



Full wwPDB EM Validation Report ⓘ

Nov 20, 2022 – 04:39 am GMT

PDB ID : 6H3C
EMDB ID : EMD-0132
Title : Cryo-EM structure of the BRISC complex bound to SHMT2
Authors : Bunker, R.D.; Rabl, J.; Thoma, N.H.
Deposited on : 2018-07-18
Resolution : 3.90 Å(reported)
Based on initial models : 5V7I, 6GVW

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.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

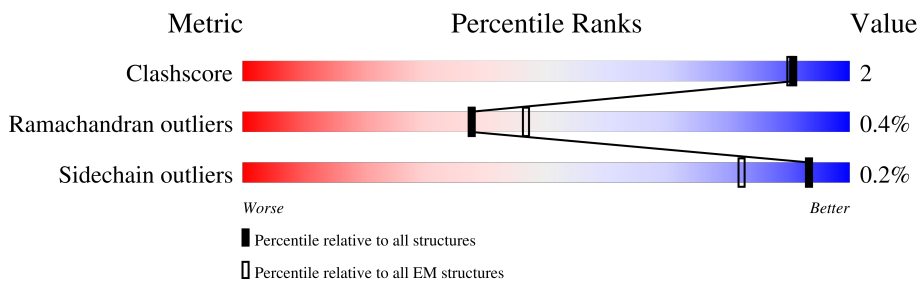
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.90 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	434	
1	F	434	
2	B	335	
2	G	335	
3	C	402	
3	H	402	
4	D	352	
4	I	352	

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Mol	Chain	Length	Quality of chain
5	E	507	 80% 7% 13%
5	J	507	 79% 7% 13%

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 49982 atoms, of which 24860 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 BRISC complex subunit Abraxas 2.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
1	A	255	4134	1305	2052	375	395	7	0	0
1	F	255	4134	1305	2052	375	395	7	0	0

There are 38 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-18	MET	-	initiating methionine	UNP Q15018
A	-17	HIS	-	expression tag	UNP Q15018
A	-16	HIS	-	expression tag	UNP Q15018
A	-15	HIS	-	expression tag	UNP Q15018
A	-14	HIS	-	expression tag	UNP Q15018
A	-13	HIS	-	expression tag	UNP Q15018
A	-12	HIS	-	expression tag	UNP Q15018
A	-11	VAL	-	expression tag	UNP Q15018
A	-10	ASP	-	expression tag	UNP Q15018
A	-9	GLU	-	expression tag	UNP Q15018
A	-8	ASN	-	expression tag	UNP Q15018
A	-7	LEU	-	expression tag	UNP Q15018
A	-6	TYR	-	expression tag	UNP Q15018
A	-5	PHE	-	expression tag	UNP Q15018
A	-4	GLN	-	expression tag	UNP Q15018
A	-3	GLY	-	expression tag	UNP Q15018
A	-2	GLY	-	expression tag	UNP Q15018
A	-1	GLY	-	expression tag	UNP Q15018
A	0	ARG	-	expression tag	UNP Q15018
F	-18	MET	-	initiating methionine	UNP Q15018
F	-17	HIS	-	expression tag	UNP Q15018
F	-16	HIS	-	expression tag	UNP Q15018
F	-15	HIS	-	expression tag	UNP Q15018
F	-14	HIS	-	expression tag	UNP Q15018
F	-13	HIS	-	expression tag	UNP Q15018
F	-12	HIS	-	expression tag	UNP Q15018

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-11	VAL	-	expression tag	UNP Q15018
F	-10	ASP	-	expression tag	UNP Q15018
F	-9	GLU	-	expression tag	UNP Q15018
F	-8	ASN	-	expression tag	UNP Q15018
F	-7	LEU	-	expression tag	UNP Q15018
F	-6	TYR	-	expression tag	UNP Q15018
F	-5	PHE	-	expression tag	UNP Q15018
F	-4	GLN	-	expression tag	UNP Q15018
F	-3	GLY	-	expression tag	UNP Q15018
F	-2	GLY	-	expression tag	UNP Q15018
F	-1	GLY	-	expression tag	UNP Q15018
F	0	ARG	-	expression tag	UNP Q15018

- Molecule 2 is a protein called Lys-63-specific deubiquitinase BRCC36.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
2	B	258	4122	1295	2053	366	394	14	0	0
2	G	258	4122	1295	2053	366	394	14	0	0

There are 38 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-18	MET	-	initiating methionine	UNP P46736
B	-17	HIS	-	expression tag	UNP P46736
B	-16	HIS	-	expression tag	UNP P46736
B	-15	HIS	-	expression tag	UNP P46736
B	-14	HIS	-	expression tag	UNP P46736
B	-13	HIS	-	expression tag	UNP P46736
B	-12	HIS	-	expression tag	UNP P46736
B	-11	VAL	-	expression tag	UNP P46736
B	-10	ASP	-	expression tag	UNP P46736
B	-9	GLU	-	expression tag	UNP P46736
B	-8	ASN	-	expression tag	UNP P46736
B	-7	LEU	-	expression tag	UNP P46736
B	-6	TYR	-	expression tag	UNP P46736
B	-5	PHE	-	expression tag	UNP P46736
B	-4	GLN	-	expression tag	UNP P46736
B	-3	GLY	-	expression tag	UNP P46736
B	-2	GLY	-	expression tag	UNP P46736
B	-1	GLY	-	expression tag	UNP P46736

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Chain	Residue	Modelled	Actual	Comment	Reference
B	0	ARG	-	expression tag	UNP P46736
G	-18	MET	-	initiating methionine	UNP P46736
G	-17	HIS	-	expression tag	UNP P46736
G	-16	HIS	-	expression tag	UNP P46736
G	-15	HIS	-	expression tag	UNP P46736
G	-14	HIS	-	expression tag	UNP P46736
G	-13	HIS	-	expression tag	UNP P46736
G	-12	HIS	-	expression tag	UNP P46736
G	-11	VAL	-	expression tag	UNP P46736
G	-10	ASP	-	expression tag	UNP P46736
G	-9	GLU	-	expression tag	UNP P46736
G	-8	ASN	-	expression tag	UNP P46736
G	-7	LEU	-	expression tag	UNP P46736
G	-6	TYR	-	expression tag	UNP P46736
G	-5	PHE	-	expression tag	UNP P46736
G	-4	GLN	-	expression tag	UNP P46736
G	-3	GLY	-	expression tag	UNP P46736
G	-2	GLY	-	expression tag	UNP P46736
G	-1	GLY	-	expression tag	UNP P46736
G	0	ARG	-	expression tag	UNP P46736

- Molecule 3 is a protein called BRISC and BRCA1-A complex member 2.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
3	C	383	6077	1993	2999	504	567	14	0	0
3	H	383	6077	1993	2999	504	567	14	0	0

There are 38 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-18	MET	-	initiating methionine	UNP Q9NXR7
C	-17	HIS	-	expression tag	UNP Q9NXR7
C	-16	HIS	-	expression tag	UNP Q9NXR7
C	-15	HIS	-	expression tag	UNP Q9NXR7
C	-14	HIS	-	expression tag	UNP Q9NXR7
C	-13	HIS	-	expression tag	UNP Q9NXR7
C	-12	HIS	-	expression tag	UNP Q9NXR7
C	-11	VAL	-	expression tag	UNP Q9NXR7
C	-10	ASP	-	expression tag	UNP Q9NXR7
C	-9	GLU	-	expression tag	UNP Q9NXR7

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-8	ASN	-	expression tag	UNP Q9NXR7
C	-7	LEU	-	expression tag	UNP Q9NXR7
C	-6	TYR	-	expression tag	UNP Q9NXR7
C	-5	PHE	-	expression tag	UNP Q9NXR7
C	-4	GLN	-	expression tag	UNP Q9NXR7
C	-3	GLY	-	expression tag	UNP Q9NXR7
C	-2	GLY	-	expression tag	UNP Q9NXR7
C	-1	GLY	-	expression tag	UNP Q9NXR7
C	0	ARG	-	expression tag	UNP Q9NXR7
H	-18	MET	-	initiating methionine	UNP Q9NXR7
H	-17	HIS	-	expression tag	UNP Q9NXR7
H	-16	HIS	-	expression tag	UNP Q9NXR7
H	-15	HIS	-	expression tag	UNP Q9NXR7
H	-14	HIS	-	expression tag	UNP Q9NXR7
H	-13	HIS	-	expression tag	UNP Q9NXR7
H	-12	HIS	-	expression tag	UNP Q9NXR7
H	-11	VAL	-	expression tag	UNP Q9NXR7
H	-10	ASP	-	expression tag	UNP Q9NXR7
H	-9	GLU	-	expression tag	UNP Q9NXR7
H	-8	ASN	-	expression tag	UNP Q9NXR7
H	-7	LEU	-	expression tag	UNP Q9NXR7
H	-6	TYR	-	expression tag	UNP Q9NXR7
H	-5	PHE	-	expression tag	UNP Q9NXR7
H	-4	GLN	-	expression tag	UNP Q9NXR7
H	-3	GLY	-	expression tag	UNP Q9NXR7
H	-2	GLY	-	expression tag	UNP Q9NXR7
H	-1	GLY	-	expression tag	UNP Q9NXR7
H	0	ARG	-	expression tag	UNP Q9NXR7

- Molecule 4 is a protein called BRISC and BRCA1-A complex member 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
4	D	237	3761	1206	1872	306	359	18	0	0
4	I	237	3761	1206	1872	306	359	18	0	0

There are 46 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	-22	MET	-	initiating methionine	UNP Q9NWX8
D	-21	ALA	-	expression tag	UNP Q9NWX8

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-20	SER	-	expression tag	UNP Q9NWX8
D	-19	TRP	-	expression tag	UNP Q9NWX8
D	-18	SER	-	expression tag	UNP Q9NWX8
D	-17	HIS	-	expression tag	UNP Q9NWX8
D	-16	PRO	-	expression tag	UNP Q9NWX8
D	-15	GLN	-	expression tag	UNP Q9NWX8
D	-14	PHE	-	expression tag	UNP Q9NWX8
D	-13	GLU	-	expression tag	UNP Q9NWX8
D	-12	LYS	-	expression tag	UNP Q9NWX8
D	-11	VAL	-	expression tag	UNP Q9NWX8
D	-10	ASP	-	expression tag	UNP Q9NWX8
D	-9	GLU	-	expression tag	UNP Q9NWX8
D	-8	ASN	-	expression tag	UNP Q9NWX8
D	-7	LEU	-	expression tag	UNP Q9NWX8
D	-6	TYR	-	expression tag	UNP Q9NWX8
D	-5	PHE	-	expression tag	UNP Q9NWX8
D	-4	GLN	-	expression tag	UNP Q9NWX8
D	-3	GLY	-	expression tag	UNP Q9NWX8
D	-2	GLY	-	expression tag	UNP Q9NWX8
D	-1	GLY	-	expression tag	UNP Q9NWX8
D	0	ARG	-	expression tag	UNP Q9NWX8
I	-22	MET	-	initiating methionine	UNP Q9NWX8
I	-21	ALA	-	expression tag	UNP Q9NWX8
I	-20	SER	-	expression tag	UNP Q9NWX8
I	-19	TRP	-	expression tag	UNP Q9NWX8
I	-18	SER	-	expression tag	UNP Q9NWX8
I	-17	HIS	-	expression tag	UNP Q9NWX8
I	-16	PRO	-	expression tag	UNP Q9NWX8
I	-15	GLN	-	expression tag	UNP Q9NWX8
I	-14	PHE	-	expression tag	UNP Q9NWX8
I	-13	GLU	-	expression tag	UNP Q9NWX8
I	-12	LYS	-	expression tag	UNP Q9NWX8
I	-11	VAL	-	expression tag	UNP Q9NWX8
I	-10	ASP	-	expression tag	UNP Q9NWX8
I	-9	GLU	-	expression tag	UNP Q9NWX8
I	-8	ASN	-	expression tag	UNP Q9NWX8
I	-7	LEU	-	expression tag	UNP Q9NWX8
I	-6	TYR	-	expression tag	UNP Q9NWX8
I	-5	PHE	-	expression tag	UNP Q9NWX8
I	-4	GLN	-	expression tag	UNP Q9NWX8
I	-3	GLY	-	expression tag	UNP Q9NWX8
I	-2	GLY	-	expression tag	UNP Q9NWX8

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Chain	Residue	Modelled	Actual	Comment	Reference
I	-1	GLY	-	expression tag	UNP Q9NWX8
I	0	ARG	-	expression tag	UNP Q9NWX8

- Molecule 5 is a protein called Serine hydroxymethyltransferase, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
5	E	440	6893	2172	3452	616	638	15	0	0
5	J	440	Total	C	H	N	O	S	0	0
			6893	2172	3452	616	638	15		

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	-23	MET	-	initiating methionine	UNP P34897
E	-22	GLY	-	expression tag	UNP P34897
E	-21	SER	-	expression tag	UNP P34897
E	-20	SER	-	expression tag	UNP P34897
E	-19	HIS	-	expression tag	UNP P34897
E	-18	HIS	-	expression tag	UNP P34897
E	-17	HIS	-	expression tag	UNP P34897
E	-16	HIS	-	expression tag	UNP P34897
E	-15	HIS	-	expression tag	UNP P34897
E	-14	HIS	-	expression tag	UNP P34897
E	-13	SER	-	expression tag	UNP P34897
E	-12	SER	-	expression tag	UNP P34897
E	-11	GLY	-	expression tag	UNP P34897
E	-10	LEU	-	expression tag	UNP P34897
E	-9	VAL	-	expression tag	UNP P34897
E	-8	PRO	-	expression tag	UNP P34897
E	-7	ARG	-	expression tag	UNP P34897
E	-6	GLY	-	expression tag	UNP P34897
E	-5	SER	-	expression tag	UNP P34897
E	264	THR	ALA	cloning artifact	UNP P34897
J	-23	MET	-	initiating methionine	UNP P34897
J	-22	GLY	-	expression tag	UNP P34897
J	-21	SER	-	expression tag	UNP P34897
J	-20	SER	-	expression tag	UNP P34897
J	-19	HIS	-	expression tag	UNP P34897
J	-18	HIS	-	expression tag	UNP P34897
J	-17	HIS	-	expression tag	UNP P34897
J	-16	HIS	-	expression tag	UNP P34897

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Chain	Residue	Modelled	Actual	Comment	Reference
J	-15	HIS	-	expression tag	UNP P34897
J	-14	HIS	-	expression tag	UNP P34897
J	-13	SER	-	expression tag	UNP P34897
J	-12	SER	-	expression tag	UNP P34897
J	-11	GLY	-	expression tag	UNP P34897
J	-10	LEU	-	expression tag	UNP P34897
J	-9	VAL	-	expression tag	UNP P34897
J	-8	PRO	-	expression tag	UNP P34897
J	-7	ARG	-	expression tag	UNP P34897
J	-6	GLY	-	expression tag	UNP P34897
J	-5	SER	-	expression tag	UNP P34897
J	264	THR	ALA	cloning artifact	UNP P34897

- Molecule 6 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	AltConf
6	B	1	Total Zn 1 1	0
6	G	1	Total Zn 1 1	0

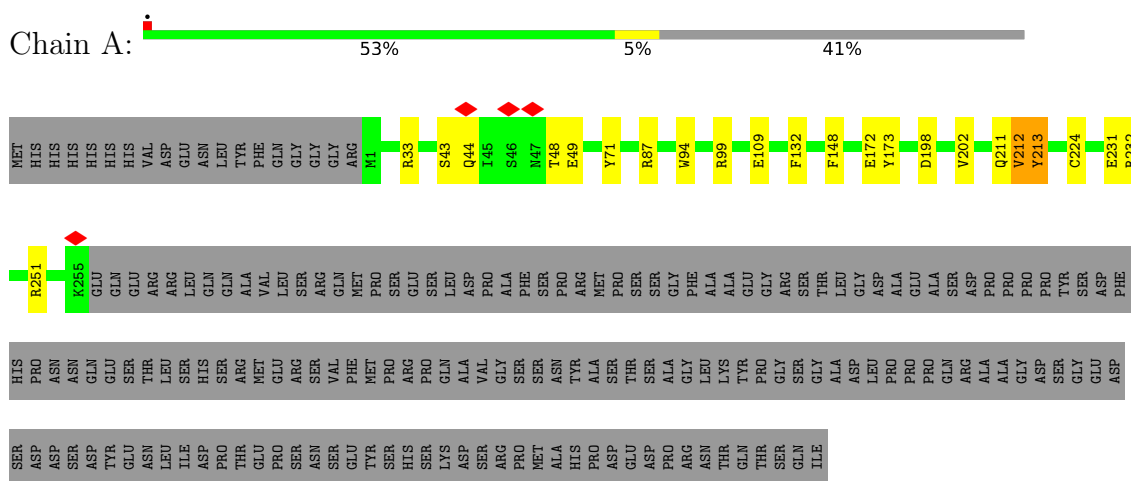
- Molecule 7 is water.

Mol	Chain	Residues	Atoms	AltConf
7	B	1	Total H O 3 2 1	0
7	G	1	Total H O 3 2 1	0

3 Residue-property plots i

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: BRISC complex subunit Abraxas 2

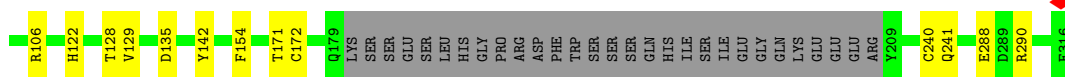


- Molecule 1: BRISC complex subunit Abraxas 2

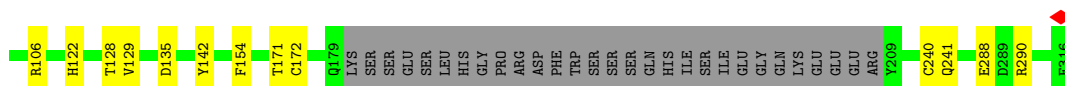


- Molecule 2: Lys-63-specific deubiquitinase BRCC36

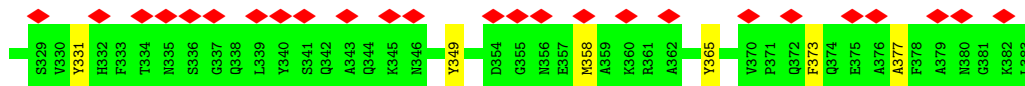
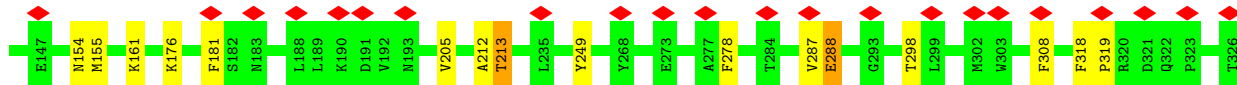
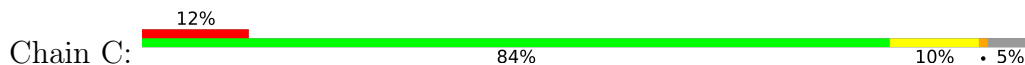




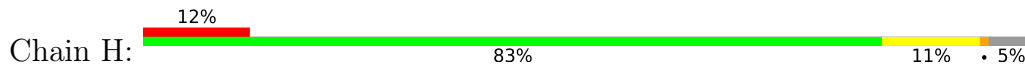
• Molecule 2: Lys-63-specific deubiquitinase BRCC36



• Molecule 3: BRISC and BRCA1-A complex member 2

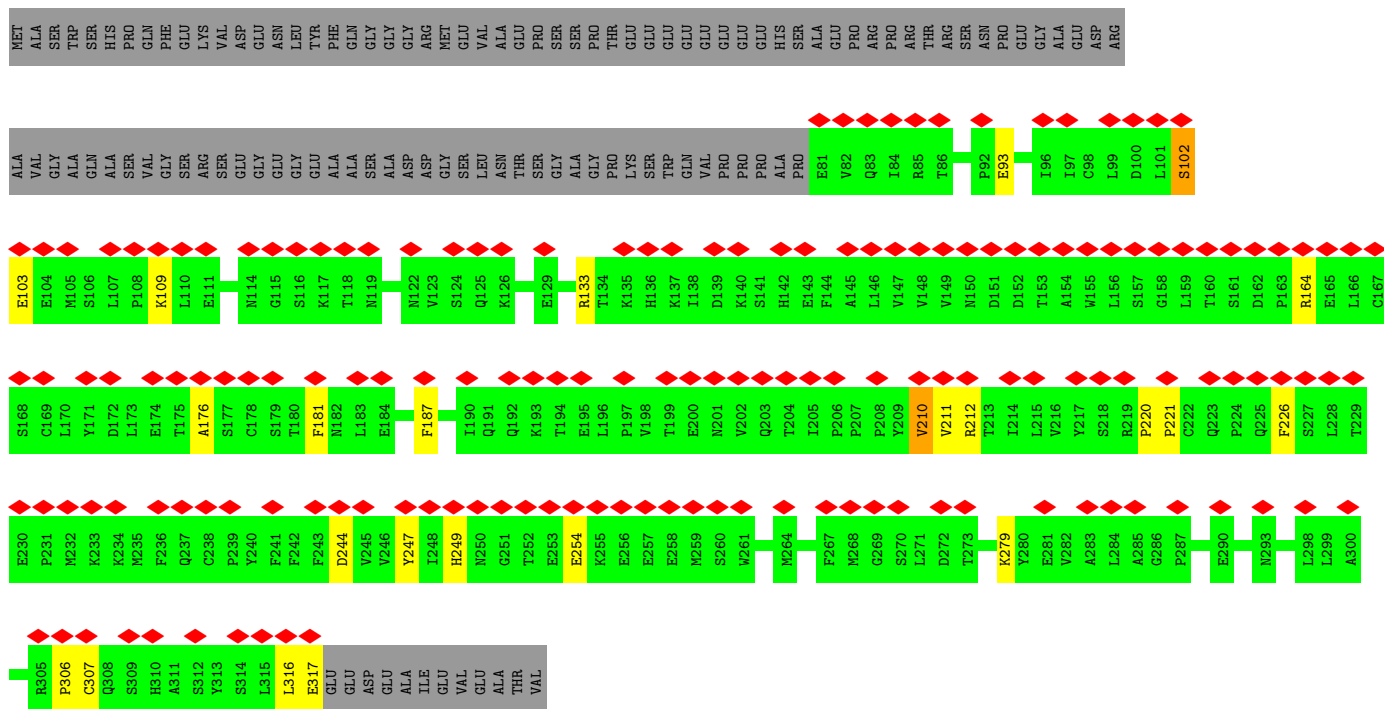


• Molecule 3: BRISC and BRCA1-A complex member 2

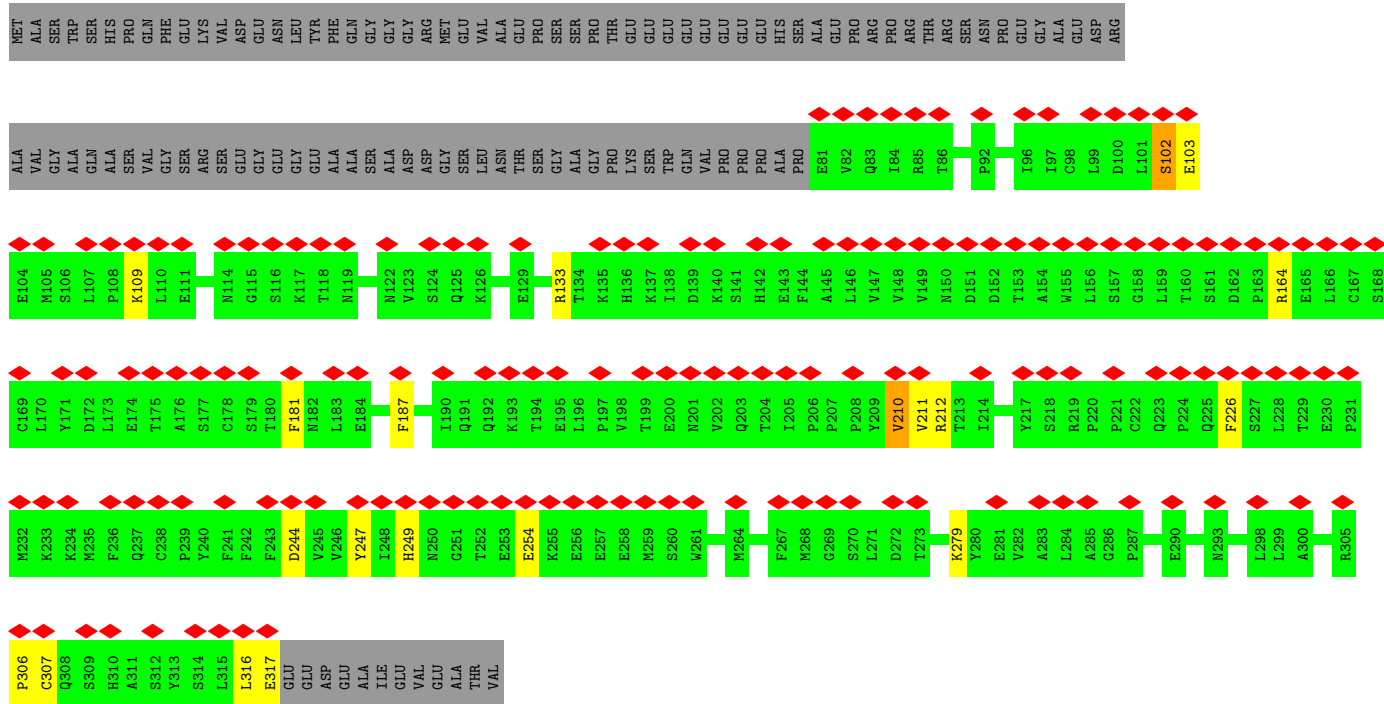
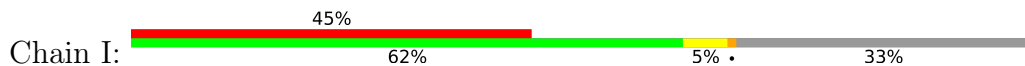


• Molecule 4: BRISC and BRCA1-A complex member 1

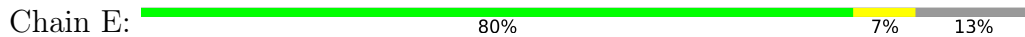




• Molecule 4: BRISC and BRCA1-A complex member 1



• Molecule 5: Serine hydroxymethyltransferase, mitochondrial



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	35595	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION; CTF was determined using GCTF. CTF was corrected within RELION.	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	45	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	58140	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.131	Depositor
Minimum map value	-0.066	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.00816	Depositor
Map size (\AA)	301.0, 301.0, 301.0	wwPDB
Map dimensions	350, 350, 350	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.86, 0.86, 0.86	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	1.16	9/2120 (0.4%)	0.95	8/2856 (0.3%)
1	F	1.15	9/2120 (0.4%)	0.95	8/2856 (0.3%)
2	B	1.15	5/2105 (0.2%)	0.89	3/2845 (0.1%)
2	G	1.15	5/2105 (0.2%)	0.89	3/2845 (0.1%)
3	C	1.08	13/3169 (0.4%)	1.01	10/4310 (0.2%)
3	H	1.08	13/3169 (0.4%)	1.02	10/4310 (0.2%)
4	D	1.08	4/1934 (0.2%)	1.09	7/2623 (0.3%)
4	I	1.08	3/1934 (0.2%)	1.09	7/2623 (0.3%)
5	E	1.08	4/3508 (0.1%)	0.99	15/4744 (0.3%)
5	J	1.08	5/3508 (0.1%)	0.99	14/4744 (0.3%)
All	All	1.10	70/25672 (0.3%)	0.99	85/34756 (0.2%)

All (70) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	141	GLU	CD-OE2	-7.21	1.17	1.25
3	H	141	GLU	CD-OE2	-7.19	1.17	1.25
2	B	288	GLU	CG-CD	-7.16	1.41	1.51
1	A	224	CYS	CB-SG	-7.12	1.70	1.82
1	F	224	CYS	CB-SG	-7.10	1.70	1.82
2	G	288	GLU	CG-CD	-7.08	1.41	1.51
5	J	447	PHE	CG-CD2	-7.03	1.28	1.38
5	E	447	PHE	CG-CD2	-7.02	1.28	1.38
3	C	288	GLU	CD-OE1	-6.99	1.18	1.25
3	H	288	GLU	CD-OE1	-6.99	1.18	1.25
5	E	447	PHE	CB-CG	-6.91	1.39	1.51
5	J	447	PHE	CB-CG	-6.90	1.39	1.51
3	H	124	TYR	CB-CG	-6.76	1.41	1.51
3	C	124	TYR	CB-CG	-6.73	1.41	1.51
5	E	359	HIS	CB-CG	-6.32	1.38	1.50
5	J	359	HIS	CB-CG	-6.32	1.38	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	142	TYR	CB-CG	-6.31	1.42	1.51
3	H	142	TYR	CB-CG	-6.31	1.42	1.51
4	I	181	PHE	CB-CG	6.14	1.61	1.51
4	D	181	PHE	CB-CG	6.12	1.61	1.51
4	D	102	SER	CB-OG	-6.11	1.34	1.42
4	I	102	SER	CB-OG	-6.11	1.34	1.42
3	C	278	PHE	CB-CG	-6.09	1.41	1.51
3	H	278	PHE	CB-CG	-6.07	1.41	1.51
1	A	132	PHE	CB-CG	-5.98	1.41	1.51
1	F	132	PHE	CB-CG	-5.94	1.41	1.51
3	C	349	TYR	CG-CD2	-5.82	1.31	1.39
3	H	349	TYR	CG-CD2	-5.80	1.31	1.39
4	I	247	TYR	CB-CG	5.79	1.60	1.51
4	D	247	TYR	CB-CG	5.78	1.60	1.51
3	H	308	PHE	CB-CG	-5.71	1.41	1.51
2	B	41	GLU	CD-OE2	-5.68	1.19	1.25
3	C	308	PHE	CB-CG	-5.66	1.41	1.51
2	G	122	HIS	CB-CG	-5.65	1.39	1.50
2	B	122	HIS	CB-CG	-5.59	1.40	1.50
2	G	41	GLU	CD-OE2	-5.58	1.19	1.25
1	A	231	GLU	CD-OE1	-5.57	1.19	1.25
5	E	314	VAL	CB-CG2	-5.55	1.41	1.52
5	J	314	VAL	CB-CG2	-5.54	1.41	1.52
1	F	231	GLU	CD-OE1	-5.49	1.19	1.25
2	G	22	CYS	CB-SG	-5.48	1.72	1.81
3	H	287	VAL	CB-CG2	-5.44	1.41	1.52
2	B	22	CYS	CB-SG	-5.43	1.73	1.81
1	A	94	TRP	CB-CG	-5.42	1.40	1.50
1	F	94	TRP	CB-CG	-5.42	1.40	1.50
3	C	287	VAL	CB-CG2	-5.41	1.41	1.52
1	A	109	GLU	CD-OE2	-5.34	1.19	1.25
1	F	109	GLU	CD-OE2	-5.32	1.19	1.25
3	C	65	GLU	CD-OE2	-5.29	1.19	1.25
1	F	231	GLU	CD-OE2	-5.29	1.19	1.25
3	C	111	GLU	CD-OE2	-5.28	1.19	1.25
1	A	231	GLU	CD-OE2	-5.27	1.19	1.25
2	B	154	PHE	CB-CG	-5.27	1.42	1.51
2	G	154	PHE	CB-CG	-5.26	1.42	1.51
1	F	148	PHE	CB-CG	-5.24	1.42	1.51
1	A	109	GLU	CD-OE1	-5.24	1.19	1.25
1	F	109	GLU	CD-OE1	-5.24	1.19	1.25
1	A	148	PHE	CB-CG	-5.22	1.42	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	213	TYR	CE2-CZ	-5.21	1.31	1.38
3	H	111	GLU	CD-OE2	-5.20	1.20	1.25
1	F	213	TYR	CE2-CZ	-5.18	1.31	1.38
3	H	65	GLU	CD-OE2	-5.18	1.20	1.25
3	H	205	VAL	CB-CG1	-5.18	1.42	1.52
3	C	205	VAL	CB-CG1	-5.13	1.42	1.52
3	C	141	GLU	CD-OE1	-5.06	1.20	1.25
3	H	141	GLU	CD-OE1	-5.06	1.20	1.25
4	D	93	GLU	CD-OE2	-5.05	1.20	1.25
3	C	92	PHE	CB-CG	-5.04	1.42	1.51
3	H	92	PHE	CB-CG	-5.04	1.42	1.51
5	J	222	GLU	CD-OE1	-5.03	1.20	1.25

All (85) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	212	ARG	NE-CZ-NH2	-11.28	114.66	120.30
4	I	212	ARG	NE-CZ-NH2	-11.27	114.67	120.30
5	J	288	TYR	CB-CG-CD2	-9.70	115.18	121.00
5	E	288	TYR	CB-CG-CD2	-9.68	115.19	121.00
3	C	142	TYR	CB-CG-CD2	-8.58	115.85	121.00
3	H	142	TYR	CB-CG-CD2	-8.58	115.85	121.00
5	E	196	ARG	NE-CZ-NH2	-8.15	116.23	120.30
5	J	196	ARG	NE-CZ-NH2	-8.11	116.25	120.30
4	I	133	ARG	NE-CZ-NH2	-8.06	116.27	120.30
2	G	135	ASP	CB-CG-OD1	7.97	125.47	118.30
2	B	135	ASP	CB-CG-OD1	7.97	125.47	118.30
4	D	133	ARG	NE-CZ-NH2	-7.96	116.32	120.30
4	I	164	ARG	NE-CZ-NH2	-7.69	116.46	120.30
5	J	329	TYR	CB-CG-CD2	-7.62	116.43	121.00
4	D	164	ARG	NE-CZ-NH2	-7.61	116.50	120.30
5	E	329	TYR	CB-CG-CD2	-7.58	116.45	121.00
5	E	83	ARG	NE-CZ-NH1	7.31	123.96	120.30
5	E	217	ARG	NE-CZ-NH2	-7.31	116.65	120.30
5	J	83	ARG	NE-CZ-NH1	7.29	123.95	120.30
5	J	217	ARG	NE-CZ-NH2	-7.27	116.67	120.30
5	J	61	ARG	NE-CZ-NH2	-7.20	116.70	120.30
5	E	61	ARG	NE-CZ-NH2	-7.18	116.71	120.30
1	A	232	ARG	NE-CZ-NH2	-7.01	116.80	120.30
5	E	83	ARG	NE-CZ-NH2	-7.01	116.79	120.30
5	E	174	TYR	CB-CG-CD1	-7.01	116.80	121.00
5	J	83	ARG	NE-CZ-NH2	-7.00	116.80	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	232	ARG	NE-CZ-NH2	-6.99	116.81	120.30
5	J	174	TYR	CB-CG-CD1	-6.96	116.83	121.00
1	A	251	ARG	NE-CZ-NH2	-6.84	116.88	120.30
5	J	139	ARG	NE-CZ-NH2	-6.82	116.89	120.30
1	A	71	TYR	CB-CG-CD2	-6.81	116.91	121.00
2	G	290	ARG	NE-CZ-NH2	-6.74	116.93	120.30
2	B	290	ARG	NE-CZ-NH2	-6.74	116.93	120.30
1	F	251	ARG	NE-CZ-NH2	-6.73	116.94	120.30
1	F	71	TYR	CB-CG-CD2	-6.69	116.98	121.00
5	E	139	ARG	NE-CZ-NH2	-6.67	116.97	120.30
5	E	130	TYR	CB-CG-CD1	-6.57	117.06	121.00
5	J	130	TYR	CB-CG-CD1	-6.52	117.09	121.00
1	F	212	VAL	N-CA-C	-6.26	94.10	111.00
1	A	212	VAL	N-CA-C	-6.24	94.17	111.00
3	H	124	TYR	CB-CG-CD1	-6.22	117.27	121.00
3	C	124	TYR	CB-CG-CD1	-6.22	117.27	121.00
2	G	106	ARG	NE-CZ-NH2	-6.16	117.22	120.30
5	J	272	ARG	NE-CZ-NH2	-6.16	117.22	120.30
5	E	272	ARG	NE-CZ-NH2	-6.15	117.22	120.30
2	B	106	ARG	NE-CZ-NH2	-6.13	117.24	120.30
4	I	244	ASP	CB-CG-OD1	6.01	123.71	118.30
3	H	349	TYR	CB-CG-CD2	-5.99	117.41	121.00
4	D	244	ASP	CB-CG-OD1	5.98	123.68	118.30
3	C	349	TYR	CB-CG-CD2	-5.92	117.45	121.00
3	H	365	TYR	CB-CG-CD1	-5.75	117.55	121.00
5	J	288	TYR	CB-CG-CD1	5.66	124.39	121.00
1	A	213	TYR	CB-CG-CD2	-5.65	117.61	121.00
3	C	365	TYR	CB-CG-CD1	-5.64	117.62	121.00
5	E	288	TYR	CB-CG-CD1	5.63	124.38	121.00
1	F	87	ARG	NE-CZ-NH2	-5.62	117.49	120.30
1	F	213	TYR	CB-CG-CD2	-5.60	117.64	121.00
1	A	87	ARG	NE-CZ-NH2	-5.59	117.50	120.30
1	F	99	ARG	NE-CZ-NH2	-5.49	117.56	120.30
3	H	331	TYR	CB-CG-CD2	-5.48	117.71	121.00
4	I	226	PHE	CB-CG-CD2	-5.40	117.02	120.80
5	E	209	ARG	NE-CZ-NH2	-5.40	117.60	120.30
4	D	226	PHE	CB-CG-CD2	-5.39	117.02	120.80
3	C	331	TYR	CB-CG-CD2	-5.38	117.77	121.00
5	J	209	ARG	NE-CZ-NH2	-5.37	117.61	120.30
1	A	99	ARG	NE-CZ-NH2	-5.36	117.62	120.30
4	I	249	HIS	CA-CB-CG	5.33	122.65	113.60
4	D	249	HIS	CA-CB-CG	5.31	122.63	113.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	187	PHE	CB-CG-CD1	5.26	124.48	120.80
3	C	181	PHE	CB-CG-CD2	5.25	124.48	120.80
4	I	187	PHE	CB-CG-CD1	5.25	124.48	120.80
1	F	33	ARG	NE-CZ-NH2	-5.24	117.68	120.30
3	H	358	MET	CG-SD-CE	5.24	108.58	100.20
3	C	358	MET	CG-SD-CE	5.24	108.58	100.20
5	J	347	ARG	NE-CZ-NH2	-5.24	117.68	120.30
3	C	127	PHE	CB-CG-CD2	-5.24	117.13	120.80
3	H	181	PHE	CB-CG-CD2	5.24	124.47	120.80
1	A	33	ARG	NE-CZ-NH2	-5.22	117.69	120.30
5	E	347	ARG	NE-CZ-NH2	-5.22	117.69	120.30
3	C	92	PHE	CB-CG-CD2	-5.20	117.16	120.80
3	H	92	PHE	CB-CG-CD2	-5.19	117.17	120.80
3	C	249	TYR	CB-CG-CD2	-5.16	117.90	121.00
3	H	249	TYR	CB-CG-CD2	-5.16	117.91	121.00
3	H	127	PHE	CB-CG-CD2	-5.11	117.22	120.80
5	E	265	ARG	NE-CZ-NH1	5.02	122.81	120.30

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	2082	2052	2054	6	0
1	F	2082	2052	2054	5	0
2	B	2069	2053	2051	4	0
2	G	2069	2053	2051	4	0
3	C	3078	2999	3001	14	0
3	H	3078	2999	3001	16	0
4	D	1889	1872	1871	8	0
4	I	1889	1872	1871	5	0
5	E	3441	3452	3451	10	0
5	J	3441	3452	3451	13	0
6	B	1	0	0	0	0
6	G	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	B	1	2	0	0	0
7	G	1	2	0	0	0
All	All	25122	24860	24856	82	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 2.

All (82) 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:F:43:SER:O	1:F:44:GLN:C	2.43	0.56
5:J:359:HIS:ND1	5:J:359:HIS:N	2.53	0.55
4:D:210:VAL:HG12	4:D:211:VAL:H	1.73	0.54
1:A:43:SER:O	1:A:44:GLN:C	2.43	0.54
4:D:316:LEU:O	4:D:317:GLU:C	2.47	0.53
4:I:109:LYS:NZ	4:I:254:GLU:OE2	2.42	0.53
4:I:210:VAL:HG12	4:I:211:VAL:H	1.73	0.53
4:D:109:LYS:NZ	4:D:254:GLU:OE2	2.42	0.52
1:F:212:VAL:O	1:F:213:TYR:HB3	2.09	0.52
4:I:316:LEU:O	4:I:317:GLU:C	2.47	0.52
1:F:211:GLN:C	1:F:212:VAL:O	2.45	0.52
1:A:212:VAL:O	1:A:213:TYR:HB3	2.09	0.51
4:D:102:SER:OG	4:D:103:GLU:N	2.44	0.50
3:H:60:ILE:N	3:H:66:THR:O	2.45	0.50
3:C:60:ILE:N	3:C:66:THR:O	2.45	0.50
5:J:480:PHE:O	5:J:481:ASP:C	2.51	0.50
4:I:102:SER:OG	4:I:103:GLU:N	2.44	0.49
1:F:198:ASP:N	1:F:198:ASP:OD1	2.45	0.49
5:E:480:PHE:O	5:E:481:ASP:C	2.51	0.49
1:A:198:ASP:OD1	1:A:198:ASP:N	2.45	0.48
3:C:288:GLU:HG2	3:C:298:THR:HB	1.95	0.48
3:H:68:LYS:NZ	5:J:218:GLU:OE2	2.47	0.48
3:H:288:GLU:HG2	3:H:298:THR:HB	1.96	0.48
3:C:68:LYS:NZ	5:E:218:GLU:OE2	2.47	0.47
1:A:211:GLN:C	1:A:212:VAL:O	2.45	0.47
4:D:102:SER:OG	4:D:176:ALA:O	2.22	0.47
3:C:27:VAL:H	3:C:33:ASN:HD21	1.62	0.46
1:A:48:THR:OG1	1:A:49:GLU:N	2.49	0.46
2:B:92:ILE:N	2:B:142:TYR:OH	2.45	0.46
5:J:271:TYR:CE1	5:J:291:GLU:HB3	2.51	0.46
5:J:366:ARG:N	5:J:367:PRO:CD	2.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:171:THR:OG1	2:B:172:CYS:N	2.48	0.46
3:H:27:VAL:H	3:H:33:ASN:HD21	1.62	0.45
4:I:306:PRO:O	4:I:307:CYS:C	2.54	0.45
5:E:359:HIS:ND1	5:E:359:HIS:N	2.53	0.45
5:E:271:TYR:CE1	5:E:291:GLU:HB3	2.51	0.45
2:G:171:THR:OG1	2:G:172:CYS:N	2.48	0.45
5:E:366:ARG:N	5:E:367:PRO:CD	2.79	0.45
2:G:128:THR:OG1	2:G:129:VAL:N	2.49	0.45
4:D:306:PRO:O	4:D:307:CYS:C	2.54	0.45
2:B:128:THR:OG1	2:B:129:VAL:N	2.49	0.45
3:H:73:PHE:HB3	3:H:82:PRO:HA	1.99	0.45
5:E:121:SER:N	5:E:266:SER:HA	2.32	0.44
1:F:48:THR:OG1	1:F:49:GLU:N	2.49	0.44
4:D:102:SER:OG	4:D:176:ALA:N	2.45	0.44
5:J:121:SER:N	5:J:266:SER:HA	2.33	0.44
3:C:73:PHE:HB3	3:C:82:PRO:HA	1.98	0.43
2:G:92:ILE:N	2:G:142:TYR:OH	2.45	0.43
5:J:376:GLU:OE1	5:J:388:LYS:NZ	2.44	0.43
3:C:318:PHE:N	3:C:319:PRO:CD	2.81	0.43
3:H:318:PHE:N	3:H:319:PRO:CD	2.81	0.43
3:C:91:GLU:OE1	3:C:161:LYS:NZ	2.51	0.43
3:H:212:ALA:O	3:H:213:THR:CB	2.68	0.42
5:E:440:LYS:NZ	5:E:454:ASP:OD2	2.53	0.42
5:J:413:ARG:NH2	5:J:472:ALA:O	2.53	0.42
2:G:240:CYS:SG	2:G:241:GLN:N	2.92	0.42
3:C:30:ASP:OD1	3:C:31:ALA:N	2.53	0.42
5:E:35:MET:HE1	5:J:315:ALA:HB3	2.01	0.42
2:B:240:CYS:SG	2:B:241:GLN:N	2.92	0.41
5:E:413:ARG:NH2	5:E:472:ALA:O	2.53	0.41
3:C:62:TYR:O	3:C:63:ALA:C	2.57	0.41
3:C:212:ALA:O	3:C:213:THR:CB	2.68	0.41
4:D:220:PRO:HA	4:D:221:PRO:HD3	1.77	0.41
3:C:138:LEU:O	3:C:139:MET:C	2.58	0.41
5:J:440:LYS:NZ	5:J:454:ASP:OD2	2.53	0.41
3:H:30:ASP:OD1	3:H:31:ALA:N	2.53	0.41
3:H:62:TYR:O	3:H:63:ALA:C	2.57	0.41
3:C:373:PHE:CD1	3:C:377:ALA:HB3	2.56	0.41
3:H:91:GLU:OE1	3:H:161:LYS:NZ	2.51	0.41
3:H:138:LEU:O	3:H:139:MET:C	2.58	0.41
5:J:300:PRO:O	5:J:301:SER:HB2	2.21	0.41
3:H:177:LEU:HA	3:H:178:PRO:HD3	1.90	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:J:135:GLN:O	5:J:138:ASP:HB2	2.21	0.41
3:C:154:ASN:HB3	3:C:176:LYS:H	1.86	0.40
3:H:373:PHE:CD1	3:H:377:ALA:HB3	2.56	0.40
1:A:172:GLU:O	1:A:173:TYR:C	2.60	0.40
3:C:138:LEU:O	3:C:142:TYR:HB3	2.20	0.40
3:H:66:THR:O	3:H:67:LEU:C	2.60	0.40
3:H:138:LEU:O	3:H:142:TYR:HB3	2.20	0.40
3:H:154:ASN:HB3	3:H:176:LYS:H	1.86	0.40
5:E:394:ASP:OD2	5:E:400:PRO:HA	2.22	0.40
5:J:394:ASP:OD2	5:J:400:PRO:HA	2.22	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	253/434 (58%)	238 (94%)	14 (6%)	1 (0%)	34	71
1	F	253/434 (58%)	237 (94%)	15 (6%)	1 (0%)	34	71
2	B	252/335 (75%)	248 (98%)	4 (2%)	0	100	100
2	G	252/335 (75%)	248 (98%)	4 (2%)	0	100	100
3	C	381/402 (95%)	352 (92%)	26 (7%)	3 (1%)	19	57
3	H	381/402 (95%)	353 (93%)	25 (7%)	3 (1%)	19	57
4	D	235/352 (67%)	212 (90%)	22 (9%)	1 (0%)	34	71
4	I	235/352 (67%)	212 (90%)	22 (9%)	1 (0%)	34	71
5	E	436/507 (86%)	417 (96%)	17 (4%)	2 (0%)	29	67
5	J	436/507 (86%)	417 (96%)	17 (4%)	2 (0%)	29	67
All	All	3114/4060 (77%)	2934 (94%)	166 (5%)	14 (0%)	38	71

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	75	ALA
3	C	213	THR
3	H	75	ALA
3	H	213	THR
4	D	210	VAL
4	I	210	VAL
5	E	137	HIS
5	E	301	SER
5	J	137	HIS
5	J	301	SER
1	A	202	VAL
1	F	202	VAL
3	C	155	MET
3	H	155	MET

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	232/386 (60%)	232 (100%)	0	100	100
1	F	232/386 (60%)	232 (100%)	0	100	100
2	B	235/302 (78%)	234 (100%)	1 (0%)	91	94
2	G	235/302 (78%)	234 (100%)	1 (0%)	91	94
3	C	337/353 (96%)	336 (100%)	1 (0%)	92	95
3	H	337/353 (96%)	336 (100%)	1 (0%)	92	95
4	D	219/309 (71%)	218 (100%)	1 (0%)	88	93
4	I	219/309 (71%)	218 (100%)	1 (0%)	88	93
5	E	364/416 (88%)	364 (100%)	0	100	100
5	J	364/416 (88%)	364 (100%)	0	100	100
All	All	2774/3532 (78%)	2768 (100%)	6 (0%)	93	96

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	82	ARG
3	C	55	ARG
4	D	279	LYS
2	G	82	ARG
3	H	55	ARG
4	I	279	LYS

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

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

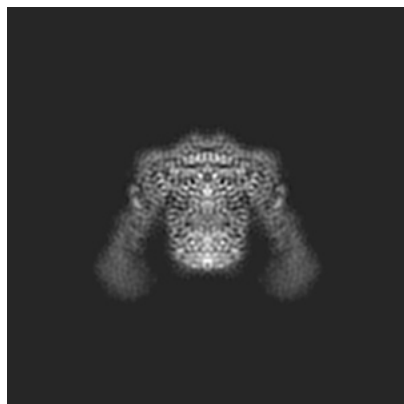
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0132. These allow visual inspection of the internal detail of the map and identification of artifacts.

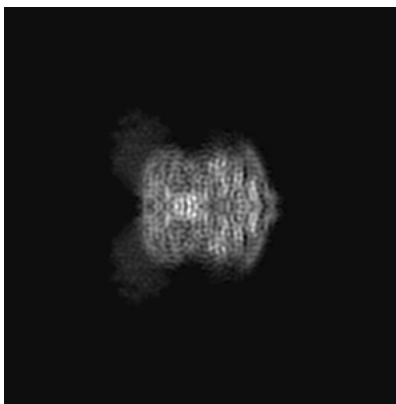
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

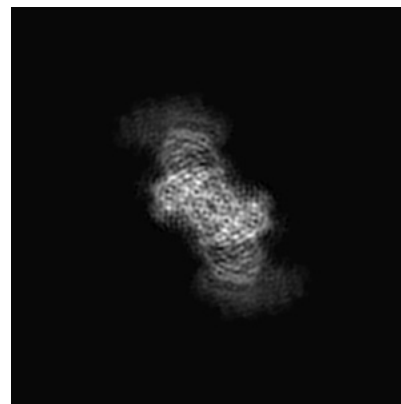
6.1.1 Primary map



X

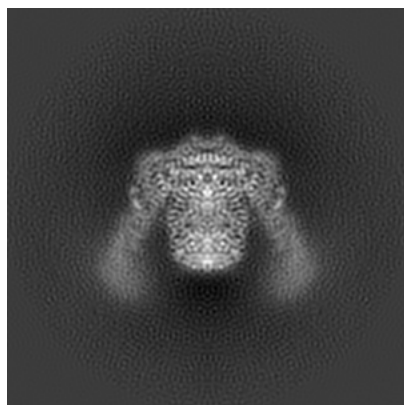


Y

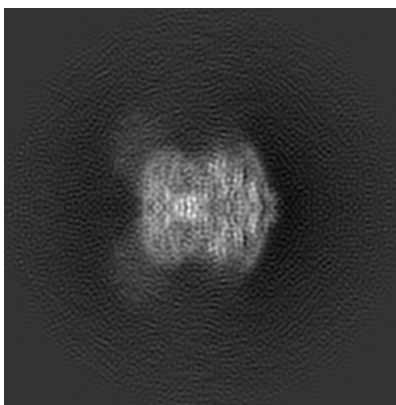


Z

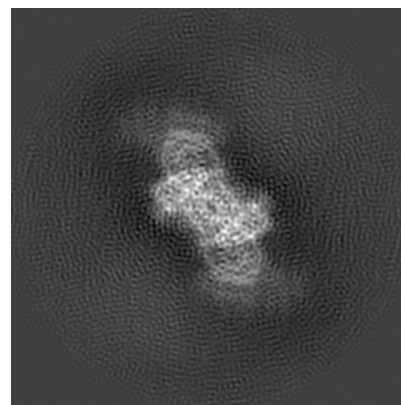
6.1.2 Raw map



X



Y

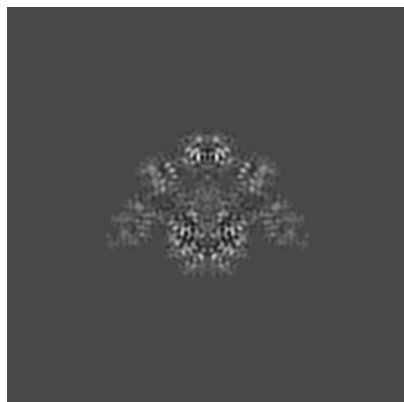


Z

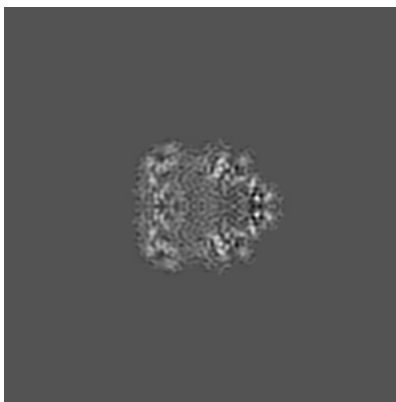
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

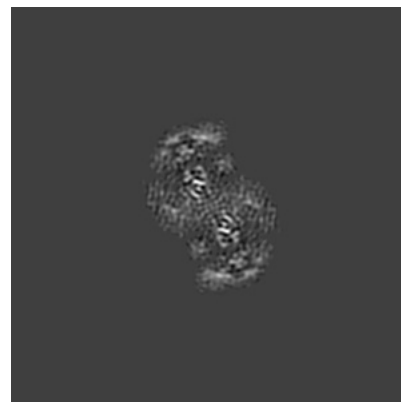
6.2.1 Primary map



X Index: 175

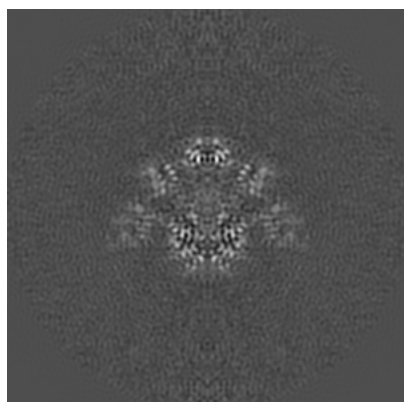


Y Index: 175

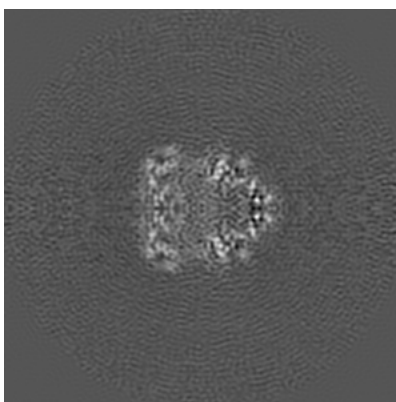


Z Index: 175

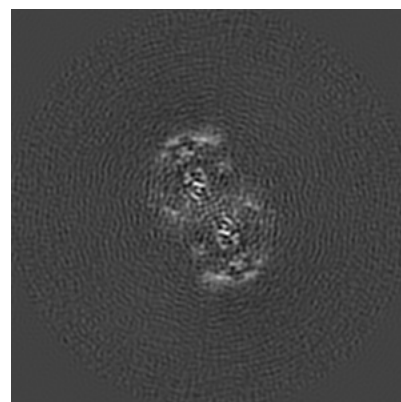
6.2.2 Raw map



X Index: 175



Y Index: 175

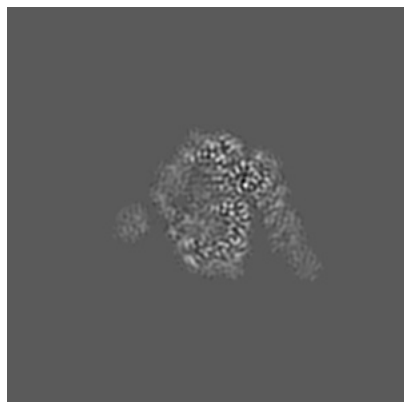


Z Index: 175

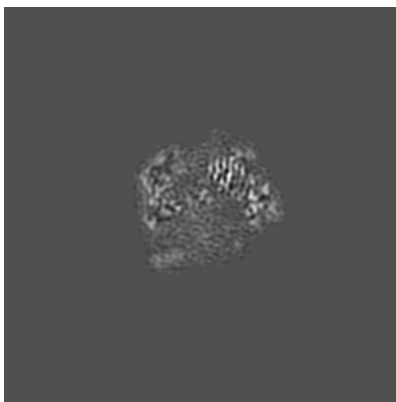
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

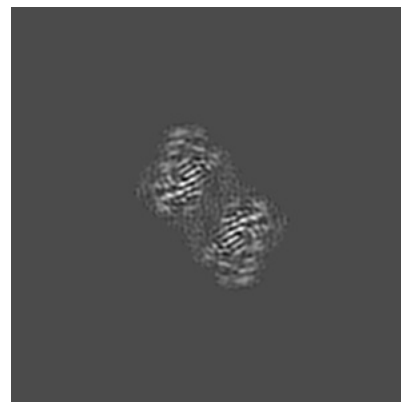
6.3.1 Primary map



X Index: 164

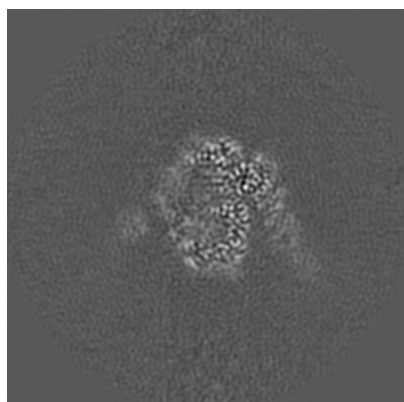


Y Index: 166

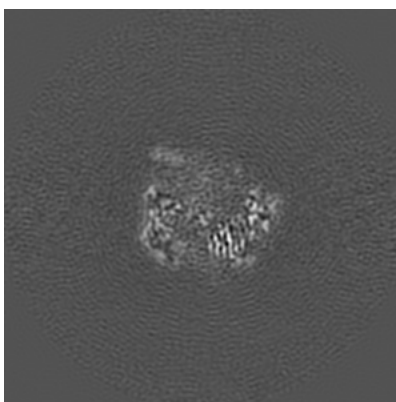


Z Index: 192

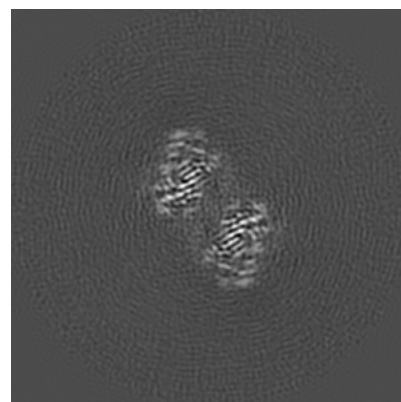
6.3.2 Raw map



X Index: 164



Y Index: 184

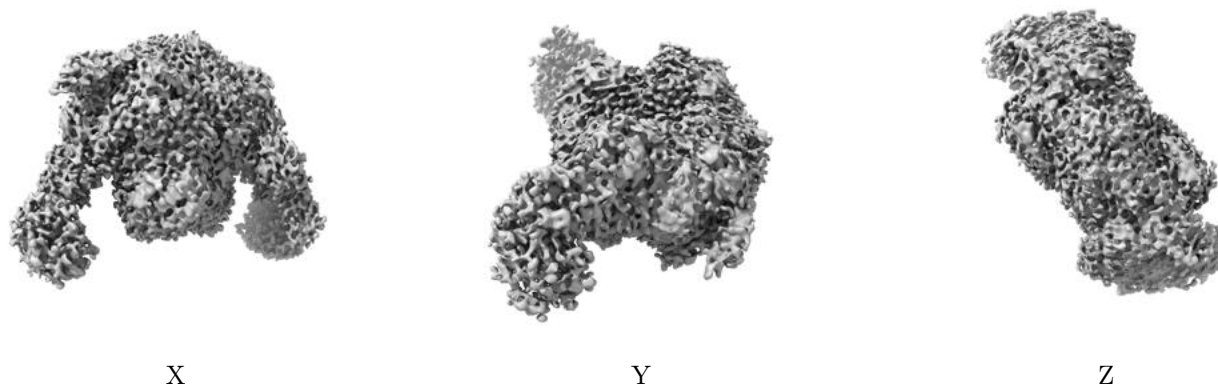


Z Index: 192

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

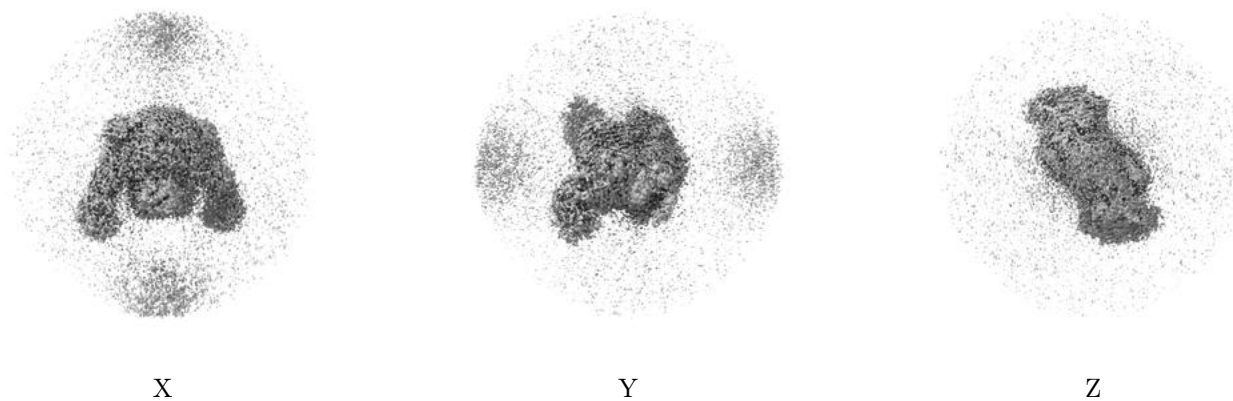
6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.00816. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 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.

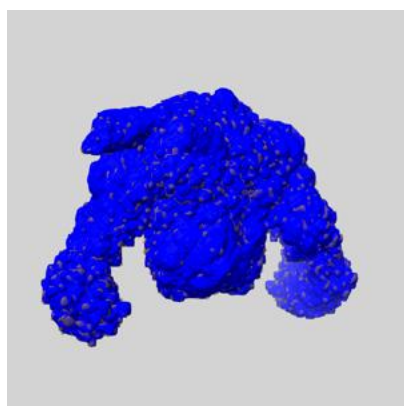
6.5 Mask visualisation [i](#)

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

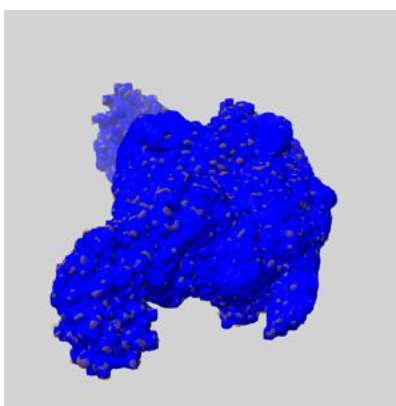
A mask typically either:

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

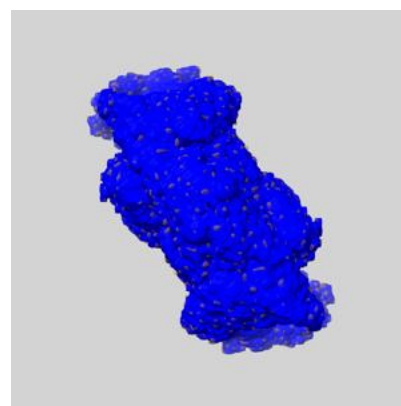
6.5.1 emd_0132_msk_1.map [i](#)



X



Y

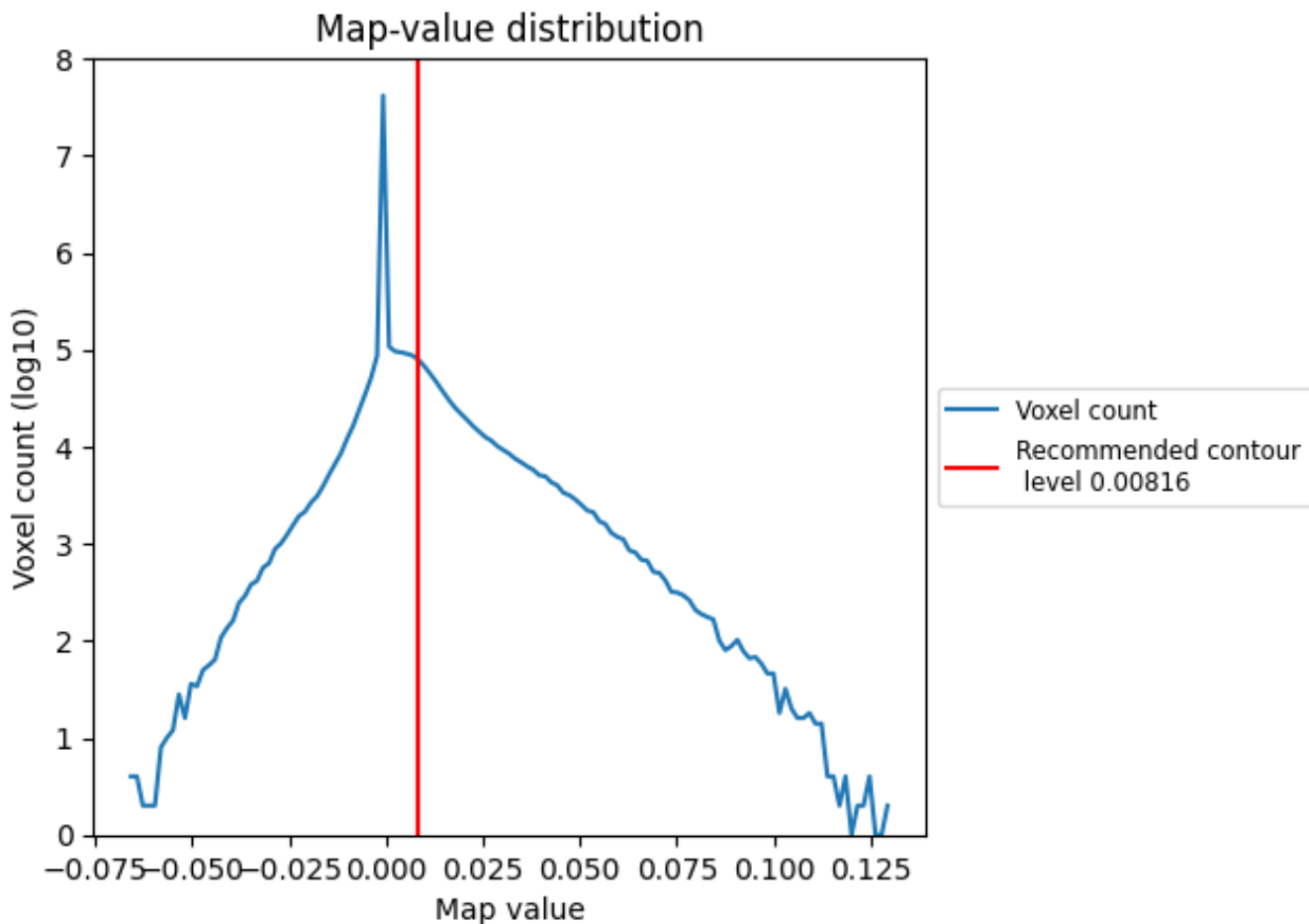


Z

7 Map analysis [i](#)

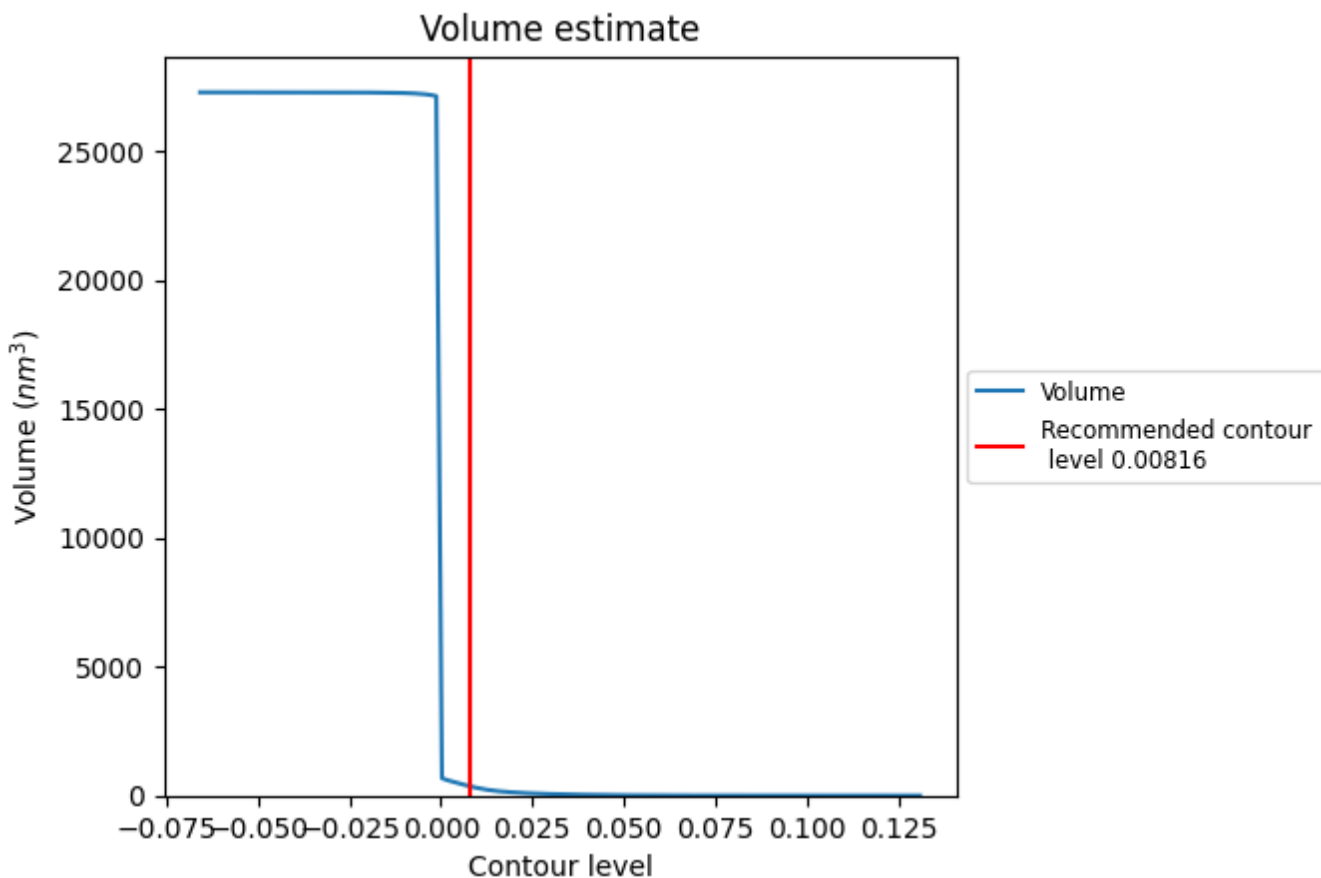
This section contains the results of statistical analysis of the map.

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.

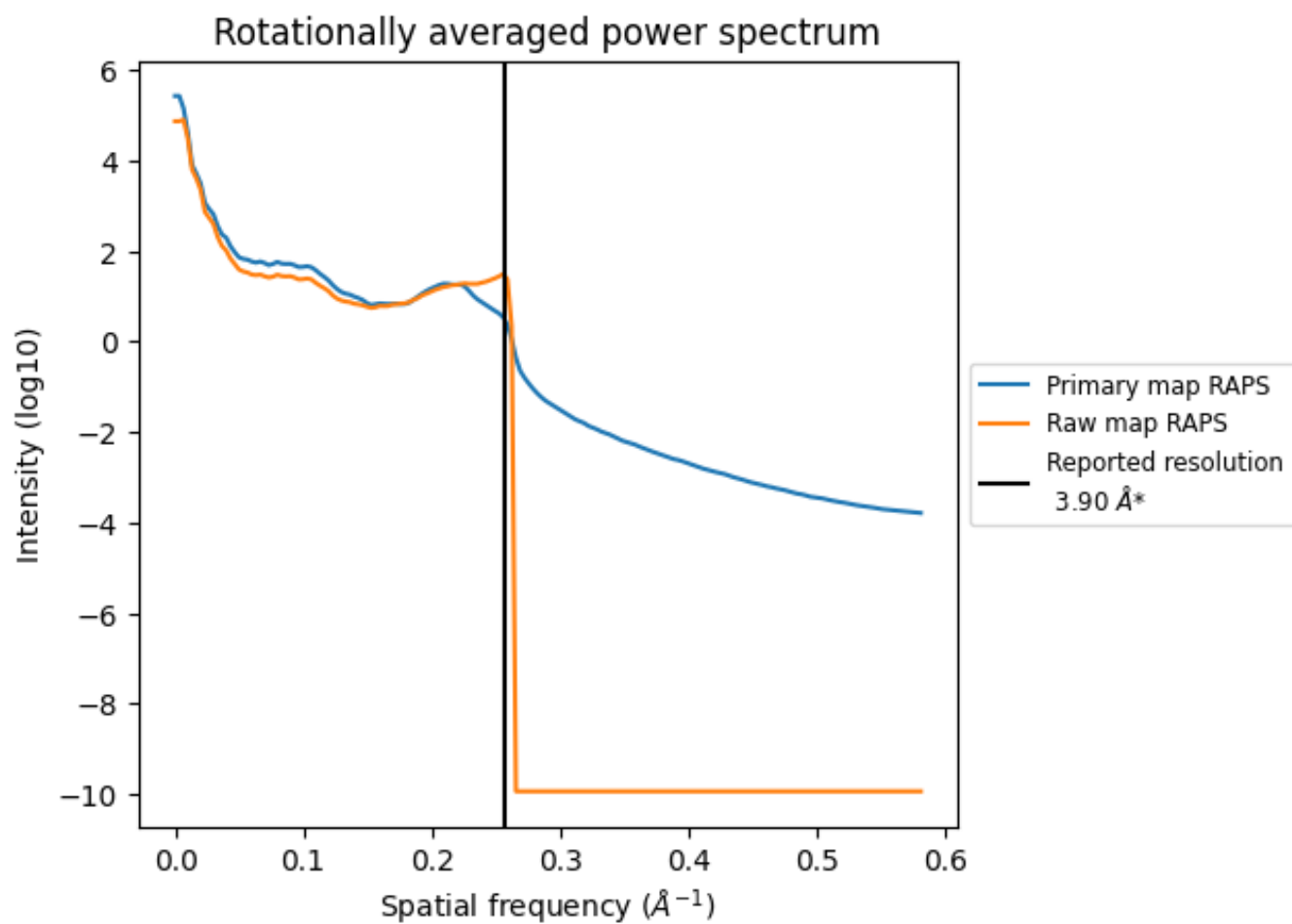
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 354 nm^3 ; this corresponds to an approximate mass of 320 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](#)

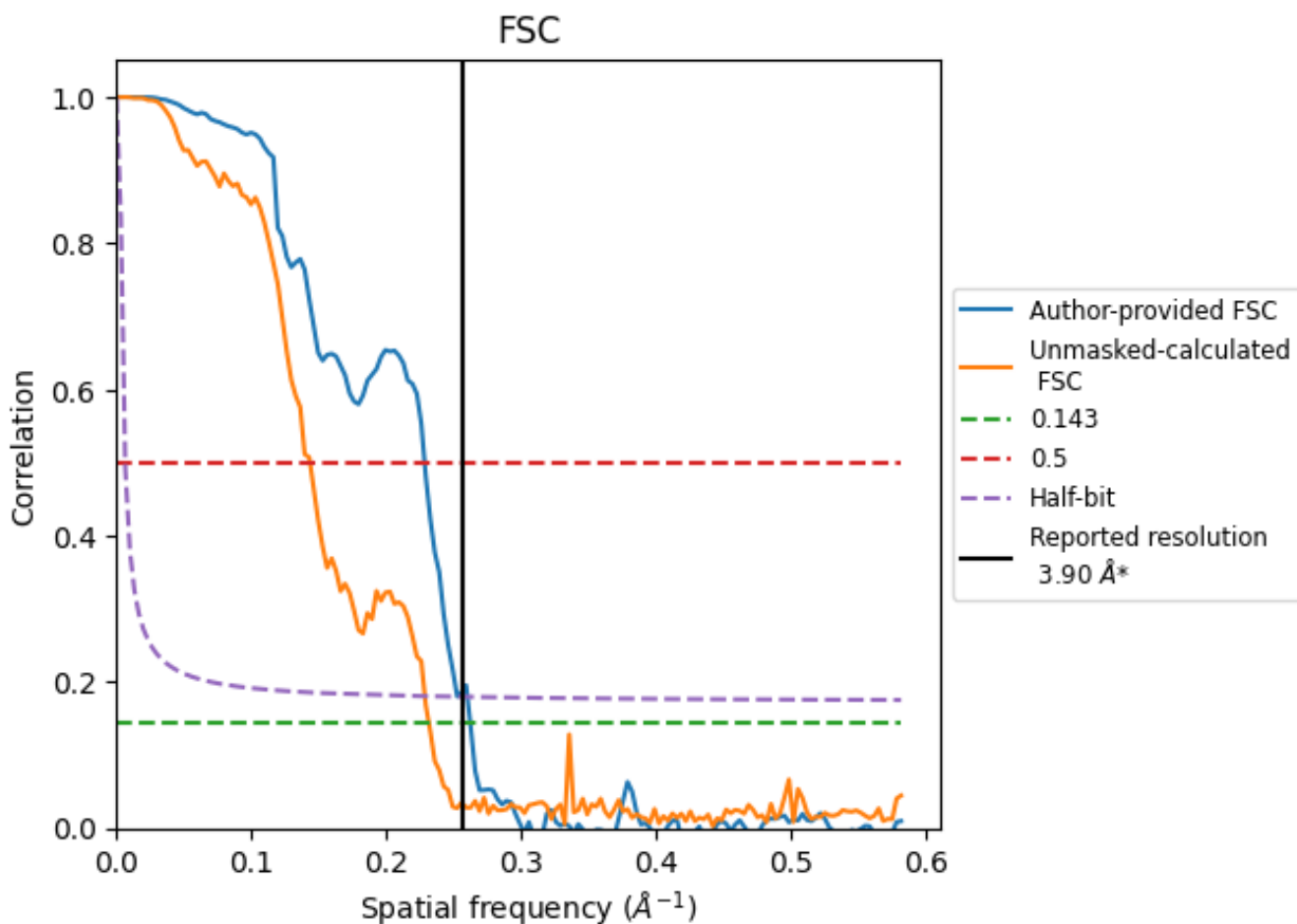


*Reported resolution corresponds to spatial frequency of 0.256 Å⁻¹

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 0.256\AA^{-1}

8.2 Resolution estimates [i](#)

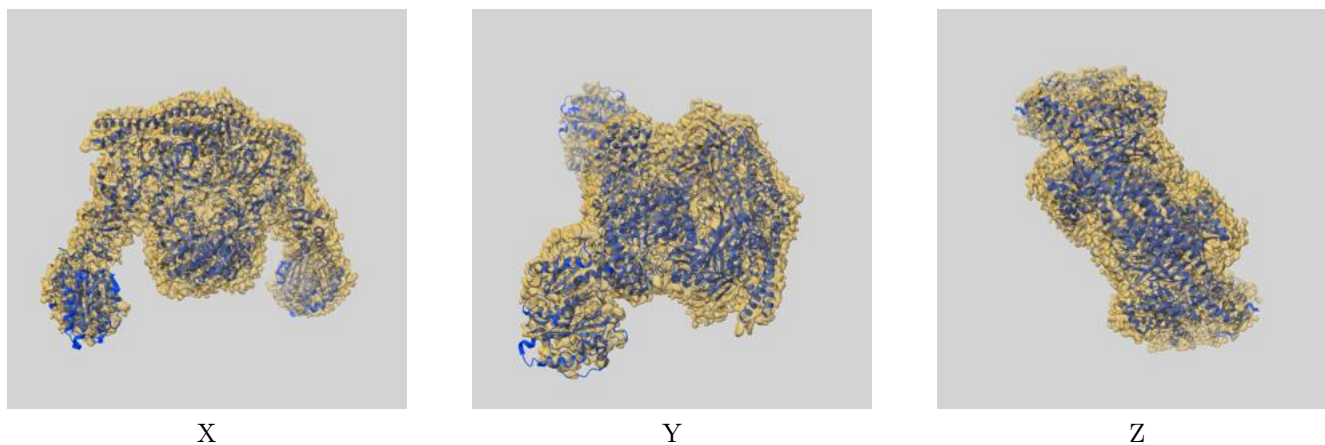
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.90	-	-
Author-provided FSC curve	3.81	4.38	3.84
Unmasked-calculated*	4.32	6.97	4.37

*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 4.32 differs from the reported value 3.9 by more than 10 %

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-0132 and PDB model 6H3C. Per-residue inclusion information can be found in section 3 on page 11.

9.1 Map-model overlay [i](#)



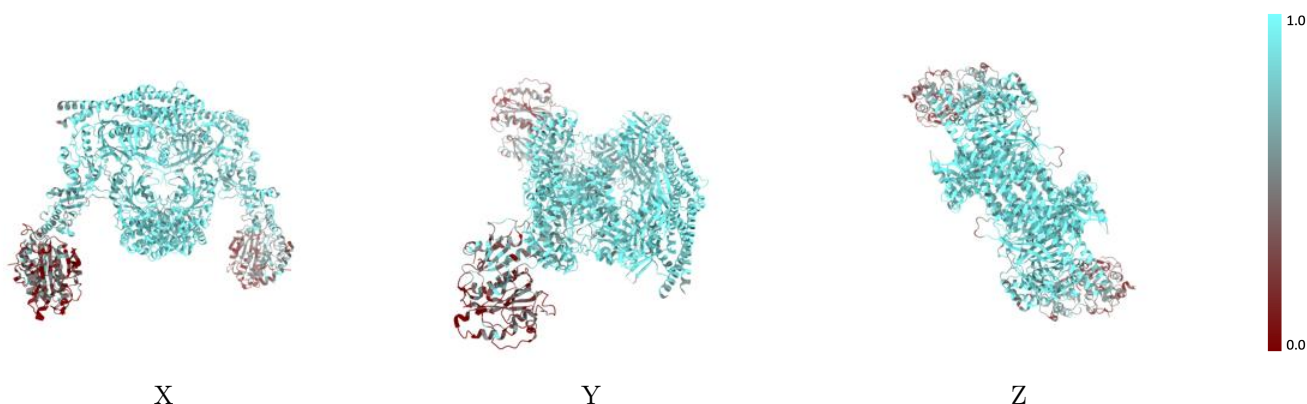
The images above show the 3D surface view of the map at the recommended contour level 0.00816 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



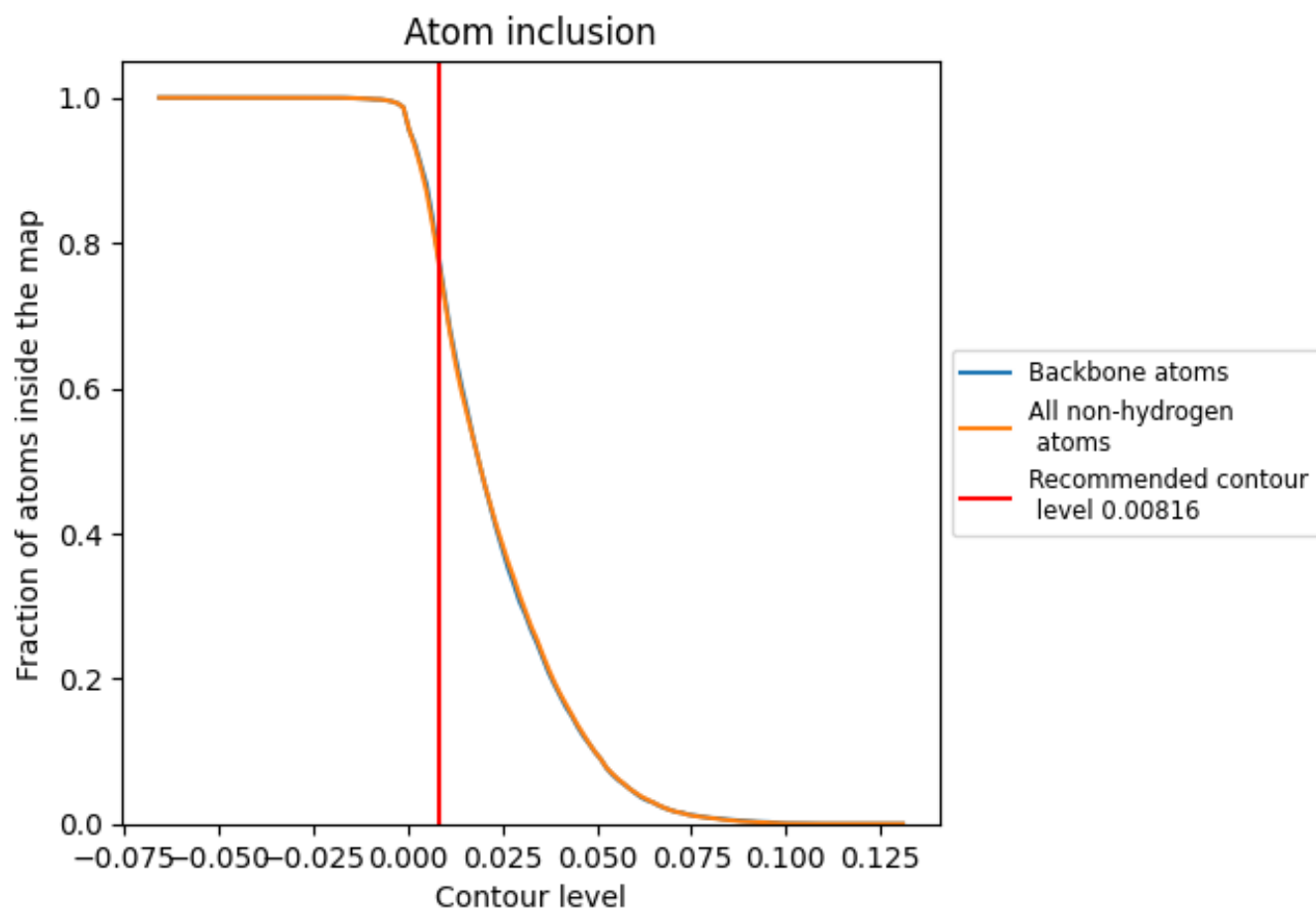
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.00816).























9.4 Atom inclusion [i](#)



At the recommended contour level, 78% of all backbone atoms, 77% 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 (0.00816) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7726	 0.2780
A	 0.9022	 0.3630
B	 0.9154	 0.3780
C	 0.7376	 0.2010
D	 0.2804	 0.0640
E	 0.9132	 0.3540
F	 0.9027	 0.3640
G	 0.9154	 0.3770
H	 0.7386	 0.2020
I	 0.2820	 0.0630
J	 0.9123	 0.3510

