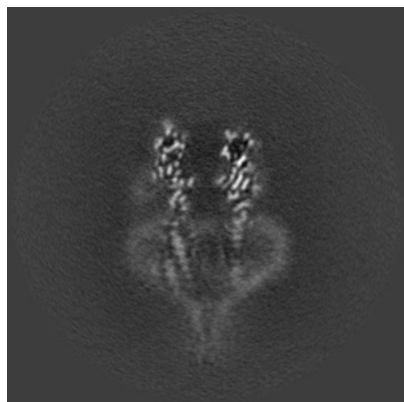


Y Index: 160

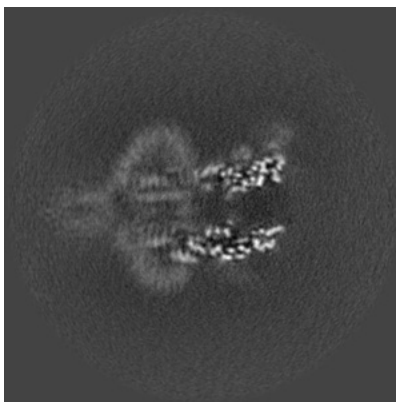


Z Index: 160

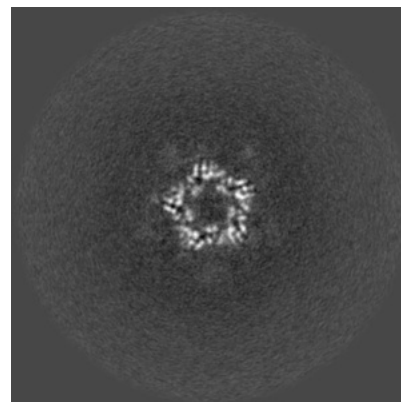
6.2.2 Raw map



X Index: 160



Y Index: 160



Z Index: 160

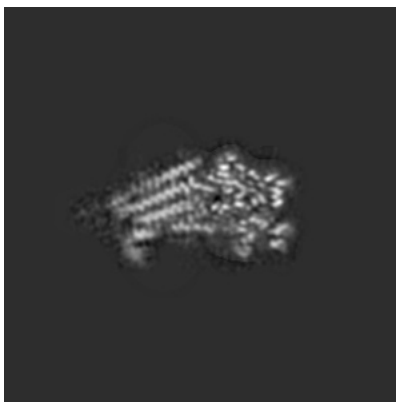
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 143

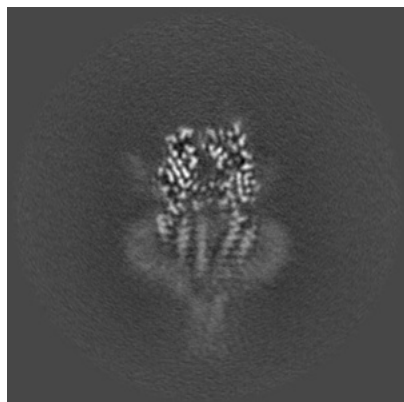


Y Index: 182

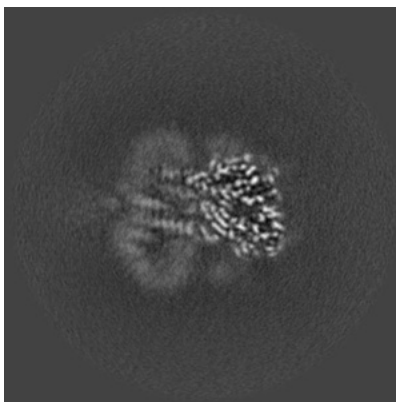


Z Index: 180

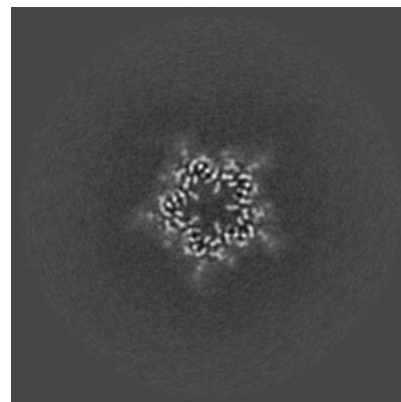
6.3.2 Raw map



X Index: 144



Y Index: 141

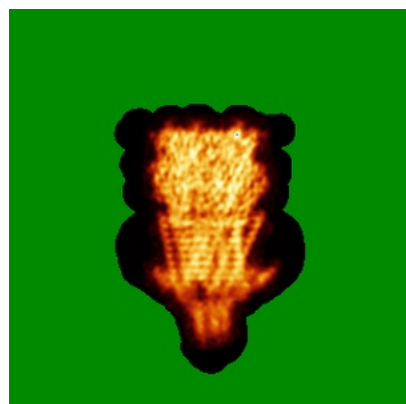


Z Index: 191

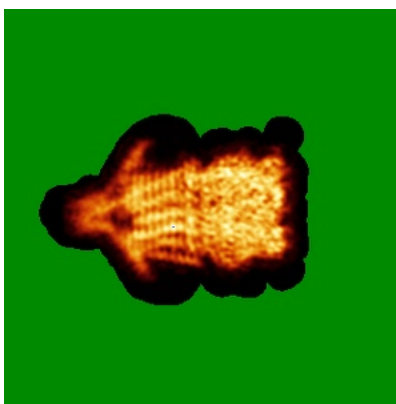
The images above show the largest variance slices of the map in three orthogonal directions.

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

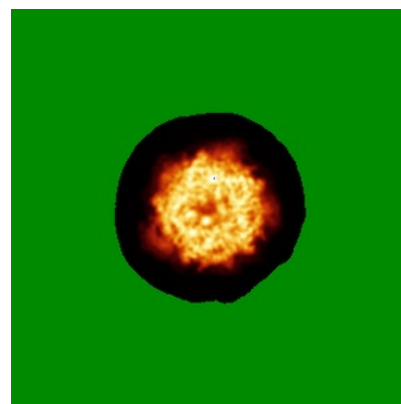
6.4.1 Primary map



X

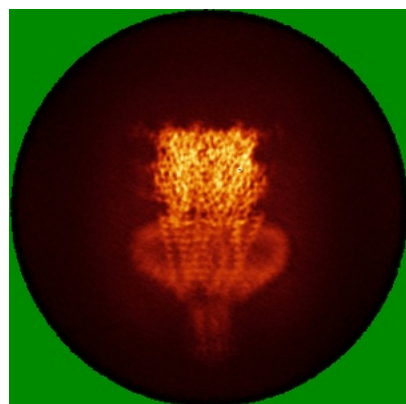


Y

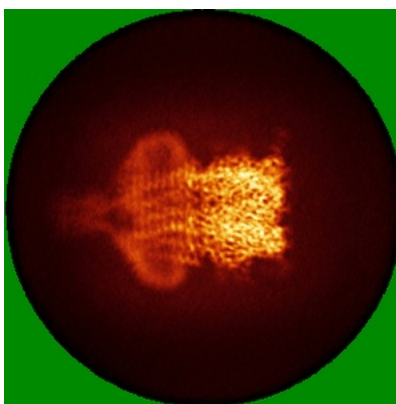


Z

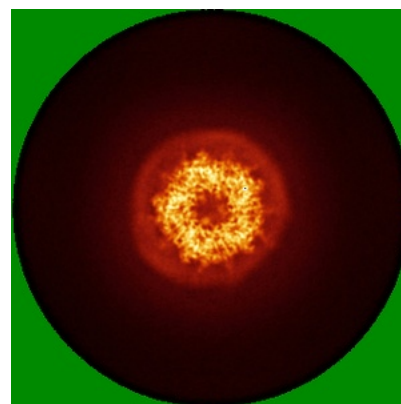
6.4.2 Raw map



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](#)

This section was not generated.

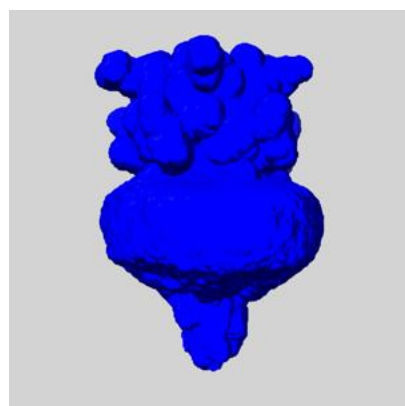
6.6 Mask visualisation [i](#)

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

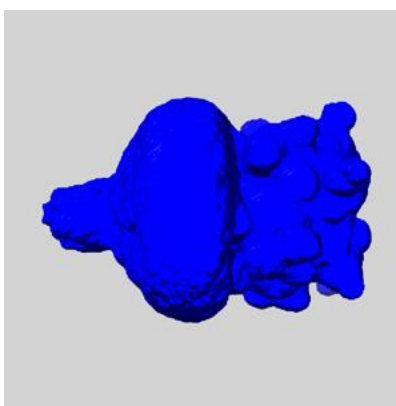
A mask typically either:

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

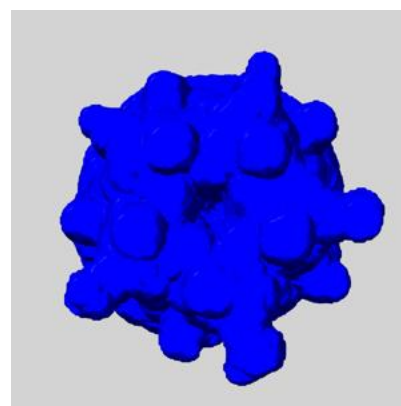
6.6.1 emd_10693_msk_1.map [i](#)



X



Y

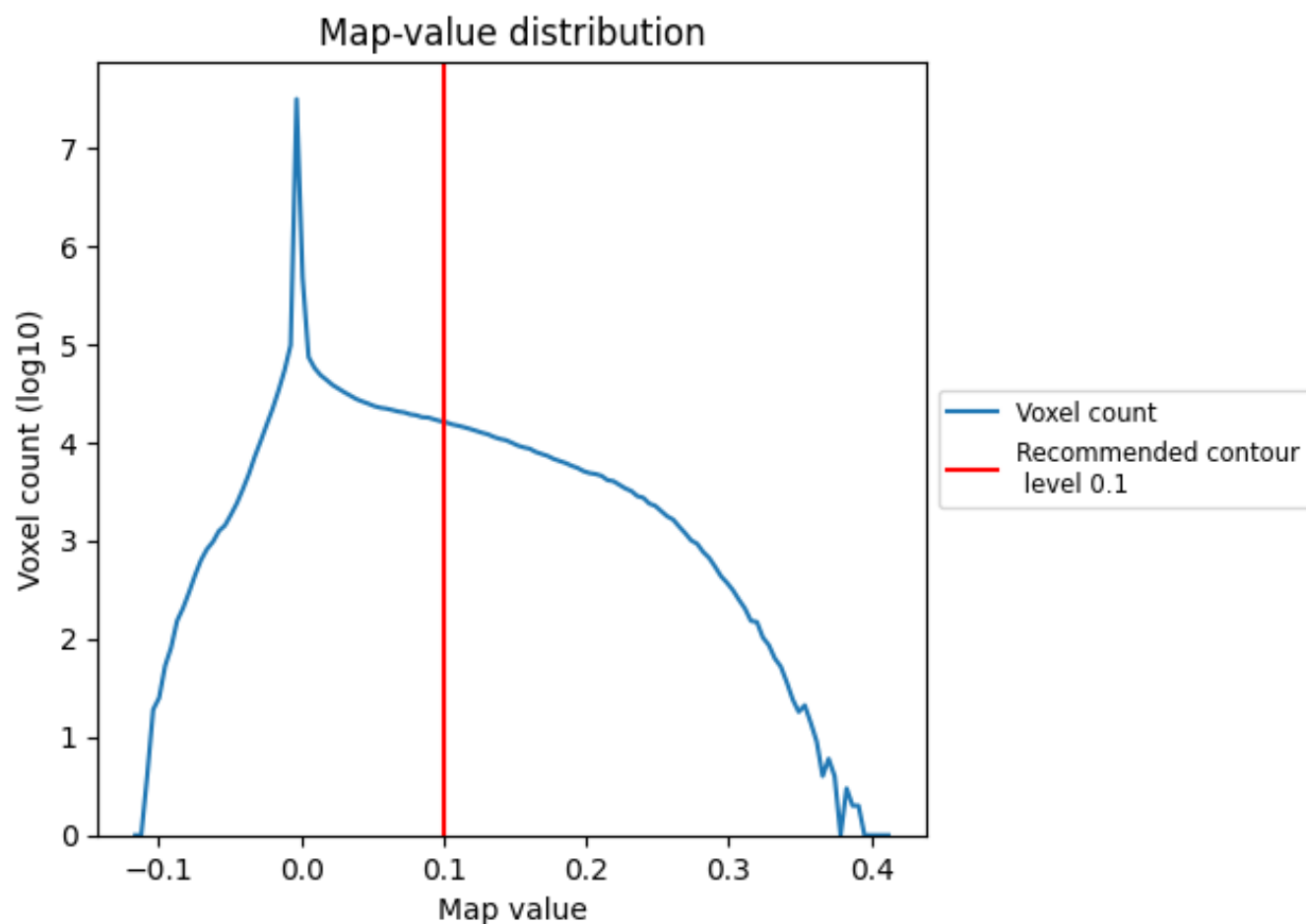


Z

7 Map analysis [i](#)

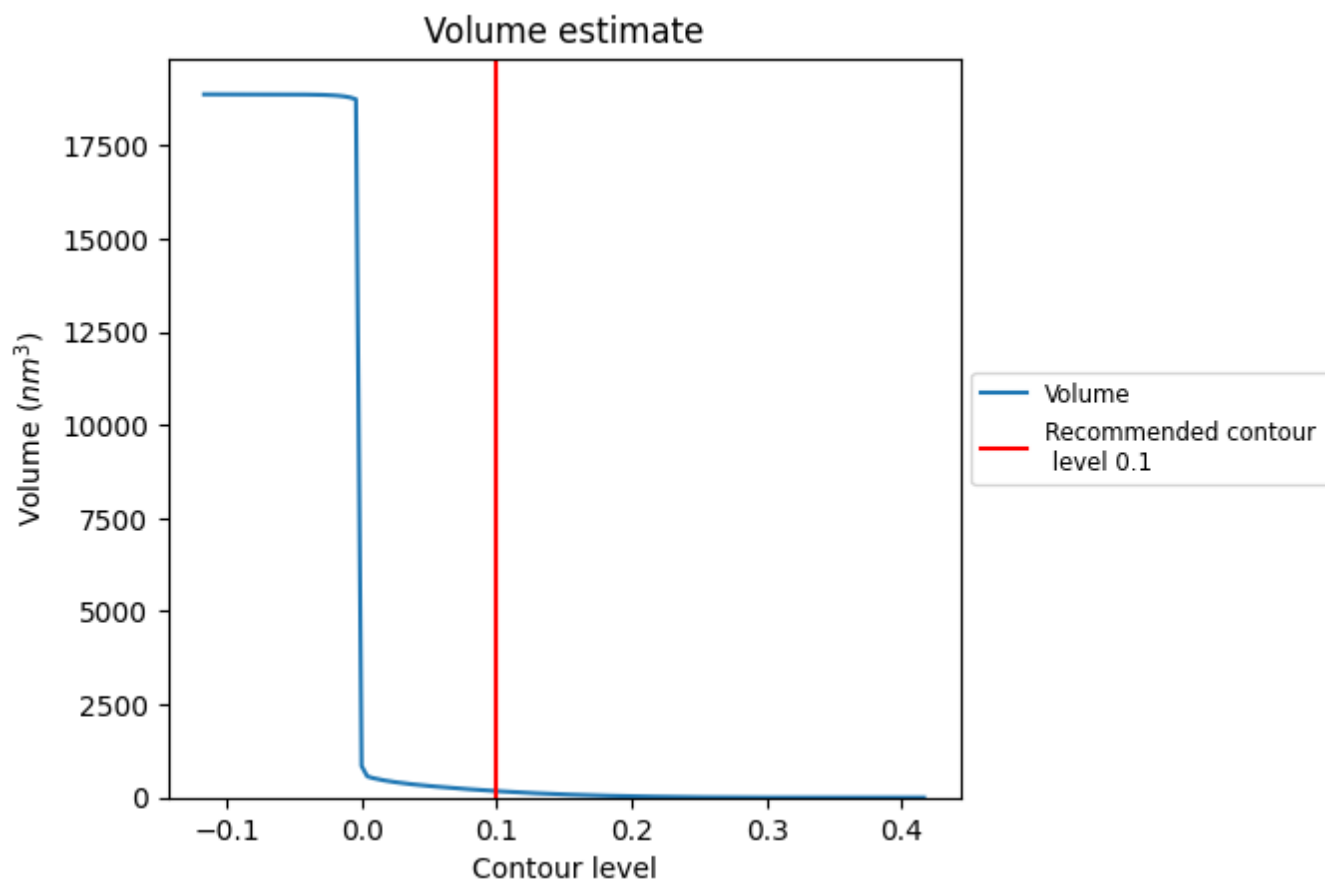
This section contains the results of statistical analysis of the map.

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.

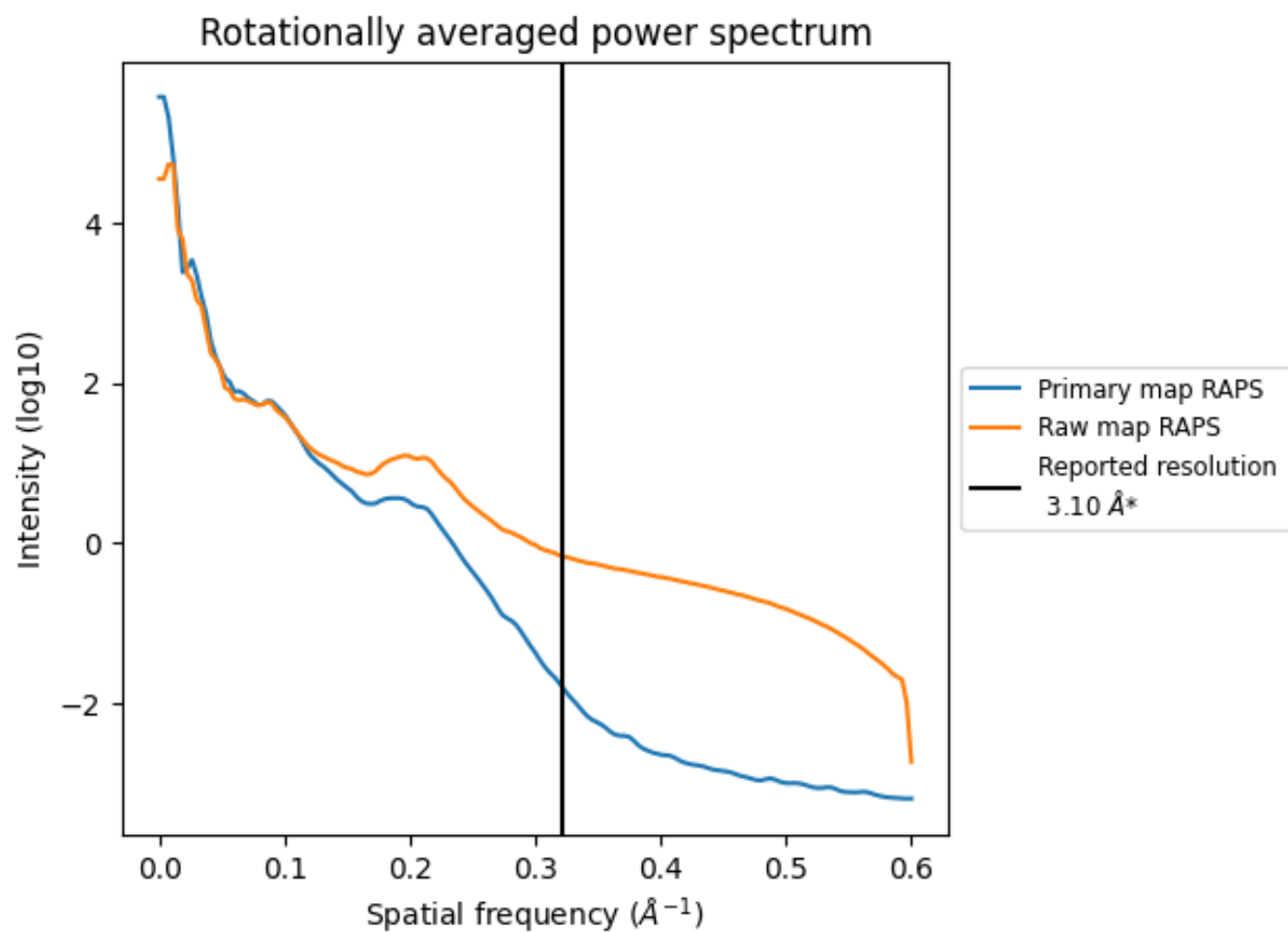
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 174 nm^3 ; this corresponds to an approximate mass of 157 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 ⓘ

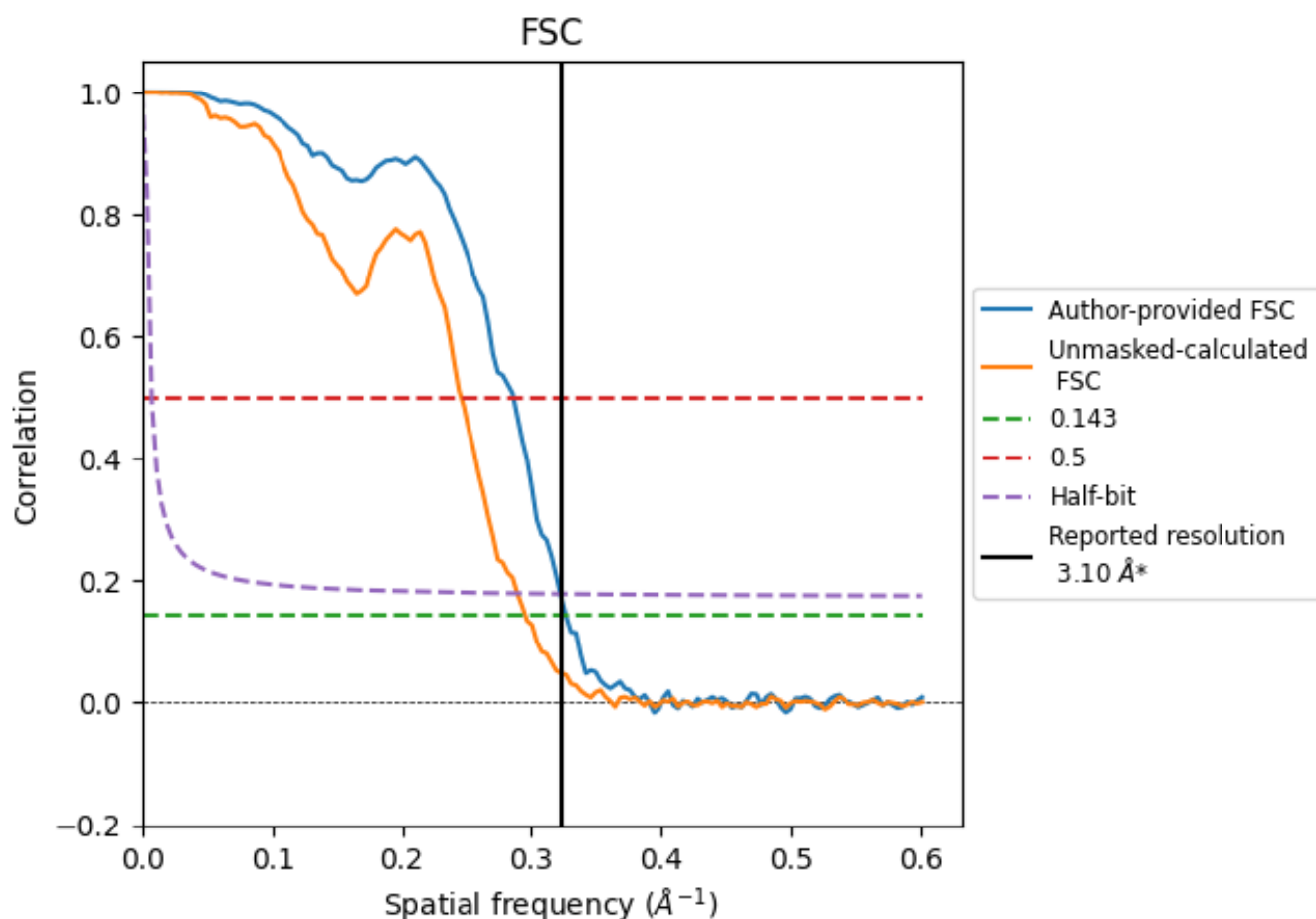


*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

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 0.323 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.06	3.50	3.10
Unmasked-calculated*	3.39	4.07	3.46

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

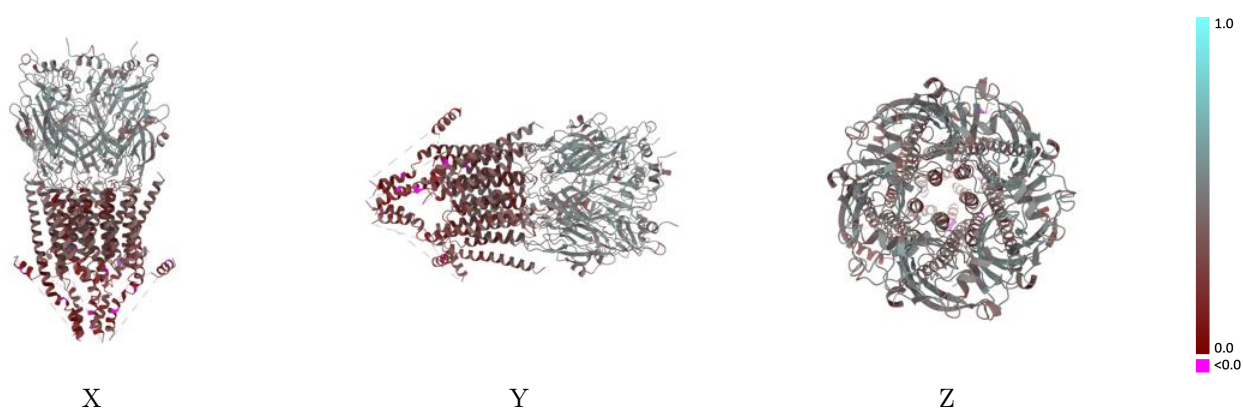
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-10693 and PDB model 6Y5B. Per-residue inclusion information can be found in section 3 on page 15.

9.1 Map-model overlay [i](#)

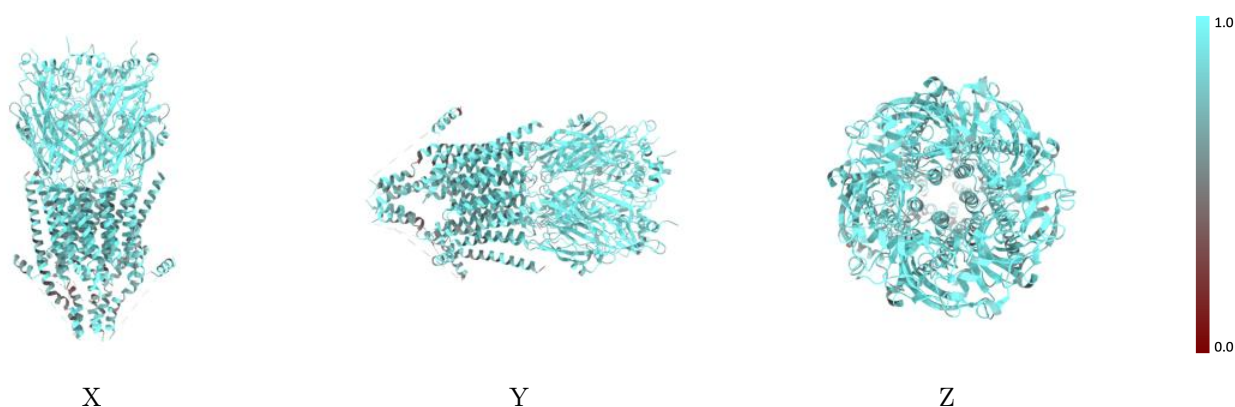
This section was not generated.

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



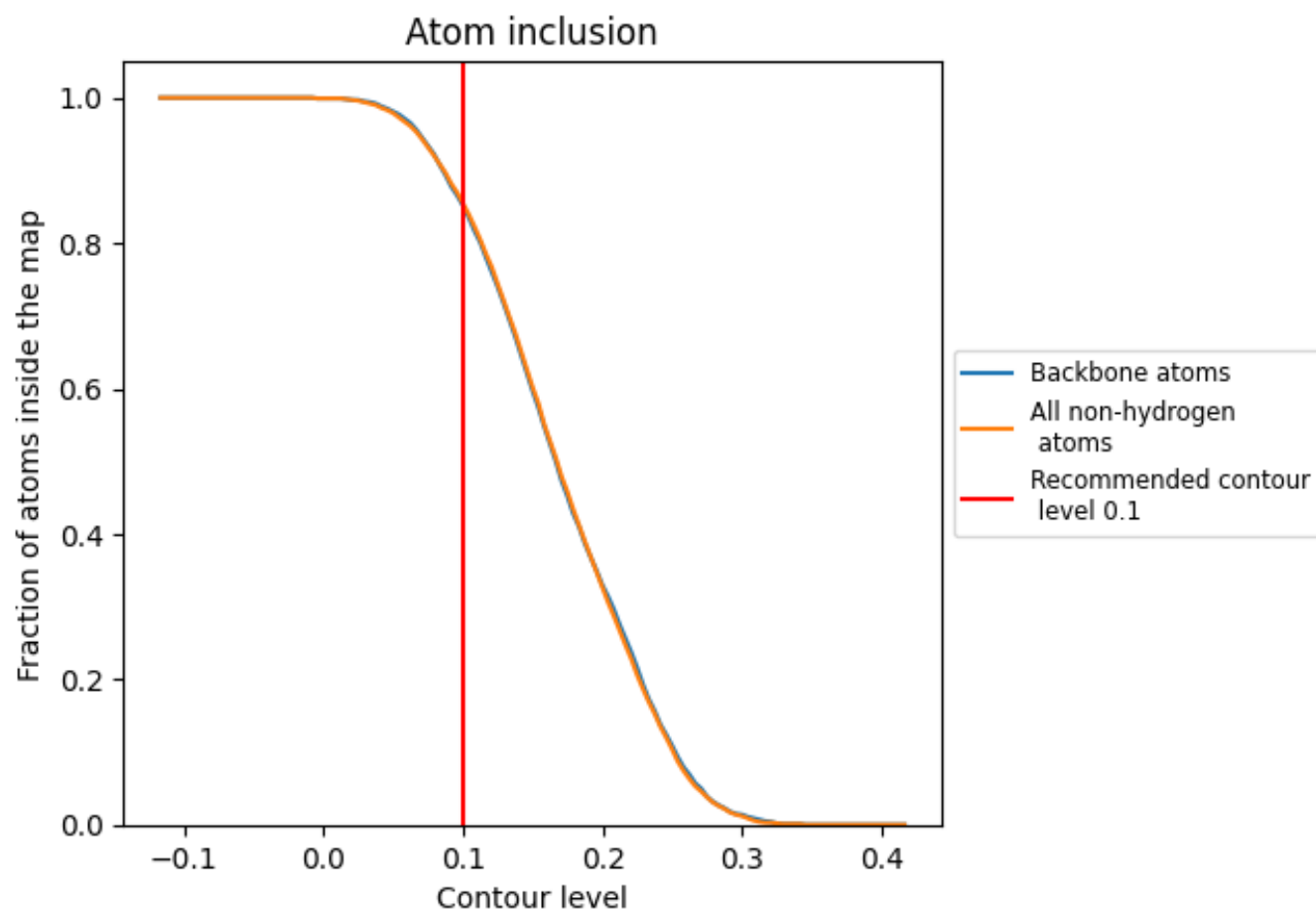
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.1).

9.4 Atom inclusion [i](#)



At the recommended contour level, 85% of all backbone atoms, 86% 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 (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8550	0.3880
A	0.8550	0.3850
B	0.8630	0.3930
C	0.8770	0.3870
D	0.8860	0.3960
E	0.8650	0.3810

